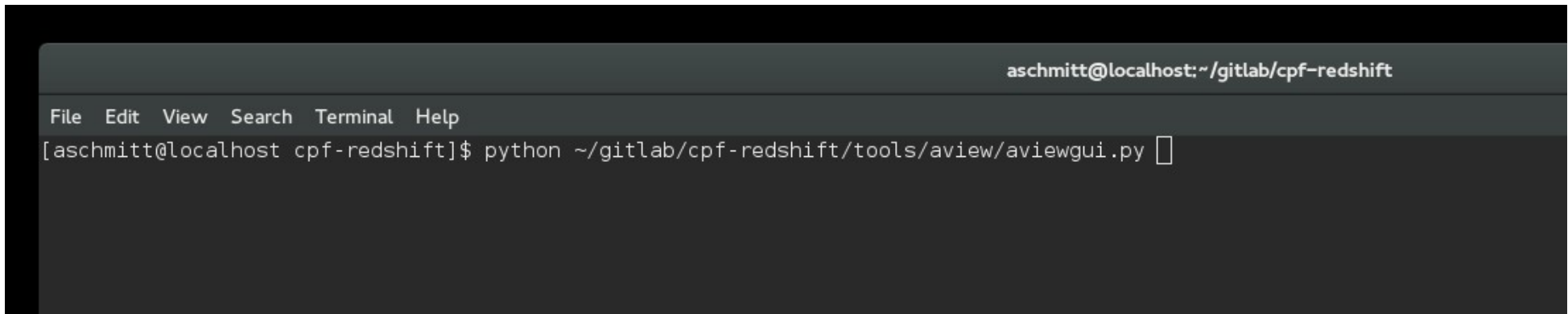


# aviewgui.py

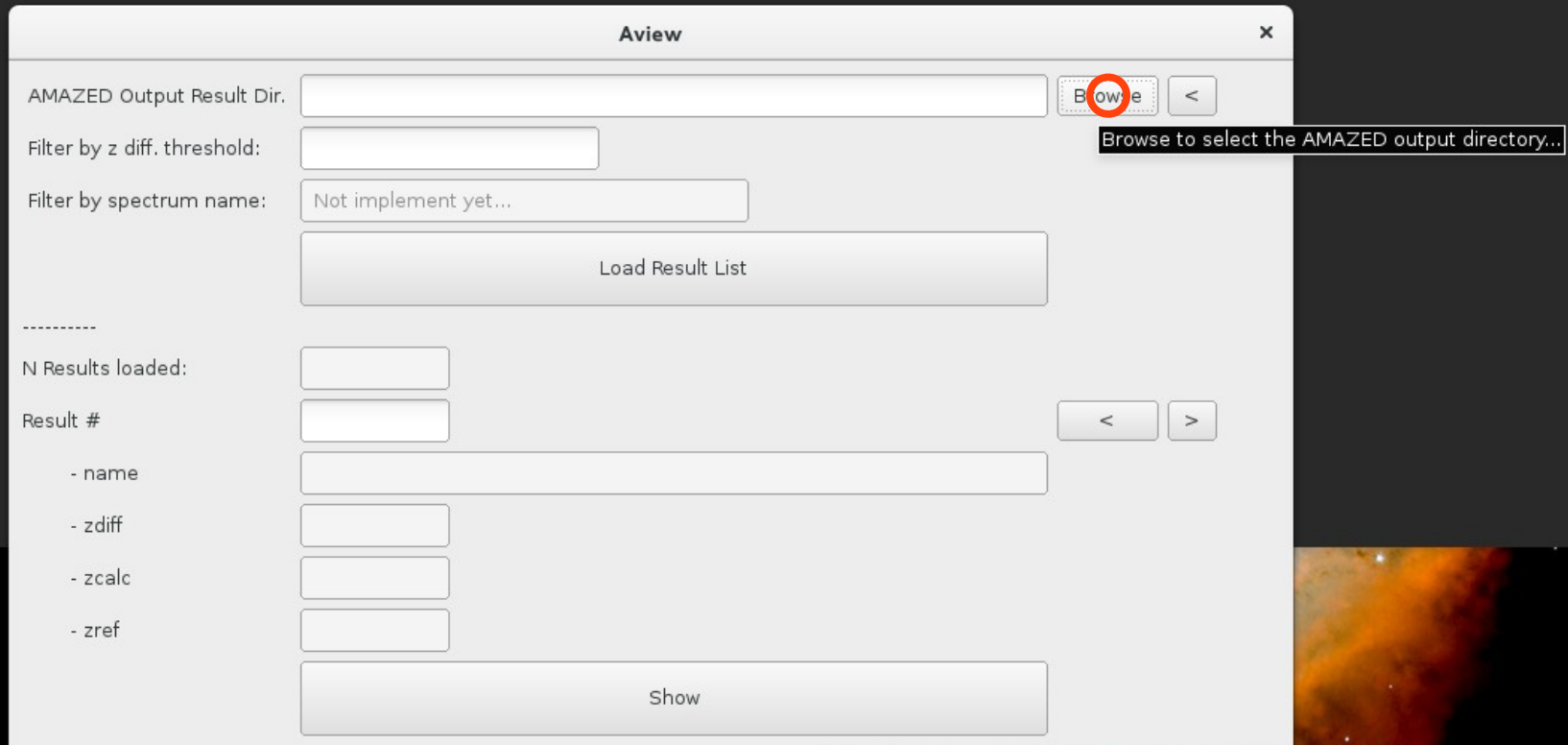
Quick Start  
2016/01/05

# Start the script

A terminal window with a dark background. The title bar at the top reads "aschmitt@localhost: ~/gitlab/cpf-redshift". Below the title bar is a menu bar with the options "File", "Edit", "View", "Search", "Terminal", and "Help". The main area of the terminal shows a command prompt "[aschmitt@localhost cpf-redshift]" followed by the command "python ~/gitlab/cpf-redshift/tools/aview/aviewgui.py" and a cursor icon.

```
aschmitt@localhost: ~/gitlab/cpf-redshift
File Edit View Search Terminal Help
[aschmitt@localhost cpf-redshift]$ python ~/gitlab/cpf-redshift/tools/aview/aviewgui.py
```

