SPIRE spectrum analysis with CASSIS-2.9.6 in HIPE

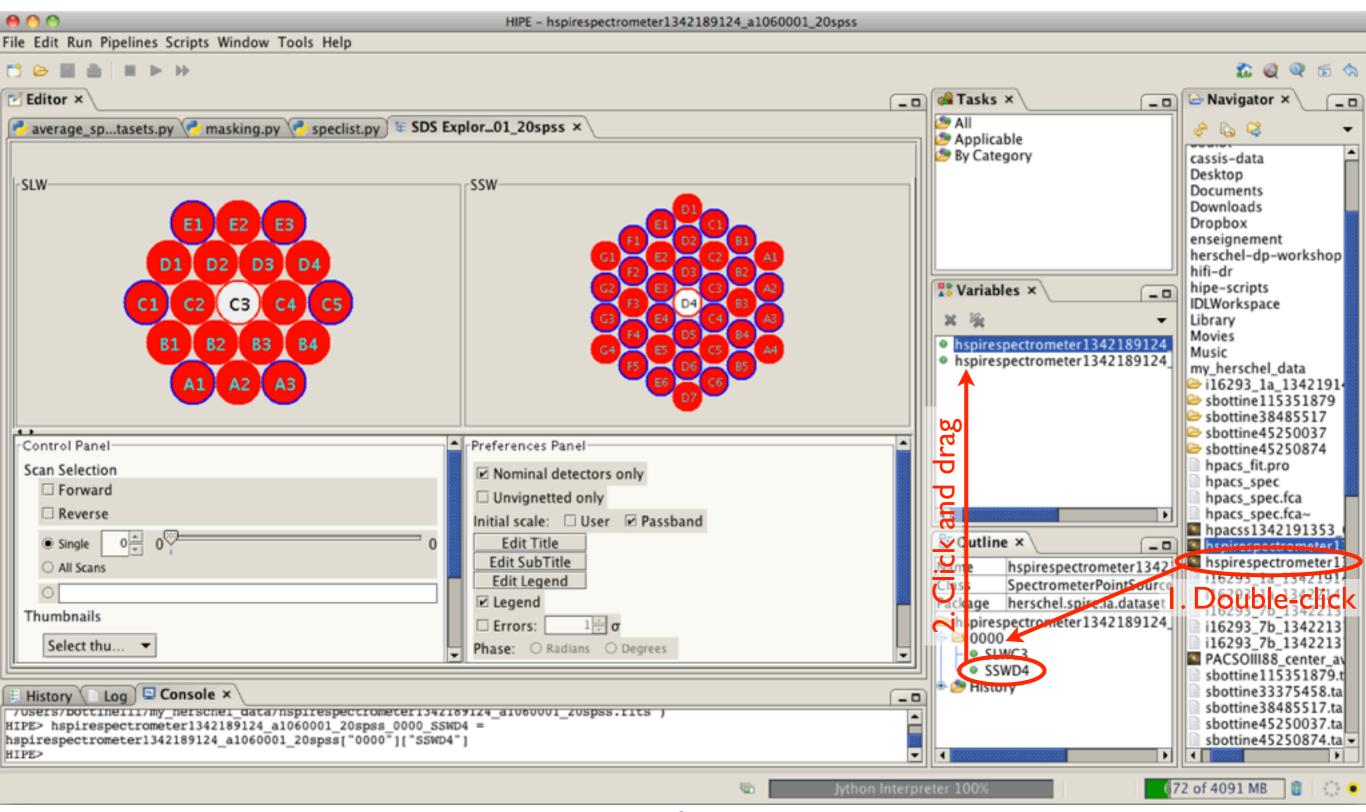


Contents:

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4.1.Line identification	
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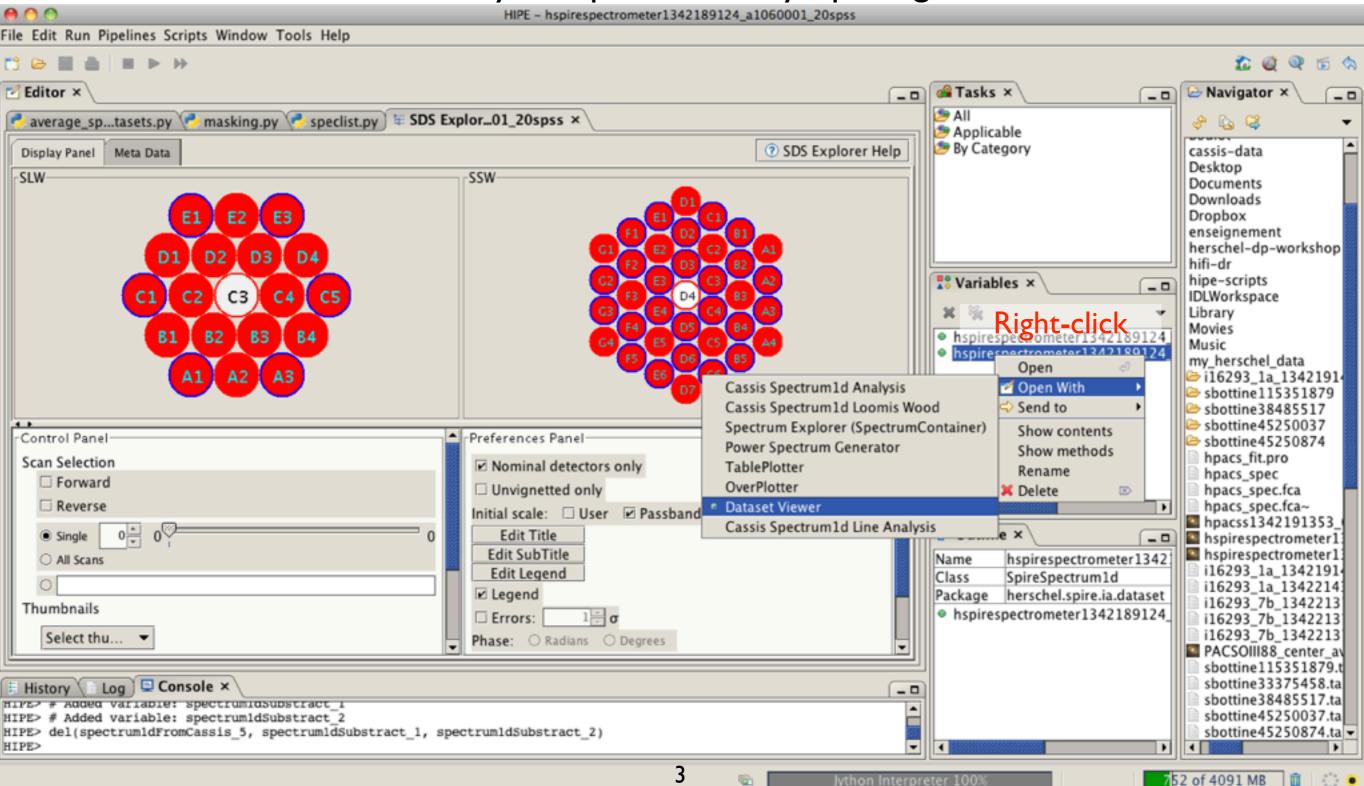
Note: Spectrum I d Line Analysis is currently not working with SPIRE data.

I. Create a spectrum I d variable



2

In order for CASSIS to recognize your data's units and hence to work correctly, you need to check the metadata of your spectrum I d by opening with Dataset Viewer.



Check the 'waveunit' and 'wavename' fields ; defaults in CASSIS for SPIRE data are: waveunit = cm-I

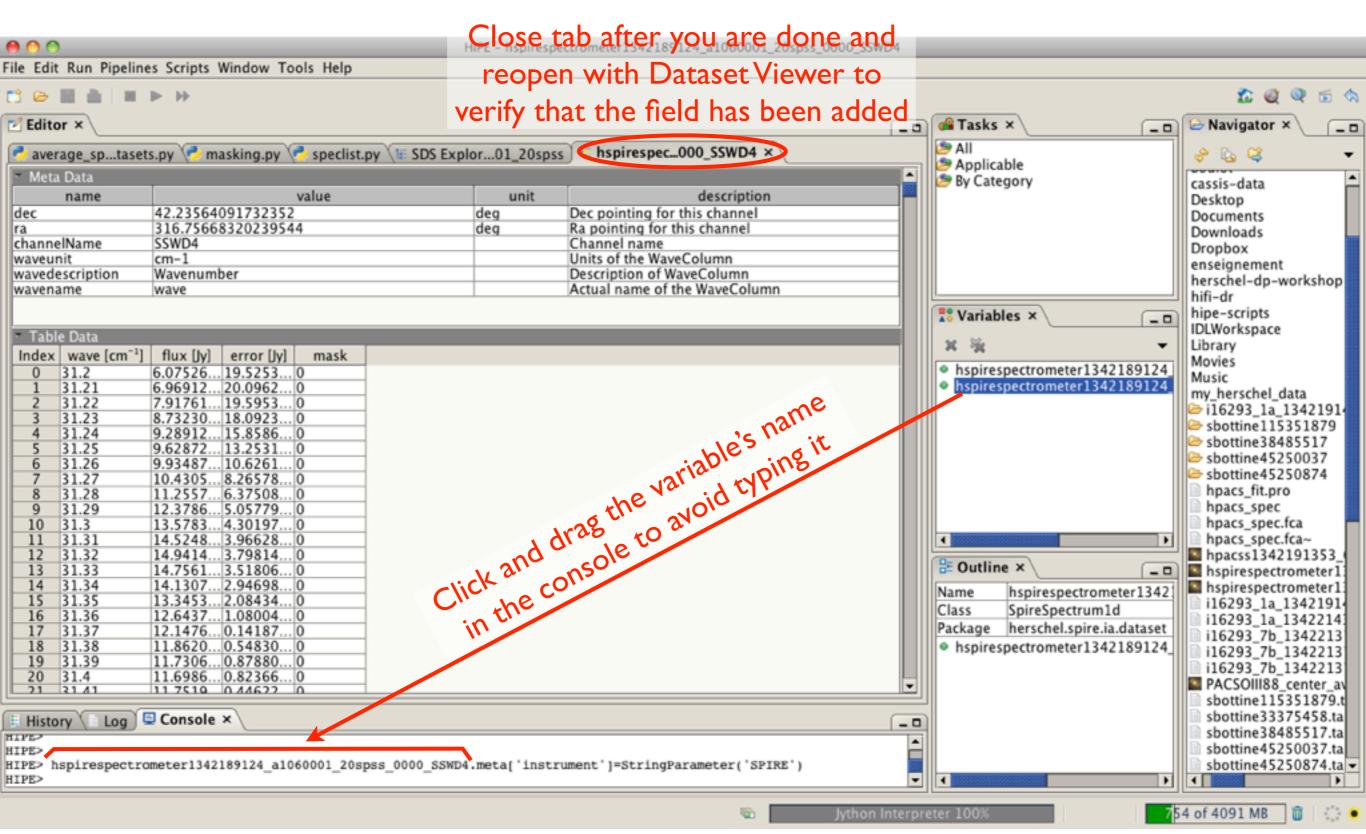
wavename = wave

(Note: the values 'cm-I' and 'wave' must match the column header of the table data as shown in the screenshot)

In this case, you are in principle good to go. However, for consistency/good practice, we recommend that you add an 'instrument' field in the metadata by typing the following command in the console (see also next page):

HIPE> variable_name_of_spectrum I d.meta['instrument'] = StringParameter('SPIRE')

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2 31.22	7.91761 19.5953 0				i16293_1a_1342191
3 31.23	8.73230 18.0923 0				sbottine115351879
4 31.24	9.28912 15.8586 0				bottine38485517
5 31.25	9.62872 13.2531 0		4		sbottine35465517
6 31.26	9.9348710.62610				chottine45250874



2. Check your metadata

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 If waveunit ≠ cm-I, or wavename ≠ wave (or if they are missing - cf. next point), then you *must* add the 'instrument' field:

HIPE> variable_name_of_spectrum I d.meta['instrument'] = StringParameter('SPIRE')

• If 'waveunit' or 'wavename' are missing, you must add the corresponding field in the metadata by typing the following command(s) (with the appropriate corresponding value) in the console:

HIPE> variable_name_of_spectrum I d.meta['waveunit'] = StringParameter('unit') HIPE> variable_name_of_spectrum I d.meta['wavename'] = StringParameter('name') where unit and name are the values from the column header of the table data.

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2. Check your metadata

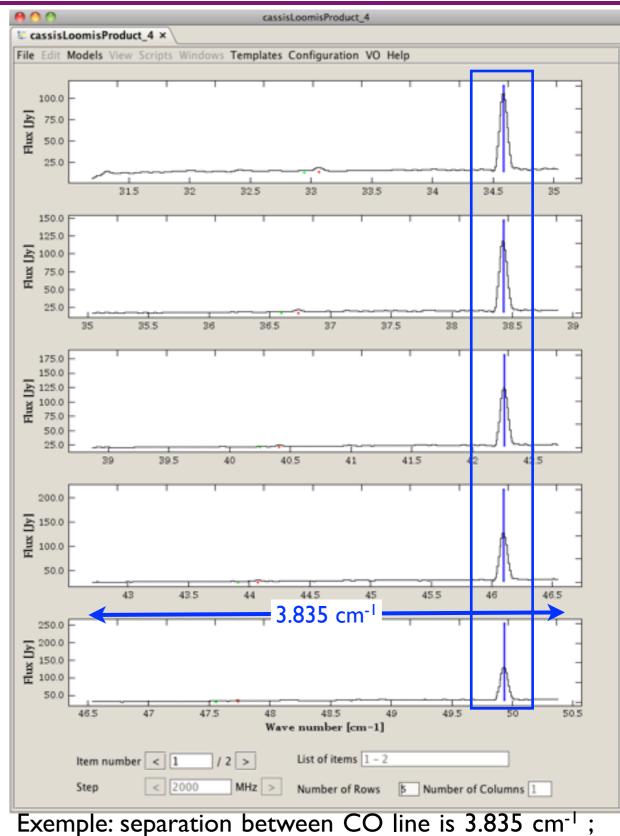
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A Loomis-Wood diagram is a two-dimensional peak diagram in which:

- the occurrence of a transition is plotted versus frequency/wavenumber/wavelength, in segments of a given width
- the height of a line is proportional to the column density, weighted by the partition function at the chosen excitation temperature

Interactive Loomis-Wood assignment programs help assign spectra, and estimate column densities.

Note that, **at the moment**, for the calculation of the line intensity (and hence the estimate of the column density) to be correct, **the data must be in Jy**. Any other unit will only allow you to determine relative column densities (assuming you look at more than one species).



setting the segment width to this value yields a

Loomis-Wood diagram with aligned CO transitions.

