

# Contents

## ↳ Contents

- ↳ *Introduction: Navigator, Flow Editor and Job Viewer*
  - ↳ *Navigator*
  - ↳ *Flow Editor*
  - ↳ *Job Table*
- ↳ *General User Interface Functions*
  - ↳ *Pull Down menus and icons*
  - ↳ *Mouse Buttons*
  - ↳ *Copying Flows and how Dataset Addressing is Handled*
  - ↳ *Sorting the Navigator Tables*
  - ↳ *Quick search in a column*
  - ↳ *Column widths*
  - ↳ *Column Re-ordering*
  - ↳ *Column Show/Hide and Size*
  - ↳ *Filtering tables*
  - ↳ *Selecting Multiple Entries in a table*
- ↳ *Working with the Navigator*
  - ↳ *The Tree and Table views*
  - ↳ *Projects (or Data Homes)*
  - ↳ *Linking the Tree and Table views*
  - ↳ *Setting Permissions*
  - ↳ *Dataset Types and Icon Descriptions*
  - ↳ *Dataset Properties / Inventory / Fold Map*
    - ↳ *Dataset Properties*
    - ↳ *Dataset Inventory*
    - ↳ *Dataset Fold Map*
  - ↳ *Setting Preferences*
    - ↳ *Navigator Tab*
    - ↳ *Flow Editor tab*
    - ↳ *Log Viewer tab*
    - ↳ *Defaults tab*
    - ↳ *Exec Tab*
- ↳ *Working with the Job Table*
  - ↳ *Overview*
  - ↳ *Job Viewer Column Headings*
  - ↳ *Job Viewer Icon Bar*

- ↳ Refresh job listing icon
- ↳ View job listing icon
- ↳ Query Status of Joblets icon
- ↳ Monitor data flow of running job icon
- ↳ Display final job report
- ↳ Multiple job printout search
- ↳ Pause job and Resume Pause job icons
- ↳ Stop input and finish flow normally icon
- ↳ Kill the job ASAP icon
- ↳ Delete job from Job Manager permanently or Remove from the Queue icon
- ↳ Output Thread Dump for debugging
- ↳ Row Filter icon
- ↳ Column Show/Hide icon
- ↳ Archive and Restore
  - ↳ Toggle Archive View icon
  - ↳ Archive Wizard icon
  - ↳ Restore Wizard icon
- ↳ Archive Data Home
- ↳ Archive View
- ↳ Archive Wizard
- ↳ Restore Wizard
- ↳ Working with the Flow Editor
  - ↳ Multiple Flow Editor Tabs
  - ↳ Opening Flows for editing
  - ↳ Saving flows
  - ↳ Adding Processes to a flow
  - ↳ The Processes List
  - ↳ The Processes List (Development Status Processes)
  - ↳ The Options Menu for Processes in a Flow
  - ↳ The Options Menus in the white spaces in the Flow Editor Tab
  - ↳ The Options Menus on dataset names in IO processes
  - ↳ Online help for the Processes
  - ↳ ProMAX® process Icons and hybrid parallelization
  - ↳ Adding Comments to Processes
  - ↳ User Defined Header Management
  - ↳ Data Context and Header Catalog at any point in a flow
  - ↳ Setting site and user defaults for SeisSpace® and ProMAX® tool menus
  - ↳ Object Grouping and Group Copying

- ↳ *The Flow Viewer*
- ↳ *Printing a flow to HTML*
- ↳ *Submitting a Job for Execution*
  - ↳ *Direct Submit*
  - ↳ *Queue and custom node list submit*
  - ↳ *Resubmit*
  - ↳ *General Rules - for job submission*
- ↳ *Purging Flows*
- ↳ *Restore a flow to its original state*
- ↳ *Overlaying menus*
- ↳ *Dataset Processing History*
- ↳ *Area, Line, Flow, Table, Dataset name restrictions*
- ↳ *Adding a new Projects and Subprojects (AREAs and LINEs)*
- ↳ *Properties for existing ProMAX® Projects*
- ↳ *Configuration for a ProMAX® development environment*
  - ↳ *User Processes List*
- ↳ *Configuration for a SeisSpace development environment*
  - ↳ *User Processes List*
- ↳ *Using user-defined icons for user-defined processes*
  - ↳ *Refreshing the processes lists*
- ↳ *SeisSpace® 3D Prestack Time Migration Workflows*
- ↳ *Replicating Flows*
  - ↳ *Supported functionality*
    - ↳ *Flow Replication Components*
  - ↳ *Building Templates*
    - ↳ *Converting a flow to a template and back to a flow*
    - ↳
    - ↳ *Selecting parameters to change from job to job*
  - ↳ *Opening and Editing The Replica Table*
    - ↳ *Adding Rows and Columns*
    - ↳ *Deleting Rows and Columns*
    - ↳ *Populating Integer or Float Columns*
    - ↳ *Populating the Constants Table*
    - ↳ *Saving the Replica Table*
  - ↳ *Special replica table syntax for some parameters*
  - ↳ *Choosing Replica Parameters in the Template Editor*
    - ↳ *Naming Conventions*
    - ↳ *Reading data from other Area / Line's in DDI*
    - ↳ *Template Editor and String Validation Table*
  - ↳ *Build and Submit jobs using the Replica Job Table*

- ↳ *Replica Job Table Overview*
- ↳ *Building jobs*
- ↳ *Flow Replication Information Storage*
- ↳ *Viewing Replicas in the Navigator*
- ↳ *Automatic Dataset Generation*
- ↳ *Building New Subprojects*
- ↳ *Submitting jobs*
- ↳ *Deleting Replicas*
- ↳ *Flow Chaining*
  - ↳ *Chained Flows*
  - ↳ *Chained Replicas (one to one)*
  - ↳ *Chained Replicas (many to one) or (many to fewer)*
  - ↳ *Chained Replicas - "one to many"*
  - ↳ *Chained Replicas - previous sequence number*
  - ↳ *Enabling and Disabling Replicas*
  - ↳ *Chained Replicas - alternate areas/lines*
- ↳ *Glossary*

# ***Using the SeisSpace® Processing System***

[Other Docs](#)

[Search Page](#)

[Known Problems](#)

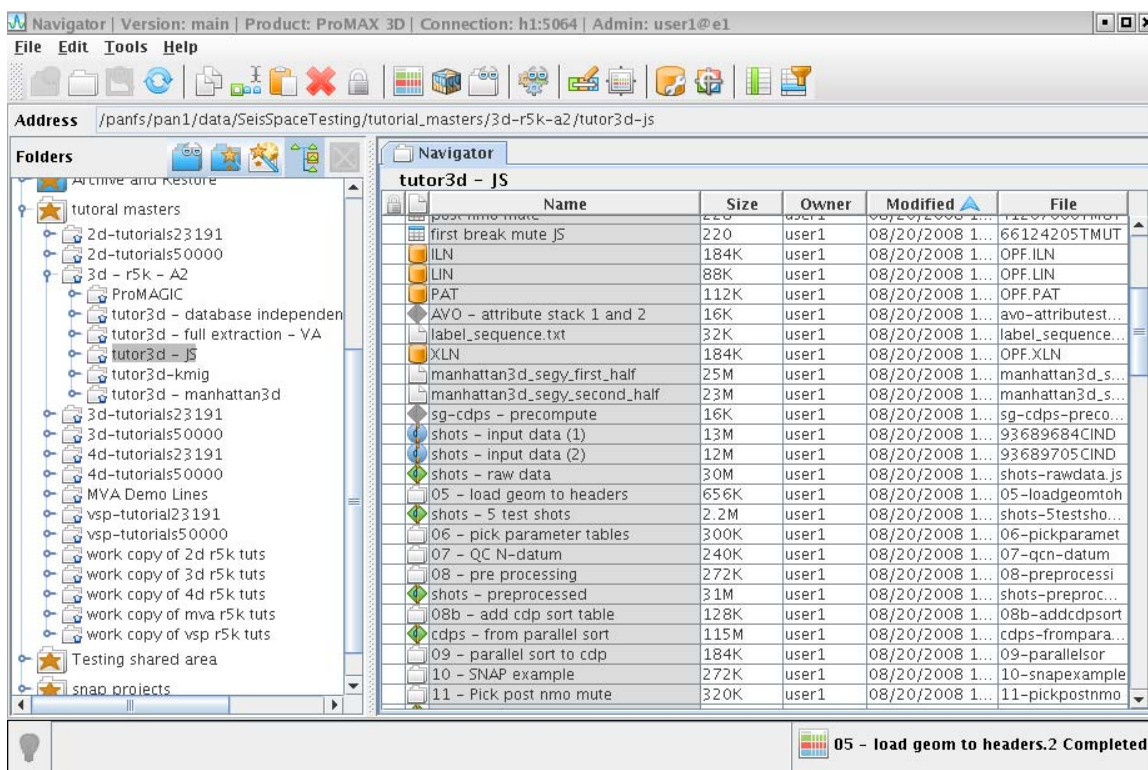
# Introduction: Navigator, Flow Editor and Job Viewer

This chapter discusses using the SeisSpace® interface: the Navigator, Flow Editor and the Job Viewer. It also offers a simple workflow example to help explain a few of the features.

Prior to following the steps in this chapter, you must first install and complete some configuration procedures. Installing and starting the SeisSpace user interface is discussed in the SeisSpace® Release Notes and configuring the SeisSpace system in the System Administration guide.

## Navigator

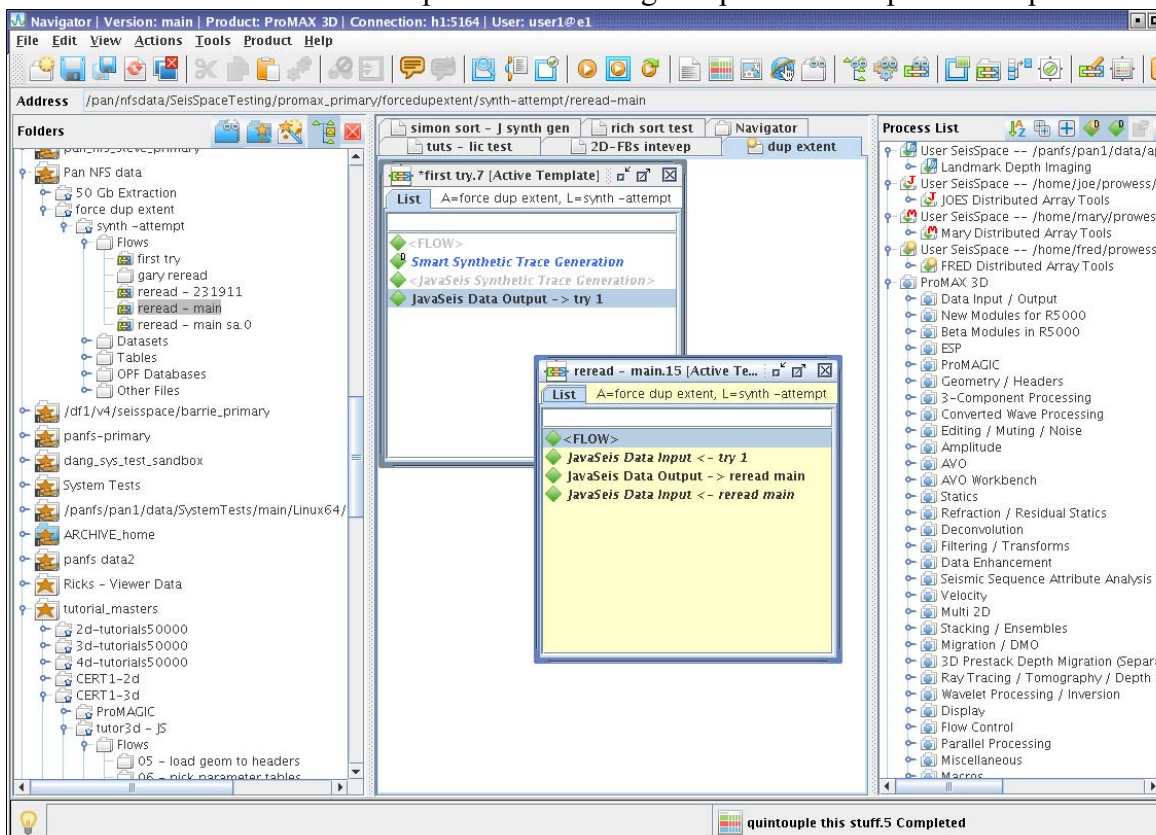
When you configure the SeisSpace system, you will define one or more Data Homes, and each will appear in the Navigator tree view. If the tree view in the left hand frame is blank, see [Configuring the SeisSpace® Processing System](#) in the SeisSpace® System Administration guide.



By default, when the Navigator is restarted, it will return to the location where you were when you exited and it will also load any flows that were open back into the flow editor. This behavior can be controlled by settings in the Navigator preferences dialog from the **Edit > Preference > Navigator**.

## Flow Editor

The SeisSpace® Flow Editor is used to create, edit and submit flows for execution. In the flow editor you will choose which processing steps, or processes to include in a flow and then select process parameters. The Flow Editor offers comprehensive editing and process manipulation capabilities.



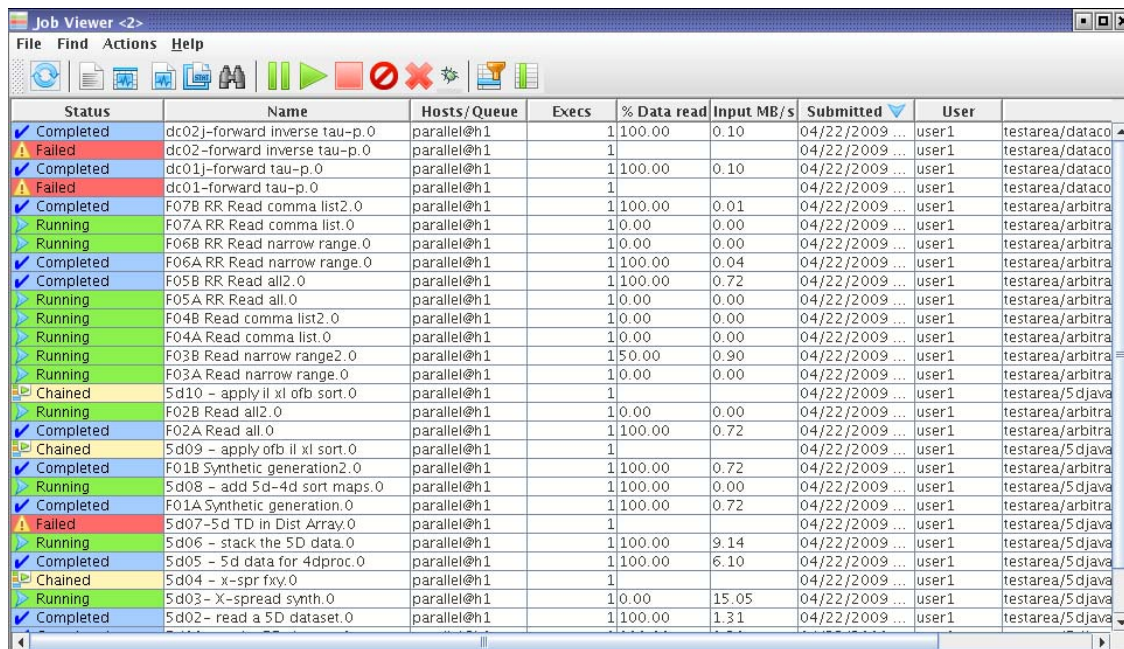
## Job Table

The Job Table tracks jobs that are submitted manually from the Flow Editor or from the tree or table lists. You can launch the Job Table by clicking in the Notification frame at the bottom right edge of the Navigator or by clicking the Job Viewer icon on the icon bar.

**Note:** Jobs submitted via the Flow Replication Job Table are not automatically tracked in the Job Table by default. In order to monitor the

replica jobs in the Job Table you must select the **Find > Show Replicas** option from the Job Table tool bar.

With the Job Table active, you can select a flow in the table and use the tool bar icons or the menu bar to view the job output, kill the flow, or get other information about the jobs.



The screenshot shows the Job Viewer application window with a table of job execution details. The table has the following columns: Status, Name, Hosts/Queue, Execs, % Data read, Input MB/s, Submitted, and User. The rows list various job flows with their respective statuses and execution metrics.

Status	Name	Hosts/Queue	Execs	% Data read	Input MB/s	Submitted	User
Completed	dc02j-forward inverse tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1 testarea/dataco
Failed	dc02-forward inverse tau-p.0	parallel@h1	1			04/22/2009 ...	user1 testarea/dataco
Completed	dc01j-forward tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1 testarea/dataco
Failed	dc01-forward tau-p.0	parallel@h1	1			04/22/2009 ...	user1 testarea/dataco
Completed	F07B RR Read comma list2.0	parallel@h1	1	100.00	0.01	04/22/2009 ...	user1 testarea/arbitra
Running	F07A RR Read comma list.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Running	F06B RR Read narrow range.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Completed	F06A RR Read narrow range.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F05B RR Read all2.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1 testarea/arbitra
Running	F05A RR Read all.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Running	F04B Read comma list2.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Running	F04A Read comma list.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Running	F03B Read narrow range2.0	parallel@h1	1	50.00	0.90	04/22/2009 ...	user1 testarea/arbitra
Running	F03A Read narrow range.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Chained	5d10 - apply il xl ofb sort.0	parallel@h1	1			04/22/2009 ...	user1 testarea/5djava
Running	F02B Read all2.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1 testarea/arbitra
Completed	F02A Read all.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1 testarea/arbitra
Chained	5d09 - apply ofb il xl sort.0	parallel@h1	1			04/22/2009 ...	user1 testarea/5djava
Completed	F01B Synthetic generation2.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1 testarea/arbitra
Running	5d08 - add 5d-4d sort maps.0	parallel@h1	1	100.00	0.00	04/22/2009 ...	user1 testarea/5djava
Completed	F01A Synthetic generation.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1 testarea/arbitra
Failed	5d07-5d TD in Dist Array.0	parallel@h1	1			04/22/2009 ...	user1 testarea/5djava
Running	5d06 - stack the 5D data.0	parallel@h1	1	100.00	9.14	04/22/2009 ...	user1 testarea/5djava
Completed	5d05 - 5d data for 4dproc.0	parallel@h1	1	100.00	6.10	04/22/2009 ...	user1 testarea/5djava
Chained	5d04 - x-spr fixy.0	parallel@h1	1			04/22/2009 ...	user1 testarea/5djava
Running	5d03 - X-spread synth.0	parallel@h1	1	0.00	15.05	04/22/2009 ...	user1 testarea/5djava
Completed	5d02 - read a 5D dataset.0	parallel@h1	1	100.00	1.31	04/22/2009 ...	user1 testarea/5djava

For more information refer to [Working with the Job Viewer](#).

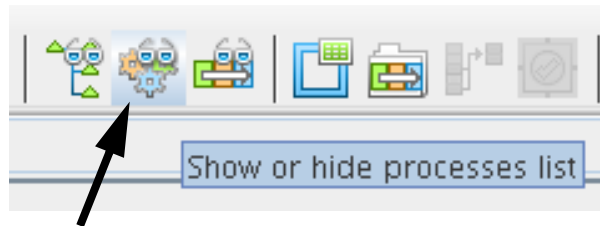


# General User Interface Functions

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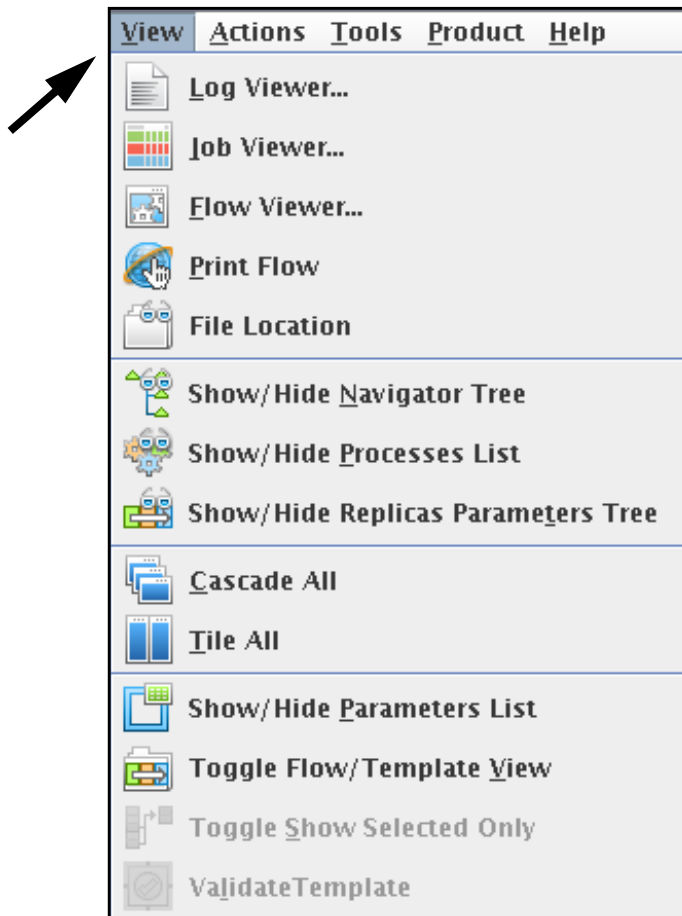
## Pull Down menus and icons

The pulldown menus and icon bars change continuously as you traverse throughout the Navigator and Flow Editor. If you hover the mouse on an icon, a description of its functionality appears.



You can also learn the icons by using the pulldown menus or the MB3 options menus to see a text description of the action associated with its

icon. You will also see some hot key combination shortcuts are associated with these actions.



Many of the main pulldown menus can be expanded using the keyboard combination of Alt-key where the key corresponds to the underlined letter of the top level pulldown. For example, Alt-F displays the File pulldown. Some of the hot keys are activated by CTRL-key combinations such as CTRL-C CTRL-X and CTRL-V for standard Copy, Cut and Paste operations. Other hot key combinations are activated by the Alt-key combination. You will find that only the appropriate hot key combinations are available depending on which tab view is currently being displayed.

## Mouse Buttons

### MB1

MB1 selects items. Items selected with MB1 will usually be highlighted. A single MB1 click also clears the screen in certain instances such as in the flow editor tab. MB1 is also used for general Drag and Drop functions.

## MB2

In the Navigator from the table view of a list of datasets, MB2 will open the Properties dialog. MB2 does have functionality in the Flow editor and, based on preference settings, MB2 can be used to open process parameter dialog boxes. MB2 can also be used in the Job Viewer or Replica Job Table to get a quick look at the end of a printout of a job.

## MB3

MB3 displays options or actions that can be performed on a selected item. These options or actions are different depending on what type of item you select. Different option lists also appear depending on where you click.

## Drag and Drop

Drag and Drop is enabled throughout the Navigator and Flow Editor. Drag and Drop is primarily a Copy operation and not a Move operation. Drag and Drop is only a move operation when you use it to rearrange the order of processes within a flow in the flow editor.

Drag and Drop makes it easy to perform tasks such as:

- Copying Datasets
- Copying Flows
- Copying Processes from one flow to another
- Moving Processes around within a flow
- Selecting Processes from the Processes lists
- Copying Tables
- Copying ProMAX® Areas
- Copying ProMAX® Lines

In the Table pane you must drop the item into the empty space below the table, onto the **Name** column header, or into the white "informational" column space.

You can also drop an item from the table pane into the tree view. For example, copying a ProMAX® flow, dataset or table from one line to another. The drop location is sensitive to the location you are trying to drop an object. You should also only be able to drop a Line onto an Area for example.

## Copying Flows and how Dataset Addressing is Handled

When you copy a flow containing Disk Data Input, Disk Data Insert, Disk Data Output, JavaSeis Framework Create, JavaSeis Data Input, JavaSeis Sort\* or JavaSeis Data Output, the dataset addressing in the flow is adjusted as follows:

- **IF** a flow is copied inside the same subproject (or Line), **THEN** the dataset addressing is not changed in the copied flow.
- **IF** a flow is copied to a different subproject (or Line) and the selected dataset was in the same project as the original flow **AND** the same dataset name exists in the project the flow is copied to, **THEN** the dataset information is altered to address the local dataset in the project into which the flow was copied.
- **IF** a flow is copied to a different subproject (or Line) and the selected dataset is in the same project as the original flow **AND** the same dataset name does not exist in the project that the flow is being copied to, **THEN** the dataset information is reset to the default "NONE" value.
- **IF** a flow is copied to a different project and the datasets were selected from a different project than the project from which the flow originated, **THEN** the dataset addressing is not changed in the copied flow.

## Sorting the Navigator Tables

The table pane can be sorted by clicking MB1 on any of the column headers.





















- Click a selected column once to sort alphabetically (or numerically) in ascending order. Additional clicks will reverse the sort order.
- CTRL-MB1 is used to set multiple column sort criteria and a additional CTRL-MB1 clicks will reverse the direction of the sort.
- Shift-MB1 removes the sort specifications.

## Quick search in a column

A MB3 click on a column header opens an options menu which includes quick search.

Search Column	
	Sort Ascending
	Sort Descending
	Sort Ascending 2nd Level
	Sort Descending 2nd Level
Reset Sort	

The quick search feature will allow you to find the first instance in the column starting with the characters typed into the column header. For example if you select **Search Column** and then enter a character (such as the number "2"), the first flow that starts with 2 is highlighted.

Flows		
	da23	Owned
	da01-XspreadSynthGen	prowess
	da02-RailRoadSynthGen	prowess
	da03-Marine3dShots	prowess
	da05-FKK (Expl Tool) - Hybrid	prowess
	da06-FKK (Prod Tool) - Hybrid	prowess
	da07-FXY - PostStack	prowess
	da08-FKK running	prowess
	da09-FKK padding tests	prowess
	da10-RunMix1	prowess
	da11-RunMix2	prowess
	da12-SNAP-minmax1000	prowess
	da13-SNAP1	prowess
	da21 - time slice transpose	prowess
	da22 - pm in dist arr	prowess
	da23 - pm b4 dist arr	prowess
	da24-TimeSlice132	prowess
	da25-Wavelet transform1	prowess
	da26-Windowed Processes1	prowess
	da27-3dAgc1	prowess

Pressing the **ESC** (escape) key dismisses the Search mode.

## Column widths

Column widths can be adjusted by dragging the separators between the column headers.

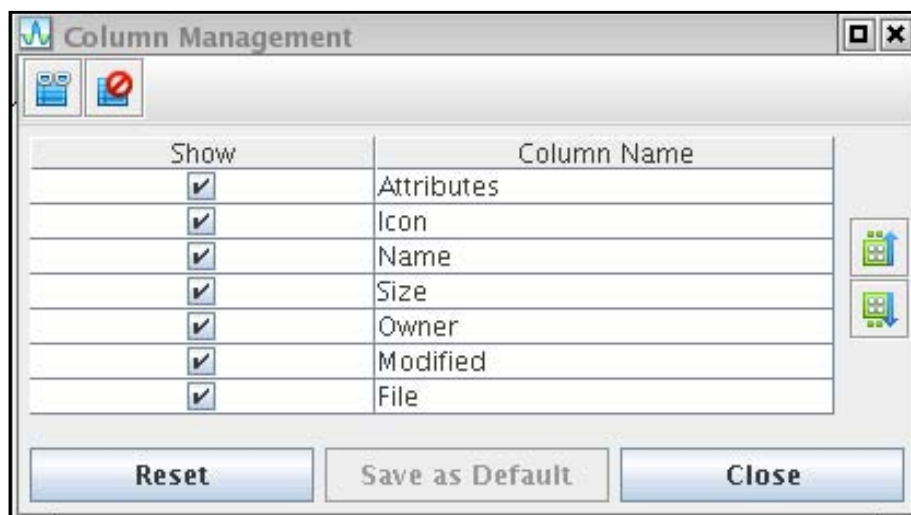
## Column Re-ordering

You can re-order the columns by dragging the column headers to their new locations.

## Column Show/Hide and Size



You can select to show or hide columns. Use the **Column Selector** icon to choose which columns to show.

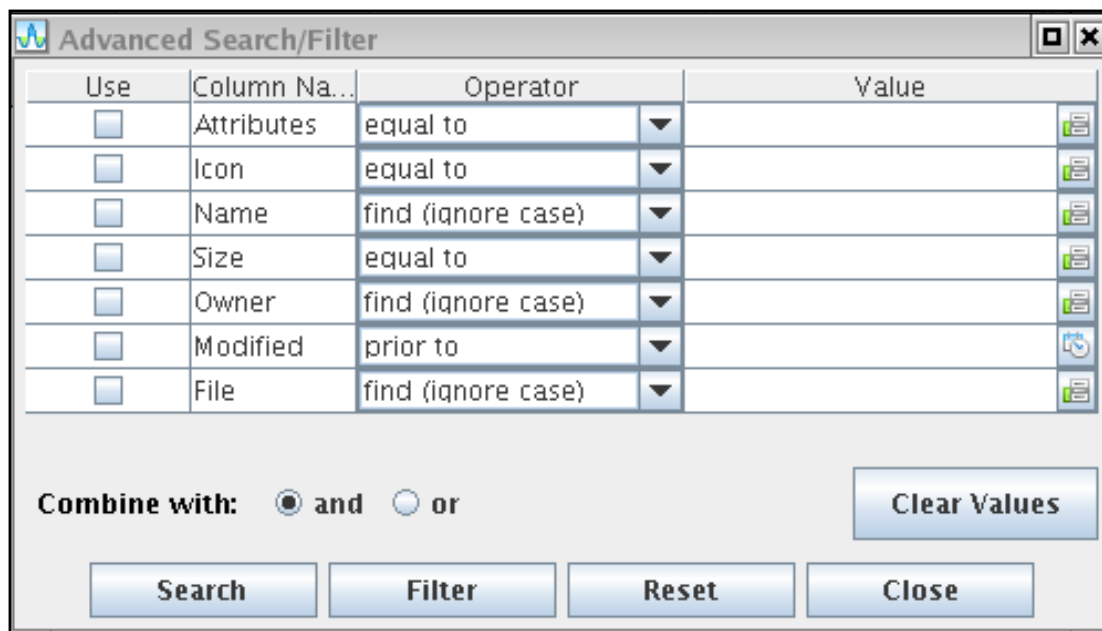


*Note:* Each tab pane is treated as a separate entity. You can set different column visibility, widths, order and sort criteria for each of the different tab panes. The default is to have a single Navigator tab pane, but you may elect to set the user preference to have separate tab panes for Flows, Datasets and Tables in addition to the single Navigator tab pane.

## Filtering tables



You can select which entries to display in a table using the Row Filter option. For example, you can select only the datasets or flow of interest to you. Use the **Row Filter** icon to choose criteria for selecting what to show.



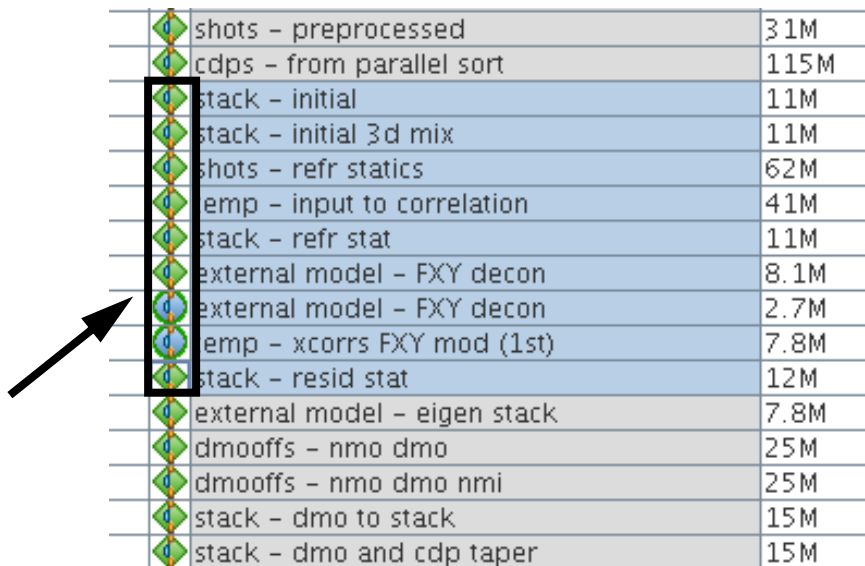
## Selecting Multiple Entries in a table

















You can select multiple entries and perform the same operation on them. For example you can delete several flows in one step, or select multiple flows to load into the editor simultaneously, or submit several jobs to the job queue without opening the flows in the Flow Editor.

There are two ways to select multiple objects in the table. A single MB1 click will select the first, single item,

- **CTRL-MB1** selects a second item.
- **SHIFT-MB1** selects all of the items between the previous selection and the current selection.

You may also select a continuous set of objects in the table by holding down MB1 while "painting" down the data type column. (the second column by default). The selected objects will inherit the light blue color.



	shots - preprocessed	31M
	cdps - from parallel sort	115M
	stack - initial	11M
	stack - initial 3d mix	11M
	shots - refr statics	62M
	temp - input to correlation	41M
	stack - refr stat	11M
	external model - FXY decon	8.1M
	external model - FXY decon	2.7M
	temp - xcorrs FXY mod (1st)	7.8M
	stack - resid stat	12M
	external model - eigen stack	7.8M
	dmooffs - nmo dmo	25M
	dmooffs - nmo dmo nmi	25M
	stack - dmo to stack	15M
	stack - dmo and cdp taper	15M



# Working with the Navigator

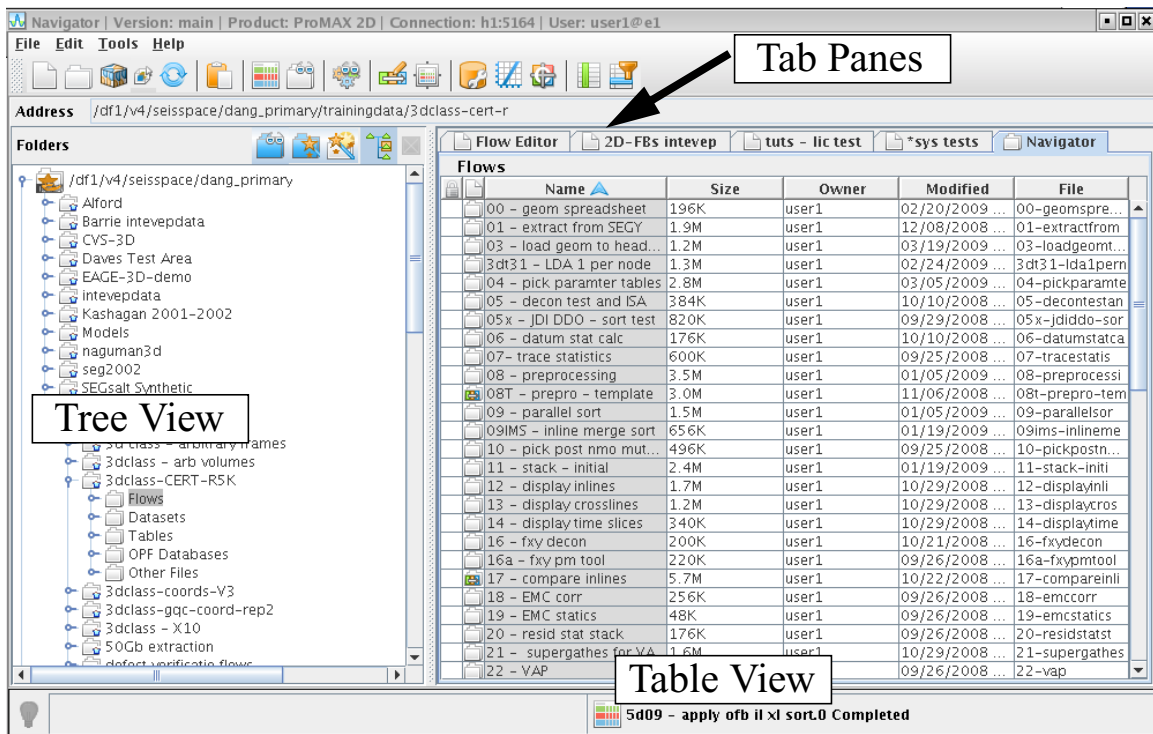
## The Tree and Table views

The Navigator has two main frames. The tree view in the left frame and the table view in the right frame.

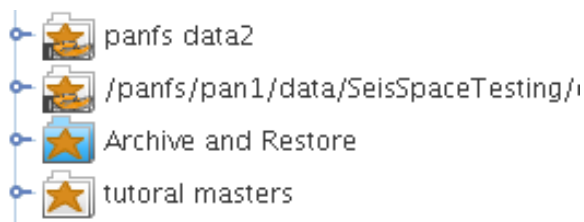
The tree view shows the contents of Data Homes and their associated project databases. Expand the projects to see their subprojects and associated flows, datasets and tables. Open the folder in the tree view to display the subprojects and associated files in the table pane.

The right pane displays a variety of tab pane combinations such as **Navigator**, **Job Table**, **Replica Editor** and **Flow Editor** depending on preferences you have selected. If you choose the preference you can have separate tabs for **Flows**, **Tables**, and **Datasets**. You can use these tabs to quickly move from one list of objects to another or to the flow editor.

**Note:** By default there is only one Navigator tab for all types of objects. You can change this behavior by altering a setting in the Navigator tab of the preferences dialog.



Expand and contract the entries in the tree view by clicking on the symbol to the left of the folder name.



You will see the highest level is a list of “Data Homes”. The icon with the gray bar at the bottom indicates that this is a project that is shared by the administrator and the properties are locked.

All other folders are shown with the standard project icon.

The one example above showing the standard icon with the Blue shading indicates that the data home is the ARCHIVE\_DATA\_HOME that is used as the default location for working with archive and restore flows.

## Projects (or Data Homes)

As you continue to expand the projects, you see a list of Areas (or Projects) under the ProMAX® data homes, Lines (or Sub-Projects) under the Areas, and Flows, Datasets, and Tables under the Lines. Note that in the SeisSpace® user interface, the Areas and Lines are referred to as Projects and Subprojects.

## Linking the Tree and Table views



The Tree view can be either locked or dynamically repositioned with respect to what is selected in the Navigator table or Replica Table or Replica Job Table views using the "Tree Lock" icon.

When this icon is "unselected" (with a gray background) the tree is locked to the other views so that when you select something in the Table or a flow in the flow editor, the tree will dynamically reposition to show you the location of the selected item.

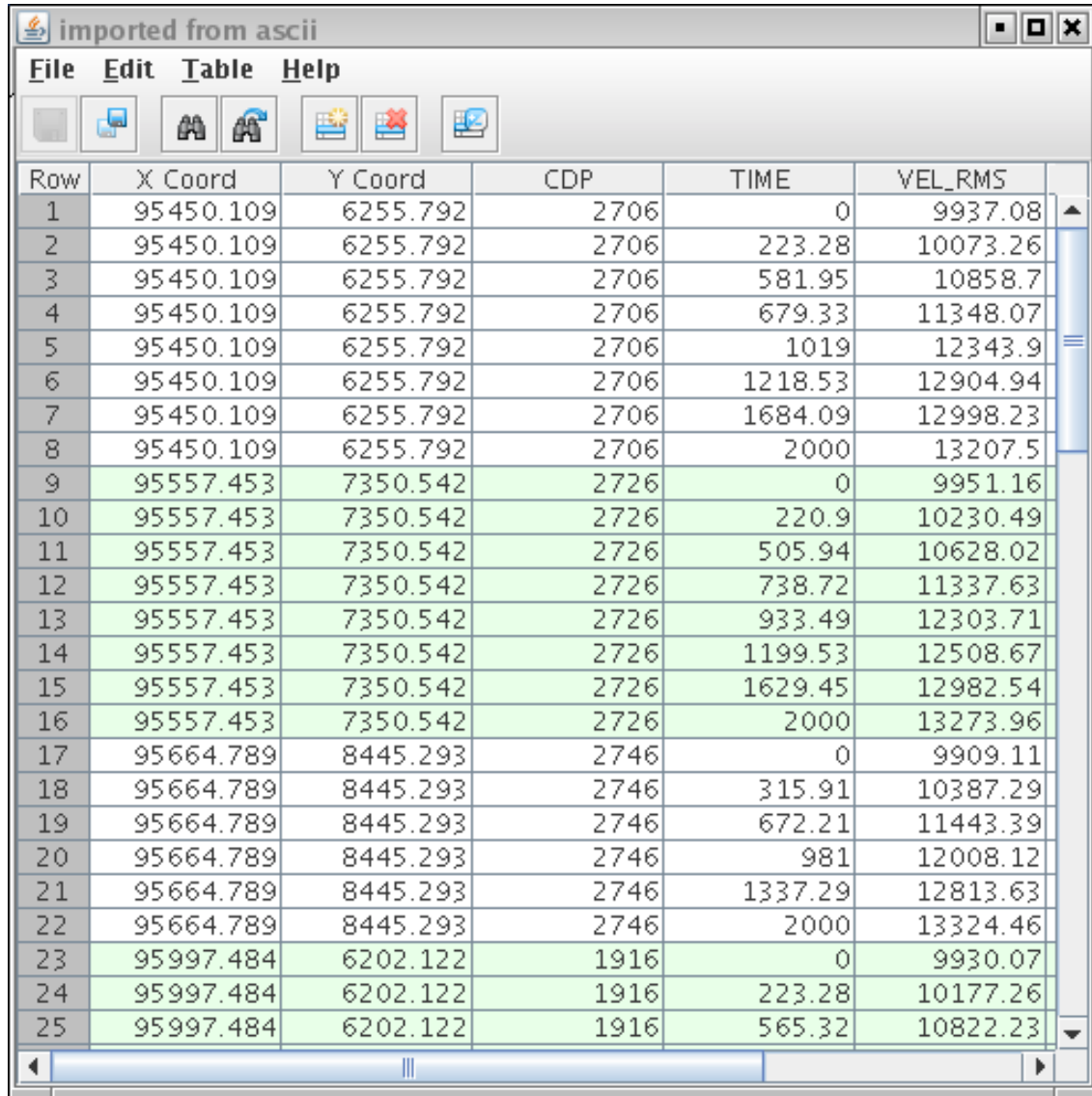


Sometimes you may not want the tree view changing as you are working. In this case you can turn the lock off by clicking on this icon giving it a white background.

In this mode the tree view will remain stationary as you select different objects in the other Navigator panels.

## Editing Parameter Tables

Table editing is performed using either ProTab or geomsread (the original ProMAX® table editor) and is enabled by choosing the Edit option from the MB3 options menu when MB3 is depressed on a table name in the tree or table.



Row	X Coord	Y Coord	CDP	TIME	VEL_RMS
1	95450.109	6255.792	2706	0	9937.08
2	95450.109	6255.792	2706	223.28	10073.26
3	95450.109	6255.792	2706	581.95	10858.7
4	95450.109	6255.792	2706	679.33	11348.07
5	95450.109	6255.792	2706	1019	12343.9
6	95450.109	6255.792	2706	1218.53	12904.94
7	95450.109	6255.792	2706	1684.09	12998.23
8	95450.109	6255.792	2706	2000	13207.5
9	95557.453	7350.542	2726	0	9951.16
10	95557.453	7350.542	2726	220.9	10230.49
11	95557.453	7350.542	2726	505.94	10628.02
12	95557.453	7350.542	2726	738.72	11337.63
13	95557.453	7350.542	2726	933.49	12303.71
14	95557.453	7350.542	2726	1199.53	12508.67
15	95557.453	7350.542	2726	1629.45	12982.54
16	95557.453	7350.542	2726	2000	13273.96
17	95664.789	8445.293	2746	0	9909.11
18	95664.789	8445.293	2746	315.91	10387.29
19	95664.789	8445.293	2746	672.21	11443.39
20	95664.789	8445.293	2746	981	12008.12
21	95664.789	8445.293	2746	1337.29	12813.63
22	95664.789	8445.293	2746	2000	13324.46
23	95997.484	6202.122	1916	0	9930.07
24	95997.484	6202.122	1916	223.28	10177.26
25	95997.484	6202.122	1916	565.32	10822.23

Detailed documentation on using ProTab is available from the ProTab Help menu pulldown.

## Setting Permissions

You will notice that some items may have the Lock icon next to them in the table view.

Testing shared area		Name ▲
		Barrie
		Barrie Naguman 3D
		EAGE
		Hal
		MEXY
		Magnesium
		Naguman3D
		SEGsalt Synthetic
		Salt3D
		Steve
		Steve C
		manhattan-kmig tests
		md-wemr
		watsonrise-kmig tsts

In general, an item in the table that has a Lock icon indicates that you do not have write permission for some major component of that item.

For Projects (Data Homes), the lock icon appears when the main project directory does not have sufficient write permissions for your user.

A ProMAX® dataset that is annotated with the Lock icon indicates that the xxxxxxxxCIND file does not have write permission. **Note:** The CIND file is the only file that is checked for ProMAX® datasets.

A JavaSeis dataset that is annotated with the lock icon indicates that the dataset-name.js directory does not have write permission. **Note:** This directory is the only check for JavaSeis datasets.

For Flows, the lock icon appears when the main flow directory does not have sufficient write permissions for your user. **Note:** The main flow directory is the only check for flows.

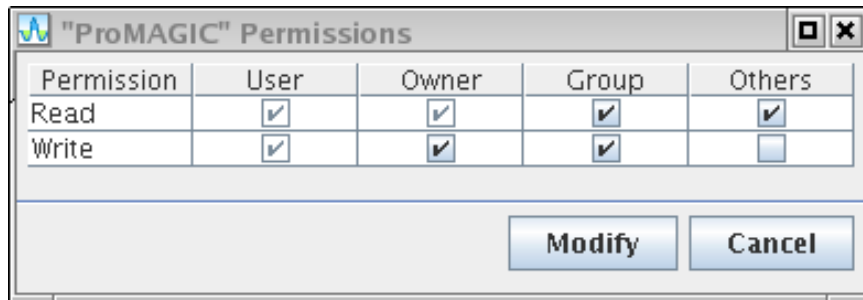
Tables follow the same convention. All files associated with the table must have sufficient permissions or the entry in the list is annotated as locked. The file that is checked is the #####XXXX file.

## Changing permissions



Use the lock icon or select **Edit > Permissions** from the pulldown menu or click MB3 on the item and select **Permissions** from the popup to view or modify the permissions on entire projects or subproject. You can also change the permission on individual objects such as datasets, flows or tables.

*Note:* You must be the owner of all of the files under the selected directory for all of the permission changes to take place successfully. If you are not the owner you will be presented with a non-editable dialog.



Files associated with datasets and flows can be owned by many different users and the permission change is only applied to the files owned by you.








*Note:* The SeisSpace® user interface does not offer the ability to do batch commands as the root user to change global ownerships.

The Permissions window shows the standard Owner, Group, and Other read and write permissions and allows you to change the permission.

To change the permission, click the boxes that describe the desired permissions and then click the **Modify** button.

## Dataset Types and Icon Descriptions

When you look a list of dataset in the Navigator in either the tree or table view you can see a variety of different dataset types.

	shots - prepro - from 23191	shots-prepro-from23191.js
	shots - preprocessed	shots-preprocessed.js
	cdps - output from parallel so	cdps-outputfromparallelso.js
	precompute output	precomputeoutput.js
	pstm gathers - carl test	pstmgathers-carltest.js
	pstm gathers - pm ddi	pstmgathers-pmddi.js
	shots - 5 test shots	shots-5testshots.js
	shots - extract	shots-extract.js
	shots - geom	shots-geom.js
	shots - geom (multi job)	shots-geommultijob.js
	shots - prepro (multi job)	shots-prepromultijob.js
	stack - initial	stack-initial.js
	supergathres	supergathres.js
	cdps - JDI sort input	cdps-jdisortinput.js
	shots - geom	02745406CIND
	shots - prepro - pstm input	73801106CIND
	shots - extract	32334578CIND
	small3d_initial.vol	small3d_initial.vol
	empty ProMAX dataset	19619303CIND
	empty JavaSeis dataset	emptyjavaseisdataset.is



JavaSeis dataset that is simply a stub (Dataset added to the list with no framework or trace data).



JavaSeis dataset that has had it's framework defined or has been "Emptied". Dataset has no trace or header extent files.



JavaSeis dataset that has had it's framework defined and has trace/header data.



JavaSeis dataset that has had it's framework defined, has trace/header data and has at least one sort map generated for it.



JavaSeis dataset that has been "Emptied" but still has pre-existing sort map(s) associated with it.



ProMAX® dataset that is simply a stub (dataset added to the list with no framework or trace data) or a ProMAX® dataset that has been “Emptied.”



ProMAX® dataset that has Trace and Header extent files.



ProMAX® dataset that has Trace and Header extent files and has also had a framework file added using the Scanning tool.



GeoProbe .vol file. or Hybrid model file

## Dataset Properties / Inventory / Fold Map

From the **MB3 > menu** or from the icon bar you can get information about the datasets. Of particular interest are the Dataset Properties, Inventory and Fold Map. ProMAX® vs. JavaSeis vs. ProMAX® with framework will have different options.

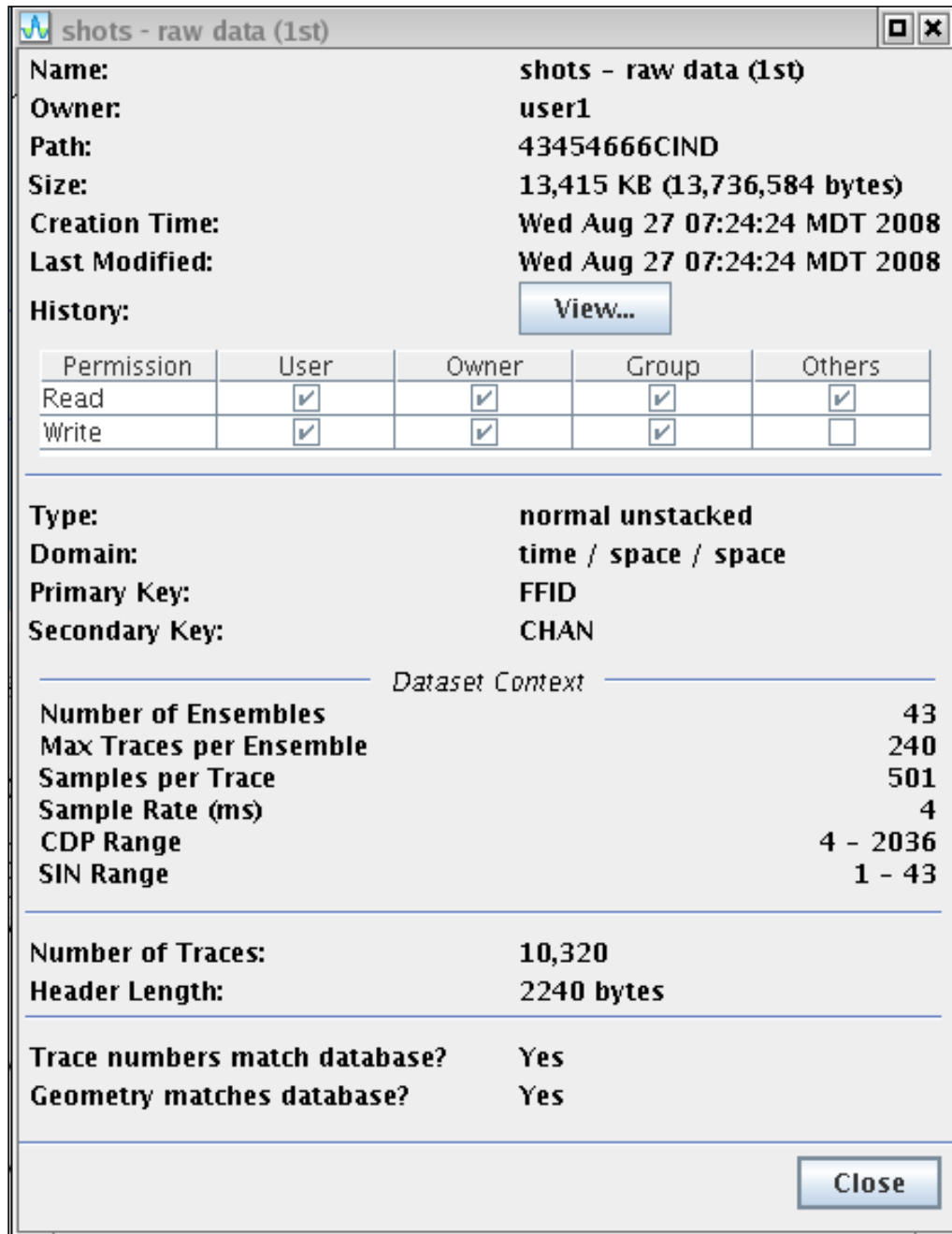
### Dataset Properties

The properties information dialogs show general information about the datasets. The properties dialog will be different for ProMAX®, ProMAX® with framework and JavaSeis Datasets.