# Browse to the AMAZED output directory

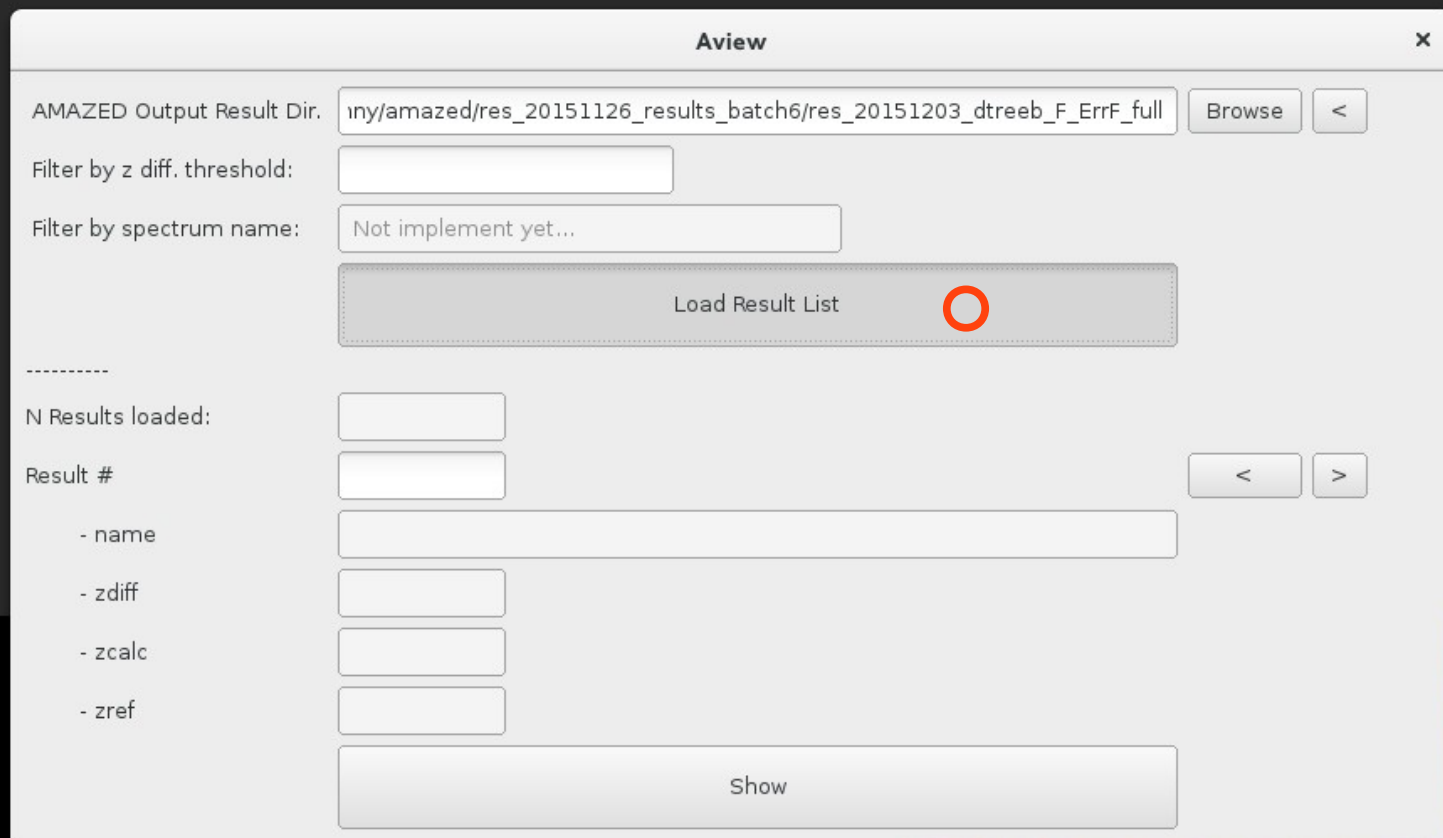


The screenshot shows the 'Aview' application window. The title bar reads 'Aview' with a close button. The main interface includes several input fields and buttons:

- AMAZED Output Result Dir.:** A text input field followed by a 'Browse' button (circled in red) and a '<' button. A tooltip points to the 'Browse' button with the text 'Browse to select the AMAZED output directory...'.
- Filter by z diff. threshold:** A text input field.
- Filter by spectrum name:** A text input field containing the text 'Not implement yet...'.
- Load Result List:** A large button.
- 
- N Results loaded:** A text input field.
- Result #:** A text input field.
- name:** A text input field.
- zdiff:** A text input field.
- zcalc:** A text input field.
- zref:** A text input field.
- Show:** A large button.

Navigation buttons '<' and '>' are located to the right of the 'Result #' field.

# Load the result list



The screenshot shows a window titled "Aview" with a close button (x) in the top right corner. The window contains several input fields and buttons:

- AMAZED Output Result Dir.**: A text box containing the path `iny/amazed/res_20151126_results_batch6/res_20151203_dtreeb_F_ErrF_full`, followed by a **Browse** button and a left arrow button (**<**).
