



File Edit View Workflow Tools Window Help
Advanced Workflow Editor for Spectroscopy Data (v. 5.3.31)

Workflow Instructions Setup Directories Global Parameters

Modifying a Reflex Workflow

Public

0 results found

Execution Finished: 647489 ms. Memory: 871424K. Free: 421223K (49%)

John Pritchard



ESO-Reflex and Kepler

- **EsoReflex** is the *ESO Recipe Flexible Execution Workbench*, an environment to run ESO VLT pipelines which employs a workflow engine (**Kepler**) to provide a real-time visual representation of a data reduction cascade, called a workflow, which can be easily understood by most astronomers.



■ Actors:

- (mostly) Green folder like things...
- ‘things’ that act on ‘stuff’, in an EsoReflex workflow, the important actors are the **recipe executors** and the graphical display actors.

■ Connections:

- The lines joining things up
- connect ‘things’ allowing the ‘stuff’ coming out of one ‘thing’ to ‘flow’ to another ‘thing’

■ Relations:

- The black diamonds here and there...
- allow ‘stuff’ to be sent to/from multiple ‘things’

- The following is being done on a Mac, with fors-5.3.31 and giraf-2.16.2 workflows, installed via MacPorts

- If working on RPM based installation replace:

`/opt/local/ → /usr/`

- If working on a install-script based installation replace:

`/opt/local/ → <dir_spec>/install/`



SOFs – The ‘stuff’ that flows...

■ SOFs: Set Of Files

- original concept from esorex, a Filename+Category, e.g. bias.fits MASTER_BIAS
- Extended for esoReflex by adding “purposes”, checksums, class...

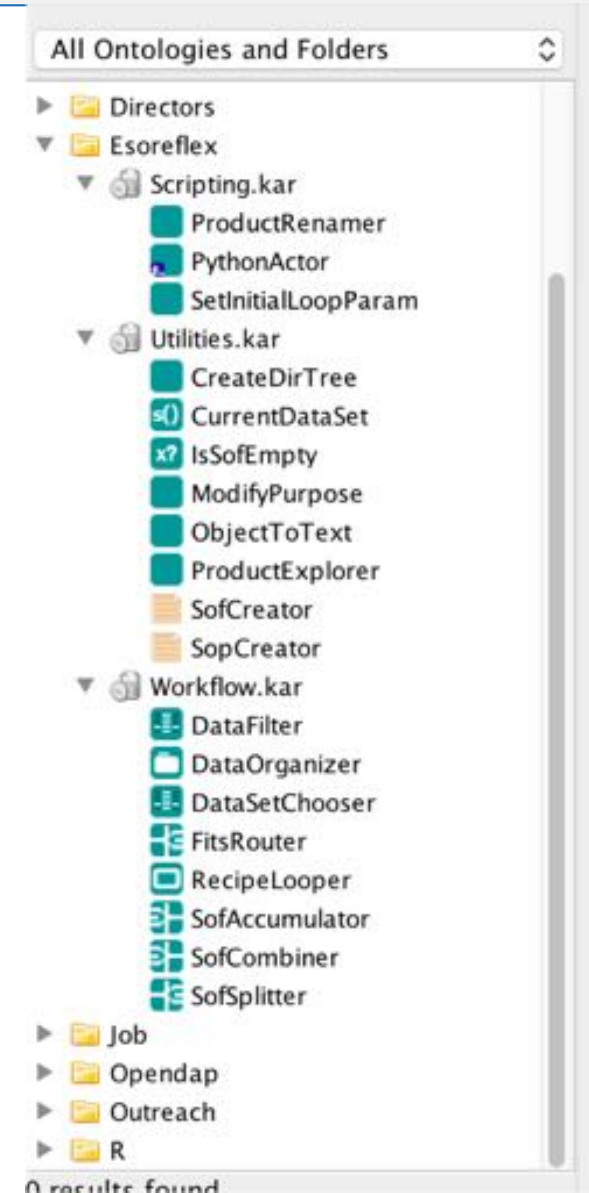
■ SOFs are the main objects that flow around an esoReflex workflow

- they are passed from the output port of one actor to the input port one or more other actors “via” the connectors.
- The actors act on the input SOF(s), processing the files and/or modifying the SOF that they then output



“Kepler” & ESO Actors

- A number of the standard Kepler actors are useful, e.g. to set variables, or to replicate objects...
- But, most of the actors used in the esoReflex workflows are ESO specific and are found in the “Esoreflex” folder
- To add an actor to a work flow, simply drag and drop from the side bar onto the workflow...

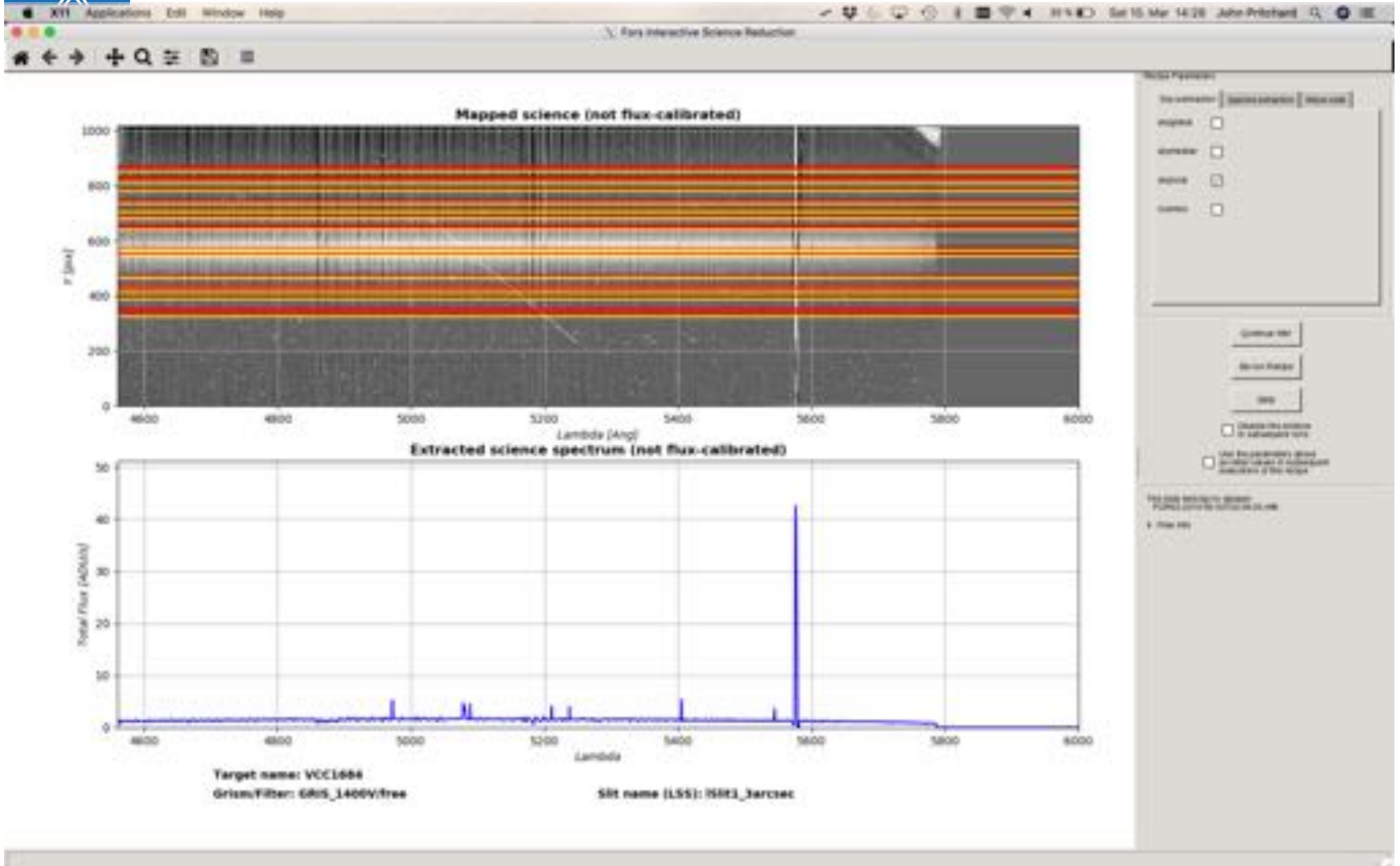




Step 0: open the WKF and export as...

- Open the standard fors_spec workflow and then export as XML to a new directory.
- Then run the recipe selecting just the 4th dataset (which has a nice set of cosmic rays...)







Step 1: add a 'simple' actor

- Select the 'DataFilter' actor from the Esoreflex/Workflows.kar folder
- Drag it on to the workflow under the ForsCalib actor
- Disconnect the Connection from the 'sci' port of the master FitsRouter and re-connect it to the 'sof out' port of the DataFilter actor.
- Create a new connection between the 'sci' port of the master FitsRouter and the 'sof in' port of the DataFilter actor

FORS Workflow For Spectroscopy Data (v. 5.3.31)


Search Components

Advanced ... Sources ...

All Ontologies and Folders

- Components
- Disciplines
- Projects
- Demos
- Actions
- Data Folders
- Directors
- Executives
 - Scripting bar
 - Utilities bar
 - Workflow bar
 - Workflow**
 - DataOrganizer
 - DataSetChanger
 - FileRouter
 - KeepLoopover
 - SoftAccumulator
 - SoftCombiner
 - SoftFilter
- Jobs
 - OpenJob
 - Outreach
 - ...

0 results found



Workflow Instructions

To run this workflow on the demo data:

- Turn on highlighting, "Doing 'Tricks'" -> "Workshop at Runtime"
- Press the "Run" button on the left to start the workflow.

To run on a different data set:

- Click on "Data" (DATA) and set up appropriate file introductions of your DATA, and will be searched for data.
- If desired, change SMO, PRODUCTS, SMO.
- Press the "Run" button on the left to start the workflow.

The general concepts of files are described in Action, Introduction, TTT, SMO. Please credit this paper in publications on research that used FORS.

Workflow manual and more detailed manual can be found here: http://www.esa.org/for/software/pipelines/for_workflow

Setup Directories

Input

- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000

Output

- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000

Working Directories

- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000

Global Parameters

- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000
- 4 1000_0000_0000_0000_0000_0000

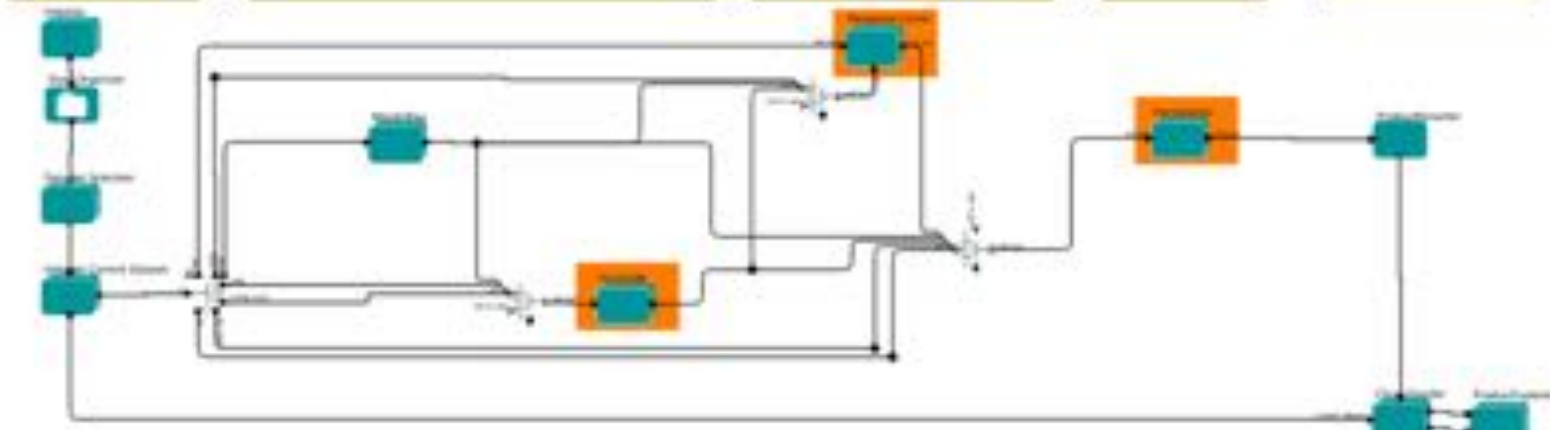
Step 1:
Data Organisation
and Selection

Step 2:
Creation of Master
Calibration Files

Step 3:
Response computation

Step 4:
Science
Reduction

Step 5:
Output
Organisation



1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000 1000_0000_0000_0000_0000_0000

pausing execution



Data Outline



FORS Workflow For Spectroscopy Data (v. 5.3.31)

Search Components

Advanced Sources

- All Ontologies and Folders
- Components
 - Disciplines
 - Projects
 - Demos
 - Actors
 - Data Folders
 - Directors
 - Executives
 - Scripting Kit
 - ProductRenamer
 - PythonActor
 - SetInitialLoopParam
 - Utilities Kit
 - CreateDirTree
 - CurrentDirGet
 - ISoftcopy
 - ModifyPurpose
 - ObjectOfText
 - ProductExpater
 - SoftCreator
 - SoftCreator
 - Workflow Kit
 - Workflow
 - DataOrganizer
 - DataSetChanger
 - FileReader
 - RecipeLumper
 - SoftAccumulator
 - SoftContainer
 - SoftFilter

0 results found



Workflow Instructions

To run this workflow on the demo data:

- Point on highlighting "Doing 'Tests'" in "Workflow at Runtime" from top menu bar on in in "1"
- Press the "Run" button on view it to start the workflow

To run on a different data set:

- Click on "Data" tab in "Data" and set up appropriate set of directories of data (DATA_001 will be searched for data, if desired change END_PRODUCT_001).
- Press the "Run" button on view it to start the workflow

The general concepts of Refex are described in Refex Introduction, TTS, etc. Please refer to the application or publications on research that used Refex.

Workflow manual and more detailed manual can be found here: <http://www.oxford-journals.org/doi/full/10.1093/bioinformatics/btt001>

Setup Directories

Input

- 4 END_DATA_001 - path to demo data directory
- 4 END_PRODUCT_001 - path to demo product directory
- 4 END_DATA_002 - path to demo data directory
- 4 END_PRODUCT_002 - path to demo product directory

Output

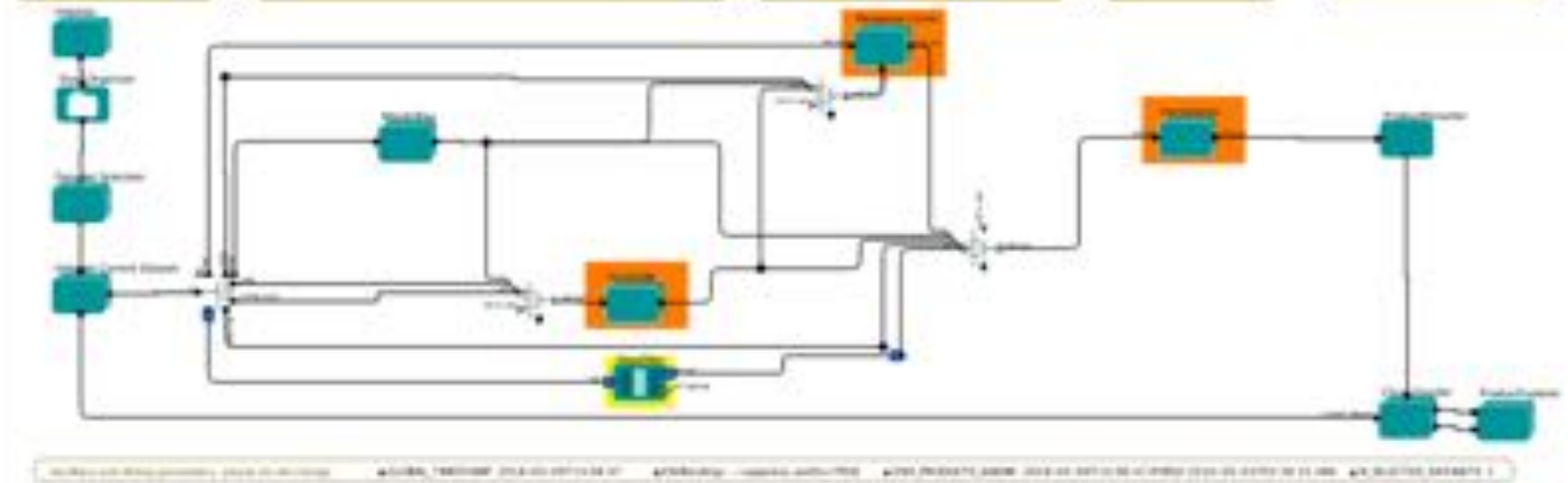
- 4 END_PRODUCT_001 - path to demo product directory
- 4 END_PRODUCT_002 - path to demo product directory
- 4 END_PRODUCT_003 - path to demo product directory
- 4 END_PRODUCT_004 - path to demo product directory

Working Directories

- 4 END_PRODUCT_001 - path to demo product directory
- 4 END_PRODUCT_002 - path to demo product directory
- 4 END_PRODUCT_003 - path to demo product directory
- 4 END_PRODUCT_004 - path to demo product directory

Global Parameters

- 4 END_PRODUCT_001 - path to demo product directory
- 4 END_PRODUCT_002 - path to demo product directory
- 4 END_PRODUCT_003 - path to demo product directory
- 4 END_PRODUCT_004 - path to demo product directory
- 4 END_PRODUCT_005 - path to demo product directory
- 4 END_PRODUCT_006 - path to demo product directory
- 4 END_PRODUCT_007 - path to demo product directory
- 4 END_PRODUCT_008 - path to demo product directory
- 4 END_PRODUCT_009 - path to demo product directory
- 4 END_PRODUCT_010 - path to demo product directory



WorkflowEngine - 2023 - 1000 - 1000

FORS Workflow For Spectroscopy Data (v. 5.3.31)

Search Components
Advanced Search

- All Ontologies and Folders
- Components
 - Disciplines
 - Projects
 - Demos
 - Actions
 - Data Pipeline
 - Directors
 - Executives
 - Scripting Kit
 - ProductRenderer
 - PythonEditor
 - ScriptWorkflowParam
 - Utilities Kit
 - CreateDirTree
 - CurrentDirGet
 - FileCopy
 - ModifyPurpose
 - ObjectExist
 - ProductExist
 - SrcCreator
 - SrcCreator
 - Workflow Kit
 - DataOrganiser
 - DataSetChanger
 - FileReader
 - RecipeLoader
 - SoftwareCompiler
 - SoftwareCompiler
 - SoftwareCompiler
 - SoftwareCompiler
 - Job
 - Operator
 - Outreach
 - R

Workflow Instructions Setup Director Global Parameters

To set up this workflow on the demo data:
- From the demo data folder
- Press the 'Data Organiser' button
- Click on 'Data Organiser' button
- Press the 'Data Organiser' button

Select Frames

File	Category	Purpose
FORS_2010-05-01701_16-15-488.Au	SCIENCE_L3A	(NCL)3A

Select All Deselect All Save as... Inspect

Pause Continue

Global parameter for the behaviour when a source file has been processed. The process is continued to step 4 or 5. Customer may want the workflow to skip errors and continue. This means the workflow will stop.

