8. MaNGA TRM: Setting up and running the MANGA DR13 pipeline

Outlined here are the steps necessary to set up the MANGA pipeline. In this example, we'll set up the v1_5_4 version. It is assumed that you already have a working version of IDL 7.1 or later.

8.1. Set up Directory Structure

Create a main MaNGA data directory inside which all data will be placed. This folder will be your MANGA_DIR [e.g. !/Users/dlaw/MANGApipe/] in your bash or cshrc files. Note that the path to this root MaNGA data directory must not include the '-' character anywhere.

```
mkdir Manga [e.g. /Users/dlaw/MANGApipe/]
```

Inside this folder create the spectro and gcam subfolders. Inside the spectro subfolder, create folders for data and redux. Data is the directory where the raw data will be stored. Redux is the directory where the 2d output of the full MANGA pipeline will be stored.

```
mkdir data redux [e.g. /Users/dlaw/MANGApipe/spectro/data/, etc ..]
```

Note: Inside your data and gcam directories, the subdirectory structure must be [MJD] where each subdirectory is the MJD of the raw observations. [e.g. !/Users/dlaw/MANGApipe/spectro/data/56290/]

8.2. Checking Out the Necessary Products

From the SDSS4 SVN, you need to check out a number of different products that contain various codes and reference files. The default below checks out the product into the directory you ran the svn command in.

I like to separate the MaNGA pipeline data from the svn products, so I install all of the svn products into a separate SDSS_DIR directory:

```
setenv SDSS_DIR /Users/dlaw/sdss
```

8.2.1. Note on versions

Many of the SVN products will continually be updated over the lifetime of the survey, and as such you'll need to check out different versions as the project evolves. The detailed instructions below are given for the DR13 tagged software versions.

mangadrp: v1_5_4

mangacore: v1_2_3
idlutils: v5_5_23
specflat: v1_26
dust: v0_2
platedesign: v2_52
mangatarget: v1_2_14
mangatile: v2_3
preimaging: v2_1

8.2.2. Download instructions for svn products

Note that the PDF format unfortunately splits things across lines, the following commands should be all on one line for a given product, e.g.,
svn co remotepath localpath

- **MANGADRP**

MaNGA data reduction pipeline code

```
svn co https://svn.sdss.org/public/repo/manga/mangadrp/tags/v1_5_4
$SDSS_DIR/mangadrp/v1_5_4
```

- **MANGACORE**

MaNGA metadata files (~ 1 GB)

```
svn co https://svn.sdss.org/public/repo/manga/mangacore/tags/v1_2_3
$SDSS_DIR/mangacore/v1_2_3
```

- **IDLUTILS**

Shared code between all SDSS projects

```
svn co https://svn.sdss.org/public/repo/sdss/idlutils/tags/v5_5_23
$SDSS_DIR/idlutils/v5_5_23
```

- **SPECFLAT**

This product is ~3 GB and contains files necessary for bias subtraction and pixel flat-fielding, of the 2d raw data.

```
svn co https://svn.sdss.org/public/data/sdss/specflat/tags/v1_26
$SDSS_DIR/specflat/v1_26
```

- **DUST**

This product is ~1 GB and contains dust catalogs (needed for flux calibration).

```
svn co https://svn.sdss.org/public/data/sdss/catalogs/dust/tags/v0_2/
$SDSS_DIR/dust/v0_2
```

- **PLATEDESIGN**

This product is ~10 MB and contains plate design code (needed for astrometry).

svn co https://svn.sdss.org/public/repo/sdss/platedesign/tags/v2_52
$SDSS_DIR/platedesign/v2_52

- **MANGAPREIM**

MaNGA preimaging files (~ 2 GB)

svn co https://svn.sdss.org/public/data/manga/mangapreim/tags/v2_1
$SDSS_DIR/mangapreim/v2_1

8.3. Set up Environment Variables and Path Dependencies

In this step, you need to set up your environment variables and path dependencies in your .bashrc file or .cshrc file to find all of the downloaded products and input/output directories. The following example is for a .cshrc file.

- Make sure a directory and path to IDL exists. IDL_DIR is your path to where IDL is installed on your machine. IDL_PATH is any folder where your IDL files are located. IDL searches for code files inside this path. In these examples, we'll assume default install locations for all products from Step 1, modify these as appropriate

```
   setenv IDL_DIR /usr/local/itt/idl
   setenv IDL_PATH +/usr/local/itt/idl
```

Note that the '+' sign in the above path is important, since it specifies that IDL should descend into subdirectories when looking for code.

