Quantitative Life Sciences Ph.D. Program Proposal

Draft Version 5 - October 2016

Prepared By:

Peter Grutter	Chair of QLS Committee, Physics
Mathieu Blanchette	Computer Science
Guillaume Bourque	Human Genetics
Erik Cook	Physiology
Celia M T Greenwood	Oncology/Epidemiology and Biostatistics
Frédéric Guichard	Biology
Sabine Dhir	Graduate and Postdoctoral Studies

CONTENTS

Executive Summary **4**

1. Program identification **6**

2. Rationale for the proposed program **6**

2.1 Academic and cultural **6**

2.1.1 Evolution of the Quantitative Life Science Discipline 6

2.1.2 Originality of the proposal 7

2.1.3 Definition of body knowledge 7

2.1.4 Links to the traditional life and medical science discipline 8

2.1.5 Future developments in Quantitative Life Sciences 9

2.1.6 History and strength of Quantitative Life Sciences at McGill 11

2.1.7 Priority area as defined by government or other organizations 14

2.2 Academic/Professorial staff **14**

2.2.1 Staff resources required, available and projected 14

2.3 Institutional orientations **34**

2.3.1 Faculty and University development plan 34

2.3.2 Vertical and horizontal integration 35

2.4 Relevance to the University networks **35**

2.4.1 Related Programs 35

2.4.2 Similar programs offered elsewhere 36

2.4.3 Originality and anticipated contribution of the proposed program 39

2.4.4 Student mobility 40

2.4.5 Inter-university collaboration and relevance to Quebec network 40

2.5 Timetable of program implementation and projected student enrolment **40**

2.6 Socioeconomic motives **41**

2.6.1 Clientele 41

2.6.2 Labour Market 41

2.7 References and documents cited **43**

3. Academic Dossier **47**

3.1 Objectives **47**

3.1.1 General objective 47
3.1.2 Specific objectives 47
3.2 Structure and academic regulations 47
3.2.1 Admission requirements and selection process 48
3.2.2 Length of program 50
3.2.3 Academic regulations and environment 51
3.2.4 Program administration 51
3.3 Required academic activities 55
3.3.1 Academic requirements 55
3.3.2 Advisory Committee 56
3.3.3 Courses 56
3.3.4 Community building activities 58
3.3.5 Thesis 59
3.4 SPECIALIZED areas of research/streams 59
3.4.1 Computational and Statistical Molecular Biology Stream 60
3.4.2 Biophysics Stream 61
3.4.3 Ecosystems Stream 62
3.5 Examples of typical coursework 63
4. Resources 66
4.1 Staff resources required, available and projected 66
4.1.1 Teaching staff 66
4.1.2 Administrative and support staff 67
4.1.2.1 Staff in place 67
4.2 Physical and other resources 67
4.2.1 Library resources 67
4.2.2 Computer facilities 69
4.2.3 Laboratories 70
4.2.4 Space 71
4.2.5 Financial Support for Ph.D. Students 71
4.3 Required funding 72
APPENDICES 73

APPENDIX A: Foundational Course Syllabus 74
APPENDIX B: List of Complementary Courses..... 82
APPENDIX C: Letters of Interested Faculty (in progress) 83
APPENDIX D: Letters of Support..... 85
APPENDIX E: List of Grants Awarded to Teaching Faculty Members..... 91
APPENDIX F: List of Publications of Teaching Faculty Members 106

EXECUTIVE SUMMARY

We propose a novel inter-department and inter-faculty Ph.D. training program in Quantitative Life Sciences to produce the next generation of leaders in the rapidly changing world of biology, medicine and biotechnology. This program has been designed from the ground-up with close consultation with all stakeholders to produce graduates with the quantitative and interdisciplinary skills that Quebec and Canada need to maintain their positions as world-leaders in bio- and life-science research. It builds on, integrates and expands many currently loosely connected initiatives at McGill and will enable a stimulating, sustained and exciting interdisciplinary training environment.

The **Quantitative Life Sciences Program** (Figure 1) fits centrally into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics among others. Overall, the goal of these research fields is to understand the *biological whole*: how the complex interactions among the individual components (e.g., molecules, genes, cells) underlie entire living systems (e.g., cells, organisms, environments). To achieve this goal, active research lies at the interface between biological processes and advanced mathematics, physics, statistics and computer science. Here we are proposing an interdisciplinary doctoral level program to support this endeavor.

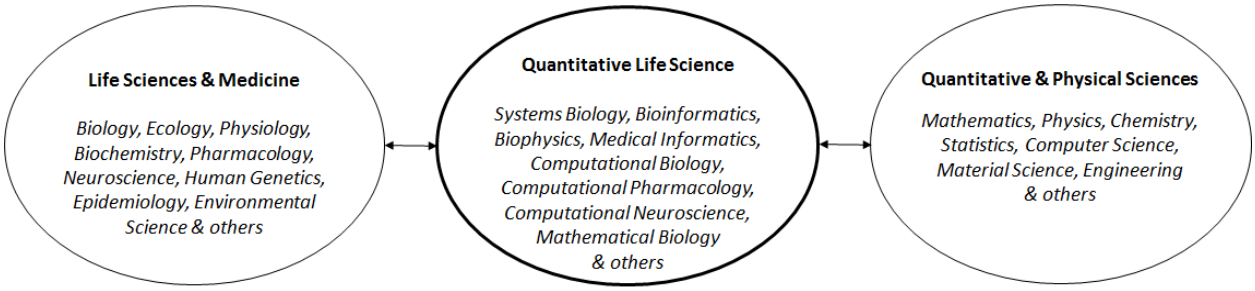


Figure 1. The Quantitative Life Science Program will train the next generation of multidisciplinary researchers needed to bridge the life and quantitative sciences. In addition, this new graduate program will facilitate collaborative life science research that cuts across departments and faculties at McGill University.

At the core of this proposal is a large multidisciplinary group of McGill researchers focused on quantitative approaches to understanding genetic, molecular & physiological systems, global ecosystems and disease interactions. McGill University has been very successful in hiring and bringing together interdisciplinary researchers to tackle the most important life science questions. The University has also taken first steps toward facilitating interdisciplinary training (e.g. through department specific graduate options and several research Centres or NSERC/CIHR funded training programs), but it still lacks a cohesive, cross-department and cross-faculty graduate program to train our students in this essential multidisciplinary field. We thus propose an interdisciplinary Ph.D. training program engaged in applied mathematical, statistical, physical and computational research that connects to all aspects of the life sciences, and capitalizes on the commonalities in quantitative methods in disparate fields.

Key elements of the proposed program have been designed to broaden the contextual knowledge of students, to encourage interactions between traditional fields of research and to create a sense of community. For example, a core course including a series of in-depth case studies will demonstrate links between quantitative methods and life sciences research in many different contexts. The depth of the proposed Ph.D. program is built around three different areas of research, or streams, defined by the type of biological questions being addressed and the quantitative approach being used (additional streams may be added later depending on the evolution of the field and demonstrated sufficient interest). Co-supervision of graduate students between life and quantitative researchers will be strongly encouraged. The program's streams are:

- **Computational and statistical molecular biology**: Quantitative methods in genetics/genomics and molecular biology
- **Biophysics**: Application of physical principles, development of tools and modeling approaches to quantitatively study biological systems, including biomolecules.
- **Ecosystems**: Mathematical and computational approaches in ecology and evolution.

The interest and the demand for interdisciplinary research in quantitative life sciences has led to the formation of new international graduate programs in the US and Europe, which emphasize quantitative research skills applied to the life sciences. Worldwide, governments and industry have begun to invest in quantitative life science and many top research universities worldwide have launched similar themed programs. This proposal is timely, and already in demand by McGill University students and researchers.

1. PROGRAM IDENTIFICATION

Program title: Quantitative Life Sciences
Degree title: Ph.D.
Unit responsible: Interfaculty Studies (IFS); Participating units: Medicine and Science.

2. RATIONALE FOR THE PROPOSED PROGRAM

2.1 ACADEMIC AND CULTURAL

2.1.1 Evolution of the Quantitative Life Science Discipline

Quantitative Life Sciences is the broad application of mathematical, computational and other quantitative methods to study biological systems at all scales - from single molecules to the environment[1-4]. It is part of a rapidly expanding field that includes such specializations as systems biology, bioinformatics, biophysics, medical informatics, computational biology, computational pharmacology, computational neuroscience and mathematical biology. The motivation for establishing a training program in Quantitative Life Sciences is the recognition that the most important and challenging problems in biology, medicine and the environment, will not be solved without a highly interdisciplinary approach that brings together students and researchers across all scientific disciplines and university faculties. This new Ph.D. program will train the future generation of researchers in the quantitative methods (mathematics, statistics, measurement, computer simulation and data analysis) needed to advance the rapidly changing landscape of the life sciences.

There are several major forces driving the need for quantitative methods in the life sciences. First, the high cost and slow timeline of translational bioscience research has become a serious concern for all stakeholders. For example, a conservative estimate for bringing a new drug to market is over one billion USD[5], and major funding agencies, including CIHR, NIH and UK's MRC, have targeted computer-based predictive models in drug development as a "critical path" for the future[6-8.] Second, we lack the quantitative tools needed to translate the vast amounts of data now generated by high-throughput bioanalysis systems into useful outcomes[9]. A promising solution to reduce cost, accelerate development and illuminate existing data is to apply powerful mathematical and computational tools to life science research. For example, entire ecosystems can be modeled, expression products of gene networks can be predicted, and drug interactions can be explored more cost effectively and quickly using mathematics and computer science[10]. Finally, new technologies and quantitative tools are rapidly changing the way traditional bioscience research is performed. For example, new imaging technologies have provided unprecedented views of living cells[11] while computational methods have revolutionized genomics[12]. Hence, developing and applying novel methods in physics, computer science, mathematics, and chemistry to solve the most pressing biological and medical challenges is a societal priority for future generations. As a demonstration of societal interest, a Pan-Canadian thematic program on Models and Methods in Ecology, Epidemiology and Public Health, was recently held as part of the international Mathematics of Planet Earth 2013 project[13.]

2.1.2 Originality of the proposal

Given the need to combine different theoretical orientations, methodologies and methods, creating an Interdisciplinary Program in Quantitative Life Sciences requires a highly original approach that spans departments and faculties across the University. There are only a few graduate programs in Canada that emphasize interdisciplinary life science research (for further clarification, see section 2.4.2.), and these programs are mostly limited to degree options within a single faculty or department.

Although there is a clearly recognized need for the life and health sciences at McGill to become more interdisciplinary, many of McGill University's current graduate programs do not attract undergraduate students outside of the traditional life science fields. For example, of the 35 graduate students newly recruited in 2014 to McGill's basic science biomedical departments (Anatomy & Cell Biology, Biochemistry, Microbiology & Immunology, Pharmacology & Therapeutics, and Physiology), only one student had undergraduate training in the quantitative or physical sciences. As described below (section 2.4.2), there are now many new interdisciplinary graduate programs in the Quantitative Life Sciences in the US and Europe. These new programs offer competing opportunities for the best McGill, Quebec and Canadian undergraduate students with quantitative science backgrounds to pursue graduate training in the quantitative life sciences abroad. With our new interdisciplinary graduate program, we hope to retain many of these excellent students at McGill.

As documented below (section 2.1.6), during the last decade McGill University has successfully developed several department specific graduate options, research centres, and NSERC/CIHR funded training programs that facilitate interdisciplinary training in the life and quantitative sciences. Unfortunately, these existing programs lack the ability to train students outside of existing departments and faculties. In addition, many of these NSERC/CIHR externally funded programs will be ending in the next few years. Our proposed Ph.D. program expands upon these successful McGill initiatives to create a permanent cross-department and cross-faculty graduate program to train our students in this multidisciplinary field.

2.1.3 Definition of body knowledge

In the proposed Quantitative Life Sciences Ph.D. Program, students will learn the broad application of mathematical, computational and other quantitative methods to study life science systems at all scales - from molecules to ecosystems. Specifically, students will gain skills and knowledge in the following key areas:

- Foundations of life science, with a focus on how quantitative approaches can best contribute to scientific advancement.
- Application and understanding of advanced technologies and tools used to measure living systems.
- Experimental techniques in relation to analysis methods, including how to analyze large life science data sets.
- Quantitative models and computer simulations of life science systems.
- Identification of similar mathematical, computational and statistical techniques that can be applied across life science levels.
- Effective communication and collaboration between traditional and quantitative life scientist.

This Quantitative Life Sciences Ph.D. program will span departments and faculties, and provide breadth of understanding as well as depth of knowledge to core aspects of bioscience research.

2.1.4 Links to the traditional life and medical science discipline

The Quantitative Life Sciences Ph.D. Program will address several critical limitations in McGill University's current training and research environment.

2.1.4.1 Links to the traditional life and medical science disciplines

McGill University's traditional department-centered graduate programs in the Faculties of Science and Medicine do not provide the needed breadth of training to optimally prepare the next generation of students for this interdisciplinary field. We anticipate that the proposed regular interactions between researchers across faculties and departments will lead to synthesis of similar concepts used in different fields, and hence to novel insights and new fruitful collaborations. Furthermore, gathering these cross-disciplinary areas of research under one program will increase visibility, ensure high standards and quality control of the training at the interface between two fields, and attract and retain superb graduate students and researchers at McGill University. By creating a bridge between disciplines (Figure 1 above) we expect our new Ph.D. program to enhance and extend the viability of existing life and quantitative science disciplines at McGill University.

2.1.4.2 Links to the bio- and biomedical engineering disciplines

McGill University is currently integrating its existing Biological and Biomedical Engineering training programs between the Faculties of Medicine and Engineering. With their emphasis on the application of methods, paradigms, technologies and devices from engineering to problems in medicine and biology, the Biological and Biomedical Engineering programs complement the proposed training program in Quantitative Life Sciences (QLS). Broadly speaking, Biological and Biomedical Engineering focusses on (i) the design of devices and approaches to measure aspects of biological systems (microscopes, DNA sequencers, microfluidics, etc.), (ii) the design of engineered biological systems (proteins, cells, bacterial communities, etc.) to perform specific functions, and (iii) the design of engineering solutions to medical problems (e.g. artificial tissues). In contrast, QLS is centered on the data analysis aspects of the study of fundamental questions about biological systems. Although these analyses are often based on measurements obtained from devices built by bioengineers, they usually offer their own, distinct set of challenges, both in terms of the approaches used (mathematics, statistics, computer science), and in terms of the biological interpretation of their results. The Biological and Biomedical Engineering and Quantitative Life Science fields are thus highly synergetic: many aspects of QLS would be impossible without devices to measure biological systems, while the impact of these devices would be limited without sophisticated approaches to make use of their measurements.

Most of the newly formed and successful graduate programs in Quantitative Life Sciences in North America exist alongside equally successful Biological or Biomedical Engineering training programs (also see Section 2.4.1). This is because experience has taught us that the broad differences in terms of the nature of the questions addressed, the background required to make a contribution, and the type of education provided, require both educational environments. Thus, Quantitative Life Science and Biological and Biomedical Engineering programs

are highly complementary and together provide a beneficial research and training environment for students and faculty across the university research environment. At McGill, the proposed Program in Quantitative Life Sciences will maintain strong links with Biological and Biomedical Engineering and be open to participation from all researchers in the Faculty of Engineering.

2.1.5 Future developments in Quantitative Life Sciences

In 2006, a group of 111 interdisciplinary researchers from universities across Canada published an important and influential paper that highlighted the need to strengthen the Quantitative Life Sciences[14]. The main conclusion of their analysis was that the blending of the physical, computational and biological sciences had now become critical to all new advances in biology and medicine, with enormous economic and social impacts. It was also noted that Canada lagged significantly behind in terms of government and academic initiatives needed to promote this new field. Since then many small initiatives have been developed, including several at McGill and in Quebec, that have helped move Canada closer to the forefront of this important trend. In this section, we present evidence that quantitative methods have become an integral part of health and life science research.

Across all life science disciplines, it is commonly accepted that quantitative approaches improve research outcomes by bringing powerful new methods for understanding biological processes that range from biomolecules to the environment. For example, mathematical and computational approaches are needed to support traditional research methods in order to make sense of the thousands of genetic alterations now shown to be associated with cancer[15]. This type of interdisciplinary research now commonly appears in all major academic journals and there are currently over 650 journals specifically dedicated to multidisciplinary research in chemistry, computer science, engineering, physics and psychology alone according to the scientific citation indexing service Web of Science.

Recently, new scholarly societies have been formed that highlight quantitative life sciences, such as the International Society for Systems Biology, International Society for Computational Biology, Canadian Genetics and Genomics Society, and Canadian Society for Systems Biology. These new societies join existing organizations such as the Society for Mathematical Biology, Institute for Electrical and Electronics and Engineers, and the Biomedical Engineering Society that have traditionally included computational bioscience and bioinformatics as part of their membership domain. In Quebec, the multi-institutional Centre de Recherches Mathématiques regularly supports workshops and meetings that focus on life science applications[13]. At McGill, the Centre for Nonlinear Dynamics and the newer Centre for Applied Mathematics in Bioscience and Medicine (CAMBAM)[18] has organized numerous meetings and summer schools in Montreal that focus on the link between quantitative methods and life science research.

2.1.5.1 Importance to future environmental resource management

Computer models have become a critical component for predicting the behaviour of essential environmental resources. The complexity of environmental problems, such as pollution and climate change, and the loss of biodiversity, require quantitative approaches that can cope with the inter-connectivity of our planet[63, 64]. For example, measuring only temperature or the population of a single species is not enough to capture the

biological whole of the ecosystem. We need better quantitative tools to predict environmental damage from human activity and to develop bioremediation programs. In agriculture, computational models are used to predict crop performance as well as other resources that support human populations[19, 20]. The availability of water supplies is now a critical concern of many parts of the world, including North America. Predicting water resources requires sophisticated models that combine long-term weather forecasting, human usage patterns, and population growth estimates. Locally, McGill's CAMBAM Ecology group has ongoing collaborations with Environment Canada and Fisheries and Oceans Canada to create computational models of the tight link between water-based resources and human activity.

2.1.5.2 Importance to future industry-based research

Quantitative approaches have become a critical component for advancing life science research in industry. Many non-bioscience industrial sectors have already fully integrated mathematical and computational techniques in product development. For example, electrical circuits, automobiles and buildings are now completely designed and simulated using computer aided design techniques before physical manufacturing. While the impact of new computational techniques, such as predictive computer modeling, has affected many bioscience and health sectors including agriculture, medical devices, biodefense, bioremediation and cosmetics, the pharmaceutical industry has particular potential for benefit. The cost of developing a new drug is over one billion USD, and more than six out of seven drugs that undergo human testing ultimately fail[5, 22-24]. Both in vitro cell-line models and in-vivo animal models fall short of capturing the complexity of human physiology[25]. Thus, even a modest improvement in predicting drug-discovery outcomes using computational methods would produce a substantial cost impact on the pharmaceutical industry[26-30.] For example, researchers at Astrazeneca use predictive computer models to facilitate cancer immunotherapy research[31]. Many other companies, such as Chemical Computing Group based in Montreal[32], now specialize in delivery of the quantitative and data-analysis methods needed for this new era of pharmaceutical research.

The BiologicalIT sector, a rapidly expanding area within the traditional information technology industry, is another area where quantitative methods are increasingly applied to problems in the life and health sciences. For example, Google has demonstrated its ability to alert healthcare professionals of developing pandemics in real time, with the potential to save thousands of lives per year[33]. Microsoft has launched initiatives in bioinformatics and computational bioscience research to speed drug development[34]. IBM has also embraced life science research with new initiatives dedicated to medical informatics, computational biology and biologically-inspired cognitive computing[35]. Much of this research emphasis is directed at helping traditional life science researchers make sense of the vast amount of life science data generated. In a recent example of how quantitative data-analysis can generate new life science discoveries, IBM's new cognitive-computing supercomputer system revealed exciting new relationships that were unknown in the existing cancer literature[36].

2.1.5.3 Importance to future healthcare

Quantitative life sciences approaches have provided governmental agencies with new tools for predicting and tracking disease outbreaks. Mathematics and computation are also rapidly improving how healthcare is delivered. Personalized medicine refers to the revolutionary idea that individuals respond differently to therapeutic interventions depending on their unique physiology[37]. Thus, a patient may have hundreds (or thousands) of unique biomarkers (for example, genomic or proteomic identifiers) that can be used to predict how he/she responds to a given treatment or drug. The plummeting costs of generating biomarkers, a result of technological advances and improved analysis methods, means that the reality of personalized medicine is imminent. In addition, transformation of medical records to digital formats allows computational and data mining methods to identify promising treatment programs that would have gone unnoticed by individual healthcare professionals[38], and to identify unanticipated drug interactions[62]. Research in the IT industry is now focused on achieving the full potential of personalized medicine. For example, Apple has launched research efforts with the Mayo Clinic to enhance healthcare delivery with its new HealthKit development system[39]. Canada's health delivery sector lags far behind many other industries and countries in adopting quantitative methods, and thus, CIHR has recently announced an eHealth initiative to advance the development and application of information systems in health delivery[65].

2.1.6 History and strength of Quantitative Life Sciences at McGill

There is a strong demand among undergraduate students at McGill for a graduate program in Quantitative Life Sciences. The current cohort of undergraduate university students has been quick to respond to this ongoing paradigm shift, but current disciplinary boundaries guiding academic education fail to embrace this exciting challenge. At McGill University, students can choose among 16 undergraduate programs or options that offer training in biological and other quantitative sciences such as physics, chemistry, computer science and mathematics (Table 1). The success of these Quantitative Life Sciences undergraduate initiatives has been remarkable: the number of participating undergraduate students has increased from approximately 650 in 2010 to 909 in 2016. Nevertheless, current disciplinary boundaries make it challenging for these graduating students, and those from other institutions, to find and choose appropriate graduate programs, since the opportunities are spread across so many departments and faculties.

Table 1. Enrollment in multidisciplinary undergraduate programs at McGill in quantitative life sciences.

Interdisciplinary Program	Fall 2010	Winter 2011	Fall 2011	Winter 2012	Fall 2012	Winter 2013	Fall 2013	Winter 2014	Fall 2014	Winter 2015	Fall 2015	Winter 2016	Fall 2016
Bachelor of Science													
BIOL & MATH Major	15	13	20	20	25	24	29	24	32	31	26	25	31
CS & BIOL Major	24	25	38	38	49	52	63	54	61	63	71	72	81
MATH & CS Honours	9	11	19	19	29	27	38	40	39	40	41	35	35
MATH & CS Major	17	14	18	17	22	21	30	32	45	42	43	43	50
MATH & PHYS Honours	59	56	64	62	64	64	83	69	68	64	77	71	67
NEUR Honours							14	14	16	16	22	21	21
NEUR Major	170	158	175	171	186	184	180	168	167	157	147	145	151
PHYS & CS Major	14	14	17	15	19	21	25	23	26	28	33	32	37
PHYS & CHEM Honours	2	2	6	5	6	5	9	10	7	6	5	5	6
PHYS & GEPHYS Major	5	4	2	2	2	2	3	2	9	8	7	7	8
PHGY & MATH Major	17	15	19	17	11	14	16	15	21	24	30	26	22
PHGY & PHYS Major	18	15	34	35	33	34	30	27	22	18	25	26	21
QB Honours								5	2	4	3	3	6
QB Major			8	7	12	12	15	11	12	8	18	16	16
ENVIR Honours	3	4	8	9	13	10	9	11	10	7	8	7	4
ENVIR Major	105	99	111	108	100	91	100	94	93	86	79	75	56
Bachelor of Science Total	458	430	539	525	571	561	644	599	630	602	635	609	612
Bachelor of Arts and Science													
COG SCI Honours	24	26	23	28	35	39	39	43	32	34	37	39	34
COG SCI Interfaculty	76	71	110	100	124	112	142	139	178	172	185	178	195
ENVIR Interfaculty	43	39	46	44	37	41	28	26	33	29	30	25	32
Sustainability, Sci & Soc -H Honours							4	4	5	6	8	9	7
Sustainability, Sci & Soc	2	5	11	13	19	17	20	20	27	24	29	21	29

Interfaculty Program													
Bachelor of Arts and Science Total	145	141	190	185	215	209	233	232	275	265	289	272	297
Grand Total	**603**	**571**	**729**	**710**	**786**	**770**	**877**	**831**	**905**	**867**	**924**	**881**	**909**

CS - computer science. BIOL - Biology. GEPHYS - Geophysics. MATH - Mathematics. NEUR - Neurology. PHGY - Physiology. PHYS - Physics. QB - quantitative biology. COGSCI - Cognitive science

We believe that the strong demand among undergraduates at McGill reflects similar demands at other universities in Quebec and Canada. In addition, the creation of many new interdisciplinary life science graduate programs in the US and Europe during the last decade (see section 2.4.2 below) suggests a market demand for this type of education, and without a dedicated program, McGill is currently unable to attract graduate students interested in this emerging field.

A diversity of programs, centres and networks at McGill could be envisaged as falling under a quantitative life sciences umbrella. In fact, the existence of so many different groups and departments working at the interface of quantitative methods and biology or medicine (Table 2) speaks strongly to the interest in this area, and to the fact that there are many interested students and faculty. However, many of the externally-funded training programs are reaching the end of their terms soon. Thus, the proposed Quantitative Life Science Program builds upon the success of these initiatives to create a vibrant and sustainable educational environment.

Table 2. Programs, Centres and Networks in existence at McGill with relevance to Quantitative Life Sciences

Centres and Networks	● Centre for Applied Mathematics in Bioscience and Medicine (CAMBAM): Mathematics in Biology and biophysics (www.mcgill.ca/cambam) ● Centre for Bioinformatics (www.mcgill.ca/mcb). Modelling biological systems using non-linear dynamics, networks, genomics, population genetics, etc. ● McConnell Brain Imaging Centre (www.bic.mni.mcgill.ca/Research/Homepage). ● Cell Imaging and Analysis Network (biology.mcgill.ca/CIAN/index.htm/) high throughput imaging and analysis of images ● Canadian Center for Computational Genomics (computationalgenomics.ca/)
Grant funded graduate- level training programs	● Systems Biology Training Program (www.mcgill.ca/osb/introduction) Applying a range of quantitative techniques to address large-scale research projects. This is a CIHR-funded training grant. (2009-2015)

	● CREATE training program BioNanoMachines: (bionano.ca/en/). Bionanotechnology involving protein engineering, structural biology, bioinformatics (2011-2017) ● CREATE Canadian Astrobiology Training Program (create-astrobiology.mcgill.ca/). Geology, chemistry, physics, astronomy, microbiology. (2009-2015) ● CREATE Integrated Sensor Systems (www.mcgill.ca/miam/iss) Physics, biomedical engineering, medicine (2010-2016) ● CREATE Neuroengineering (www.neuroengineering.ca/) chemists, physicists, engineers, neuroscientists (2011-2017) ● CREATE Program in Medical Image Analysis www.cim.mcgill.ca/create-mia) Mathematical modelling, image processing. (2012-2018)
Inter-disciplinary Graduate programs within existing departments	● Integrated program in Neuroscience (www.mcgill.ca/brain/welcome) ● Department of Epidemiology, Biostatistics and Occupational Health ● Graduate Option in Bioinformatics

2.1.7 Priority area as defined by government or other organizations

The increasingly interdisciplinary nature of academic bioscience research has motivated government funding agencies to reconsider the traditional segregation of the biological, medical and physical sciences. For example, NIH has targeted both Systems Biology and Computational Biology as focus areas in its intramural research program[7]. The UK's Medical Research Council prominently highlights computational and system approaches in each stage of its 2014-19 Strategic Plan[8]. In CIHR's Three Year Implementation Plan and Progress Report 2013-15, bioinformatics and computational biology are highlighted as recent successes[6] and are part of the Institute of Genetics' research priorities[16]. Finally, Génome Canada has promoted computational and bioinformatics-based methods to maintain Canada as a world-leader in genomic research[17].

2.2 ACADEMIC/PROFESSORIAL STAFF

2.2.1 Staff resources required, available and projected

2.2.1.1 Full time Academic and Professorial Staff

All fifteen professorial staff associated with the Quantitative Life Science Ph.D. Program are actively engaged in research in one or more of the three streams that together form the proposed Ph.D. Program. The following table lists the participating professors, their position and their major areas of research focus.

Table 3: Faculty members participating in the Quantitative Life Sciences Ph.D. Program

Name and Academic Training	Position	Research Focus
Mathieu BLANCHETTE, Ph.D. Post-doctoral fellow (University of California in Santa Cruz). Ph.D. - Computer Science (University of Washington) MSc - Computer Science, (Université de Montréal). BSc - Mathematics and Computer Science (Université de Montréal).	Associate Professor Dept. of Computer Science	Computational genomics; Bioinformatics with applications in genomics, epigenomics, evolution, phylogenetics, gene regulation and proteomics (Ancestral genomics, 3D genomics, epigenetic and gene regulation, mRNA localization, transposable element annotation, plant genome assembly and evolution)
Guillaume BOURQUE, Ph.D. Postdoctoral fellow (Centre de Recherches Mathématiques) Ph.D. - Applied Mathematics (Université de Montréal) MA - Applied Mathematiccs (University of Southern California) BSc- Computer Science and Mathematics (Université de Montréal)	Associate Professor Dept. of Human Genetics	Comparative functional genomics; evolution of regulatory sequences; role of transposable elements in host gene regulation; impact of genome rearrangements in evolution and in cancer.
Erik COOK, Ph.D. Postdoctoral fellow (Harvard University) Postdoctoral fellow (Baylor College of Medicine) Ph.D. – Neuroscience (Baylor College of Medicine) MEng – Electrical Engineering (Rice University) BSc – Electrical & Computer Engineering (Arizona State University)	Associate Professor Dept. of Physiology	Neuronal communication and neurotransmission; computational modeling of the visual system, neuronal and synaptic activity
Ken DEWAR, Ph.D. Postdoctoral fellow (University of Pennsylvania) Ph.D.- Sciences Forestières (Université Laval)	Associate Professor Dept. of Human Genetics Dept. of Experimental Medicine	Advanced DNA sequencing technologies; bioinformatics; genome architecture; comparative genomics

MSc - Forestry (University of Toronto) BSc - Forestry (University of Toronto)		
Paul FRANÇOIS, Ph.D. Postdoctoral fellow (Rockefeller University) Ph.D. – Theoretical Physics (École Normale Supérieure Paris, France) MSc - Theoretical Physics (École Normale Supérieure Paris, France) Diplôme d'Ingénieur – Physics (École Polytechnique Palaiseau, France)	Associate Professor Dept. of Physics	Biological physics; theoretical and computational modeling; theoretical aspects of evolution; signaling networks; vertebrate axis elongation
Simon GRAVEL, Ph.D. Postdoctoral fellow (Stanford University) Postdoctoral fellow (Universität zu Köln, Germany & Kavli Institute for Theoretical Physics, UCSB) Ph.D. – Physics (Cornell University) MSc – Physics (Université de Montréal) BSc – Mathematics & Physics (Université de Montréal)	Assistant Professor Dept. of Human Genetics	Population genomics; integration of biological, historical and archaeological information; analysis and genetics of complex population cohorts (settlement of the Americas and Caribbean)
Celia M T GREENWOOD, Ph.D. Postdoctoral fellow (McGill University) Ph.D. – Biostatistics (University of Toronto) MMath – Mathematics in Statistics (University of Waterloo) BSc – Mathematics (McGill University)	Associate Professor Dept. of Oncology Dept. of Epidemiology, Biostatistics and Occupational Health	Analysis of rare genetic variation; high dimensional data analysis; development of statistical methodology for genetic and genomics data
Peter GRUTTER, Ph.D. Habilitation (University of Basel) Postdoctoral fellow (IBM Almaden Research Lab) Ph.D. (University of Basel)	Professor Dept. of Physics	Nanoscience and scanning probe technology; development of atomic force microscopes; electron behaviour; molecular charge transport; solid-liquid

Diploma – Experimental Physics (University of Basel)		interface dynamics; synapse formation
Frédéric GUICHARD, Ph.D. Postdoctoral fellow (Princeton University) Ph.D. – Biology (Laval University) BSc – Biology (Université de Montréal)	Professor Dept. of Biology	maintenance of biological diversity; mathematical ecology and dynamics of complex systems; impact of global change on biodiversity; spatial modeling
Anmar KHADRA, Ph.D. Postdoctoral fellow (Institute for Theoretical Biology, Humboldt University) Postdoctoral fellow (University of British Columbia) Ph.D. – Applied Mathematics (University of Waterloo) MMath – Applied Mathematics (University of Waterloo) BSc – Pure Mathematics (Concordia University)	Assistant Professor Dept. of Physiology	Mathematical modeling; quantitative immunology; computational electrophysiology and endocrinology; neuronal synchrony; applied nonlinear and stochastic dynamics; stability theory and differential equations; impulsive control and delayed impulsive systems
Sabrina LESLIE, Ph.D. Postdoctoral fellow (Harvard University) Ph.D. – Physics (University of California, Berkeley) Hon BSc – Physics & Mathematics (University of British Columbia)	Assistant Professor Dept. of Physics	Nano scale microscopy; Biomedical diagnostics; DNA dynamics; DNA confirmation kinetics; DNA-protein interactions
Judith MANDL, Ph.D. Postdoctoral fellow (National Institute of Allergy and Infectious Diseases, NIH) Postdoctoral fellow (Yerkes Primate Research Center, Emory University) Ph.D. – Population Biology, Ecology & Evolution (Emory University) Hon. BSc – Computational Biology	Assistant Professor Dept. of Physiology	Immunology; cellular defence; infectious and immune diseases; immune mediators; cytokines and chemokines; immunodeficiencies; T cell homeostasis
Christopher PACK, Ph.D.	Associate Professor	Visual cortex; visual neurophysiology; neuronal

Research Fellow (Harvard University) Ph.D. – Cognitive and Neural Systems (Boston University) BSc – Computer Science (Tufts University)	Dept. of Neurology and Neurosurgery	communication; eye movement behaviour; electrophysiology
Tomi Markku PASTINEN, MD Ph.D. Postdoctoral fellow (McGill University) Ph.D. – Human Genetics (University of Helsinki) MD – General Practitioner (University of Helsinki)	Associate Professor Dept. of Human Genetics	Large-scale epigenome mapping; functional genomics of pediatric cancers; Genome-wide characterization of regulatory variation in human cells; human disease trait oriented population cell models; impact of perturbation on cis-regulatory variation; identification of causal and disease associated non-coding variants.
Paul William WISEMAN, Ph.D. Postdoctoral fellow (University of California, San Diego) Postdoctoral fellow (University of Tokyo) Ph.D. – Chemistry (University of Western Ontario) Hon BSc – Chemistry (St. Francis Xavier University)	Professor Dept. of Chemistry Dept. of Physics	Imaging based fluorescence fluctuation methods; characterization of cellular signaling, receptor transport and protein interactions in living cells and neurons; application of new nonlinear microscopic techniques; application of nanoparticles for fluorescence fluctuation and single molecule measurements

2.2.1.2 Funded research

All professors associated with the Ph.D. Program in Quantitative Life Sciences are actively engaged in externally funded research projects. As Table 4 indicates, QLS Teaching Faculty are successful in securing multiple research grants, often holding numerous multi-year awards from a variety of funding agencies at the same time. It is worth noting that many awards are from provincial, federal and internationally recognized bodies (ie. FQRNT, Genome Canada, CIHR, NIH) and are awarded individually (ie. the NSERC Accelerator Grant) or to collaborative research efforts (ie. CIHR Team Grants, NSERC Create Grants). The following Table, lists research funding and grants held from 2011 onwards (including grants awarded before 2011 but still ongoing in 2011 or later).

Table 4: Research grants held by QLS Teaching Faculty (* indicates PI or Co-PI)

Mathieu Blanchette		
Grant	**Year(s)**	**Total**
Multilateral France-Germany-Canada call on Epigenomics of Complex Diseases	2015-2019	$1,623,720
Genome Canada Disruptive Innovation in Genomics Competition	2016-2018	$250,000
NSERC Accelerator*	2013-2017	$160,000
NSERC Discovery*	2013-2017	$276,000
Canadian Foundation for Innovation – Leader Edge Fund	2013-2017	$2,312,056
CIHR Canadian Epigenetics, Environment, and Health Research Consortium (CEEHRC) Epigenomics platform – Data coordination Center	2012-2017	$1,098,980
CIHR Canadian Epigenetics, Environment, and Health Research Consortium (CEEHRC) Epigenomics platform – Epigenomics Mapping Center	2012-2017	$4,532,000
Genome Canada Bioinformatics and Computational Biology Competition	2013-2016	$375,000
FQRNT Team Grant	2013-2016	$144,000
Genome Canada Bioinformatics and Computational Biology Competition*	2013-2015	$250,000
Genome Canada Bioinformatics and Computational Biology Competition	2013-2015	$250,000
NSERC Research Tools and Instrumentation*	2012-2013	$40,385
Genome Québec Health Program	2010-2013	$1,273,155

Genome Canada Competition IV	2009-2013	$4,709,132
NSERC Discovery Grant*	2008-2013	$155,000
CIHR Team Grant	2008-2012	$3,315,976
Guillaume Bourque		
Grant	**Year(s)**	**Total**
CFI, Cyber-infrastructure	2016-2020	$5,000,000
CIHR, CEEHRC Consortium Network*	2015-2019	$2,000,000
CFI, Innovation Fund	2015-2019	$58, 435,000
CFI, Innovation Fund	2015-2019	$2,893,000
NSERC, Discovery Frontiers*	2014-2018	$6,000,000
Genome Canada, GIN – Tech. Development	2015-2017	$527,000
Genome Canada, Genomics Innovation Network	2015-2017	$1,050,000
Genome Canada, Genomics Innovation Network	2015-2017	$2,000,000
Genome Canada, Genomics Innovation Network – Tech Development	2015-2017	$1,000,000
CIHR, CEEHRC (Canadian Epigenetics, Environment, and Health Research Consortium) Epigenomics Platform*	2012-2017	$1,500,000
CIHR, CEEHRC (Canadian Epigenetics, Environment, and Health Research Consortium) Epigenomics Platform*	2012-2017	$6,000,000
Genome Canada, Large-scale Applied Research*	2013-2016	$6,000,000
Brain Canada	2013-2016	$1,494,900

CIHR, Operating Grant	2011-2016	$426,482
CIHR, Team Grant: Childhood Cancer*	2011-2016	$2,445,054
CANARIE, Research Middleware Program*	2011-2014	$771,000
Genome Quebec, Human Health Competition*	2011-2014	$2,000,000
CIHR, Advancing Technology Innovation*	2011-2012	$1,550,000
Erik Cook		
Grant	**Year(s)**	**Total**
Infrastructure CFI Innovation fund	2016-2026	$1,400,000
Operating NSERC Discovery grant*	2012-2017	$200,000
Fellowship Canada Research Chairs (CRC) Tier 2 Salary Award*	2009-2014	$500,000
CIHR Operating grant*	2009-2013	$370,000
EJLB Foundation Scholar Research Program*	2009-2011	$350,000
Operating Mathematics of Information Technology and Complex Systems (MITACS) Centre of Excellence	2009-2011	$67,000
CIHR Meetings, Plannings and Dissemination grant	2010-2011	$6,000
NSERC Discovery Grant*	2006-2011	$157,000
Ken Dewar		
Grant	**Year(s)**	**Total**
Canada Foundation for Innovation Leading Edge Fund (infrastructure)*	2011-2016	$1,051,010
McGill University Discretionary fund*	2008-2014	$21,4290

Genome Quebec*	2010-2013	$620,880
National Institutes of Health Public Health Service Grant	2009-2013	$2,943,072
Genome Canada	2009-2013	$17,400,000
McGill University Faculty of Medicine Infrastructure grant*	2009-2012	$187,500
Paul François		
Grant	**Year(s)**	**Total**
NSERC Discovery grant	2016-2021	$240,000
Simons Investigator: Mathematical Modeling of Living Systems	2014-2019	$500,000 USD
FQRNT*	2015-2018	$144,000
NSERC Discovery grant	2011-2016	$100,000
FQRNT	2013-2015	$40,000
Human Frontier Science Program (HFSP) Program Grant	2012-2015	$1,050,000 USD
Simon Gravel		
Grant	**Year(s)**	**Total**
CIHR Operating Grant	2014-2018	$289,886
Réseau de Médecine Génétique Appliquée (RMGA) Pilot Project Grant	2016 – 2017	$50,000
Sloan Research Fellowship	2014-2016	$50,000 USD
National Science Foundation	2012-2016	$227,565
Celia Greenwood		

Grant	Year(s)	Total
CIHR Project Grant	2016-2021	$1,496,217
CIHR Team Grant: Developmental Origins of Health and Disease	2016-2021	$1,496,217
CIHR Project Grant	2016-2019	$1,246,135
CIHR Project Grant*	2016-2019	$236, 995
Canadian Statistical Sciences Institute (CANSSI) Collaborative Research Team Project	2016-2019	$180,000
Cancer Research Society	2016-2018	$120,000
CIHR Team Grant: Canadian Epigenetics, Environment, and Health Research Consortium (CEEHRC)	2013-2018	$1,250,000
NSERC Discovery Grant*	2013-2017	$50,000
Ludmer Centre for Neuroinformatics and Mental Health	2013-2017	$13,200,000
CIHR*	2013-2017	$402,148
CIHR Transitional Operating Grant	2015-2016	$60,000
CIHR Operating Grant	2012-2015	$816,608
CIHR Operating Grant	2012-2015	$339,000
CIHR Operating Grant*	2011-2014	$216,327
NSERC Discovery Grant*	2009-2014	$75,000
CIHR Operating Grant	2010-2013	$458,100
The Lady Davis (LDI) Clinical Research Pilot (CLiPP) Competition	2012-2013	$49,670

The Week-End to End Women's Cancer Pilot Projects Grant*	2011-2012	$38,866
Peter Grutter		
Grant	**Year(s)**	**Total**
NSERC Discovery*	2016-2021	$69,000
FQRNT RS	2015-2021	$576,000
NSERC SPG	2016-2019	$171,000
MEIE (PSR-SIIRI)	2016-2019	$49,973
NSERC CRD	2014-2018	$150,000
McGill University Dawson/James McGill Chair research stipend	2013-2018	$15,000
McGill University Chair's research stipend	2013-2018	$10,000
FQRNT RS	2015-2017	$100,000
NSERC CRD	2014-2017	$100,000
FRQNT Team Grant	2013-2016	$43,000
FRQNT Team	2013-2016	$43,000
NSERC Discovery*	2011-2016	$98,000
NSERC CREATE	2011-2016	$300,000
NSERC CREATE	2011-2016	$300,000
CFI	2014-2015	$697,595
FQRNT RS	2013-2015	$300,000
CFI LEF*	2013-2015	$11,300,370
NSERC CREATE	2010-2015	$300,000
CIHR Training Program	2010-2015	$325,000

FQRNT RS*	2009-2015	$930,000
NSERC ENGAGE*	2014	$25,000
NanoQuebec*	2013-2014	$70,000
NSERC ENGAGE*	2013	$25,000
FQRNT Team*	2013	$44,050
NanoQuebec*	2012-2013	$57,000
NanoQuebec*	2011-2013	$140,000
FQRNT Team*	2010-2013	$58,000
CIfAR*	2010-2013	$75,000
FQRNT RS	2008-2013	$385,000
NSERC Strategic	2010-2012	$135,000
FQRNT Team	2009-2012	$55,550
NSERC RTI	2011	$139,419
Frédéric Guichard		
Grant	**Year(s)**	**Total**
FRQNT Strategic Cluster Program	2015-2021	$3,045,200
NSERC CREATE	2015-2021	$1,650,000
Coastal Healthy Ocean Network II (CHONe II). Strategic NSERC Network*	2015-2018	$164,000
NSERC Discovery Grant	2012-2017	$165,000
NSERC Strategic Project	2013-2016	$600,000
FRQNT Strategic Cluster	2009-2016	$3,630,000
NSERC Emerging Opportunity Fund, Coastal Healthy Ocean Network (CHONe)	2011-2012	$50,000

NSERC. Discovery Grant	2007-2012	$96,250
Coastal Healthy Ocean Network (CHONe)	2009-2011	$120,000
NSERC. MITACS Centers	2009-2011	$300,000
Coastal Healthy Ocean Network (CHONe). Strategic NSERC Network*	2009-2011	$150,000
Anmar Khadra		
Grant	**Year(s)**	**Total**
NSERC Canada*	2013-2018	$160,00
Canadian Foundation for Innovation CFI	2015-2018	$11,400,000
McGill University	2016-2017	$31,000
McGill University NSERC	2014-2015	$27,500
Mathematical Biosciences Institute (MBI) *	2014-2015	$30,000 (MBI) $10,000 (McGill) $10,000 (NIMBioS)
McGill University*	2012-2014	$70,000
R01 DK53456 (NIH)	2013-2014	$3,200,000
The Fields Institute*	2013-2014	$12,000
National Institutes of Health (NIH) *	2011-2012	$20,000
Sabrina Leslie		
Grant	**Year(s)**	**Total**
NSERC Collaborative Research and Development Grant (CRD)*	2016-2018	$467,940
FRQNT Team	2015-2018	$184,000
NSERC Collaborative Research and Development Grant (CRD)	2015-2017	$239,411

NSERC Discovery Grant	2012-2017	$25,000
CFI Infrastructure and Operating Fund	2012-2017	$125,000
Physics Start-up Funding	2012-2017	$170,000
NSERC Idea to Innovation	2015-2016	$12,000
NSERC RTI	2015-2016	$150,000
ZSGenetics	2014-2016	$113,819
Collaborative Health Research Project (CHRP)*	2013-2016	$428,370
NSERC Engage	2012-2016	$25,000
NSERC Engage	2012-2016	$61,000
NSERC Engage	2015	$25,000
NSERC Engage	2015	$25,000
CFI Leaders Opportunity Fund	2012-2015	$980,000
NSERC Research Tools and Instruments Grant	2012	$147,686
Judith Mandl		
Grant	**Year(s)**	**Total**
CIHR Project Grant	2016-2021	$905, 000
NSERC Discovery Grant	2016-2021	$170,000
CRC in Immune Cell Dynamics Canada Research Chairs (CRC)	2015-2020	$500,000
Startup Funds McGill University	2015-2016	$250,000
CFI Leaders Opportunity Fund	2015-2016	$450,000
McGill University Total Funding	2015	$225,000

McGill Endowment Fund Phyllis Butterworth Endowment	2015	$250,000
National Institutes of Health (NIH) (USA) Office of AIDS Research*	2010-2011	$122,000
Christopher Pack		
Grant	**Year(s)**	**Total**
Defense Advanced Research Projects Agency (DARPA) BAA-15-35*	2016-2017	$415,255
FRQS Senior Scholar	2016-2017	$40,233
U.S. Department of Defense Psychological Health/Traumatic Brain Injury (PH/TBI) Research Program	2014-2017	$180,000
NSERC Discovery Grant	2012-2017 (renewal)	$280,000
Killam Scholar	2007-2017	$0
CIHR Operating Grant	2011-2016	$594,635
Defense Advanced Research Projects Agency (DARPA) BAA-14-38	2014-2015	$598,471
Ministère du Développement économique, de l'Innovation et de l'Exportation (MDEIE) Grant: Programme de Soutien à la Recherche	2012-2015	$150,000
Canada Research Chair	2005-2015 (renewed 2010)	$125,000
Neuro Early Career Award	2013	$0
National Science Foundation Collaborative Research in Computational Neuroscience Grant	2010-2013	$270,895

MITACS Centre Grant	2009-2012	$40,000
NSERC Discovery Grant	2007-2012	$133,710
Ministère du Développement économique, de l'Innovation et de l'Exportation (MDEIE) Grant Programme de Soutien à la Recherche	2008-2011	$150,000
EJLB Scholar Research Program	2008-2011	$350,000
CIHR Operating Grant	2006-2011	$492,450
Tomi Pastinen		
Grant	**Year(s)**	**Total**
CIHR, FRQS, ANR, BMBF*	2016-2019	$2,273,208
NIH*	2015-2019	$12,382,880
CIHR	2015-2019	$2,000,000
CIHR*	2014-2019	$1,026,630
The EU Joint Programme – Neurodegenerative Disease Research (JPND)*	2016-2018	$333,000
CIHR	2014-2018	$1,195,200
Réseau de médecine génétique appliquée (RMGA)	2014-2018	$2,700,000
CIHR	2013-2018	No direct funds
Department of Defense*	2016-2017	$142,500
Genome Canada*	2015-2017	$3,293,976
Merck & Co. Inc*	2015-2017	$195,000
Genome Canada*	2015-2017	$4,000,000
Crohn's & Colitis Foundation of Canada*	2014-2017	$371,460

CIHR	2013-2017	No direct funds
Genome Canada*	2013-2017	$6,772,000
Multidimensional Epigenome Mapping Centre McGill. CIHR*	2012-2017	$5,850,000
Compute Canada Resource Allocation*	2015-2016	$198,000
Finnish Funding Agency for Innovation (TEKES)	2015-2016	€80,000
CIHR*	2012-2016	$850,000
NIH	2012-2016	~$125,000
Academy of Finland	2015	$629,280
Genome Canada	2013-2015	$9,610,984
Compute Canada*	2014	$0
CIHR	2013-2014	$20,000
FRSQ*	2010-2014	$2,400,000
CIHR*	2010-2014	$716,000
CIHR	2010-2013	$2,048,322
Genome Quebec	2010-2011	$100,000
Genome Quebec	2009-2011	$304,000
CIHR	2008-2011	$408,000
Paul Wiseman		
Grant	**Year(s)**	**Total**
Canadian Institute for Advanced Research (CIFAR) Global Call for Ideas	2015-2021	$1,100,000

NIH National Institute on Deafness and Other Communication Disorders R01 – DC005788-10	2014-2019	$439,000 (2014)
Brain Canada Platform Grant	2015-2018	$120,250
NSERC CREATE	2012-2018	$300,000
NSERC CREATE	2012-2018	$300,000
CFI Innovation Fund	2016-2017	$12,560,000
NSERC Discovery Grant*	2012-2017	$101,000
FRQS- Groupe d'étude des proteins membranaires (GEPROM) GEPROM Research Stimulus Grants	2016	$15,000
NSERC CREATE	2010-2016	$300,000
CFI Leading Edge Fund	2013-2015	$12,100,000
CIHR Strategic Training Grant	2009-2015	$375,000
CFI Innovation Grant	2009-2014	$26,600,000
FQRNT Team Grant	2009-2012	$84,000
NSERC Discovery Grant*	2007-2012	$53,400
American Academy of Otolaryngology Training grant	2011	$9,976
Canadian Institute for Photonic Innovations (CIPI) Technology Exploitation & Networking	2010-2011	$25,000

Table 5 shows research funding received by QLS Teaching Faculty from four major sources of funding in Quebec and Canada for research in quantitative, physical and biological life sciences. In some cases, research projects are proposed and undertaken by a single principal investigator, but in many cases successful research grants are the result of multidisciplinary projects and the collaboration of many researchers. For example, Guillaume Bourque, Erik Cook, Ken Dewar, Peter Grutter, Anmar Khadra, Sabrina Leslie, Judith Mandl and Paul Wiseman

have been involved in securing over $149,000,000 in funding for innovation research, infrastructure and operating grants from the Canadian Foundation for Innovation (CFI). Many of these are large scale grants that benefit not only the individual research groups, but the research field within the university as a whole.