Despite the similarities, there are several important differences between the Properties view is for ProMAX® and JavaSeis datasets.



For ProMAX® datasets the properties information dialog looks like this:



For ProMAX® datasets with a framework added, the properties information dialog looks like this:

**merge sort to cdp**

**Name:** merge sort to cdp  
**Owner:** sangelov  
**Path:** 06805951CIND  
**Size:** 2,386,569 KB (2,443,847,036 bytes)  
**Creation Time:** Mon Jan 05 17:28:18 MST 2009  
**Last Modified:** Mon Jan 05 17:28:18 MST 2009  
**History:** [View...](#)

Permission	User	Owner	Group	Others
Read	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Write	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Type:** normal unstacked  
**Domain:** time / space / space / space  
**Primary Key:** FFID  
**Secondary Key:** CHAN

**Sort Map** [<NONE>](#) [Delete](#)

---

*4D Dataset Framework*

**Data type** SOURCE  
**Trace format** unknown

**Axis coordinate** [Logical](#) [Physical](#)

[V] 3D inline number range (LINE\_NO) range 1-308 (1) : 308  
[F] 3D crossline number range (XLINE\_NO) range 1-390 (1) : 390  
[T] Sequence number in ensemble range (SEQNO) range 1-41 (1) : 41  
[S] Time range (milliseconds) 0.0-4000.0 (8.0) : 501

**Number of Traces in Framework** 4,924,920

---

**Number of Traces:** 1,699,444  
**Header Length:** 396 bytes

---

**Trace numbers match database?** Yes  
**Geometry matches database?** Yes

[Close](#)

For JavaSeis datasets the properties information dialog looks like this:

**cdps - dmo gathers**

**Name:** cdps - dmo gathers  
**Owner:** user1  
**Path:** cdps-dmogathers.js  
**Size:** 91,872 KB (94,076,928 bytes)  
**Last Modified:** Tue Apr 21 16:51:50 MDT 2009  
**History:** [View...](#)

Permission	User	Owner	Group	Others
Read	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Write	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

**Type:** normal unstacked  
**Domain:** time / space / space / space  
**Primary Key:** CDP  
**Secondary Key:** OFB\_NO

**Sort Map**  [Delete](#)

---

*4D Dataset Framework*

**Data type** CMP  
**Trace format** COMPRESSED\_INT16

Axis coordinate	Logical	Physical
[V] 3D inline number range (ILINE_NO) range	50-250 (50)	: 5
[F] 3D crossline number range (XLINE_NO) range	1-390 (1)	: 390
[T] Offset bin number range (OFB_NO) range	1-23 (1)	: 23
[S] Time range (milliseconds)	0.0-4000.0 (8.0)	: 501

**Number of Traces in Framework** 44,850

---

**Number of Traces:** 44,850  
**Header Length:** 820 bytes

---

**Trace numbers match database?** No  
**Geometry matches database?** Yes

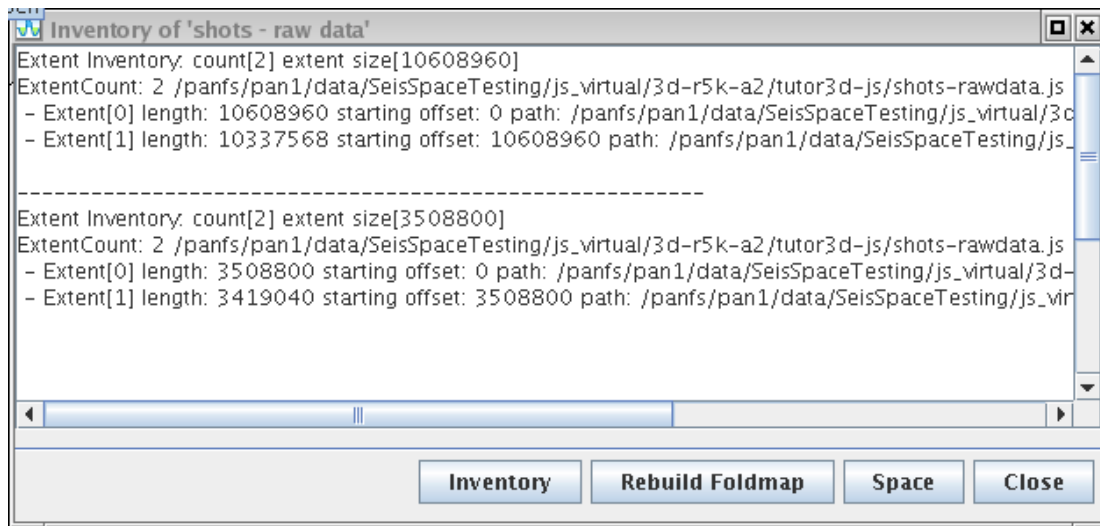
[Close](#)

The main difference in these dialogs is that the information for a ProMAX® dataset includes the minimum and maximum SIN and CDP ranges of the datasets and the JavaSeis Framework is shown for ProMAX® datasets with a framework and JavaSeis datasets.

If a sort table exists for a dataset you can select the sort table and then the framework summary will change to reflect the framework of the chosen sort table.

## Dataset Inventory

JavaSeis datasets are usually distributed over several different physical files on a number of different disk file systems. The Inventory dialog shows a summary of the distribution of the extents over the file systems.



**Inventory:** Shows the locations and distribution of the dataset extent files.

**Rebuild Foldmap:** If required, you can rebuild the traceMap file based on the actual contents of the extents. We found during development that there were cases where the traceMap file was updated as if the traces were written, but the traces were not actually written to the file. The Rebuild Foldmap option was added to help diagnose and fix this problem.

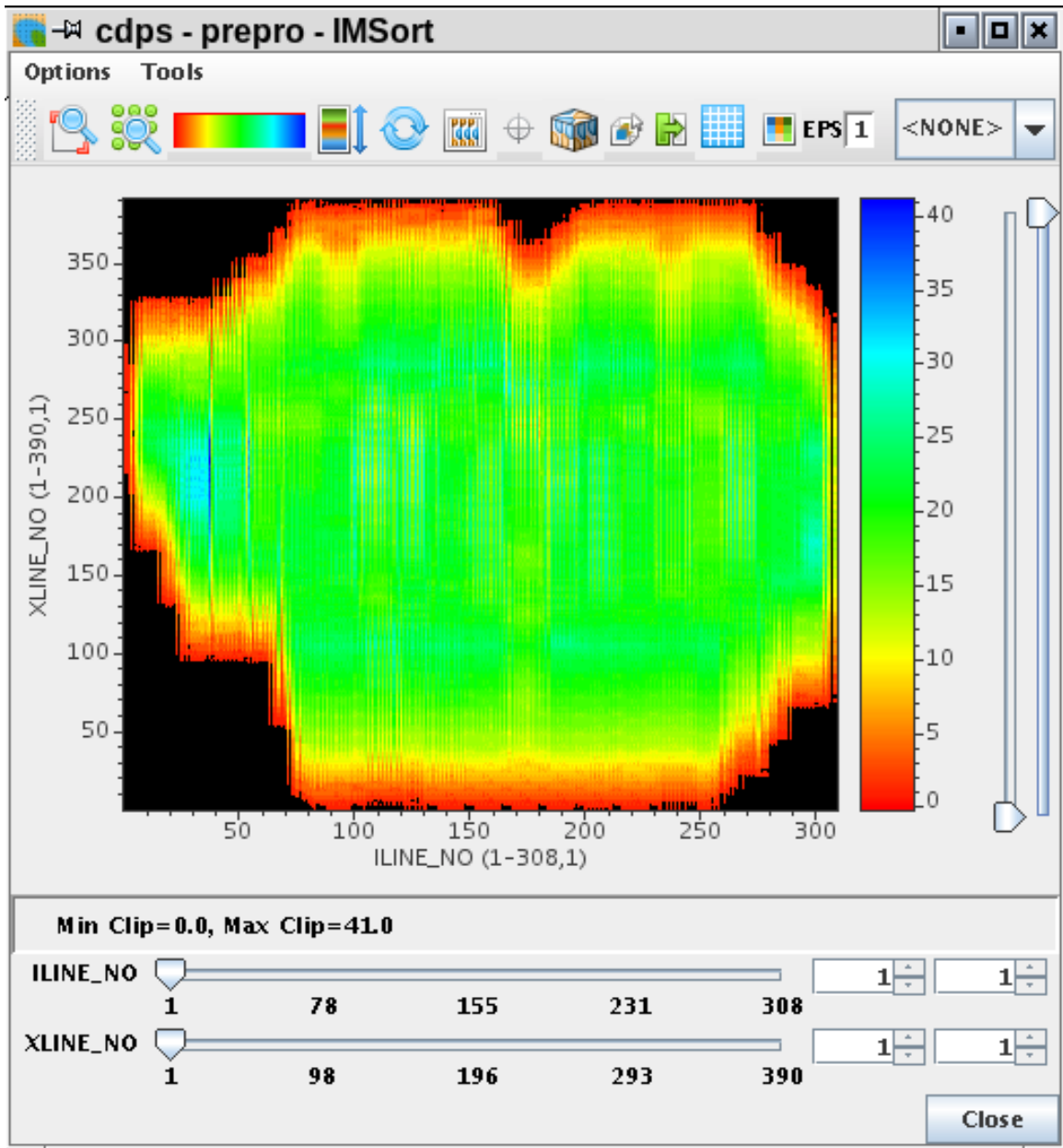
**Space:** Space can be used to get a listing of the free space available on the secondary storage disks.

**Close:** Exits the dialog.

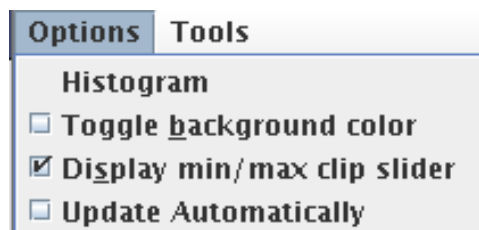
## Dataset Fold Map

The Fold map is available for JavaSeis and ProMAX® datasets with JavaSeis frameworks. This tool can be used to monitor a JavaSeis dataset as it is being populated or as a quality control tool after a dataset write

operation is completed. The Fold Map can also be used to check the integrity of a dataset to see if all of the data is in the file.

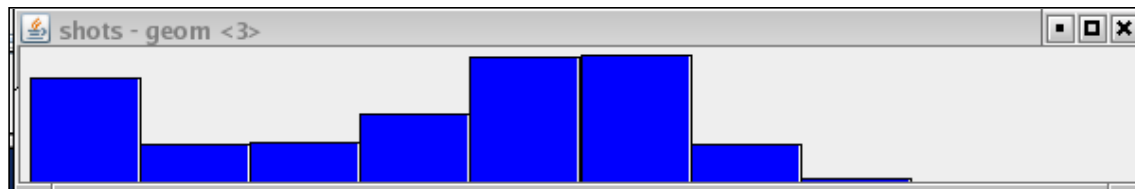


Fold map Options menu:



**Histogram:**

Generate a histogram plot that shows the distribution of the data values.

**Toggle background color:**

Alternate between background colors of black and white.

**Display min/max clip slider:**

Choose to display or not display the clip limit slider bars on the right side of the fold map display.

**Update Automatically:**

With this option checked "ON" the display will automatically refresh every few seconds and update the display with the data population.

**Fold map Icon Bar:**

Zoom Unzoom

Color Table

Color Clipping

Refresh

TraceDisplay

Pick mark control

3D Display

3D picking

Connect to Message Server

Shot Receiver CDP plot

Trace Fold for post stack data

Ensembles per Screen

SortMap selection

**Zoom:**

Enables the zooming function. Use MB1 to drag a box inside the display or outside the display in the axis for one dimensional zoom.

**UnZoom:**

Click on this icon to restore the display to its original size

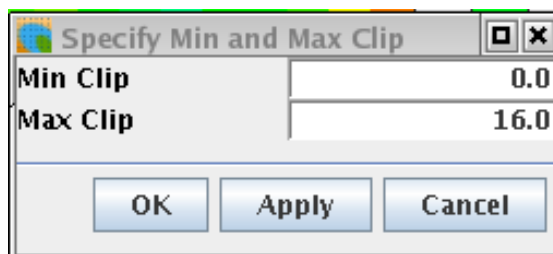
[Other Docs](#)
[Search Page](#)
[Known Problems](#)

**Color Table:**

Choose a color table from a list.

**Specify min/max clipping:**

Manually set the color clipping limits.

**Reload and refresh:**

Refreshes the display by rereading the input dataset from disk. If you recreate the dataset you can use this button to force a hard restart and relocate the files and re-initialize the display.

**Trace Display:**

Clicking on this icon will start a SeisSpace® Trace Display. You can display "frames" from the JavaSeis dataset selecting the locations with MB1 clicks.

**Change pick mark and cross hair appearance:**

Used in the 3D picking mode to control the size of the pick marks and the crosshair locators.

**3D Viewer:**

Start the 3D viewer to look at the data in the file in 3D.

**3D Picking:**

Start the 3D viewer and a 2D Trace display to pick mutes and design gates using the Fold map for navigation, the 3D viewer for QC of the table in a 3d display and the 2D viewer to pick the functions.

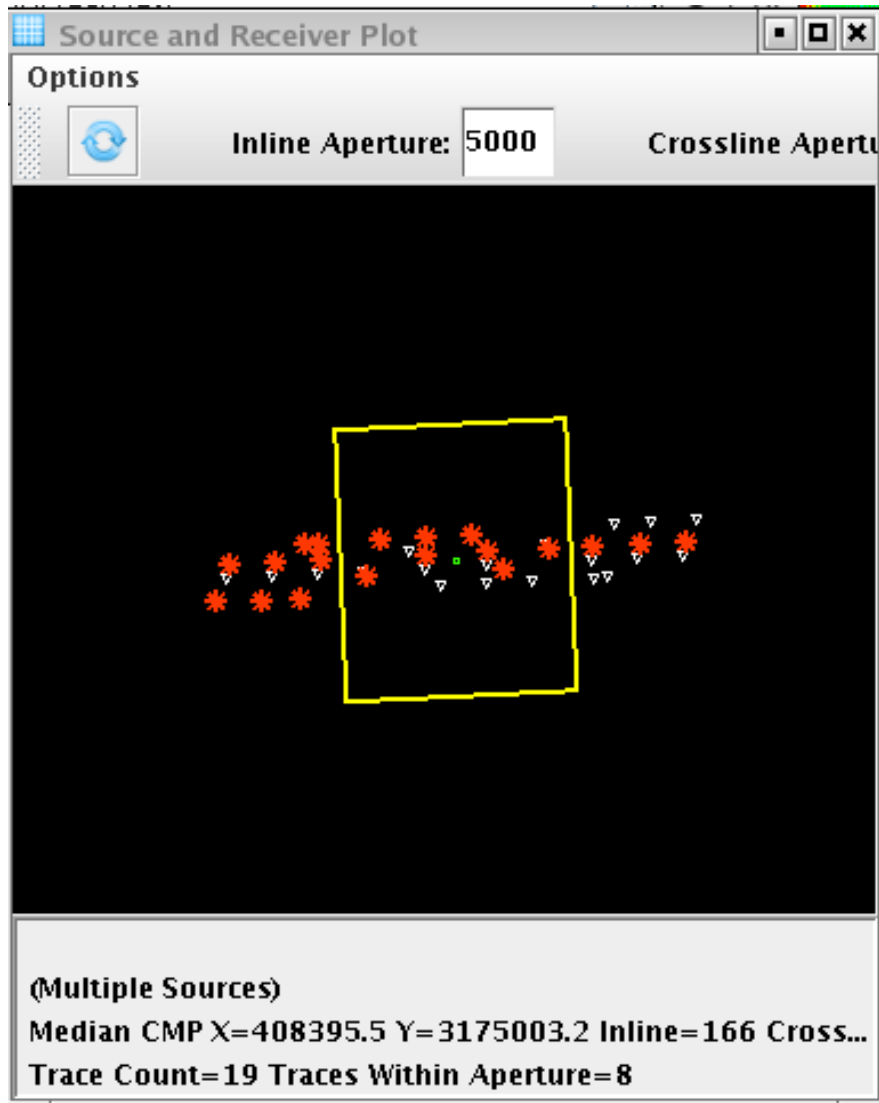
**Turn Locator and Pick Messages On/Off:**

When the Trace Display, Fold map, 3D viewer and Seismic Compare are running together in different modes, there is a Message Server that sends location information from one application to another. This icon can be used to turn the message passing on and off for this instance of the fold map so that it does not send location information to the other application or receiver location information from other

applications.

### Display the bin grid geometry...:

For pre-stack frames this option will show a map of all of the shot, receiver and cdp positions for all of the traces in the frame. You can also use this feature to help define aperture distances for the prestack imaging modules.



### Display TRC\_FOLD for a post stack dataset:

For post stack data you can plot the actual trace fold as a secondary plot in addition to the “frame fold” normal fold map.

### EPS (Ensembles per Screen):

Combined with the 2D Trace Display viewer sets the number of



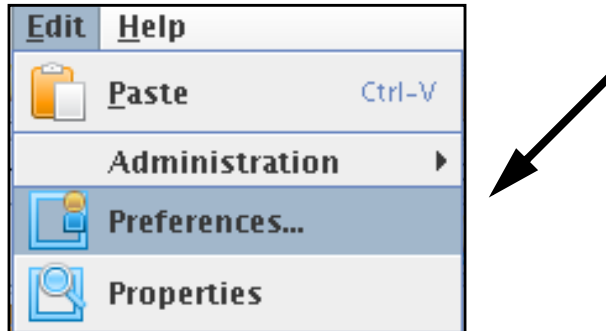
frames to display in Trace Display at each selected location.

**Additional fold map displays based on sort tables:**

The selection box allows you to choose from a list of sort tables that exist for this dataset. Select the fold map and a new fold map based on the selected sort table will be generated and displayed.

## Setting Preferences

Select **Edit > Preferences** to display the preferences window.



The tabs at the top are used to change the preferences for specific windows within the user interface. They are discussed from left to right.

## Navigator Tab

The screenshot shows the 'User Preferences' dialog box with the 'Navigator' tab selected. The dialog has a title bar with a maximize button and a close button. Below the title bar are five tabs: 'Navigator', 'Flow Editor', 'Log Viewer', 'Defaults', and 'Exec'. The 'Navigator' tab is active and contains the following settings:

- Automatically increment flow version when flow is saved
- Overwrite instead of append to existing log files
- Automatically purge old flow versions
  - Number of instances to keep after purge:
- Automatically purge old replicas
  - Number of replicas to keep after purge:
  - Number of parallel replica builders:
- Use a single common tab for all data types
- Single mouse click opens latest instance of flow
- Click on single selected cell in Name column allows rename
- Prompt for the name of the copied object
- Automatically open last opened flows  Expand tree to last opened flows
- Restart at last opened location
- Restore last archive state
- Hide the job viewer after job submit
- Never calculate and display the size of data home areas
- Beep after Job completion
- Check for changes on disk when redisplaying
- Attempt to automatically sort tree nodes
- Include files whose names match this RE in a flow copy:
- Order of Tree Nodes:  ▼
- Size of the Toolbar Icons:  ▼
- Scaler for the size of the UI fonts:  ▲ ▼

At the bottom of the dialog are three buttons: 'OK', 'Cancel', and 'Help'.

The Navigator tab allows you to set preferences for the Navigator.

- **Automatically increment flow version when flow is saved** can be toggled on or off. With this set to Off, you will only have a single instance of the flow saved.
- **Overwrite instead of append to existing log files** can be toggled on or off if the previous setting is set off (or do not increment the flow instances). With this set to OFF multiple runs of the flow will concatenate into the log file. With this set to ON, the exec.0.log file will be replaced for each run of the flow.
- **Automatically purge old flow versions** can be toggled on or off. On will limit the maximum number of flow versions at any time.

Change the **Number of flow instances to keep after purge**. The default is to keep the 5 most recent versions. This also sets the maximum number of instances to have before an auto-purge takes effect if that option is chosen

- **Automatically purge old flow replicas** can be toggled on or off. On will limit the maximum number of replica versions to have at any time.

Change the **Number of replicas to keep after purge**. The default is to keep the 2 most recent versions. This also sets the maximum number of instances to have before an auto-purge takes effect if that option is chosen

- **Number of parallel replica builders** can be use to change the number of threads used to to build replica flows. The default is 7.
- **Use a single common tab for all data types**: Select to reduce the number of tabs at the top of the Navigator by using the Navigator tab only instead of having separate tabs for Datasets, Flows, Tables, and Navigator.
- **Single mouse click opens latest instance of flow**: This is a compatibility switch to make the Navigator act like the ProMAX® user interface. That is, a single click on a flow name displays it in the flow editor. This option takes fewer mouse clicks to get a flow into the editor. However, it is harder to get to the flow instance list. This option is toggled **On** when you choose ProMAX® feel from the Defaults tab.
- **Click on a single selected cell in Name column allows rename**: If this option is selected then a second click on an entry in the table view will put that item into a rename mode. (note that this is two separate single clicks which is different from a double click)
- **Prompt for the name of the copied object**: If this option is selected you will be prompted to supply a name for a copied object before the

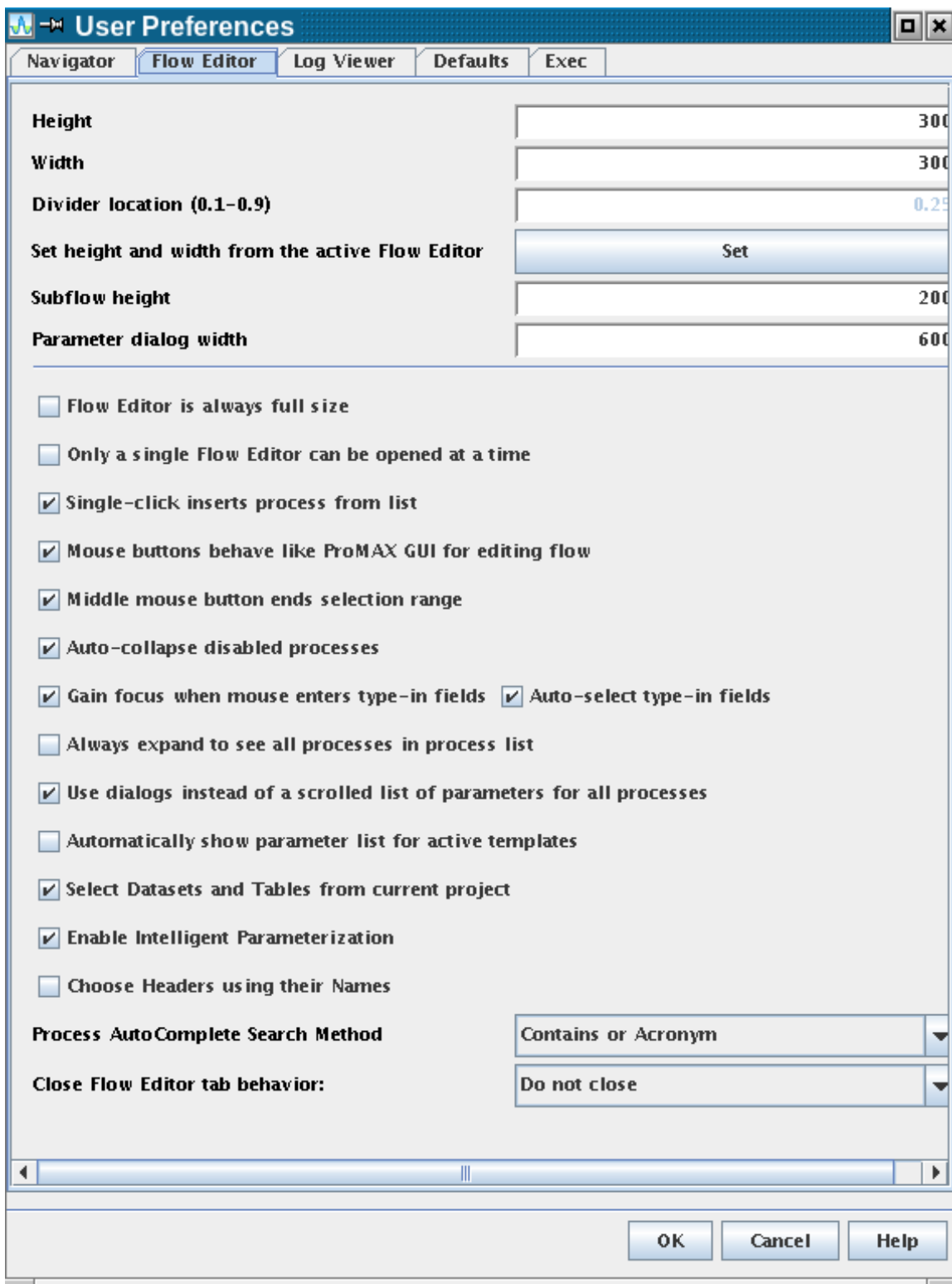
copy operation is performed. If this is unchecked, the "copy of" naming convention will be used automatically.

- **Automatically open last selected flow on startup:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. That is, the last flow you were editing when you stopped a session is opened on startup. This option is toggled **On** when you choose ProMAX® feel from the Defaults tab.
- **Expand tree to last opened flows:** If flows are opened you have the option to also expand the tree to open the lists of flows for all of the projects for which flows are opened. Leaving this box unchecked will keep the tree view in a more compressed state.
- **Restart at last opened location:** You may elect to have the Navigator automatically navigate to the last set of information you were looking at when you exited the Navigator. The default is so start the Navigator where it presents the lists of projects under the hosts where you would then select which project you wanted to work on.
- **Restore last archive state:** If you have selected objects for archiving, the last selection will be saved and restored the next time you go to archive selection.
- **Hide the job viewer after job submit:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. That is, when you submit a flow the job viewer window is hidden and the job status appears in the notification window. This option is toggled **On** when you choose ProMAX® feel from the Defaults tab.
- **Never calculate and display the size of data-home areas:** If this option is checked on then you will not compute the size of areas when you click on a data home in the tree view.
- **Beep after job completion:** You can select to turn off the notification "beep" of job completion status.
- **Check for changes on disk when redisplaying** can be toggled on or off. On will refresh the list of datasets, flows, tables etc each time the list is opened so that if other users have added items you will see them. This action is similar to clicking on a node in the tree view and then clicking the refresh icon. With this option on, the refresh icon is automatically clicked when you choose a node.
- **Attempt to automatically sort tree nodes** can be toggled on or off. On means that extra steps will be taken to try to ensure that that tree view always stays sorted.

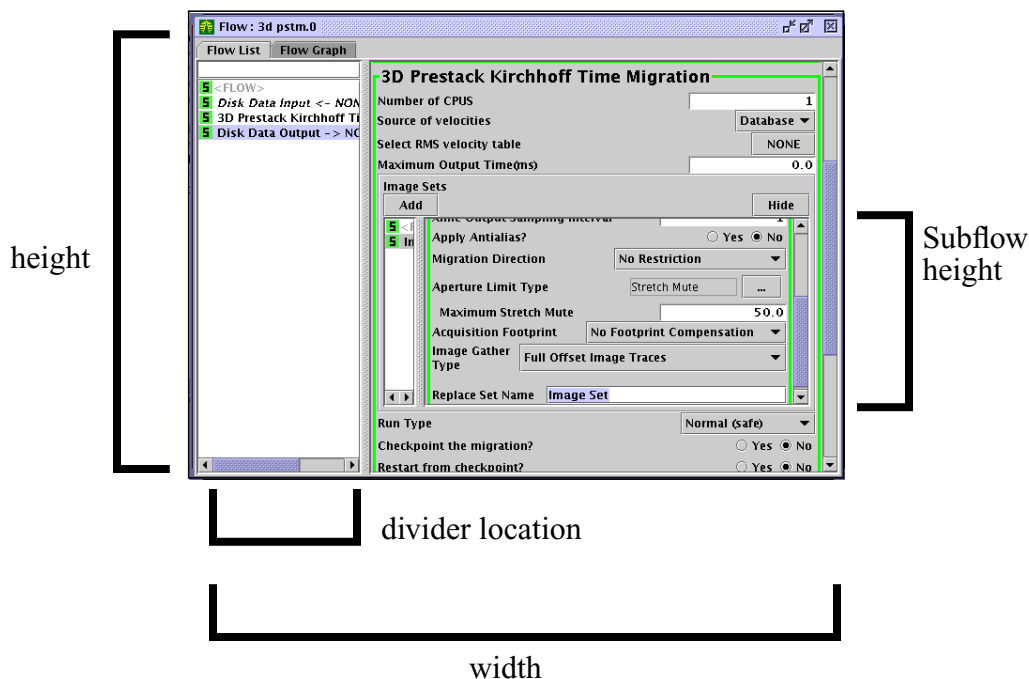
- **Include files whose names match this RE in a flow copy** can be used if there are non-standard files in a flow directory. Set the regular expression to include other files to include in the copy operation.
- **Order of Tree nodes** can be set to control how items are listed in the tree view.
- **Size of the Toolbar Icons:** Choose to use Normal or Large icons on the toolbar.
- **Scaler for the size of the UI fonts** can be used to display the text in the navigator with smaller than normal or larger than normal fonts. The navigator will need to be restarted for the change in value to take affect.

## Flow Editor tab

This window contains options for customizing the flow editing behavior.



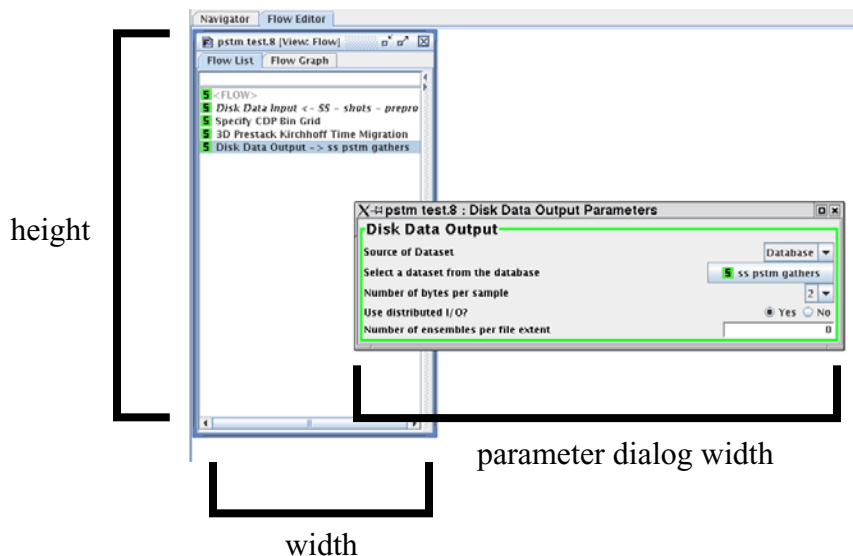
The first height and width values control the size of the flow editor window. The Divider location is active only if the “Use dialogs instead of scrolled list for parameters for all processes” is toggled off and controls the position of the divider between the process list and the scrollable parameter window components of the flow editor. You can use the “Set height and width from the active Flow Editor” to populate these values from an active flow edit session. The subflow height value is shown in the graphic below.



The Parameter dialog width value is used when the “Use dialogs instead of scrolled list for parameters of all processes” is toggled on and sets the



width of the individual parameter dialog box of parameters for each process that is shown when MB2 is clicked on a process.



## Flow Editor parameters

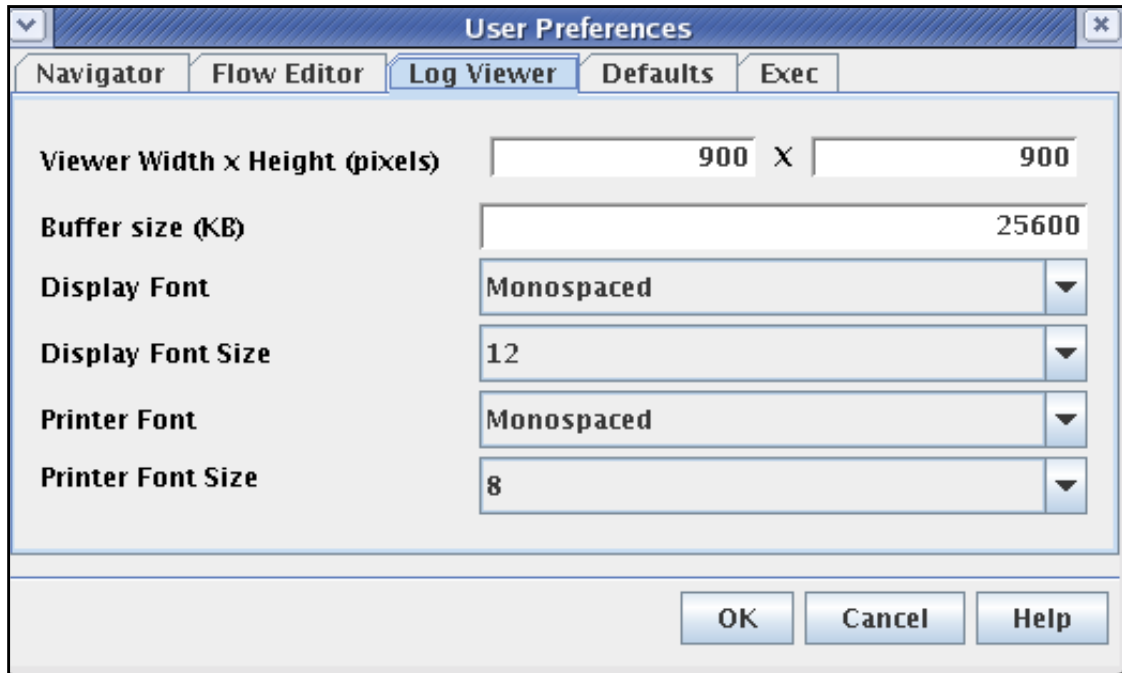
- **Flow Editor is always full size:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. The flow editor window occupies the entire flow editor window to mimic the ProMAX® look and feel.
- **Only a single Flow Editor can be opened at a time:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. Only one flow is open in the flow editor at any given time. This mimics the behavior of the ProMAX® user interface. Editing a new flow opens a new flow editor window.
- **Single-Click inserts process from list:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. Toggle **On** to add a process from the processes list with a single click. Toggle **Off** to add a process by either using Drag and Drop or a double click.
- **Mouse buttons behave like ProMAX GUI for editing a flow:** This is a compatibility switch for mouse bindings to be similar to those in the ProMAX® system. This option only affects MB3; toggle **on** for MB3 to toggle a process back and forth between active and inactive. Toggle **Off** for MB3 to popup a dialog box for the selected process.
- **Middle mouse button ends selection range:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface.

Toggle **On** to select a range of processes using MB1 and MB2 instead of using SHFT MB1 to select the range.

- **Auto-collapse disabled processes:** This option is only applicable when using the scrollable window flow editor. Toggle **On** to collapse the parameters for an inactive process.
- **Gain focus when mouse enters type-in fields :** With this option checked, typein fields in menus will automatically gain mouse and keyboard focus when you enter the field, With it un-checked you can give the typein field focus by clicking in the text dialog. NOTE: you will need to re-open existing flows in the editor or restart the navigator to see a change in behavior.
- **Auto-select type-in fields:** When the mouse moves into a type-in files you have the choice of whether or not the current text gets put into the temporary copy clipboard. With this option checked the text will be added to the clipboard, with it unchecked, the text will not be added to the clipboard. It is recommended to un-check this if you do a lot of mouse copy with MB1 drag from one source and a MB2 drop to copy the text from one location to another. NOTE: you will need to re-open existing flows in the editor or restart the navigator to see a change in behavior.
- **Always expand to see all processes in the processes list:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. Toggle **On** to show all processes in the processes selection window.
- **Use dialogs instead of a scrolled list of parameters for all processes:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. Toggle on to display the flow as a simple list of processes. MB2 is used to view the parameters for the selected process. You can have multiple parameter windows open simultaneously.
- **Automatically show parameter list for active templates:** Select this option if you want template flows to be opened with the scrollable parameterization window as the default.
- **Select Datasets and Tables from current project:** Toggle **Off** to navigate to the last list of datasets or tables that you visited. This is useful if you are selecting several datasets from a different project. This does nothing related to the general capability to select datasets from different AREA/LINE's within the same DATA\_HOME. This simply controls which datasets list is presented when you ask for a list from a data input or output menu.

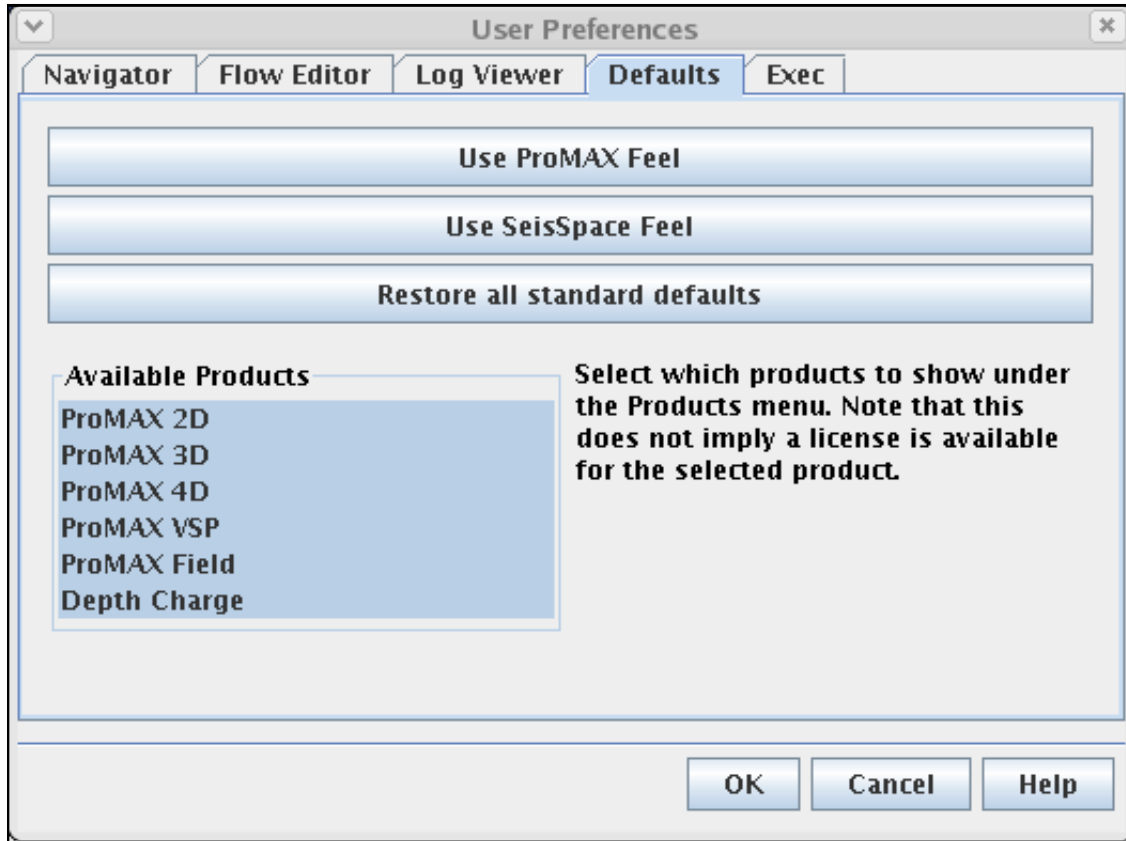
- **Enable Intelligent Parameterization:** You can have the flow builder automatically and instantly check some of the parameterization of the processes as the flows are being built. The functionality is automatically turned off for pure ProMAX® flows. The status of the IPM is shown in the light bulb icon in the lower left hand corner of the navigator.
- **Choose Headers using their names** can be toggled on or off. On indicates that headers will be shown in menus by their attribute name. Off indicates that headers will be shown in menus with their descriptive name.
- **Process AutoComplete Search Method:** This is a compatibility switch to make the Navigator act like the ProMAX® user interface. Set to **Starts With** to display processes with the characters you entered. **Contains or Acronym** mimics the ProMAX® user interface in that you can type more shortcuts for a process search.
- **Close Flow Editor tab behavior:** choose between Do not close, or Automatically close when a flow editor tab is emptied of all of its flows.

## Log Viewer tab



The Log Viewer tab configures the job printout viewer. The Buffer size entry controls the maximum size of a printout. This is handy if you are running the client remotely and you want to view a large printout. Only 1024 KB of the file is initially transferred. The remaining entries control the font sizes of the viewer.

## Defaults tab

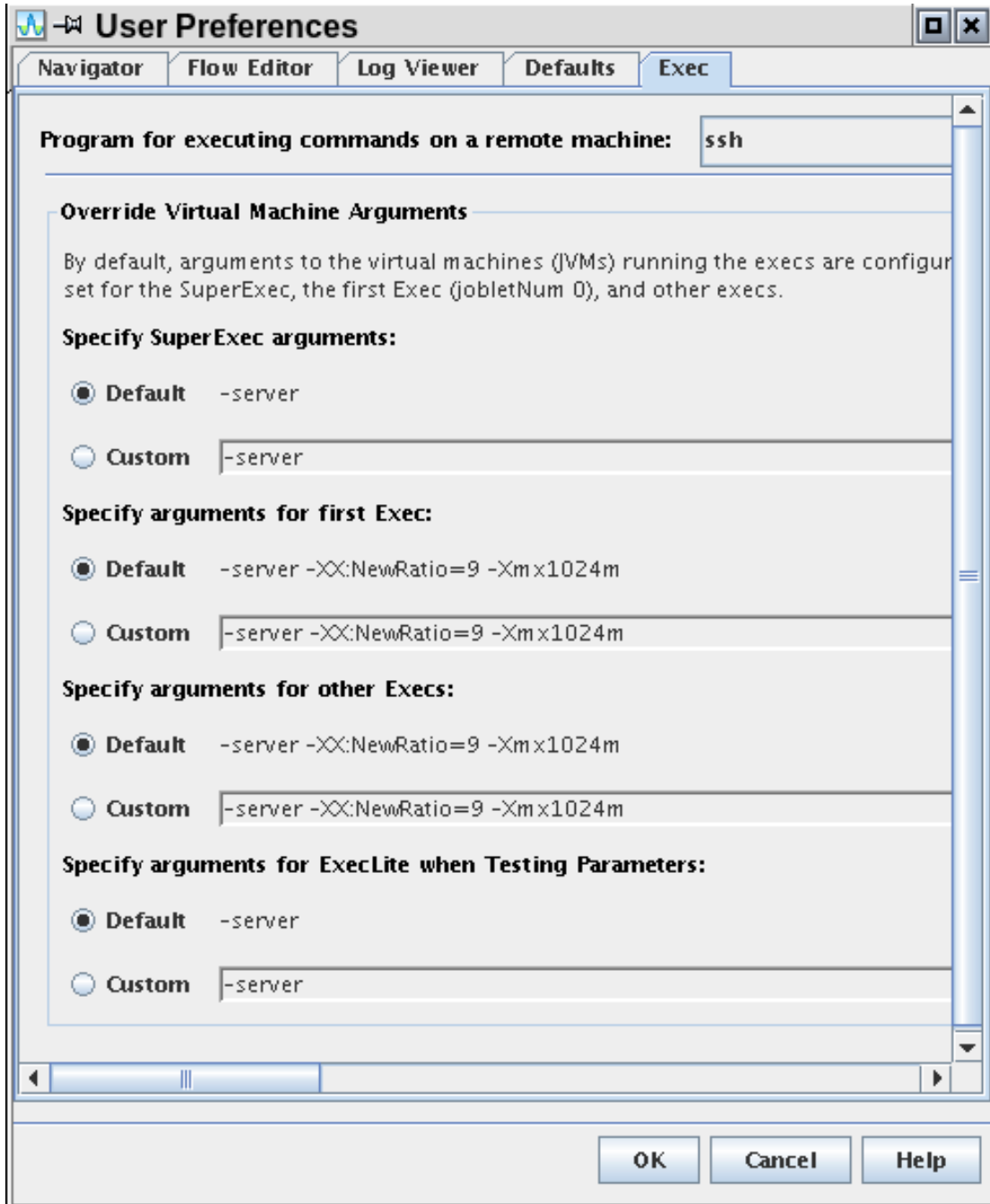


There are three basic sets of defaults: **Use ProMAX® feel**, **Use SeisSpace® feel** and you can also **Restore all standard defaults**.

Under the products selection section you can choose which products you want to make available in your product list pulldown from the Navigator. The default is to use the list that the administrator has set up. You can override that list for your personal settings here.

## Exec Tab

The Exec tab allows you to set preferences for the SeisSpace® trace processing executive program.



- **Program for executing command on remote machine:** If you do not have rsh permission to run the qsub command you can select to use ssh instead. *Note:* you must go through the ssh setup procedure to allow ssh without a password prompt. This procedure is outlined in the ProMAX® and SeisSpace® System Administration online help.
- **Override virtual machine arguments:** This is a capability added specifically for the development environment. The user has the capability to alter exec parameters to work in a debug environment. The details of this procedure is outlined in the development class notes.

# Working with the Job Table

## Overview

The Job Table shows the status of jobs submitted via the Navigator or Flow Builder. The primary purpose of this table is to monitor jobs that are submitted from the Flow Editor, or from the tree and table lists of flows. Jobs that are submitted from the Flow Replication Job Table can also be monitored here by clicking the **Find > Show replicas** check box.

Status	Name	Hosts/Queue	Execs	% Data read	Input MB/s	Submitted	User	
Completed	dc02j-forward inverse tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1	testarea/dataco
Failed	dc02-forward inverse tau-p.0	parallel@h1	1			04/22/2009 ...	user1	testarea/dataco
Completed	dc01j-forward tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1	testarea/dataco
Failed	dc01-forward tau-p.0	parallel@h1	1			04/22/2009 ...	user1	testarea/dataco
Completed	F07B RR Read comma list2.0	parallel@h1	1	100.00	0.01	04/22/2009 ...	user1	testarea/arbitra
Running	F07A RR Read comma list.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Running	F06B RR Read narrow range.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Completed	F06A RR Read narrow range.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1	testarea/arbitra
Completed	F05B RR Read all2.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1	testarea/arbitra
Running	F05A RR Read all.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Running	F04B Read comma list2.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Running	F04A Read comma list.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Running	F03B Read narrow range2.0	parallel@h1	1	150.00	0.90	04/22/2009 ...	user1	testarea/arbitra
Running	F03A Read narrow range.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Chained	5d10 - apply il xl ofb sort.0	parallel@h1	1			04/22/2009 ...	user1	testarea/5djava
Running	F02B Read all2.0	parallel@h1	1	0.00	0.00	04/22/2009 ...	user1	testarea/arbitra
Completed	F02A Read all.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1	testarea/arbitra
Chained	5d09 - apply ofb il xl sort.0	parallel@h1	1			04/22/2009 ...	user1	testarea/5djava
Completed	F01B Synthetic generation2.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1	testarea/arbitra
Running	5d08 - add 5d-4d sort maps.0	parallel@h1	1	100.00	0.00	04/22/2009 ...	user1	testarea/5djava
Completed	F01A Synthetic generation.0	parallel@h1	1	100.00	0.72	04/22/2009 ...	user1	testarea/arbitra
Failed	5d07-5d TD in Dist Array.0	parallel@h1	1			04/22/2009 ...	user1	testarea/5djava
Running	5d06 - stack the 5D data.0	parallel@h1	1	100.00	9.14	04/22/2009 ...	user1	testarea/5djava
Completed	5d05 - 5d data for 4dproc.0	parallel@h1	1	100.00	6.10	04/22/2009 ...	user1	testarea/5djava
Chained	5d04 - x-spr fxy.0	parallel@h1	1			04/22/2009 ...	user1	testarea/5djava
Running	5d03 - X-spread synth.0	parallel@h1	1	0.00	15.05	04/22/2009 ...	user1	testarea/5djava
Completed	5d02 - read a 5D dataset.0	parallel@h1	1	100.00	1.31	04/22/2009 ...	user1	testarea/5djava

The commonly occurring status values are:

- **Completed,**
- **Failed,**
- **User Terminated,**
- **Running,**
- **Chained,** and
- **Queued.**

The other status values are **Unknown, Submitted, Initializing, Unresponsive, Waiting\_on\_RSRCs, Waiting\_on\_Mount, Paused,**



**Stopping, Cancelled, Chain\_Failed and Build\_Failed.** **Stopping** occurs when the jobs are completing. Only pure ProMAX® jobs can be in a **Paused** state.

You can get a Quick View of the end of a job printout by holding down MB2 on one of the rows of the job viewer. This shows the last few lines of the printout for a quick QC of the job.

Status	Name	Hosts/Queue	Execs	% Data read	Input MB/s	Submitted	User
Completed	dc02j-forward inverse tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1 testarea/dataco
Failed	dc02-forward inverse tau-p.0	parallel@h1	1			04/22/2009 ...	user1 testarea/dataco
Completed	dc01j-forward tau-p.0	parallel@h1	1	100.00	0.10	04/22/2009 ...	user1 testarea/dataco
Failed	dc01-forward tau-p.0	parallel@h1	1			04/22/2009 ...	user1 testarea/dataco
Completed	F07B RR Read comma list.0	parallel@h1	1	100.00	0.01	04/22/2009 ...	user1 testarea/arbitra
Completed	F07A RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07D RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07C RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07E RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07F RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07G RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07H RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07I RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07J RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07K RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07L RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07M RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07N RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07O RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07P RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07Q RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07R RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07S RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07T RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07U RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07V RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07W RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07X RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07Y RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F07Z RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F080 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F081 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F082 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F083 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F084 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F085 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F086 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F087 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F088 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F089 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F090 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F091 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F092 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F093 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F094 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F095 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F096 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F097 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F098 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F099 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra
Completed	F100 RR Read comma list.0	parallel@h1	1	100.00	0.04	04/22/2009 ...	user1 testarea/arbitra

```

Tool: # traces # ensemb expected Mbytes Mbyte/s seconds
SmartInput 40 4 70 0.08 0.04 1.99
Assertion 40 4 70 0.08 9.17 0.02
END

*****
Jobid = 2825030210445386819
JobState = Completed
Traces processed = 40
Rate = 0.04 Mb/s
Submitted @ 2009/04/22 07:48:35
Initialized @ 2009/04/22 07:48:48
Finished @ 2009/04/22 07:49:15
Wait time = 12 seconds
Run time = 27 seconds
Total time = 40 seconds

*****

--- ProMAX license(s) checked out for this flow :-
--- POSTPAL
---

--- ProMAX license(s) accessed, continuing.

*** Start of STDERR ***

Exit status = 0

```

## Job Viewer Column Headings

### Name

Shows the name of the flow and its instance number.

### Host/Queue

Shows the host (or list of hosts) or Queue where a job was submitted.

**Foreman**

Show the foreman node. One Joblet is the foreman of the job. Usually the first node in the execution node list.

**Execs**

Shows the number of joblets into which the job was divided.

**Status**

Shows the current status of the job.

**% Data read**

Shows the percent of the input data passing through the **Input**.

**Input MB/s**

Shows the rate at which data is passing through the **Input**.

**Submitted**

Shows the date and time when a job was submitted.

**Initialized**

Shows the date and time when a job was initialized.

**Completed**

Shows the date and time when a job completed.

**User**

Shows the user who submitted the job.

**Area/Line**

Shows the Area/Line with which the flow is associated.

**Traces**

Shows the number of traces processed by the job.

**IsReplica**

Shows true or false depending if the flow is a replica or not.

## Queue JobID

Shows the JobID from the Queue. Shows -1 for direct submit jobs

## Job Viewer Icon Bar



The icons will be changed to a grayed out status depending on the status of the job and the type of job that is selected.

### Refresh job listing icon



The icon can be used to refresh the job listing by rereading the current jobs.\* files from the logs directory.