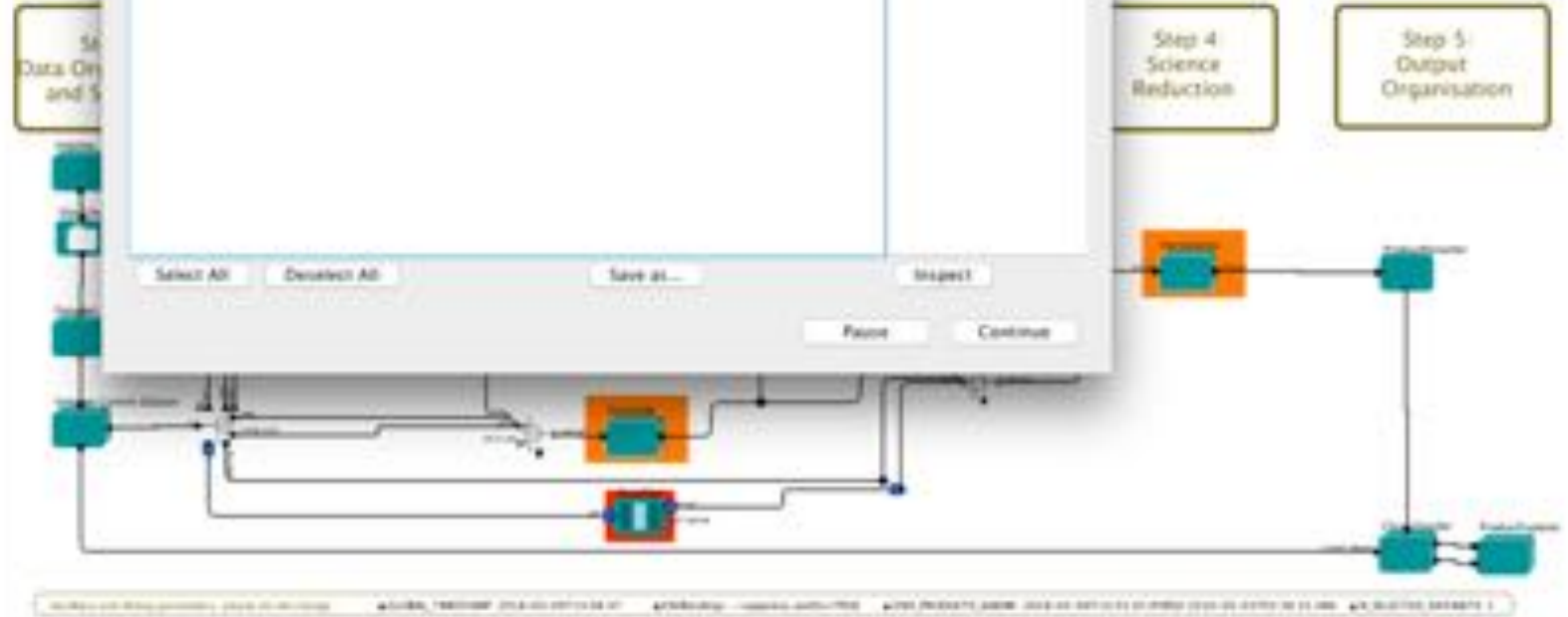
Change 'Transfer' to 'True' to allow the workflow to run many times with the same input.

Program to use for the execution of management products. The full path name is to be used in the command line.

Set to 'True' to enable interactive mode for the whole workflow. Each interactive step can specify its own setting, which overrides the global value here.

Specify how frames for processing are selected. 'All' - select all frames before. 'Random' - randomly select frames before. 'Target' - manually select frames before. 'Interactive' - for interactive selection.

Specify when you want to use the interactive system. 'On' - always. 'Off' - never. 'When' - when a file is not found. 'When' - when a file is found.



Workflow instructions: 1. Data Organiser 2. Step 4 Science Reduction 3. Step 5 Output Organisation 4. Final Output



The end...

- And that's "How to modify a workflow..."



...Not the end...

■ But seriously...



Step 2.1: Add a basic Python Actor

- Select the 'PythonActor' actor from the Esoreflex/Scripting.kar folder
- Drag it on to the workflow beside and to the left of the DataFilter actor
- Note it (currently) has no ports...
- In a terminal do:

```
cp /opt/local/share/esopipes/giraf-2.16.2/reflex/giraf_in_out.py fors_in_out.py
```
- Edit it (double click, or right click and select Edit) and set "Python script" to fors_in_out.py
- Note how the two ports appear...



Step 2.1: Add a basic Python Actor

- Disconnect the Connection from the 'sof in' port of the DataFilter actor and re-connect it to the 'sof out' port of the PythonActor actor.
- Create a new connection between the 'sof out' port of the PythonActor actor and the 'sof in' port of the DataFilter actor
- Right button Click on the PythonActor actor and select 'Customize name'.
- Set the name to InOut.
- The InOut actor doesn't do anything, except write the in and out SOFs to the bookkeeping directory.

FORS Workflow For Spectroscopy Data (v. 5.3.31)

Home Data Outline

Search Components
 Search
 Advanced Sources Found

All Strategies and Folders

- Components
- Disciplines
- Projects
- Demos
- Actions
- Data Folders
- Directors
- Executives
 - Scripting.kar
 - ProductNumber
 - ProductID**
 - SerialExpParam
 - Utilities.kar
 - Workflow.kar
- Job
- Operator
- Outreach
- 8

0 results found



Workflow Instructions

To run this workflow on the demo data:

- Turn on highlighting, "Doing 'Trails'" - "Workshop at Runtime"
- Press the "Run" button on the left to start the workflow.

To run on a different data set:

- Check on "Data" tab and set up appropriate
- All subdirectories of "Data" folder will be searched for data.
- If desired, change "Data" folder to "Data".
- Press the "Run" button on the left to start the workflow.

The general concepts of folders are described in

Alerts:Alerts@biodidac.com, basic 1.mil. Please credit this paper in publications on research that used FORS.

Workflow manual and more detailed manual can be found here:
http://www.biodidac.org/for/for_workflow_instructions_workflow

Setup Directories

Input

- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001

Output

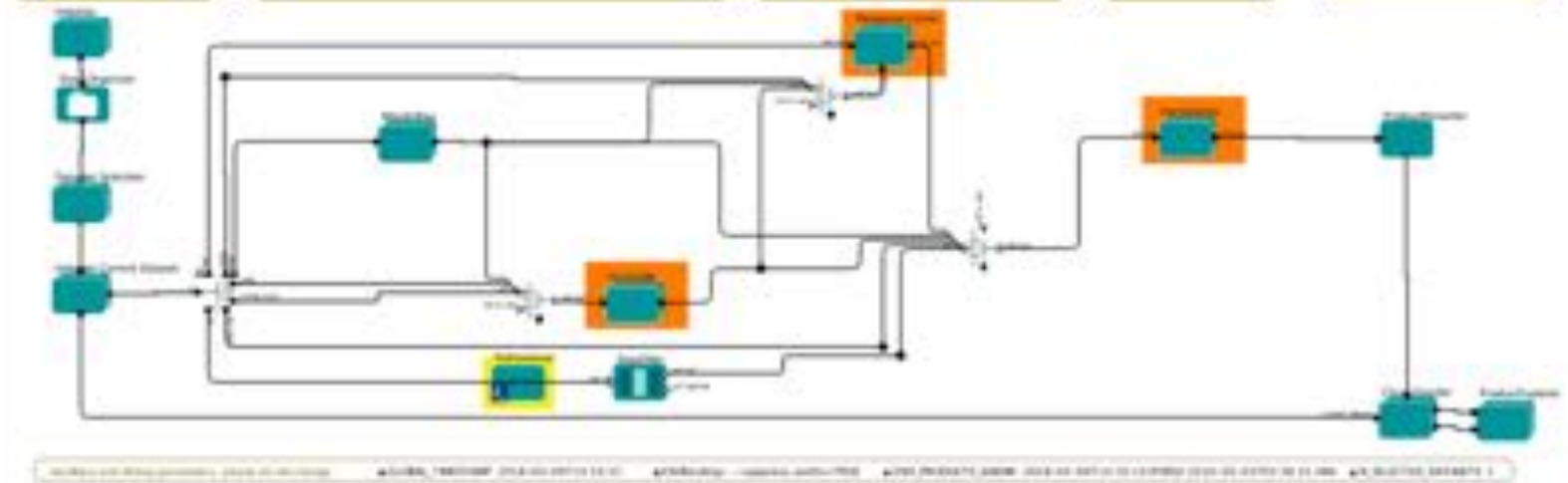
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001

Working Directories

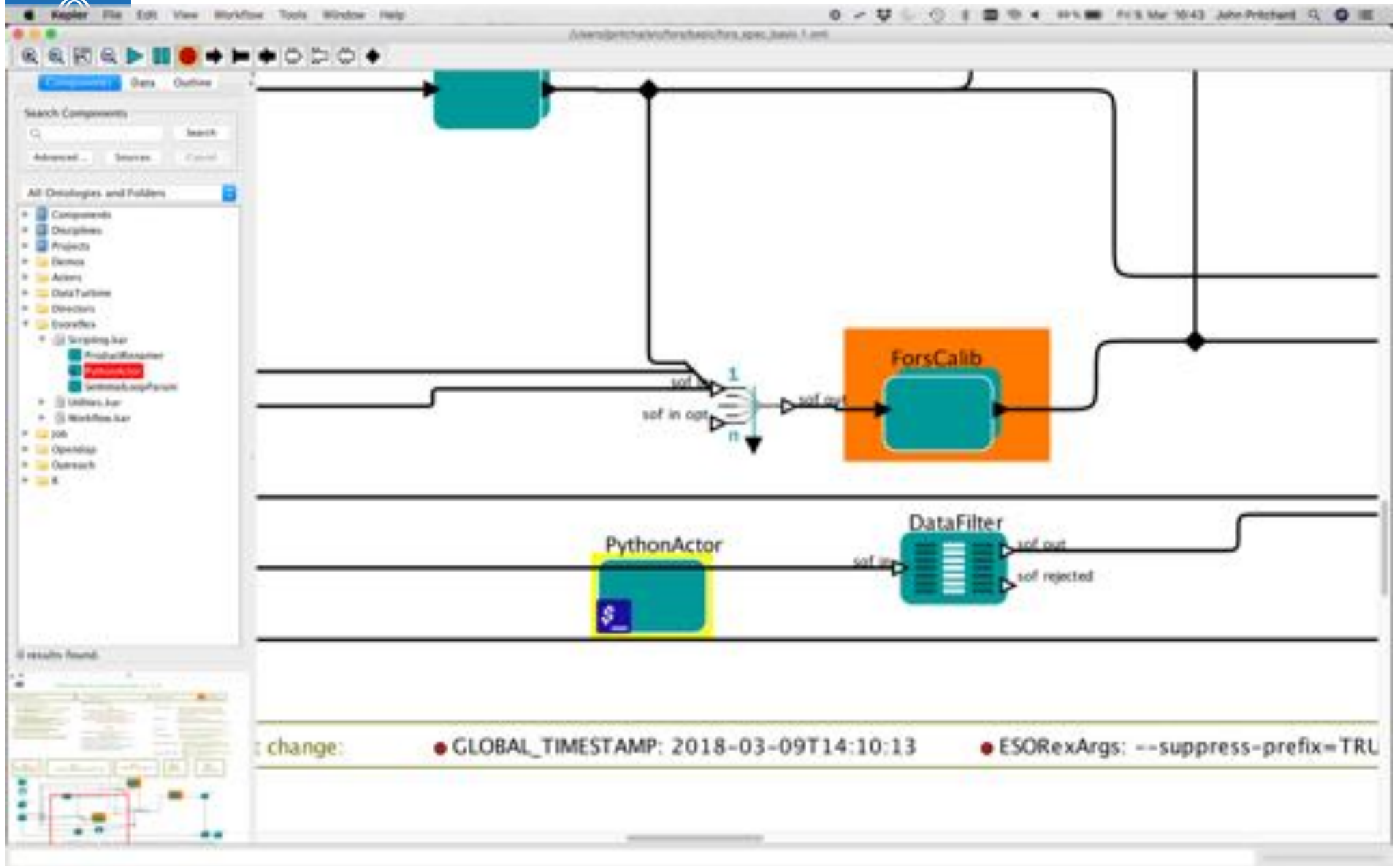
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001

Global Parameters

- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001
- 41001_2014_08_10001_0001_0001_0001



41001_2014_08_10001_0001_0001_0001 41001_2014_08_10001_0001_0001_0001 41001_2014_08_10001_0001_0001_0001 41001_2014_08_10001_0001_0001_0001 41001_2014_08_10001_0001_0001_0001 41001_2014_08_10001_0001_0001_0001



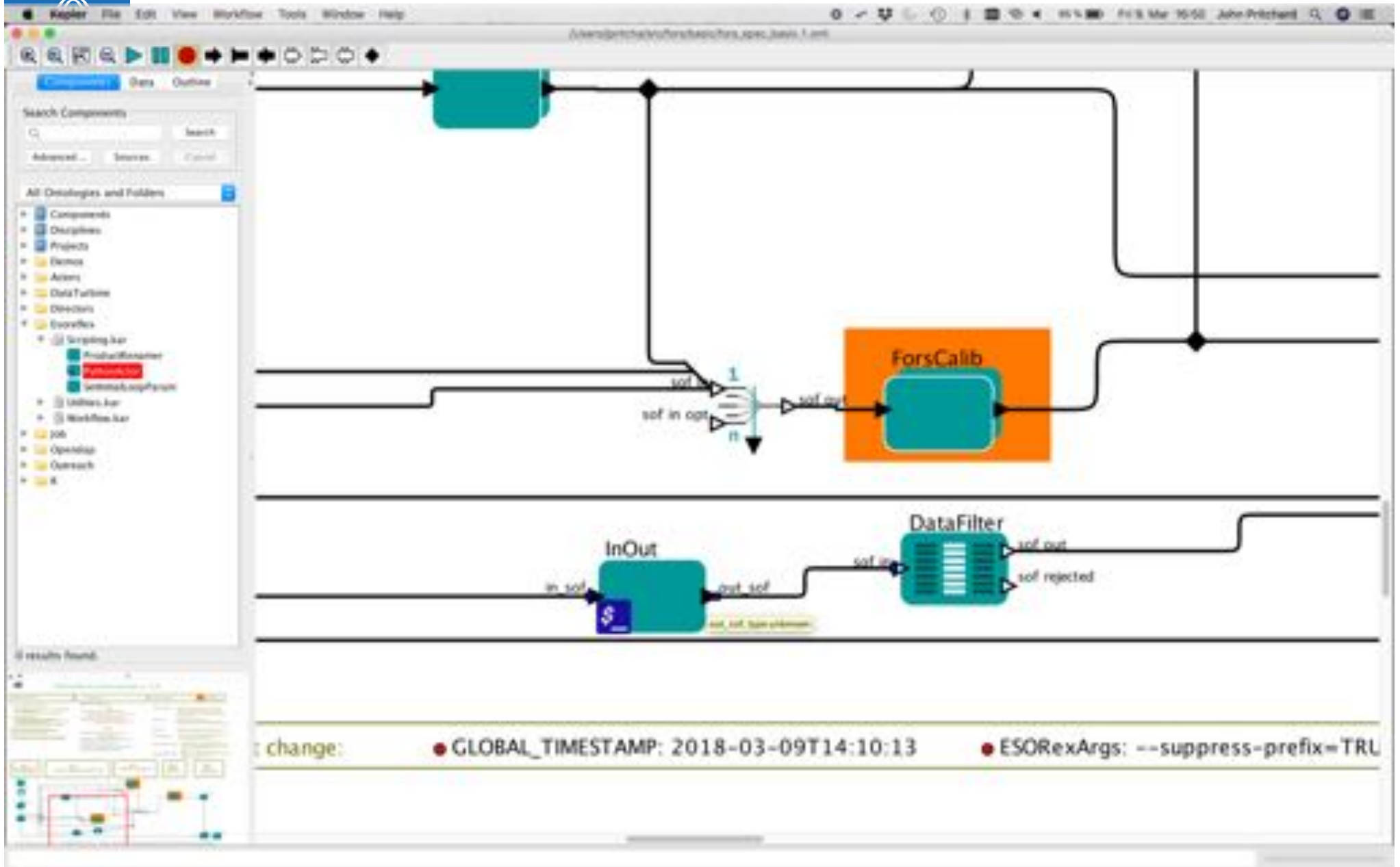


The screenshot shows the Kepler workflow editor interface. A workflow is visible with a **PythonActor** component (highlighted in yellow) and a **DataFilter** component. The **PythonActor** has an input port labeled `in_sof` and an output port labeled `out_sof`. The **DataFilter** component has an input port labeled `sof in` and two output ports labeled `sof out` and `sof rejected`. A configuration dialog titled "Edit parameters for PythonActor" is open, showing the following settings:

- Python script: `/Users/jpritcha/kepler/flow/flow_in_out.py`
- Run in terminal:
- Lazy Mode:
- Recipe Failure Mode: `Stop`
- Disable logging:
- Clean Temporary Directories:
- Products Dir: `STMP_PRODUCTS_DIR`
- Log Dir: `LOGS_DIR`
- Bookkeeping Dir: `BOOKKEEPING_DIR`
- Bookkeeping DB: `BOOKKEEPING_DB`
- FTS viewer: `FTS_VIEWER`
- state: `org.esm.pythonactor`