Table 5: Research grants received by QLS Teaching Faculty from major Quebec and Canadian funding agencies

Funding Agency	Total Amount	Faculty Members
CFI	$ 149,991,975	Guillaume Bourque, Erik Cook, Ken Dewar, Peter Grutter, Anmar Khadra, Sabrina Leslie, Judith Mandl, Paul Wiseman
CIHR	$47,216,367	Mathieu Blanchette, Guillaume Bourque, Erik Cook, Simon Gravel, Celia Greenwood, Peter Grutter, Judith Mandl, Christopher Pack, Tomi Pastinen, Paul Wiseman
FRQNT/FRQS	$12,261,033	Mathieu Blanchette, Paul François, Peter Grutter, Frédéric Guichard, Sabrina Leslie, Chris Pack, Tomi Pastinen, Paul Wiseman
NSERC	$15,404,701	Mathieu Blanchette, Guillaume Bourque, Erik Cook, Paul François, Celia Greenwood, Peter Grutter, Frédéric Guichard, Anmar Khadra, Sabrina Leslie, Judith Mandl, Christopher Pack, Paul Wiseman

2.2.1.3 Publications

The academic staff teaching in the Ph.D. Program in Quantitative Life Sciences have a consistent record of scholarly and professional publications. These professors regularly publish collaborative research findings in top tier journals, including Nature Genetics, Genome Biology, Cell, Lancet Oncology, and Nature Nanotechnology. Table 6 below lists the number of publications from 2011 onwards. For a detailed record of each publication by faculty member, please see the Appendix.

Table 6: QLS Teaching Faculty Total Publications by Year

Faculty Member		Number of Publications					
		2011	**2012**	**2013**	**2014**	**2015**	**2016**
Mathieu	Blanchette	8	3	10	6	5	0
Guillaume	Bourque	8	5	4	7	12	2
Erik	Cook	2	5	0	1	1	0
Ken	Dewar	2	3	3	1	4	6
Paul	FranÇois	1	5	6	1	3	2
Simon	Gravel	0	1	5	3	4	0
Celia	Greenwood	6	6	8	10	11	6
Peter	Grutter	12	12	14	4	5	5
Frédéric	Guichard	8	5	5	6	7	5
Anmar	Khadra	2	1	2	2	6	2
Sabrina	Leslie	0	0	3	2	2	2
Judith	Mandl	1	3	2	5	2	1
Christopher	Pack	9	4	4	3	4	4
Tomi	Pastinen	7	7	10	6	16	2
Paul	Wiseman	7	6	13	7	4	4
	TOTAL	**73**	**66**	**89**	**64**	**86**	**41**

2.2.1.4 Graduate student supervision

All members of the Quantitative Life Sciences Program are actively engaged in supervision of student and postdoctoral research. The table below highlights the number of undergraduate, graduate and postdoctoral fellow supervision undertaken since 2010.

Table 7: Student supervision from 2010 to 2016

Supervisor		Undergraduate	Graduate		Postdoctoral fellow
			Master's	Ph.D.	
Mathieu	BLANCHETTE	10	6	11	4
Guillaume	BOURQUE	4	5	2	4
Erik	COOK	8	3	4	1
Paul	FRANCOIS	22	6	3	6
Simon	GRAVEL	2	2	8	2
Celia M T	GREENWOOD	3	5	4	10
Peter	GRUTTER	45	16	21	13
Frederic	GUICHARD	11	5	10	5
Anmar	KHADRA	2	6	1	1
Sabrina Rose	LESLIE	29	5	3	4
Judith	MANDL	2	2	4	2
Christopher	PACK	10	3	15	3
Tomi	PASTINEN		3	2	7
Paul	WISEMAN	6	8	6	7
	TOTAL	**154**	**75**	**94**	**69**

2.3 INSTITUTIONAL ORIENTATIONS

2.3.1 Faculty and University development plan

The new Quantitative Life Sciences Ph.D. Program will promote multidisciplinary life science and health research at McGill University. This program will directly contribute to the success of McGill's Strategic Research Plan of bringing together the life sciences, natural sciences, and engineering[21]. It is important to emphasize that this will be a McGill University wide graduate program, not constrained to a single department and faculty. Thus, students will not have to choose between a quantitative or life science department, and faculty members will be able to recruit students from a variety of academic backgrounds to form the interdisciplinary teams needed to advance their research aims. The result of this cross-fertilization of graduate students is that it will greatly facilitate interdisciplinary research at McGill by bringing investigators and students from the physical, computational, mathematical and biological sciences together.

2.3.2 Vertical and horizontal integration

The horizontal integration of the proposed Quantitative Life Sciences Ph.D. Program is to be viewed in relation to the other programs offered by traditional disciplines in the Faculties of Medicine and Science (see Figure 1 above). Traditional disciplines that are related to this Ph.D. program include Biology, Ecology, Biochemistry, Physiology, Pharmacology, Neuroscience, Human Genetics, Mathematics, Physics, Chemistry, Statistics, Computer Science, Material Science and others. By bridging the gap between the life and quantitative science departments at McGill, this new Ph.D. program will enhance these established disciplines. Because this program will be open to researchers involved in multidisciplinary life science research, vertical integration will be satisfied by the participation of faculty members across departments and faculties. Although a new core curriculum will be organized within the Quantitative Life Sciences Ph.D. Program, appropriate elective courses will be offered in collaboration with other departments in the Faculties of Medicine and Science.

2.4 RELEVANCE TO THE UNIVERSITY NETWORKS

2.4.1 Related Programs

There are no graduate programs or graduate options at McGill that approach the breadth of the proposed Ph.D. Program in Quantitative Life Sciences, although the proposed program builds on McGill's existing Graduate Option in Bioinformatics and synergizes with the new Bioengineering and Biomedical Engineering graduate program. The proposed program also builds on several externally funded department-centered training programs (outlined in Table 2 above) that have been very successful in establishing the quantitative life sciences. Although most of these training programs are nearing their funding completion, these programs have laid the critical foundation for the new Quantitative Life Sciences Ph.D. Program. In addition, McGill has an exemplary track record in graduate training in Biomedical Engineering (now Biological and Biomedical Engineering), which is complementary to the proposed program in Quantitative Life Sciences. To capitalize on these shared interests, we intend to invite students and faculty members associated with Biological and Biomedical Engineering program to participate in the proposed QLS seminar series outlined in Section 4 and take part in any workshops offered by QLS.

2.4.1.1 Relationship to existing Graduate Option in Bioinformatics

The Graduate Option in Bioinformatics has existed at McGill since 2006, at both the Masters and Ph.D. levels. Students in the Graduate Option in Bioinformatics are registered in one of 14 departments and have to satisfy the admission and progress requirements of their home department, but can replace two of the courses they would normally take within their home department with one of five bioinformatics courses offered by this option, and need to attend a seminar series. The program currently attracts both students with very strong quantitative background from Computer Science, Math, Biostatistics, or Physics, as well as students whose background focusses on life sciences and who often lack solid quantitative skills. Because of this spectrum of quantitative skills, the depth of the training on the quantitative aspects is limited. Students learn fundamental concepts of bioinformatics and become qualified bioinformatics users, but most lack the training to push the limits of bioinformatics through the development of new approaches. Contrary to the Graduate Option in

Bioinformatics, the new Quantitative Life Sciences Ph.D. Program targets students with strong quantitative and computational skills, and aims to train future researchers who will develop innovative computational approaches to solve a variety of important life science problems that go beyond traditional bioinformatics. Thus, the Graduate Option in Bioinformatics and the Quantitative Life Sciences Ph.D. Program will be complementary in both their scope and clientele.

2.4.1.2 Relationship to existing training programs in Biological and Biomedical Engineering

McGill's Bioengineering Department in the Faculty of Engineering, and the Biomedical Engineering Department in the Faculty of Medicine, have recently been integrated to create a single graduate training program. This will provide a unique training environment for students interested in linking engineering to the biosciences. The combination of Quantitative Life Science (QLS) and Biological and Biomedical Engineering (BBME) programs at McGill will enhance student training in these two disciplines. Although students with strong quantitative or computational backgrounds could potentially enroll in either the BBME or Quantitative Life Science graduate programs, the type of students targeted by the two programs are quite different. The BBME Ph.D. program largely (though not exclusively) targets students with an engineering undergraduate degree. Its prerequisites include courses in electromagnetics, mechanics, biophysics and physical chemistry, which are not part of the standard curriculum of Science undergraduates. It also requires a Masters in BBME or equivalent, a program that mostly aims at recruiting engineering graduates. In contrast, the QLS program mostly targets students from the Science streams, with the mathematical, statistical, and computational skills needed for biological data analysis. Students that seek advanced training from a program that focuses on engineering-related skills would likely choose Biological or Biomedical Engineering, while those with more fundamental bioscience backgrounds and interests, would gravitate to the Quantitative Life Sciences Ph.D. Program.

Evidence that bioengineering and quantitative bioscience provide complementary training environments can be found in McGill's successful quantitative bioscience undergraduate programs (Table 1) and the newly created undergraduate Bioengineering program,, where demand for these programs is high. Further evidence that a graduate training program in the Quantitative Life Sciences is complementary to Biological or Biomedical Engineering arises from the large number of research-intensive universities that have both programs. For example, all universities with comparable programs to Quantitative Life Science listed in Table 8 below, also have strong Biological or Biomedical Engineering training programs. Although the QLS and BBME programs clearly differ in the types of students they aim to recruit and in the training they provide, every effort will be made to maximize the synergy between the two programs, e.g. through jointly offered seminars, cross-listing of courses, and multi-disciplinary projects. Students from the two programs will be encouraged to collaborate whenever possible, e.g. in situations where a device developed by a BBME student may be used by an QLS student who would develop approaches to analyze the data it produces.

2.4.2 Similar programs offered elsewhere

Within Canada, no degree-granting program currently exists with a similar breadth to the proposed Ph.D. program in Quantitative Life Sciences. There are, however, a number of smaller programs usually based within a faculty or department. The University of Ottawa has had a successful NSERC-CREATE training program in

Quantitative Biomedicine (http://www.qbm.uottawa.ca). For statistical methods in genetics and genomics, Toronto (http://www.stage.utoronto.ca/) has the only formal training program in Canada. There are several Bioinformatics programs across the country, such as at the University of Montreal (https://admission.umontreal.ca/programmes/doctorat-en-bio-informatique/), and the University of British Columbia (www.bioinformatics.ubc.ca/program/). One of the broadest programs with overlap in scope is the Collaborative Program in Genome Biology and Bioinformatics at the University of Toronto which provides a unifying genomic theme for students in 10 departments ranging from Engineering to Ecology to Physics. Students are first admitted to their home departments and then request admission to the Collaborative Program (http://gbb.utoronto.ca/index.php/Main_Page). Although broad, this program is focused around genetic and genomic research.

Elsewhere, as at McGill, there are numerous research groups with interests overlapping those in the Quantitative Life Sciences, but most are not degree granting Programs. To give a few examples, research interests at the Donnelly Centre for Cellular and Biomolecular Research at the University of Toronto (http://tdccbr.med.utoronto.ca/) span integrative biology, bioengineering and structural biology, and models of disease. At UBC, the Mathematical Biology group (http://www.math.ubc.ca/Research/MathBio/graduate.php), unites faculty with interests in research applying mathematics to various fields within biology. Similarly, the Centre for Mathematical Biology at the University of Alberta (http://www.math.ualberta.ca/~mathbio/index.html), the Pacific Institute for the Mathematical Sciences (https://www.pims.math.ca/), and the University of Waterloo Applied Mathematics, Mathematical Medicine and Biology (https://math.uwaterloo.ca/applied-mathematics/ research-areas/mathematical-medicine-and-biology) each represent centres or groups of faculty or researchers with interests in mathematical biology.

In many Quebec universities, there are programs or options that overlap with some elements of the proposed Ph.D. Program in Quantitative Life Sciences program. As mentioned above, a Graduate Option in Bioinformatics already exists at McGill (https://www.mcgill.ca/mcb/academic), while a complete degree-granting bioinformatics program exists at Université de Montréal (http://www.bioinfo.umontreal.ca/home/). There is a graduate diploma in Biotechnology and Genomics at Concordia (http://www.concordia.ca/artsci/biology/programs/graduate/diploma- biotechnology-genomics.html), and a Physiology and Biophysics program at the University of Sherbrooke (http://www.usherbrooke.ca/dep-physiologie-biophysique/en/). For other quantitative life science topics outside of bioinformatics at McGill, many active research groups exist, and students registered in an appropriate department can get involved in their area of interest by linking with such groups. However, these research groups cannot facilitate cross-topic interactions, through courses or through peer groups that allow comparisons of similar quantitative research methods applied to a variety of areas.

Outside of Canada, the interest and the demand for interdisciplinary research in quantitative life sciences has led to the formation of various programs, both nationally and internationally, that emphasize quantitative research skills applied to biology. These programs span a wide variety of different administrative structures, and vary in the breadth addressed. Among comprehensive degree-granting programs focused at the doctoral level, several examples can be found in the US, mostly among top-ranking universities with which McGill is competing (Table 8). It is notable that all of these programs were recently formed and this reflects the fact that quantitative life science is a new and evolving discipline. In addition to the programs in Table 8, several

universities have created informal groupings of disciplines to facilitate interdisciplinary research in these fields. University of California, Irvine has a gateway year prior to Ph.D. degrees in 6-7 departments and UC San Francisco groups 3 Ph.D. programs in quantitative biology. Internationally, the same trend can be seen, for example at the University of Munich, Germany (Graduate Program in Quantitative Bioscience) and Imperial College London (MSc in Computational Methods in Ecology and Evolution).

Table 8. A selection of comparable programs outside Canada

University	Name of program	Degree(s)	Fields of focus	Year started: # per year: Total cohort:
Princeton (USA)	Quantitative and Computational Biology www.princeton.edu/qcbgrad	Ph.D.	Genomics, computational biology, systems biology, biophysics, quantitative genetics, molecular evolution, microbial interactions	Started: 2009 Per year: 5-9 Total: ~30
Harvard (USA)	Systems Biology SysbioPh.D..harvard.edu	Ph.D.	Understanding complex biological systems. There is also a Bioinformatics/Computational Biology Masters program linked with Biostatistics	Started: 2008 Per year: 10-15 Total: 60
University of California Merced (USA)	Quantitative and systems biology qsb.ucmerced.edu	Ph.D. and MSc	Integration of systems at molecular, cellular, organ, organismal or ecological levels to better understand the overall function of biological systems as a whole	Started: 2007 Per year: 10-25 (13 in 2013) Total: 59
Carnegie Mellon (USA)	Carnegie Mellon Ph.D. in Computational Biology www.compbio.cmu.edu	Ph.D.	Cellular systems modeling, computational genomics, computational structural biology, bioimage informatics.	Started: 2005 Per year: 10-15
University of Pennsylvania (USA)	Graduate group in genomics and computational biology	Ph.D.	Require synthesis and integration of biology, computer science, mathematics, statistics and	Started: 2002 Per year: 5-8

	www.med.upenn.edu/gcb		engineering	
Rice University	Program in Systems, Synthetic, and Physical Biology sspb.rice.edu	Ph.D.	Fundamental and applied problems in the biosciences, biotechnology and medicine	Started: 2011 Per year: 8 Total: 16

It is worth noting (see section 2.1.4.2) that all the Universities listed above have separate Biological or Biomedical Engineering programs or streams, often more focused on development of devices or technology than the Quantitative Life Science, Biology or Systems groups.

2.4.3 Originality and anticipated contribution of the proposed program

The Interdisciplinary Program in Quantitative Life Science is original and makes several important contributions that are distinct from existing programs at McGill. First, this new program provides a common teaching framework by uniting the subdomains of the discipline (e.g., computational biology, bioinformatics, biophysics, mathematical biology, and computational ecology) that share many of the same mathematical and quantitative methods. Second, although there are many smaller initiatives in quantitative life sciences at McGill, they are independent and located locally within departments or faculties. Thus, the proposed program enhances collaborative interactions among researchers and students. Third, this new program facilitates interdisciplinary life science research at McGill by providing a mechanism for researchers in the faculties of science and medicine to recruit students for joint graduate supervision. Fourth, the Quantitative Life Sciences Ph.D. Program will prepare a new breed of Ph.D. researchers that are in high demand and provide an academic community in which they can thrive and develop. Finally, this new program allows McGill to retain and recruit highly-talented graduate students that would have enrolled in similar programs that are currently only available outside of Quebec and Canada.

A hypothetical example may clearly illustrate the original contributions this new program will have on life science research at McGill. Suppose a professor in biochemistry has extensive experimental results that defy traditional methods of analysis. Through the Quantitative Life Sciences Ph.D. Program, this professor establishes a collaboration with a professor in computer science, and together, they recruit and co-supervise a Ph.D. student with an undergraduate background in physics. Thus, an interdisciplinary team of experts in biochemistry, computer science and physics has been established to develop the novel solutions and interpretations needed for a successful outcome. In the process, a new Ph.D. scientist has been uniquely trained in the interdisciplinary skills that will contribute to the future advancements of the life sciences.

2.4.4 Student mobility

Students in the Quantitative Life Sciences Ph.D. Program will have mobility both within McGill University and through various international summer schools. By establishing an interdisciplinary community, our students will be encouraged to participate in a variety of seminars and symposiums that allows them to "break out" of their comfort zone and experience new research directions. Our graduate students will be encouraged to participate in the many international summer schools that now focus on topics in quantitative life science. This includes the yearly summer schools organized by McGill's Centre for Applied Mathematics in Bioscience and Medicine in collaboration with Ohio State University's Mathematical Biosciences Institute and US National Institute for Mathematical and Biological Synthesis. Other examples include the Frontiers in Neurophotonics at Université Laval and the Cold Spring Harbor Laboratory (CSHL) Summer School in Computational Cell Biology in New York.

2.4.5 Inter-university collaboration and relevance to Quebec network

The proposed Ph.D. Program in Quantitative Life Sciences will facilitate inter-university collaborations in Quebec. For example, many McGill faculty that will take part in this training program belong to multi-university centers or networks. Examples include the Centre de Recherches en Mathématiques (of which McGill's Centre for Applied Mathematics in Bioscience and Medicine belongs), that spans 12 universities in Quebec and Ontario including Université de Montréal, Université du Québec à Montréal, Concordia University, Université Laval, Université de Sherbrooke, École Polytechnique, HEC Montréal, Université du Québec à Trois-Rivières, University of Ottawa, Carleton University and Queen's University. Each of the laboratories hosts an average of 20 professors, 50 graduate students, and 7 postdoctoral fellows, organizes workshops and inter-university seminars on a regular basis, and coordinates a unified graduate school (involving five, six or seven universities), with funding coming from a wide variety of sources. Another example is Le Regroupement Québécois sur les Matériaux de Pointe, an FRQNT sponsored network in advanced materials, which includes a strong biophysics stream. Both the Neurophotonics and Biophotonics centres at Université Laval have close interactions with faculty at McGill. In addition, the Bioinformatics program at Université de Montréal will provide many opportunities for local collaborations with the Quantitative Life Sciences Ph.D. Program. Finally, quantitative life science research has become an important component of Calcul Québec, which is part of Canada's national high performance computing network and Génome Quebec's research mission in bioinformatics and computational biology.

2.5 TIMETABLE OF PROGRAM IMPLEMENTATION AND PROJECTED STUDENT ENROLMENT

Forecast growth of student enrolment for the Ph.D. Program Quantitative Life Science is presented in Table 9 below. Beginning with the first year of implementation and approximately 10 to 20 new Ph.D. students per year over the next five years, for a total of approximately 80 enrolled students. This is based on the assumption that the program will receive approval from the Ministère de l'Éducation et de l'Enseignement supérieur (MEES) to enable us to enroll students starting in the 2017-2018 academic year. If a 10% attrition rate is forecast, we expect to award about 10 Ph.D. per year starting in the year 2021. Thus, we expect a steady-state enrollment of between 70 to 80 students when the program reaches equilibrium. Based on a survey of the potential undergraduate

clientele at McGill (see section 2.1.6 above), we expect most of our new graduate students from Quebec will come from the current cohort of top students that have been leaving the province to attend similar graduate programs in the US and Europe. Along with attracting new students from outside of Quebec, the Interdisciplinary Program in Quantitative Life Science will produce a net gain in life science graduates students with no reduction from other graduate programs at McGill.

Table 9. Expected program enrollment during the program's first five years.

Student details	2017/18	2018/19	2019/20	2020/21	2021/22
New students from Quebec	7	8	10	12	12
New students from Canada	2	2	4	4	4
New international students	1	2	4	4	4
Annual total enrolled	**10**	**22**	**40**	**60**	**80**

2.6 SOCIOECONOMIC MOTIVES

2.6.1 Clientele

As discussed in Section 2.1.6 above (and outlined in Table 1) there is a strong student demand for an interdisciplinary Quantitative Life Sciences Program at McGill University, as well as other universities in Quebec and Canada. Similar programs offered in the United States and Europe are well developed, having been created within the last 10 years, indicating McGill University must act swiftly to attract students interested in this dynamic and innovative research area.

2.6.2 Labour Market

McGill University's proposed Ph.D. Program in Quantitative Life Sciences has broad applicability to academia, government and industry and will contribute to economic growth in key sectors of the economy. Recent market studies have estimated that the global quantitative life science market is growing from USD $760 million in 2011 to a projected $4.2 billion in 2020[40,41]. This does not include the related pharmaceutical and medical devices market which are more than 50 times larger[42]. Importantly, the quantitative life science sectors are expanding at a compounded annual growth rate of over 20%[40,41] and will form a substantial component of the "green economy" that is central to the economic development of Quebec and Canada[43]. In this section, we present evidence that students trained in the Quantitative Life Sciences will be in high demand by academia,

government and industry.

2.6.2.1 Employment opportunities in the academic and government sectors

Graduates of the Ph.D. Program in Quantitative Life Sciences will be part of the next generation of academic and government researchers that will change how life science research is conducted. As evident by the number of new and expanding graduate programs in the quantitative life sciences at the top research universities in North America (outlined in section 2.4.2 below), there will be ample opportunities for academic employment. As research becomes more interdisciplinary, traditional life science departments will seek individuals with quantitative backgrounds. For example, Genome Quebec and Genome Canada rely heavily on computer-based bioinformatic analysis to advance their genomic innovation mandate[44]. Other academic opportunities for graduates of the quantitative life sciences can be found in university engineering departments and faculties. In addition, the quantitative skills acquired by our graduates will also be applicable to academic research in non-bio related fields such as computational chemistry and computational material science.

Quantitative analysis of life science data is routinely performed by many different government agencies when developing public policy. Government agencies benefit from the application of predictive models of future health care demand and agricultural resources. For example, Fisheries and Oceans Canada rely on computational biologists to construct mathematical models of changing environments and its impact on food supply. Our graduates will have developed the skills needed to collect the relevant data and then create predictive models to explain complex, interlinked biological systems.

2.6.2.2 Employment opportunities in the life science industrial sectors

The industrial demand for mathematical and computational life scientists is expanding rapidly[2,14,22,40,41,45] and with it the need for graduates with relevant research expertise. Examples of this new demand is evident in the large-enterprise pharmaceutical sector such as Novartis, which has recently established a modeling and simulation group which tackles a wide range of translational problems,[46] and AstraZeneca where the new predictive sciences group is focused on developing computational solutions to improve traditional research and development[47]. Other examples include Eli Lilly, Pfizer and Merck that have placed greater emphasis on their system and computational biology efforts, and have corresponding positions available[48-50]. Worldwide, there are numerous examples of small companies applying new quantitative approaches to a variety of life science and health services such as personalized medicine (Selventa[51] and GNS Healthcare[52]), predictive biosimulation (Entelos[53]) and data-mining (Genedata[54]).

With strong life sciences and biotechnology industries in Quebec and Canada, our graduates will have many career opportunities in the pharmaceutical, medical devices, and sustainable environment sectors[42,55]. Canadian employment opportunities for our graduates will be at both multinational as well as small and medium sized enterprises (SMEs), which account for 60% of Canada's economic output and 80% of national employment[56]. Increasingly, the SMEs in the Canadian life science sectors are looking for personnel capable of performing a wide-range of research activities. For example, Chemical Computing Group, an SME with an office in Montreal,

focuses on computational methods for drug discovery and is interested in recruiting graduate students with the interdisciplinary skills our program will provide[32]. Another example is Rogue Research in Quebec, who need personnel with interdisciplinary training to develop state-of-the-art computational techniques to link brain imaging to real-time surgical intervention[57]. Overall, the large and growing national and global biotechnology sector[42] will offer many employment opportunities for graduates of our Quantitative Life Sciences Ph.D. Program.

2.6.2.3 Employment opportunities in the technology industrial sector

It is important to emphasize that the skills developed by the students in the Ph.D. Program in Quantitative Life Sciences will go beyond the immediate application of life science research, since many technology sectors share similar quantitative methods. An example is the United States National Science Foundation (NSF) and National Institutes of Standards and Technology (NIST) funded 'Materials Genome Initiative' which aims to translate data mining and other techniques developed for life-science 'omics' research to discover, develop and deploy new material systems deemed critical for advanced manufacturing[58]. The students who graduate from our program will be experts in describing and understanding complex systems using a variety of quantitative tools and techniques. They will also acquire valuable multidisciplinary teamwork, communication, and project management skills. Because graduates of the Ph.D. Program in Quantitative Life Sciences will have a strong foundation of mathematical, computer programming and data analysis abilities, they will have skills that are highly desired by almost all employers and government organizations throughout Quebec, Canada and the world. For example, according to a recent report from the International Labour Organization[59] employment opportunities in the information and communication technology sectors will continue to outpace the supply of qualified University graduates throughout the developed economies of North America and Europe.

2.6.2.4 Employment examples of multidisciplinary trained McGill graduate students

An example of how a multidisciplinary training program leads to successful employment is McGill graduate student Ali Yehia who received his Ph.D. in Physiology (1998)[60]. As part of the Center for Nonlinear Dynamics, one of McGill's earliest initiative to nurture quantitative methods in bioscience and medicine, Ali's Ph.D. research had a large computational component. The interdisciplinary graduate training that Ali received enabled him to develop a career in the biotechnology sector, where he is now director of product and business development at Fluxion Biosciences. A second example of how a student trained in both the physical and biosciences is Alan Schoen[61]. Alan received a B.Sc. in Physics (2010) and a Master's in Neuroscience (2012) from McGill and has been employed as a data scientist with technology companies Qlaym and Backtrack. Thus, the proposed Quantitative Life Sciences graduate program will produce graduates with strong interdisciplinary skills, such as Ali and Alan, that will be readily equipped to contribute to the fast growing green economy of science, technology, engineering and mathematics that are key components for the future of technology development in Quebec and Canada's broader economic action plan[43].

2.7 REFERENCES AND DOCUMENTS CITED

1. Kitano, H. Computational systems biology. Nature, 420, 206-10 (2002).

2. Nugent KL, Kulkarni, A. An interdisciplinary shift in demand for talent within the biotech industry. Nature Biotechnology 31, 853–855 (2013)
3. Noble, D. The rise of computational biology. Nature Reviews Molecular Cell Biology 3, 460-63 (2002).
4. Kitano, H. Systems Biology: A Brief Overview. Science 295, 1662-64 (2002).
5. Pharmaceutical Research and Manufacturers of America. Industry profile 2015. http://www.phrma.org/sites/default/files/pdf/2014_PhRMA_PROFILE.pdf
6. http://www.cihr-irsc.gc.ca/e/47490.html
7. http://irp.nih.gov/our-research/scientific-focus-areas
8. http://www.mrc.ac.uk/news-events/publications/strategic-plan-2014-19/
9. Eugene C Butcher, E.C., Berg, E.L. and Kunkel, E.J. Nature Biotechnology 22, 1253-59 (2004).
10. Hood, L. and Perlmutter, R.M. The impact of systems approaches on biological problems in drug discovery. Nature Biotechnology 22, 1215-17 (2004).
11. Aerts, H.J.W., et al. Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach, Nature Communications 5, 4006 (2013).
12. Savage ,N. Bioinformatics: Big data versus the big C. Nature 509, S66–S67 (2014).
13. http://www.crm.umontreal.ca/MPE/mpe.shtml
14. Integrative Systems Biology. The 21st Century Challenge to Biological, Biomedical and Biotechnological Research in Canada. Briefing paper and working recommendations (2006). The Canadian Society for Systems Biology. https://www.sysbiosociety.ca
15. Williams, R. Different Cancers, Same Mutations. The Scientist (2103). http://www.the-scientist.com/?articles.view/articleNo/37661/title/Different-Cancers--Same-Mutations/
16. http://www.cihr-irsc.gc.ca/e/20677.html
17. http://www.genomecanada.ca/en
18. http://www.mcgill.ca/cambam/
19. Dorigo, W.A., Zurita-Milla, R., de Wit, A.J.W., Brazile, J., Singh, R. and Schaepman, M.E. A review on reflective remote sensing and data assimilation techniques for enhanced agroecosystem modeling. International Journal of Applied Earth Observation and Geoinformation 9, 165-93 (2007).
20. Pascual M. Computational Ecology: From the Complex to the Simple and Back. PLoS Computational Biology 1 (2005).
21. http://www.mcgill.ca/research/about/srp
22. Fisher, H.P. Towards quantitative biology: integration of biological information to elucidate disease pathways and to guide drug discovery. Biotechnology Annual Reviews 11, 1-60 (2005).
23. Scannell, J. W., Blanckley, A., Boldon, H. and Warrington, B. Diagnosing the decline in pharmaceutical R&D efficiency. Nature Reviews Drug Discovery 11, 191-200 (2012).
24. Herper, M. The Cost Of Creating A New Drug Now $5 Billion, Pushing Big Pharma To Change. Forbes (2013). http://www.forbes.com/sites/matthewherper /2013/ 08/11/how-the-staggering-cost-of-inventing-new-drugs-is-shaping-the-future-of-medicine/
25. Chua, H.N. and Roth, F.P. Discovering the Targets of Drugs Via Computational Systems Biology. The Journal of Biological Chemistry 286, 23653–58 (2011).
26. Enhancing the Vitality of the National Institutes of Health: Organizational Change to Meet New

Challenges. National Research Council (US) and Institute of Medicine (US) Committee on the Organizational Structure of the National Institutes of Health (2003).
27. Gwynne, P. and Heebner, G. Pharmaceutical and biopharmaceutical firms need to reduce the cost and lead time of drug development. A range of recently developed technologies makes that goal possible. Science. http://www.sciencemag.org/ site/products/ddbt_0207_Final.xhtml
28. Kraljevic,S., Stambrook, P.J. and Pavelic, K. Accelerating drug discovery. EMBO Reports 5, 837-42 (2004).
29. Saha, D., Emran, T.B. and Paul, S. Bioinformatics: The effects on the cost of drug discovery. Galle Medical Journal 18, 44-50 (2013).
30. Okinawa Institute of Science and Technology. Using computers to speed up drug discovery. ScienceDaily, 20 (2014). Http://www.sciencedaily.com/releases/2014/02/140220083259.htm
31. Cook, D., Scherrer, D., Onsum. M., and Henney A. Systems Biology: A Multi- Disciplinary Approach to Improve the Drug Discovery and Development Process. American Drug Discovery 2, 1-5 (2007).
32. http://www.chemcomp.com
33. Ginsberg, J., Mohebbi, M.H., Patel, R.S., Brammer, L., Smolinski, M.S. and Brilliant, L. Detecting influenza epidemics using search engine query data. Nature 457, 1012-15 (2009).
34. Microsoft Research Connections Blog, Cloud Computing Unlocks Drug Discovery (2012). http://blogs.msdn.com/b/msr_er/archive/2012/11/16/big-data-and-drug-discovery.aspx
35. http://researcher.watson.ibm.com/researcher/view_group.php?id=1718
36. IBM Watson Ushers in a New Era of Data-Driven Discoveries, New York Times, September 16 (2014).
37. Weston, A.D. and Hood, L. Systems Biology, Proteomics, and the Future of Health Care: Toward Predictive, Preventative, and Personalized Medicine . Journal of Proteome Research 3, 179-196 (2004).
38. Song, M. Opinion: Text Mining in the Clinic, The Scientist (2013) http://www.the-scientist.com/?articles.view/articleNo/34820/title/Opinion--Text-Mining-in-the-Clinic/
39. http://www.apple.com/ca/pr/library/2014/06/02Apple-Releases-iOS-8-SDK-With- Over-4-000-New-APIs.html
40. http://www.fiercebiotech.com/press-releases/global-computational-biology-market- application-cellular-biological-simulat
41. https://www.linkedin.com/pulse/computational-biology-market-expected-reach-usd-42851-pawar
42. http://www.statista.com/topics/1634/biotechnology-industry/
43. Canada's economic action plan. Government of Canada. 2014
44. Meeting Report from the Bioinformatics & Computational Biology Workshop. Genome Canada (2011). http://www.genomecanada.ca/medias/pdf/en/bioinformatics-meeting-report.pdf
45. Levine A.G. An Explosion Of Bioinformatics Careers. Science 344: 1303-1306 (2014).
46. https://www.novartis.com/our-work/innovation/modeling-simulation.
47. http://www.labtalk.astrazeneca.com/hot-topics/the-role-of-modelling-and-simulation-in-the-modern-world-of-drug-development/
48. http://www.fiercebiotechit.com/story/eli-lilly-ceo-sees-computational-tools-key-rd- boost/2011-11-22
49. http://www.pfizer.com
50. http://www.merck.com/licensing/areas-of-interest/research.html
51. http://selventa.com

52. http://www.gnshealthcare.com
53. http://www.entelos.com
54. https://www.genedata.com
55. Industry Canada. https://www.ic.gc.ca/eic/site/lsg-pdsv.nsf/eng/home
56. Canadian e-Business Initiative (CeBI). Net Impact Study Canada: The SME Experience. Industry Canada (2002).
57. https://www.rogue-research.com
58. http://materialsinnovation.tms.org/genome.aspx
59. Global Employment Trends 2013: Recovering from a second jobs dip. International Labour Organization.
60. http://www.linkedin.com/in/aliyehia
61. http://ca.linkedin.com/in/alanschoen
62. http://www.cnodes.ca/
63. Marquet, Pablo A., Allen, Andrew P., Brown, James H., Dunne, Jennifer A., Enquist, Brian J., Gillooly, James F., Gowaty, Patricia A., Green, Jessica L., Harte, John, Hubbell, Steve P., O'Dwyer, James, Okie, Jordan G., Ostling, Annette, Ritchie, Mark, Storch, David & West, Geoffrey B. On Theory in Ecology. Bioscience 64: 701-710 (2014).
64. Chitnis, Nakul & Smith, Thomas A. Mathematical illiteracy impedes progress in biology. Proceedings of the National Academy of Sciences 109: E3055 (2012).
65. http://www.cihr-irsc.gc.ca/e/48614.html

3. ACADEMIC DOSSIER

3.1 OBJECTIVES

3.1.1 General objective

The general objective of the Ph.D. Program in Quantitative Life Science is to educate students on quantitative approaches (technological, computational, and statistical) for the collection, analysis, and interpretation of complex data from life sciences. Our students will ask questions that will drive biology and medicine tomorrow, and will be equipped to answer them.

3.1.2 Specific objectives

1. To understand the challenges facing and the opportunities afforded by quantitative approaches in life sciences.
2. To communicate and collaborate across areas, from physics and technological development, to computer science, statistics, and life sciences.
3. To have an in-depth understanding of one area of life science (genetics, molecular biology, physiology, neuroscience, ecology, etc) and of the quantitative approaches that pertain to that field.
4. To enable breakthroughs in specific aspects of life science through the development of cutting-edge quantitative approaches.
5. To develop skills that contribute to solving life science problems of societal importance.

3.2 STRUCTURE AND ACADEMIC REGULATIONS

The proposed Ph.D. program is structured so as to educate scientists who will be able to have a significant impact on life sciences through the development and use of quantitative approaches. Students wishing to specialize in one of the main areas of quantitative life sciences can follow an area of research or stream (computational and statistical molecular biology, biophysics, or ecosystems) that allows students to specialize while maintaining contacts with students in other areas. Following a stream is not mandatory, although it is expected that most students will.

The academic structure of the program includes the following elements (described in more detail in section 3.3). At the center of the program is a **two semester core foundations course**, required for all students in the program, that will ensure that they receive the necessary breadth of knowledge to be able to communicate effectively across fields, to comprehend the methodological commonalities across fields, and to understand the challenges faced and fundamental techniques used in each of the streams.

Beyond this, students will be required to take a set of specialized quantitative and life science courses. Students enrolled in specific areas of research will be required to select their courses from predefined lists of quantitative and life science courses, thus ensuring that they receive the depth required. Students who do not enroll in any of the program's streams will select their courses in conjunction with their supervisory committee. In all cases, students will have the opportunity to learn about existing and upcoming technologies for data collection, the

computational and statistical approaches required for their analysis, and the biological interpretation of the results.

Breadth of knowledge and communication skills will be further enhanced through attendance at a regular seminar series. A comprehensive exam within the first year and a half will ensure quality control and a research thesis will demonstrate original scholarship.

Contact between students in different research areas and streams is critical in order to ensure the cross-fertilization of ideas between students working in very different areas. To build a community of students and researchers working in quantitative life sciences a number of student centric events will be organized, including monthly journal clubs (before research seminars) and an annual research retreat to ensure regular meetings of all cohorts.

Each student will be advised and mentored by an interdisciplinary supervisory committee. Co-supervision is encouraged, but not mandated. Progress tracking and program compliance will be performed by the Graduate Program Director.

3.2.1 Admission requirements and selection process

Applications will be welcomed from individuals who have prior education and/or training in many different fields. Applicants are expected to have demonstrated strong quantitative skills and a background in mathematics, statistics and computer science. In addition, all potential students must have a strong interest in interdisciplinary research in quantitative life sciences. It is expected that applicants have prior research experience and have taken advanced, in depth training courses at the undergraduate or Master's level.