The icon can be used to open the Workpile Manager dialog for a template or a replica.

### View job listing icon



The icon can be used to view the printout of the selected job while it is running or after it has completed.

### Query Status of Joblets icon



This icon is only used for pure SeisSpace® or Hybrid jobs, it has no use for pure ProMAX® jobs. The joblet status window that is started using the "Query status of joblets" icon displays the detail of a job. The window is a matrix display with one column per thread and several rows per process.




Job Summary @ 2008/05/19 16:20:21 : 3dt3-loadgeom.1				
name	0	1	2	3
01--tool 'SmartInput' % active	12.604	14.788	13.082	13.583
01--tool 'SmartInput' % waiting for input	0	0	0	0
01--tool 'SmartInput' % waiting to output	87.396	85.212	86.918	86.417
01->port below 'SmartInput' apparent mb/...	0	0	0	0
01->port below 'SmartInput' ensembles pa...	386	597	584	511
01->port below 'SmartInput' megabytes pa...	134.995	224.308	218.936	180.347
01->port below 'SmartInput' seconds elaps...	52.061	82.161	86.085	66.075
02--tool 'SSHybrid' % active	30.937	31.767	28.535	29.728
02--tool 'SSHybrid' % waiting for input	2.214	2.861	2.381	2.279
02--tool 'SSHybrid' % waiting to output	66.849	65.372	69.085	67.993
02->port below 'SSHybrid' apparent mb/sec	0	0	0	0
02->port below 'SSHybrid' ensembles pass...	386	597	584	511
02->port below 'SSHybrid' megabytes pas...	134.995	224.308	218.936	180.347
02->port below 'SSHybrid' seconds elapsed	54.065	84.167	88.089	70.081
03--tool 'JavaSeisOut' % active	74.614	74.801	75.978	75.788
03--tool 'JavaSeisOut' % waiting for input	25.386	25.193	24.021	24.212
03--tool 'JavaSeisOut' % waiting to output	0	0.006	0.001	0
03->port below 'JavaSeisOut' apparent mb...	0	0	0	0
03->port below 'JavaSeisOut' ensembles p...	386	597	584	511
03->port below 'JavaSeisOut' megabytes p...	134.995	224.308	218.936	180.347
03->port below 'JavaSeisOut' seconds elap...	51.579	80.826	85.138	67.875
Host name	q8	a5	s4	q12
Input mb/sec	2.593	2.73	2.543	2.729
Input percent complete	100	100	100	100
Joblet index	0	1	2	3
Joblets in job	4	-	-	-
Memory Java heap size	61	60	44	48
Memory reuse table	8	8	8	8

Process 1

Process 2

Process 3

Job Summary

Monitor    Refresh    Transpose    Close

Each group of rows displays statistics for a process.

Watch for large values in **waiting for input** or **waiting to output**. For example, when a job has a low percent active and a high value in waiting for input, it indicates that you cannot feed the data to the processors fast enough. High values for waiting to output are very typical for all of the processes proceeding the Prestack migration. PSTM is a very compute intensive process and is generally in a very high CPU utilization and high waiting for input mode.

### Monitor data flow of running job icon



The job summary displays statistics about a job.

For SeisSpace® and Hybrid jobs, an example job status monitor is shown:

Job is Completed

Thread 0:

Host(s): q8; 2008/05/19 16:20:24

Tool:	# traces	# ensemb	expected	Mbytes	Mbyte/s	seconds
SmartInput	297380	386	30225	135.0	2.59	6.56
GEOM_LOAD	297380	0	0	130.46	2.41	994.0
JavaSeisOut	297380	386	30225	135.0	2.62	40.34
END						

Thread 1:

Host(s): a5; 2008/05/19 16:20:24

Tool:	# traces	# ensemb	expected	Mbytes	Mbyte/s	seconds
SmartInput	494127	597	30225	224.31	2.73	12.15
GEOM_LOAD	494127	0	0	216.77	2.58	1452.0
JavaSeisOut	494127	597	30225	224.31	2.78	62.96
END						

Thread 2:

Host(s): s4; 2008/05/19 16:20:24

Tool:	# traces	# ensemb	expected	Mbytes	Mbyte/s	seconds
SmartInput	482293	584	30225	218.94	2.54	11.26
GEOM_LOAD	482293	0	0	211.58	2.4	1257.0
JavaSeisOut	482293	584	30225	218.94	2.57	66.93
END						

Thread 3:

Host(s): q12; 2008/05/19 16:20:24

Tool:	# traces	# ensemb	expected	Mbytes	Mbyte/s	seconds
SmartInput	397285	511	30225	180.35	2.73	8.98
GEOM_LOAD	397285	0	0	174.29	2.49	1173.0
JavaSeisOut	397285	511	30225	180.35	2.66	53.11
END						

:

Host(s): ; 2008/05/19 16:20:24

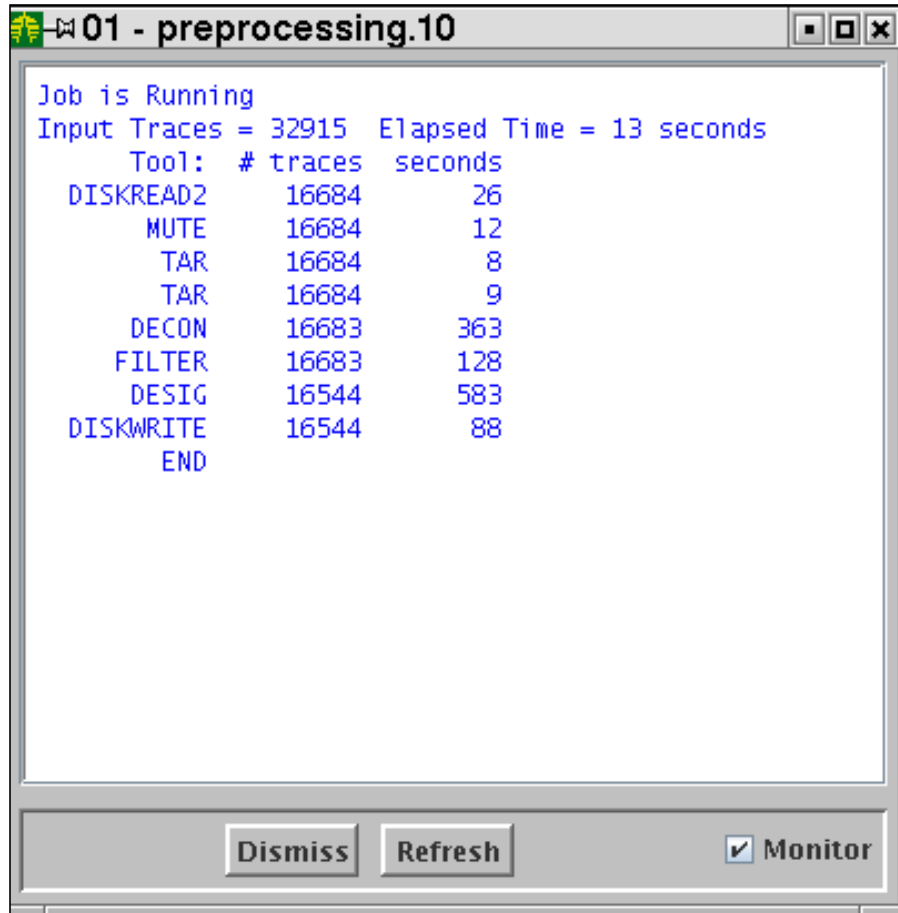
Tool:	# traces	# ensemb	expected	Mbytes	Mbyte/s	seconds
SmartInput	1671085	2078	30225	758.59	8.81	9.74
GEOM_LOAD	1671085	0	0	733.09	8.32	1219.0
JavaSeisOut	1671085	2078	30225	758.59	8.91	55.83
END						

Monitor  Refresh Close

Each thread has a set of statistics for each process in the thread. You can see bottlenecks in this window or those jobs consuming the most CPU time.

For PSTM jobs it is very common to see that the PSTM is using a high percentage of the CPU and causing a high percentage delay in the previous processes.

For ProMAX® jobs, an example job status monitor is shown:



### Display final job report



Display the final job report that is available after the job completes.

### Multiple job printout search



You can select multiple jobs in the table and then search all of the most recent printout files for the same string.

After the printout viewer starts, click on the refresh icon to view the results.

### Pause job and Resume Pause job icons



These icons can be used to temporarily halt a job that can be started again later. **Note:** Pausing a job that was released from the Queue does NOT



mean that another job will be released while this one is paused. This operation is valid for all types of jobs.

### Stop input and finish flow normally icon



The "Stop" icon is only available for Hybrid or SeisSpace® jobs. This icon will stop the input step of the flow but the remainder of the flow will complete as if the input had read all of the available data. There will generally be a delay between the time the icon is clicked and the job stops, especially jobs that are doing a lot of computation between data reads.

### Kill the job ASAP icon



This icon will terminate a ProMAX®, SeisSpace® or Hybrid job as soon as possible. The job will not complete normally after having shut off the input stream of data using the Stop icon.

### Delete job from Job Manager permanently or Remove from the Queue icon



This icon can be used to permanently remove jobs from the viewer. This icon can also be used to remove jobs from the queue that are in queued status.

### Output Thread Dump for debugging



For debugging some jobs it is useful to do a thread dump on the job so that development can try to determine where a job is having a problem.

### Row Filter icon

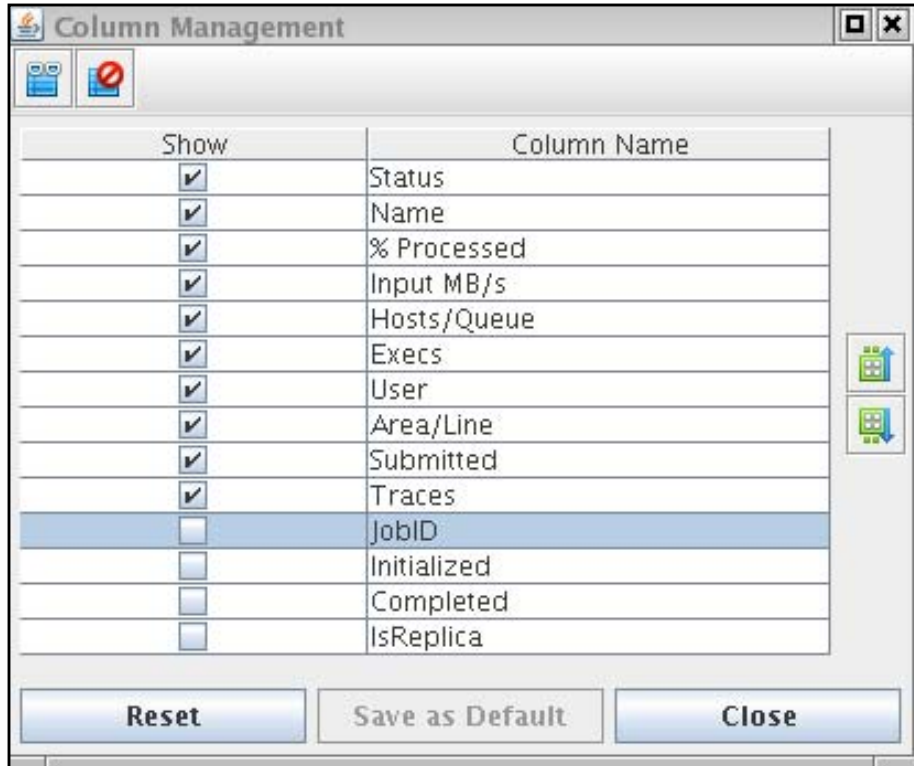


You can select which entries to display in a table using the Row Filter option. For example, you can select only the datasets or flow of interest to you. Use the **Row Filter** icon to choose criteria for selecting what to show.

### Column Show/Hide icon



You can select to show or hide columns. Use the **Column Selector** icon to choose which columns to show.



**Note:** Each tab pane is treated as a separate entity. You can set different column visibility, widths, order and sort criteria for each of the different tab panes. The default is to have a single Navigator tab pane, but you may elect to set the user preference to have separate tab panes for Flows, Datasets and Tables in addition to the single Navigator tab pane.



**Advanced Search/Filter**

Use	Column Na...	Operator	Value
<input type="checkbox"/>	Status	find (ignore case) ▼	
<input type="checkbox"/>	Name	find (ignore case) ▼	
<input type="checkbox"/>	% Processed	find (ignore case) ▼	
<input type="checkbox"/>	Input MB/s	find (ignore case) ▼	
<input type="checkbox"/>	Hosts/Que...	find (ignore case) ▼	
<input type="checkbox"/>	Execs	find (ignore case) ▼	
<input type="checkbox"/>	User	find (ignore case) ▼	
<input type="checkbox"/>	Area/Line	find (ignore case) ▼	
<input type="checkbox"/>	Submitted	find (ignore case) ▼	
<input type="checkbox"/>	Traces	find (ignore case) ▼	

Combine with:  and  or

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# Archive and Restore

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The original ProMAX® Archive to Tape module has been removed from the processes list as of release 5000.0.0.0. The “List/Restore from Tape” remains in the system so you can restore legacy ctar files created in earlier versions.

The Archive and Restore procedures are driven by selecting what you want to archive and what you want to restore using user interface components built into the Navigator. The Archive and Restore are driven by a restructured “tar” protocol that handles sparse files and properly understands the secondary storage directories.

Both the Archive and Restore procedures are driven by “wizards” to guide you through the required steps.

There are three icons above the tree view of the Navigator related to the Archive and Restore wizards and choosing/viewing what you want to archive.

## Toggle Archive View icon



The icon can be used to toggle the tree view between the normal view and the Archive view which allows you to select objects to include in the archive.

## Archive Wizard icon



The icon can be used to start the Archive Wizard.

## Restore Wizard icon

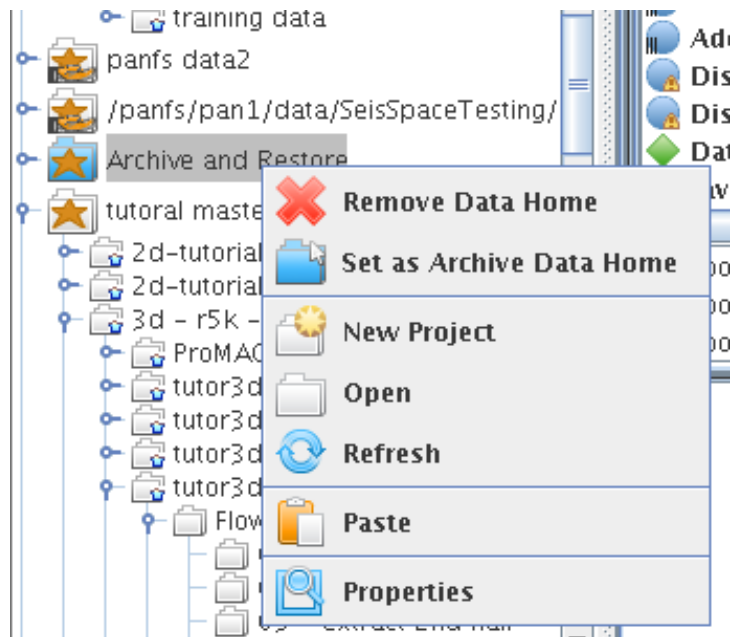


The icon can be used to start the Restore Wizard.

## Archive Data Home

You will need to designate some Data\_Home as the Archive Data Home. There is nothing special about this Data\_Home except that it has an

Archive and Restore area in it where the archive and restore jobs are built and saved by the Wizards. You can add an Archive Data Home using the **Edit > Administration > Add Archive Data Home** pulldown menus. This will start the standard Data Home addition dialog. If you choose an existing project, replacing it will add the Archive and Restore areas. You can make many Archive and Restore Areas in the different projects and then set any of the projects to the archive data home using the MB3 - Set as Archive Data Home option.



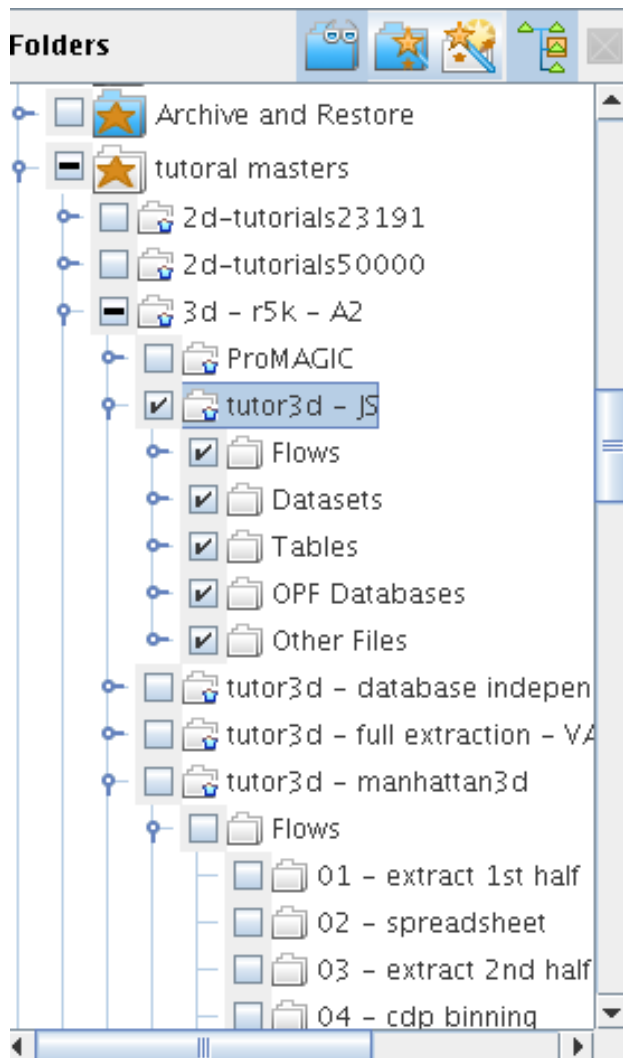
You must set one project as the default archive data home.

The Data Home that is the current Archive Data Home is annotated with the Blue shaded project icon as shown above.

## Archive View

Archive View can be used at any time during a Navigator session to add or remove objects from the list of objects to be archived. A file is stored in the users preference directory (either ~/SeisSpace or \$PROWESS\_PREFS\_DIR) called “.archive\_state.xml”. When you run the Archive Wizard, the first guess at what you want to archive is retrieved from this file. This file is saved when you exit the Navigator.

As you are using the Navigator you can toggle to the Archive View and add something to the list while you are thinking about it, or remove things that have either already been archived or you no longer want to archive.



You can click MB1 in the box next to the items you want to archive. A “-” sign indicates that not everything under that directory has been chosen. A “check mark” indicates objects that have been chosen. A check in a directory or a datatype, such as Flows indicates that all flows, or database files, tables, datasets, and other files below the checked object will be archived.

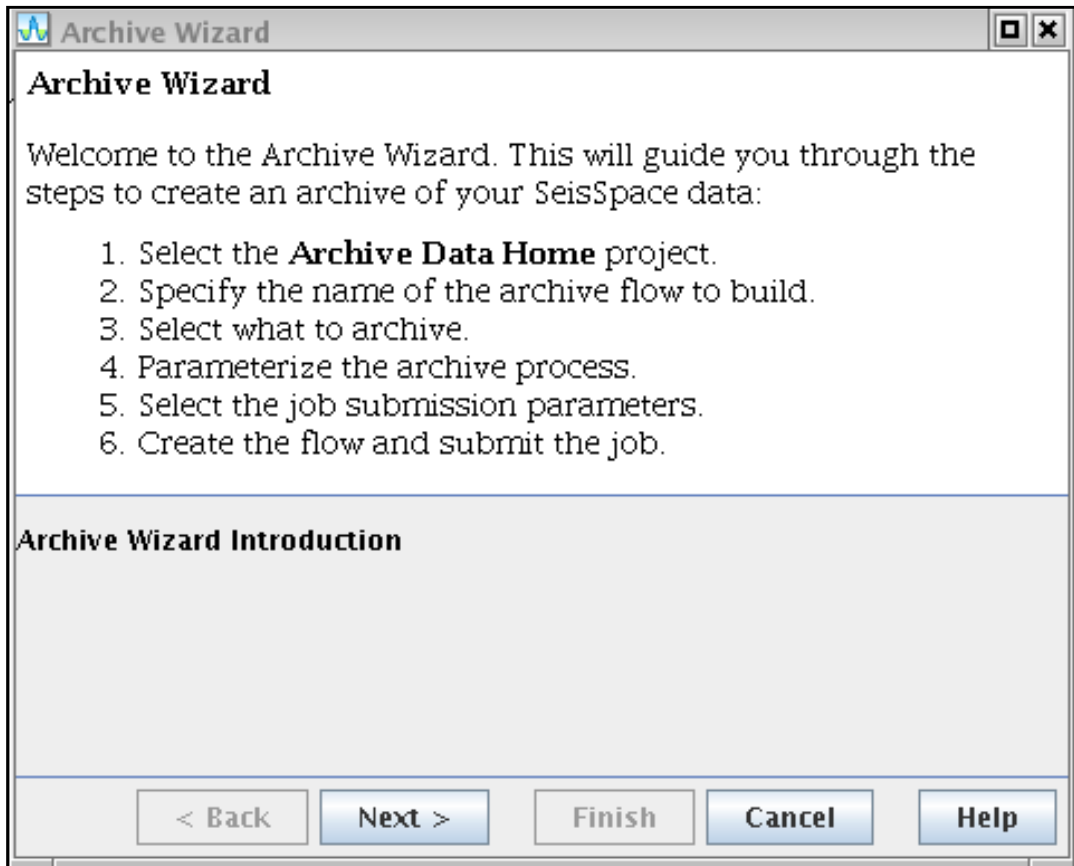
Notice that there is the “Other Files” section. This will show other files that are in the Line directory that are not recognized as system files that you can choose to archive. If any flow is selected then the replica\* files associated with that flow will also be automatically chosen for archival. Similarly, if

any database object is chosen then the PromaxGeom\* files will automatically be included in the archive.

You can continue to use the Navigator as normal while in the archive view mode. Be careful where you click so you don't accidentally include things in the archive list you did not want or delete items that you did want.

## Archive Wizard

The six steps in running the Archive Wizard are listed in the first window.



Click on **Next>** to go to step 1 to select the Archive Data Home project.

In this panel you are asked to select the Archive Data Home project and also give a descriptive name to the archive flow that will be constructed and executed by the wizard.

**Archive Wizard**

### Archive Selection and Description

Specify the location and description of the archive flow to execute:

1. Select the **Archive Data Home** from the tree, by right-clicking on a **Data Home** then selecting **Set as Archive Data Home**.
2. Enter a unique name for the archive flow directory. The default is the current **dd-hhmmss** where **dd**=date, **hh**=hour, **mm**=minute, **ss**=second

Archive Data Home: /panfs/pan1/data/SeisSpaceTesting/Archive

Archive flow description: 27-144609

< Back   Next >   Finish   Cancel   Help

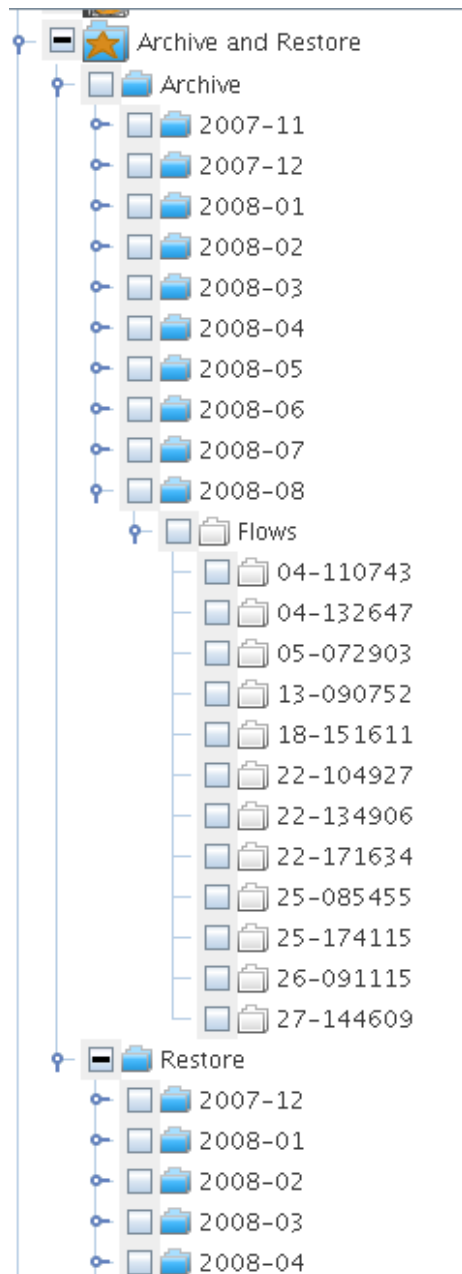
As the text describes, you can choose any project as the archive data home using the MB3 option, but it must have already been set up as a valid Archive Data Home with the “archive” and “restore” areas. The flows will be written to Lines where the Line name is the current calendar year-month.

The Line name is not under user control, but the flow names are.

After running a few archive and restore flows you will see the flows listed in the tree view as shown in the following diagram. Notice that Project (Area) level is Archive, the Subproject (Line) level is the current year-



month, and the Flow names are the day of month and hour-minute-second when the Wizard created the flow.



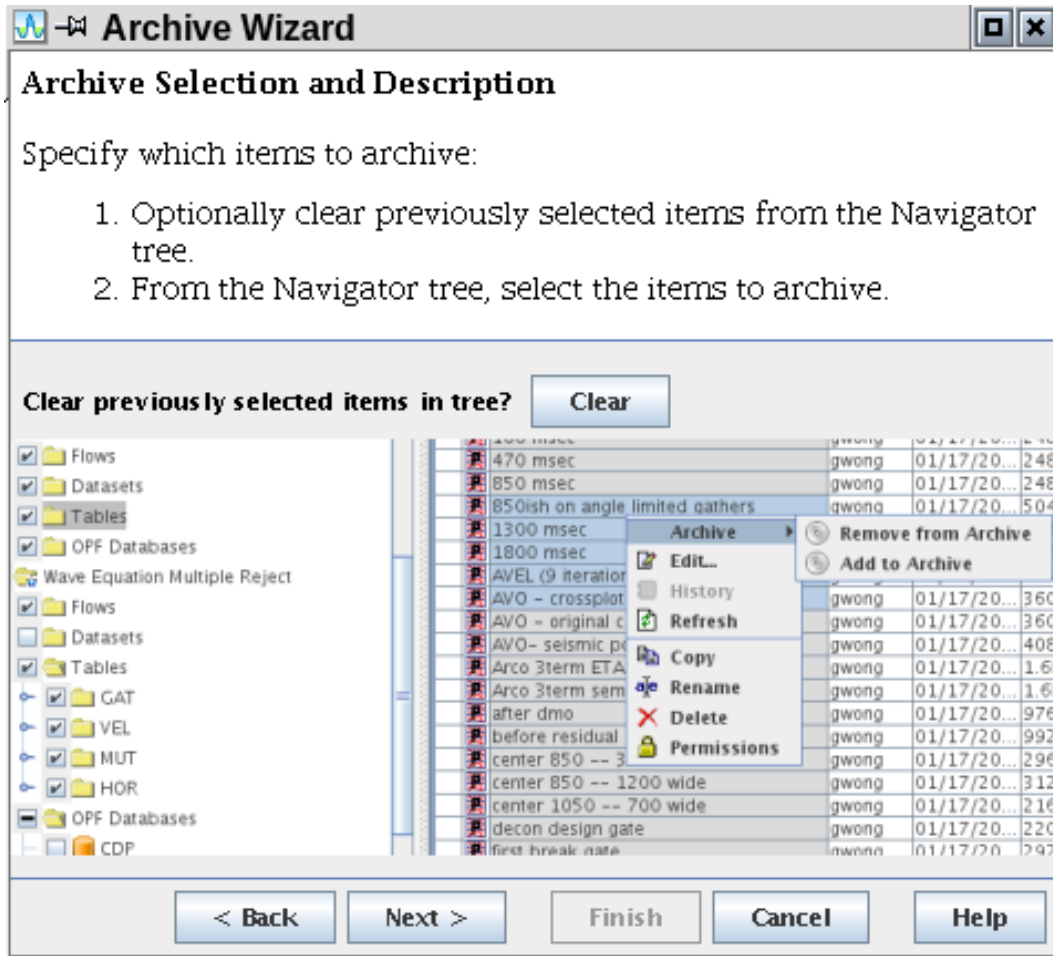
Click **Next>** to go to the next panel.

At this point you will have a new flow in the Archive Data Home/archive/year-month/date-time directory. In the date-time flow directory there will be a DescName file only.

In this step you are asked to finalize your selection of what you want to archive by selecting the check boxes next to the items in the tree view. This

list is initially populated with the selections that are stored in the users **.archive\_state.xml file** which is in the user's \$PROWESS\_PREFS\_DIR directory which by default is ~/SeisSpace.

The “Clear” button can be used to reset the selections back to an All Off state so that you can start over and or prevent including things in an archive that you did not intend to include.



Finalize the selections in the Tree view of the main Navigator display. An “inventory.xml” file is written to the flow directory. This file is an XML file that lists the files to be archived and a directory structure on the archive that it will be mapped to. All of the absolute path names are removed and replaced by a relative pathname structure. This allows the restore to place the archived objects into a different directory structure than where they originated.

Click **Next>** to go to the next panel.

At this point, no additional files have been generated in the flow or output archive directories.

**Archive Wizard**

**Archive Parameters**

Specify the parameters used for archiving.

**Archive**

Use TTS to write the archive ?  Yes  No

Number of 512 byte blocks per output buffer ?

Scan files for sparseness ?  Yes  No

Attempt additional compression ?  ▼

Skip the traces and headers ?  Yes  No

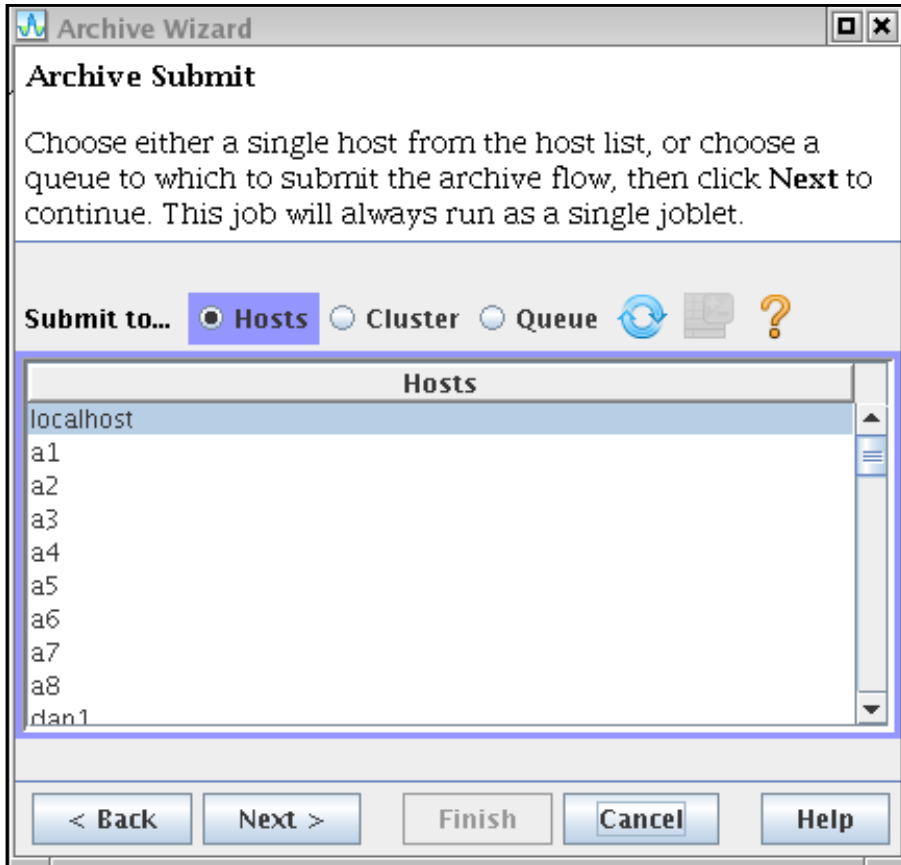
How much detail in printout ?  ▼

Enter DISK file path name

< Back   Next >   Finish   Cancel   Help

In this panel you are asked to parameterize the flow that will run to perform the archive of the selected objects. Click the Help button to get full documentation for the Archive process. The menu defaults to writing the archive files to disk. The default disk file system use to write the disk archive files to is defined by setting the PROMAX\_ARCHIVE\_HOME environment variable (documented in the PROWESS\_HOME/etc/SSclient example start script).

Click **Next>** to go to the next panel.



**Archive Submit**

Choose either a single host from the host list, or choose a queue to which to submit the archive flow, then click **Next** to continue. This job will always run as a single joblet.

Submit to...  Hosts  Cluster  Queue

Queue server: h

Queue name: parallel

===== NODES =====

Queue Node Properties

Overrides the default ppn (processes per node) 0

Additional job attributes

===== PRIORITY =====

Batch Priority 10

Batch Job Start Time

=====

Number of nodes	×	Execs per node	=	Total joblets
1		1		1

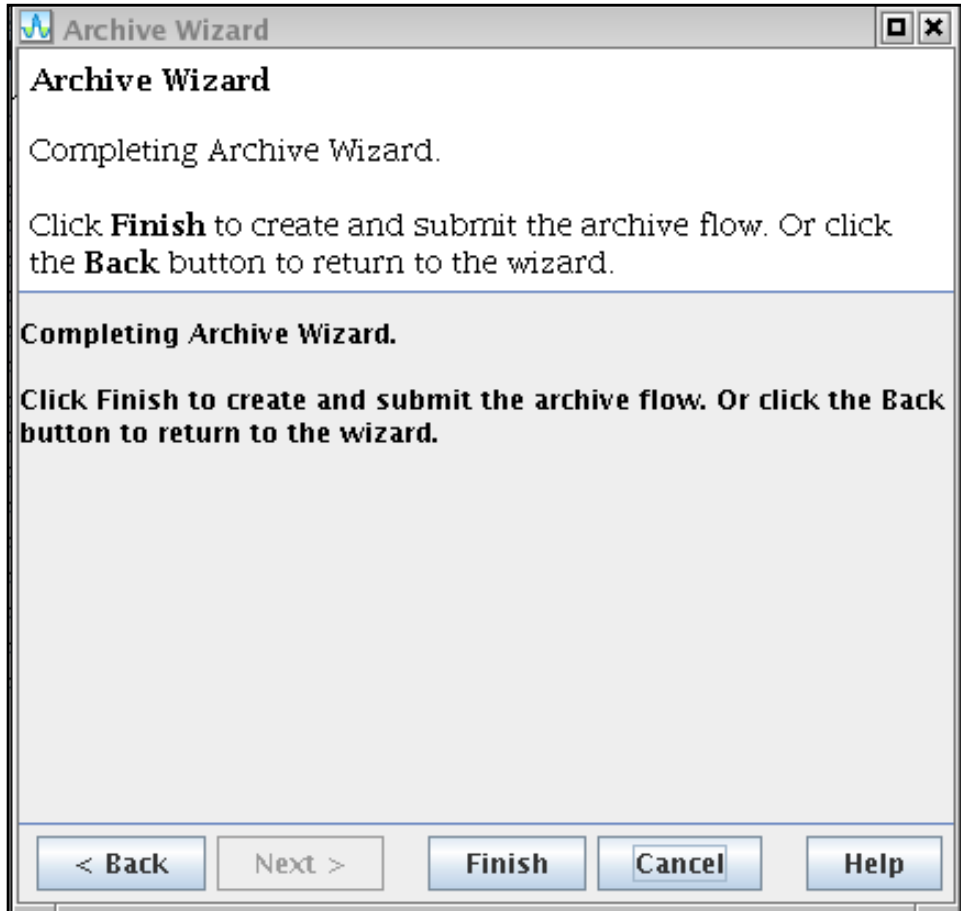
< Back   Next >   Finish   Cancel   Help

In this panel select how you want to run the job either selecting a single host or send the job to a queue.

Click **Next>** to go to the next panel.

At this point, no additional files have been generated in the flow or output archive directories.

This is the last panel of the wizard.



Click **Finish** to write the flow and submit the job for execution.

At this point the flow files are written to the flow directory including the inventory.xml file.

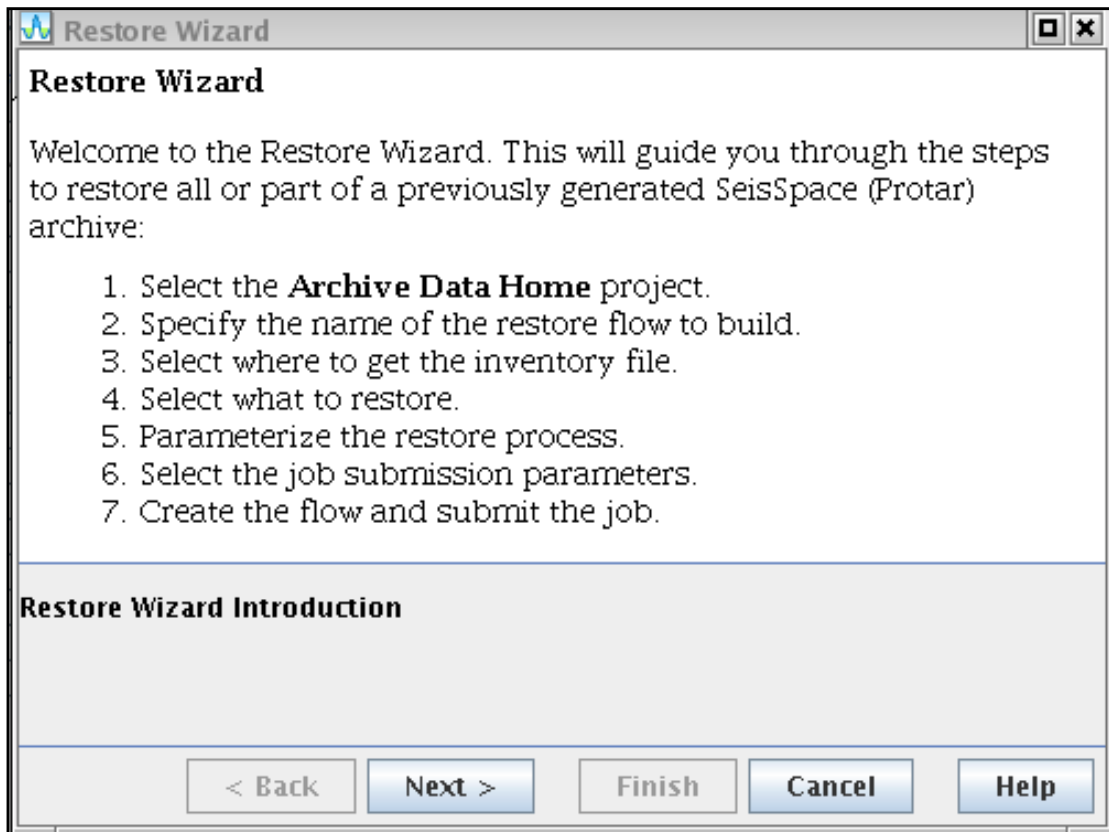
```
-rw-rw-r-- 1 user1 users 10 Feb 28 10:37 DescName
-rw-rw-r-- 1 user1 users 3030 Feb 28 10:43 exec.0.log
-rw-rw-r-- 1 user1 users 38504 Feb 28 10:43 exec.0.pwflow
-rwxrw-r-- 1 user1 users 12733 Feb 28 10:43 exec.0.qsh
-rw-rw-r-- 1 user1 users 21304 Feb 28 10:43 inventory.xml
-rw-rw-rw- 1 user1 users 156 Feb 28 10:43 jobs.stat
-rw-rw-r-- 1 user1 users 28280 Feb 28 10:43 packet.0.job
-rw-rw-r-- 1 user1 users 28280 Feb 28 10:43 packet.job
-rw-rw---- 1 user1 users 6 Feb 28 10:43 .promax_pid
```

After the flow completes, the following list of files will be in the flow directory.

```
-rw-rw-r-- 1 user1 users 10 Feb 28 10:37 DescName
-rw-rw-r-- 1 user1 users 86381 Feb 28 10:43 exec.0.log
-rw-rw-r-- 1 user1 users 38504 Feb 28 10:43 exec.0.pwflow
-rwxrw-r-- 1 user1 users 12733 Feb 28 10:43 exec.0.qsh
-rw-rw-r-- 1 user1 users 21505 Feb 28 10:43 inventory.xml
-rw-rw-rw- 1 user1 users 156 Feb 28 10:43 jobs.stat
-rw-rw-r-- 1 user1 users 28280 Feb 28 10:43 packet.job
```

## Restore Wizard

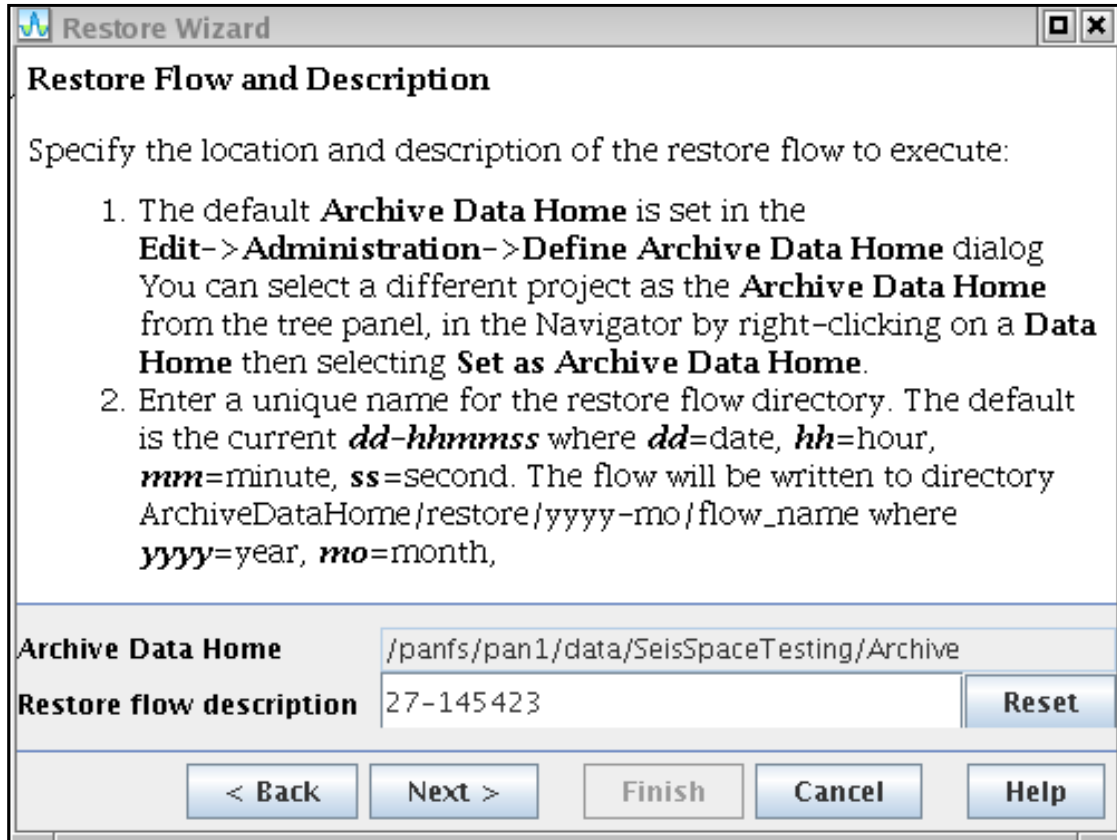
The seven steps to running the the Restore wizard are listed in the first window.



Click **Next >** to go to step 1 to select the Archive Data Home project.



In this panel you are asked to select the Archive Data Home project and also give a descriptive name to the restore flow that will be constructed and executed by the wizard.



The screenshot shows a window titled "Restore Wizard" with a tab labeled "Restore Flow and Description". The main text reads: "Specify the location and description of the restore flow to execute:". Below this, there are two numbered instructions:

1. The default **Archive Data Home** is set in the **Edit->Administration->Define Archive Data Home** dialog. You can select a different project as the **Archive Data Home** from the tree panel, in the Navigator by right-clicking on a **Data Home** then selecting **Set as Archive Data Home**.
2. Enter a unique name for the restore flow directory. The default is the current *dd-hhmmss* where *dd*=date, *hh*=hour, *mm*=minute, *ss*=second. The flow will be written to directory `ArchiveDataHome/restore/yyyy-mo/flow_name` where *yyyy*=year, *mo*=month,

At the bottom of the dialog, there are two input fields:

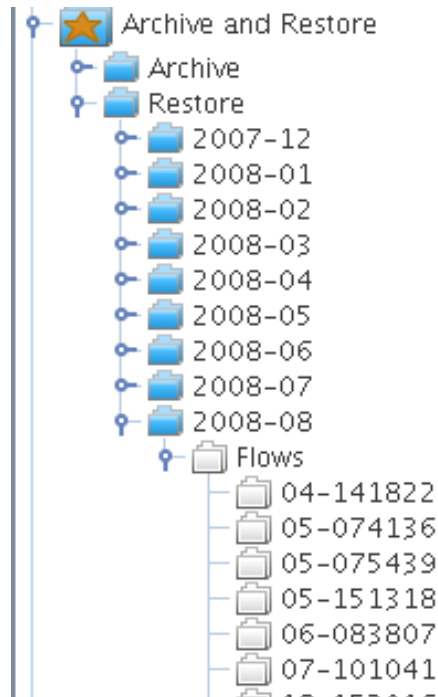
- Archive Data Home**: `/panfs/pan1/data/SeisSpaceTesting/Archive`
- Restore flow description**: `27-145423`

There is a "Reset" button next to the "Restore flow description" field. At the very bottom, there are five buttons: "< Back", "Next >", "Finish", "Cancel", and "Help".

As the text describes, you can choose any project as the archive data home using the MB3 option, but it must have already been set up as a valid Archive Data Home with the Archive and Restore areas. The flows will be written to Lines where the Line name is the current calendar year-month.

The Line name is not under user control, but the flow names are.

After running a few archive and restore flows you will see the flows listed in the tree view as shown below:



Click **Next >** to go to the next panel.

At this point you will have a new flow in the Archive Data Home/restore/year-month/date-time directory. In the date-time flow directory there will be a DescName file only.

The next step is to locate the inventory file for an archive file. When an archive file is written, the first file within the archive is the inventory file that was used to create it. The inventory file is the file that was created in the Archive step when you selected the areas, lines, flows, datasets or whatever you chose to archive. In the restore wizard you will be asked in the next step to select what you want to restore from the archive by looking at a listing of what is on the archive based on the contents of the inventory file that was used to create it.

There are two places where you may find the original inventory files.

- In the archive protar file
- Stored on disk in a user specified location.

The inventory file is written to the flow directory that was used to create the archive. You may choose to browse down the ARCHIVE\_DATA\_HOME/archive/ directory and locate the inventory file that you want to use.

You may have chosen to collect all of your inventory files into a specific directory of your choosing.

Alternatively, you may elect to extract the inventory file from the archive file.

The default and most foolproof method is to extract the inventory file from the archive file. This way you are confident that you have the inventory file that was actually used to create the archive (the inventory is embedded within the archive file itself).

**Restore Wizard**

**Source of Inventory**

Specify from where you want to get the archive inventory file. The inventory file is used to present the contents of the archive so that you can select the items that you want to restore. You can either recover the inventory file from an existing archive tar (on disk, tape, CD or DVD) or select an inventory file from disk:

Extract the inventory file from an existing archive tar  
 Select an inventory file from disk

To get the file out of an existing archive file you need to run a job to extract it. The job will be run as part of this wizard. Parameterize the menu to read the archive file from the media on which it was recorded. Click **Next** to extract the inventory file from the archive.

**Inventory Archive**

Use TTS to read the archive ?  Yes  No  
Number of 512 byte blocks per read ?   
Skip any traces and headers ?  Yes  No  
Suppress warnings about an attempt to override an existing file ?  Yes  No  
How much detail in printout ?   
Type of storage to use   
Select files using a pattern?  Yes  No  
Enter DISK file path name(s)    
Browse for DISK file path name(s)

< Back   Next >   Finish   Cancel   Help

In this panel you are asked to parameterize the flow that will run to perform the restore of the inventory file. Click the Help button to get full documentation for the Restore process. The menu defaults to reading the inventory file from a previously written archive file on disk. The default disk file system use to retrieve the disk archive files from is defined by setting the `PROMAX_ARCHIVE_HOME` environment variable (documented in the `PROWESS_HOME/etc/SSclient` example start script).

Click **Next>** to go to the next panel.

This will start a local job running that will extract the inventory file from the archive file. You may experience a brief delay while this happens.