At the bottom of the interface, there is a status bar with the following information:

- change: ● GLOBAL_TIMESTAMP: 2018-03-09T14:10:13
- ESORexArgs: --suppress-prefix=TRU





```
Terminal Shell Edit View Window Help
fery-spec -- jpritcha@ml14017-reflex_data/reflex_book_keeping/fery-spec -- bash - cd -- 2018-03
jpritcha@ml14017-reflex_data:~$ cd /Users/jpritcha/reflex_data/reflex_book_keeping/fery-spec
jpritcha@ml14017-reflex_data:~/reflex_book_keeping/fery-spec$ ls -l
total 6176
drwxr-xr-x 17 jpritcha users 544 Mar 12 09:21
drwxr-xr-x 4 jpritcha users 128 Mar 9 08:49 ...
drwxr-xr-x 8 jpritcha users 256 Mar 10 14:24 Addressbook
drwxr-xr-x 4 jpritcha users 128 Mar 10 14:24 DatabaseSpec
drwxr-xr-x 17 jpritcha users 544 Mar 10 14:24 FeryDataInteraction
drwxr-xr-x 10 jpritcha users 320 Mar 10 14:24 FeryDataInteractionSpec
drwxr-xr-x 18 jpritcha users 576 Mar 10 14:24 FeryDataInteractionSpec
drwxr-xr-x 4 jpritcha users 128 Mar 9 09:21 FeryDataInteractionSpec
drwxr-xr-x 14 jpritcha users 448 Mar 10 14:24 Input
drwxr-xr-x 8 jpritcha users 256 Mar 10 14:24 InputSpec
drwxr-xr-x 15 jpritcha users 480 Mar 10 14:24 InputSpec
drwxr-xr-x 15 jpritcha users 480 Mar 10 14:24 InputSpec
drwxr-xr-x 1 jpritcha users 160 Mar 10 14:24 InputSpec
-rw-r--r-- 1 jpritcha users 212126 Mar 10 14:15 bookkeeping.db
drwxr-xr-x 5 jpritcha users 160 Mar 10 14:24 FeryData_1
drwxr-xr-x 5 jpritcha users 160 Mar 10 14:24 FeryData_2
drwxr-xr-x 8 jpritcha users 256 Mar 10 14:24 FeryData_3
jpritcha@ml14017-reflex_data:~/reflex_book_keeping/fery-spec$ ls -l /InOut/
total 0
drwxr-xr-x 14 jpritcha users 448 Mar 10 14:24
drwxr-xr-x 17 jpritcha users 544 Mar 12 09:21
drwxr-xr-x 9 jpritcha users 288 Mar 9 08:55 2018-03-09T08:55:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 08:58 2018-03-09T08:58:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 09:06 2018-03-09T09:06:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 09:25 2018-03-09T09:25:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 09:26 2018-03-09T09:26:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 09:49 2018-03-09T09:49:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 16:18 2018-03-09T16:18:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 16:34 2018-03-09T16:34:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 17:14 2018-03-09T17:14:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 9 20:50 2018-03-09T20:50:14.288
drwxr-xr-x 9 jpritcha users 288 Mar 10 14:24 2018-03-09T14:24:14.288
drwxr-xr-x 1 jpritcha users 87 Mar 10 14:24 latest -> /Users/jpritcha/reflex_data/reflex_book_keeping/fery-spec/InOut/2018-03-20T14:24:29.947
jpritcha@ml14017-reflex_data:~/reflex_book_keeping/fery-spec$ ls -l /InOut/latest/
total 40
drwxr-xr-x 8 jpritcha users 288 Mar 10 14:24
drwxr-xr-x 14 jpritcha users 448 Mar 10 14:24 ...
-rw-r--r-- 1 jpritcha users 3833 Mar 10 14:24 refFlex.ch
-rw-r--r-- 1 jpritcha users 1 Mar 10 14:24 extracode.txt
-rw-r--r-- 1 jpritcha users 371 Mar 10 14:24 input_parameters.json
drwxr-xr-x 1 jpritcha users 79 Mar 10 14:24 log_dir -> /Users/jpritcha/reflex_data/reflex_logs/fery-spec/InOut/2018-03-20T14:24:29.947
-rw-r--r-- 1 jpritcha users 357 Mar 10 14:24 output_parameters.json
drwxr-xr-x 1 jpritcha users 87 Mar 10 14:24 products_dir -> /Users/jpritcha/reflex_data/reflex_logs_products/fery-spec/InOut/2018-03-20T14:24:29.947
-rw-r--r-- 1 jpritcha users 30 Mar 10 14:24 script.closure
jpritcha@ml14017-reflex_data:~/reflex_book_keeping/fery-spec$ cat /InOut/latest/input_parameters.json
{"Title": "Fery", "Date": "14 Mar 2018", "DatabaseName": "FOCKL_2018-03-09T16:34:14.288", "Files": [{"purpose": "SQL", "name": "/opt/local/share/cockpit/databases/fery/fery/fery-dbg-reflex-0.3.0/fockl_2018-03-09T16:34:14.288_files", "checksum": "8C74A38406A0938D78C8C0E117", "category": "SOURCE", "class": "org.ees.dawin.FocklFile"}, {"class": "org.ees.dawin.SourceFile"}]}jpritcha@ml14017-reflex_data:~/reflex_book_keeping/fery-spec$
```



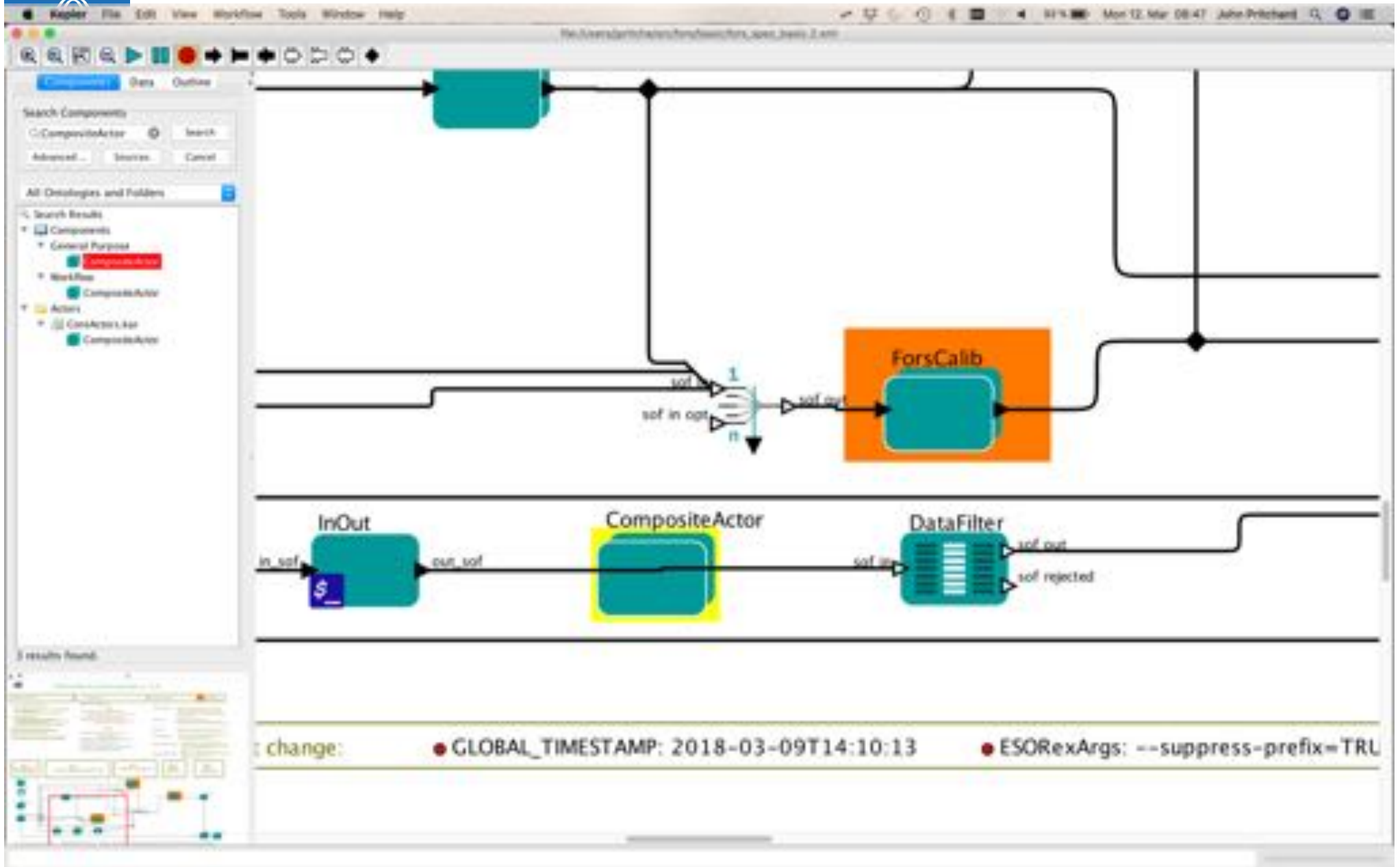


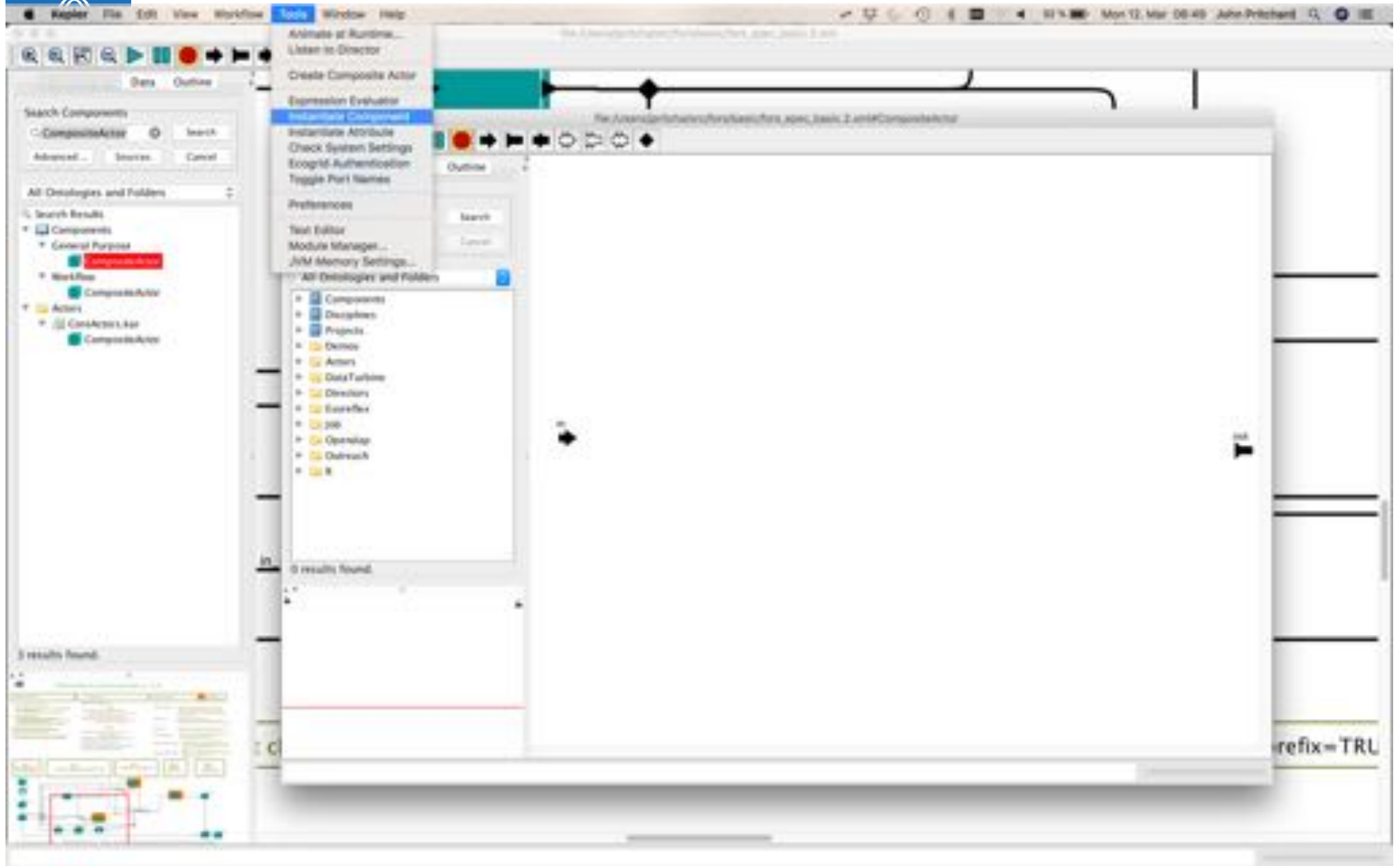
Step 2.2: Add a Recipe Executor

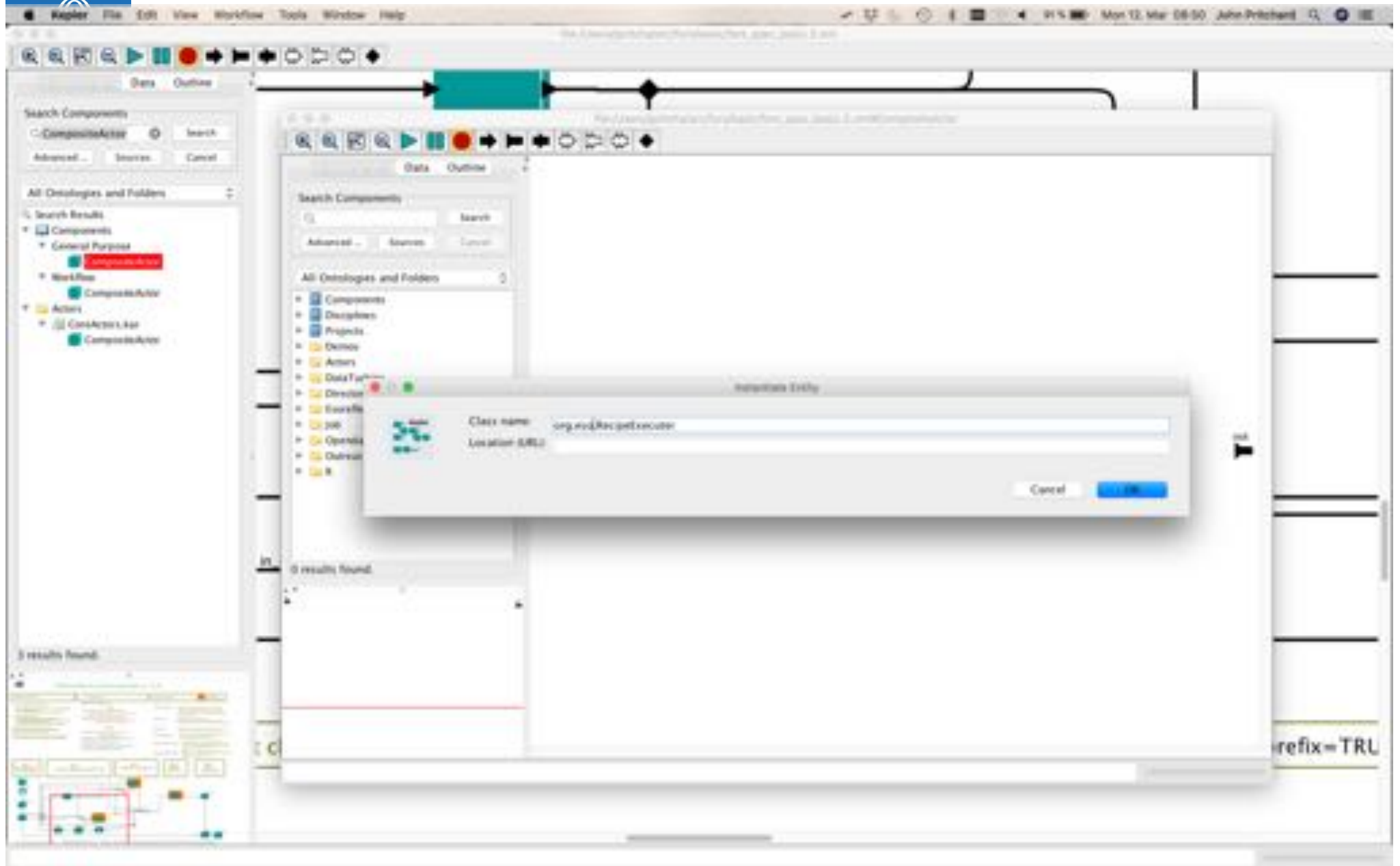
- The Esoreflex Recipe Executor is a special case.
- There is no template actor to drag and drop.
- Instead... as per the [Reflex Workflow Development Guide](https://www.eso.org/sci/software/reflex) (<https://www.eso.org/sci/software/reflex>):

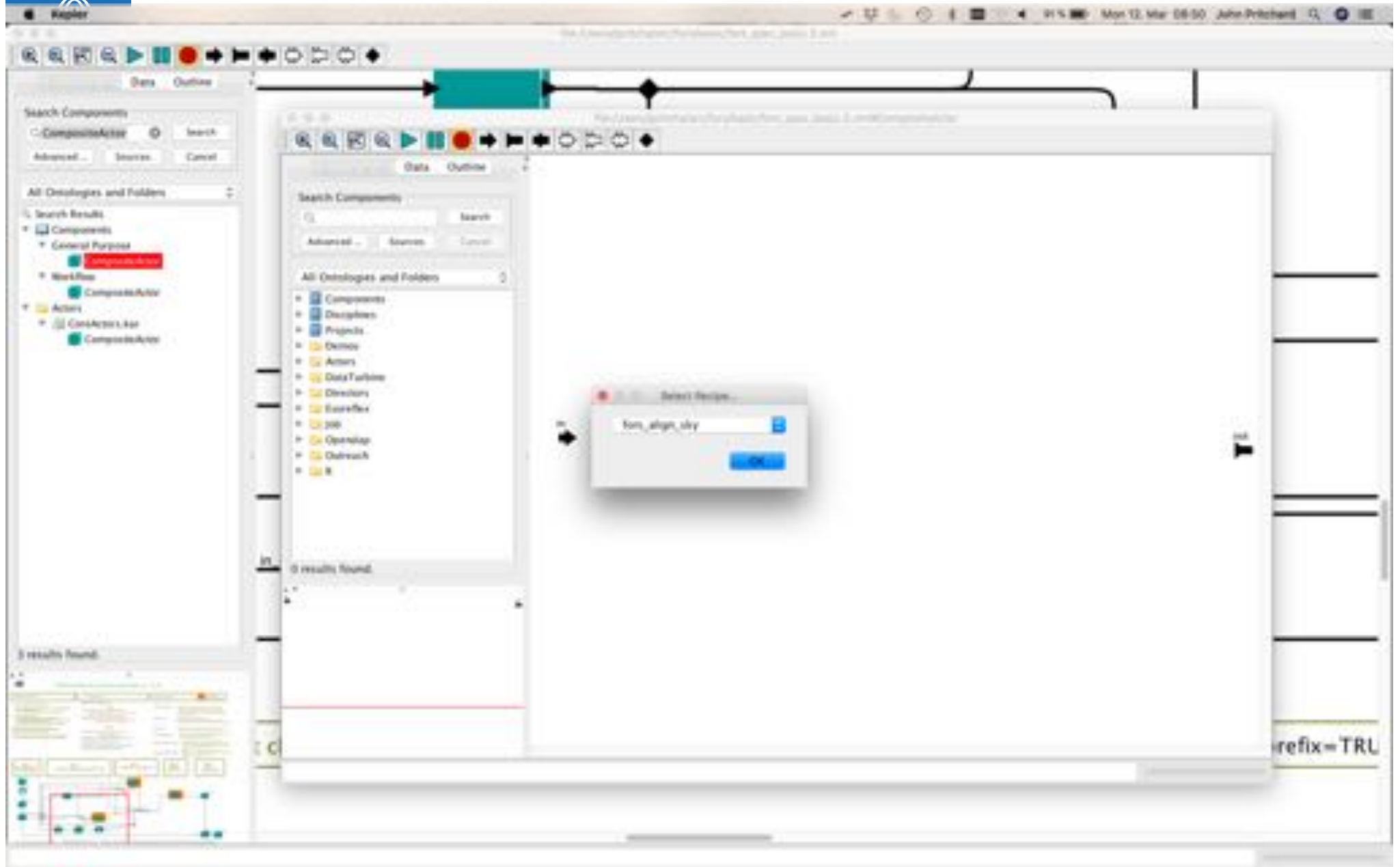
The RecipeExecutor should be instantiated using the Tools -> Instantiate Component option. The component should be called org.eso.RecipeExecutor. This will show a list of available recipes as seen by the esorex command which is in the current path. If your recipe is not shown there, check your esorex and pipeline installation.