3.2.1.1 General and specific requirements

1. Applicants are expected to hold an undergraduate degree in one of the following areas (or equivalent): Biology, chemistry, physiology, genetics, engineering, computer science, mathematics, statistics, physics, or chemistry.
2. Applicants must have a *strong quantitative background*. Such a background may be obtained by having at least the equivalent of a minor in computer science, mathematics, statistics, physics, chemistry or engineering.
3. Applicants who do not have a formal education in life sciences need to have a demonstrated interest for that field, for example in the form of an undergraduate research project or the completion of life-science courses.

Applicants need to satisfy the following *program-wide* prerequisites or their equivalents (focused on foundations in quantitative approaches). Students who wish to follow in one of the program's streams (Section 3.4) may need to satisfy additional admission prerequisites. Applicants who may be missing one prerequisite may still be admitted to the program but would be required to take an additional course during their first year in the program.

Program-wide prerequisites:

A. Computer science
- Entry-level algorithms (McGill course COMP 250 or equivalent)
- Entry-level programming (McGill course COMP 206 or equivalent)

B. Mathematics and Statistics
- Advanced Calculus (McGill course MATH 314 or equivalent)
- Entry-level Linear Algebra (McGill course MATH 223 or 236 or equivalent)
- Entry-level Probabilities (McGill course MATH 323 or equivalent) or Statistics (McGill course MATH 324 or equivalent)

C. Biology
- Entry Level Molecular or Cell Biology (McGill courses BIOL 200 or 201 or equivalent)

3.2.1.2 Selection criteria

Two letters of reference will be required, both of which should attest to the candidate's strong aptitude for research, quantitative skills and interest in quantitative life sciences. Applicants must submit a copy of their most recent curriculum vitae and a 1-2 page personal statement describing their background, research interests and reasons for wishing to undertake the proposed program. Top candidates may be invited to an interview with faculty members who are interested in potentially supervising each candidate.

Applications are selected on the basis of the following criteria: superior academic performance (CGPA of 3.4 or higher), level of relevant research experience, motivation for graduate study, demonstration of a high interest in interdisciplinary research, and awards received for scholarly excellence. Strong letters of support attesting the applicant's aptitude in conducting research are closely considered.

3.2.1.3 Selection process

Each applicant's dossier will be carefully reviewed by the Admissions Committee (see section 3.4.2.6 for a detailed description). Applicants who do not meet the program criteria are not considered further in the review process. The remaining applicants will be evaluated on the basis of letters of recommendations, academic performance and relevant work experience. The number of students accepted will depend on the number of open spots that are available with each supervisor in the program. Students will be admitted to the program through one of two mechanisms:

- Students without external or internal scholarships. The admission committee will forward to potential supervisors the files of applicants who satisfy the program's requirements in terms of background and excellence. If at least one supervisor (or group of supervisors) wants to admit and fund the student, he/she will be admitted. The student would then join the supervisor(s) lab(s) immediately upon starting in the program.

- Students with external or internal scholarships. Exceptional students, e.g. those with their own scholarships or to whom funding from the program will be offered, will be given the possibility of being admitted to the program without an assigned supervisor. We do not anticipate that these students will have significant difficulties finding a supervisor, because of the excellence of their dossier and the fact that they have access to independent sources of funding.

3.2.2 Length of program

3.2.2.1 Total number of credits

The Interdisciplinary Program in Quantitative Life Sciences is a Ph.D. program and is expected to last 4 to 5 years, similar to other Ph.D. programs at McGill. To graduate, students will generally need to take a minimum of 4 courses, for a total of 15 credits (including a two-semester required foundational course, as well as stream-specific complementary courses), attend regular research seminars, successfully pass a comprehensive exam, perform original, scholarly research and write a Thesis. Some students, upon the recommendation of the student's supervisory committee, may take up to two 600-level "directed reading" courses required to address gaps in a student's background.

3.2.2.2 Credit distribution by term

The credit distribution by term will be the same for all students who enter the program in the fall of each year. However, some students may take more courses than others due to the research topic and the supervision committee's discretion.

3.2.2.3 Study mode

Students must enroll on a full-time basis and complete the two term foundational course that is "cohort based". Students can take other courses at their own discretion and within a two-year time frame. The comprehensive exam must be passed within the first two years.

3.2.2.4 Student supervision and evaluation

Each student will be required to form a supervisory committee consisting of the supervisor(s) and at least two other professors. The supervisory committee will need to include researchers representing a broad spectrum of the proposed program with complementary expertise, from biology to quantitative approaches. The student will meet with his/her committee at least annually. The role of the supervisory committee is to help guide the student through his/her studies, identify issues and propose approaches to fix them, and ensure that the student's research program remains at the intersection of life and quantitative science.

Students are evaluated in each course, according to standard evaluation procedures for these courses; these include a combination of exams, term papers, essays, and problem-based questions, etc. For graduate studies, Grades A through B- are deemed satisfactory passes, and F is a failure. Students must obtain grades of B- or better in courses used to fulfill program requirements. Grades of C and D do not exist in graduate studies. The

Ph.D. Thesis will be evaluated according to the rules set by the Office of Graduate and Postdoctoral Studies at McGill University, i.e. external and internal review by experts as well as an oral defence.

Grades	Grade points	Numerical scale of marks
A	4	85 - 100%
A-	3.7	80 - 84%
B+	3.3	75 - 79%
B	3	70 - 74%
B-	2.7	65- 69%
F	0	0-64%

3.2.3 Academic regulations and environment

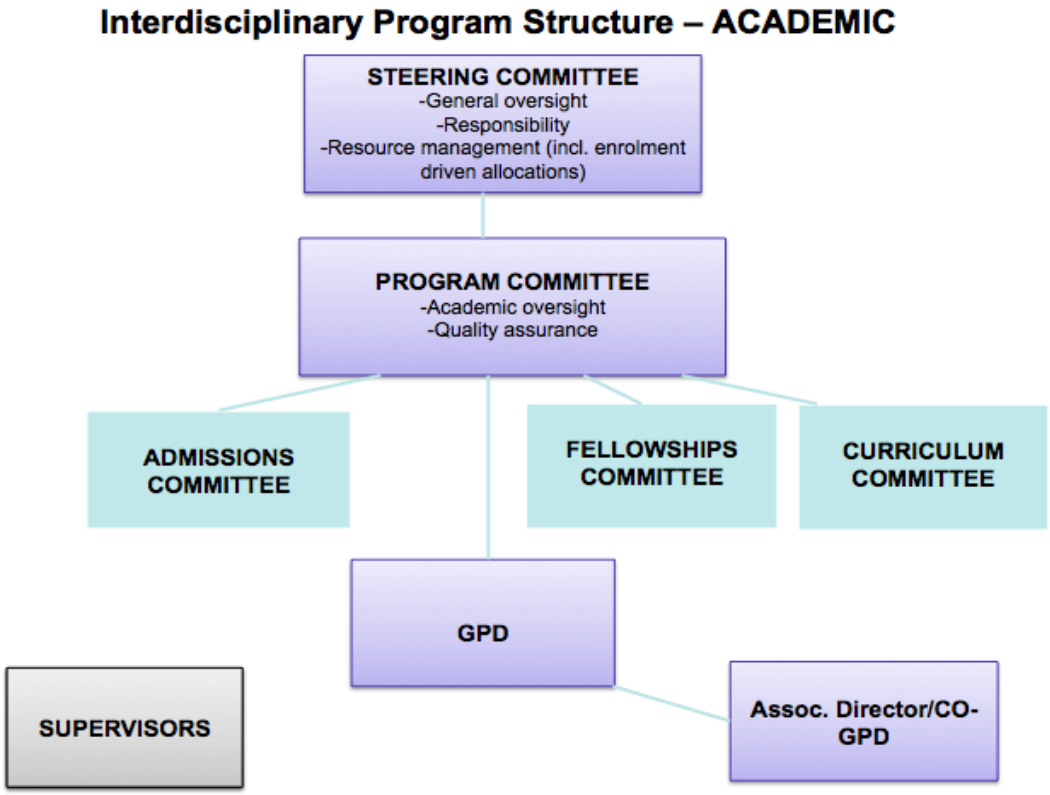
Academic regulations are determined by the Office of Graduate and Postdoctoral Studies and those regulations will be applied to this program. All other academic regulations comply with those of the University as a whole, which are available on the website.[1]

3.2.4 Program administration

The Quantitative Life Sciences Ph.D. Program will be an Interfaculty program comprised of the participating faculties (i.e. Science, Medicine) and will be directed by a Steering Committee and Program Executive Committee with representation from all faculties involved. Its structure follows that of all interdisciplinary programs at McGill.

[1] coursecalendar.mcgill.ca/gps201011/wwhelp/wwhimpl/js/html/wwhelp.htm

3.2.4.1 Academic Program Administration



Supervisory Membership

- Members of any Faculty (ie. Medicine, Science, Engineering and Agricultural & Environmental Science) interested in obtaining supervisory privilege within this program must submit their CV to the Program Executive Committee for approval.
- The potential supervisor's home unit must approve the participation of the faculty member's involvement as an associate member in writing. Written approval by the home unit must accompany the faculty member's CV when submitted for consideration of supervisory privilege. QLS program participation must be acknowledged by the home unit in faculty member workload, merit, promotion, etc.
- Continuation of supervisory privileges is contingent on adequate participation and involvement in the program.

Steering Committee

- *Mandate*. The Steering Committee provides the overall program governance and administration for the QLS Ph.D. program.
- *Composition*. The Steering Committee is composed of
    - the Dean of Graduate and Postdoctoral Studies (GPS)
    - Deans of participating faculties
    - QLS program representatives (2)
    - QLS Graduate Program Director (GPD)

- *Meetings*. The Steering Committee meets at least once per year. More frequent meetings may be necessary until the program is fully established.
- *Assignments (non-exclusive).* The Steering Committee appoints the GPD and Associate GPD, upon the recommendation of the Program Executive Committee.
    - The Steering Committee reaches decisions with regard to space allocation, program budget and staff recruitment for the QLS Ph.D. Program.
- *Representation*. When not in session, the Steering Committee is represented by the Chair (Dean of GPS)

Program Executive Committee

- *Mandate*. The Program Executive Committee provides academic oversight, quality assurance and establishes academic policy subject to approval of Steering Committee.
- *Composition*. The Program Executive Committee is composed of
    - The Graduate Program Director, who chairs the Committee and sets the agenda for meetings of the committee;
    - The Associate GPD (if appointed)
    - One member representing the Biophysics Stream
    - One member representing the Computational and Statistical Molecular Biology Stream One member representing the Ecosystems Stream
    - If adequate representation of participating faculties is not achieved with the GPD, Associate GPD and Stream representatives, additional members will be nominated by the respective faculty.
    - Two student representatives by special invitation
- *Meetings*. The Program Committee should meet at least once per term, or as required.
- *Decisional Process*. Whenever possible, the decisions are reached by consensus. If the general consensus cannot be reached, decisions are reached by the vote of all members except the GPD. The GPD only votes in the case of a tie.
- *Assignments (non-exclusive).*
    - The Program Executive Committee nominates the GPD and the Associate GPD to the Steering Committee.
    - The Program Executive Committee appoints the chairs of the Curriculum, the Admissions and the Fellowship sub-committees, and any other sub-committees needed.
    - The Program Executive Committee approves and reviews supervisory privileges.
    - The Program Executive Committee receives and approves reports and policy recommendations from GPD and all sub-committees.
    - The Program Executive Committee approves award recommendations by the Fellowships and Awards committee

Graduate Program Director (GPD)

- *Mandate*. The GPD manages the day-to-day operations of the QLS graduate program, with consultation from the Associate GPD, according to the policies set by the Program Executive Committee.
- *Role term and rotation*. The term of the GPD and associate GPD is normally 3 years. This is renewable at the discretion of the Steering Committee.
- *Assignments* (non-exclusive).
    - Overall responsibility for management of QLS graduate program

- Chairs the Program Executive Committee
- Responsible for detecting student/supervisor issues at an early stage and taking corrective action
- Implements academic policies as defined by the Program Executive Committee for academic management of QLS graduate program
- Establishes administrative procedures for operational management of QLS graduate program.
- Monitors supervisor performance and takes corrective actions if needed (can recommend removal of supervisor rights, as needed, to the Program Executive Committee)
- Approves student leaves
- Selects Chair's representative for all Ph.D. committees
- Monitors student progress and reviews minutes of Ph.D. meetings
- Approves choice of examiners for thesis review
- Approves makeup of Oral Examination Committees
- Organizes and chairs the Annual Faculty Meeting at the QLS retreat.

- *Delegation*
  - Any of the roles listed above can be delegated to the Associate GPD as needed by the GPD.

Admissions Committee

- *Mandate*. Devise policies and regulations regarding admissions, which are proposed to the Program Committee for approval. Review applications to determine if the student meets all entrance requirements.
- *Composition*. The Admissions Committee is composed of three members (at minimum) in addition to the Student Affairs officer (ex officio member without vote).
- *Membership*: The chair of the admissions committee selects members for the committee with approval from the respective departmental chair.
- *Meetings*. The Committees meet as necessary or as requested by the GPD.
- *Assignments* (non-exclusive).
  - Reviews applications to determine if the student meets all entrance requirements
  - Determines whether or not to accept a student who does not meet all requirements (e.g. missing prerequisites, GPA too low)
  - Determines prerequisites (if any) student must fulfill if accepted
  - Determines any other admission requirements
  - Approves all acceptances

Curriculum Committee

- *Mandate*. Devise policies and regulations regarding the QLS curriculum, which are proposed to the Program Executive Committee for approval
- *Composition*. The Curriculum Committee is composed of a three members (at minimum)
- *Meetings.* The Committees meet as necessary or as requested by the GPD.
- *Assignments (non-exclusive).*
  - Reviews course proposals and makes recommendations to the Program Executive Committee
  - Reviews and approves list of suggested non program courses
  - Advises GPD/Program Executive Committee w.r.t. course consultations

- Develops proposal for modifications to the curriculum of program

Fellowships and Awards Committee

- *Mandate*. Develops policy for distribution of GPS funds for graduate support and submits to Program Executive Committee for approval of policy. Evaluates student dossiers for internal and external awards.
- *Composition*. The Fellowships and Awards Committee is composed of five (at minimum) members in addition to the QLS Student Affairs officer (ex officio member without vote).
- *Meetings*. The Committees meet as necessary or as requested by the GPD.
- *Assignments (non-exclusive).*
  - Implements approved policies for allocation of GPS awards
  - Reviews candidate applications and recommends to the GPD and associate GPD for:
    - Student Recruitment Awards
    - Student Excellence Awards
    - Graduate Research Enhancement and Travel (GREAT) Awards
    - External fellowships
    - Awards for graduate student funding

3.2.4.2. Administrative Resources

Resources at McGill tend to be distributed through existing Faculty mechanisms and since multi-Faculty interdisciplinary graduate programs are outside of Faculty resource networks, independent interdisciplinary programs require different bases for gaining and distributing resources. The Quantitative Life Sciences Ph.D. Program requires:

- Budgetary unit identification so that graduate programs can control and report financial resources
- Human resources mechanism to provide permanent operational resources to support director stipend and staff salaries

Initially, operational resources to support the program will be provided in-kind by the units involved in the program. Once success of the Quantitative Life Sciences Ph.D. Program has been established (one full year of operation), permanent resources will be secured by the Steering Committee and managed by IFS.

3.3 REQUIRED ACADEMIC ACTIVITIES

3.3.1 Academic requirements

The program will include 5 basic elements:

1. [Breadth] One two-semester required foundational course (shared across streams).
2. [Breadth] A research seminar with invited speakers (shared across streams).
3. [Depth] Complementary courses, including both life science courses and quantitative courses, to be selected based on the student's area of research or conjunction with the student's supervisory

committee, to fill gaps in a student's background and allow depth in a desired area.

4. [Breadth + Depth] A comprehensive exam.
5. [Depth] A research thesis.

Students enrolled in one of the program's streams may need to satisfy additional requirements (see Section 3.4).

3.3.2 Advisory Committee

Within one month of entry to the Ph.D. Program, each student, in conjunction with their supervisor, will select an advisory committee comprised of the supervisor and at least one faculty member from each of the relevant Quantitative and Life Science departments with expertise and knowledge in the intended area of research. Within 3 months of entry, students will be expected to have an initial meeting with their advisory committee to determine the rationale and overall objectives of the planned research project. The advisory committee will also review the student's academic background and training and recommend course work to complement and/or strengthen the student's knowledge base. Advisory committee meetings will take place on an annual basis to evaluate the student's progress towards completion of the thesis.

3.3.3 Courses

Students will be required to take a minimum of 4 courses, for a total of 15 credits (but see below for course reductions):

- 1 two-semester foundational course, shared across streams [6 credits]
- 1 to 2 "quantitative" courses [3 - 6 credits]
- 1 to 2 "life science" courses [3 - 6 credits]

In addition, and upon the recommendation of the student's supervisory committee, up to two 600-level "directed reading" courses may be required to address gaps in a student's background. Such courses may take the form of a combination of the course material from an undergraduate course and additional reading or project.

Course load reduction: Students entering the program with a Masters or having taken extra graduate courses during their undergraduate degree will have the opportunity to apply for a course reduction, if they have taken courses that are analogous to those listed below. Up to three stream-specific courses may be waived, leaving at a minimum the foundational 2-semester course.

3.3.3.1 Required Course -" Foundations of Quantitative Life Sciences"

All students will take the "Foundations of Quantitative Life Sciences" course (6 credits), offered over two consecutive semesters. The main topics to be addressed in these two courses are:

- Foundations of life science, with a focus on how quantitative approaches can best contribute to scientific advancement.
- Advanced technologies and tools used to measure living systems and their limitations.

- Linking experimental techniques to analysis methods, including how to analyze large life science data sets.
- Quantitative models and computer simulations of life science systems.
- Identifying similar mathematical, computational and statistical techniques that can be applied across life science levels.
- Effective communication and collaboration between traditional and quantitative life scientist.

The course will be divided into 3 week modules that will each focus on specific applications of and methods for quantitative life science. During the first few weeks of the term, depending on demand and need, a series of intensive workshops and/or bootcamps will be offered to train students in specific software programs, and to build community. A detailed course outline and description of the Foundations of Quantitative Life Sciences course is included in the Appendix.

3.3.3.2 Comprehensive Exam

Students will be required to pass a Comprehensive Exam early in their graduate careers. Before the end of the second year (18-24 months since entering the program), students must be prepared to complete the Comprehensive Exam. The Comprehensive Exam is evaluated by the student's advisory committee, in addition to two members external to the committee. One external committee member must be from a Quantitative discipline, while the other from a Life Sciences discipline. The Comprehensive Exam consists of the following three components:

Written Thesis Proposal: The student must present a written Thesis Proposal and circulate it to the members of the advisory committee. The proposal should be between ten and twenty pages long, and address the following topics:

- Central hypothesis, main research question, specific objectives
- Review of relevant literature, rationale
- New findings and knowledge to be gained, how this research will advance science and/or health
- Work plan, timelines, analysis of results, potential limiting factors, contingency plans and alternatives
- Preliminary data and initial findings supporting the proposed project

Thesis Proposal Presentation: The student will deliver a 30 minute oral presentation of their Thesis Proposal to the advisory committee

Oral Examination: The oral examination portion of the Comprehensive Exam will include both a breadth component (knowledge of applications of and methods in QLS, i.e. material covered in the two foundational courses), and field-specific depth component. For students enrolled in a stream, the Comprehensive Exam will evaluate the understanding of the biological phenomena under study as well as the fundamental quantitative approaches in their stream. For students who are not enrolled in a stream, the Comprehensive Exam will

similarly test depth of understanding of the specific biological concepts and quantitative approaches related to the student's research topic. In addition, students will be expected to answer questions relating directly to the material presented in the Thesis Proposal.

3.3.3.3 Complementary courses

The choice of the complementary courses will be made by the student and his/her supervisory committee, but should include at least one course on "quantitative methods" and one course on "Life sciences". Students enrolled in an existing stream will need to select courses from stream-specific lists of complementary courses. Those not enrolled in a stream will need to get their course selection approved by their supervisory committee and by the program director. We note that it is not expected that every incoming student will have sufficient background to take every complementary course listed. It will be the student's and supervisory committee's responsibility to ensure that he/she has the prerequisites for the selected courses.

3.3.4 Community building activities

Contact between students in different research areas and streams is critical in order to ensure cross-fertilization of ideas between students working in very different areas. Therefore, we propose several complementary elements in order to build a community of students and faculty and to facilitate interactions.

3.3.4.1 Monthly half-day research seminar

- Once a month during the academic year, one high-profile researcher will be invited to give a seminar. Topic areas for the invited speakers will rotate across the streams, so there will be approximately 2 speakers from each stream within each academic year. Students will nominate potential speakers to be invited in the following academic year.
- Prior to the seminar, there will be a student-led journal club, where one or two papers, relevant to the seminar, will be read and discussed. The students will choose the papers to be discussed.
- Following the seminar, the speaker will be invited to join an informal discussion with the students over lunch.
- Student attendance at the monthly research half-day will be mandatory for the first 3 years of the Ph.D. program. Students with course conflicts may apply for a temporary exemption. Faculty members will also be encouraged to attend.

3.3.4.2 Annual retreat

A full-day retreat for all students and supervisors in the program will occur once a year. QLS students will be required to present their research to the academic community through short talks and presentations. An annual meeting of all faculty members with supervisory privilege in the QLS program will also occur at the retreat as a forum for discussions regarding the status and progress of the QLS graduate program. This event will strengthen and maintain interdisciplinary discussions and encourage new collaborations.

3.3.4.3 Dissemination of relevant events and seminars

The Program coordinator will collate seminars or workshops of potential interest across the campus (and city-wide), and send an announcement each week to students and associated faculty. This information will also be posted on the Program web site.

3.3.4.4 Round tables

From time to time, an opportunity to meet with potential employers will be facilitated through a Round Table. Representatives from companies or agencies with applications and interest in quantitative life sciences will be invited to speak and to be available for questions from students.

3.3.5 Thesis

The thesis expectations follow the guidelines established by Graduate and Postdoctoral Studies at McGill University. In general, the thesis must demonstrate a mastery of appropriate research as well as contributing original scholarship relating to the area of specialization. An oral examination of the content and implications of the thesis will be held in a public forum to determine the quality of the written thesis document and the student's oral defence of the thesis.

The following table provides an overview of the typical 5 year timeline for a student enrolled in the QLS PhD Program

	Year 1 Fall	**Year 1 Winter**	**Year 2 Fall**	**Year 2 Winter**	**Year 3 Fall**	**Year 3 Winter**	**Year 4 Fall**	**Year 4 Winter**	**Year 5 Fall**	**Year 5 Winter**
Courses	Foundations of QLS Complement Course 1	Foundations of QLS Complement Course 2	Complement Course 3	Complement Course 4						
Community Building Activities		QLS Retreat		QLS Retreat		QLS Retreat		QLS Retreat		QLS Retreat
Program Benchmark	Initial Advisory Committee Meeting		Thesis Proposal and Comp Exam		Advisory Committee Meeting		Advisory Committee Meeting		Submit Thesis	Defend Thesis

3.4 SPECIALIZED AREAS OF RESEARCH/STREAMS

Students will have the opportunity to follow one of several well-defined streams, although participation in a stream of research is not mandatory. A stream represents a course of study that is focused on a well-defined research discipline, and furthermore is of sufficient interest to attract multiple interested students. Each stream provides a structured complement to the basic program requirements, training around cohesive themes.

Initially, three streams are proposed and program requirements for these streams are described in detail below (Computational and Statistical Molecular Biology, Biophysics, Ecosystems). As knowledge and fields of research evolve, new streams may be created to suit demand. Such flexibility is essential to staying at the forefront of evolving methods and fields of application in quantitative life sciences. However, it is important to note that for students whose research interests do not align with one of these three streams, or where the research topic crosscuts multiple streams in a significant manner, a personalized program can be designed, guided by the basic program requirements, and the student's supervisory committee.

The proposed streams are divided according to the scale of biological phenomena and systems being studied:

- **Computational and Statistical Molecular Biology**: Computational, statistical and mathematical approaches for the study of genetic and molecular biology questions.
- **Biophysics**: Applications of physics to the design of cutting edge tools to study biological questions, and to model biomolecules, molecular machines, cellular processes, and complete cells.
- **Ecosystems**: Mathematical and computational approaches in ecology, evolution, and infectious disease.

We note that the streams are conceptually interconnected, which is why it makes sense to include them under the same program. For example, cancer is an area that is fruitfully studied at all scales (search for driver mutations that alter the function of the cell division machinery, identification of key pathways, regulators and targets, competitive interactions between tumor and normal cells within organ systems, and the evolution of tumor cells- e.g. from benign to metastatic). The boundaries between the three streams are meant to be malleable and a student whose project would lie at the boundary of two or three of these streams would be allowed to select courses for each of them, under the guidance of his/her progress committee.

3.4.1 Computational and Statistical Molecular Biology Stream

Computational and Statistical Molecular Biology includes the fields of computer science, statistics and mathematics applied to the analysis of data from molecular biology and genetics. As biological assays become increasingly high-throughput (while often remaining quite noisy), sophisticated algorithms and efficient computational analyses are now intrinsic part of biology. Key challenges include: (i) How to store and retrieve huge data sets (e.g. those produced by a massively parallel sequencing machine)? (ii) how to process, normalize, and analyze such data sets? (iii) How to translate biological questions into algorithmic questions, and how to solve them efficiently while keeping in mind the potential sources of bias and error? (iv) how to develop high-dimensional predictive models and machine learning approaches to gain insights leading to formulate testable biological hypotheses?

Students in the Computational and Statistical Molecular Biology stream will receive training in databases, computational biology algorithms, biostatistics, and machine learning. They will also be required to train in the life science field of their choice (genomics, structural biology, evolution, proteomics, cancer, etc.) and become expert in both the specific computational and statistical aspects of their area of application, but also in their biological aspects. With time, we expect graduates from the Computational and Statistical Molecular Biology

stream to be able to (i) formulate new, cutting-edge biological questions, (ii) understand the experimental approaches needed to acquire the relevant data, (iii) understand existing approaches for their analysis, and be equipped to develop new approaches when necessary, (iv) be able to interpret the results of their analyses in a biological context. Co-supervision between bioinformatics researchers and life scientists will be encouraged.

3.4.1.1 Computational and Statistical Molecular Biology Stream admission requirement

- One of the following: Entry-level computational biology (COMP 462), Regression and ANOVA (MATH 423), or Biophysics (BIOL/PHYS 319).

3.4.1.2 Computational and Statistical Molecular Biology Stream program requirements

Students will be required to take one or two courses from each of the Quantitative and Life Science blocks below, for a total of three courses.

Complementary Courses

Quantitative Block	Life Sciences Block
BMDE 502 BME Modelling & Identification **BIOS 601** Epidemiology: Introduction and statistical models. **MATH 523** Generalized Linear Models **HGEN 677** Advanced statistical methods in genetics and genomics. **COMP 561** Computational Biology Methods and Research **COMP 598:** Topics in Computer Science: Advanced Computational Biology Methods **MATH 680** Computation Intensive Statistics	**BIOC 603** Genomics and Gene Expression. **HGEN 661** Population Genetics **HGEN 692** Human Genetics. **EXMD 602** Techniques in Molecular Genetics. **BIOL 551** Principles of Cellular Control

3.4.2 Biophysics Stream

The increasingly quantitative nature of biology requires a physical understanding of the organization of cellular structures, from macromolecules to organelles, from biopolymers to cytoskeleton. Specific tools have been designed to probe properties of this living matter, including sophisticated imaging techniques and algorithms, micro and nanofluidics, force microscopy, along with biophysical models at the nexus of soft condensed matter and out of equilibrium physics.

Students in the biophysical stream will receive a broad training in physical approaches applied to biology, both on the experimental and theory side. Life science training will focus on necessary techniques from molecular

biology and concepts from systems biology for physical applications. They will also conduct research within biophysical groups or cross-departmental teams between physics and life-science departments.

3.4.2.1 Biophysics stream admission requirement

- One of the following: Thermal and Statistical Physics (PHYS 333), Statistical Mechanics (PHYS 362), or Introduction to Biophysics (BIOL/319) or equivalent.

3.4.2.2 Biophysics stream program requirements

Students will be required to take one or two courses from each of the Quantitative and Life Science blocks below, for a total of three courses.

Complementary Courses

Quantitative Block	Life Sciences Block
BIEN 530 Imaging and Bioanalytical Instrumentation **BMDE 519** Biomedical Signals & Systems **BMDE 512** Finite-Element Modelling: BME **CHEM 514** Biophysical Chemistry. **CHEM 520** Methods in Chemical Biology **COMP 551** Applied Machine Learning **PHYS 519** Advanced Biophysics **PHYS 559** Advanced Statistical Mechanics	**BIOC 604** Macromolecular Structure. **PHGY 520** Ion Channels **PHGY 518** Artificial Cells **BIOL 551** Principles of Cellular Control

3.4.3 Ecosystems Stream

Ecosystems can be contained in a vial or they can extend over the biosphere, but they represent the highest level of biological organization. They constitute a great scientific challenge and define many of our goals for a sustainable planet. Ecological, evolutionary, and epidemiological systems have provided many historical case studies in quantitative fields such as mathematics and computer sciences. However, the large complexity of natural ecosystems has repeatedly limited their quantitative study in favor of more observational methods. Students participating in the Ecosystem stream will receive an in-depth training in classic quantitative methods such as statistics and dynamical systems that have been historically adopted by mathematicians to study ecosystems. They will also be trained in statistical physics and advanced molecular methods that have been more recently applied to the study of whole-ecosystems. They will conduct their research under the guidance of scientists working across these areas and will apply cutting edge physical and mathematical methods to the understanding and forecasting of ecosystem response to natural and human impacts.

3.4.3.1 Ecosystems stream admission requirements

- One of the following: Ecological Dynamics (BIOL 308), Evolution (BIOL 304), Conservation Biology (BIOL 465), or equivalent.

3.4.3.2 Ecosystems stream program requirements

Students will be required to take one or two courses from each of the Quantitative and Life Science blocks below, for a total of three courses.

Complementary Courses

Quantitative Block	Life Sciences Block
ENVB 506 Quantitative Methods in Ecology **MATH 556** Mathematical Statistics 1 **MATH 525** Sampling Theory and Applications **MATH 533** Honours Regression and Analysis of Variance **MATH 537** Mathematical Models in Biology **MATH 547** Stochastic Processes **MATH 523** Generalized Linear Models	**BIOL 509** Methods in Molecular Ecology **BIOL 510** Community Ecology **BIOL 594** Advanced Evolutionary Ecology **ENVR/BIOL 540** Ecology of Species Invasion

3.5 EXAMPLES OF TYPICAL COURSEWORK

Here, we give four examples of the coursework that may be assigned to students entering the program with different types of backgrounds, as a function of their stream and their specific research program, and as determined by the student and his/her supervisory committee.

Example 1. Computational and Statistical Molecular Biology stream.

A student is admitted with a major in statistics and a minor in biology. He wants to develop new statistical approaches for the analysis of population genomics data. He lacks background in computer science.

Semester 1	Semester 2	Semester 3
Foundation course - part 1 Reading course (based on COMP 250 - Intro.to comp. sci.) HGEN 692: Human Genetics	Foundation course - part 2 MATH 680 Computation Intensive Statistics HGEN 661 Population Genetics	COMP 561: Computational Biology Methods and Research.

Example 2. Biophysics stream.

A student is admitted with a major in physics and a Masters in Biology. He wants to model the stochastic aspects of microtubule assembly during cell divisions, under the supervision of a biologist expert in imaging and a physicist.

Semester 1	Semester 2	Semester 3
Foundation course - part 1 BIOL 551: Principles of Cellular Control PHYS 519: Advanced Biophysics	Foundation course - part 2 BIEN 530 Imaging and Bioanalytical Instrumentation	

Example 3. Ecosystems stream.

A student is admitted with a major in biology and a minor in mathematics. She wants to model the impact of climate change on the arrival of invasive species in the St-Lawrence River.

Semester 1	Semester 2	Semester 3
Foundation course - part 1 Reading course (based on COMP 350: Numerical computing) BIOL 594: Advanced Evolutionary Ecology	Foundation course - part 2 BIOL 509: Methods in Molecular Ecology. ENVR/BIOL 540 Ecology of Species Invasion	MATH 525 Sampling Theory and Applications

Example 4. Cross-cut of computational molecular biology and ecosystems (no Stream)

A student admitted with an undergraduate degree in physics wants to work on developing a microfluidics device to analyze the human gut microbiome. She lacks background in microbiology.

Semester 1	Semester 2	Semester 3
Foundation course - part 1 Reading course (based on MIMM 211 - Intro. microbiology) BMDE 519 Biomedical Signals and Systems	Foundation course - part 2 PHYS 519: Advanced Biophysics. BIOL 540: Ecology of Species Invasions.	PARA 655: Host-Parasite Interactions.

4. RESOURCES

4.1 STAFF RESOURCES REQUIRED, AVAILABLE AND PROJECTED

4.1.1 Teaching staff

4.1.1.1 Academic Staff in Place

The proposed program has adequate faculty for teaching and supervision at McGill University.

The following McGill University faculty members will be teaching the required two semester capstone course. This selection of professors from across a variety of departments highlights the true interdisciplinary and collaborative nature of the proposed program.

Table 10: List of Academic Staff in Place

Departmental Affiliation	Faculty Member
Biology	Frederic Guichard, Ph.D.
Computer Science	Mathieu Blanchette, Ph.D.
Epidemiology & Biostatistics/Oncology	Celia Greenwood, Ph.D.
Human Genetics	Guillaume Bourque, Ph.D. Ken Dewar, Ph.D. Simon Gravel, Ph.D. Tomi Pastinen, Ph.D.
Neurology & Neurosurgery	Christopher Pack, Ph.D.
Physiology	Erik Cook, Ph.D. Anmar Khadra, Ph.D. Judith Mandl, Ph.D.
Physics	Paul François, Ph.D. Sabrina Leslie, Ph.D. Paul Wiseman, Ph.D.

4.1.1.2 New Staff Required

No new teaching staff are required or requested for the proposed program.

4.1.2 Administrative and support staff

4.1.2.1 Staff in place

McGill University will eventually appoint the required full-time Program Director, Associate Program Director and Graduate Program Coordinator. Their responsibilities are outlined in sections 3.2.4.4. - 3.2.4.7.

4.2 PHYSICAL AND OTHER RESOURCES

4.2.1 Library resources

4.2.1.1 Quality of collections and quantity

The McGill Library consists of 12 branches covering all subjects taught at McGill, and includes 5.6 million print and electronic items in a variety of different formats. Of particular interest to students in the Quantitative Life Sciences Program are the Schulich Library of Science & Engineering and the Macdonald Campus Library, both part of the McGill Library system. The Schulich Library of Science and Engineering supports the teaching and research activities of all departments in the Faculties of Engineering, Science, Medicine, and Dentistry. The Macdonald Campus Library supports the teaching and research activities of the Faculty of Agricultural and Environmental Sciences, the School of Dietetics and Human Nutrition, the McGill School of Environment, the Institute of Parasitology, the Morgan Arboretum, and the Macdonald Farm. The collections of these libraries include books, journals, government publications, standards, and technical reports in engineering and the sciences.

McGill students, faculty, and staff can borrow from any of the Library's branches with their university ID card and have 24/7 access to the Library's electronic information resources. The latter includes use of approximately 2.2 million electronic books, circa 126 000 electronic journals, and EndNote and RefWorks citation software. The McGill community has access to many of the large, aggregated e-journal packages, including: the American Chemical Society, the American Medical Association, BMJ, Elsevier Science, the Institute of Physics, Nature Publishing Group, Springer, Taylor & Francis, Wiley-Blackwell, and Wolters Kluwer. In addition, the library subscribes to research databases that enable searching for references to the published literature such as: BIOSIS Previews, CAB Abstracts, Cochrane Library, Compendex, Embase, Inspec, Medline (via Ovid), SciFinder, Scopus, Web of Science, ProQuest Dissertations & Theses, and Derwent Innovations Index (for patent literature).

4.2.1.2 Accessibility; assistance and reference services provided; access to resources available at other institutions.

The Macdonald Campus Library and the Schulich Library of Science & Engineering are open for service 6 days per week (52 hours and 57 hours a week respectively) in the Fall and Winter semesters, and 5 days per week (40

hours a week) in the summer. During service hours, there are professional librarians available to help library users whether in person, by phone, email or online chat. Both libraries also have extended study hours throughout the Fall and Winter semesters. Faculty members and graduate students can request permanent, 24/7 after-hours access to the Schulich Library, which is valid for the duration of their employment or studies at McGill. The auto-loan machines in the library enable individuals to borrow items themselves outside of service hours. Off-campus or remote access to all of the Library's electronic resources is available to students, faculty, and staff via McGill's EZproxy service or Virtual Private Network (VPN) connection. The McGill Library also participates in Eduroam ("education roaming"), which allows students and staff to use their McGill credentials to obtain Internet connectivity at other participating universities for the purpose of accessing McGill Library's electronic resources on their own laptops.

The Macdonald Campus Library and the Schulich Library have seating for approximately 230 and 635 people respectively, including group and quiet study areas that together house 155 computers, 14 photocopiers, and 9 scanners available for use. Some of this equipment is located in the libraries' three electronic classrooms which are each equipped with 19-25 desktop computers, a built-in projector, podium and screen. These classrooms are used by librarians for teaching, and by students on a daily basis for work and access the library's electronic resources. Wireless network access is available throughout the library. Many desk carrels and tables in the library contain power outlets for personal laptops. Individuals can access any of the McGill Library's 12 branches for similar physical resources.

Fourteen librarians (11 at the Schulich Library and 3 at the Macdonald Campus Library) support the learning, research, and teaching needs of the departments they serve in numerous ways including assisting students, faculty, and staff with finding specific information, developing optimal database search strategies, identifying highly influential journals in their fields, and managing their citations; providing library orientation and hands-on information literacy instruction to students (both inside and outside the classroom); purchasing books and other materials; creating and maintaining online subject guides that pull together resources in a specific area; and communicating updates on library services and resources.

McGill students and researchers working at any of the university's affiliated teaching hospitals also have access to libraries on site that are equipped with computers, study spaces, and staffed with their own librarians and library assistants. All electronic resources provided by the McGill Library system are accessible to McGill students, faculty and research staff of the affiliated hospitals and research institutes. These include:

Douglas Mental Health University Institute

McGill University Health Centre:

- Montreal Chest Institute
- Montreal Children's Hospital
- Montreal General Hospital
- Montreal Neurological Institute & Hospital
- Royal Victoria Hospital

Lachine Hospital & Camille-Lefebvre Pavilion

Sir Mortimer B. Davis Jewish General Hospital,

St. Mary's Hospital Center

McGill University's Graduate and Postdoctoral Studies unit in partnership with Teaching and Learning Services and McGill University librarians also offer a 4-part "MyResearch" workshop series (totaling 8 hours) for graduate students to advance their library research skills. Graduate students discover how to use the citation software EndNote; understand and locate different types of information produced at each stage of the research cycle; learn advanced search strategies and techniques to make the best use of specialized resources for their disciplines; and gain a better understanding of citation analysis tools and metrics. Students who complete all 4 of these modules receive a certificate signed by both the Trenholme Dean of Libraries and the Dean of Graduate and Postdoctoral Studies. The MyResearch workshop series is also added to the students' co-curricular records upon completion.

Graduate students, faculty, and staff can directly borrow materials in person from other Canadian libraries with a BCI (*Bureau de Coopération Interuniversitaire*) card, which can be obtained from the service desk of any McGill Library branch. Furthermore, a worldwide interlibrary loan/document delivery service is available to obtain materials that are not in the McGill Library's print or electronic collections. The McGill community is also encouraged to submit comments, suggestions, and request book purchases. McGill librarians continually monitor use of the library system's services, facilities, and resources, as well as acquire new and/or more relevant resources to allow efficient and timely access to information. In 2016, as in previous years, the Library has also sent out the LibQual+ survey to students, faculty, and staff to collect feedback about its services, facilities, and resources. The McGill Library system implements changes in response to emerging trends and concerns as identified in the survey

4.2.2 Computer facilities

4.2.2.1 Quality and quantity

McGill Library offers over 500 computer work stations throughout the Library system for use by McGill student and faculty members. These workstations are in addition to the hundreds of computers available to students in individual hospital, laboratory and office settings. Wireless network connectivity is accessible to students, faculty and staff through the McGill Wireless Zone on campus, and remote wireless access to the network and its resources can be easily configured with a username and password. Users of the McGill wireless network can attain speeds of up to 54 Mbps using the 802.11g or 802.11a standards

4.2.2.2 Accessibility; technical support; training and maintenance), networks.

Participants in the QLS Program will have access to significant state-of-the-art advanced research computing (ARC) systems, storage and software solutions through Compute Canada (https://www.computecanada.ca) in partnership with its regional partner organization, Calcul Quebec (http://www.calculquebec.ca/en/). Compute

Canada helps researchers who need ARC in all disciplines and at all scales; from individual researchers to some of the largest international research collaborations in the world. Compute Canada serves several disciplines as diverse as computational criminology, chemistry, aerospace engineering, medicine, and analysis of great works of fiction. Powered by a nationally coordinated network of hardware and software resources, Compute Canada provides a broad spectrum of advanced computing services in support of research, including technical support, training, application and development. Compute Canada supports an extensive range of research computing needs on a case-by-case basis, including (but not limited to):

- large scale computation
- large memory machines
- accelerated systems (GPUs)
- scientific gateways, portals, etc.
- cloud services
- high-throughput storage and compute systems
- archival storage

Calcul Quebec provides world class High Performance Computing (HPC) infrastructures to its member institutions and industry, and provides support and training to researchers in areas of code development, code optimization, numerical methods and others so as to help researchers efficiently exploit modern computational and data analytics resources. The computational platforms accessible within Calcul Quebec include large scale multi-processor systems. The Calcul Quebec centre at McGill University (McGill HPC) offers various courses on high performance computing, computer programming, Big Data Analytics techniques and high performance computing methods. Topics include: MPI, OpenMP, Linux, Python, C++, R, CUDA, Matlab, Hadoop and MapReduce and others. The McGill HPC Centre also develops customized courses around these and other topics of advanced computing in partnership with McGill and other university units. The McGill HPC Centre is able to offer class participants access to all elements of the HPC platform for the duration of the course period, providing students with the resources for direct, hands-on learning via exercises and related course projects.

Many Principal Investigators at McGill have accounts for their research groups at Compute Canada and Calcul Quebec. Access to these resources is through desktops located in the supervisor's labs or through student laptops.

4.2.3 Laboratories

Supervisors in the QLS Ph.D. Program will be expected to provide their students access to all necessary research equipment, tools and laboratory space to effectively collect their data and perform their research. McGill University assigns and supports laboratory spaces for all faculty members whose research requires such specialized infrastructure. The QLS Ph.D. Program encourages active collaboration across different disciplines and hence, students can potentially have access to multiple laboratories and research tools in their graduate career.

4.2.4 Space

4.2.4.1 Teaching space

The required core course for students in the QLS Ph.D. Program will be taught in a classroom associated with either the Faculty of Medicine, Science or Engineering. Classrooms in these faculties are well designed to accommodate the needs of course instructors and students, and equipped with all the equipment necessary (furniture, overhead projectors, chalkboards and audio visual connections). There will be no need to renovate or design new classroom space. The teaching spaces of complementary courses are similarly well organized and capable of accommodating the lecture material and resources necessary to effectively deliver course content within the departments of Biology, Biochemistry, Epidemiology, Mathematics, Computer Science, Biomedical Engineering, Human Genetics, Experimental Medicine, Physics, Chemistry, Physiology and Environmental Biology.

4.2.4.2 Office and Study Space

Many laboratories at McGill University incorporate desk and study space within the laboratory environment, providing students convenient work space in close proximity to their research. If desk space is not available in the supervisor's laboratory, it will be made available in a nearby office or study room alongside other graduate students. Students also have access to the various libraries on both McGill's Downtown and Macdonald campuses. Six of the 12 library branches feature private, quiet, and secure working spaces dedicated to graduate students. These include a Ph.D. study room with 36 desks equipped with two lockable drawers and two book shelves each, study carrels that can be reserved for an entire semester, locked cubicles, graduate study rooms for thesis and comprehensive exam preparation, and semi-private desks with locking cabinets. As discussed above, QLS Ph.D. students can request permanent, 24/7 after-hours access to the Schulich Library, which is valid for the duration of their studies at McGill.

Laboratories and libraries located on campus or within hospitals and research institutes are part of a collective of academic units that feature seminars and departmental activities on a regular, ongoing basis. Students whose laboratories and offices are physically located at these sites will have access to these offerings, especially those highlighting related and relevant topics. Moreover, in an effort to build a sense of community amongst participants of the QLS Ph.D. Program, the mandatory monthly half day seminar series will be held at various locations throughout the university campus and the city of Montreal to ensure all students are familiar with the laboratories and physical spaces associated with the QLS program.