At this point if you extracted the inventory file from the archive file you will have some new files in the restore flow directory. The extraction of the inventory file required that a job be run to read the archive file and extract the inventory file. You will see the following list of files in the flow directory:

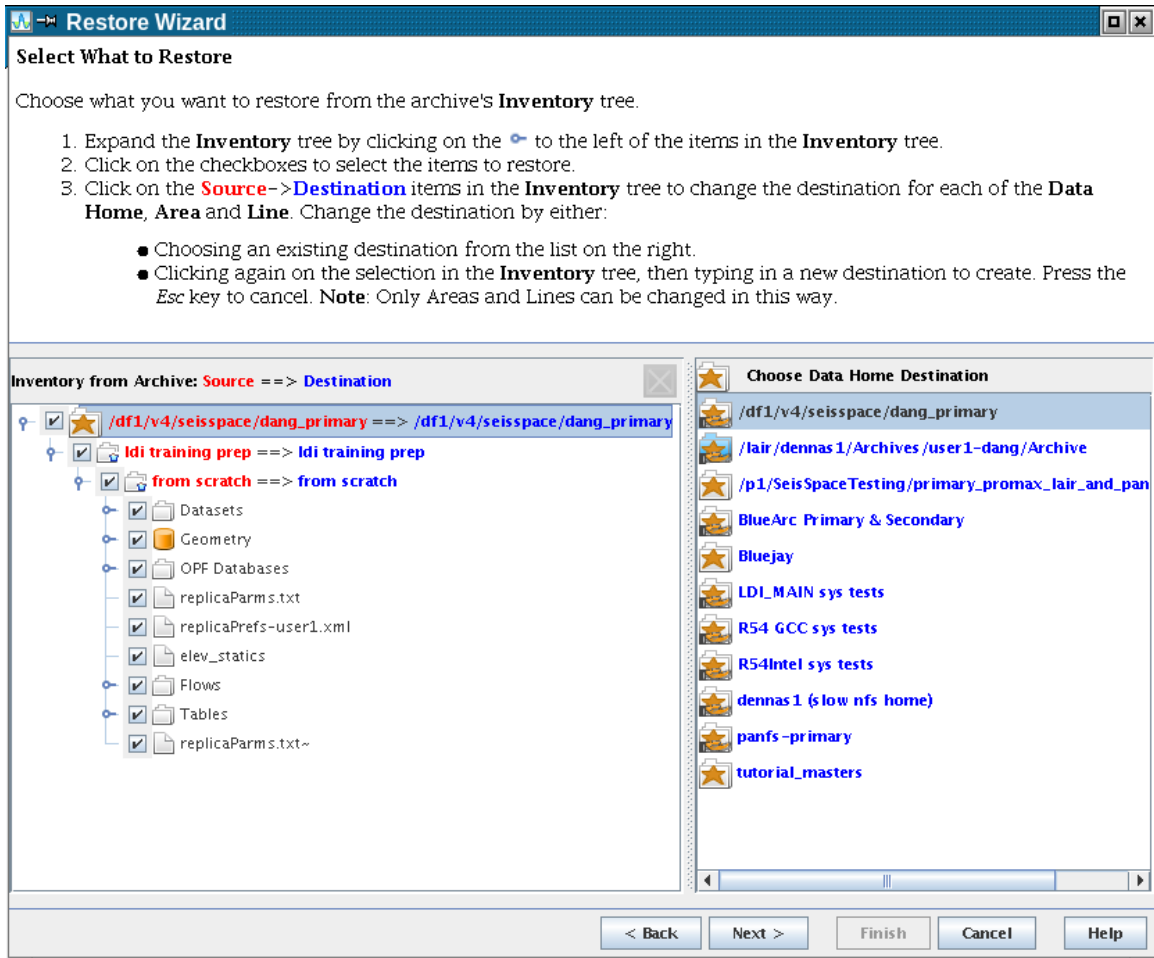
```
-rw-rw-r-- 1 user1 users 10 Feb 29 07:50 DescName
-rw-rw-r-- 1 user1 users 46028 Feb 29 08:10 exec.0.pwflow
-rw-rw-r-- 1 user1 users 21505 Feb 28 10:43 inventory.xml
-rw-rw-r-- 1 user1 users 34560 Feb 29 08:10 packet.0.job
-rw-rw-r-- 1 user1 users 34560 Feb 29 08:10 packet.job
```

In this next step you are asked to finalize your selection of what you want to restore by selecting the check boxes next to the items in the left hand side tree view. This list is populated with the contents of the inventory file that was chosen in the last step. You are also presented with a second selection list on the right side that is your current project listing. This panel has two steps that need to be completed:

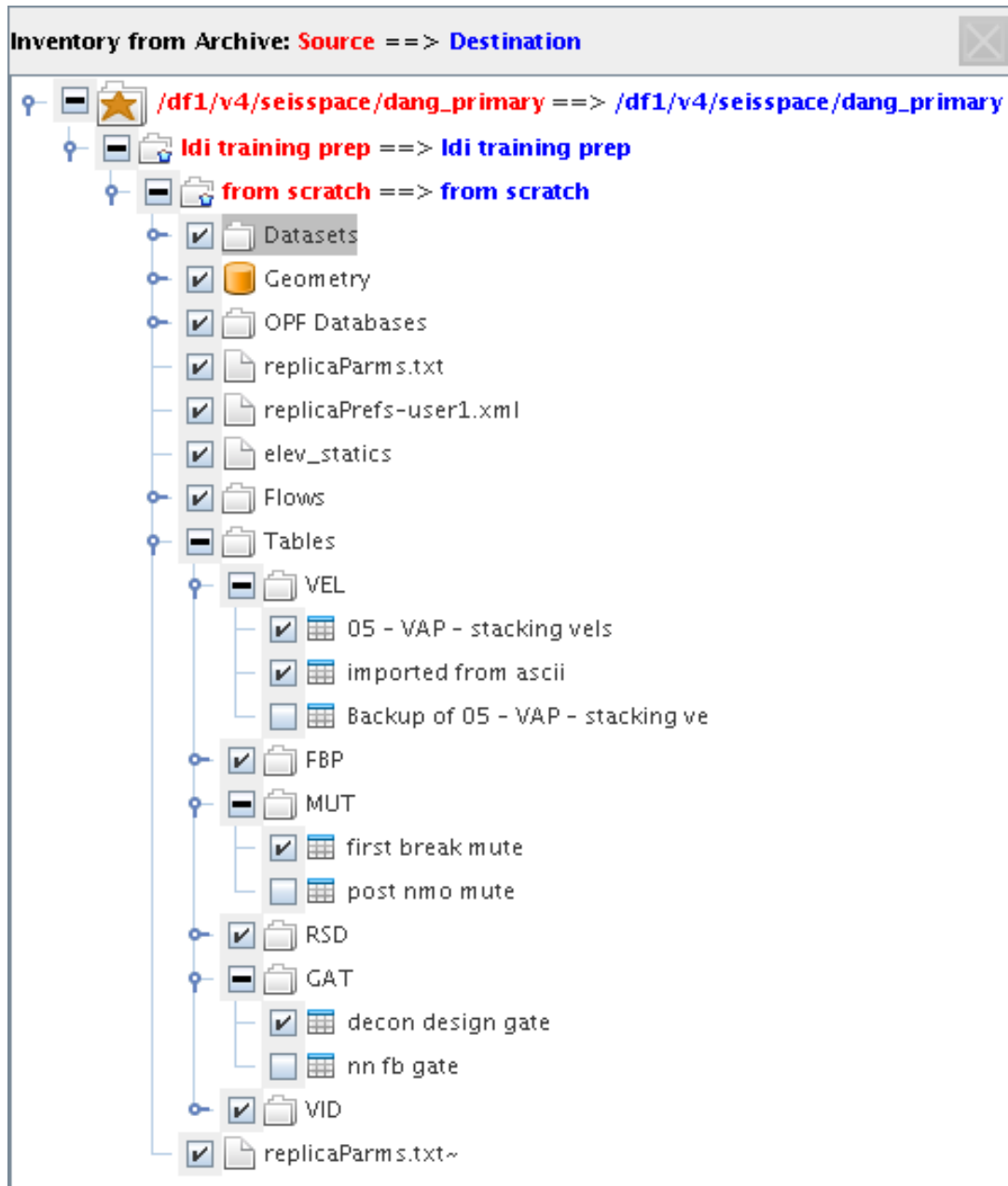
- Select what you want to restore.
- Select where you want the selected items restored.

This example will show how to select a single dataset from an existing archive and put it back into a different `DATA_HOME/Area/Line` than it came from originally.

The main dialog looks as shown below:



First look at the left side where you will select what you want to restore. In this example choose one dataset to restore.



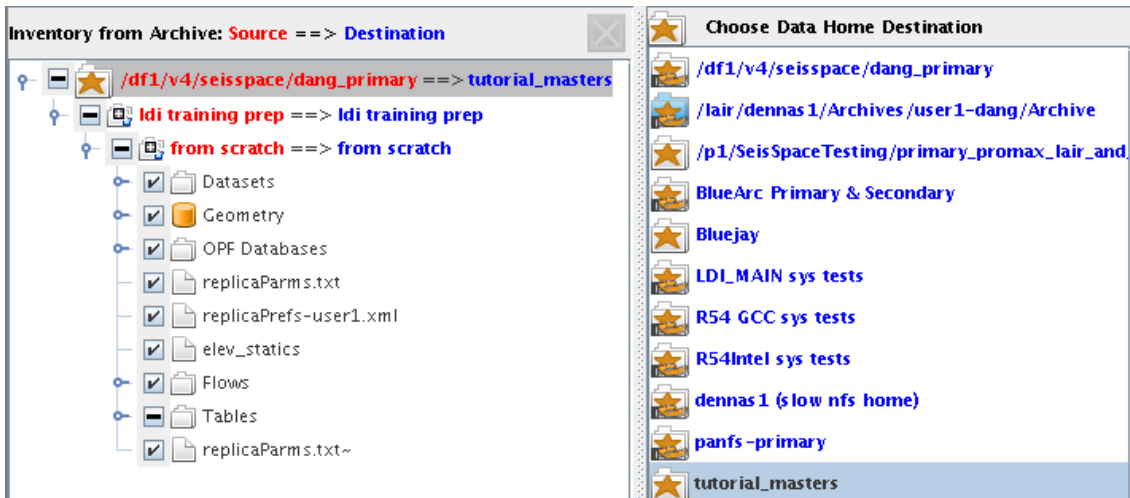
Click in the box next to the items that you want to restore and it will get the check mark. Looking up the tree you will see the “-” signs indicating that part of a list has been chosen, but not the entire list.

The next step is to change the mapping between the original Data\_Home/Area/Line names on the left panel to the destination Data\_Home/Area/Line on the right panel.

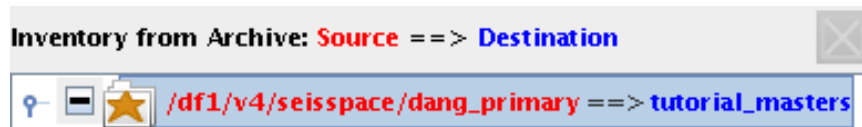
Looking at the **red** text of the data home, area and line directories you will see **text -> text** which indicates the current selection of origin to destination locations. The default is to put the chosen objects back into the same directory structure from where they originated. If this is the goal then you are done and don't need to make any new selections. But there are many occasions where you will not have the same directory structure when you want to do the restore. So you have to change the **original** -> **destination** mapping.

- select the data\_home level on the left side. All of the available data\_homes in the current environment will show up in the right panel.
- select the destination data\_home from the right panel (as seen below)

You must choose the Data\_Home project level from the list on the right.

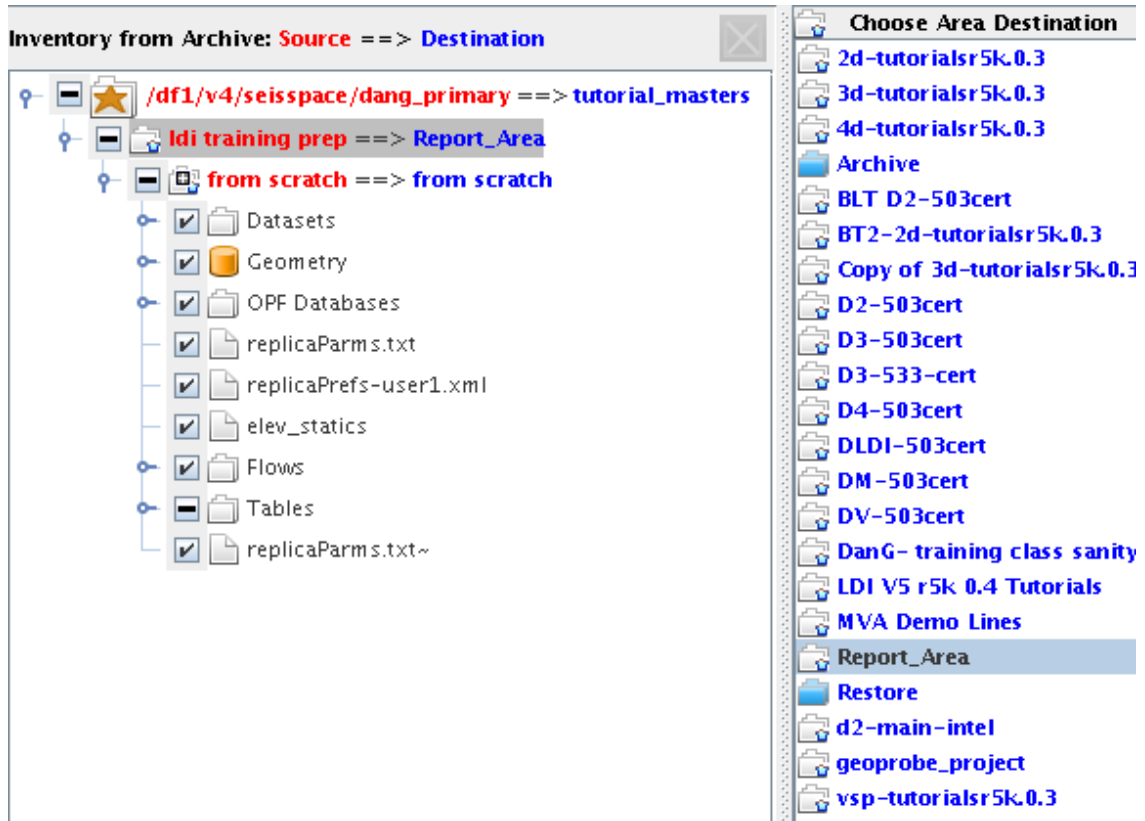


The mapping in the left pane will update to show the original data home -> the target data home for the restore operation.

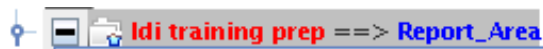


For the Area selection you have a choice to either, do nothing and leave the name the same, select an existing area or line or create a new one. If you leave it the same and it does not already exist - it will be created. Similarly, if you choose the Rename option by double clicking on the entry in the left side tree view the new area or line will be created by the restore process.

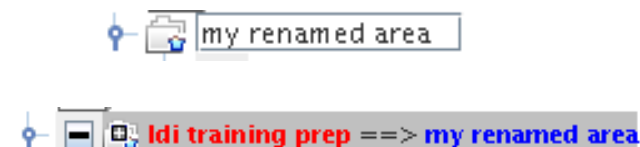
You can either select an existing area from the Choose Area Destination view on the right side with MBI or click on the name twice in the left hand tree view button to change the name to something else. The Areas under the project you have chosen will be shown in **blue** text identifying them as selectable objects.:



If you want to select an existing area you can choose one of the Areas in the project that you selected previously.. The mapping text will update in the left tree view.



The Rename option allows you to change the name of the target output area by putting you into an edit mode where you can type in a new name of a new area to create. Click on the area name twice to enter manual rename mode, enter the desired text and press Enter.





Selecting the target LINE name for the restore is the same procedure as for the AREA selection. Either do not change it, select an existing line, or type in a new line name. If you leave it the same and it does not already exist - it will be created. Similarly, if you choose the Rename option the new area or line will be created by the restore process.

At this point, no additional files have been generated in the flow or output restore directories.

Click **Next >** to go to the next panel.

The screenshot shows a Windows-style dialog box titled "Restore Wizard" with a subtitle "Restore Parameters". The main instruction is "Specify the parameters to access the archive file for the restore job." The panel is titled "Restore from Archive" and contains the following settings:

- Use TTS to read the archive ? :  Yes  No
- Number of 512 byte blocks per read ? : 20
- Use primary storage for trace data files ? : No
- Use primary storage for OPF pagefiles ? : No
- Use size information from inventory map file ? :  Yes  No
- Skip any traces and headers ? :  Yes  No
- Suppress warnings about an attempt to override an existing file ? :  Yes  No
- How much detail in printout ? : Medium
- Type of storage to use : Disk
- Select files using a pattern? :  Yes  No
- Enter DISK file path name(s) : g:/Archive/ldi-train-from-scratch-v2.arc
- Browse for DISK file path name(s) : Browse

At the bottom of the dialog are five buttons: "< Back", "Next >", "Finish", "Cancel", and "Help".

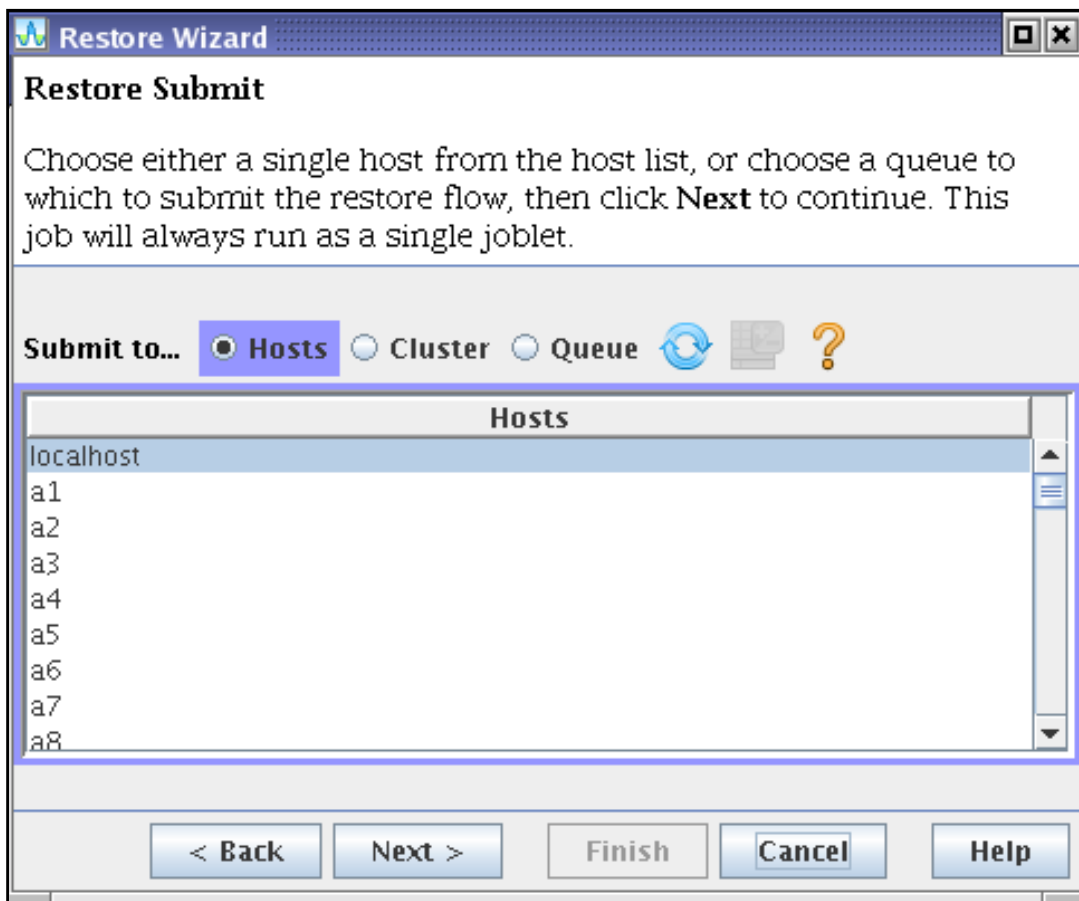
In this panel you are asked to parameterize the flow that will run to perform the restore of the selected objects. Click on the Help button to get full documentation for the restore process. The menu defaults to reading the archive file from disk. The default disk file system use to locate the disk archive files is defined by setting the PROMAX\_ARCHIVE\_HOME

environment variable (documented in the PROWESS\_HOME/etc/SSclient example start script).

Click **Next >** to go to the next panel.

[Other Docs](#)

[Known Problems](#)



**Restore Submit**

Choose either a single host from the host list, or choose a queue to which to submit the restore flow, then click **Next** to continue. This job will always run as a single joblet.

Submit to...  Hosts  Cluster  Queue

Queue server:

Queue name:

=====  
**NODES**  
 Queue Node Properties

Overrides the default ppn (processes per node)

Additional job attributes

=====  
**PRIORITY**  
 Batch Priority

Batch Job Start Time

=====  

Number of nodes	x	Execs per node	=	Total joblets
<input type="text" value="1"/>		<input type="text" value="1"/>		<input type="text" value="1"/>

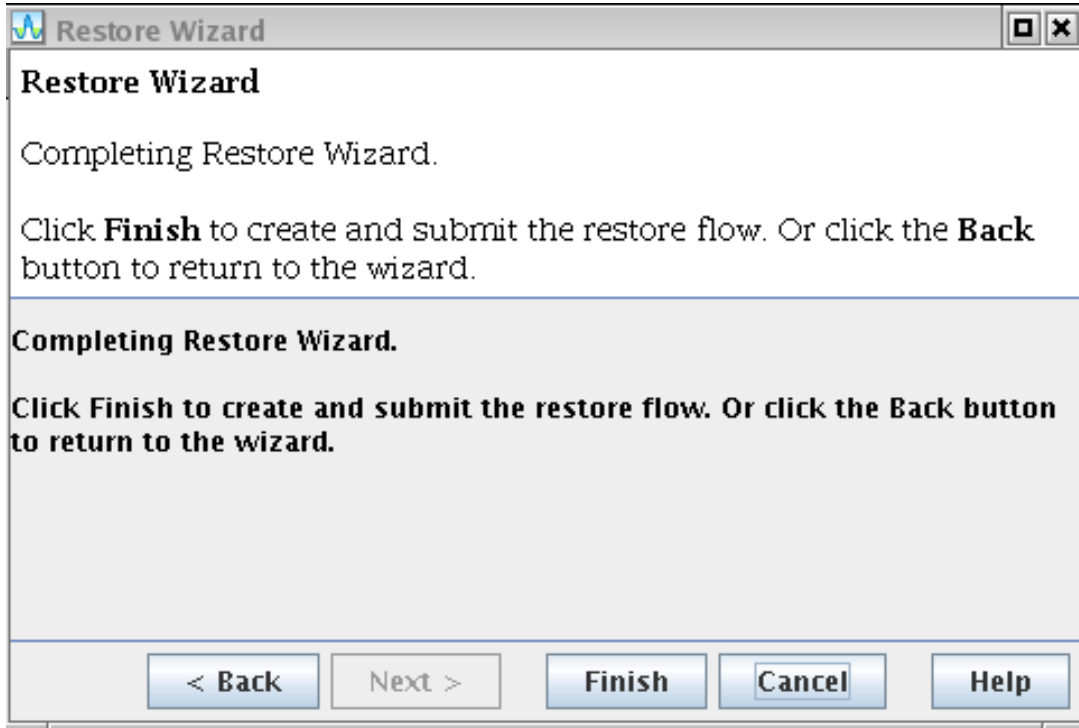
< Back    Next >    Finish    Cancel    Help

In this panel select how you want to run the job either selecting a single host or send the job to a queue.

Click **Next >** to go to the next panel.

At this point, no additional files have been generated in the flow or output archive directories.

This last panel of the Wizard.



Click **Finish** to write the flow and submit the job to be run.

At this point the flow files are written to the flow directory including the restore.xml file.

```
-rw-rw-r-- 1 user1 users 10 Feb 29 07:50 DescName
-rw-rw-r-- 1 user1 users 38 Feb 29 10:35 exec.0.log
-rw-rw-r-- 1 user1 users 46635 Feb 29 10:35 exec.0.pwflow
-rwxrw-r-- 1 user1 users 12733 Feb 29 10:35 exec.0.qsh
-rw-rw-r-- 1 user1 users 21505 Feb 28 10:43 inventory.xml
-rw-rw-rw- 1 user1 users 156 Feb 29 10:35 jobs.stat
-rw-rw-r-- 1 user1 users 34560 Feb 29 10:35 packet.0.job
-rw-rw-r-- 1 user1 users 34560 Feb 29 10:35 packet.job
-rw-rw-r-- 1 user1 users 1902 Feb 29 10:35 restore.xml
```

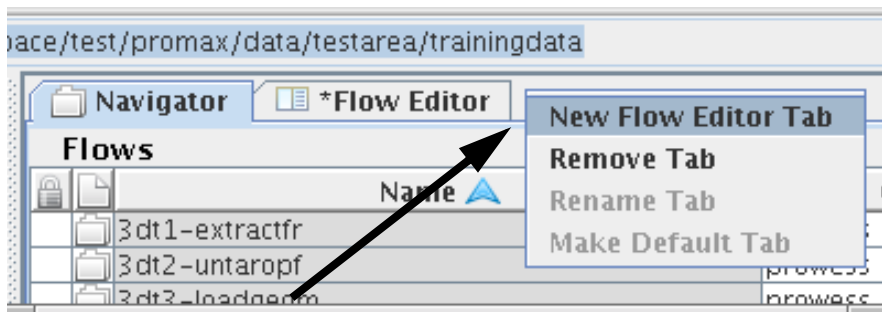
After the flow completes, the following list of files will be in the flow directory:

```
-rw-rw-r-- 1 user1 users 10 Feb 29 07:50 DescName
-rw-rw-r-- 1 user1 users 8117 Feb 29 10:35 exec.0.log
-rw-rw-r-- 1 user1 users 46635 Feb 29 10:35 exec.0.pwflow
-rwxrw-r-- 1 user1 users 12733 Feb 29 10:35 exec.0.qsh
-rw-rw-r-- 1 user1 users 21505 Feb 28 10:43 inventory.xml
-rw-rw-rw- 1 user1 users 156 Feb 29 10:35 jobs.stat
-rw-rw-r-- 1 user1 users 34560 Feb 29 10:35 packet.job
-rw-rw-r-- 1 user1 users 1902 Feb 29 10:35 restore.xml
```

# Working with the Flow Editor

## Multiple Flow Editor Tabs

You may find it useful to open multiple flow editor tabs to help separate work from one line to another or one processing task to another. To open multiple flow editor tabs you can use the MB3 option menu from the tab list area of the Navigator.



You can copy processes from one flow to another on different tabs using the pulldown copy and paste or the Ctrl-C and Ctrl-V hot keys. There is no facility to drag and drop between the tab panes.

Tab pane closing behavior when a tab pane becomes empty is controlled as a preference in the flow editor tab of the preferences dialog. Options are to Not close, Automatically close, or prompt for a choice.

A special History tab will appear if you select Display Flows from the History dialog for a dataset.


The tabs are restored when the Navigator is restarted as they were when the navigator was shut down.

You can also remove tabs that are empty, Rename a tab, or make a selected tab the default tab which allows you to preselect a tab before you edit a flow from the navigator table view. For example if you have a table displayed with multiple flow editor tabs available, you can choose any of the tabs as the default tab so that flows you select will be put into the selected tab when they are chosen to be edited,

## Opening Flows for editing

From the tree view or table panes you can open a flow into the flow editor by:

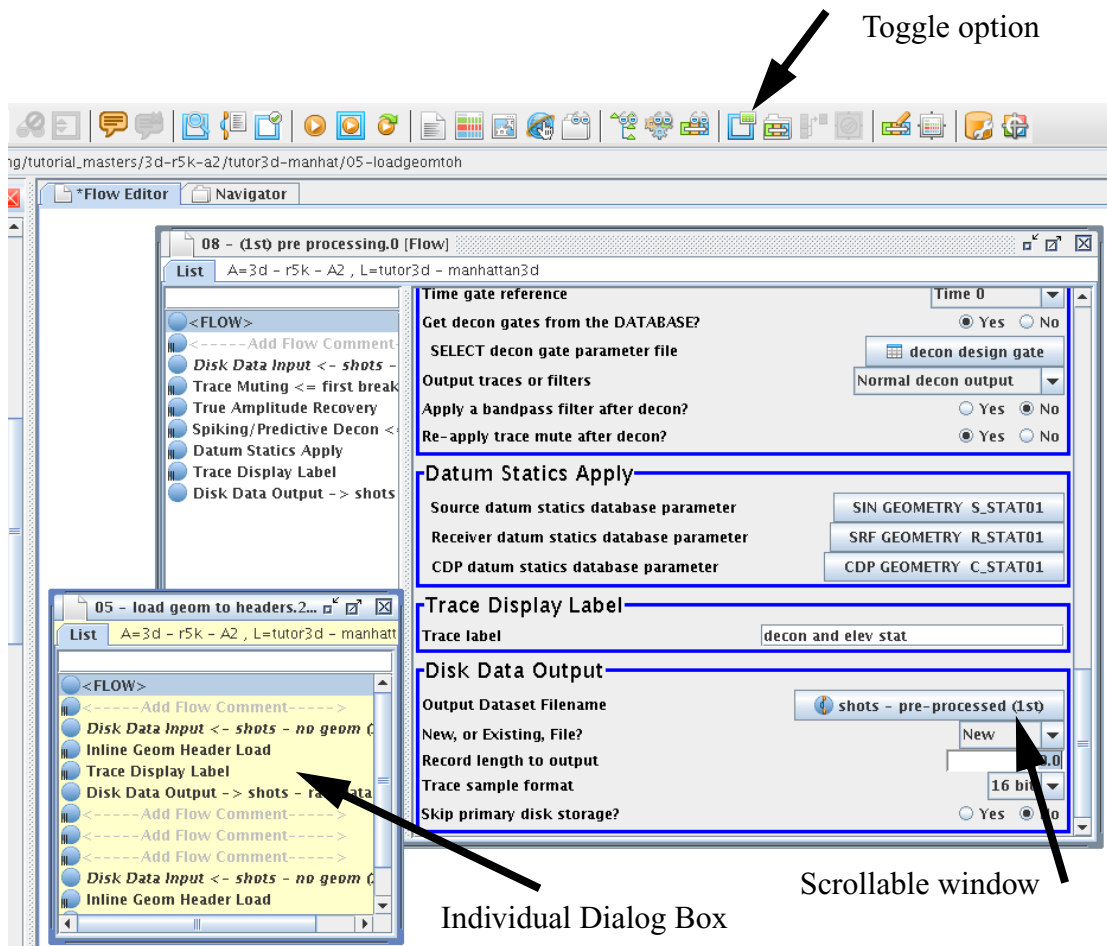
- Double-clicking the flow name from the table list of flows.

- Single-clicking the flow name from the tree view list (this is the default setting that preference in the Navigator preferences). (Single-click is not an option from the table)
- MB3 > Open.
- Using the Open File Icon. 
- Using the File > Open pulldown menus.

If you use the MB3--> Navigate option from the tree view, the table view will show the "instances" of the flow. You can open older versions. The instance labeled "-1" is the packet file that will be read by the conventional ProMAX® user interface or the last version saved by the ProMAX® user interface.

You can set the flow editor appearance and operational preferences with the Flow Editor tab of the preferences dialog box.

There are two ways of viewing flows: the Individual Dialog box mode (the default) and the Scrollable window mode.







You can switch back and forth using the Toggle Parameter List Icon.

You can also choose which mode to use as your default from the Edit > Preferences dialog box by checking or unchecking the "Use Dialogs instead of scrolled list of parameters for all processes" option.

**Note:** When you select a flow for editing from the tree or the table listing, you will always get the most recent menu (or highest numbered instance). You do not have to select the highest numbered instance from the instance list.

If you want a specific instance, an older version for example, select the desired instance from the instance list in the table pane.

If you have edited the flow in the ProMAX® user interface, you will need to go to the instance list and choose the -1th instance to get the most recent version of the packet file.

## Saving flows

Every time a flow is edited and saved or submitted, the flow is saved twice: once as an XML file (exec.#.pflow) and again as the binary file; packet.job.

New instances are generated when a flow is submitted for execution or edited and saved.

An instance saves all components of the flow including the job file and the printout.

## Adding Processes to a flow

There are many ways to add processes to a flow:

- Drag and Drop a process into the flow from the processes list. You can add (or remove) the processes list from the flow editor tab using



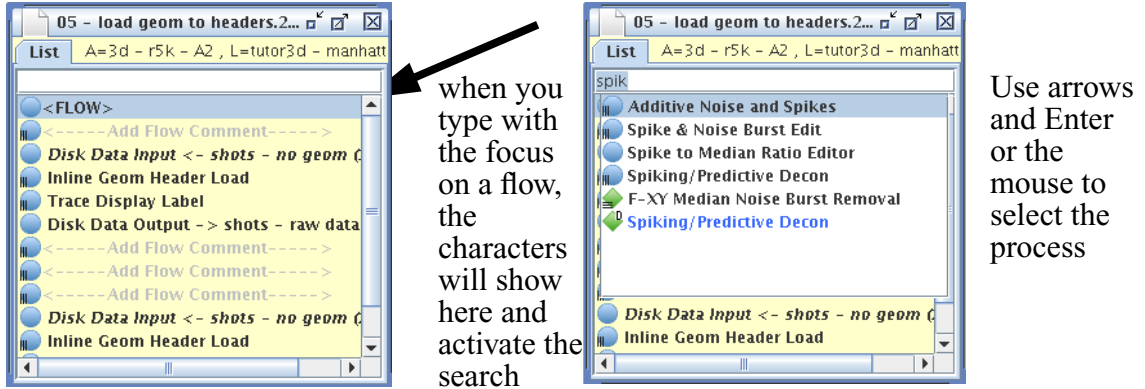
the "show or hide processes list" icon.

- Click MB1 on a process and it will be added after the process that is currently selected in the flow's list of processes. **Note:** this is controlled by a user preference.
- Use the quick search option. This option is enabled by typing in the flow window in the flow editor. **Note:** you do not have to position the

mouse in the text box. Keystrokes will be reflected in the text box of the currently active flow.

- Drag and Drop a process from another flow that is open in the editor.

Flows can be built very rapidly using the quick search capability and the arrow and Enter keys to select the processes.



There is a subtle functionality difference here depending on where keyboard focus is when you use the up and down arrow keys. If focus is given to the small search window at the top of the flow edit window by clicking in it with the mouse, the up and down arrow keys will repeat the last search. This is useful if you are selecting the same process multiple times or if the processes you are looking for all have some characters in common. The more general use here would be just give keyboard focus to the main edit window and just start typing. The up and down arrows and enter keys can still be used to find and select the process. After the process is selected you can then use the up and down arrow keys to select the next process you want to add new processes after. This is useful while you are building a flow and realize that you have forgotten to add in a process earlier in the flow.

The first entry in the returned list is automatically highlighted so that as you get better at narrowing down the search characters you can just hit enter to select the single (or first) process in the list.

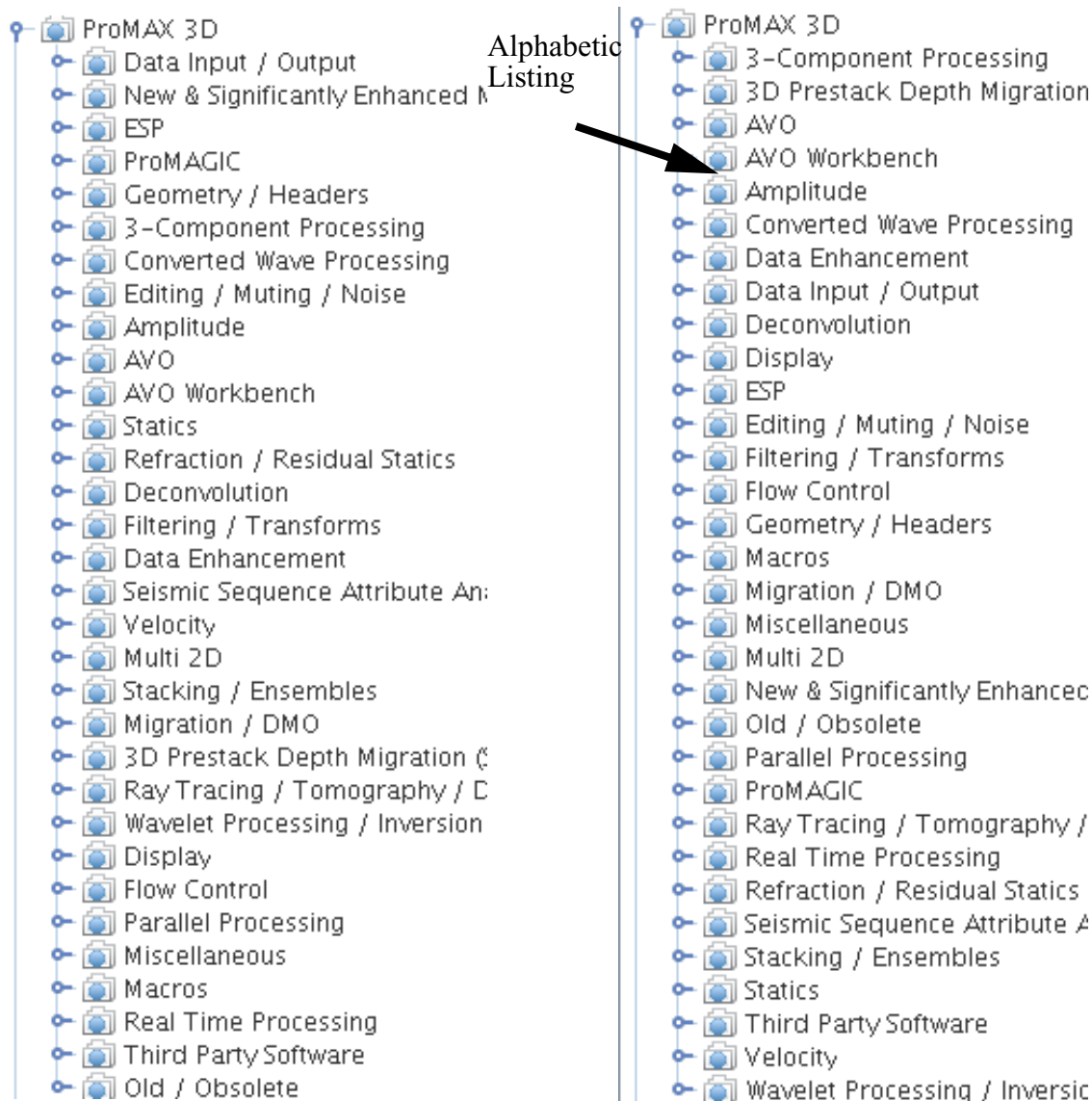
### The Processes List

There are a few functional icons at the top of the processes list:



From Left to Right:

- a/z : Select to alphabetically sort the list of processes. The default displays processes in the same manner as the conventional ProMAX® user interface. That is, processes are shown in the exact order that they are listed in the Processes list. Sorting alphabetically sorts the categories alphabetically as well as the processes in the category.



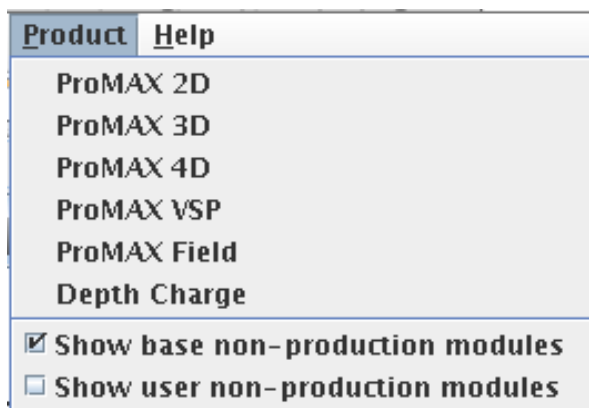
- The double + icon will expand the list to show all processes in all categories
- The single + icon will expand/compress to show only the major process categories

- The refresh icon can be used to refresh the processes list with a full reread from disk for the specified product.
- The X icon will close the processes list panel.

## The Processes List (Development Status Processes)

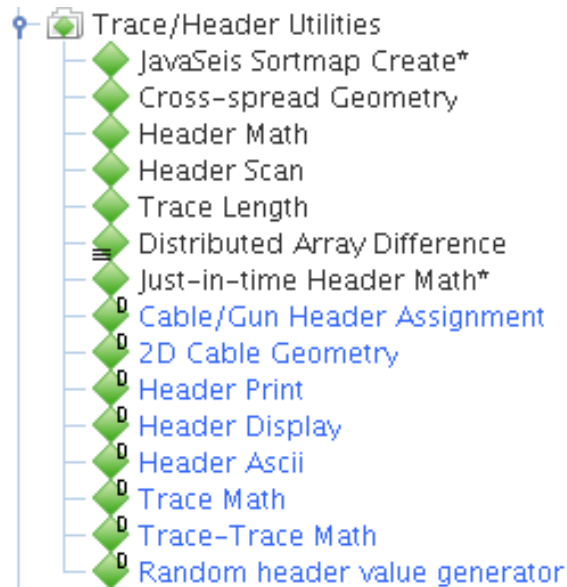
There are two major types of SeisSpace tools: those that have been deemed ready to use in production and those that are in a development status. Production tools are supported, development status tools are not, but we would still appreciate feedback on these tools so that we can eventually get them to production/supported status.

To view the list of development status tools you can toggle them on and off using the Product > Show non production Tools pulldown from the top of the Navigator screen, or the icons on top of the processes lists.



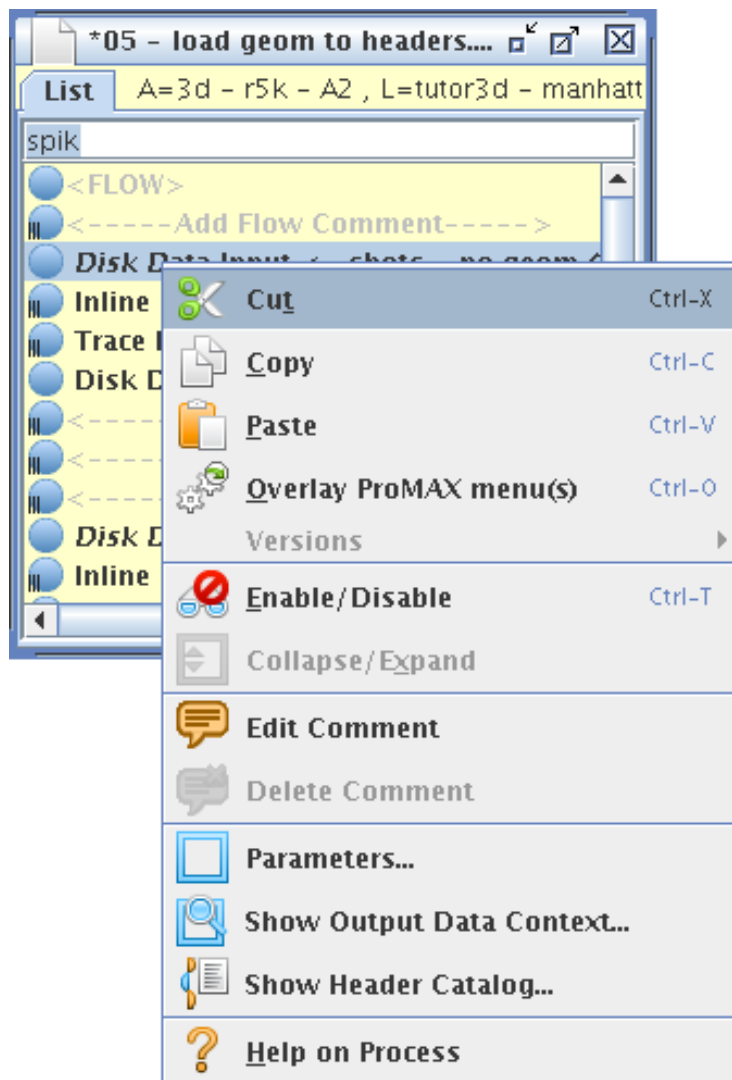
With the toggle selected, the Development status tools will be available in the Processes list and the quick search utility in the flow builder. When active, the icons will be highlighted in a blue background and the pulldown menu will be "checked". The first icon on the processes list icon bar is for the user development processes and the one on the right is for the base system development processes delivered by Landmark.

The Development status tools will be annotated with the D overlay on the Green Diamond icon.



## The Options Menu for Processes in a Flow

There is an options menu available for all process in a flow.



This options menu can be enabled using either MB3 on the process or CTRL-MB3 on the process depending on your preference setting. In the flow editor tab of the preferences dialog there is an option:

**Mouse buttons behave like ProMAX GUI for editing flow**

If this option is checked "ON" then you can enable the options menu using CTRL-MB3. While editing flows, the most probable reasons for needing this options list is to have access the online help documentation or to edit comments.

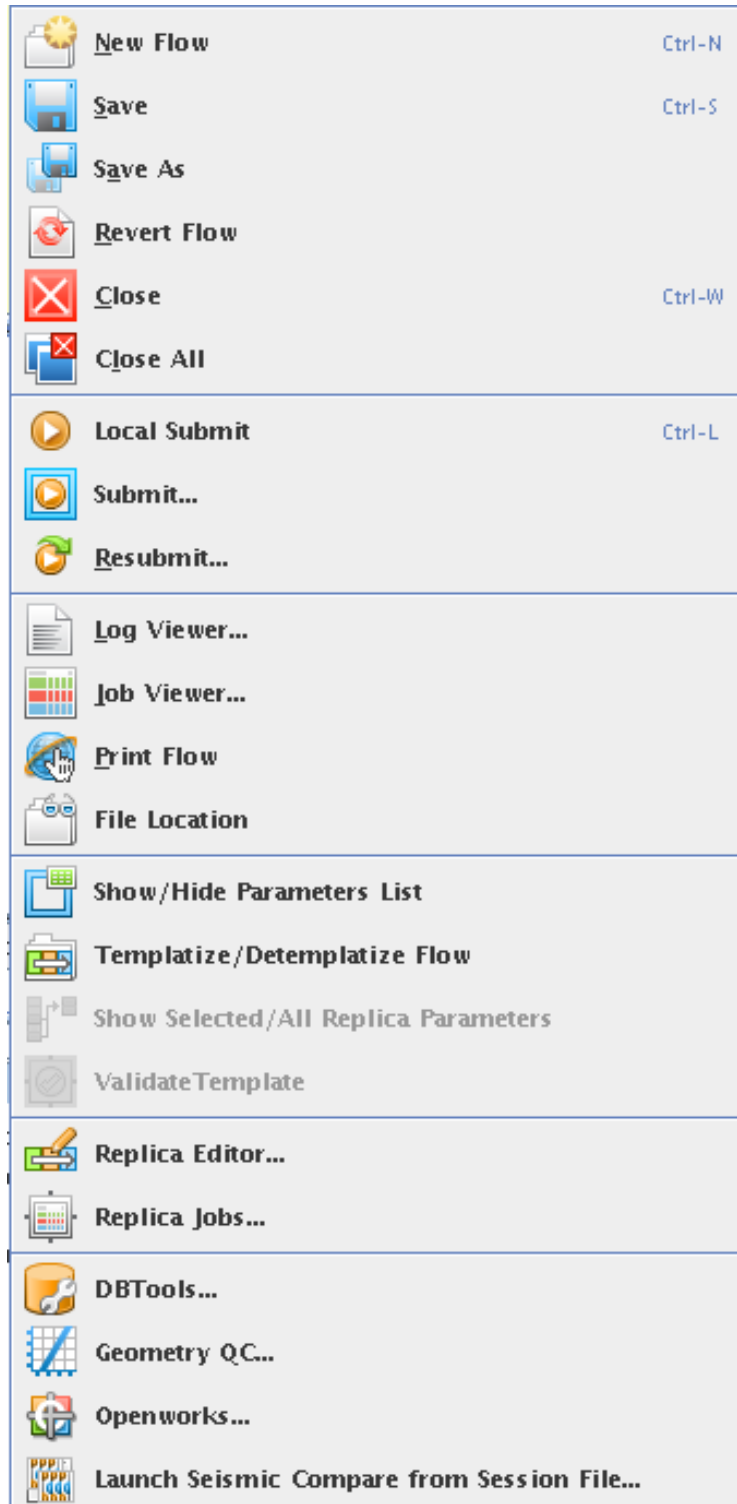
The "Versions" option will be discussed in the development environment section of the documentation.

[Other Docs](#)[Search Page](#)[Known Problems](#)

## The Options Menus in the white spaces in the Flow Editor Tab

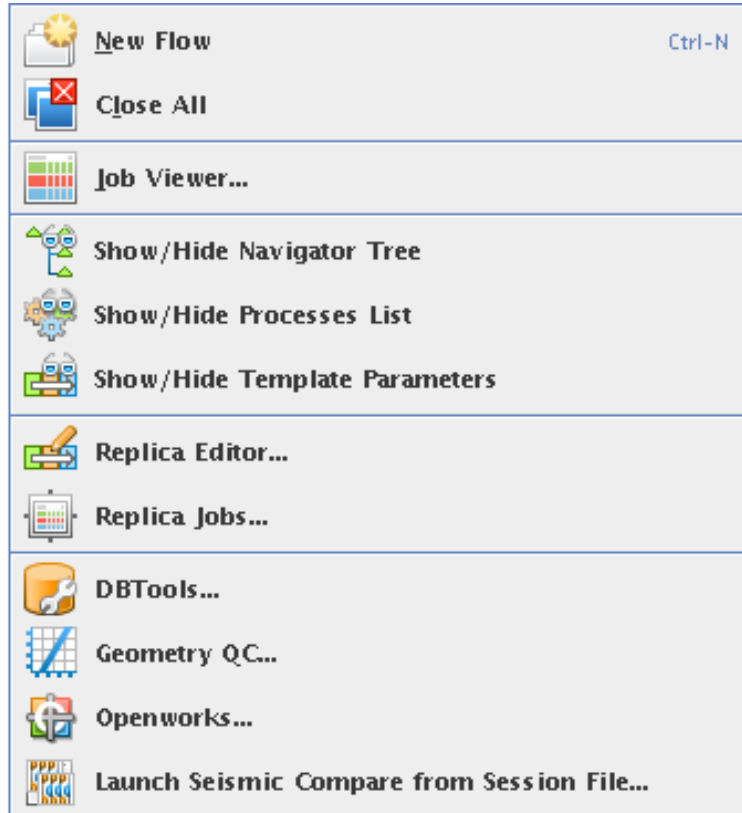
There are two additional options menu available in the flow editor:

- one in the white space inside a flow,



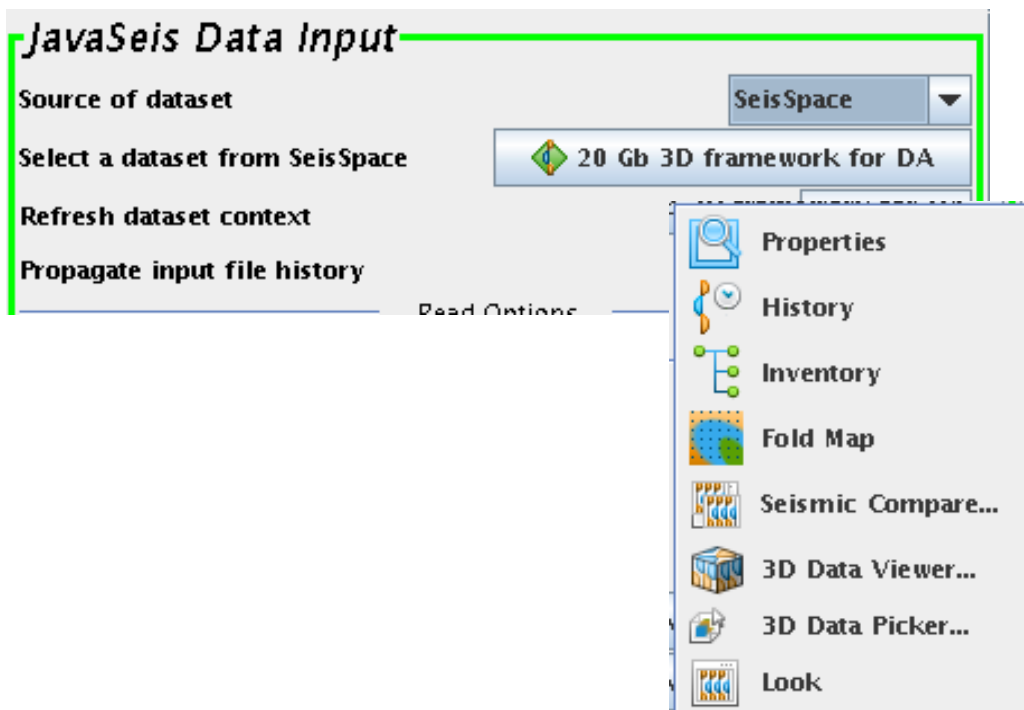


- and another in the white space outside of all the open flows.



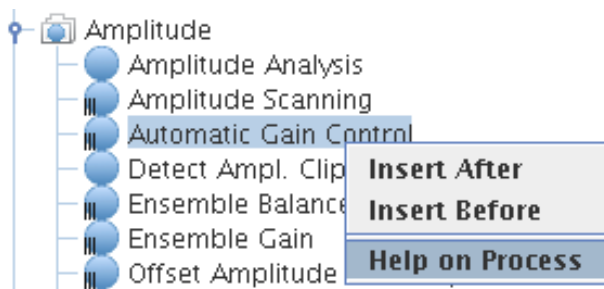
## The Options Menus on dataset names in IO processes

For any process that allows you to select datasets you can MB3 on the dataset in the menu to get a list of options. The list will vary depending on what type of dataset it is.



## Online help for the Processes

While building flows or parameterizing processes in a flow you may want access to some help to describe the process and guide you through parameters. One way to get the help files is to press the F1 key after selecting the process with MB1 in the flow editor. If a parameter selection dialog is open for a process, F1 will open the help document for the process. For access to the complete help document for a process in the processes list you can use the **MB3 > Help on Process** option:



If a process is in a flow you can get help using the **MB3** (or CTRL-MB3) > **Help on Process** option. You can select the process with MB1 and then press the F1 key. The **Edit > Help** on Process pulldown menu is another option that can be used to get help on a selected process.

## ProMAX® process icons and hybrid parallelization

The list of ProMAX® modules that can be run in a Hybrid environment is a subset of the entire processes list. For example, no ProMAX® process that writes trace data or writes attribute data to the database can be run in a multi-joblet hybrid flow. There are other exceptions. The processes that have been tested and have shown to produce correct output from a multi-node multi-joblet distributed hybrid job have been annotated with a

"parallel ProMAX®" icon in the processes list and in the flow editor.



Some ProMAX® processes are annotated with a "ProMAX® x" icon indicating that they are illegal in a Hybrid environment. You will not be able to submit these jobs.