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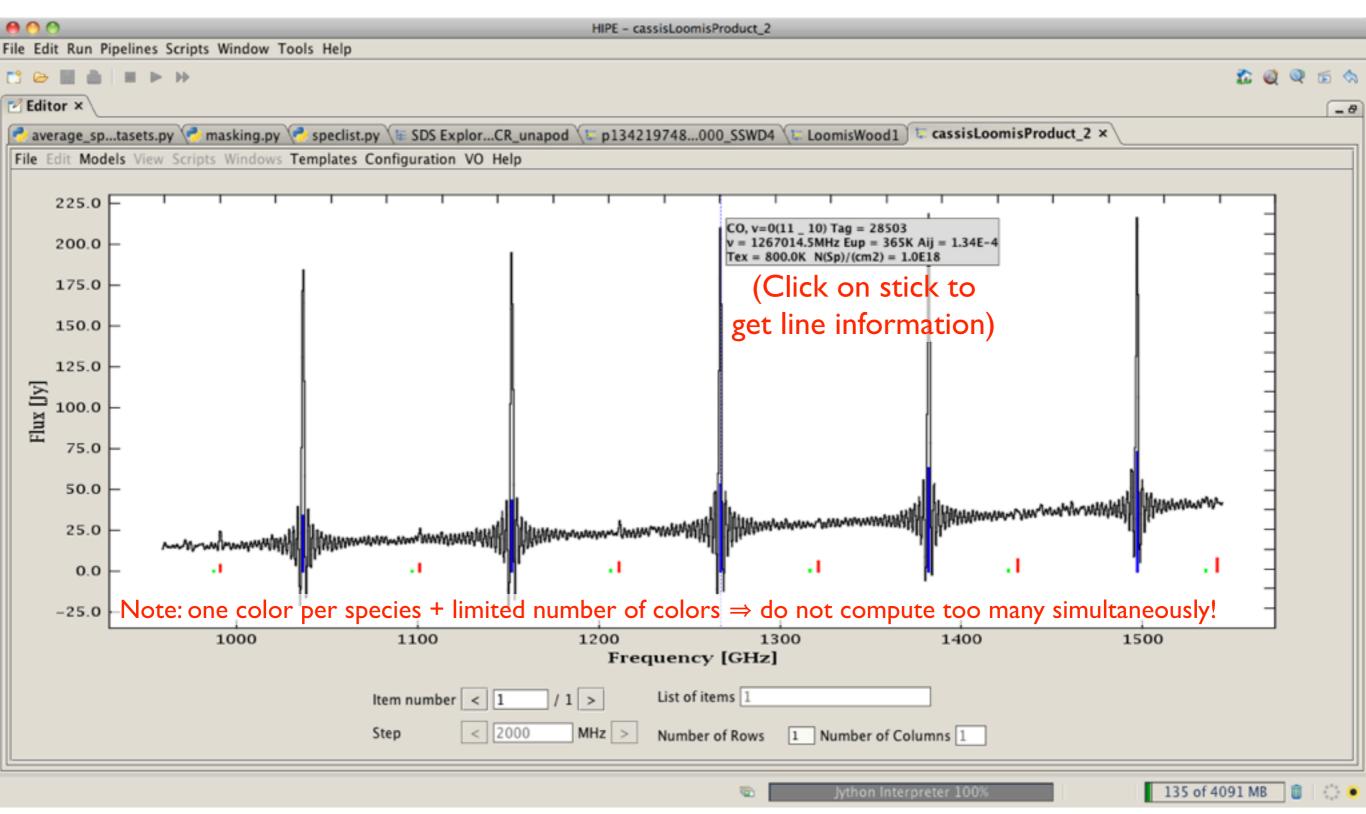
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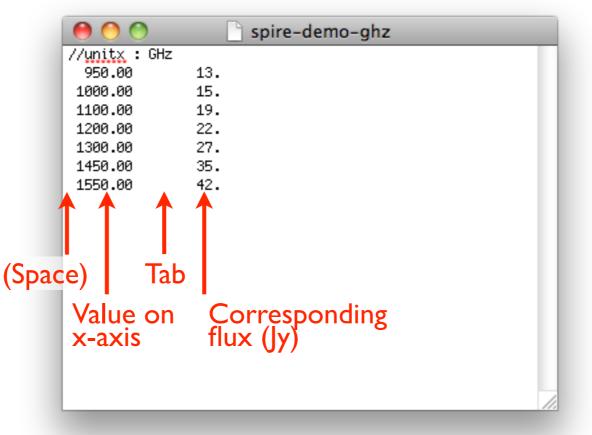
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- I. In YOUR_CASSIS_DIR/user/continuum/, create an ascii file with the name of your choice, no extension
- 2. Fill it in with the continuum information, following the format below:



3. Close and re-open your spectrum I d with "Cassis Spectrum I d Loomis Wood"



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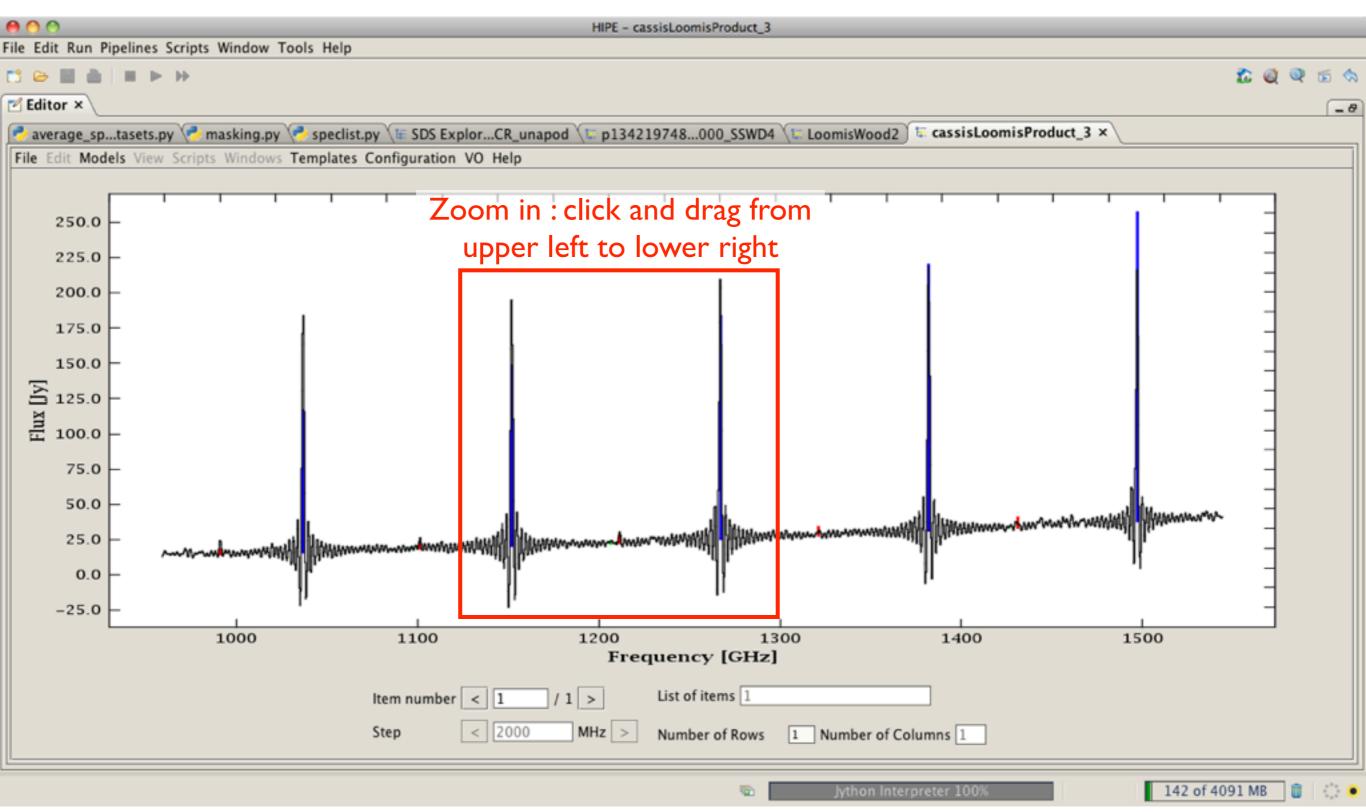
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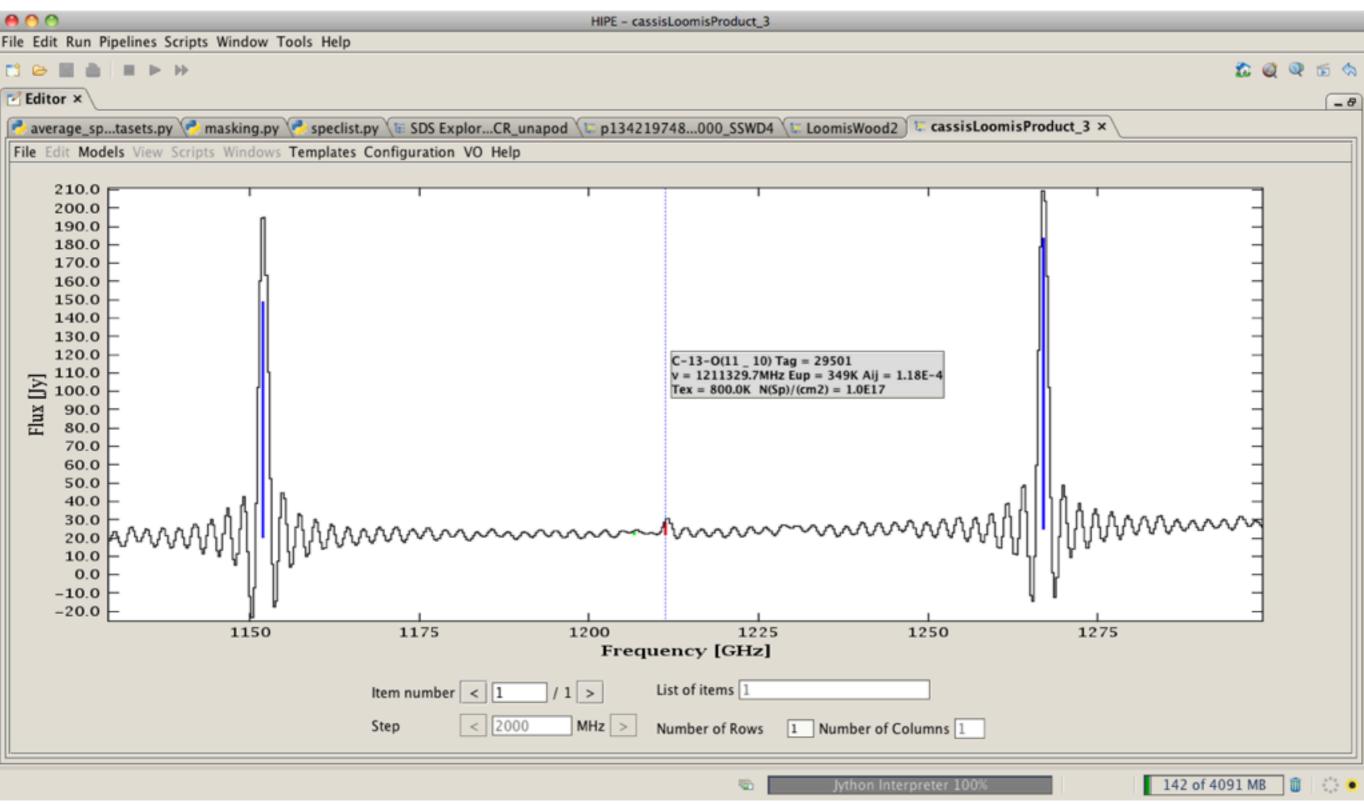
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A-3. Creating your template within L-W

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CH+	13503 CDMS		7.0E14	100.0
CH2 C-13-H+	14501 CDMS 14502 CDMS		7.0E14 7.0E14	100.0
C-13-H+, v=1-0	14504 CDMS		7.0E14	100.0
CD+, v=1-0	14505 CDMS		7.0E14	100.0
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NH2	16501 CDMS		7.0E14	100.0
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OH+	17501 CDMS		7.0E14	100.0
NH2D	18501 CDMS	Ĭ.	7.0E14	100.0 -

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A-3. Creating your template within L-W

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Repeat the search and selection steps for isotopologues of CO : ${}^{13}CO$, C ${}^{18}O$, C ${}^{17}O$, ${}^{13}C{}^{18}O$, ${}^{13}C{}^{17}O$. Note that, for example, ${}^{13}CO$ and C ${}^{18}O$ are listed as C-13-O and CO-18



A-3. Creating your template within L-W

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D.

A-3. Creating your template within L-W

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A-3. Creating your template within L-W

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4. Spectrum I d Analysis

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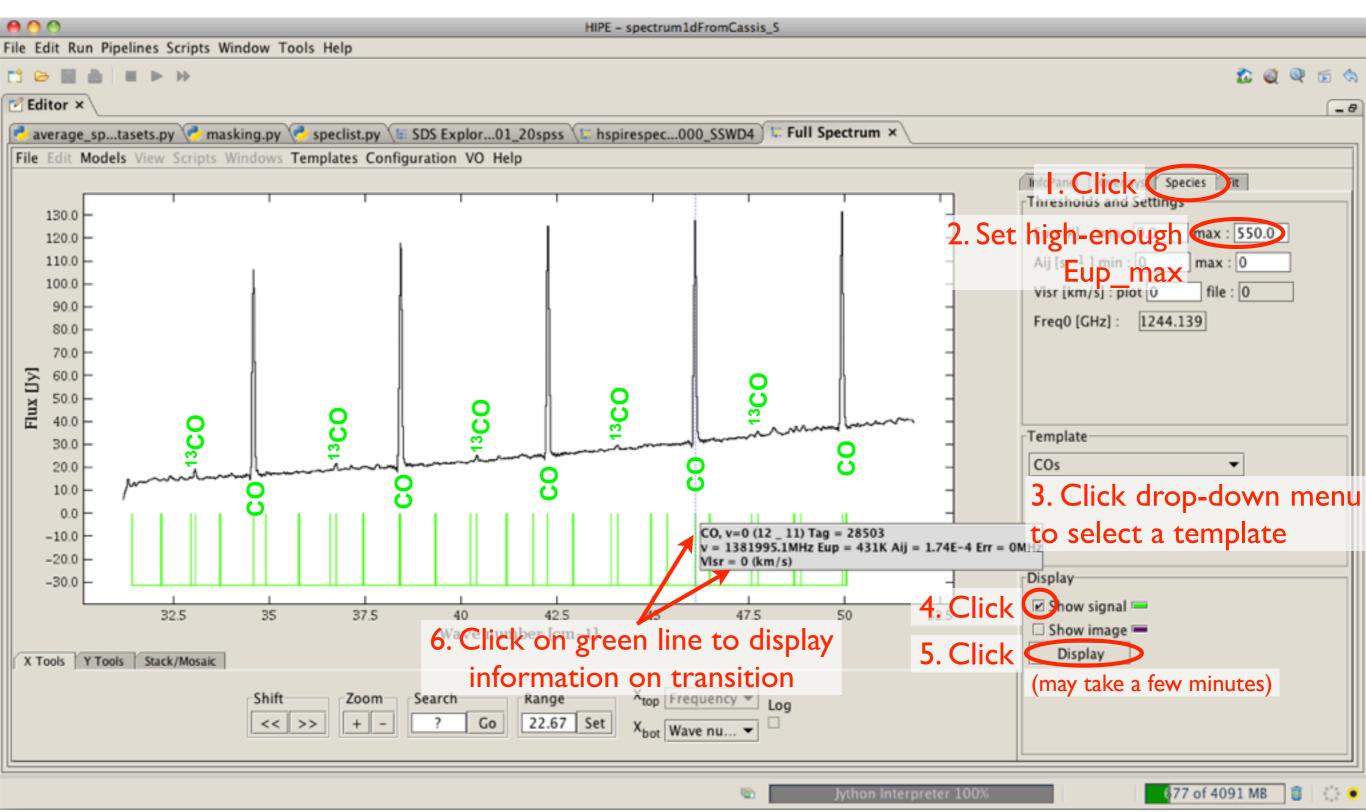