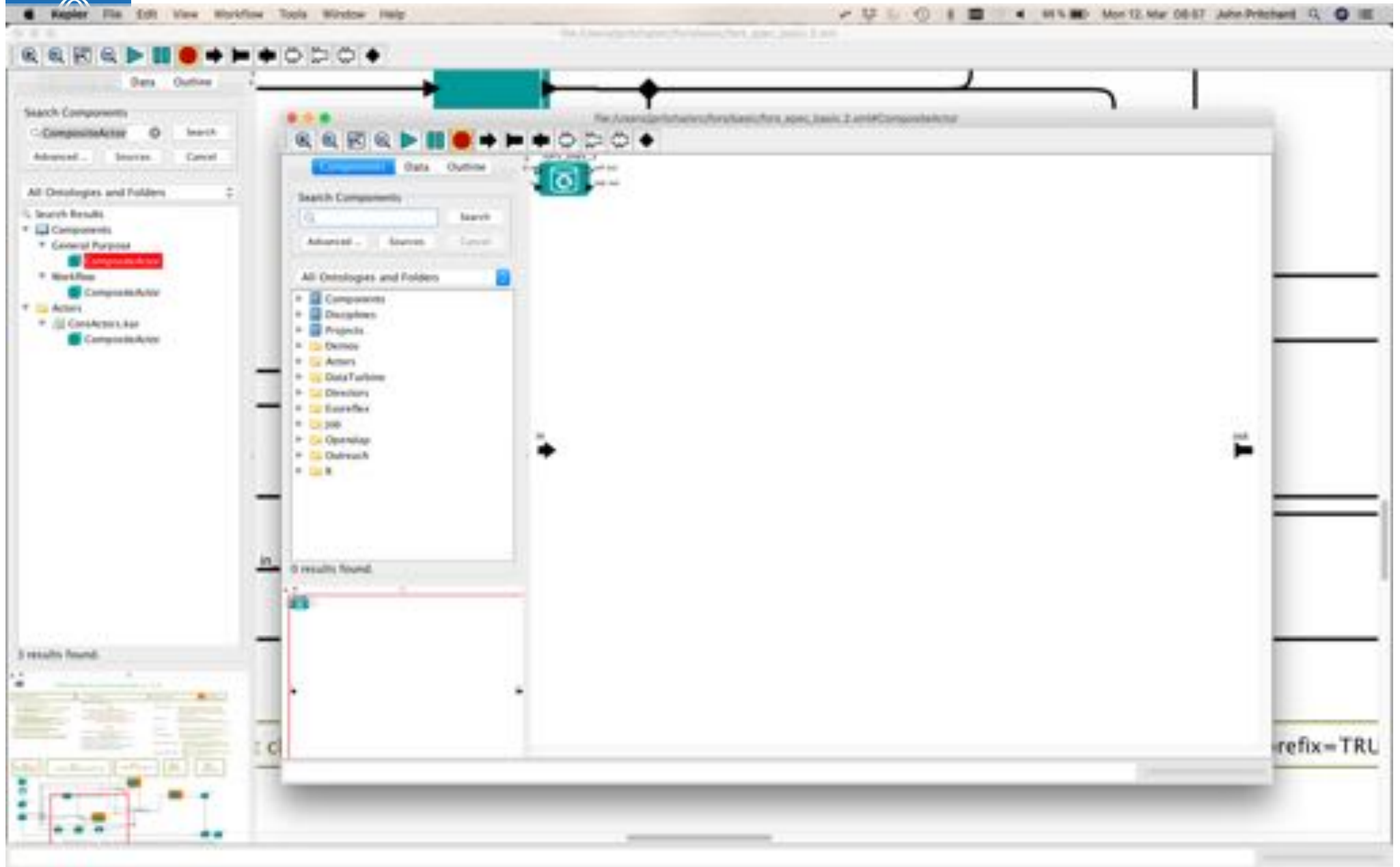
- Add inside a CompositeActor, together with a sofSplitter and a sofAccumulator.