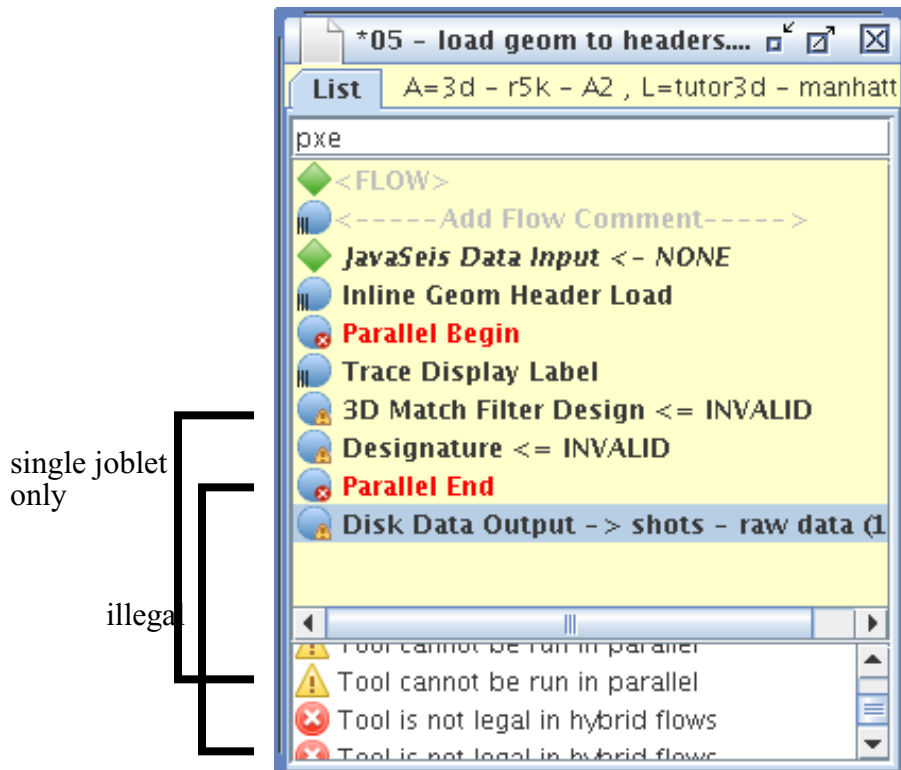


Other ProMAX® processes are annotated with a "ProMAX® yield" icon

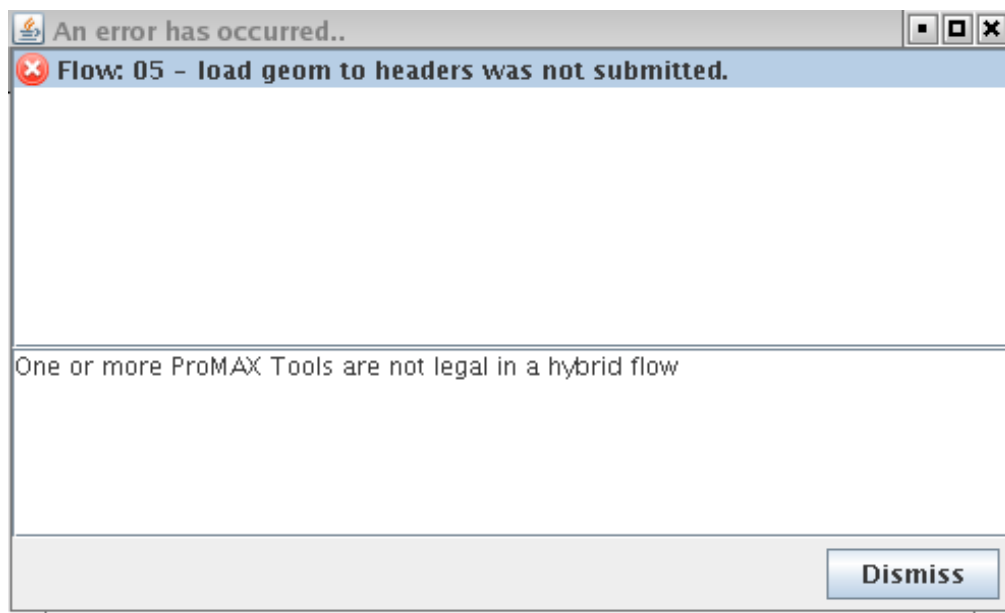


indicating that they can only be run in a single joblet hybrid job.

Hybrid flows are also expanded in the flow editor with warnings about the ProMAX® processes in them.

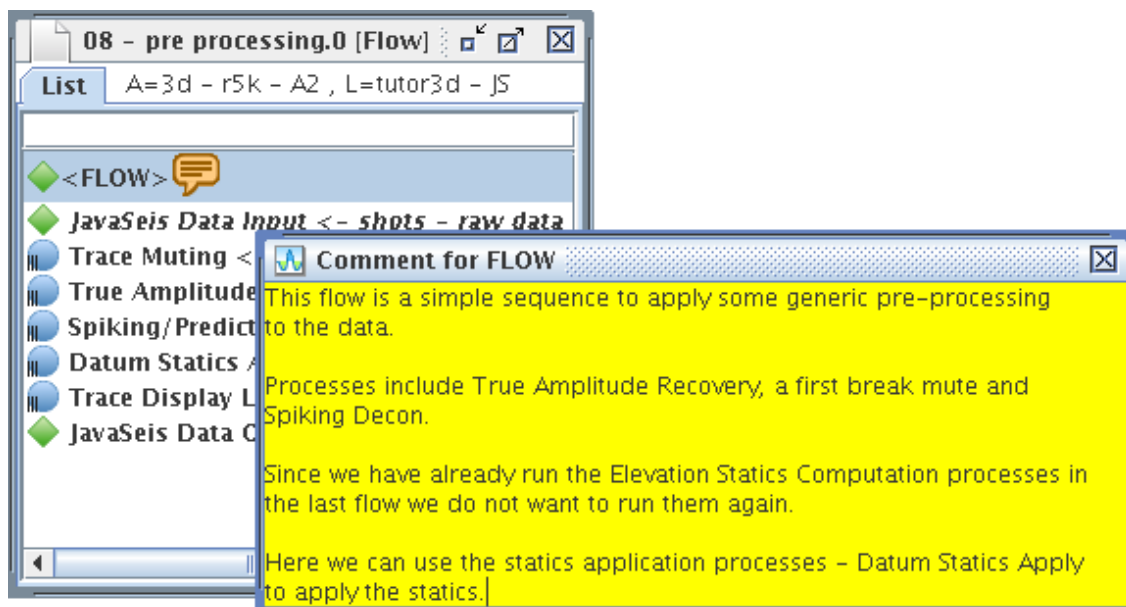


If you try to execute a hybrid flow that has illegal processes in it you will receive the following dialog box:



## Adding Comments to Processes

You can add comments to processes in flows using ----- **Add Flow Comment** ----- or using the comment editor. This is applicable for both ProMAX® or SeisSpace® processes. Enter your comments in the dialog box. You can also edit or delete comments.



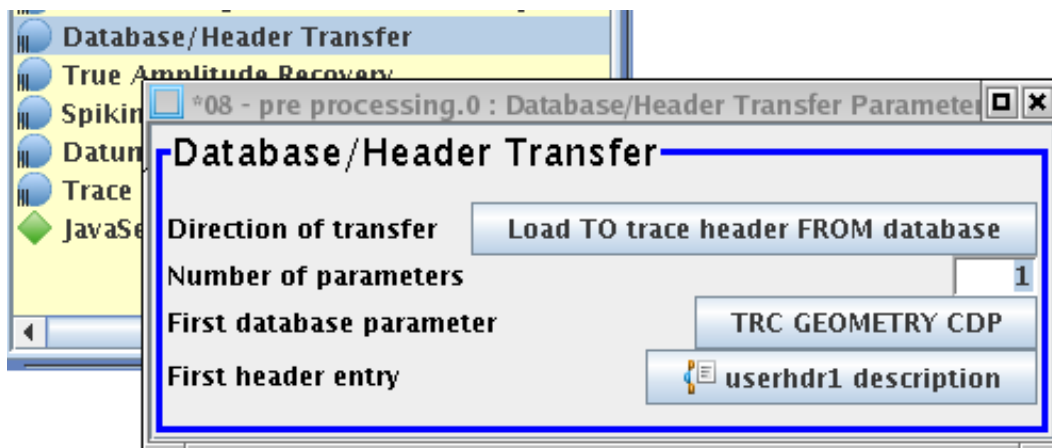
## User Defined Header Management

The user defined headers list is kept in a file called `.user_headers` which can be stored at any or all of the `DATA_HOME` directory level, the `AREA` directory level, or the `LINE` directory level. The Header list will be the concatenation of all of the user headers found in the files at all three levels if they exist. The administrator can control which level can be used by the users and where the default location will be. This procedure is outlined in the SeisSpace System Administration Document. Any tool that accesses the "SeisSpace/ProMAX® Headers" selection dialog can add, delete, or relocated headers to this different lists. The user defined headers are listed together with the standard headers for selection.

**Note:** Not all tools that add headers use this dialog. There are cases where user defined headers will show up as "transient" values in the list. ProMAX® Trace Header Math does not access the header selector so new attributes generated by this tool will not be added automatically to the `.user_headers` file, but they will show up in the header selector as long as

the Intelligent Parameterization is active or the init phase has been run in the Flow Builder.

A simple example of how this works would be to use the ProMAX® Database/Header Transfer tool.



When you add the new header in the header selector it is added to a ..user\_headers file at the selected directory level. The header is added to the

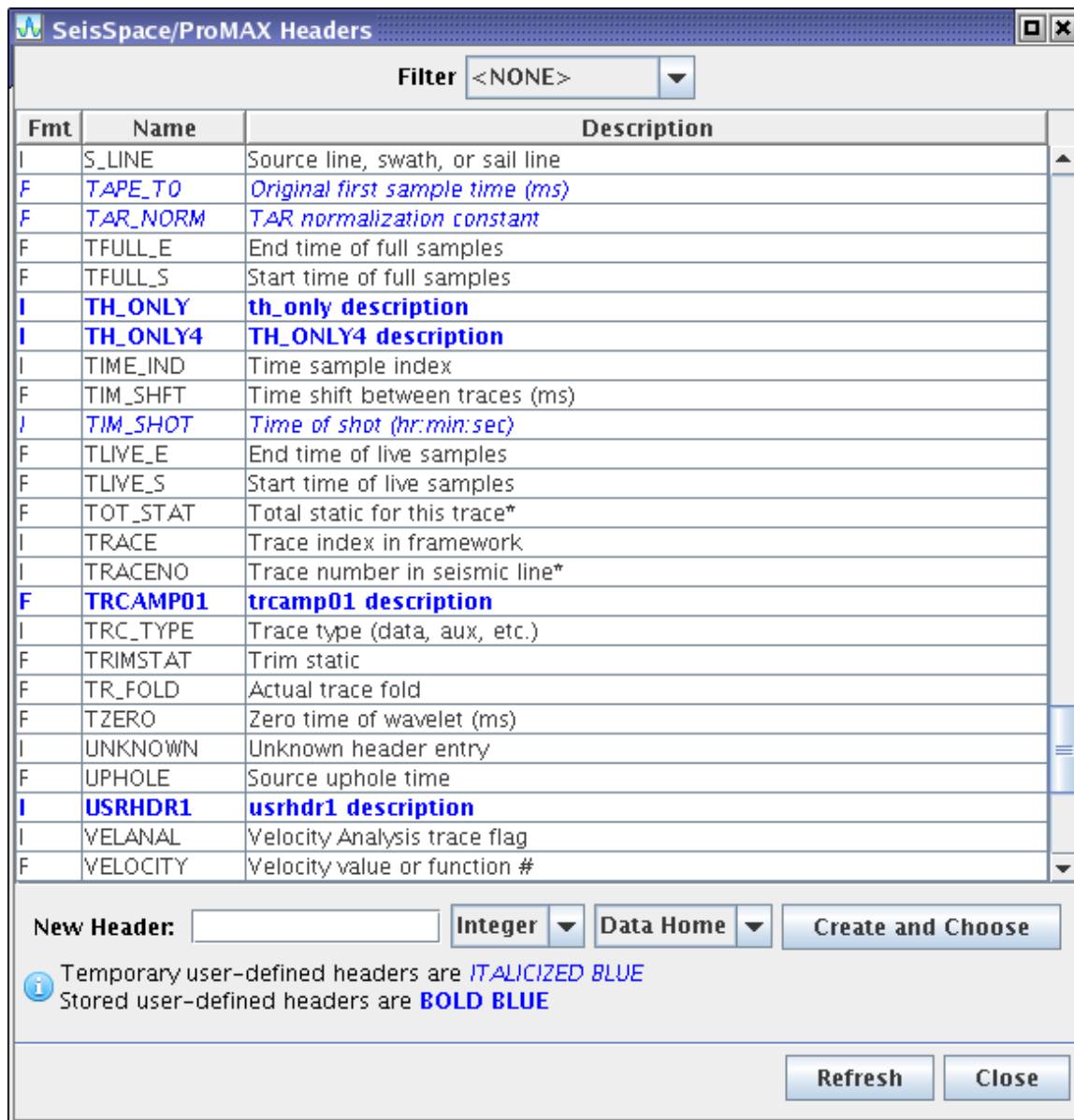
New Header:

**i** Temporary user-defined headers are *ITALICIZED BLUE*  
 Stored user-defined headers are **BOLD BLUE**

list when the Create and Choose button is clicked.

**Note:** depending on the setting in the prowess.properties file you may or may not have the choice of Data Home, Area, or Line for saving the header entry. If the option is grayed out and inactive, the administrator has elected to not give users this privilege.

When you choose the header entry dialog again you will be presented with the SeisSpace®/ProMAX® Headers dialog where you can choose existing headers or add new ones.



The user defined headers that have already been added appear in the BOLD/Italic text.

The headers that are in italicized blue are "transient" headers that are added by processes in the open flows. These are temporary headers that are only in memory in the available data contexts and do not exist in the .user\_headers files. All transient headers from all open flows will be shown in the list and are available for selection if desired. You may also use the MB3 - option menu to save these permanently. Other option in the MB3

options menu include the ability to move a header from one .user\_header file to another, or delete entries in the .user\_headers files.

Fmt	Name	Description
I	S_LINE	Source line, swath, or sail line
F	TAPE_TO	Original first sample time (ms)
F	TAR_NORM	TAR m
F	TFULL_E	End ti
F	TFULL_S	Start t
I	TH_ONLY	th_on
I	TH_ONLY4	TH_ONCT+ description
I	TIME_IND	Time sample index

The file that stores the information is the .user\_headers file and is an editable XML file. If you want to change the default description of the user defined header you can edit this file manually.


```

user1@e1:/panfs/pan1/data/SeisSpaceTesting/promax_primary
File Edit View Terminal Tabs Help
<parset name="UserDefinedHeaders">
  <parset name="USERCDP">
    <par name="format" type="int"> 1 </par>
    <par name="description" type="string"> CDP+100 </par>
    <par name="nvals" type="int"> 1 </par>
  </parset>
  <parset name="SSUSRCDP">
    <par name="format" type="int"> 1 </par>
    <par name="description" type="string"> "ssusrcdp description"
  </parset>
  <par name="nvals" type="int"> 1 </par>
</parset>
1,1 Top

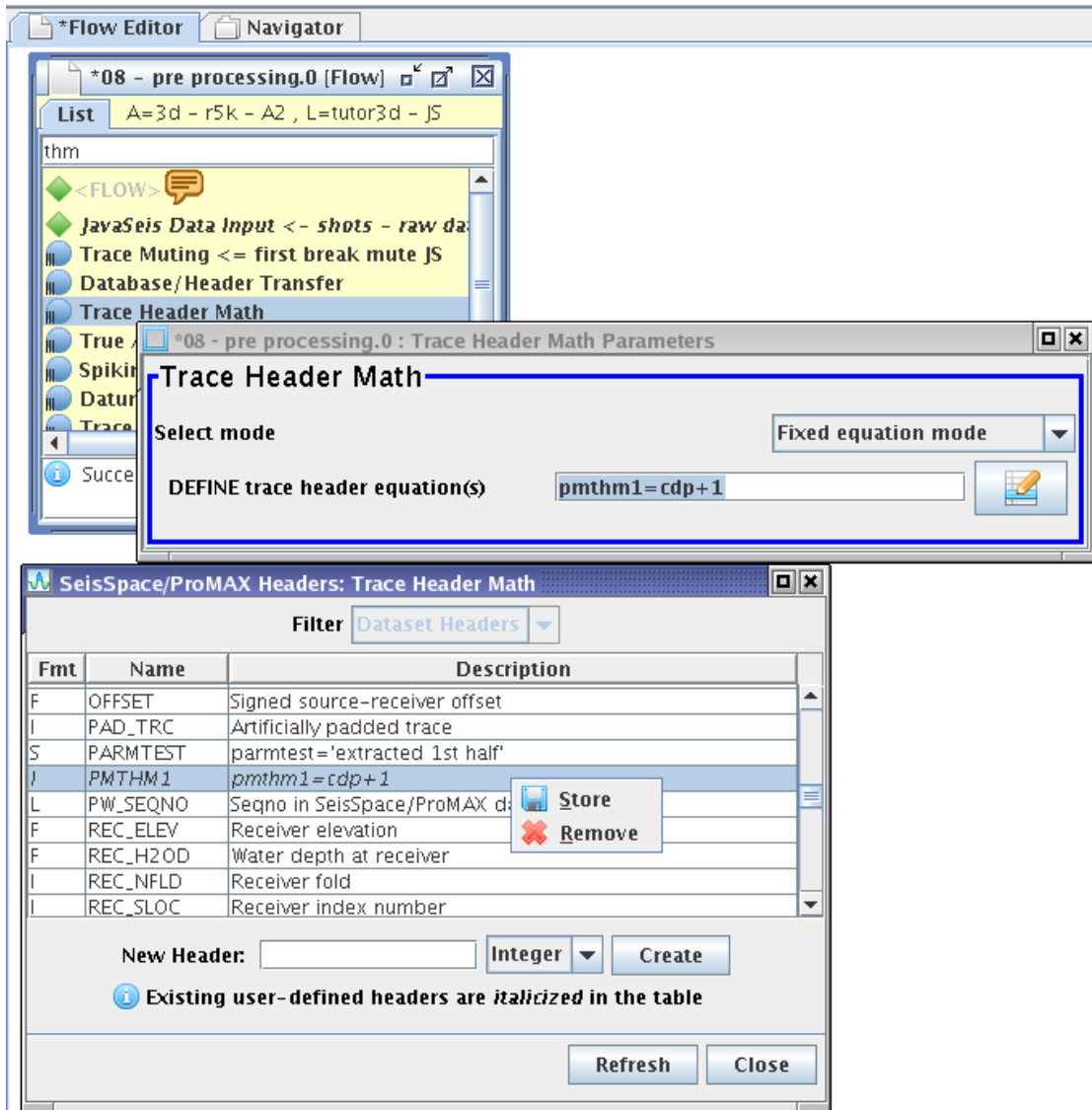
```

## Data Context and Header Catalog at any point in a flow


As you are working on a flow you may want to know what the header catalog and/or the data context is at any point in the flow. For SeisSpace® flows (as long as Intelligent Parameterization is on) you can always get the context and header list at any point in the flow. For ProMAX® or Hybrid flows you need to run the Intelligent Parameterization (Init Phase) manually

by clicking on the "init phase" icon.  After running the init phase, the header catalog and data context are available.



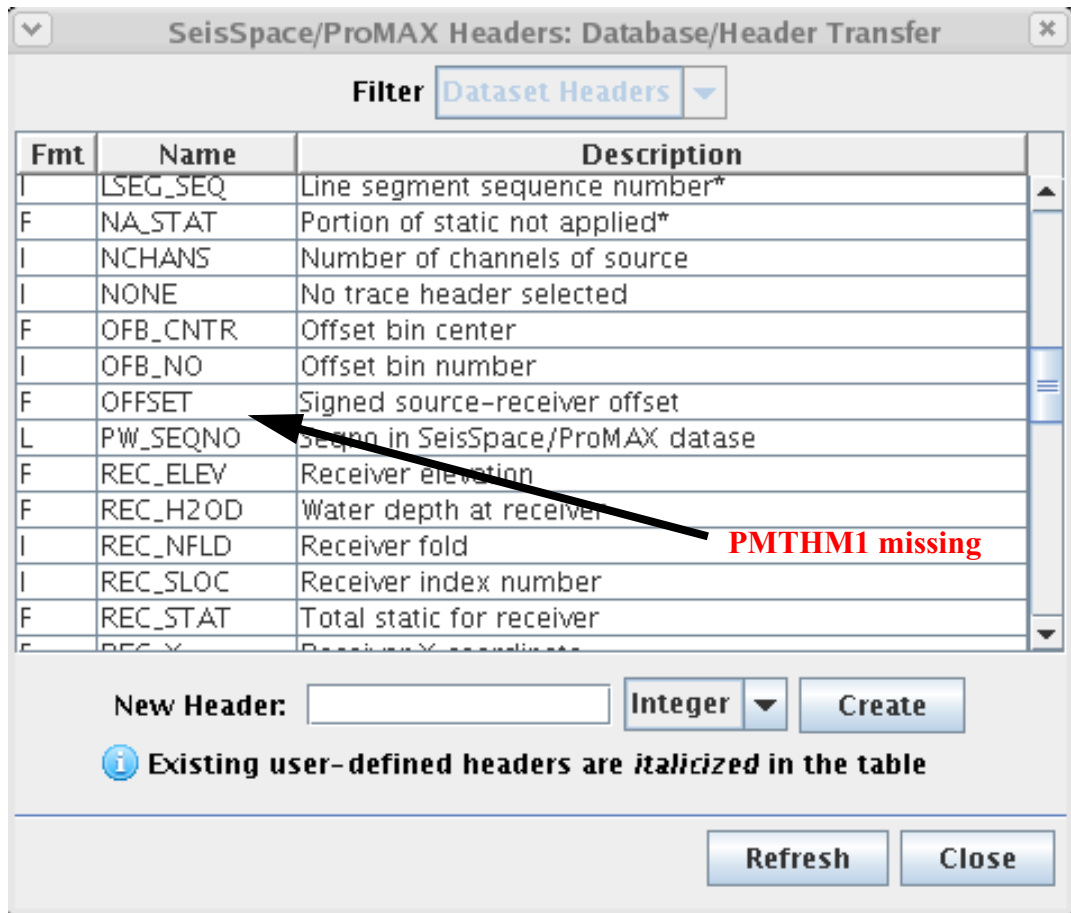


In this example, the ProMAX® trace header math is adding header "pmthm1". If you look at the header list after the Trace Header Math using

the Inline Show Header Catalog Icon:  you will see this header in the list in a *blue/italic* font. This means that it is a non-standard header but is not cataloged in the .user\_headers file. You can save it to the .user\_headers file by MB3-Store on the header from the list.

MB3-Remove can be used to remove headers from the .user\_headers file.

If you then click on the Database/Header Transfer process you will see that the "pmthm1" header is not in the header catalog at that point in the flow.




SeisSpace/ProMAX Headers: Database/Header Transfer

Filter: Dataset Headers


Fmt	Name	Description
I	LSEG_SEQ	Line segment sequence number*
F	NA_STAT	Portion of static not applied*
I	NCHANS	Number of channels of source
I	NONE	No trace header selected
F	OFB_CNTR	Offset bin center
I	OFB_NO	Offset bin number
F	OFFSET	Signed source-receiver offset
L	PW_SEQNO	Seqno in SeisSpace/ProMAX datase
F	REC_ELEV	Receiver elevation
F	REC_H2OD	Water depth at receiver
I	REC_NFLD	Receiver fold
I	REC_SLOC	Receiver index number
F	REC_STAT	Total static for receiver
F	REC_X	Receiver X coordinate

New Header:  Integer Create

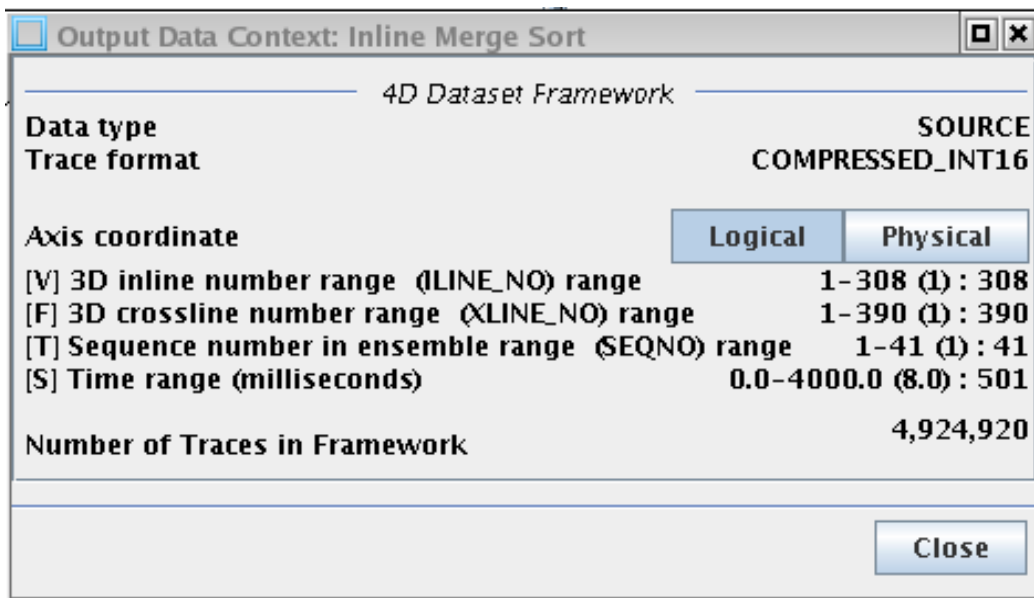
 Existing user-defined headers are *italicized* in the table

Refresh Close

Similar to the header catalog you can interrogate the data context at any

point in the flow if you click on the context icon . The context

summary is in a separate dialog and you can ask for the header list from this dialog if so desired.



## Setting site and user defaults for SeisSpace® and ProMAX® tool menus

There are cases where some sites want to set the defaults for parameters in processes that are more appropriate than the defaults set by Landmark. Typical examples include setting the data output tools to use secondary storage or to use full 32-bit floating point storage. In the past, ProMAX® modules have been user configurable after the installation by manually editing the text menu files. SeisSpace tools were not user configurable except for a couple of default settings in the `promess.properties` file.

There are now two levels of user configurable defaults that are available in the flow builder: Site level defaults that are managed by the administrative user and User level defaults that are managed by each individual user. Both levels are stored as flows where the general methodology is simply to build a flow that contains the processes of interest, setting the default values and marking the parameters to be used as overriding defaults.

The Default flows are stored in different locations by default:

The Site level (or administrative) default flow is stored in a flow directory `$PROWESS_ETC_HOME/defaultdatahom/defaultarea/defaultline/site` or `$PROWESS_HOME/etc/defaultdatahom/defaultarea/defaultline/site`.

The user default flow is stored in a flow directory:

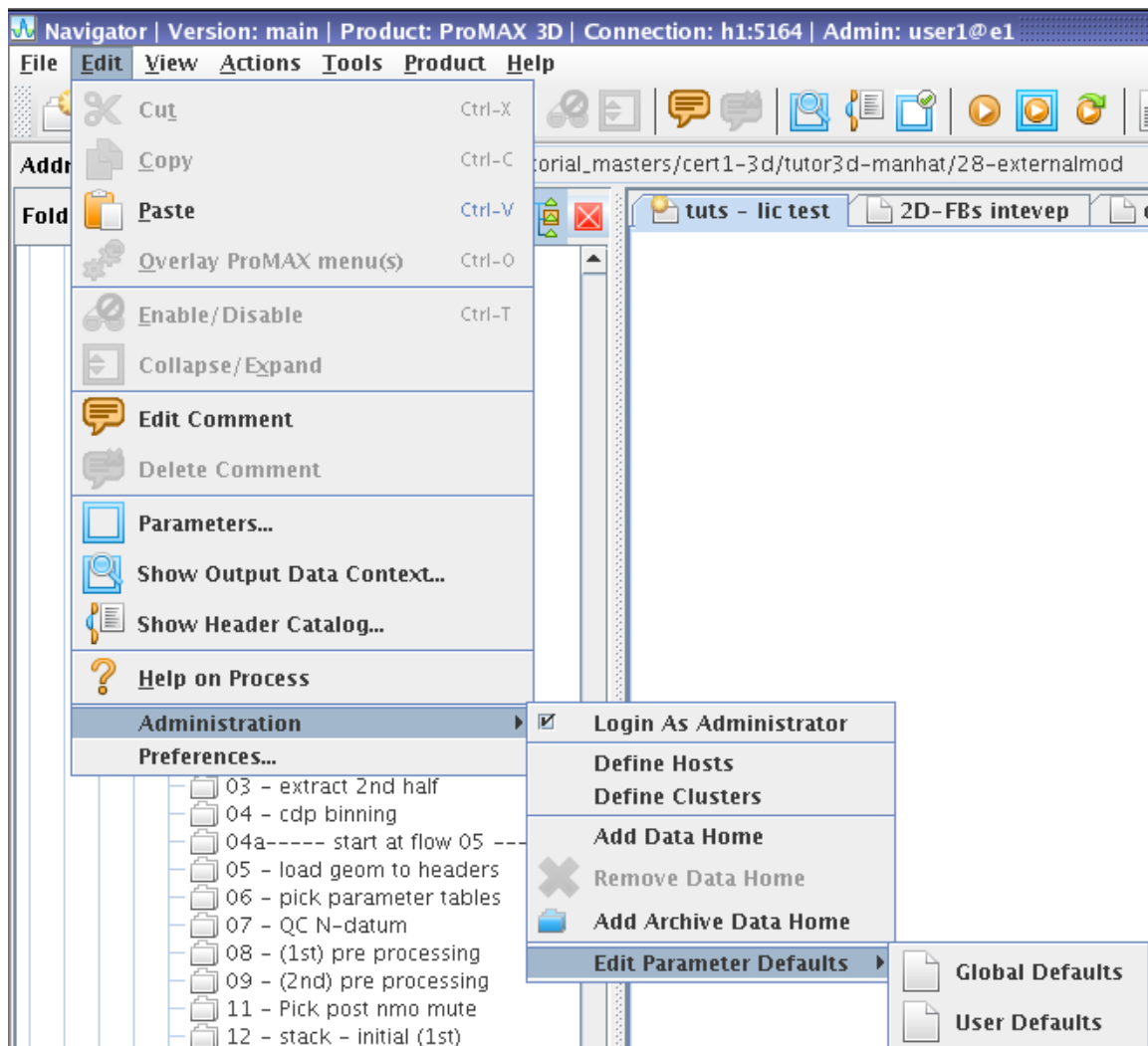
`$HOME/SeisSpace/defaultdatahom/defaultarea/defaultline/user` or  
`$PROWESS_PREFS_DIR/defaultdatahome/defaultarea/defaultline/user`.

The administrator may want to use a setting in the `PROWESS_HOME/etc` (or `PROWESS_ETC_HOME`) `/prowess.properties` file for where the user default flows are being stored. The stanza can be set to point the user defaults to the same general directory as the site level defaults for example:

```
# You can define a common location under which to create a hierarchy for  
# user parameter defaulting flows. For example, you can set this to  
# the value of $PROWESS_HOME/etc or $PROWESS_ETC_HOME  
if this variable is set.  
# The default is $HOME/SeisSpace or $PROWESS_PREFS_DIR if  
this variable is set.  
# the directory structure under this is  
.../defaultdatahom/defaultarea/defaultline  
#com.lgc.prodesk.navigator.userDefaultsDir=$PROWESS_ETC_HO  
ME
```

If the above property is set to the default value, the user default flows are named `$PROWESS_ETC_HOME/defaultdatahome/defaultarea/defaultline/userusername`

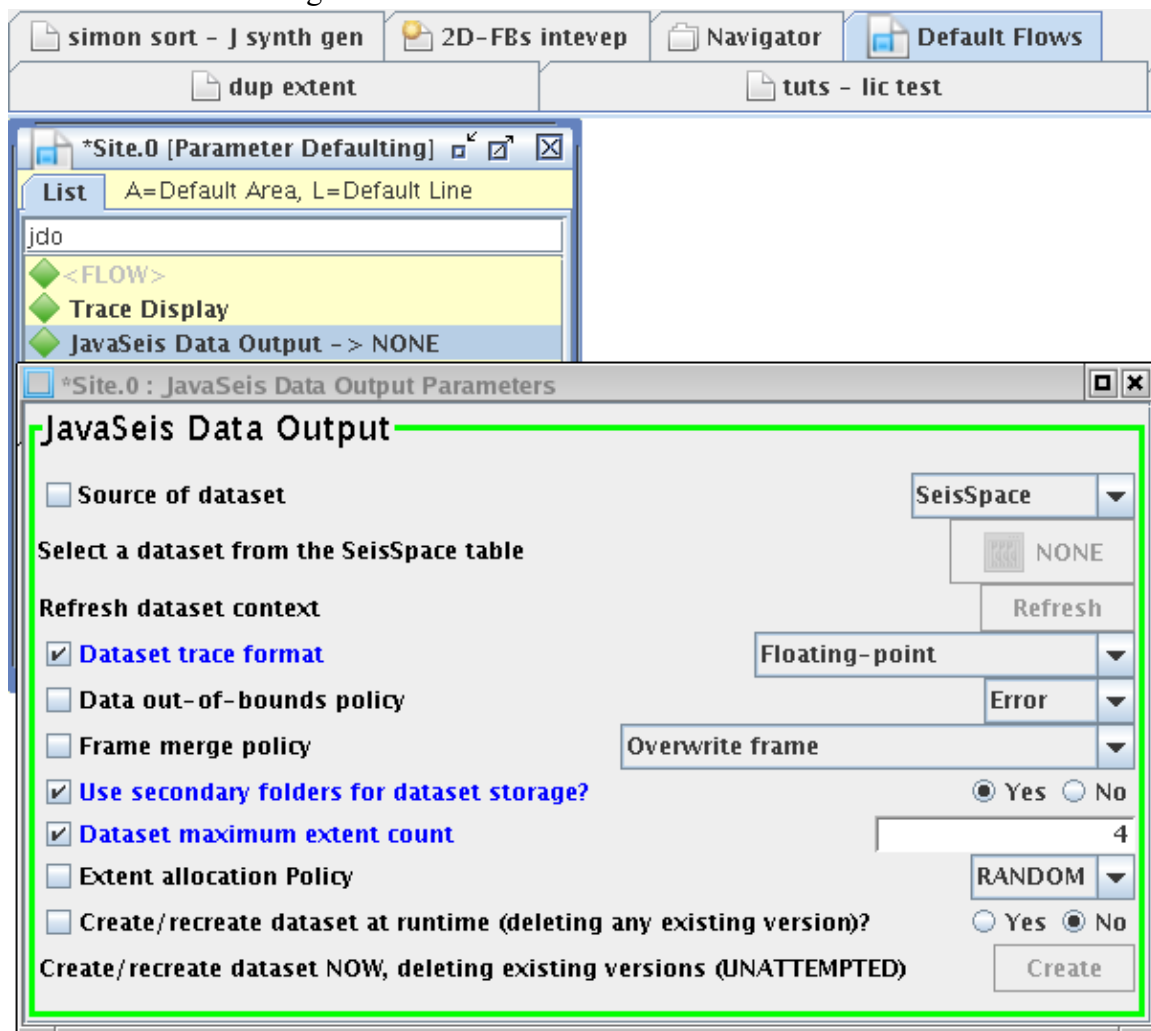
To build the flow that is used solely to set parameter defaults you would use the Edit > Administration > Edit Parameter Defaults pulldown menu.



If you are currently set as the administrative user, the Global Defaults option will be enabled.

When you select either the Global (or Site) default flow or the User default flow, the flow will be added to a Default Flows tab in the flow builder. You will not be able to add any other flows to this tab or submit any flows for execution from this tab.

To set a parameter default, add the process to the flow, set the parameter value and **check the box** next to the parameter in the menu dialog. Checking the box is the indicator to use the value as the default.



You can add as many processes to the flow as you like and set as many parameter defaults as are required. There are some parameter types where defaulting has been disabled such as the dataset name selector and some informational parameters.

User defaults override the Site level defaults.

Both ProMAX® and SeisSpace® processes can be defaulted in this manner.

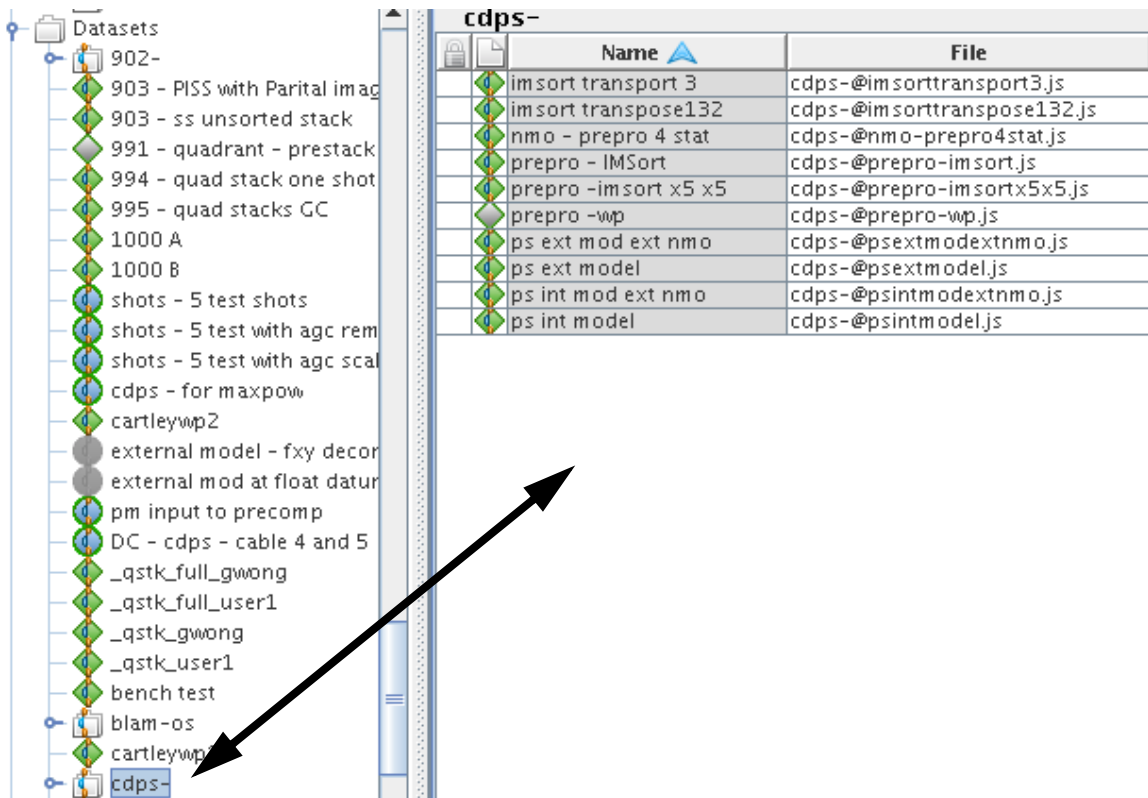
Parameter defaults will not be used for processes in a Disabled state in the flows.

## Object Grouping and Group Copying

Object Grouping was implemented to help support the data explosion of flows, datasets and tables for a project by grouping like named objects into a sub-view to shorten the lists in the tree and table views of the navigator.

Object grouping allows you to apply a constant prefix to like named objects and display them in a sub-list on their own. This may help reduce a long list of flows or datasets to a more manageable list with sub-lists.

For example, you may have several different versions of CDP gather datasets. You may elect to "group" them together so that in the main datasets list you see "cdps-", but you can further expand that list into the table to see all of the cdps-\* datasets.



cdps-		
	Name	File
	imsort transport 3	cdps-@imsorttransport3.js
	imsort transpose132	cdps-@imsorttranspose132.js
	nmo - prepro 4 stat	cdps-@nmo-prepro4stat.js
	prepro - IMSort	cdps-@prepro-imsort.js
	prepro -imsort x5 x5	cdps-@prepro-imsortx5x5.js
	prepro -wp	cdps-@prepro-wp.js
	ps ext mod ext nmo	cdps-@psextmodextnmo.js
	ps ext model	cdps-@psextmodel.js
	ps int mod ext nmo	cdps-@psintmodextnmo.js
	ps int model	cdps-@psintmodel.js

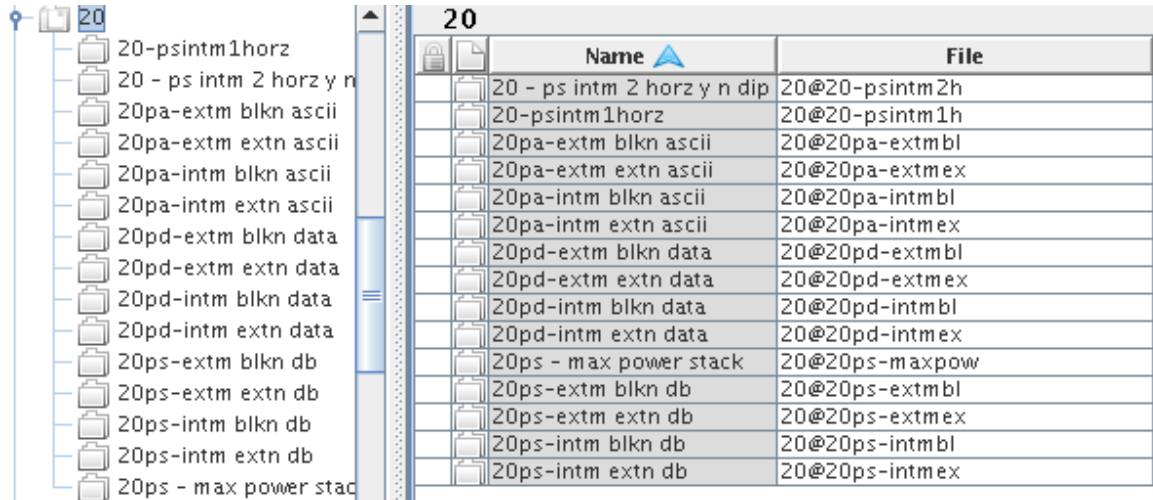
NOTE the actual dataset name of the file on disk. `cdps-@xxxxxxxxxx`. The `@` symbol is the designator for separating a common prefix from a more descriptive suffix. Also note that only the suffix is used as the descriptive name in the navigator.

For datasets you can control the groupings in either a manual dataset create mode or in a flow-replication auto create mode by including a common "prefix@" before the descriptive name.

The same methodology can be applied to flows and tables.

Remember that flow replication already does this replica compression so you do not see all of the individual replicas in the flows list.

Below is a picture showing a group of similarly named flows that are grouped into the 20\* group. This example also shows that the group can be expanded in the tree view if so desired.

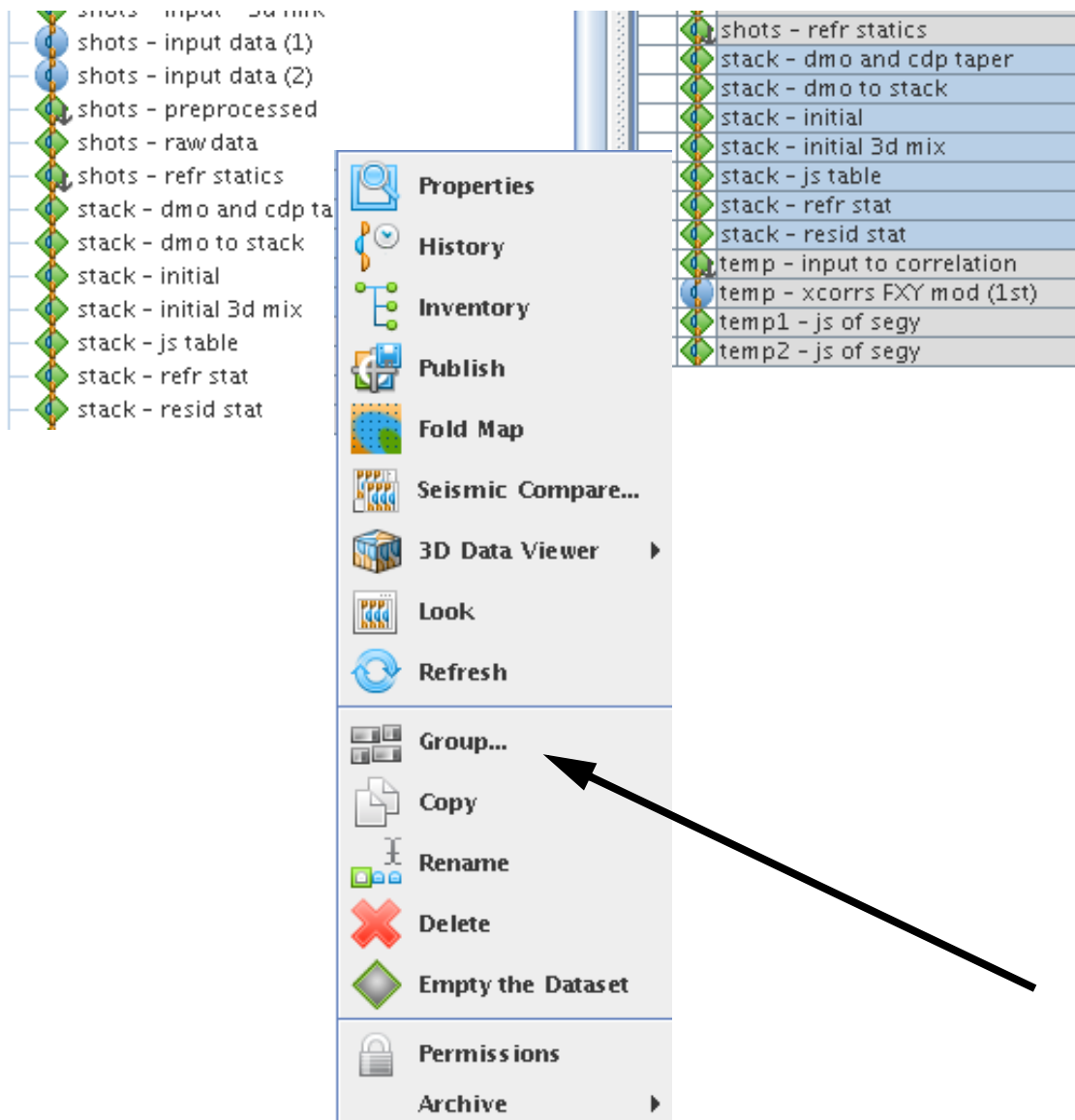


20		Name	File
		20 - ps intm 2 horz y n dip	20@20-psintm2h
		20-psintm1horz	20@20-psintm1h
		20pa-extm blkn ascii	20@20pa-extmbl
		20pa-extm extrn ascii	20@20pa-extmex
		20pa-intm blkn ascii	20@20pa-intmbl
		20pa-intm extrn ascii	20@20pa-intmex
		20pd-extm blkn data	20@20pd-extmbl
		20pd-extm extrn data	20@20pd-extmex
		20pd-intm blkn data	20@20pd-intmbl
		20pd-intm extrn data	20@20pd-intmex
		20ps - max power stack	20@20ps-maxpow
		20ps-extm blkn db	20@20ps-extmbl
		20ps-extm extrn db	20@20ps-extmex
		20ps-intm blkn db	20@20ps-intmbl
		20ps-intm extrn db	20@20ps-intmex

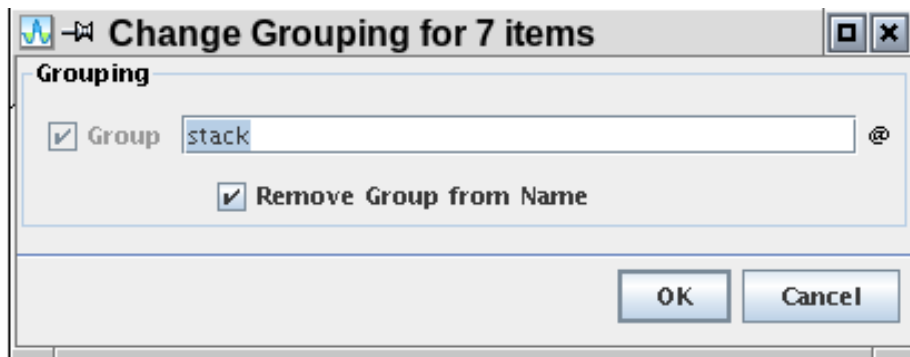


## Grouping and Un-Grouping existing objects

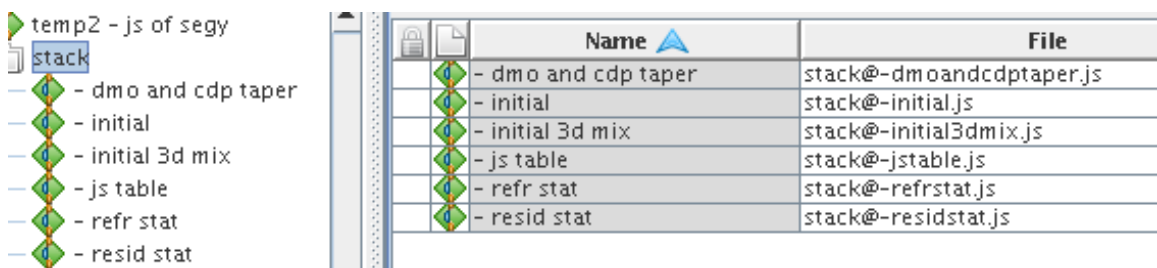
If you have a series of existing datasets that you want to group you can choose them all in the table view and use the MB3 - Group option



You will be presented with a dialog asking for the group name with an option to remove the group name from the existing names.