4. Spectrum I d Analysis

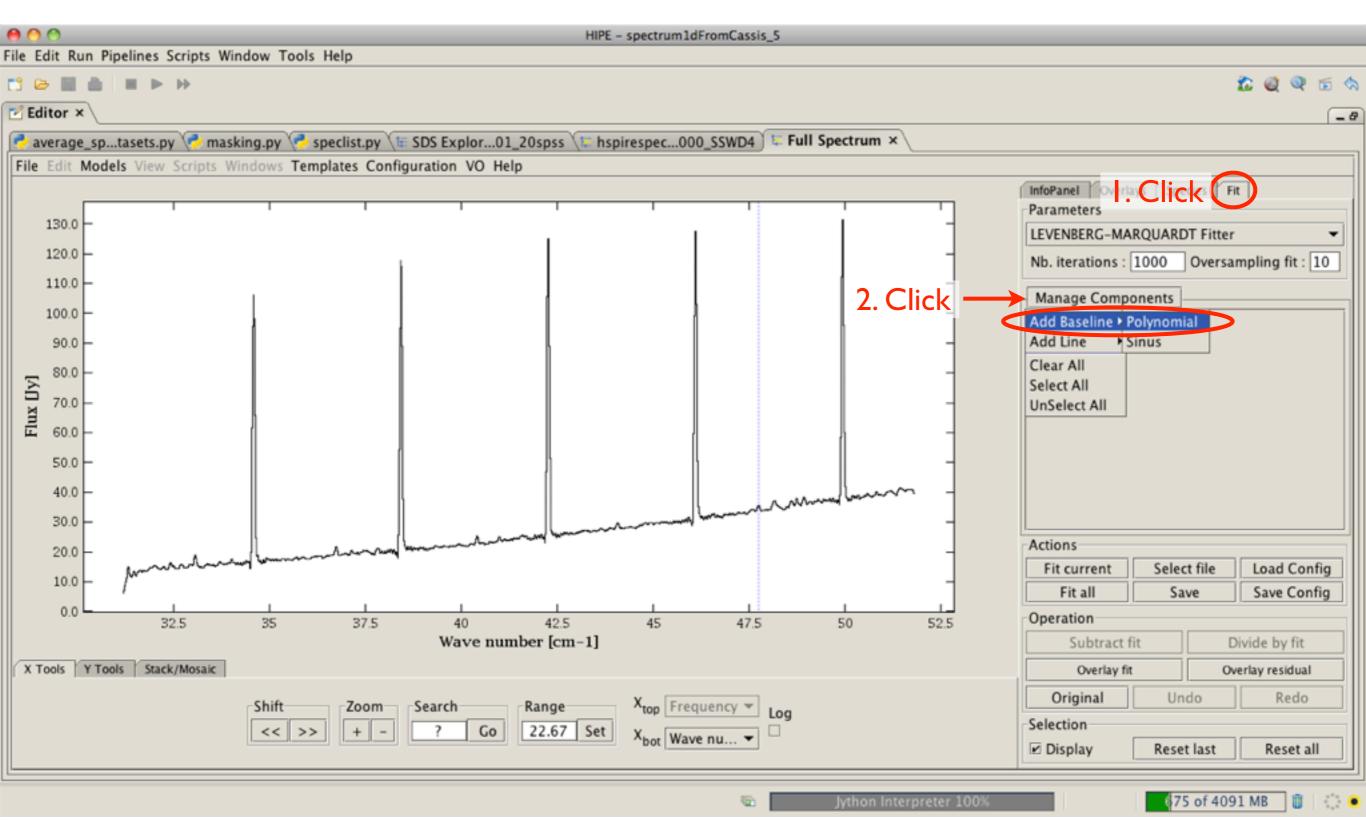
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Can change these to display a restricted range			Variables ×	 hspirespectrometer1: i16293_1a_1342191- i16293_1a_1342214: i16293_7b_1342213 i16293_7b_1342213 i16293_7b_1342213 PACSOIII88_center_av sbottine115351879.t
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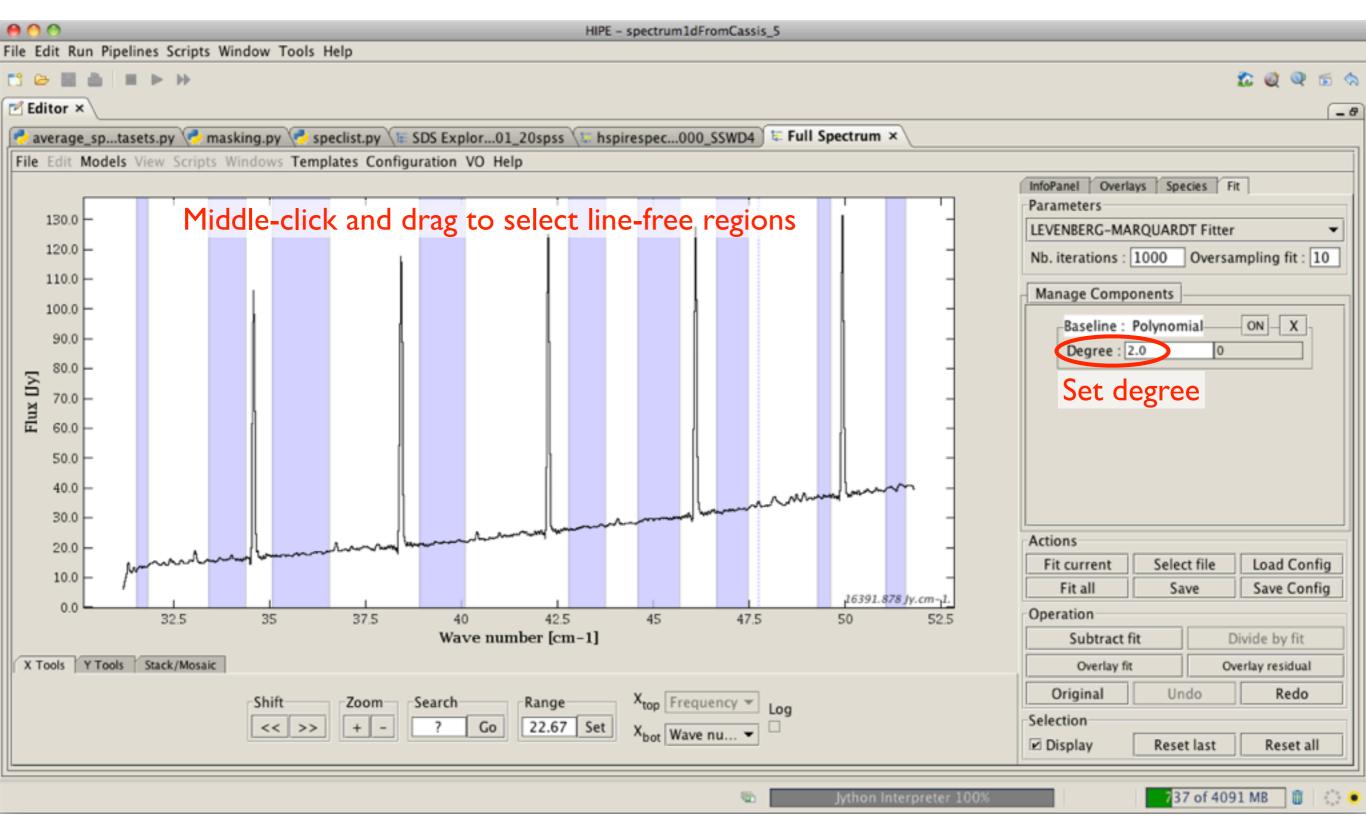
4.1. Line identification



