
pyspeckit Documentation

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Adam Ginsburg

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An extensible spectroscopic analysis toolkit for astronomy.

If you're just getting started, see the *[examples page](#)*.

To cite pyspeckit, use <http://adsabs.harvard.edu/abs/2011ascl.soft09001G>.

Part I

Downloads

- March 2015 version
- latest commit from bitbucket (see *Installation and Requirements*)
- latest commit from github (same as above)
- pypi entry.

Supported file types and their formats:

- *FITS*
- *Plain Text*
- *hdf5*

Part II

Guides / Getting Started

- *Guide for GILDAS-CLASS users*
A simple getting started guide aimed at Gildas-CLASS users
- *Guide for IRAF users*
Intended for users of IRAF's splot interactive fitting routine.

Part III

Classes and API

At the core, PySpecKit runs on a ‘Spectroscopic Object’ class called [Spectrum](#). Therefore everything interesting about PySpecKit can be learned by digging into the properties of this class.

- [spectrum](#) can read a variety of individual spectra types
 - [Spectrum](#) The Spectrum class, which is the core of pyspeckit. The `__init__` procedure opens a spectrum file.
 - [Spectra](#) A group of [Spectrum](#)s. Generally for when you have multiple wavelength observations you want to stitch together (e.g., two filterbanks on a heterodyne system, or the red/blue spectra from a multi-band spectrometer like the Double Imaging Spectrograph)
 - [ObsBlock](#) An Observation Block - multiple spectra of different objects or different times covering the same wavelength range
- [Cubes](#) is used to deal with data cubes and has functionality similar to [GAIA](#) and [ds9](#).
 - [Cube](#) A Cube of Spectra. Has features to collapse the cube along the spectral axis and fit spectra to each element of the cube. Is meant to replicate [Starlink’s GAIA](#) in some ways, but with less emphasis on speed and much greater emphasis on spectral line fitting.

Part IV

Features

- *Baseline Fitting* describes baseline & continuum fitting.
- *Model Fitting* describes the general process of model fitting.
- *Measurements* is a toolkit for performing EQW, column, and other measurements...
- *Units* contains the all-important `SpectroscopicAxis` class that is used to deal with coordinate transformations
- *Registration* describes the extensible qualities of pyspeckit

Installation and Requirements

Hint: You can *easy_install* or *pip_install* pyspeckit:

```
pip install pyspeckit
easy_install pyspeckit
```

PySpecKit requires at least the basic scientific packages:

- `numpy`
- `matplotlib`
- `mpfit` is included
- `scipy` is optional. It is only required for RADEX grid interpolation and certain types of optimization
- `python2.7` or `ordereddict` for model parameter storage

You'll most likely want at least one of the following packages to enable file reading

- `astropy` ≥ 0.4
- `pyfits` ≥ 2.4
- `atpy` (which depends on `asciitable` [[github link](#)])
- `hdf5`

If you have `pip` (see <http://pypi.python.org/pypi/pyspeckit>), you can install with:

```
pip install pyspeckit
```

Or the most recent version:

```
pip install https://bitbucket.org/pyspeckit/pyspeckit/get/master.tar.gz
```

You can acquire the code with this clone command:

```
git clone git@bitbucket.org:pyspeckit/pyspeckit.git pyspeckit
cd pyspeckit
python setup.py install
```

Or you can [Download the latest tarball version](#), then extract and install using the standard python method (but the `pip` install version of this is easier):

```
wget --no-check-certificate https://bitbucket.org/pyspeckit/pyspeckit/get/master.tar.gz
tar -xzf master.tar.gz
cd pyspeckit-pyspeckit-[commit]
python setup.py install
```

You can also check out the [source code](#)

Note: If you use `easy_install pyspeckit` with the Enthought Python Distribution, you will most likely get a `SandboxViolation` error. You can get around this by using `python setup.py install` or `pip install pyspeckit`.

Models

See [Parameters](#) for information on how to restrict/modify model parameters. The generic `SpectralModel` class is a wrapper for model functions. A model should take in an X-axis and some number of parameters. In order to declare a `SpectralModel`, you give `SpectralModel` the function name and the number of parameters it requires. The rest of the options are optional, though `parnames` & `shortvarnames` are strongly recommended. If you do not specify `fitunits`, your fitting code must deal with units internally.

Here are some examples of how to make your own fitters:

```
hill5_fitter = model.SpectralModel(hill5_model, 5,
    parnames=['tau', 'v_lsr', 'v_infall', 'sigma', 'tpeak'],
    parlimited=[(True,False),(False,False),(True,False),(True,False), (True,False)],
    parlimits=[(0,0), (0,0), (0,0), (0,0), (0,0)],
    # specify the parameter names (TeX is OK)
    shortvarnames=("\\tau", "v_{lsr}", "v_{infall}", "\\sigma", "T_{peak}"),
    fitunits='Hz' )

gaussfitter = model.SpectralModel(gaussian, 3,
    parnames=['amplitude', 'shift', 'width'],
    parlimited=[(False,False),(False,False),(True,False)],
    parlimits=[(0,0), (0,0), (0,0)],
    shortvarnames=('A', r'\Delta x', r'\sigma'))
```

Then you can register these fitters.

2.1 API Documentation for Models

```
class pyspeckit.spectrum.models.model.SpectralModel(modelfunc, npars, shortvarnames=('A',
    '\Delta x', '\sigma'), fitunits=None,
    centroid_par=None, fwhm_func=None,
    fwhm_pars=None, integral_func=None,
    use_lmfit=False, **kwargs)
```

A wrapper class for a spectra model. Includes internal functions to generate multi-component models, annotations, integrals, and individual components. The declaration can be complex, since you should name individual variables, set limits on them, set the units the fit will be performed in, and set the annotations to be used. Check out some of the hyperfine codes (hcn, n2hp) for examples.

Spectral Model Initialization

Create a Spectral Model class for data fitting

Parameters**modelfunc** : function

the model function to be fitted. Should take an X-axis (spectroscopic axis) as an input followed by input parameters. Returns an array with the same shape as the input X-axis

npars : int

number of parameters required by the model

parnames : list (optional)

a list or tuple of the parameter names

parvalues : list (optional)

the initial guesses for the input parameters (defaults to ZEROS)

parlimits : list (optional)

the upper/lower limits for each variable (defaults to ZEROS)

parfixed : list (optional)

Can declare any variables to be fixed (defaults to ZEROS)

parerror : list (optional)

technically an output parameter... hmm (defaults to ZEROS)

partied : list (optional)

not the past tense of party. Can declare, via text, that some parameters are tied to each other. Defaults to zeros like the others, but it's not clear if that's a sensible default

fitunits : str (optional)

convert X-axis to these units before passing to model

parsteps : list (optional)

minimum step size for each parameter (defaults to ZEROS)

npeaks : list (optional)

default number of peaks to assume when fitting (can be overridden)

shortvarnames : list (optional)

TeX names of the variables to use when annotating

Returns

A tuple containing (model best-fit parameters, the model, parameter : errors, χ^2 value) :

analytic_centroids(*centroidpar=None*)

Return the *analytic* centroids of the model components

Parameters**centroidpar** : None or string

The name of the parameter in the fit that represents the centroid *some models have default centroid parameters - these will be used if centroidpar is unspecified*

Returns

List of the centroid values (even if there's only 1) :

analytic_fwhm(*parinfo=None*)

Return the FWHM of the model components *if* a `fwhm_func` has been defined

Done with incomprehensible list comprehensions instead of nested for loops... readability sacrificed for speed and simplicity. This is unpythonic.

analytic_integral(*modelpars=None, npeaks=None, npars=None*)

Placeholder for analytic integrals; these must be defined for individual models

annotations(*shortvarnames=None, debug=False*)

Return a list of TeX-formatted labels

The values and errors are formatted so that only the significant digits are displayed. Rounding is performed using the decimal package.

Parameters

shortvarnames : list

A list of variable names (tex is allowed) to include in the annotations. Defaults to `self.shortvarnames`

Examples

```
>>> # Annotate a Gaussian
>>> sp.specfit.annotate(shortvarnames=['A', '\Delta x', '\sigma'])
```

component_integrals(*xarr, dx=None*)

Compute the integrals of each component

components(*xarr, pars, **kwargs*)

Return a numpy ndarray of shape [npeaks x modelshape] of the independent components of the fits

computed_centroid(*xarr=None*)

Return the *computed* centroid of the model

Parameters

xarr : None or np.ndarray

The X coordinates of the model over which the centroid should be computed. If unspecified, the centroid will be in pixel units

fitter(*xax, data, err=None, quiet=True, veryverbose=False, debug=False, parinfo=None, **kwargs*)

Run the fitter using mpfit.

kwargs will be passed to `_make_parinfo` and mpfit.

Parameters

xax : SpectroscopicAxis

The X-axis of the spectrum

data : ndarray

The data to fit

err : ndarray (optional)

The error on the data. If unspecified, will be uniform unity

parinfo : ParinfoList

The guesses, parameter limits, etc. See `pyspeckit.spectrum.parinfo` for details

quiet : bool

pass to mpfit. If False, will print out the parameter values for each iteration of the fitter

veryverbose : bool

print out a variety of mpfit output parameters

debug : bool

raise an exception (rather than a warning) if χ^2 is nan

get_emcee_ensemblesampler(*xarr, data, error, nwalkers, **kwargs*)

Get an emcee walker ensemble for the data & model

Parameters

data : np.ndarray

error : np.ndarray

nwalkers : int

Number of walkers to use

Examples

```
>>> import pyspeckit
>>> x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10,10,50), unit='km/s')
>>> e = np.random.randn(50)
>>> d = np.exp(-np.asarray(x)**2/2.)*5 + e
>>> sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
>>> sp.specfit(fittype='gaussian')
>>> nwalkers = sp.specfit.fitter.npars * 2
>>> emcee_ensemble = sp.specfit.fitter.get_emcee_ensemblesampler(sp.xarr, sp.data, sp.error, nwalkers)
>>> p0 = np.array([sp.specfit.parinfo.values] * nwalkers)
>>> p0 *= np.random.randn(*p0.shape) / 10. + 1.0
>>> pos, logprob, state = emcee_ensemble.run_mcmc(p0, 100)
```

get_emcee_sampler(*xarr, data, error, **kwargs*)

Get an emcee walker for the data & model

Parameters

xarr : pyspeckit.units.SpectroscopicAxis

data : np.ndarray

error : np.ndarray

Examples

```
>>> import pyspeckit
>>> x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10,10,50), unit='km/s')
>>> e = np.random.randn(50)
>>> d = np.exp(-np.asarray(x)**2/2.)*5 + e
>>> sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
>>> sp.specfit(fittype='gaussian')
>>> emcee_sampler = sp.specfit.fitter.get_emcee_sampler(sp.xarr, sp.data, sp.error)
>>> p0 = sp.specfit.parinfo
>>> emcee_sampler.run_mcmc(p0, 100)
```

get_pymc(*xarr*, *data*, *error*, *use_fitted_values=False*, *inf=inf*, *use_adaptive=False*, *return_dict=False*, ***kwargs*)

Create a pymc MCMC sampler. Defaults to ‘uninformative’ priors

Parameters

data : np.ndarray

error : np.ndarray

use_fitted_values : bool

Each parameter with a measured error will have a prior defined by the Normal distribution with $\sigma = \text{par.error}$ and $\mu = \text{par.value}$

Examples

```
>>> x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10,10,50), unit='km/s')
>>> e = np.random.randn(50)
>>> d = np.exp(-np.asarray(x)**2/2.)*5 + e
>>> sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
>>> sp.specfit(fittype='gaussian')
>>> MCuninformed = sp.specfit.fitter.get_pymc(sp.xarr, sp.data, sp.error)
>>> MCwithpriors = sp.specfit.fitter.get_pymc(sp.xarr, sp.data, sp.error, use_fitted_values=True)
>>> MCuninformed.sample(1000)
>>> MCuninformed.stats()['AMPLITUDE0']
>>> # WARNING: This will fail because width cannot be set <0, but it may randomly reach that...
>>> # How do you define a likelihood distribution with a lower limit?!
>>> MCwithpriors.sample(1000)
>>> MCwithpriors.stats()['AMPLITUDE0']
```

integral(*modelpars*, *dx=None*, ***kwargs*)

Extremely simple integrator: IGNORES modelpars; just sums self.model

lmfitfun(*x*, *y*, *err=None*, *debug=False*)

Wrapper function to compute the fit residuals in an lmfit-friendly format

lmfitter(*xax*, *data*, *err=None*, *parinfo=None*, *quiet=True*, *debug=False*, ***kwargs*)

Use lmfit instead of mpfit to do the fitting

Parameters

xax : SpectroscopicAxis

The X-axis of the spectrum

data : ndarray

The data to fit

err : ndarray (optional)

The error on the data. If unspecified, will be uniform unity

parinfo : ParinfoList

The guesses, parameter limits, etc. See `pyspeckit.spectrum.parinfo` for details

quiet : bool

If false, print out some messages about the fitting

logp(*xarr*, *data*, *error*, *pars=None*)

Return the log probability of the model

mpfitfun(*x*, *y*, *err=None*)

Wrapper function to compute the fit residuals in an mpfit-friendly format

n_modelfunc(*pars=None*, *debug=False*, ***kwargs*)

Simple wrapper to deal with N independent peaks for a given spectral model

slope(*xinp*)

Find the local slope of the model at location *x* (*x* must be in *xax*'s units)

Ammonia inversion transition TKIN fitter translated from Erik Rosolowsky's <http://svn.ok.ubc.ca/svn/signals/nh3fit/>

2.1.1 Module API

```
pyspeckit.spectrum.models.ammonia.ammonia(xarr, tkin=20, tex=None, ntot=100000000000000.0,  
                                             width=1, xoff_v=0.0, fortho=0.0, tau=None, fillingfrac-  
                                             tion=None, return_tau=False, background_tb=2.7315,  
                                             thin=False, verbose=False, return_components=False,  
                                             debug=False)
```

Generate a model Ammonia spectrum based on input temperatures, column, and gaussian parameters

Parameters

xarr: 'pyspeckit.spectrum.units.SpectroscopicAxis' :

Array of wavelength/frequency values

ntot: float :

can be specified as a column density (e.g., 10^{15}) or a log-column-density (e.g., 15)

tex: float or None :

Excitation temperature. Assumed LTE if unspecified (None), if $\text{tex} > \text{tkin}$, or if *thin* is specified.

ntot: float :

Total column density of NH₃. Can be specified as a float in the range 5-25 or an exponential ($1\text{e}5$ - $1\text{e}25$)

width: float :

Line width in km/s

xoff_v: float :

Line offset in km/s

fortho: float :

Fraction of NH₃ molecules in ortho state. Default assumes all para (*fortho*=0).

tau: None or float :

If *tau* (optical depth in the 1-1 line) is specified, *ntot* is NOT fit but is set to a fixed value. The optical depths of the other lines are fixed relative to *tau_oneone*

fillingfraction: None or float :

fillingfraction is an arbitrary scaling factor to apply to the model

return_tau: bool :

Return a dictionary of the optical depths in each line instead of a synthetic spectrum

thin: bool :

uses a different parametrization and requires only the optical depth, width, offset, and `tkin` to be specified. In the ‘thin’ approximation, `tex` is not used in computation of the partition function - LTE is implicitly assumed

return_components: bool :

Return a list of arrays, one for each hyperfine component, instead of just one array

background_tb : float

The background brightness temperature. Defaults to TCMB.

verbose: bool :

More messages

debug: bool :

For debugging.

Returns

spectrum: ‘numpy.ndarray’ :

Synthetic spectrum with same shape as `xarr`

component_list: list :

List of `numpy.ndarray`’s, one for each hyperfine component

tau_dict: dict :

Dictionary of optical depth values for the various lines (if `return_tau` is set)

Adds a variable height (background) component to any model. This is a formaldehyde 1₁₁-1₁₀ / 2₁₂-2₁₁ fitter. It includes hyperfine components of the formaldehyde lines and has both LTE and RADEX LVG based models

```
pyspeckit.spectrum.models.formaldehyde.formaldehyde(xarr, amp=1.0, xoff_v=0.0, width=1.0,
                                                    return_hyperfine_components=False, texscale=0.01, tau=0.01, **kwargs)
```

Generate a model Formaldehyde spectrum based on simple gaussian parameters

the “amplitude” is an essentially arbitrary parameter; we therefore define it to be `Tex` given `tau=0.01` when passing to the fitter. The final spectrum is then rescaled to that value

```
pyspeckit.spectrum.models.formaldehyde.formaldehyde_pyradex(xarr, density=4, column=13, temperature=20, xoff_v=0.0, opr=1.0,
                                                            width=1.0, tbackground=2.73,
                                                            grid_vwidth=1.0, debug=False,
                                                            verbose=False, **kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because `tau = modeltau / width` (see, e.g., Draine 2011 textbook pgs 219-230)

```
pyspeckit.spectrum.models.formaldehyde.formaldehyde_radex(xarr,          density=4,          col-  
ummn=13,          xoff_v=0.0,  
width=1.0,          grid_vwidth=1.0,  
grid_vwidth_scale=False,          tex-  
grid=None,          taugrid=None,  
hdr=None,          path_to_texgrid='',  
path_to_taugrid='',          tempera-  
ture_gridnumber=3,          debug=False,  
verbose=False, **kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because $\tau = \text{modeltau} / \text{width}$ (see, e.g., Draine 2011 textbook pgs 219-230) `grid_vwidth_scale` is True or False: False for LVG, True for Sphere

```
pyspeckit.spectrum.models.formaldehyde.formaldehyde_radex_orthopara_temp(xarr,          density=4,  
column=13,          or-  
thopara=1.0,          tem-  
perature=15.0,  
xoff_v=0.0,  
width=1.0,          Tback-  
ground1=2.73,  
Tback-  
ground2=2.73,  
grid_vwidth=1.0,  
grid_vwidth_scale=False,  
texgrid=None,  
taugrid=None,  
hdr=None,  
path_to_texgrid='',  
path_to_taugrid='',  
debug=False,  
verbose=False,  
getpars=False,  
**kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because $\tau = \text{modeltau} / \text{width}$ (see, e.g., Draine 2011 textbook pgs 219-230) `grid_vwidth_scale` is True or False: False for LVG, True for Sphere


```
pyspeckit.spectrum.models.formaldehyde.formaldehyde_radex_tau(xarr,      density=4,      col-
                                                                umn=13,      xoff_v=0.0,
                                                                width=1.0,      grid_vwidth=1.0,
                                                                grid_vwidth_scale=False,
                                                                taugrid=None,      hdr=None,
                                                                path_to_taugrid='',      tem-
                                                                perature_gridnumber=3,      de-
                                                                bug=False,      verbose=False,      re-
                                                                turn_hyperfine_components=False,
                                                                **kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

- uses hyperfine components
- assumes *tau* varies but *tex* does not!

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because $\tau = \text{modeltau} / \text{width}$ (see, e.g., Draine 2011 textbook pgs 219-230) `grid_vwidth_scale` is True or False: False for LVG, True for Sphere

The simplest and most useful model.

Until 12/23/2011, gaussian fitting used the complicated and somewhat bloated `gaussfitter.py` code. Now, this is a great example of how to make your own model! Just make a function like `gaussian` and plug it into the `SpectralModel` class.

```
pyspeckit.spectrum.models.inherited_gaussfitter.gaussian(x, A, dx, w, return_components=False,
                                                                normalized=False,      re-
                                                                turn_hyperfine_components=False)
```

Returns a 1-dimensional gaussian of form $A * \text{numpy.exp}(-(x-dx)**2/(2*w**2))$

Area is $\sqrt{2*\pi*\sigma^2} * \text{amplitude}$ - i.e., this is NOT a normalized gaussian, unless `normalized=True` in which case $A = \text{Area}$

Parameters

x : np.ndarray

array of x values

A : float

Amplitude of the Gaussian, i.e. its peak value, unless `normalized=True` then A is the area of the gaussian

dx : float

Center or “shift” of the gaussian

w : float

Width of the gaussian (sigma)

return_components : bool

dummy variable; `return_components` does nothing but is required by all fitters

return_hyperfine_components : bool

dummy variable; does nothing but is required by all fitters

normalized : bool

Return a normalized Gaussian?

`pyspeckit.spectrum.models.inherited_gaussfitter.gaussian_fitter()`

Generator for Gaussian fitter class

`pyspeckit.spectrum.models.inherited_gaussfitter.gaussian_integral(amplitude, sigma)`

Integral of a Gaussian

`pyspeckit.spectrum.models.inherited_gaussfitter.gaussian_vheight_fitter()`

Generator for Gaussian fitter class

This is an HCN fitter... ref for line params: <http://www.strw.leidenuniv.nl/~moldata/datafiles/hcn@hfs.dat>

`pyspeckit.spectrum.models.hcn.aval_dict = {'10-01': 2.4075e-05, '12-01': 2.4075e-05, '11-01': 2.4075e-05}`

Line strengths of the 15 hyperfine components in J = 1 - 0 transition. The thickness of the lines indicates their relative weight compared to the others. Line strengths are normalized in such a way that summing over all initial J = 1 levels gives the degeneracy of the J = 0 levels, i.e., for JF1F = 012, three for JF1F = 011, and one for JF1F = 010. Thus, the sum over all 15 transitions gives the total spin degeneracy

`pyspeckit.spectrum.models.hcn.hcn_radex(xarr, density=4, column=13, xoff_v=0.0, width=1.0, grid_vwidth=1.0, grid_vwidth_scale=False, texgrid=None, taugrid=None, hdr=None, path_to_texgrid='', path_to_taugrid='', temperature_gridnumber=3, debug=False, verbose=False, **kwargs)`

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because $\tau = \text{modeltau} / \text{width}$ (see, e.g., Draine 2011 textbook pgs 219-230) `grid_vwidth_scale` is True or False: False for LVG, True for Sphere

Code translated from: https://bitbucket.org/devries/analytic_infall/overview

Original source: <http://adsabs.harvard.edu/abs/2005ApJ...620..800D>

`pyspeckit.spectrum.models.hill5infall.hill5_model(xarr, tau, v_lsr, v_infall, sigma, tpeak, TBG=2.73)`

The rest of this needs to be translated from C

`pyspeckit.spectrum.models.hill5infall.jfunc(t, nu)`

t- kelvin nu - Hz?

`class pyspeckit.spectrum.models.hyperfine.hyperfinemodel(line_names, voff_lines_dict, freq_dict, line_strength_dict, relative_strength_total_degeneracy)`

Wrapper for the hyperfine model class. Specify the offsets and relative strengths when initializing, then you've got yourself a hyperfine modeler.

There are a wide variety of different fitter attributes, each designed to free a different subset of the parameters. Their purposes should be evident from their names.

Initialize the various parameters defining the hyperfine transitions

Parameters

line_names: list :

list of the line names to be used as indices for the dictionaries

voff_lines_dict: dict :

a linename:v_off dictionary of velocity offsets for the hyperfine components. Technically, this is redundant with freq_dict

freq_dict: dict :

frequencies of the individual transitions

line_strength_dict: dict :

Relative strengths of the hyperfine components, usually determined by their degeneracy and Einstein A coefficients

hyperfine(*xarr*, *Tex*=5.0, *tau*=0.1, *xoff_v*=0.0, *width*=1.0, *return_hyperfine_components*=False, *Tbackground*=2.73, *amp*=None, *return_tau*=False, *tau_total*=None, *vary_hyperfine_tau*=False, *vary_hyperfine_width*=False)

Generate a model spectrum given an excitation temperature, optical depth, offset velocity, and velocity width.

Parameters

return_tau : bool

If specified, return just the tau spectrum, ignoring Tex

tau_total : bool

If specified, use this *instead of tau*, and it tries to normalize to the *peak of the line*

vary_hyperfine_tau : bool

If set to true, allows the hyperfine transition amplitudes to vary and does not use the line_strength_dict. If set, tau must be a dict

hyperfine_addbackground(*xarr*, *Tbackground*=2.73, *Tex*=5.0, *tau*=0.1, *xoff_v*=0.0, *width*=1.0, *return_tau*=False, ***kwargs*)

Identical to hyperfine, but adds Tbackground as a constant continuum level

hyperfine_amp(*xarr*, *amp*=None, *xoff_v*=0.0, *width*=1.0, *return_hyperfine_components*=False, *Tbackground*=2.73, *Tex*=5.0, *tau*=0.1)

wrapper of self.hyperfine with order of arguments changed

hyperfine_tau(*xarr*, *tau*, *xoff_v*, *width*, ***kwargs*)

same as hyperfine, but with arguments in a different order, AND tau is returned instead of exp(-tau)

hyperfine_tau_total(*xarr*, *tau_total*, *xoff_v*, *width*, ***kwargs*)

same as hyperfine, but with arguments in a different order, AND tau is returned instead of exp(-tau), AND the *peak* tau is used

hyperfine_varyhf(*xarr*, *Tex*, *xoff_v*, *width*, **args*, ***kwargs*)

Wrapper of hyperfine for using a variable number of peaks with specified tau

hyperfine_varyhf_amp(*xarr*, *xoff_v*, *width*, **args*, ***kwargs*)

Wrapper of hyperfine for using a variable number of peaks with specified amplitude (rather than tau). Uses some opaque tricks: Tex is basically ignored, and return_tau means you're actually returning the amplitude, which is just passed in as tau

hyperfine_varyhf_amp_width(*xarr*, *xoff_v*, **args*, ***kwargs*)

Wrapper of hyperfine for using a variable number of peaks with specified amplitude (rather than tau). Uses some opaque tricks: Tex is basically ignored, and return_tau means you're actually returning the amplitude, which is just passed in as tau

The simplest and most useful model.

Until 12/23/2011, lorentzian fitting used the complicated and somewhat bloated gaussfitter.py code. Now, this is a great example of how to make your own model!

```
pyspeckit.spectrum.models.inherited_lorentzian.lorentzian(x, A, dx, w, re-
    turn_components=False)
    Returns a 1-dimensional lorentzian of form  $A*2*\pi*w/((x-dx)**2 + ((w/2)**2))$ 
```

[amplitude,center,width]

return_components does nothing but is required by all fitters

```
pyspeckit.spectrum.models.inherited_lorentzian.lorentzian_fitter()
    Generator for lorentzian fitter class
```

Fit a line based on parameters output from a grid of models

```
pyspeckit.spectrum.models.modelgrid.gaussian_line(xax, maxamp, tau, offset, width)
    A Gaussian line function in which the
```

```
pyspeckit.spectrum.models.modelgrid.line_model_2par(xax, center, width, gridval1, gridval2,
    griddim1, griddim2, maxampgrid, taugrid,
    linefunction=<function gaussian_line at
    0x7f0b334d2ed8>)
```

Returns the spectral line that matches the given x-axis

xax, center, width must be in the same units!

```
pyspeckit.spectrum.models.modelgrid.line_params_2D(gridval1, gridval2, griddim1, griddim2, value-
    grid)
```

Given a 2D grid of modeled line values - the amplitude, e.g. excitation temperature, and the optical depth, tau - return the model spectrum

griddims contains the names of the axes and their values... it should have the same number of entries as gridpars

2.1.2 N2H+ fitter

Reference for line params: Daniel, F., Dubernet, M.-L., Meuwly, M., Cernicharo, J., Pagani, L. 2005, MNRAS 363, 1083

<http://www.strw.leidenuniv.nl/~moldata/N2H+.html>

<http://adsabs.harvard.edu/abs/2005MNRAS.363.1083D>

Does not yet implement: <http://adsabs.harvard.edu/abs/2010ApJ...716.1315K>

```
pyspeckit.spectrum.models.n2hp.n2hp_radex(xarr, density=4, column=13, xoff_v=0.0, width=1.0,
    grid_vwidth=1.0, grid_vwidth_scale=False,
    texgrid=None, taugrid=None, hdr=None,
    path_to_texgrid='', path_to_taugrid='', tempera-
    ture_gridnumber=3, debug=False, verbose=False,
    **kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))

xarr must be a SpectroscopicAxis instance xoff_v, width are both in km/s

grid_vwidth is the velocity assumed when computing the grid in km/s this is important because tau = modeltau / width (see, e.g., Draine 2011 textbook pgs 219-230) grid_vwidth_scale is True or False: False for LVG, True for Sphere

`pyspeckit.spectrum.models.inherited_voigtfitter.v \mathbf{voigt} (xarr, amp, xcen, sigma, gamma, normalized=False)`

$$z = (x + i \cdot \text{gam}) / (\text{sig} \cdot \sqrt{2}) \quad V(x, \text{sig}, \text{gam}) = \text{Re}(w(z)) / (\text{sig} \cdot \sqrt{2 \cdot \pi})$$

Original implementation converted from <http://mail.scipy.org/pipermail/scipy-user/2011-January/028327.html>
(had an incorrect normalization and strange treatment of the input parameters)

Parameters

The X values over which to compute the Voigt profile

Amplitude of the voigt profile if normalized = True, amp is the AREA

The X-offset of the profile

The width / sigma parameter of the Gaussian distribution

The width / shape parameter of the Lorentzian distribution

Determines whether “amp” refers to the area or the peak of the voigt profile

Generator for voigt fitter class

Approximation to the Voigt FWHM from wikipedia

Parameters

The width / sigma parameter of the Gaussian distribution

The width / shape parameter of the Lorentzian distribution

Get the spectral moments from the moments package. Use the gaussian width for the lorentzian width (not a great guess!)

2.1.3 Hydrogen Models

Hydrogen in HII regions is typically assumed to follow Case B recombination theory.

The values for the Case B recombination coefficients are given by [Hummer & Storey \(1987\)](#). They are also computed in [Hummer \(1994\)](#) and tabulated at a [wiki](#). I had to OCR and pull out by hand some of the coefficients.

`pyspeckit.spectrum.models.hydrogen.add_to_registry(sp)`

Add the Hydrogen model to the Spectrum's fitter registry

`pyspeckit.spectrum.models.hydrogen.find_lines(xarr)`

Given a `pyspeckit.units.SpectroscopicAxis` instance, finds all the lines that are in bounds. Returns a list of line names.

`pyspeckit.spectrum.models.hydrogen.hydrogen_fitter(sp, temperature=10000, tiedwidth=False)`

Generate a set of parameters identifying the hydrogen lines in your spectrum. These come in groups of 3 assuming you're fitting a gaussian to each. You can tie the widths or choose not to.

temperature [5000, 10000, 20000]

The case B coefficients are computed for 3 temperatures

tiedwidth [bool]

Should the widths be tied?

Returns a list of tied and guesses in the `xarr`'s units

`pyspeckit.spectrum.models.hydrogen.hydrogen_model(xarr, amplitude=1.0, width=0.0, velocity=0.0, a_k=0.0, temperature=10000)`

Generate a set of parameters identifying the hydrogen lines in your spectrum. These come in groups of 3 assuming you're fitting a gaussian to each. You can tie the widths or choose not to.

Parameters

sp : `pyspeckit.Spectrum`

The spectrum to fit

temperature : [5000, 10000, 20000]

The case B coefficients are computed for 3 temperatures

a_k : float

The K-band extinction normalized to 2.2 microns. Simple exponential.

width : float

Line width in km/s

velocity : float

Line center in km/s

amplitude : float

arbitrary amplitude of the first line (all other lines will be scaled to this value)

Returns

np.ndarray with same shape as `sp.xarr` :

`pyspeckit.spectrum.models.hydrogen.rrl(n, dn=1, amu=1.007825)`

compute Radio Recomb Line freqs in GHz from Brown, Lockman & Knapp ARAA 1978 16 445

2.2 Model Documentation Table of Contents

2.2.1 Parameters

Model parameters are very flexible, and can be accessed and modified in many parallel ways.

The `parinfo` class is built on top of `lmfit-py`'s `parameters` for compatibility with `lmfit-py`, but it builds on that. The code for the parameter overloading is in `parinfo.py`.

Simple Example

Start with a simple example: if you want to limit parameters to be within some range, use the `limits` and `limited` parameters.

```
# define shorthand first:
T,F = True,False
sp.specfit(fittype='gaussian', guesses=[-1,5,1,0.5,2,1],
           limits=[(0,0), (0,0), (0,0), (0,0), (0,0), (0,0)],
           limited=[(F,T), (F,F), (T,F), (T,F), (F,F), (T,F)])
```

In this example, there are two gaussian components being fitted because a Gaussian takes 3 parameters, an amplitude, a center, and a width, and there are 6 parameters in the input guesses.

The first line is forced to be an absorption line: its limits are $(0,0)$ but `limited=(F,T)` so only the 2nd parameter, the upper limit, is respected: the amplitude is forced to be $A \leq 0$.

The second line has its amplitude (the 4th parameter in guesses) forced *positive* since its limits are also $(0,0)$ but its `limited=(T,F)`.

Both lines have their *widths* forced to be positive, which is true by default: there is no meaning to a negative width, since the width enters into the equation for a gaussian as σ^2 .

Note that the need to limit parameters is the main reason for the existence of `lmfit-py` and `mpfit`.

Tying Parameters

It is also possible to explicitly state that one parameter depends on another. If, for example, you want to fit two gaussians, but they must be at a fixed wavelength separation from one another (e.g., for fitting the [S II] doublet), use `tied`:

```
sp.specfit(fittype='gaussian', guesses=[1,6716,1,0.5,6731,1],
           tied=['','','','p[1]','])
```

If you use `lmfit-py` by specifying `use_lmfit=True`, you can use the more advanced `mathematical constraints` permitted by `lmfit-py`.

Optical fitting: The $H\alpha$ -[NII] complex of a type-I Seyfert galaxy shows a more complete example using `tied`.

Making your own parinfo

You can also build a `parinfo` class directly. Currently, the best example of this is in `tests/test_formaldehyde_mm_radex.py`.

Here's an example of how you would set up a fit using `parinfo` directly.

Warning: There is a bug in the use_lmfit section of this code that keeps it from working properly. =(

```
amplitude0 = pyspeckit.parinfo.Parinfo(n=0, parname='Amplitude0',
    shortparname='$A_0$', value=1, limits=[0, 100], limited=(True,True))
width0 = pyspeckit.parinfo.Parinfo(n=2, parname='Width0',
    shortparname='$\sigma_0$', value=1, limits=(0, 0), limited=(True,False))
center0 = pyspeckit.parinfo.Parinfo(n=1, parname='Center0',
    shortparname='$\Delta x_0$', value=6716, limits=(0, 0), limited=(False,False))
amplitude1 = pyspeckit.parinfo.Parinfo(n=3, parname='Amplitude1',
    shortparname='$A_1$', value=1, limits=[0, 100], limited=(True,True))
width1 = pyspeckit.parinfo.Parinfo(n=5, parname='Width1',
    shortparname='$\sigma_1$', value=1, limits=(0, 0), limited=(True,False))
center1 = pyspeckit.parinfo.Parinfo(n=4, parname='Center1',
    shortparname='$\Delta x_1$', value=6731, limits=(0, 0),
    limited=(False,False), tied=center0)

parinfo = pyspeckit.parinfo.ParinfoList([amplitude0,center0,width0,amplitude1,center1,width1])

sp.specfit(parinfo=parinfo, use_lmfit=True)
```


3.1 Baseline Fitting

There are a number of cool features in baselining that aren't well-described below, partly due to Sphinx errors as of 12/22/2011.

`exclude` and `include` allow you to specify which parts of the spectrum to use for baseline fitting. Enter values as pairs of coordinates.

`Excludefit` makes use of an existing fit and excludes all points with signal above a (very low) threshold when fitting the baseline. Going back and forth between `baseline(excludefit=True)` and `specfit()` is a nice way to iteratively measure the baseline & emission/absorption line components.

3.1.1 API

class `pyspeckit.spectrum.baseline.Baseline(Spectrum)`

Class to measure and subtract baselines from spectra.

While the term 'baseline' is generally used in the radio to refer to broad-band features in a spectrum not necessarily associated with a source, in this package it refers to general continuum fitting. In principle, there's no reason to separate 'continuum' and 'spectral feature' fitting into different categories (both require some model, data, and optional weights when fitting). In practice, however, 'continuum' is frequently something to be removed and ignored, while spectral features are the desired measurable quantity. In order to accurately measure spectral features, it is necessary to allow baselines of varying complexity.

The Baseline class has both interactive and command-based data selection features. It can be used to fit both polynomial and power-law continua. Blackbody fitting is not yet implemented [12/21/2011]. Baseline fitting is a necessary prerequisite for Equivalent Width measurement.

As you may observe in the comments on this code, this has been one of the buggiest and least adequately tested components of `pyspeckit`. Bug reports are welcome. (as of 1/15/2012, a major change has probably fixed most of the bugs, and the code base is much simpler)

`__call__`(**args*, ***kwargs*)

Fit and remove a polynomial from the spectrum. It will be saved in the variable "self.basespec" and the fit parameters will be saved in "self.order"

Parameters

order: int :

Order of the polynomial to fit

excludefit: bool :

If there is a spectroscopic line fit, you can automatically exclude the region with signal above some tolerance set by `exclusionlevel` (it works for absorption lines by using the absolute value of the signal)

exclusionlevel: float :

The minimum value of the spectroscopic fit to exclude when fitting the baseline

save: bool :

Write the baseline fit coefficients into the spectrum's header in the keywords `BLCOEFnn`

interactive: bool :

Specify the include/exclude regions through the interactive plot window

fit_original: bool :

Fit the original spectrum instead of the baseline-subtracted spectrum. If disabled, will overwrite the original data with the baseline-subtracted version.

Warning: If this is set False, behavior of `unsubtract` may be unexpected

fit_plotted_area: bool :

Will respect user-specified zoom (using the pan/zoom buttons) unless `xmin/xmax` have been set manually

reset_selection: bool :

Reset the selected region to those specified by this command only (will override previous `xmin/xmax` settings)

select_region: bool :

Run the region selection procedure? If false, will leave 'includemask' untouched

baseline_fit_color: color name (string) :

[plot parameter] Color to plot the baseline

clear_all_connections: bool :

[plot parameter] Disable any previous interactive sessions

highlight_fitregion: bool :

[plot parameter] Highlight the selected region for baseline fitting (default green)

`__init__(Spectrum)`

`__module__ = 'pyspeckit.spectrum.baseline'`

`annotate(loc='upper left')`

`button2action(event=None, debug=False, subtract=True, powerlaw=None, fit_original=False, spline=False, spline_sampling=None, spline_downsampler=<function median at 0x7f0b415b7050>, baseline_fit_color='orange', **kwargs)`

Do the baseline fitting and save and plot the results.

`button3action(*args, **kwargs)`

Wrapper - same as `button2action`, but with `subtract=False`

clearlegend()

copy(*parent=None*)

Create a copy of the baseline fit

[**parent**]

A spectroscopic axis instance that is the parent of the specfit instance. This needs to be specified at some point, but defaults to None to prevent overwriting a previous plot.

crop(*x1pix, x2pix*)

When spectrum.crop is called, this must be too

downsample(*factor*)

fit(*powerlaw=None, order=None, includemask=None, spline=False, spline_sampling=10, spline_downsampler=<function median at 0x7f0b415b7050>, **kwargs*)

Run the fit and set self.basespec

get_model(*xarr=None, baselinepars=None*)

plot_baseline(*annotate=True, baseline_fit_color=(1, 0.65, 0, 0.75), use_window_limits=None, linewidth=1, alpha=0.75, plotkwargs={}, **kwargs*)

Overplot the baseline fit

Parameters

annotate : bool

Display the fit parameters for the best-fit baseline on the top-left of the plot

baseline_fit_color : matplotlib color

What color to use for overplotting the line (default is slightly transparent orange)

use_window_limits : None or bool

Keep the current window or expand the plot limits? If left as None, will use self.use_window_limits

savefit()

set_basespec_frompars(*baselinepars=None*)

Set the baseline spectrum based on the fitted parameters

set_spectofit(*fit_original=True, fit_residuals=False*)

Reset the spectrum-to-fit from the data

unsubtract(*replot=True, preserve_limits=True*)

Restore the spectrum to “pristine” state (un-subtract the baseline)

replot [**True**]

Re-plot the spectrum? (only happens if unsubsctraction proceeds, i.e. if there was a baseline to unsubtract)

preserve_limits [**True**]

Preserve the current x,y limits

3.2 Model Fitting

class pyspeckit.spectrum.fitters.**Specfit**(*Spectrum, Registry=None*)

Bases: pyspeckit.spectrum.interactive.Interactive

EQW(*plot=False, plotcolor='g', fitted=True, continuum=None, components=False, annotate=False, alpha=0.5, loc='lower left', xmin=None, xmax=None, xunits='pixel', continuum_as_baseline=False, verbose=False*)

Returns the equivalent width (integral of “baseline” or “continuum” minus the spectrum) over the selected range (the selected range defaults to self.xmin:self.xmax, so it may include multiple lines!)

Parameters

plot : bool

Plots a box indicating the EQW if plot==True (i.e., it will have a width equal to the equivalent width, and a height equal to the measured continuum)

fitted : bool

Use the fitted model? If false, uses the data

continuum : None or float

Can specify a fixed continuum with this keyword, otherwise will use the fitted baseline. WARNING: continuum=0 will still “work”, but will give numerically invalid results. Similarly, a negative continuum will work, but will yield results with questionable physical meaning.

continuum_as_baseline : bool

Replace the baseline with the specified continuum when computing the absorption depth of the line

components : bool

If your fit is multi-component, will attempt to acquire centroids for each component and print out individual EQWs

xmin : float

xmax : float

The range over which to compute the EQW

xunits : str

The units of xmin/xmax

Returns

Equivalent Width, or widths if components=True :

add_sliders(*parlimitdict=None, **kwargs*)

Add a Sliders window in a new figure appropriately titled

Parameters

parlimitdict: dict :

Each parameter needs to have displayed limits; these are set in min-max pairs. If this is left empty, the widget will try to guess at reasonable limits, but the guessing is not very sophisticated yet.

.. todo:: Add a button in the navbar that makes this window pop up :

<http://stackoverflow.com/questions/4740988/add-new-navigate-modes-in-matplotlib> :

annotate(*loc='upper right', labelspacing=0.25, markerscale=0.01, borderpad=0.1, handlelength=0.1, handletextpad=0.1, frameon=False, chi2=None, optimal_chi2_kwargs={}, **kwargs*)
 Add a legend to the plot showing the fitted parameters

`_clearlegend()` will remove the legend

`chi2`: {True or 'reduced' or 'optimal' or 'allthree'}

kwargs passed to legend

button3action(*event, debug=False, nwidths=1*)
 Disconnect the interactiveness Perform the fit (or die trying) Hide the guesses

clear(*legend=True, components=True*)
 Remove the fitted model from the plot

Also removes the legend by default

clear_all_connections(*debug=False*)
 Prevent overlapping interactive sessions

clear_highlights()
 Hide and remove "highlight" colors from the plot indicating the selected region

copy(*parent=None*)
 Create a copy of the spectral fit - includes copies of the `_full_model`, the registry, the fitter, parinfo, modelpars, modelerrs, model, npeaks

[**parent**]

A Spectrum instance that is the parent of the specfit instance. This needs to be specified at some point, but defaults to None to prevent overwriting a previous plot.

crop(*x1pix, x2pix*)
 When `spectrum.crop` is called, this must be too

downsample(*factor*)
 Downsample the model spectrum (and the specfit spectra) This should only be done when `Spectrum.smooth` is called

event_manager(*event, debug=False*)
 Decide what to do given input (click, keypress, etc.)

firstclick_guess()
 Initialize self.guesses

fullsizemodel()
 If the model was fit to a sub-region of the spectrum, expand it (with zeros wherever the model was not defined) to fill the spectrum.

Examples

```
>>> noise = np.random.randn(100)
>>> xarr = np.linspace(-50,50,100)
>>> signal = np.exp(-(xarr-5)**2/(2*3.**2))
>>> sp = pyspeckit.Spectrum(data=noise + signal, xarr=xarr, xarrkwargs={'units':'km/s'})
>>> sp.specfit(xmin=-25,xmax=25)
>>> sp.specfit.model.shape
(48,)
>>> sp.specfit.fullsizemodel()
>>> sp.specfit.model.shape
(100,)
```

get_components(**kwargs)

If a model has been fitted, return the components of the model

Parameters

kwargs are passed to `self.fitter.components` :

get_emcee(nwalkers=None, **kwargs)

Get an emcee walker ensemble for the data & model using the current model type

Parameters

data : np.ndarray

error : np.ndarray

nwalkers : int

Number of walkers to use. Defaults to $2 * \text{self.fitters.npars}$

Examples

```
>>> import pyspeckit
>>> x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10,10,50), unit='km/s')
>>> e = np.random.randn(50)
>>> d = np.exp(-np.asarray(x)**2/2.)*5 + e
>>> sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
>>> sp.specfit(fittype='gaussian')
>>> emcee_ensemble = sp.specfit.get_emcee()
>>> p0 = emcee_ensemble.p0 * (np.random.randn(*emcee_ensemble.p0.shape) / 10. + 1.0)
>>> pos, logprob, state = emcee_ensemble.run_mcmc(p0,100)
```

get_full_model(debug=False, **kwargs)

compute the model over the full axis

get_model(xarr, pars=None, debug=False, add_baseline=None)

Compute the model over a given axis

get_model_frompars(xarr, pars, debug=False, add_baseline=None)

Compute the model over a given axis

get_model_xlimits(threshold='auto', peak_fraction=0.01, add_baseline=False, units='pixels')

Return the x positions of the first and last points at which the model is above some threshold

Parameters

threshold : 'auto' or 'error' or float

If 'auto', the threshold will be set to `peak_fraction * the peak model value`. If 'error', uses the error spectrum as the threshold

peak_fraction : float

ignored unless `threshold == 'auto'`

add_baseline : bool

Include the baseline when computing whether the model is above the threshold? default FALSE. Passed to `get_full_model`.

units : str

A valid unit type, e.g. 'pixels' or 'angstroms'

get_pymc(**kwargs)

Create a pymc MCMC sampler from the current fitter. Defaults to ‘uninformative’ priors

kwargs are passed to the fitter’s get_pymc method, with parameters defined below.

Parameters

data : np.ndarray

error : np.ndarray

use_fitted_values : bool

Each parameter with a measured error will have a prior defined by the Normal distribution with $\sigma = \text{par.error}$ and $\mu = \text{par.value}$

Examples