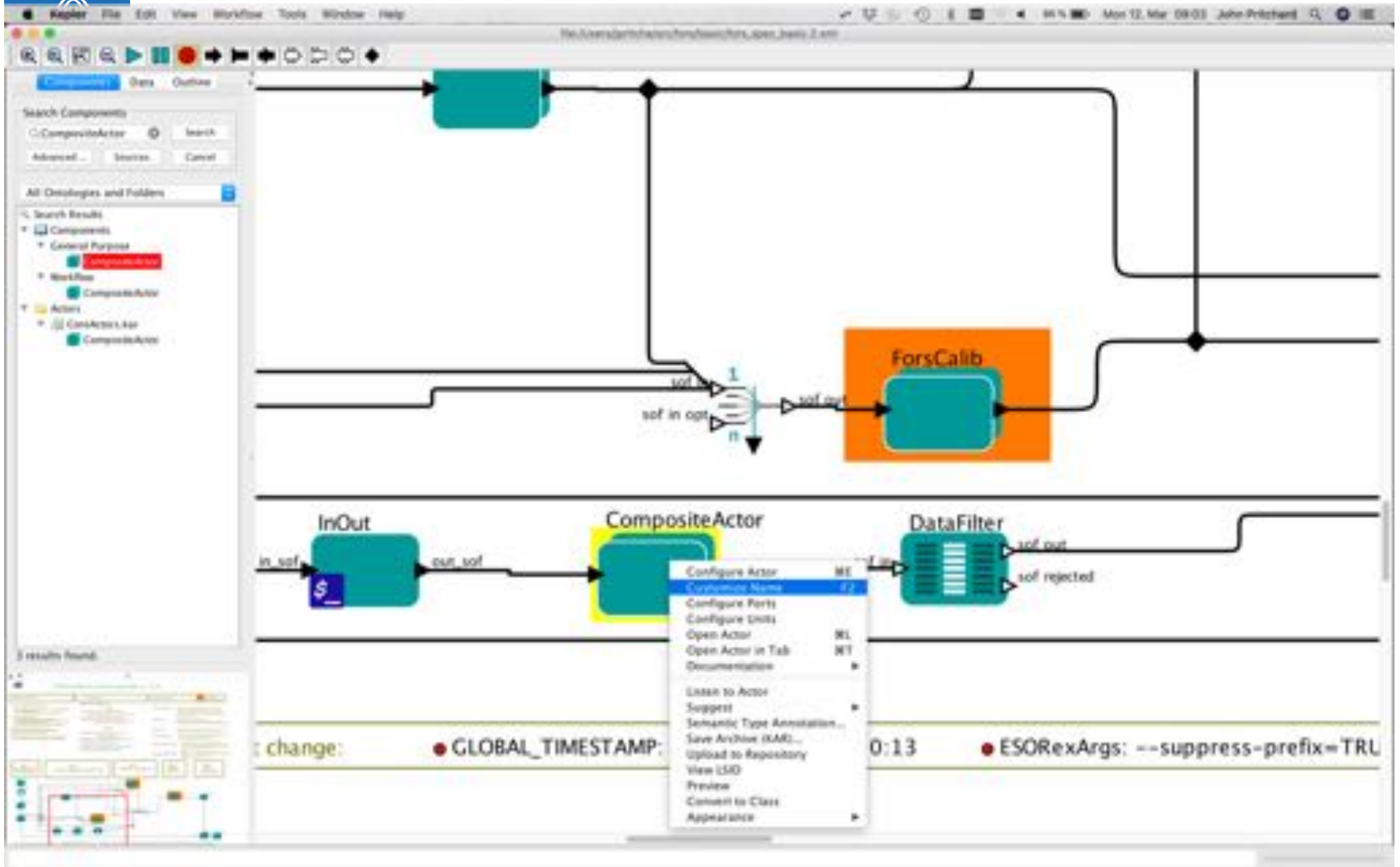


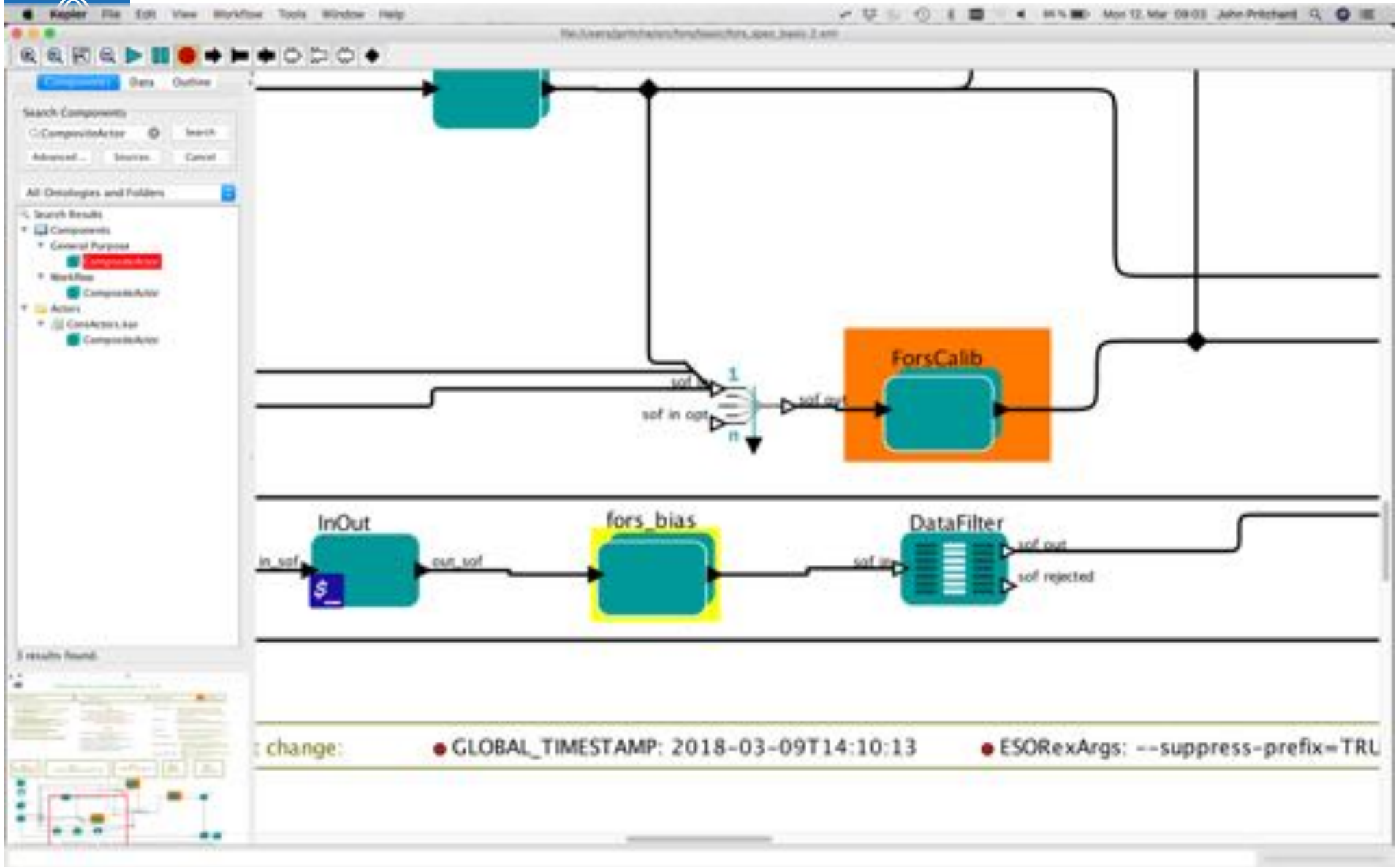


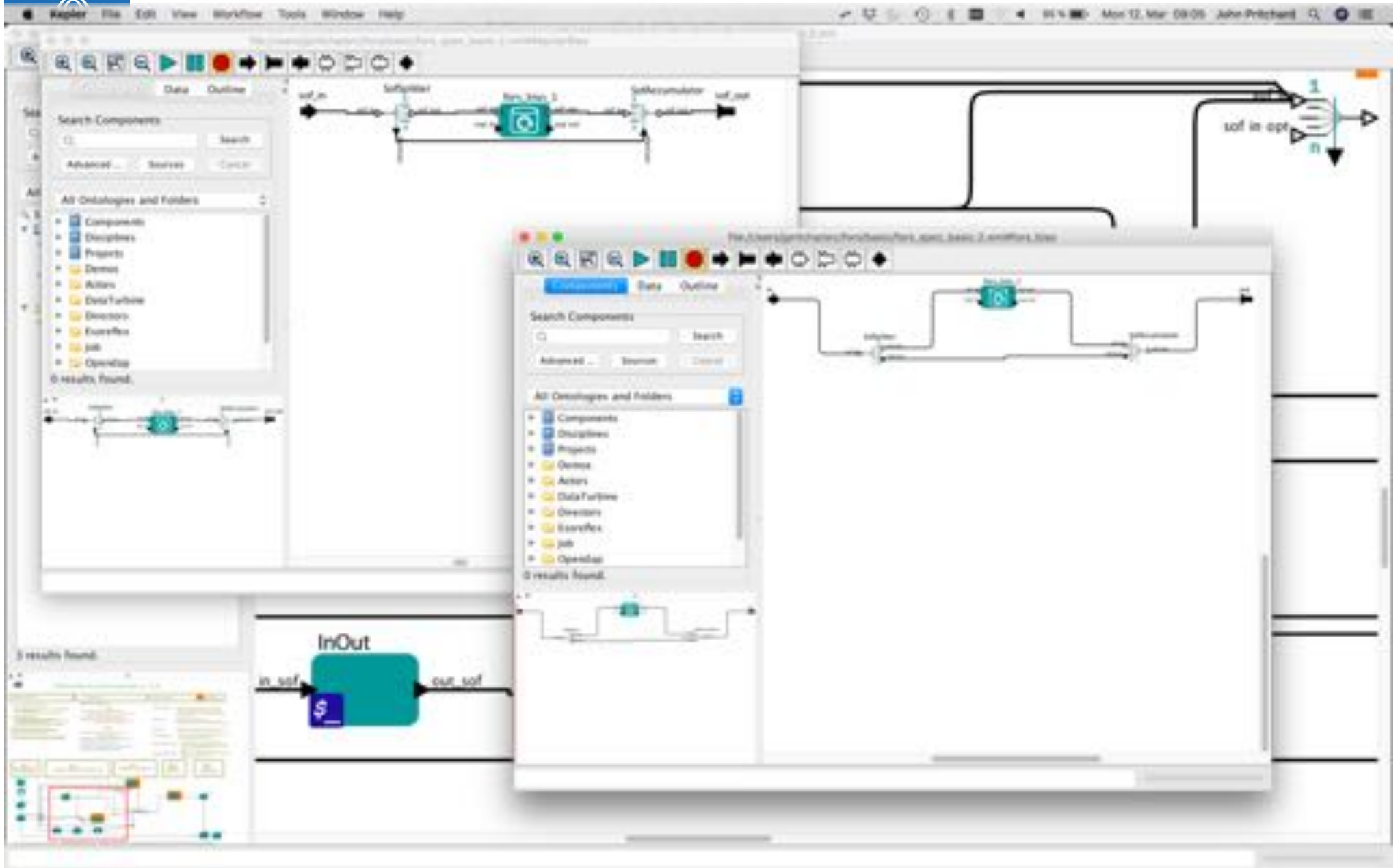


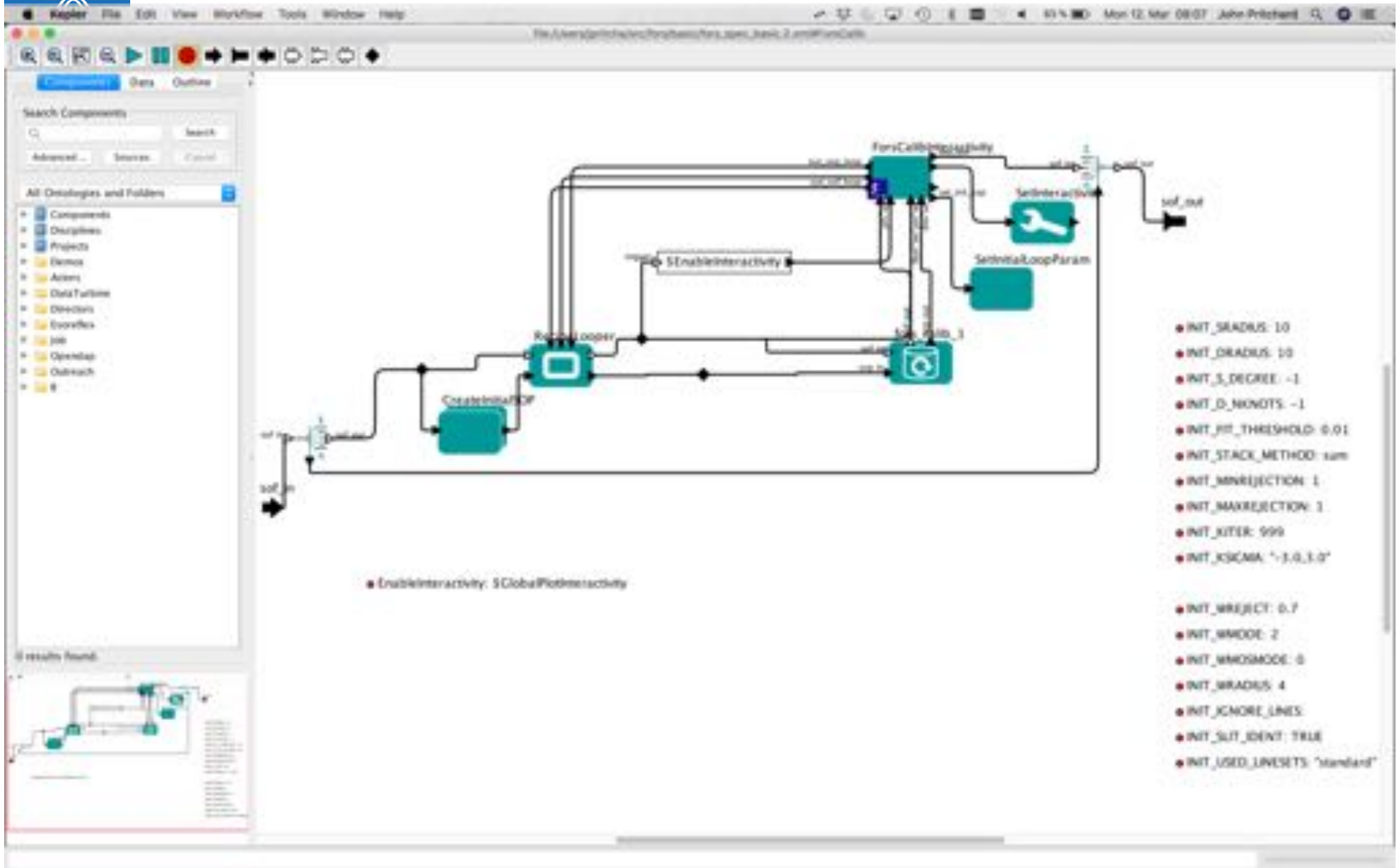
The screenshot shows the Repl IDE interface. At the top, the menu bar includes 'Repl', 'File', 'Edit', 'View', 'Workflow', 'Tools', 'Window', and 'Help'. The main workspace displays a workflow diagram with several components connected by arrows. A search window is open in the foreground, showing search results for 'Component'. The search results are organized into folders: 'General Purpose', 'Workflow', and 'Actors'. Under 'Workflow', there are sub-folders for 'Component', 'CompositeActor', and 'Workflow'. The search results list includes 'Component', 'CompositeActor', 'Workflow', 'Workflow.kar', 'Workflow.kar', 'Workflow.kar', 'Workflow.kar', and 'Workflow.kar'. The search window also shows a search bar, a search button, and a search filter. The workflow diagram in the background shows a 'New Item 2' component and a 'Workflow.kar' component. The search window is titled 'Component' and has a search bar containing 'Component'. The search results are displayed in a list view with icons and text. The search window is also showing a search filter and a search button. The search results are displayed in a list view with icons and text. The search window is titled 'Component' and has a search bar containing 'Component'. The search results are displayed in a list view with icons and text. The search window is also showing a search filter and a search button. The search results are displayed in a list view with icons and text.

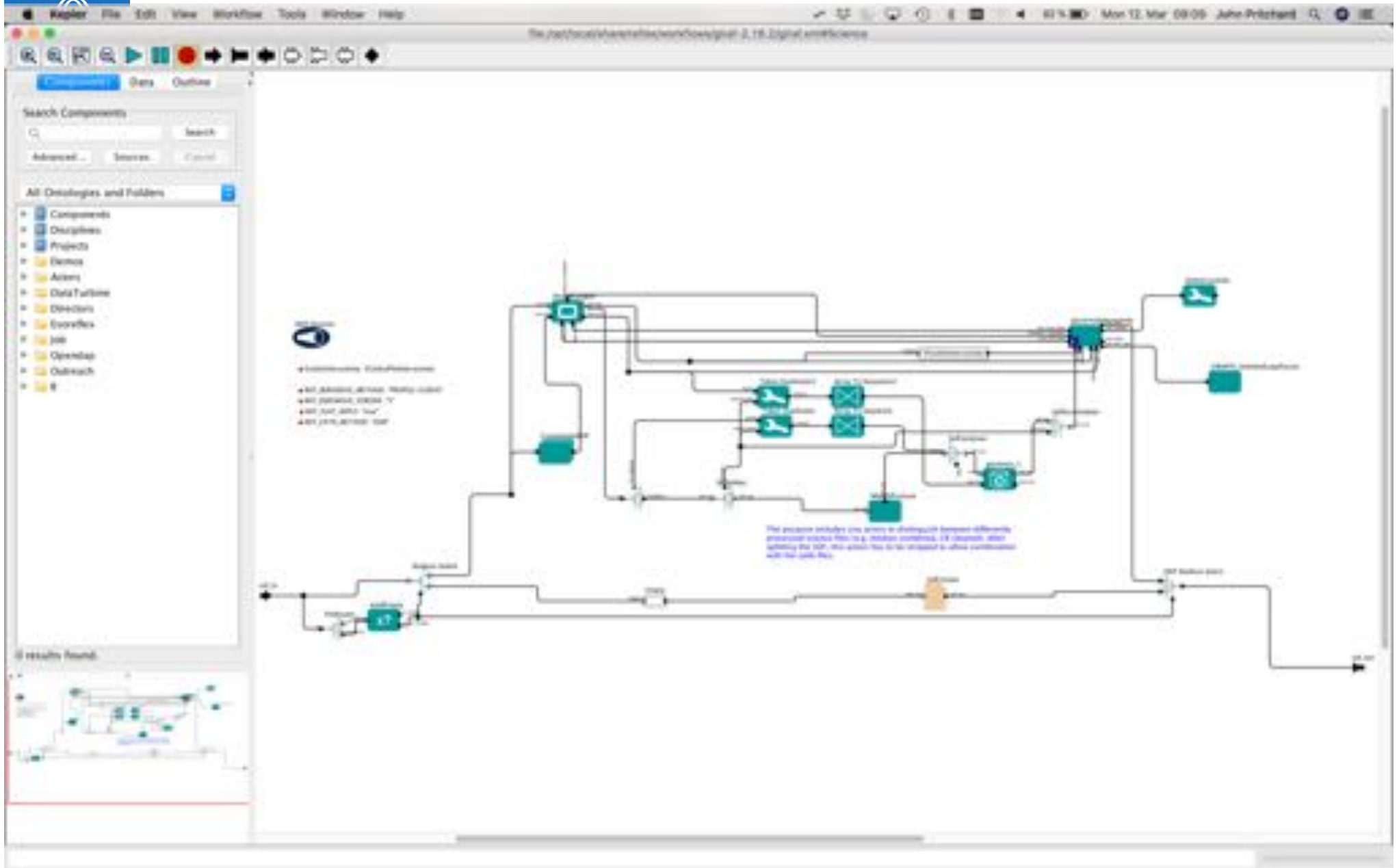














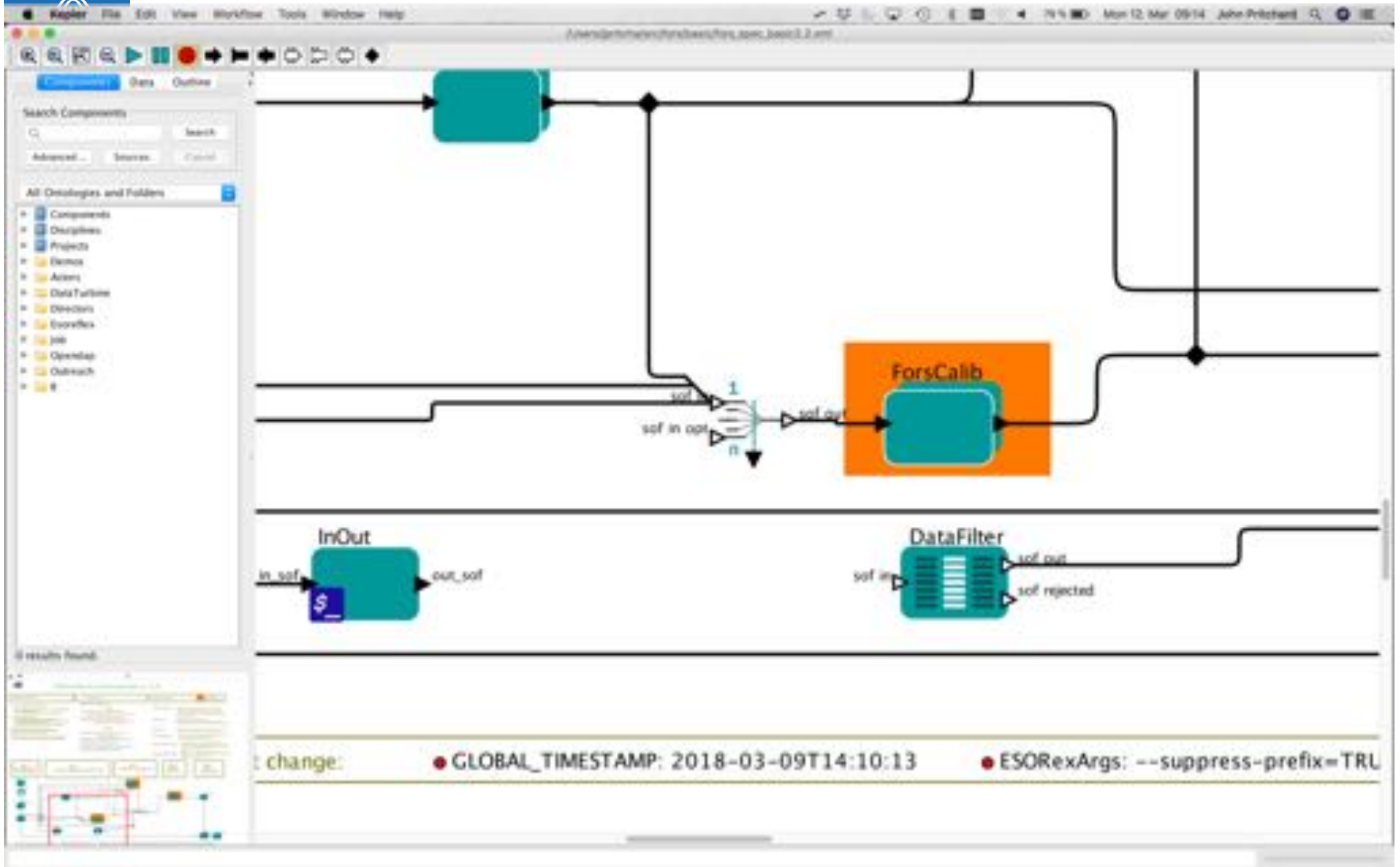
Step 3: Copy paste giraf CRC

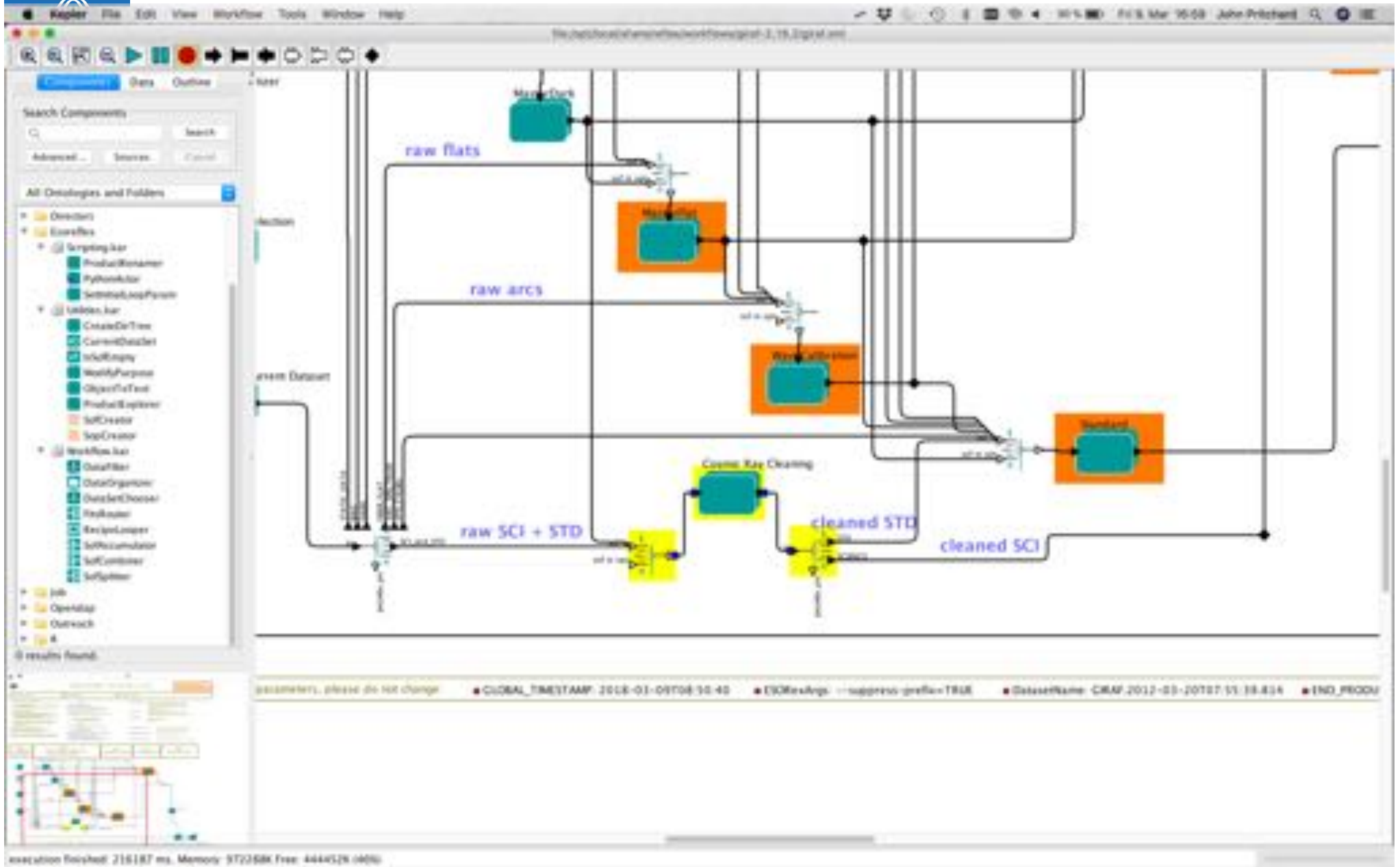
- Remove the `fors_bias` actor.
- Open the giraf workflow
- Select and copy the 'Cosmic Ray Cleaning', the SofCombiner and the FitsRouter actors just before and just after the CRC actor, and the connections between these three
- Paste into the `fors_spec` workflow, and move into position below the DataFilter actor.