4.2.5 Financial Support for Ph.D. Students

Students in the QLS Ph.D. Program will be supported financially in several ways. All students registered in the program will draw a guaranteed minimum annual stipend from their supervisor's research grants that will cover the cost of tuition and living expenses in Montreal. In any given semester, students will also have the option of being hired as a teaching assistant for complementary courses related to their field of study. In this case, students will gain valuable teaching experience as well as financial support. These arrangements will be in observance of McGill University's regulations concerning maximum hours that can be worked weekly by the

student.

It is also anticipated that students in the QLS Ph.D. Program will be competitive applicants for fellowships and awards. McGill University has almost $1 million in internal funding endowments for graduate students engaged in medical and scientific research. In many cases students are automatically considered for, and offered, internal funding throughout their graduate careers. These awards include multidisciplinary research fellowships such as the Tomlinson Doctoral Fellowships (valued at $35,000 a year and held for up to three years), the Max Stern Recruitment Fellowships (valued at $14,000) and the Schulich Graduate Fellowships (minimum stipend of $25,000).

Students applying for external federal and provincial funding are well supported during the application process. McGill University's Graduate and Postdoctoral Studies unit offers a number of information sessions that are in-person presentations followed by a live question and answer period. Each session focuses on the application process for a particular federal or provincial agency award, and covers everything from eligibility and deadlines to supporting documents and best practices. A staff of four graduate funding specialists at McGill University handle all questions and concerns regarding graduate funding opportunities throughout the year and regularly assist individual students for all matters pertaining to graduate funding fellowships and awards.

The McGill Writing Centre offers two fellowship writing workshops for students to develop their writing skills and write with the fellowship selection committee in mind. McGill University's Teaching and Learning Services, through the SKILLSETS Program, offers a further layer of application review with the "Would You Fund It? Fellowship Consultation Session" open to graduate students applying for external funding opportunities. Students in the workshop have their two page project summary reviewed by a former Tri-Council or Quebec committee reviewer who provides feedback on the structure, relevance and language accuracy with suggestions on how to improve the draft.

4.3 REQUIRED FUNDING

The tables provided in Appendix provide an estimated cost of the program expenses projected over the first five years (2017-2021) as well as a cost analysis of the predicted revenue to the university. The expenses for the first year include administrative salaries, office supplies, promotional materials (e.g., website, pamphlets), webinars, software licensing, travel costs related to guest speakers for graduate seminars and promotional materials.

APPENDICES

A: Foundational Course Syllabus
B: List of Complementary Courses
C: List of Interested Faculty (in progress)
D: Letters of Support (in progress)
E: List of Grants Awarded to Teaching Faculty Members
F: List of Publications of Teaching Faculty Members

APPENDIX A: FOUNDATIONAL COURSE SYLLABUS

FOUNDATIONS OF QUANTITATIVE LIFE SCIENCE

Duration: 2 semesters

Course Schedule: Two 90-minute sessions per week

Course Credits: 6 (three per semester)

RATIONAL

This graduate course will train the next generation of multidisciplinary researchers needed to bridge the life and quantitative sciences. Quantitative life science is the broad application of mathematical, computational and other quantitative methods to study life science and biological systems. This course fits centrally into the rapidly expanding interdisciplinary field where mathematical and computer algorithms are becoming just as important as traditional approaches in biology and medicine. Worldwide, governments, universities and industries have begun to invest in quantitative life science, and these skills are already in high demand.

COURSE SUMMARY AND ORGANIZATION

Objectives

1. Give students an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches combined with cutting-edge measurement technologies.
2. Introduce students to the modern technologies for biological data acquisition.
3. Identify the key challenges related to the analysis of these data and provide a sample of the key set of mathematical, computational, and statistical approaches involved in their solution.
4. Teach students a common language to communicate across biological, physical, mathematical, and computational sciences.
5. Build a community of student scientists with an appreciation for the breadth of quantitative approaches in the life sciences.

Prerequisites (or equivalent)

BIOL 200 Molecular Biology or BIOL 201 Cell Biology and Metabolism
COMP 250 Introduction to Computer Science
COMP 206 Introduction to Software Systems
MATH 314 Advanced Calculus
MATH 223 Linear Algebra or MATH 236 Algebra 2
MATH 323 Probability or MATH 324 Statistics

Students without the prerequisites can register with approval from the course director upon demonstration of the above knowledge and skills.

Format

This course is divided into eight modules, with each module 3 weeks long. Modules will be taught by one or two professors who will present students with a broad view of the key biological questions in the topic area and of the quantitative approaches available to address them.

Methods of Evaluation

Project Based Homework Assignments. Each module will have a set of homework assignments that will include data analysis and computer programming. Assignments are due approximately one week after they are assigned.

Small Group Presentation. Students will participate in at least one small group presentation each semester. At the beginning of each module, two relevant research papers will be assigned for class reading. At the end of the module one group will briefly present the relative strengths and weaknesses of each paper utilizing ideas and concepts from the module.

Critical Reviewer Questions. Students not involved in the Small Group Presentation for the module will submit five critical questions analyzing the two research papers of the module. Questions should focus on topics such as rationale, methodology, research findings or conclusions that could be posed as critical reviewers of the research articles. Questions should be submitted to the module instructors the day before the presentation and will be posted to the class website.

Discussion & Class Participation. Participation in lecture sessions and small group presentations is considered beneficial to generating discussion and ideas in the course, and as such will be part of the overall grade.

Peer Collaboration

Students will be assigned to work in groups for the assignments and the small group presentation. Groups will change for each module. However each student must write his/her own assignment report and individually present a portion of the journal club presentation in class.

Grading scheme

Project Based Assignments	70%
Journal Club Presentation	10%
Critical Reviewer Questions	10%
Discussion & Class Participation	10%

COURSE CONTENT

BOOTCAMPS

In conjunction with the Foundations of Quantitative Life Sciences course, a "Bootcamp" skill series will be offered in the first week of each semester. This skill series offers incoming students the opportunity to learn or brush-up on software relevant to the course.

Fall Semester

Bootcamp 1: *Introduction to scientific computing in Python and R* (Week 1 Fall Semester)

Instructor: Mathieu Blanchette (Computer Science)

Interactive exercises in a computer-lab that review basic programming in Python and statistical analysis in R. These hands-on exercises will help the students understand Python's visualization of data, functions, and programmatic elements (loops and conditional statements), while statistical testing and model fitting will be demonstrated in R.

Winter Semester

Bootcamp 2: *Introduction to scientific computing in MATLAB* (Week 1 Winter Semester)

Instructor: Sabrina Leslie (Physics)

Interactive exercises in a computer-lab that review basic programming in MATLAB. These hands-on exercises will help the students understand MATLAB's visualization of data, functions, and programmatic elements (loops and conditional statements) by focusing on random walks, along with their statistical properties, by directly simulating the walks, and then comparing simulated observations to the theory.

MODULES

Eight modules will introduce students to the diverse set of quantitative approaches used to address a variety of current life science questions. Modules will be 3 weeks and share a common organizational structure. Modules are presented in an order that reflects the progression of scales in the life sciences: from genes to systems to ecosystems.

First, each module will introduce a specific instance of a cutting-edge biological question. Second, a review of the relevant biological concepts will be provided. Third, the module will discuss the technologies that allow collecting data relevant to the question at hand, focussing not only on the techniques themselves but also on their limitations that will need to be taken into consideration at the analysis step. Fourth, each module will

introduce the mathematical formalism that describes the data, which together with the computational approaches, solve the resulting biological problem. Modules will use a combination of lectures, presentations of recent scientific papers, computer-based assignments and small group discussion.

Fall Semester Modules

Module 1: *Genome sequencing and annotation* (Weeks 2-4 Fall Semester)

Instructors: Mathieu Blanchette (Computer Science) and Ken Dewar (Human Genetics)

Question	What is the genetic makeup of an organism?
Biological concepts	Genome architecture and function
Technology	High-throughput sequencing
Quantitative analyses	Quality assessment; read mapping and genome assembly; gene prediction

Module 2: *Genetic links to disease* (Weeks 5-7 Fall Semester)

Instructors: Celia Greenwood (Oncology and Epidemiology) and Simon Gravel (Human Genetics)

Question	How are genes associated with ancestry and disease?
Biological concepts	Population genetics; links between genotype and phenotype; linkage disequilibrium
Technology	Genome sequencing; genotyping
Quantitative analyses	Estimating haplotypes; imputation; genome-wide association studies; population structure; genomic ancestry; multiple testing

Module 3: *Gene regulation* (Weeks 8-10 Fall Semester)

Instructors: Guillaume Bourque (Human Genetics) and Tomi Pastinen (Human Genetics)

Question	What are the mechanisms that govern gene expression and how do mutations in non-coding sequences contribute to disease?
Biological concepts	Chromatin; protein-DNA interactions; regulation of transcription; splicing; allelic expression; eQTLs; mRNA stability; lncRNAs and micro-RNAs

Technology	RNA-seq; Chip-seq; Methyl-seq; Hi-C; single cell sequencing, gene editing; synthetic cell models
Quantitative analyses	Statistical analysis of gene expression and Chip-seq data; integration and visualization of publicly available data; regulatory networks; chromatin-state identification; hidden Markov models; chromatin structure inference; statistical motif analysis

Module 4: *Nonlinear dynamics in biological systems* (Weeks 11-13 Fall Semester)

Instructors: Anmar Khadra (Physiology) and Judith Mandl (Physiology)

Question	How do the different components of biological systems interact?
Biological concepts	Immune and autoimmune cell responses; population dynamics; interaction dynamics (cell-cell, protein-protein, virus-host); positive feedback loops in cellular migration; spatio-temporal heterogeneity
Technology	Single cell tracking; imaging cellular dynamics in live organisms
Quantitative analyses	Deterministic models and differential equations; bifurcation theory in low dimension to pattern formation in high dimension; simulating finite-populations; Markov processes

Winter Semester Modules

Module 5: *Biological and neural time series* (Weeks 2-4 Winter Semester)

Instructors: Erik Cook (Physiology) and Christopher Pack (Neurology & Neurosurgery)

Question	How do we model biological and neural signals that vary in time?
Biological concepts	Membrane biophysics; ion channels; neural systems; Hodgkin-Huxley equations
Technology	Electrophysiological measurements
Quantitative analyses	Nyquist sampling; filtering; Fourier transform; linear models; nonlinear models; Volterra and Weiner model frameworks

Module 6: *Biophysical imaging* (Weeks 5-7 Winter Semester)

Instructors: Paul Wiseman (Physics) and Sabrina Leslie (Physics)

Question	How do we image subcellular biological components and molecules?
Biological concepts	Biophysics of DNA, proteins and organelles
Technology	Optical microscopy; photon detectors; super-resolution molecular localization; structured illumination microscopy; light sheet and lattice sheet microscopy
Quantitative analyses	Image formation; diffraction and the resolution limit; Abbe's criterion; Fourier optics and the spatial frequency bandwidth; photon detection statistics; PALM and STORM methods; molecular localization; Fluorescence fluctuation techniques

Module 7: *Biophysical networks* (Weeks 8-10 Winter Semester)

Instructor: Paul Francois (Physics)

Question	How do interacting agents form networks and what is their emergent behavior?
Biological concepts	Regulatory protein-protein interaction; signaling dynamics; metabolic networks; subcellular networks during development
Technology	Yeast two-hybrid; metabolomics; fluorescence-activated cell sorting; fluorescent in situ hybridization
Quantitative analyses	Dynamical systems; control theory; self-organization; information theory; graph theory

Module 8: *Ecosystem dynamics* (Weeks 11-13 Winter Semester)

Instructor: Fred Guichard (Biology)

Question	How do the different components of an ecosystem interact?

Biological concepts	Population regulation; mutualistic interactions; niche differentiation; community structure; trophic interactions in lake ecosystems; metrics to food web stability
Technology	Experimental ecology; morphometrics; stock assessment; stable isotopes analysis
Quantitative analyses	Numerical analysis of dynamical systems; continuation analysis; derive null expectations from statistics; linearization and local stability; analysis of species assemblages of increasing size and complexity

PRELIMINARY SCHEDULE

Fall 2017

Mathieu Blanchette
Bootcamp 1: *Introduction to scientific computing in Python and R*
Sessions 1-2, Week 1, Early Sept 2017

Mathieu Blanchette & Ken Dewar
Module 1: *Genome sequencing and annotation*
Sessions 3-8, Weeks 2-4, Mid Sept to early Oct 2017

Celia Greenwood & Simon Gravel
Module 2: *Genetic links to disease*
Sessions 9-14, Weeks 5-7, Early Oct to late Oct 2017

Guillaume Bourque & Tomi Pastinen
Module 3: *Gene regulation*
Sessions 15-20, Weeks 8-10, Late Oct to Mid Nov 2017

Anmar Khadra & Judith Mandl
Module 4: *Nonlinear dynamics in biological systems*
Sessions 21-26, Weeks 11-13, Mid Nov to early Dec 2017

Winter 2018

Sabrina Leslie
Bootcamp 2: *Introduction to scientific computing in Matlab*

Sessions 1-2, Week 1, Early Jan 2018

Erik Cook & Chris Pack
Module 5: *Biological and neural time series*
Sessions 3-8, Weeks 2-4, Mid Jan to early Feb 2018

Paul Wiseman & Sabrina Leslie
Module 6: *Biophysical imaging*
Sessions 9-14, Weeks 5-7, Early Feb to late Feb 2018

Paul Francois
Module 7: *Network biophysics*
Sessions 15-20, Weeks 8-10, Late Feb to Mid March 2018

Fred Guichard
Module 8: *Ecosystem dynamics*
Sessions 21-26, Weeks 11-13, Mid March to early April 2018

APPENDIX B: LIST OF COMPLEMENTARY COURSES

Students will be required to take one or two courses from each of the Quantitative and Life Science Blocks, for a total of three courses.

Biophysics Stream

Quantitative Block	Life Sciences Block
BIEN 530 Imaging and Bioanalytical Instrumentation **BMDE 519** Biomedical Signals & Systems **BMDE 512** Finite-Element Modelling: BME **CHEM 514** Biophysical Chemistry. **CHEM 520** Methods in Chemical Biology **COMP 551** Applied Machine Learning **PHYS 519** Advanced Biophysics **PHYS 559** Advanced Statistical Mechanics	**BIOC 604** Macromolecular Structure. **PHGY 520** Ion Channels **PHGY 518** Artificial Cells **BIOL 551** Principles of Cellular Control

Computational and Statistical Molecular Biology Stream

Quantitative Block	Life Sciences Block
BMDE 502 BME Modelling & Identification **BIOS 601** Epidemiology: Introduction and statistical models. **MATH 523** Generalized Linear Models **HGEN 677** Advanced statistical methods in genetics and genomics. **COMP 561** Computational Biology Methods and Research **COMP 598** Topics in Computer Science: Advanced Computational Biology Methods **MATH 680** Computation Intensive Statistics	**BIOC 603** Genomics and Gene Expression. **HGEN 661** Population Genetics **HGEN 692** Human Genetics. **EXMD 602** Techniques in Molecular Genetics. **BIOL 551** Principles of Cellular Control

Ecosystems Stream

Quantitative Block	Life Sciences Block
ENVB 506 Quantitative Methods in Ecology **MATH 556** Mathematical Statistics 1 **MATH 525** Sampling Theory and Applications **MATH 533** Honours Regression and Analysis of Variance **MATH 537** Mathematical Models in Biology **MATH 547** Stochastic Processes **MATH 523** Generalized Linear Models	**BIOL 509** Methods in Molecular Ecology **BIOL 510** Community Ecology **BIOL 594** Advanced Evolutionary Ecology **ENVR/BIOL 540** Ecology of Species Invasion

APPENDIX C: LETTERS OF INTERESTED FACULTY (IN PROGRESS)

List of McGill Faculty members who have expressed interest in obtaining supervisory privilege in the QLS Ph.D. Program

Name	Professorial Rank	Department
Robert Nadon	Associate Professor	Human Genetics
Heungsun Hwang	Associate Professor	Psychology
Alan Evans	Professor	Neurology and Neurosurgery; Biomedical Engineering
Rob Sladek	Associate Professor	Experimental Medicine; Human Genetics
Dave Alan Stephens	Professor	Mathematics & Statistics
Jacek Majewski	Associate Professor	Human Genetics
Alexandra Schmidt	Associate Professor	Epidemiology, Biostatistics & Occupational Health
Jérôme Waldispühl	Associate Professor	Computer Science
Joëlle Pineau	Associate Professor	Computer Science
Daniel Schoen	Professor	Biology
Melania Cristescu	Associate Professor	Biology
Jackie Vogel	Associate Professor	Biology
Uri David Akavia	Assistant Professor	Biochemistry
Nicolas Moitessier	Associate Professor	Chemistry
Claudia Kleinman	Assistant Professor	Human Genetics
Robert Kearney	Professor	Biomedical Engineering
Paul Harrison	Associate Professor	Biology
Leon Glass	Professor	Physiology
Hamed S. Najafabadi	Assistant Professor	Human Genetics
Mark Lathrop	Professor	Human Genetics
Brian Leung	Associate Professor	Biology and School of Environment
Rodrigo Reyes	Assistant Professor	Biology

Gregor Fussmann	Professor	Biology
Gary Brouhard	Associate Professor	Biology
Stephanie Weber	Assistant Professor	Biology
Brent Richards	Associate Professor	Experimental Medicine; Human Genetics; Epidemiology & Biostatistics
Ian Robert Watson	Assistant Professor	Biochemistry

APPENDIX D: LETTERS OF SUPPORT (IN PROGRESS)

UNIVERSITY OF TORONTO
DALLA LANA SCHOOL OF PUBLIC HEALTH

16 September 2016

Celia Greenwood
Senior Investigator, Lady Davis Institute for Medical Research
Associate Professor, McGill University

RE: Interdisciplinary McGill PhD program in Quantitative Life Sciences

Dear Celia,

This program in Quantitative Life Sciences looks very exciting and you have our strongest support for this initiative. We at STAGE are strong proponents of fostering and nurturing young scientists to develop strong quantitative skills and solid foundation in life sciences to become talented scientists well equipped to answer complex biological questions. We strongly believe that this can be best achieved through interdisciplinary mentoring research teams.

As you know, we are co-Directors of the Toronto CIHR STAGE program (Strategic Training for Advanced Genetic Epidemiology), which has been in operation since 2010 training students in genetic epidemiology and statistical methods in genetics and genomics. From the beginning, our training program has included strong interdisciplinary aspects, so that every STAGE trainee has a research project supervision committee containing at least 3 members from different disciplinary fields. We have found this setup to be very successful; students have done extremely well in obtaining scholarships, postdoctoral fellowships at prestigious institutions, or excellent jobs.

To exemplify the success this interdisciplinary mentorship team format has on the development of trainees as well-rounded scientists, we note:

1. Originating from a CIHR investment of less than $1.8M, STAGE trainees have generated over $2M in external funding in the first four years of the training program alone;
2. Practically every trainee has received some form of external funding;
3. Several trainees have received highly competitive awards and recognitions, including Vanier Canada Graduate Scholarship, CIHR Clinical Investigatorship Award (ranking first), International Genetic Epidemiology Society Williams Award, and Connaught International Scholarship.
4. All trainees have found positions in their discipline: post-docs moving into faculty positions, clinical-scientist positions, and leadership positions in the

industry; PhD students pursuing their training in high profile international research teams (e.g. at Vanderbilt University, University of Michigan).

We look forward to hearing about the progress of this new program.

Warm regards,

France Gagnon, MSc, PhD
Canada Research Chair in Genetic Epidemiology
Co-Director, CIHR STAGE (Strategic Training for Advanced Genetic Epidemiology)
Associate Professor, Division of Epidemiology, Dalla Lana School of Public Health
University of Toronto

Shelley B. Bull, PhD
Senior Investigator, Lunenfeld-Tanenbaum Research Institute, Sinai Health System
Co-Director, CIHR STAGE (Strategic Training for Advanced Genetic Epidemiology)
Professor, Division of Biostatistics, Dalla Lana School of Public Health
University of Toronto

Guy Rouleau, M.D., Ph.D., F.R.C.P.(C)., O.Q.

Chaire de neurosciences Wilder-Penfield
Directeur, Institut et hôpital neurologiques de Montréal
Directeur, Département de neurologie et neurochirurgie, Université McGill
Chef intérim, Département de génétique, CUSM

Wilder Penfield Chair in Neuroscience
Director, Montreal Neurological Institute and Hospital
Chair, Department of Neurology and Neurosurgery, McGill University
Interim Chief, Department of Medical Genetics, MUHC

August 30, 2016

Celia Greenwood, PhD
Senior Investigator
Lady Davis Institute Associate Professor, McGill University
H414 - 3755 Cote Ste Catherine, Montreal, QC H3T 1E2
celia.greenwood@mcgill.ca

Re: Proposed McGill graduate program in Integrative Quantitative Life Sciences.

Dear Celia,

It is a great pleasure to write a letter of support for the proposed graduate program in Integrative Quantitative Life Sciences (IQLS). As Director of the Montreal Neurological Institute, I come into contact with many graduate students who work in highly interdisciplinary research areas, many of which require advanced mathematics and physics knowledge.

For some years now, McGill has had an Integrative Program in Neuroscience (IPN), which has proven to be extremely popular with both students and supervisors, and has enriched the training experience for all involved. Interdisciplinary programs, when well designed, are needed to develop the next generation of researchers able to work at the interface of traditional disciplines.

After examining the proposed program, I can see that it requires all students to have a very strong quantitative background at enrollment, and then builds on this base to encourage rigorous quantitative research. Given the ground-breaking advances in imaging that are ongoing at the MNI, together with the ever-increasing data sharing resources that we are putting in place, the need for excellent training in quantitative life sciences has never been greater.

Sincerely,

Dr. Guy Rouleau

Hôpital général juif
Jewish General Hospital

McGill

Institut Lady Davis de recherches médicales | Lady Davis Institute for Medical Research

August 25, 2016

Celia Greenwood, PhD
Senior Investigator, Lady Davis Institute
Associate Professor, McGill University
H414 - 3755 Cote Sainte Catherine
Montreal, QC H3T 1E2

Dear Celia,

I have had the chance to review the excellent proposal for a new interdisciplinary graduate program in Quantitative Life Sciences, and I am delighted to write this letter of support.

As Director of the Lady Davis Institute at the Jewish General, and as former Scientific Director of the Institute of Genetics of CIHR, I am intimately aware that the advances in technology in the laboratory are challenging all biological researchers to become more quantitatively competent. Terabytes of data are now routinely generated, and trainees often must spend more time at their computers than at the bench.

I am very enthusiastic about the possibility of McGill training new researchers who not only have the quantitative skills to develop new approaches, but who also are capable of communicating and working synergistically with those from other disciplines in life sciences.

Let me know if I can provide any further support for this excellent initiative.

Sincerely,

Roderick R. McInnes, CM, MD, PhD, FRSC
Director, Lady Davis Institute
Jewish General Hospital
Alva Chair in Human Genetics
Canada Research Chair in Neurogenetics
Professor of Human Genetics, Professor of Biochemistry
McGill University

THE UNIVERSITY OF CHICAGO

The Grossman Institute for Neuroscience, Quantitative Biology and Human Behavior

September 22, 2016

Erik P. Cook, Ph.D.
Co-director, Centre for Applied Mathematics in Biosciences and Medicine
Department of Physiology
McGill University
3655 Sir William Osler
Montreal, QC H3G 1Y6
Canada

Re: Proposed graduate training program in Quantitative Life Sciences at McGill University

Dear Erik,

I am delighted to write in support of McGill University's new interdisciplinary graduate training program in Quantitative Life Sciences. As the Director of the Grossman Institute for Neuroscience, Quantitative Biology and Human Behavior at the University of Chicago, I know first hand of the importance of training new interdisciplinary researchers.

There is a shortage of scientists able to harness the power of both modern computation and biological techniques necessary to advance research and education across all areas of the life sciences. Many new high-throughput technologies are generating staggering volumes of biological data, creating the need for researchers who are thoroughly versed with quantitative methods. These skills are a critical component for the successful translation of life-science research into beneficial solutions.

Like your proposed program in Quantitative Life Science, the Grossman Institute takes to heart the idea that an interdisciplinary approach is critical for solving the most challenging and complex problems in the biological sciences. Although our Institute was established primarily to serve the Neuroscience community at the University of Chicago, we work alongside faculty in Chemistry, Psychology, Computer Science, Human Genetics, Cellular and Molecular Biology, and Statistics to foster an interdisciplinary research environment. An exciting component of your program is its bridging of traditional Departments and Divisions to facilitate research partnerships and enhance student training.

I am very supportive of McGill's new initiative to train graduate students in the Quantitative Life Sciences. I expect that your new program will make McGill competitive with similar programs across North America that are now actively recruiting students with quantitative backgrounds. I wish you much success in the launch of your new training program.

Sincerely,

John H.R. Maunsell, PhD

John H.R. Maunsell, Ph.D.
Director
Albert D. Lasker Professor in Neurobiology

P-423, MC0912
5841 South Maryland Avenue
Chicago, Illinois 60637
773.702.3203 • maunsell@uchicago.edu

APPENDIX E: LIST OF GRANTS AWARDED TO TEACHING FACULTY MEMBERS

Mathieu Blanchette

Eric Lécuyer, Mathieu Blanchette, Jérôme Waldispühl. Identification and design of RNA localization zipcodes: new tools to manipulate cellular function. Genome Canada Disruptive Innovation in Genomics Competition. $125,000 annually (2016 – 2018)

Tomi Pastinen, Mathieu Blanchette, Catherine Laprise, Renee Siebert, Ezio Bonifacio, Florence Demenais, Pierre Bougneres, Delphine Fradin. RESET-AID Consortium. Multilateral France-Germany-Canada call on Epigenomics of Complex Diseases. $ 405,930 annually (2015-2019)

Mathieu Blanchette, Thomas Bureau. User-friendly application for high-resolution transposable element identification and characterization. Genome Canada Bioinformatics and Computational Biology Competition. $125,000 annually (2013-2015)

Jérôme Waldispühl, Mathieu Blanchette, Derek Ruths. : A development and deployment platform for citizen science games in biology. Genome Canada Bioinformatics and Computational Biology Competition. $125,000 annually (2013-2015)

Nicholas Provart. Genomics Large Data Sets and Novel Tools for Plant Biology for use International Infrastructure-Tier Data Repositories and Portals. Genome Canada Bioinformatics and Computational Biology Competition. $125,000 annually (2013-2016)

Mathieu Blanchette. Inference and analysis of ancestral genomes. NSERC Accelerator. $40,000 annually (2013-2017).

Mathieu Blanchette. Inference and analysis of ancestral genomes. NSERC Discovery. $69,000 annually (2013-2017).

Mathieu Blanchette, Eric Lecuyer, Jerome Waldispuhl. Évolution des gènes d'ARN de transfert à l'échelle génomique. FQRNT Team grant. $48,000 annually (2013-2016)

Mark Prentki, Pavel Hamet, Benoit Coulombe, Rob Sladek, Remi Rabasa-Lhoret, Mathieu Blanchette, Vincent Poitout, Shant Dersakissian, Erik Joly, Nabil Seidah. The Montreal CardioMet Biomarker and Drug Discovery Consortium. Canadian Foundation for Innovation – Leader Edge Fund. $2,312,056 (2013-2017)

Guillaume Bourque. Integrative Epigenomic Data Coordination Centre (EDCC) at McGill. CIHR CEEHRC Epigenomics platform – Data coordination Center. $219,796 annually (2012-2017)

Mark Lathrop. Epigenomics Mapping Centre (EMC) at McGill. CIHR CEEHRC Epigenomics platform – Epigenomics Mapping Center. $906,400 annually (2012-2017)

Mathieu Blanchette, Derek Ruths and Jérôme Waldispuhl. Computing infrastructure for bioinformatics web services. NSERC Research Tools and Instrumentation. $40,173 annually (2012-2013)

John White, Mathieu Blanchette, Rob Sladek. Host macrophage transcriptomic responses to M. tuberculosis infection. Genome Québec Health Program. $424, 385 annually (2010-2013)

Thomas Bureau, Mathieu Blanchette, Stephen Wright, John Stinchcomb, Alan Moses, Paul Harrison, Daniel Schoen, Anwar Naseem and Ken Dewar. Bridging comparative, population and functional genomics to identify and experimentally validate novel regulatory regions and genes for crop improvement. Genome Canada Competition IV. $ 1,177,283 annually (2009-2013)

Silvia Vidal, Mathieu Blanchette, Philippe Gros, Danielle Malo, Maya Saleh, Salman Qureshi. An integrative forward genetic approach to identify novel pathways in host response to infection: from mouse models to patients. CIHR Team grant. $ 828, 994 annually (2008-2012)

Mathieu Blanchette. Algorithms for whole-genome comparative and regulatory genomics. NSERC Discovery Grant. $ 31, 000 annually (2008-2013)

Guillaume Bourque
2016 – 2020 CFI, Cyber-infrastructure *$ 5,000,000*
Role: co-Project Lead. Title: CanDIG: Canadian Distributed cyber-Infrastructure for Genomics

2015 – 2017 Genome Canada, GIN – Tech. Development *$ 527,000* Role: Project Lead
Title: Canadian Center for Computational Genomics (C3G)

2015 – 2017 Genome Canada, Genomics Innovation Network *$ 1,050,000* Role: Project Lead
Title: Canadian Center for Computational Genomics (C3G)

2012 – 2017 CIHR, CEEHRC Epigenomics Platform *$ 1,500,000* Role: Principal Investigator

Title: Integrative Epigenomic Data Coordination Centre (EDCC) at McGill

2011 – 2016 CIHR, Operating Grant *$ 426,482* Role: Principal Investigator Title: Functional characterization of the endogenous retrovirus HERV-H family in human embryonic stem cells

2015 – 2019 CIHR, CEEHRC Consortium Network *$ 2,000,000* Role: Principal Applicant (NPA Hirst, share 7%)
Title: Canadian Epigenetics, Environment and Health Research Consortium Network

2015 – 2019 CFI, Innovation Fund *$ 58,435,000* Role: Principal User (PL Jones, share 8%)
Title: Canada's Genomics Enterprise (CGEn): A national genomic tools network for transforming life science research

2015 – 2019 CFI, Innovation Fund *$ 2,893,000* Role: Principal User (PL Meaney, share 0%)
Title: Treatment Outcomes in Mood Disorders

2015 – 2017 Genome Canada, Genomics Innovation Network *$ 2,000,000* Role: co-Lead (PL Lathrop, share 15%) Title: McGill University and Génome Québec Innovation Center

2015 – 2017 Genome Canada, GIN – Tech. Development *$ 1,000,000* Role: co-Lead (PL Lathrop, share 10%) Title: McGill University and Génome Québec Innovation Center

2014 – 2018 NSERC, Discovery Frontiers *$ 6,000,000* Role: co-Investigator (PI Stein, share 7%)
Title: The Cancer Genome Collaboratory

2013 – 2017 Genome Canada, Large-scale Applied Research *$ 6,000,000* Role: co-Investigator (PIs Jabado – Majewski, share 5%) Title: Biomarkers for Pediatric Glioblastoma through Genomics and Epigenomics

2013 – 2016 Brain Canada *$ 1,494,900* Role: co-Investigator (PI Meaney, share 0%) Title: Epigenetics and Mental Health

2012 – 2017 CIHR, CEEHRC Epigenomics Platform *$ 6,000,000* Role: co-Investigator (PI Lathrop, share 15%) Title: Multidimensional Epigenomics Mapping Centre (EMC) at McGill

2011 – 2016 CIHR, Team Grant: Childhood Cancer *$ 2,445,054* Role: co-Investigator (PI Sinnett, share 0%) Title: Genomic determinants of common long-term treatment effects in childhood acute lymphoblastic leukemia survivors

2013 – 2015 CANARIE, Research Middleware Program *$ 771,000* Role: Principal Investigator Title: Genetics and Genomics Analysis Platform (GenAP)

2011 – 2014 Genome Quebec, Human Health Competition *$ 2,000,000* Role: co-Inv (PI Moreau, share 10%)
Title: Development of comprehensive diagnostic assays for scoliosis

2011 – 2012 CIHR, Advancing Technology Innovation *$ 1,550,000* Role: co-Inv (PI Sorensen, share 10%) Title: The Canadian Pediatric Cancer Genome Consortium: Translating next-generation se- quencing technologies into improved therapies for high-risk childhood cancer.

Erik Cook

2016/4 - 2026/3 Co-applicant Targeted Manipulation of Neural Microcircuits for Understanding and Correcting Brain Dysfunction, Grant, Infrastructure Canada Foundation for Innovation (CFI)
Innovation fund Total Funding - 5,600,000 (Canadian dollar) Principal Applicant: Kathleen Cullen

2012/4 - 2017/3 Principal Investigator Information coding in neurons: bridging the gap between cellular and behavioral neuroscience, Grant, Operating Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery grant Total Funding - 200,000 (Canadian dollar)

2009/4 - 2014/3 Principal Investigator Physiology of Visual Perception, Fellowship Canada Research Chairs (CRC) Tier 2 Salary Award Total Funding - 500,000 (Canadian dollar)

2009/10 - 2013/9 Principal Investigator Neural encoding in the visual cortex: engineering principles for advanced neural prosthetics, Grant, Canadian Institutes of Health Research (CIHR) Operating grant Total Funding - 370,000 (Canadian dollar)

2009/1 - 2011/12 Principal Investigator Neural correlates of time perception in visual cortex, Grant, EJLB Foundation Scholar Research Program Total Funding - 350,000 (Canadian dollar)

2009/4 - 2011/3 Collaborator Centre for Applied Mathematics in Bioscience and Medicine, Grant, Operating Mathematics of Information Technology and Complex Systems (MITACS)
Centre of Excellence Total Funding - 67,000 (Canadian dollar). Principal Investigator: Mackey, Michael

2010/4 - 2011/3 Principal Applicant Joint CPS/CAPnet winter meeting: Physiological mechanisms of perception, cognition and action, Grant, Operating Canadian Institutes of Health Research (CIHR) Meetings, plannings and dissemination grant Total Funding - 6,000 (Canadian dollar) Co-applicant : Doug Crawford; Randy Flanagan; Jody Culham; Paul Cisek

2006/4 - 2011/3 Principal Investigator Information coding in neurons: bridging the gap between cellular and behavioral neuroscience, Grant, Operating Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant Total Funding - 157,500 (Canadian dollar)

Ken Dewar

CV Pending

Paul François

Fonds Québecois de Recherche Nature Technologie (FQRNT, Québec natural science research fund) Projet de recherche en équipe (2015-2018), $ 144,000 (CAD total) main PI in collaboration with Jackie Vogel, Gary Brouhard (McGill) and Steve Michnick (Université de Montreal). Share: 50 %.

Simons Investigator: Mathematical Modeling of Living Systems (2014-2019), $500,000 (US) total

Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery grant (2016-2021), $ 240,000 (CAD) total.

Human Frontier Science Program (HFSP) Program grant (2012-2015), $ 1,050,000 (US) total for our research team in collaboration with O. Pourquié (IGBMC Strasbourg), Rusty Lansford (Caltech). Share : 30 %.

Fonds Québecois de Recherche Nature Technologie (FQRNT, Québec natural science research fund) Nouveaux Chercheurs grant (2013-2015), $ 40,000 (CAD) total.

Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery grant (2011-2016), $ 100,000 (CAD) total.

Simon Gravel

Simon Gravel. Modelling recent genetic events in complex cohorts. CIHR Operating Grant. $289,886 (2014-2018).

Simon Gravel. Statistical Methods for Enabling Medical and Population Genomics of Admixed Human Populations (Subaward to Gravel). National Science Foundation. $227,565 (2012-2016).

Celia Greenwood

A. Wazana et al. How the early environment interacts with prenatal adversity and genetic susceptibility to moderate the risk for anxious and depressive disorders. CIHR Team Grant: Developmental Origins of Health and Disease—Implications for Men, Women, Boys, and Girls. $462,665 (2016-2021)

A Bureau , A Labbe (PI), K Burkett, J Graham, C Greenwood, MJ Lakhal Chaieb, F Larribe, K Oualkacha, M-H Roy-Gagnon, I Ruczinski, E Zeggini, A Brooks-Wilson, C Laprise, M Maziade, B Richards, J Simard. Rare DNA variants and human complex traits: improving analyses of family studies by better modeling the dependence structures. CANSSI Collaborative Research Team Project. $180, 000 (2016-2019)

JB Richards, C. Greenwood, G. Thanassoulis. Mendelian randomization: Testing the causality of clinically-relevant biomarkers. CIHR Transitional Operating Grant. $60,000 (2015-2016)

C Greenwood. Finding important associations in genetic and genomic data. NSERC Discovery grant. $10, 000 annually (2014-2019)

M Meaney, A Evans, C Greenwood. Ludmer Centre for Neuroinformatics and Mental Health $ 3.3 million annually: $870,000 to Jewish General Hospital (2013 – 2017).

C Greenwood, A Labbe, A Ciampi, D Stephens. Analysis of DNA methylation data. Canadian Institute of Health Research. $100, 537 annually (2013 – 2017)

D Daley, C Greenwood, M Kobor, A Kozyrskyj, A Labbe, C Laprise, P Pare, A Sandford. Epigenetic mechanisms for the development of asthma. CIHR Team Grant: Canadian Epigenetics, Environment, and Health Research Consortium (CEEHRC). $250,000 annually (2013 – 2018)

B Richards, T Pastinen, C Greenwood. Pinpointing causal variants for osteoporosis. CIHR Operating Grant. $816,608 annually (2012 – 2015)

D Bickel, C Greenwood. Statistical methods of detecting and estimating associations with uncommon genetic variants. CIHR Operating Grant. $113,000 annually (2012- 2015)

C Greenwood, A Ciampi. Modeling the relationship between genotypic configurations and traits. CIHR Operating Grant. $72,109 annually (2011 – 2014)

C Greenwood. Identifying useful predictors from genome-wide SNP association studies. NSERC Discovery Grant. $15,000 annually (2009 – 2014)

M Cotterchio, S Gallinger, C Greenwood. Association between allergy history, immunologic genetic variants and pancreatic cancer risk. CIHR Operating grant. $485, 100 annually (2010 – 2013)
M. Hudson, C Greenwood. Epigenetic Signatures of Systemic Autoimmune Rheumatic Diseases- A Pilot Study. LDI CLiPP competition. $49, 670 (2012-2013)

C Greenwood, P Tonin. How to measure the impact of copy number aberrations in ovarian cancer. The Week-End to End Women's Cancer Pilot Projects Grant. $38,866 annually (2011 – 2012)

Peter Grutter

$ 98,000 2011-2016 NSERC Discovery Scanning Probe Microscopy Applied to Nanoscience (PI)

$ 43,000 2013-2016 FRQNT Team Grant Contrale et organisation d'assemblages discrets de nanoparticules d'or avec l'ADN (PI)

$ 43,000 2013-2016 FRQNT Team La comprehension des processus photogeneration des porteurs de charge dans des cellules solaires organiques (PI Cook)

$100,000 2014-2018 NSERC CRD The Design and Mapping of Next Generation Nano Lithium-ion Battery Cathodes

$25,000 2013 NSERC ENGAGE Combined Scanning Kelvin Probe Force Microscopy and Scanning Maxwell Stress Microscopy for Improved Semiconductor Dopant Profiling (PI)

$25,000 2014 NSERC ENGAGE Development of new micropositioner systems compatible with high resolution optical microscopy

$15,000 2013-2018 McGill University Dawson/James McGill Chair research stipend

$10,000 2013-2018 McGill University Chair's research stipend

$300,000 2010-2016 NSERC CREATE Integrated Sensor Systems (PI Kirk, 9 others)

$300,000 2011-2017 NSERC CREATE Neuroengineering (PI Lennox, 9 others)

$300,000 2011-2017 NSERC CREATE NanoBioMachines (PI Gehring, 9 others)

$325,000 2009-2015 CIHR Training Pgm Neurophysics; Setting new frontiers in neuroscience with Material Sciences, Photonics and Computational Sciences (PI de Koninck)

$ 576,000 2015-2021 FQRNT *Le Regroupement québécois sur les matériaux de pointe* (RQMP)

$ 925,000 2009-2015 FQRNT *Le Regroupement québécois sur les matériaux de pointe* (RQMP) (PI)

$ 300,000 2013-2015 FQRNT *INstitut TRansdisciplinaire d'Informatique Quantique* (INTRIQ) (PI Hilke)

$ 697,595 2014-2016 CFI LEF *System to study the mechanics of single molecules with high spatial and temporal resolution* (PI D. Rassier)

$ 11,300,370 2013-2016 CFI LEF *Tools for Nanoscience and Technology upgrade ('Nanotools 2')* (PI)

$ 44,050 2013-2015 FRQNT Team Controle et organisation d'assemblages discrets de nanoparticules d'or avec l'ADN

Fred Guichard

FRQNT. Strategic Cluster program. *Centre de Recherches Mathématiques (CRM)*. Luc Vinet (PI), Frederic Guichard and 14 others (Lab Directors), and 104 other co-PIs. 2015-21. $3,045,200.

NSERC. CREATE (graduate training grant). *Biodiversity, Ecosystem Services and Sustainability* (BESS). Andrew Hendry (PI) and 10 co-PIs. 2015-21. $1,650,000.

Coastal Healthy Ocean Network II (CHONe II). Strategic NSERC network. *Optimization of MPA selection based on spatial connectivity and on metapopulation and metacommunity dynamics*. $164,000. Frederic Guichard (Co-PI) and Marie-Josée Fortin (PI, University of Toronto). 2015-2018 (3 years).

NSERC. Strategic Project. Impact of genetic connectivity for marine protected areas. Frederic Guichard (co-PI), Marie-Josée Fortin (PI), Isabelle Côté (co-PI). 2013-2016. $600,000.

NSERC. Discovery Grant. $165,000. *Non-equilibrium dynamics of marine metaecosystems*.
2012-2017

NSERC. Emerging Opportunity Fund, Coastal Healthy Ocean Network (CHONe). Metaanalysis of biodiversity and ecosystem function in oceans. 2011-12. $50,000.

FRQNT. Strategic Cluster program. *Quebec-Ocean Centre*. Maurice Levasseur (PI) and ~50 co-PI. 2009-16. $3,630,000.

Coastal Healthy Ocean Network (CHONe). Strategic NSERC network. *Ecosystem-based design of marine reserve networks*. $120,000. 2009-2011.

NSERC. MITACS Centers. Center for Applied Mathematics in Biosciences and Medicine (CAMBAM). Michael Mackey (PI) with 30 co-PIs. 2009-2011. $300,000.

Coastal Healthy Ocean Network (CHONe). Strategic NSERC network. *Larval transport and metacommunity dynamics: a graph-theoretical approach*. $150,000. Frederic Guichard (PI) and David Pike (Co-PI, Memorial University). 2009-2011 (3 years).

NSERC. Discovery Grant. $96,250. *Variability across scales in coastal ecosystems*. 2007- 2012 (5 years).

James S. McDonnell Foundation. 21st Century Science Initiative Research Award. US$304,500. *Metacommunity dynamics across scales and the design of marine reserve networks*. 2006-2010.

Anmar Khadra

Grant/Agency: NSERC Canada/RGPIN Khadra (PI) 04/01/13–03/31/18. Title: Computational Models for the Study of Various Immunological and Electrophysiological Systems. Amount: CAN$32,000/year [Total = CAN$160,000] Role: PI

Grant/Agency: Canadian Foundation for Innovation CFI Vogel (PI) 09/01/15–08/31/18. Title: Integrated Quantitative Bioscience of Adaptation. Amount: ~CAN$11.4M. Role: User

Grant/Agency: McGill University CFI-JELF Brown (PI) 04/30/16–03/31/17. Title: Photo-Manipulation & Increased Throughput for a Combined TIRF/SDCM. Amount: CAN$31,000. Role: Co-PI

Grant/Agency: McGill University NSERC GRF-RTI Brown (PI) 04/30/14–03/31/15. Title: Spinning Disk Confocal Microscope for Measuring Protein Dynamics and Interactions. Amount: CAN$27,500. Role: Co-PI

Grant/Agency: Mathematical Biosciences Institute (MBI) Khadra (PI) 07/01/14–06/30/15. McGill University. National Institute for Mathematical and Biological Synthesis (NIMBioS). Title: The Montreal 2015 CAMBAM/MBI/NIMBioS Summer School in Quantitative Biosciences. Amount: US$30,000 (MBI) + CAN$10,000 (McGill University) + US$10,000 (NIMBioS). Role: Organizer

Grant/Agency: McGill University Khadra (PI) 01/01/12–12/31/14. Title: Startup Fund. Amount: CAN$20,000/(year 1) + CAN$50,000/(year 2) [Total = CAN$70,000]. Role: PI

Grant/Agency: R01 DK53456 (NIH) Pietropaolo (PI) 01/01/13–12/31/14. Title: Enhancement of Biomarkers for Type 1 Diabetes. Amount: US$40,000/year [Total: US$3.2M; US$80,000 was allocated to my project]. Role: Co-investigator

Grant/Agency: The Fields Institute Khadra (PI) 04/30/13–03/31/14. Title: 2014 Workshop on Diabetes Systems Biology Anmar Khadra Curriculum Vitae. 10 Amount: CAN$12,000. Role: Organizer

Grant/ Agency: National Institutes of Health (NIH) Khadra (CoPI) 07/31/11–06/30/12. Title: Dynamics in Neural, Endocrine and Metabolic Systems: A Symposium in Honor of Arthur Sherman. Amount: US$20,000. Role: Co-organizer

Sabrina Leslie

NSERC Collaborative Research and Development Grant (CRD). Identify and Quantitate Biomarkers using Nanopores Fabricated by Controlled Breakdown. Tabard-Cossa, Leslie, Slater, Godin. Industry partner Abbott Laboratories. 4/2016 - 3/2018.