```
>>> x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10,10,50), unit='km/s')
>>> e = np.random.randn(50)
>>> d = np.exp(-np.asarray(x)**2/2.)*5 + e
>>> sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
>>> sp.specfit(fittype='gaussian')
>>> MCuninformed = sp.specfit.get_pymc()
>>> MCwithpriors = sp.specfit.get_pymc(use_fitted_values=True)
>>> MCuninformed.sample(1000)
>>> MCuninformed.stats()['AMPLITUDE0']
>>> # WARNING: This will fail because width cannot be set <0, but it may randomly reach that...
>>> # How do you define a likelihood distribution with a lower limit?!
>>> MCwithpriors.sample(1000)
>>> MCwithpriors.stats()['AMPLITUDE0']
```

guesspeakwidth(event, debug=False, nwidths=1, **kwargs)

Interactively guess the peak height and width from user input

Width is assumed to be half-width-half-max

highlight_fitregion(drawstyle='steps-mid', color=(0, 0.8, 0, 0.5), linewidth=2, alpha=0.5, clear_highlights=True, **kwargs)

Re-highlight the fitted region

kwargs are passed to matplotlib.plot

history_fitpars()**integral**(analytic=False, direct=False, threshold='auto', integration_limits=None, integration_limit_units='pixels', return_error=False, **kwargs)

Return the integral of the fitted spectrum

Parameters

analytic : bool

Return the analytic integral of the fitted function? .. WARNING:: This approach is only implemented for some models .. todo:: Implement error propagation for this approach

direct : bool

Return the integral of the *spectrum* (as opposed to the *fit*) over a range defined by the *integration_limits* if specified or *threshold* otherwise

threshold : ‘auto’ or ‘error’ or float

Determines what data to be included in the integral based off of where the model is greater than this number. If 'auto', the threshold will be set to `peak_fraction * the peak model value`. If 'error', uses the error spectrum as the threshold. See `self.get_model_xlimits` for details.

integration_limits : None or 2-tuple

Manually specify the limits in `integration_limit_units` units

return_error : bool

Return the error on the integral if set. The error computed by `sigma = sqrt(sum(sigma_i^2)) * dx`

kwargs :

passed to `self.fitter.integral` if not(`direct`)

Returns

np.scalar or np.ndarray with the integral or integral & error :

mask

Mask: True means "exclude"

mask_sliced

Sliced (subset) Mask: True means "exclude"

measure_approximate_fwhm(*threshold='error', emission=True, interpolate_factor=1, plot=False, grow_threshold=2, **kwargs*)

Measure the FWHM of a fitted line

This procedure is designed for multi-component *blended* lines; if the true FWHM is known (i.e., the line is well-represented by a single gauss/voigt/lorentz profile), use that instead. Do not use this for multiple independently peaked profiles.

This MUST be run AFTER a fit has been performed!

Parameters

threshold : 'error' | float

The threshold above which the spectrum will be interpreted as part of the line. This threshold is applied to the *model*. If it is 'noise', `self.error` will be used.

emission : bool

Is the line absorption or emission?

interpolate_factor : integer

Magnification factor for determining sub-pixel FWHM. If used, "zooms-in" by using linear interpolation within the line region

plot : bool

Overplot a line at the FWHM indicating the FWHM. `kwargs` are passed to `matplotlib.plot`

grow_threshold : int

Minimum number of valid points. If the total # of points above the threshold is \leq to this number, it will be grown by 1 pixel on each side

Returns

The approximated FWHM, if it can be computed :

If there are ≤ 2 valid pixels, a fwhm cannot be computed :

model_mask(**kwargs)

Get a mask (boolean array) of the region where the fitted model is significant

Parameters

threshold : 'auto' or 'error' or float

The threshold to compare the model values to for selecting the mask region.

- auto: uses peak_fraction times the model peak
- error: use the spectrum error
- float: any floating point number as an absolute threshold

peak_fraction : float

Parameter used if threshold=='auto' to determine fraction of model peak to set threshold at

add_baseline : bool

Add the fitted baseline to the model before comparing to threshold?

Returns

mask : ndarray

A boolean mask array with the same size as the spectrum, set to True where the fitted model has values above a specified threshold

moments(fittype=None, **kwargs)

Return the moments

see the moments module

Parameters

fittype : None or str

The registered fit type to use for moment computation

multifit(fittype=None, renormalize='auto', annotate=None, show_components=None, verbose=True, color=None, guesses=None, parinfo=None, reset_fitspec=True, use_window_limits=None, use_lmfit=False, plot=True, **kwargs)

Fit multiple gaussians (or other profiles)

Parameters

fittype : str

What function will be fit? fittype must have been Registryed in the peakbgfitters dict. Uses default ('gaussian') if not specified

renormalize : 'auto' or bool

if 'auto' or True, will attempt to rescale small data (<1e-9) to be closer to 1 (scales by the median) so that the fit converges better

parinfo : parinfo structure

Guess structure; supercedes guesses

guesses : list or 'moments'

Either a list of guesses matching the number of parameters * the number of peaks for the model, or 'moments' to fit a single spectrum with the moments as guesses

optimal_chi2(reduced=True, threshold='error', **kwargs)

Compute an "optimal" χ^2 statistic, i.e. one in which only pixels in which the model is statistically significant are included

Parameters**reduced** : boolReturn the reduced χ^2 **threshold** : 'auto' or 'error' or float

If 'auto', the threshold will be set to `peak_fraction` * the peak model value, where `peak_fraction` is a kwarg passed to `get_model_xlimits` reflecting the fraction of the model peak to consider significant. If 'error', uses the error spectrum as the threshold.

kwargs : dictpassed to `get_model_xlimits()`**Returns****chi2** : float χ^2 statistic or reduced χ^2 statistic (χ^2/n)

$$\chi^2 = \sum ((d_i - m_i)^2 / e_i^2)$$

peakbgfit(*usemoments=True, annotate=None, vheight=True, height=0, negamp=None, fitype=None, renormalize='auto', color=None, use_lmfit=False, show_components=None, debug=False, use_window_limits=True, guesses=None, nsigcut_moments=None, plot=True, parinfo=None, **kwargs*)

Fit a single peak (plus a background)

Parameters**usemoments** : bool

The initial guess will be set by the fitter's 'moments' function (this overrides 'guesses')

annotate : bool

Make a legend?

vheight : bool

Fit a (constant) background as well as a peak?

height : float

initial guess for background

negamp : bool

If True, assumes amplitude is negative. If False, assumes positive. If None, can be either.

fitype : boolWhat function will be fit? `fitype` must have been Registered in the `peakbgfitters` dict**renormalize** : 'auto' or bool

if 'auto' or True, will attempt to rescale small data ($<1e-9$) to be closer to 1 (scales by the median) so that the fit converges better

nsigcut_moments : bool

pass to moment guesser; can do a sigma cut for moment guessing

```
plot_components(xarr=None, show_hyperfine_components=None, component_yoffset=0.0, component_lw=0.75, pars=None, component_fit_color='blue', component_kwargs={}, add_baseline=False, plotkwargs={}, **kwargs)
```

Overplot the individual components of a fit

Parameters

xarr : None

If none, will use the spectrum's xarr. Otherwise, plot the specified xarr. This is useful if you want to plot a well-sampled model when the input spectrum is undersampled

show_hyperfine_components : None | bool

Keyword argument to pass to component codes; determines whether to return individual (e.g., hyperfine) components of a composite model

component_yoffset : float

Vertical (y-direction) offset to add to the components when plotting

component_lw : float

Line width of component lines

component_fitcolor : color

Color of component lines

component_kwargs : dict

Keyword arguments to pass to the `fitter.components` method

add_baseline : bool

Add the fit to the components before plotting. Makes sense to use if `self.Spectrum.baseline.subtracted == False`

pars : parinfo

A parinfo structure or list of model parameters. If none, uses best-fit

```
plot_fit(xarr=None, annotate=None, show_components=None, composite_fit_color='red', lw=0.5, composite_lw=0.75, pars=None, offset=None, use_window_limits=None, show_hyperfine_components=None, plotkwargs={}, **kwargs)
```

Plot the fit. Must have fitted something before calling this!

It will be automatically called whenever a spectrum is fit (assuming an axis for plotting exists)

kwargs are passed to the fitter's components attribute

Parameters

xarr : None

If none, will use the spectrum's xarr. Otherwise, plot the specified xarr. This is useful if you want to plot a well-sampled model when the input spectrum is undersampled

annotate : None or bool

Annotate the plot? If not specified, defaults to `self.autoannotate`

show_components : None or bool

show_hyperfine_components : None or bool

Show the individual gaussian components overlaid on the composite fit

use_window_limits : None or bool

If False, will reset the window to include the whole spectrum. If True, leaves the window as is. Defaults to self.use_window_limits if None.

pars : parinfo

A parinfo structure or list of model parameters. If none, uses best-fit

offset : None or float

Y-offset. If none, uses the default self.Spectrum.plotter offset, otherwise, uses the specified float.

plot_model(*pars, offset=0.0, annotate=False, clear=False, **kwargs*)

Plot a model from specified input parameters (see plot_fit for kwarg specification)

annotate is set to “false” because arbitrary annotations are not yet implemented

plotresiduals(*fig=2, axis=None, clear=True, color='k', linewidth=0.5, drawstyle='steps-mid', yoffset=0.0, label=True, pars=None, zeroline=None, set_limits=True, **kwargs*)

Plot residuals of the fit. Specify a figure or axis; defaults to figure(2).

Parameters

fig : int

Figure number. Overridden by axis

axis : axis

The axis to plot on

pars : None or parlist

If set, the residuals will be computed for the input parameters

zeroline : bool or None

Plot the “zero” line through the center of the residuals. If None, defaults to “True if yoffset!=0, False otherwise”

kwargs are passed to matplotlib plot :

print_fit(*print_baseline=True, **kwargs*)

Print the best-fit parameters to the command line

refit(*use_lmfit=False*)

Redo a fit using the current parinfo as input

register_fitter(**args, **kwargs*)

Register a model fitter

Register a fitter function.

Parameters

name: string :

The fit function name.

function: function :

The fitter function. Single-fitters should take npars + 1 input parameters, where the +1 is for a 0th order baseline fit. They should accept an X-axis and data and standard fitting-function inputs (see, e.g., gaussfitter). Multi-fitters should take N * npars, but should also operate on X-axis and data arguments.

npars: int :

How many parameters does the function being fit accept?

savefit()

Save the fit parameters from a Gaussian fit to the FITS header

selectregion(*xmin=None, xmax=None, xtype='wcs', highlight=False, fit_plotted_area=True, reset=False, verbose=False, debug=False, use_window_limits=None, exclude=None, **kwargs*)

Pick a fitting region in either WCS units or pixel units

Parameters

xmin / xmax : [float]

The min/max X values to use in X-axis units (or pixel units if xtype is set). TAKES PRECEDENCE ALL OTHER BOOLEAN OPTIONS

xtype : [string]

A string specifying the xtype that xmin/xmax are specified in. It can be either 'wcs' or any valid xtype from [pyspeckit.spectrum.units](#)

reset : [bool]

Reset the selected region to the full spectrum? Only takes effect if xmin and xmax are not (both) specified. TAKES PRECEDENCE ALL SUBSEQUENT BOOLEAN OPTIONS

fit_plotted_area : [bool]

Use the plot limits *as specified in :class:'pyspeckit.spectrum.plotters'?* Note that this is not necessarily the same as the window plot limits!

use_window_limits : [bool]

Use the plot limits *as displayed*. Defaults to self.use_window_limits (pyspeckit.spectrum.interactive.use_window_limits). Overwrites xmin,xmax set by plotter

exclude: {list of length 2n,'interactive', None} :

- interactive: start an interactive session to select the include/exclude regions
- list: parsed as a series of (startpoint, endpoint) in the spectrum's X-axis units. Will exclude the regions between startpoint and endpoint
- None: No exclusion

selectregion_interactive(*event, mark_include=True, debug=False, **kwargs*)

select regions for baseline fitting

seterrspec(*usestd=None, useresiduals=True*)

Simple wrapper function to set the error spectrum; will either use the input spectrum or determine the error using the RMS of the residuals, depending on whether the residuals exist.

setfitspec()

Set the spectrum that will be fit. This is primarily to remove NaNs from consideration: if you simply remove the data from both the X-axis and the Y-axis, it will not be considered for the fit, and a linear X-axis is not needed for fitting.

However, it may be possible to do this using masked arrays instead of setting errors to be 1e10....

shift_pars(*frame=None*)

Shift the velocity / wavelength / frequency of the fitted parameters into a different frame

Right now this only takes care of redshift and only if redshift is defined. It should be extended to do other things later

```
start_interactive(debug=False, LoudDebug=False, reset_selection=False, print_message=True,  
                  clear_all_connections=True, **kwargs)
```

Initialize the interactive session

Parameters

print_message : bool

Print the interactive help message?

clear_all_connections : bool

Clear all matplotlib event connections? (calls `self.clear_all_connections()`)

reset_selection : bool

Reset the include mask to be empty, so that you're setting up a fresh region.

3.3 Measurements

```
class pyspeckit.spectrum.measurements.Measurements(Spectrum, z=None, d=None, fluxnorm=None,  
                                                  miscline=None, misctol=10.0, ignore=None,  
                                                  derive=True, debug=False, restframe=False,  
                                                  ptol=2, sort=False)
```

Bases: `object`

This can be called after a fit is run. It will inherit the specfit object and derive as much as it can from modelpars. Just do: `spec.measure(z, xunits, fluxnorm)`

Notes: If `z` (redshift) or `d` (distance) are present, we can compute integrated line luminosities rather than just fluxes. Provide distance in cm.

Only works with Gaussians. To generalize:

1. make sure we manipulate modelpars correctly, i.e. read in entries corresponding to wavelength/frequency/whatever correctly.

Parameters

z: float or None :

redshift

d: float or None :

distance in cm (used for luminosities)

fluxnorm: bool :

Normalize the fluxes?

miscline: dictionary :

`miscline = [{'name': 'H_alpha', 'wavelength': 6565}]`

misctol: tolerance (in Angstroms) for identifying an unmatched line :

to the line(s) we specify in `miscline` dictionary.

sort: bool :

Sort the entries in order of observed wavelength (or velocity or frequency)

bisection(*f, x_guess*)

Find root of function using bisection method. Absolute tolerance of 1e-4 is being used.

bracket_root(*f*, *x_guess*, *atol*=0.0001)

Bracket root by finding points where function goes from positive to negative.

compute_amplitude(*pars*)

Calculate amplitude of emission line. Should be easy - add multiple components if they exist. Currently assumes multiple components have the same centroid.

compute_flux(*pars*)

Calculate integrated flux of emission line. Works for multi-component fits too. Unnormalized.

compute_fwhm(*pars*)

Determine full-width at half maximum for multi-component fit numerically, or analytically if line has only a single component. Uses bisection technique for the former with absolute tolerance of 1e-4.

compute_luminosity(*pars*)

Determine luminosity of line (need distance and flux units).

derive()

Calculate luminosity and FWHM for all spectral lines.

identify_by_position(*ptol*)

Match observed lines to nearest reference line. Don't use spacing at all.

ptol = tolerance (in angstroms) to accept positional match

identify_by_spacing()

Determine identity of lines in *self.modelpars*. Fill entries of *self.lines* dictionary.

Note: This method will be infinitely slow for more than 10 or so lines.

separate()

For multicomponent lines, separate into broad and narrow components (assume only one of components is narrow).

to_tex()

Write out fit results to tex format.

3.4 Units

Unit parsing and conversion tool. The `SpectroscopicAxis` class is meant to deal with unit conversion internally

Open Questions: Are there other FITS-valid projection types, unit types, etc. that should be included? What about for other fields (e.g., wavenumber?)

class `pyspeckit.spectrum.units.SpectroscopicAxis`

Bases: `astropy.units.quantity.Quantity`

A Spectroscopic Axis object to store the current units of the spectrum and allow conversion to other units and frames. Typically, units are velocity, wavelength, frequency, or redshift. Wavenumber is also hypothetically possible.

WARNING: If you index a `SpectroscopicAxis`, the resulting array will be a `SpectroscopicAxis` without a `dxarr` attribute! This can result in major problems; a workaround is being sought but subclassing numpy arrays is harder than I thought

as_unit(*unit*, *equivalencies*=[], *velocity_convention*=None, *refX*=None, *refX_unit*=None, *center_frequency*=None, *center_frequency_unit*=None, ***kwargs*)

Convert the spectrum to the specified units. This is a wrapper function to convert between frequency/velocity/wavelength and simply change the units of the X axis. Frame conversion is... not necessarily implemented.

Parameters**unit** : string

What unit do you want to ‘view’ the array as? None returns the x-axis unchanged (NOT a copy!)

frame : string

NOT IMPLEMENTED. When it is, it will allow you to convert between LSR, topocentric, heliocentric, rest, redshifted, and whatever other frames we can come up with. Right now the main holdup is finding a nice python interface to an LSR velocity calculator... and motivation.

center_frequency: float :

The reference frequency for determining a velocity. Required for conversions between frequency/wavelength/energy and velocity.

center_frequency_unit: string :

If converting between velocity and any other spectroscopic type, need to specify the central frequency around which that velocity is calculated. I think this can also accept wavelengths....

cdelt(*tolerance=1e-08, approx=False*)

Return the channel spacing if channels are linear

Parameters**tolerance** : float

Tolerance in the difference between pixels that determines how near to linear the xarr must be

approx : bool

Return the mean DX even if it is inaccurate

convert_to_unit(*unit, **kwargs*)

Return the X-array in the specified units without changing it Uses as_unit for the conversion, but changes internal values rather than returning them.

coord_to_x(*xval, xunit*)

Given an X-value assumed to be in the coordinate axes, return that value converted to xunit e.g.: xarr.units = ‘km/s’ xarr.refX = 5.0 xarr.refX_unit = GHz xarr.coord_to_x(6000,’GHz’) == 5.1 # GHz

classmethod find_equivalencies(*velocity_convention=None, center_frequency=None, equivalencies=[]*)

Utility function to add equivalencies from the velocity_convention and the center_frequency

Parameters**velocity_convention** : str

‘optical’, ‘radio’ or ‘relativistic’

center_frequency : float | astropy.units.Quantity

The reference frequency for determining a velocity. Required for conversions between frequency/wavelength/energy and velocity.

equivalencies : list

astropy equivalencies list containing tuples of the form: (from_unit, to_unit, forward, backward) forward and backward are functions that convert values between those units

in_range(*xval*)

Given an X coordinate in SpectroscopicAxis' units, return whether the pixel is in range

make_dxarr(*coordinate_location*='center')

Create a "delta-x" array corresponding to the X array.

Parameters

coordinate_location : ['left', 'center', 'right']

Does the coordinate mark the left, center, or right edge of the pixel? If 'center' or 'left', the *last* pixel will have the same dx as the second to last pixel. If right, the *first* pixel will have the same dx as the second pixel.

refX_units

set_unit(*unit*, *bad_unit_response*='raise')

umax(*unit*=None)

Return the maximum value of the SpectroscopicAxis. If units specified, convert to those units first

umin(*unit*=None)

Return the minimum value of the SpectroscopicAxis. If units specified, convert to those units first

units

classmethod validate_unit(*unit*, *bad_unit_response*='raise')

x_to_coord(*xval*, *xunit*, *verbose*=False)

Given a wavelength/frequency/velocity, return the value in the SpectroscopicAxis's units e.g.: `xarr.unit = 'km/s' xarr.refX = 5.0 xarr.refX_unit = GHz xarr.x_to_coord(5.1,'GHz') == 6000 # km/s`

x_to_pix(*xval*, *xval_units*=None)

Given an X coordinate in SpectroscopicAxis' units, return the corresponding pixel number

class `pyspeckit.spectrum.units.SpectroscopicAxes`

Bases: `pyspeckit.spectrum.units.SpectroscopicAxis`

Counterpart to Spectra: takes a list of SpectroscopicAxis's and concatenates them while checking for consistency and maintaining header parameters

3.5 Registration

PySpecKit is made extensible by allowing user-registered modules for reading, writing, and fitting data.

For examples of registration in use, look at the source code of `pyspeckit.spectrum.__init__` and `pyspeckit.spectrum.fitters`.

The registration functions can be accessed directly:

```
pyspeckit.register_reader
pyspeckit.register_writer
```

However, models are bound to individual instances of the Spectrum class, so they must be accessed via a specfit instance

```
sp = pyspeckit.Spectrum('myfile.fits')
sp.specfit.register_fitter
```

Alternatively, you can access and edit the default Registry

```
pyspeckit.fitters.default_Registry.add_fitter
```

If you've already loaded a Spectrum instance, but then you want to reload fitters from the default_Registry, or if you want to make your own Registry, you can use the semi-private method

```
MyRegistry = pyspeckit.fitters.Registry()
sp._register_fitters(registry=MyRegistry)
```

3.5.1 API

`pyspeckit.spectrum.__init__.register_reader(filetype, function, suffix, default=False)`

Register a reader function.

Parameters

filetype: str :

The file type name

function: function :

The reader function. Should take a filename as input and return an X-axis object (see `units.py`), a spectrum, an error spectrum (initialize it to 0's if empty), and a pyfits header instance

suffix: int :

What suffix should the file have?

`pyspeckit.spectrum.__init__.register_writer(filetype, function, suffix, default=False)`

Register a writer function.

Parameters

filetype: string :

The file type name

function: function :

The writer function. Will be an attribute of Spectrum object, and called as `spectrum.Spectrum.write_hdf5()`, for example.

suffix: int :

What suffix should the file have?

class `pyspeckit.spectrum.fitters.Registry`

This class is a simple wrapper to prevent fitter properties from being globals

add_fitter(name, function, npars, override=False, key=None, multisingle=None)

Register a fitter function.

Parameters

name: string :

The fit function name.

function: function :

The fitter function. Single-fitters should take `npars + 1` input parameters, where the +1 is for a 0th order baseline fit. They should accept an X-axis and data and standard

fitting-function inputs (see, e.g., `gaussfitter`). Multi-fitters should take $N * npars$, but should also operate on X-axis and data arguments.

npars: int :

How many parameters does the function being fit accept?

3.6 Classes

3.6.1 spectrum

The spectrum module consists of the `Spectrum` class, with child classes `ObsBlock` and `Spectra` for multi-spectrum analysis of different types.

The `Spectrum` class is the main functional code. `ObsBlocks` are containers of multiple spectra of different objects. The `Spectra` class is a container of multiple spectra of the *same* object at different wavelengths/frequencies.

class `pyspeckit.spectrum.classes.Spectrum`(*filename=None, filetype=None, xarr=None, data=None, error=None, header=None, doplot=False, maskdata=True, unit=None, plotkwargs={}, xarrkwargs={}, **kwargs*)

Bases: `object`

The core class for the spectroscopic toolkit. Contains the data and error arrays along with wavelength / frequency / velocity information in various formats.

Create a `Spectrum` object.

Must either pass in a filename or ALL of `xarr`, `data`, and `header`, plus optionally `error`.

`kwargs` are passed to the file reader

Parameters

filename : string

The file to read the spectrum from. If `data`, `xarr`, and `error` are specified, leave `filename` blank.

filetype : string

Specify the file type (only needed if it cannot be automatically determined from the `filename`)

xarr : `units.SpectroscopicAxis` or `np.ndarray`

The X-axis of the data. If it is an `np.ndarray`, you must pass `xarrkwargs` or a valid header if you want to use any of the unit functionality.

data : `np.ndarray`

The data array (must have same length as `xarr`)

error : `np.ndarray`

The error array (must have same length as the `data` and `xarr` arrays)

header : `pyfits.Header` or dict

The header from which to read unit information. Needs to be a `pyfits.Header` instance or another dictionary-like object with the appropriate information

maskdata : boolean

turn the array into a masked array with all nan and inf values masked

doplot : boolean

Plot the spectrum after loading it?

plotkwargs : dict

keyword arguments to pass to the plotter

xarrkwargs : dict

keyword arguments to pass to the SpectroscopicAxis initialization (can be used in place of a header)

unit : str

The data unit

Examples

```
>>> sp = pyspeckit.Spectrum(data=np.random.randn(100),
                             xarr=np.linspace(-50, 50, 100), error=np.ones(100)*0.1,
                             xarrkwargs={'unit':'km/s', 'refX':4.829, 'refX_unit':'GHz',
                                           'xtype':'VLSR-RAD'}, header={})

>>> xarr = pyspeckit.units.SpectroscopicAxis(np.linspace(-50,50,100),
                                              units='km/s', refX=6562.83, refX_unit='angstroms')
>>> data = np.random.randn(100)*5 + np.random.rand(100)*100
>>> err = np.sqrt(data/5.)*5. # Poisson noise
>>> sp = pyspeckit.Spectrum(data=data, error=err, xarr=xarr, header={})

>>> # if you already have a simple fits file
>>> sp = pyspeckit.Spectrum('test.fits')
```

copy(*deep=True*)

Create a copy of the spectrum with its own plotter, fitter, etc. Useful for, e.g., comparing smoothed to unsmoothed data

crop(*x1, x2, unit=None, **kwargs*)

Replace the current spectrum with a subset from x1 to x2 in current units

Fixes CRPIX1 and baseline and model spectra to match cropped data spectrum

downsample(*dsfactor*)

Downsample the spectrum (and all of its subsidiaries) without smoothing

Parameters

dsfactor : int

Downsampling Factor

flux

The data in the spectrum (flux = data, for compatibility with astropy's Spectrum1D object).

classmethod from_hdu(*hdu*)

Create a pyspeckit Spectrum object from an HDU

classmethod from_spectrum1d(*spec1d*)

Tool to load a pyspeckit Spectrum from a specutils object

(this is intended to be temporary; long-term the pyspeckit Spectrum object will inherit from a specutils Spectrum1D object)

getlines(*linetype*='radio', ***kwargs*)

Access a registered database of spectral lines. Will add an attribute with the name *linetype*, which then has properties defined by the *speclines* module (most likely, a table and a “show” function to display the lines)

interpans(*spec*)

Interpolate over NAN values, replacing them with values interpolated from their neighbors using linear interpolation.

measure(*z=None*, *d=None*, *fluxnorm=None*, *miscline=None*, *misctol=10.0*, *ignore=None*, *derive=True*, ***kwargs*)

Initialize the measurements class - only do this after you have run a fitter otherwise pyspeckit will be angry!

moments(*unit='km/s'*, ***kwargs*)

Return the moments of the spectrum. In order to assure that the 1st and 2nd moments are meaningful, a ‘default’ unit is set. If unit is not set, will use current unit.

Documentation imported from the moments module:

Returns the gaussian parameters of a 1D distribution by calculating its moments. Depending on the input parameters, will only output a subset of the above.

Theory, from first principles (in the absence of noise): $\text{integral}(\text{gaussian}) = \sqrt{2\pi}\sigma^2 * \text{amp}$
 $\sigma = \text{integral} / \text{amp} / \sqrt{2\pi}$

In the presence of noise, this gets much more complicated. The noisy approach is inspired by [mpfit](#)

Parameters

height: :

is the background level

amplitude: :

is the maximum (or minimum) of the data after background subtraction

x: :

is the first moment

width_x: :

is the second moment

estimator: function :

A function to estimate the “height” or “background level” of the data, e.g. mean or median. If masked arrays are being used, use the *np.ma* versions of the numpy functions

negamp: bool or None :

Force the peak negative (True), positive (False), or the sign of the peak will be “autodetected” (negamp=None)

nsigcut: float or None :

If specified, the code will attempt to estimate the noise and only use data above/below *n-sigma* above the noise. The noise will be estimated from the data unless the noise is specified with *noise_estimate*

noise_estimate: float or None :

Guess for the noise value. Only matters if *nsigcut* is specified.

Returns**(height, amplitude, x, width_x) :****parse_hdf5_header(*hdr*)**

HDF5 reader will create a *hdr* dictionary from HDF5 dataset attributes if they exist. This routine will convert that dict to a *pyfits* header instance.

parse_header(*hdr*, *specname=None*)

Parse parameters from a *.fits* header into required spectrum structure parameters

parse_text_header(*Table*)

Grab relevant parameters from a table header (*xaxis* type, etc)

This function should only exist for *Spectrum* objects created from *.txt* or other *atpy* table type objects

shape

Return the data shape (a property of the *Spectrum*)

slice(*start=None*, *stop=None*, *unit='pixel'*, *copy=True*, *preserve_fits=False*)

Slicing the spectrum

Warning: this is the same as cropping right now, but it returns a copy instead of cropping inplace

Parameters**start** : *numpy.float* or *int*

start of slice

stop : *numpy.float* or *int*

stop of slice

unit : *str*

allowed values are any supported physical unit, 'pixel'

copy : *bool*

Return a 'view' of the data or a copy?

preserve_fits : *bool*

Save the fitted parameters from *self.fitter*?

smooth(*smooth*, *downsample=True*, *kwargs*)**

Smooth the spectrum by factor *smooth*.

Documentation from the *smooth* module:

Parameters**smooth** : *float*

Number of pixels to smooth by

smoothtype : ['gaussian', 'hanning', or 'boxcar']

type of smoothing kernel to use

downsample : *bool*

Downsample the data?

downsample_factor : *int*

Downsample by the smoothing factor, or something else?

convmode : ['full', 'valid', 'same']

see `numpy.convolve`. 'same' returns an array of the same length as 'data' (assuming data is larger than the kernel)

stats(*statrange*=(), *interactive*=False)

Return some statistical measures in a dictionary (somewhat self-explanatory)

Parameters

statrange : 2-element tuple

X-range over which to perform measures

interactive : bool

specify range interactively in plotter

unit

units

write(*filename*, *type*=None, ***kwargs*)

Write the spectrum to a file. The available file types are listed in `spectrum.writers.writers`

type - what type of file to write to? If not specified, will attempt to determine type from suffix

class `pyspeckit.spectrum.classes.Spectra`(*speclist*, *xunit*='GHz', ***kwargs*)

Bases: `pyspeckit.spectrum.classes.Spectrum`

A list of individual Spectrum objects. Intended to be used for concatenating different wavelength observations of the SAME OBJECT. Can be operated on just like any Spectrum object, including fitting. Useful for fitting multiple lines on non-contiguous axes simultaneously. Be wary of plotting these though...

Can be indexed like python lists.

X array is forcibly sorted in increasing order

fiteach(***kwargs*)

Fit each spectrum within the Spectra object

ploteach(*xunit*=None, *inherit_fit*=False, *plot_fit*=True, *plotfitkwargs*={}, ***plotkwargs*)

Plot each spectrum in its own window *inherit_fit* - if specified, will grab the fitter & fitter properties from Spectra

smooth(*smooth*, ***kwargs*)

Smooth the spectrum by factor "smooth". Options are defined in `sm.smooth`

because 'Spectra' does not have a header attribute, don't do anything to it...

class `pyspeckit.spectrum.classes.ObsBlock`(*speclist*, *xtype*='frequency', *xarr*=None, *force*=False, ***kwargs*)

Bases: `pyspeckit.spectrum.classes.Spectra`

An Observation Block

Consists of multiple spectra with a shared X-axis. Intended to hold groups of observations of the same object in the same setup for later averaging.

ObsBlocks can be indexed like python lists.

average(*weight*=None, *inverse_weight*=False, *error*='erravgtrn', *debug*=False)

Average all scans in an ObsBlock. Returns a single Spectrum object

Parameters**weight** : string

a header keyword to weight by. If not specified, the spectra will be averaged without weighting

inverse_weight : bool

Is the header keyword an inverse-weight (e.g., a variance?)

error : ['scanrms', 'erravg', 'erravgrtn']

estimate the error spectrum by one of three methods. 'scanrms' : the standard deviation of each pixel across all scans 'erravg' : the average of all input error spectra 'erravgrtn' : the average of all input error spectra divided by $\sqrt{n_obs}$

smooth(*smooth*, ***kwargs*)

Smooth the spectrum by factor "smooth". Options are defined in sm.smooth

pyspeckit.spectrum.**register_reader**(*filetype*, *function*, *suffix*, *default=False*)

Register a reader function.

Parameters**filetype**: str :

The file type name

function: function :

The reader function. Should take a filename as input and return an X-axis object (see units.py), a spectrum, an error spectrum (initialize it to 0's if empty), and a pyfits header instance

suffix: int :

What suffix should the file have?

pyspeckit.spectrum.**register_writer**(*filetype*, *function*, *suffix*, *default=False*)

Register a writer function.

Parameters**filetype**: string :

The file type name

function: function :

The writer function. Will be an attribute of Spectrum object, and called as spectrum.Spectrum.write_hdf5(), for example.

suffix: int :

What suffix should the file have?

3.6.2 Cubes

Pyspeckit can do a few things with spectral cubes. The most interesting is the spectral line fitting.

Cube objects have a `fiteach()` method that will fit each spectral line within a cube. It can be made to do this in parallel with the `multicore` option.

As of version 0.16, pyspeckit cubes can be read from `SpectralCube` objects:


```
>>> pcube = pyspeckit.Cube(cube=mySpectralCube)
```

Otherwise, they can be created from FITS cubes on disk:

```
>>> pcube = pyspeckit.Cube(filename="mycube.fits")
```

or from arrays:

```
>>> mycube = np.random.randn(250,50,50)
>>> myxaxis = np.linspace(-100,100,250)
>>> pcube = pyspeckit.Cube(cube=mycube, xarr=myxaxis, xunit='km/s')
```

The most interesting features of the `Cube` object are the `fiteach()` method, which fits a model spectrum to each element of the cube, and `mapplot`, which plots up various projections of the cube.

`Cube.mapplot` will create an interactive plot window. You can click on any pixel shown in that window and pull up a second window showing the spectrum at that pixel. If you've fitted the cube, the associated best-fit model will also be shown. This interactive setup can be a bit fragile, though, so please report bugs aggressively so we can weed them out!

The interactive viewer has a few button interactions described [here](#).

Cubes

Tools to deal with spectroscopic data cubes.

Some features in Cubes require additional packages:

- smoothing - requires `agpy`'s `smooth` and `parallel_map` routines
- pyregion

The 'grunt work' is performed by the `cubes` module

```
class pyspeckit.cubes.SpectralCube.Cube(filename=None, cube=None, xarr=None, xunit=None, error-
                                         cube=None, header=None, x0=0, y0=0, maskmap=None,
                                         **kwargs)
```

Bases: `pyspeckit.spectrum.classes.Spectrum`

A `pyspeckit Cube` object. Can be created from a FITS file on disk or from an array or a `spectral_cube.SpectralCube` object. If an array is used to instantiate the cube, the `xarr` keyword must be given, specifying the X-axis units

Parameters

filename : str, optional

The name of a FITS file to open and read from. Must be 3D

cube : `np.ndarray`, `spectral_cube.SpectralCube`, or `astropy.units.Quantity`

The data from which to instantiate a `Cube` object. If it is an array or an `astropy Quantity` (which is an array with attached units), the X-axis must be specified. If this is given as a `SpectralCube` object, the X-axis and units should be handled automatically.

xarr : `np.ndarray` or `astropy.units.Quantity`, optional

The X-axis of the spectra from each cube. This actually corresponds to axis 0, or what we normally refer to as the Z-axis of the cube, but it indicates the X-axis in a plot of intensity vs wavelength. The units for this array are specified in the `xunit` keyword unless a `Quantity` is given.

xunit : str, optional

The unit of the `xarr` array if `xarr` is given as a numpy array

errorcube : np.ndarray, spectral_cube.SpectralCube, or Quantity, optional

A cube with the same shape as the input cube providing the 1-sigma error for each voxel. This can be specified more efficiently as an error map for most use cases, but that approach has not yet been implemented. However, you can pass a 2D error map to `fiteach`.

header : fits.Header or dict, optional

The header associated with the data. Only needed if the cube is given as an array or a quantity.

x0, y0 : int

The initial spectrum to use. The `Cube` object can be treated as a `pyspeckit.Spectrum` object, with all the associated tools (plotter, fitter) using the `set_spectrum` method to select a pixel from the cube to plot and fit. However, it is generally more sensible to extract individual spectra and treat them separately using the `get_spectrum` method, so these keywords MAY BE DEPRECATED in the future.

maskmap : np.ndarray, optional

A boolean mask map, where True implies that the data are good. This will be used for both plotting using `mapplot` and fitting using `fiteach`.

copy(*deep=True*)

Create a copy of the spectrum with its own plotter, fitter, etc. Useful for, e.g., comparing smoothed to unsmoothed data

crop(*x1, x2, unit=None, **kwargs*)

Replace the current spectrum with a subset from `x1` to `x2` in current units

Fixes CRPIX1 and baseline and model spectra to match cropped data spectrum

cubes = <module 'pyspeckit.cubes.cubes' from '/var/build/user_builds/pyspeckit-keflavich/checkouts/toctree_sidebar/pysp

downsample(*dsfactor*)

Downsample the spectrum (and all of its subsidiaries) without smoothing

Parameters

dsfactor : int

Downsampling Factor

fiteach(*errspec=None, errmap=None, guesses=(), verbose=True, verbose_level=1, quiet=True, signal_cut=3, usemomentcube=False, blank_value=0, integral=True, direct=False, absorption=False, use_nearest_as_guess=False, start_from_point=(0, 0), multicore=0, continuum_map=None, **fitkwargs*)

Fit a spectrum to each valid pixel in the cube

For guesses, priority is `use_nearest_as_guess`, `usemomentcube`, `guesses`, None

Parameters

use_nearest_as_guess: bool :

Unless the fitted point is the first, it will find the nearest other point with a successful fit and use its best-fit parameters as the guess

start_from_point: tuple(int,int) :

Either start from the center or from a point defined by a tuple. Work outward from that starting point.

guesses: tuple or ndarray[naxis=3] :

Either a tuple/list of guesses with `len(guesses) = npars` or a cube of guesses with shape `[npars, ny, nx]`. NOT TRUE, but a good idea in principle: You can also use a dictionary of the form `{(y,x): [list of length npars]}`, where `(y,x)` specifies a pixel location. If the dictionary method is used, `npars` must be specified and it sets the length of the first parameter axis

signal_cut: float :

Minimum signal-to-noise ratio to “cut” on (i.e., if peak in a given spectrum has `s/n` less than this value, ignore it)

blank_value: float :

Value to replace non-fitted locations with. A good alternative is `numpy.nan`

verbose: bool :

verbose_level: int :

Controls how much is output. 0,1 - only changes frequency of updates in loop 2 - print out messages when skipping pixels 3 - print out messages when fitting pixels 4 - specfit will be verbose

multicore: int :

if `>0`, try to use multiprocessing via `parallel_map` to run on multiple cores

continuum_map: np.ndarray :

Same shape as error map. Subtract this from data before estimating noise.

flux

The data in the spectrum (`flux = data`, for compatibility with `astropy`’s `Spectrum1D` object).

classmethod from_hdu(hdu)

Create a `pyspeckit Spectrum` object from an HDU

classmethod from_spectrum1d(spec1d)

Tool to load a `pyspeckit Spectrum` from a `specutils` object

(this is intended to be temporary; long-term the `pyspeckit Spectrum` object will inherit from a `specutils Spectrum1D` object)

get_apspec(aperture, coordsys=None, method='mean', **kwargs)

Extract an aperture using `cubes.extract_aperture` (defaults to Cube pixel coordinates)

aperture [tuple or list] (x, y, radius)

The aperture to use when extracting the data

coordsys ['celestial' | 'galactic' | None]

the coordinate system the aperture is specified in None indicates pixel coordinates (default)

wunit [str]

arcsec, arcmin, or degree

get_modelcube(update=False)

get_spectrum(x, y)

Very simple: get the spectrum at coordinates `x,y`

(inherits fitter from self)

Returns a `SpectroscopicAxis` instance

getlines(*linetype*='radio', ***kwargs*)

Access a registered database of spectral lines. Will add an attribute with the name *linetype*, which then has properties defined by the *speclines* module (most likely, a table and a “show” function to display the lines)

interpans(*spec*)

Interpolate over NAN values, replacing them with values interpolated from their neighbors using linear interpolation.

load_fits(*fitsfile*)

load_model_fit(*fitsfilename*, *npars*, *npeaks*=1, *fittype*=None, *_temp_fit_loc*=(0, 0))

Load a parameter + error cube into the *.parcube* and *.errcube* attributes.

Parameters

fitsfilename : str

The filename containing the parameter cube written with `write_fit`

npars : int

The number of parameters in the model fit for a single spectrum

npeaks : int

The number of independent peaks fit toward each spectrum

fittype : str, optional

The name of the *fittype*, e.g. ‘gaussian’ or ‘voigt’, from the *pyspeckit* fitter registry. This is optional; it should have been written to the FITS header and will be read from there if it is not specified

_temp_fit_loc : tuple (int,int)

The initial spectrum to use to generate components of the class. This should not need to be changed.

load_spectral_cube(*cube*)

Load the cube from a *spectral_cube.SpectralCube* object

measure(*z*=None, *d*=None, *fluxnorm*=None, *miscline*=None, *misctol*=10.0, *ignore*=None, *derive*=True, ***kwargs*)

Initialize the measurements class - only do this after you have run a fitter otherwise *pyspeckit* will be angry!

momenteach(*verbose*=True, *verbose_level*=1, *multicore*=0, ***kwargs*)

Return a cube of the moments of each pixel

Parameters

multicore: int :

if >0, try to use multiprocessing via `parallel_map` to run on multiple cores

moments(*unit*='km/s', ***kwargs*)

Return the moments of the spectrum. In order to assure that the 1st and 2nd moments are meaningful, a ‘default’ unit is set. If unit is not set, will use current unit.

Documentation imported from the moments module:

Returns the gaussian parameters of a 1D distribution by calculating its moments. Depending on the input parameters, will only output a subset of the above.

Theory, from first principles (in the absence of noise): $\text{integral}(\text{gaussian}) = \sqrt{2\pi\sigma^2} * \text{amp}$
 $\sigma = \text{integral} / \text{amp} / \sqrt{2\pi}$

In the presence of noise, this gets much more complicated. The noisy approach is inspired by [mpfit](#)

Parameters

height: :

is the background level

amplitude: :

is the maximum (or minimum) of the data after background subtraction

x: :

is the first moment

width_x: :

is the second moment

estimator: function :

A function to estimate the “height” or “background level” of the data, e.g. mean or median. If masked arrays are being used, use the np.ma versions of the numpy functions

negamp: bool or None :

Force the peak negative (True), positive (False), or the sign of the peak will be “autodetected” (negamp=None)

nsigcut: float or None :

If specified, the code will attempt to estimate the noise and only use data above/below n-sigma above the noise. The noise will be estimated from the data unless the noise is specified with noise_estimate

noise_estimate: float or None :

Guess for the noise value. Only matters if nsigcut is specified.

Returns

(height, amplitude, x, width_x) :

parse_hdf5_header(hdr)

HDF5 reader will create a hdr dictionary from HDF5 dataset attributes if they exist. This routine will convert that dict to a pyfits header instance.

parse_header(hdr, specname=None)

Parse parameters from a .fits header into required spectrum structure parameters

parse_text_header(Table)

Grab relevant parameters from a table header (xaxis type, etc)

This function should only exist for Spectrum objects created from .txt or other atpy table type objects

plot_apspec(aperture, coordsys=None, reset_ylimits=True, wunit='arcsec', method='mean', **kwargs)

Extract an aperture using cubes.extract_aperture (defaults to Cube coordinates)

Parameters

aperture : list

A list of aperture parameters, e.g.

- For a circular aperture, `len(ap)=3`: + `ap = [xcen,ycen,radius]`
- For an elliptical aperture, `len(ap)=5`: + `ap = [xcen,ycen,height,width,PA]`

coordsys : None or str

The coordinate system of the aperture (e.g., galactic, fk5, None for pixel)

method : 'mean' or 'sum'

Either average over parallel spectra or sum them.

plot_fit(*x, y, silent=False, **kwargs*)

If fiteach has been run, plot the best fit at the specified location

Parameters

x : int

y : int

The x, y coordinates of the pixel (indices 2 and 1 respectively in numpy notation)

plot_spectrum(*x, y, plot_fit=False, **kwargs*)

Fill the .data array with a real spectrum and plot it

set_apspec(*aperture, coordsys=None, method='mean'*)

Extract an aperture using `cubes.extract_aperture` (defaults to Cube coordinates)

set_spectrum(*x, y*)

shape

Return the data shape (a property of the Spectrum)

show_fit_param(*parnumber, **kwargs*)

If pars have been computed, display them in the mapplot window

Parameters

parnumber : int

The index of the parameter in the parameter cube

show_moment(*momentnumber, **kwargs*)

If moments have been computed, display them in the mapplot window

slice(*start=None, stop=None, unit='pixel', preserve_fits=False, copy=True*)

Slice a cube along the spectral axis (equivalent to “spectral_slab” from the `spectral_cube` package)

Parameters

start : numpy.float or int

start of slice

stop : numpy.float or int

stop of slice

unit : str

allowed values are any supported physical unit, 'pixel'

smooth(*smooth, **kwargs*)

Smooth the spectrum by factor `smooth`.

Documentation from the `cubes.spectral_smooth` module:

stats(*statrange=()*, *interactive=False*)

Return some statistical measures in a dictionary (somewhat self-explanatory)

Parameters

statrange : 2-element tuple

X-range over which to perform measures

interactive : bool

specify range interactively in plotter

unit

units

write(*filename*, *type=None*, ***kwargs*)

Write the spectrum to a file. The available file types are listed in `spectrum.writers.writers`

type - what type of file to write to? If not specified, will attempt to determine type from suffix

write_cube()

write_fit(*fitcubefilename*, *clobber=False*)

Write out a fit cube using the information in the fit's `parinfo` to set the header keywords

Parameters

fitcubefilename: string :

Filename to write to

clobber: bool :

Overwrite file if it exists?

class `pyspeckit.cubes.SpectralCube.CubeStack`(*cubelist*, *xunit='GHz'*, *x0=0*, *y0=0*, *maskmap=None*, ***kwargs*)

Bases: `pyspeckit.cubes.SpectralCube.Cube`

The Cube equivalent of `Spectra`: for stitching multiple cubes with the same spatial grid but different frequencies together

Initialize the Cube. Accepts FITS files.

x0,y0 - initial spectrum to use (defaults to lower-left corner)

MapPlot

Make plots of the cube and interactively connect them to spectrum plotting. This is really an interactive component of the package; nothing in here is meant for publication-quality plots, but more for user interactive analysis.

That said, the plotter makes use of `APLpy`, so it is possible to make publication-quality plots.

author

Adam Ginsburg

date

03/17/2011

class `pyspeckit.cubes.mapplot.MapPlotter(Cube=None, figure=None, doplot=False, **kwargs)`

Bases: `object`

Class to plot a spectrum

See `mapplot` for use documentation; this docstring is only for initialization.

Create a map figure for future plotting

circle(*x1, y1, x2, y2, **kwargs*)

Plot the spectrum of a circular aperture

click(*event*)

Record location of downclick

copy(*parent=None*)

Create a copy of the map plotter with blank (uninitialized) axis & figure

[**parent**]

A spectroscopic axis instance that is the parent of the specfit instance. This needs to be specified at some point, but defaults to None to prevent overwriting a previous plot.

makeplane(*estimator=<function mean at 0x7f0b41830aa0>*)

Create a “plane” view of the cube, either by slicing or projecting it or by showing a slice from the best-fit model parameter cube.

Parameters

estimator : [function | ‘max’ | ‘int’ | FITS filename | integer | slice]

A non-pythonic, non-duck-typed variable. If it’s a function, apply that function along the cube’s spectral axis to obtain an estimate (e.g., mean, min, max, etc.). ‘max’ will do the same thing as passing `np.max` ‘int’ will attempt to integrate the image (which is why I didn’t duck-type) (integrate means sum and multiply by dx) a .fits filename will be read using `pyfits` (so you can make your own cover figure) an integer will get the n’t slice in the parcube if it exists If it’s a slice, slice the input data cube along the Z-axis with this slice

mapplot(*convention=‘calabretta’, colorbar=True, useaplpy=True, vmin=None, vmax=None, cmap=None, plotkwargs={}, **kwargs*)

Plot up a map based on an input data cube.

The map to be plotted is selected using `makeplane`. The estimator keyword argument is passed to that function.

The plotted map, once shown, is interactive. You can click on it with any of the three mouse buttons.

Button 1 or keyboard ‘1’:

Plot the selected pixel’s spectrum in another window. Mark the clicked pixel with an ‘x’

Button 2 or keyboard ‘o’:

Overplot a second (or third, fourth, fifth...) spectrum in the external plot window

Button 3:

Disconnect the interactive viewer

You can also click-and-drag with button 1 to average over a circular region. This same effect can be achieved by using the ‘c’ key to set the /c/enter of a circle and the ‘r’ key to set its /r/adius (i.e., hover over the center and press ‘c’, then hover some distance away and press ‘r’).

Parameters

convention : ‘calabretta’ or ‘griesen’

The default projection to assume for Galactic data when plotting with `aplpy`.

colorbar : bool

Whether to show a colorbar

plotkwargs : dict, optional

A dictionary of keyword arguments to pass to `aplpy.show_colourscale` or `matplotlib.pyplot.imshow`

useaplpy : bool

Use `aplpy` if a FITS header is available

vmin, vmax: float or None :

Override values for the `vmin/vmax` values. Will be automatically determined if left as `None`

.. todo: :

Allow `mapplot` in subfigure

plot_spectrum(*event*, *plot_fit=True*)

Connects map cube to Spectrum...

refresh()

cubes.py

From `agpy`, contains functions to perform various transformations on data cubes and their headers.

`pyspeckit.cubes.cubes.aper_world2pix`(*ap*, *wcs*, *coordsys='galactic'*, *wunit='arcsec'*)

Converts an elliptical aperture (*x,y,width,height,PA*) from WCS to pixel coordinates given an input *wcs* (an instance of the `pywcs.WCS` class). Must be a 2D WCS header.

`pyspeckit.cubes.cubes.baseline_cube`(*cube*, *polyorder=None*, *cubemask=None*, *splineorder=None*,
numcores=None, *sampling=1*)

Given a cube, fit a polynomial to each spectrum

Parameters

cube: np.ndarray :

An ndarray with `ndim = 3`, and the first dimension is the spectral axis

polyorder: int :

Order of the polynomial to fit and subtract

cubemask: boolean ndarray :

Mask to apply to cube. Values that are `True` will be ignored when fitting.

numcores : None or int

Number of cores to use for parallelization. If `None`, will be set to the number of available cores.

`pyspeckit.cubes.cubes.blfunc_generator`(*x=None*, *polyorder=None*, *splineorder=None*, *sampling=1*)

Generate a function that will fit a baseline (polynomial or spline) to a data set. Either `splineorder` or `polyorder` must be set

Parameters

x : np.ndarray or None

The X-axis of the fitted array. Will be set to `np.arange(len(data))` if not specified

polyorder : None or int

The polynomial order.

splineorder : None or int

sampling : int

The sampling rate to use for the data. Can set to higher numbers to effectively down-sample the data before fitting

`pyspeckit.cubes.cubes.coords_in_image(fitsfile, lon, lat, system='galactic')`

Determine whether the coordinates are inside the image

`pyspeckit.cubes.cubes.extract_aperture(cube, ap, r_mask=False, wcs=None, coordsys='galactic', wunit='arcsec', debug=False, method='mean')`

Extract an aperture from a data cube. E.g. to acquire a spectrum of an outflow that is extended.

Cube should have shape [z,y,x], e.g. `cube = fits.getdata('datacube.fits')`

Apertures are specified in PIXEL units with an origin of 0,0 (NOT the 1,1 fits standard!) unless `wcs` and `coordsys` are specified

Parameters

ap : list

For a circular aperture, len(ap)=3:

`ap = [xcen,ycen,radius]`

For an elliptical aperture, len(ap)=5:

`ap = [xcen,ycen,height,width,PA]`

wcs : wcs

a `pywcs.WCS` instance associated with the data cube

coordsys : str

the coordinate system the aperture is specified in. Options are 'celestial' and 'galactic'. Default is 'galactic'

wunit : str

units of width/height. default 'arcsec', options 'arcmin' and 'degree'

method : str

'mean' or 'sum' (average over spectra, or sum them) or 'error' for `sqrt(sum-of-squares / n)`

`pyspeckit.cubes.cubes.flatten_header(header, delete=False)`

Attempt to turn an N-dimensional fits header into a 2-dimensional header Turns all `CRPIX[>2]` etc. into new keywords with suffix 'A'

header must be a `fits.Header` instance

`pyspeckit.cubes.cubes.getspec(lon, lat, rad, cube, header, r_fits=True, inherit=True, wunit='arcsec')`

Given a longitude, latitude, aperture radius (arcsec), and a cube file, return a .fits file or a spectrum.

Parameters

lon: float :

lat: float :

longitude and latitude center of a circular aperture in WCS coordinates must be in coordinate system of the file

rad: float :

radius (default degrees) of aperture

`pyspeckit.cubes.cubes.getspec_reg(cubefilename, region, **kwargs)`

Aperture extraction from a cube using a pyregion circle region

The region must be in the same coordinate system as the cube header

Warning: The second argument of `getspec_reg` requires a pyregion region list, and therefore this code depends on pyregion.

`pyspeckit.cubes.cubes.integ(file, vrange, xcen=None, xwidth=None, ycen=None, ywidth=None, **kwargs)`

wrapper of `subimage_integ` that defaults to using the full image

`pyspeckit.cubes.cubes.plane_smooth(cube, cubedim=0, parallel=True, numcores=None, **kwargs)`

parallel-map the smooth function

Parameters

parallel: bool :

defaults True. Set to false if you want serial (for debug purposes?)

numcores: int :

pass to `parallel_map` (None = use all available)

`pyspeckit.cubes.cubes.speccen_header(header, lon=None, lat=None, proj='TAN', system='celestial', spectral_axis=3, celestial_axes=[1, 2])`

Turn a cube header into a spectrum header, retaining RA/Dec vals where possible (speccen is like flatten; spec-ify would be better but, specify? nah)

Assumes 3rd axis is velocity

`pyspeckit.cubes.cubes.spectral_smooth(cube, smooth_factor, downsample=True, parallel=True, numcores=None, **kwargs)`

Smooth the cube along the spectral direction

`pyspeckit.cubes.cubes.subcube(cube, xcen, xwidth, ycen, ywidth, header=None, dvmult=False, return_HDU=False, units='pixels', widthunits='pixels')`

Crops a data cube

All units assumed to be pixel units

cube has dimensions (velocity, y, x)

xwidth and ywidth are “radius” values, i.e. half the length that will be extracted

if dvmult is set, multiple the average by DV (this is useful if you set average=sum and dvmul=True to get an integrated value)

`pyspeckit.cubes.cubes.subimage_integ(cube, xcen, xwidth, ycen, ywidth, vrange, header=None, average=<function mean at 0x7f0b41830aa0>, dvmult=False, return_HDU=False, units='pixels', zunits=None)`

Returns a sub-image from a data cube integrated over the specified velocity range

All units assumed to be pixel units

cube has dimensions (velocity, y, x)

xwidth and ywidth are “radius” values, i.e. half the length that will be extracted

if `dvmult` is set, multiply the average by DV (this is useful if you set `average=sum` and `dvmul=True` to get an integrated value)

4.1 Plain Text

Text files should be of the form:

```
wavelength flux err
3637.390 0.314 0.000
3638.227 0.717 0.000
3639.065 1.482 0.000
```

where there 'err' column is optional but the others are not. The most basic spectrum file allowed would have no header and two columns, e.g.:

```
1 0.5
2 1.5
3 0.1
```

If the X-axis is not monotonic, the data will be sorted so that the X-axis is in ascending order.

4.1.1 API

Routines for reading in ASCII format spectra. If atpy is not installed, will use a very simple routine for reading in the data.

```
pyspeckit.spectrum.readers.txt_reader.open_1d_txt(filename, xaxcol=0, datacol=1, errorcol=2,
                                                    text_reader='simple', atpytype='ascii',
                                                    **kwargs)
```

Attempt to read a 1D spectrum from a text file assuming wavelength as the first column, data as the second, and (optionally) error as the third.

Reading can be done either with atpy or a 'simple' reader. If you have an IPAC, CDS, or formally formatted table, you'll want to use atpy.

If you have a simply formatted file of the form, e.g. # name name # unit unit data data data data

kwargs are passed to atpy.Table

```
pyspeckit.spectrum.readers.txt_reader.simple_txt(filename, xaxcol=0, datacol=1, errorcol=2,
                                                    skiplines=0, **kwargs)
```

Very simple method for reading columns from ASCII file.

4.2 FITS

A minimal header should look like this:

```
SIMPLE =          T / conforms to FITS standard
BITPIX =         -32 / array data type
NAXIS  =          2 / number of array dimensions
NAXIS1 =         659
NAXIS2 =          2
CRPIX1 =          1.0
CRVAL1 =   -4953.029632560421
CDELT1 =    212.5358581542998
CTYPE1 = 'VRAD-LSR'
CUNIT1 = 'm/s'
BUNIT  = 'K'
RESTFRQ =    110.20137E9
SPECSYS = 'LSRK'
END
```

A fits file with a header as above should be easily readable without any user effort:

```
sp = pyspeckit.Spectrum('test.fits')
```

If you have multiple spectroscopic axes, e.g.

```
CRPIX1A =          1.0
CRVAL1A =   110.2031747948101
CTYPE1A = 'FREQ-LSR'
CUNIT1A = 'GHz'
RESTFRQA=    110.20137
```

you can load that axis with the 'wcstype' keyword:

```
sp = pyspeckit.Spectrum('test.fits', wcstype='A')
```

If you have a .fits file with a non-linear X-axis that is stored in the .fits file as data (as opposed to being implicitly included in a header), you can load it using a custom .fits reader. An example implementation is given in the [tspec_reader](#). It can be registered using [Registration](#):

```
tspec_reader = check_reader(tspec_reader.tspec_reader)
pyspeckit.register_reader('tspec', tspec_reader, 'fits')
```

4.2.1 API

`pyspeckit.spectrum.readers.fits_reader.open_1d_fits(filename, hdu=0, **kwargs)`

Grabs all the relevant pieces of a simple FITS-compliant 1d spectrum

Inputs:

wcstype - the suffix on the WCS type to get to
velocity/frequency/whatever

specnum - Which # spectrum, along the y-axis, is
the data?

errspecnum - Which # spectrum, along the y-axis,
is the error spectrum?

```
pyspeckit.spectrum.readers.fits_reader.open_1d_pyfits(pyfits_hdu, specnum=0, wcstype='',
specaxis='1', errspecnum=None,
autofix=True, scale_keyword=None,
scale_action=<built-in function div>,
verbose=False, apnum=0, **kwargs)
```

This is open_1d_fits but for a pyfits_hdu so you don't necessarily have to open a fits file

```
pyspeckit.spectrum.readers.fits_reader.read_echelle(pyfits_hdu)
```

Read an IRAF Echelle spectrum

<http://iraf.noao.edu/iraf/ftp/iraf/docs/specwcs.ps.Z>

4.3 hdf5

(work in progress)

4.3.1 API

Routines for reading in spectra from HDF5 files.

Note: Current no routines for parsing HDF5 headers in classes.py.

```
pyspeckit.spectrum.readers.hdf5_reader.open_hdf5(filename, xaxkey='xarr', datakey='data',
rkey='error')
```

This reader expects three datasets to exist in the hdf5 file 'filename': 'xarr', 'data', and 'error', by default. Can specify other dataset names.

4.4 Gildas CLASS files

Pyspeckit is capable of reading files from some versions of CLASS. The CLASS developers have stated that the GILDAS file format is private and will remain so, and therefore there are no guarantees that the CLASS reader will work for your file.

Nonetheless, if you want to develop in python instead of SIC, the `read_class` module is probably the best way to access CLASS data.

The `CLASS file specification` is incomplete, so much of the data reading is hacked together. The code style is based off of Tom Robitaille's `idlsave` package.

An example usage. Note that telescope and line are NOT optional keyword arguments, they are just specified as such for clarity

```
n2hp = class_to_obsblocks(fn1, telescope=['SMT-F1M-HU', 'SMT-F1M-VU'],
line=['N2HP(3-2)', 'N2H+(3-2)'])
```

This will generate a ObsBlock from all data tagged with the 'telescope' flags listed and lines matching either of those above. The data selection is equivalent to a combination of

```
find /telescope SMT-F1M-HU
find /telescope SMT-F1M-VU
find /line N2HP(3-2)
find /line N2H+(3-2)
```

ALL of the data matching those criteria will be included in an ObsBlock. They will then be accessible through the ObsBlock's `speclist` attribute, or just by indexing the ObsBlock directly.

4.4.1 An essentially undocumented API

GILDAS CLASS file reader

Read a CLASS file into an `pyspeckit.spectrum.ObsBlock`

`class pyspeckit.spectrum.readers.read_class.LazyItem(parent)`
Simple lazy spectrum-retriever wrapper

`pyspeckit.spectrum.readers.read_class.class_to_obsblocks(*arg, **kwargs)`
Load an entire CLASS observing session into a list of `ObsBlocks` based on matches to the ‘telescope’, ‘line’ and ‘source’ names

Parameters

filename : string

The Gildas CLASS data file to read the spectra from.

telescope : list

List of telescope names to be matched.

line : list

List of line names to be matched.

source : list (optional)

List of source names to be matched. Defaults to None.

imagfreq : bool

Create a `SpectroscopicAxis` with the image frequency.

`pyspeckit.spectrum.readers.read_class.class_to_spectra(*arg, **kwargs)`
Load each individual spectrum within a CLASS file into a list of `Spectrum` objects

`pyspeckit.spectrum.readers.read_class.downsample_1d(myarr, factor, estimator=<function mean at 0x7f0b41830aa0>, weight=None)`
Downsample a 1D array by averaging over *factor* pixels. Crops right side if the shape is not a multiple of factor.
This code is pure numpy and should be fast.

keywords:

estimator - default to mean. You can downsample by summing or

something else if you want a different estimator (e.g., downsampling error: you want to sum & divide by \sqrt{n})

weight: np.ndarray

An array of weights to use for the downsampling. If None, assumes uniform 1

`pyspeckit.spectrum.readers.read_class.gi8_dicho(ninp, lexn, xval, ceil=True)`
! @ public ! Find ival such as ! $X(ival-1) < xval \leq X(ival)$ (ceiling mode) ! or ! $X(ival) \leq xval < X(ival+1)$ (floor mode) ! for input data ordered. Use a dichotomic search for that. call `gi8_dicho(nex, file%desc%lexn, entry_num, true, kex, error)`

`pyspeckit.spectrum.readers.read_class.make_axis(header, imagfreq=False)`
Create a `pyspeckit.spectrum.units.SpectroscopicAxis` from the CLASS “header”

`pyspeckit.spectrum.readers.read_class.print_timing(func)`
Prints execution time of decorated function. Included here because CLASS files can take a little while to read; this should probably be replaced with a progressbar

`pyspeckit.spectrum.readers.read_class.read_class(*arg, **kwargs)`
Read a binary class file. Based on the [GILDAS CLASS file type Specification](#)

Parameters

filename: str :

downsample_factor: None or int :

Factor by which to downsample data by averaging. Useful for overresolved data.

sourcename: str or list of str :

Source names to match to the data (uses regex)

telescope: str or list of str :

‘XTEL’ or ‘TELE’ parameters: the telescope & instrument

flag_array: np.ndarray :

An array with the same shape as the data used to flag out (remove) data when down-sampling. True = flag out

`pyspeckit.spectrum.readers.read_class.tests()`
Tests are specific to the machine on which this code was developed.

4.5 GBTIDL FITS files

GBTIDL SDFITS sessions can be loaded as `pyspeckit.ObsBlock` objects using the `GBTSession` reader:

```
gbtsession = pyspeckit.readers.GBTSession('AGBTsession.fits')
```

4.5.1 API

GBTIDL SDFITS file

GBTIDL SDFITS files representing GBT observing sessions can be read into `pyspeckit`. Additional documentation is needed. Nodding reduction is supported, frequency switching is not.

class `pyspeckit.spectrum.readers.gbt.GBTSession(sdfitsfile)`

A class wrapping all of the above features

Load an SDFITS file or a pre-loaded FITS file

load_target(*target*, **kwargs)

Load a Target...

reduce_all()

reduce_target(*target*, **kwargs)

Reduce the data for a given object name

class `pyspeckit.spectrum.readers.gbt.GBTTarget(Session, target, **kwargs)`

A collection of `ObsBlocks` or `Spectra`

Container for the individual scans of a target from a GBT session

reduce(*obstype='nod'*, **kwargs)

Reduce noddred observations (they should have been read in `__init__`)

`pyspeckit.spectrum.readers.gbt.average_IF(block, debug=False)`
Average the polarizations for each feed in each IF

`pyspeckit.spectrum.readers.gbt.average_pols(block)`
Average the polarizations for each feed in each IF

`pyspeckit.spectrum.readers.gbt.count_integrations(sdfitsfile, target)`
Return the number of integrations for a given target (uses one sampler; assumes same number for all samplers)

`pyspeckit.spectrum.readers.gbt.dcmeantsys(calon, caloff, tcal, debug=False)`
from GBTIDL's `dcmeantsys.py` ; `mean_tsys = tcal * mean(nocal) / (mean(withcal-nocal)) + tcal/2.0`

`pyspeckit.spectrum.readers.gbt.find_feeds(block)`
Get a dictionary of the feed numbers for each sampler

`pyspeckit.spectrum.readers.gbt.find_matched_freqs(reduced_blocks, debug=False)`
Use frequency-matching to find which samplers observed the same parts of the spectrum

WARNING These IF numbers don't match GBTIDL's! I don't know how to get those to match up!

`pyspeckit.spectrum.readers.gbt.find_pols(block)`
Get a dictionary of the polarization for each sampler

`pyspeckit.spectrum.readers.gbt.identify_samplers(block)`
Identify each sampler with an IF number, a feed number, and a polarization

`pyspeckit.spectrum.readers.gbt.list_targets(sdfitsfile, doprint=True)`
List the targets, their location on the sky...

`pyspeckit.spectrum.readers.gbt.read_gbt_scan(sdfitsfile, obsnumber=0)`
Read a single scan from a GBTIDL SDFITS file

`pyspeckit.spectrum.readers.gbt.read_gbt_target(sdfitsfile, objectname, verbose=False)`
Give an object name, get all observations of that object as an 'obsblock'

`pyspeckit.spectrum.readers.gbt.reduce_gbt_target(sdfitsfile, objectname, nbeams, verbose=False)`
Wrapper - read an SDFITS file, get an object, reduce it (assuming noddod) and return it

`pyspeckit.spectrum.readers.gbt.reduce_nod(blocks, verbose=False, average=True, fdid=(1, 2))`
Do a noddod on/off observation given a dict of observation blocks as produced by `read_gbt_target`

Parameters
fdid : 2-tuple

`pyspeckit.spectrum.readers.gbt.reduce_totalpower(blocks, verbose=False, average=True, fdid=1)`
Reduce a total power observation

`pyspeckit.spectrum.readers.gbt.round_to_resolution(frequency, resolution)`
kind of a hack, but round the frequency to the nearest integer multiple of the resolution, then multiply it back into frequency space

`pyspeckit.spectrum.readers.gbt.sigref(nod1, nod2, tsys_nod2)`
Signal-Reference ('nod') calibration ; $((\text{dcsig}-\text{dcres})/\text{dcres}) * \text{dcres.tsys}$ see GBTIDL's `dosigref`

`pyspeckit.spectrum.readers.gbt.totalpower(calon, caloff, average=True)`
Do a total-power calibration of an on/off data set (see `dototalpower.pro` in GBTIDL)

`pyspeckit.spectrum.readers.gbt.uniq(seq)`
from <http://stackoverflow.com/questions/480214/how-do-you-remove-duplicates-from-a-list-in-python-whilst-preserving-order>

Wrappers

These are wrappers to simplify some of the more complicated (and even some of the simpler) functions in PySpecKit

5.1 Cube Fitting

Complicated code for fitting of a whole data cube, pixel-by-pixel

```
pyspeckit.wrappers.cube_fit.cube_fit(cubefilename, outfilename, errfilename=None,
                                     scale_keyword=None, vheight=False, verbose=False, signal_cut=3, verbose_level=2, clobber=True, **kwargs)
```

Light-weight wrapper for cube fitting

Takes a cube and error map (error will be computed naively if not given) and computes moments then fits for each spectrum in the cube. It then saves the fitted parameters to a reasonably descriptive output file whose header will look like

```
PLANE1 = 'amplitude'
PLANE2 = 'velocity'
PLANE3 = 'sigma'
PLANE4 = 'err_amplitude'
PLANE5 = 'err_velocity'
PLANE6 = 'err_sigma'
PLANE7 = 'integral'
PLANE8 = 'integral_error'
CDEL3   = 1
CTYPE3  = 'FITPAR'
CRVAL3  = 0
CRPIX3  = 1
```

Parameters

errfilename: [None | string name of .fits file] :

A two-dimensional error map to use for computing signal-to-noise cuts

scale_keyword: [None | Char] :

Keyword to pass to the data cube loader - multiplies cube by the number indexed by this header kwarg if it exists. e.g., if your cube is in T_A units and you want T_A*

vheight: [bool] :

Is there a background to be fit? Used in moment computation

verbose: [bool] :

verbose_level: [int] :

How loud will the fitting procedure be? Passed to momenteach and fiteach

signal_cut: [float] :

Signal-to-Noise ratio minimum. Spectra with a peak below this S/N ratio will not be fit and will be left blank in the output fit parameter cube

clobber: [bool] :

Overwrite parameter .fits cube if it exists?

'kwargs' are passed to :class:'pyspeckit.Spectrum.specfit' :

```
pyspeckit.wrappers.fit_gaussians_to_simple_spectra.fit_gaussians_to_simple_spectra(filename,
                                                                 units='km/s',
                                                                 do-
                                                                 plot=True,
                                                                 base-
                                                                 line=True,
                                                                 plotresid-
                                                                 u-
                                                                 als=False,
                                                                 figure-
                                                                 save-
                                                                 name=None,
                                                                 cro-
                                                                 prange=None,
                                                                 save-
                                                                 name=None,
                                                                 **kwargs)
```

As stated in the name title, will fit Gaussians to simple spectra!

kwargs will be passed to specfit

figuresavefilename [None | string]

After fitting, save the figure to this filename if specified

croprange [list of 2 floats]

Crop the spectrum to (min,max) in the specified units

savefilename [None | string]

After fitting, save the spectrum to this filename

Note that this wrapper can be used from the command line:

python fit_gaussians_to_simple_spectra.py spectrum.fits

5.2 NH3 fitter wrapper

Wrapper to fit ammonia spectra. Generates a reasonable guess at the position and velocity using a gaussian fit

Example use:

```
import pyspeckit
sp11 = pyspeckit.Spectrum('spec.nh3_11.dat', errorcol=999)
sp22 = pyspeckit.Spectrum('spec.nh3_22.dat', errorcol=999)
```

```
sp33 = pyspeckit.Spectrum('spec.nh3_33.dat', errorcol=999)
sp11.xarr.refX = pyspeckit.spectrum.models.ammonia.freq_dict['oneone']
sp22.xarr.refX = pyspeckit.spectrum.models.ammonia.freq_dict['twotwo']
sp33.xarr.refX = pyspeckit.spectrum.models.ammonia.freq_dict['threethree']
input_dict={'oneone':sp11,'twotwo':sp22,'threethree':sp33}
spf = pyspeckit.wrappers.fitnh3.fitnh3tkin(input_dict)
```

```
pyspeckit.wrappers.fitnh3.BigSpectrum_to_NH3dict(sp, vrang=None)
```

A rather complicated way to make the spdicts above given a spectrum...

```
pyspeckit.wrappers.fitnh3.fitnh3(spectrum, vrang=[-100, 100], vrangunits='km/s', quiet=False,
    Tex=20, Tkin=15, column=1000000000000000.0, fortho=1.0,
    tau=None)
```

```
pyspeckit.wrappers.fitnh3.fitnh3tkin(input_dict, dobaseline=True, baselinekwargs={}, crop=False,
    guessline='twotwo', tex=15, tkin=20, column=15.0,
    fortho=0.66, tau=None, thin=False, quiet=False, do-
    plot=True, fignum=1, guessfignum=2, smooth=False,
    scale_keyword=None, rebase=False, npeaks=1, guesses=None,
    **kwargs)
```

Given a dictionary of filenames and lines, fit them together e.g. {'oneone': 'G000.000+00.000_nh3_11.fits'}

```
pyspeckit.wrappers.fitnh3.plot_nh3(spdict, spectra, fignum=1, show_components=False, resid-
    fignum=None, **plotkwargs)
```

Plot the results from a multi-nh3 fit

spdict needs to be dictionary with form:

'oneone': spectrum, 'twotwo': spectrum, etc.

```
pyspeckit.wrappers.fitnh3.plotter_override(sp, vrang=None, **kwargs)
```

Do plot_nh3 with syntax similar to plotter()

5.3 N2H+ fitter wrapper

Wrapper to fit N2H+ using RADEX models. This is meant to be used from the command line, e.g.

```
python n2hp_wrapper.py file.fits
```

and therefore has no independently defined functions.

```
pyspeckit.wrappers.n2hp_wrapper.make_n2hp_fitter(path_to_radex='/Users/adam/work/n2hp',
    fileprefix='1-2_T=5to55_lvg')
```

Create a n2hp fitter using RADEX data cubes. The following files must exist:

```
path_to_radex+fileprefix+'_tex1.fits'
path_to_radex+fileprefix+'_tau1.fits'
path_to_radex+fileprefix+'_tex2.fits'
path_to_radex+fileprefix+'_tau2.fits'
```

e.g. /Users/adam/work/n2hp/1-2_T=5to55_lvg_tau1.fits

5.4 N2H+ extras

In place of the actual contents of N2H+ fitter, here are the modules used to make the wrapper

```
class pyspeckit.spectrum.models.model.SpectralModel(modelfunc, npars, shortvarnames=('A',
                                         '\Delta x', '\sigma'), fitunits=None,
                                         centroid_par=None, fwhm_func=None,
                                         fwhm_pars=None, integral_func=None,
                                         use_lmfit=False, **kwargs)
```

A wrapper class for a spectra model. Includes internal functions to generate multi-component models, annotations, integrals, and individual components. The declaration can be complex, since you should name individual variables, set limits on them, set the units the fit will be performed in, and set the annotations to be used. Check out some of the hyperfine codes (hcn, n2hp) for examples.

Spectral Model Initialization

Create a Spectral Model class for data fitting

Parameters

modelfunc : function

the model function to be fitted. Should take an X-axis (spectroscopic axis) as an input followed by input parameters. Returns an array with the same shape as the input X-axis

npars : int

number of parameters required by the model

parnames : list (optional)

a list or tuple of the parameter names

parvalues : list (optional)

the initial guesses for the input parameters (defaults to ZEROS)

parlimits : list (optional)

the upper/lower limits for each variable (defaults to ZEROS)

parfixed : list (optional)

Can declare any variables to be fixed (defaults to ZEROS)

parerror : list (optional)

technically an output parameter... hmm (defaults to ZEROS)

partied : list (optional)

not the past tense of party. Can declare, via text, that some parameters are tied to each other. Defaults to zeros like the others, but it's not clear if that's a sensible default

fitunits : str (optional)

convert X-axis to these units before passing to model

parsteps : list (optional)

minimum step size for each parameter (defaults to ZEROS)

npeaks : list (optional)

default number of peaks to assume when fitting (can be overridden)

shortvarnames : list (optional)

TeX names of the variables to use when annotating

Returns

A tuple containing (model best-fit parameters, the model, parameter : errors, χ^2 value) :

```
static n2hp.n2hp_radex(xarr, density=4, column=13, xoff_v=0.0, width=1.0, grid_vwidth=1.0,
                      grid_vwidth_scale=False, texgrid=None, taugrid=None, hdr=None,
                      path_to_texgrid='', path_to_taugrid='', temperature_gridnumber=3, debug=False,
                      verbose=False, **kwargs)
```

Use a grid of RADEX-computed models to make a model line spectrum

The RADEX models have to be available somewhere. OR they can be passed as arrays. If as arrays, the form should be: `texgrid = ((minfreq1,maxfreq1,texgrid1),(minfreq2,maxfreq2,texgrid2))`

`xarr` must be a `SpectroscopicAxis` instance `xoff_v`, `width` are both in km/s

`grid_vwidth` is the velocity assumed when computing the grid in km/s this is important because $\tau = \text{modeltau} / \text{width}$ (see, e.g., Draine 2011 textbook pgs 219-230) `grid_vwidth_scale` is True or False: False for LVG, True for Sphere

Examples

Check out the [flickr gallery](#).

Want your image or example included? [E-mail us](#).

6.1 Creating a Spectrum from scratch

This example shows the initialization of a pyspeckit object from numpy arrays.

```
import numpy as np
import pyspeckit

xaxis = np.linspace(-50,150,100.)
sigma = 10.
center = 50.
synth_data = np.exp(-(xaxis-center)**2/(sigma**2 * 2.))

# Add noise
stddev = 0.1
noise = np.random.randn(xaxis.size)*stddev
error = stddev*np.ones_like(synth_data)
data = noise+synth_data

# this will give a "blank header" warning, which is fine
sp = pyspeckit.Spectrum(data=data, error=error, xarr=xaxis,
                        xarrkwargs={'unit':'km/s'},
                        unit='erg/s/cm^2/AA')

sp.plotter()

# Fit with automatic guesses
sp.specfit(fittype='gaussian')

# Fit with input guesses
# The guesses initialize the fitter
# This approach uses the 0th, 1st, and 2nd moments
amplitude_guess = data.max()
center_guess = (data*xaxis).sum()/data.sum()
width_guess = data.sum() / amplitude_guess / np.sqrt(2*np.pi)
guesses = [amplitude_guess, center_guess, width_guess]
sp.specfit(fittype='gaussian', guesses=guesses)
```

```
sp.plotter(errstyle='fill')
sp.specfit.plot_fit()
```

6.2 Radio Fitting: H₂CO RADEX example

Because an LVG model grid is being used as the basis for the fitting in this example, there are fewer free parameters. If you want to create your own model grid, there is a set of tools for creating RADEX model grids (in parallel) at the [agpy RADEX page](#). The model grids used below are available on the [pyspeckit bitbucket download page](#).

```
import pyspeckit
import numpy as np
import pyfits
from pyspeckit.spectrum import models

# create the Formaldehyde Radex fitter
# This step cannot be easily generalized: the user needs to read in their own grids
texgrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_greenscaled/1-1_2-2_T5to55_lvg_greenscaled_tex1.fits')
taugrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_greenscaled/1-1_2-2_T5to55_lvg_greenscaled_tau1.fits')
texgrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_greenscaled/1-1_2-2_T5to55_lvg_greenscaled_tex2.fits')
taugrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_greenscaled/1-1_2-2_T5to55_lvg_greenscaled_tau2.fits')
hdr = pyfits.getheader('/Users/adam/work/h2co/radex/grid_greenscaled/1-1_2-2_T5to55_lvg_greenscaled_tau2.fits')

# this deserves a lot of explanation:
# models.formaldehyde.formaldehyde_radex is the MODEL that we are going to fit
# models.model.SpectralModel is a wrapper to deal with parinfo, multiple peaks,
# and annotations
# all of the parameters after the first are passed to the model function
formaldehyde_radex_fitter = models.model.SpectralModel(
    models.formaldehyde.formaldehyde_radex, 4,
    parnames=['density', 'column', 'center', 'width'],
    parvalues=[4, 12, 0, 1],
    parlimited=[(True, True), (True, True), (False, False), (True, False)],
    parlimits=[(1, 8), (11, 16), (0, 0), (0, 0)],
    parsteps=[0.01, 0.01, 0, 0],
    fitunits='Hz',
    texgrid=((4, 5, texgrid1), (14, 15, texgrid2)), # specify the frequency range over which the grid is valid (in GHz)
    taugrid=((4, 5, taugrid1), (14, 15, taugrid2)),
    hdr=hdr,
    shortvarnames=("n", "N", "v", "\\sigma"), # specify the parameter names (TeX is OK)
    grid_vwidth_scale=False,
)

# sphere version:
texgrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_aug2011_sphere/grid_aug2011_sphere_tex1.fits')
taugrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_aug2011_sphere/grid_aug2011_sphere_tau1.fits')
texgrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_aug2011_sphere/grid_aug2011_sphere_tex2.fits')
taugrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/grid_aug2011_sphere/grid_aug2011_sphere_tau2.fits')
hdr = pyfits.getheader('/Users/adam/work/h2co/radex/grid_aug2011_sphere/grid_aug2011_sphere_tau2.fits')

formaldehyde_radex_fitter_sphere = models.model.SpectralModel(
    models.formaldehyde.formaldehyde_radex, 4,
    parnames=['density', 'column', 'center', 'width'],
    parvalues=[4, 12, 0, 1],
    parlimited=[(True, True), (True, True), (False, False), (True, False)],
    parlimits=[(1, 8), (11, 16), (0, 0), (0, 0)],
    parsteps=[0.01, 0.01, 0, 0],
```

```

        fitunits='Hz',
        texgrid=((4,5,texgrid1),(14,15,texgrid2)),
        taugrid=((4,5,taugrid1),(14,15,taugrid2)),
        hdr=hdr,
        shortvarnames=("n", "N", "v", "\\sigma"),
        grid_vwidth_scale=True,
    )

sp1 = pyspeckit.Spectrum('G203.04+1.76_h2co.fits', wcstype='D', scale_keyword='ETAMB')
sp2 = pyspeckit.Spectrum('G203.04+1.76_h2co_Tastar.fits', wcstype='V', scale_keyword='ETAMB')

sp1.crop(-50,50)
sp1.smooth(3) # match to GBT resolution
sp2.crop(-50,50)

sp1.xarr.convert_to_unit('GHz')
sp1.specfit() # determine errors
sp1.error = np.ones(sp1.data.shape)*sp1.specfit.residuals.std()
sp1.baseline(excludefit=True)
sp2.xarr.convert_to_unit('GHz')
sp2.specfit() # determine errors
sp2.error = np.ones(sp2.data.shape)*sp2.specfit.residuals.std()
sp2.baseline(excludefit=True)
sp = pyspeckit.Spectra([sp1,sp2])

sp.Registry.add_fitter('formaldehyde_radex',
    formaldehyde_radex_fitter,4)
sp.Registry.add_fitter('formaldehyde_radex_sphere',
    formaldehyde_radex_fitter_sphere,4)

sp.plotter()
sp.specfit(fittype='formaldehyde_radex', multifit=None, guesses=[4,12,3.75,0.43], quiet=False)

# these are just for pretty plotting:
sp1.specfit.fitter = sp.specfit.fitter
sp1.specfit.modelpars = sp.specfit.modelpars
sp1.specfit.model = np.interp(sp1.xarr, sp.xarr, sp.specfit.model)
sp2.specfit.fitter = sp.specfit.fitter
sp2.specfit.modelpars = sp.specfit.modelpars
sp2.specfit.model = np.interp(sp2.xarr, sp.xarr, sp.specfit.model)

# previously, xarrs were in GHz to match the fitting scheme
sp1.xarr.convert_to_unit('km/s')
sp2.xarr.convert_to_unit('km/s')

sp1.plotter(xmin=-5,xmax=15,errstyle='fill')
sp1.specfit.plot_fit(show_components=True)
sp2.plotter(xmin=-5,xmax=15,errstyle='fill')
sp2.specfit.plot_fit(show_components=True)

sp.plotter(figure=5)
sp.specfit(fittype='formaldehyde_radex_sphere', multifit=None, guesses=[4,13,3.75,0.43], quiet=False)

# these are just for pretty plotting:

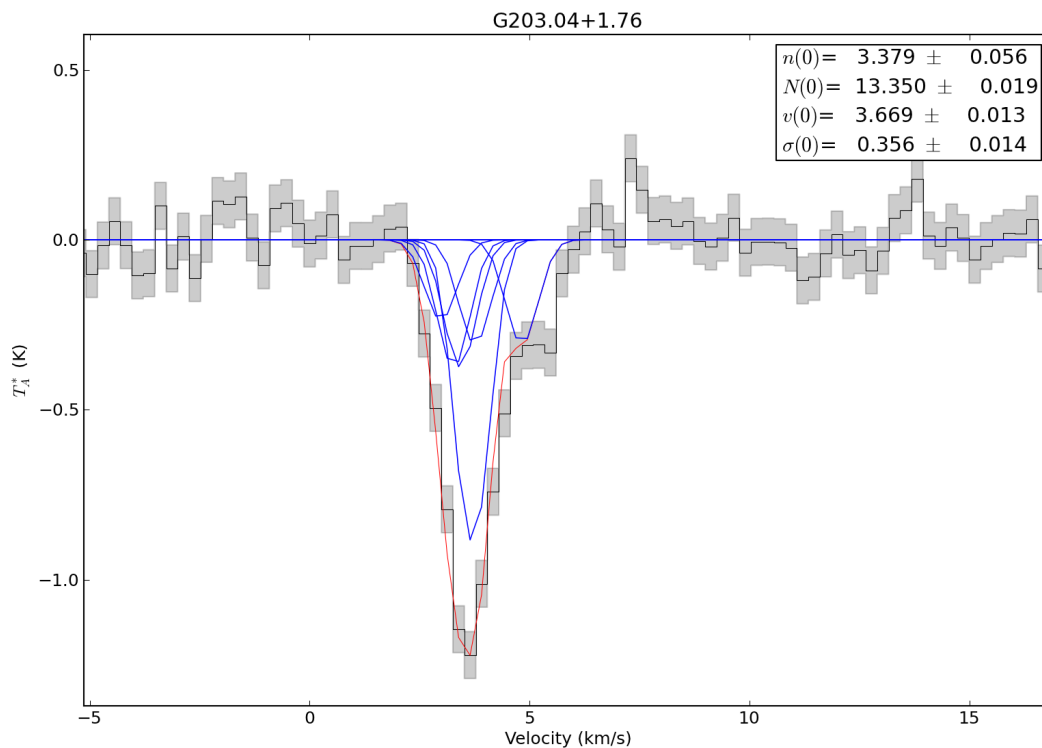
```

```

sp1.specfit.fitter = sp.specfit.fitter
sp1.specfit.modelpars = sp.specfit.modelpars
sp1.specfit.model = np.interp(sp1.xarr.as_unit('GHz'), sp.xarr, sp.specfit.model)
sp2.specfit.fitter = sp.specfit.fitter
sp2.specfit.modelpars = sp.specfit.modelpars
sp2.specfit.model = np.interp(sp2.xarr.as_unit('GHz'), sp.xarr, sp.specfit.model)

sp1.plotter(xmin=-5, xmax=15, errstyle='fill', figure=6)
sp1.specfit.plot_fit(show_components=True)
sp2.plotter(xmin=-5, xmax=15, errstyle='fill', figure=7)
sp2.specfit.plot_fit(show_components=True)

```



6.3 Radio Fitting: H₂CO millimeter thermometer lines

Example hyperfine line fitting of a data cube for the H₂CO 303-202, 321-220, and 322-221 lines.

```

import pyspeckit
try:
    import astropy.io.fits as pyfits
except ImportError:
    import pyfits
from pyspeckit.spectrum import models

# create the Formaldehyde Radex fitter
# This step cannot be easily generalized: the user needs to read in their own grids
# Some of these grids can be acquired from:

```

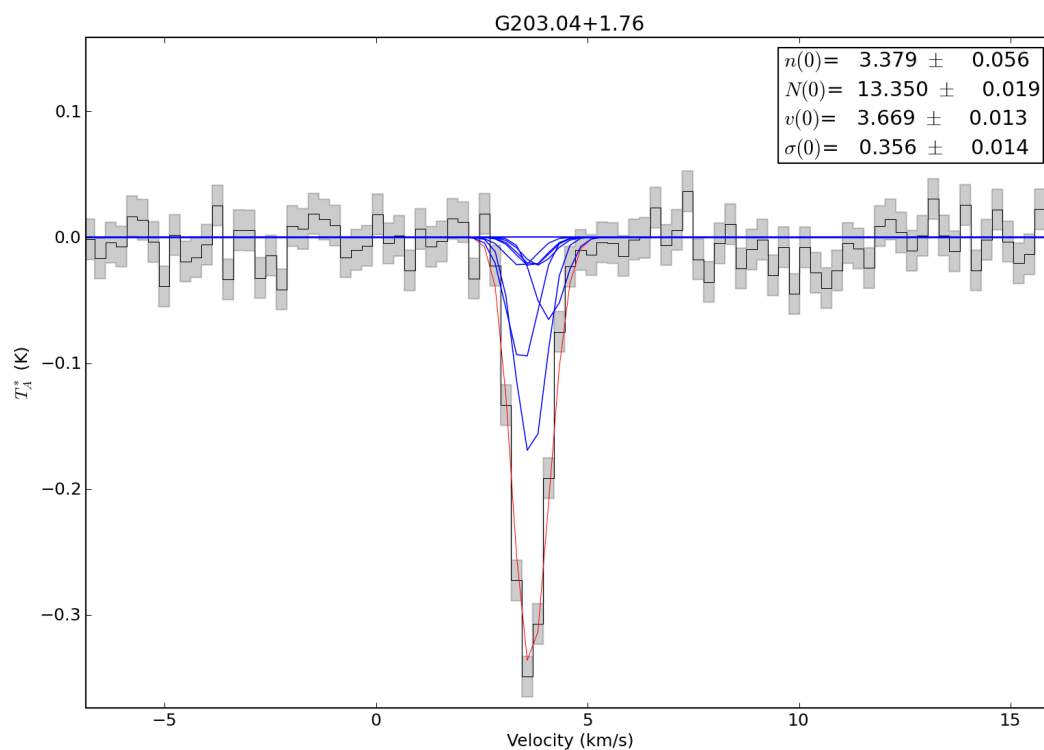


Figure 6.1: Both transitions are fit simultaneously using a RADEX model. The input (fitted) parameters are therefore density, column density, width, and velocity.