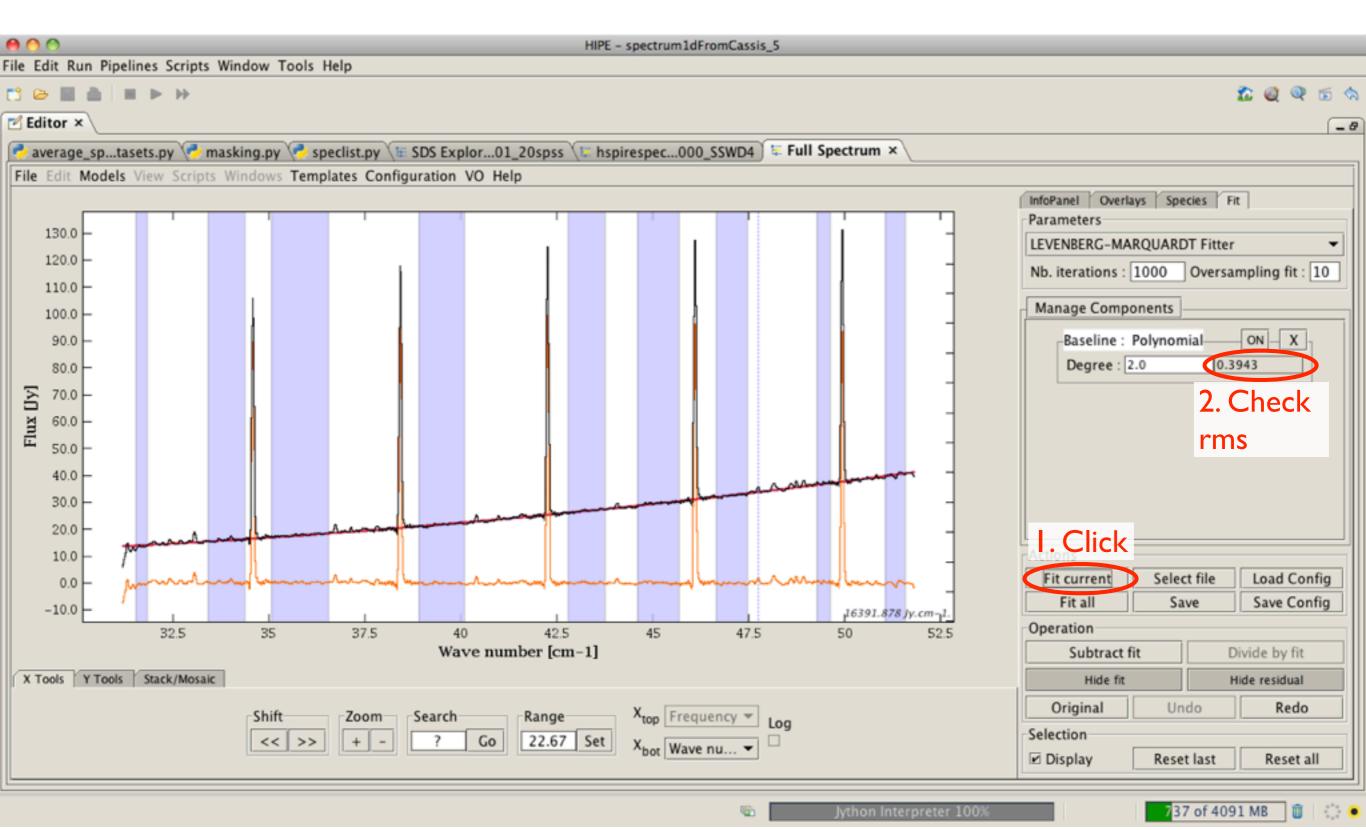




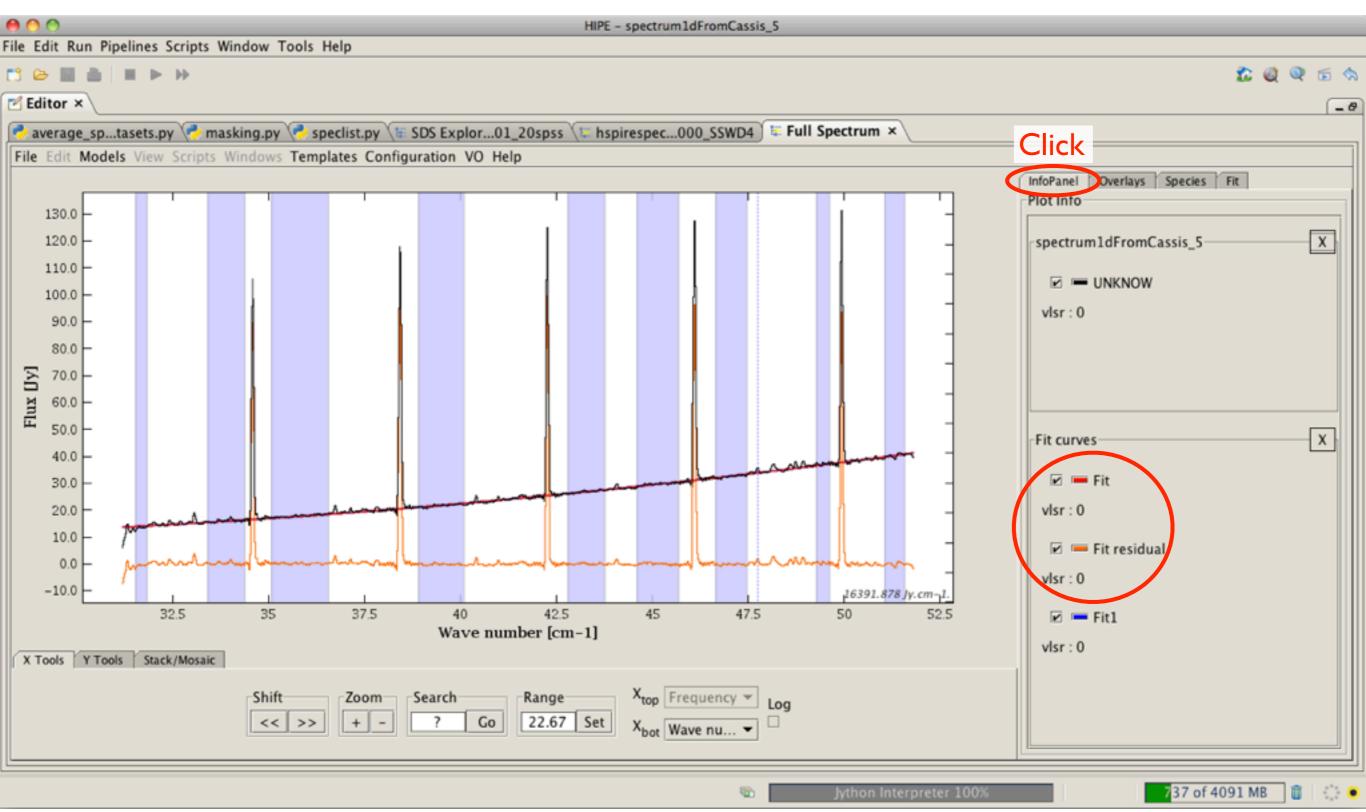




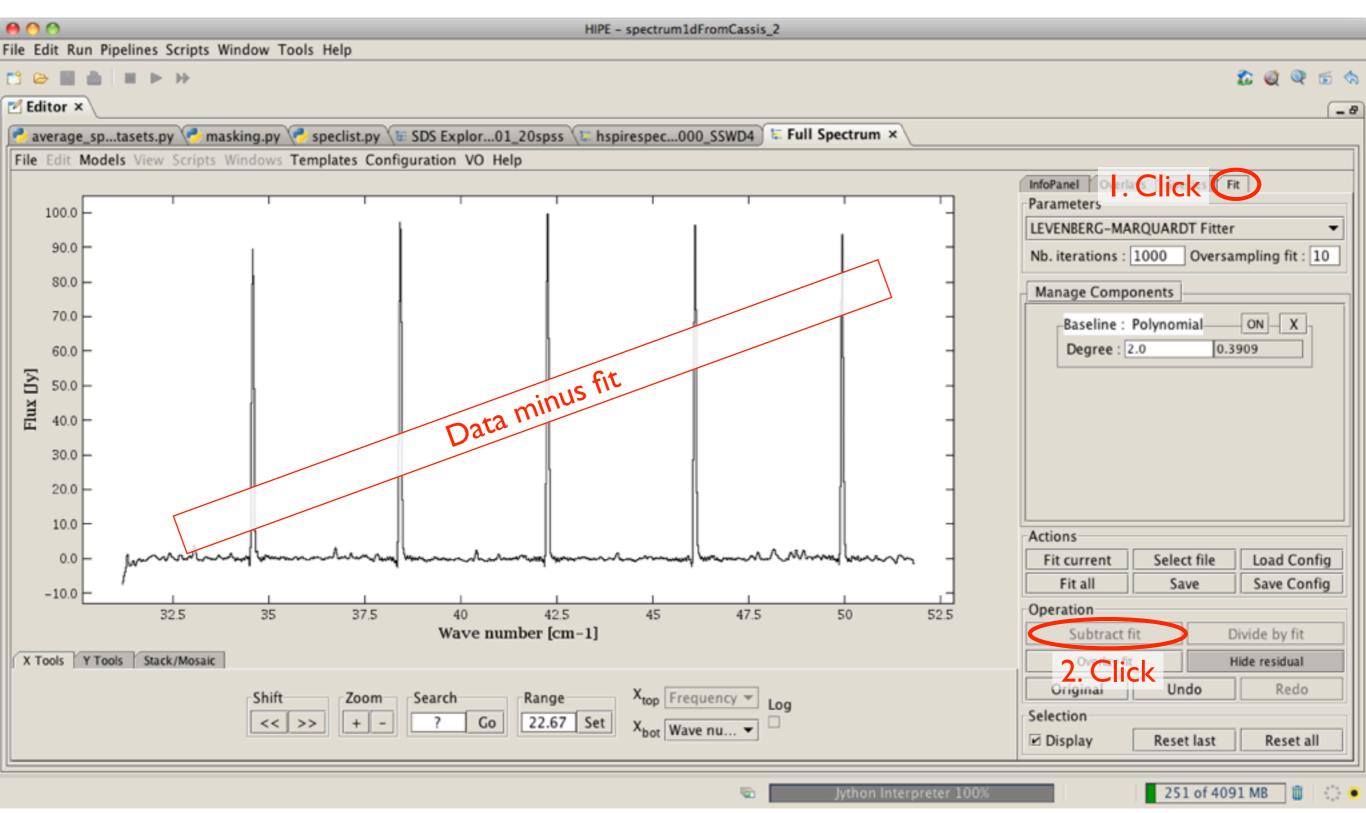










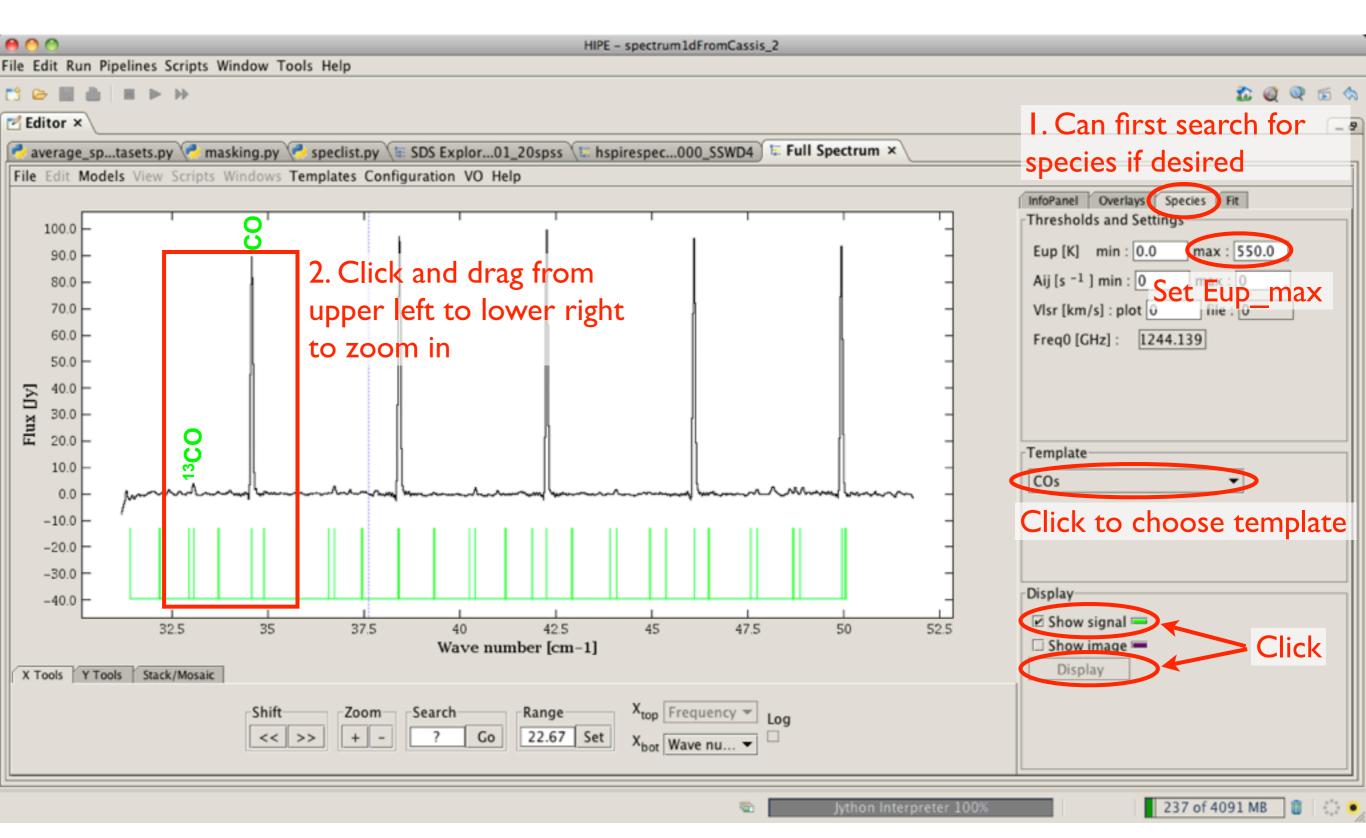




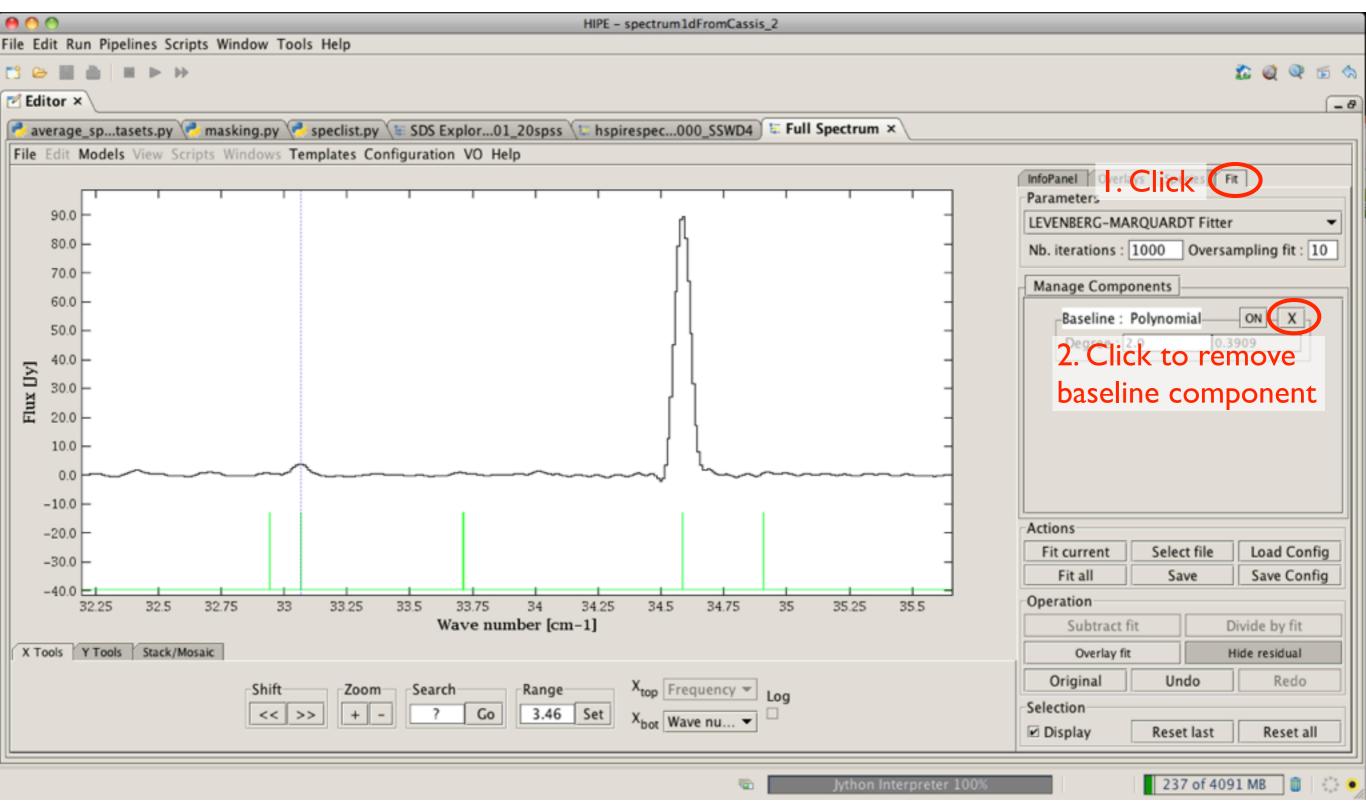
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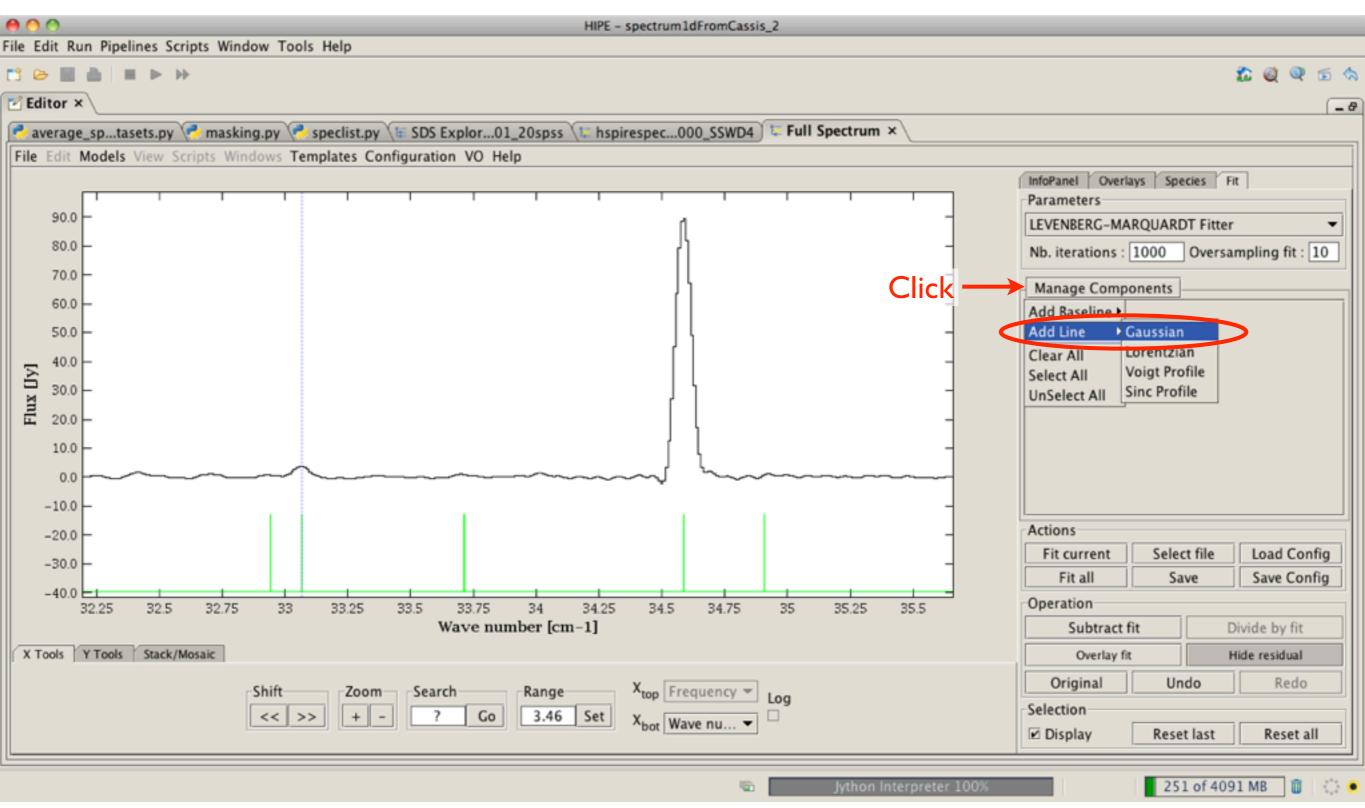
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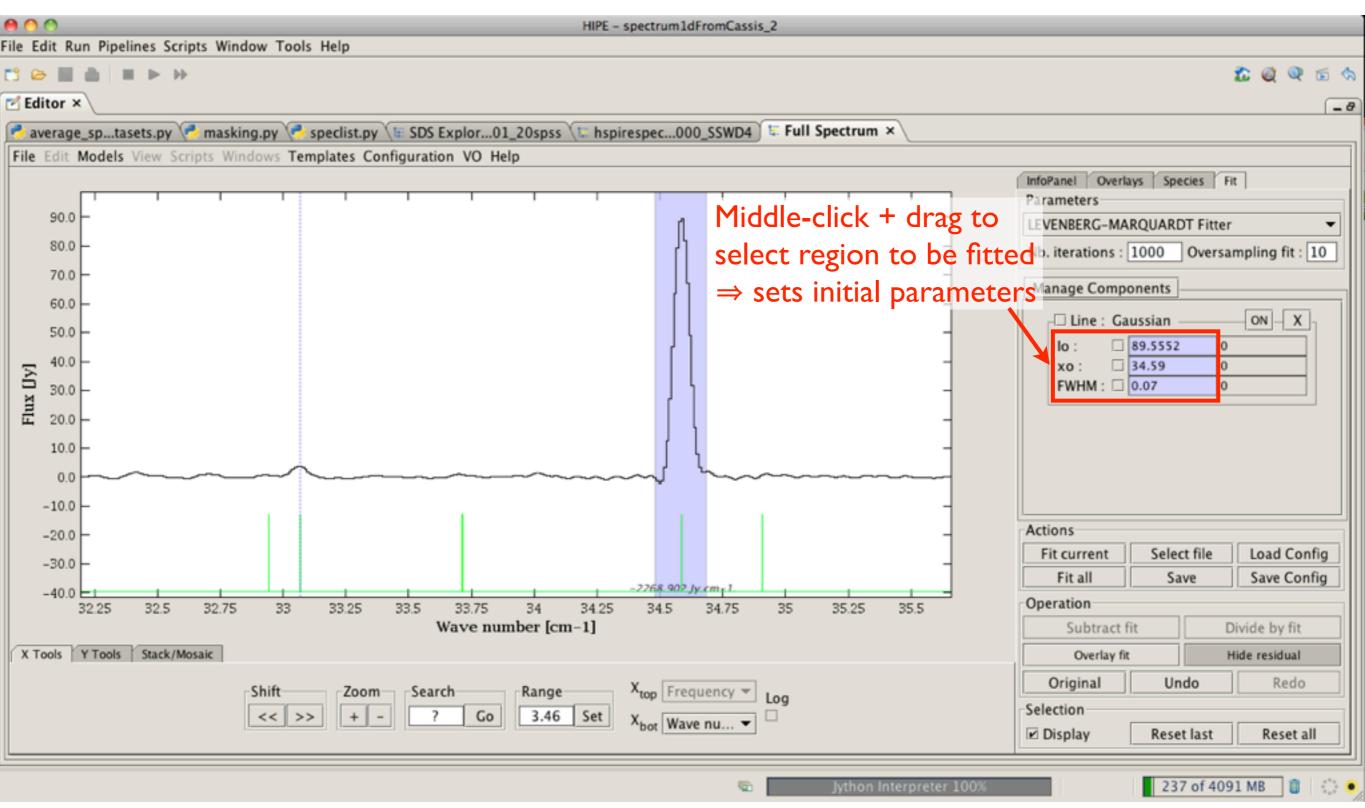
4.2. Line fitting