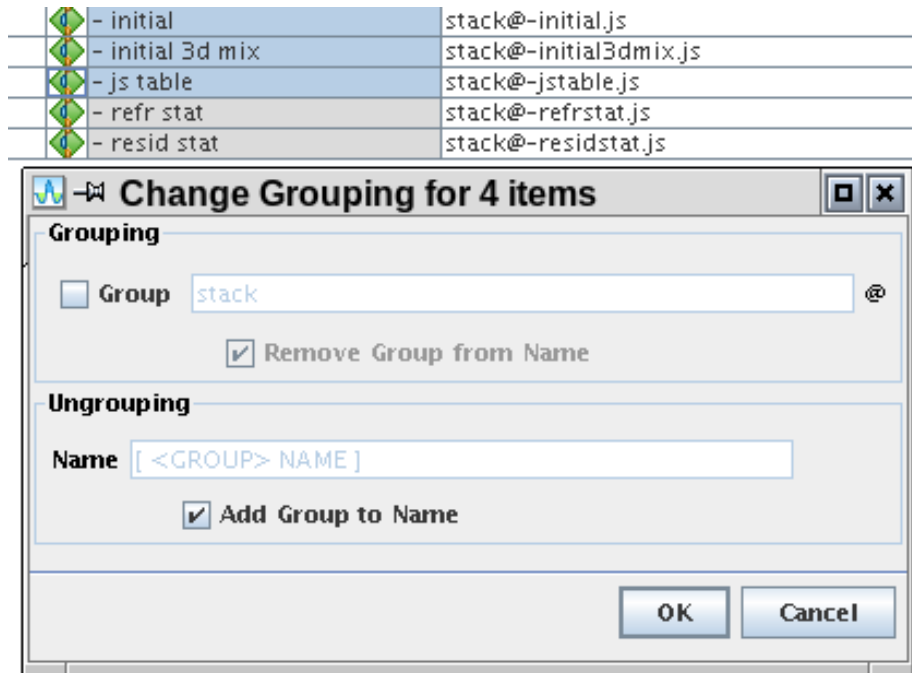


This will result in the creation of the "stack" group with the dataset descriptive names having the "stack" text removed and a rename of the file directories to stack@\*



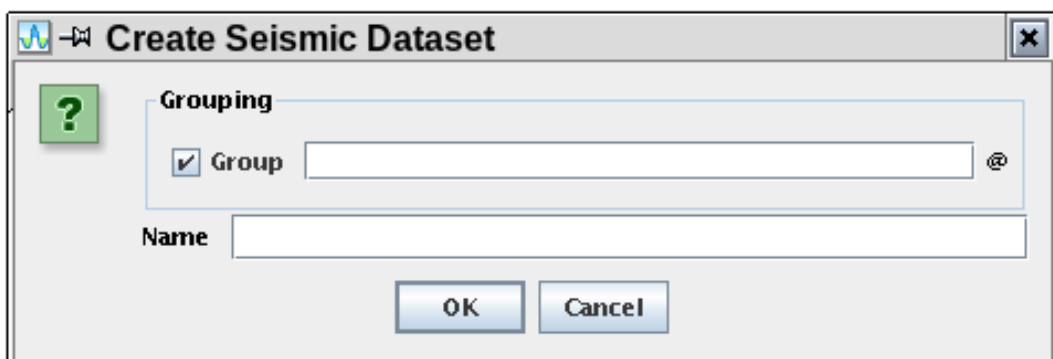
Objects that belong to a group can be un-grouped by a similar procedure of selecting the objects in a group that you want to un-group, choose the

Group option from the MB3 options menu and then un-select the "Group" option. The un-grouping options will then be enabled:

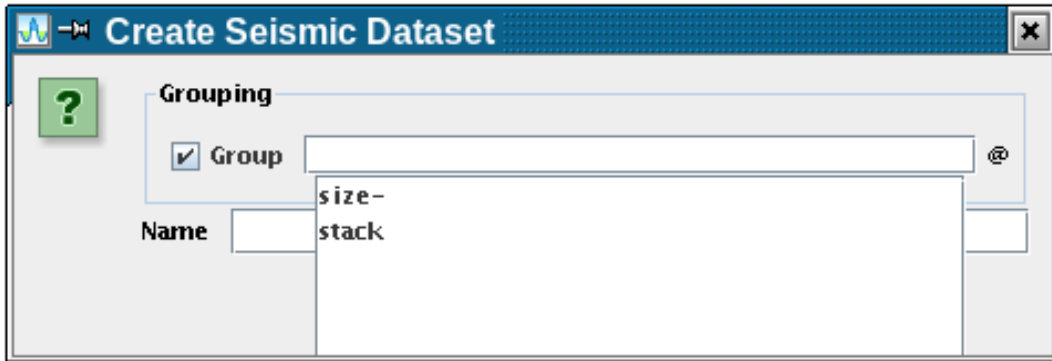


### Adding new objects to a group

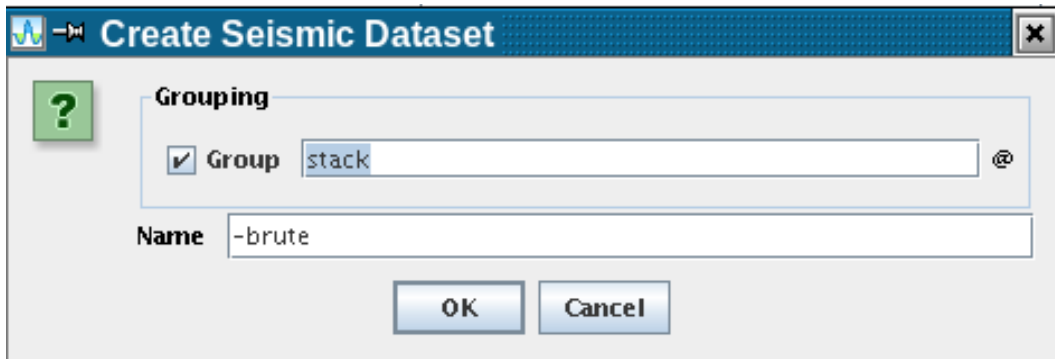
When adding new datasets, the dialog prompts you to choose or enter a new group if you check the Group check box



Double click in the group entry box to get a list of the existing groups or type in a new group prefix name.



Then add the descriptive part of the file name



This will result in a dataset being added to the "stack" group with a file name on disk of stack@-brute and a descriptive name of "-brute"

Grouping and Un-grouping of existing flows and tables follows the exact same procedures as does the generation of new flows and tables.

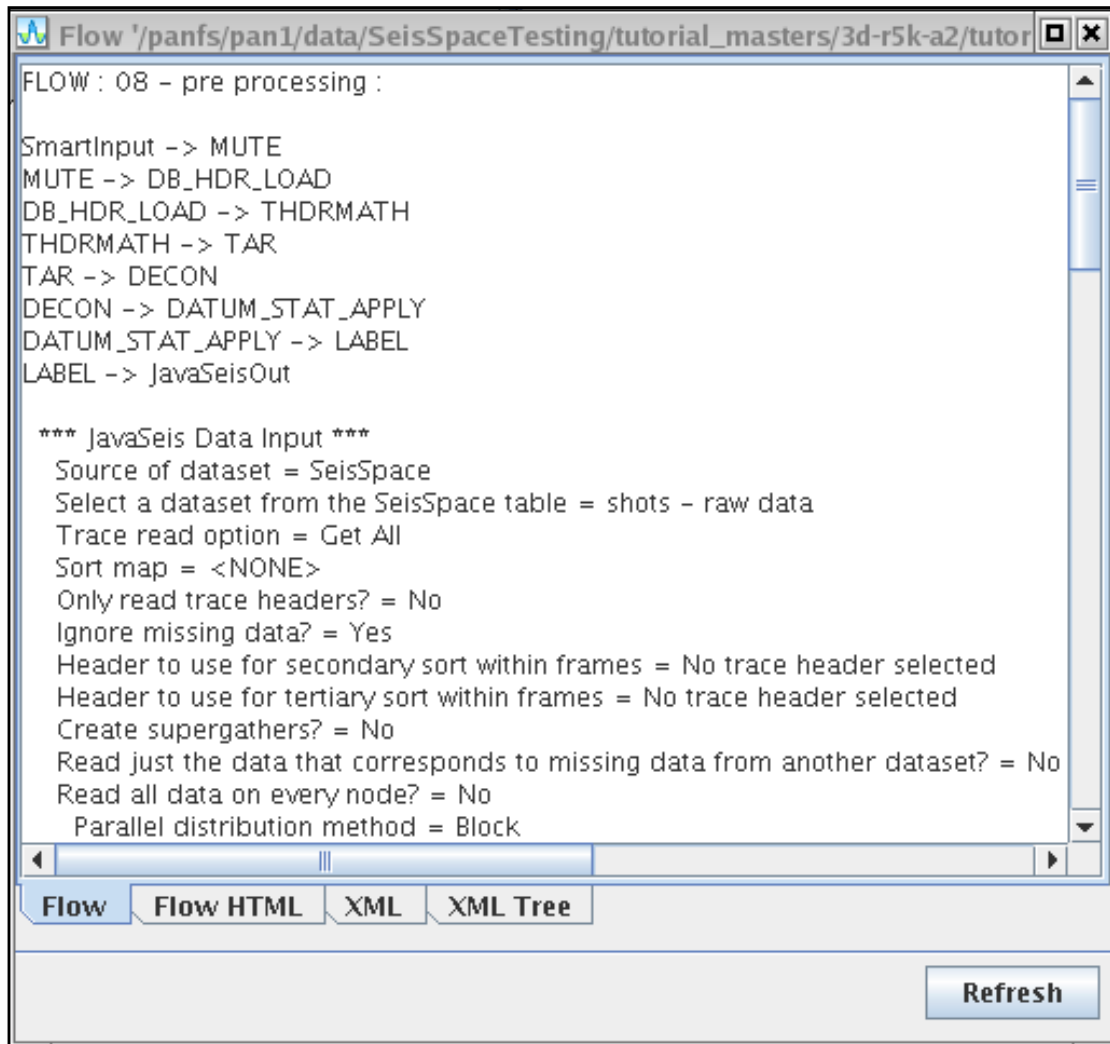
## The Flow Viewer

The Flow Viewer can be used as an alternative to loading the flow into the editor to see what is in the flow. The Flow Viewer is started by using the

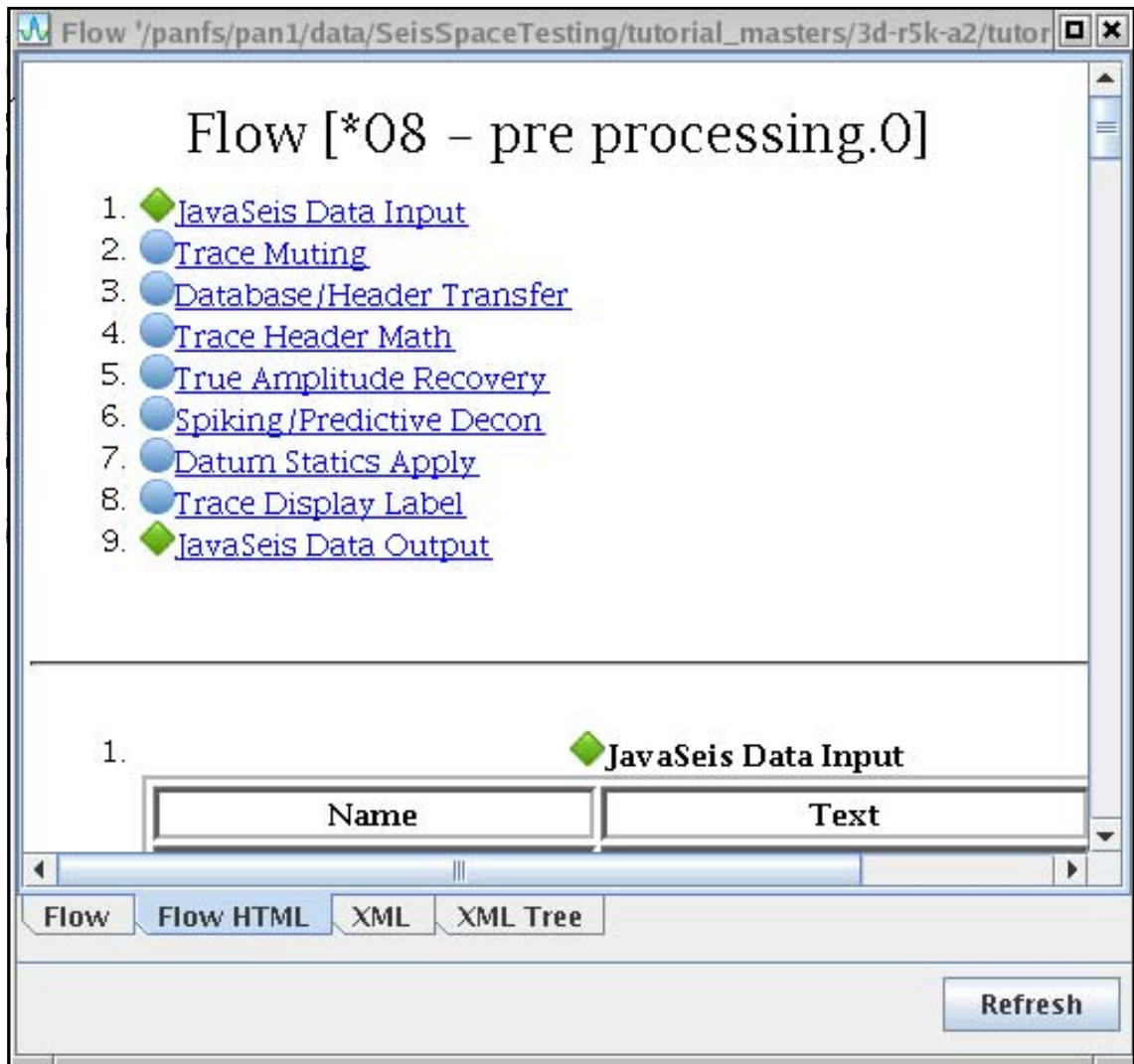


. There are four different views available in the Flow Viewer:










- **Flow**- A text "pretty print" of the processes and parameters




- **Flow HTML** - A formatted HTML printout.



The screenshot displays a window titled "Flow '/panfs/pan1/data/SeisSpaceTesting/tutorial\_masters/3d-r5k-a2/tutor'". The main content area shows a flowchart titled "Flow [\*08 - pre processing.0]". The flowchart consists of nine steps, each with a diamond-shaped icon and a text label:

1.  [JavaSeis Data Input](#)
2.  [Trace Muting](#)
3.  [Database/Header Transfer](#)
4.  [Trace Header Math](#)
5.  [True Amplitude Recovery](#)
6.  [Spiking/Predictive Decon](#)
7.  [Datum Statics Apply](#)
8.  [Trace Display Label](#)
9.  [JavaSeis Data Output](#)

Below the list, a detailed view of the first step is shown:

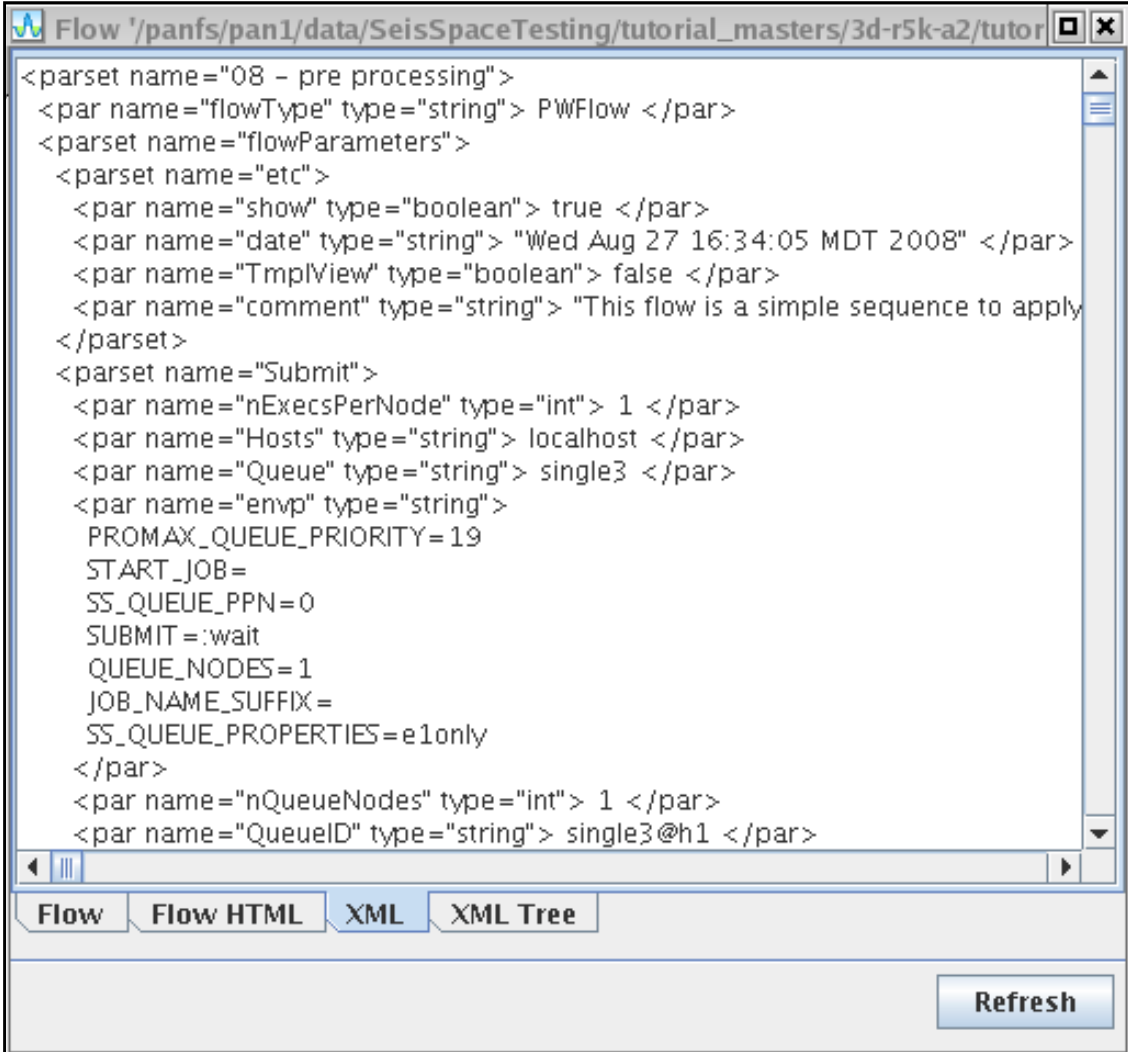
1.  **JavaSeis Data Input**

This view includes a table with two columns: "Name" and "Text".

Name	Text
------	------

At the bottom of the window, there are four tabs: "Flow", "Flow HTML", "XML", and "XML Tree". The "Flow HTML" tab is currently selected. A "Refresh" button is located in the bottom right corner of the window.

- **XML** - Shows the actual XML contents of the pworkflow file for the flow.

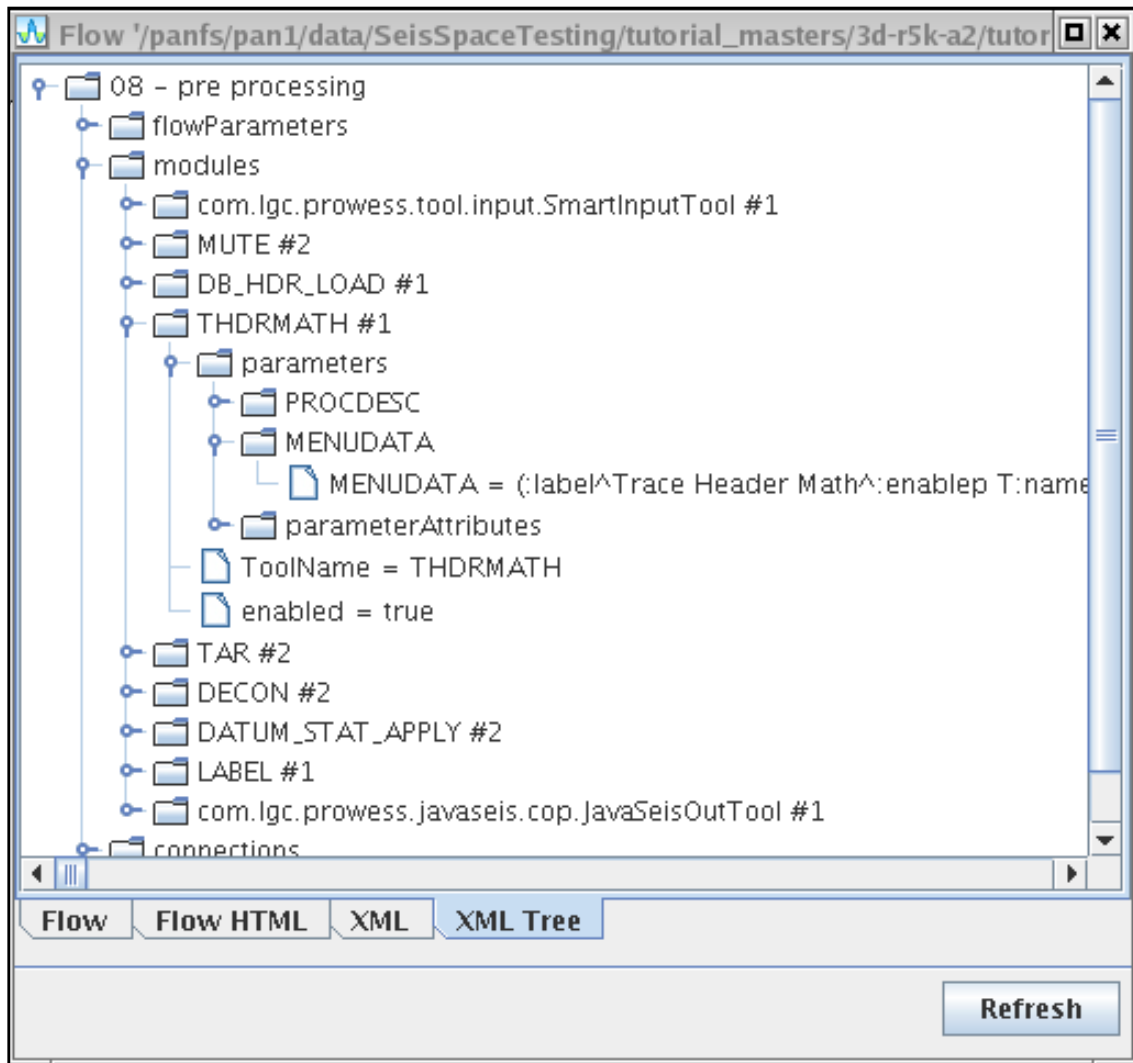


The screenshot shows a window titled "Flow '/panfs/pan1/data/SeisSpaceTesting/tutorial\_masters/3d-r5k-a2/tutor" with a tab labeled "XML". The XML content is as follows:

```
<parset name="08 - pre processing">
<par name="flowType" type="string"> PWorkflow </par>
<parset name="flowParameters">
  <parset name="etc">
    <par name="show" type="boolean"> true </par>
    <par name="date" type="string"> "Wed Aug 27 16:34:05 MDT 2008" </par>
    <par name="TmpView" type="boolean"> false </par>
    <par name="comment" type="string"> "This flow is a simple sequence to apply
  </parset>
  <parset name="Submit">
    <par name="nExecsPerNode" type="int"> 1 </par>
    <par name="Hosts" type="string"> localhost </par>
    <par name="Queue" type="string"> single3 </par>
    <par name="envp" type="string">
      PROMAX_QUEUE_PRIORITY=19
      START_JOB=
      SS_QUEUE_PPN=0
      SUBMIT=:wait
      QUEUE_NODES=1
      JOB_NAME_SUFFIX=
      SS_QUEUE_PROPERTIES=e1only
    </par>
    <par name="nQueueNodes" type="int"> 1 </par>
    <par name="QueueID" type="string"> single3@h1 </par>
  </parset>
</parset>
```

At the bottom of the window, there are four tabs: "Flow", "Flow HTML", "XML" (selected), and "XML Tree". A "Refresh" button is located in the bottom right corner of the window.

- **XML tree** - generally only used by developers for debugging. This is not very useful to users.





## Printing a flow to HTML

You can print the flow to a HTML file and view it in a browser. If you select



the browser icon when working with a flow or a flow list. The browser that is used is controlled by the PROMAX\_HOME/port/bin/PromaxFlowPrinter script and defaults to Netscape for Operating systems other than Linux. For Linux it defaults to Mozilla.

### Flow [\*08 - preprocessing.154]

1. [JavaSeis Input](#)
2. [Database/Header Transfer](#)
3. [Trace Kill/Reverse](#)
4. [Trace Muting](#)
5. [Spiking/Predictive Decon](#)
6. [Datum Statics Apply](#)
7. [Trace Display Label](#)
8. [JavaSeis Data Output](#)

#### JavaSeis Input

Name	Text	Value
DATA_SOURCE	Source of Dataset	<i>SeisSpace</i>
DATA_SELECTOR	Select a dataset from the SeisSpace table	<i>shots - geom</i>
refresh	Refresh dataset context	<i>Refresh</i>
READ_OPT	Trace read option	<i>Read All sequentially</i>
IGNORE_OPT	Ignore missing data?	<i>Yes</i>
READALL_ON_EVERY_NODE	Read all data on every node?	<i>No</i>
SECONDARY_SORT_HDR	Header to use for secondary sort within frames	<i>No trace header selected</i>
TERTIARY_SORT_HDR	Header to use for tertiary sort within frames	<i>No trace header selected</i>
PARALLEL_DIST_METHOD	Parallel distribution method	<i>Block</i>
PARALLEL_DIST_AXIS	Parallel distribution axis	<i>S_LINE</i>

1.

#### Database/Header Transfer

Name	Text	Value
DIRECT	Direction of transfer	<i>Load TO trace header FROM database</i>
NUMPARMS	Number of parameters	<i>1</i>

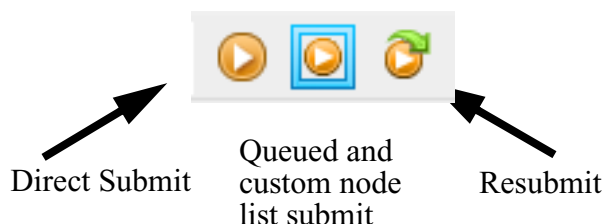
The HTML file is saved in the flow directory as the packet.html file.

## Submitting a Job for Execution

You can submit jobs for execution from

- the tree view of a list of Flows,
- the table view of a list of Flows,
- the Flow Editor tab, and
- the Replica Job Table (when working with replicated flows).

In all cases, the following three job submit icons provide a variety of job submit options:



There are three fundamental methods available to submit jobs:

- direct submit on the machine where the navigator is running as a single joblet job
- a directed submit to either a user specified host list or to a Queue for either single joblet, multi joblet, or PVM jobs, and
- resubmit as the job was submitted previously.

**Note:** there are two stanzas in the `SeisSpace/etc/prowess.properties` file that you may want to set for your specific Q behavior. If you are using the delivered capabilities without any additional user modified q scripts, you should not change the settings for these values in the `prowess.properties` file.

```
# Whether or not show the joblet specification (number of nodes, number of  
# execs per node, number of joblets) in the Submit dialog; the default  
# is to show it. If you customize your queue menu and submit scripts in such  
# a way that you take responsibility for how to obtain the number of joblets,  
# you may want to hide these parameters in the Submit dialog.
```

```
com.lgc.prodesk.jobviewer.showJobletsSpec=true
```

```
# Indicates whether the submit dialog will automatically load the default  
# submit parameters or the resubmit parameters when it is displayed.
```

```
com.lgc.prodesk.jobviewer.autoload=true
```

## Direct Submit

This option directly submits a job as a single node - single joblet job. The job will run on the machine where the Navigator/Flow Builder is running.

## Queue and custom node list submit

This option allows you to customize the submit parameters of a job or set of jobs and also allows you to set up a job submission default. A common use would be to set up a default queue for most jobs.

General usage would be to parameterize the default Queued submit and then save this configuration and optionally set it as the DEFAULT.

A Ctrl-MB1 combination on this icon will submit the selected job(s) using the saved DEFAULT job submit configuration. If you want to do something else, then you can click MB1 on this icon and the submit user interface will present itself and you can choose the submit parameters as you desire.

The main job submission user interface has three major options: Hosts, Cluster, and Queue.

All of these options allow you to reorder selected jobs for submission if you have selected multiple jobs from the table list in the Navigator. That is, you can put them in the Queue in a different order than they were selected.



Select the "reorder" icon to enable this feature. First Select the flow (or flows) that you want to move with MB1 and Ctrl or Shift MB1 combinations and then drag the selection to the location where you want to drop them. They will be dropped below the dark bold line. To move a single flow to first select the flow with a click and release with MB1 and then hold and drag with MB1.

The joblet count (or parallelization) part of the user interface is the same for all of the options. See each individual section for details.

## Submit (button)

This button will submit the job(s) with the selected submit configuration.

## Cancel (button)

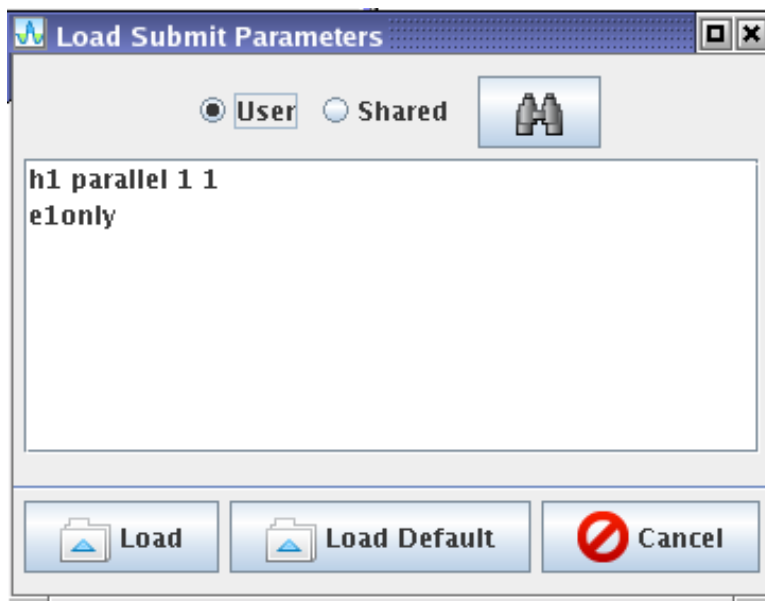
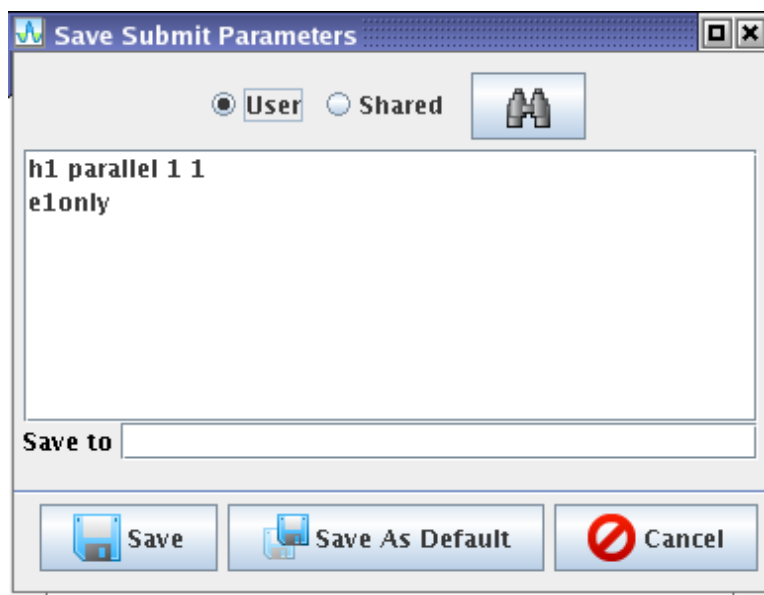
This will cancel the job submit operation.

## Save and Load (buttons)

This option will allow you to save different job submit configuration as defaults which can then be accessed later. The DEFAULT saved

configuration is accessed when using the Ctrl-MB1 option on the job submit icon from the flow editor or the table view of the Navigator.

You may elect to save multiple submission variations for easy access later. There is the one main DEFAULT configuration that is what is recalled if you use the Ctrl-MB1 option on the second job submit icon. You can SAVE additional submit configurations and then reload them using the LOAD button in the submit dialog box.



The "binocular" icon can be toggle from blue to gray background. When in a blue background, as you select the different configuration choices in the list, the Submit dialog will update with the parameters for inspection before

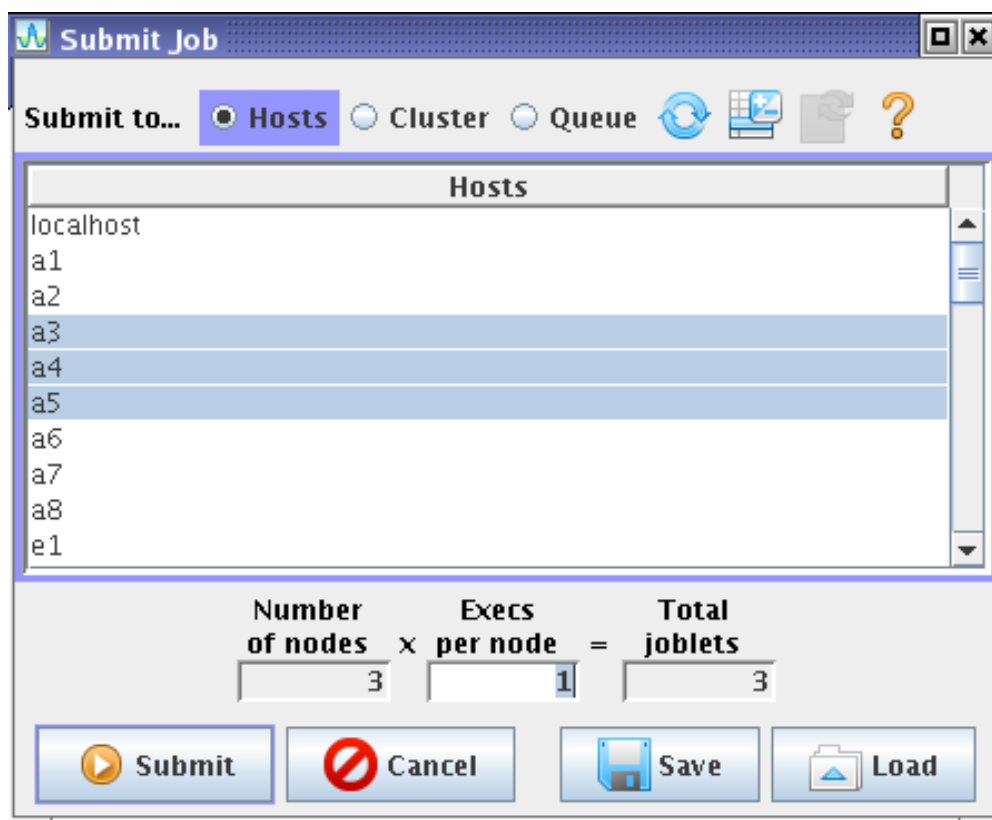
you actually choose one. When in light blue/shaded background the Submit dialog will not update as you click on the different choices in the list.

When set to User mode - the different job submit configurations are store in the users user\_prefs directory.

When set to Shared mode - the different job submit configurations are stored in the "logs" directory. General users may not have permission to write to this directory.

## Hosts option

The host option will present a list of the machines that have been added to the hosts list.



You can select multiple hosts on which to run the job in parallel. Select multiple nodes with Ctrl-MB1 to select individual nodes from the list or Shift-MB1 to select a range of nodes.

### ***Number of nodes***

This parameter is automatically filled in based on the number of hosts that were selected from the list.

### ***Execs per node***

Specify the number of execs per node to use to run the job.

### **Cluster option**

You can select from a list of predefined cluster definitions. These cluster aliases are defined in the Administrator Tool.

Submit Job

Submit to...  Hosts  Cluster  Queue

Cluster	Shared	Foreman	# Hosts

Number of nodes × Execs per node = Total joblets

×  =

Submit Cancel Save Load

This option is not available for simple single exec ProMAX® jobs or any combination of jobs that include single exec ProMAX® jobs.

### ***Number of nodes***

The "number of nodes" option is not user configurable in this mode. The number of nodes will be set to the number of hosts that make up the cluster definition for combinations of SeisSpace®, Hybrid or ProMAX® Parallel Begin/ Parallel End jobs.

## ***Execs per node***

Specify the number of execs per node to use to run the job.

## **Queue option**

For all types of jobs, select the Queue for submission. The contents of the central box may vary depending on which queue system you are using and how they have been customized by your administrators.

Submit Job

Submit to...  Hosts  Cluster  Queue

Queue server: h1

Queue name: parallel

===== NODES =====

Queue Node Properties q

Overrides the default ppn (processes per node) 0

===== PRIORITY =====

Batch Priority 19

Batch Job Start Time

Number of nodes	Execs per node	Total joblets
1	1	1

Submit Cancel Save Load

### **Queue server:**

Select the Queue server from the available list. This action reads the \$PROMAX\_HOME/etc/qconfig or \$PROMAX\_ETC\_HOME/qconfig file and presents the list of servers found on the "machine" lines in the qconfig file.

### **Queue name:**

This presents a list of the known queues for the selected server. The list of Queues can be initiated by clicking on the "refresh" icon in the submit user interface. This action reads the \$PROMAX\_HOME/etc/qconfig or

\$PROMAX\_ETC\_HOME/qconfig file and presents the list of queues found in that file for the specified server.

## Queue Node Properties

You can specify a property to add to the queue directive line that is built for submitting the jobs. You will need to know the options here, consult your administrator for the list of properties at your site.

### Overrides the default ppn (processes per node)

This does not control the number of processors for ProMAX® jobs or SeisSpace® jobs. This is used only to specify the ppn specification on the QSUB directives to tell PBS/Torque how many processors (or mom units) to allocate for this job. With this set to 1, you will most likely get multiple ProMAX® jobs per node. With this set to the number or cpus as configured in the server\_priv/nodes file you will most likely get 1 ProMAX® job per node. Do not specify a number higher than the actual number of processors per node that you have. (Hyperthreading may allow you to specify more nodes as long as the server\_priv/nodes file in the PBS / Torque configuration also reflects the higher number of virtual nodes). The default ppn value (0) is reset to the number of joblets per node (execs/node \* joblets/exec). If you are working in a pure ProMAX® environment and you want to restrict the number of jobs per node to 1. Then you can use this override to set the ppn to the maximum number of cpus per node for each job.

## Main Dialog

### *number of nodes*

The "number of nodes" option is user configurable in this mode. If the job is parallelizable, the user parameters will be honored, If the job or some of the jobs in a group selected from the table are not parallelizable, those jobs will be "dumbed-down" to execute one node - one joblet.

For multi-node ProMAX® Parallel Begin/ Parallel End jobs, leave the host list blank in Parallel Begin. The host list will be filled with the list of nodes that was returned by the Q system when the job was released.

### *execs per node*

Specify the number of execs per node to use to run the job. If the job or some of the jobs in a group selected from the table are not parallelizable, those jobs will be "dumbed-down" to execute one node - one joblet.



## Resubmit

Use this option if you want to resubmit a job exactly the same what it was submitted previously. This icon also has CTRL-MB1 and MB1 options. This is handy if you have selected a specific list of nodes for a SeisSpace® job and the first attempt fails for some reason. You can fix the problem in the flow editor and CTRL-MB1 click this icon to resubmit with the previously chosen submit parameters.

MB1 displays the job submit dialog box populated with the last submit parameters.

CTRL-MB1 resubmits using the same parameters as the last submit, bypassing the job submit dialog box.

## Reset

Use this option to restore the original parameters.

## General Rules - for job submission

The rules surrounding job submit parameterization can be quite complex especially when you select multiple jobs of multiple types from the table list of flow. The general rules of parallelization can be summarized as follows:

ProMAX® single exec jobs - can run on one CPU of one node. Number of nodes and execs per node are forced to be 1.

ProMAX® Parallel Begin/End PVM jobs can be run on multiple nodes, with multiple execs per node.

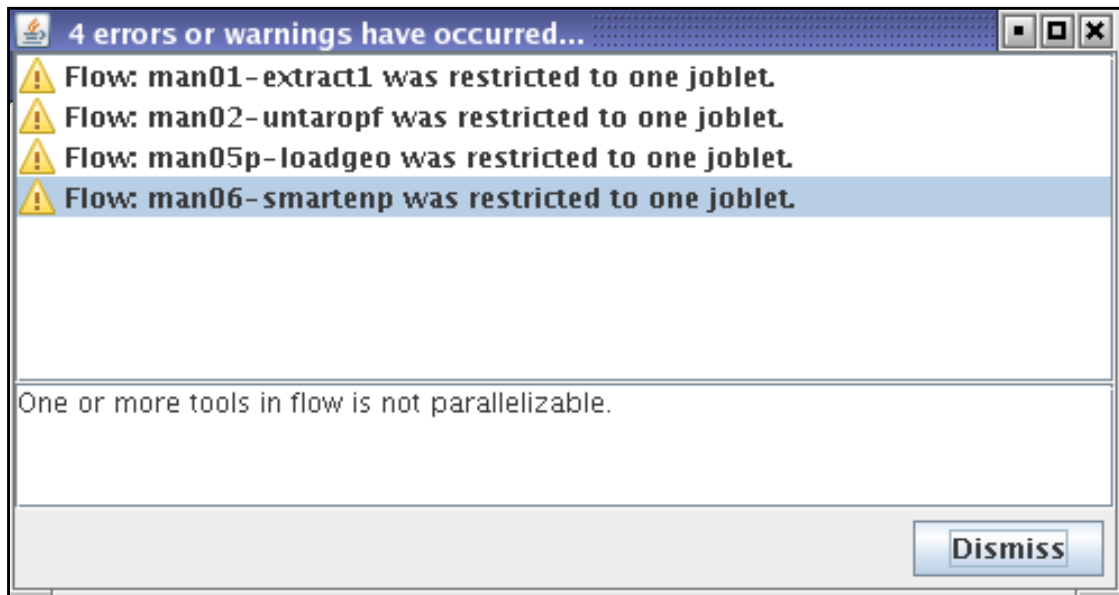
Hybrid jobs can be run on multiple nodes with multiple execs per node.

SeisSpace® jobs can be run on multiple nodes with multiple execs per node.

Hybrid jobs are screened to determine if they can be processed in parallel. That is, there are many ProMAX® processes and a couple of SeisSpace® processes that can only be run in a single joblet Hybrid flow. The Job submit protocols will treat a Hybrid flow with non-parallelizable ProMAX® processes in it as if it were a single exec ProMAX® job. That is, it can only be submitted to a single node with one joblet.

You will always be allowed to choose multiple nodes and multiple execs per node. If the job you are submitting or any of a group of jobs selected from the table are not parallelizable, those jobs will be downgraded in the

submit process to run on a single joblet on a single node. You will be notified as to which jobs were downgraded in an information dialog box.



For multi-node ProMAX® Parallel Begin/ Parallel End jobs, leave the host list blank in Parallel Begin. The host list will be filled with the list of nodes that you selected with additional instances for the number of execs per node that was selected.

## Purging Flows

The SeisSpace® Flow Builder will keep an user configurable number of copies of flow files and printouts from previous executions.

You can purge (delete) the oldest instances of the flow by using the



**Edit >Purge** pulldown menu or the Purge Icon.

For example, a flow with 25 instances can be purged down to only instances 21 through 25 using the default of five. The -1th instance is retained as the packet.job. The number of instances remaining after a purge can be configured in the preferences dialog.

You can also select multiple flows or even complete subprojects to apply the purge option.

*Note:* Purging cannot be undone.

## Restore a flow to its original state

If you have a flow in the editor that has been changed but you want to revert it back to its original state without closing it and not saving the changes and then re-opening it, you can use the "Revert Flow" icon



You can select **File > Revert Flow** or use the "Revert Flow" Icon.

## Overlaying menus

With each new release, the parameters in some processes change. A feedback dialog box will tell you which parameters are new or have been removed from a process. You can update ProMAX® processes in an existing flow using the overlay option. You can also select multiple processes and overlay an entire flow in a single operation.

You can select **Edit > Overlay ProMAX menu(s)**, use the Overlay



ProMAX® Menu(s) Icon., or use SHFT-MB2 as you have used in the past with the ProMAX® user interface.

*Note:* SeisSpace® processes do not need updating in this manner.

## Dataset Processing History

ProMAX® datasets use the original ProMAX® history viewer.

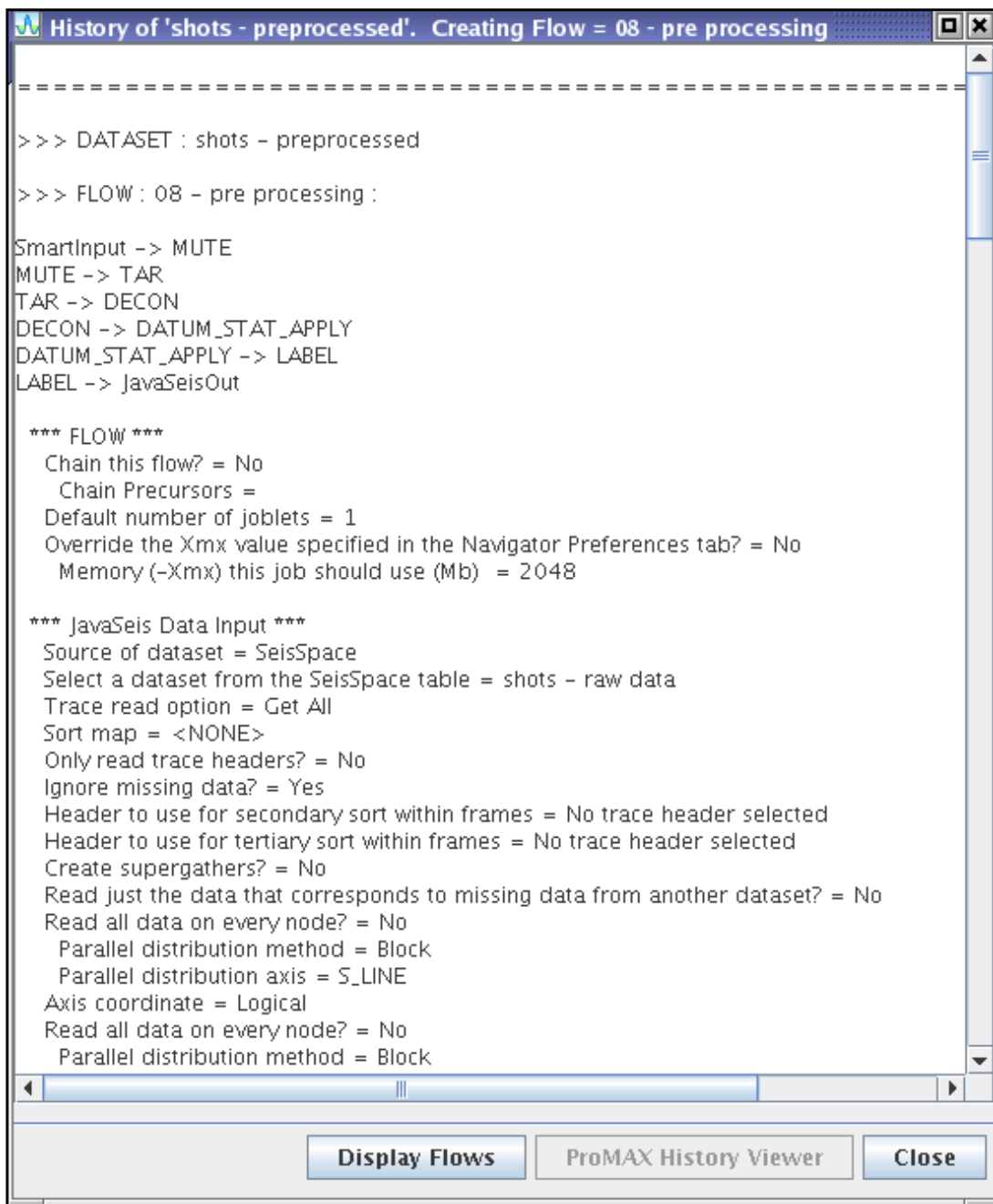
[Other Docs](#)[Search Page](#)[Known Problems](#)

JavaSeis dataset history is stored with the dataset in the History.xml file in the primary storage (project) directory.

In both cases you can see the history using the MB3-History option from the options menu.

The ProMAX® history viewer is documented in the ProMAX® documentation.

The JavaSeis history viewer shows the text "pretty print" concatenation of the flows and processes and parameters that were used to create the dataset.



You may choose to rebuild the flows from the history using the "Display Flows" button. These flows will be added to the History tab in the flow editor pane and added to the list of flows for the project.

The ProMAX® History Viewer button will be active for ProMAX® datasets that were written using ProMAX® Disk Data Output from a Pure ProMAX® Flow.

## Area, Line, Flow, Table, Dataset name restrictions

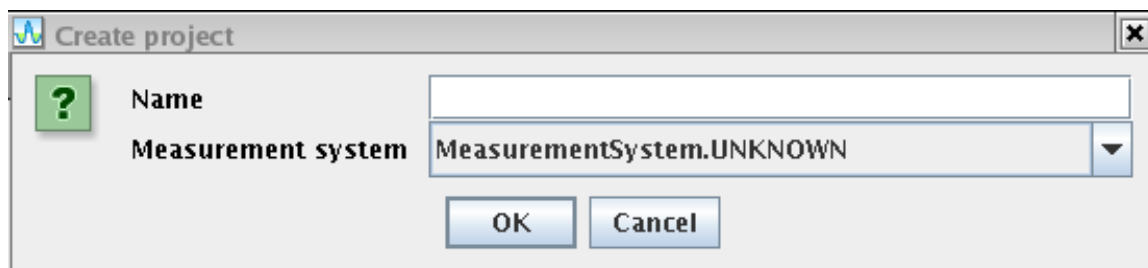
ProMAX® and SeisSpace® projects, subprojects, flows, tables and dataset names can have spaces, as well as mixed case, but are limited to 30 characters. Actual UNIX paths are all lower case, and where all of the blanks and certain other characters are removed.

ProMAX® database object naming has the same restrictions as the conventional ProMAX® system.

The length of the name can be controlled by setting the value of the parameter length entry in the PROWESS\_HOME/etc/prowess.properties file. The default is set to enforce the 30 character limit for backwards compatibility with the ProMAX® user interface. The alternative is to have unlimited length. For this property change to take effect you will need to exit from the Client, edit the prowess.properties file and then restart the client.

## Adding a new Projects and Subprojects (AREAs and LINEs)

You can add a new Project (or AREA) by placing the cursor on the project in the tree view and using the MB3--> New Project option.



Enter the new Project name and select the coordinate system for this project. Landmark recommends selecting UNKOWN for the coordinate system at this time.

The procedure for adding Subprojects (or lines) is identical.

## Properties for existing ProMAX® Projects

When you set up a "Data\_Home" in the Admin tool you were asked to enter information about the project, such as the path to the Data Home directory and required environment variables. These variables include the path to a config\_file and a scratch directory. You can review to the list of system environment variables and append environment variables for different users by using the Properties dialog. Select **MB3 > Properties** to display the dialog. This dialog may or may not be editable depending on

whether this is a shared or a private project and if you are logged in as an administrator or not.

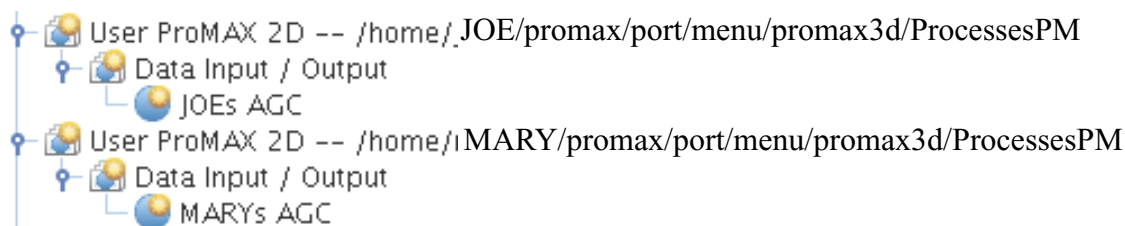
## Configuration for a ProMAX® development environment

In a standard development environment, a user's directory mirrors the path to the production directory. For example, if the ProMAX® software is installed in the directory `/apps/vendors/landmark/ProMAX` then the developer should have `~/apps/vendors/landmark/ProMAX` in the home directory. This mirror directory is usually created by the `$PROMAX_HOME/port/bin/Makeadvance` script.

Users would set the `MY_PROMAX_HOME` environment variable in the SSclient start script to access user menus, executables and documentation files.

### User Processes List

The ProMAX® development environment is slightly different in the SeisSpace® software relative to the ProMAX® software. The main difference is how the Processes list is handled. In the legacy ProMAX® development environment, the developer must maintain a Processes list that is the combination of the production Processes list delivered with the release and the developer's Processes list. In the SeisSpace® software, the developer need only maintain the list of developer processes. The SeisSpace® software appends the processes found in the developer's processes list to the production list under a new folder called the concatenation of the text `User ProMAX xx --` and the exact name of the processes file that it found and is displaying the contents of. You can specify multiple development environments to enable access to processes under development by a number of different users



This is enabled by setting an environment variable `MY_PROMAX_HOME` in your SSclient start up script to a multi-pathed list of development directories, where the entries are separated by a `" : "`. Each colon separated entry will be a separate folder at the top of the processes list.

```
MY_PROMAX_HOME=/home/JOE/promax:/home/MARY/promax
```

As a general rule, make sure that multiple developers do not use the same names for different processes. For example make sure that Joe does not have a process A that does scaling and Mary has a process A that does decon.

