

# Reducing spectral line data

The raw data (in MBFITS format) are converted to CLASS format automatically. This is done using the method described in Winkel, Kraus, & Bach, *Unbiased flux calibration methods for spectral-line radio observations*, [A&A 540, A140, 2012](#) (Section 3.4 and Section 4.5) - assuming a *constant system temperature* ( $T_{\text{sys}}$ ) and *flat calibration signal* ( $T_{\text{cal}}$ ). The latter is produced by a noise diode the power of which is in most cases directly fed into the waveguide within the receiver. *Neglecting the frequency-dependence of  $T_{\text{sys}}$  and  $T_{\text{cal}}$  introduces a bias, especially for wide-band observations!* (For more information see Winkel, Kraus, & Bach 2012 where we also show ways to do it better.)

The data files can be found on the *observer4* or *observer3* in the directory **/daten/Class/class\_YYYY\_MM\_DD.100m**. There might be a short delay until the data is processed and is visible in the class file after the observation has finished

**Spectra in Class are always in units of  $T_{\text{cal}}$ !** To obtain Kelvins or Jy/Beam you have to multiply with the temperature of the noise diode ( $T_{\text{cal}}$ ) and appropriate antenna sensitivities/efficiencies. Approximate values for this can be found on our receiver website [receiver website](#). However, it is highly recommended to do calibration measurements during your observation for better accuracy. Furthermore, the automatic Class pipeline does not account for atmospheric opacity, elevation-gain curve, and antenna efficiency. Information about these steps can be found in Kraus 2009 (calibration memo).

Of course it is also possible to use the raw data directly, should one wish to do so.

## Using class

To reduce your (spectroscopic and pointing) data with `class` one should use the **observer3** or **observer4** computer. Everyone with an account in the mpifr network can login to this computer with his/her account. It is connected to the `/homes` server. It is also connected to `/homes/astro/gag`, so your `gildas` package of choice should work. It is also possible to use a local version of `class`, which is used to write the spectroscopic and pointing data. To enable this, change to the `bash` shell by typing `bash` and source the init file:

```
source /opt/EffelsbergPipeline/init_classwriter.sh
```

afterward you can run

```
class
```

The Data from the Class pipeline is stored in `/daten/Class`. To open the file with Class use

```
las90> file in "/daten/Class/class_2010_10_20.100m"
las90> find
```

For pointings you have to switch to continuum mode first:

```
las90> set type c
las90> find
```

One can switch back to line observations with:

```
las90> set type l
las90> find
```

To look for new data in the file:

```
las90> new
```

(Note: This doesn't always work. In such cases simply reopen the file, using `file open`.)

Printing is possible using:

```
las90> hardcopy /dev eps color /plot HP-RECH
```

In some cases, a file permission error may occur, in that case create a temporary eps file, please

```
las90> hardcopy "/tmp/tmp.eps" /dev eps color /plot HP-RECH /overwrite
```

A list of available printer names is obtained using

```
sh> lpstat -p -d
```

For more information on how to use Class have a look into the [Gildas documentation](#).

## Frequency switching

Note that in frequency switching mode the Class pipeline already performs the folding (since the `fold` command of Class produces incorrect results for some cases). Details can be found in the [News section](#) and [Winkel, Kraus & Bach 2012](#).

## Reprocessing spectra using the Class pipeline

Sometimes it may be necessary to re-reduce the data with the Class pipeline. This can be done on the observer5 computer. The necessary software is installed in `/opt/EffelsbergSpecPipeline`. There is a bash script to set all the necessary paths. tcsh shell users should change to bash by typing `bash` (the `teleskop` and `obs2` account are already bash accounts). Launch the following command:

```
source /opt/EffelsbergSpecPipeline/init_classwriter.sh
```

Now you should be ready to run the Offline Calibration pipeline. Type

```
OfflinePipeline
```

Now you are in an ipython interface to reduce the data. There are the following commands to reduce the data:

```
setFitsDir('/daten/Raw')
```

which sets the source directory for the rawdata. The program will look in this directory for the raw mbfits files.

```
setClassName('Filename','Directory')
```

This sets the output gildas, class file. If only:

```
setClassName('Filename')
```

is given, the named file is created in the current dictionary. Without this command a file name e.g. like class\_2010\_10\_20.100m is created in the current directory. To write the files one has to know the scan number and must give the subscan number. Subscan numbers are 1 based. If the subscan is not in the file an error is plotted.

```
reduceSubscan(scannumber,subscannumber)
```

If you reduce the same scan twice, it is written twice to the class file with the same scan number. You can investigate the result with using\_class\_on\_observer3\_computer\_in\_effelsberg.

Before February 2011 the reference channel of the FFTS was wrong and has to be shifted by +0.5 channels if the spectrum was not flipped, otherwise -0.5 channels. This can be performed automatically using

```
fixFFTSRefChannel(shiftFFTSRefChannel=True)
flipArrayOrientation(reverseArrayOrientation=True)
```

The latter function flips the dataArrays for the following reduce operations, in case the IF flip needs to be applied (receiver dependent). You may ask local staff for help.

For projects involving lots of scan numbers, one may want to speed up things by using a small piece of python code such that one doesn't have to type in all scan numbers manually:

```
setClassName('myfile.100m')
setFitsDir('/daten/Raw')

# choose the desired scan numbers, using the python range function (the
# second number is exclusive!)
scannums = range(6901, 6930)

# alternatively, you can also use a shell-glob pattern and do some python
# magic to obtain associated scan numbers
import glob, re
filenames = sorted(glob.glob('/daten/Raw/*_27-13_*.FITS'))
scannums = [re.search(r'20\d{6,6}_(\d{4,4})_*', f).group(1) for f in
filenames]

for scannr in scannums:
    info = getScanInfo(scannr)
```

```
print scannr
subscanList = info.getSubscanNumList()
for subscan in subscanList:
    try:
        reduceSubscan(scannr, subscan)
    except:
        pass
```

(In python it is important to keep indentation!)

From:  
<https://eff100mwiki.mpifr-bonn.mpg.de/> - Effelsberg 100m Teleskop

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Last update: 2014/11/30 13:58