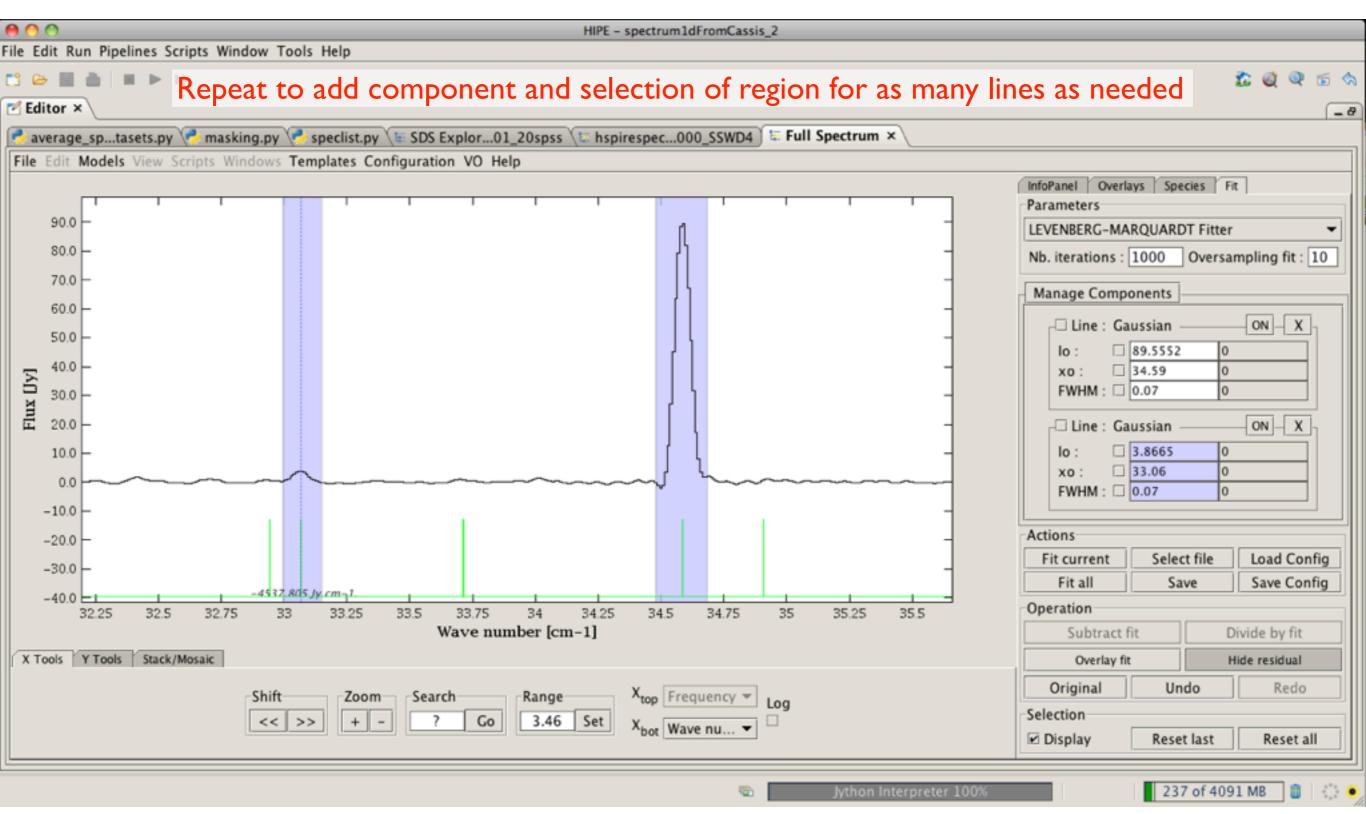




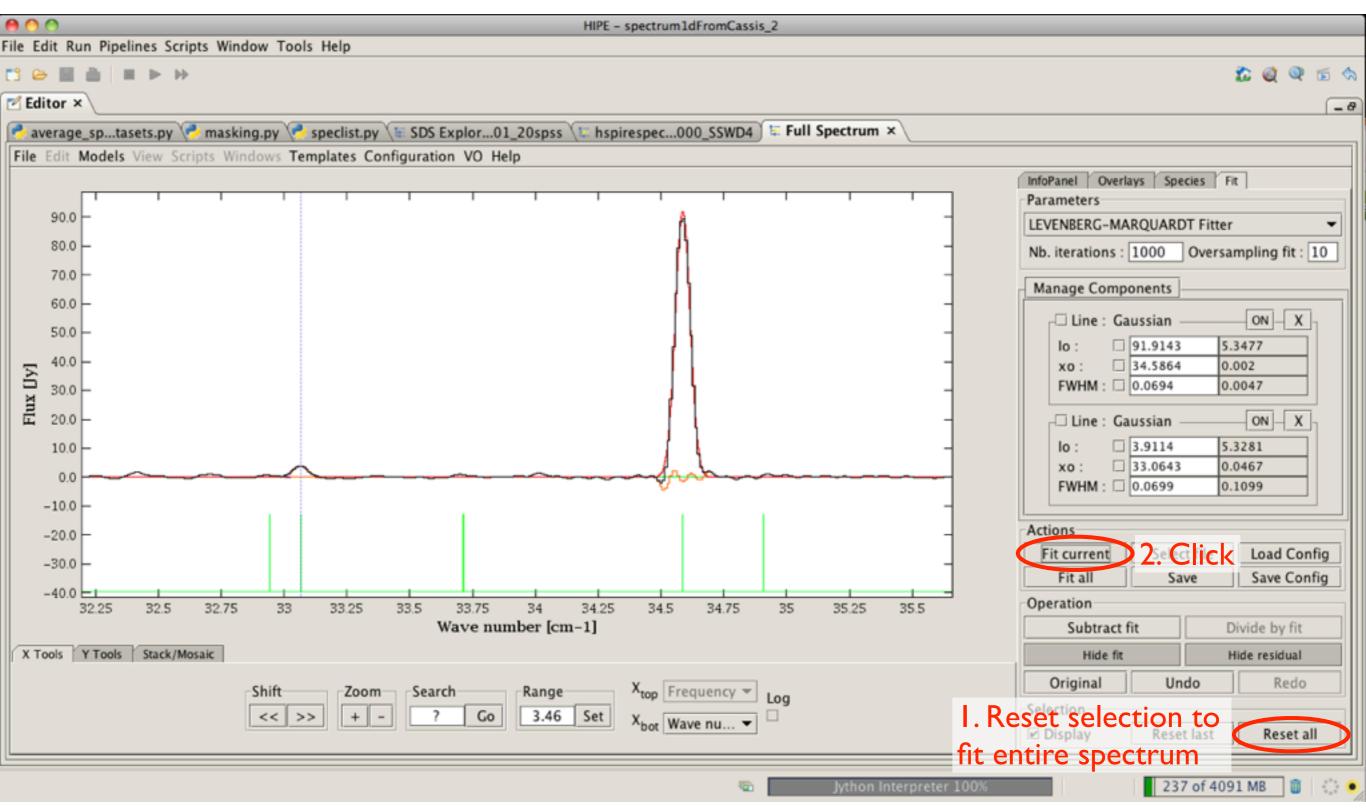




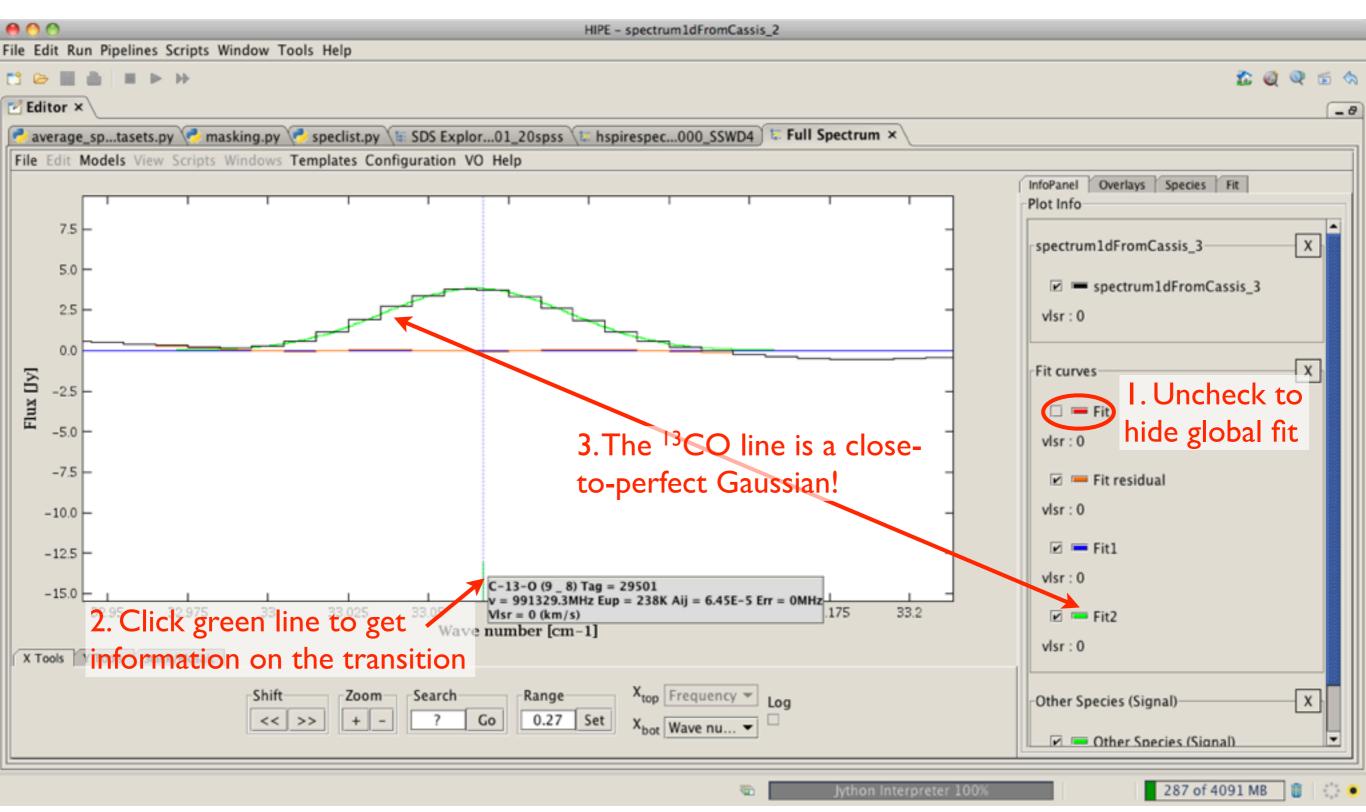
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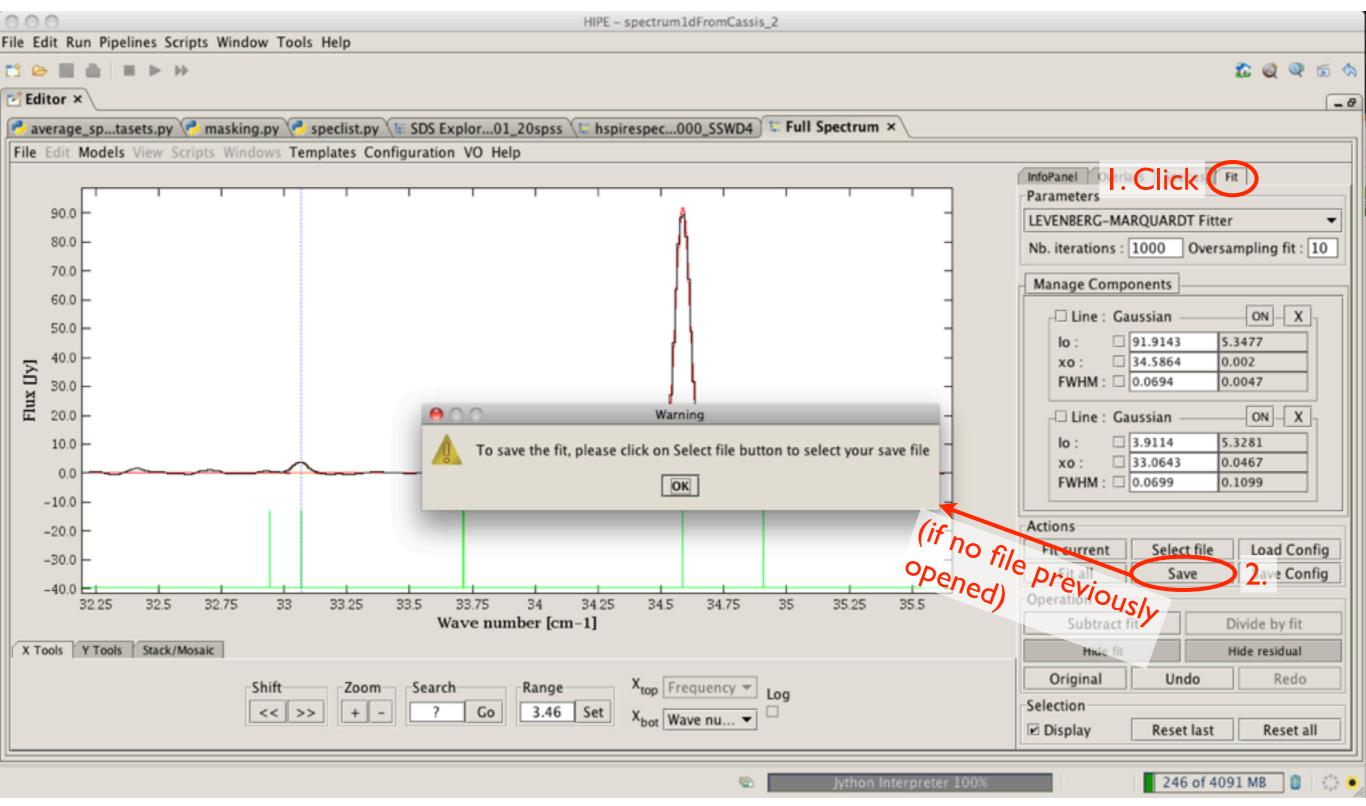