Step 3: Copy paste giraf CRC

- Make a new connection from the 'sof in' port of the SofCombiner to the relation just after the MasterBias actor
- Reconnect the 'sof out' port of the InOut actor to the 'sof in' port of the SofCombiner
- Make a new connection from the 'SCIENCE' port of the FitsRouter to the 'sof in' port of the DataFilter







Workflow instructions

Setup Directories

Global Parameters

Step 1: Data Organisation and Selection

Step 2: Creation of Master Calibration Files

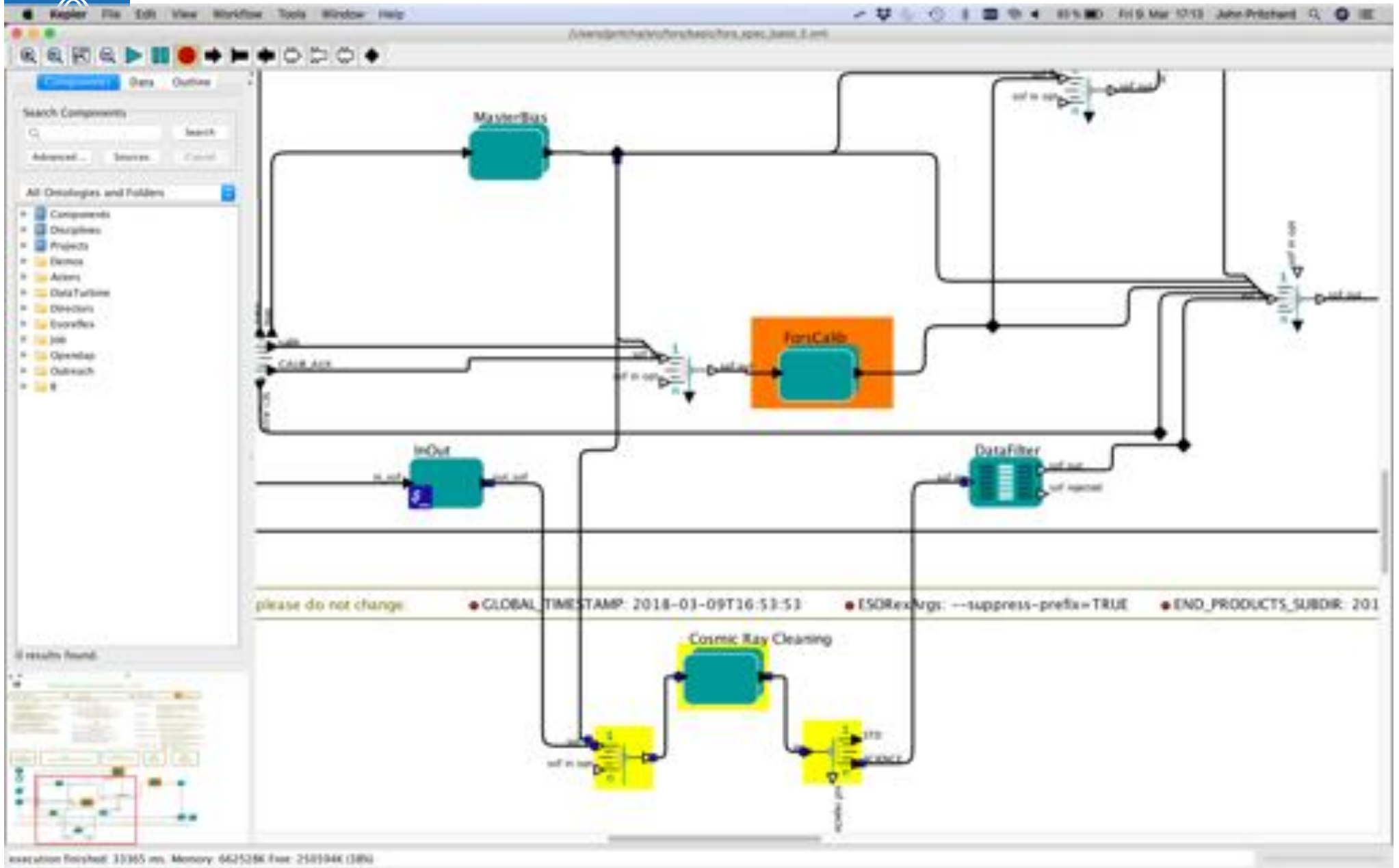
Step 3: Response computation

Step 4: Science Reduction

Step 5: Output Organisation

execution finished: 33365 ms, Memory: 662528K Free: 218194K (38%)





Step 4: adapt giraf to fors

- Ok so it ran past the CRC actor without crashing, but then the DataFilter is empty and continuing the science recipe crashes because there is no science file. So what's wrong?
- In a nutshell, the GIRAF science data have category SCIENCE, while the FORS spec' data have one of SCIENCE_MXU, SCIENCE_MOS or SCIENCE_LSS. So this needs to be fixed in the workflow and the python script.
- Check the categories of the science coming out of the master FitsRouter

Step 4: adapt giraf to fors

- Edit the parameters of the FitsRouter just after the CRC actor
- Add a parameter:
 - Class = `ptolemy.data.expr.Parameter`
 - Name = `SCIENCE_config` (the name of the port plus “_config”)
 - Default value = `"SCIENCE_MXU,SCIENCE_MOS,SCIENCE_LSS"`
- Open (not edit) the CRC actor and do the same to the FitsRouter actor just after the Input port

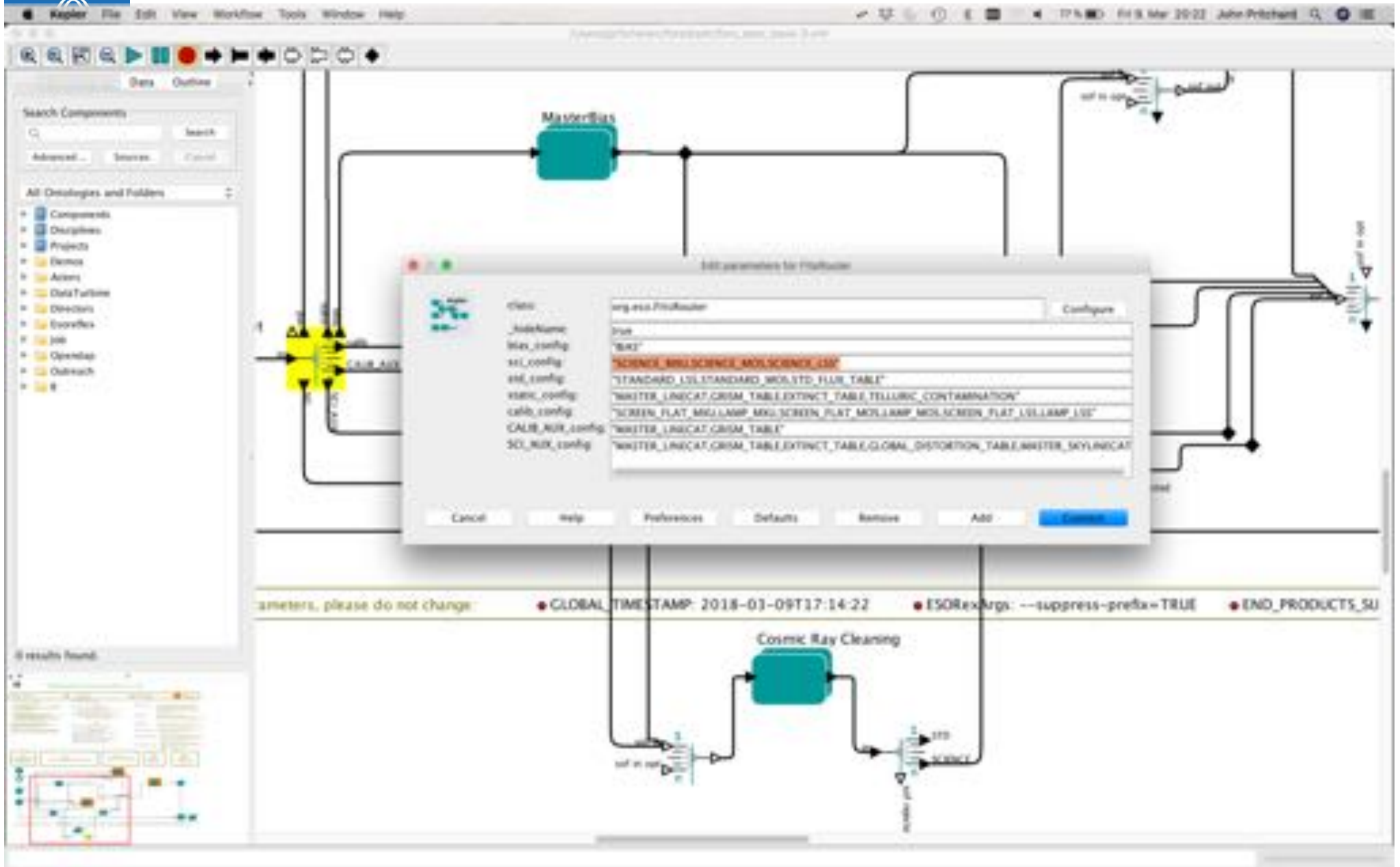


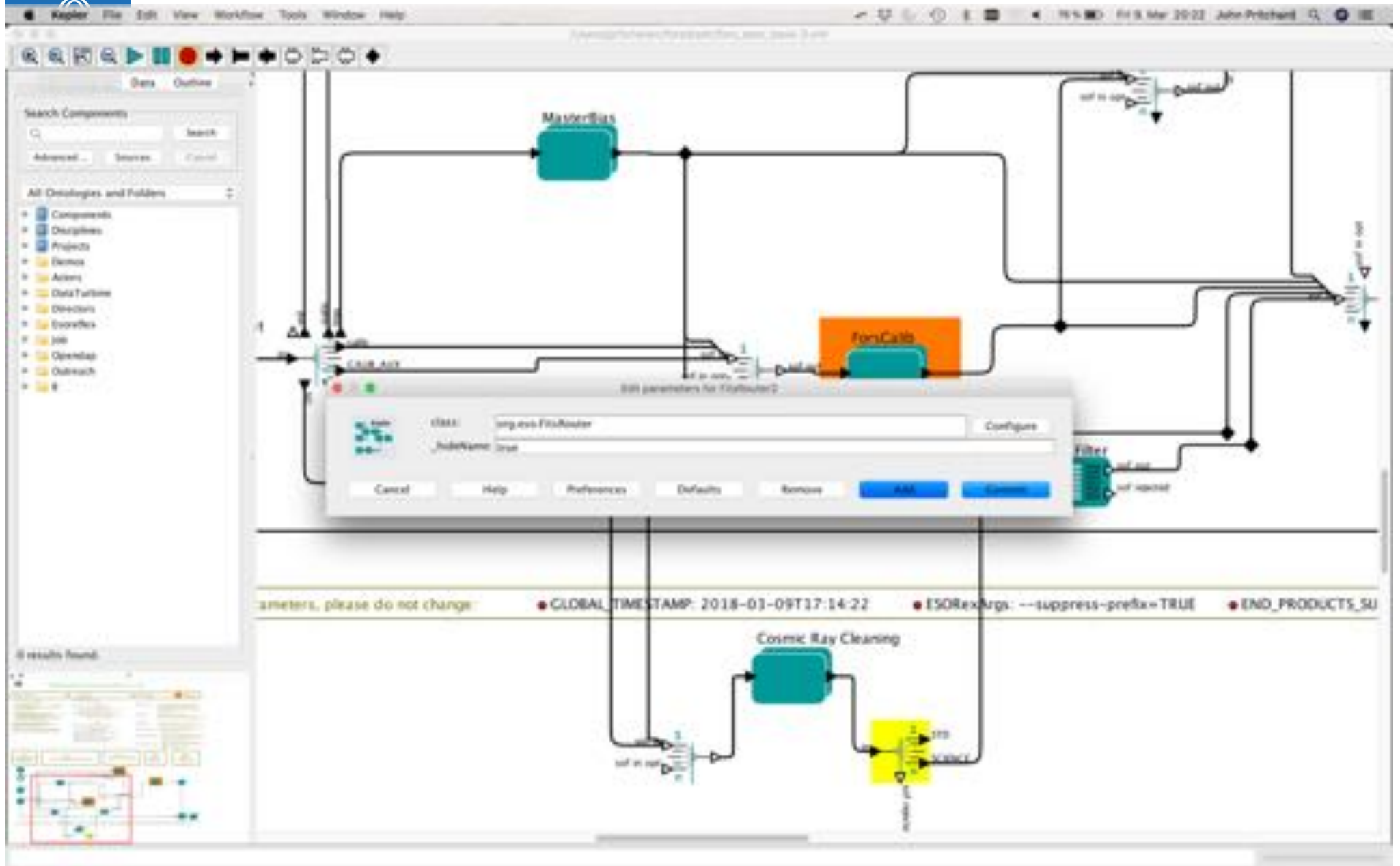
Step 4: adapt giraf to fors

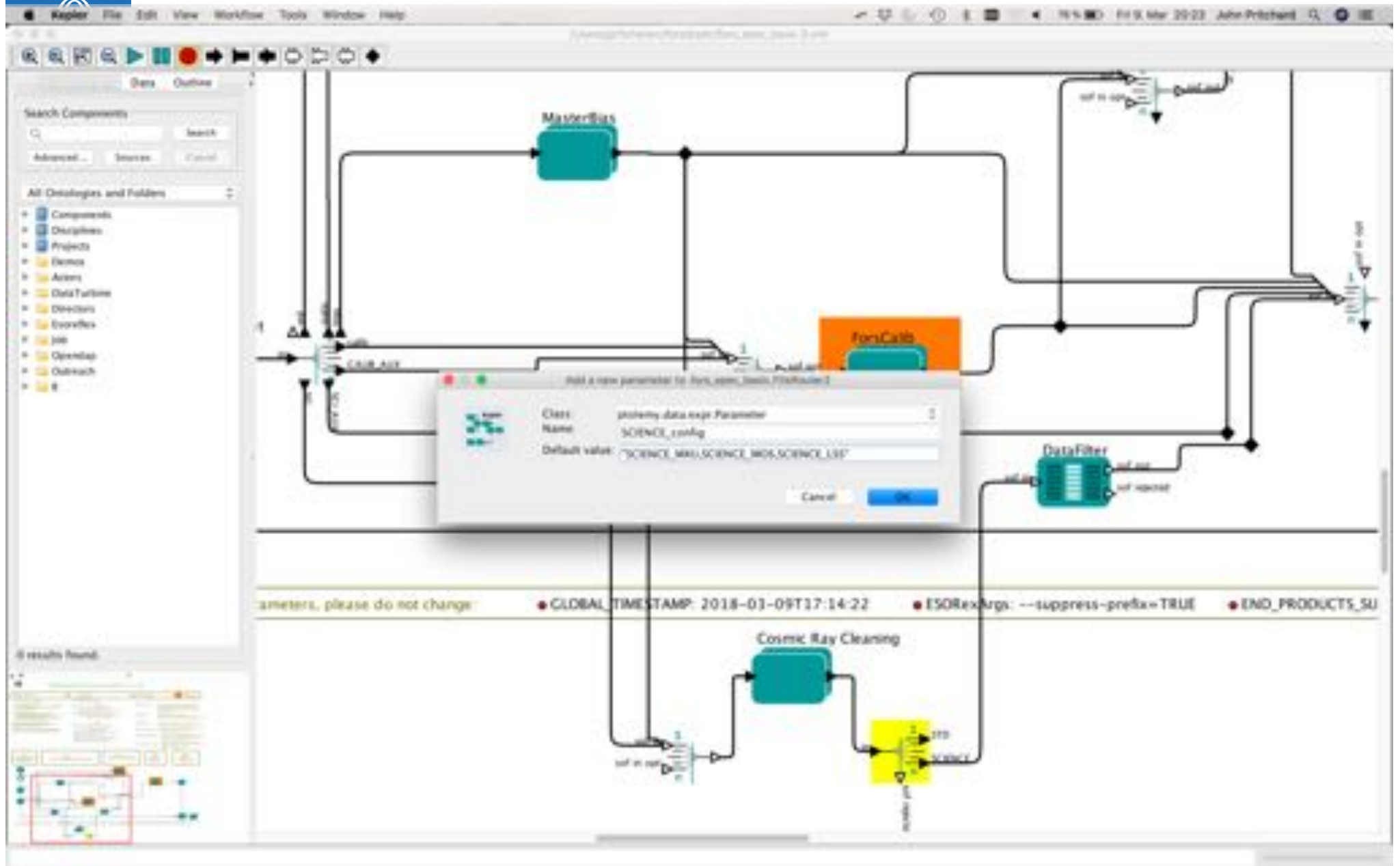
- Edit the parameters of the Astroscrappy actor
- Copy the name of the Python script.
- In a terminal, copy that python script file to the local directory:

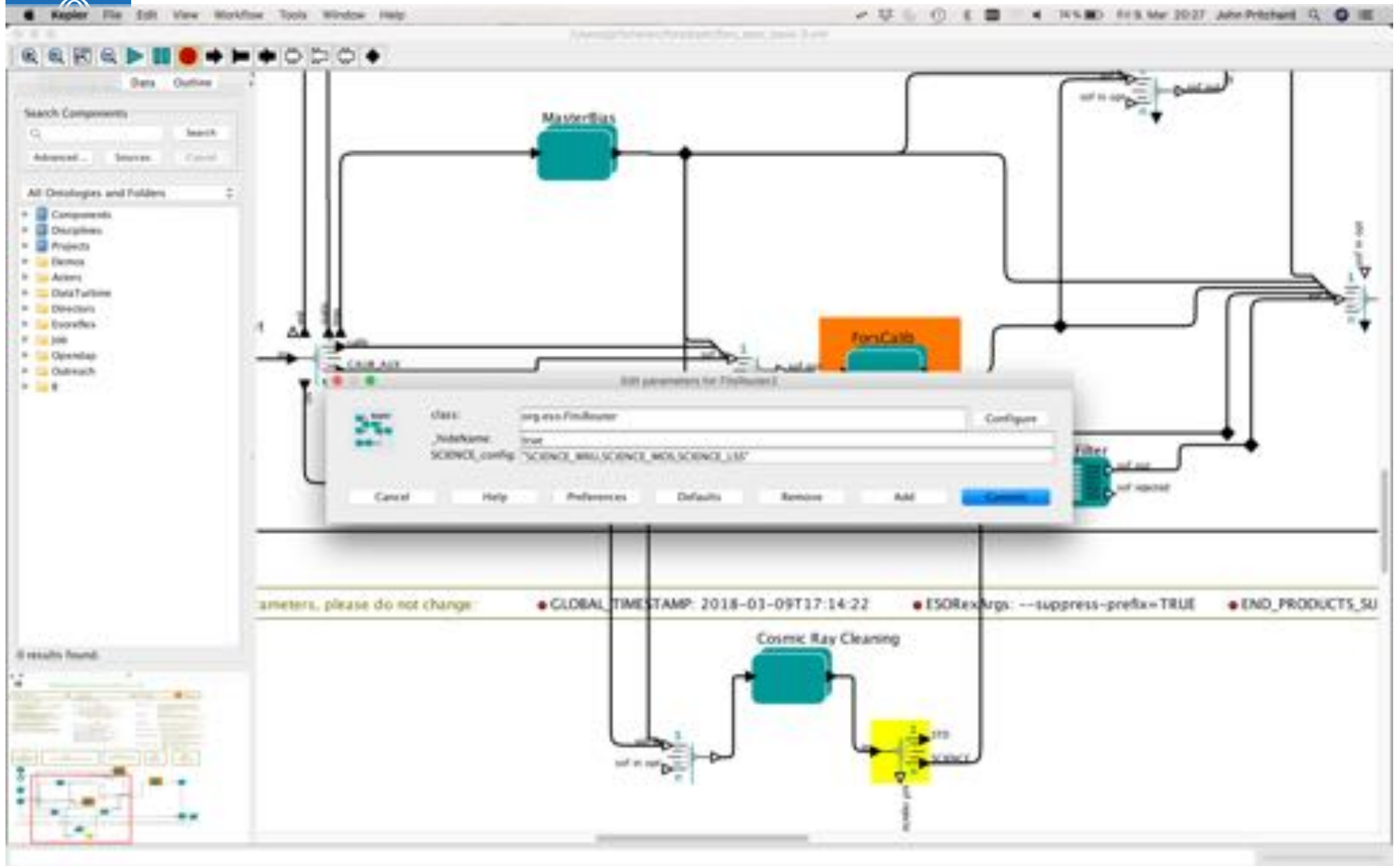
```
cp /opt/local/share/esopipes/giraf-2.16.2/reflex/giraf_astroscrappy_multi.py fors_astroscrappy_multi.py
```

- Adapt the python script appropriately... 😊
- Set the Python script to the fors_astroscrappy_multi.py, make sure that it has the full path to the file.