```
# https://github.com/keflavich/radex_data_grids
texgrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_321-220_5kms_temperature_para_tex1.fits')
taugrid1 = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_321-220_5kms_temperature_para_tau1.fits')
texgrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_321-220_5kms_temperature_para_tex2.fits')
taugrid2 = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_321-220_5kms_temperature_para_tau2.fits')
hdr = pyfits.getheader('/Users/adam/work/h2co/radex/thermom/303-202_321-220_5kms_temperature_para_tau2.fits')

texgrid1b = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_322-221_5kms_temperature_para_tex1.fits')
taugrid1b = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_322-221_5kms_temperature_para_tau1.fits')
texgrid2b = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_322-221_5kms_temperature_para_tex2.fits')
taugrid2b = pyfits.getdata('/Users/adam/work/h2co/radex/thermom/303-202_322-221_5kms_temperature_para_tau2.fits')
hdrb = pyfits.getheader('/Users/adam/work/h2co/radex/thermom/303-202_322-221_5kms_temperature_para_tau2.fits')

# this deserves a lot of explanation:
# models.formaldehyde.formaldehyde_radex is the MODEL that we are going to fit
# models.model.SpectralModel is a wrapper to deal with parinfo, multiple peaks,
# and annotations
# all of the parameters after the first are passed to the model function
# This first one fits only the 303-202 and 322-221 lines
formaldehyde_radex_fitter_b = models.model.SpectralModel(
    models.formaldehyde_mm.formaldehyde_mm_radex, 5,
    parnames=['temperature', 'column', 'density', 'center', 'width'],
    parvalues=[50, 12, 4.5, 0, 1],
    parlimited=[(True, True), (True, True), (True, True), (False, False), (True, False)],
    parlimits=[(5, 205), (10, 17), (2, 7), (0, 0), (0, 0)],
    parsteps=[0.01, 0.01, 0.1, 0, 0],
    fitunits='Hz',
    texgrid=((218.2, 218.3, texgrid1b), (218.4, 218.55, texgrid2b)), # specify the frequency range over which the grid is valid
    taugrid=((218.2, 218.3, taugrid1b), (218.4, 218.55, taugrid2b)),
    hdr=hdrb,
    shortvarnames=("T", "N", "n", "v", "\\sigma"), # specify the parameter names (TeX is OK)
    grid_vwidth=5.0,
)

# This second fitter fits only the 303-202 and 321-220 lines
formaldehyde_radex_fitter = models.model.SpectralModel(
    models.formaldehyde_mm.formaldehyde_mm_radex, 5,
    parnames=['temperature', 'column', 'density', 'center', 'width'],
    parvalues=[50, 12, 4.5, 0, 1],
    parlimited=[(True, True), (True, True), (True, True), (False, False), (True, False)],
    parlimits=[(5, 205), (10, 17), (2, 7), (0, 0), (0, 0)],
    parsteps=[0.01, 0.01, 0.1, 0, 0],
    fitunits='Hz',
    texgrid=((218.2, 218.3, texgrid1), (218.7, 218.8, texgrid2)), # specify the frequency range over which the grid is valid
    taugrid=((218.2, 218.3, taugrid1), (218.7, 218.8, taugrid2)),
    hdr=hdr,
    shortvarnames=("T", "N", "n", "v", "\\sigma"), # specify the parameter names (TeX is OK)
    grid_vwidth=5.0,
)

# This third fitter fits all three of the 303-202, 322-221, and 321-220 lines
# Since it has no additional free parameters, it's probably best...
formaldehyde_radex_fitter_both = models.model.SpectralModel(
    models.formaldehyde_mm.formaldehyde_mm_radex, 5,
    parnames=['temperature', 'column', 'density', 'center', 'width'],
    parvalues=[50, 12, 4.5, 0, 1],
    parlimited=[(True, True), (True, True), (True, True), (False, False), (True, False)],
    parlimits=[(5, 205), (10, 17), (2, 7), (0, 0), (0, 0)],
```

```

parsteps=[0.01,0.01,0.1,0,0],
fitunits='Hz',
texgrid=((218.2,218.3,texgrid1b),(218.4,218.55,texgrid2b),(218.7,218.8,texgrid2)), # specify the frequency range over
taugrid=((218.2,218.3,taugrid1b),(218.4,218.55,taugrid2b),(218.7,218.8,taugrid2)),
hdr=hdrb,
shortvarnames=("T","N","n","v","\\sigma"), # specify the parameter names (TeX is OK)
grid_vwidth=5.0,
)

if __name__ == "__main__":

    sp = pyspeckit.readers.read_class.class_to_spectra('example_h2co_mm_spectrum.apex',apex=True)
    sp.data *= 1/0.75 # T_A* -> T_MB
    sp.unit = "$T_{MB}$"
    # estimate the error from the data
    sp.error[:] = sp.stats((2.183e2,2.184e2))['std']

    # register the fitters
    sp.Registry.add_fitter('formaldehyde_mm_radex',
                           formaldehyde_radex_fitter,5)
    sp.Registry.add_fitter('formaldehyde_mm_radex_b',
                           formaldehyde_radex_fitter_b,5)
    sp.Registry.add_fitter('formaldehyde_mm_radex_both',
                           formaldehyde_radex_fitter_both,5)

    # make 3 copies so that we can view independent fits
    # This step isn't really necessary, but it's a nice way to compare the fits
    # side-by-side
    sp1 = sp.copy()
    sp2 = sp.copy()
    sp3 = sp.copy()

    sp1.plotter(figure=1)
    sp1.specfit(fittype='formaldehyde_mm_radex',
                multifit=None,
                guesses=[100,13.2,4.5,0,7.0],
                limits=[(20,200),(11,15),(3,5.5),(-5,5),(2,15)],
                limited=[(True,True)]*5,
                fixed=[False,False,True,False,False],
                quiet=False,)
    sp1.plotter.savefig('h2co_mm_fit_303-202_321-220.png')

    sp2.plotter(figure=2)
    sp2.specfit(fittype='formaldehyde_mm_radex_b',
                multifit=None,
                guesses=[100,13.2,4.5,0,7.0],
                limits=[(20,200),(11,15),(3,5.5),(-5,5),(2,15)],
                limited=[(True,True)]*5,
                fixed=[False,False,True,False,False],
                quiet=False,)
    sp2.plotter.savefig('h2co_mm_fit_303-202_322-221.png')

    # Do two versions of the fit with different input guesses
    sp3.plotter(figure=3)
    sp3.specfit(fittype='formaldehyde_mm_radex_both',
                multifit=None,
                guesses=[95,13.2,4.5,0,7.0],

```

```

limits=[(20,200),(11,15),(3,5.5),(-5,5),(2,15)],
limited=[(True,True)]*5,
fixed=[True,False,False,False,False],
quiet=False,)
sp3.plotter.savefig('h2co_mm_fit_303-202_322-221_and_303-202_321-220_try1.png')

sp3.plotter.figure=4
sp3.specfit(fittype='formaldehyde_mm_radex_both',
            multifit=None,
            guesses=[105,13.2,4.5,0,7.0],
            limits=[(20,200),(11,15),(3,5.5),(-5,5),(2,15)],
            limited=[(True,True)]*5,
            fixed=[False,True,False,False,False],
            quiet=False,)
sp3.plotter.savefig('h2co_mm_fit_303-202_322-221_and_303-202_321-220_try2.png')

# An illustration of the degeneracy between parameters
sp3.plotter.figure=5
sp3.specfit.plot_model([95,13.5,4.75,2.89,6.85])
sp3.specfit.plot_model([165,13.5,7.0,2.89,6.85],composite_fit_color='b')
sp3.specfit.plot_model([117,13.15,5.25,2.89,6.85],composite_fit_color='g')
sp3.plotter.savefig("h2co_mm_fit_degeneracy_example.png")

```

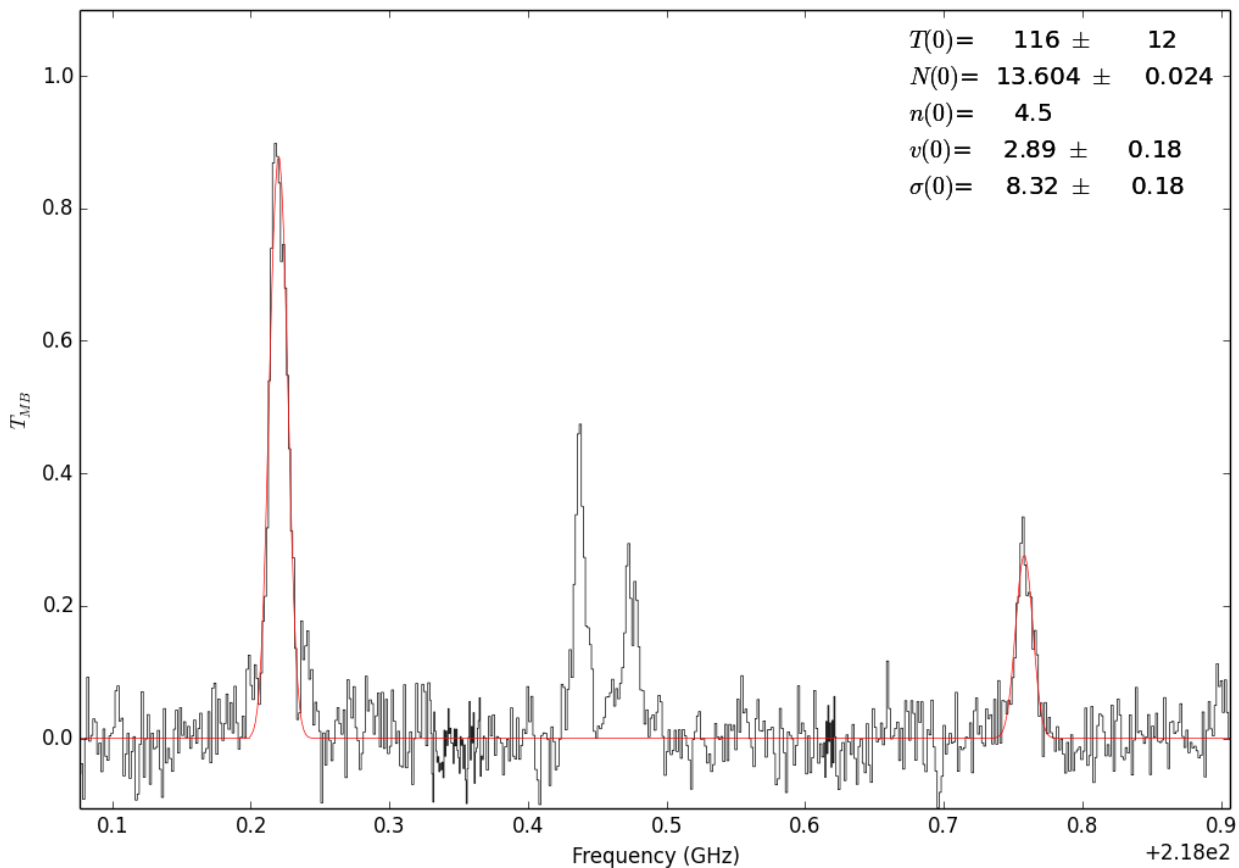


Figure 6.2: Fit with the 302-202 and 321-220 lines

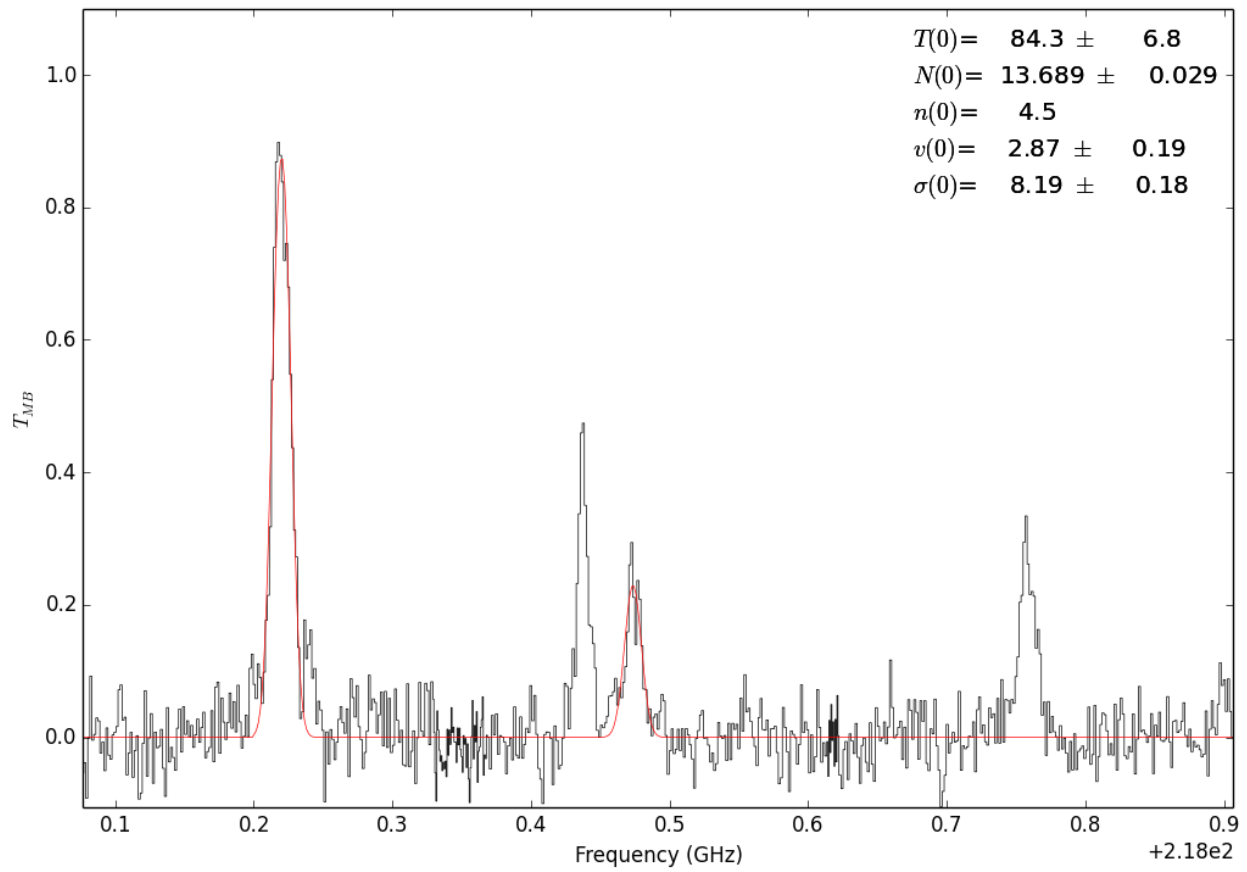


Figure 6.3: Fit with the 302-202 and 321-220 lines

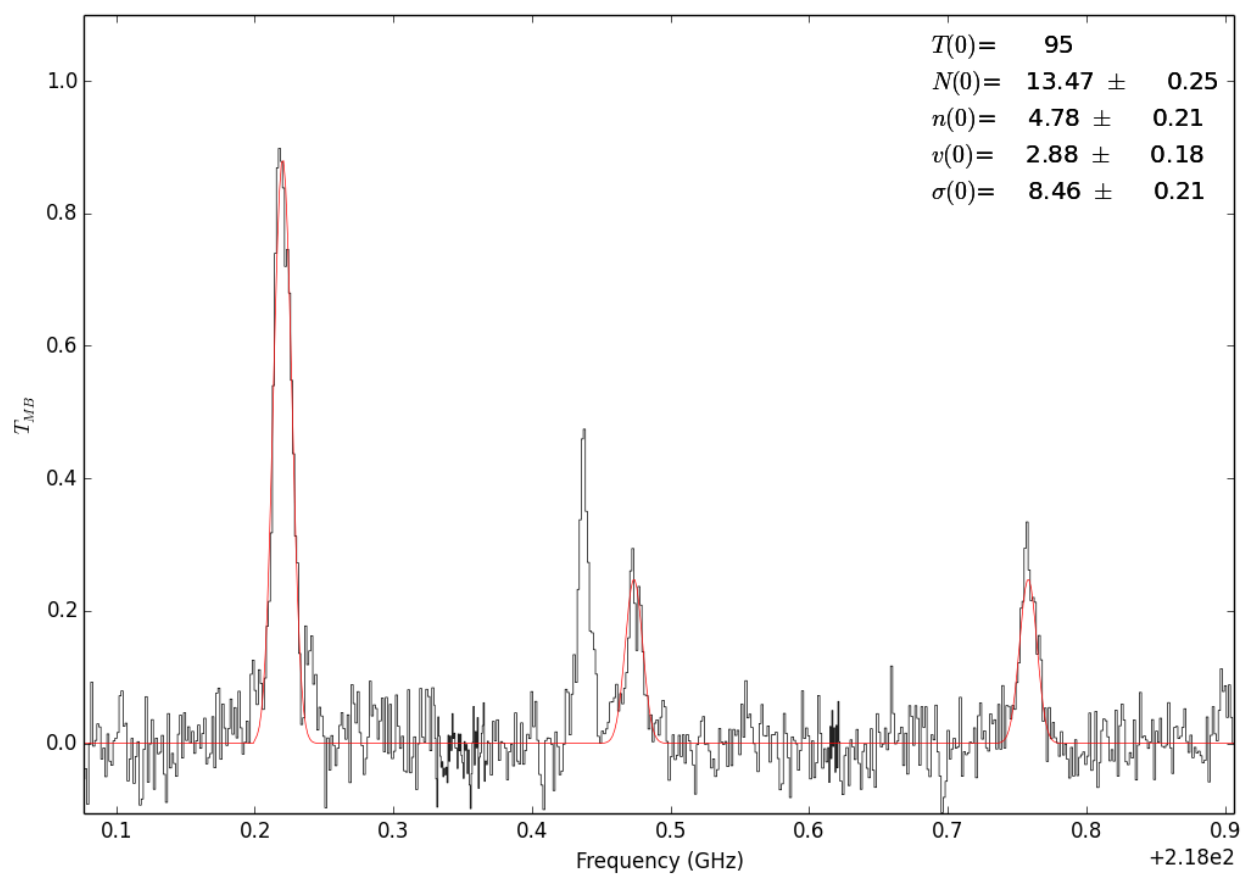


Figure 6.4: Fit with all 3 lines. In this case, the temperature is unconstrained.

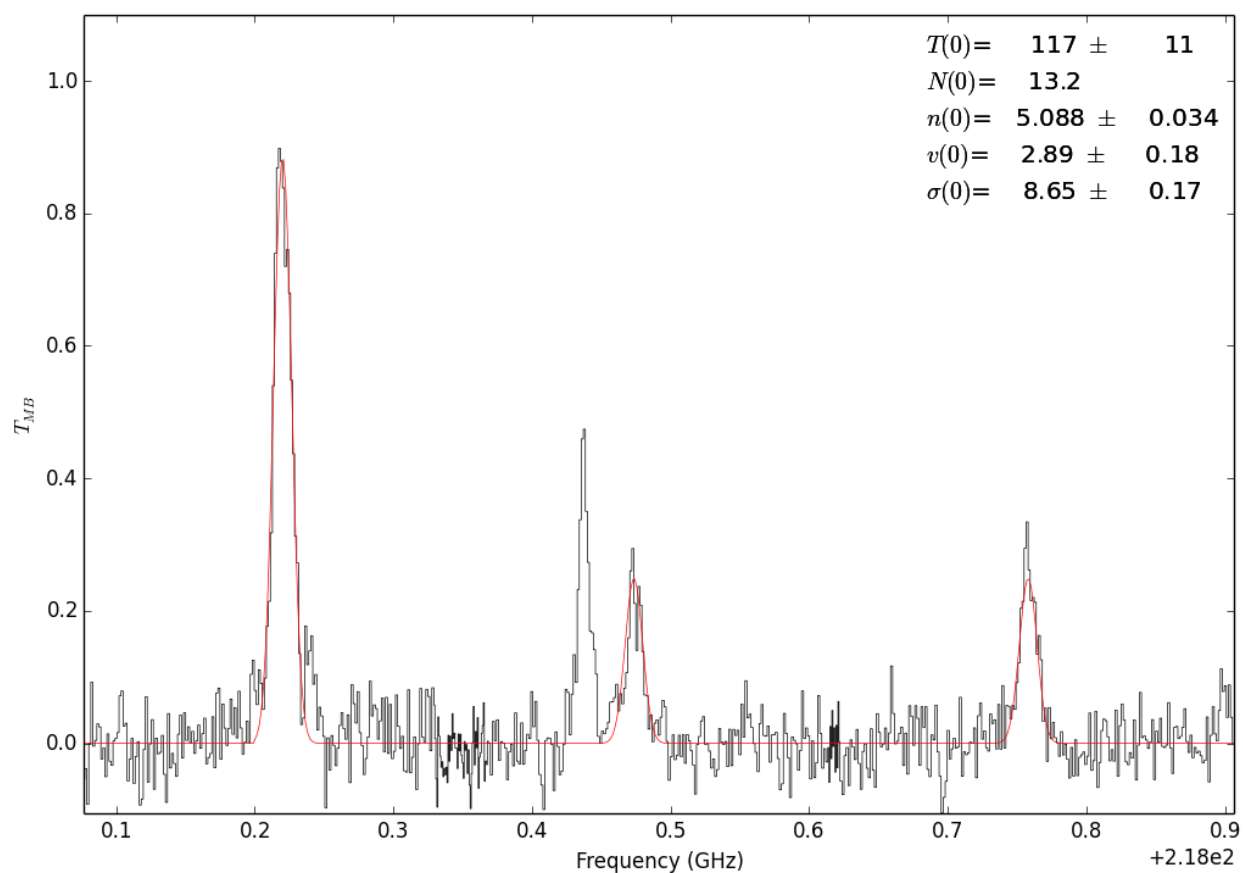


Figure 6.5: Fit with all 3 lines. In this case, the column is unconstrained.

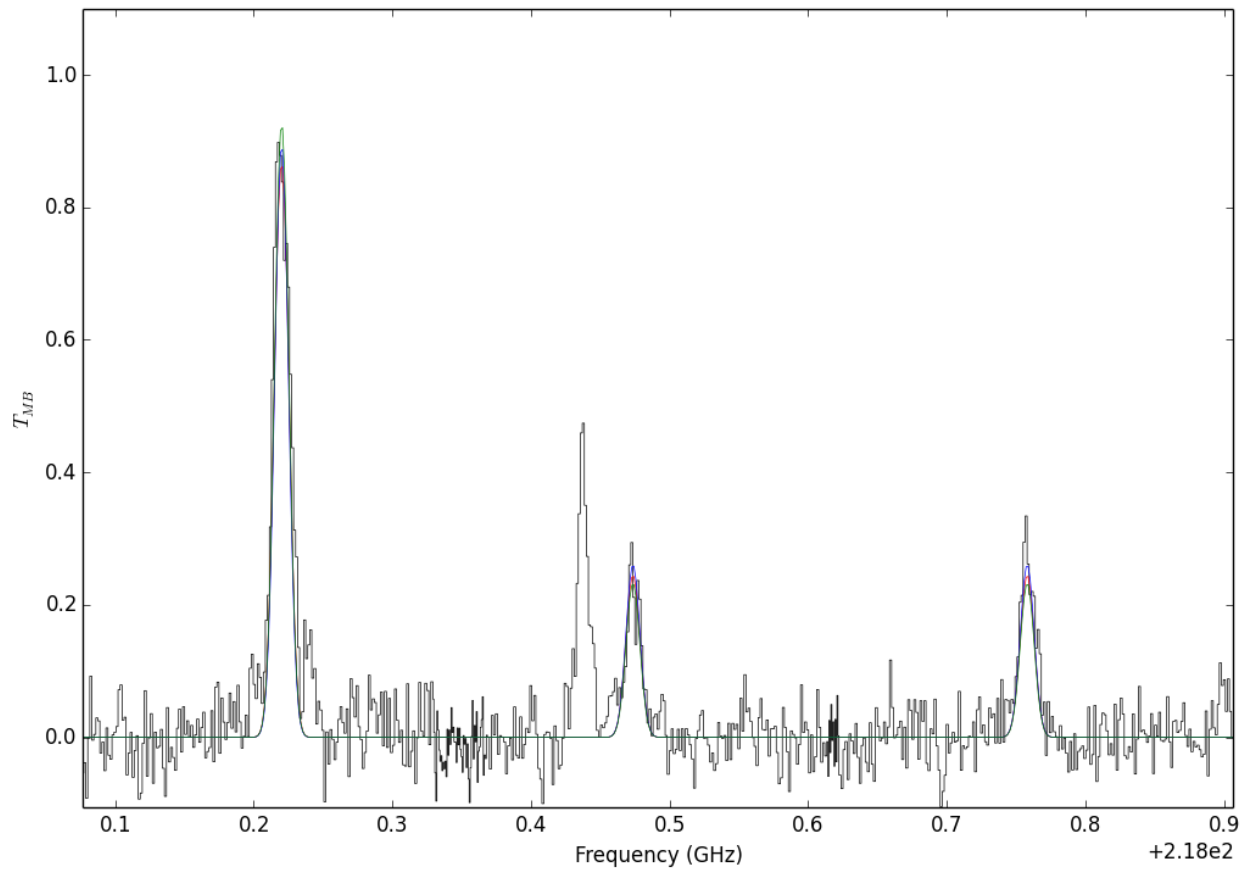


Figure 6.6: A demonstration of degenerate parameters. The parameters used are:

- Blue: $T, N, n = 95, 13.5, 4.75$
- Green: $T, N, n = 165, 13.5, 7.0$
- Red: $T, N, n = 117, 13.15, 5.25$

6.4 Radio Fitting: NH₃ example

```
import pyspeckit
```

```
# The ammonia fitting wrapper requires a dictionary specifying the transition name
# (one of the four specified below) and the filename. Alternately, you can have the
# dictionary values be pre-loaded Spectrum instances
```

```
filenames = {'oneone': 'G032.751-00.071_nh3_11_Tastar.fits',
             'twotwo': 'G032.751-00.071_nh3_22_Tastar.fits',
             'threethree': 'G032.751-00.071_nh3_33_Tastar.fits',
             'fourfour': 'G032.751-00.071_nh3_44_Tastar.fits'}
```

```
# Fit the ammonia spectrum with some reasonable initial guesses. It is
# important to crop out extraneous junk and to smooth the data to make the
# fit proceed at a reasonable pace.
```

```
spdickt1,spectra1 = pyspeckit.wrappers.fitnh3.fitnh3tkin(filenames,crop=[0,80],tkin=18.65,tex=4.49,column=15.5,fortho=0.9,
```

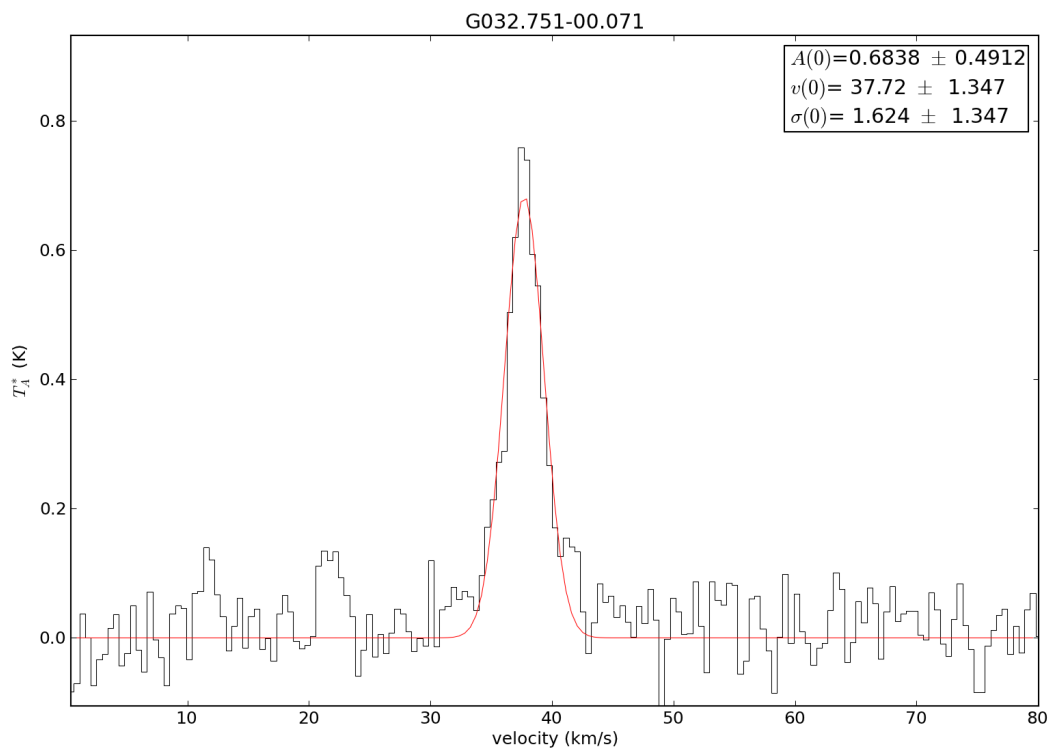


Figure 6.7: The 2-2 transition is used to guess the central velocity and width via gaussian fitting because its hyperfine lines are weaker

6.5 Radio Fitting: NH₃ CUBE example

```
"""
Fit NH3 Cube
=====
```

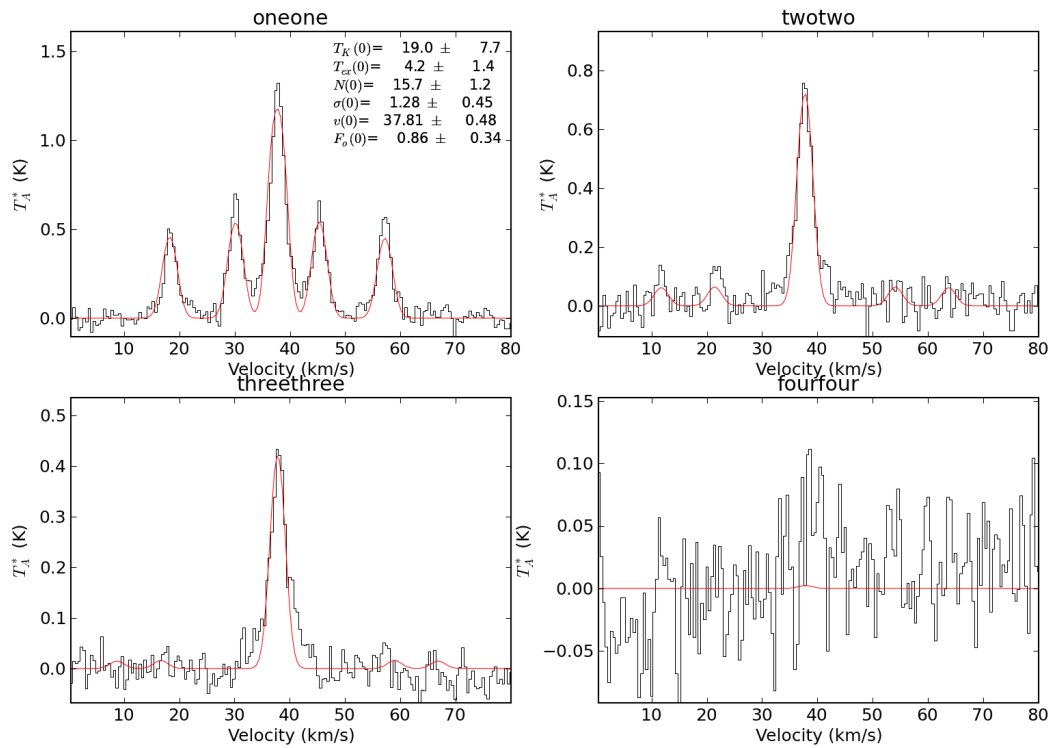


Figure 6.8: Then all 4 lines are simultaneously fit. Even upper limits on the 4-4 line can provide helpful constraints on the model

Example script to fit all pixels in an NH₃ data cube.

This is a bit of a mess, and fairly complicated (intrinsically), but if you have matched 1-1 + 2-2 + ... NH₃ cubes, you should be able to modify this example and get something useful out.

.. WARNING:: Cube fitting, particularly with a complicated line profile ammonia, can take a long time. Test this on a small cube first!

.. TODO:: Turn this example script into a function. But customizing the fit parameters will still require digging into the data manually (e.g., excluding bad velocities, or excluding the hyperfine lines from the initial guess)

"""

```
import pyspeckit
try:
    import astropy.io.fits as pyfits
except ImportError:
    import pyfits
import numpy as np
import os
from astropy.convolution import convolve_fft, Gaussian2DKernel

# set up CASA-like shortcuts
F=False; T=True

# Some optional parameters for the script
# (if False, it will try to load an already-stored version
# of the file)
fitcube = True

# Mask out low S/N pixels (to speed things up)
mask = pyfits.getdata('hotclump_11_mask.fits')
mask = np.isfinite(mask) * (mask > 0)

# Load the data using a mask
# Then calibrate the data (the data we're loading in this case are in Janskys,
# but we want surface brightness in Kelvin for the fitting process)
cube11 = pyspeckit.Cube('hotclump_11.cube_r0.5_rerun.image.fits', maskmap=mask)
cube11.cube *= (13.6 * (300.0 /
    (pyspeckit.spectrum.models.ammonia.freq_dict['oneone']/1e9))**2 *
    1./cube11.header.get('BMAJ')/3600. * 1./cube11.header.get('BMIN')/3600. )
cube11.unit = "K"
cube22 = pyspeckit.Cube('hotclump_22.cube_r0.5_contsub.image.fits', maskmap=mask)
cube22.cube *= (13.6 * (300.0 /
    (pyspeckit.spectrum.models.ammonia.freq_dict['twotwo']/1e9))**2 *
    1./cube22.header.get('BMAJ')/3600. * 1./cube22.header.get('BMIN')/3600. )
cube22.unit = "K"
cube44 = pyspeckit.Cube('hotclump_44.cube_r0.5_contsub.image.fits', maskmap=mask)
cube44.cube *= (13.6 * (300.0 /
    (pyspeckit.spectrum.models.ammonia.freq_dict['fourfour']/1e9))**2 *
    1./cube44.header.get('BMAJ')/3600. * 1./cube44.header.get('BMIN')/3600. )
cube44.unit = "K"

# Compute an error map. We use the 1-1 errors for all 3 because they're
# essentially the same, but you could use a different error map for each
# frequency
oneonemomentfn = 'hotclump_11.cube_r0.5_rerun.image.moment_linefree.fits'
```

```
errmap11 = (pyfits.getdata(oneonemomentfn).squeeze() * 13.6 *
            (300.0 /
             (pyspeckit.spectrum.models.ammonia.freq_dict['oneone']/1e9))**2
            * 1./cube11.header.get('BMAJ')/3600. *
            1./cube11.header.get('BMIN')/3600.)
# Interpolate errors across NaN pixels
errmap11[errmap11 != errmap11] = convolve_fft(errmap11,
                                              Gaussian2DKernel(3),
                                              interpolate_nan=True)[errmap11 != errmap11]

# Stack the cubes into one big cube. The X-axis is no longer linear: there
# will be jumps from 1-1 to 2-2 to 4-4.
cubes = pyspeckit.CubeStack([cube11, cube22, cube44], maskmap=mask)
cubes.unit = "K"

# Make a "moment map" to contain the initial guesses
# If you've already fit the cube, just re-load the saved version
# otherwise, re-fit it
if os.path.exists('hot_momentcube.fits'):
    momentcubefile = pyfits.open('hot_momentcube.fits')
    momentcube = momentcubefile[0].data
else:
    cube11.mapplot()
    # compute the moment at each pixel
    cube11.momenteach()
    momentcube = cube11.momentcube
    momentcubefile = pyfits.PrimaryHDU(data=momentcube, header=cube11.header)
    momentcubefile.writeto('hot_momentcube.fits', clobber=True)

# Create a "guess cube". Because we're fitting physical parameters in this
# case, we want to make the initial guesses somewhat reasonable
# As above, we'll just reload the saved version if it exists
guessfn = 'hot_guesscube.fits'
if os.path.exists(guessfn):
    guesscube = pyfits.open(guessfn)
    guesses = guesscube[0].data
else:
    guesses = np.zeros((6,) + cubes.cube.shape[1:])
    guesses[0, :, :] = 20 # Kinetic temperature
    guesses[1, :, :] = 5 # Excitation Temp
    guesses[2, :, :] = 14.5 # log(column)
    guesses[3, :, :] = momentcube[3, :, :] / 5 # Line width / 5 (the NH3 moment overestimates linewidth)
    guesses[4, :, :] = momentcube[2, :, :] # Line centroid
    guesses[5, :, :] = 0.5 # F(ortho) - ortho NH3 fraction (fixed)

    guesscube = pyfits.PrimaryHDU(data=guesses, header=cube11.header)
    guesscube.writeto(guessfn, clobber=True)

# This bit doesn't need to be in an if statement
if fitcube:
    # excise guesses that fall out of the "good" range
    guesses[4, :, :][guesses[4, :, :] > 100] = 100.0
    guesses[4, :, :][guesses[4, :, :] < 91] = 95

    # do the fits
    # signal_cut means ignore any pixel with peak S/N less than this number
    # In this fit, many of the parameters are limited
    # start_from_point selects the pixel coordinates to start from
```



```

# use_nearest_as_guess says that, at each pixel, the input guesses will be
# set by the fitted parameters from the nearest pixel with a good fit
# HOWEVER, because this fitting is done in parallel (multicore=12 means
# 12 parallel fitting processes will run), this actually means that EACH
# core will have its own sub-set of the cube that it will search for good
# fits. So if you REALLY want consistency, you need to do the fit in serial.
cubes.fiteach(fittype='ammonia', multifit=None, guesses=guesses,
             integral=False, verbose_level=3, fixed=[F,F,F,F,T], signal_cut=3,
             limitedmax=[F,F,F,F,T,T],
             maxpars=[0,0,0,0,101,1],
             limitedmin=[T,T,F,F,T,T],
             minpars=[2.73,2.73,0,0,91,0],
             use_nearest_as_guess=True, start_from_point=(94,250),
             multicore=12,
             errmap=errmap11)

# Save the fitted parameters in a data cube
fitcubefile = pyfits.PrimaryHDU(data=np.concatenate([cubes.parcube,cubes.errcube]), header=cubes.header)
fitcubefile.header.update('PLANE1','TKIN')
fitcubefile.header.update('PLANE2','TEX')
fitcubefile.header.update('PLANE3','COLUMN')
fitcubefile.header.update('PLANE4','SIGMA')
fitcubefile.header.update('PLANE5','VELOCITY')
fitcubefile.header.update('PLANE6','FORTH0')
fitcubefile.header.update('PLANE7','eTKIN')
fitcubefile.header.update('PLANE8','eTEX')
fitcubefile.header.update('PLANE9','eCOLUMN')
fitcubefile.header.update('PLANE10','eSIGMA')
fitcubefile.header.update('PLANE11','eVELOCITY')
fitcubefile.header.update('PLANE12','eFORTH0')
fitcubefile.header.update('CDELTA3',1)
fitcubefile.header.update('CTYPE3','FITPAR')
fitcubefile.header.update('CRVAL3',0)
fitcubefile.header.update('CRPIX3',1)
fitcubefile.writeto("hot_fitcube_try6.fits")
else: # you can read in a fit you've already done!
    cubes.load_model_fit('hot_fitcube_try6.fits', 6, 'ammonia', _temp_fit_loc=(94,250))
    cubes.specfit.parinfo[5]['fixed'] = True

# Now do some plotting things
import pylab as pl

# Set the map-to-plot to be the line centroid
cubes.mapplot.plane = cubes.parcube[4,:,:]
cubes.mapplot(estimator=None,vmin=91,vmax=101)

# Set the reference frequency to be the 1-1 line frequency
cubes.xarr.refX = pyspeckit.spectrum.models.ammonia.freq_dict['oneone']
cubes.xarr.refX_unit='Hz'

# If you wanted to view the spectra in velocity units, use this:
#cubes.xarr.convert_to_unit('km/s')
#cubes.plotter.xmin=55
#cubes.plotter.xmax=135

# Now replace the cube's plotter with a "special" plotter
# The "special" plotter puts the 1-1, 2-2, and 4-4 lines in their own separate

```

```
# windows

cubes.plot_special = pyspeckit.wrappers.fitnh3.plotter_override
cubes.plot_special_kwargs = {'fignum':3, 'vrange':[55,135]}
cubes.plot_spectrum(160,99)

# make interactive
pl.ion()
pl.show()

# At this point, you can click on any pixel in the image and see the spectrum
# with the best-fit ammonia profile overlaid.
```

6.6 Radio fitting: NH3 multiple lines with independent tau, Tex

Example hyperfine line fitting for the NH3 1-1 through 3-3 lines, including making up a synthetic spectrum

```
import numpy as np
import pyspeckit
from astropy import units as u
from pyspeckit.spectrum.models import ammonia_constants, ammonia, ammonia_hf
from pyspeckit.spectrum.models.ammonia_constants import freq_dict
from pyspeckit.spectrum.units import SpectroscopicAxis, SpectroscopicAxes

# Step 1. Generate a synthetic spectrum.  Already have a real spectrum?  Skip
# to step 2!
# Generate a synthetic spectrum based off of 3 NH3 lines
# Note that they are converted to GHz first
xarr11 = SpectroscopicAxis(np.linspace(-30, 30, 100)*u.km/u.s,
                           velocity_convention='radio',
                           refX=freq_dict['oneone']).as_unit(u.GHz)
xarr22 = SpectroscopicAxis(np.linspace(-40, 40, 100)*u.km/u.s,
                           velocity_convention='radio',
                           refX=freq_dict['twotwo']).as_unit(u.GHz)
xarr33 = SpectroscopicAxis(np.linspace(-50, 50, 100)*u.km/u.s,
                           velocity_convention='radio',
                           refX=freq_dict['threethree']).as_unit(u.GHz)
# Merge the three X-axes into a single axis
xarr = SpectroscopicAxes([xarr11,xarr22,xarr33])

# Compute a synthetic model that is made of two temperature components with
# identical velocities
synthspec = (ammonia.ammonia(xarr, tkin=20, ntot=15, fortho=0.5, xoff_v=0.0,
                             width=1.0) +
             ammonia.ammonia(xarr, tkin=50, ntot=14, fortho=0.5, xoff_v=0.0,
                             width=1.0))

# Create the Spectrum object
spectrum = pyspeckit.Spectrum(xarr=xarr, data=synthspec)

# Step 2.  You have a spectrum.
# plot it
spectrum.plotter()

# Use the multi-tex/multi-tau model generator to build up a model function
```

```

# You can use any set of oneone, twotwo, ..., eighteight (no 9-9 or higher)
# This sets the number of parameters to be fit: 2+2*(n_transitions)
fitter = ammonia_hf.nh3_vtau_multimodel_generator(['oneone', 'twotwo',
                                                  'threethree'])

# Register the fitter - i.e., tell pyspeckit where it is and how to use it
spectrum.specfit.Registry.add_fitter('nh3_vtau_123', fitter, fitter.npars)
# These are the parameter names, approximately:
# parnames=['center', 'width', 'Tex11', 'tau11', 'Tex22', 'tau22', 'Tex33', 'tau33'],

# Need to give some input guesses. We start with something wrong-ish: -5 km/s,
# 1.2 km/s width, and 15 K + 0.5 tau for all 3 lines
guesses = [-5, 1.2, 15, 0.5, 15, 0.5, 15, 0.5,]

# Plot up the guessed model
spectrum.plotter.axis.plot(spectrum.xarr,
                          fitter.n_modelfunc(guesses)(spectrum.xarr), 'b')

# Run the fit!
spectrum.specfit(fittype='nh3_vtau_123', guesses=guesses)

# display the correct and fitted answers
print "Low column version:"
print "Real optical depths of component 1: ", [ammonia.ammonia(xarr, tk=20,
                                                             ntot=15,
                                                             forto=0.5,
                                                             xoff_v=0.0,
                                                             width=1.0,
                                                             return_tau=True)[x]
                                                             for x in ['oneone', 'twotwo',
                                                             'threethree']]
print "Real optical depths of component 2: ", [ammonia.ammonia(xarr, tk=50,
                                                             ntot=14,
                                                             forto=0.5,
                                                             xoff_v=0.0,
                                                             width=1.0,
                                                             return_tau=True)[x]
                                                             for x in ['oneone', 'twotwo',
                                                             'threethree']]

print "Fitted parameters: ", spectrum.specfit.parinfo

# It works, but the covariances between tex and tau are large.
# So, another example with higher tau (and therefore... less degenerate?)

synthspec = (ammonia.ammonia(xarr, tk=20, ntot=16, forto=0.5, xoff_v=0.0,
                             width=1.0) +
             ammonia.ammonia(xarr, tk=50, ntot=15, forto=0.5, xoff_v=0.0,
                             width=1.0))

spectrum2 = pyspeckit.Spectrum(xarr=xarr, data=synthspec)
spectrum2.plotter()
spectrum2.specfit.Registry.add_fitter('nh3_vtau_123', fitter, fitter.npars)
spectrum2.specfit(fittype='nh3_vtau_123', guesses=guesses)

# We can also examine what tau really should have been... kinda.
print "High column version:"
print "Real optical depths of component 1: ", [ammonia.ammonia(xarr, tk=20,
                                                             ntot=16,
                                                             forto=0.5,

```

```
        xoff_v=0.0,
        width=1.0,
        return_tau=True)[x]
    for x in ['oneone', 'twotwo',
              'threethree']]
print "Real optical depths of component 2: ",[ammonia.ammonia(xarr, tkin=50,
        ntot=15,
        fortho=0.5,
        xoff_v=0.0,
        width=1.0,
        return_tau=True)[x]
    for x in ['oneone', 'twotwo',
              'threethree']]
print "Fitted parameters: ",spectrum2.specfit.parinfo
```

6.7 Radio Fitting: N₂H⁺ example

Example hyperfine line fitting for the N₂H⁺ 1-0 line.

```
import pyspeckit

# Load the spectrum
sp = pyspeckit.Spectrum('n2hp_opha_example.fits')

# Register the fitter
# The N2H+ fitter is 'built-in' but is not registered by default; this example
# shows how to register a fitting procedure
# 'multi' indicates that it is possible to fit multiple components and a
# background will not automatically be fit
# 4 is the number of parameters in the model (excitation temperature,
# optical depth, line center, and line width)
sp.Registry.add_fitter('n2hp_vtau', pyspeckit.models.n2hp.n2hp_vtau_fitter,4)

# Run the fitter
sp.specfit(fittype='n2hp_vtau',guesses=[15,2,4,0.2])

# Plot the results
sp.plotter()
# Re-run the fitter (to get proper error bars) and show the individual fit components
sp.specfit(fittype='n2hp_vtau', guesses=[15,2,4,0.2], show_hyperfine_components=True)

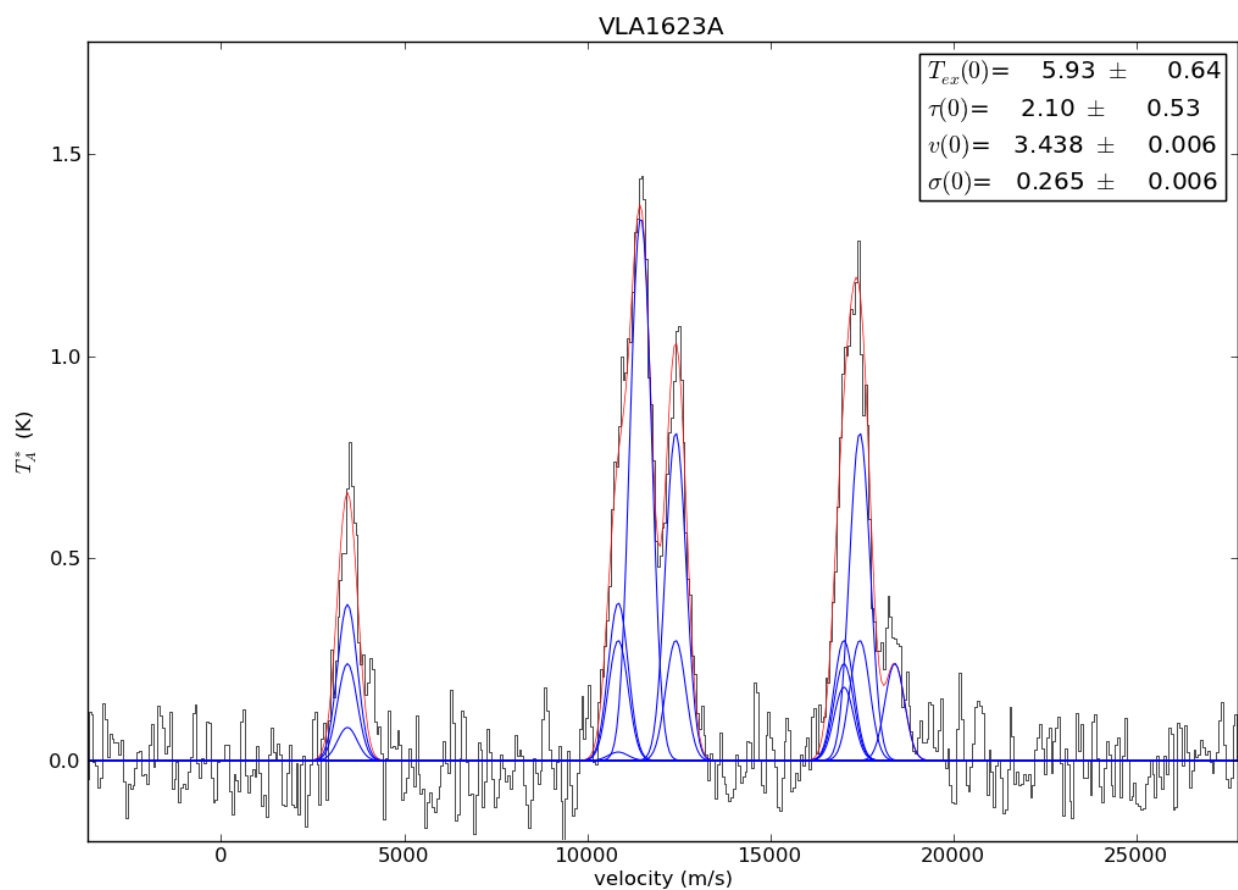
# Save the figure (this step is just so that an image can be included on the web page)
sp.plotter.savefig('n2hp_ophA_fit.png')
```

6.8 Radio Fitting: N₂H⁺ cube example

Example hyperfine line fitting of a data cube for the N₂H⁺ 1-0 line.