- Filter by z diff. threshold:**: An empty text box.
- Filter by spectrum name:**: A text box containing the text "Not implement yet...".
- Load Result List**: A large button with a red circle around it, indicating it is the focus of the instruction.
- : A horizontal separator line.
- N Results loaded:**: An empty text box.
- Result #**: An empty text box, followed by left (**<**) and right (**>**) arrow buttons.
- name**: A long empty text box.
- zdiff**: An empty text box.
- zcalc**: An empty text box.
- zref**: An empty text box.
- Show**: A button at the bottom of the form.

# See the loaded results...

Terminal window showing the execution of a script and the resulting output:

```
aschmitt@localhost:~/gitlab/cpf-redshift
File Edit View Search Terminal Help

name is: 71021050047882vacLine_F
zref is: 2.70774
zcalc is: 2.7114
self.difftreshold is: -1.0
method is: dtreeb_3.1
460/460 results loaded

name is: 71021050060542vacLine_F
zref is: 2.70885
zcalc is: 2.7106
self.difftreshold is: -1.0
method is: dtreeb_3.1
461/461 results loaded

name is: 71025054000072vacLine_F
zref is: 2.71775
zcalc is: 2.8028
self.difftreshold is: -1.0
method is: dtreeb_3.1
462/462 results loaded

name is: 71025054000456vacLine_F
zref is: 2.71722
zcalc is: 2.7873
self.difftreshold is: -1.0
method is: dtreeb_3.1
463/463 results loaded.

463 results loaded.
```