NSERC Collaborative Research and Development Grant (CRD). Massively parallel linearization and chemical treatment of DNA molecules in arrays using tunable nanoscale con_nement Leslie. Industry Partners Micralyne and ZSGenetics. 12/2015 - 12/2017.

Research Agreement. Convex Lens-induced Con_nement (CLiC) microscopy of polymer complexes. Industry partner ZSGenetics. Leslie, 12/2014-01/2016.

NSERC Idea to Innovation, Market Assessment. Market Assessment of Molecular Manipulation and Nanoscopy Platform. Leslie. Partner is CEIM. 11/2015-04/2016.

FRQNT Team. Microscopie de con_nement a l'echelle nanometrique pour l'observation de la dynamique et des interactions de l'ADN et des proteines. Leslie, Michnick (Biochemistry, University of Montreal), Sutton. Collaborators Levens, Benham, Sleiman, Wiseman. 04/2015-03/2018.

NSERC RTI. Visualizing and Directing Dynamic DNA Nanostructure Assembly with Single-Molecule Resolution. Leslie, Sleiman, Wiseman, Juncker, Tabard-Cossa. 04/2015-04/2016.

NSERC Engage. Single-DNA manipulation above a suspended membrane using tunable nanoscale con_nement. Leslie, 01/2015-06/2015. With Abbot Laboratories.

NSERC Engage. Strain Imaging of Thin Patterned Films Using Convex Lens-induced Con_nement Microscopy. Leslie, 11/2015-04/2015. With Rolls Royce.

Collaborative Health Research Project (CHRP). Nanocon_nement Based Single-Cell Cytogenetic Platform for Pre-/Post-Implantation Genetic Diagnosis. Reisner, Leslie, Sladek (Genome Center), Ao (Montreal Children's Hospital), 05/2013-05/2016. With Quorum Technologies.

NSERC Engage. A Custom Inexpensive Versatile Microscope. Leslie, 05/2013-11/2013. With Aurora Scienti_c.

NSERC Engage. Dramatically improved single-molecule imaging of thin molecular _lms. Leslie, 09/2012-09/2016. With Quorum Technologies.

NSERC Research Tools and Instruments Grant. Force-And-Fluorescence Microscopy Of DNA

Repair. Leslie, 04/2012-05/2012.

NSERC Discovery Grant. Single-molecule investigations of fast biomolecular search processes initiating DNA repair. Leslie, 04/2012-04/2017.

CFI Leaders Opportunity Fund. Single-molecule investigations of fast biomolecular search processes initiating DNA repair. Leslie, 04/2012-04/2015.

CFI Infrastructure and Operating Fund. Single-molecule investigations of fast biomolecular search processes initiating DNA repair. Leslie, 04/2012-04/2017.

Physics Start-up Funding. Leslie, 04/2012-04/2017.

Judith Mandl

2015/4 - 2020/4 Principal Applicant CRC in Immune Cell Dynamics Canada Research Chairs (CRC). Tier 2 Canada Research Chair (CRC). Total Funding - 500,000 (Canadian dollar)

2015/1 - 2016/12 Principal Applicant Startup Funds McGill University Total Funding - 250,000 (Canadian dollar)

2015/7 - 2016/12 Principal Applicant CFI Leaders Opportunity Fund: Program in T cell interaction and migration dynamics in health and immunodeficiency. Canada Foundation for Innovation (CFI). Leaders Opportunity Fund. Total Funding - 450,000 (Canadian dollar)

2015/1 - 2015/12 Principal Applicant Equipment Funds. McGill University Total Funding - 225,000 (Canadian dollar).
2015/6 – 2015/12 Principal Applicant Phyllis Butterworth Endowment for Intravital Imaging Laboratory (McGill University). McGill Endowment Fund Phyllis Butterworth Endowment. Total Funding - 250,000 (Canadian dollar)

2010/9 - 2011/9 Co-investigator Visualizing in vivo effector T cell killing and surveillance to quantify dynamics relevant to HIV vaccine design Co-investigator : Germain, Ronald National Institutes of Health (NIH) (USA) Office of AIDS Research Total Funding - 122,000 (United States dollar)

Christopher Pack

DARPA BAA-15-35 (2016-2017)

FRQS Senior Scholar (2016 – 2017)

Merck, Sharpe & Dohme Corporation (2014-2016; co-applicant)

DARPA BAA-14-38 (2014-2015)

U.S. Department of Defense PH/TBI RP (2014-2017; co-PI)

Neuro Early Career Award (2013)

NSERC Discovery Grant (2012-2017 [renewal])

MDEIE Grant: Programme de Soutien à la Recherche (2012-2015)

CIHR Operating Grant (2011-2016 [renewal])

Canada Research Chair (2005-2015 [renewed 2010])

NSF Collaborative Research in Computational Neuroscience Grant (2010-2013)

MITACS Centre Grant (2009-2012; P.I.: M. Mackey)

CNIB E.A. Baker New Researcher (2008-2009)

NARSAD Young Investigator (2008-2010)

MDEIE Grant: Programme de Soutien à la Recherche (2008-2011)

EJLB Scholar Research Program (2008-2011)

NSERC Discovery Grant (2007-2012)

Killam Scholar (2007-2012)

Alfred P. Sloan Foundation Research Fellow (2006- 2008)

CIHR Operating Grant (2006-2011)

CFI Infrastructure Grant (2005-2010)

NSF Cognitive Neuroscience Grant (2003-2007)

NIH Postdoctoral Training Grant (2001-2003)

McDonnell-Pew Fellowship in Cognitive Neuroscience (1998-2001)

Tomi Pastinen

Oncohistones: Role of Histone H3 Mutations in the Oncogenesis of Pediatric Cancer. NIH (USA). $3,095,720/yr. 2015-2019 Role: Co-PI (my lab receives $120K USD per year)

Father's lasting influence: Molecular foundations of intergenerational transmission of the paternal environment. CIHR. $298,800/yr. 2014-2018 Role: Co-I ($25K to my lab)

Dietary Gluten-induced Disease Entities -from Genomics to Personalized Health and Well-being. Academy of Finland. $629,280/yr. 2015-Role: Co-I (my lab receives $100K per year)

CEEHRC (Epigenetics): Research Consortium. CIHR and Genome Canada. 2015-2019 $500,000/yr. Role: Principal Applicant (my lab receives $238K per year)

Genomic risk in asthma susceptibility accessed by next-generation integrative tools. CIHR. $205,326/yr. Role: Co-PI (my lab receives $80K per year)

FRSQ Network: Reseau de Medecine Genetique Appliquee RMGA. Role co-PI Pastinen. 2014-2018 $2.7M (my lab receives $30K per year)

Resolving Systems Epigenomes of T-cells in Autoimmune and Inflammatory Diseases. CIHR, FRQS, ANR, BMBF. 2016-2019 $757,736/yr. Role: PI, Consortium Coordinator

Pollution, Epigenetics, and Serologic Markers of Rheumatoid Arthritis. Department of Defense (USA). 2016-2017 $142,500/yr. Role: Co-PI (my lab receives $40K per year)

Brain Imaging, cognition, Dementia and next generation GEnomics: a Transdisciplinary approach to search for risk and protective factors of neurodegenerative disease. JPND and CIHR. $111,000/yr. Role: PI for Canadian program

Genomics Innovation Network Technology Development. Genome Canada. $1,646,988/yr. 2015-2017 Role: Co-PI (my lab receives $400K per year)

Orthogonal genomic tools to pinpoint causal variants for multiple sclerosis as potential therapeutic targets. Merck & Co. Inc. 2015-2017 $97,500/yr. Role: PI

Comprehensive discovery of functional variants in inflammatory bowel disease leveraging genome-wide maps of human immune cell function. Crohn's & Colitis Foundation of Canada (CCFC). $123,820/yr. Role: Co-PI

Genomics Innovation Network. Genome Canada. 2015-2017 $2,000,000/yr. Role: Co-PI (no direct funds to my lab)

Multidimensional Epigenome Mapping Centre McGill. CIHR. 2012-2017 $1,170,000/yr. Role: PI

The ICHANGE (International CHildhood Astrocytomas iNtegrated Genomics and Epigenomics) Consortium. Genome Canada. $1,693,000/yr. 2013-2017 Role: Co-PI (my lab receives $180K per year)

2016 Compute Canada Resource Allocation. 2015-2016 $198,000/yr. Role: PI.

TEKES/Finland: “Individualized diagostics and care: Subcontract for sequencing non-coding variants in graft-vs.-host disease and IBD” 2014-2017. Principal Investigator(s): PASTINEN, Tomi (for subcontract) €80K per year.

Analysis of DNA Methylation Data. CIHR. 2013-2017 My role: Co-investigator (no direct funds to my group)

“ Role of chromatin remodeling in the genesis of pediatric and young adult astrocytomas” CIHR 2013-2018 My role: Co-investigator (no direct funds to my group)

CIHR “Pinpointing Causal Variants for Osteoporosis” 2012 – 2016. **My role:** PI with Dr. B. Richards ($850,000 CDN)

National Institutes of Health (NIH) (USA) R01 (subcontract). “Allele-specific Mapping in Alzheimer's Disease” 2010 – 2015. **My role:** Principal Investigator for subcontract (~$125,000 CDN)

FRSQ “Réseau de Médecine Génétique Appliquée” 2010 – 2014. **My role:** Co-PI ($2,400,000 CDN)

CIHR “CIHR Training Program in Integrative Approaches to Human Health” **My role:** Co-Applicant ($1,766,127 CDN)

Genome Canada “RENEWAL OF SCIENCE AND TECHNOLOGY INNOVATION CENTRE OPERATIONS SUPPORT for McGill University and Génome Québec Innovation Centre” 2013-2015. **My role:** Head of Integrated Genomics (one of five named applicants for the Centre) ($9,610,984CDN)

CIHR “ImmunoSeq: novel immunogenetic discovery tool and its translation to personalized medicine in Finnish and Canadian partnership” 2013-2014. Principal Investigator(s): PASTINEN, Tomi; LATHROP, Mark **My role** PI

Compute Canada “HPC Resource Allocation” 2014-2014. **My Role:** PI

CIHR “Map of cis-regulatory variants in human genome” 2010 – 2014. **My role:** PI ($716,000 CDN)

CIHR “CAN-STAR - CAnadian Network for SysTemic Autoimmune Rheumatic diseases” 2013-2014. **My role** Co-Principal Investigator with Drs. HUDSON, Marie; BARON, Murray; BERNATSKY, Sasha R; COLMEGNA, Ines

CIHR operating grant and Terry Fox team grant. “Investigation of the genomic determinants of childhood leukemia using next-generation sequencing” 2010 – 2013. **My role:** Co-applicant ($2,048,322 CDN; $600,000 CDN for my group)

Genome Quebec “High Throughput Genotyping and Sequencing Using Pooled DNA/RNA” 2010 – 2011. Co-Applicant ($100,000 CDN; $10,000 CDN for my group)

Canadian Institutes of Health Research “Genomewide analysis of functional polymorphisms affecting human bone phenotypes” 2008 – 2011. Principal Investigator ($408,000 CDN)

Genome Quebec “International Collaboration Initiatives in Functional Population Genomics” 2009-2011 Principal Investigator ($304,000 CDN)

Paul Wiseman

2016-2017 CFI Innovation Fund J. Vogel McGill U. + 9 coapplicants +20 collaborators An integrated quantitative biology initiative (IQBI) $12.56 M $684 k

2014-2019 (noncompeting renewal annually) NIH National Institute on Deafness and Other Communication Disorders R01 – DC005788-10 L. Mongeau McGill U. + x others Design, construction, and evaluation of implants for vocal fold alteration and reconstruction $439 k USD (2014) $15 k USD (2014)

2015-? Brain Canada Brain Canada Platform Grant Y. DeKoninck (Laval U. + 9 others) The Canadian Neurophotonics Platform TBD TBD

2015-2021 Canadian Institute for Advanced Research (CIFAR) Global Call for Ideas (4 funded out of 262 LOIs) RJD Miller (Max Planck Institute) + 11 others Molecular Architecture of Life ~1.1M ~45 k

2010- 2016 NSERC CREATE P. DeKoninck (Laval U. + x others) Training Program in Biophotonics $300k $21k

2012-2018 NSERC CREATE R. B. Lennox (McGill U. + 10 others) Training Program in Neuroengineering $300k $21k

2012-2018 NSERC CREATE K. Gehring (McGill U. + 10 others) Training Program in Bionanomachines $300k $21k

2016 FRQS-GEPROM GEPROM research stimulus grants Wiseman (+ 1 other) Understanding the nature of GPCR dimerization using biophysical approaches $15 k $7.5 k

2012-2017 NSERC Discovery Grant Wiseman Image correlation studies of distributions and dynamics of macromolecules in cells $101 k $101 k

2013-2015 CFI Leading Edge Fund K. Gehring (McGill U. + 20 others) Structural Biology at the Crossroads of Biology and Medicine $12.1 M (total) $346k (total)

2011 American Academy of Otolaryngology Training grant for medical scientists Wiseman Ultrafast laser blation of tissue $9976 $9976

2010-2011 CIPI Technology Exploitation & Networking Wiseman Ultrafast laser ablation of tissue $25k $25k

2007-2012 NSERC Discovery Grant Wiseman Image correlation methods for biophysical chemistry tudies of living cells $53.4 k $53.4 k

2009-2014 CFI Innovation Grant D. Thomas (+ 30 others) McGill University Life Sciences Complex: Disease to therapy initiative $26.6 M (total) $200k (total)

2009-2012 FQRNT Team Grant A. Geitmann (U. Montreal) Quantification of secretory vesicle trafficking in plant cells using high temporal resolution confocal imaging and spatio-temporal image $84k $42k correlation spectroscopy

2009-2015 CIHR Strategic Training Grant Y. DeKoninck (Laval U.) (+ 14 others) Neurophysics; Setting new frontiers in Neuroscience with Material Sciences, Photonics and Computational Sciences $375 k $30 k

2006-2010 CIHR New Emerging Team Grant D. Colman (McGill U.) (+8 others) Neuro-engineering $295 k $42.2 k

2005- 2010 CIHR New Emerging Team Grant Y. DeKoninck (Laval U.) (+ 4 others) Nanotools for Neuropharmacology $300 k $50 k

APPENDIX F: LIST OF PUBLICATIONS OF TEACHING FACULTY MEMBERS

Mathieu Blanchette

Busche S., Shao X., Caron M., Kwan T., Allum F., Cheung W.A., Ge B., Westfall S., Simon M.M.; Multiple Tissue Human Expression Resource, Barrett A., Bell J.T., McCarthy M.I., Deloukas P., **Blanchette M.**, Bourque G., Spector T.D., Lathrop M., Pastinen T., Grundberg E. 2015. Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology. 16(290):1-18.

Malina A., Cameron C.J., Robert F., **Blanchette M.**, Dostie J., Pelletier J. 2015. PAM multiplicity marks genomic target sites as inhibitory to CRISPR-Cas9 editing. Nature Communications. 6(10124):1-6.

Cingolani P., Sladek R., **Blanchette M**. 2015. BigDataScript: a scripting language for data pipelines. Bioinformatics. 31(1):10-16.

Hoen D.R., Hickey G., Bourque G., Casacuberta J., Cordaux R., Feschotte C., Fiston-Lavierm A.S., Hua-Van A., Hubley R., Kapusta A., Lerat E., Maumus F., Pollock D.D., Quesneville H., Smit A., Wheeler T.J., Bureau T.E., **Blanchette M**. 2015. A call for benchmarking transposable element annotation methods. Mobile DNA. 6(13):1-9.

Edger P.P., Heidel-Fischer H.M., Bekaert M., Rota J., Glöckner G., Platts A.E., Heckel D.G., Der J.P., Wafula E.K., Tang M., Hofberger J.A., Smithson A., Hall J.C., **Blanchette M**., Bureau T.E., Wright S.I., dePamphilis C.W., Eric Schranz M., Barker M.S., Conant G.C., Wahlberg N., Vogel H., Pires J.C., Wheat C.W. 2015. The butterfly plant arms-race escalated bygene and genome duplications. Proceding of the National Academy of Sciences of United States of America. 112(27):8362-8366.

Fodil N., Langlais D., Moussa P., Boivin G.A., Di Pietrantonio T., Radovanovic I., Dumaine A., **Blanchette M**., Schurr E., Gros P., Vidal SM. 2014. Specific dysregulation of IFNγ production by natural killer cells confers susceptibility to viral infection. PLOS Pathogens. 10(12) e1004511:1-14.

Williamson R.J., Josephs E.B., Platts A.E., Hazzouri K.M., Haudry A., **Blanchette M**., Wright S.I. 2014. Evidence for widespread positive and negative selection in coding and conserved noncoding regions of Capsella grandiflora. PLOS Genetics. 10(9) e1004622:1-12.

Rousseau M., Ferraiuolo M.A., Crutchley J.L., Wang X.Q., Miura H., **Blanchette M**., Dostie J. 2014. Classifying leukemia types with chromatin conformation data. Genome Biology 2014.15(R60):1-12.

Wagner J.R., Busche S., Ge B., Kwan T., Pastinen T., **Blanchette M**. 2014. The relationship between DNA methylation, genetic and expression inter-individual variation in untransformed human fibroblasts. Genome Biology 2014. 15(R37):1-17.

Cloutier P., Lavallée-Adam M., Faubert D., **Blanchette M**., Coulombe B. 2014. Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. Journal of Proteomics. 100:115-124.

Rousseau M., Crutchley J.L., Miura H., Suderman M., **Blanchette M**., Dostie J. 2014. Hox in motion: tracking HoxA conformation during differentiation. Nucleic Acids Research. 42(3):1524-1540.

Caignard G., Leiva-Torres G.A., Leney-Greene M., Charbonneau B., Dumaine A., Fodil-Cornu N., Pyzik M., Cingolani P., Schwartzentruber J., Dupaul-Chicoine J., Guo H., Saleh M., Veillette A., Lathrop M., **Blanchette M**., Majewski J., Pearson A., Vidal S.M. 2013. Genome-Wide Mouse Mutagenesis Reveals CD45-Mediated T Cell Function as Critical in Protective Immunity to HSV-1. PLOS Pathogens. 9(9) e1003637:1-17.

Kwak D., Kam A., Becerra D., Zhou Q., Hops Q., Zarour E., Sarmenta L., **Blanchette M**., Waldispühl J. 2013. Open-Phylo: a customizable crowd-computing platform for multiple sequence alignment. Genome Biology 2013. 14(R116):1-12.

Haudry A., Platts A.E., Vello E., Hoen D., Leclercq M., Williamson R., Forczek E., Joly-Lopez Z., Steffen J., Hazzouri K.M., Dewar K., Stinchcombe J.R., Schoen D.J., Wang X, Schmutz J., Town J.D., Edger P.P., Pires J.C., Schumaker K.S., Jarvis D.E., Mandáková T., Lysak M.A., Schranz M.E., van den Bergh E., Harrison P., Moses A.M., Bureau T.E., Wright S.I., **Blanchette M**. 2013. An Atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics. 45(8): 891-898.

Zhang Y., Ponty Y., **Blanchette M**., Lecuyer E., Waldispuhl J. 2013. SPARCS: a web server to analyze (un)structured regions in coding RNA sequences. Nucleic Acids Research. 41:W480-W485.

Leclercq M., Diallo A.B., **Blanchette M**. 2013. Computational prediction of the localization of microRNAs within their pre-miRNA. Nucleic Acids Research. 41(15):7200-7211.

Forget D., Lacombe A.A., Cloutier P., Lavallée-Adam M., **Blanchette M**., Coulombe B. 2013. Nuclear import of RNA polymerase II is coupled with nucleocytoplasmic shuttling of the RNA polymerase II-associated protein 2. Nucleic Acids Research. 41(14):6881-6891.

Slotte T., Hazzouri K.M., Ågren J.A., Koenig D., Maumus F., Guo Y.L., Steige K., Platts A.E., Escobar J.S., Newman L.K., Wang W., Mandáková T., Vello E., Smith L.M., Henz S.R., Steffen J., Takuno S., Brandvain Y., Coop G., Andolfatto P., Hu T.T., **Blanchette M**., Clark R.M., Quesneville H., Nordborg M., Gaut B.S., Lysak M.A., Jenkins J., Grimwood J., Chapman J., Prochnik S., Shu S., Rokhsar D., Schmutz J., Weigel D., Wright S.I. 2013. The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics. 45(7):831-835.

Meunier C., Van Der Kraak L., Turbide C., Groulx N., Labouba I., Cingolani P., **Blanchette M**., Yeretssian G., Mes-Masson A.M., Saleh M., Beauchemin N., Gros P. 2013. Positional mapping and candidate gene analysis of the mouse Ccs3 locus that regulates differential susceptibility to carcinogen-induced colorectal cancer. PLoS ONE. 8(3) e58733:1-12.

Cloutier P., Lavallée-Adam M., Faubert D., **Blanchette M**., Coulombe B. 2013. A newly uncovered group of distantly related lysine methyltransferases preferentially interact with molecular chaperones to regulate their activity. PLoS Genetics. 9(1) e1003210:1-13.

Lavallée-Adam M., Rousseau J., Domecq C., Bouchard A., Forget D., Faubert D., **Blanchette M**., Coulombe B. 2013. Discovery of Cell Compartment Specific Protein-Protein Interactions using Affinity Purification Combined with Tandem Mass Spectrometry. Journal of Proteome Research. 12(1):272-281.

Blanchette M. 2012. Exploiting ancestral mammalian genomes for the prediction of human transcription factor binding sites. BioMed Central (BMC) Bioinformatics. 13 (Suppl 19):S2:1-13.

Gagnon Y., **Blanchette M**., El-Mabrouk, N. 2012. A Flexible Ancestral Genome Reconstruction Method based on Gapped Adjacencies. BioMed Central (BMC) Bioinformatics. 13 (Suppl 19):S4:1-12.

Bongfen S.E., Rodrigue-Gervais I.G., Berghout J., Cingolani P., Torre S., Sladek R., **Blanchette M**., Behr M., Gruenheid S., Vidal S., Saleh M., Gros P. 2012. An N-Ethyl-N-Nitrosourea (ENU)-induced mutation in JAK3 protects against cerebral malaria but causes susceptibility to mycobacteria. PLoS ONE. 7(2) e31012:1-13.

Kawrykow A., Roumanis G., Kam A., Leung C., Wu C., Zarour E., Phylo players, Sarmenta L., **Blanchette M**., Waldispühl J. 2011. Phylo: A citizen science approach for improving multiple sequence alignment. PLoS One. 7(3) e31362:1-9.

Hickey G., **Blanchette M**., Carmi P. Maheshwari A. Zeh N. 2011. An Approximation Algorithm for the Noah's Ark Problem with Random Feature Loss. IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB). 8(2), 551-556.

Rousseau M., Fraser J., Ferraiuolo M.A., Dostie J. **Blanchette M**. 2011. Three-dimensional modeling of chromatin structure from interaction frequency data using Markov chain Monte Carlo sampling. BioMed Central (BMC) Bioinformatics. 12(414):1-16

Hickey G., **Blanchette M**. 2011. A Probabilistic Model for Sequence Alignment with Context-Sensitive Indels. Journal of Computational Biology. 18(11):1449-1464.

Mongin E., Dewar K., **Blanchette M**. 2011. Mapping association between long-range cis-regulatory regions and their target genes using synteny. Journal of Computational Biology. 18(9):1115-30

Mongin E., Auer T.O., Bourrat F., Gruh l.F., Dewar K., **Blanchette M**., Wittbrodt J., Ettwiller L. 2011. Combining computational prediction of cis-regulatory elements with a new enhancer assay to efficiently label neuronal structures in the medaka fish. PLoS One. 6(5) e19747:1-10.

Sadri J., Diallo A.B., **Blanchette M**. 2011. Predicting site-specific human selective pressure using evolutionary signatures. Bioinformatics (Proceedings of ISMB 2011). 27(13):i266-i274.

Lavallée-Adam, M., Cloutier, P., Coulombe, B., and **Blanchette, M**. 2011. Modeling contaminants in AP-MS/MS experiments. Journal of Proteome Research, 10(2):886-95.

Guillaume Bourque

Audet-Walsh É., Papadopoli D.J., Gravel S.P., Yee T., Bridon G., Caron M., **Bourque G.**, Giguère V., St-Pierre J. 2016. The PGC-1α/ERRα Axis Represses One-Carbon Metabolism and Promotes Sensitivity to Anti-folate Therapy in Breast Cancer. Cell Reports. 14(4):920-31.

Ramsay L., **Bourque G.** 2016. In Silico Methods to Identify Exapted Transposable Element Families. Methods in Molecular Biology. 1400:33-45.

Hocking T.D., Rigaill G., **Bourque G.** 2015. PeakSeg: constrained optimal segmentation and supervised penalty learning for peak detection in count data. Proceedings of the 32nd International Conference on Machine Learning. ICML-15 324-332.

Hocking T.D., **Bourque G.** 2015. PeakSegJoint: fast supervised peak detection via joint segmentation of multiple count data samples. arXiv:1506.01286.

Busche S., Shao X., Caron M., Kwan T., Allum F., Cheung W.A., Ge B., Westfall S., Simon M.M.; Multiple Tissue Human Expression Resource, Barrett A., Bell J.T., McCarthy M.I., Deloukas P., Blanchette M., **Bourque G.**, Spector T.D., Lathrop M., Pastinen T., Grundberg E. 2015. Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology. 16(290):1-18.

Aarabi M., San Gabriel M.C., Chan D., Behan N.A., Caron M., Pastinen T., **Bourque G.**, MacFarlane A.J., Zini A., Trasler J. 2015. High dose folic acid supplementation alters the human sperm methylome and is influenced by the MTHFR C677T polymorphism. Human Molecular Genetics. 24(22):6301-13.

Nicolas G., Charbonnier C., Wallon D., Quenez O., Bellenguez C., Grenier-Boley B., Rousseau S., Richard A.C., Rovelet-Lecrux A., Le Guennec K., Bacq D., Garnier J.G., Olaso R., Boland A., Meyer V., Deleuze J.F., Amouyel P., Munter H.M., **Bourque G.**, Lathrop M., Frebourg T., Redon R., Letenneur L., Dartigues J.F., Génin E., Lambert J.C., Hannequin D., Campion D.; CNR-MAJ collaborators. 2015. SORL1 rare variants: a major risk factor for familial early-onset Alzheimer's disease. Molecular Psychiatry. 21(6):831-6.

Hoen D.R., Hickey G., **Bourque G.**, Casacuberta J., Cordaux R., Feschotte C., Fiston-Lavier A.S., Hua-Van A., Hubley R., Kapusta A., Lerat E., Maumus F., Pollock D.D., Quesneville H., Smit A., Wheeler T.J., Bureau T.E., Blanchette M. 2015. A call for benchmarking transposable element annotation methods. Mobile DNA. Aug 4;6:13.

Nicolas G., Wallon D., Charbonnier C., Quenez O., Rousseau S., Richard A.C., Rovelet-Lecrux A., Coutant S., Le Guennec K., Bacq D., Garnier J.G., Olaso R., Boland A., Meyer V., Deleuze J.F., Munter H.M., **Bourque G.**, Auld D., Montpetit A., Lathrop M., Guyant-Maréchal L., Martinaud O., Pariente J., Rollin-Sillaire A., Pasquier F., Le Ber I., Sarazin M., Croisile B., Boutoleau-Bretonnière C., Thomas-Antérion C., Paquet C., Sauvée M., Moreaud O., Gabelle A., Sellal F., Ceccaldi M., Chamard L., Blanc F., Frebourg T., Campion D., Hannequin D. 2015. Screening of dementia genes by whole-exome sequencing in early-onset Alzheimer disease: input and lessons. European Journal of Human Genetics. 24(5):710-6.

Sayadi A., Jeyakani J., Seet S.H., Wei C.L., **Bourque G.**, Bard F.A., Jenkins N.A., Copeland N.G., Bard-Chapeau E.A. 2015. Functional features of EVI1 and EVI1Δ324 isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. Oncogene. 35(18):2311-21.

Dyke S.O., Cheung W.A., Joly Y., Ammerpohl O., Lutsik P., Rothstein M.A., Caron M., Busche S., **Bourque G.**, Rönnblom L., Flicek P., Beck S., Hirst M., Stunnenberg H., Siebert R., Walter J., Pastinen T. 2015. Epigenome data release: a participant-centered approach to privacy protection. Genome Biology. 16:142.

Tang Q.L., Julien C., Eveleigh R., **Bourque G.**, Franco A., Labelle H., Grimard G., Parent S., Ouellet J., Mac-Thiong J.M., Gorman K.F., Moreau A. 2015. A Replication Study for Association of 53 Single Nucleotide Polymorphisms in ScoliScoreTM Test with Adolescent Idiopathic Scoliosis in French-Canadian Population. Spine. 40(8):537-43.

McGraw S., Zhang J.X., Farag M., Chan D., Caron M., Konermann C., Oakes C.C., Mohan K.N., Plass C., Pastinen T., **Bourque G.**, Chaillet J.R., Trasle r J.M. 2015. Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research. 43(3):1485-97.

Scelo G., Riazalhosseini Y., Greger L., Letourneau L., Gonzàles Porta M., Wozniak M.B., Rung J., Bourgey M., Harnden P., Egevad L., Jackson S.M., Karimzadeh M., Arseneault M., Lepage P., How-Kit A., Daunay A., Renault V., Blanché H., Viksna J., Celms E., Opmanis M., Zarins A., Vasudev N.S., Seywright M., Abedi-Ardekani B., Carreira C., Selby P.J., Cartledge J.J., Byrnes G., Zavadil J., Su J., Holcatova I., Brisuda A., Zaridze D., Moukeria A., Foretova L., Navratilova M., Mates D., Jinga V., Heath S., Gut M., Bihoreau M.-T., Lechner D., Foglio M., Gut I.G., Skryabin K., Prokhortchouk E., Cambon-Thomsen A., **Bourque G.**, Brennan P., Tost J., Banks R.E., Brazma A., Lathrop G.M. 2014. Variation in the genomic landscape of clear cell renal cell carcinoma in Europe. Nature Communications. 5:5135.

Hocking T.D., Goerner-Potvin P., Morin A., Shao X., **Bourque G.** 2015. Visual annotations and a supervised learning approach for evaluating and calibrating ChIP-seq peak detectors. arXiv:1409.6209.

Chen E.S., Gigek C.O., Rosenfeld J.A., Diallo A.B., Maussion G., Chen G.G., Vaillancourt K., Lopez J.P., Crapper L., Poujol R., Shaffer L.G., **Bourque G.**, Ernst C. 2014. Molecular convergence of neurodevelopmental disorders. American Journal of Human Genetics. 95(5):490-508.

Caignard G., Eva M.M., van Bruggen R., Eveleigh R., **Bourque G.**, Malo D., Gros P., Vidal S.M. 2014. Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples and Perspectives. Genes. 5(4):887-925.

Lu X., Sachs F., Ramsay L., Jacques P.E., Göke J., **Bourque G.**, Ng H.H. 2014. The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. Nature Structural & Molecular Biology. 21(4):423-5.

Salem S., Langlais D., Lefebvre F., **Bourque G.**, Bigley V., Haniffa M., Casanova J.L., Burk D., Berghuis A., Butler K.M., Leahy T.R., Hambleton S., Gros P. 2014. Functional characterization of the human dendritic cell immunodeficiency associated with the IRF8K108E mutation. Blood. 124(12):1894-904.

Buczkowicz P., Hoeman C., Rakopoulos P., Pajovic S., Letourneau L., Dzamba M., Morrison A., Lewis P., Bouffet E., Bartels U., Zuccaro J., Agnihotri S., Ryall S., Barszczyk M., Chornenkyy Y., Bourgey M., **Bourque G.,** Montpetit A., Cordero F., Castelo-Branco P., Mangerel J., Tabori U., Ho K.C., Huang A., Taylor K.R., Mackay A., Bendel A.E., Nazarian J., Fangusaro J.R., Karajannis M.A., Zagzag D., Foreman N.K., Donson A., Hegert J.V., Smith A., Chan J., Lafay-Cousin L., Dunn S., Hukin J., Dunham C., Scheinemann K., Michaud J., Zelcer S., Ramsay D., Cain J., Brennan C., Souweidane M.M., Jones C., Allis C.D., Brudno M., Becher O., Hawkins C. 2014. Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. Nature Genetics. 46(5):451-6.

Magnus N., Garnier D., Meehan B., McGraw S., Lee T.H., Caron M., **Bourque G.**, Milsom C., Jabado N., Trasler J., Pawlinski R., Mackman N., Rak J. 2014. Tissue factor expression provokes escape from tumor dormancy and leads to genomic alterations. Proceedings of the National Academy of Sciences of the United States of America. 111(9):3544-9.

Jacques P.E., Jeyakani J., **Bourque G.** 2013. The majority of primate-specific regulatory sequences are derived from transposable elements. PLoS Genetics. 9(5):e1003504.

Kapusta A., Kronenberg Z., Lynch V.J., Zhuo X., Ramsay L., **Bourque G.**, Yandell M., Feschotte C. 2013. Transposable elements are major contributors to the origin, diversification, and regulation of vertebrate long noncoding RNAs. PLoS Genetics. 9(4):e1003470.

Lu X., Göke J., Sachs F., Jacques P.E., Liang H., Feng B., **Bourque G.**, Bubulya P.A., Ng H.H. 2013. SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. Nature Cell Biology. 15(10):1141-1152.0

Chaveroux C., Eichner L.J., Dufour C.R., Shatnawi A., Khoutorsky A., **Bourque G.**, Sonenberg N., Giguère V. 2013. Molecular and genetic crosstalks between mTOR and ERRα are key determinants of rapamycin-induced nonalcoholic fatty liver. Cell Metabolism. 17(4):586-98.

Nagarajan N., Bertrand D., Hillmer A.X., Zang Z.J., Yao F., Jacques P.E., Teo A.S.M., Cutcutache I., Zhang Z., Lee W.H., Sia Y.Y., Gao S., Ariyaratne P.N., Ho A., Woo X.Y., Veeravali L., Ong C.K., Deng N., Desai K.V., Khor C.C., Hibberd M.L., Shahab A., Rao J., Wu M., The M., Zhu F., Chin S.Y., Pang B., So J.B.Y., **Bourque G.**, Soong R., Sung W.K., Teh B.T., Rozen S., Ruan X., Yeoh K.G., Tan P.B.O., Ruan Y. 2012. Whole-genome reconstruction of host and pathogen sequences and mutational signatures in gastric cancer. Genome Biology. 13(12):R115.

Khuong-Quang D.A., Buczkowicz P., Rakopoulos P., Liu X.Y., Fontebasso A.M., Bouffet E., Bartels U., Albrecht S., Schwartzentruber J., Letourneau L., Bourgey M., **Bourque G**., Montpetit A., Bourret G., Lepage P., Fleming A., Lichter P., Kool M., von Deimling A., Sturm D., Korshunov A., Faury D., Jones D.T., Majewski J., Pfister S.M., Jabado N., Hawkins C. 2012. K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. Acta Neuropathologica. 124(3):439-47.

Pott S., Kamrani N.K., **Bourque G.**, Pettersson S., Liu E.T. 2012. PPARG Binding Landscapes in Macrophages Suggest a Genome-Wide Contribution of PU.1 to Divergent PPARG Binding in Human and Mouse. PLoS One. 7(10):e48102.

Bard-Chapeau E.A., Jeyakani J., Kok C.H., Muller J., Chua B.Q., Gunaratne J., Batagov A., Jenjaroenpun P., Kuznetsov V.A., Wei C.L., D'Andrea R.J., **Bourque G.**, Jenkins N.A., Copeland N.G. 2012. Ecotopic viral integration site 1 (EVI1) regulates multiple cellular processes important for cancer and is a synergistic partner for FOS protein in invasive tumors. Proceedings of the National Academy of Sciences of the United States of America. 109(6):2168-73.

Yao F., Ariyaratne P.N., Hillmer A.M., Lee W.H., Li G., Teo A.S., Woo X.Y., Zhang Z., Chen J.P., Poh W.T., Zawack K.F., Chan C.S., Leong S.T., Neo S.C., Choi P.S., Gao S., Nagarajan N., Thoreau H., Shahab A., Ruan X., Cacheux-Rataboul V., Wei C.L., **Bourque G.**, Sung W.K., Liu E.T., Ruan Y. 2012. Long span DNA paired-end-tag (DNA-PET) sequencing strategy for the interrogation of genomic structural mutations and fusion-point-guided reconstruction of amplicons. PLoS One. 7(9):e46152.

Handoko L., Xu H., Li G., Ngan C.Y., Chew E., Schnapp M., Lee C.W., Ye C., Ping J.L., Mulawadi F., Wong E., Sheng J., Zhang Y., Poh T., Chan C.S., Kunarso G., Shahab A., **Bourque G.**, Cacheux-Rataboul V., Sung W.K., Ruan Y., Wei C.L. 2011. CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics. 43(7):630-8.

Zemojtel T., Kielbasa S.M., Arndt P.F., Behrens S., **Bourque G.**, Vingron M. 2011. CpG deamination creates transcription factor binding sites with high efficiency. Genome Biology and Evolution. 3:1304-11.

Chatterjee S., **Bourque G.**, Lufkin T. 2011. Conserved and Non-Conserved Enhancers Direct Tissue Specific Transcription in Ancient Germ Layer Specific Developmental Control Genes. BMC Developmental Biology. 11(1):63.

Hillmer A.M., Yao F., Inaki K., Lee W.H., Ariyaratne P.N., Teo A.S., Woo X.Y., Zhang Z., Zhao H., Ukil L., Chen J.P., Zhu F., So J.B., Salto-Tellez M., Poh W.T., Zawack K.F., Nagarajan N., Gao S., Li G., Kumar V., Lim H.P., Sia Y.Y., Chan

C.S., Leong S.T., Neo S.C., Choi P.S., Thoreau H., Tan P.B., Shahab A., Ruan X., Bergh J., Hall P., Cacheux-Rataboul V., Wei C.L., Yeoh K.G., Sung W.K., **Bourque G.**, Liu E.T., Ruan Y. 2011. Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research. 21(5):665-75.

Inaki K., Hillmer A.M., Ukil L., Yao F., Woo X.Y., Vardy L.A., Zawack K.F., Lee C.W., Ariyaratne P.N., Chan Y.S., Desai K.V., Bergh J., Hall P., Putti T.C., Ong W.L., Shahab A., Cacheux-Rataboul V., Karuturi R.K., Sung W.K., Ruan X., **Bourque G.**, Ruan Y., Liu E.T. 2011. Transcriptional consequences of genomic structural aberrations in breast cancer. Genome Research. 21(5):676-87.

Aanes H., Winata C.L., Lin C.H., Chen J.P., Srinivasan K.G., Lee S.G., Lim A.Y., Hajan H.S., Collas P., **Bourque G.**, Gong Z., Korzh V., Alestrom P., Mathavan S. 2011. Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. Genome Research. 21(8):1328-38.

Lam S.H., Lee S.G., Lin C.Y., Thomsen J.S., Fu P.Y., Murthy K.R., Li H., Govindarajan K.R., Nick L.C., **Bourque G.**, Gong Z., Lufkin T., Liu E.T., Mathavan S. 2011. Molecular conservation of estrogen-response associated with cell cycle regulation, hormonal carcinogenesis and cancer in zebrafish and human cancer cell lines. BMC Medical Genomics. 4:41.

Cheong C.Y., Lon Ng P.M., Ponnampalam R., Tsai H.H., **Bourque G.**, Lufkin T. 2011. In silico tandem affinity purification refines an Oct4 interaction list. Stem Cell Research & Therapy. 2(3):26.

Erik Cook

Smith J.E., Beliveau V., Schoen A., Remz J., Zhan C.A., **Cook E.P.** 2015. Dynamics of the functional link between area MT LFPs and motion detection. Journal of neurophysiology. 114(1): 80-98.

Farah K., Smith J.E.T., **Cook E.P.** 2014. ROC-Based Estimates of Neural-Behavioral Covariations Using Matched Filters. Neural Computation. 26(8): 1667-89.

Schoen A., Salehiomran A., Larkum ME., **Cook E.P.** 2012. A compartmental model of linear resonance and signal transfer in dendrites. Neural computation. 24(12):3126-44.

Cook E.P., Pack C.C. 2012. Parietal cortex signals come unstuck in time. PLoS biology. 10(10):e1001414.

Hacking S.A., Boyraz P., Powers B.M., Sen-Gupta E., Kucharski W., Brown C.A., **Cook E.P.** 2012. Surface roughness enhances the osseointegration of titanium headposts in non-human primates. Journal of neuroscience methods. 211(2):237-44.

Masse N.Y., Herrington T.M., **Cook E.P.** 2012. Spatial attention enhances the selective integration of activity from area MT. Journal of neurophysiology. 108(6):1594-606.

Smith J.E., Masse N.Y., Zhan C.A., **Cook E.P.** 2012. Linking neural activity to visual perception: separating sensory and attentional contributions. Visual Cortex.

Sadeghi N.G., Pariyadath V., Apte S., Eagleman D.M., **Cook E.P.** 2011. Neural correlates of subsecond time distortion in the middle temporal area of visual cortex. Journal of cognitive neuroscience. 23(12):3829-40.

Smith J.E., Zhan C.A., **Cook E.P.** 2011. The functional link between area MT neural fluctuations and detection of a brief motion stimulus. The Journal of neuroscience: the official journal of the Society for Neuroscience. 31(38):13458-68.

Masse N.Y., **Cook E.P.** 2010. Behavioral time course of microstimulation in cortical area MT. Journal of neurophysiology. 103(1):334-45.

Ken Dewar

Xiong J., Déraspe M., Iqbal N., Ma J., Jamieson F.B., Wasserscheid J., **Dewar K.**, Hawkey P.M., Roy P.H. 2016. Genome and Plasmid Analysis of blaIMP-4 -Carrying Citrobacter freundii B38. Antimicrobial Agents and Chemotherapy. pii: AAC.00588-16.

Teatero S., Lemire P., **Dewar K.**, Wasserscheid J., Calzas C., Mallo G.V., Li A., Athey T.B., Segura M., Fittipaldi N. 2016. Genomic Recombination Leading to Decreased Virulence of Group B Streptococcus in a Mouse Model of Adult Invasive Disease. Pathogens. 5(3): E54.

Vincent C., Miller M.A., Edens T.J., Mehrotra S., **Dewar K.**, Manges A.R. 2016. Bloom and bust: intestinal microbiota dynamics in response to hospital exposures and Clostridium difficile colonization or infection. Microbiome. 4:12

Athey T.B., Teatero S., Takamatsu D., Wasserscheid J., **Dewar K.**, Gottschalk M., Fittipaldi N. 2016. Population Structure and Antimicrobial Resistance Profiles of Streprococcus suis Serotype 2 Sequence Type 25 Strains. PLoS One. 11(3):e0150908.

Rao C., Guyard C., Pelaz C., Wasserscheid J., Bondy-Denomy J., **Dewar K.**, Ensminger A.W. 2016. Active and adaptive Legionella CRISPR-Cas reveals a recurrent challenge to the pathogen. Cellular Microbiology. 18(10):1319-38.

Vincent C., Mehrotra S., Loo V.G., **Dewar K.**, Manges A.R. 2015. Excretion of Host DNA in Feces Is Associated with Risk of Clostridium difficile Infection. Journal of Immunology Research. doi: 10.1155/2015/246203.