```
import pyspeckit
import os

if not os.path.exists('n2hp_cube.fit'):
    import astropy.utils.data as aud
    from astropy.io import fits
```



```
f = aud.download_file('ftp://cdsarc.u-strasbg.fr/pub/cats/J/A%2BA/472/519/fits/opha_n2h.fit')
with fits.open(f) as ff:
    ff[0].header['CUNIT3'] = 'm/s'
    for kw in ['CTYPE4', 'CRVAL4', 'CDELTA4', 'CRPIX4']:
        del ff[0].header[kw]
    ff.writeto('n2hp_cube.fit')

# Load the spectral cube
spc = pyspeckit.Cube('n2hp_cube.fit')

# Register the fitter
# The N2H+ fitter is 'built-in' but is not registered by default; this example
# shows how to register a fitting procedure
# 'multi' indicates that it is possible to fit multiple components and a
# background will not automatically be fit 4 is the number of parameters in the
# model (excitation temperature, optical depth, line center, and line width)
spc.Registry.add_fitter('n2hp_vtau', pyspeckit.models.n2hp.n2hp_vtau_fitter, 4)

# Get a measurement of the error per pixel
errmap = spc.slice(20, 28, unit='km/s').cube.std(axis=0)

# A good way to write a cube fitter is to have it load from disk if the cube
# fit was completed successfully in the past
if os.path.exists('n2hp_fitted_parameters.fits'):
    spc.load_model_fit('n2hp_fitted_parameters.fits', npars=4, npeaks=1)
else:
    # Run the fitter
    # Estimated time to completion ~ 2 minutes
    spc.fiteach(fittype='n2hp_vtau', multifit=True,
               guesses=[5, 0.5, 3, 1], # Tex=5K, tau=0.5, v_center=12, width=1 km/s
               signal_cut=6, # minimize the # of pixels fit for the example
               start_from_point=(16, 13), # start at a pixel with signal
               errmap=errmap,
               )
    # There are a huge number of parameters for the fiteach procedure. See:
    # http://pyspeckit.readthedocs.org/en/latest/example_nh3_cube.html
    # http://pyspeckit.readthedocs.org/en/latest/cubes.html?highlight=fiteach#pyspeckit.cubes.SpectralCube.Cube.fiteach
    #
# Unfortunately, a complete tutorial on this stuff is on the to-do list;
# right now the use of many of these parameters is at a research level.
# However, pyspeckit@gmail.com will support them! They are being used
# in current and pending publications

# Save the fitted parameters to a FITS file, and overwrite one if one exists
spc.write_fit('n2hp_fitted_parameters.fits', clobber=True)

# Show an integrated image
spc.mapplot()
# you can click on any pixel to see its spectrum & fit

# plot one of the fitted spectra
spc.plot_spectrum(14, 27, plot_fit=True)
# spc.parcube[:, 27, 14] = [ 14.82569198,  1.77055642,  3.15740051,  0.16035407]
# Note that the optical depth is the "total" optical depth, which is
# distributed among 15 hyperfine components. You can see this in
# pyspeckit.spectrum.models.n2hp.line_strength_dict
# As a sanity check, you can see that the brightest line has 0.259 of the total
# optical depth, so the peak line brightness is:
```

```
# (14.825-2.73) * (1-np.exp(-1.77 * 0.259)) = 4.45
# which matches the peak of 4.67 pretty well

# Show an image of the best-fit velocity
spc.mapplot.plane = spc.parcube[2,:,:]
spc.mapplot(estimator=None)

# running in script mode, the figures won't show by default on some systems
import pylab as pl
# pl.draw()
# pl.show()
```

6.9 Radio Fitting: HCN example with freely varying hyperfine amplitudes

Example hyperfine line fitting for the HCN 1-0 line.

```
import pyspeckit
import pylab as pl
import astropy.units as u

# Load the spectrum & properly identify the units
# The data is from http://adsabs.harvard.edu/abs/1999A%26A...348..600P
sp = pyspeckit.Spectrum('02232_plus_6138.txt')
sp.xarr.set_unit(u.km/u.s)
sp.xarr.refX = 88.63184666e9 * u.Hz
sp.xarr.velocity_convention = 'radio'
sp.xarr.xtype='velocity'
sp.unit='$T_A^{*}$'

# set the error array based on a signal-free part of the spectrum
sp.error[:] = sp.stats((-35,-25))['std']
# Register the fitter
# The HCN fitter is 'built-in' but is not registered by default; this example
# shows how to register a fitting procedure
# 'multi' indicates that it is possible to fit multiple components and a
# background will not automatically be fit
# 5 is the number of parameters in the model (line center,
# line width, and amplitude for the 0-1, 2-1, and 1-1 lines)
sp.Registry.add_fitter('hcn_varyhf', pyspeckit.models.hcn.hcn_varyhf_amp_fitter, 5)

# This one is the same, but with fixed relative amplitude hyperfine components
sp.Registry.add_fitter('hcn_fixedhf', pyspeckit.models.hcn.hcn_amp, 3)

# Plot the results
sp.plotter()
# Run the fixed-amplitude fitter and show the individual fit components
sp.specfit(fittype='hcn_fixedhf',
           multifit=None,
           guesses=[1,-48,0.6],
           show_hyperfine_components=True)
# Now plot the residuals offset below the original
sp.specfit.plotresiduals(axis=sp.plotter.axis, clear=False, yoffset=-1, color='g', label=False)
sp.plotter.reset_limits(ymin=-2)
```

```
# Save the figure (this step is just so that an image can be included on the web page)
sp.plotter.savefig('hcn_fixedhf_fit.png')

# Run the variable-amplitude fitter and show the individual fit components
# Note the different order of the arguments (velocity, width, then three amplitudes)
sp.specfit(fittype='hcn_varyhf',
           multifit=None,
           guesses=[-48,1,0.2,0.6,0.3],
           show_hyperfine_components=True,
           clear=True)

# Again plot the residuals
sp.specfit.plotresiduals(axis=sp.plotter.axis,clear=False,yoffset=-1,color='g',label=False)
sp.plotter.reset_limits(ymin=-2)

# Save the figure
sp.plotter.savefig('hcn_freehf_fit.png')

# now do the same thing, but allow the widths to vary too
# there are 7 parameters:
# 1. the centroid
# 2,3,4 - the amplitudes of the 0-1, 2-1, and 1-1 lines
# 5,6,7 - the widths of the 0-1, 2-1, and 1-1 lines
sp.Registry.add_fitter('hcn_varyhf_width',pyspeckit.models.hcn.hcn_varyhf_amp_width_fitter,7)

# Run the fitter
sp.specfit(fittype='hcn_varyhf_width',
           multifit=None,
           guesses=[-48,0.2,0.6,0.3,1,1,1],
           show_hyperfine_components=True,
           clear=True)

# print the fitted parameters:
print sp.specfit.parinfo
# Param #0      CENTER0 =      -51.865 +/-      0.0525058
# Param #1      AMP10-010 =      1.83238 +/-      0.0773993   Range:  [0,inf)
# Param #2      AMP12-010 =      5.26566 +/-      0.0835981   Range:  [0,inf)
# Param #3      AMP11-010 =      3.02621 +/-      0.0909095   Range:  [0,inf)
# Param #4      WIDTH10-010 =      2.16711 +/-      0.118651   Range:  [0,inf)
# Param #5      WIDTH12-010 =      1.90987 +/-      0.0476163   Range:  [0,inf)
# Param #6      WIDTH11-010 =      1.64409 +/-      0.076998   Range:  [0,inf)

sp.specfit.plotresiduals(axis=sp.plotter.axis,clear=False,yoffset=-1,color='g',label=False)
sp.plotter.reset_limits(ymin=-2)

# Save the figure (this step is just so that an image can be included on the web page)
sp.plotter.savefig('hcn_freehf_ampandwidth_fit.png')

# Finally, how well does a 2-component fit work?
sp.specfit(fittype='hcn_fixedhf',
           multifit=None,
           guesses=[1,-48,0.6,0.1,-46,0.6],
           show_hyperfine_components=True,
           clear=True)
sp.specfit.plotresiduals(axis=sp.plotter.axis,clear=False,yoffset=-1,color='g',label=False)
sp.plotter.reset_limits(ymin=-2)
```



```
# Save the figure (this step is just so that an image can be included on the web page)
sp.plotter.savefig('hcn_fixedhf_fit_2components.png')
```

The green lines in the following figures all show the residuals to the fit

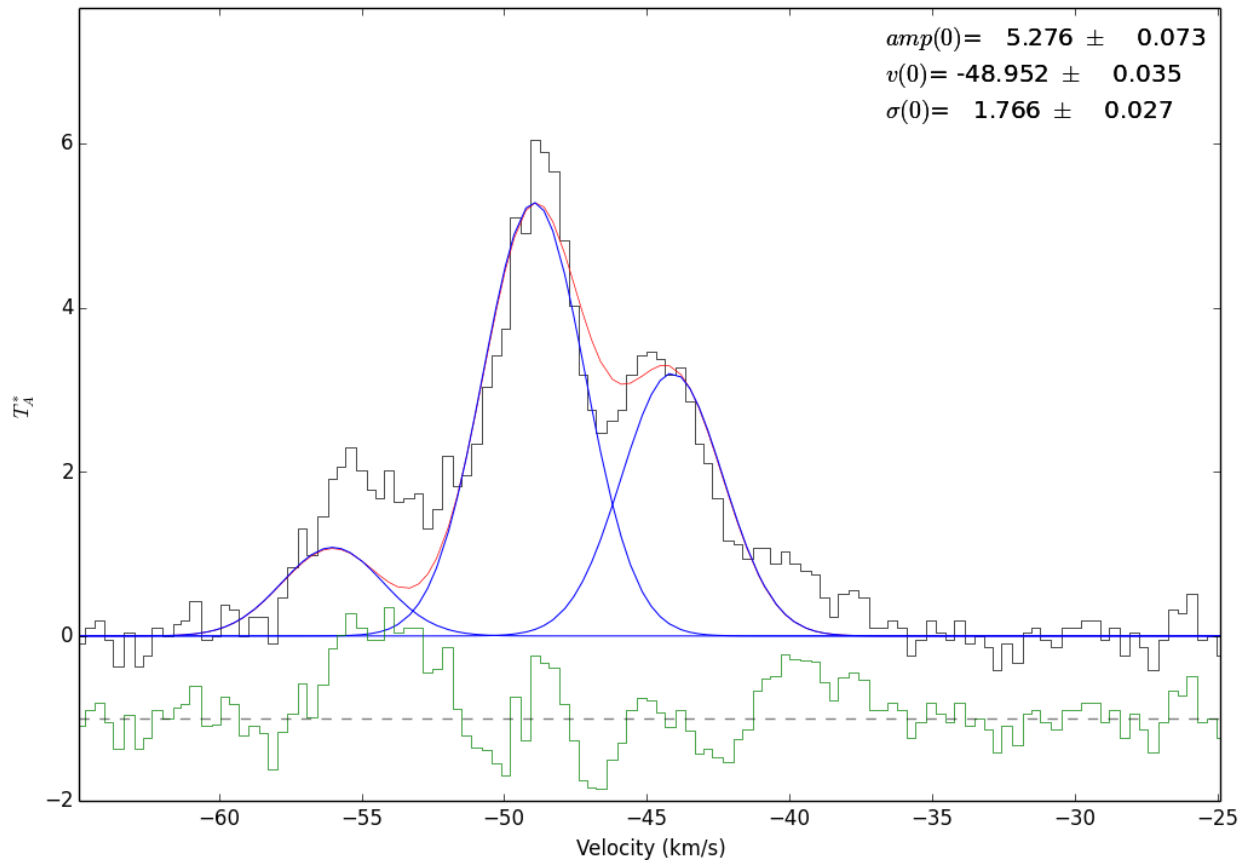


Figure 6.9: Fit to the 3 hyperfine components of HCN 1-0 simultaneously with fixed amplitudes. The (0)'s indicate that this is the 0'th velocity component being fit (though that velocity corresponds to the 12-01 component of the line)

6.10 Simple Radio Fitting: HCO+ example

```
import pyspeckit
```

```
# load a FITS-compliant spectrum
spec = pyspeckit.Spectrum('10074-190_HCOp.fits')
# The units are originally frequency (check this by printing spec.xarr.units).
# I want to know the velocity. Convert!
# Note that this only works because the reference frequency is set in the header
spec.xarr.frequency_to_velocity()
# Default conversion is to m/s, but we traditionally work in km/s
spec.xarr.convert_to_unit('km/s')
# plot it up!
spec.plotter()
# Subtract a baseline (the data is only 'mostly' reduced)
```

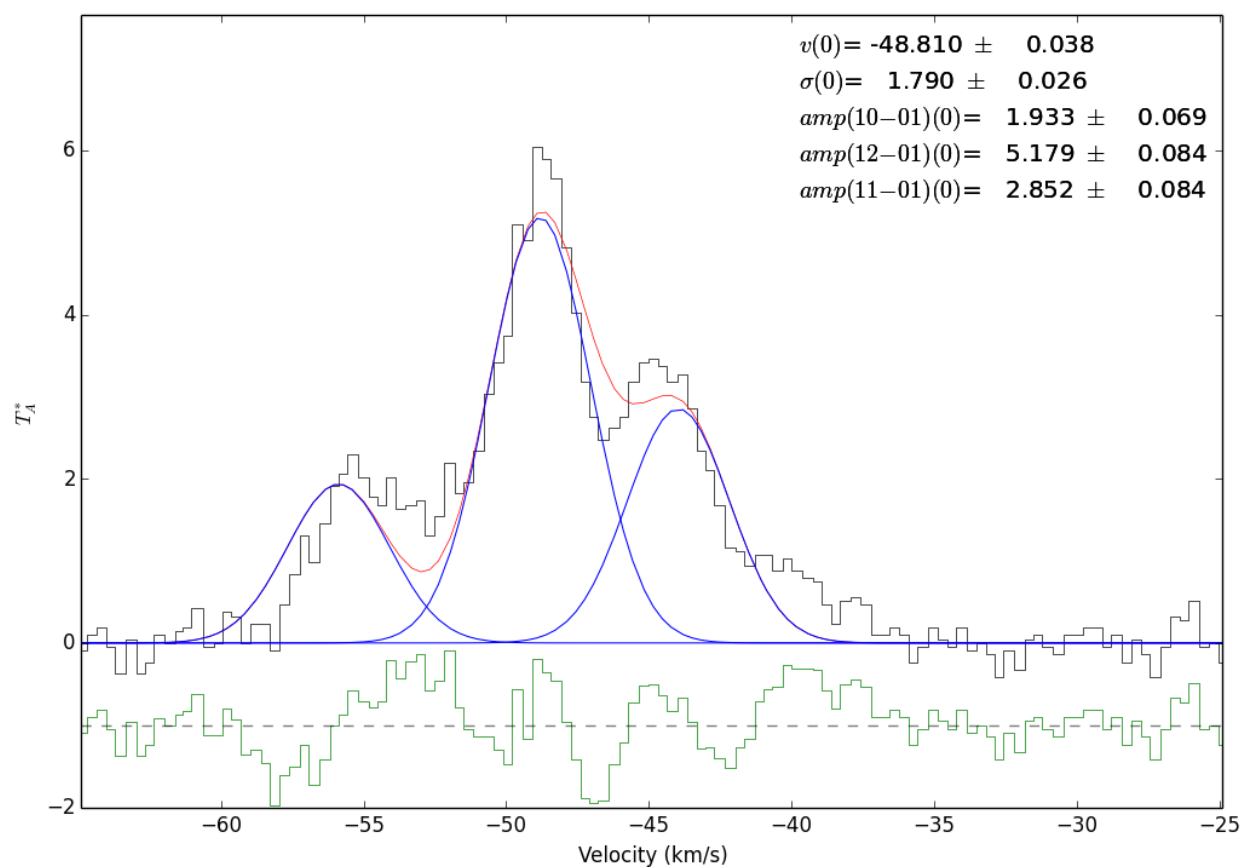


Figure 6.10: Fit to the 3 hyperfine components of HCN 1-0 simultaneously with freely varying amplitudes. The (0)'s indicate that this is the 0'th velocity component being fit

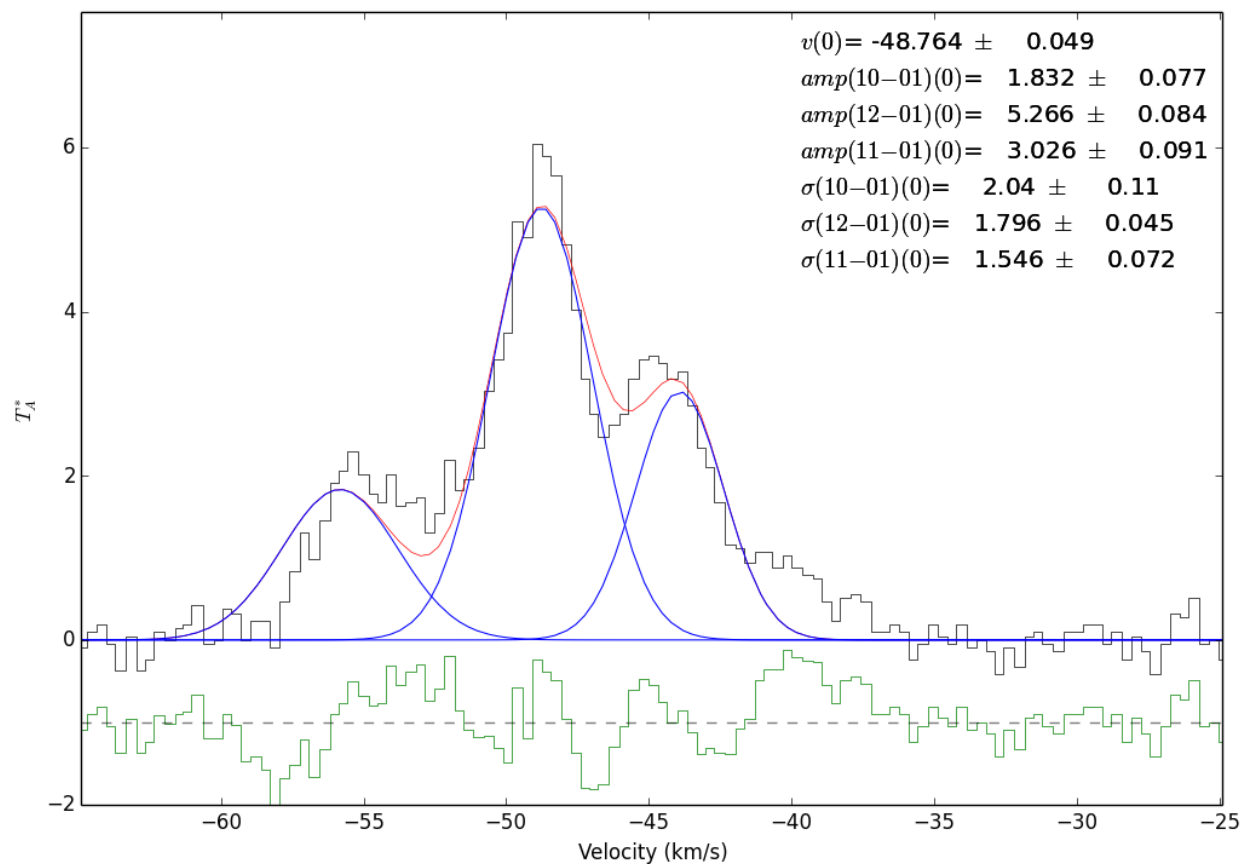


Figure 6.11: Fit to the 3 hyperfine components of HCN 1-0 simultaneously. The widths are allowed to vary in this example.

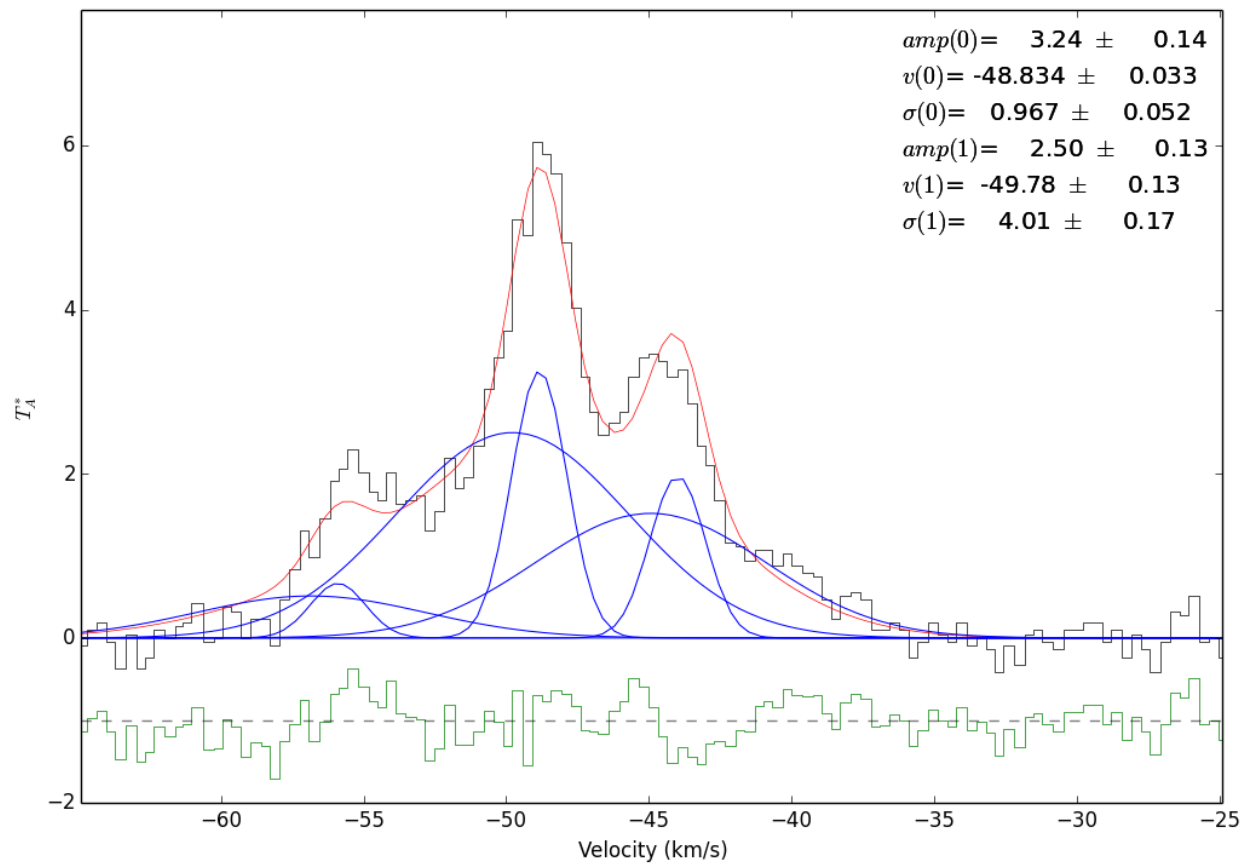


Figure 6.12: A two-component fit to the same spectrum. It appears to be a much better fit, hinting that there are indeed two components (though the fit is probably not unique)

```

spec.baseline()
# Fit a gaussian. We know it will be an emission line, so we force a positive guess
spec.specfit(negamp=False)
# Note that the errors on the fits are larger than the fitted parameters.
# That's because this spectrum did not have an error assigned to it.
# Let's use the residuals:
spec.specfit.plotresiduals()
# Now, refit with error determined from the residuals:
# (we pass in guesses to save time / make sure nothing changes)
spec.specfit(guesses=spec.specfit.modelpars)

# Save the figures to put on the web...
spec.plotter.figure.savefig("simple_fit_example_HCOp.png")
spec.specfit.residualaxis.figure.savefig("simple_fit_example_HCOp_residuals.png")

# Also, let's crop out stuff we don't want...
spec.crop(-100,100)
# replot after cropping (crop doesn't auto-refresh)
spec.plotter()
# replot the fit without re-fitting
spec.specfit.plot_fit()
# show the annotations again
spec.specfit.annotate()
spec.plotter.figure.savefig("simple_fit_example_HCOp_cropped.png")

```

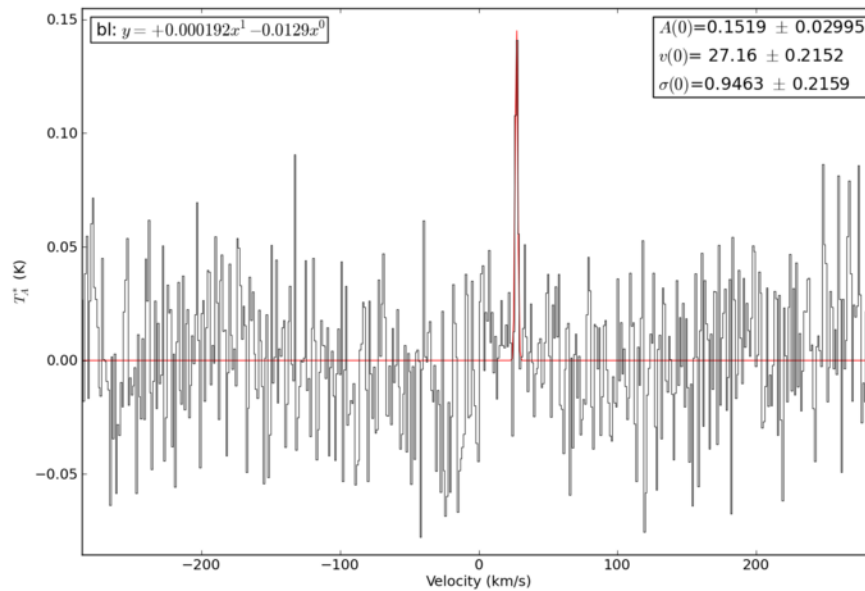


Figure 6.13: Sample HCO+ spectrum fitted with a gaussian

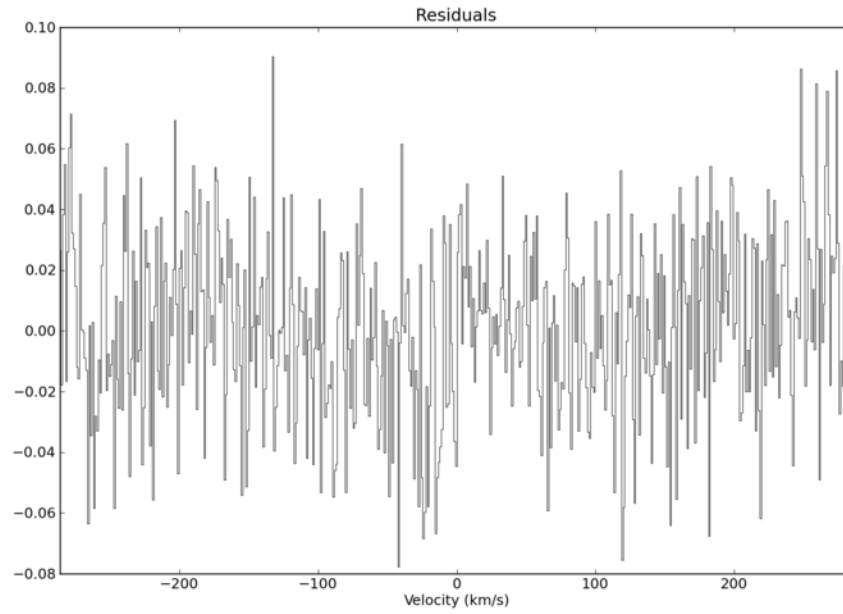


Figure 6.14: Residuals of the gaussian fit from the previous figure

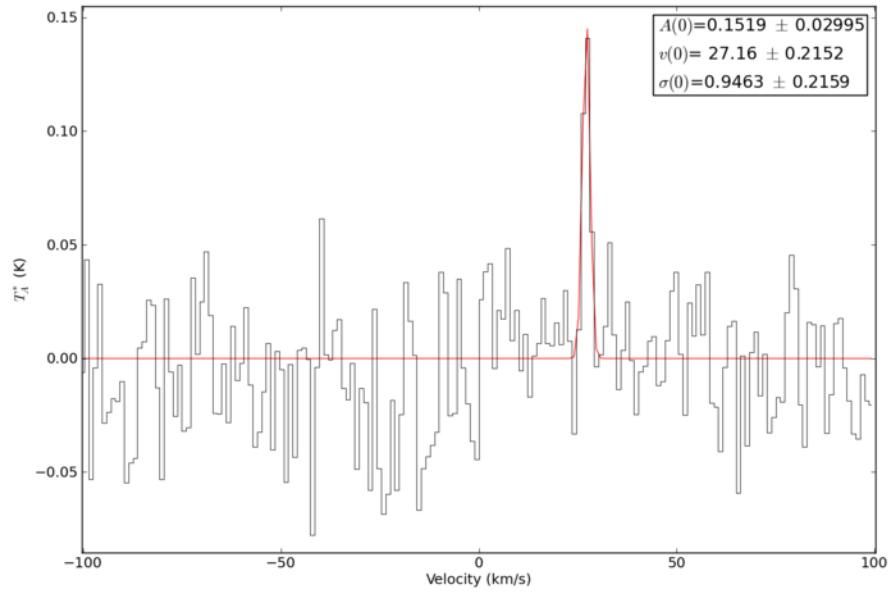


Figure 6.15: A zoomed-in, cropped version of the spectrum. With the ‘crop’ command, the excess data is discarded.

6.11 Optical fitting: The $H\alpha$ -[NII] complex of a type-I Seyfert galaxy

```
import pyspeckit

# Rest wavelengths of the lines we are fitting - use as initial guesses
NIIa = 6549.86
NIIb = 6585.27
Halpha = 6564.614
SIIa = 6718.29
SIIb = 6732.68

# Initialize spectrum object and plot region surrounding Halpha-[NII] complex
spec = pyspeckit.Spectrum('sample_sdss.txt', errorcol=2)
spec.plotter(xmin = 6450, xmax = 6775, ymin = 0, ymax = 150)

# We fit the [NII] and [SII] doublets, and allow two components for Halpha.
# The widths of all narrow lines are tied to the widths of [SII].
guesses = [50, NIIa, 5, 100, Halpha, 5, 50, Halpha, 50, 50, NIIb, 5, 20, SIIa, 5, 20, SIIb, 5]
tied = ['', '', 'p[17]', '', '', 'p[17]', '', 'p[4]', '', '3 * p[0]', '', 'p[17]', '', '', 'p[17]', '', '', '']

# Actually do the fit.
spec.specfit(guesses = guesses, tied = tied, annotate = False)
spec.plotter.refresh()

# Let's use the measurements class to derive information about the emission
# lines. The galaxy's redshift and the flux normalization of the spectrum
# must be supplied to convert measured fluxes to line luminosities. If the
# spectrum we loaded in FITS format, 'BUNITS' would be read and we would not
# need to supply 'fluxnorm'.
spec.measure(z = 0.05, fluxnorm = 1e-17)

# Now overplot positions of lines and annotate

y = spec.plotter.ymax * 0.85 # Location of annotations in y

for i, line in enumerate(spec.measurements.lines.keys()):

    # If this line is not in our database of lines, don't try to annotate it
    if line not in spec.speclines.optical.lines.keys(): continue

    x = spec.measurements.lines[line]['modelpars'][1] # Location of the emission line
    spec.plotter.axis.plot([x]*2, [spec.plotter.ymin, spec.plotter.ymax], ls = '--', color = 'k') # Draw dashed line to
    spec.plotter.axis.annotate(spec.speclines.optical.lines[line][-1], (x, y), rotation = 90, ha = 'right', va = 'center')

# Make some nice axis labels
spec.plotter.axis.set_xlabel(r'Wavelength $(\AA)$')
spec.plotter.axis.set_ylabel(r'Flux $(10^{-17} \text{ erg/s/cm}^2/\AA)$')
spec.plotter.refresh()

# Print out spectral line information
print "Line   Flux (erg/s/cm^2)   Amplitude (erg/s/cm^2)   FWHM (Angstrom)   Luminosity (erg/s)"
for line in spec.measurements.lines.keys():
    print line, spec.measurements.lines[line]['flux'], spec.measurements.lines[line]['amp'], spec.measurements.lines[line]['lum']

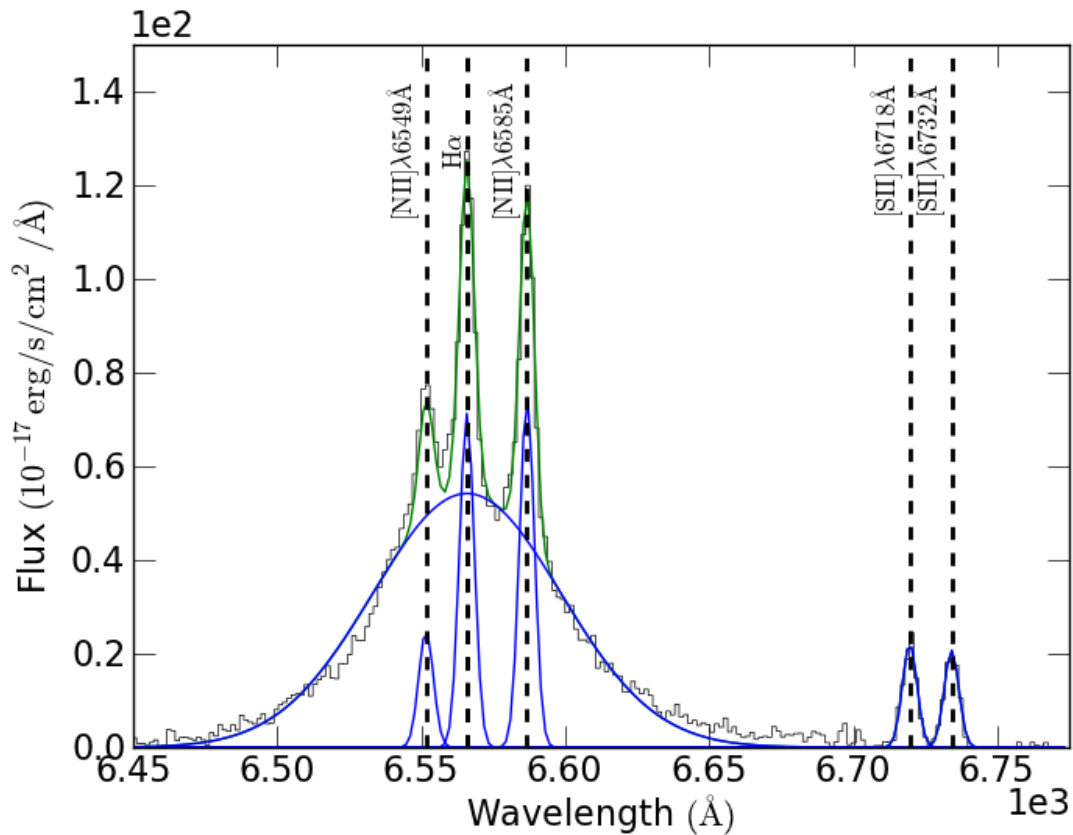
# Had we not supplied the objects redshift (or distance), the line
# luminosities would not have been measured, but integrated fluxes would
# still be derived. Also, the measurements class separates the broad and
```

```
# narrow H-alpha components, and identifies which lines are which. How nice!
```

```
spec.specfit.plot_fit()
```

```
# Save the figure
```

```
spec.plotter.figure.savefig("sdss_fit_example.png")
```



6.12 Optical Plotting - Echelle spectrum of Vega (in color!)

```
import pyspeckit
from pylab import *
import wav2rgb
```

```
speclist = pyspeckit.wrappers.load_IRAF_multispec('evega.0039.rs.ec.dispcor.fits')
```

```
for spec in speclist:
    spec.units="Counts"
```

```
SP = pyspeckit.Spectra(speclist)
```

```
SPa = pyspeckit.Spectra(speclist,xunits='angstroms',quiet=False)
```

```
SP.plotter(figure=figure(1))
```



```

SPa.plotter(figure=figure(2))

figure(3)
clf()
figure(4)
clf()

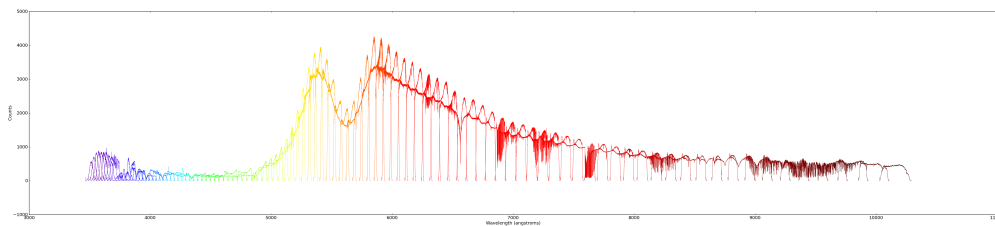
#clr = [list(clr) for clr in matplotlib.cm.brg(linspace(0,1,len(speclist)))]
clr = [wav2rgb.wav2RGB(c) + [1.0] for c in linspace(380,780,len(speclist))][::-1]
for ii,(color,spec) in enumerate(zip(clr,speclist)):
    spec.plotter(figure=figure(3), clear=False, reset=False, color=color, refresh=False)

    fig4=figure(4)
    fig4.subplots_adjust(hspace=0.35,top=0.97,bottom=0.03)
    spec.plotter(axis=subplot(10,1,ii%10+1), clear=False, reset=False, color=color, refresh=False)
    spec.plotter.axis.yaxis.set_major_locator( matplotlib.ticker.MaxNLocator(4) )

    if ii % 10 == 9:
        spec.plotter.refresh()
        spec.plotter.savefig('vega_subplots_%03i.png' % (ii/10+1))
        clf()

spec.plotter.refresh()

```



6.13 A guide to interactive fitting

A step-by-step example of how to use the interactive fitter.

In short, we will do the following:

```

# 1. Load the spectrum
sp = pyspeckit.Spectrum('hr2421.fit')

# 2. Plot a particular spectral line
sp.plotter(xmin=4700,xmax=5000)

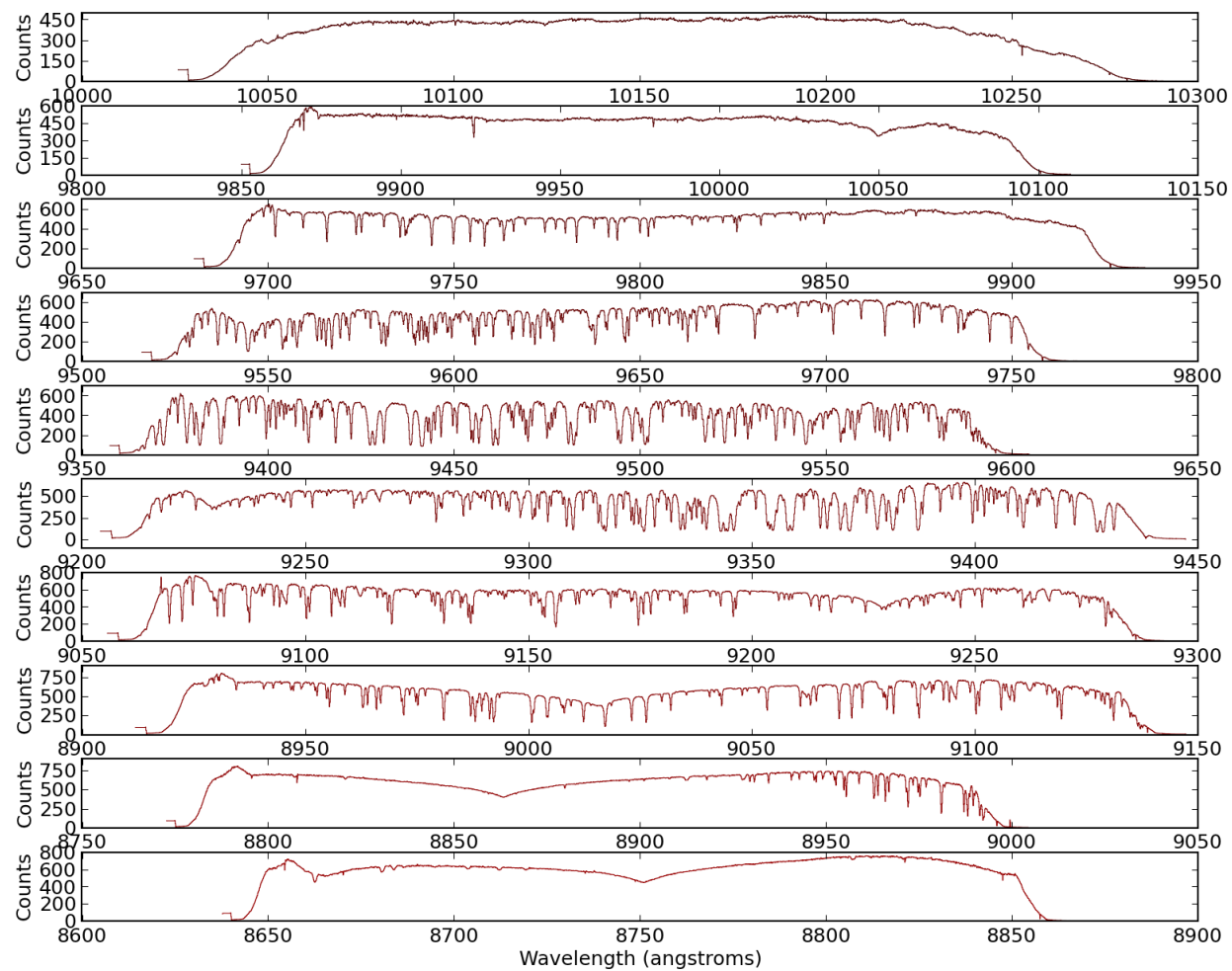
# 3. Need to fit the continuum first
sp.baseline(interactive=True, subtract=False)

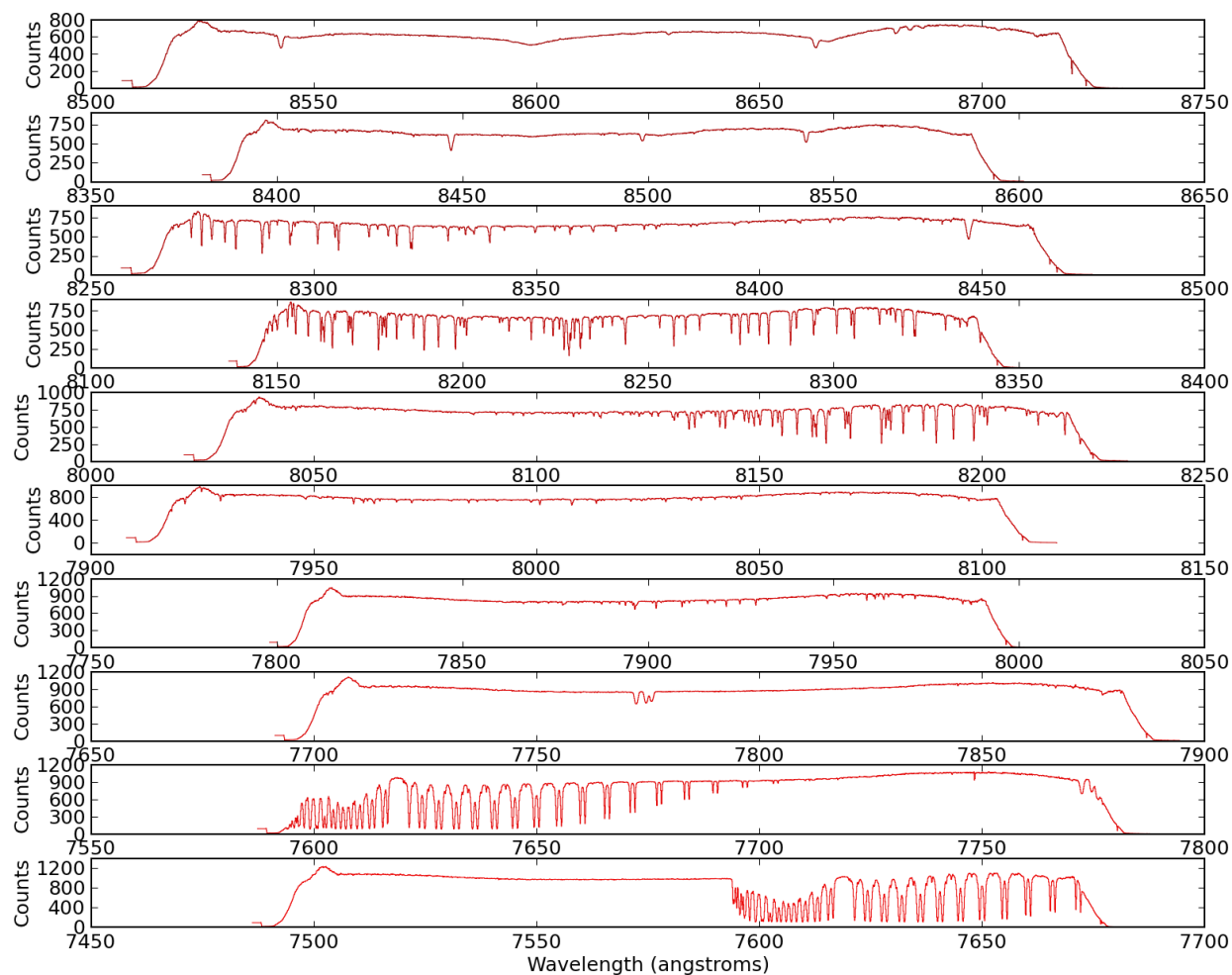
# 4... (much work takes place interactively at this stage)