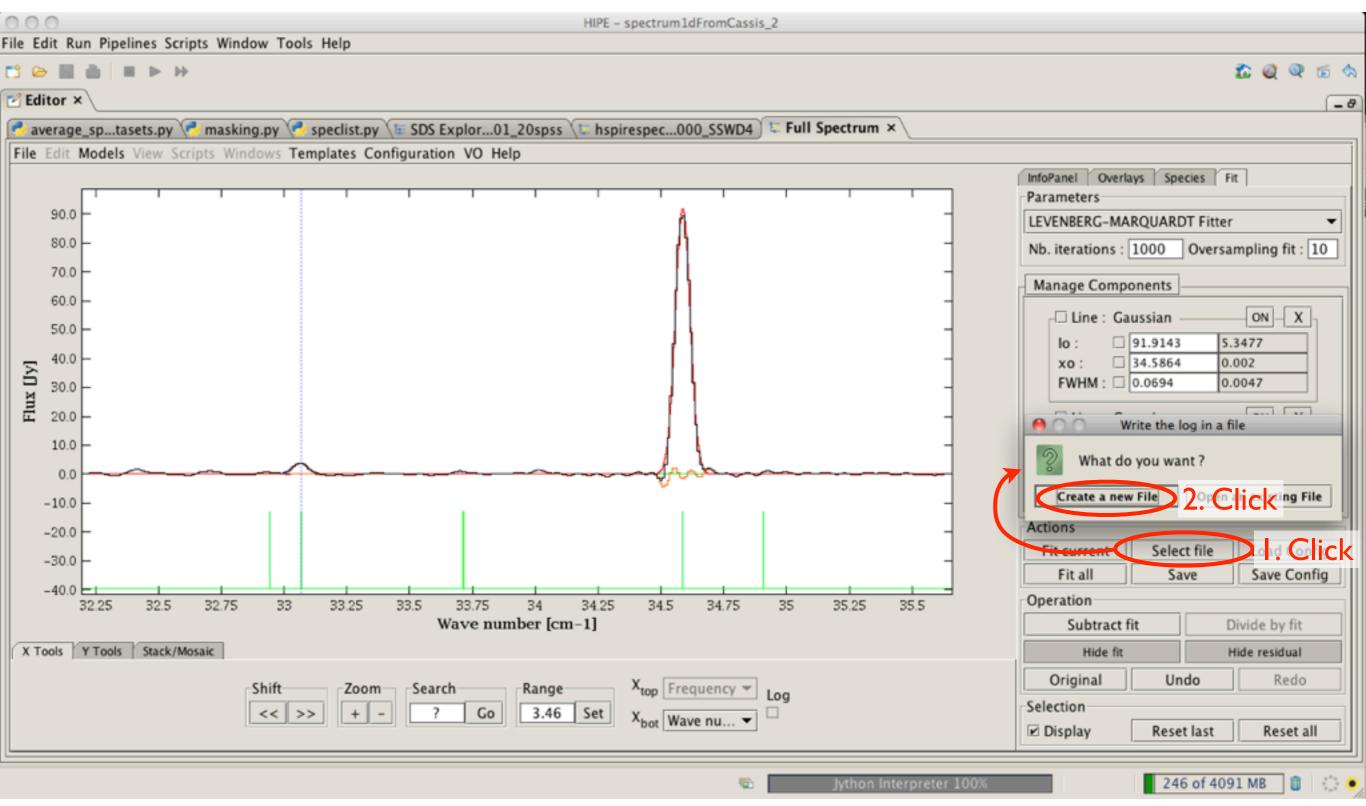




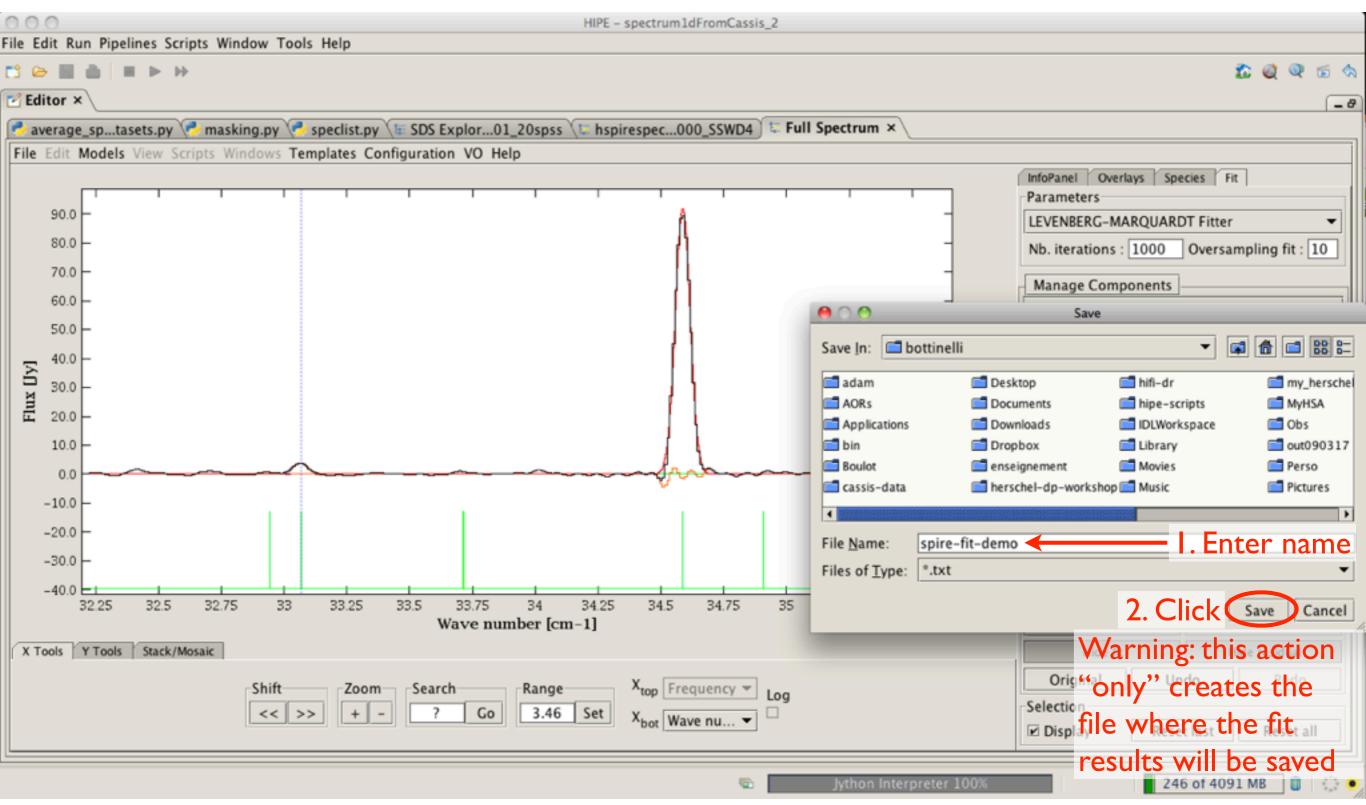




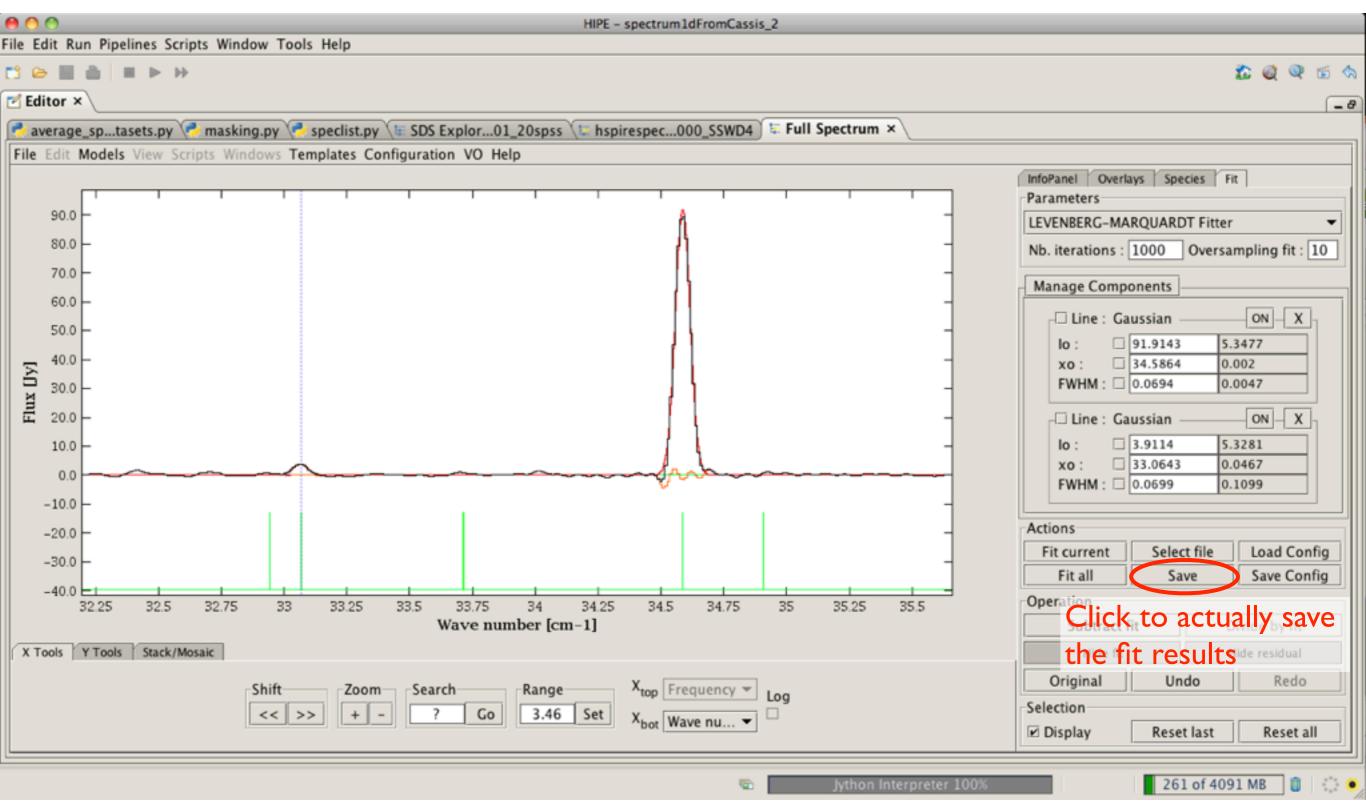














Import in / open with spreadsheet for easier viewing

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Notes:

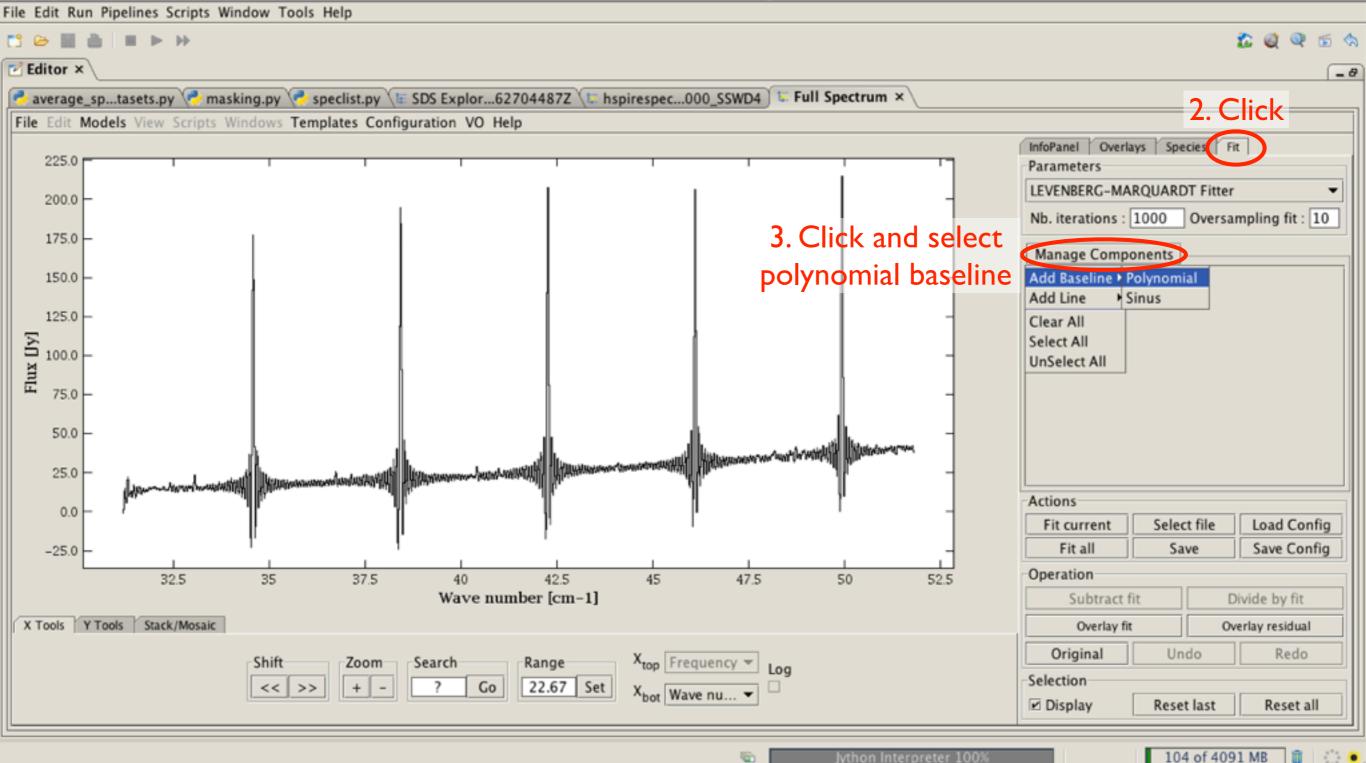
- columns C, D, K, L are not relevant for Gaussian fitting and are therefore empty here
- units are not written (here cm⁻¹ and Jy)