An "Aview" window is open, displaying the loaded results for the selected file:

AMAZED Output Result Dir:

Filter by z diff. threshold:

Filter by spectrum name:

N Results loaded:

Result #

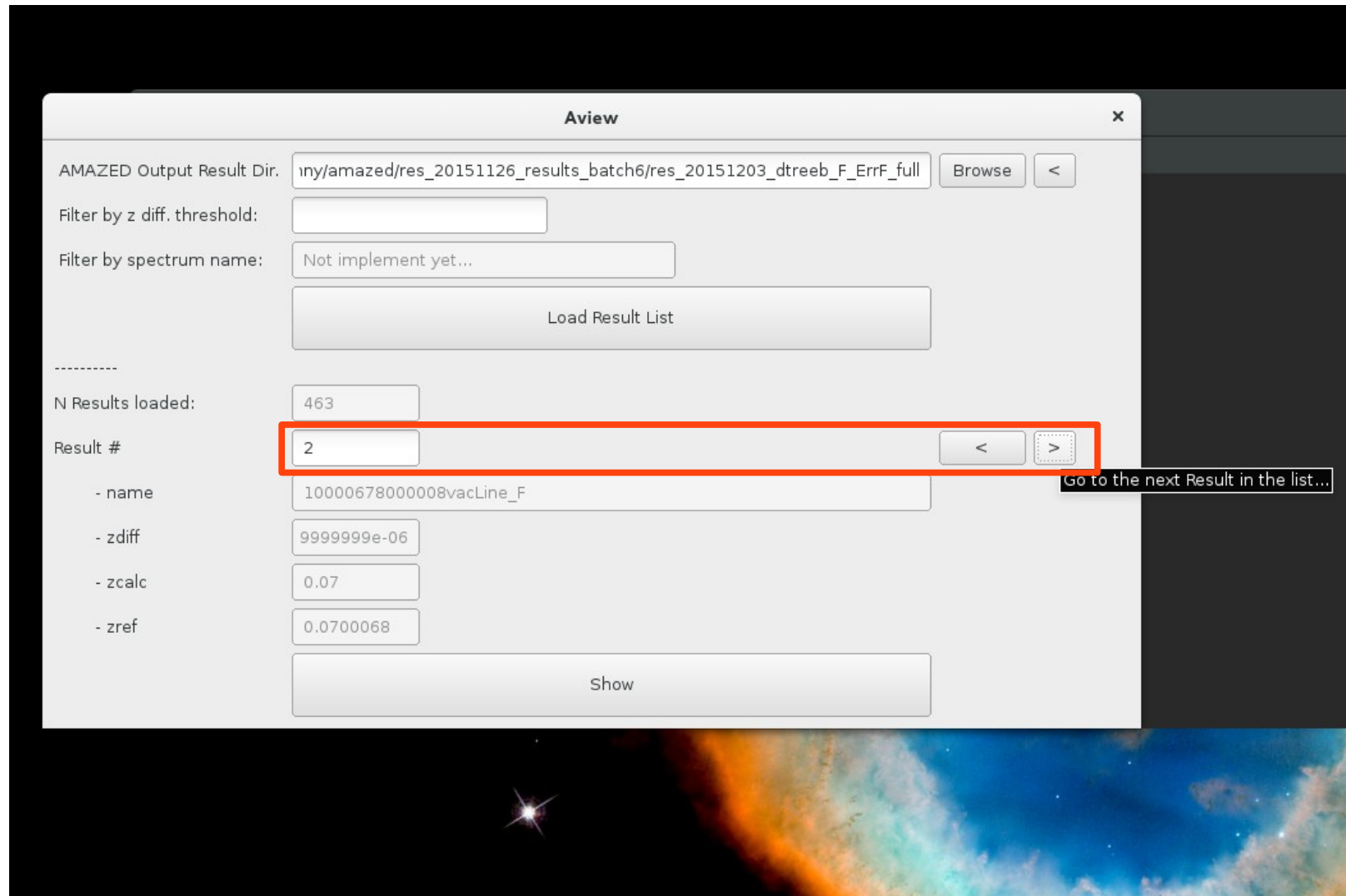
- name

- zdiff

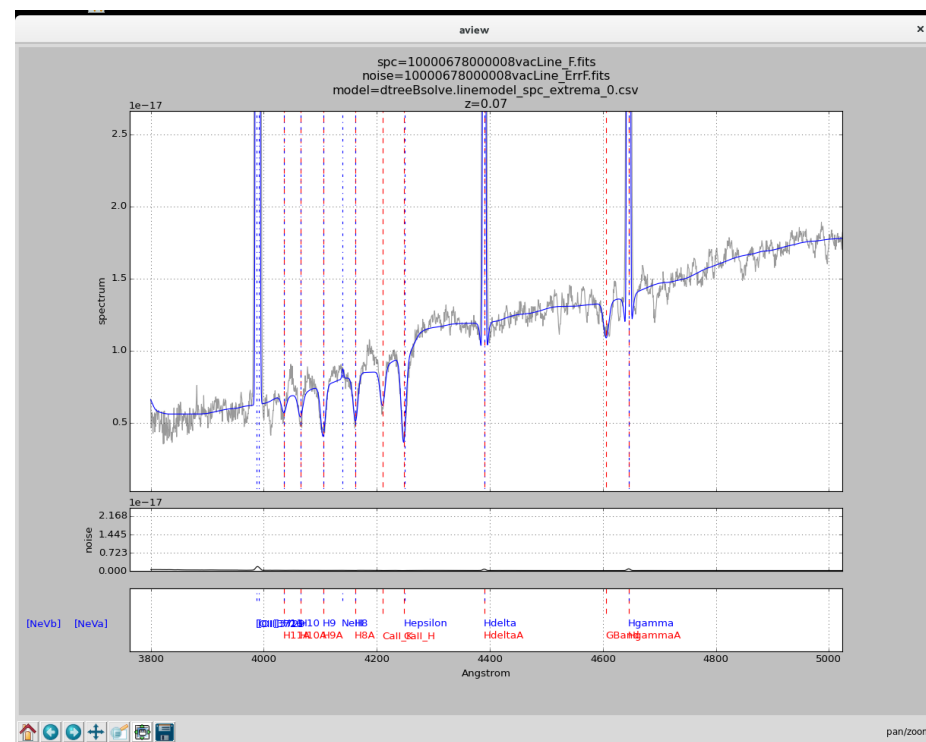
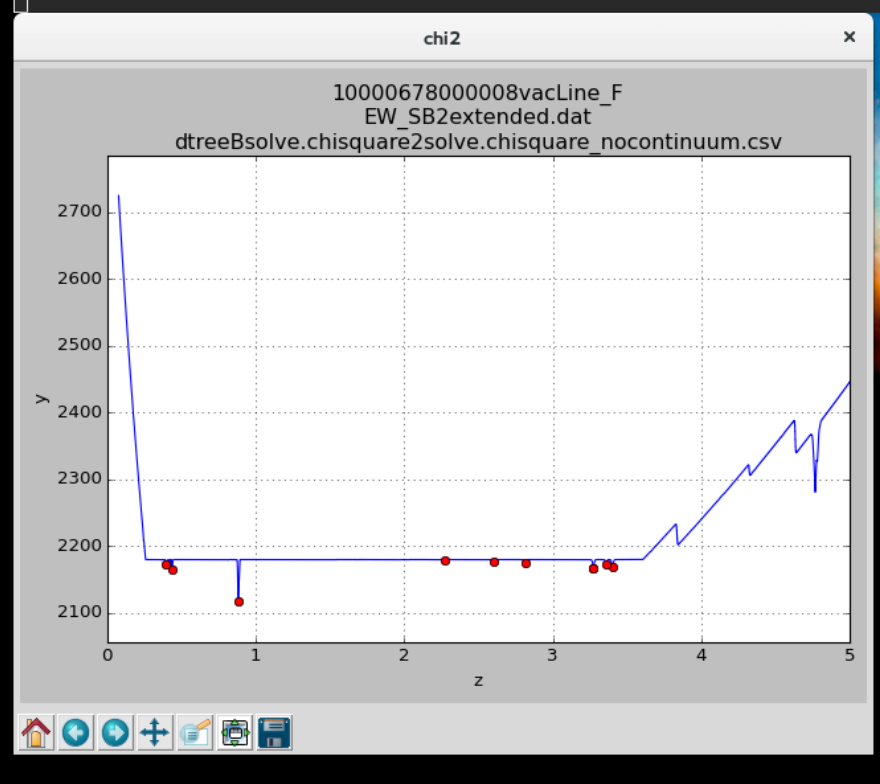
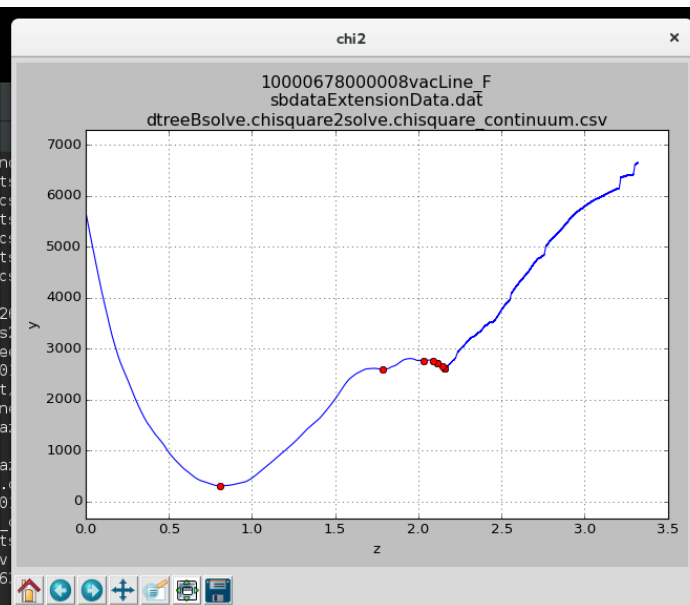