Labrie S.J., Tremblay D.M., Plante P.L., Wasserscheid J., **Dewar K.**, Corbeil J., Moineau S. 2015. Complete Genome Sequence of Streptococcus thermophilus SMQ-301, a Model Strain for Phage-Host Interactions. Genome Announcements. 3(3): e00480

Wang J., McIntosh F., Radomski N., **Dewar K.**, Simeone R., Enninga J., Brosch R., Rocha E.P., Veyrier F.J., Behr M.A. 2015. Insights on the emergence of Mycobacterium tuberculosis from the analysis of Mycobacterium kansasii. Genome Biology and Evolution. 7(3):856-70.

Labrie S.J., El Haddad L., Tremblay D.M., Plante P.L., Wasserscheid J., Dumaresq J., **Dewar K.**, Corbeil J., Moineau S. 2014. First Complete Genome Sequence of Staphylococcus xylosus, a Meat Starter Culture and a Host to Propagate Staphylococcus aureus Phages. Genome Announcements. 2(4): e00671-14.

Vincent C., Stephens D.A., Loo V.G., Edens J. V., Behr M.A., **Dewar K.**, Manges A.R. 2013. Reductions in intestinal Clostridiales precede the development of nosocomial Clostridium difficile infection. Microbiome. 1(1):18.

Forgetta V., Leveque G., Dias J., Grove D., Lyons R. Jr, Genik S., Wright C., Singh S., Peterson N., Zianni M., Kieleczawa J., Steen R., Perera A., Bintzler D., Adams S., Hintz W., Jacobi V., Bernier L., Levesque R., **Dewar K**. 2013. Sequencing of the Dutch elm disease fungus genome using the Roche/454 GS-FLX Titanium System in a comparison of multiple genomics core facilities. Journal of Biomolecular Techniques. 24(1):39-49.

Welch R.L., Sladek R., **Dewar K.**, Reisner W.W. 2012. Denaturation mapping of Saccharomyces cerevisiae. Lab Chip. 12(18):3314-21.

Forgetta V., Oughton M.T., Marquis P., Brukner I., Blanchette R., Haub K., Magrini V., Mardis E.R., Gerding D.N., Loo V.G., Miller M.A., Mulvey M.R., Rupnik M., Dascal A., **Dewar K**. 2011. Fourteen-genome comparison identifies DNA markers for severe-disease-associated strains of Clostridium difficile. Journal of Clinical Microbiology. 49(6):2230-8.

Zhang R., Martinez D.R., Nguyen Q.N., Pollara J., Arifin T., Stolarchuk C., Foulger A., Amos J.D., Parks R., Himes J.E., Wang M., Edwards R.W., Trama A.M., Vandergrift N., Colvin L., **Dewar K.**, Juretic N., Wasserscheid J., Ferrari G., Liao H.X., Permar S.R. 2016. Envelope-specific B-cell populations in African green monkeys chronically infected with simian immunodeficiency virus. Nature Communications. 7:12131.

Warren W.C., Jasinska A.J., García-Pérez R., Svardal H., Tomlinson C., Rocchi M., Archidiacono N., Capozzi O., Minx P., Montague M.J., Kyung K., Hillier L.W., Kremitzki M., Graves T., Chiang C., Hughes J., Tran N., Huang Y., Ramensky V., Choi O.W., Jung Y.J., Schmitt C.A., Juretic N., Wasserscheid J., Turner T.R., Wiseman R.W., Tuscher J.J., Karl J.A., Schmitz J.E., Zahn R., O'Connor D.H., Redmond E., Nisbett A., Jacquelin B., Müller-Trutwin M.C., Brenchley J.M., Dione M., Antonio M., Schroth G.P., Kaplan J.R., Jorgensen M.J., Thomas G.W., Hahn M.W., Raney B.J., Aken B., Nag R., Schmitz J., Churakov G., Noll A., Stanyon R., Webb D., Thibaud-Nissen F., Nordborg M., Marques-Bonet T., **Dewar K.**, Weinstock G.M., Wilson R.K., Freimer N.B. 2015. The genome of the vervet (Chlorocebus aethiops sabaeus). Genome. 25(12):1921-33.

Haudry A1., Platts A.E., Vello E., Hoen D.R., Leclercq M., Williamson R.J., Forczek E., Joly-Lopez Z., Steffen J.G., Hazzouri K.M., **Dewar K.**, Stinchcombe J.R., Schoen D.J., Wang X., Schmutz J., Town C.D., Edger P.P., Pires J.C., Schumaker K.S., Jarvis D.E., Mandáková T., Lysak M.A., van den Bergh E., Schranz M.E., Harrison P.M., Moses A.M., Bureau T.E., Wright S.I., Blanchette M. 2013. An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics. 45(8):891-8.

Levesque S., Morin C., Guay S-P., Villeneuve J., Marquis P., Yik W.Y., Jiralerspong S., Bouchard L., Steinberg S., Hacia J.G., **Dewar K.**, Braverman N.E. 2012. A founder mutation in the PEX6 gene is responsible for increased incidence of Zellweger syndrome in a French Canadian population. BMC Medical Genetics. 13:72.

Santa-Maria I1., Haggiagi A., Liu X., Wasserscheid J., Nelson P.T., **Dewar K.**, Clark L.N., Crary J.F. 2012. The MAPT H1 haplotype is associated with tangle-predominant dementia. Acta Neuropathologica. 124(5):693-704.

Raincrow J.D.1, **Dewar K.**, Stocsits C., Prohaska S.J., Amemiya C.T., Stadler P.F., Chiu C.H. 2011. Hox clusters of the bichir (Actinopterygii, Polypterus senegalus) highlight unique patterns of sequence evolution in gnathostome phylogeny. Journal of Experimental Zoology Part B Molecular and Developmental Evolution. 316(6):451-64.

Paul François

Rothschild J., Tsimiklis P., Siggia E.D., **François P.** 2016. Predicting Ancestral Segmentation Phenotypes from *Drosophila* to *Anopheles* Using In Silico Evolution. PLoS Genetics**.** 12(5):e1006052.

François P., Altan-Bonnet G. 2016. The case for absolute ligand discrimination modeling information processing and decision by immune T cells. Journal of Statistical Physics. 62 (5):1130-1152.

Tufcea D., François P. 2015. Critical timing without timer for embryonic development. Biophysical Journal. 109(8):1724-34.

Shih N., **François P.**, Delaune E., Amacher S. 2015. In vivo Zebrafish Segmentation Clock Dynamics Reveal a Two-Segment Periodicity in the Anterior Presomitic Mesoderm. Development. 142(10):1785-93.

Lalanne J.B., François P. 2015. Chemodetection in fluctuating environments: receptor coupling, buffering and antagonism. Proceedings of the National Academy of Sciences of the United States of America. 112(6):1898-903.

François P. 2014. Evolving phenotypic networks in silico. Seminars in Cell & Developmental Biology. 2014 35:90-7

Nazarova E., O'Toole E., Chen D., Kaitna S., Yen E., Jones M., Keck J., **François P.**, Winey M., Vogel J. 2013. Distinct roles for antiparallel microtubule pairing and overlap during early spindle assembly. Molecular Biology of the Cell**.** 24(20):3238-50.

Lalanne J.B., **François P.** 2013. Principles of adaptive sorting revealed by evolution in silico. Physical Review Letters. 110(21):218102.

François P., Voisinne G., Siggia E.D., Altan-Bonnet G., Vergassola M. 2013. A phenotypic model for early T-cell activation displaying sensitivity, specificity and antagonism. Proceedings of the National Academy of Sciences of the United States of America. 110(10):E888-97

Lauschke V.M., Tsiairis C.D., **François P.**, Aulehla A. 2013. Scaling of embryonic patterning based on phase-gradient encoding. Nature. 493(7430):101-5.

François P., Siggia E.D. 2012. Phenotypic Models of Evolution and Development: Geometry as Destiny. Current Opinion in Genetics & Development. 22(6):627-33.

Delaune E., **François P.**, Shih N.P., Amacher S.L. 2012. Visualizing segmentation clock dynamics with single cell resolution. Developmental Cell**.** 23(5):995-1005.

Warmflash A., **François P.**, Siggia E.D. 2012. Pareto Evolution of Gene Networks. Physical Biology. 9(5):056001.

François P., Despierre N., Siggia E.D. 2012. Adaptive Temperature Compensation in Circadian Oscillations. PLoS Computational Biology. 8(7):e1002585.

François P. 2012. Evolution in silico: from network structure to bifurcation theory. Advances in Experimental Medecine and Biology. 751:157-82.

François P. 2013. Adaptation d'échelle et gradient de phase dans un modèle ex vivo de somitogenèse. Médecine Sciences (Paris). 29(8-9):696-8.

Delaune E., **François P.**, Shih N.P., Amacher S.L. 2013. Une avancée technique pour comprendre la dynamique de l'horloge de segmentation. Médecine Sciences (Paris). 29(4):355-8.

Benazeraf B., **François P.**, Baker R., Denans N., Little C., Pourquié O. 2011. A non directional cell migration gradient in the presomitic mesoderm contributes to axis elongation in chicken embryos. Biologie Aujourdhui. 205(2):95-103.

Simon Gravel

Gravel S., Steel M. 2015. The existence and abundance of ghost ancestors in bi-parental populations. Theoretical population biology. 101: 47-53.

1000 Genomes Consortium (843 Collaborators). 2015. A global reference for human genetic variation. Nature 526 (7571):68 -74.

Homburger J.R., Moreno-Estrada A., Gignoux C.R., Nelson D., Sanchez E., Ortiz-Tello P., Pons-Estel B.A., Acevedo-Vasquez E., Miranda P., Langefeld C.D., **Gravel S.**, Alarcón-Riquelme M.E., Bustamante C.D. 2015. Genomic Insights into the Ancestry and Demographic History of South America. PLoS Genetcs. 11(12):e1005602.

Coffman A.J., Hsieh P.H., **Gravel S.**, Gutenkunst R.N. 2015. Computationally efficient composite likelihood statistics for demographic inference. Molecular Biology and Evolution. 33(2):591-3.

Perry G.H., Foll M., Grenier J.C., Patin E., Nédélec Y., Pacis A., Barakatt M., **Gravel S.**, Zhou X., Nsobya S.L., Excoffier L., Quintana-Murci L., Dominy N.J., Barreiro L.B. 2014. Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America. 111(35):E3596-603.

Gravel S. 2014. Predicting Discovery Rates of Genomic Features. Genetics. 197(2):601-10.

Patin E., Siddle K.J., Laval G., Quach H., Harmant C., Becker N., Froment A., Régnault B., Lemée L., **Gravel S.**, Hombert J.M., Van der Veen L., Dominy N.J., Perry G.H., Barreiro L.B., Verdu P., Heyer E., Quintana-Murci L. 2014. The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. Nature Communications. 5: 3163.

Gravel S., Zakharia F., Moreno-Estrada A., Byrnes J.K., Muzzio M., Rodriguez-Flores J.L., Kenny E.E., Gignoux C.R., Maples B.K., Guiblet W., Dutil J., Via M., Sandoval K., Bedoya G., The 1000 Genomes Project, Oleksyk T.K., Ruiz-Linares A., Burchard E.G., Martinez-Cruzado J.C., Bustamante C.D. 2013. Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics. 9(12): e1004023.

Moreno-Estrada A., **Gravel S.**, Zakharia F., McCauley J.L., Byrnes J.K., Gignoux C.R., Ortiz-Tello P.A., Martínez R.J., Hedges D.J., Morris R.W., Eng C., Sandoval K., Acevedo-Acevedo S., Norman P.J., Layrisse Z., Parham P., Martínez-Cruzado J.C., Burchard E.G., Cuccaro M.L., Martin E.R., Bustamante C.D. 2013. Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics. 9(11): e1003925.

Carpenter M.L., Buenrostro J.D., Valdiosera C., Schroeder H., Allentoft M.E., Sikora M., Rasmussen M., **Gravel S.**, Guillén S., Nekhrizov G., Leshtakov K., Dimitrova D., Theodossiev N., Pettener D., Luiselli D., Sandoval K., Moreno-Estrada A., Li Y., Wang J., Gilbert M.T., Willerslev E., Greenleaf W.J., Bustamante C.D. 2013. Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. American journal of human genetics. 93(5):852-64.

Botigué L.R., Henn B.M. **Gravel S.**, Maples B.K., Gignoux C.R., Corona E., Atzmon G., Burns E., Ostrer H., Flores C., Bertranpetit J., Comas D., Bustamante C.D. 2013. Gene flow from North Africa contributes to differential genetic diversity in Southern Europe. Proceedings of the National Academy of Sciences of the United States of America. 110(29):11791-6.

Maples B.K., **Gravel S.**, Kenny E.E., Bustamante C.D. 2013. RFMix: a discriminative modeling approach for rapid and robust local ancestry inference. American Journal of Human Genetics. 93(2):278.

Gravel S. 2012. Population genetics models of local ancestry. Genetics. 191(2):607.

Celia M T Greenwood

Assouline S.E., Nielsen T.H., Yu S., Alcaide M., Chong L., MacDonald D., Tosikyan A., Kukreti V., Kezouh A., Petrogiannis-Haliotis T., Albuquerque M., Fornika D., Alamouti S., Froment R., Greenwood C.M., Oros K.K., Camglioglu E., Sharma A., Christodoulopoulos R., Rousseau C., Johnson N., Crump M., Morin R.D., Mann K.K. 2016. Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. Blood. 128(2):185-94.

McGregor K., Bernatsky S., Colmegna I., Hudson M., Pastinen T., Labbe A, **Greenwood C.** 2016. An evaluation of methods correcting for cell-type heterogeneity in DNA methylation studies. Genome Biology. 17:84.

Lakhal-Chaieb L., Oualkacha K., Richards J.B., **Greenwood C.** 2016. A rare variant association test in family-based designs and non-normal quantitative traits. Statistics in Medicine. 35(6):905-21

Oualkacha K., Lakhal-Chaieb L., **Greenwood C**. 2016. Software Application Profile: RVPedigree: A suite of family-based rare-variant association tests for normally- and non-normally-distributed quantitative traits. International Journal of Epidemiology. 45(2):402-7.

Rivera B., Gayden T., Carrot-Zhang J., Nadaf J., Boshari T., Faury D., Zeinieh M., Blanc R., Burk D.L., Fahiminiya S., Bareke E., Schüller U., Monoranu C.M., Sträter R., Kerl K., Niederstadt T., Kurlemann G., Ellezam B., Michalak Z., Thom M., Lockhart P.J., Leventer R.J., Ohm M., MacGregor D., Jones D., Karamchandani J., **Greenwood C.**, Berghuis A.M., Bens S., Siebert R., Zakrzewska M., Liberski P.P., Zakrzewski K., Sisodiya S.M., Paulus W., Albrecht S., Hasselblatt M., Jabado N., Foulkes W.D., Majewski J. 2016. Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. Acta Neuropathologica. 131(6):847-63.

Sun J., Oualkacha K., Forgetta V., Zheng H.-F., Richards J.B., Ciampi A., **Greenwood C.**, UK10K Consortium. 2016. A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. European Journal of Human Genetics. doi: 10.1038/ejhg.2016.8.

Castellsagué E., Liu J., Volenik A., Giroux S., Gagné R., Maranda B., Roussel-Jobin A., Latreille J., Laframboise R., Palma L., Kasprzak L., Marcus V.A., Breguet M., Nolet S., El-Haffaf Z., Australie K., Gologan A., Aleynikova O., Oros-

Klein K., **Greenwood C.**, Mes-Masson A.M., Provencher D., Tischkowitz M., Chong G., Rousseau F., Foulkes W.D. 2015. Characterization of a novel founder MSH6 mutation causing Lynch syndrome in the French Canadian population. Clinical Genetics. 87(6):536-42.

Arseneault M., Camlioglu E., Constantin A., Qiang-Hammarstrom P., Peng Q.R., Mann K.K., Johnson N. 2015. Genetic landscapes of relapsed or refractory diffuse large B cell lymphomas. Clinical Cancer Research. 22(9):2290-300.

Morin R.D., Assouline S.E., Alcaide M., Mohajeri A., Johnston R.L., Chong L., Grewal J., Yu S., Fornika D., Bushell K., Nielsen T.H., Haliotis T., Crump M., Tosikyan A., Grande B., Macdonald D., Rousseau C., Bayat M., Sesques P., Froment R., Albuquerque M., Monczak Y.I., Oros K.K., **Greenwood C.**, Riazalhosseini Y.,

Oros Klein K., Grinek S., Bernatsky S., Bouchard L., Ciampi A., Colmegna I., Fortin J.P., Gao L., Hivert M.F., Hudson M., Kobor M.S., Labbe A., MacIsaac J.L., Meaney M.J., Morin A.M., O'Donnell K.J., Pastinen T., Van Ijzendoorn M.H., Voisin G., **Greenwood C.** 2015. funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. Bioinformatics. 32(4):593-5.

Mokry L.E., Ross S., Ahmad O.S., Forgetta V., Davey-Smith G., Leong A., **Greenwood C.**, Thanassoulis G., Richards J.B. 2015. Vitamin D and risk of Multiple Sclerosis: A Mendelian Randomization Study. PLOS Medicine. 12(8):e1001866.

Zheng H.F., Forgetta V., Hsu Y.H., Estrada K., Rosello-Diez A., Leo P.J., Dahia C.L., Park-Min K.H., Tobias J.H., Kooperberg C., Kleinman A., Styrkarsdottir U., Liu C.T., Uggla C., Evans D.S., Nielson C.M., Walter K., Pettersson-Kymmer U., McCarthy S., Eriksson J., Kwan T., Jhamai M., Trajanoska K., Memari Y., Min J., Huang J., Danecek P., Wilmot B., Li R., Chou W.C., Mokry L.E., **[Greenwood C., 113 co-authors]**, Jackson R.D., Rowe D.W., Loomis C.A., Evans D.M., Ackert-Bicknell C.L., Joyner A.L., Duncan E.L., Kiel D.P., Rivadeneira F., Richards J.B., GEFOS Consortia, UK10K Consortia. 2015. Whole-genome sequence-based identification of EN1 as a determinant of bone density and fracture. Nature. 526(7571):112-117.

UK10K Consortium, Walter K., Min J.L., Huang J., Crooks L., Memari Y., McCarthy S., Perry J.R., Xu C., Futema M., Lawson D., Iotchkova V., Schiffels S., Hendricks A.E., Danecek P., Li R., Floyd J., Wain L.V., Barroso I., Humphries S.E., Hurles M.E., Zeggini E., Barrett J.C., Plagnol V., Richards J.B., **Greenwood C.**, Timpson N.J., Durbin R., Soranzo N. 2015. The UK10K project: rare variants in health and disease. Nature. 526(7571):82-90.

Cotterchio M., Lowcock B., Lemire M., **Greenwood C.**, Gallinger S., Hudson T. 2015. Association between variants in atopy-related immunologic candidate genes and pancreatic cancer risk. PLoS ONE. 10(5):e0125273.

Ahmad O.S., Morris J.A., Mujammami M., Forgetta V., Li R., **Greenwood C.**, Thanassoulis G., Meigs J., Sladek R., Richards J.B. 2015. A Mendelian randomization study of the effect of type-2 diabetes on coronary heart disease. Nature Communications. 6:7060.

Bhatnagar S., **Greenwood C**., Labbe A. 2015. Assessing transmission ratio distortion in extended families: a comparison of analysis methods. BMC Proceedings. 9(8):S24.

Arabzadeh A., Dupaul-Chicoine J., Breton V., Haftchenary S., Yumeen S., Turbide C., Saleh M., McGregor K., **Greenwood C.**, Akavia U.D., Blumberg R.S., Gunning P.T., Beauchemin N. 2015. Carcinoembryonic Antigen Cell Adhesion Molecule 1 long isoform impedes metastasis of colon cancer cells. Gut. 65(5):821-9.

Woltersdorf W., Zeggini E., Zheng H.F., Toniolo D., Dayan C.M., Naitza S., Walsh J.P., Spector T., Davey Smith G., Durbin R., Richards J.B., Sanna S., Soranzo N., Timpson N.J., Wilson S.G., UK0K Consortium. 2015. Whole genome based analysis of thyroid function. Nature Communications. 6:5681.

Taylor P.N., Porcu E., Chew S., Campbell P.J., Traglia M., Brown S.J., Mullin B.H., Shihab H.A., Min J., Walter K., Memari Y., Huang J., Barnes M.R., Beilby J.P., Charoen P., Danecek P., Dudbridge F., Forgetta V., **Greenwood C.**, Grundberg E., Johnson A.D., Hui J., Lim E.M., McCarthy S., Muddyman D., Panicker V., Perry J.R., Bell J.T., Yuan W., Relton C., Gaunt T., Schlessinger D., Abecasis G., Cucca F., Surdulescu G.L.,

Leong A., Goltzman D., Hanley D., Rehman W., Dastani Z., **Greenwood C.**, Timpson N., Langsetmo L., Berger C., Malik S., Cole D. 2014. The causal effect of vitamin D binding protein levels on calcemic and cardiometabolic diseases: A Mendelian randomization study. PLoS Medicine. 11(10):e1001751.

Fortin J.P., Labbe A., Lemire M., Zanke B.W., Hudson T.J., Fertig E.J., **Greenwood C.**, Hansen K.D. 2014. Functional normalization of 450K methylation array data improves replication in large cancer studies. Genome Biology. 15(11):503.

Przybytkowski E., Lenkiewicz E., Barrett M.T., Klein K., **Greenwood C.**, Basik M. 2014. Chromosome-breakage genomic instability and chromothripsis in breast cancer. BMC Genomics. 15(1):579.

Burkett K.M., McNeney B., Graham J., **Greenwood C.** 2014. Using gene genealogies to detect rare variants associated with complex traits. Human Heredity. 78:117-130.

Jarry J., Schadendorf D., **Greenwood C.**, Spatz A., van Kempen L.C. 2014. The validity of circulating microRNAs in oncology: five years of challenges and contradictions. Molecular Oncology. 8(4):819-29.

Xu C., Ciampi A., **Greenwood C.**, the UK10K Consortium. 2014. Exploring the potential benefits of stratified false discovery rates for region based testing of association with rare genetic variation. Frontiers in Genetics: Statistical Genetics and Methodology. (5):11.

Xu C., Tachmazidou I., UK10K Consortium, Ciampi A., Zeggini E., **Greenwood C**. 2014. Estimating genome-wide significance for whole genome sequencing studies**.** Genetic Epidemiology. 38(4): 281-290.

Cotterchio M., Lowcock E., Hudson T., **Greenwood C.**, Gallinger S. 2014. Association between allergies and risk of pancreatic cancer. Cancer Epidemiology, Biomarkers and Prevention. 23(3): 469-480.

Lui R., Montpetit A., Rousseau M., Wu S.Y.M., **Greenwood C.**, Spector T.D., Pollak M., Polychronakos C., Richards J.B. 2014. Somatic Mutations Occurring in Early Development: A Monozygotic Twin Study. Journal of Medical Genetics**.** 51(1):28-34.

Haghighi A., Melka M.G., Bernard M., Abrahamowicz M., Leonard G.T., Richer L., Perron M., Veillette S., Xu C.J., **Greenwood C.**, Dias A., El-Sohemy A., Gaudet D., Paus T., Pausova Z. 2014. Opioid receptor mu 1 gene, fat intake and obesity in adolescence. Molecular Psychiatry. 19(1):63-8.

Burkett K., **Greenwood C.**, McNeney B., J Graham J. 2013. Gene genealogies for genetic association mapping, with application to Crohn's disease. Frontiers in Genetics: Statistical Genetics and Methodology. 4:260.

Burkett K., **Greenwood C.** 2013. A sequence of methodological changes due to sequencing. Current Opinion in Allergy and Clinical Immunology. 13(5):470-7.

Basik M., Aguilar-Mahecha A., Rousseau C., Diaz Z., Tejpar S., Spatz A., **Greenwood C.**, Gerald Batist G. 2013. Metastatic biopsies – next-generation biospecimens for tailoring therapy. Nature Reviews Clinical Oncology. 10(8):437-50.

Chen Z., **Greenwood C.**, Isaacs W.B., Foulkes W.D., Sun J., Zheng S.L., Condreay L.D., Xu J. 2013. The G84E mutation of HOXB13 is associated with increased risk for prostate cancer: Results from the REDUCE trial. Carcinogenesis. 34(6):1260-4.

Oualkacha K., Dastani Z., Li R., Cingolani P.E., Spector T.D., Hammond C.J., Richards J.B., Ciampi A. **Greenwood C.** 2013. Adjusted Sequence Kernel Association Test for Rare Variants Controlling for Cryptic and Family Relatedness. Genetic Epidemiology. 37(4): 366–376.

Oros K.K., Arcand S.L., Squire J.A., Mes-Masson A.-M., Tonin P.N., **Greenwood C.** 2013. Analysis of genomic abnormalities in tumours: a review of available methods for Illumina two-color SNP genotyping and evaluation of performance. Cancer Genetics. 206(4):103-15.

Ladouceur M., **Greenwood C.**, Richards J.B., Zheng H.F. 2013. Empirical Power of Very Rare Variants for Common Traits and Disease: Results from Sanger Sequencing 1,998 Individuals. European Journal of Human Genetics. 21(9): 1027-1030.

Asai Y., **Greenwood C.**, Hull P.R., Alizadehfar R., Ben-Shoshan M., Brown S.J., Campbell L., Michel D.L., Bussières J., Rousseau F., Fujiwara T.M., Morgan K., Irvine A.D., McLean W.H., Clarke A. 2013. Filaggrin gene mutation associations with peanut allergy persist despite variations in peanut allergy diagnostic criteria or asthma status. Journal of Allergy and Clinical Immunology. 132(1):239-42.

Hu P., Wang X., Haitsma J.J., Furmli S., Masoom H., Liu M., Imai Y., Slutsky A.S., Beyene J., **Greenwood C.**, dos Santos C. 2012. Microarray meta-analysis identifies acute lung injury biomarkers in donor lungs that predict development of primary graft failure in recipients. PLoS ONE. 7(10):e45506.

Wojnarowicz P.M., Oros K.K., Quinn M.C., Arcand S.L., Gambaro K., Madore J., Birch A.H., de Ladurantaye M., Rahimi K., Provencher D.M., Mes-Masson A.M., **Greenwood C.**, Tonin P.N. 2012. The Genomic Landscape of *TP53* and p53 Annotated High Grade Ovarian Serous Carcinomas from a Defined Founder Population Associated with Patient Outcome. PLoS ONE. 7(9):e45484.

Zheng H.F., Ladouceur M., **Greenwood C.,** Richards J.B. 2012. Effect of genome-wide genotyping array density on rare variant imputation. Journal of Genetics and Genomics. 39(10):545-50.

Xu C., Ladouceur M., Richards J.B., Ciampi A., **Greenwood C.** 2012. Multiple regression methods show great potential for rare variant association tests. PLoS ONE. 7(8):e41694.

Dastani Z., Hivert M.-F., Timpson N., Perry J.R.B., Yuan X., Scott R.A., Henneman P., Heid I.M., Kizer J.R., Lyytikainen L.-P., Fuchsberger C., Tanaka T., Morris A.P., Small K., Isaacs A., Beekman M., Coassin S., Lohman K., Qi L., Kanoni S., Pankow J.S., Uh H.-W., Wu Y., Bidulescu A., Rasmussen-Torvik L.J., **Greenwood C.**, Ladouceur M., Grimsby J.,

Manning A.K., Liu C.-T., Kooner J., Mooser V.E., Vollenweider P., Kapur K.A., Chambers J., Wareham N.J., Langenberg C., Frants R., Willems-Vandijk K., Oostra B.A., Willems S.M., Lamina C., Winkler T.W., Psaty B.M., Tracy R.P., Brody J., Chen I., Viikari J., Kähönen M., Pramstaller P.P., Evans D.M., St Pourcain B., Sattar N., Wood A.R., Bandinelli S., Carlson O.D., Egan J.M., Böhringer S., van Heemst D., Kedenko L., Kristiansson K., Nuotio M.L., Loo B.M., Harris T., Garcia M., Kanaya A., Haun M., Klopp N., Wichmann H.E., Deloukas P., Katsareli E., Couper D.J., Duncan B.B., Kloppenburg M., Adair L.S., Borja J.B., DIAGRAM+ Consortium, MAGIC Consortium, GLGC Investigators, MuTHER Consortium, Wilson J.G., Musani S., Guo X., Johnson T., Semple R., Teslovich T.M., Allison M.A., Redline S., Buxbaum S.G., Mohlke K.L., Meulenbelt I., Ballantyne C.M., Dedoussis G.V., Hu F.B., Liu Y., Paulweber B., Spector T.D., Slagboom P.E., Ferrucci L., Jula A., Perola M., Raitakari O., Florez J.C., Salomaa V., Eriksson J.G., Frayling T.M., Hicks A.A., Lehtimäki T., Smith G.D., Siscovick D.S., Kronenberg F., van Duijn C., Loos R.J., Waterworth D.M., Meigs J.B., Dupuis J., Richards J.B. 2012. Novel Loci for Adiponectin Levels and their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics. 8(3):e1002607.

Hamid J.S., **Greenwood C.**, Beyene J. 2012. Weighted kernel Fisher discriminant analysis for Integrating Heterogeneous Data. Computational Statistics and Data Analysis. 56:2031-2040.

Ladouceur M., Dastani Z., Aulchenko Y.S., Ehm M.G., **Greenwood C.**, Richards J.B. 2011. The empirical power of rare variant association methods: Results from Sanger sequencing in 1,998 individuals. PLoS GenetIcs. 8(2): e1002496.

Greenwood C., Paterson A.D., Linton L., Andrulis I.L., Apicella C., Dimitromanolakis A., Kriukov V., Martin L.J., Salleh A., Samiltchuk E., Parekh R.V., Southey M.C., John E.M., Hopper J.L., Boyd N.F., Rommens J.M. 2011. A genome-wide linkage study of mammographic density, a risk factor for breast cancer. Journal of Breast Cancer Research. 13(6):R132.

Birch A.H., Arcand S.L., Oros K.K., Rahimi K., Watters A.K., Provencher D., **Greenwood C.**, Mes-Masson A.M., Tonin P.N 2011. Chromosome 3 anomalies investigated by genome wide SNP analysis of benign, low malignant potential and low grade ovarian serous tumours. PLoS One. 6(12):e28250.

McCuaig J.M., **Greenwood C.**, Shuman C., Chitayat D., Murphy J., Rosen B., Armel S.R. 2011. Breast and ovarian cancer: the forgotten paternal contribution. Journal of Genetic Counselling. 20 (5): 442-449.

Hamel N., Feng B.J., Foretova L., Stoppa-Lyonnet D., Narod S.A., Imyanitov E., Sinilnikova O., Tihomirova L., Lubinski J., Gronwald J., Gorski B., Hansen T.V., Nielsen F.C., Thomassen M., Yannoukakos D., Konstantopoulou I., Zajac V., Ciernikova S., Couch F.J., **Greenwood C.**, Goldgar D.E., Foulkes W.D. 2011. On the origin and diffusion of BRCA1 c.5266dupC (5382insC) in European populations. European Journal of Human Genetics. 19(3):300-6.

Rahman P., Roslin N.M., Lemire M., **Greenwood C.**, Beyene J., Pope A., Peddle L., Paterson D, Uddin M., Gladman D.D. 2011. High resolution mapping in the MHC region identifies multiple independent novel loci for psoriatic arthritis. Annals of the Rheumatic Diseases. 70(4):690-4.

Mrkonjic M., Roslin N.M., **Greenwood C.**, Raptis S., Pollett A., Laird P.W., Pethe V.V., Chiang T., Daftary D., Dicks E., Thibodeau S.N., Gallinger S., Parfrey P.S., Younghusband H.B., Potter J.D., Hudson T.J., McLaughlin J.R., Green R.C., Zanke B.W., Newcomb P.A., Paterson A.D., Bapat B. 2010. Specific variants in the MLH1 Gene Region May Drive DNA Methylation, Loss of Protein Expression and MSI-H Colorectal Cancer. PLoS One. 13:5(10):e13314.

McCuaig J., **Greenwood C.**, Shuman C., Chitayat D., Murphy J., Rosen B., Armel S. 2010. Breast and Ovarian Cancer: Y do we forget about dad? Lancet Oncology. 11(12):1115-7.

Greenwood C., Sun S., Veenstra J., Hamel N., Niell B., S Gruber S., Foulkes W.D. 2010. How old is this mutation? - a study of three Ashkenazi Jewish founder mutations. BMC Genetics 11:39.

Husted J., Bassett A., **Greenwood C.** 2010. Familial aggregation of clinical and neurocognitive features in sibling pairs with and without schizophrenia. Schizophrenia Research. 116:289-290.

Hawken S.J., **Greenwood C.**, Hudson T.J., Kustra R., McLaughlin J., Yang Q., Zanke B.W., Little J. 2010. The utility and predictive value of combinations of low penetrance genes for screening and risk prediction of colorectal cancer. Human Genetics. 128(1):89-101.

Peter GRÜTTER

Xing S., Grol M.W., **Grütter P.**, Dixon S.J., Komarova S.V. 2016. Modeling the interactions among individual P2 receptors to explain complex response patterns over a wide range of ATP concentrations. Frontiers in Physiology. 7:294.

Schumacher Z., Miyahara Y., Spielhofer A., **Grütter P.** 2016. Accurate Measurement of Surface Photovoltage by Atomic Force Microscopy under pulsed illumination. Physical Review Applied. 5:044018.

Jia Q., Hu Z.X., Ji W., Burke S.A., Gao H.J., **Grütter P.** and Guo H., 2016. Adsorption of PTCDA and C 60 on KBr (001): electrostatic interaction versus electronic hybridization. Physical Chemistry Chemical Physics. 18(16):11008-16.

Magdesian M.H., Lopez-Ayon,G.M., Mori M., Boudreau D., Goulet-Hanssens A., Sanz R., Miyahara Y., Barrett C.J., Fournier A.E., De Koninck Y., **Grütter P.** 2016. Rapid Mechanically Controlled Rewiring of Neuronal Circuits. The Journal of Neuroscience. 36(3):979-87.

Jia Q., Hu Z.X., Ji W., Burke S.A., Gao H.J., **Grütter P.**, Guo, H. 2016. Adsorption of PTCDA and C 60 on KBr (001): electrostatic interaction versus electronic hybridization. Physical Chemistry Chemical Physics. 18(16):11008-16.

Miyahara Y., Topple J., Schumacher Z, **Grütter P.** 2015. Kelvin Probe Force Microscopy by Dissipative Electrostatic Force Modulation. Physical Review Applied. 4(5):054011.

Schumacher Z., Miyahara Y., Aeschimann L., **Grütter P.** 2015. Improved atomic force microscopy cantilever performance by partial reflective coating. Beilstein journal of nanotechnology. 6(1):1450-56.

Roy-Gobeil A., Miyahara Y., Grütter P. 2015. Revealing energy level structure by tunneling rate measured by single-electron sensitive electrostatic force spectroscopy. Nano Letters. 15(4):2324-28.

Haag A.L., Nagai Y., Lennox R.B., **Grütter P.** 2015. Characterization of a gold coated cantilever surface for biosensing applications. EPJ techniques and instrumentation. 2(1):1.

Paul W., **Grütter P.** 2015. Field Ion Microscopy for the Characterization of Scanning Probes. In Surface Science Tools for Nanomaterials Characterization. Springer Berlin Heidelberg. 159-198.

Zhou X., Hedberg J., Miyahara Y., **Grütter P.**, Ishibashi, K. 2014. Scanning gate imaging of two coupled quantum dots in single-walled carbon nanotubes. Nanotechnology. 25(49):495703.

Lopez-Ayon G.M., Liu H.Y., Xing S., Maria O.M., LeDue J.M., Bourque H., **Grütter P.**, Komarova, S.V. 2014. Local membrane deformation and micro-injury lead to qualitatively different responses in osteoblasts. F1000Research. 3:162

Paul W., Oliver D., **Grütter P.** 2014. Indentation-formed nanocontacts: an atomic-scale perspective. Physical Chemistry Chemical Physics. 16(18):8201-8222.

Paul W., Oliver D., Miyahara Y., **Grütter P.** 2014. FIM tips in SPM: Apex orientation and temperature considerations on atom transfer and diffusion. Applied Surface Science. 305:124-132.

Oliver D.J., Paul W., El Ouali M., Hagedorn T., Miyahara Y., Qi Y., **Grütter P.** 2013. One-to-one spatially matched experiment and atomistic simulations of nanometre-scale indentation. Nanotechnology. 25(2):025701.

Goldman J.S., Ashour M.A., Magdesian M.H., Tritsch N.X., Harris S.N., Christofi N., Chemali R., Stern Y.E., Thompson-Steckel G., Gris P., Glasgow S.D., **Grütter P**., Bouchard J.F., Ruthazer E.S., Stellwagen D., Kennedy T.E. 2013. Netrin-1 Promotes Excitatory Synaptogenesis between Cortical Neurons by Initiating Synapse Assembly. Journal of Neuroscience. 33(44):17278-89.

Paul W., Oliver D., Miyahara Y., **Grütter P.** 2013. Transient adhesion and conductance phenomena in initial nanoscale mechanical contacts between dissimilar metals. Nanotechnology. 24(47):475704.

Nagai Y., Carbajal J.D., White J.H., Sladek R., **Grütter P.**, Lennox R.B. 2013. Electrochemically Controlled Microcantilever Biosensor. Langmuir 29(32):9951-7.

Schumacher Z., Topple J., Tekiel A., **Grütter P**. 2013. Photovoltaics at the nanoscale. SPIE Proceedings Physical Chemistry of Interfaces and Nanomaterials XII. **8811**: 881116-1–881116-6.

Tekiel A., Miyahara Y., Topple J.M., **Grütter P.** 2013. Room-Temperature Single-Electron Charging Detected by Electrostatic Force Microscopy. ACS Nano. 7(5):4683-90.

Paul W., Miyahara Y., **Grütter P.** 2013. Simple Si (111) surface preparation by thin wafer cleavage. Journal of Vacuum Science & Technology A. 31(2):023201.

Paul W., Oliver D., Miyahara Y., **Grütter P.** 2013. Incipient plasticity and pop-ins in the atomic-scale nanoindentation of Au(111). Physical Review Letters. 110(13):135506.

Tekiel A., Fostner S., Topple J., Miyahara Y., **Grütter, P**. 2013. Reactive growth of MgO overlayers on Fe (001) surfaces studied by low-energy electron diffraction and atomic force microscopy. Applied Surface Science. 273:247-252.

Ricoult S.G., Pla-Roca M., Safavieh R., Lopez-Ayon G.M., **Grütter P.**, Kennedy T.E., Juncker D. 2013. Large Dynamic Range Digital Nanodot Gradients of Biomolecules Made by Low-Cost Nanocontact Printing for Cell Haptotaxis. Small. 9(19):3308-3313.

Bates J.R., Miyahara Y., Burgess J.A., Iglesias-Freire O., **Grütter P.** 2013. Effect of using stencil masks made by focused ion beam milling on permalloy (Ni81Fe19) nanostructures. Nanotechnology 24(11):115301.

Iglesias-Freire O., Bates J.R., Miyahara Y., Asenjo A., **Grütter P.** 2013. Tip-induced artifacts in magnetic force microscopy images. Applied Physics Letters. 102(2):022417.

Suarez F., Thostrup P., Colman D., **Grütter P.** 2013. Dynamics of presynaptic protein recruitment induced by local presentation of artificial adhesive contacts. Developmental Neurobiology. 73(1):98-106.

Labuda A., Kobayashi K., Suzuki K., Yamada H., **Grütter P.** 2013. Monotonic damping in nanoscopic hydration experiments. Physical Review Letters. 110(6):066102.

Paul W., Miyahara Y., **Grütter P.** 2012. Implementation of atomically defined field ion microscopy tips in scanning probe microscopy. Nanotechnology. 23(33)**:**335702.

Tekiel A., Topple J., Miyahara Y., **Grütter P.** 2012. Layer-by-layer growth of sodium chloride overlayers on an Fe(001)-p(1x1)O surface. Nanotechnology. 23(50):505602.

Labuda A., Lysy M., **Grütter P.** 2012. Stochastic simulation of tip-sample interactions in atomic force microscopy. Applied Physics Letters. 101(11):113105.

Labuda A., Lysy M., Paul W., Miyahara Y., **Grütter P.**, Bennewitz R., Sutton M. 2012. On stochastic noise in atomic force microscopy. Physical Review E. 86(3 Pt 1):031104.

Magdesian M.H., Sanchez F.S., Lopez M., Thostrup P., Durisic N., Belkaid W., Liazoghli D., **Grütter P.**, Colman D.R. 2012. Atomic force microscopy reveals important differences in axonal resistance to injury. Biophysical journal. 103(3):405-414.

Oliver D.J., Maassen J., El Ouali M., Paul W., Hagedorn T., Miyahara Y., Qi Y., Guo H., **Grütter P.** 2012. Conductivity of an atomically defined metallic interface. Proceedings of the National Academy of Sciences of the United States of America. 109(47):19097-19102.

Labuda A., Kobayashi K., Miyahara Y., **Grütter P.** 2012. Retrofitting an atomic force microscope with photothermal excitation for a clean cantilever response in low Q environments. Review of Scientific Instruments. 83(5):053703.

Lopez-Ayon G.M., Oliver D.J., **Grütter P.**, Komarova S.V. 2012. Deconvolution of calcium fluorescent indicator signal from AFM cantilever reflection. Microscopy and Microanalysis. 18(04):808-815.

Labuda A., **Grütter P.** 2012. Atomic force microscopy in viscous ionic liquids. Langmuir. 28(12):5319-5322.

Grütter P. 2012. Seeing the charge within. Nature Nanotechnology. 7(4):210-1.

Cockins L., Miyahara Y., Bennett S.D., Clerk A.A., **Grütter P.** 2012. Excited-State Spectroscopy on an Individual Quantum Dot Using Atomic Force Microscopy. Nano letters. 12(2):709-713.

Stöffler D., Fostner S., **Grütter P.**, Hoffmann-Vogel R. 2012. Scanning probe microscopy imaging of metallic nanocontacts. Physical Review B. 85(3):033404.

Labuda A., Bates J.R., **Grütter P.** 2011. The noise of coated cantilevers. Nanotechnology. 23(2):025503.

Mahimwalla Z.S., Nagai Y., **Grütter P.**, Barrett C.J. 2011. Photomechanical Effect of Azobenzene Thin Polymer Films Measured with an AFM Cantilever Based Sensor. SPIE Nanophotonics. 7712:76.

Miyahara Y., Cockins L., **Grütter P**. 2011. Electrical characterization of low dimensional systems (quantum/nano-structures) in *Kelvin Probe Force Microscopy - Measuring and Compensating Electrostatic Forces* Springer Series in Surface Sciences. Springer. 48: 175-195.

Lalanne J.-B., Paul W., Oliver D., **Grütter P.** 2011. Electrochemical etching of sharp iridium tips. Review of Scientific Instruments. 82:116105.

Durisic N., Godin A.G., Walters D., **Grütter P.**, Wiseman P.W., Heyes C.D. 2011. Probing the "Dark" Fraction of Core–Shell Quantum Dots by Ensemble and Single Particle pH-Dependent Spectroscopy. ACS nano. 5(11):9062-9073.

Labuda A., Miyahara Y., Cockins L., **Grütter P.** 2011. Decoupling conservative and dissipative forces in frequency modulation atomic force microscopy. Physical Review B. 84(12):125433.

Hagedorn T., El Ouali M., Paul W., Oliver D., Miyahara Y., **Grütter P.** 2011. Refined tip preparation by electrochemical etching and ultrahigh vacuum treatment to obtain atomically sharp tips for scanning tunneling microscope and atomic force microscope. Review of Scientific Instruments. 82(11):113903.

Fostner S., Tekiel A., Topple J.M., Miyahara Y., **Grütter P.** 2011. Field deposition from metallic tips onto insulating substrates. Nanotechnology. 22(46):465301.

Labuda A., Kobayashi K., Kiracofe D., Suzuki K., **Grütter P.**, Yamada H. 2011. Comparison of photothermal and piezoacoustic excitation methods for frequency and phase modulation atomic force microscopy in liquid environments. AIP Advances. 1(2):p.022136.

Risse P.A., Jo T., Suarez F., Hirota N., Tolloczko B., Ferraro P., **Grütter P.**, Martin J.G. 2011. Interleukin-13 inhibits proliferation and enhances contractility of human airway smooth muscle cells without change in contractile phenotype. American Journal of Physiology-Lung Cellular and Molecular Physiology. 300(6):L958-L966.

Labuda A., Hausen F., Gosvami N.N., **Grütter P.**, Lennox R.B., Bennewitz R. 2011. Switching atomic friction by electrochemical oxidation. Langmuir. 27(6):2561-2566.