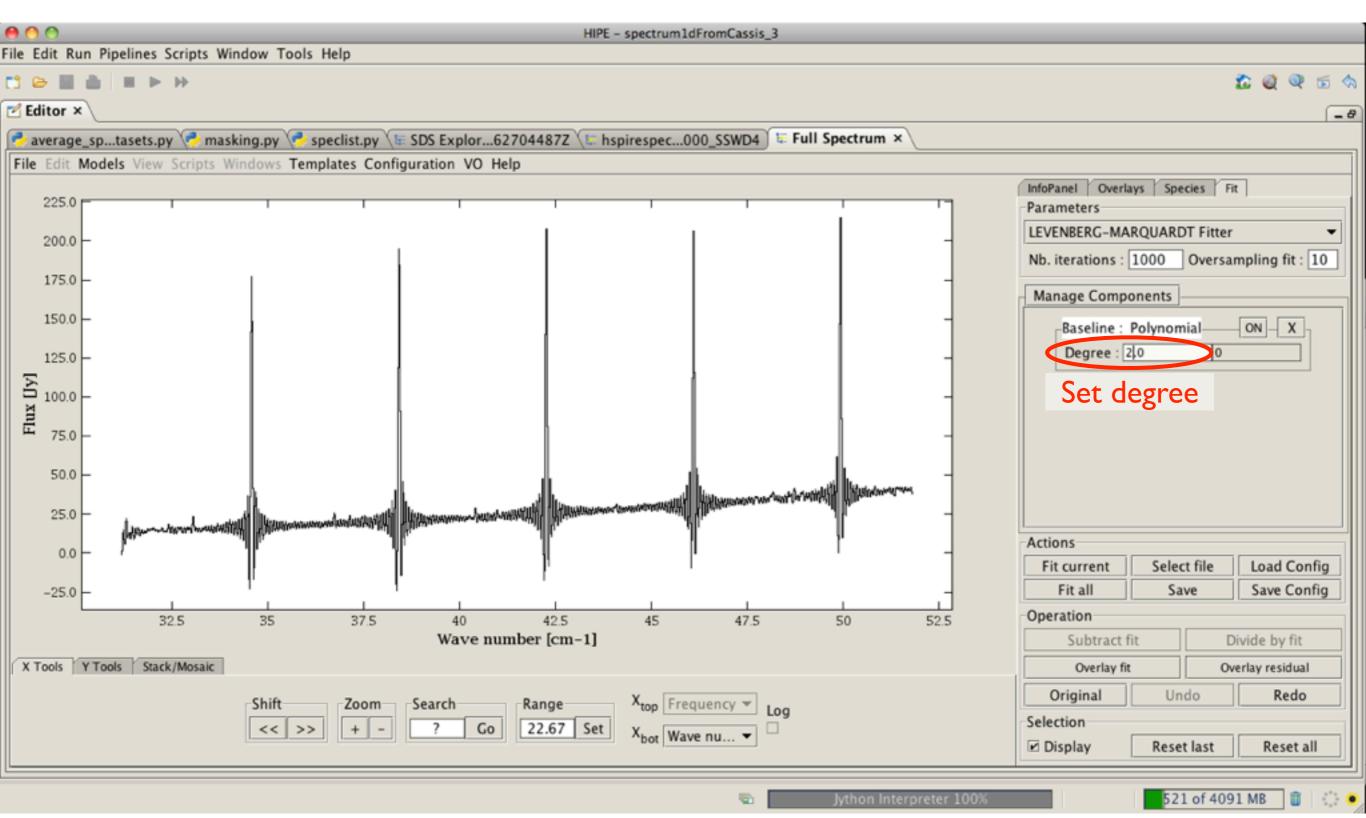
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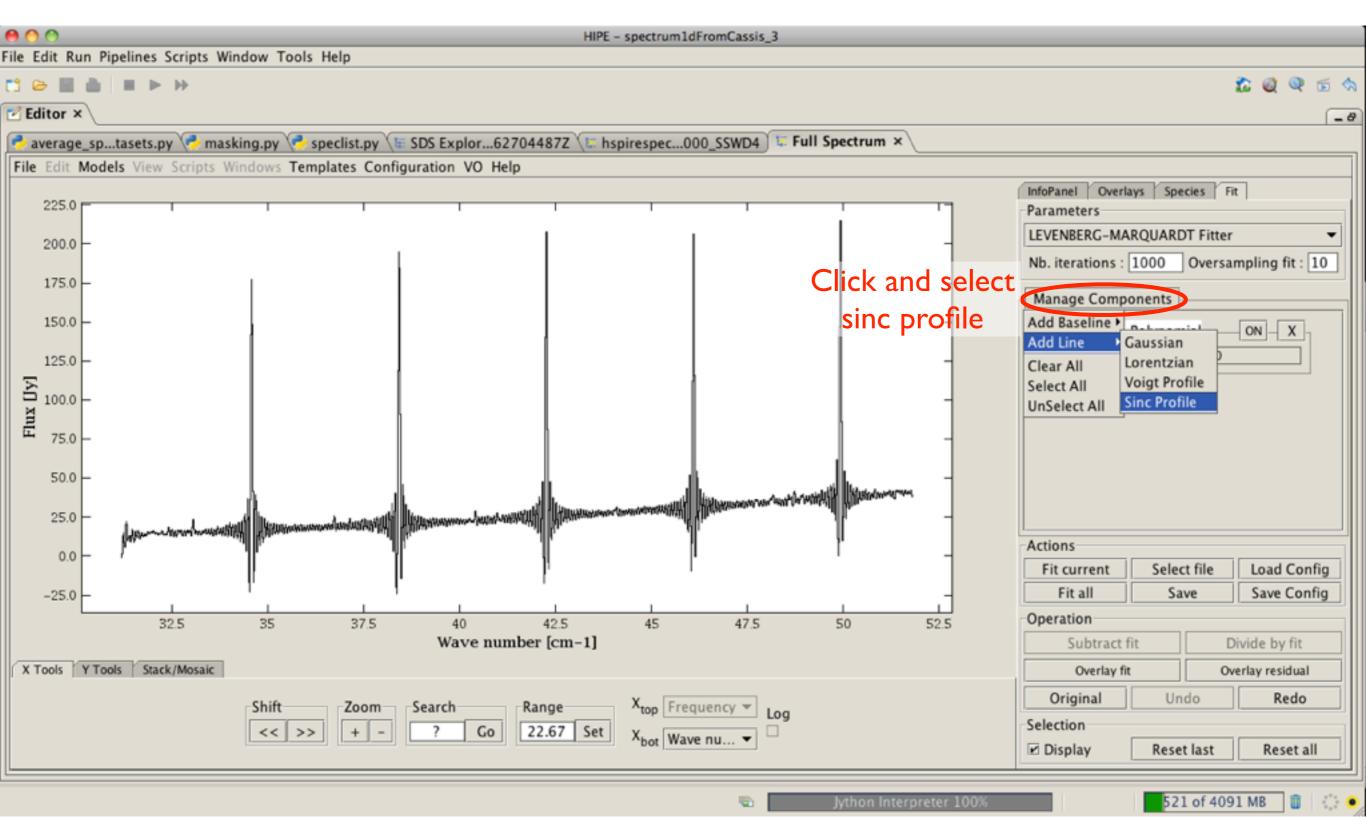
4.3. Sinc profile removal

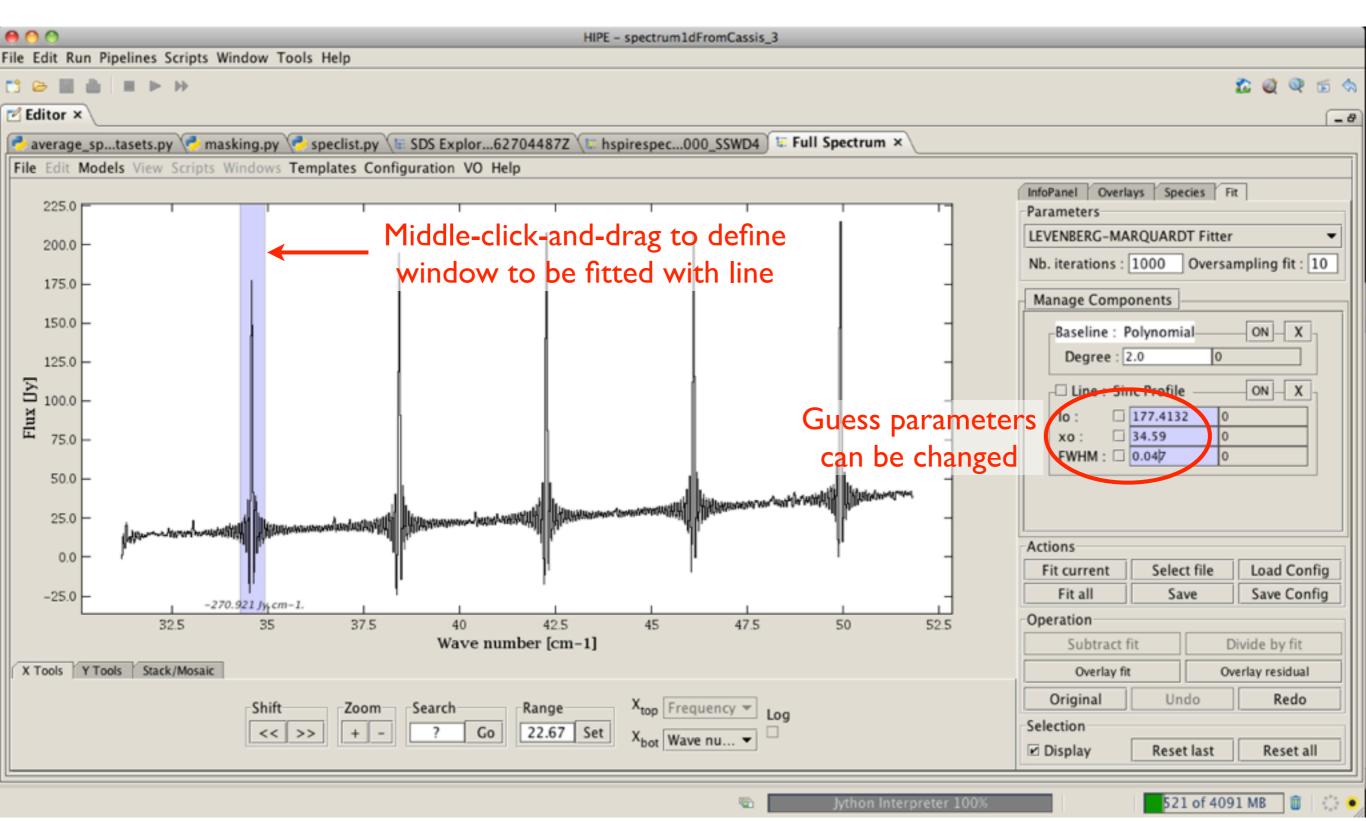
I. Start with a spectrum I d of an unapodized spectrum, and open+display it with Cassis Spectrum I d Analysis