Given a multi-pathed MY\_PROMAX\_HOME as shown above and where promax(xxx) = promax3d for example:

### Search order for Processes List

All Processes lists found in all of the directory entries in MY\_PROMAX\_HOME plus the installation will be presented

```
/home/JOE/promax/port/menu/promax(xxx)/ProcessesPM  
/home/JOE/promax/port/menu/promax(xxx)Processes
```

and

```
/home/MARY/promax/port/menu/promax(xxx)/ProcessesPM  
/home/MARY/promax/port/menu/promax(xxx)Processes
```

and

```
$PROMAX_HOME/port/menu/promax(xxx)/ProcessesPM
```

and

```
$PROWESS_HOME/etc/flowbuilder/PROWESS.xml
```

### Search order for menus

If a valid absolute path is specified in the Processes list, it will be used, Otherwise, the system will search for an appropriately named menu in the following order:

```
/home/JOE/promax/port/menu/promax(xxx)
```

then

```
/home/MARY/promax/port/menu/promax(xxx)
```

then

```
$PROMAX_HOME/port/menu/promax(xxx)
```



### Search order for ProMAX® executables

/home/JOE/promax/sys/exe

then

/home/MARY/promax/sys/exe

then

\$PROMAX\_SYS\_EXE\_HOME first path

\$PROMAX\_SYS\_EXE\_HOME second path etc...

then

\$PROMAX\_HOME/sys/exe

### Search order for ProMAX® libraries

/home/JOE/promax/sys/lib/syslibs

/home/JOE/promax/sys/lib

then the second path in MY\_PROMAX\_HOME

/home/MARY/promax/sys/lib/syslibs

/home/MARY/promax/sys/lib

then the SeisSpace® and ProMAX® installations

\$PROWESS\_HOME/sys/linux(64)/lib

\$PROMAX\_HOME/sys/linux(64)/lib

\$PROMAX\_HOME/jre/lib

then the base system library directories

/lib

/usr/lib

/usr/local/lib

/syslibs

### Search order for documentation.

/home/JOE/promax/port/help/promax/toolname.pdf

then

/home/MARY/promax/port/help/promax/toolname.pdf

then

\$PROMAX\_HOME/port/help/promax/toolname.pdf

Help files for user developed modules may be prepared as pdf, html, text, or FrameMaker files with extensions of pdf, html, help, and lok

respectively. The \$PROMAX\_HOME/port/bin/PromaxHelp script is called to determine which application is started for the various different types of help files.

## Configuration for a SeisSpace development environment

In a standard development environment, a user's directory mirrors the path to the production directory. For example, if SeisSpace® is installed in the directory `/apps/vendors/landmark/SeisSpace` then the developer should have `~/apps/vendors/landmark/prowess` in the home directory. NOTE that the last directory is "prowess" and not "SeisSpace". this is different from the standard ProMAX® development environment. Users would set the MY\_PROWESS\_HOME environment variable in the SSclient start script to access user tools and documentation files.

### User Processes List

In the SeisSpace® software, the developer need only maintain the list of developer processes. The SeisSpace® software appends the processes found in the developer's processes list to the production list under a new folder called the concatenation of the text User SeisSpace -- xx and the exact name of the processes file that it found and is displaying the contents of. You can specify multiple development environments to enable access to processes under development by a number of different users



This is enabled by setting an environment variable MY\_PROWESS\_HOME in your SSclient start up script to a multi-pathed

list of development directories, where the entries are separated by a " : ". Each colon separated entry will be a separate folder at the top of the processes list.

```
MY_PROWESS_HOME=/home/JOE/prowess:/home/MARY/prowess
```

As a general rule, make sure that multiple developers do not use the same names for different processes. For example make sure that Joe does not have a process A that does scaling and Mary has a process A that does decon.

Given a multi-pathed MY\_PROWESS\_HOME as shown above:

### **Search order for Processes List**

All Processes lists found in all of the directory entries in MY\_PROWESS\_HOME plus the installation will be presented

```
/home/JOE/prowess/etc/flowbuilder/PROWESS.xml
```

and

```
/home/MARY/prowess/etc/flowbuilder/PROWESS.xml
```

and

```
$PROWESS_HOME/etc/flowbuilder/PROWESS.xml
```

### **Search order for menus**

The system will search for an appropriately named menu in the following order:

```
/home/JOE/prowess
```

then

```
/home/MARY/prowess
```

then

```
$PROWESS_HOME
```

### **Search order for executables and libraries**

```
/home/JOE/prowess
```

then

```
/home/MARY/prowes
```

```
then  
$PROWESS_HOME
```

### **Search order for documentation.**

```
/home/JOE/prowess/port/help/seisspace/toolname.pdf
```

```
then  
/home/MARY/prowess/port/help/seisspace/toolname.pdf
```

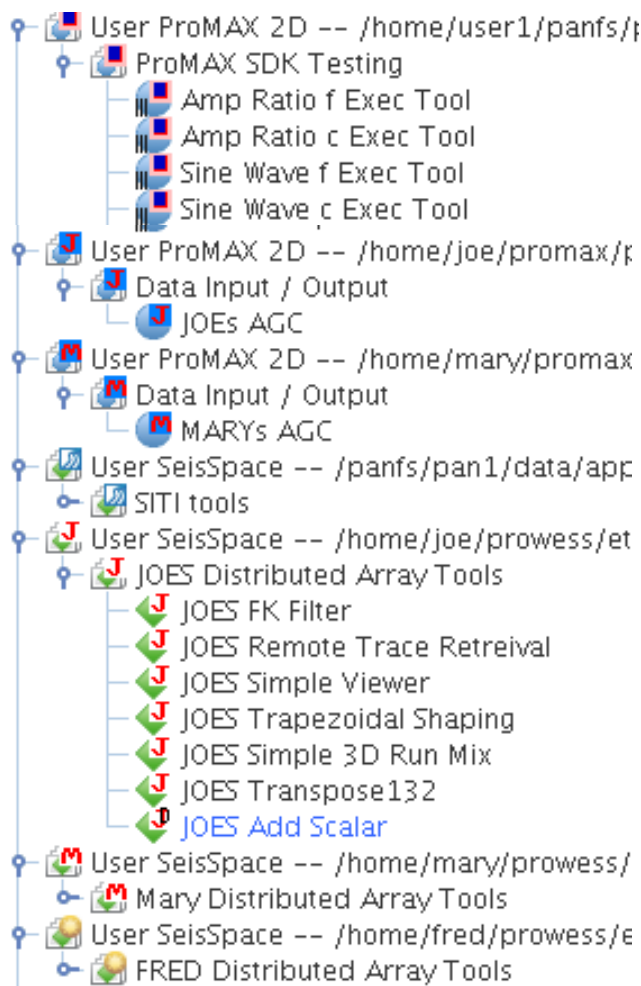
```
then  
$PROMAX_HOME/port/help/seisspace/toolname.pdf
```

Help files for user-developed modules may be prepared as pdf, html, text, or FrameMaker files with extensions of pdf, html, help, and lok respectively. The \$PROMAX\_HOME/port/bin/PromaxHelp script is called to determine which application is started for the various different types of help files. All help files delivered by Landmark are under the \$PROMAX\_HOME/port/help directory.

## **Using user-defined icons for user-defined processes**

You may find it useful to annotate the processes from different MY\_PROMAX\_HOME's and MY\_PROWESS\_HOME's with different icons so that you can tell which "library" of tools a particular tool came

from. The picture belows shows a variety of different source directories with different icons:



To achieve this you can add your user defined icon to your user defined MY\_PROMAX\_HOME and MY\_PROWESS\_HOME directories.

For the ProMAX® system, add a file called user\_tool.png (or gif) to the directory MY\_PROMAX\_HOME/port/menu/promax(xx)/user\_tool.png.

For SeisSpace, add a file called user\_tool.png (or gif) to the directory MY\_PROWESS\_HOME/etc/flowbuilder.

These icons should be 8x8 or a maximum of 10x10 and they will work better if they are "pastel" or low intensity colors so that the D (development) flag can appear on top of them if they are Development of Alpha testing status user tools.

You will need to restart the Navigator after adding or replacing these icons to see the changes.

### **Refreshing the processes lists**

The PROWESS.xml lists are cached to memory in the Flow Builder as they are read and used. You can refresh the cache by forcing a reread of the file by using MB3 > Refresh on the top level folder in the tree view of the processes list or click on the refresh icon on the icon bar of the processes list.

# SeisSpace® 3D Prestack Time Migration Workflows

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The following is the supported 3D Prestack Time Migration workflow:

The SS- prefix indicates that these are SeisSpace® processes that will appear green in the flow builder.

Build a SeisSpace® job to create gathers on velocity lines.

SS-JavaSeis Input --> SS-Specify CDP Bin Grid --> SS-JavaSeis Create (PSTM gathers)

SS-JavaSeis Input --> SS-Specify CDP Bin Grid --> SS-3D Prestack Kirchhoff Time Migration --> SS-JavaSeis Output (PSTM gathers)

Build jobs to perform NMO or RMO velocity analysis and generate a QC stack.

JavaSeis Input --> NMO (inverse) --> Supergather Select --> Disk Data Output

Disk Data Input --> PreCompute --> Disk Data Output

Disk Data Input --> Velocity Analysis with PD connection to VVE

VVE with PD connection to VA

JavaSeis Input --> NMO (inverse) --> NMO (forward) --> Stack3D --> JavaSeis Output

Run the full project PSTM to gathers jobs using the updated velocity fields from the NMO or RMO analysis step

JavaSeis Input --> SS-Specify CDP Bin Grid --> JavaSeis Create

JavaSeis Input --> SS-Specify CDP Bin Grid --> SS-3D Prestack Kirchhoff Time Migration --> JavaSeis Output

JavaSeis Input --> Stack3D --> Disk Data Output

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# Replicating Flows

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## Supported functionality

The following functionality for flow replication is supported:

- building template flows
- selecting parameters that change from one replica to another (limited to numeric values, strings and sort lists. Boolean values like Yes/No switches and multiple choice variables are not supported in this release).
- building a table of replacement parameter values
- creating replica flows with automatic dataset name generation
- managing the replication and job submit in a job status matrix
- chaining flows based on successful completion of pre-requisite flows

Flow replication values are stored in flat files in the Project and Template flow directories.

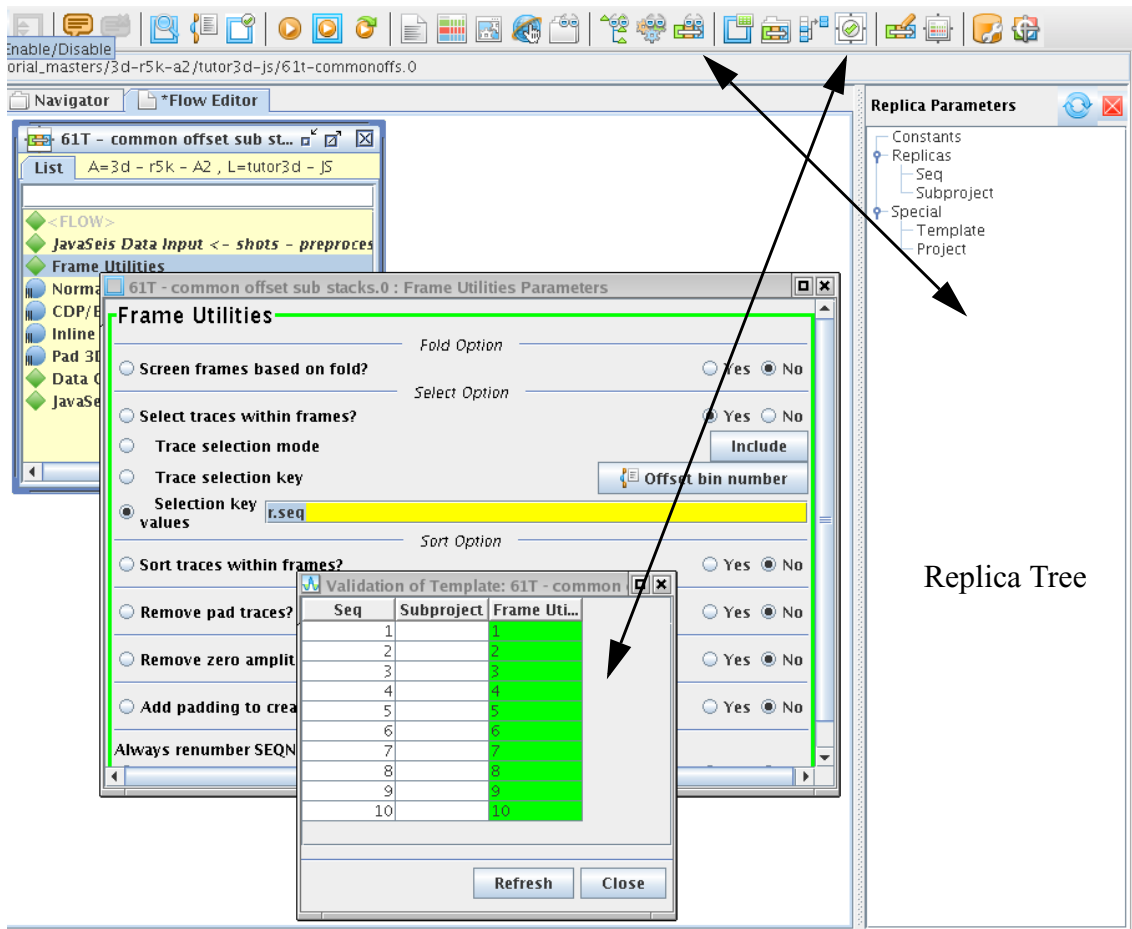
The flow replication attempts to keep the information in the flat files and the actual replica flow information synchronized. As you create and delete flows and datasets on disk, the corresponding information is also created and deleted in the flat files (as long as you do all creating and deleting in the SeisSpace® User Interface.)

We have attempted to keep this synchronization in place for a variety of things that users may decided to do, such as renaming templates or renaming lines, etc. We believe that many of these types of activities can be handled but recommend that you try to keep these actions to a minimum.

**Note:** The synchronization will not remain intact if you delete directories and/or files off of disk outside of the navigator. At this time, it is difficult to delete information in the flat files that is left stranded there by manually deleting information from disk.

## Flow Replication Components

Many of the Flow Replication components are shown below. These include a flow in template mode in the editor, a tree view of the columns in the replica table and a validation table. The other components, not shown here, are the replica table of replacement values, and the job status table.




Validation Table


The tree view of the contents of the replica table can be opened with the

**Replica Tree** icon. 

The validation table can be opened with the **Validate Template**

**Parameters (V)** icon. 

A general workflow is:

- Convert a flow to a template using the toggle icon. 
- Select the parameters in the flow that will change from job to job,
- Populate the replica table columns with the parameter values for each job,

- Set the values of the parameters in the template flow by select the replica table column heading names from the Replica Tree view pane of the Flow Editor,
- Validate that the replacement strings are correct, and
- Generate (build) and execute the replicated flows.

## Building Templates

A template is a flow that is used as a master to make copies from. The template flow is copied and the selected parameters are changed in each copy (or Replica). It is always a good idea to run the template flow as a test and make sure that the flow runs and generates the desired results given one set of replica parameters.

*Note:* When a Template flow is submitted, it will use the parameters behind the yellow boxed replacement strings. i.e. the value in the menu if the yellow replacement box is not there.

### Converting a flow to a template and back to a flow

In the flow editor, you can toggle the status of a flow between being a normal Flow and a Template using the **View > Templatize / Detemplatize Flow** pulldown menu, or the **Templatize or detemplatize flow**

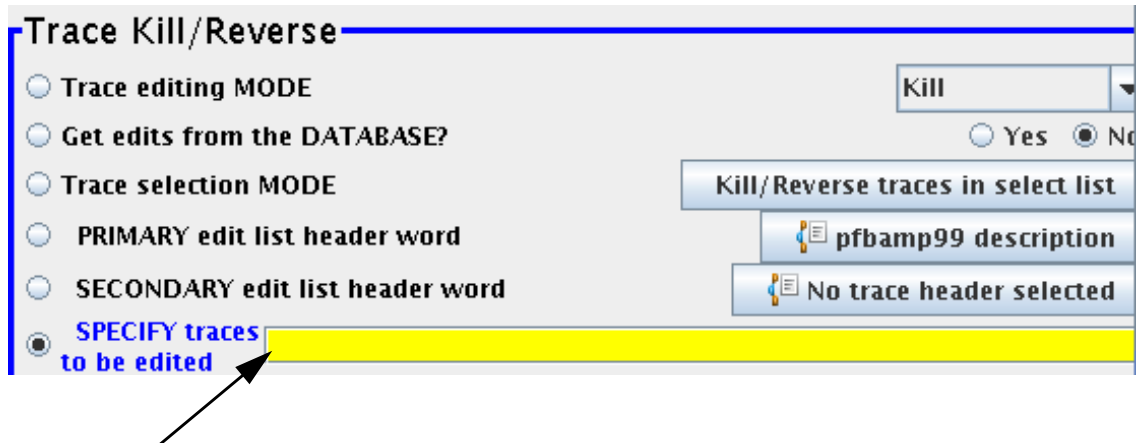


icon.

When you change a template back to a normal flow, all components of any previously created replica flows will be deleted and the template column will be deleted from the Replica Job Table.

## Selecting parameters to change from job to job

To select a parameter as one that will have its value changed from job to job, click on the circle next to the parameter name. A yellow box will replace the standard parameter input.



The screenshot shows a dialog box titled "Trace Kill/Reverse". It contains several radio button options:

- Trace editing MODE
- Get edits from the DATABASE?
- Trace selection MODE
- PRIMARY edit list header word
- SECONDARY edit list header word
- SPECIFY traces to be edited

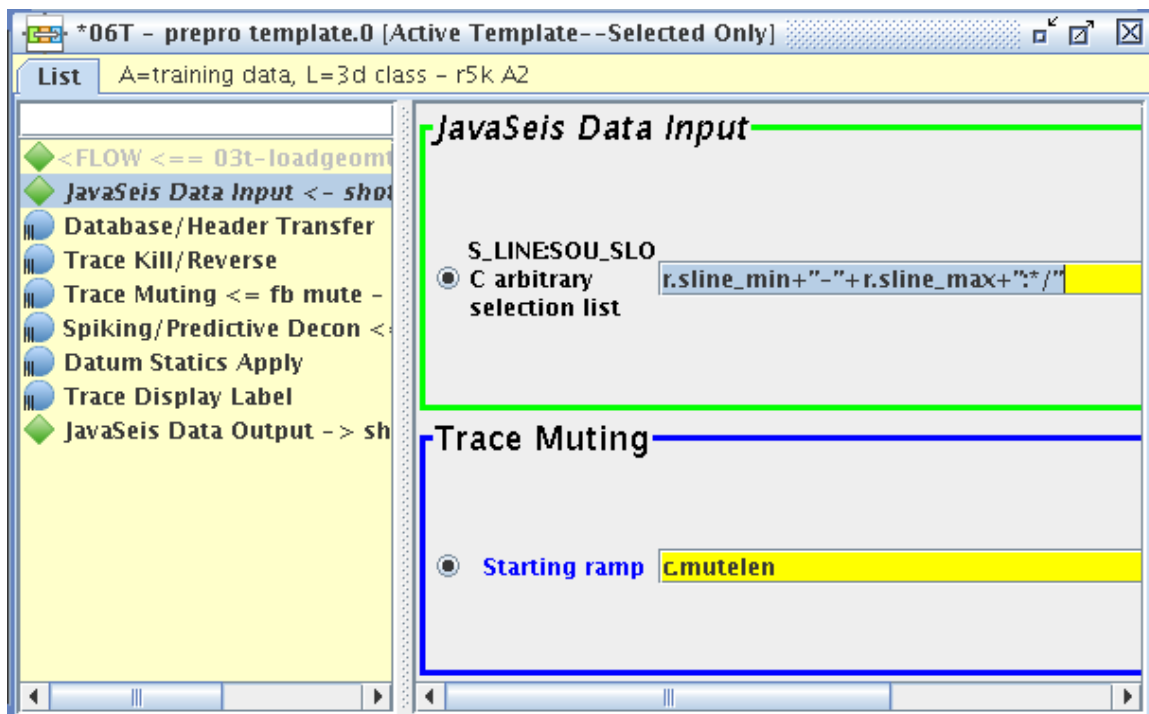
Next to the "SPECIFY traces to be edited" option, there is a yellow rectangular box. An arrow points to this box. To the right of the dialog, there are several buttons and a dropdown menu:

- A dropdown menu with "Kill" selected.
- Radio buttons for "Yes" and "No", with "No" selected.
- A button labeled "Kill/Reverse traces in select list".
- A button labeled "pfbamp99 description".
- A button labeled "No trace header selected".

Populate this yellow box with the values that will change by using a combination of text and column selections from the replica table spreadsheet. The replica table will be described in the next section.

To display only selected parameters in table view or in individual process dialogs, select **View > Toggle Show Selected Only** pulldown menu or the

**Toggle Show Selected Only** icon.




The first time you convert a flow to a template and set some replication parameters, you will need to save the flow. The flow will also be annotated

as a "Template" flow icon in the tree and table views.

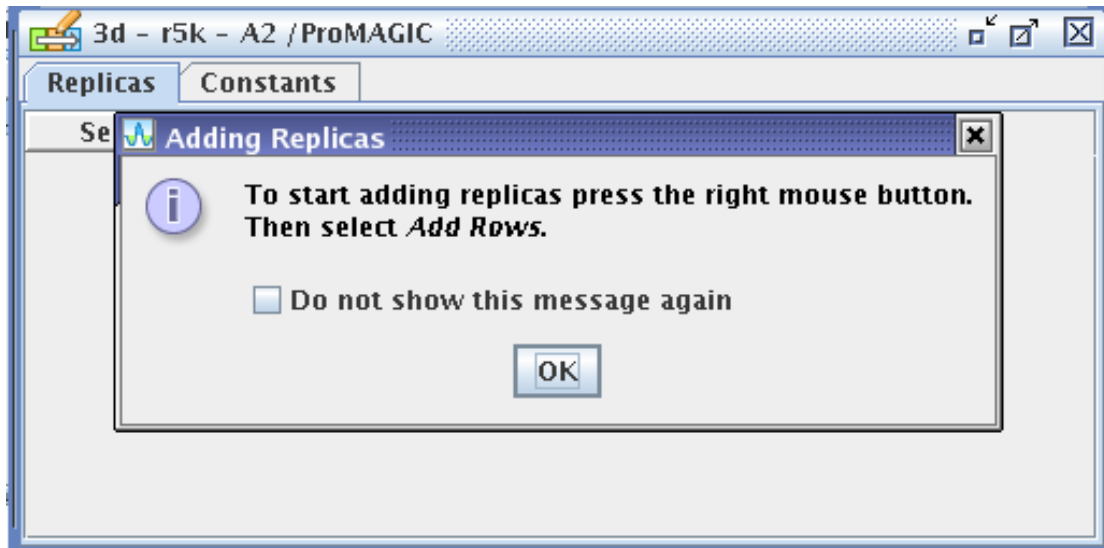


All of the replication information is saved with the flow. The folder icon in the tree and table views will revert back to a standard folder if the flow is no longer considered to be a template.

## Opening and Editing The Replica Table

To open a replica table for a line click the **Replica Editor** icon . If this is a new table, a new replica table containing no values is opened and you are prompted to add rows. Click **OK** to dismiss the window. The **R** icon is available when a Line level project, datasets, flows, or tables folder is selected in the Tree view or the table view or from the flow editor. **Note:** A different replica table exists for each line and you can have multiple

replica tables open at the same time. The replica table for the line that is active in the navigator or flow editor will be active in the replica editor tab.

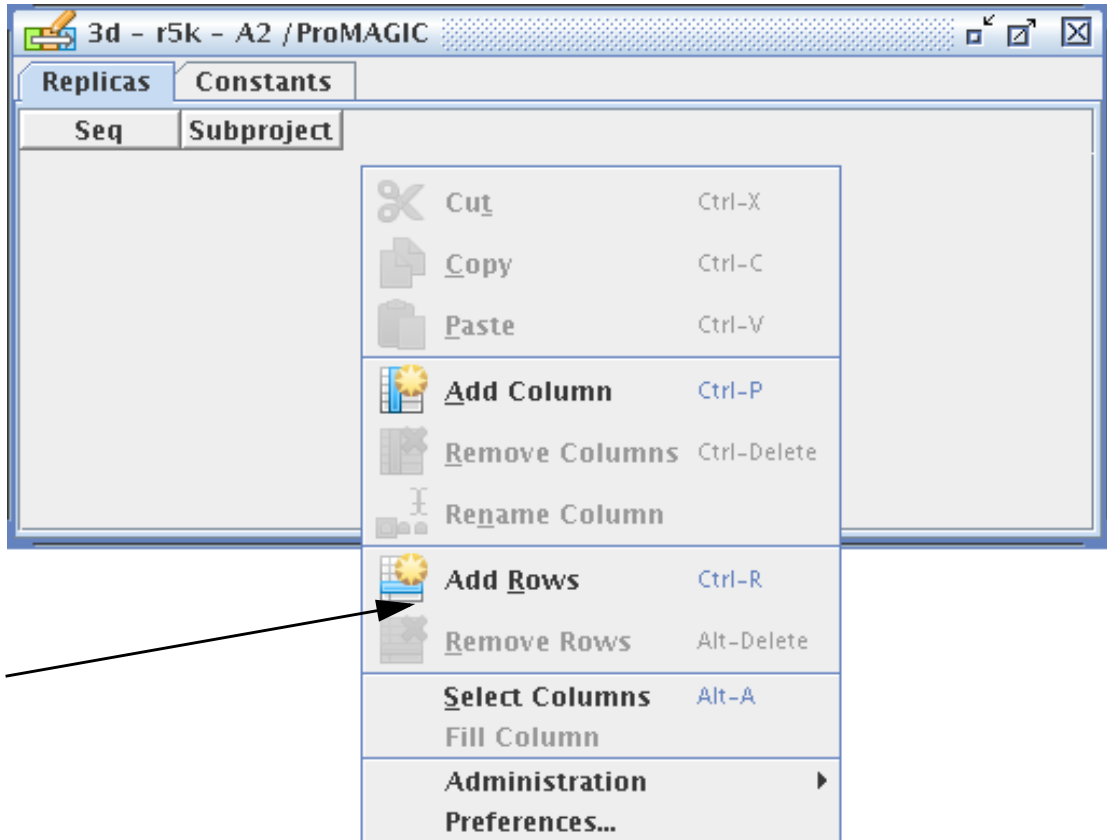


The replica table has two tabs: the Replicas tab and the Constants tab. The constants tab can be used to set values you want everyone to use all the time that differ from the menu defaults. Examples might include a specific ramp length for mutes or a specific stretch percentage value for NMO. The replica tab will be populated with the values that will change for the parameters you want to change from job to job.

The Subproject column is used for setting the names of the lines (or subprojects) for writing the replica flows to if you select that option in the Job Table tab. This is common for 2D work where you need to put the replicated flows in *different lines*.

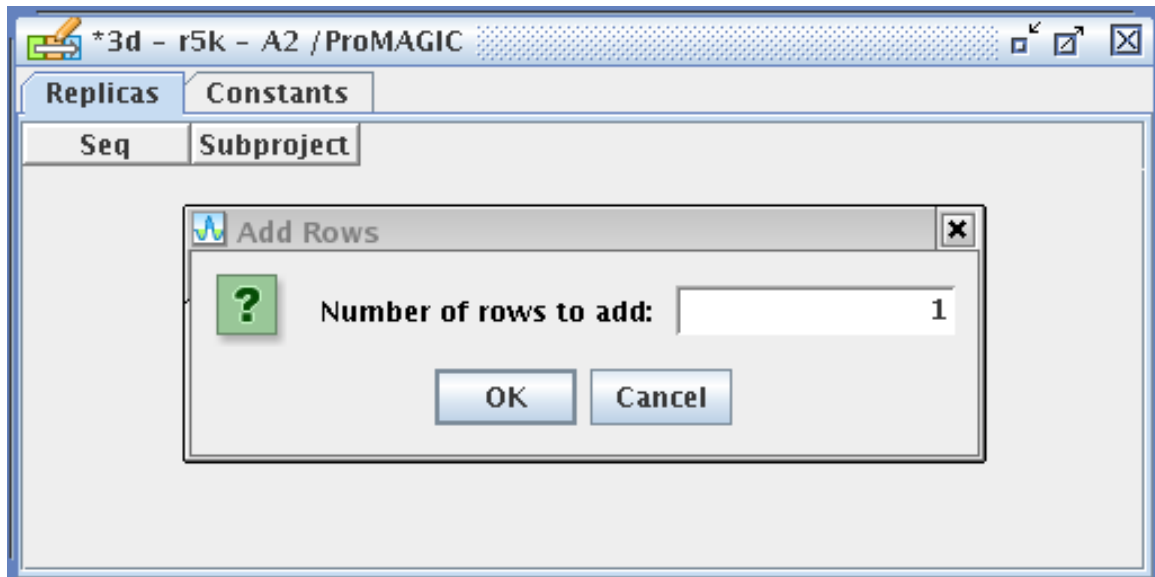
## Adding Rows and Columns

Use MB3 inside the empty replica table for the options menu.



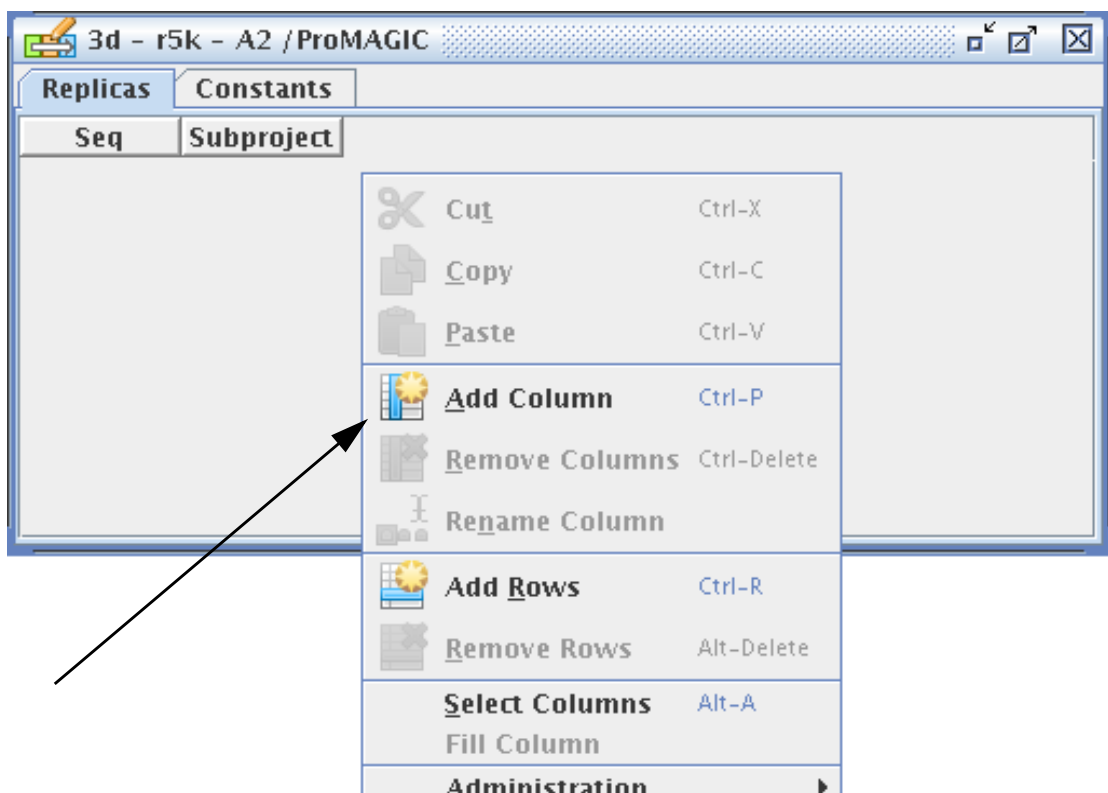
### Adding rows

Click **Add Rows** and enter a number of rows to add for your table.



## Adding Columns

Use MB3 to open the options menu and select **Add Column**.



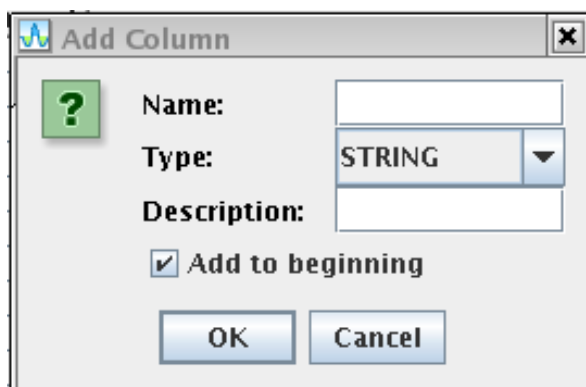


Enter the column name and type into the **Add Column** dialog. The name of the column may reflect the process and/or parameter that will have different values from job to job. Typical column names might be min\_shot, max\_shot, min\_cdp, max\_cdp. The three types are: **String**, **Integer** or **Float**. You can also add a text description of the column. You cannot change the data type of a column after it is created.

**Note:** The replica table will allow you to use column names with blank spaces, but it may help with formatting later to avoid using blanks. For example:

instead of using a name like: line min

use a name like: line\_min or min\_line



You can add the column to the left side or right side of the table. The default is set to add new columns to the left. This means that the older columns will be pushed off the right side of the display as time progresses and as you add more and more columns.

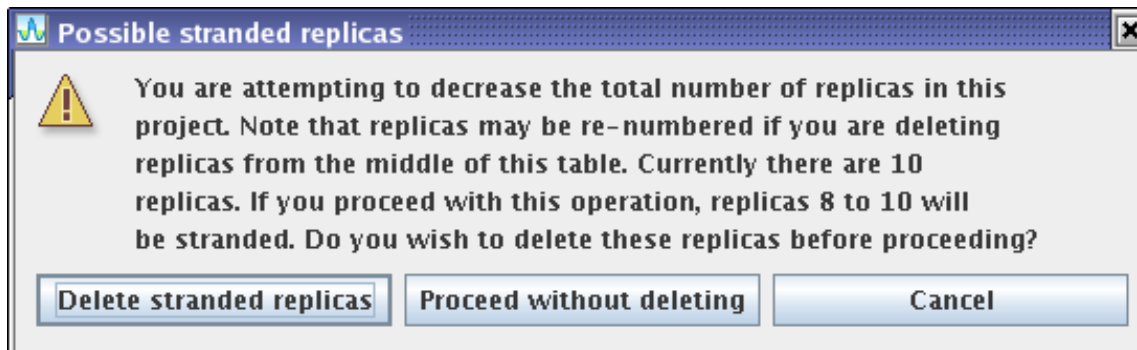
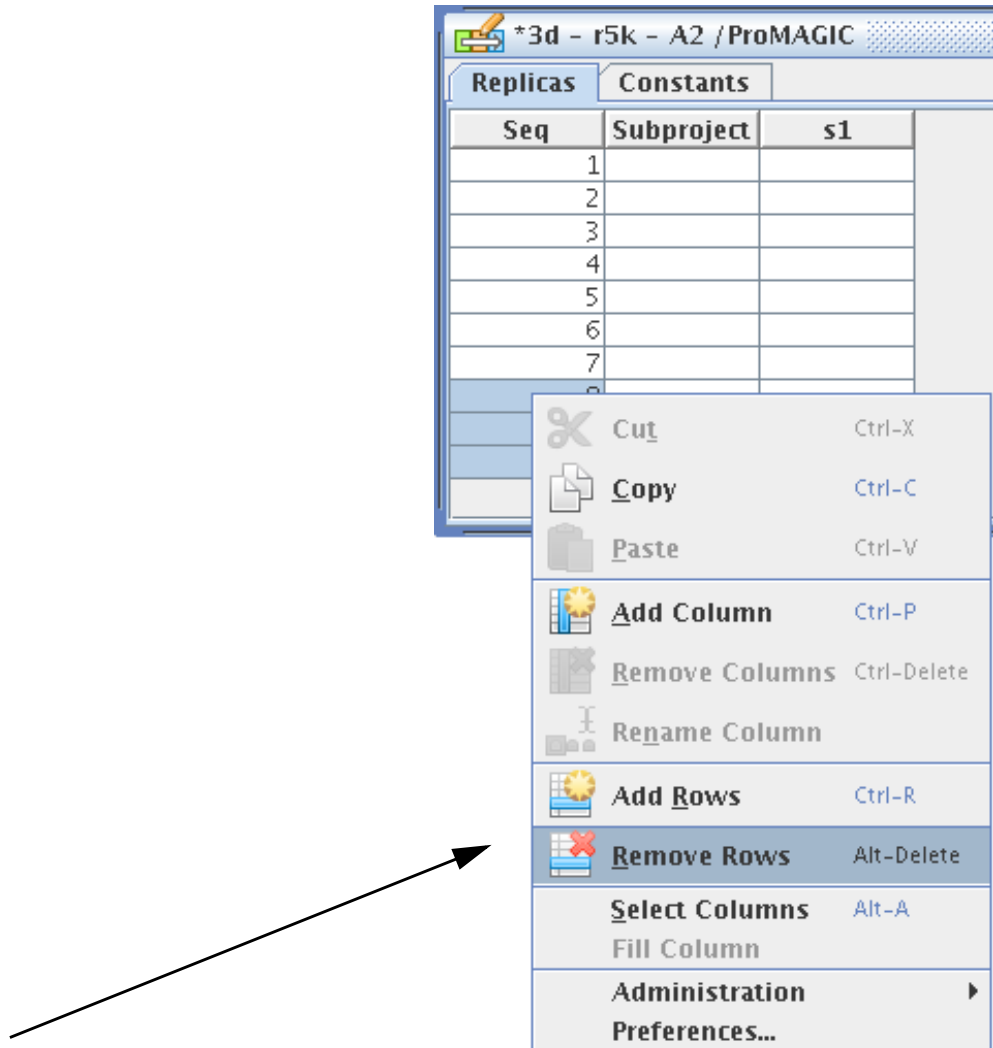
## Deleting Rows and Columns

### Deleting rows

Select some cells in the rows that you want to remove and then choose the **Remove Rows** option from the MB3 menu or use the Icons to delete the



rows in the replica table spreadsheet.



When you delete rows you are prompted for a response on what to do with Replica flows that may have been built against these rows for some templates.

## Delete stranded replicas

Delete any replica flows for these sequence numbers when you delete the rows. In general, to make sure that there are no replica flow files left over on disk, this option should be selected.

## Proceed without deleting


Delete the rows but do not delete any replica flows that may exist for any template for these rows. The replica flow files will remain on disk but will become "stranded" and will not be presented in the Replica Job Table.

## Cancel

Cancel the row delete operation and do nothing.

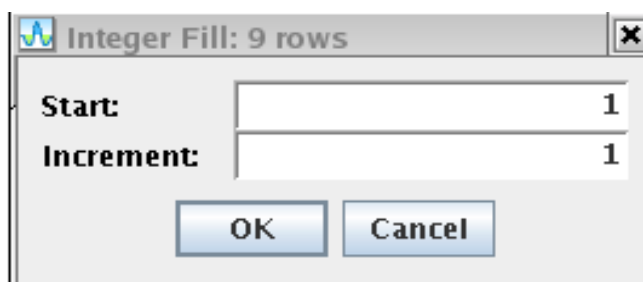
## Deleting Columns

Select some cells in the column that you want to remove and then choose the **Remove Columns** option from the MB3 menu or use the Icons to delete the columns in the replica table

spreadsheet. 

## Populating Integer or Float Columns

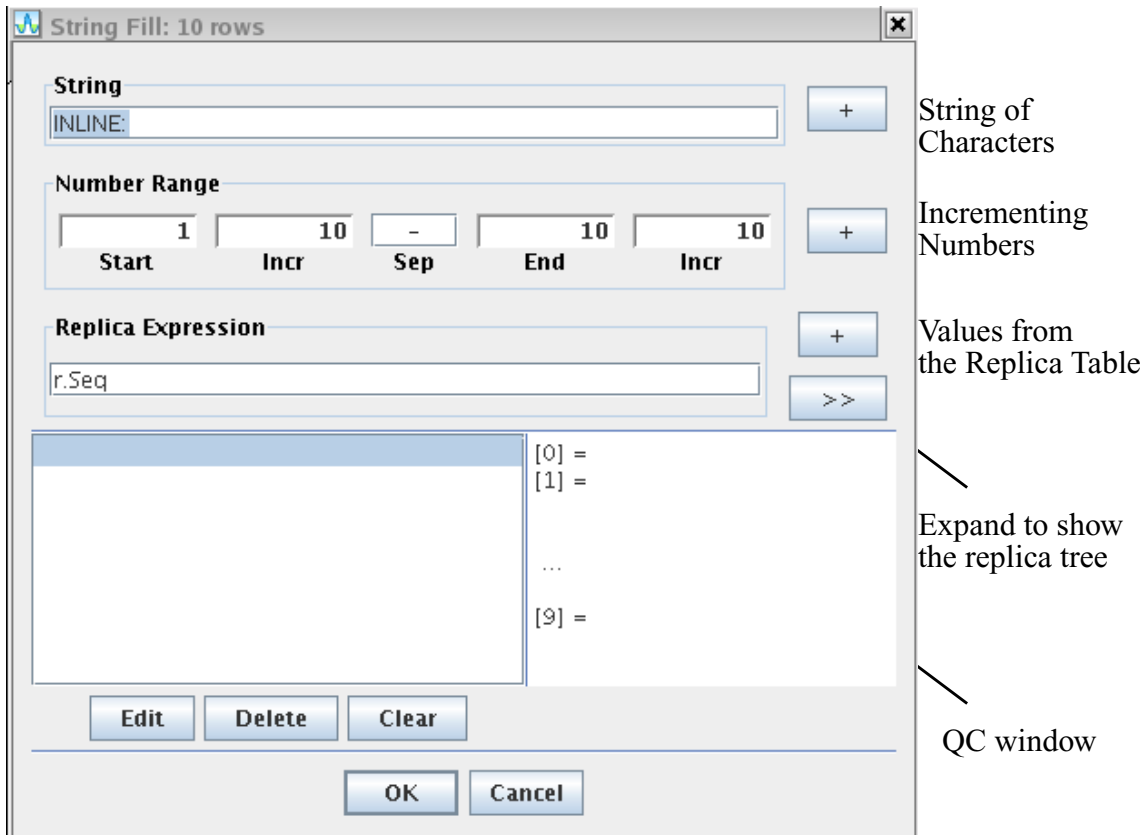
Enter a starting value and increment into the **Fill Column** dialog. Starting values can be either integer or floating point.



## Populating String Columns

The **Fill Column** dialog allows you to build an expression based on text constants, numerical sequences and other values in the replica table. You can use the >> and << icons to toggle the tree view on and off where you can choose to use values that exist in the replica table.

There are three ways that you can add in text or numerical sequences to build the strings that you want to populate the column with: String of Characters, Incrementing Numbers and Values from the Replica Table.



The best way to learn to use this tool is to experiment with adding in string, numeric and replica table values and watch the way the strings build up in the QC window.

Add expressions to the final string by using the + icons.

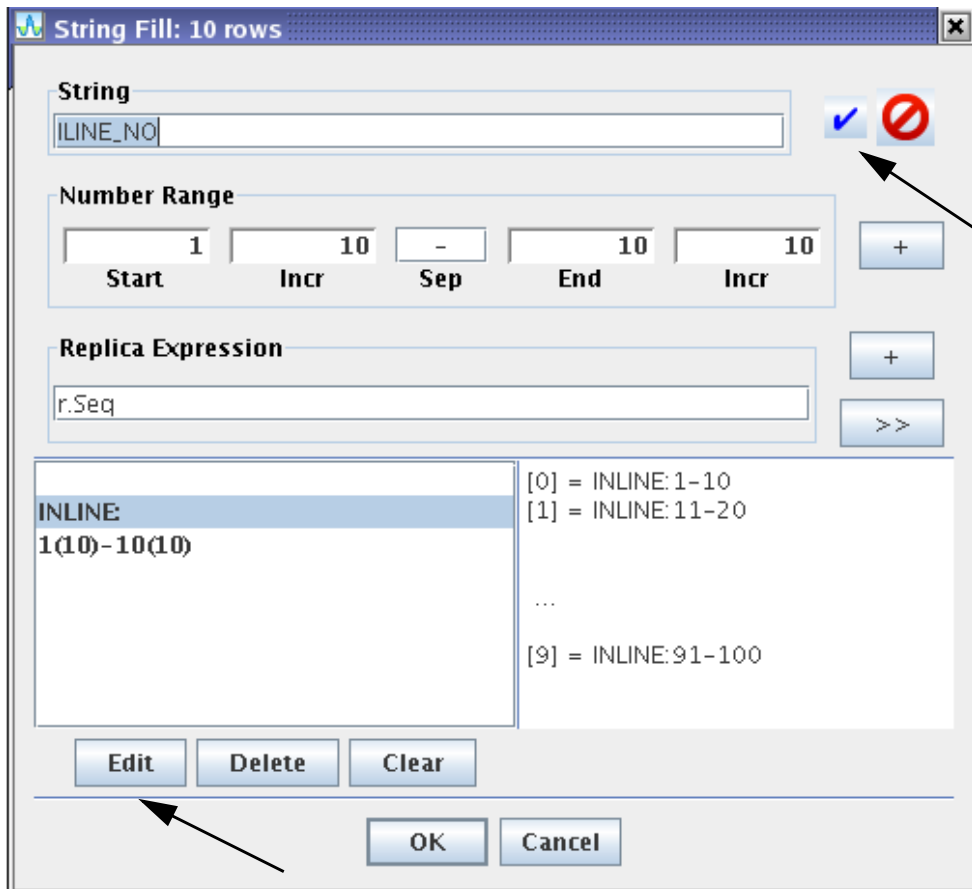
You can Edit, Delete, or Clear values and arrange the text and numerical sequences.

Select **OK** to fill the cells with the current strings and close the fill window.

Select **Apply** to fill the cells with the current strings.

Select **Cancel** to cancel the fill operation.

If you want to edit an existing entry, you will find that there is a check mark and an X next to it. You can accept your changes using the check mark and abort the edit with the X.



## Populating the Constants Table

The Constants Table is a single value per variable.

Name	Value	Descripti...
mutelen	24	mute length

Give the constant a Name and a value and an optional description. For example: you may choose a constant name of mutelen and a value of 24 with a description of "mute length".

## Saving the Replica Table

The Replica Table is stored in a flat file. You are required to Save the contents of the Replica Table manually. An "\*" will appear in the title bar of a replica table pane if un-saved edits exist in the table.

## Special replica table syntax for some parameters

Some parameters requires special syntax for the replacement strings. These include multiple choose and pop-choose parameters.

For choose parameters such as pop choose and circular choose

Type in the descriptive name of choice presented in menu. Case and whitespace are ignored. For example:

If the choices are:

"RMS", "Mean", "Median" or "Time variant"

Then to choose "RMS" any of these specifications are equivalent:

RMS , rms or rmS

To choose "Time variant" any of these specifications are equivalent:

Time Variant , TimeVariant or Time variant

For Multiple choose parameter: (such as the attribute to choose in Trace Statistics)

This is the same as single choose except that you specify multiple choices delimited by one or more space. If you want to specify a choice that has embedded blanks you need to quote it with a ^. Note that we use a ^ instead of a double quote. For example, if the choices are the same as above.

Then to choose "RMS", "Median", and "Time variant", any of these specifications are equivalent:

Rms Median timevariant

median RMS ^time variant^

^Time Variant^ Median RMS

For Boolean parameters. Like the others, case is ignored.

To choose "Yes", specify:

Yes or true

To choose "No", specify:

No or false

## Choosing Replica Parameters in the Template Editor

After you have chosen which parameters will change from job to job and have populated the replica table, you need to tell the template which parameters to use. This is all accomplished in the Flow Editor tab.

The screenshot shows the Flow Editor interface with the 'Replica Parameters' tab selected. The main window displays the 'JavaSeis Data Input' and 'Trace Muting' sections. The 'C arbitrary selection list' is highlighted in yellow with the value 'r.sline\_min+\"-\"+r.sline\_max+\"\*/\"'. The 'Starting ramp' is also highlighted in yellow with the value 'c.mutelen'. A 'Validation of Template' dialog box is open in the foreground, showing a table of replica parameters.

Seq	Subproject	JavaSeis ...	Trace Mut...
1		1-16 */	24
2		17-32 */	24
3		33-48 */	24
4		49-64 */	24
5		65-80 */	24
6		81-96 */	24
7		97-112 */	24
8		113-128 */	24
9		129-144 */	24
10		145-154 */	24

This example shows that two process parameters have been selected to change from job to job. One "yellow box" is populated with a combination of text and replica values or constants. The other is a constant.

You can drag and drop the replica table column names into the template from the tree view. To enable the tree view click on the Replica Tree



icon.

Click **Refresh** on the Validation table to verify the changes and then check the value that will be used for each flow replica to be built.

## Naming Conventions

Replacement values have the following naming conventions:

c.xxxxxx is a constant

r.xxxxxx is a replica table column

s.xxxxxx have the template name and project name available

Add additional text by including it in double quotes and + signs as separators.

Selections are concatenated together with + signs. For example, a Replica Table with columns of **min\_line** and **max\_line**, can be used to name the output data files based on a line range. The the following string can be used for the output naming convention:

"output" + r.min\_line + "-" + r.max\_line

This creates the following output dataset names:

```
output1-10
output11-20
...
output91-100
```

## Reading data from other Area / Line's in DDI

There is a special case for setting up a series of replicated flows where the input step in each flow will read a different dataset from a series of different Area / Lines. To build the input string to handle this case build a string in the Disk Data Input - Select Dataset parameter that has the Area Line and Dataset information separated by the "pipe" or "|" symbol. For example:

If you have a series of datasets called Data under a series of different lines under the same area,

```
AREA
    / Line1 ----> Data
    / Line2 ----> Data
```



```

/ Line3 ----> Data
.....
/ Linen ----> Data

```

you can build a template in a different line to read these datasets by specifying the string "AREA "|" + "Line"+r.seq +"|" + "Data". Make sure that you don't have any extra blank spaces around the pipe symbols.

**Select dataset**      "AREA "|" + "Line"+r.seq +"|" + "Data"

Propagate input

Trace read option

Read the data from

Process trace header

Override input data

---

**-Disk Data Output**

Seq	Subproject	DISKREAD2:1
1		AREA  Line1 Data
2		AREA  Line2 Data
3		AREA  Line3 Data
4		AREA  Line4 Data
5		AREA  Line5 Data
6		AREA  Line6 Data
7		AREA  Line7 Data
8		AREA  Line8 Data
9		AREA  Line9 Data
10		AREA  Line10 Data

## Template Editor and String Validation Table

The validation table can be opened with the **Validation Table** icon.



If you select a cell or series of cells in the replica table, that parameter in the flow editor where it will be outlined in a white box.

The screenshot shows the SeisSpace interface with a flow editor and a validation table. The flow editor has two sections: 'JavaSeis Data Input' and 'Trace Muting'. The 'JavaSeis Data Input' section has a radio button for 'C arbitrary selection list' and a text field containing 'r.sline\_min+"-"+r.sline\_max+'. The 'Trace Muting' section has a radio button for 'Starting ramp' and a text field containing 'Emutelen'. The validation table has columns for Seq, Subproject, JavaSeis, and Trace Mut... with rows 1-10. The 'Trace Mut...' column is highlighted in green. Arrows point from the table to the flow editor.

Seq	Subproject	JavaSeis ...	Trace Mut...
1		1-16:*/	24
2		17-32:*/	24
3		33-48:*/	24
4		49-64:*/	24
5		65-80:*/	24
6		81-96:*/	24
7		97-112:*/	24
8		113-128:*/	24
9		129-144:*/	24
10		145-154:*/	24

## Build and Submit jobs using the Replica Job Table

### Replica Job Table Overview

The **Replica Job Table** is used to build, submit and monitor replicated flows. Open the Replica Job Table by clicking on the **Replica jobs**

icon. 

If no templates exists, the table is initialized with two columns: the sequence number and the subproject columns. The subproject is blank if you did not populate it in the Replica Table.