Labuda A., **Grütter P.** 2011. Exploiting cantilever curvature for noise reduction in atomic force microscopy. Review of Scientific Instruments. 82(1):013704.

Topple J.M., Burke S.A., Ji W., Fostner S., Tekiel A., **Grütter P.** 2010. Tailoring the morphology and dewetting of an organic thin film. The Journal of Physical Chemistry C. 115(1):217-224.

Hedberg J.A., Lal A., Miyahara Y., **Grütter P.**, Gervais G., Hilke M., Pfeiffer L., West K.W. 2010. Low temperature electrostatic force microscopy of a deep two-dimensional electron gas using a quartz tuning fork. Applied Physics Letters. 97(14):143107.

Labuda A., Paul W., Pietrobon B., Lennox R.B., **Grütter P.**, Bennewitz R. 2010. High-resolution friction force microscopy under electrochemical control. The Review of Scientific Instruments. 81(8):083701.

LeDue J.M., Lopez-Ayon M., Miyahara Y., Burke S.A., **Grütter P.** 2010. Noise in combined optical microscopy and dynamic force spectroscopy: Toward in vivo hydration measurements. Journal of Vacuum Science & Technology B. 28(3):C4C15-C4C20.

Cockins L., Miyahara Y., Bennett S.D., Clerk A.A., Studenikin S., Poole P., Sachrajda A., **Grütter P.** 2010. Filling of Few Electron Quantum Dots Imaged and Characterized By Scanning Force Microscopy. Proceedings of the National Academy of Sciences of the United States of America. 107(21):9496-501.

Godin M., Tabard-Cossa V., Miyahara Y., Monga T., Williams P.J., Beaulieu L.Y., Bruce Lennox R., **Grütter P.** 2010. Cantilever-Based Sensing: Origin of the Surface Stress and Optimization Strategies. Nanotechnology. 21(7):75501.

Fostner S., Burke S.A., Topple J., Mativetsky J.M., Beerens J., **Grütter P**. 2010. Silicon nanostencils with integrated support structures. Microelectronic Engineering. 87(4):652-657.

Frédéric GUICHARD

Eger A., Curtis J.M.R., Fortin M.-J., Côté I.M., **Guichard, F.** 2016. Transferability and scalability of species distribution models: A test with sedentary marine invertebrates. Canadian Journal of Fisheries and Aquatic Sciences. *in press.*

Lacoursière-Roussel A., Bock D.G., **Guichard F**., McKinsey C.W. 2016. Effect of shipping traffic on biofouling invasion success at population and community levels. Biological Invasions. *in press.*

Pedersen E., **Guichard, F**. 2016. At what scales does aggregated dispersal lead to coexistence? Oikos. *in press.*

Pedersen E., Marleau J., Granados M., Moeller H., **Guichard F.** 2016. Nonhierarchical movement promotes stability and resilience in a tri-trophic metacommunity. The American Naturalist. 187(5):E116-28.

Spiecker B., Gouhier T.C., **Guichard F.** 2016. Reciprocal feedbacks between spatial subsidies and reserve networks in coral reef meta-ecosystems. Ecological Applications. 26(1):264-78.

Marleau J., **Guichard F.**, Loreau M. 2015. Emergence of nutrient colimitation in stoichiometric meta-ecosystems. Ecology Letters. 18(11):1163-1173

Lecorre N., **Guichard F.**, Johnson L.E. 2015. Patterns and scales of metapopulation connectivity: Temporal stability and variation within a marine metapopulation. Ecology. 96(8):2245-56

Kerr K., Collin R., **Guichard F.** 2015. Seasonal variation in planktonic predation risk depends on prey life history stage. Journal of Plankton Research. 37(2):452-461.

Xue Z., **Guichard F.**, Costopoulos A. 2015. The supply of phenotypic variation can drive long-term evolutionary trends even with strong natural selection. Complexity. DOI: 10.1002/cplx.21660

Zhang Y., Lutscher F., **Guichard F.** 2015. How robust is dispersal-induced spatial synchrony? Chaos. 25(3):036402.

Zhang Y., Lutscher F., **Guichard F.** 2015. The effect of predator avoidance and travel time delay on the stability of predator-prey metacommunities. Theoretical Ecology. 8(3):273-283.

Xue Z., Kaznatcheev A., Costopoulos A., **Guichard F.** 2015. Fidelity drive: a mechanism for chaperone proteins to maintain stable mutation rates in prokaryotes over evolutionary time. Journal of Theoretical Biology. 364:162-167.

Gounand I., Mouquet N., Canard E., **Guichard F.**, Hauzy C., Gravel D. 2014. The paradox of enrichment in metaecosystems. The American Naturalist. 184:752-763.

Kerr K.A. Collin R. Christy J., **Guichard F.** 2014. Timing reproduction when temperature varies: behavioral mechanisms in fiddler crabs. PLoS One. 9(5):e97593.

Gouhier T.C., **Guichard F.** 2014. Synchrony: quantifying variability in space and time. Methods in Ecology and Evolution. 5:524-533.

Kerr K.A., Cornejo A., **Guichard F.**, Collin R. 2014. Planktonic predation risk varies with prey life history stage and diurnal phase. Marine Ecology Progress Series. 503:99-109.

Guichard F., Gouhier T.C. 2014. Non-equilibrium ecological dynamics across spatial and temporal scales. Mathematical Biosciences. 255:1-10.

Marleau J.N., **Guichard F.**, Loreau M. 2014. Meta-ecosystem dynamics and functioning on finite spatial networks. Proceedings of Royal Society of London B. 281(1777):20132094.

Gouhier T.C., **Guichard F.**, Menge B.A. 2013. Designing effective marine reserve networks for non-equilibrium metacommunities. Ecological Applications. 23:1488–1503.

Wall E., **Guichard F.**, Humphries A.R. 2013. Synchronization in ecological systems by weak dispersal coupling with time delay. Theoretical Ecology. 6:405-418.

Le Corre N., Martel A.L., **Guichard F.**, Johnson L.E. 2013. Variation in recruitment: differentiating the roles of primary and secondary settlement of blue mussels (Mytilus spp.). Marine Ecology Progress Series. 481:133-146.

Loreau M., Daufresne T., Gonzalez A., Gravel D., **Guichard F.**, Leroux S., Loeuille N., Massol F., Mouquet N. 2013. Unifying sources and sinks in ecology, evolution and Earth sciences. Biological Reviews of the Cambridge Philosophical Society. 88(2):365-79.

Lutscher F., **Guichard F.** 2013. The Aisenstadt lectures by Simon Levin. CRM bulletin. 19(2): 7-8.

Lacoursière-Roussel A., McKindsey C.W., Bock D., Cristescu M., **Guichard F.**, Girard P., Legendre P. 2012. Disentangling invasion processes in a dynamic shipping-boating network. Molecular Ecology. 21:4227-41.

Lacoursière-Roussel A., Forrest B.M., **Guichard F.**, Piola R.F., McKindsey C.W. 2012. Modeling biofouling from boat and source characteristics: A comparative study between Canada and New Zealand. Biological Invasions. 14:2301-2413.

Kerr K.A., Christy J.H., Collin R., Guichard F. 2012. Reducing error in reproductive timing caused by temperature variation: Interspecific differences in behavioural adjustment by fiddler crabs. Marine Ecology Progress Series. 459:1-16.

Pillai P., **Guichard F.** 2012. Competition-Colonization Trade-offs, Competitive Uncertainty, and the Evolutionary Assembly of Species. PLoS One. 7(3):e33566.

Largaespada C., **Guichard F.**, Archambault P. 2012. Meta-ecosystemsengineering: Nutrient fluxes reveal intra-specific and inter-specific feedbacks in fragmented mussel beds. Ecology. 93:324-333.

Puebla O., Bermingham E., **Guichard F.** 2011. Pairing dynamics and the origin of species. Proceedings of the Royal Society of London B. 279:1085-1092.

Xue J.Z., Costopoulos A., **Guichard F.** 2011. Choosing fitness-enhancing innovations can be detrimental under fluctuating environments. PLoS One. 6(1):e26770.

Gravel D., Hochberg M., **Guichard F.** 2011. Coexistence in a variable world. Ecology Letters. 14:828-39.

Gravel D., Canard E., **Guichard F.**, Mouquet N. 2011. Persistence increases with diversity and connectance in trophic metacommunities. PLoS One. 6(5): e19374.

Puebla O., Bermingham E., **Guichard F.** 2011. Perspective: matching, mate choice and speciation. Integrative and Comparative Biology. 51: 485-491.

Lecorre N., Johnson L.E., **Guichard F.** 2011. Connectivity as a tool to manage coastal ecosystems in changing oceans. in: Oceanography. Intech Publisher. ISBN: 978-953-51-0301-1

Jessen S., Chan K., Côté I., Dearden P., De Santo E., Fortin M.J., **Guichard F.**, Haider W., Jamieson G., Kramer D.L., McCrea-Strub A., Mulrennan M., Montevecchi W.A., Roff J., Salomon A., Gardner J., Honka L., Menafra R., Woodley A. 2011. Sciencebased Guidelines for MPAs and MPA Networks in Canada. Vancouver: Canadian Parks and Wilderness Society. 58 pp.

Puebla O., **Guichard F.**, Bermingham E. 2011. Pairing dynamics and the origin of species. Integrative and Comparative Biology. 279(1731):1085-92.

Anmar KHADRA

Mitre T.M., Mackey M.C., **Khadra A.** 2016. Mathematical Model of Galactose Regulation and Metabolic Consumption in Yeast. Journal of Theoretical Biology. 407:238-258.

Moran S., Moenter S.M., **Khadra A**. 2016. A Unified Model for Two Modes of Bursting in GnRH Neurons. Journal of Computational Neuroscience. 40(3):297-315.

Khadra A., Schnell S. 2015. Development, Growth and Maintenance of Beta-Cell Mass: Models are also Part of the Story. Molecular Aspects of Medicine. 42:78-90.

Morran M.P., Vonberg A., **Khadra A.**, Pietropaolo M. 2015. Immunogenetics of Type 1 Diabetes Mellitus. Molecular Aspects of Medicine. 42:42-60.

Jaberi-Douraki M., Pietropaolo M., **Khadra A**. 2015. Continuum Model of T-Cell Avidity: Understanding Autoreactive and Regulatory T-Cell Responses in Type 1 Diabetes. Journal of Theoretical Biology. 383:93-105.

Jaberi-Douraki M., Schnell S., Pietropaolo M., **Khadra A**. 2015. Unraveling the Contribution of Pancreatic Beta-Cell Suicide in Autoimmune Type 1 Diabetes. Journal of Theoretical Biology. 375:77-87.

Michels A., Zhang L., **Khadra A.**, Redondo M.J., Pietropaolo M. 2015. Prediction and Prevention of T1DM:Update on Success of Prediction and Struggles at Prevention. Pediatric Diabetes. 16:465-84.

Zemkova H., **Khadra A.**, Rokic M.B., Tvrdonova V., Sherman A., Stojilkovic S. 2015. Allosteric Regulation of the P2X4 Receptor Channel Pore Dilation. Pflügers Archiv: European Journal of Physiology. 467(4):713-726.

Jaberi-Douraki M., Liu S.W., Pietropaolo M., **Khadra A.** 2014. Autoimmune Responses in T1DM: Quantitative Methods to Understand Onset, Progression and Prevention of Disease. Pediatric Diabetes 15(3):162-174.

Jaberi-Douraki M., Pietropaolo M., **Khadra A**. 2014. Predictive Models of Type 1 Diabetes Progression: Understanding T-Cell Cycles and their Implications on Autoantibody Release. PLoS ONE. 9(4):e93326.

Sugarman J., Tsai S., Santamaria P., **Khadra A.**, 2013. Quantifying the Relative Importance of pMHC Valency, Total pMHC Dose and Frequency on Nanoparticle Therapeutic Efficacy. Immunology and Cell Biology. 91:350-359.

Khadra A., Tomić M., Yan Z., Zemkova H., Sherman A., Stojilkovic S.S. 2013. Dual Gating Mechanism and Function of P2X7 Receptor Channels. Biophysical Journal. 104:2612-2621.

Khadra A., Yan Z., Coddou C., Tomić M., Sherman A. Stojilkovic S.S. 2012. Gating Properties of the P2X2a and P2X2b Receptor Channels: Experiments and Mathematical Modeling. Journal of General Physiology. 139:333-348.

Khadra A., Pietropaolo M., Nepom G.T., Sherman A. 2011. Investigating the Role of T-Cell Avidity and Killing Efficacy in Relation to Type 1 Diabetes Prediction. PLoS ONE. 6:e14796.

Yan Z., **Khadra A.**, Sherman A., Stojilkovic S.S. 2011. Calcium-Dependent Block of P2X7 Receptor Channel Function is Allosteric. Journal of General Physiology. 138:437-452.

Khadra A., Tsai S., Santamaria P., Edelstein-Keshet L. 2010. On How Monospecific Memory-Like Autoregulatory CD8+ T Cells Can Blunt Diabetogenic Autoimmunity: A Computational Approach. Journal of Immunology. 185:5962-5972.

Khadra A., Santamaria P., Edelstein-Keshet L. 2010. The Pathogenicity of Self-Antigen Decreases at High Levels of Autoantigenicity: A Computational Approach. International Immunology. 22:571-582.

Yan Z., **Khadra A.**, Li S., Tomić M., Sherman A., Stojilkovic S.S. 2010. Experimental Characterization and Mathematical Modeling of the P2X7 Receptor Channel Gating. Journal of Neuroscience. 30:14213-14224.

Zhang X., **Khadra A.**, Yang D., Li D. 2010. Unified Impulsive Fuzzy-Model-Based Controllers for Chaotic Systems with Parameter Uncertainties via LMI. Communications in Nonlinear Science and Numerical Simulations. 15:105-114.

Sabrina Leslie

Ahamed M.J., Mahshid S., Berard D.J., Michaud F., Sladek R., Reisner W.W., **Leslie S.R.** 2016. Continuous Confinement Fluidics: Getting Lots of Molecules into Small Spaces with High Fidelity. Macromolecules. 49(7):2853-2859.

Jia B., Wee T.-L., Berard D.J., Mallik A., Juncker D., Brown C.M., **Leslie S.R.**, 2016. Parallelized Cytoindentation Using Convex Micropatterned Surfaces. Biotechniques. 61(2):73-82.

Mahshid S., Ahamed M.J., Berard D., Amin S., Sladek R., **Leslie S.R.**, Reisner W. 2015. Development of a platform for single cell genomics using convex lens-induced confinement. Lab on a Chip. 15(14):3013-3020.

Arsenault A., Leith J.S., Henkin G., McFaul C.M., Tarling M., Talbot R., Berard D., Michaud F., Scott S., **Leslie S.R.** 2015. Open-frame system for single-molecule microscopy. Review of Scientific Instruments. 86(3):033701.

Berard D.J., Michaud F., Mahshid S., Ahamed M.J., McFaul C.M., Leith J.S., Bérubé P., Sladek R., Reisner W., **Leslie S.R.** 2014. Convex lens-induced nanoscale templating. Proceedings of the National Academy of Sciences of the United States of America. 111(37):13295-13300.

Leslie S.R. 2014. CLiC to Enhance. The Pathologist. 214(11).

Berard D., McFaul C.M., Leith J.S., Arsenault A.K., Michaud F., **Leslie S.R.** 2013. Precision platform for convex lens-induced confinement microscopy. Review of Scientific Instruments. 84(10):103704.

Elting M.W., **Leslie S.R.**, Churchman L.S., Korlach J., McFaul C.M., Leith J.S., Levene M.J., Cohen A.E., Spudich J.A. 2013. Single-molecule fluorescence imaging of processive myosin with enhanced background suppression using linear zero-mode waveguides (ZMWs) and convex lens induced confinement (CLIC). Optics express. 21(1):1189-1202.

McFaul C.M., Leith J., Jia B., Michaud F., Arsenault A., Martin A., Berard D., **Leslie S.** 2013. Single-molecule microscopy using tunable nanoscale confinement. In SPIE NanoScience+ Engineering. 881102.

Judith Mandl

Lippens C., Duraes F.V., Guery L., Dubrot J., Brighouse D., Irla M., Aubry-Lachainaye J., Reith W., **Mandl J.N.**, Hugues S. 2016. IDO-orchestrated crosstalk between pDCs and Tregs inhibits autoimmunity. Journal of Autoimmunity. pii: S0896-8411(16)30112-3.

Mandl J.N., Feinberg M.B. 2015. Robust and sustained immune activation in human Ebola virus infection. Proceedings of the National Academy of Sciences of the United States of America. 112(15):4518-4519.

Mandl J.N., Ahmed R., Barreiro L.B., Daszak P., Epstein J.H., Virgin H.W., Feinberg M.B. 2015. Reservoir Host Immune Responses to Emerging Zoonotic Viruses. Cell. 160(1-2):20-35.

Zhang Q., Dove C., Strauss-Albee D., Garcia J., **Mandl J.N.**, Grodick R., Chandler-Brown D., Jing H., Kim E., Lenardo T.E., Matthews H.F., Freeman A.F., Cornall R.J., Germain R.N., Mueller S., Su H. 2014. DOCK8 regulates lymphocyte shape integrity for skin antiviral immunity. Journal of Experimental Medicine. 211(13):2549-66.

Vrisekoop N., Monteiro J.P., **Mandl J.N.**, Germain R.N. 2014. Revisiting thymic positive selection and the mature T cell repertoire for antigen. Immunity. 41(2): 181-190.

Textor J., Hendrickson S.E., **Mandl J.N.**, von Andrian U.H., Westermann J., de Boer R.J., Beltman J.B. 2014. Random Migration and Signal Integration Promote Rapid and Robust T cell Recruitment. PLoS Computational Biology. 10(8):e1003752.

Mandl J.N., Germain R.N. 2014. Focusing in on T cell cross-reactivity. Cell. 157(5):1006-8.

Mandl J.N., Torabi-Parizi P., Germain R.N. 2014. Visualization and dynamic analysis of host-pathogen interactions. Current Opinion Immunology. 29:8-15.

Bouma H.R., **Mandl J.N.**, Strijkstra A.M., Boerema A.S., Kok J.W., van Dam A., Ijzerman A., Kroese F.G., Henning R.H. 2013. 5'-AMP impacts lymphocyte recirculation through activation of A2B receptors. Journal of Leukocyte Biology. 94(1):89-98.

Mandl J.N., Monteiro J.P., Vrisekoop N., Germain R.N. 2013. T cell-positive selection uses self-ligand binding strength to optimize repertoire recognition of foreign antigens. Immunity. 38(2):263-74.

Meteyer C.U., Barber D., **Mandl J.N.** 2012. Pathology in euthermic bats with white nose syndrome suggests a natural manifestation of immune reconstitution inflammatory syndrome. Virulence. 3(7):583-8.

Mandl J.N., Liou R., Klauschen F., Vrisekoop N., Monteiro J.P., Yates A.J., Huang A.Y., Germain R.N. 2012. Quantification of lymph node transit times reveals differences in antigen surveillance strategies of naïve CD4+ and CD8+ T cells. Proceedings of the National Academy of Sciences of the United States of America. 109(44):18036-41.

Lee M., **Mandl J.N.**, Germain R.N., Yates A.J. 2012. The race for the prize: T-cell trafficking strategies for optimal surveillance. Blood. 120(7):1432-8.

Mandl J.N., Akondy R., Lawson B., Kozyr N., Staprans S.I., Ahmed R., Feinberg M.B. 2011. Distinctive TLR7 signaling, type I IFN production, and attenuated innate and adaptive immune responses to yellow fever virus in a primate reservoir host. Journal of Immunology. 186(11):6406-16.

Christopher Pack

Liu L.D., Haefner R., **Pack C.C.** 2016. Neural basis of the spatial suppression of visual motion perception. eLife. 5:e16167.

Neupane S., Guitton D., **Pack C.C.** 2016. Dissociation of forward and convergent remapping in primate visual cortex. Current Biology. 26(12):R491-2.

Cui Y., Liu L.D., McFarland J.M., **Pack C.C.,** Butts D.A. 2016. Inferring cortical variability from local field potentials. Journal of Neuroscience. 3:4121-4135.

Neupane S., Guitton D., **Pack C.C.** 2016. Two distinct types of remapping in primate visual cortex. Nature Communications, 7:10402.

Simard F., **Pack C.C.** 2015. Dissociation of sensory facilitation and decision bias in statistical learning. Visual Cognition. 6:758-780.

Zanos T.P., Mineault P.J., Nasiotis K., Guitton D., **Pack C.C.** 2015. A sensorimotor role for traveling waves in primate visual cortex. Neuron. 85:615-627.

Farah C.A., Naqib F., Weatherill D.B., **Pack C.C.**, Sossin W.S. 2015. Synapse formation changes the rules for desensitization of PKC translocation in Aplysia. European Journal of Neuroscience. 41:328-340.

Pack C.C., Bensmaia S.J. 2015. Seeing and feeling motion: Canonical computations in vision and touch. PLoS Biology. 13(9):e1002271.

Pack C.C. 2014. Eye movements as a probe of corollary discharge function in schizophrenia. ACS Chemical Neuroscience. 5:326-328.

Krause M.R., **Pack C.C.** 2014. Contextual modulation and stimulus selectivity in the extrastriate visual cortex. Vision Research. 104:36-46.

Richard A.G., Churan J., Whitford V., O'Driscoll G.A., Titone D., **Pack C.C.** 2014. Perisaccadic perception of visual space in people with schizophrenia. Journal of Neuroscience. 34:4760-4765.

Cui Y., Liu L., Khawaja F.A., **Pack C.C.,** Butts D.A. 2013. Diverse suppressive influences in area MT and selectivity to complex motion features. Journal of Neuroscience. 33:16715-16728.

Khawaja F.A., Liu L., **Pack C.C.** 2013. Responses of MST neurons to plaid stimuli. Journal of Neurophysiology. 110:63-74.

Mineault P.J., Zanos T.P., **Pack C.C.** 2013. Local field potentials reflect multiple spatial scales in V4. Frontiers in Computational Neuroscience. 7(21):1-15.

Whitford V., O'Driscoll G. A., **Pack C. C.**, Joober R., Malla A., Titone D. 2013. Reading impairments in schizophrenia relate to individual differences in phonological processing and oculomotor control: Evidence from a gaze-contingent moving window paradigm. Journal of Experimental Psychology: General. 142:57-75.

Churan J., Guitton D., **Pack C.C.** 2012. Remapping and rescaling of visual responses in macaque superior colliculus. PLoS One. 7(12):e52195.

Churan J., Guitton D., **Pack C.C.** 2012. Spatiotemporal structure of visual receptive fields in macaque superior colliculus. Journal of Neurophysiology. 108:2653-2667.

Jadauji J., Djordjevic J., Lundström J., **Pack C.C.** 2012. Modulation of olfactory processing by visual cortex stimulation. Journal of Neuroscience. 32:3095-3100.

Mineault P.J., Khawaja F.A., Butts D.A., **Pack C.C.** 2012. Hierarchical processing of complex motion stimuli along the dorsal visual pathway. Proceedings of the National Academy of Sciences of the United States of America. 109:E972-980.

Naqib F., Farah C.A., **Pack C.C.**, Sossin W.S. 2011. The rates of protein synthesis and degradation account for the differential response of neurons to spaced and massed training protocols. PLoS Computational Biology. 7(12):1-21.

Churan J., Guitton D., **Pack C.C.** 2011. Context dependence of receptive field remapping in macaque superior colliculus. Journal of Neurophysiology. 106:1862-1874.

Tsui J.M.G., **Pack C.C.** 2011. Contrast sensitivity of MT receptive field centers and surrounds. Journal of Neurophysiology. 106:1888-1900.

Glasser D.M., Tsui J.M.G, **Pack C.C.**, Tadin D. 2011. Perceptual and neural consequences of rapid motion adaptation. Proceedings of the National Academy of Sciences United States of America. 108:E1080-1088.

Zanos T.P., Mineault P.J., Monteon J.A., **Pack C.C.** 2011. Functional connectivity during surround suppression in macaque area V4. IEEE Engineering in Medicine and Biology Society. 3342-3345.

Richard A.G., Churan J., Guitton D., **Pack, C.C.** 2011. Perceptual compression of visual space during eye-head gaze shifts. Journal of Vision. 11(12):1-17.

Ponce C.R., Hunter J.N., **Pack C.C.**, Lomber S.G., Born R.T. 2011. Contributions of indirect pathways to visual response properties in macaque cortical area MT. Journal of Neuroscience. 313894-3903.

Thompson B., Richard A.G., Churan J., Hess R.F., Stockdale C.A., **Pack C.C.** 2011. Impaired spatial and binocular summation for motion direction discrimination in strabismic amblyopia. Vision Research. 51:577-584.

Zanos T., Mineault P.J., **Pack C.C.** 2011. Removal of spurious correlations between spikes and local field potentials. Journal of Neurophysiology. 105:474-486.

Tomi Pastinen

McGregor K., Bernatsky S., Colmegna I., Hudson M., **Pastinen T.**, Labbe A., Greenwood C. 2016. An evaluation of methods correcting for cell-type heterogeneity in DNA methylation studies. Genome biology. 17:84.

Oros Klein K., Grinek S., Bernatsky S., Bouchard L., Ciampi A., Colmegna I., Fortin J.P., Gao L., Hivert M.F., Hudson M., Kobor M.S., Labbe A., MacIsaac J.L., Meaney M.J., Morin A.M., O'Donnell K.J., **Pastinen T.**, Van Ijzendoorn M.H., Voisin G., Greenwood C. 2016. funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. Bioinformatics. 32(4):593-5.

Busche S., Shao X., Caron M., Kwan T., Allum F., Cheung W.A., Ge B., Westfall S., Simon M.M., Multiple Tissue Human Expression Resource, Barrett A., Bell J.T., McCarthy M.I., Deloukas P., Blanchette M., Bourque G., Spector T.D., Lathrop M., **Pastinen T.**, Grundberg E. 2015. Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology. 16(1):290.

Siuko M., Valori M., Kivelä T., Setälä K., Morin A., Kwan T., **Pastinen T.**, Tienari P. 2015. Exome and regulatory element sequencing of neuromyelitis optica patients. Journal of Neuroimmunology. 289:139-42.

Pacis A., Tailleux L., Morin A.M., Lambourne J., MacIsaac J.L., Yotova V., Dumaine A., Danckaert A., Luca F., Grenier J.C., Hansen K.D., Gicquel B., Yu M., Pai A., He C., Tung J., **Pastinen T.**, Kobor M.S., Pique-Regi R., Gilad Y., Barreiro L.B. 2015. Bacterial infection remodels the DNA methylation landscape of human dendritic cells. Genome Research. 25(12):1801-11.

Zheng H.F., Forgetta V., Hsu Y.H., Estrada K., Rosello-Diez A., Leo P.J., Dahia C.L., Park-Min K.H., Tobias J.H., Kooperberg C., Kleinman A., Styrkarsdottir U., Liu C.T., Uggla C., Evans D.S., Nielson C.M., Walter K., Pettersson-Kymmer U., McCarthy S., Eriksson J., Kwan T., Jhamai M., Trajanoska K., Memari Y., Min J., Huang J., Danecek P., Wilmot B., Li R., Chou W.C., Mokry L.E., Moayyeri A., Claussnitzer M., Cheng C.H., Cheung W., Medina-Gómez C., Ge B., Chen S.H., Choi K., Oei L., Fraser J., Kraaij R., Hibbs M.A., Gregson C.L., Paquette D., Hofman A., Wibom C., Tranah G.J., Marshall M., Gardiner B.B., Cremin K., Auer P., Hsu L., Ring S., Tung J.Y., Thorleifsson G., Enneman A.W., van Schoor N.M., de Groot L.C., van der Velde N., Melin B., Kemp J.P., Christiansen C., Sayers A., Zhou Y., Calderari S., van Rooij J., Carlson C., Peters U., Berlivet S., Dostie J., Uitterlinden A.G., Williams S.R., Farber C., Grinberg D., LaCroix A.Z., Haessler J., Chasman D.I., Giulianini F., Rose L.M., Ridker P.M., Eisman J.A., Nguyen T.V., Center J.R., Nogues X., Garcia-Giralt N., Launer L.L., Gudnason V., Mellström D., Vandenput L., Amin N., van Duijn

C.M., Karlsson M.K., Ljunggren Ö., Svensson O., Hallmans G., Rousseau F., Giroux S., Bussière J., Arp P.P., Koromani F., Prince R.L., Lewis J.R., Langdahl B.L., Hermann A.P., Jensen J.E., Kaptoge S., Khaw K.T., Reeve J., Formosa M.M., Xuereb-Anastasi A., Åkesson K., McGuigan F.E., Garg G., Olmos J.M., Zarrabeitia M.T., Riancho J.A., Ralston S.H., Alonso N., Jiang X., Goltzman D., **Pastinen T.**, Grundberg E., Gauguier D., Orwoll E.S., Karasik D., Davey-Smith G., AOGC Consortium, Smith A.V., Siggeirsdottir K., Harris T.B., Zillikens M.C., van Meurs J.B., Thorsteinsdottir U., Maurano M.T., Timpson N.J., Soranzo N., Durbin R., Wilson S.G., Ntzani E.E., Brown M.A., Stefansson K., Hinds D.A., Spector T., Cupples L.A., Ohlsson C., Greenwood C., UK10K Consortium, Jackson R.D., Rowe D.W., Loomis C.A., Evans D.M., Ackert-Bicknell C.L., Joyner A.L., Duncan E.L., Kiel D.P., Rivadeneira F., Richards J.B. 2015. Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature. 526(7571):112-7.

Aarabi M., San Gabriel M.C., Chan D., Behan N.A., Caron M., **Pastinen T.**, Bourque G., MacFarlane A.J., Zini A., Trasler J. 2015. High-dose folic acid supplementation alters the human sperm methylome and is influenced by the MTHFR C677T polymorphism. Human Molecular Genetics. 24(22):6301-13.

Dyke S.O., Cheung W.A., Joly Y., Ammerpohl O., Lutsik P., Rothstein M.A., Caron M., Busche S., Bourque G., Rönnblom L., Flicek P., Beck S., Hirst M., Stunnenberg H., Siebert R., Walter J., **Pastinen T**. 2015. Epigenome data release: a participant-centered approach to privacy protection. Genome Biology. 16:142.

Laxman N., Rubin C.J., Mallmin H., Nilsson O., **Pastinen T.**, Grundberg E., Kindmark A. 2015. Global miRNA expression and correlation with mRNA levels in primary human bone cells. RNA. 21(8):1433-43.

Labreche K., Simeonova I., Kamoun A., Gleize V., Chubb D., Letouzé E., Riazalhosseini Y., Dobbins S.E., Elarouci N., Ducray F., de Reyniès A., Zelenika D., Wardell C.P., Frampton M., Saulnier O., **Pastinen T.**, Hallout S., Figarella-Branger D., Dehais C., Idbaih A., Mokhtari K., Delattre J.Y., Huillard E., Mark Lathrop G., Sanson M., Houlston R.S., POLA Network. 2015. TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications. 6:7207.

Park H.W., Ge B., Tse S., Grundberg E., **Pastinen T.**, Kelly H.W., Tantisira K.G. 2015. Genetic risk factors for decreased bone mineral accretion in children with asthma receiving multiple oral corticosteroid bursts. Journal of Allergy and Clinical Immunology. 136(5):1240-6.e1-8.

Allum F., Shao X., Guénard F., Simon M.M., Busche S., Caron M., Lambourne J., Lessard J., Tandre K., Hedman Å.K., Kwan T., Ge B.;, Multiple Tissue Human Expression Resource Consortium, Rönnblom L., McCarthy M.I., Deloukas P., Richmond T., Burgess D., Spector T.D., Tchernof A., Marceau S., Lathrop M., Vohl M.C., **Pastinen T.**, Grundberg E. 2015. Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications. 2015 May 29;6:7211

Hudson M., Baron M., Colmegna I., Bernatsky S., Klein Oros K., **Pastinen T.**, Greenwood C. 2015. Novel approaches to discovery of biomarkers in rheumatoid arthritis: comment on the article by Oswald et al. Arthritis Rheumatol. 67(8):2276-7.

Joly Y., Dyke S.O., Cheung W.A., Rothstein M.A., **Pastinen T**. 2015. Risk of re-identification of epigenetic methylation data: a more nuanced response is needed. Clinical Epigenetics. 7(1):45.

Lemire M., Zaidi S.H., Ban M., Ge B., Aïssi D., Germain M., Kassam I., Wang M., Zanke B.W., Gagnon F., Morange P.E., Trégouët D.A., Wells P.S., Sawcer S., Gallinger S., **Pastinen T.**, Hudson T.J. 2015. Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. Nature Communications. 6:6326.

Liang L., Willis-Owen S.A., Laprise C., Wong K.C., Davies G.A., Hudson T.J., Binia A., Hopkin J.M., Yang I.V., Grundberg E., Busche S., Hudson M., Rönnblom L., **Pastinen T.**, Schwartz D.A., Lathrop G.M., Moffatt M.F., Cookson W.O. 2015. An epigenome-wide association study of total serum immunoglobulin E concentration. Nature. 520(7549):670-4.

McGraw S., Zhang J.X., Farag M., Chan D., Caron M., Konermann C., Oakes C.C., Mohan K.N., Plass C., **Pastinen T.**, Bourque G., Chaillet J.R., Trasler J.M. 2015. Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research. 43(3):1485-97.

Adoue V., Schiavi A., Light N., Almlöf J.C., Lundmark P., Ge B., Kwan T., Caron M., Ronnblom L., Wang C., Chen S.H., Goodall A.H., Cambien F., Deloukas P., Ouwehand W., Syvanen A.C., **Pastinen T.** 2014. Allelic expression mapping across cellular lineages to establish impact of non-coding SNPs. Molecular Systems Biology. 10:754.

Almlöf J.C., Lundmark P., Lundmark A., Ge B., **Pastinen T.**, Cardiogenics Consortium, Goodall A.H., Cambien F., Deloukas P., Ouwehand W.H., Syvänen A.C. 2014. Single nucleotide polymorphisms with cis-regulatory effects on long non-coding transcripts in human primary monocytes. PLoS One. 15:e102612.

Light N., Adoue V., Ge B., Chen S.H., Kwan T., **Pastinen T**. 2014. Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. Epigenetics. 9(9):1238-1251.

Wagner J.R., Busche S., Ge B., Kwan T., **Pastinen T.,** Blanchette M. 2014. The relationship between DNA methylation, genetic and expression inter-individual variation in untransformed human fibroblasts. Genome Biol. 15(2):R37.

Zhang K., Huentelman M.J., Rao F., Sun E.I., Corneveaux J.J., Schork A.J., Wei Z., Waalen J., Miramontes-Gonzalez J.P., Hightower C.M., Maihofer A.X., Mahata M., **Pastinen T.**, Ehret GB, International Consortium for Blood Pressure Genome-Wide Association Studies, Schork N.J., Eskin E., Nievergelt C.M., Saier M.H. Jr, O'Connor D.T. 2014. Genetic implication of a novel thiamine transporter in human hypertension. Journal of American College Cardiology. 63:1542-55.

Kleinman C.L., Gerges N., Papillon-Cavanagh S., Sin-Chan P., Pramatarova A., Quang D.A., Adoue V., Busche S., Caron M., Djambazian H., Bemmo A., Fontebasso A.M., Spence T., Schwartzentruber J., Albrecht S., Hauser P., Garami M., Klekner A., Bognar L., Montes J.L., Staffa A., Montpetit A., Berube P., Zakrzewska M., Zakrzewski K., Liberski P.P., Dong Z., Siegel P.M., Duchaine T., Perotti C., Fleming A., Faury D., Remke M., Gallo M., Dirks P., Taylor M.D., Sladek R., **Pastinen T.**, Chan J.A., Huang A., Majewski J., Jabado N. 2014. Fusion of Ttyh1 with the C19mc Microrna Cluster Drives Expression of a Brain-Specific Dnmt3b Isoform in the Embryonal Brain Tumor Etmr. Nature Genetics. 46(1):39-44.

Busche S., Ge B., Vidal R., Spinella J.F., Saillour V., Richer C., Healy J., Chen S.H., Droit A., Sinnett D., **Pastinen T.** 2013. Integration of High-Resolution Methylome and Transcriptome Analyses to Dissect Epigenomic Changes in Childhood Acute Lymphoblastic Leukemia. Cancer Research. 73(14):4323-36.

CARDIoGRAMplusC4D Consortium, Deloukas P., Kanoni S., Willenborg C., Farrall M., Assimes T.L., Thompson J.R., Ingelsson E., Saleheen D., Erdmann J., Goldstein B.A., Stirrups K., König I.R., Cazier J.B., Johansson A., Hall A.S., Lee J.Y., Willer C.J., Chambers J.C., Esko T., Folkersen L., Goel A., Grundberg E., Havulinna A.S., Ho W.K., Hopewell J.C., Eriksson N., Kleber M.E., Kristiansson K., Lundmark P., Lyytikäinen L.P., Rafelt S., Shungin D., Strawbridge R.J., Thorleifsson G., Tikkanen E., Van Zuydam N., Voight B.F., Waite L.L., Zhang W., Ziegler A., Absher D., Altshuler D.,

Balmforth A.J., Barroso I., Braund P.S., Burgdorf C., Claudi-Boehm S., Cox D., Dimitriou M., Do R., DIAGRAM Consortium, CARDIOGENICS Consortium, Doney A.S., El Mokhtari N., Eriksson P., Fischer K., Fontanillas P., Franco-Cereceda A., Gigante B., Groop L., Gustafsson S., Hager J., Hallmans G., Han B.G., Hunt S.E., Kang H.M., Illig T., Kessler T., Knowles J.W., Kolovou G., Kuusisto J., Langenberg C., Langford C., Leander K., Lokki M.L., Lundmark A., McCarthy M.I., Meisinger C., Melander O., Mihailov E., Maouche S., Morris A.D., Müller-Nurasyid M., MuTHER Consortium, Nikus K., Peden J.F., Rayner N.W., Rasheed A., Rosinger S., Rubin D., Rumpf M.P., Schäfer A., Sivananthan M., Song C., Stewart A.F., Tan S.T., Thorgeirsson G., van der Schoot C.E., Wagner P.J., Wellcome Trust Case Control Consortium, Wells G.A., Wild P.S., Yang T.P., Amouyel P., Arveiler D., Basart H., Boehnke M., Boerwinkle E., Brambilla P., Cambien F., Cupples A.L., de Faire U., Dehghan A., Diemert P., Epstein S.E., Evans A., Ferrario M.M., Ferrières J., Gauguier D., Go A.S., Goodall A.H., Gudnason V., Hazen S.L., Holm H., Iribarren C., Jang Y., Kähönen M., Kee F., Kim H.S., Klopp N., Koenig W., Kratzer W., Kuulasmaa K., Laakso M., Laaksonen R., Lee J.Y., Lind L., Ouwehand W.H., Parish S., Park J.E., Pedersen N.L., Peters A., Quertermous T., Rader D.J., Salomaa V., Schadt E., Shah S.H., Sinisalo J., Stark K., Stefansson K., Trégouët D.A., Virtamo J., Wallentin L., Wareham N., Zimmermann M.E., Nieminen M.S., Hengstenberg C., Sandhu M.S., **Pastinen T.**, Syvänen A.C., Hovingh G.K., Dedoussis G., Franks P.W., Lehtimäki T., Metspalu A., Zalloua P.A., Siegbahn A., Schreiber S., Ripatti S., Blankenberg S.S., Perola M., Clarke R., Boehm B.O., O'Donnell C., Reilly M.P., März W., Collins R., Kathiresan S., Hamsten A., Kooner J.S., Thorsteinsdottir U., Danesh J., Palmer C.N., Roberts R., Watkins H., Schunkert H., Samani N.J. 2013. Large-Scale Association Analysis Identifies New Risk Loci for Coronary Artery Disease. Nature Genetics. 45(1):25-33.

Cotton A. M., Ge B., Light N., Adoue V., **Pastinen T.**, Brown C.J. 2013. Analysis of Expressed Snps Identifies Variable Extents of Expression from the Human Inactive X Chromosome. Genome Biology. 14(11):R122.

Couch F.J., Wang X., McGuffog L., Lee A., Olswold C., Kuchenbaecker K.B., Soucy P., Fredericksen Z., Barrowdale D., Dennis J., Gaudet M.M., Dicks E., Kosel M., Healey S., Sinilnikova O.M., Lee A., Bacot F., Vincent D., Hogervorst F.B., Peock S., Stoppa-Lyonnet D., Jakubowska A., kConFab Investigators, Radice P., Schmutzler R.K. SWE-BRCA, Domchek S.M., Piedmonte M., Singer C.F., Friedman E., Thomassen M., Ontario Cancer Genetics Network, Hansen T.V., Neuhausen S.L., Szabo C.I., Blanco I., Greene M.H., Karlan B.Y., Garber J., Phelan C.M., Weitzel J.N., Montagna M., Olah E., Andrulis I.L., Godwin A.K., Yannoukakos D., Goldgar D.E., Caldes T., Nevanlinna H., Osorio A., Terry M.B., Daly M.B., van Rensburg E.J., Hamann U., Ramus S.J., Toland A.E., Caligo M.A., Olopade O.I., Tung N., Claes K., Beattie M.S., Southey M.C., Imyanitov E.N., Tischkowitz M., Janavicius R., John E.M., Kwong A., Diez O., Balmaña J., Barkardottir R.B., Arun B.K., Rennert G., Teo S.H., Ganz P.A., Campbell I., van der Hout A.H., van Deurzen C.H., Seynaeve C., Gómez Garcia E.B., van Leeuwen F.E., Meijers-Heijboer H.E., Gille J.J., Ausems M.G., Blok M.J., Ligtenberg M.J., Rookus M.A., Devilee P., Verhoef S., van Os T.A., Wijnen J.T., HEBON, EMBRACE, Frost D., Ellis S., Fineberg E., Platte R., Evans D.G., Izatt L., Eeles R.A., Adlard J., Eccles D.M., Cook J., Brewer C., Douglas F., Hodgson S., Morrison P.J., Side L.E., Donaldson A., Houghton C., Rogers M.T., Dorkins H., Eason J., Gregory H., McCann E., Murray A., Calender A., Hardouin A., Berthet P., Delnatte C., Nogues C., Lasset C., Houdayer C., Leroux D., Rouleau E., Prieur F., Damiola F., Sobol H., Coupier I., Venat-Bouvet L., Castera L., Gauthier-Villars M., Léoné M., Pujol P., Mazoyer S., Bignon Y.J., GEMO Study Collaborators, Złowocka-Perłowska E., Gronwald J., Lubinski J., Durda K., Jaworska K., Huzarski T., Spurdle A.B., Viel A., Peissel B., Bonanni B., Melloni G., Ottini L., Papi L., Varesco L., Tibiletti M.G., Peterlongo P., Volorio S., Manoukian S., Pensotti V., Arnold N., Engel C., Deissler H., Gadzicki D., Gehrig A., Kast K., Rhiem K., Meindl A., Niederacher D., Ditsch N., Plendl H., Preisler-Adams S., Engert S., Sutter C., Varon-Mateeva R., Wappenschmidt B., Weber B.H., Arver B., Stenmark-Askmalm M., Loman N., Rosenquist R., Einbeigi

Z., Nathanson K.L., Rebbeck T.R., Blank S.V., Cohn D.E., Rodriguez G.C., Small L., Friedlander M., Bae-Jump V.L., Fink-Retter A., Rappaport C., Gschwantler-Kaulich D., Pfeiler G., Tea M.K., Lindor N.M., Kaufman B., Shimon Paluch S., Laitman Y., Skytte A.B., Gerdes A.M., Pedersen I.S., Moeller S.T., Kruse T.A., Jensen U.B., Vijai J., Sarrel K., Robson M., Kauff N., Mulligan A.M., Glendon G., Ozcelik H., Ejlertsen B., Nielsen F.C., Jønson L., Andersen M.K., Ding Y.C., Steele L., Foretova L., Teulé A., Lazaro C., Brunet J., Pujana M.A., Mai P.L., Loud J.T., Walsh C., Lester J., Orsulic S., Narod S.A., Herzog J., Sand S.R., Tognazzo S., Agata S., Vaszko T., Weaver J., Stavropoulou A.V., Buys S.S., Romero A., de la Hoya M., Aittomäki K., Muranen T.A., Duran M., Chung W.K., Lasa A., Dorfling C.M., Miron A., BCFR, Benitez J., Senter L., Huo D., Chan S.B., Sokolenko A.P., Chiquette J., Tihomirova L., Friebel T.M., Agnarsson B.A., Lu K.H., Lejbkowicz F., James P.A., Hall P., Dunning A.M., Tessier D., Cunningham J., Slager S.L., Wang C., Hart S., Stevens K., Simard J., **Pastinen T.**, Pankratz V.S., Offit K., Easton D.F., Chenevix-Trench G., Antoniou A.C., CIMBA. 2013. Genome-Wide Association Study in Brca1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics. 9(3):e1003212.