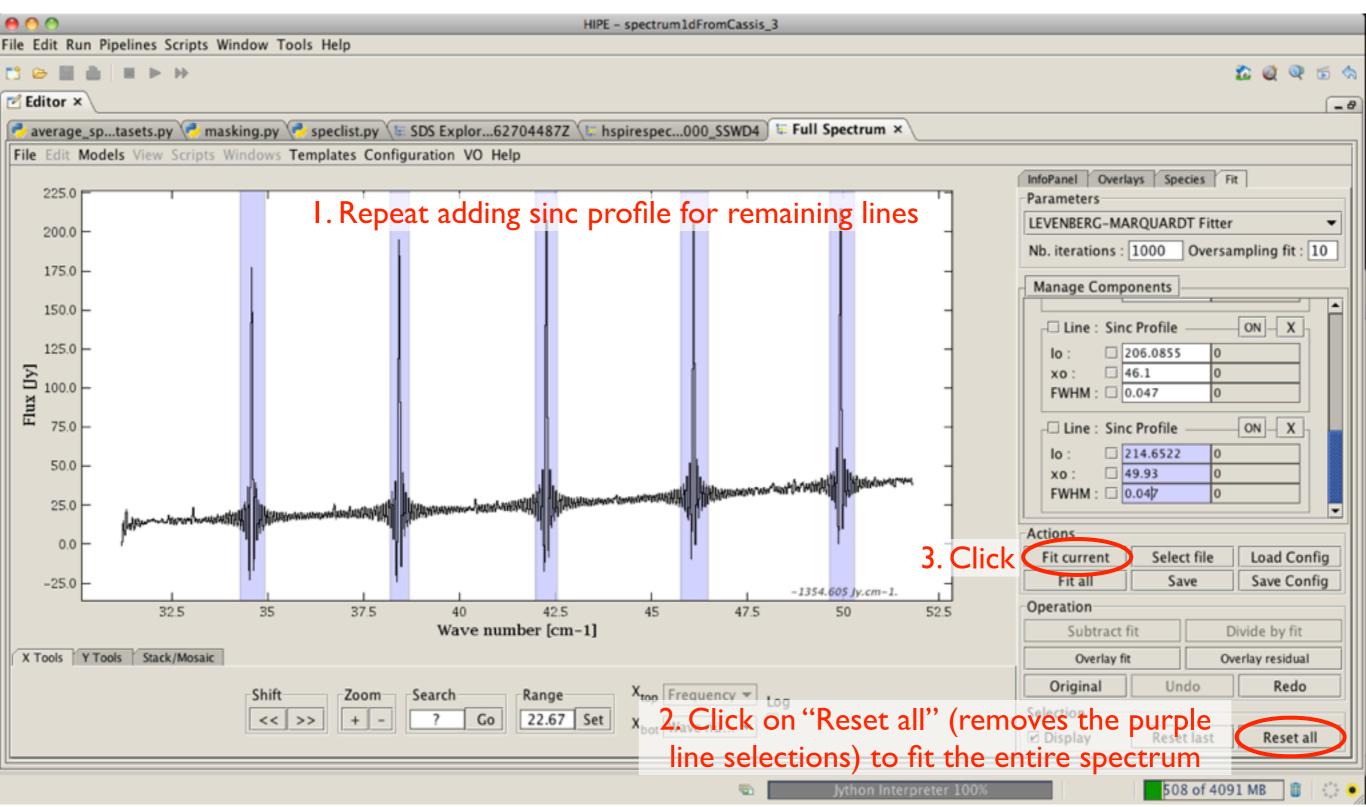
HIPE - spectrum1dFromCassis_3

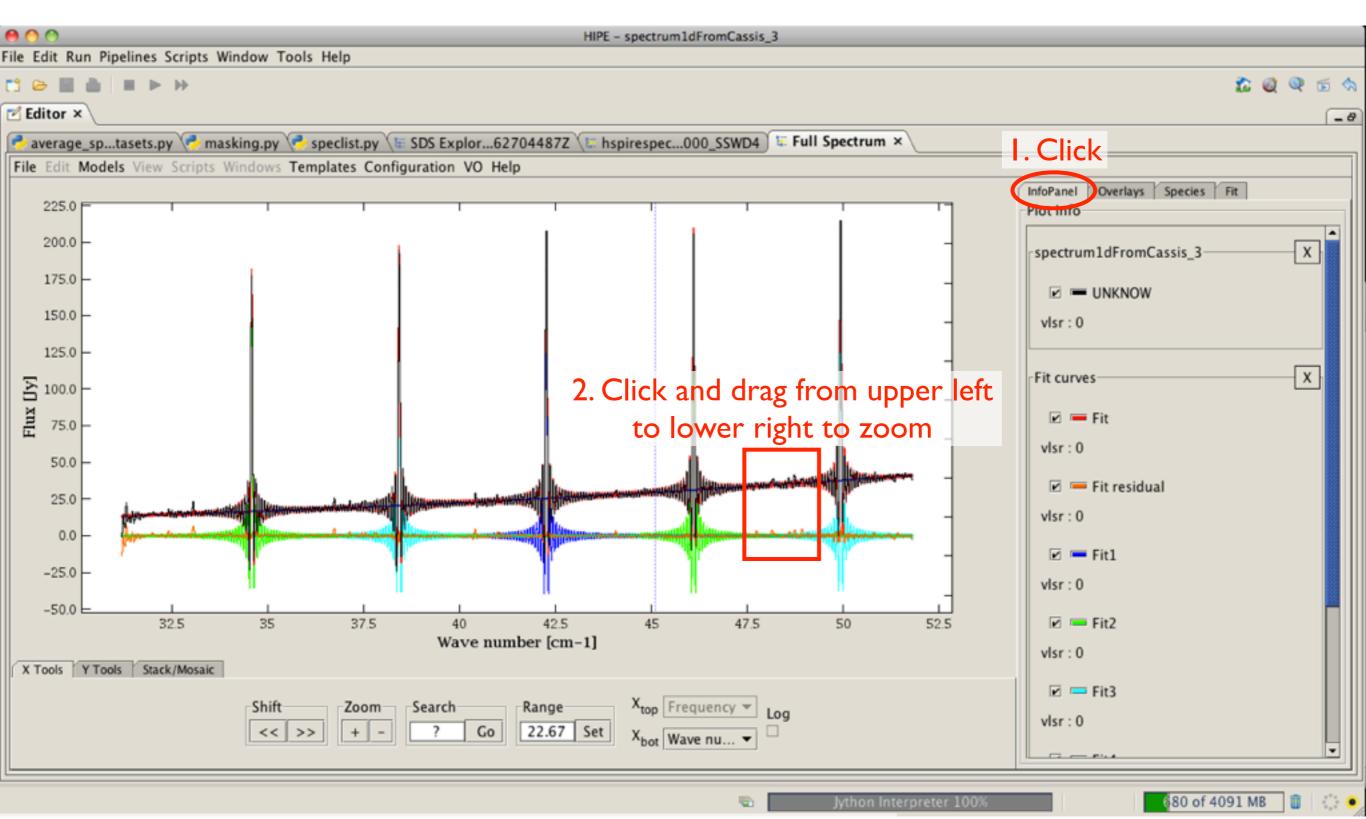




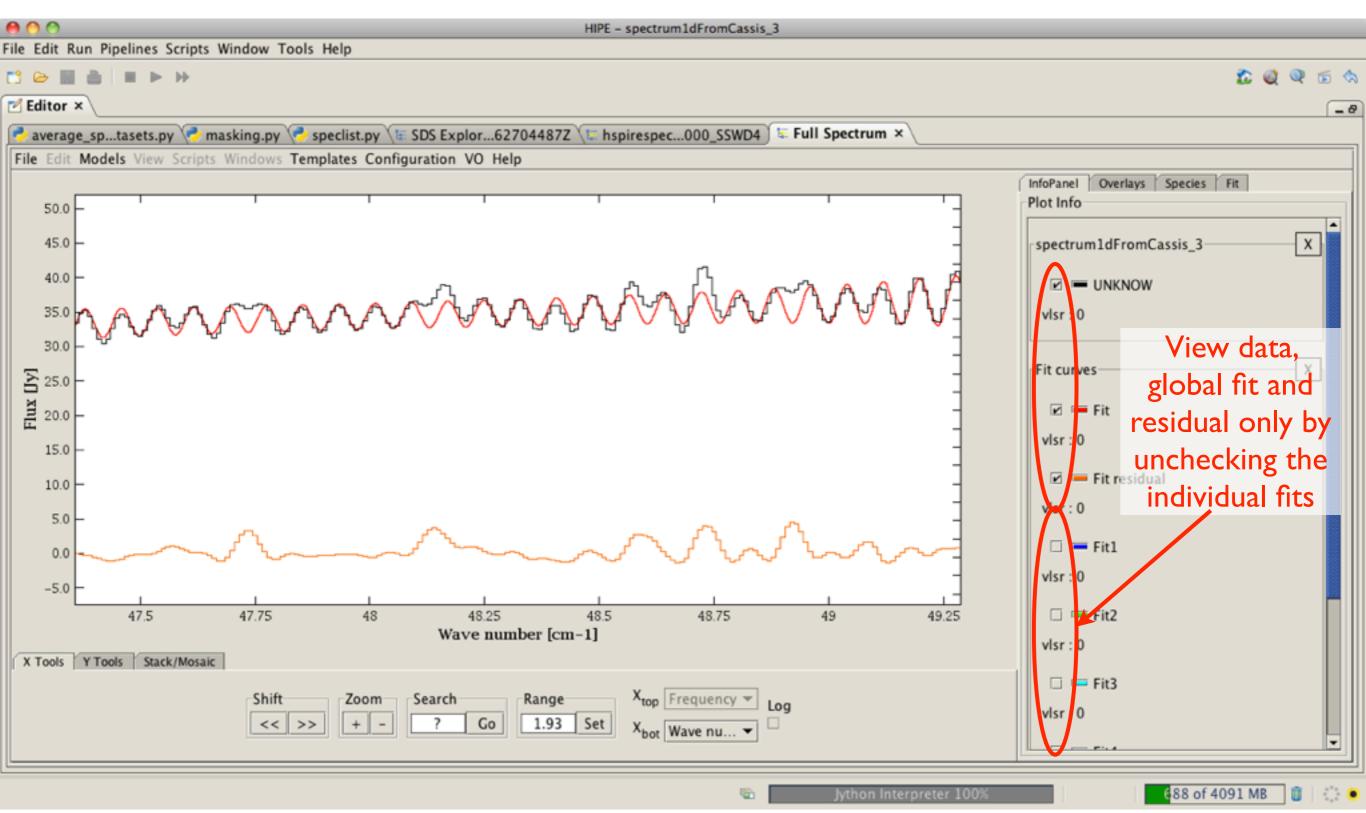








(Note: Click and drag from lower right to upper left to unzoom)



4.3. Sinc profile removal

Back to the fit tab, full spectrum ; click on "Subtract fit" 00 HIPE - spectrum1dFromCassis 3 File Edit Run Pipelines Scripts Window Tools Help 🏠 🍭 🍳 🗟 🥎 📑 🗁 📓 👜 Editor × - 8 everage_sp...tasets.py 🥐 masking.py 🥐 speclist.py 👍 SDS Explor...62704487Z 🐚 hspirespec...000_SSWD4 ቹ Full Spectrum 🗙 I. Click File Edit Models View Scripts Windows Templates Configuration VO Help InfoPanel Overlays Species Fit 225.0 Parameters LEVENBERG-MARQUARDT Fitter 200.0 -Nb. iterations : 1000 Oversampling fit : 10 175.0 -Manage Components 150.0 Line : Sinc Profile ON X 125.0 178.6336 0.6721 lo: Flux [Jy] 46.0952 8.10146E-5 xo: 100.0 FWHM : 0.0472 2.732637E-5 75.0 Line : Sinc Profile ON X lo : 173.9618 0.7365 50.0 49.9294 8.316004E-5 xo: FWHM : 0.0472 8.636457E-5 25.0 Actions 0.0 Select file Load Config Fit current Fit all Save Save Config -25.0 Operation 37.5 52.5 32.5 35 40 42.5 45 47.5 50 2. Click Wave number [cm-1] Subtract fit X Tools Y Tools Stack/Mosaic Hide fit Hide residual Original Undo Redo Xtop Frequency -Shift Zoom Search Range Log Selection Go 22.67 Set << >> + X_{bot} Wave nu... -Display Reset last Reset all

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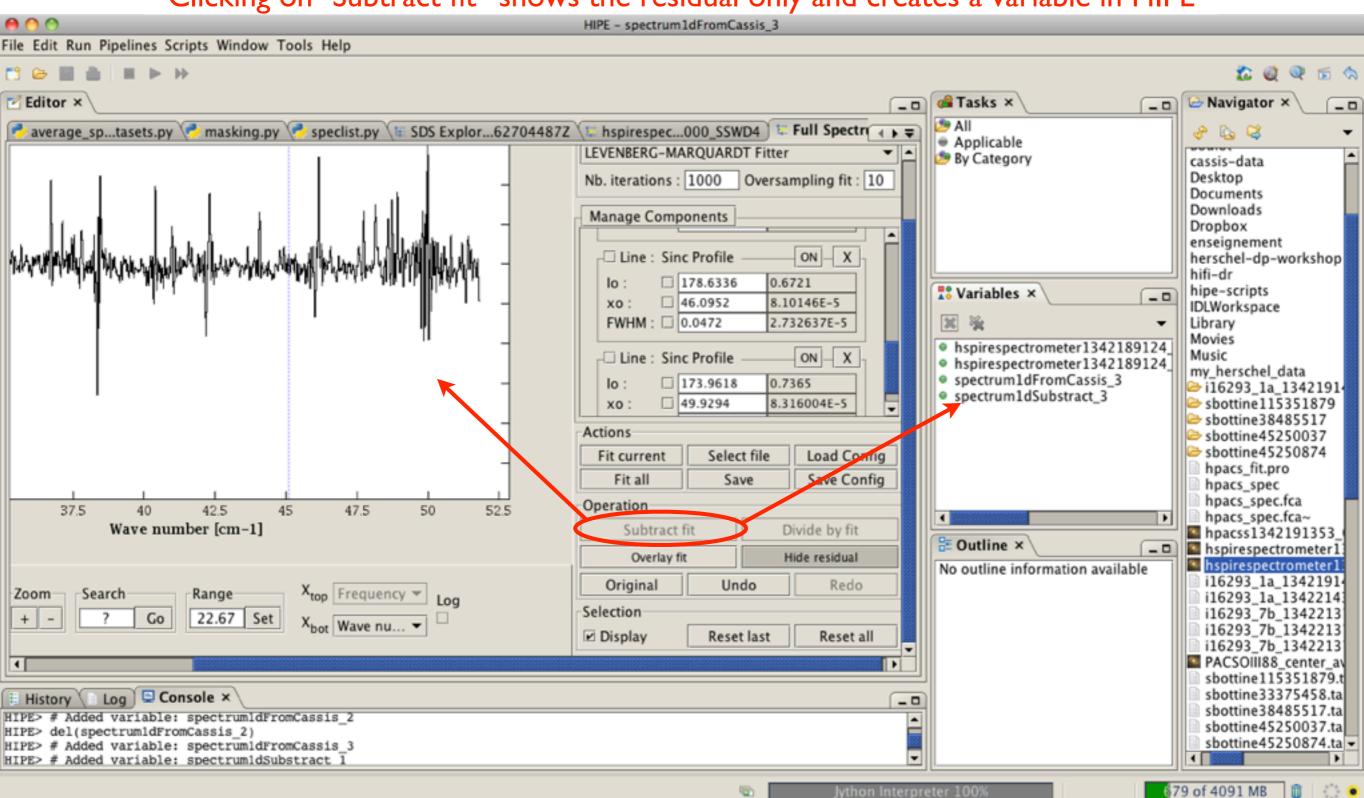
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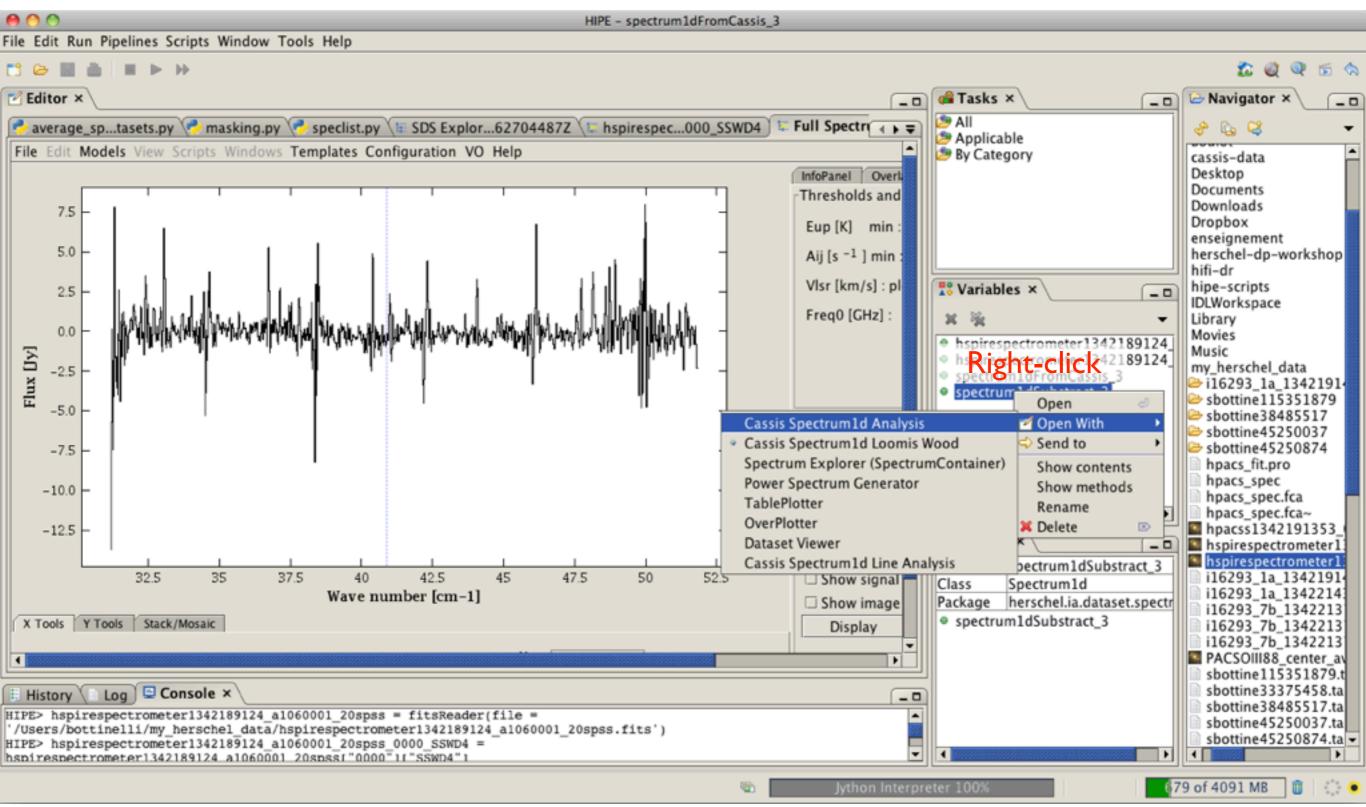
4

4.3. Sinc profile removal

Clicking on "Subtract fit" shows the residual only and creates a variable in HIPE



4.3. Sinc profile removal : line identification

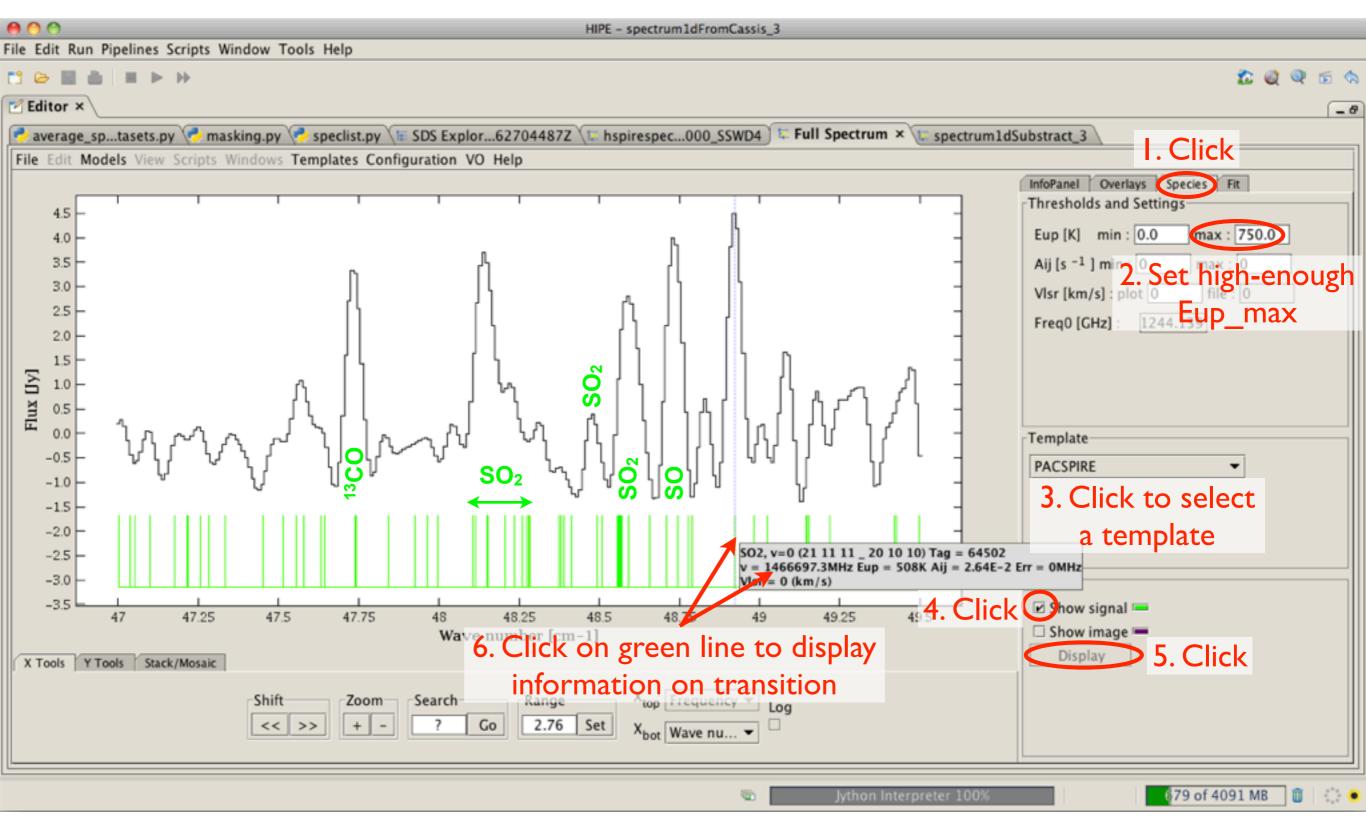


4.3. Sinc profile removal : line identification

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4.3. Sinc profile removal : line identification



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