Workflow to clean Cosmic Rays

Three strategies are used to clean Cosmic Rays (bad pixels). The first one is to median combine all incoming frames. The second and third perform Cosmic Ray detection and interpolation of each individual frame using Python modules PyCosmic and Astrocrappy.

Note that a (different) action is added to the purpose of each output frame so that they can later be separated for separate science processing.

- EnablePyCosmic: true
- EnableAstrocrappy: true

Workflow diagram showing the process of cleaning Cosmic Rays. The workflow starts with 'sof_in' and goes through a 'MedianCombine' block, then a 'FixAstrocrappy' block, and finally an 'Astrocrappy' block. A 'Cosmic Ray Cleaning' block is also shown. A configuration window for 'org.ana.FixRouter' is open, showing 'SCIENCE_CONFIG' set to 'SCIENCE_NRS/SCIENCE_MOS/SCIENCE_LIST'.



The screenshot displays the Kepler software interface. A configuration dialog box titled "Edit parameters for Astroscopy" is open, showing various settings for a Python script. The dialog includes fields for "Python script" (with a browse button), "Run in terminal", "Lazy Mode" (set to "Stop"), "Recipe Failure Mode", "Disable logging", "Clean Temporary Directories", "Products Dir" (17MP_PRODUCTS_DIR), "Logs Dir" (LOGS_DIR), "Bookkeeping Dir" (BOOKKEEPING_DIR), "Bookkeeping DB" (BOOKKEEPING_DB), "FITS Viewer" (FITS_VIEWER), and "Data" (org.esa.pythonactor). The dialog also has buttons for "Cancel", "Help", "Preferences", "Defaults", "Remove", "Add", and "Connect".

The background shows a workflow editor with several components connected by lines. A component labeled "Astroscopy" is highlighted in yellow. Other components include "FixAstroscopy", "1EnableAstroscopy", and "Cosmic Ray Cleaning". The workflow is connected to a "ToleranceUpdate" component, which is connected to an "out" port.



```
Terminal Shell Edit View Window Help
base: ~/groch@mac02407-chemforchem -- ssh -- 208x57
groch@mac02407-chemforchem: ~$
# "ROK ID: glraf_astromcrazy_wlrl.py 201312 2017-04-21 12:18:472 rpa1sa F"
# Report the needed modules
try:
    import reflex
    import sys
    import os
    try:
        from astropy.io import fits as pyfits
    except:
        import pyfits
    import numpy
    import logging
    import astromcrazy
    report_success = True

def astromcrazy_wlrl():

    # get Kepler parameters:
    parameters= []
    for p in sys.argv[1:]:
        parameters(p.split("-")[0])> p.split("-")[1]

    #Define one output file for every input file:
    outputs_out_wlrl = inputs_in_wlrl
    files = outputs_out_wlrl.files

    masterblases=[]
    subblases=[]
    for file in files:
        if file.category == 'MASTER_BIAS':
            for p in file.purposes:
                masterblases[p]=file
        if file.category == 'NO_PDCL_MAP':
            for p in file.purposes:
                subblases[p]=file

    outfiles=list()
    for file in files:
        #select a file category:
        purpose=file.purposes[0]
        try:
            HDU=pyfits.open(file.name)
        except:
            try:
                logging.error("Could not open file %s" %file.name)
            except:
                pass
            sys.exit()
        if purpose in masterblases:
            try:
                HDU=pyfits.open(masterblases[purpose].name)
            except:
                try:
                    # "ROK ID: glraf_astromcrazy_wlrl.py 201312 2017-04-21 12:18:472 rpa1sa F"
                    # Report the needed modules
                    try:
                        import reflex
                        import sys
                        import os
                        try:
                            from astropy.io import fits as pyfits
                        except:
                            import pyfits
                        import numpy
                        import logging
                        import astromcrazy
                        report_success = True

                    def astromcrazy_wlrl():

                        # get Kepler parameters:
                        parameters= []
                        for p in sys.argv[1:]:
                            parameters(p.split("-")[0])> p.split("-")[1]

                        #Define one output file for every input file:
                        outputs_out_wlrl = inputs_in_wlrl
                        files = outputs_out_wlrl.files

                        masterblases=[]
                        subblases=[]
                        for file in files:
                            if file.category == 'MASTER_BIAS':
                                for p in file.purposes:
                                    masterblases[p]=file
                            if file.category == 'NO_PDCL_MAP':
                                for p in file.purposes:
                                    subblases[p]=file

                        outfiles=list()
                        for file in files:
                            #select a file category:
                            purpose=file.purposes[0]
                            try:
                                HDU=pyfits.open(file.name)
                            except:
                                try:
                                    logging.error("Could not open file %s" %file.name)
                                except:
                                    pass
                                sys.exit()
                            if purpose in masterblases:
                                try:
                                    HDU=pyfits.open(masterblases[purpose].name)
                                except:
                                    try:

```


Kepler File Edit View Workflow Tools Window Help

Workflow Instructions

Setup Directories

Global Parameters

FORS Workflow For Spectroscopy Data (v. 5.3.31)

Workflow Instructions

To update workflow to the latest version:

- Click on "Help/Getting Started" -> "Workflow at Kepler"
- Click on "Help/Getting Started" -> "Workflow at Kepler"
- Click on "Help/Getting Started" -> "Workflow at Kepler"

To create a different data set:

- Click on "Help/Getting Started" -> "Workflow at Kepler"
- Click on "Help/Getting Started" -> "Workflow at Kepler"
- Click on "Help/Getting Started" -> "Workflow at Kepler"

The general operation of Kepler can be described as follows:

Workflow updated with new parameters (see the Global Parameters section)

Setup Directories

Global Parameters

Workflow Diagram:

Step 1: Data Organisation and Selection

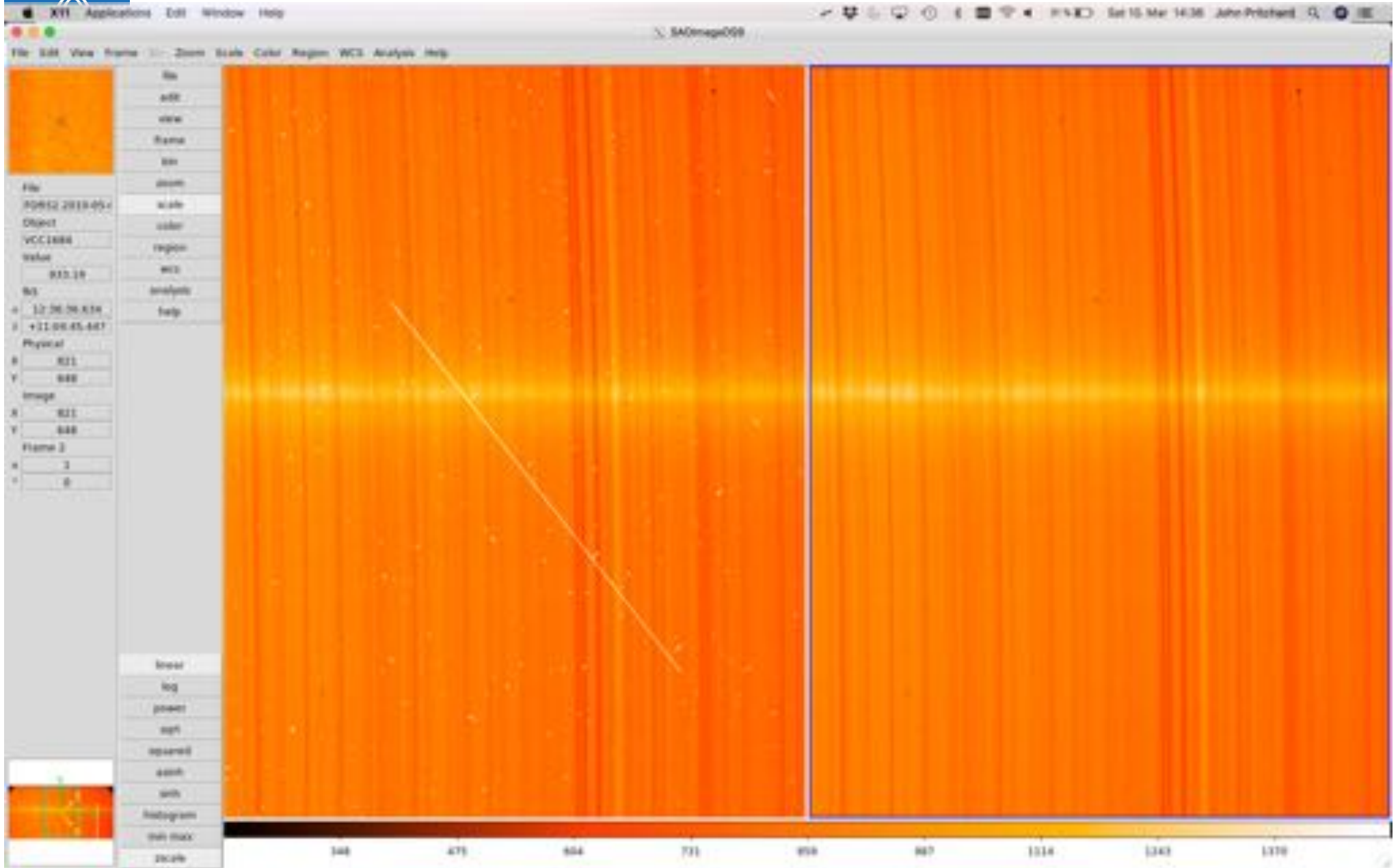
Step 2: Creation of Master Calibration Files

Step 3: Response computation

Step 4: Science Reduction

Step 5: Output Organisation

execution finished: 647489 ms. Memory: 871424K Free: 421223K (49%)





X11 Applications Edit Window Help

FORIS Workflow For Spectroscopy Data (v. 5.3.31)

FORIS Interactive Science Reduction

Search Components

Advanced ... Sources Cancel

All Ontologies and Folders

- Components
- Disciplines
- Projects
- Explan
- Actions
- Data/Tutorials
- Directors
- Exercises
- Jobs
- Operations
- Outreach
- 8

0 results found

Mapped science (not flux-calibrated)

Extracted science spectrum (not flux-calibrated)

Target name: VCC3484
Grism/Filter: GRIS_1600V/free slit name (LSS): IRIS1_3arcsec

NOISE FILTERING

Use extension: [Spectroscopy] [None]

skipped
removed
masked
center

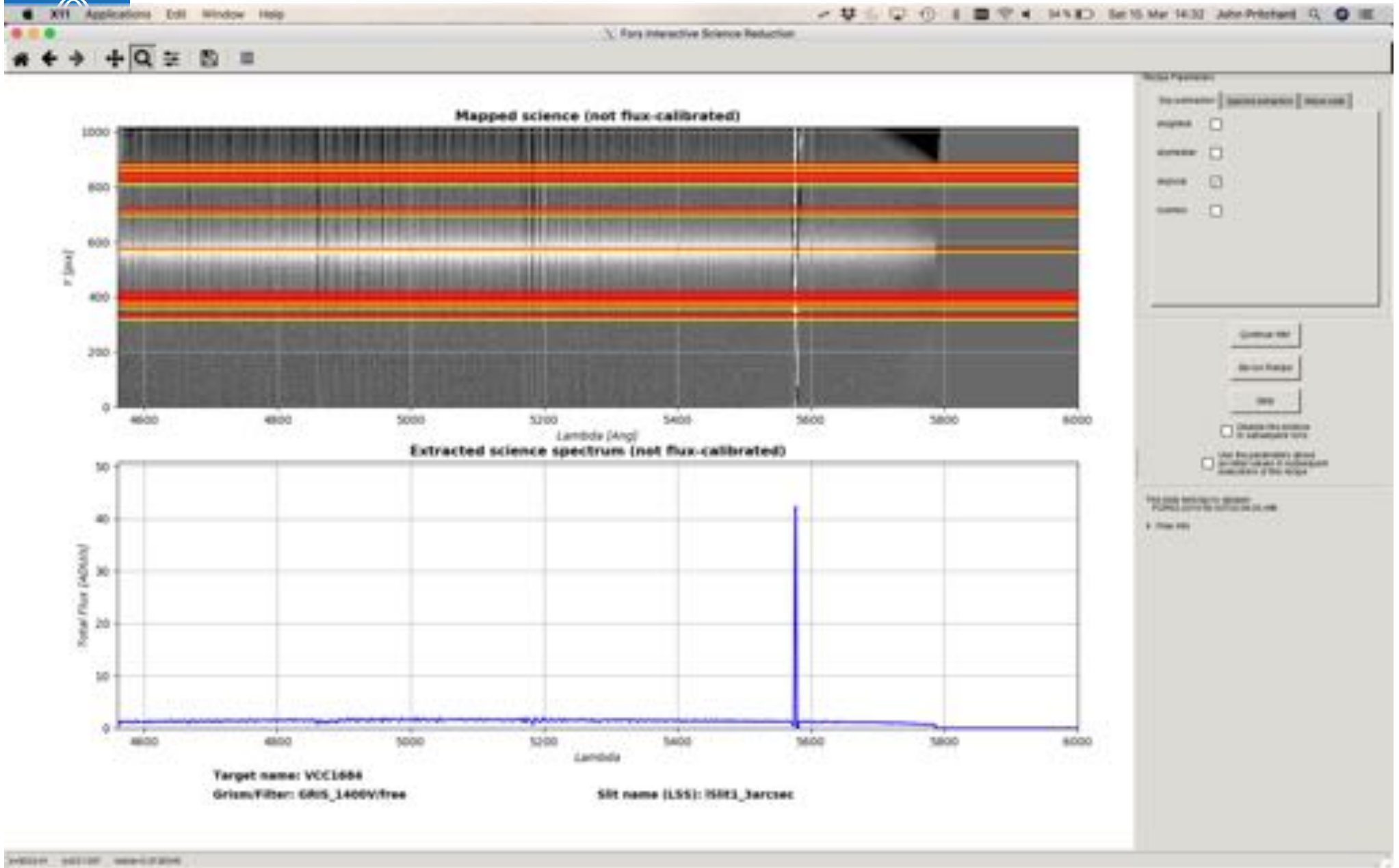
Continue All
Reset Filter
OK

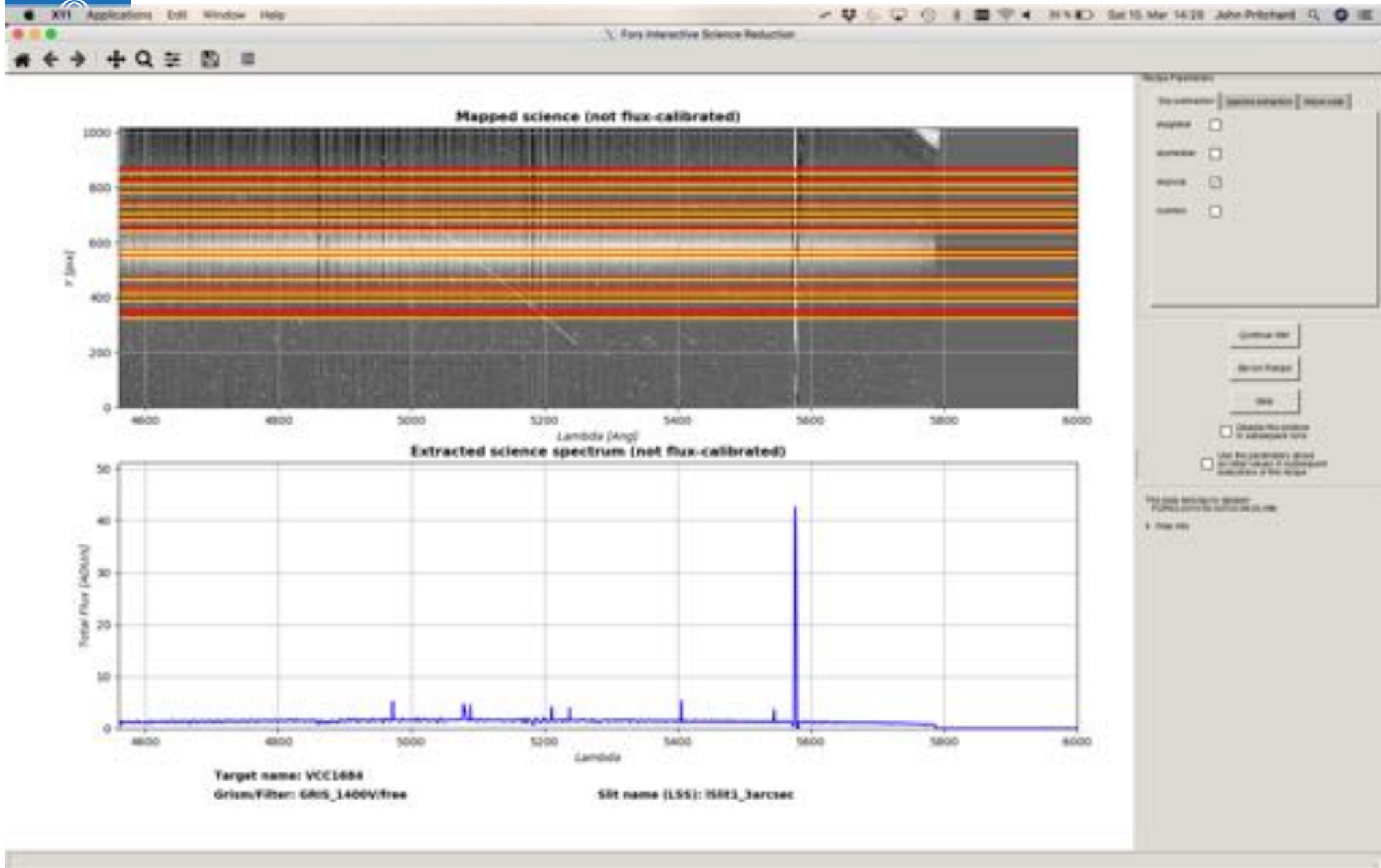
Search procedure in subsequent runs
 Use the coordinates above as filter values in subsequent iterations of this step