Demerath E.W., Liu C.T., Franceschini N., Chen G., Palmer J.R., Smith E.N., Chen C.T., Ambrosone C.B., Arnold A.M., Bandera E.V., Berenson G.S., Bernstein L., Britton A., Cappola A.R., Carlson C.S., Chanock S.J., Chen W., Chen Z., Deming S.L., Elks C.E., Evans M.K., Gajdos Z., Henderson B.E., Hu J.J., Ingles S., John E.M., Kerr K.F., Kolonel L.N., Le Marchand L., Lu X., Millikan R.C., Musani S.K., Nock N.L., North K., Nyante S., Press M.F., Rodriquez-Gil J.L., Ruiz-Narvaez E.A., Schork N.J., Srinivasan S.R., Woods N.F., Zheng W., Ziegler R.G., Zonderman A., Heiss G., Gwen Windham B., Wellons M., Murray S.S., Nalls M., **Pastinen T.**, Rajkovic A., Hirschhorn J., Adrienne Cupples L., Kooperberg C., Murabito J.M., Haiman C.A. 2013. Genome-Wide Association Study of Age at Menarche in African-American Women. Human Molecular Genetics. 22(16):3329-46.

Li Q., Makri A., Lu Y., Marchand L., Grabs R., Rousseau M., Ounissi-Benkalha H., Pelletier J., Robert F., Harmsen E., Hudson T.J., **Pastinen T.**, Polychronakos C., Qu H.Q. 2013. Genome-Wide Search for Exonic Variants Affecting Translational Efficiency. Nature Communications. 4:2260.

Najafabadi H.S., Lu Z., MacPherson C., Mehta V., Adoue V., **Pastinen T.**, Salavati R. 2013. Global Identification of Conserved Post-Transcriptional Regulatory Programs in Trypanosomatids. Nucleic Acids Research. 41(18):8591-600.

Nordlund J., Bäcklin C.L., Wahlberg P., Busche S., Berglund E.C., Eloranta M.L., Flaegstad T., Forestier E., Frost B.M., Harila-Saari A., Heyman M., Jónsson O.G., Larsson R., Palle J., Rönnblom L., Schmiegelow K., Sinnett D., Söderhäll S., **Pastinen T.**, Gustafsson M.G., Lönnerholm G., Syvänen A.C. 2013. Genome-Wide Signatures of Differential DNA Methylation in Pediatric Acute Lymphoblastic Leukemia. Genome Biology. 14(9):r105.

Sanseau P., Agarwal P., Barnes M.R., **Pastinen T.**, Richards J.B., Cardon L.R., Mooser V. 2013. 'Reply to Rational Drug Repositioning by Medical Genetics. Nature Biotechnology, 31(12):1082.

Deloukas P., Kanoni S., Willenborg C., Farrall M., Assimes T.L., Thompson J.R., Ingelsson E., Saleheen D., Erdmann J., Goldstein B.A., Stirrups K., König I.R., Cazier J.B., Johansson A., Hall A.S., Lee J.Y., Willer C.J., Chambers J.C., Esko T., Folkersen L., Goel A., Grundberg E., Havulinna A.S., Ho W.K., Hopewell J.C., Eriksson N., Kleber M.E., Kristiansson K., Lundmark P., Lyytikäinen L.P., Rafelt S., Shungin D., Strawbridge R.J., Thorleifsson G., Tikkanen E., Van Zuydam N., Voight B.F., Waite L.L., Zhang W., Ziegler A., Absher D., Altshuler D., Balmforth A.J., Barroso I., Braund P.S., Burgdorf C., Claudi-Boehm S., Cox D., Dimitriou M., Do R., DIAGRAM Consortium, CARDIOGENICS Consortium, Doney A.S., El Mokhtari N., Eriksson P., Fischer K., Fontanillas P., Franco-Cereceda A., Gigante B., Groop L.,

Gustafsson S., Hager J., Hallmans G., Han B.G., Hunt S.E., Kang H.M., Illig T., Kessler T., Knowles J.W., Kolovou G., Kuusisto J., Langenberg C., Langford C., Leander K., Lokki M.L., Lundmark A., McCarthy M.I., Meisinger C., Melander O., Mihailov E., Maouche S., Morris A.D., Müller-Nurasyid M. MuTHER Consortium, Nikus K., Peden J.F., Rayner N.W., Rasheed A., Rosinger S., Rubin D., Rumpf M.P., Schäfer A., Sivananthan M., Song C., Stewart A.F., Tan S.T., Thorgeirsson G., van der Schoot C.E., Wagner P.J., Wellcome Trust Case Control Consortium, Wells G.A., Wild P.S., Yang T.P., Amouyel P., Arveiler D., Basart H., Boehnke M., Boerwinkle E., Brambilla P., Cambien F., Cupples A.L., de Faire U., Dehghan A., Diemert P., Epstein S.E., Evans A., Ferrario M.M., Ferrières J., Gauguier D., Go A.S., Goodall A.H., Gudnason V., Hazen S.L., Holm H., Iribarren C., Jang Y., Kähönen M., Kee F., Kim H.S., Klopp N., Koenig W., Kratzer W., Kuulasmaa K., Laakso M., Laaksonen R., Lee J.Y., Lind L., Ouwehand W.H., Parish S., Park J.E., Pedersen N.L., Peters A., Quertermous T., Rader D.J., Salomaa V., Schadt E., Shah S.H., Sinisalo J., Stark K., Stefansson K., Trégouët D.A., Virtamo J., Wallentin L., Wareham N., Zimmermann M.E., Nieminen M.S., Hengstenberg C., Sandhu M.S., **Pastinen T.**, Syvänen A.C., Hovingh G.K., Dedoussis G., Franks P.W., Lehtimäki T., Metspalu A., Zalloua P.A., Siegbahn A., Schreiber S., Ripatti S., Blankenberg S.S., Perola M., Clarke R., Boehm B.O., O'Donnell C., Reilly M.P., März W., Collins R., Kathiresan S., Hamsten A., Kooner J.S., Thorsteinsdottir U., Danesh J., Palmer C.N., Roberts R., Watkins H., Schunkert H., Samani N.J. 2013. Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics. 45:25-33.

Almlöf J.C., Lundmark P., Lundmark A., Ge B., Maouche S., Göring H.H., Liljedahl U., Enström C., Brocheton J., Proust C., Godefroy T., Sambrook J.G., Jolley J., Crisp-Hihn A., Foad N., Lloyd-Jones H., Stephens J., Gwilliam R., Rice C.M., Hengstenberg C., Samani N.J., Erdmann J., Schunkert H., **Pastinen T.**, Deloukas P., Goodall A.H., Ouwehand W.H., Cambien F., Syvänen A.C. 2012. Powerful Identification of Cis-regulatory SNPs in Human Primary Monocytes Using Allele-Specific Gene Expression. PLoS One. 7:e52260.

Lefebvre J.F., Vello E., Ge B., Montgomery S.B., Dermitzakis E.T., **Pastinen T.**, Labuda D. 2012. Genotype-based test in mapping cis-regulatory variants from allele-specific expression data. PLoS One. 7:e38667.

Liu C.T., Estrada K., Yerges-Armstrong L.M., Amin N., Evangelou E., Li G., Minster R.L., Carless M.A., Kammerer C.M., Oei L., Zhou Y., Alonso N., Dailiana Z., Eriksson J., García-Giralt N., Giroux S., Husted L.B., Khusainova R.I., Koromila T., Kung A.W., Lewis J.R., Masi L., Mencej-Bedrac S., Nogues X., Patel M.S., Prezelj J., Richards J.B., Sham P.C., Spector T., Vandenput L., Xiao S.M., Zheng H.F., Zhu K., Balcells S., Brandi M.L., Frost M., Goltzman D., González-Macías J., Karlsson M., Khusnutdinova E.K., Kollia P., Langdahl B.L., Ljunggren O., Lorentzon M., Marc J., Mellström D., Ohlsson C., Olmos J.M., Ralston S.H., Riancho J.A., Rousseau F., Urreizti R., Van Hul W., Zarrabeitia M.T., Castano-Betancourt M., Demissie S., Grundberg E., Herrera L., Kwan T., Medina-Gómez C., **Pastinen T.**, Sigurdsson G., Thorleifsson G., Vanmeurs J.B., Blangero J., Hofman A., Liu Y., Mitchell B.D., O'Connell J.R., Oostra B.A., Rotter J.I., Stefansson K., Streeten E.A., Styrkarsdottir U., Thorsteinsdottir U., Tylavsky F.A., Uitterlinden A., Cauley J.A., Harris T.B., Ioannidis J.P., Psaty B.M., Robbins J.A., Zillikens M.C., Vanduijn C.M., Prince R.L., Karasik D., Rivadeneira F., Kiel D.P., Cupples L.A., Hsu Y.H. 2012. Assessment of gene-by-sex interaction effect on bone mineral density. Journal of Bone and Mineral Research. 27:2051-64.

Verlaan D.J., Ouimet M., Adoue V., Sirois-Gagnon D., Larivière M., Ge B., Beaulieu P., Dias J., Lam K.C., Koka V., Laprise C., **Pastinen T.**, Sinnett D. 2012. Promoter polymorphisms in CHI3L1 are associated with asthma. Journal of Allergy and Clinical Immunology. 130:533-5.

Estrada K., Styrkarsdottir U., Evangelou E., Hsu Y.H., Duncan E.L., Ntzani E.E., Oei L., Albagha O.M., Amin N., Kemp J.P., Koller D.L., Li G., Liu C.T., Minster R.L., Moayyeri A., Vandenput L., Willner D., Xiao S.M., Yerges-Armstrong

L.M., Zheng H.F., Alonso N., Eriksson J., Kammerer C.M., Kaptoge S.K., Leo P.J., Thorleifsson G., Wilson S.G., Wilson J.F., Aalto V., Alen M., Aragaki A.K., Aspelund T., Center J.R., Dailiana Z., Duggan D.J., Garcia M., Garcia-Giralt N., Giroux S., Hallmans G., Hocking L.J., Husted L.B., Jameson K.A., Khusainova R., Kim G.S., Kooperberg C., Koromila T., Kruk M., Laaksonen M., Lacroix A.Z., Lee S.H., Leung P.C., Lewis J.R., Masi L., Mencej-Bedrac S., Nguyen T.V., Nogues X., Patel M.S., Prezelj J., Rose L.M., Scollen S., Siggeirsdottir K., Smith A.V., Svensson O., Trompet S., Trummer O., van Schoor N.M., Woo J., Zhu K., Balcells S., Brandi M.L., Buckley B.M., Cheng S., Christiansen C., Cooper C., Dedoussis G., Ford I., Frost M., Goltzman D., González-Macías J., Kähönen M., Karlsson M., Khusnutdinova E., Koh J.M., Kollia P., Langdahl B.L., Leslie W.D., Lips P., Ljunggren O., Lorenc R.S., Marc J., Mellström D., Obermayer-Pietsch B., Olmos J.M., Pettersson-Kymmer U., Reid D.M., Riancho J.A., Ridker P.M., Rousseau F., Lagboom P.E., Tang N.L., Urreizti R., Van Hul W., Viikari J., Zarrabeitia M.T., Aulchenko Y.S., Castano-Betancourt M., Grundberg E., Herrera L., Ingvarsson T., Johannsdottir H., Kwan T., Li R., Luben R., Medina-Gómez C., Th Palsson S., Reppe S., Rotter J.I., Sigurdsson G., van Meurs J.B., Verlaan D., Williams F.M., Wood A.R., Zhou Y., Gautvik K.M., **Pastinen** T., Raychaudhuri S., Cauley J.A., Chasman D.I., Clark G.R., Cummings S.R., Danoy P., Dennison E.M., Eastell R., Eisman J.A., Gudnason V., Hofman A., Jackson R.D., Jones G., Jukema J.W., Khaw K.T., Lehtimäki T., Liu Y., Lorentzon M., McCloskey E., Mitchell B.D., Nandakumar K., Nicholson G.C., Oostra B.A., Peacock M., Pols H.A., Prince R.L., Raitakari O., Reid I.R., Robbins J., Sambrook P.N., Sham P.C., Shuldiner A.R., Tylavsky F.A., van Duijn C.M., Wareham N.J., Cupples L.A., Econs M.J., Evans D.M., Harris T.B., Kung A.W., Psaty B.M., Reeve J., Spector T.D., Streeten E.A., Zillikens M.C., Thorsteinsdottir U., Ohlsson C., Karasik D., Richards J.B., Brown M.A., Stefansson K., Uitterlinden A.G., Ralston S.H., Ioannidis J.P., Kiel D.P., Rivadeneira F. 2012. Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics. 44:491-501.

Sanseau P., Agarwal P., Barnes M.R., **Pastinen T.**, Richards J.B., Cardon L.R., Mooser V. 2012. Use of Genome-Wide Association Studies for Drug Repositioning**.** Nature Biotechnology. 30:317-20.

Berlivet, S., Moussette, S., Ouimet, M., Verlaan, D.J., Koka, V., Al Tuwaijri, A., Kwan, T., Sinnett, D., Pastinen, T. and Naumova, A.K. 2012. Interaction between genetic and epigenetic variation defines gene expression patterns at the asthma-associated locus 17q12-q21 in lymphoblastoid cell lines. Human Genetics. Jan 24. 131(7):1161-1171.

Schiavi A., Light N., Adoue V., Busche S., **Pastinen T**. 2011. Human Genetics in full resolution. Genome Biology. 12:309.

M. Labuda M., S. Laberge S., J. Briere J., D. Berube D., P. Beaulieu P., **T. Pastinen T.**, M. Krajinovic M. 2011. Phosphodiesterase type 4D gene polymorphism - association with the response to short acting bronchodilators in paediatric asthma patients. Mediators of Inflammation. 2011:301695.

N'Diaye A., Chen G.K., Palmer C.D., Ge B., Tayo B., Mathias R.A., Ding J., Nalls M.A., Adeyemo A., Adoue V., Ambrosone C.B., Atwood L., Bandera E.V., Becker L.C., Berndt S.I., Bernstein L., Blot W.J., Boerwinkle E., Britton A., Casey G., Chanock S.J., Demerath E., Deming S.L., Diver W.R., Fox C., Harris T.B., Hernandez D.G., Hu J.J., Ingles S.A., John E.M., Johnson C., Keating B., Kittles R.A., Kolonel L.N., Kritchevsky S.B., Le Marchand L., Lohman K., Liu J., Millikan R.C., Murphy A., Musani S., Neslund-Dudas C., North K.E., Nyante S., Ogunniyi A., Ostrander E.A., Papanicolaou G., Patel S., Pettaway C.A., Press M.F., Redline S., Rodriguez-Gil J.L., Rotimi C., Rybicki B.A., Salako B., Schreiner P.J., Signorello L.B., Singleton A.B., Stanford J.L., Stram A.H., Stram D.O., Strom S.S., Suktitipat B., Thun M.J., Witte J.S., Yanek L.R., Ziegler R.G., Zheng W., Zhu X., Zmuda J.M., Zonderman A.B., Evans M.K., Liu Y., Becker D.M., Cooper R.S., **Pastinen T.**, Henderson B.E., Hirschhorn J.N., Lettre G., Haiman C.A. 2011. Identification,

replication and fine-mapping of loci associated with adult height in individuals of African ancestry. PLoS Genetics. 7(10):e1002298.

Grundberg E., Adoue V., Kwan T., Ge B., Duan Q.L., Lam K.C.L., Koka V., Kindmark A., Weiss S.T., Tantisira K., Mallmin H., Raby B.A., Nilsson O., **Pastinen T.** 2011. Global analysis of the impact of environmental perturbation on cis-regulation of gene expression. PLoS Genetics. 20:e1001279.

Morcos L., Verlaan D.J., Ge B., Koka V., Lam K.C.L., Pokholok D., Gunderson K.L., Montpetit A., **Pastinen T**. 2011. Genome-wide assessment of imprinted expression in human cells. Genome Biology. 12:R25.

Majewski J., **Pastinen T.** 2011. The study of eQTL variations by RNA-seq: from SNPs to phenotype. Trends in Genetics. 27:72-9.

Lalonde E., Ha K.C.H., Wang Z., Bemmo A., Kwan T., **Pastinen T.**, Majewski J. 2011. High Throughput RNA Sequencing Reveals Genetic Determinants and Mechanisms Regulating Human Expression Quantitative Traits Loci. Genome Research. 21:545-554.

Paul Wiseman

Rappaz B., Sun K.L.W., Correia J.P., **Wiseman P.W.**, Kennedy T.E. 2016. FLIM FRET Visualization of Cdc42 Activation by Netrin-1 in Embryonic Spinal Commissural Neuron Growth Cones. PLoS One. 11(8):0159405.

Klein H., Abu-Arish A., Trinh N.T.N., Luo Y., **Wiseman P.W.**, Hanrahan J.W., Brochiero E., Sauvé R. 2016. Investigating CFTR and KCa3. 1 Protein/Protein Interactions. PloS one. 11(4):e0153665.

Gopal A.A., Rappaz B., Rouger V., Martyn I.B., Dahlberg P.D., Meland R.J., Beamish I.V., Kennedy T.E., **Wiseman P.W.** 2016. Netrin-1-Regulated Distribution of UNC5B and DCC in Live Cells Revealed by TICCS. Biophysical journal. 110(3):623-634.

Miraucourt L.S., Tsui J., Gobert D., Desjardins J.F., Schohl A., Sild M., Spratt P., Castonguay A., De Koninck Y., Marsh-Armstrong N., **Wiseman P.W.**, Ruthazer E.S. 2016. Endocannabinoid signaling enhances visual responses through modulation of intracellular chloride levels in retinal ganglion cells. Elife. 5:e15932.

Meddens M.B., van den Dries K., Guillet D., Figdor C.G., **Wiseman P.**, Cambi A. 2013. Mesoscale Coordinated Dynamics of Cytoskeletal Components at Mechanosensory Podosomes Shown by Time Resolved STICS. Biophysical Journal. 104(2):143a.

Ashdown G., Pandžić E., Cope A., **Wiseman P.**, Owen D. 2015. Cortical Actin Flow in T Cells Quantified by Spatio-temporal Image Correlation Spectroscopy of Structured Illumination Microscopy Data. Journal of Visualized Experiments: JoVE. (106):e53749.

Godin A.G., Rappaz B., Potvin-Trottier L., Kennedy T.E., De Koninck Y., **Wiseman P.W.** 2015. Spatial intensity distribution analysis reveals abnormal oligomerization of proteins in single cells. Biophysical journal. 109(4):710-21.

Abu-arish A., Pandzic E., Goeppe J., Matthes E., Hanrahan J.W., **Wiseman P.W.** 2015. Cholesterol modulates CFTR confinement in the plasma membrane of primary epithelial cells. Biophysical Journal. 109(1):85-94.

Heris H.K., Miri A.K., Ghattamaneni N.R., Li N.Y.K., Thibeault S.L., Wiseman P.W., Mongeau L. 2015. Microstructural and mechanical characterization of scarred vocal folds. Journal of Biomechanics. 48(4):708-711.

Ashdown G.W., Cope A., **Wiseman P.W.**, Owen D.M. 2014. Molecular flow quantified beyond the diffraction limit by spatio-temporal image correlation of structured illumination microscopy data. Biophysical Journal. 107(9):L21-L23.

Khazaei M.R., Girouard M.-P., Alchini R., Tone S.O., Shimada T., Bechstedt S., Cowan M., Guillet D., **Wiseman P.W.**, Brouhard G., Cloutier J.F., Fournier A.E.. 2014. Collapsin response mediator protein 4 regulates growth cone dynamics through the actin and microtubule cytoskeleton. Journal of Biological Chemistry. 289:30133-30143.

Lorenzo L.-E., Godin A.G., Wang F., Saint-Louis M., Carbonetto S., **Wiseman P.W.**, Ribeiro-da-Silva A., DeKoninck Y. 2014. Gephyrin clusters are absent from small diameter primary afferent terminals despite the presence of GABAA receptors. Journal of Neuroscience. 34(24):8300-8317.

Bujold K.E., Fakhoury J., Edwardson T.G., Carneiro K.M., Briard J.N., Godin A.G., Amrein L., Hamblin G.D., Panasci L.C., **Wiseman P.W.**, Sleiman H.F. 2014. Sequence-responsive unzipping DNA cubes with tunable cellular uptake profiles. Chemical Science. 5(6):2449-2455.

Jowett N., Wöllmer W., Reimer R., Zustin J., Schumacher U., **Wiseman P.**, Mlynarek A., Böttcher A., Dalchow C., Lörincz B., Knecht R., Miller R.J.D. 2014. Bone ablation without thermal or acoustic mechanical injury via a novel picoseconds infrared laser (PIRL). Otolaryngology - Head & Neck Surgery. 150(3):385-393.

Arnspang E.C., Koffman J.S., Marlar S., **Wiseman P.W.**, Nejsum L.N. 2014. Easy measurement of diffusion coefficients of EGFP-tagged plasma membrane proteins using k-Space Image Correlation Spectroscopy. Journal of Visualized Experiments: JoVE. 10:87.

Godin A.G., Rappaz B., Potvin-Trottier L., De Koninck Y., **Wiseman P.W.** 2014. Spatial Intensity Distribution Analysis (SpIDA): A method to probe membrane receptor organization in intact cells in *Cell Membrane Nanodomains: from Biochemistry to Nanoscopy.* CRC Press. Pages 239-260.

Arnspang E.C., Schwartzentruber J., Clausen M.P., Lyngsø C., Hansen J.L., **Wiseman P.W.**, Lagerholm B.C. 2013. Bridging the gap between single molecule and ensemble methods for measuring lateral dynamics in the plasma membrane. PLoS ONE. 8(12):e78096.

Wiseman P.W. 2013. Fluctuation Imaging Spiced Up with a Piece of PIE. Biophysical Journal. 105:831.

Brandao H.B., Sangji H., Pandzic E., Bechstedt S., Brouhard G.J., **Wiseman P.W.** 2013. Measuring ligand-receptor binding kinetics and dynamics using k-space image correlation spectroscopy. Methods. 66(2):273-282.

Barbeau A., Swift J.L., Godin A.G., De Koninck Y., **Wiseman P.W.**, Beaulieu J.-M. 2013. Spatial Intensity Distribution Analysis (SpiDA), a new tool for receptor tyrosine kinase activation and transactivation quantification. Methods in Cell Biology. 117:1-19.

Potvin-Trottier L., Chen L., Horwitz A.R., **Wiseman P.W.** 2013. A nu-space for ICS: characterization and application to measure protein transport in live cells. New Journal of Physics. 15(8):085006.

Hossein Heris K., Miri A.K., Tripathy U., Wiseman P.W., Mongeau L. 2013. Microstructural Characterization of Vocal Folds toward a Strain-Energy Formulation. Acta Biomaterialia. 9(8):7957-7967.

Tripathy U., Giguère-Bisson M., Sangji M.H., Bellemare M.-J., Bohle D.S., George E., Wiseman P.W. 2013. Optimization of the third harmonic generation response for imaging detection of the malaria pigment hemozoin. Analytical and Bioanalytical Chemistry. 405:5431-5440.

Wiseman P.W. 2013. Image correlation spectroscopy: mapping correlations in space, time, and reciprocal space. Methods in Enzymology. 518:245-267.

Rappaz B., **Wiseman P.W.** 2013. Image Correlation Spectroscopy for measurements of particle densities and colocalization. Current Protocols-Cell Biology. 4(27):1-15.

Jowett N., Woellmer W., Mlynarek A.M., **Wiseman P.W.**, Segal B., Franjic K., Kroetz P., Boettcher A., Knecht R., Miller R.J.D. 2013. Heat generation during ablation of porcine skin with Er:YAG laser versus a novel picosecond infrared laser (PIRL). JAMA Otolaryngology— Head & Neck Surgery. 139(8):828-833.

Barbeau A., Godin A.G., Swift J.L., De Koninck Y., **Wiseman P.W**., Beaulieu J.-M. 2013. Ligand-induced clustering of EGF receptors: Quantification of receptor tyrosine kinase activation and transactivation by G Protein Coupled receptors using Spatial Intensity Distribution Analysis (SpIDA). Methods in Enzymology. 522:109-131.

Wiseman P.W. 2013. Image Correlation Spectroscopy: Mapping Correlations in Space, Time, and Reciprocal Space in *Methods in Enzymology: Fluorescence Fluctuation Spectroscopy, Part A*. Elsevier. Volume 518, pages 245-267.

Toplak T., Pandzic E., Chen L., Vicente-Manzanares M., Horwitz A.R., **Wiseman P.W.** 2012. STICCS Reveals Matrix-Dependent Adhesion Slipping and Gripping in Migrating Cells. Biophysical Journal. 103:1672-1682.

Chen L., Vicente-Manzanares M., Potvin-Trottier L., **Wiseman P.W.**, Horwitz A.R. 2012. The integrin-ligand interaction regulates adhesion and migration through a molecular clutch. PLoS ONE 7(7):e40202.

M. Sergeev, A. G. Godin A.G., Kao L., Abuladze N., **Wiseman P.W.**, Kurtz I.. 2012. Determination of membrane protein transporter oligomerization in native tissue using spatial fluorescence intensity fluctuation analysis. PLoS ONE. 7(4):e26215.

Sergeev M., Swift J.L., Godin A.G., **Wiseman P.W.** 2012. Ligand-induced clustering of EGF receptors: A quantitative study by fluorescence image moment analysis. Biophysical Chemistry. 161:50-53.

Miri K., Tripathy U., Mongeau L., **Wiseman P.W.** 2012. Nonlinear Laser Scanning Microscopy of Human Vocal Folds. The Laryngoscope. 122(2):356-363.

Wiseman P.W. 2012. Image Correlation Spectroscopy in *Compreshensive Biophysics*. Academic Press; 1st edition Volume 2, pages 246-259.

Durisic N., Godin A.G., Walters D., Grütter P., **Wiseman P.W.**, Heyes C. 2011. Probing the "dark" fraction of core-shell quantum dots by ensemble and single particle pH-dependent spectroscopy. ACS Nano. 5(11):9062-9073.

Boyle S., Kolin D., Bieler J.G., Schneck J.P., **Wiseman P.W.**, Edidin M. 2011. Quantum dot fluorescence characterizes the nanoscale organization of T cell receptors for antigen. Biophysical Journal. 101(11):L57-L59.

Balghi H., Robert R., Rappaz B., Zhang X., Wohlhuter-Haddad A., Evagelidis A., Luo Y., Goepp J., Ferraro P., Roméo P., Trebak M., **Wiseman P.W.**, Thomas D.Y., Hanrahan J.W. 2011. Enhanced Ca2+ entry due to Orai1 plasma membrane insertion increases IL-8 secretion by cystic fibrosis airways. FASEB Journal. 25(12):4274-4291.

Mesnage B., Gaillard S., Godin A.G., Rodeau J.-L., Hammer M., von Engelhardt J., Wiseman P.W., De Koninck Y., Schlichter R., Cordero-Erausquin M. 2011. Morphological and functional characterization of cholinergic interneurons in the dorsal horn of the mouse spinal cord. Journal of Comparative Neurology. 519:3139-3158.

Swift J.L., Godin A.G., Doré K., Freland L., Bouchard N., Nimmo C.M., Sergeev M., De Koninck Y., **Wiseman P.W.**, Beaulieu J.M. 2011. Quantitative analysis of receptor tyrosine kinase transactivation via direct dimerization and surface density measurements in single cells. Proceedings of the National Academy of Sciences of the United States of America. 108(17):7016-7021.

Godin A.G., Costantino S., Lorenzo L.E., Swift J.L., Sergeev M., Ribeiro-da-Silva A., De Koninck Y., **Wiseman P.W.** 2011. Revealing protein oligomerization and densities in situ using spatial intensity distribution analysis. Proceedings of the National Academy of Sciences of the United States of America. 108(17):7010-7015.

Baumgärtel V., Ivanchenko S., Dupont A., Sergeev M., **Wiseman P.W.**, Kräusslich H.-G., Bräuchle C., Müller B., Lamb D.C.. 2011. Dynamics of HIV budding site interactions with an ESCRT component visualized in live-cells. Nature Cell Biology. 13(4):469-474.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Bioengineering – Dan Nicolau (For/acting chair)

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

____√____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: Marie A. Kaelin.

Date: Feb. 23, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Biology – Graham Bell

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

___X___ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):
This proposal for QLSC600 was reviewed by Irene Gregory-Eaves (Chair, Curriculum Committee, Biology) and Lauren Chapman (Chair, Graduate Training Committee, Biology). The proposed course seems like an excellent capstone course for the Quantitative Life Science program. It might be valuable if the bootcamp skill series could be made available more broadly to students outside QLSC600, depending on availability, but we have no objections to the course proposal.

Signature: Lauren Chapman, Graduate Program Director, Biology

Date: February 29th, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM RE NEW COURSE PROPOSAL QLSC 600 Foundations of Quantitative Life Sciences

DATE: August 5, 2016

TO: Biomedical Engineering – Dr. Robert Kearney

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response at your earliest convenience.**

X NO OBJECTIONS SOME OBJECTIONS

COMMENTS (included here or emailed separately):

An interesting and very ambitious course.

Signature: 

Date: 15 Aug 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email sabine.dhir@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: June 22, 2016

TO: Computer Science – Gregory Dudek

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

____X____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS:

We would like to thank you for your revised QLS graduate program proposal which we received on May 10, 2016. We have engaged in extensive and spirited debate since then. The revised proposal better explains the context of the current proposed course.

There is much support in spirit for the new course, and in general for the new program which creates a mechanism for PhD students to do interdisciplinary work. As a department we support this effort and hope we can participate fully.

Signature: 

Date: June 17, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Epidemiology & Biostatistics – Gilles Paradis

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

✓ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: _____

Date: 22-2-2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Human Genetics – Eric Shoubridge

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

____x____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Excellent course that will take quantitative biology to a new level at McGill. Essential to train the next generation of computational scientists.

Signature: _____

Date: 23 February, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: March 11, 2016

TO: Dr. Jim Fyles – Natural Resource Sciences

FROM: Dr. Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response at your earliest convenience.**

____X____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

We agree that this course is appropriate to the program and that the program is appropriate to the anticipated student body. We continue to feel, as expressed in previous communications, that the program and course could be more broadly oriented to make it more accessible to students with a biological background. Nevertheless, we agree that this may be something for consideration in a future version of the course/program.

Signature: _____

Date: 15 mar 2016

Please return to Sabine Dhir, PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Neurology & Neurosurgery – Guy Rouleau

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

✓ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: _____

Date: Feb 25, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Peter Grutter (Physics)

FROM: Sabine Dhir

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

____x____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Excellent course!

Signature: 

Date: 22.2.2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE NEW COURSE PROPOSAL
QLSC 600 Foundations of Quantitative Life Sciences

DATE: February 22, 2016

TO: Physiology – John Orlowski

FROM: Peter Grutter

We are requesting a consultation on a new course: QLSC 600 Foundations of Quantitative Life Sciences.

The goal of this course is to provide graduate students in the life and quantitative sciences an overview of the different types of biological questions that can be addressed using mathematical, computational and statistical approaches. This course will also introduce students to modern technologies used in acquisition of biological data and the key challenges associated with complex data analyses.

QLSC 600 will also serve as a capstone (or required) course for students in a multidisciplinary quantitative life sciences graduate program currently being developed at McGill University.

Would you kindly review the attached proposal and let us know whether or not your department has any objections to, or comments regarding, the course proposal. **We would be grateful to receive your response by February 26th 2016.**

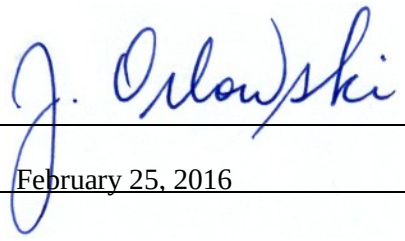
_____NO OBJECTIONS _____X_____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Very impressive line-up for the course. The course appears to be designed for students with a quantitative background (i.e. who were in programs with multiple math and compsci courses). However, there are some concerns that the students will not have grasped the biology adequately by the end of the course. They need to have some biological background going in or be spoon-fed one by the program before taking the course.

The program needs a basic biology course for people with purely quantitative backgrounds; i.e. a stand-alone course that gives students an overview of physiology/biochemistry/genetics. The boot camps will be more of the same for quantitative students and largely about the technology and not the biology. It would be important that students have the basics of DNA-RNA-protein before diving into modules 1-3. I would also argue that module 2 should come after module 3. The students should have a more "organic" grasp of what a gene is and how it is regulated before diving into more abstract concepts like linkage disequilibrium, etc. In other words, they may need another bootcamp first, which should be the basics of DNA-RNA-protein (2 lectures),

basic organelle biology (1-2 lectures), immunology (innate and adaptive; 1-2 lectures), basic neuroscience (2 lectures). As it stands, the first two bootcamps will be essentially completely out of context.

Signature: 

Date: February 25, 2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: March 10, 2016

TO: **Dr. Albert M. Berghuis**
Chair, Department of Biochemistry

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

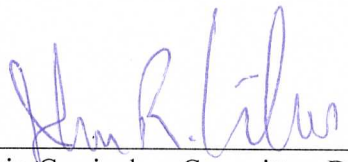
We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- BIOC 603: Genomics and Gene Expression.
- BIOC 605: Protein Biology and Proteomics

Would you kindly review the attached proposal and let us know whether or not you any objections or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response at the earliest.**

_____X_____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: 
(Prof. John Silvius, Chair, Curriculum Committee, Dept of Biochemsisry)

Date: Mar. 10, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St.West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Dan Nicolau** /Interim
Chair, Department of Bioengineering

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following course from your department in the list of complementary courses that students could register for as part of the PhD Program:

- BIEN 530 Imaging and Bioanalytical Instrumentation

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

___X___ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

The Department of Bioengineering is pleased to support, with no objections, the inclusion of BIEN 530 Imaging and Bioanalytical Instrumentation as a complementary course in the Quantitative Life Sciences curriculum.

The Bioengineering Department will be happy to contribute more courses to the curriculum if needed, for example, BIEN 570 Active Mechanics in Biology, and BIEN 550 Biomolecular Devices.

Signature: Andrée A. Kaller

Date: Feb, 24, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Graham Bell**
Chair, Department of Biology

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. This program will be presented at an upcoming meeting of the Faculty of Science. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

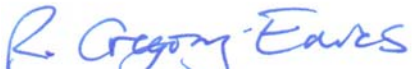
We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- BIOL 551 Principles of Cellular Control
- BIOL 509 Methods in Molecular Ecology
- BIOL 510 Community Ecology
- BIOL 540 Ecology of Species Invasion
- BIOL 434 Theoretical Ecology
- BIOL 594 Advanced Evolutionary Ecology
- BIOL 551 Principles of Cellular Control

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

_____X_____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):
Our only minor comment is that we have the capacity to absorb a few more students in the proposed courses (indicated above). I suspect that that is in the neighborhood of what the program is anticipating as Peter Grutter previously indicated on his foundations course proposal for this program that it has an anticipated enrollment of 10 students (and there are 3 streams, of which only one includes Biology).

Signature: 
Date: April 13, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: March 11, 2016

TO: **Dr. Robert Kearney**
Chair, Department of Biological

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- BMDE 502 BME Modelling & Identification
- BMDE 519 Biomedical Signals & Systems
- BMDE 512 Finite-Element Modelling: BME

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response at your earliest convenience.**

__X__ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: _____

Date: _____

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Masad Damha**
Chair, Department of Chemistry

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. This program will be presented at an upcoming meeting of the Faculty of Science. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- CHEM 514 Biophysical Chemistry
- CHEM 520 Methods in Chemical Biology

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

✓ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

We might also recommend CHEM 555 NMR spectroscopy and CHEM 575 Chemical Kinetics as suitable complementary courses.

Signature: _____

Date: March 16, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec,

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Gregory Dudek**
Chair, Department of Computer Science

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. This program will be presented at an upcoming meeting of the Faculty of Science. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- COMP 652 Machine Learning
- COMP 561 Computational Biology Methods and Research
- COMP 618 Functional Genomics
- COMP 522 Modeling and Simulations

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

_____NO OBJECTIONS _____X_____SOME OBJECTIONS

COMMENTS:

- COMP 652 is advanced course which concentrates more on theory than practice, and as such we do not feel it is suitable for the proposed QLS program. It should be replaced by COMP 551 Applied Machine Learning (taught by Prof. Joelle Pineau) which will be offered starting Fall 2016.
- COMP 618 should be dropped from the list, since its future is uncertain. We are planning to replace it with a new 500 level course that would be a follow up to COMP 364 (Computer Tools for the Life Sciences). If this new course it is approved, it would be offered in Fall 2017. This new course would be more suitable for this program.
- COMP 522 is no longer offered because the instructor has left McGill, and so it should be removed from the list.

N.B. For other comments on the Proposed Program itself, please refer to our Consulation for QLSC 600.

Signature: _____

Date: Apr. 1, 2016.

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: October 3, 2016

TO: **Dr. Bettina Kemme**
Chair, Department of Computer Science

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. This program will be presented at an upcoming meeting of the Faculty of Science. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- COMP 551 Applied Machine Learning
- COMP 561 Computational Biology Methods and Research
- COMP 598 Topics in Computer Science: Advanced Computational Biology Methods

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response at your earliest convenience.**

_____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: _____

Date: _____

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email sabine.dhir@mcgill.ca

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Gilles Paradis**
Chair, Department of Epidemiology & Biostatistics

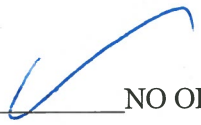
FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following course from your department in the list of complementary courses that students could register for as part of the PhD Program:

- BIOS 601 Epidemiology: Introduction and Statistical Models

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**



_____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Signature: _____

Date: Mar 17 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Eric Shoubridge**
Chair, Department of Human Genetics

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- HGEN 661 Population Genetics
- HGEN 677 Advanced Statistical Methods in Genetics and Genomics
- HGEN 692 Human Genetics

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

x
_____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

This is a terrific initiative, which I wholeheartedly support!

Signature: 

Date: 5April, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: March 16, 2016

TO: **Dr. David A. Stephens**
Chair, Department of Mathematics and Statistics

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. This program will be presented at an upcoming meeting of the Faculty of Science. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- MATH 680 Computation Intensive Statistics
- MATH 523 Generalized Linear Models
- MATH 525 Sampling Theory and Applications
- MATH 537 Mathematical Models in Biology
- MATH 547 Stochastic Processes
- MATH 533 Honours Regression and ANOVA
- MATH 556 Mathematical Statistics 1

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive at your earliest convenience.**

X NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

I am happy to support this initiative.

Signature: 

Date: 17th March 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. Anne-Marie Lauzon**
Chair, Department of Medicine

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following course from your department in the list of complementary courses that students could register for as part of the PhD Program:

- EXMD 602 Techniques in Molecular Genetics

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

✓ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Both the department and the course coordinators think this new program is a great idea. One comment which we wish to make is that, as appears from the program proposal which was sent, the course EXMD602 is part of the *Computational and Statistical Molecular Biology Stream _Life Science Block*. It should be noted that, although there are some statistical principles and computational approaches taught in EXMD-602, this is only a minor aspect of the course. The course is intended to expose the students to the most recent molecular approaches used to study human genetic diseases and their general applications to understand mechanisms of disease.

Finally, it should be noted that this course normally requires "Instructor Approval" due to the fact that students who wish to take this course must have a basic knowledge of molecular biology and at least 1 course of basic genetics.

I attach an outline of the course for the current year for your information.

Signature: Anne Marie Lauzon

Date: 25/2/2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

ADVANCED TECHNIQUES IN MOLECULAR GENETICS 2016
EXMD-602
WEDNESDAY 1h00 – 3h00 PM
McIntyre Building, ROOM 1345

DATE	TOPIC	FACULTY
January 13 2016	**Detection of gene product and quantification of gene expression**	**D. Radzioch**
January 20 2016	**Immunohistochemistry**	**D. Radzioch**
January 27 2016	**Anti-sense technology**	**D. Radzioch**
February 3 2016	**Complex Trait Genetics**	**E. Schurr**
February 10 2016	**Human Linkage and Association Studies**	**J. Engert**
February 17 2016	**Gene therapy**	**D. Cournoyer**
February 24 2016	**Students' presentations**	**Malo/Radzioch**
March 2 2016	**READING WEEK**	
March 9 2016	**Gene regulatory network**	**R. Sladek**
March 16 2016	**Next generation sequencing: technologies and applications**	**G. Bourque**
March 23 2016	**Mouse genetics**	**D. Malo**
March 30 2016	**Mouse genetics**	**D. Malo**
April 6 2016	**Mutagenesis and transgenesis**	**M. Bouchard**
April 13 2016	**Students' presentations**	**Malo/Radzioch**
April 20 2016	**EXAM_N2/2 Stewart Building**	**Malo/Radzioch**

Evaluation: Presentation 40%; Final Exam 60%

In accord with McGill University's Charter of Students' Rights, students in this course have the right to submit in English or in French any written work that is to be graded.

McGill University values academic integrity. Therefore all students must understand the meaning and consequences of cheating, plagiarism and other academic offences under the Code of Student Conduct and Disciplinary Procedures (see http://www.mcgill.ca/integrity for more information).

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: March 16, 2016

TO: **Dr. Jim Fyles**
Chair, Department of Natural Resource Sciences

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

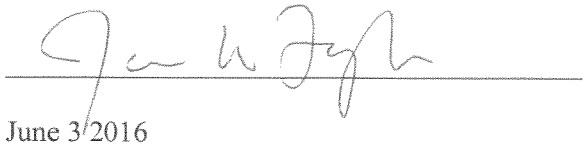
- ENVB 506 Quantitative Methods in Ecology
- ENVR 540 Ecology of Species Invasion

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response at your earliest convenience.**

____X____NO OBJECTIONS _____SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Note that ENVR 540 'Ecology of Invasion' is a course of the McGill School of Environment, jointly listed with Biology. Hence, as Chair of NRS, I cannot officially sign for this course.

Signature: 

Date: June 3/2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec, or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 22, 2016

TO: Dr. Peter Grutter
Chair, Department of Physics

FROM: Dr. Sabine Dhir

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- PHYS 519 Advanced Biophysics
- PHYS 559 Advanced Statistical Mechanics

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 26th 2016.**

___x___ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

Great program!

Signature:

Date: 22.2.2016

Please return to Sabine Dhir, PhD, GPS OFFICE ADDRESS or fax 514-398-6283 or email academicprograms.gps@mcgill.ca.

APPENDIX B

CONSULTATION REPORT FORM
RE AD HOC PROGRAM PROPOSAL
PhD Program in Quantitative Life Sciences

DATE: February 23, 2016

TO: **Dr. John Orlowski**
Chair, Department of Physiology

FROM: **Dr. Sabine Dhir**, on behalf of **Dr. Josephine Nalbantoglu,** Dean Graduate and Postdoctoral Studies

We are requesting consultation from your department regarding a new multidisciplinary quantitative life sciences graduate program currently being developed at McGill University. The proposed Ad Hoc Interdisciplinary PhD Program in Quantitative Life Sciences fits into a rapidly expanding interdisciplinary field that includes ecology, physiology, genetics, systems biology, computational biology, bioinformatics, mathematical biology, evolutionary biology and biophysics. Key elements of the program have been designed to broaden the contextual knowledge of students and to encourage interactions between different fields of research. The three areas of specialization within the program are: Computational and Statistical Molecular Biology, Biophysics and Ecosystems. There is strong interest and demand for quantitative research skills to be applied to the life sciences, and we feel this program proposal is quite timely.

We would like to include the following courses from your department in the list of complementary courses that students could register for as part of the PhD Program:

- PHGY 520 Ion Channels
- PHGY 518 Artificial Cells

Would you kindly review the attached proposal and let us know whether or not you any objections to, or comments regarding the complementary course(s) from your department to be included as part of the Ad Hoc PhD Program in Quantitative Life Sciences. **We would be grateful to receive your response by February 29th 2016.**

___X___ NO OBJECTIONS _____ SOME OBJECTIONS

COMMENTS (included here or emailed separately):

While PHGY 520 Ion Channels would provide solid training in electrophysiology and biophysics, I am not sure of the basis for recommending PHGY 518 Artificial Cells. It might be more beneficial for the students to include a more basic course in molecular and cellular biology or physiology, unless this is already addressed in prerequisite courses required for the program (or offered in the other courses).

Signature: J. Orlowski

Date: February 25, 2016

Please return to Sabine Dhir PhD, James Administration Building, Room 400, 845 Sherbrooke St. West, Montreal, Quebec,
or email academicprograms.gps@mcgill.ca.