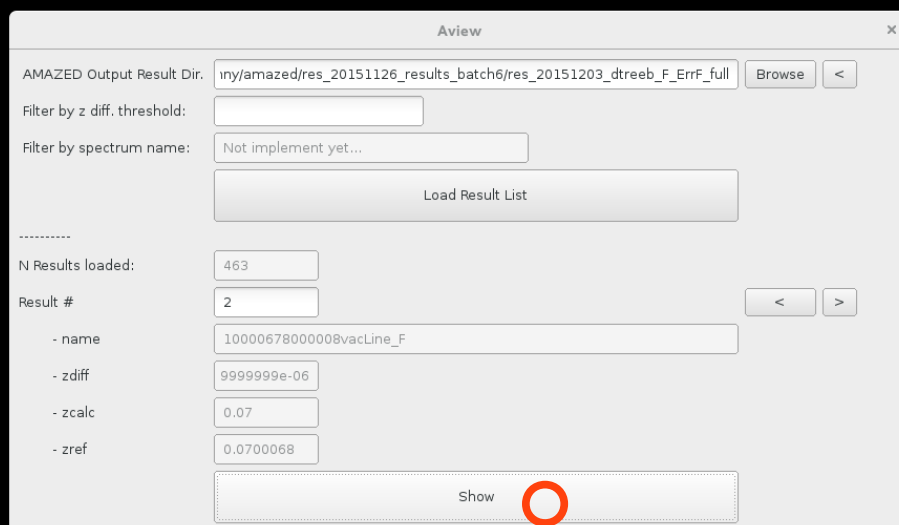
- zcalc

- zref

# Navigate between the individual spectrum results...



## Plot some results for the selected spectrum ...



# NB:

- You can use `aview.py` for a command line version of the display script. It allows to override the redshift value (default is the *zcal/c* value) used for plotting the spectrum overlaid with the template or the linemodel...
- The chisquare results are only displayed if the AMAZED pipeline has been run with the parameter :

**"SaveIntermediateResults": "all"**

- Tested methods are : `dtree7`, `dtreeB`, `chisquare`, `linemodel`, ...
- This is an early prototype version that is intended to provide a quick and easy display. Your feedback is very welcome