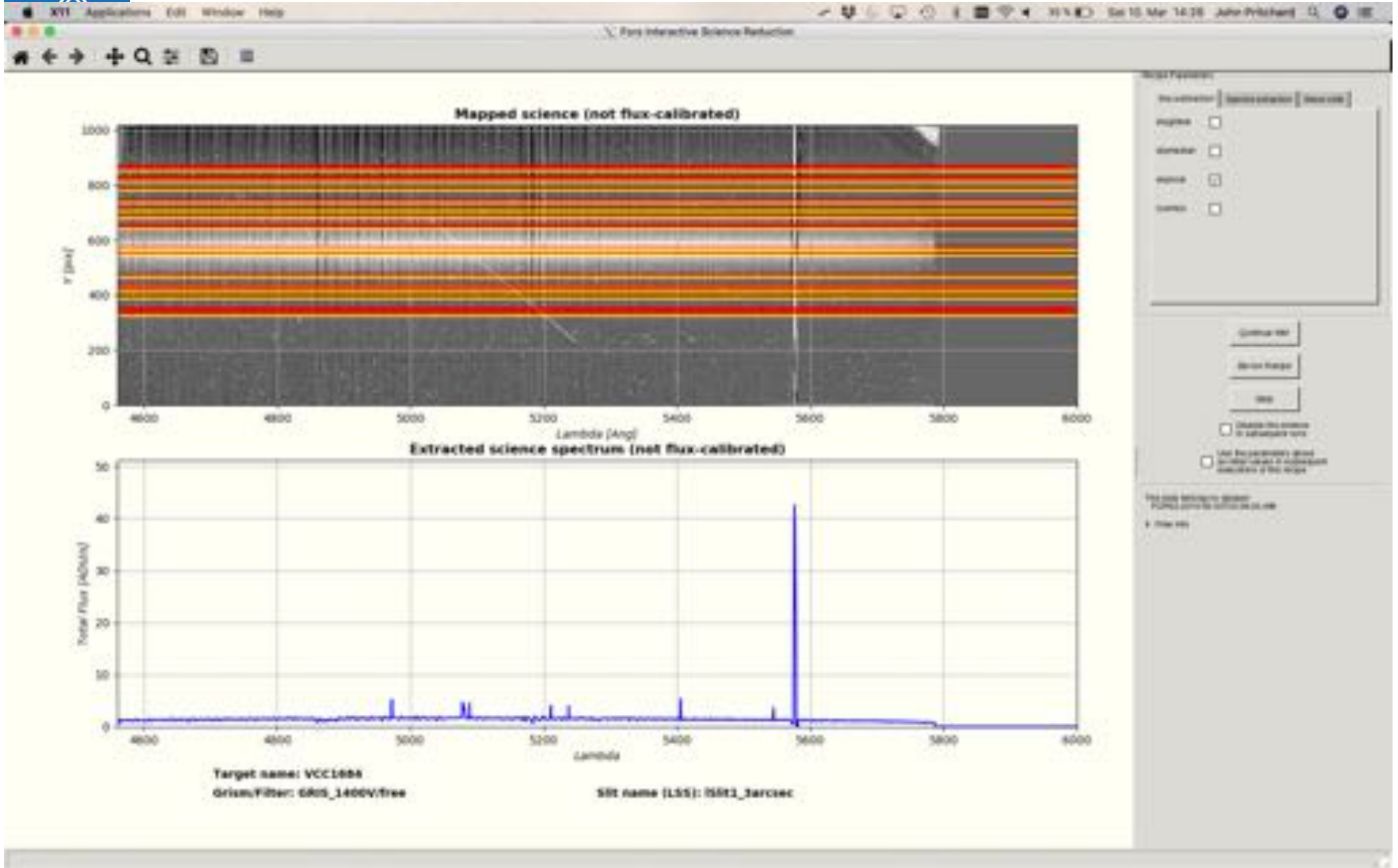
You are viewing the output of the FORIS Interactive Science Reduction

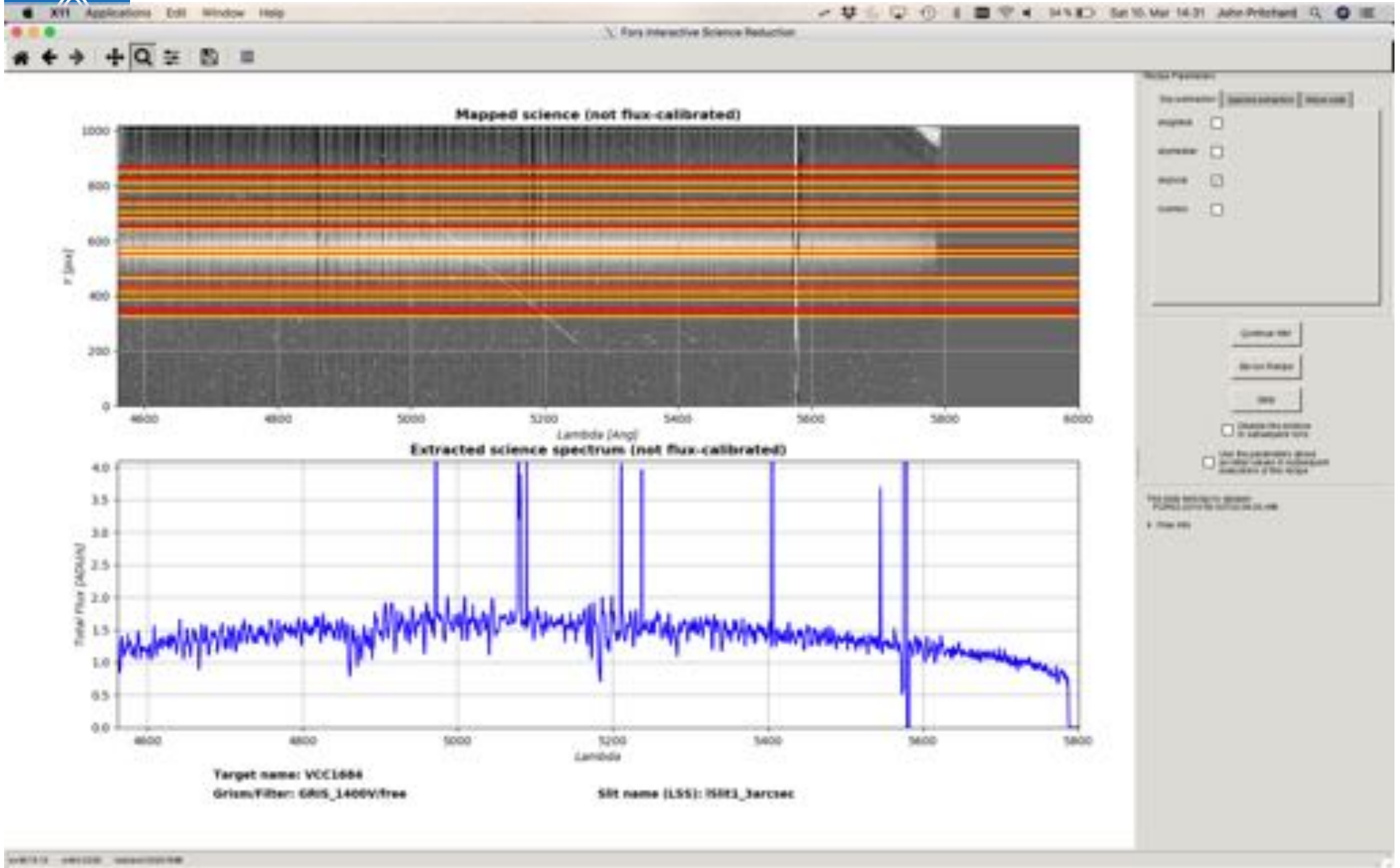
1 Run All

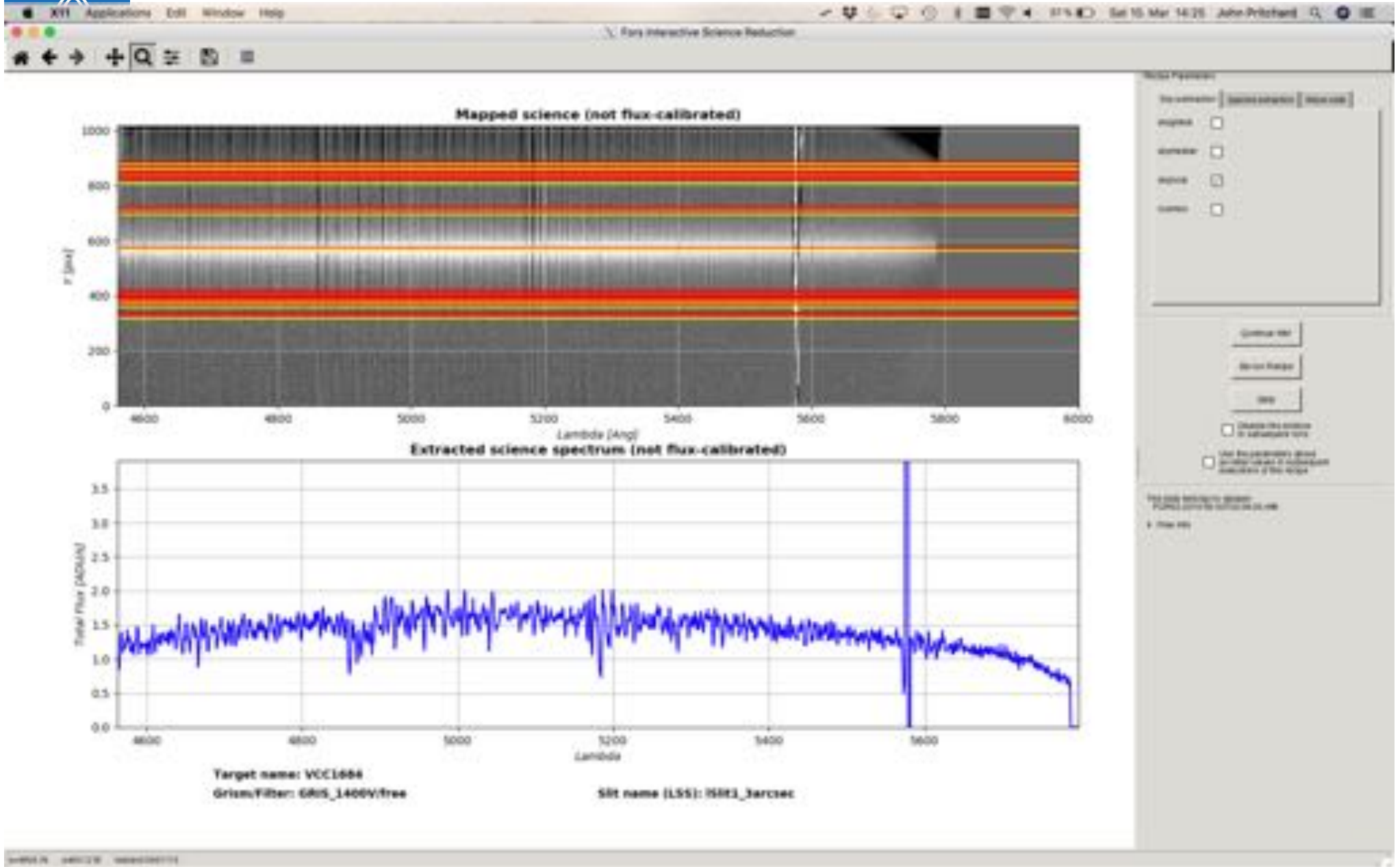
Executing

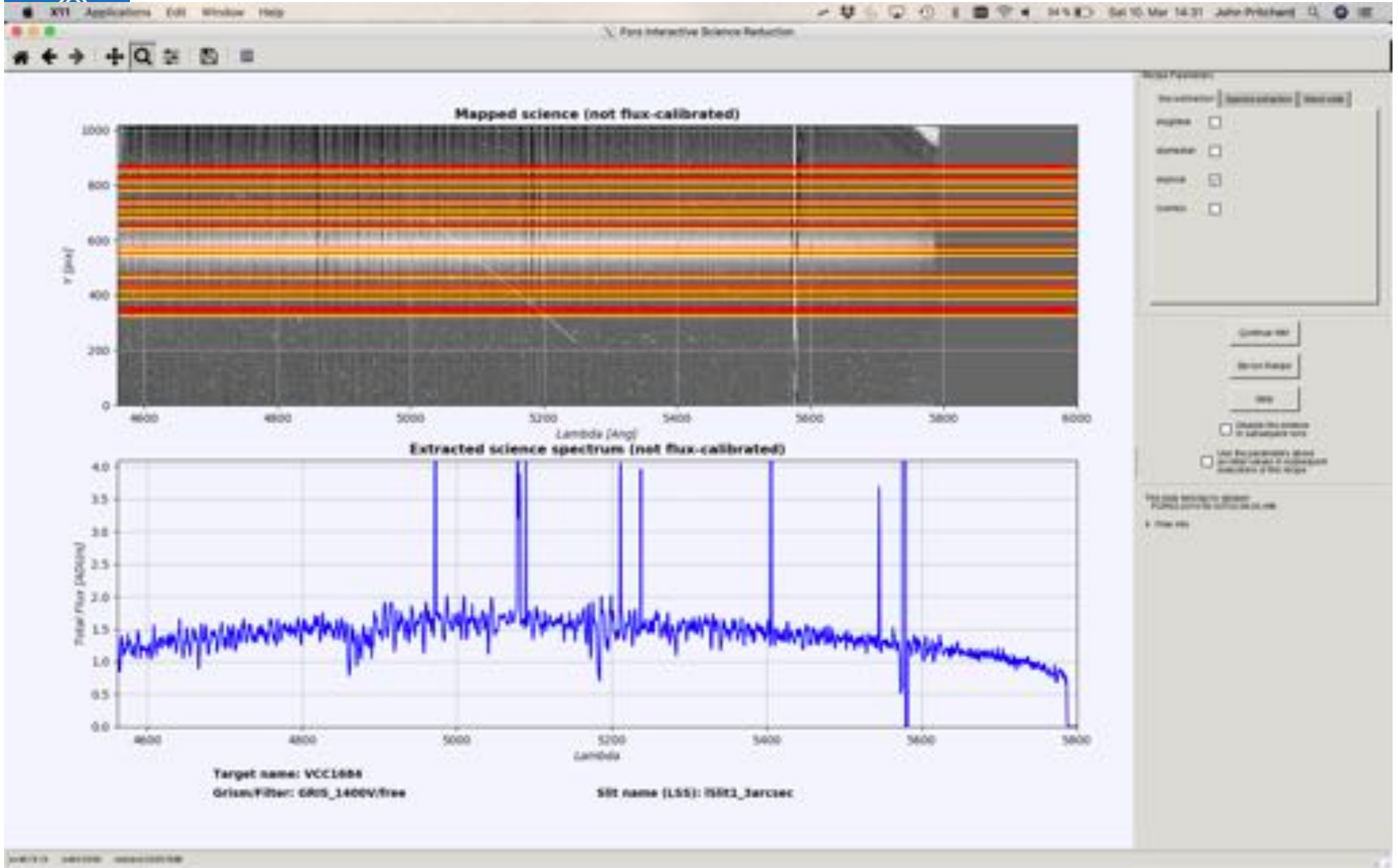






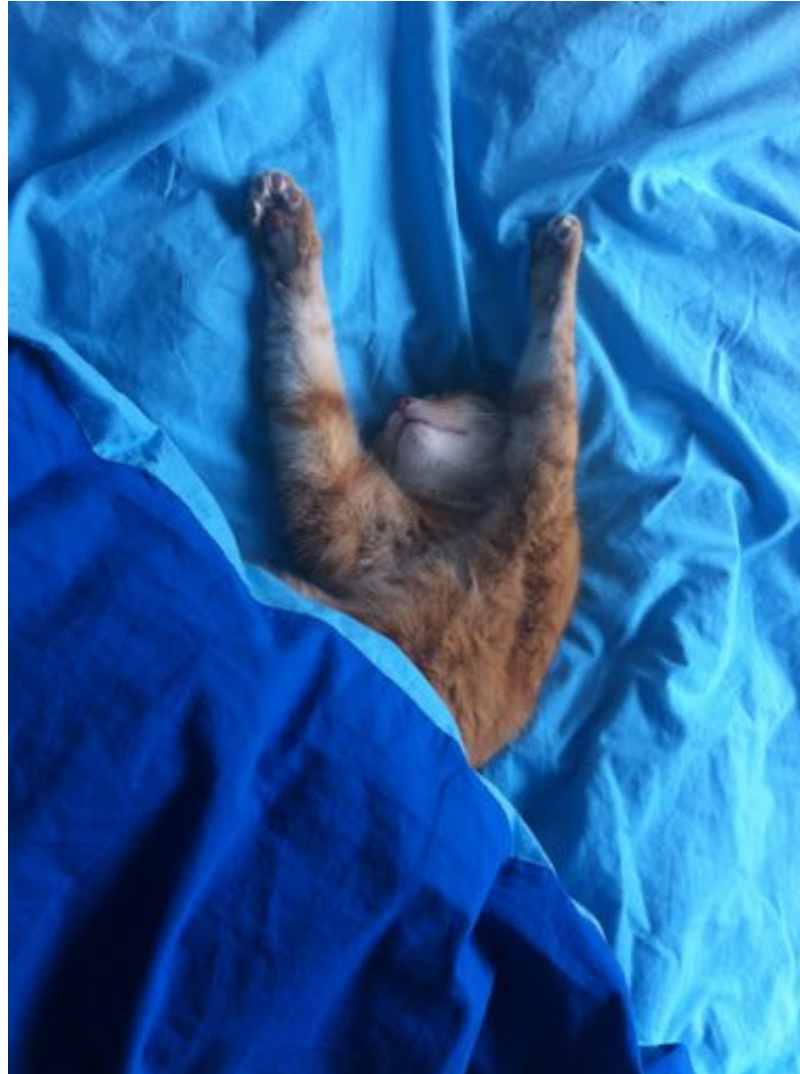






The end...really this time...

- And that really is “How to modify a workflow...”





Oh, and one more thing...

- Exercises for the workshop participants...
 - Implement the PyCosmic and Median+Pass-Thru
 - Implement the handling of multiple versions of the same RAW file in the ForsScience actor
 - Implement the handling of multiple versions of the same RAW file in the ForsScience actor GUI interface

Actually I've done all this (except the last step) but it is a bit beyond the scope of today's presentation... but I hope it will find its way – when finished with the last step – into the public release of the workflow (if not for 2018, then at least for 2019).