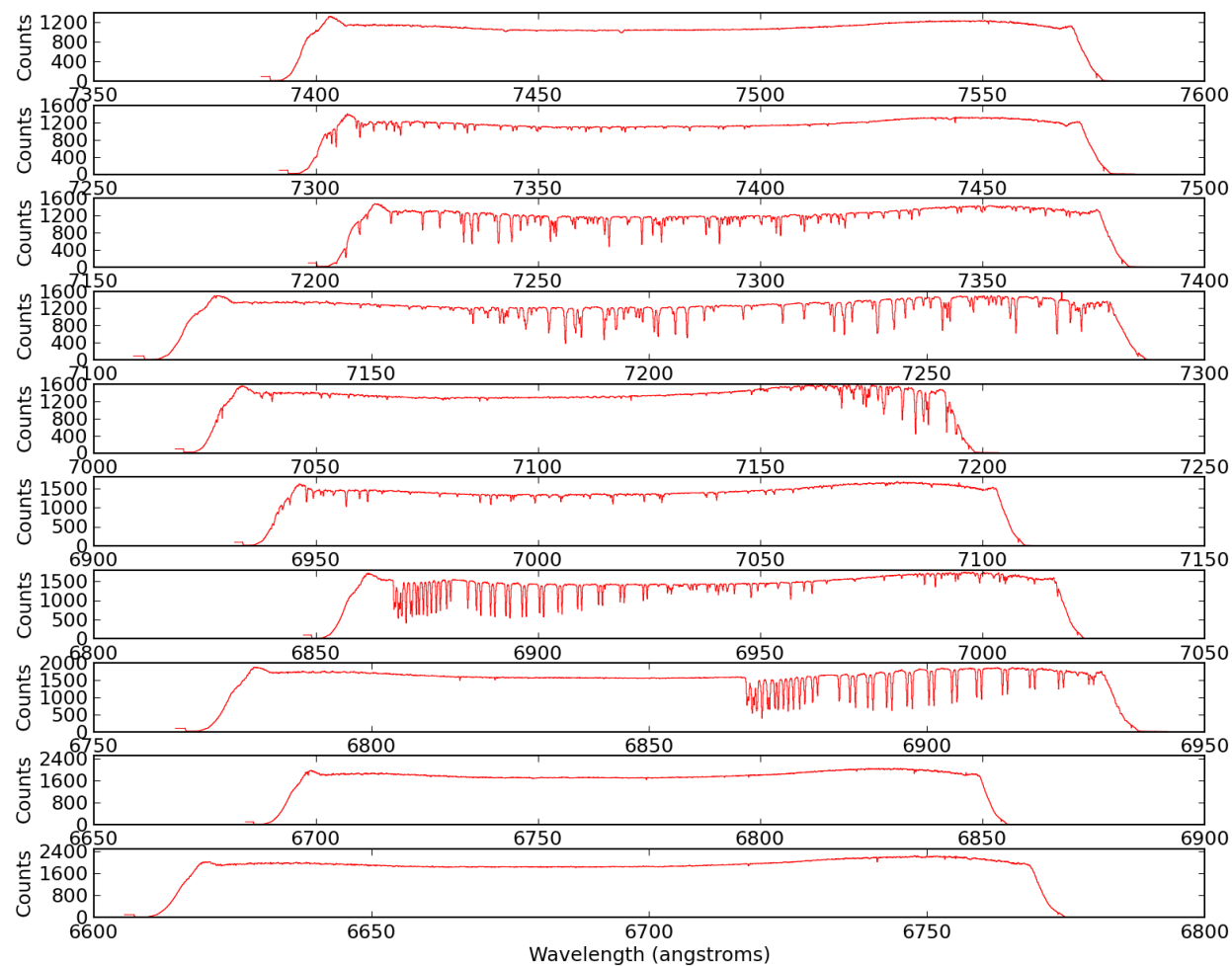
# 5. Start up an interactive line-fitting session
sp.specfit(interactive=True)

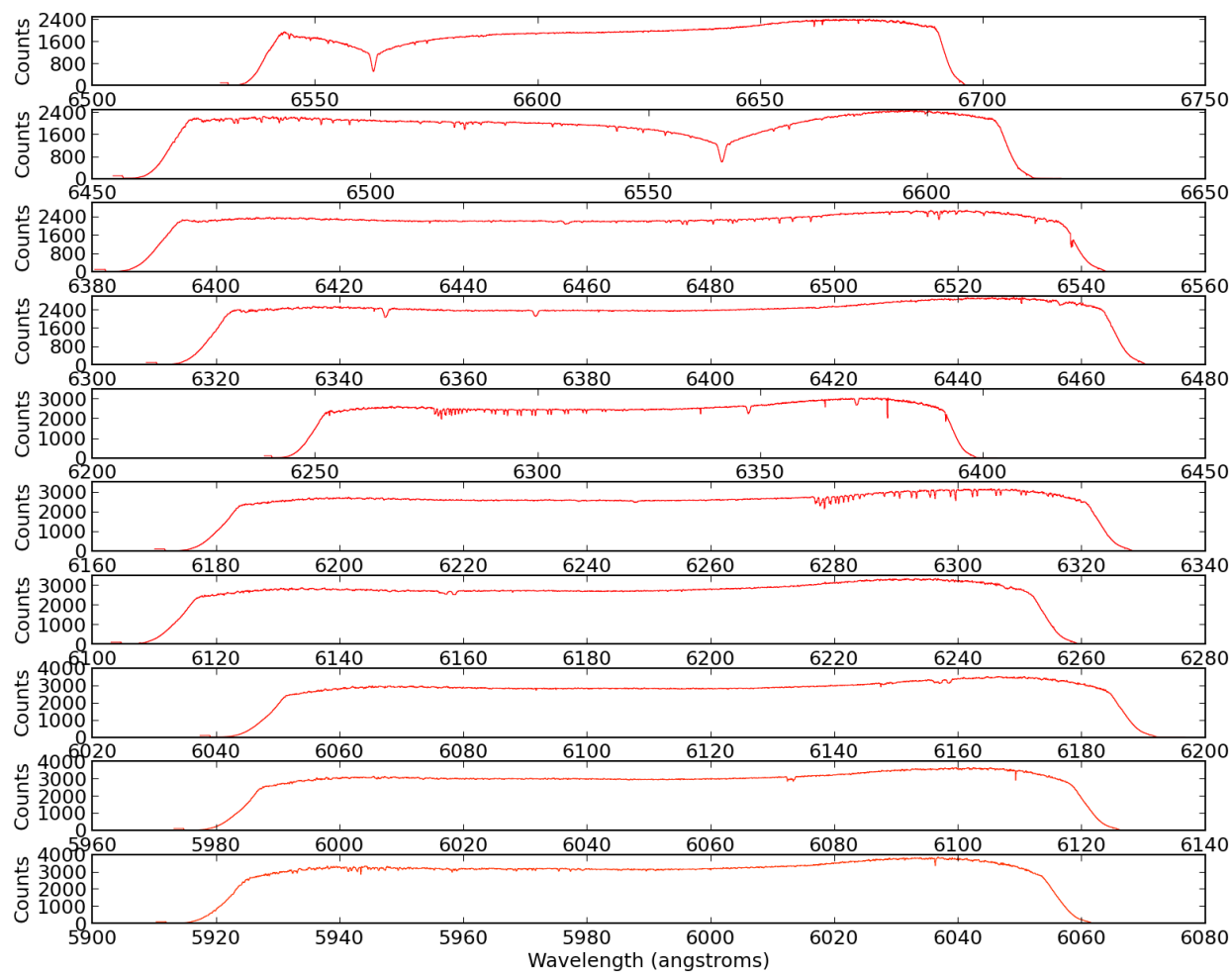
```

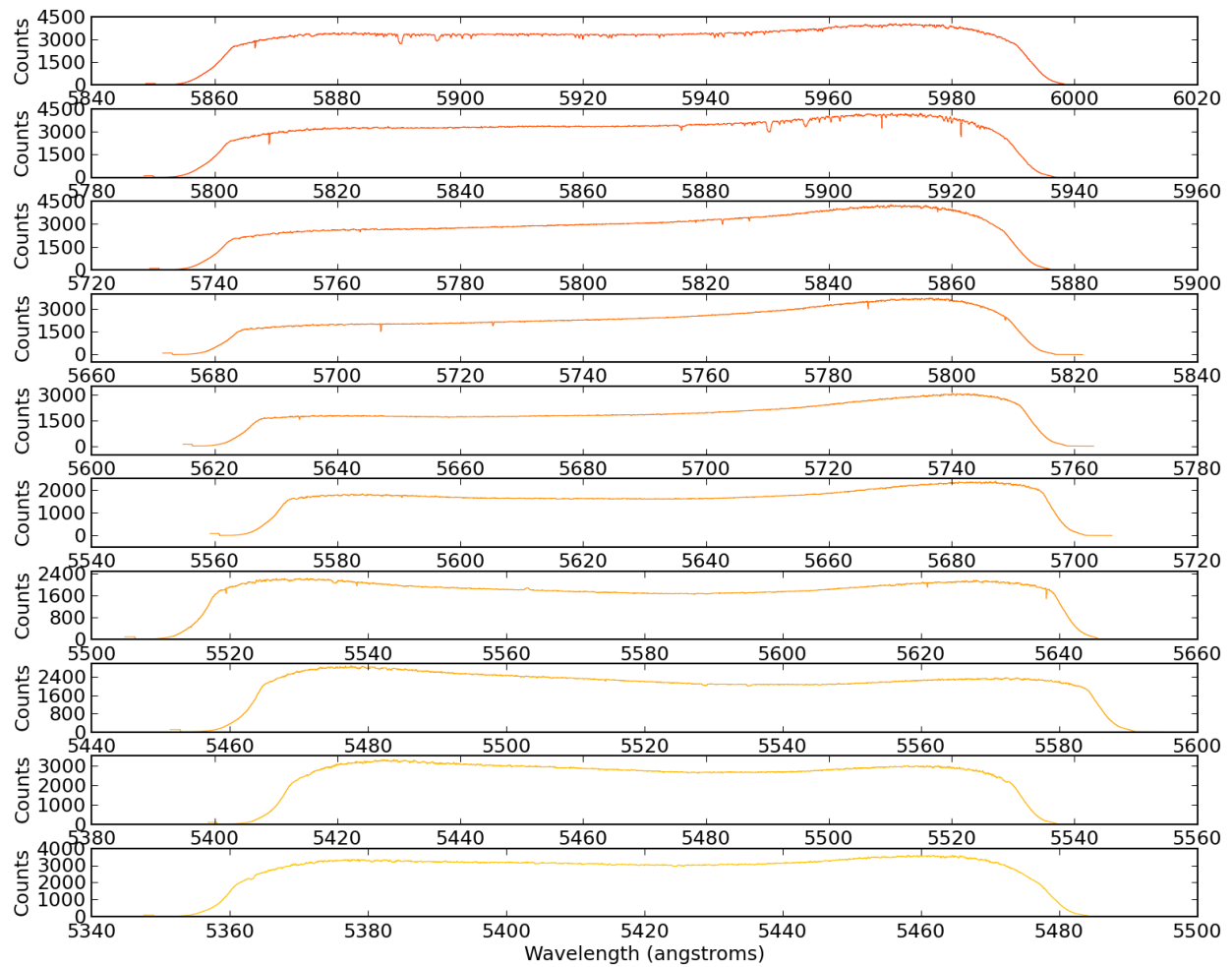
Note: If you don't see a plot window after step #2 above, make sure you're using matplotlib in interactive mode. This may require starting ipython as `ipython --pylab`

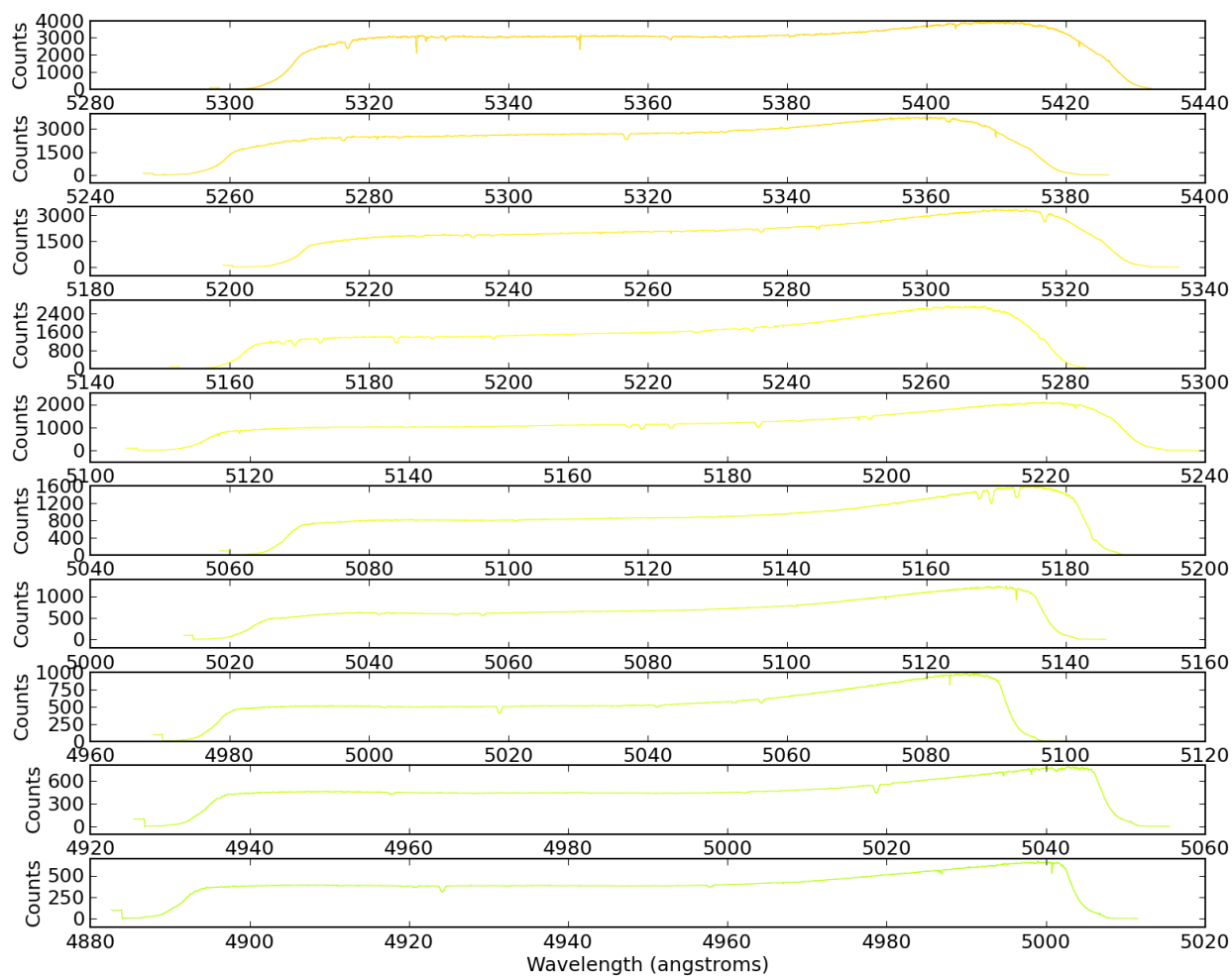


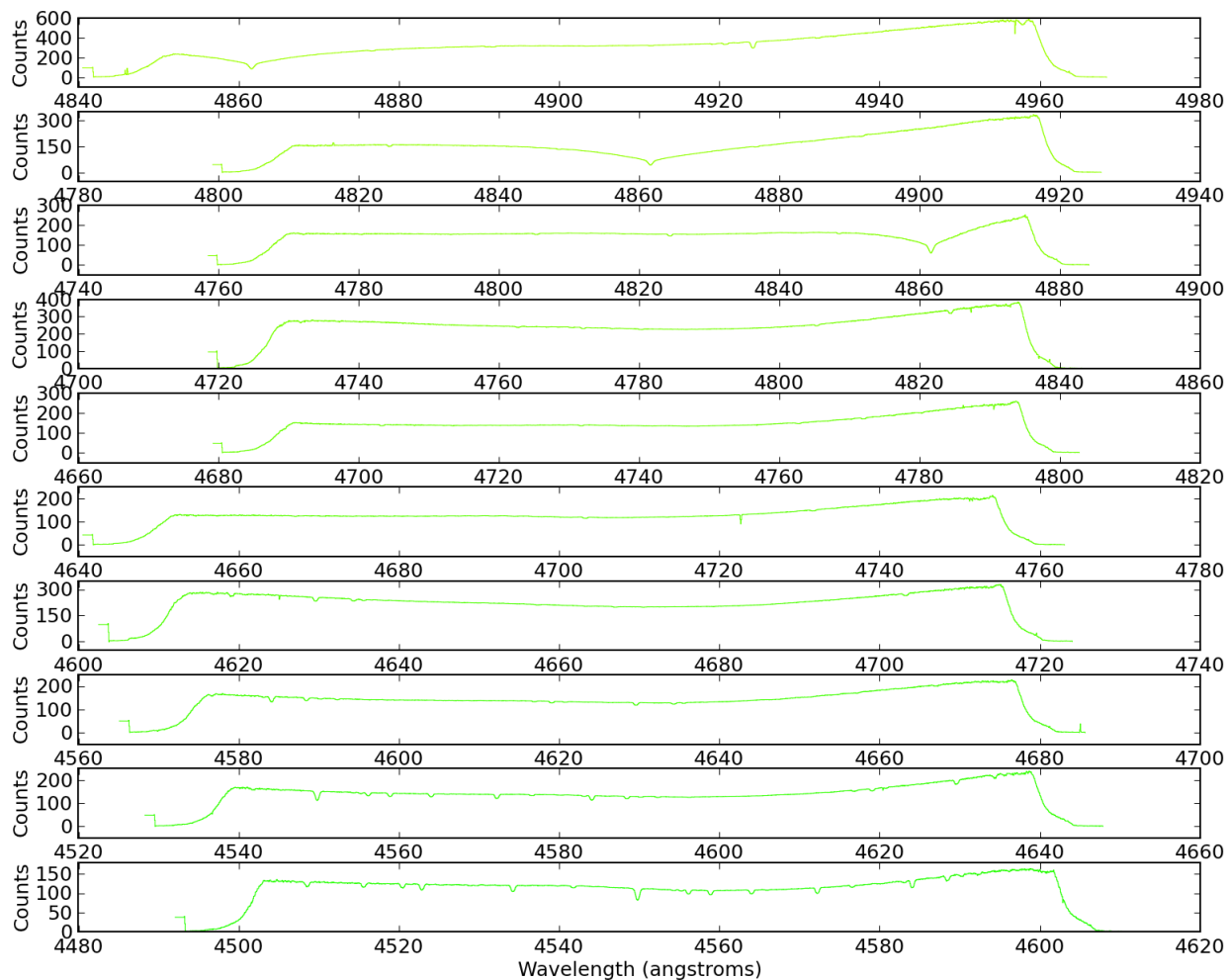


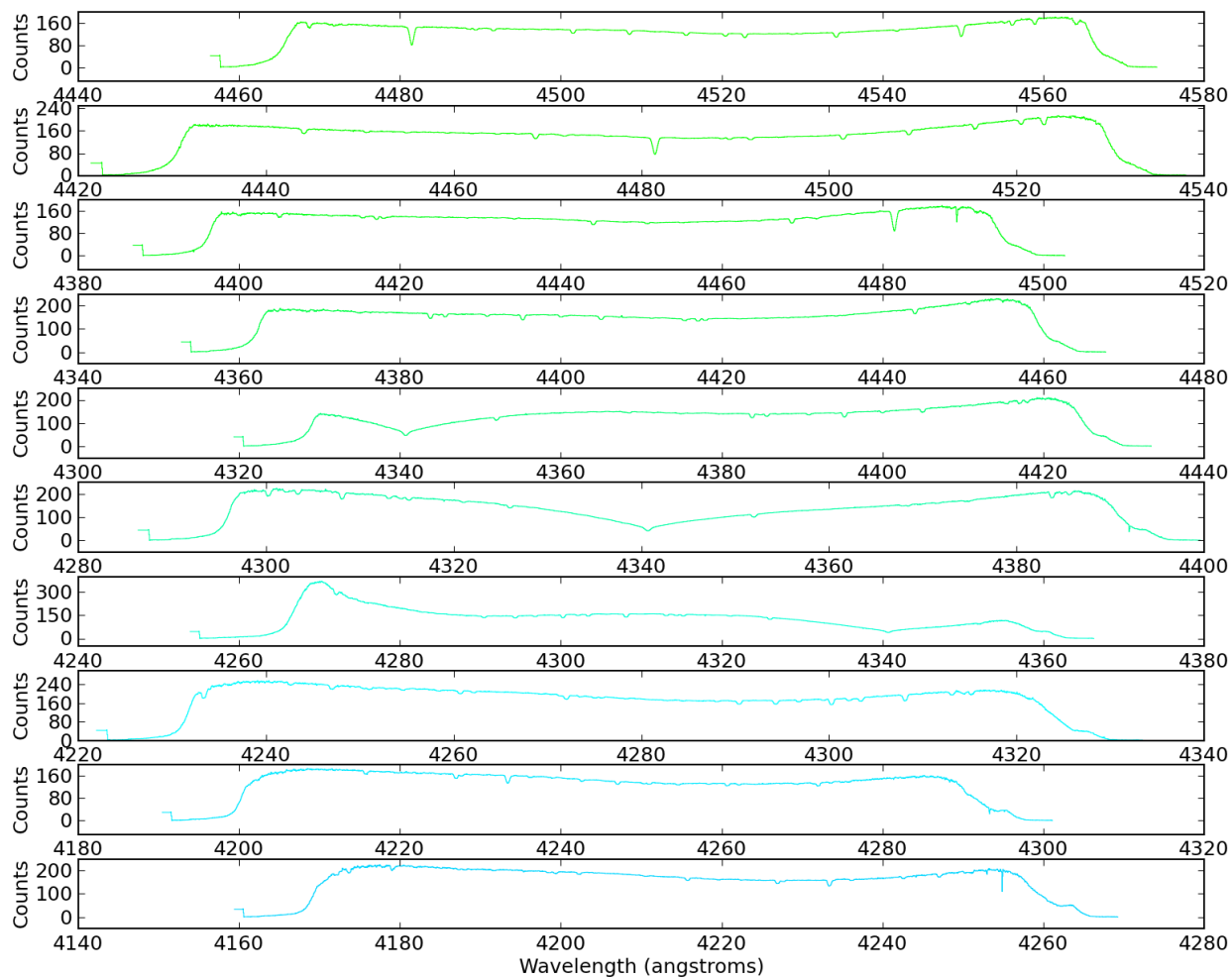


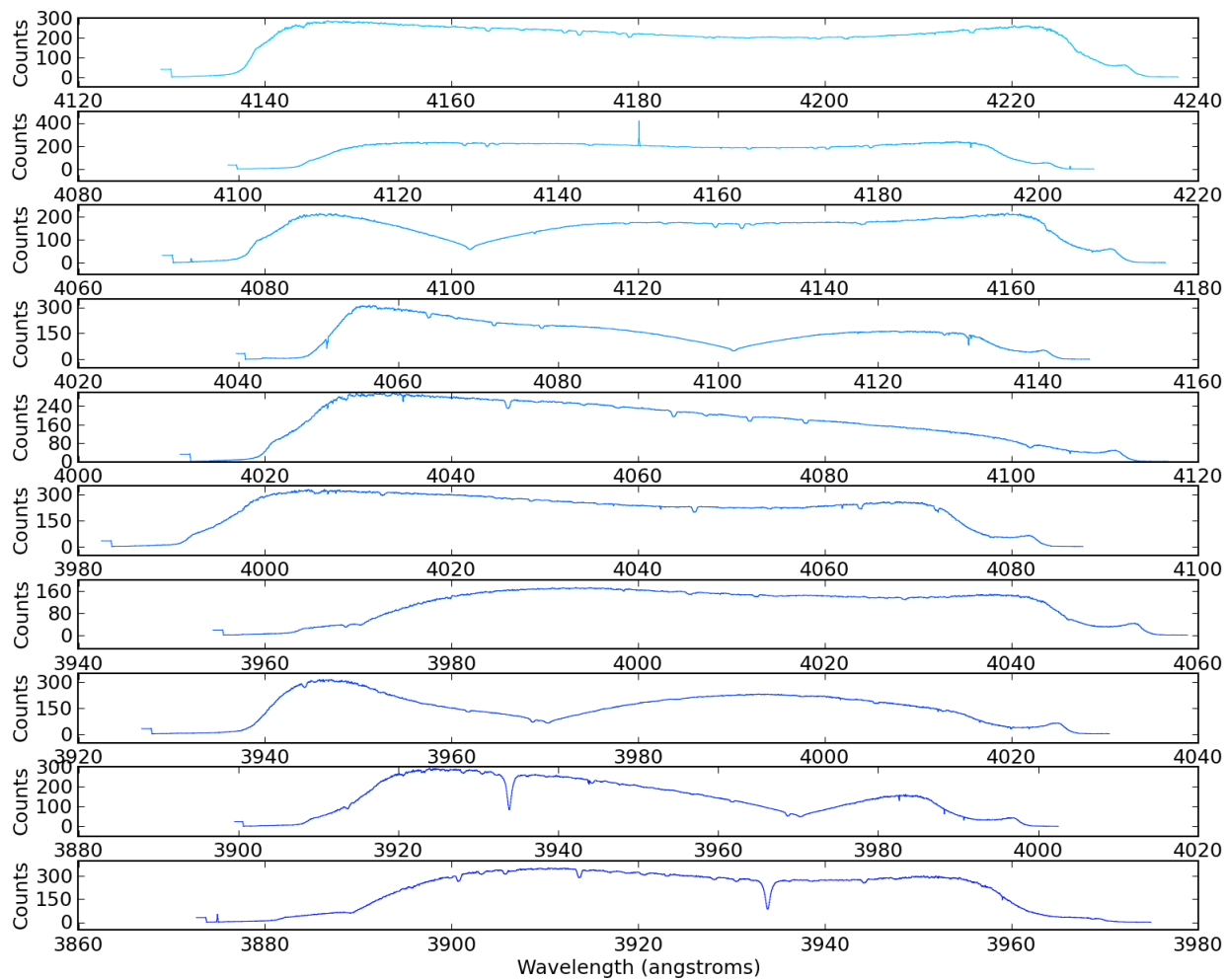


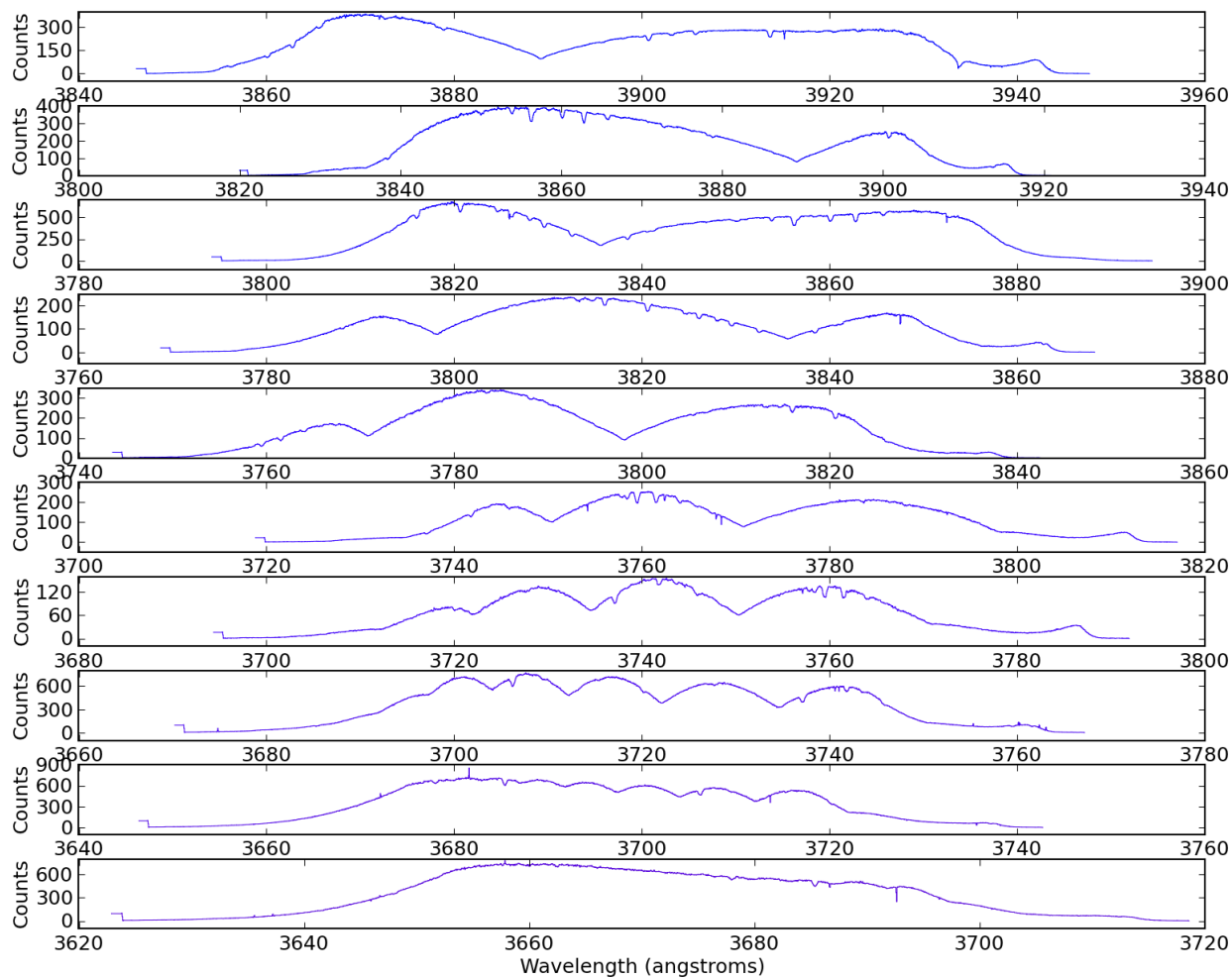


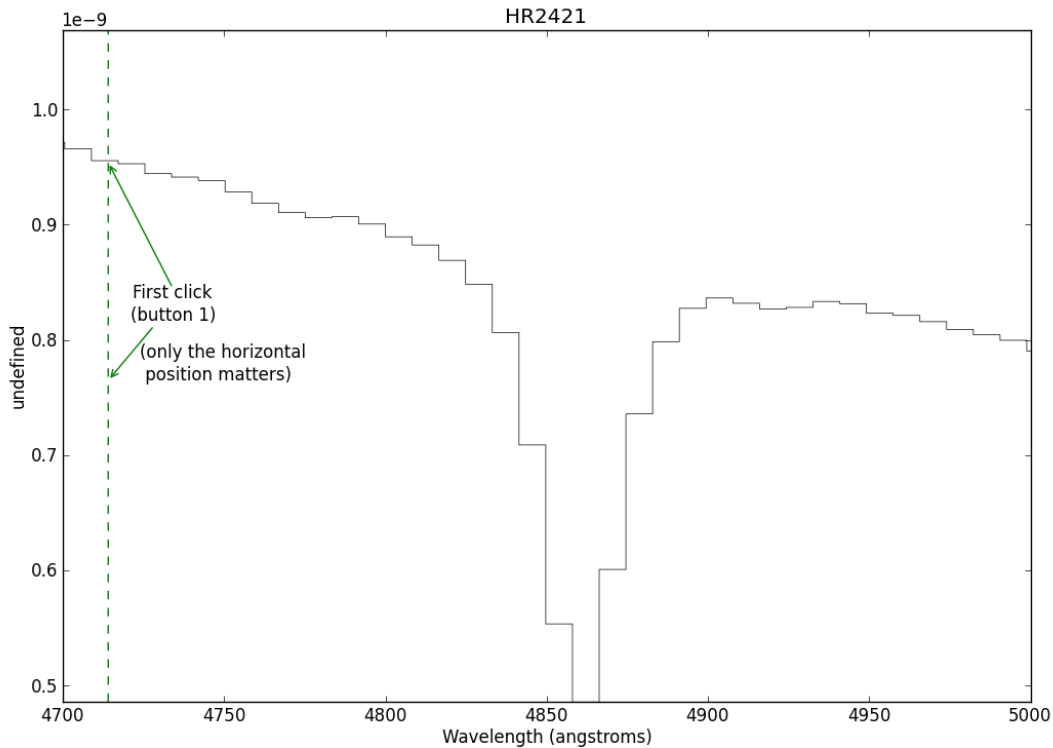












This is where you start the line-fitter:

```
# Start up an interactive line-fitting session
sp.specfit(interactive=True)
```

6.14 Complicated H-alpha Line Fitting

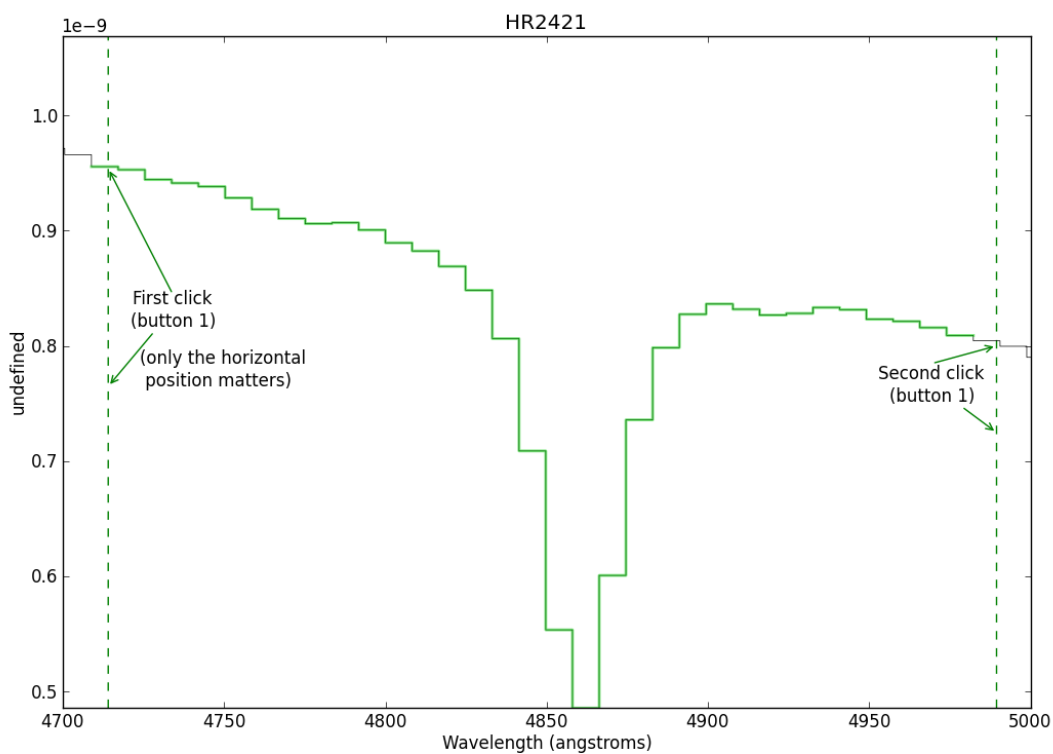
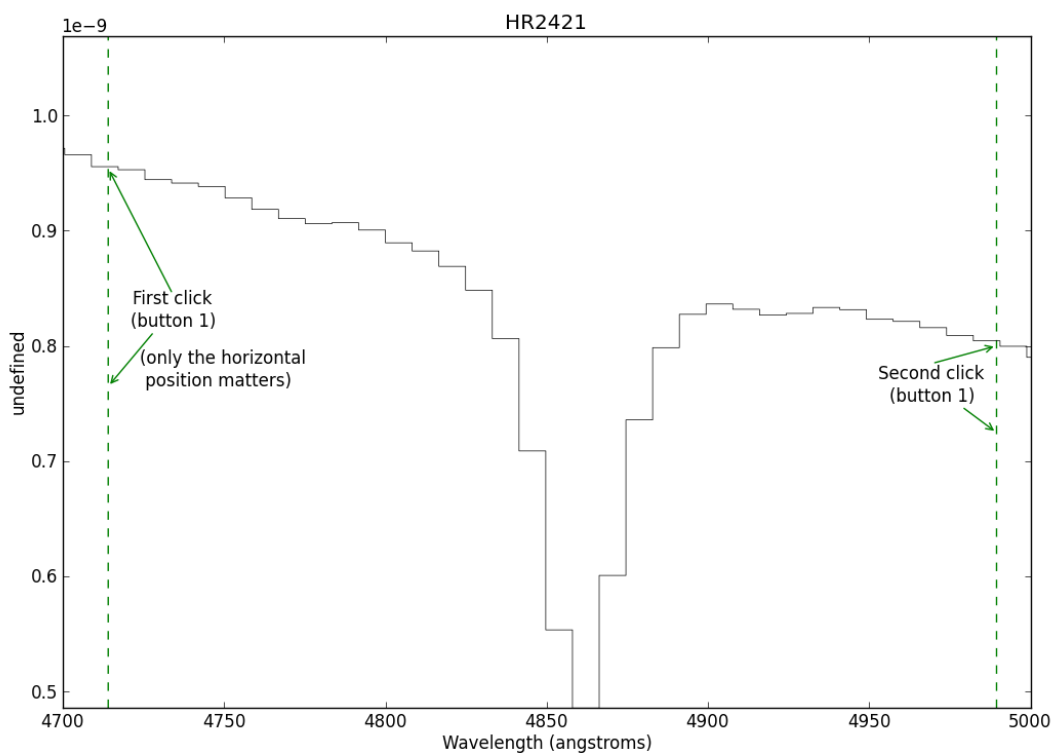
Source code for this example

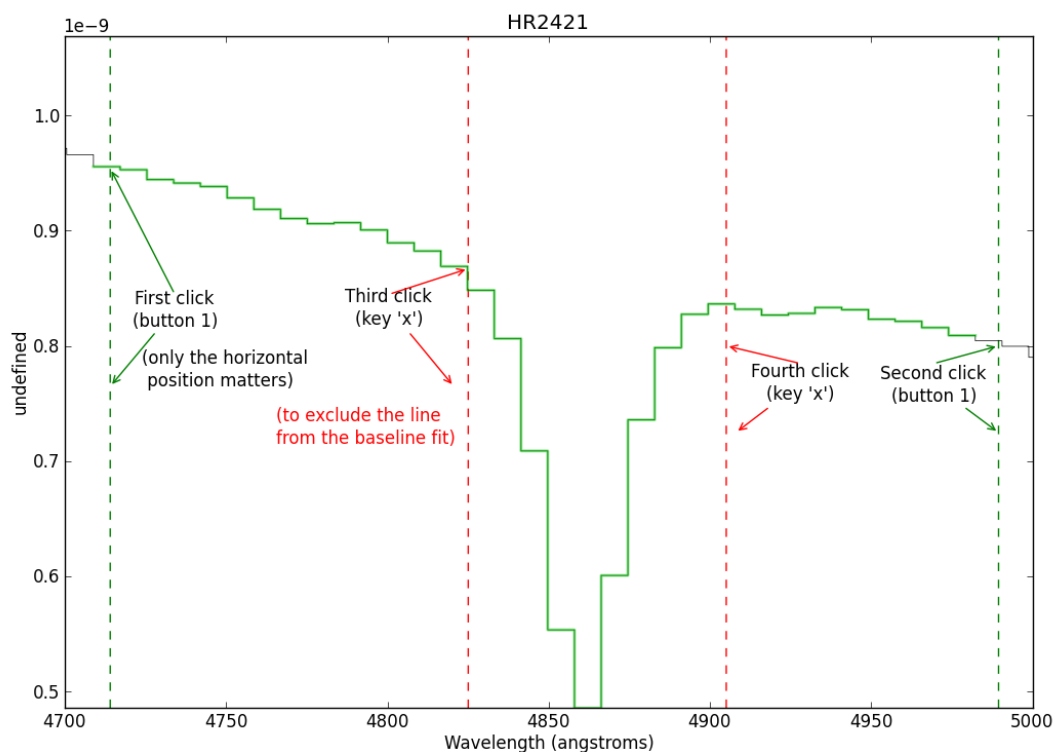
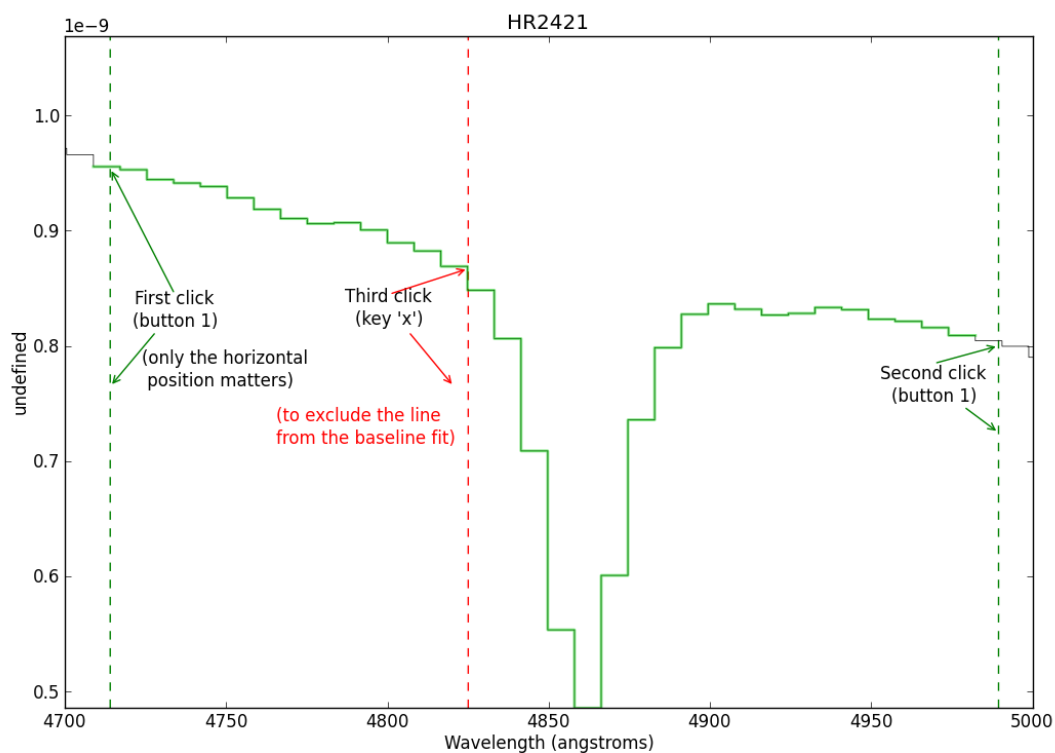
```
"""
Example demonstrating how to fit a complex H-alpha profile after subtracting off a satellite line
(in this case, He I 6678.151704)
"""
import pyspeckit

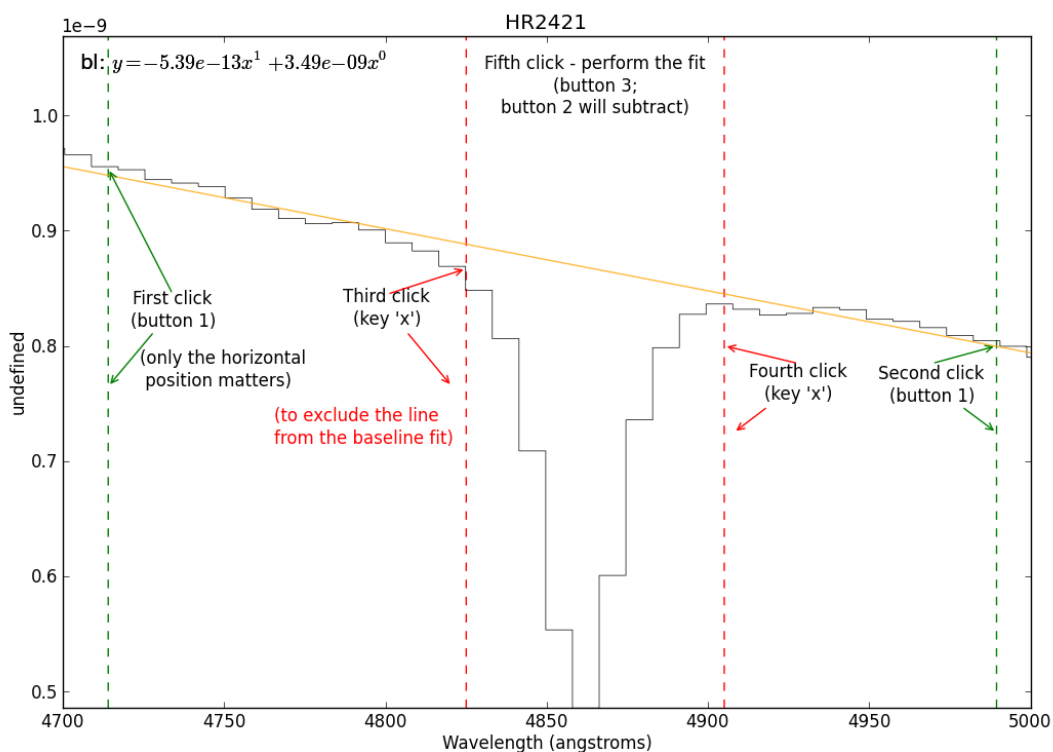
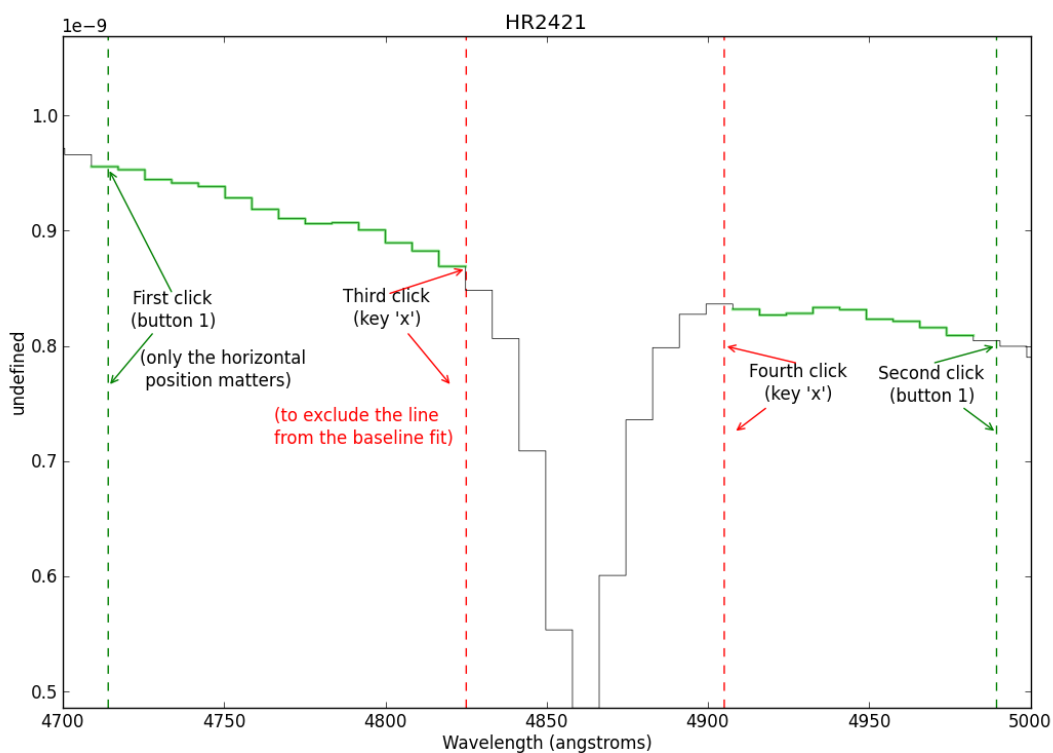
sp = pyspeckit.Spectrum('sn2009ip_halpha.fits')

