Semi-automatic reduction of spectroscopic observations

Under develpoment

This is meant as a cookbook describing the procedures for analyzing the continuum data (to get calibration information) and applying the calibration parameters automatically to the spectroscopy pipeline.

Please note, that the software is still under development, therefore, some things might change, some might not (yet) work as expected.

Compile a list of appropriate scans for the continuum pipeline. In case of just one used frequency it might be sufficient to give the first and the last scan to the pipeline. It might, however, be useful to have a file with the scans of interest.

Run the continuum pipeline with

```
eff_cont.py —scan 1234-1236 [—fdir /daten/mbfits/mbfits-2019-05/]
```

The conversion factor for going from counts to Jy is found in the subdirectory `./08-results/calibration/` separately for each receiver-baseband combination.

This value - together with the standard gain curve from the receiver pages - should be applied to the call of the spectroscopy pipeline:

```
CmdLinePipeline2 -c 20190618_cal.100m —aatm —atm-method wvr —gaincurve 0.954
3.19E-3 " -5.42E-5" —tcal 9.87
/daten/mbfits/mbfits-2019-06/EFFBG_2019-06-18*19-19*FFTS*fits >
Output_SpekPipeline.txt
```

This pipeline converts the MBFITS-data into Class data performing a calibration at the same time. The flags `—aatm` and `—atm-method wvr` make sure that an opacity correction based on data from the water vapor radiometer is used. The gaincurve parameters (to correct for the gain-elevation effect) can be taken from the webpage (or determined independently). As Tcal here the ratio Tcal/Sensitivity is chosen to get the spectra in Jy that's the values taken from the continuum data, i.e. from the subdirectory `./08-results/calibration/`. A selection of Tcal/MB_efficiency will provide the spectra in T_MB.

The output file can be freely chosen, the selection of input files should be appropriate to accelerate the calculations. It is recommend that the output of the pipeline is stored for further references - just in case.

What is left to do is:

- checking for bad spectra and deleting these
- averaging
- subtracting a baseline
- fitting the line (if appropriate)

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