



SIMPLE_RUN_GENERAL

```
# -----  
# Read in spectrum  
# -----  
datafile = "../Data/FakeData/PLcompOnly/fakepowlaw1_werr.dat"  
wavelengths, flux, flux_err = np.loadtxt(datafile, unpack=True)  
spectrum = Spectrum()  
spectrum.wavelengths = wavelengths  
spectrum.flux = flux  
spectrum.flux_error = flux_err  
  
# -----  
# Initialize model  
# -----  
model = Model()  
model.print_parameters = False  
# -----  
# Initialize components  
# -----  
nuclear_comp = NuclearContinuumComponent() model.components.append(  
nuclear_comp)  
model.data_spectrum = spectrum # add data  
  
# -----  
# Run MCMC  
# -----  
model.run_mcmc(n_walkers=n_walkers, n_iterations=n_iterations)  
print("Mean acceptance fraction: {0:.3f}".format(np.mean(model.sampler.  
acceptance_fraction)))  
  
# -----  
# save chains & model  
# -----  
with gzip.open('model.pickle.gz', 'wb') as model_output:  
    model_output.write(pickle.dumps(model))
```

SPECTRUM

- ❑ wavelength
- ❑ flux
- ❑ flux error

MODEL

- ❑ data spectrum
- ❑ list of components
- ❑ data mask
- ❑ emcee sampler

combines components into model
estimates likelihood
estimates posterior
run mcmc

PICKLE

ANALYSIS

- ❑ reads MODEL pickle
- ❑ evaluates percentiles
- ❑ plots posteriors, chains, triangle, spectra+model

COMPONENTS

NuclearContinuum

- ❑ normalization
- ❑ slope

generates component flux
estimates priors

BalmerContinuum

HostGalaxy

Emission lines

Reddening

Fe forest