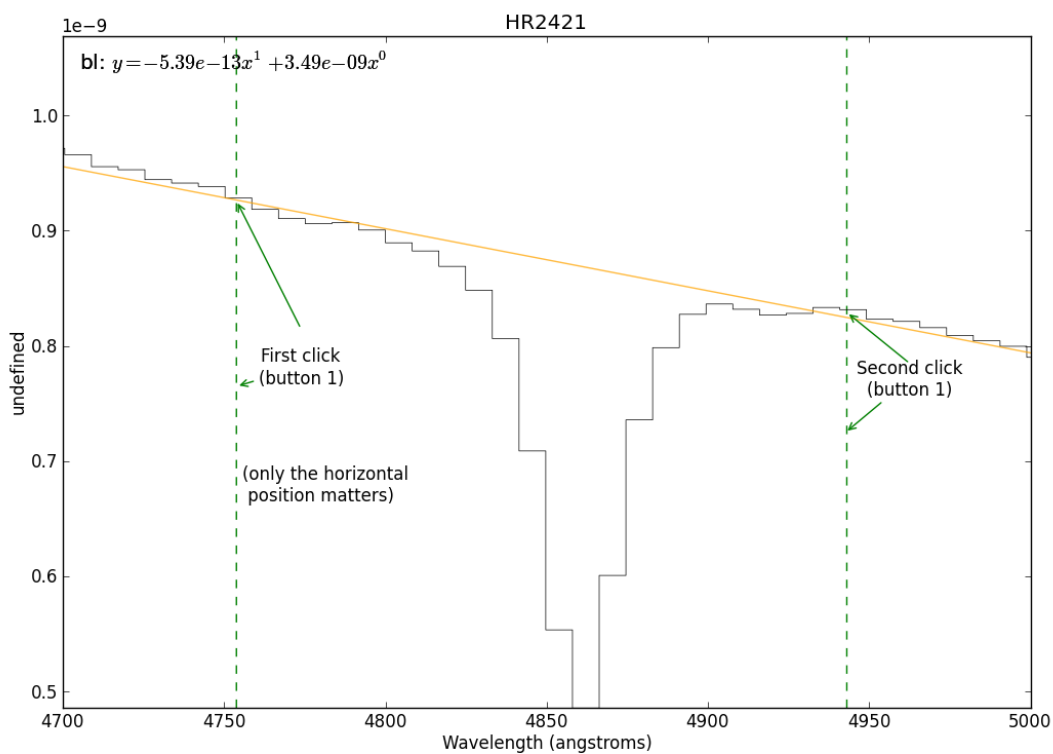
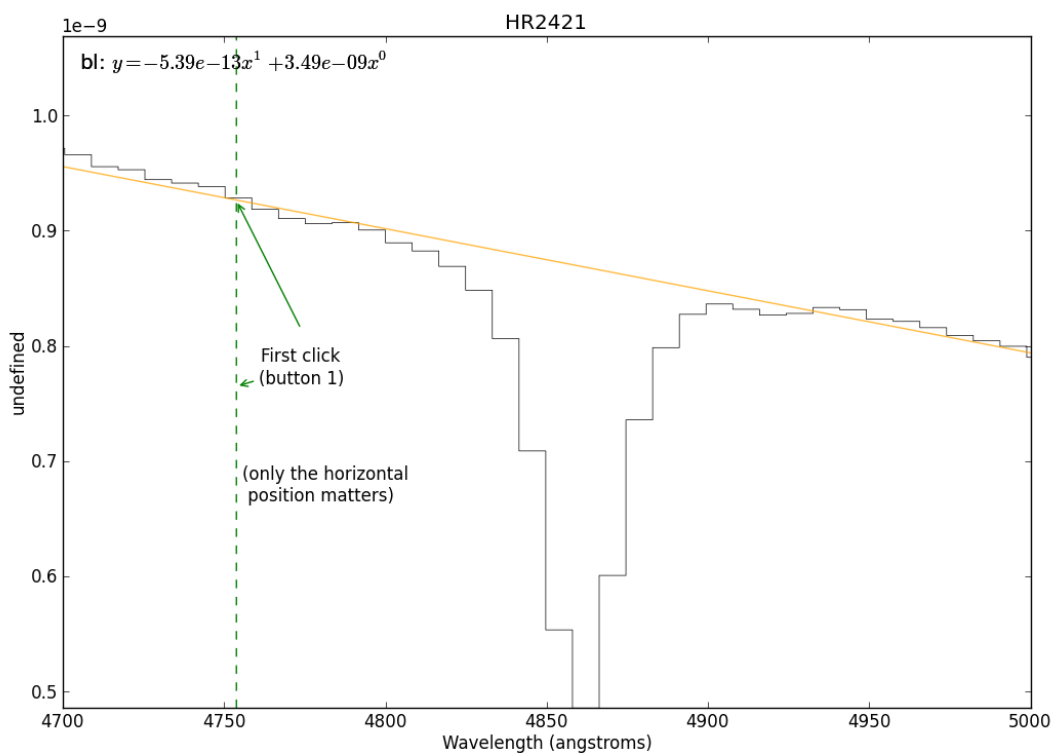
# start by plotting a small region around the H-alpha line
sp.plotter(xmin=6100, xmax=7000, ymax=2.23, ymin=0)

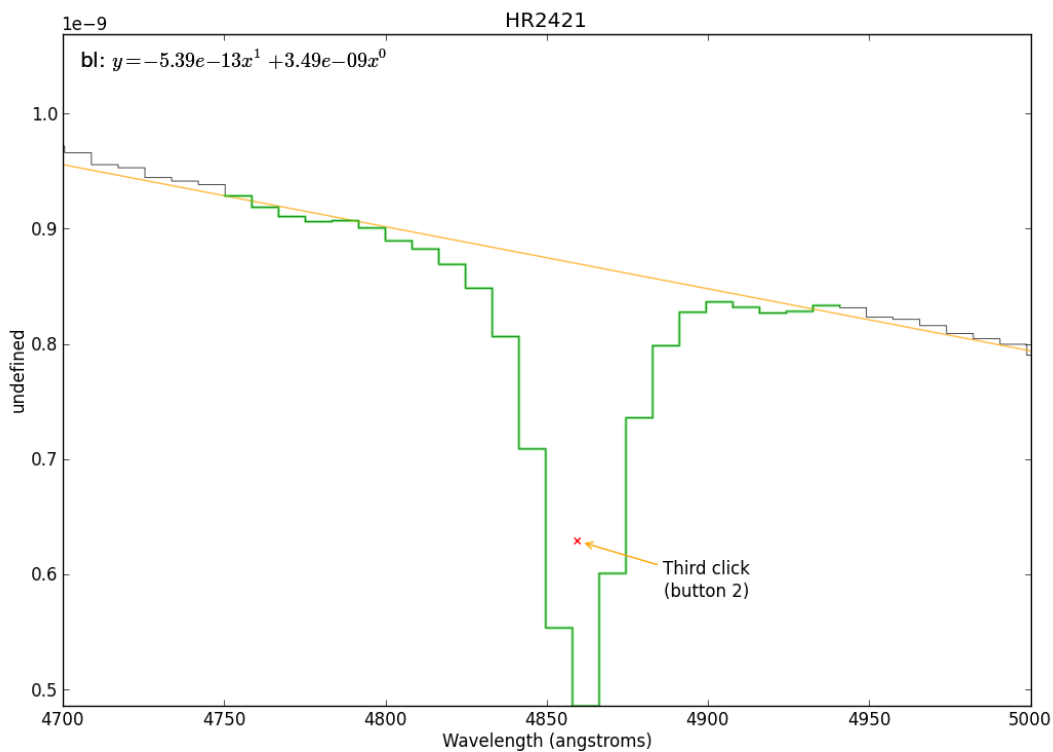
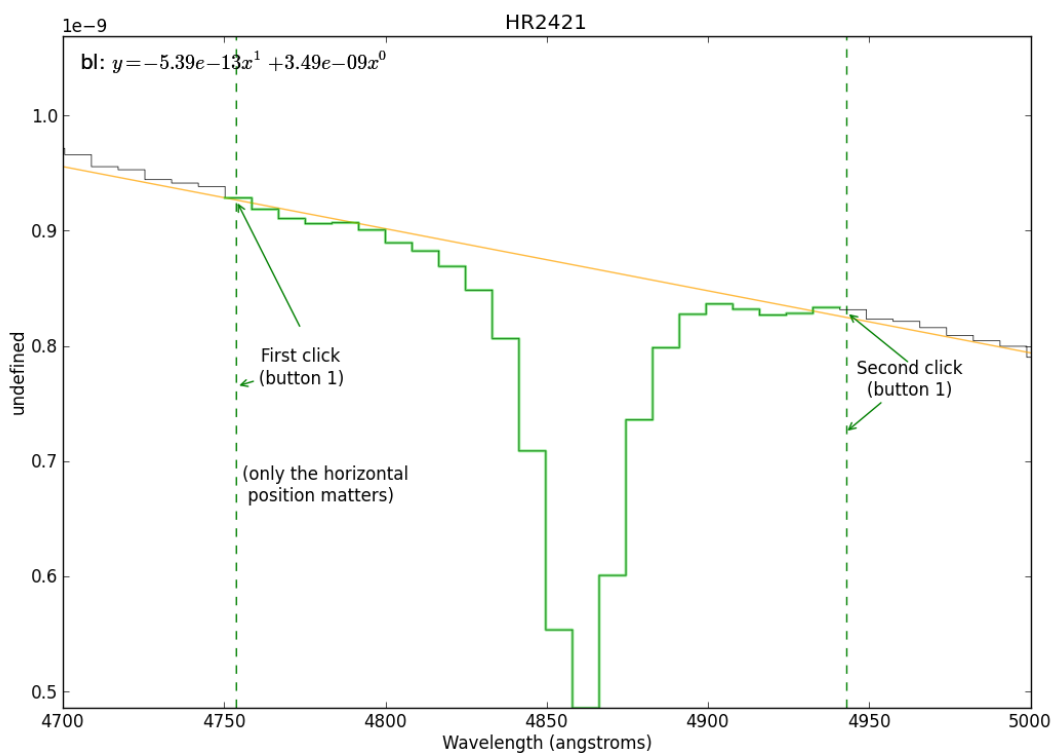
# the baseline (continuum) fit will be 2nd order, and excludes "bad"
# parts of the spectrum
# The exclusion zone was selected interactively (i.e., cursor hovering over the spectrum)
sp.baseline(xmin=6100, xmax=7000,
            exclude=[6450, 6746, 6815, 6884, 7003, 7126, 7506, 7674, 8142, 8231],
```

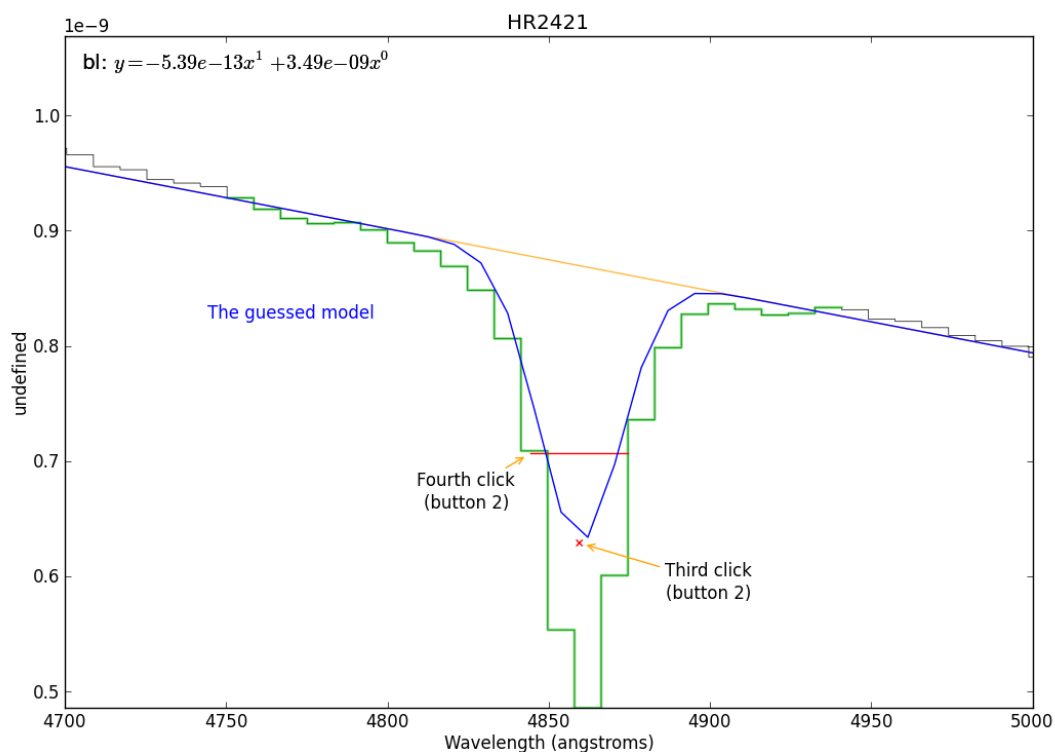
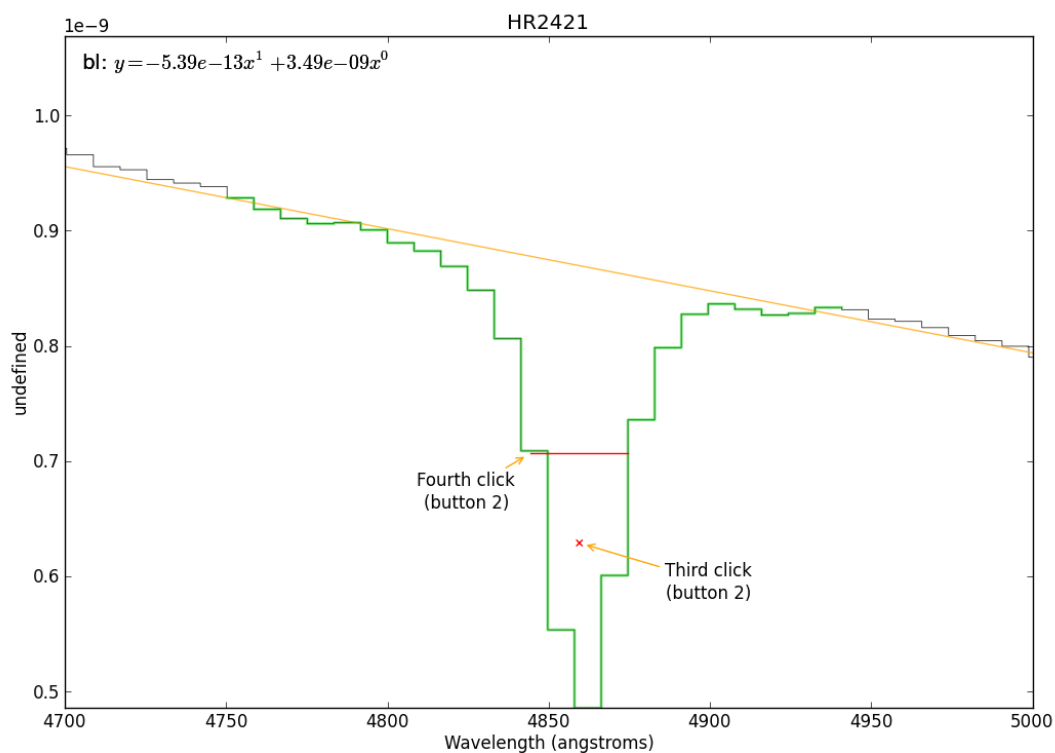


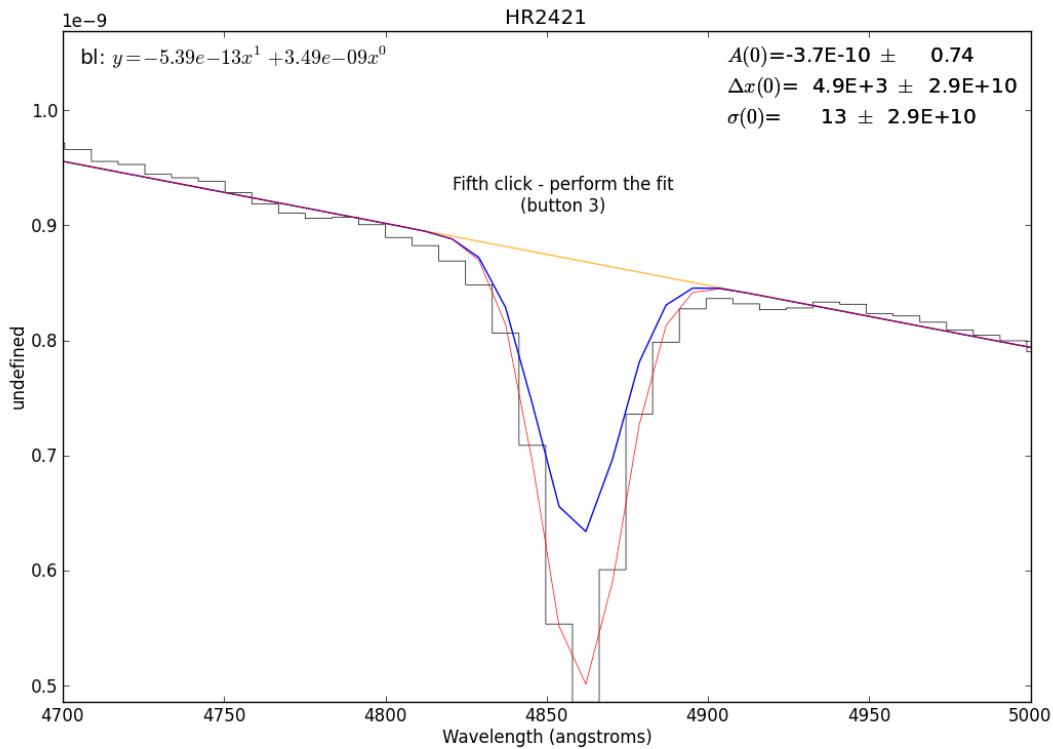












```

subtract=False, reset_selection=True, highlight_fitregion=True,
order=2)

# Fit a 4-parameter voigt (figured out through a series of guess and check fits)
sp.specfit(guesses=[2.4007096541802202, 6563.2307968382256, 3.5653446153950314, 1,
0.53985149324131965, 6564.3460908526877, 19.443226155616617, 1,
0.11957267912208754, 6678.3853431367716, 4.1892742162283181, 1,
0.10506431180136294, 6589.9310414408683, 72.378997529374672, 1,],
fittype='voigt')

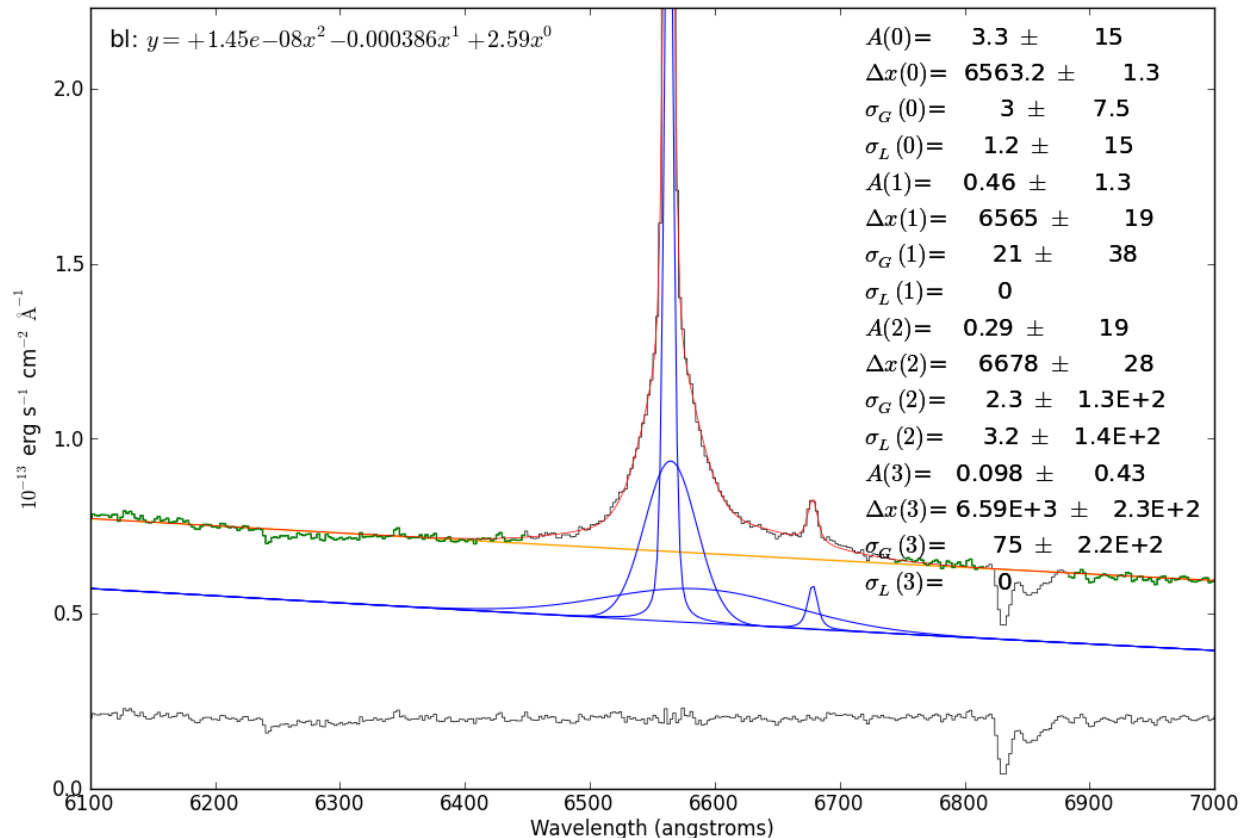
# Now overplot the fitted components with an offset so we can see them
# the add_baseline=True bit means that each component will be displayed with the "Continuum" added
# If this was off, the components would be displayed at y=0
# the component_yoffset is the offset to add to the continuum for plotting only (a constant)
sp.specfit.plot_components(add_baseline=True, component_yoffset=-0.2)

# Now overplot the residuals on the same graph by specifying which axis to overplot it on
# clear=False is needed to keep the original fitted plot drawn
# yoffset is the offset from y=zero
sp.specfit.plot_residuais(axis=sp.plotter.axis, clear=False, yoffset=0.20, label=False)

# save the figure
sp.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_zoom.png")

# print the fit results in table form
# This includes getting the equivalent width for each component using sp.specfit.EQW
print " ".join(["%15s %15s" % (s,s+"err") for s in sp.specfit.parinfo.parnames]), " ".join(["%15s" % ("EQW"+str(i)) for i in range(1,4)])
print " ".join(["%15g %15g" % (par.value,par.error) for par in sp.specfit.parinfo]), " ".join(["%15g" % w for w in sp.specfit.EQW])

```



```
# zoom in further for a detailed view of the profile fit
sp.plotter.axis.set_xlim(6562-150,6562+150)
sp.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_zoomzoom.png")

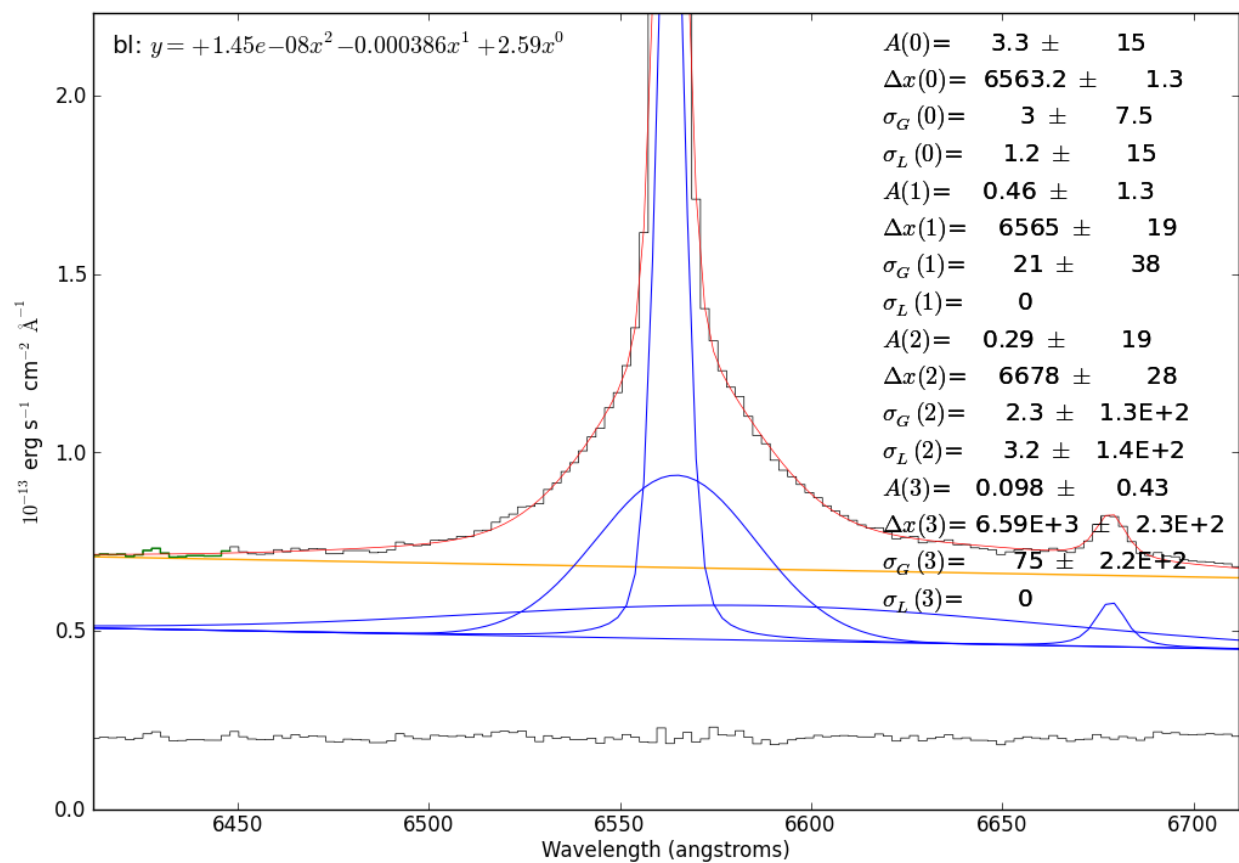
# now we'll re-do the fit with the He I line subtracted off
# first, create a copy of the spectrum
just_halpha = sp.copy()

# Second, subtract off the model fit for the He I component
# (identify it by looking at the fitted central wavelengths)
just_halpha.data -= sp.specfit.modelcomponents[2,:]

# re-plot
just_halpha.plotter(xmin=6100,xmax=7000,ymax=2.00,ymin=-0.3)

# this time, subtract off the baseline - we're now confident that the continuum
# fit is good enough
just_halpha.baseline(xmin=6100, xmax=7000,
                    exclude=[6450,6746,6815,6884,7003,7126,7506,7674,8142,8231],
                    subtract=True, reset_selection=True, highlight_fitregion=True, order=2)

# Do a 3-component fit now that the Helium line is gone
# I've added some limits here because I know what parameters I expect of my fitted line
just_halpha.specfit(guesses=[2.4007096541802202, 6563.2307968382256, 3.5653446153950314, 1,
                             0.53985149324131965, 6564.3460908526877, 19.443226155616617, 1,
                             0.10506431180136294, 6589.9310414408683, 50.378997529374672, 1,],
                    fittype='voigt',
```



```

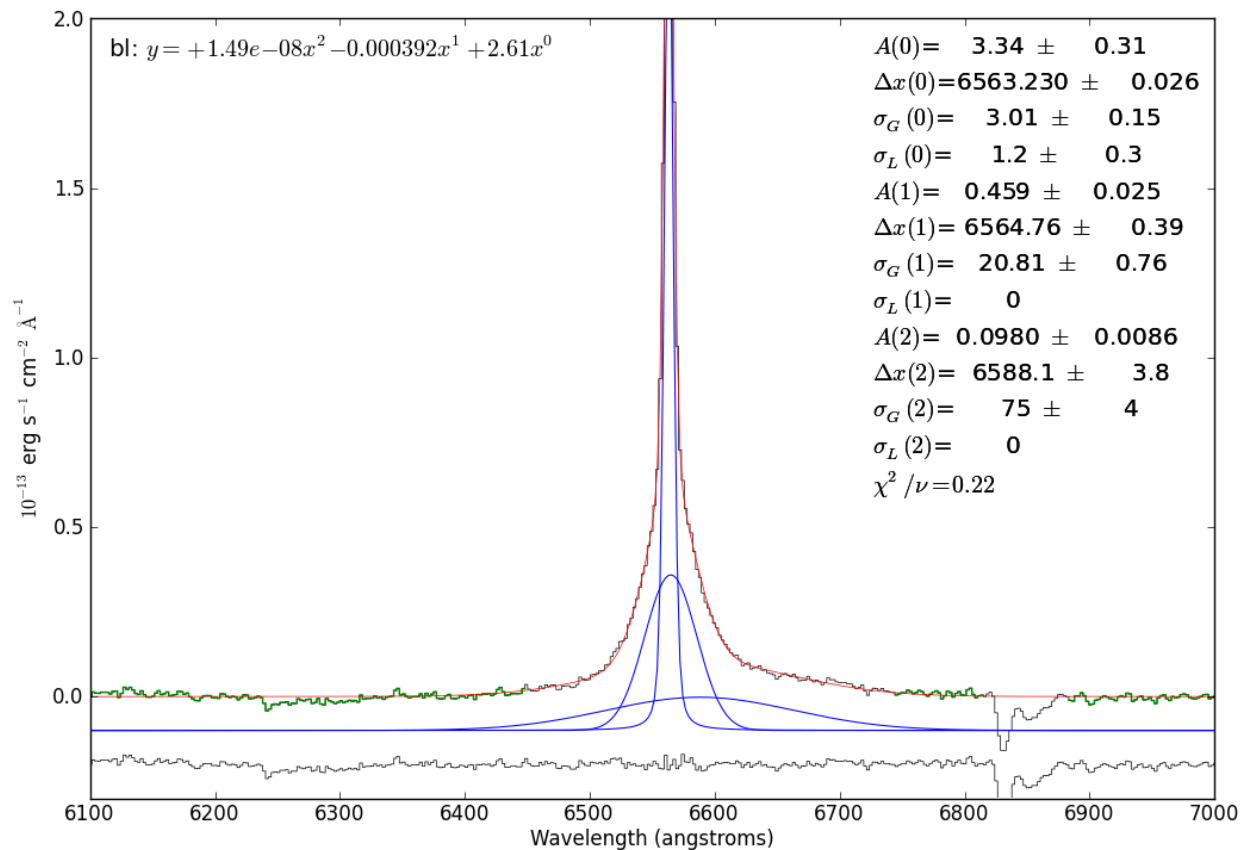
xmin=6100,xmax=7000,
limitedmax=[False,False,True,True]*3,
limitedmin=[True,False,True,True]*3,
limits=[(0,0),(0,0),(0,100),(0,100)]*3

# overplot the components and residuals again
just_halpha.specfit.plot_components(add_baseline=False,component_yoffset=-0.1)
just_halpha.specfit.plotresiduals(axis=just_halpha.plotter.axis,clear=False,yoffset=-0.20,label=False)

# The "optimal chi^2" isn't a real statistical concept, it's something I made up
# However, I think it makes sense (but post an issue if you disagree!):
# It uses the fitted model to find all pixels that are above the noise in the spectrum
# then computes chi^2/n using only those pixels
just_halpha.specfit.annotate(chi2='optimal')

# save the figure
just_halpha.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_threecomp.png")

```



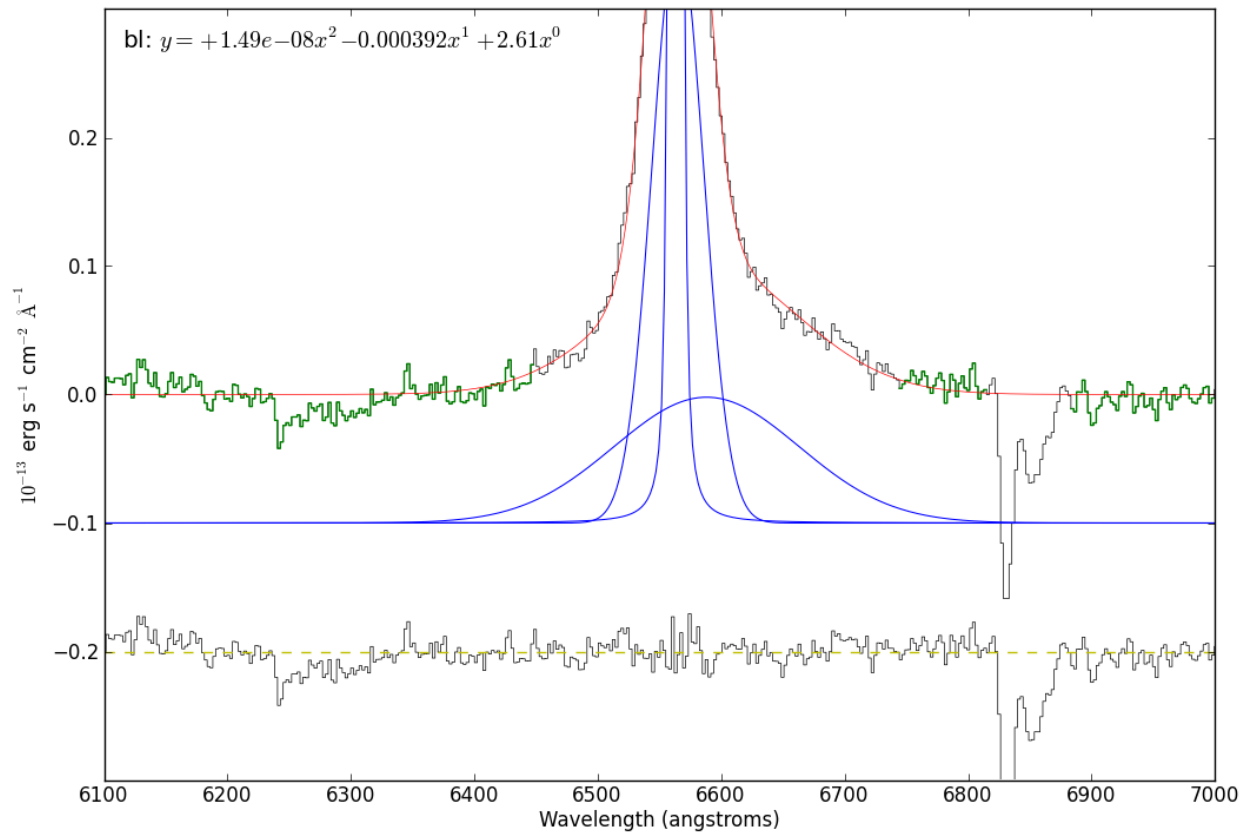
```

# A new zoom-in figure
import pylab

# now hide the legend
just_halpha.specfit.fitleg.set_visible(False)
# overplot a y=0 line through the residuals (for reference)
pylab.plot([6100,7000],[-0.2,-0.2],'y--')
# zoom vertically
pylab.gca().set_ylim(-0.3,0.3)

```

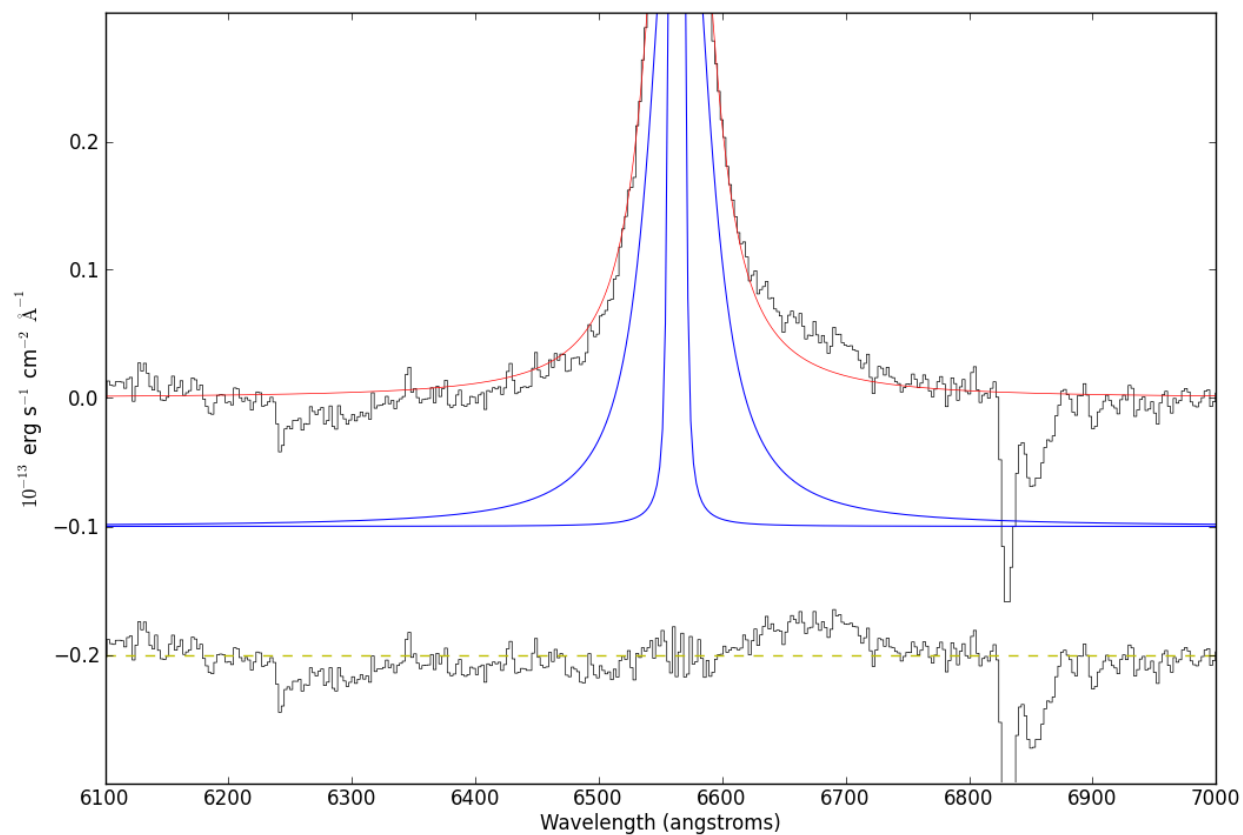
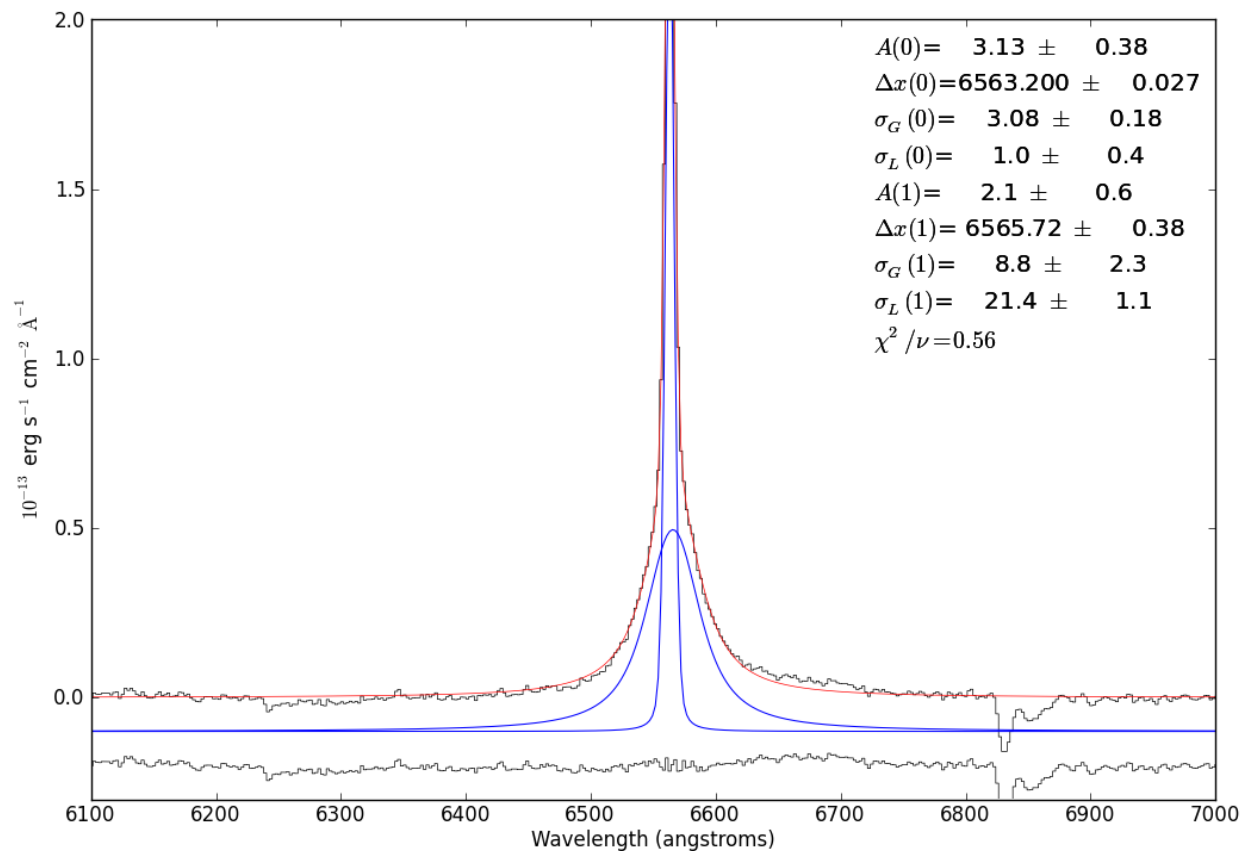
```
# redraw & save
pylab.draw()
just_halpha.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_threecomp_zoom.png")
```



```
# Part of the reason for doing the above work is to demonstrate that a
# 3-component fit is better than a 2-component fit
#
# So, now we do the same as above with a 2-component fit
```

```
just_halpha.plotter(xmin=6100,xmax=7000,ymax=2.00,ymin=-0.3)
just_halpha.specfit(guesses=[2.4007096541802202, 6563.2307968382256, 3.5653446153950314, 1,
                             0.53985149324131965, 6564.3460908526877, 19.443226155616617, 1],
                    fittype='voigt')
just_halpha.specfit.plot_components(add_baseline=False,component_yoffset=-0.1)
just_halpha.specfit.plotresiduals(axis=just_halpha.plotter.axis,clear=False,yoffset=-0.20,label=False)
just_halpha.specfit.annotate(chi2='optimal')
just_halpha.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_twocomp.png")

just_halpha.specfit.fitleg.set_visible(False)
pylab.plot([6100,7000],[-0.2,-0.2],'y--')
pylab.gca().set_ylim(-0.3,0.3)
pylab.draw()
just_halpha.plotter.savefig("SN2009ip_UT121002_Halpha_voigt_twocomp_zoom.png")
```



6.15 Fitting using a Template

Pyspeckit allows you to use a spectral template as the model to fit to your spectrum. See `pyspeckit.spectrum.models.template`.

If your model spectrum only requires a shift and a scale, it's easy to use:

```
from pyspeckit.spectrum.models.template import template_fitter

template = pyspeckit.Spectrum('template_spectrum.fits')
dataspec = pyspeckit.Spectrum("DataSpectrum.fits")

# Create the fitter from the template spectrum and "Register" it
template_fitter = template_fitter(template, xshift_units='angstroms')
dataspec.Registry.add_fitter('template', template_fitter, 2)

# The fitted parameters are amplitude & xshift
# perform the fit:
dataspec.specfit(fittype='template', guesses=[1, 0])

# print the results
print dataspec.specfit.parinfo
```

6.16 Monte Carlo examples

There are (at least) two packages implementing Monte Carlo sampling available in python: `pymc` and `emcee`. `pyspeckit` includes interfaces to both. With the `pymc` interface, it is possible to define priors that strictly limit the parameter space. So far that is not possible with `emcee`.

The examples below use a custom plotting package from `agpy`. It is a relatively simple but convenient wrapper around `numpy`'s `histogram2d`. `pymc_plotting` takes care of indexing, percentile determination, and coloring.

The example below shows the results of a gaussian fit to noisy data ($S/N \sim 6$). The parameter space is then explored with `pymc` and `emcee` in order to examine the correlation between width and amplitude.