Idi training prep/restore try LIN prob 1

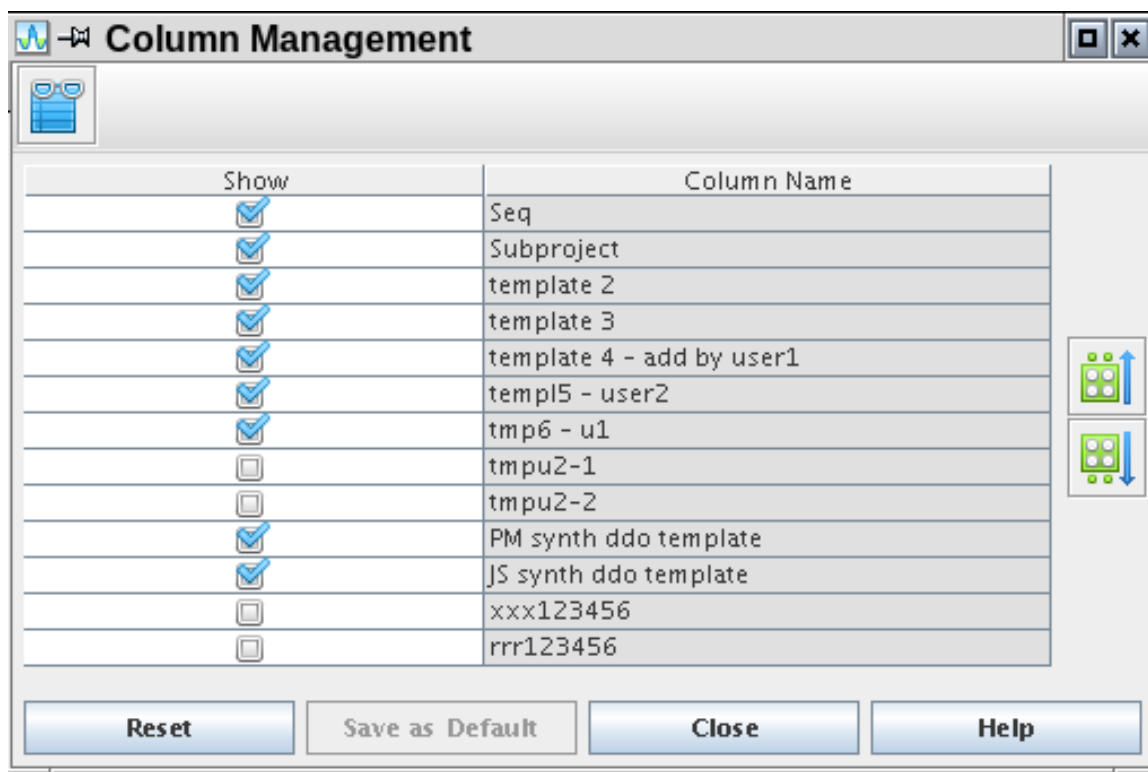
Job View: Job Status

Seq ▲	Subproject	10051a-shot rtm re...	10051c - Idi hy...	10051d= Idi hybrid ...
1		▶ Running	✓ Completed	⊘ User Terminated
2		⚠ Failed	✓ Completed	⊘ User Terminated
3		⚠ Failed	✓ Completed	⊘ User Terminated
4		⊘ User Terminated	✓ Completed	⊘ User Terminated
5		▶ Running	✓ Completed	⊘ User Terminated
6		⚠ Failed	✓ Completed	⊘ User Terminated
7		⚠ Failed	✓ Completed	⊘ User Terminated
8		⚠ Failed	✓ Completed	⊘ User Terminated
9		▶ Running	✓ Completed	⊘ User Terminated
10		⊘ User Terminated	✓ Completed	⊘ User Terminated
11		⊘ User Terminated	✓ Completed	⊘ User Terminated
12		▶ Running	✓ Completed	⊘ User Terminated
13		⚠ Failed	? Unknown	⊘ User Terminated
14		? Unknown	? Unknown	⊘ User Terminated
15		? Unknown	? Unknown	? Unknown
16		? Unknown	? Unknown	? Unknown
17		? Unknown	? Unknown	? Unknown
18		? Unknown	? Unknown	? Unknown
19		? Unknown	? Unknown	? Unknown

Any Active Template will appear as a column in the Job Table after you convert a flow to a template and save it. You do not need to save it every time you change it while it is in the editor to validate the replica parameters or make replicas from it. The validation table and job table use the information in memory related to the template in the flow editor. However, you need to save the template when you are finished with it to save all of the processes, parameters, and replication parameters. You will also find that you need to save the template if you change the chaining pre-cursor specifications.

You can remove a template from the job status table by either unchecking it

in the column selector which is activated by the  icon and presents a dialog box to choose the columns to display



or by "de-templating" the flow by clicking on the **Templatize or**

**detemplatize the flow** icon.



**Note:** Replication substitution parameters and equations are saved with the flow.

- Share this Project

This option determines where the replicas will be built. If this option is checked "ON", then the replicas are build for use in the same subproject (or LINE) as the template. If this option is not checked or "OFF" then the replicas are written to and build for use in the associated subproject. (Common for multiple 2D line work)

- Autoscroll Table

When you select a long list of flows to built, or build and submit, the

RJT can be set to autoscroll as the flows are being built or submitted. The default behavior is to not scroll the list.

There are two views of the data stored for the Replicas, The standard Replica Job Table and the Sideways-Replica Job Table. (RJT and S-RJT). In the RJT you can choose a single attribute of the jobs to display. In the S-RJT you can choose to display all attributes of the replicas for multiple templates in separate tables.

There are many different attributes you can choose to display for the replicas in the Job Table:

<b>Job Status</b>
<b>Percent Complete</b>
<b>Input Rate</b>
<b>Traces Input</b>
<b>Hostname</b>
<b>Desc Name</b>
<b>Reqid</b>
<b>Queue</b>
<b>Username</b>
<b>Replica Version</b>
<b>Submitted Time</b>
<b>Initialized Time</b>
<b>Finished Time</b>
<b>Time Running</b>

The S-RJT can be activated by selecting cells in the RJT and then clicking

on the **Detailed View** icon.  to start the S-RJT.

A separate table will be presented for each template selected.

Idi training prep/restore try LIN prob 1

Job View: Job Status

Seq	Subproject	10051a-shot rtm re...	10051c - Idi hy...	10051d=Idi hybrid ...	10051 - Shot RTM
1		Failed	Completed	User Terminated	Unknown
2		Failed	Completed	User Terminated	Unknown
3		Failed	Completed	User Terminated	Unknown
4		User Terminated	Completed	User Terminated	Unknown
5		Running	Completed	User Terminated	Unknown
6		Failed	Completed	User Terminated	Unknown
7		Failed	Completed	User Terminated	Unknown
8		Failed	Completed	User Terminated	Unknown
9		Running	Completed	User Terminated	Unknown
10		User Terminated	Completed	User Terminated	Unknown
11		User Terminated	Completed	User Terminated	Unknown
12		Running	Completed	User Terminated	Unknown
13		Failed	Unknown	User Terminated	Unknown
14		Unknown	Unknown	User Terminated	Unknown

Idi training prep/restore try LIN prob 1 10051a-shot rtm reg shots

S...	Job Status	Percent Compl...	Input Rate	Traces Input	Hostname	Desc Name
1	Failed	100.0%	0.0010 MB/s	32,078	q03	10051a-sho00
2	Failed	100.0%	0.0014 MB/s	43,137	q18	10051a-sho00
3	Failed	100.0%	0.0014 MB/s	42,139	q21	10051a-sho00
4	User Termin...	100.0%	0.0010 MB/s	32,237	q10	10051a-sho00
5	Running	100.0%	0.0010 MB/s	32,601	q04	10051a-sho00
6	Failed	100.0%	0.0014 MB/s	42,750	q19	10051a-sho00
7	Failed	100.0%	0.0010 MB/s	31,467	q08	10051a-sho00
8	Failed	100.0%	0.0011 MB/s	33,004	q01	10051a-sho00
9	Running	100.0%	0.0011 MB/s	33,692	q02	10051a-sho00
10	User Termin...	100.0%	0.0010 MB/s	32,271	q12	10051a-sho00
11	User Termin...	100.0%	0.0011 MB/s	32,963	q11	10051a-sho00
12	Running	100.0%	9.9E-4 MB/s	31,126	q06	10051a-sho00
13	Failed	100.0%	0.0013 MB/s	40,759	q24	10051a-sho00
14	Unknown	0%	0 MB/s	0		
15	Unknown	0%	0 MB/s	0		
16	Unknown	0%	0 MB/s	0		

S-RJT

There are many different values for the **Job Status** attribute. The different possible values are color coded as shown below:

- Unknown - Job status unknown - info not in sitemanager and/or jobs.stat file is not found

Unknown

- Build Pending - has been selected to be build and/or submitted, Operation in progress

Build Pending

- Built -Replica flow has been built

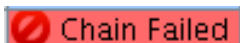
Built

- Build Failed - the build of the replica failed - usually related to a problem in the replacement strings in the template - Go back to the

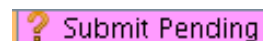
flow builder and use the Validation procedure to resolve the replacement string problem

 Build Failed

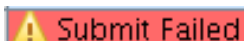
- Chain Failed - The precursor to this job failed - so the chaining was stopped. This job may still be OK.

 Chain Failed

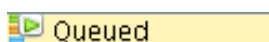
- Submit Pending - has been chosen for build/submit operation and the operation is in progress

 Submit Pending

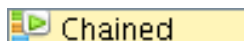
- Submit Failed - The precursor to this job is probably in an Unknown state - so the chaining was stopped. This job may still be OK.

 Submit Failed


- Queued - Job is in the Queue

 Queued

- Chained - job is waiting to be submitted pending completion of its precursor flows

 Chained

- Initializing - job has released from the Q and is in the initialization phase

 Initializing

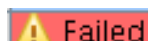
- Running - job has released from the Q and is in the running phase

 Running

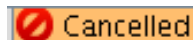
- Completed - Job has completed normally

 Completed

- Failed - Job failed - any jobs that were chained to this flow will now show Chain Failed

 Failed

- Cancelled - Job was cancelled either from a Queued or Chained state

 Cancelled

- User Terminated - Job was terminated by the user after it was in either Initialized or Running state

 User Terminated


•

If you replicated into other lines (un-checking Share this Project) then there will be a folder icon to the left of each of the above indicating that these flows are being built in another line.

All tables except the **Job Status** table show the job status only as a color code with accompanying icon but shows the alternate information.

## Building jobs

To build jobs, select cells in the Job table by "painting" them while holding

down MB1 and then select the **Build a Replica Flow** icon.  You can also use the MB3 - Build from the options menu.

You can watch the job building status in the xterm console that was used to start the Navigator and watch the cell status change. The Build Pending status indicates that the cell was selected to be built but the building process has not progressed to that point yet.

You can use the Stop icon to stop the build, build and submit or submit procedures.

To refresh the contents of the Replica Job Table, click on the **Refresh**

icon .

You will also notice that Replica Flows are visible in the navigator in the table view when a Template flow is selected in the tree.

The replicated flows have two different names, the DescName (or descriptive name that you normally address the flows by plus the actual disk directory name where the packet file and job.outputs are stored.

## Flow Replication Information Storage

All data associated with flow replication are stored in flat files in the \$PROMAX\_DATA\_HOME/AREA/LINE and \$PROMAX\_DATA\_HOME/AREA/LINE/FLOW directories

LINE/

replicaParms.txt

tab-delimited file with replica parameters--editable in Excel; can be a symbolic link

replicaParms.txt~

a backup that is generated whenever a replicaParms.txt file is successfully loaded

replicaPrefs.xml

some constants stored about the replica table such as column width and display order

LINE/FLOW (template flow)

exec.#.pwflow ---

exec.#.log |files associated with the template itself



```
exec.#.qsh          |There may be multiple versions depending
exec.#.qerr         |on how many times the template was run to test it
packet.#.job ---

jobs.stat    ---   This file is not used at this time but contains
                  the status of the main flow

exec.r#.#.pwflow  --- files associated with each replica flow
exec.r#.#.log     | The first # after the r is the sequence number
exec.r#.#.qsh    --- The second # is the replica instance number

replicas.#.stat  --- a binary file that contains all of the job status
                  information replicas of a particular version

replicasInfo.xml --- a simple XML file that indicates that the flow
                  is a template. This file also stores the user defined
                  descriptive names of the replica flows for this
                  template
```

The general methodology follows the idea that it is possible that some of the replicas will need to be rerun or rebuilt and rerun for a variety of different reasons. After you either rerun or rebuild/rerun some of the replicas you will see multiple versions of the flow, printout and qsh files for each instance of the replica and multiple replica#.stat files. In the following example replicas 1 and 2 have been built and run 4 times, replicas 3 and 4 have been run 3 times etc....

```
$ ls exec.r1.*
    exec.r1.2.log exec.r1.2.pwflow exec.r1.2.qsh exec.r1.3.log
exec.r1.3.pwflow exec.r1.3.qsh

$ ls exec.r2.*
    exec.r2.2.log exec.r2.2.pwflow exec.r2.2.qsh exec.r2.3.log
exec.r2.3.pwflow exec.r2.3.qsh

$ ls exec.r3.*
    exec.r3.1.log exec.r3.1.pwflow exec.r3.1.qsh exec.r3.2.log
exec.r3.2.pwflow exec.r3.2.qsh

$ ls exec.r4.*
    exec.r4.1.log exec.r4.1.pwflow exec.r4.1.qsh exec.r4.2.log
exec.r4.2.pwflow exec.r4.2.qsh

$ ls exec.r5.*
    exec.r5.0.log exec.r5.0.pwflow exec.r5.0.qsh exec.r5.1.log
exec.r5.1.pwflow exec.r5.1.qsh

$ ls exec.r6.*
    exec.r6.0.log exec.r6.0.pwflow exec.r6.0.qsh exec.r6.1.log
exec.r6.1.pwflow exec.r6.1.qsh

$ ls exec.r7.*
```

```

exec.r7.0.log exec.r7.0.pwflow exec.r7.0.qsh

$ ls exec.r8.*
  exec.r8.0.log exec.r8.0.pwflow exec.r8.0.qsh

$ ls exec.r9.*
  exec.r9.0.log exec.r9.0.pwflow exec.r9.0.qsh

$ ls exec.r10.*
  exec.r10.0.log exec.r10.0.pwflow exec.r10.0.qsh

$ ls -al *stat*
-rw-rw-rw- 1 user1  users          312 Jun  1 10:52 jobs.stat
-rw-rw-rw- 1 user1  users        1716 Jun  1 10:33 replicas.0.stat
-rw-rw-rw- 1 user1  users          936 Jun  1 10:40 replicas.1.stat
-rw-rw-rw- 1 user1  users          624 Jun  1 10:44 replicas.2.stat
-rw-rw-rw- 1 user1  users          312 Jun  1 10:58 replicas.3.stat

```

Notice that the earlier numbered replicas such as 1 and 2 have instance numbers 2 and 3 where as replica numbers 3 and 4 have instance numbers 1 and 2. There is a preference setting that can be used to put a limit on the number of versions of replicas to keep. In this case the preference was set to keep and automatically purge to 2 versions of the replica flows. The two most recent are retained.

The job status information for all of these versions is stored in the different replicas.#.stat files. The status that is shown in the RJT (Replica Job Table) will be the status of the flow in the matching numbered stat file. The replica.3.stat file will only have information for those flows that had a 3rd instance. The stat files contain the Job status such as Complete, Failed, User Terminated. The "Built" and "Unknown" status' are not stored. A flow is marked as Built if there is no known status for it in the matching stat file and the flow files exist on disk. If multiple versions of replicated flows exist, the status that will be shown is the status in the stat file of the highest numbered replica.

```

sequence number
                1 1 1 1 1
1 2 3 4 5 6 7 8 9 0 1 2 3 4
-----
. . . . x . . . x . . . . . 2.stat
. . . x x . . . x x x . . . 1.stat
x x x x x x x x x x x x x x 0.stat

```

If you delete a replica using the delete function in the RJT, all existing instances of the replicated flows will be deleted and the job status will be removed from all of the stat files. For example, if the replica flows for sequence 5 are deleted, the status will be removed from all existing stat

files. The status of the flow will be set to "Unknown" until the replica is rebuilt.

```

sequence number
          1 1 1 1 1
1 2 3 4 5 6 7 8 9 0 1 2 3 4
-----
. . . . . x . . . . . 2.stat
. . . x . . . x x x . . . 1.stat
x x x x . x x x x x x x x x 0.stat
    
```

If you delete all of the replicas all of the replica flow folders will be deleted but the replica#.stat files will not be deleted. All of the status values in all of the stat files will be deleted.

```

sequence number
          1 1 1 1 1
1 2 3 4 5 6 7 8 9 0 1 2 3 4
-----
. . . . . . . . . . . . . . . 2.stat
. . . . . . . . . . . . . . . 1.stat
. . . . . . . . . . . . . . . 0.stat
    
```

If you make a new set of replicas the instance numbering will start at 0 again.

If there are no replica flows left in the template flow directly you can safely delete all of the stat file is you want to.

### Viewing Replicas in the Navigator

The DescName is under user control. When you build the flows you can either use the default name which is a concatenation the first 10 squished characters of the template name with the sequence number appended, or a name that you have built in the replica job table. In either case the actual directory name is a concatenation of "exec.r#.#.pwflow" as previously described

For example, in the picture below notice that the template name is "pure pm 2 templaate". The replicated flows have a the default names that are the

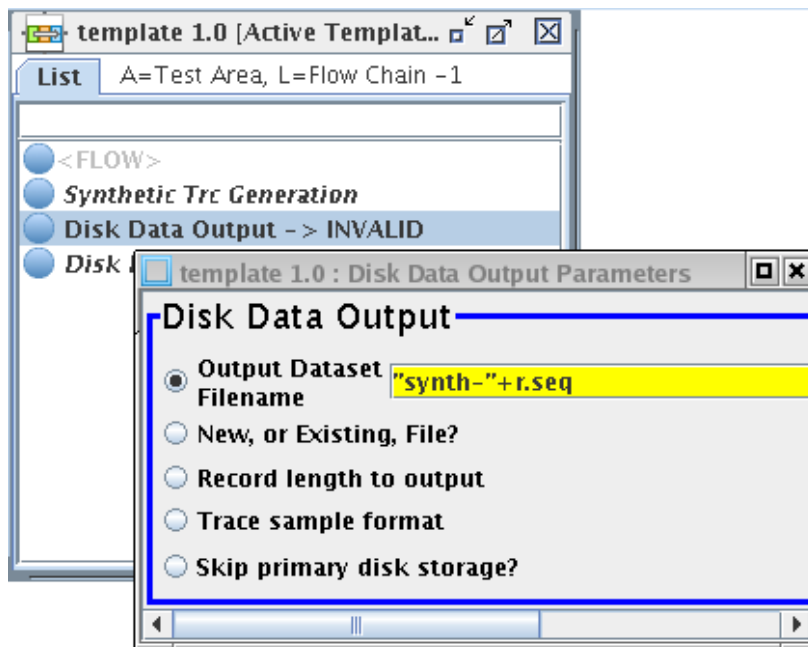
concatenation of part of the original template name and the sequence number..

pure pm2 template						
	Name	Owner	Modified	Size	File	
	-1	user1	05/08/200...	52K	packet.job	
	0	user1	05/08/200...	76K	exec.0.pwflow	
	pure pm2 t0001	user1	05/08/200...	76K	exec.r1.0.pwflow	
	pure pm2 t0001	user1	05/14/200...	76K	exec.r1.1.pwflow	
	pure pm2 t0002	user1	05/14/200...	76K	exec.r2.1.pwflow	
	pure pm2 t0002	user1	05/08/200...	76K	exec.r2.0.pwflow	
	pure pm2 t0003	user1	05/14/200...	76K	exec.r3.1.pwflow	
	pure pm2 t0003	user1	05/08/200...	76K	exec.r3.0.pwflow	
	pure pm2 t0004	user1	05/14/200...	76K	exec.r4.1.pwflow	
	pure pm2 t0004	user1	05/08/200...	76K	exec.r4.0.pwflow	
	pure pm2 t0005	user1	05/14/200...	76K	exec.r5.1.pwflow	
	pure pm2 t0005	user1	05/08/200...	76K	exec.r5.0.pwflow	

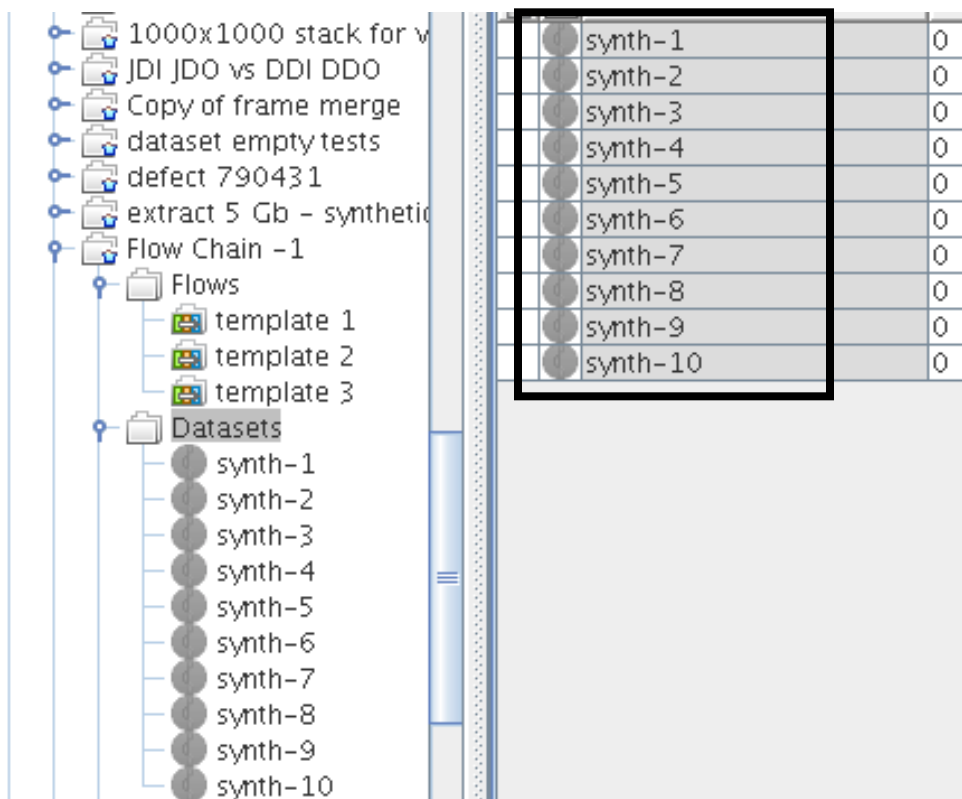


### Automatic Dataset Generation

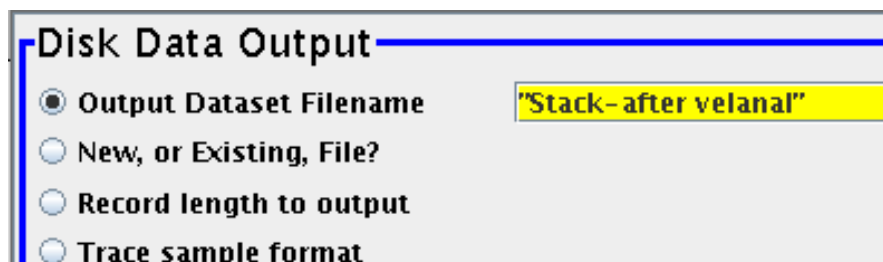
If the replicas are all to output different datasets, these datasets names will be automatically generated when the replica flows are built. Choose the Output Dataset Filename a parameter to change from one replica to the next and input the desired output dataset name string definition.



When the replica flows are built, the output datasets will be created and added to the datasets list.



You must select the output dataset name in the menu as a replacement variable for the dataset stubs to be created and added to the datasets list. (This is different behavior from ProMANAGER) . This is true for the 2D case where each replica manufactures the same dataset in the other lines (if sharing is set to no). In the case where all of the replicas write the same dataset name in each line, set the replacement value to the descriptive name of the dataset.



The datasets are not deleted when the replica flows are deleted or when the Template flow is de-templated (or turned back into a standard flow). The output datasets need to be managed manually.

## Building New Subprojects

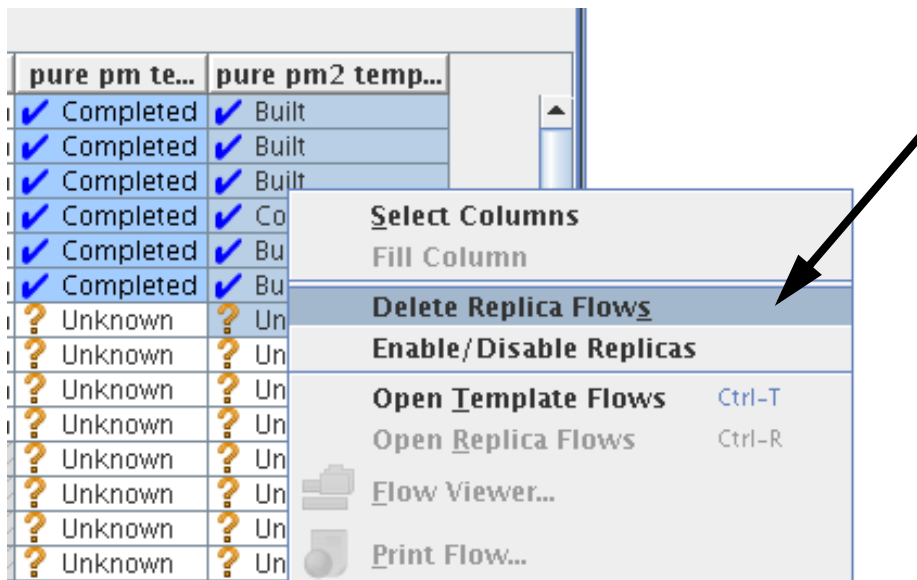
If you select to *NOT* "Share this Project" then you will create a series of new subprojects under the current project and the flows and datasets will be created in the new subprojects.

## Submitting jobs

To submit jobs, select the cells and click on one of the **Job Submit** icons. Jobs are submitted in the order they were selected. The Job Table will also display the status of the jobs as they progress through the system. You can also use MB3 to get job submit options.

## Deleting Replicas

You can delete the replica flow in the Navigator tab or you can delete them from the job status table.



Delete is an option from the MB3 options dialog.

If you delete the replicas from the Navigator table view, you will need to refresh the display of the Replica Job Table (RJT) to see that they were deleted.

## Flow Chaining

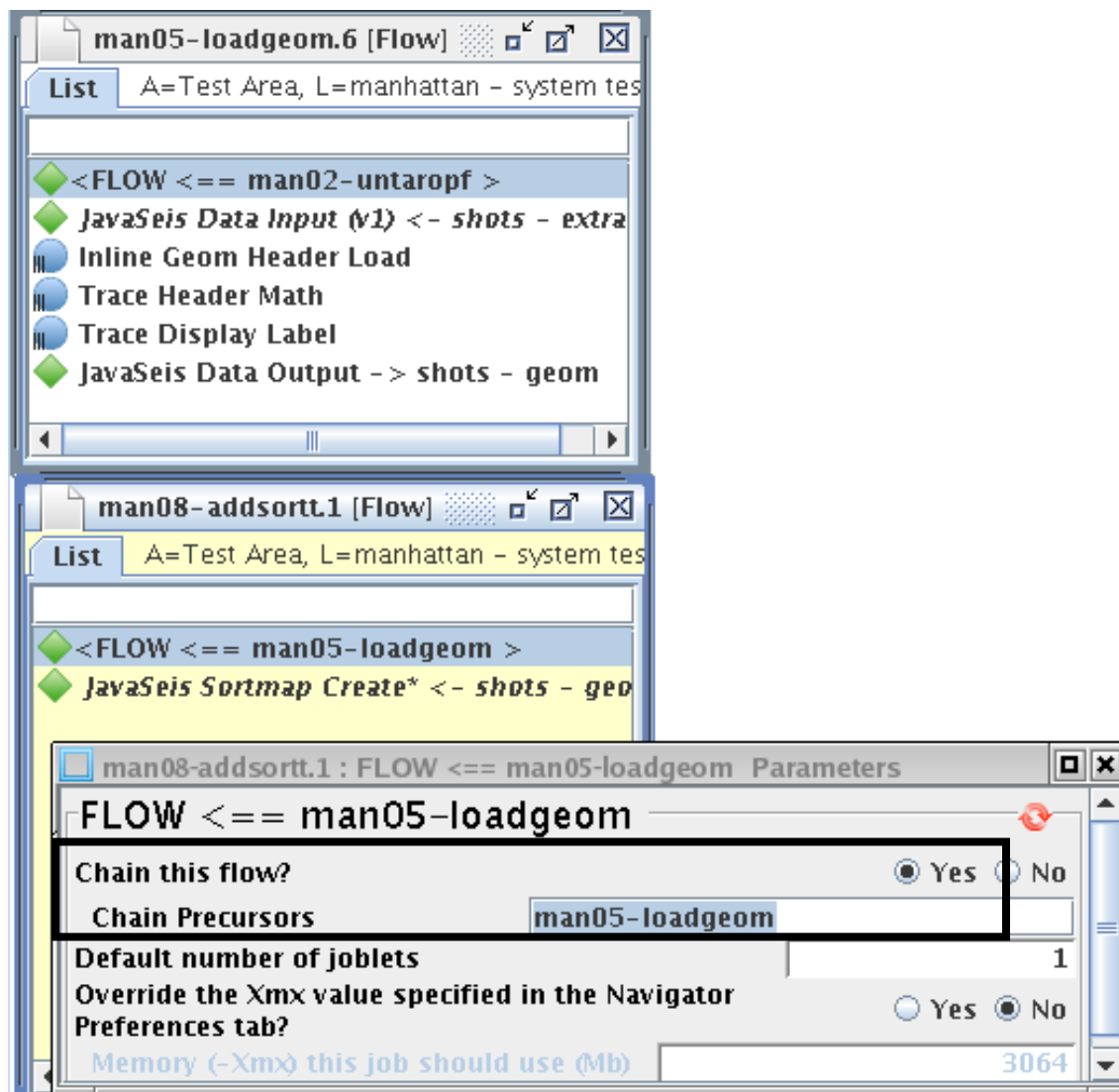
Chaining flows together means that a flow will not be submitted until another flow completes, or multiple other flows complete successfully. The concept of chaining flows together exists for normal flows as well as replicated flows build from templates.

To chain flows together you simply tell a flow which other flow (or flows) must complete before it can be submitted for execution. This list of prerequisite flows is added to the parameterization of the <Flow> executive process at the beginning of the flow list of processes.

### Chained Flows

The simplest example of flow chaining involves two flows where the first flow must complete before the second flow is submitted. In this example flow "man05..." creates an output dataset and flow "man08..." then reads that dataset for further processing work and writes a new dataset. In this

case you tell flow "man08..." that it has a pre-requisite flow called flow "man05..".



In the parameter dialog for the <Flow> "executive process" of the second flow enter the name of the first flow as the precursor flow.



When you submit the first flow to the Queue, it will run as a standard flow and will progress from Queued to Running to Completed status. When you submit the second flow to the Queue, it will not be put into the Queue until Flow 1 completes and will show in the job viewer with a "Chained" status.

▶ Chained	man08-addsortt.2	parallel@h1	1	
▶ Running	man05-loadgeom.2	parallel@h1	1	100.00

After the first flow completes, the second flow will be added to the Queue.



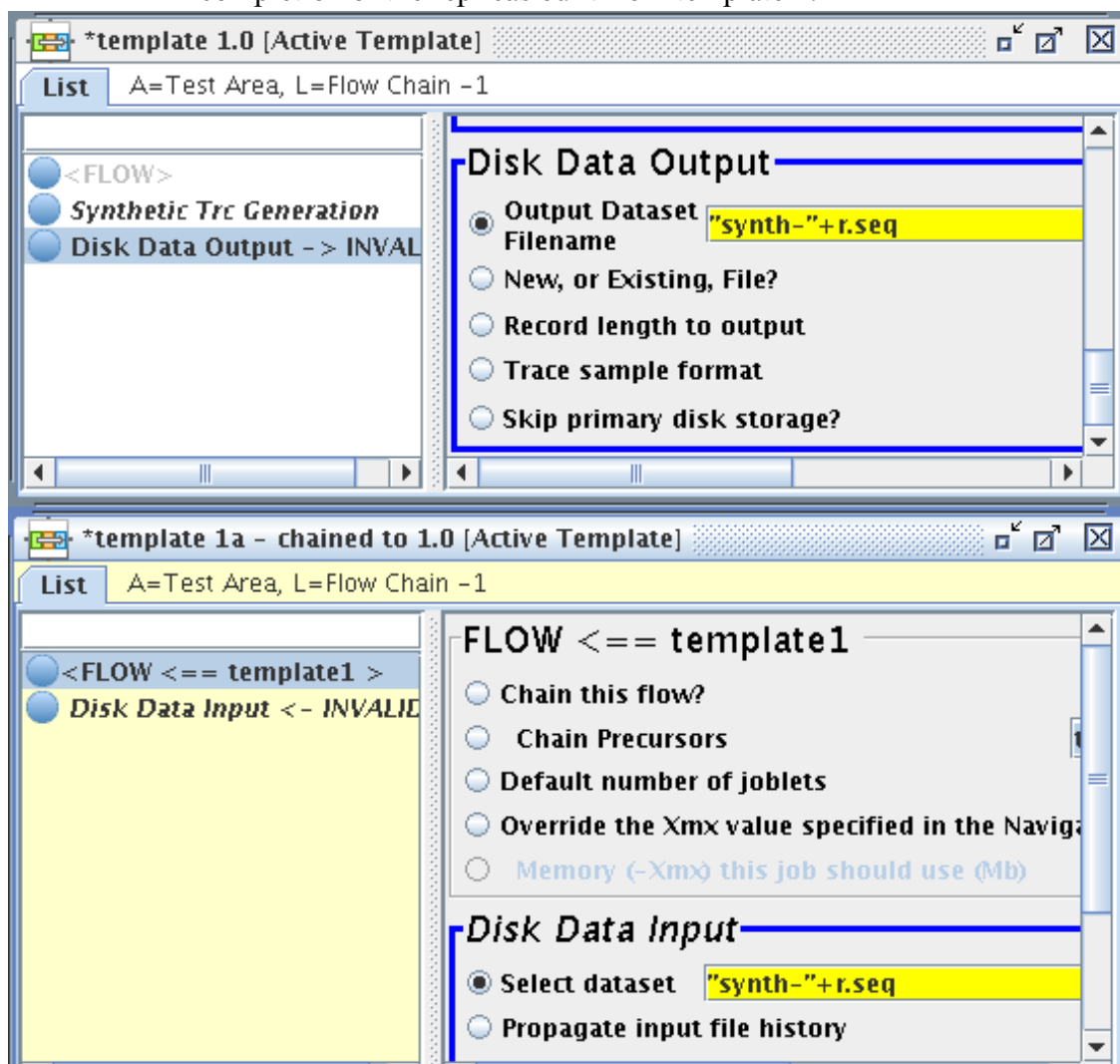
If Flow 1 fails or it is terminated, Flow 2 will receive a "Chain Failed" status and Flow 2 will not be added to the Queue.

 Chain Failed	man08-addsortt.3	parallel@h1	1
 Failed	man05-loadgeom.3	parallel@h1	1

### Chained Replicas (one to one)

The next common example of chaining flows together involves two sets of replicas where there are an EQUAL number of replicas from two different templates where the second set of replicas are dependent on the first set completing.

In this example there are two templates, "template 1" and "template 2" where the replicas built from template 2 are dependent on a successful completion of the replicas built from template 1.



The screenshot displays two windows from the SeisSpace interface. The top window, titled '\*template 1.0 [Active Template]', shows a flow chain with three flows: '<FLOW>', 'Synthetic Trc Generation', and 'Disk Data Output -> INVALID'. The 'Disk Data Output' flow is selected, and its configuration panel is visible, showing options for 'Output Dataset Filename' (set to 'synth-'+r.seq), 'New, or Existing, File?', 'Record length to output', 'Trace sample format', and 'Skip primary disk storage?'. The bottom window, titled '\*template 1a - chained to 1.0 [Active Template]', shows a flow chain with two flows: '<FLOW <== template1 >' and 'Disk Data Input <- INVALID'. The '<FLOW <== template1 >' flow is selected, and its configuration panel is visible, showing options for 'Chain this flow?', 'Chain Precursors', 'Default number of joblets', 'Override the Xmx value specified in the Navig...', and 'Memory (-Xmx) this job should use (Mb)'. Below this panel, the 'Disk Data Input' configuration is visible, showing options for 'Select dataset' (set to 'synth-'+r.seq) and 'Propagate input file history'.

In this case "template 1" is added to the Chain precursor parameter of the <Flow> process in template 2.

From the RJT (Replica Job Table) select a series of replicas to work with from both columns (template 1 and template 2). You may choose to build them and submit in a separate step or you may choose to build and submit in one step. In either case you will see that the replicas that were built for template 1 will be sent to the Queue but the replicas for template 2 will inherit the "Chained" status.

Seq ▲	Subproject	template 1	template 1a ...	template 2	template 3
1		▶ Running	▶ Chained	? Unknown	? Unknown
2		▶ Running	▶ Chained	? Unknown	? Unknown
3		▶ Running	▶ Chained	? Unknown	? Unknown
4		▶ Running	▶ Chained	? Unknown	? Unknown
5		▶ Running	▶ Chained	? Unknown	
6		▶ Running	▶ Chained	? Unknown	
7		▶ Running	▶ Chained	? Unknown	
8		▶ Running	▶ Chained	? Unknown	
9		✓ Completed	▶ Running	? Unknown	
10		✓ Completed	▶ Running	? Unknown	

Share this Project  
  Show inactive templates  
  Autoscroll Table

As the replicas for template 1 complete, the replicas for template 2 will be added to the QueueChained Replicas - "many to one" and "many to fewer"

## Chained Replicas (many to one) or (many to fewer)

There may be cases where you don't have an equal number of replicas for chained templates. An example might be where you want to run 100 replicas for one template and then run a single job that is dependent on all 100 completing. In this case you would set the chain precursor to `template1[1-100]`

Another example might be where you would run 100 jobs and output to 100 datasets and then run 50 jobs, each reading two input datasets in the next processing step. In this case you need to tell each replica of the second template that they are each dependent on multiple replicas of the first template.

Two templates and their Validation Tables are shown below. The first template is set up to make 10 replica flows and output 10 different data files. The second template is set up to make 5 replica flows each reading 2 input files from the first set of replicas. Template 2/Replica 1 is dependent on the two flows Template 1/Replica 1 and Replica 2 completing successfully. In this case the syntax:

```
"template 1["+r.seq*2-1+"-"+r.seq*2+"]"
```

is used as a value that changes from replica to replica in the <Flow> process parameterization.

The screenshot displays three windows from the SeisSpace software interface:

- \*template 1.0 [Active Template]**: Shows configuration for a template. The "Disk Data Output" section is active, with "Output Dataset Filename" set to `"synth-" + r.seq`.
- \*template many to fewer.0 [Active Template--Selected Only]**: Shows configuration for a flow. The "FLOW <== "template 1[" section is active, with "Chain Precursors" set to `"template 1[" + r.seq*2 - 1 + "-" + r.seq*2 + "]"`. Below it, "Disk Data Input" and "Disk Data Insert" sections are also active, both with "Select dataset" set to `"synth-" + r.seq*2 - 1` and `"synth-" + r.seq*2` respectively.
- Validation of Template: \*template many to fewer.0**: A table showing the validation results for 10 sequences.

Seq	Subproject	FLOW <== "temp...	Disk Data Inp...	Disk Data Inse...
1		template 1[1-2]	synth-1	synth-2
2		template 1[3-4]	synth-3	synth-4
3		template 1[5-6]	synth-5	synth-6
4		template 1[7-8]	synth-7	synth-8
5		template 1[9-10]	synth-9	synth-10
6		template 1[11-12]	synth-11	synth-12
7		template 1[13-14]	synth-13	synth-14
8		template 1[15-16]	synth-15	synth-16
9		template 1[17-18]	synth-17	synth-18
10		template 1[19-20]	synth-19	synth-20

Buttons: Refresh, Close

In this case there will be 10 jobs for the first template but only 5 jobs for the second template in the RJT.

template 1	template many ...
✓ Completed	✓ Built
✓ Completed	✓ Built
✓ Completed	✓ Built
✓ Completed	✓ Built
✓ Completed	✓ Built
✓ Completed	
✓ Completed	
✓ Completed	
✓ Completed	
✓ Completed	

## Chained Replicas - "one to many"

There may also be cases where you want a set of replicas to be sent to the Queue after a single job completes. For example, you may want to run a series of Stack jobs but you need a Velocity Manipulation job to run first.

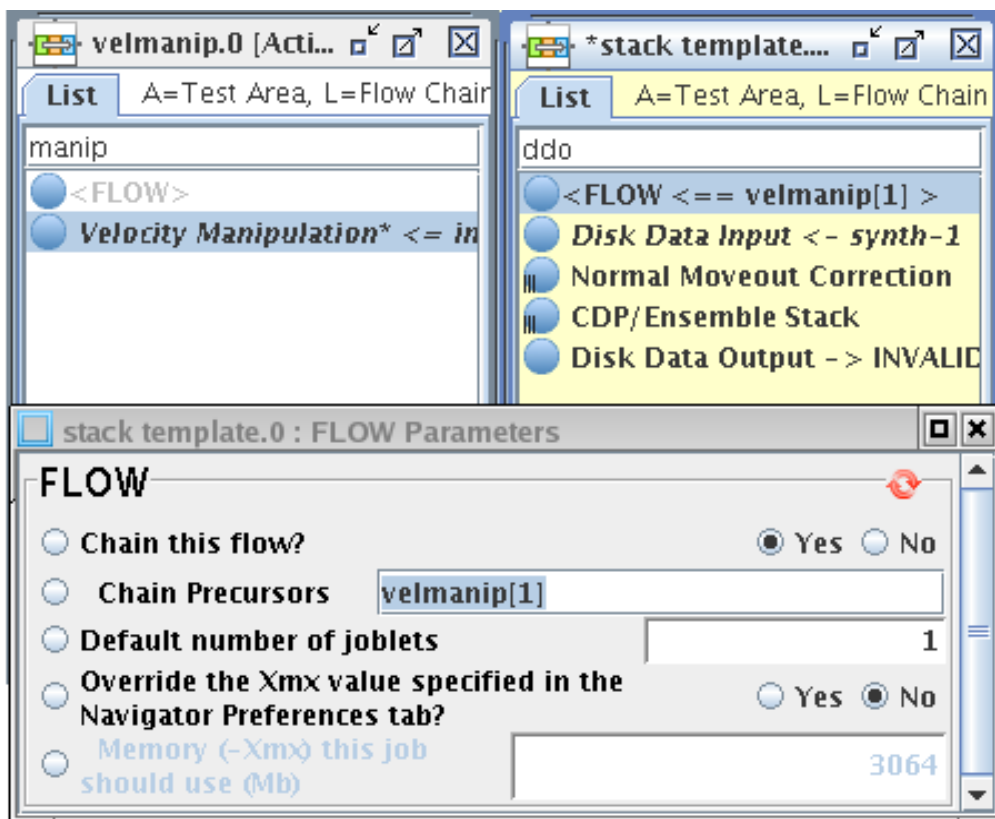
For this example you will need to build two templates: 1) for the Velocity Manipulation job where there will be only 1 replica made and 2) for the stack jobs where there will be many replicas all dependent upon the one velocity manipulation replica job completing successfully.

Note below that the Velocity Manipulation template has no replacement values since there will only be one replica manufactured from it.

Also note that the Chain precursor in the stack template is parameterized with the syntax

```
velmanip[1]
```

which means that each of the replicas produced from the stack template is dependent on the first replica sequence of the velmanip template.



In the Replica Job Table you will then built the first sequence replica of the velmanip template and all of the replicas for the stack template.

velmanip	stack tem...
✓ Built	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built
	✓ Built

The stack replicas can be submitted, to a "Chained" state after the one velmanip replica is submitted to the Queue. After the Velmanip replica job completes, the stack replicas will be added to the Queue for execution.

NOTE: the chaining is available for Flow to Flows or from Replicas to Replicas, but there is no chaining relationship for Replicas to Flows and vice versa.

## Chained Replicas - previous sequence number

Another case of flow chaining may be where you want to force the different sequence numbers of replicas from the same template to run serially and be dependent upon the previous sequence number replica completing successfully.

An example of this may be where you want to run a series of jobs to do the External Model Correlation where each job has to run separately to write to the database.

For this example the Chain precursor parameter in the Flow process is set to be dependent on the previous replica sequence from the same template. In this example the template is named "EMC picking template", with the precursor parameter is set to

```
"EMC picking template["+r.seq-1+"]"
```

Each replica will be queued up in sequence as the previous sequence completes successfully. The references to replica numbers less than or equal to 0 will be ignored so if the first line resolves to EMC picking template[0]. This job does not have any pre-cursor and the first replica will run as soon as it can be released from the Queue.

This can be used to manage a job series of 1000 jobs as an example where you can set the replication string for the precursor to:

```
"EMC picking template["+r.seq-10+"]"
```

in which case the first 10 jobs will create dependences of EMC picking template[-9] through [0]. All of these will be treated as not having precursors and the first 10 jobs will release as soon as they can. The remaining jobs will be queued up as the previous sets complete so that only 10 jobs will run at any given time but you wont clog up the Q with thousands of jobs. As 1 completes 11 will release, then 21 etc. as will all of the other sequences.





## Chained Replicas - alternate areas/lines

There may be cases where one set of replicas are dependent on another set of replicas in other lines or other area/lines. In this example template 1 is in line "Flow Chain -1" and writes datasets "synth-1 to n" into line "Flow Chain -1". The second template is the "read data template" in line "Flow Chain -2" and is dependent on the replicas in "Flow Line -1" to complete and the datasets to exist.

This example shows that the replicas for Flow Line -1 are built and the replicas for Flow Line -2 are in a Chained state waiting for the first set of replicas to complete.

The screenshot displays two job status windows. The top window, titled "Test Area/Flow Chain - 1", shows a table with 10 rows. The columns are "Seq", "Subproject", "template 1", "levelmanip", and "stack tem...". The "template 1" column contains "Built" for all rows, and the "levelmanip" column contains "Built" for all rows. The bottom window, titled "Test Area/Flow Chain - 2", shows a table with 10 rows. The columns are "Seq", "Subproject", and "read from 1". The "read from 1" column contains "Chained" for all rows. An arrow points from the "Built" state in the top window to the "Chained" state in the bottom window.

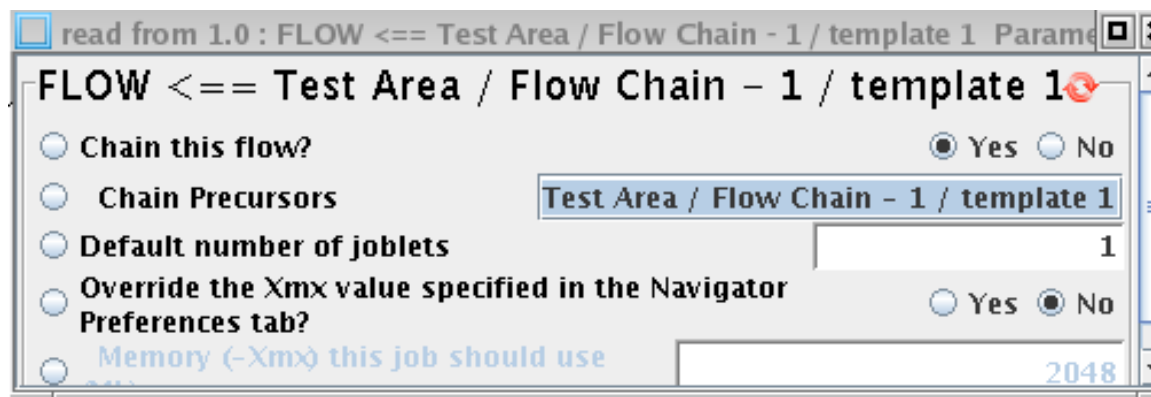
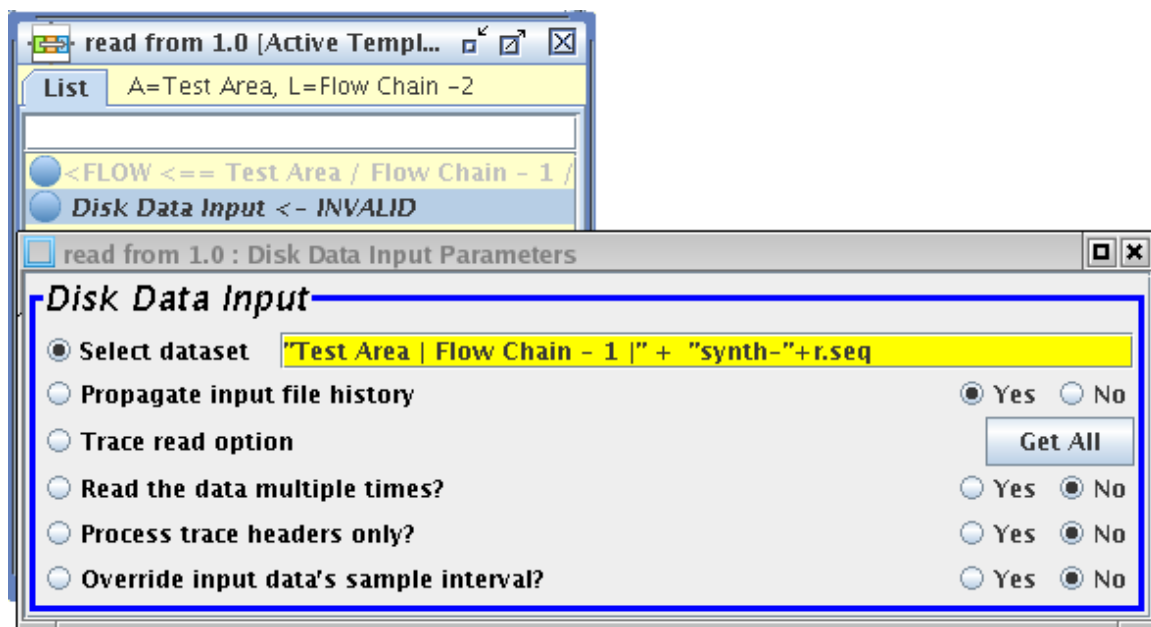
Seq	Subproject	template 1	levelmanip	stack tem...
1		✓ Built	✓ Built	✓ Built
2		✓ Built		✓ Built
3		✓ Built		✓ Built
4		✓ Built		✓ Built
5		✓ Built		✓ Built
6		✓ Built		✓ Built
7		✓ Built		✓ Built
8		✓ Built		✓ Built
9		✓ Built		✓ Built
10		✓ Built		✓ Built

Seq	Subproject	read from 1
1		Chained
2		Chained
3		Chained
4		Chained
5		Chained
6		Chained
7		Chained
8		Chained
9		Chained
10		Chained

At the bottom of the second window, there are two checkboxes:  Share this Project and  Show inactive templates.

To set the chaining pre-cursor for this scenario you can use the Area / Line / Template syntax in the chain precursor parameter:

Test Area / Flow Chain -1 / template 1



The dataset selection uses the AREA | LINE | dataset syntax to access the datasets from line "Flow Chain -1"

NOTE: in the chain precursor the AREA is optional if the alternate line is in the same AREA. In this case "Flow Chain -1 / template" is equivalent to "Training Data / Flow Chain -1 / template" since both lines Flow Chain -1 and Flow Chain -2 are under the same AREA.

## Glossary

---

Cluster	A set of nodes connected by a dedicated network.
Node	An individual computer or host in a cluster.
Mayor node Manager node Head node	A cluster node that is reserved by the manufacturer for administrating the other nodes. This node usually has more disk and more RAM than nodes reserved for distributed computation. This node is a good location to run the sitemanager and the other management daemons such as the Queue servers. Not all clusters have a specific management node, so one compute node is reserved for such tasks.
Foreman node	A foreman joblet that does any work that cannot be distributed. For instance, SEG Y input is read only by the foreman and shared with peers. The foreman should be not assigned to an already busy node, such as the manager.
iSitemanager	A server that provides information for all project and users at a given site. This is the SeisSpace® directory service. The sitemanager stores information about the jobs that have been submitted and manages the shared information in the netdir.xml file
NetDir (netdir.xml)	A database of information managed by the SiteManager. It is a file on disk that is continuously updated.
Administrator Privileges	Privileges allow you to setup cluster and project configuration.
Job Viewer	A tool on the systems menu that tracks jobs that are submitted, executing, completed or failed.
Log Viewer	A tool that presents the job output logs to the screen.
ProMAX® project	Equivalent to a PROMAX_DATA_HOME
joblet	Parallelized processing flows running on different hardware nodes. Each joblet generally processes a separate subset of the input data, but joblets can exchange information and data with their distributed peers. More than one joblet can run in a single hardware node to take advantage of dual CPUs. (You specify the number of joblets per node when submitting the job.).

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