```
import pyspeckit

# Create our own gaussian centered at 0 with width 1, amplitude 5, and
# gaussian noise with amplitude 1
x = pyspeckit.units.SpectroscopicAxis(np.linspace(-10, 10, 50), unit='km/s')
e = np.random.randn(50)
d = np.exp(-np.asarray(x)**2/2.)*5 + e

# create the spectrum object
sp = pyspeckit.Spectrum(data=d, xarr=x, error=np.ones(50)*e.std())
# fit it
sp.specfit(fittype='gaussian', multifit=None, guesses=[1, 0, 1])
# then get the pymc values
MCuninformed = sp.specfit.get_pymc()
MCwithpriors = sp.specfit.get_pymc(use_fitted_values=True)
MCuninformed.sample(101000, burn=1000, tune_interval=250)
MCwithpriors.sample(101000, burn=1000, tune_interval=250)

# MC vs least squares:
print sp.specfit.parinfo
# Param #0    AMPLITUDE0 =          4.51708 +/-          0.697514
```

```
# Param #1      SHIFT0 =      0.0730243 +/-      0.147537
# Param #2      WIDTH0 =      0.846578 +/-      0.147537   Range:   [0,inf)
```

```
print MCuninformed.stats()['AMPLITUDE0'],MCuninformed.stats()['WIDTH0']
# {'95% HPD interval': array([ 2.9593463 ,  5.65258618]),
#  'mc error': 0.0069093803546614969,
#  'mean': 4.2742994714387068,
#  'n': 100000,
#  'quantiles': {2.5: 2.9772782318342288,
#  25: 3.8023115438555615,
#  50: 4.2534542126311479,
#  75: 4.7307441549353229,
#  97.5: 5.6795448148793293},
#  'standard deviation': 0.68803712503362213},
# {'95% HPD interval': array([ 0.55673242,  1.13494423]),
#  'mc error': 0.0015457954546501554,
#  'mean': 0.83858499779600593,
#  'n': 100000,
#  'quantiles': {2.5: 0.58307734425381375,
#  25: 0.735072721596429,
#  50: 0.824695077252244,
#  75: 0.92485225882530664,
#  97.5: 1.1737067304111048},
#  'standard deviation': 0.14960171537498618}
```

```
print MCwithpriors.stats()['AMPLITUDE0'],MCwithpriors.stats()['WIDTH0']
# {'95% HPD interval': array([ 3.45622857,  5.28802497]),
#  'mc error': 0.0034676818027776788,
#  'mean': 4.3735547007147595,
#  'n': 100000,
#  'quantiles': {2.5: 3.4620369729291913,
#  25: 4.0562790782065052,
#  50: 4.3706408236777481,
#  75: 4.6842793868186332,
#  97.5: 5.2975444315549947},
#  'standard deviation': 0.46870135068815683},
# {'95% HPD interval': array([ 0.63259418,  1.00028015]),
#  'mc error': 0.00077504289680683364,
#  'mean': 0.81025043433745358,
#  'n': 100000,
#  'quantiles': {2.5: 0.63457050661326331,
#  25: 0.7465422649464849,
#  50: 0.80661741451336577,
#  75: 0.87067288601310233,
#  97.5: 1.0040591994661381},
#  'standard deviation': 0.093979950317277294}
```

```
# optional
```

```
import agpy.pymc_plotting
```

```
import pylab
```

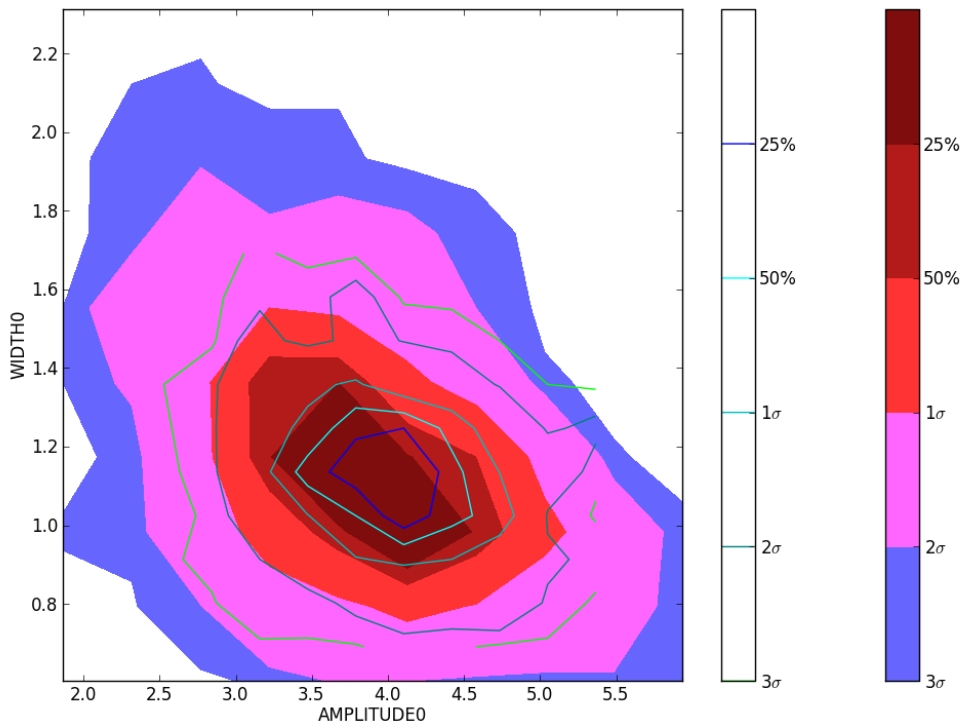
```
agpy.pymc_plotting.hist2d(MCuninformed,'AMPLITUDE0','WIDTH0',clear=True,bins=[25,25])
```

```
agpy.pymc_plotting.hist2d(MCwithpriors,'AMPLITUDE0','WIDTH0',contourcmd=pylab.contour,colors=[(0,1,0,1),(0,0.5,0.5,1),(0,
```

```
pylab.plot([5],[1], 'k+', markersize=25)
```

```
# Now do the same with emcee
emcee_ensemble = sp.specfit.get_emcee()
p0 = emcee_ensemble.p0 * (np.random.randn(*emcee_ensemble.p0.shape) / 10. + 1.0)
pos, logprob, state = emcee_ensemble.run_mcmc(p0, 100000)

plotdict = {'AMPLITUDE0': emcee_ensemble.chain[:, :, 0].ravel(),
            'WIDTH0': emcee_ensemble.chain[:, :, 2].ravel()}
agpy.pymc_plotting.hist2d(plotdict, 'AMPLITUDE0', 'WIDTH0', fignum=2, bins=[25, 25], clear=True)
pylab.plot([5], [1], 'k+', markersize=25)
```



The Amplitude-Width parameter space sampled by pymc with (lines) and without (solid) priors. There is moderate anticorrelation between the line width and the peak amplitude. The + symbol indicates the input parameters; the model does a somewhat poor job of recovering the true values (in case you're curious, there is no intrinsic bias - if you repeat the above fitting procedure a few hundred times, the mean fitted amplitude is 5.0).

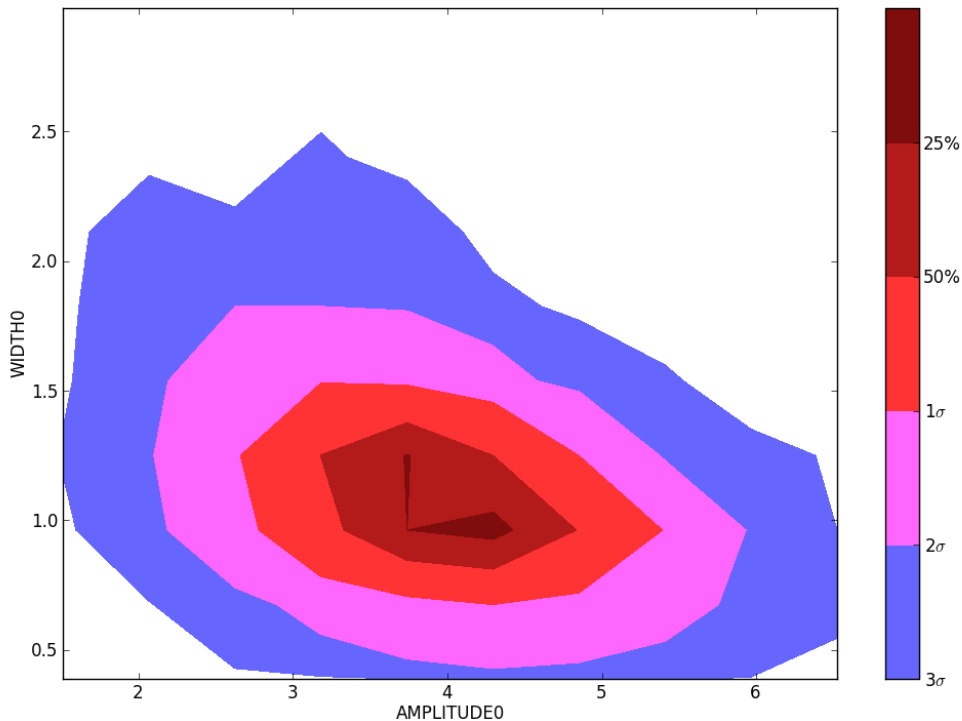
The parameter space sampled with emcee and binned onto a 25x25 grid. Note that emcee has 6x as many points (and takes about 6x as long to run) because there are 6 “walkers” for the 3 parameters being fit.

6.17 Guide for GILDAS-CLASS users

6.17.1 Reading Files

PySpecKit can read many file types including CLASS .cls files.

For example, a typical single-dish observing file will consist of a large number of individual spectra. These may be



on-the-fly spectra or multiple integrations on a single source; either way the pointing and spectral information for each individual data point should be incorporated in the data file.

The spectra are recorded from the data file into an `pyspeckit.classes.ObsBlock` object. An `ObsBlock` (Observation Block) is simply a container for many spectra; in most regards it behaves the same way as a `pyspeckit.Spectrum` object, but it has a few extra attributes built-in (e.g., spectral averaging).

A file can be loaded as a named object. The data is filtered as it is read in. The following line will ensure that the spectra in the `n2hp` `ObsBlock` contain only data from the F1M spectrometer with lines labeled 'N2HP(3-2)' or 'N2H+(3-2)':

```
from pyspeckit.spectrum.readers.read_class import class_to_obsblocks
n2hp = class_to_obsblocks(filename,
    telescope=['SMT-F1M-HU', 'SMT-F1M-VU'],
    line=['N2HP(3-2)', 'N2H+(3-2)'])
```

6.17.2 Working with the data

You can treat an `ObsBlock` like any other `pyspeckit.Spectrum` object, but there are a few unique features.

The 'smooth' function will smooth each individual spectrum in the `ObsBlock`, which can be useful if you want to smooth before averaging.

The 'average' function averages spectra. Weights for the averaging can be specified. The error is also computed either by taking the RMS of the averaged spectra or by averaging the error spectra.

You can plot each spectrum in an individual window with the `ploteach` function, or all overlaid simultaneously with the 'plotter' function. If you want to loop through each spectrum, waiting for user input after displaying, you can do something like:

```
ax = pylab.gca()
for sp in n2hp:
    sp.plotter(axis=ax)
    raw_input("Waiting for input...")
```

You can also fit a line profile to *each* spectrum in the observation block using the ‘fiteach’ command.

6.17.3 Selecting Spectra

There are 3 keywords that can be used to select spectra when reading in a file. The line and telescope keywords are required in order to make an observation block, otherwise the spectral axes will not be common to all spectra.:

```
n2hp = class_to_obsblocks(filename,
    telescope=['SMT-F1M-HU', 'SMT-F1M-VU'],
    line=['N2HP(3-2)', 'N2H+(3-2)'])
```

If you want to read in all of the data and don’t care about the line or telescope, you can instead use:

```
all_data = class_to_spectra(filename)
```

You can select data after they are read in by matching header keywords:

```
g10 = pyspeckit.ObsBlock([sp for sp in all_data if sp.specname == 'g10'])
```

6.17.4 Fitting Data

In CLASS, you would specify the data range with individual commands on the command line, e.g.:

```
[this isn't quite right]
xrange 5 25
```

In pyspeckit, you can specify the range in multiple ways, but the default is to use the plotted window. For example:

```
sp.plotter(xmin=5, xmax=25)
sp.baseline()
sp.specfit()
```

will perform a baseline fit and spectrum fit over the range 5-25 km/s (the units of xmin, xmax are the plotted units). More intricate specifications are possible:

```
sp.plotter()
# Fit a baseline over the region 5-25 km/s, excluding 7-10 km/s and 15-18 km/s
sp.baseline.selectregion(xmin=5, xmax=25, exclude=[7, 10, 15, 18])
sp.baseline()
sp.specfit()
```

6.18 Guide for IRAF users

PySpecKit is similar in intent and implementation to IRAF’s *splot* routine. IRAF users will probably want to do most of their data reduction (i.e., turning an image/cube into a 1D wavelength-calibrated spectrum) in IRAF, but will be comfortable fitting lines and making publication-quality plots using PySpecKit.

6.18.1 Loading a Spectrum

If you have an IRAF spectrum, it is straightforward to load into PySpecKit:

```
sp = pyspeckit.Spectrum('iraf_spectrum.ms.fits')
sp.plotter()
```

6.18.2 Fitting Line Profiles

Note: See *A guide to interactive fitting* for a comprehensive graphical demonstration of these instructions.

In IRAF, a line profile is fitted using *k* to start the fitter, then *k*, *l*, or *v* to perform the fit.

In PySpecKit, the continuum (*baseline*) and line profile are determined separately.

Instead of using a key twice to specify the continuum level, a continuum must be fitted from the data. This is done by pressing *b* to turn on the baseline fitter. Click or press *l* to select baseline regions - they will be highlighted in green. Press *3* to fit the baseline and display it as an orange line.

In PySpecKit, the interactive fitter is started by pressing *f* in the plot window. After pressing *f*, instructions will be provided in the terminal window telling you which line profiles are implemented. Select one of these, or use a gaussian by default.

Select the line fitting region by pressing *l* on either side of the line. Select the peak and full-width-half-maximum of the line by pressing *2* at each of these locations in turn. You may repeat this cycle indefinitely to fit multiple profiles (comparable to IRAF's *deblend* capability). Then, press *3* to perform the fit.

The fitted parameters can be accessed (as variables, or printed) through the `Spectrum.specfit.parinfo` parameter. They will also be displayed in the plot legend.

6.19 PySpecKit Projects

A few projects appropriate for a Google Summer of Code, [ESA Summer of Code in Space](#), or similar are outlined below.

6.19.1 Incorporate `astropy.units` into `pyspeckit.units`

This project is at the core of both `pyspeckit` and `specutils`.

The most important base functionality of a spectroscopic toolkit is to be able to convert between different spectroscopic systems, e.g. wavelength \leftrightarrow frequency \leftrightarrow velocity. This can be achieved using `astropy`'s [unit equivalencies](#).

The X-axis unit changes will be straightforward project that should require about 2 weeks to complete. The more complicated and interesting project is creating Y-axis units (i.e., flux units) that appropriately adjust with changes to the X-axis. These would make use of other `astropy` unit equivalencies, e.g. the [spectral density](#) equivalency.

The end goal will be to have a `Spectrum` object that will live in `specutils` and be inherited by `pyspeckit`, which will provide the interface to modeling and graphical tools.

6.19.2 Refactor and Expand the pyspeckit modeling tools

Since the development of pyspeckit, there has been substantial progress on a more general class of [modeling tools from astropy](#). Pyspeckit already has a wide variety of data fitting and modeling tools that can readily be modified to use the astropy modeling formalism.

Details of this project need to be worked out, but will include:

- refactoring `pyspeckit.models` to use `astropy.models`
- building a graphical interface to `astropy.models`

6.19.3 Expand the Unit Test suite

Pyspeckit is a complicated code suite, which has led to many bugs, particularly in the UI. An improved unit test suite would help prevent or remove these bugs. Such a project would start by breaking down the existing tests, which are really end-to-end tests, into their component units.

A guide to interactive fitting

A step-by-step example of how to use the interactive fitter.

In short, we will do the following:

```
# 1. Load the spectrum
sp = pyspeckit.Spectrum('hr2421.fit')

# 2. Plot a particular spectral line
sp.plotter(xmin=4700, xmax=5000)

# 3. Need to fit the continuum first
sp.baseline(interactive=True, subtract=False)

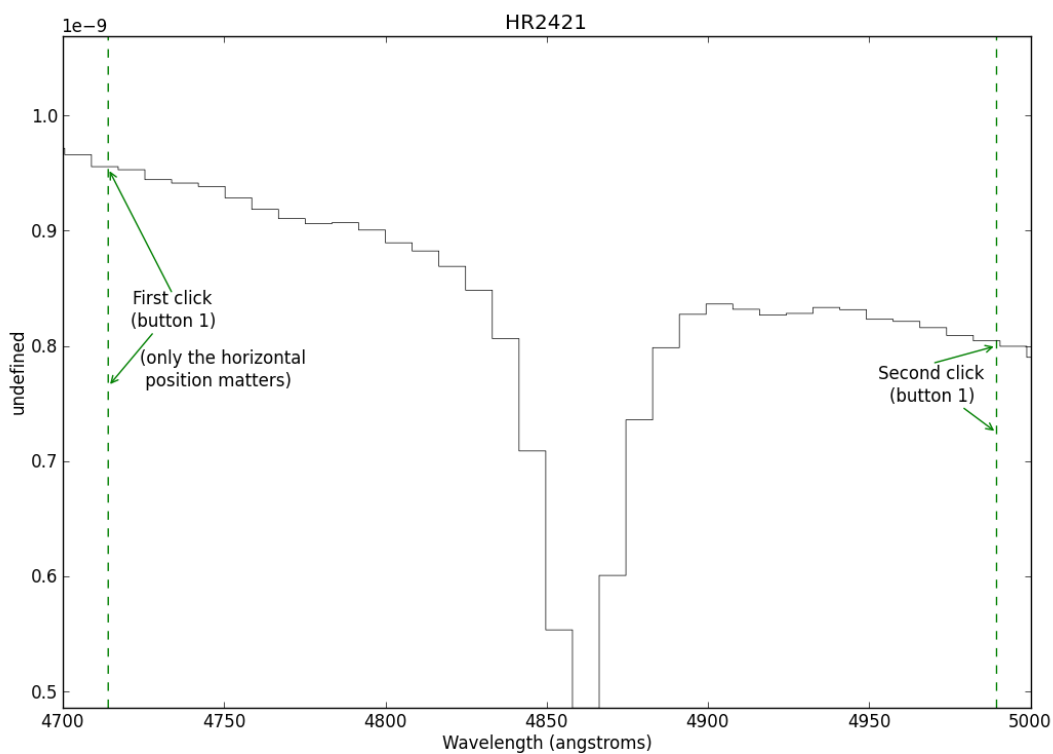
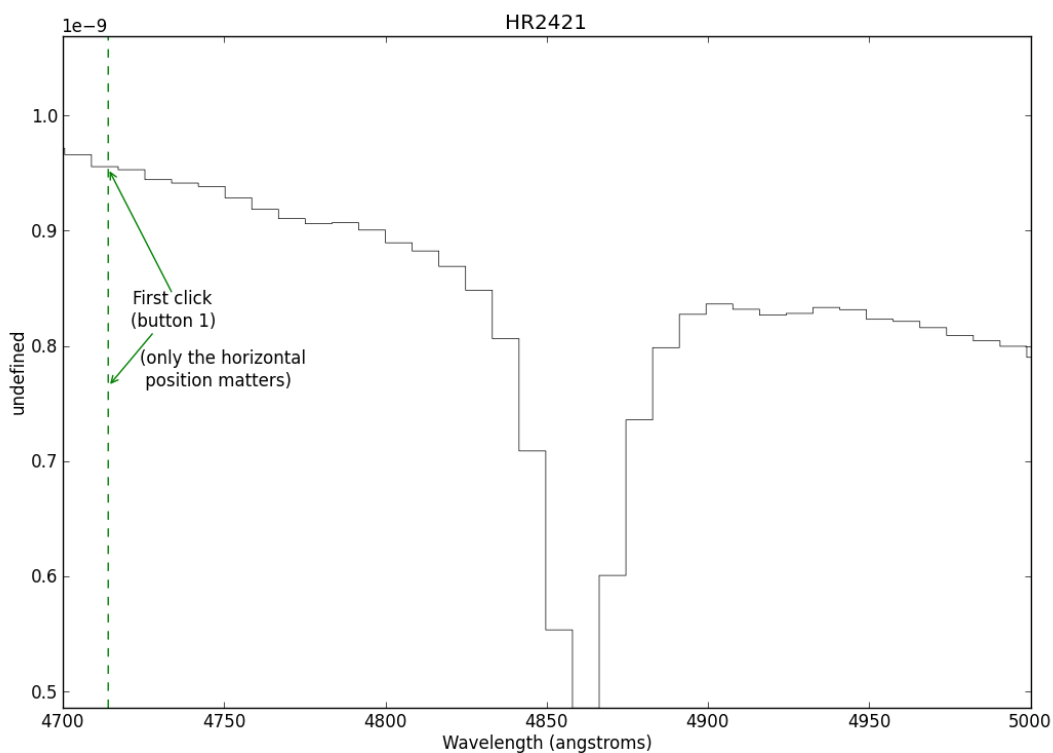
# 4... (much work takes place interactively at this stage)

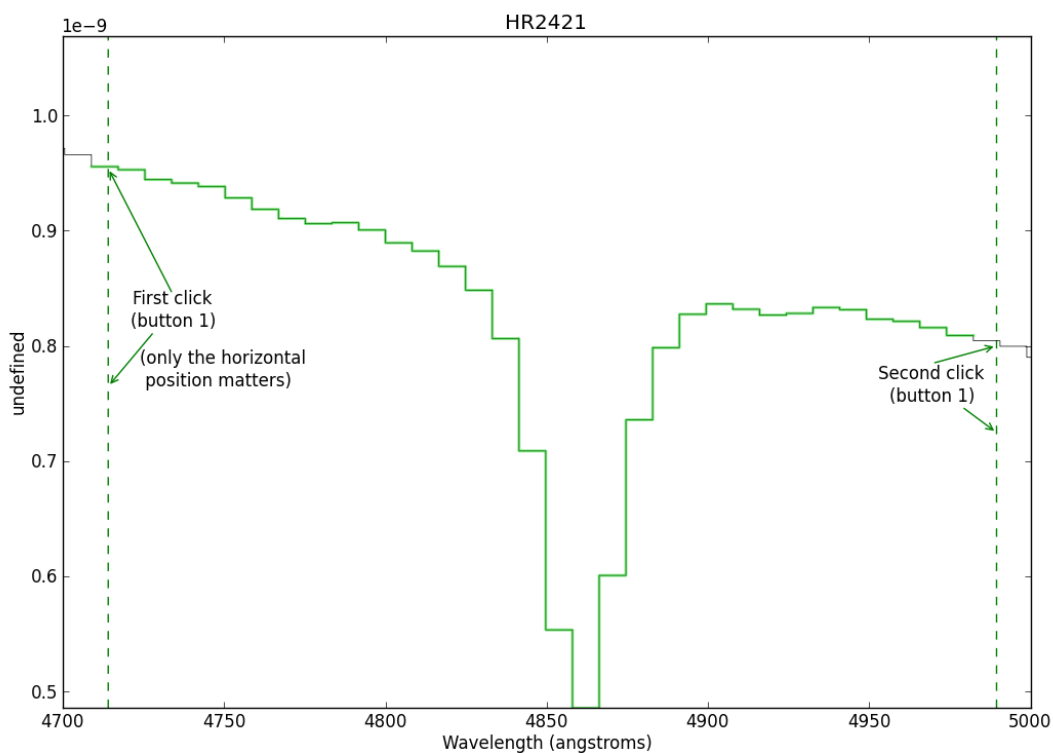
# 5. Start up an interactive line-fitting session
sp.specfit(interactive=True)
```

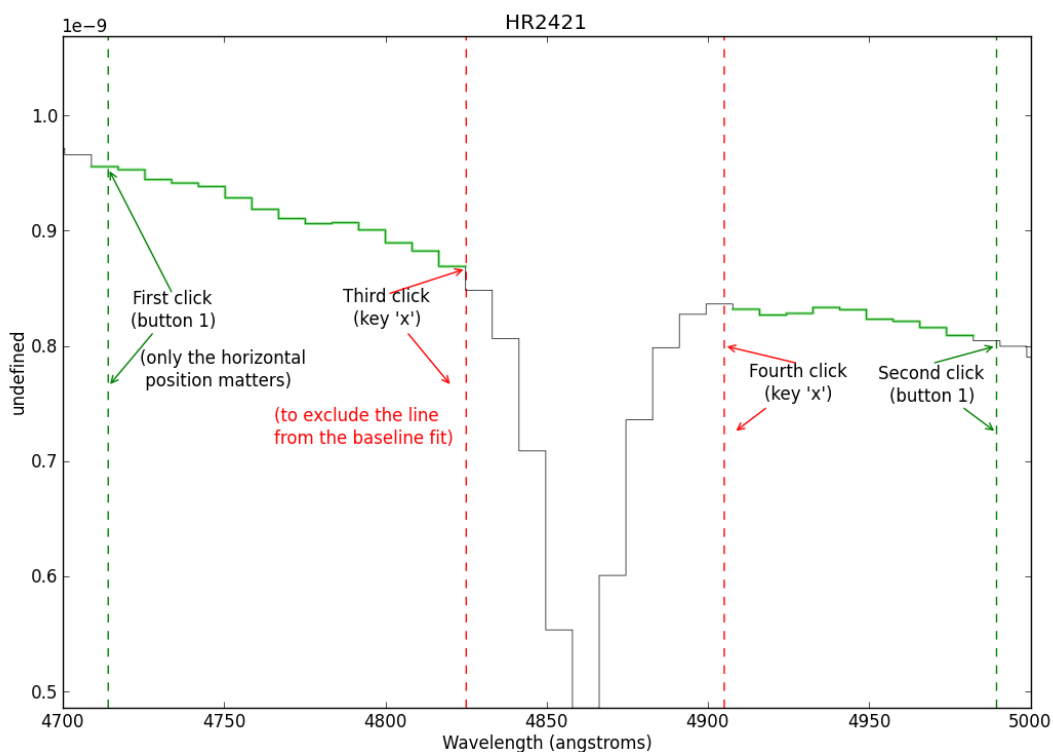
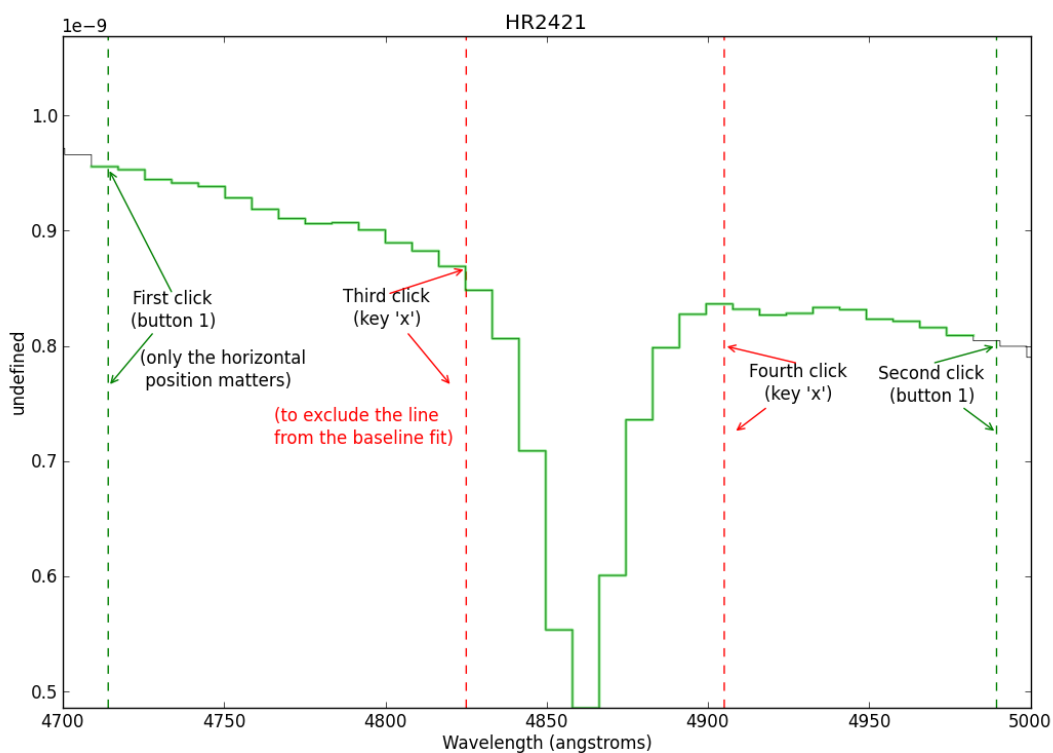
Note: If you don't see a plot window after step #2 above, make sure you're using matplotlib in interactive mode. This may require starting ipython as `ipython --pylab`

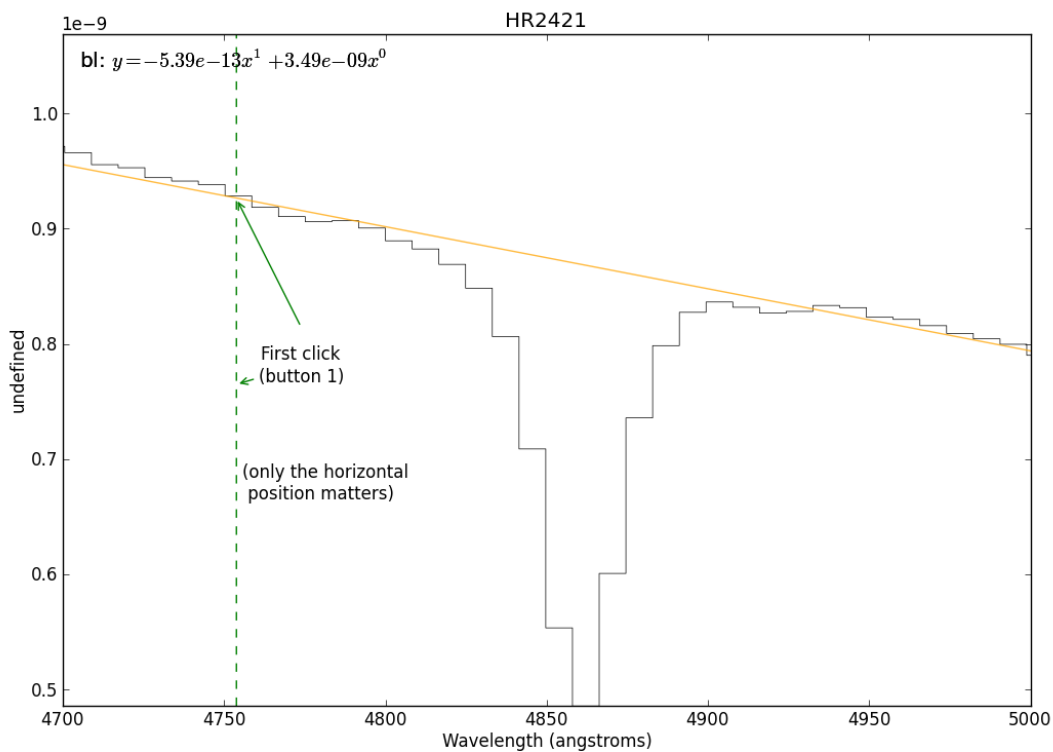
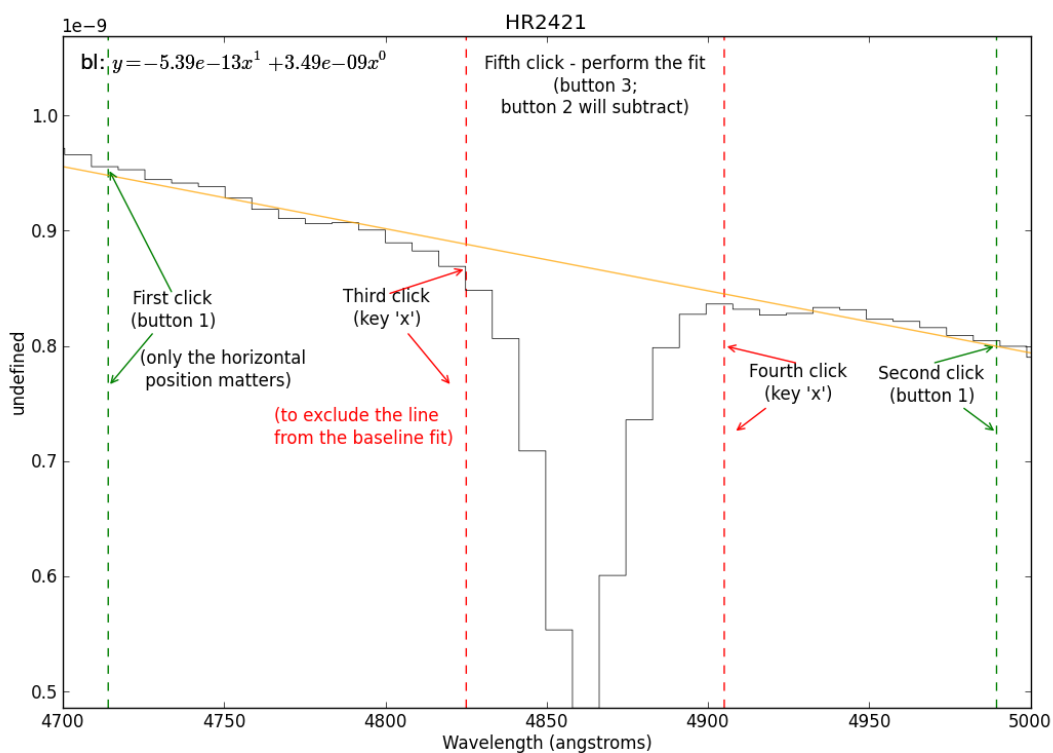
This is where you start the line-fitter:

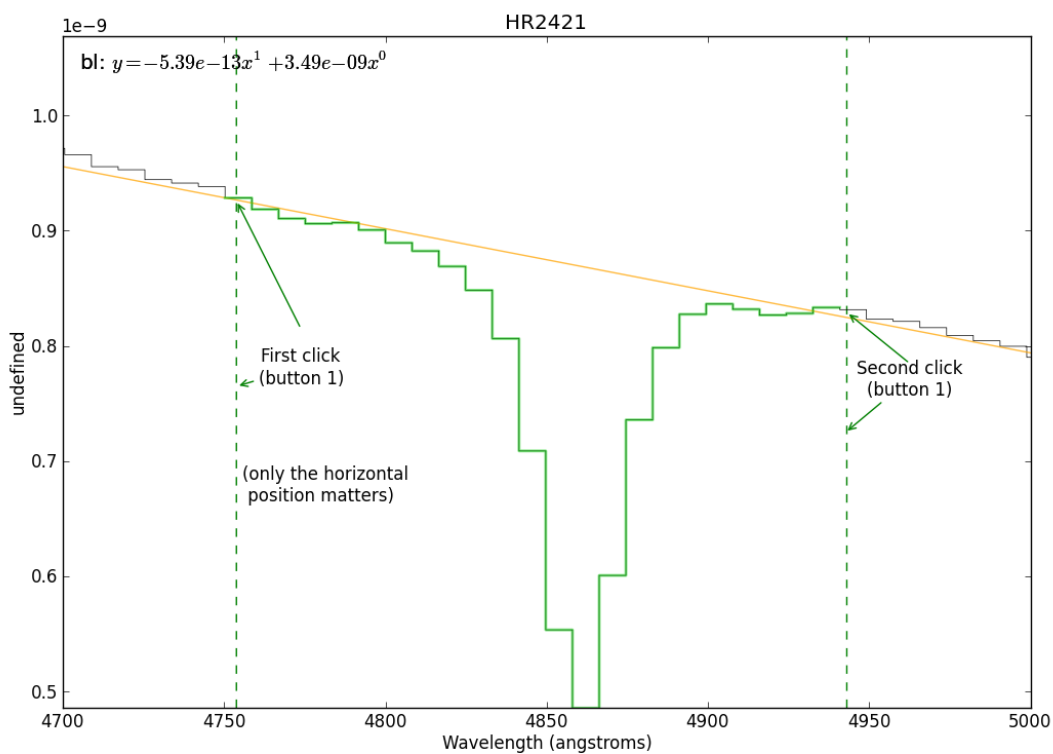
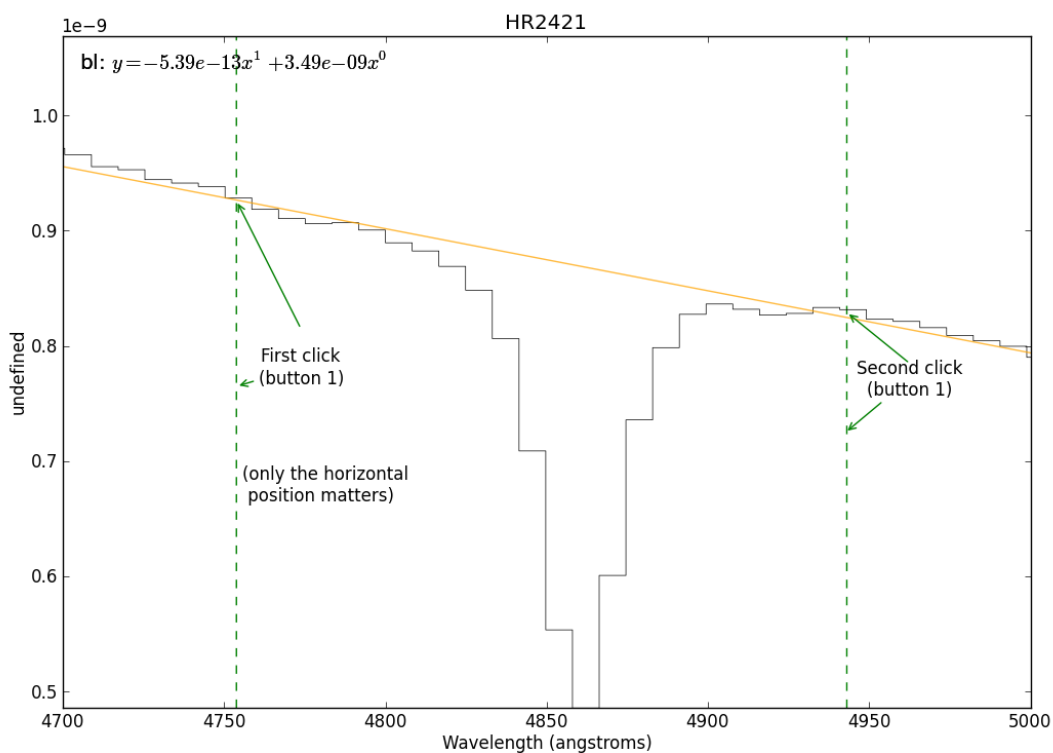
```
# Start up an interactive line-fitting session
sp.specfit(interactive=True)
```

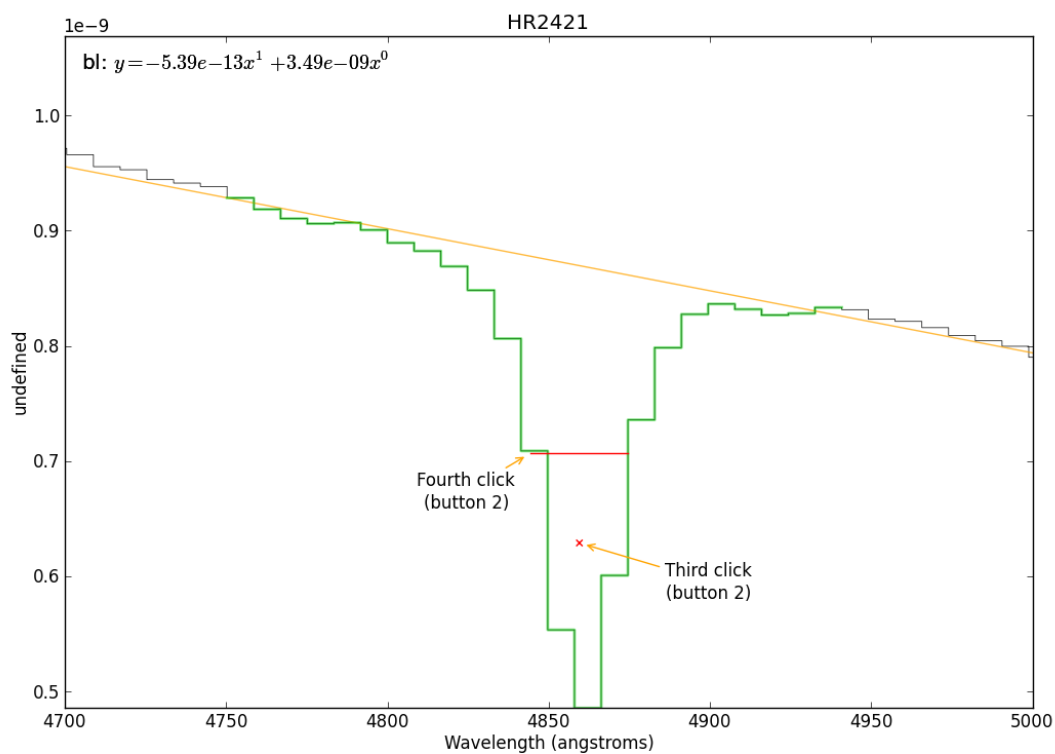
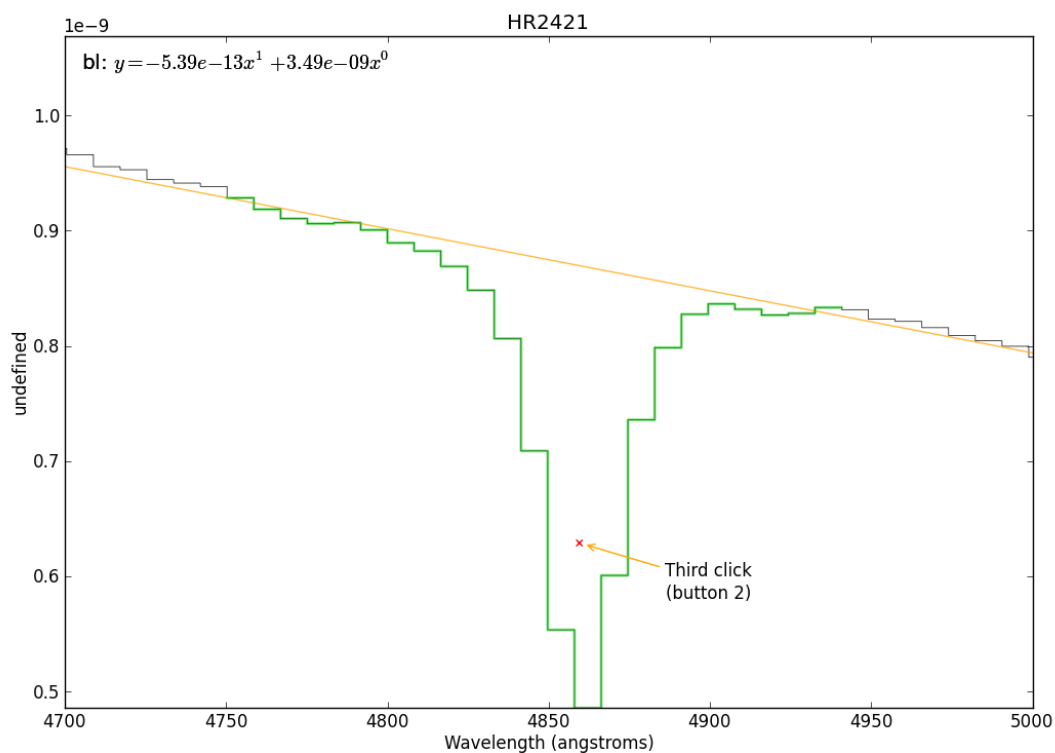


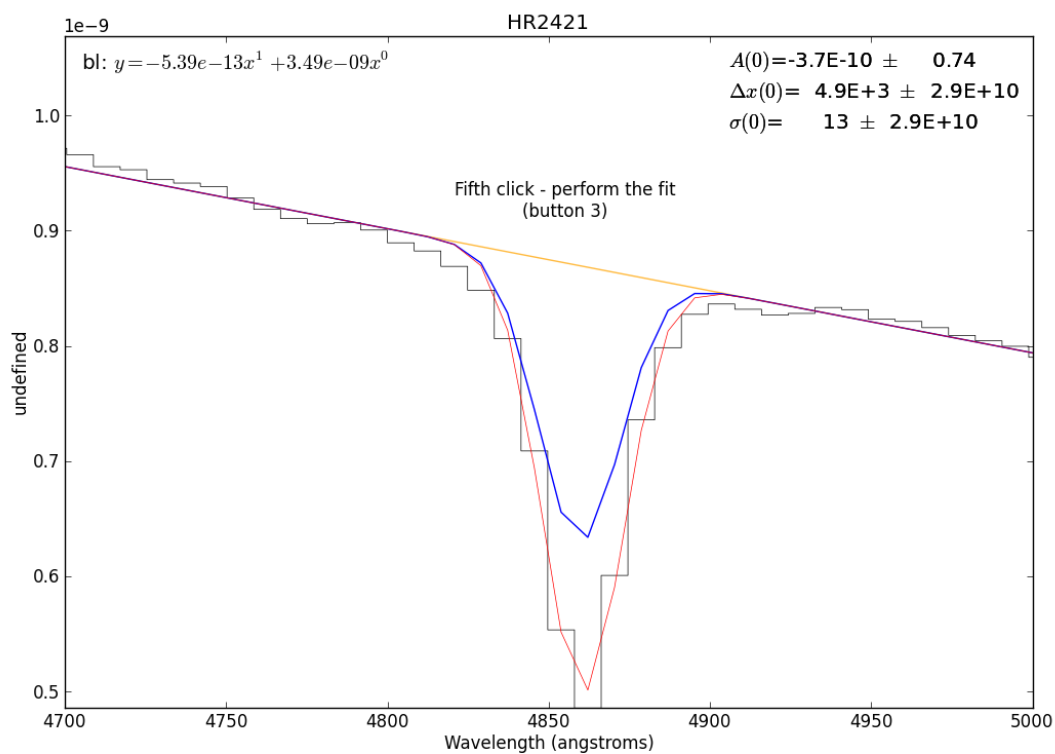
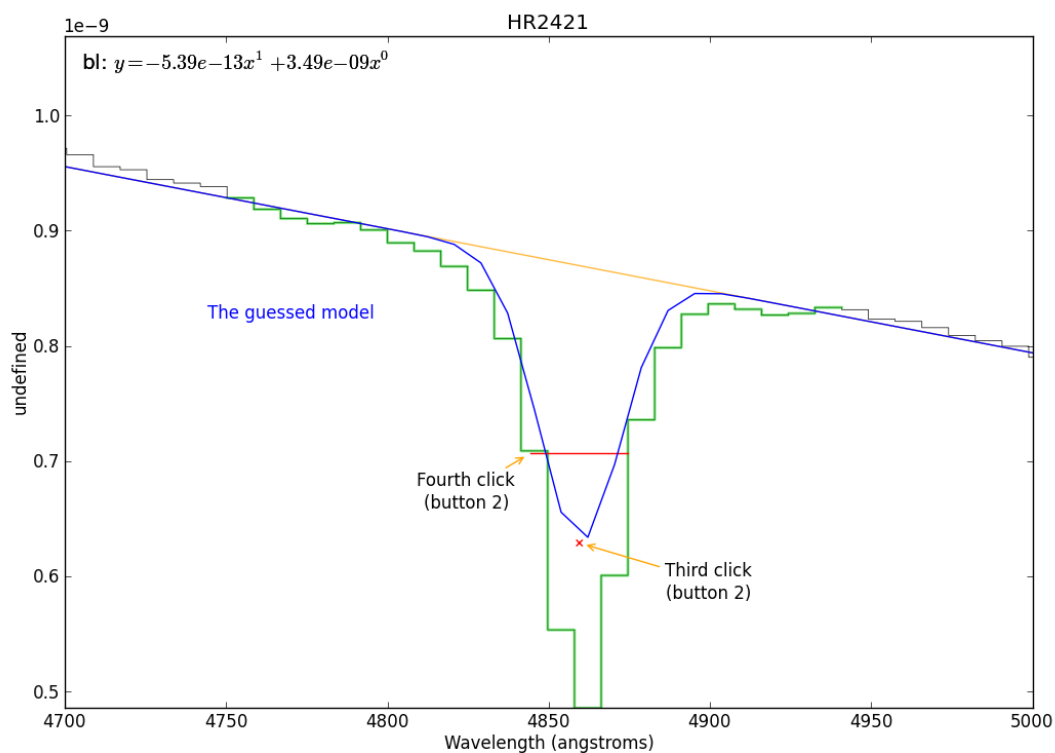












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