- Set up product aliases:

```
setenv SDSS_DIR /Users/dlaw/sdss
setenv MANGA_DIR /Users/dlaw/MANGApipe
setenv MANGA_SPECTRO_DATA $MANGA_DIR/spectro/data
setenv MANGA_SPECTRO_REDUX $MANGA_DIR/spectro/redux
setenv GCAM_DATA $MANGA_DIR/gcam

setenv MANGACORE_DIR $MANGA_DIR/mangacore/v1_2_3
setenv MANGADRP_DIR $MANGA_DIR/mangadrp/v1_5_4
setenv MANGAPREIM_DIR $MANGA_DIR/mangapreim/v2_1
setenv IDLUTILS_DIR $MANGA_DIR/idlutils/v5_5_23
setenv DUST_DIR $MANGA_DIR/dust/v0_2
setenv SPECFLAT_DIR $MANGA_DIR/specflat/v1_26
setenv PLATEDESIGN_DIR $MANGA_DIR/platedesign/v2_52
```

- Include these aliases in paths:

```
setenv IDL_PATH ${IDL_PATH}:+$MANGADRP_DIR/
setenv IDL_PATH ${IDL_PATH}:+$MANGACORE_DIR/
setenv IDL_PATH ${IDL_PATH}:+$MANGAPREIM_DIR/
setenv IDL_PATH ${IDL_PATH}:+$IDLUTILS_DIR/pro
setenv IDL_PATH ${IDL_PATH}:+$PLATEDESIGN_DIR/pro
setenv IDL_PATH ${IDL_PATH}:+$SPECFLAT_DIR/pro
setenv IDL_PATH ${IDL_PATH}:+$IDLUTILS_DIR/goddard/pro
set path = ($MANGADRP_DIR/bin $path)
set path = ($MANGACORE_DIR/bin $path)
set path = ($MANGAPREIM_DIR/bin $path)
set path = ($IDLUTILS_DIR/bin $path)
set path = ($SPECFLAT_DIR/bin $path)
set path = ($PLATEDESIGN_DIR/bin $path)
```

Note that, in some cases, the MANGADRP library uses functions with the same name as in the BOSS IDLSPEC2D library, but whose structure is slightly different. Therefore, if you also have the BOSS pipeline installed on your machine, be sure that it is not present in your IDL path to avoid the DRP grabbing the wrong version of these files.

8.4. Compile C Libraries

The Manga pipeline relies on some C routines that need to be compiled into the necessary library files. You must do this twice, once for idlutils and once for mangadrp. If you have evilmake already installed, then simply navigate to inside your idlutils and mangadrp directories and run the command evilmake. Note that for this to work you will need to have a standard set of C, C++, etc compiler functions installed. One non-standard compiler function that is needed to fully install idlutils is gfortran, which can be found at https://gcc.gnu.org/wiki/GFortranBinaries

```
cd $IDLUTILS_DIR
evilmake
cd $MANGADRP_DIR
evilmake
```

If you do not have evilmake installed, or no alias exists, evilmake is included in idlutils/bin /evilmake.

```
cd $IDLUTILS_DIR
./bin/evilmake
cd $MANGADRP_DIR
$IDLUTILS_DIR/bin/evilmake
```

Successfully running this step should produce .dylib library files inside your idlutils/lib/ directory as well as inside your mangadrp/lib/ directory. If it does not, then something has gone wrong. If you receive an error regarding the file export.h not being found, then your IDL_DIR and/or IDLUTILS_DIR and/or MANGADRP_DIR environment variable is not set, or not set correctly. Double check that this is pointing to your IDL installation, and that you've sourced your .cshrc (or equivalent) before running this command. If you still have trouble, one solution is to manually copy export.h from your $IDL_DIR/external/ directory into each subdirectory in $IDLUTILS_DIR/src/ and into $MANGADRP_DIR/src/ before running evilmake.

You have now successfully installed and set up the MANGA pipeline.

8.5. Download the necessary data

We'll assume that there are specific plate, MJD combinations for which a user wants to run the DRP. You will need to know both the MJD of your observations, and the DESIGNID of the plate if you want to run the full pipeline.

A detailed description of how to access data from the SAS can be found here: http://www.sdss.org/dr13/data_access/bulk

You can browse the MaNGA section of the DR-13 SAS by navigating to https://data.sdss.org/sas/dr13/manga

In the sections below are some specific rsync commands that can be used to pull data from the SAS for common MaNGA usage cases.

8.5.1. Raw spectroscopic data

Download the raw spectroscopic data from the SAS to your local directory for a given MJD (let's say 56741). You can do this by hand via the web browser interface (tedious), or you can grab the entire directory by doing:

```
rsync -avz rsync://data.sdss.org/dr13/manga/spectro/data/56746/ $MANGA_SPECTRO_DATA/56746/
```

8.5.2. Guider data

Guider data (which you will need for each MJD) can be obtained for MJD 56741 for instance by

```
rsync -avz rsync://data.sdss.org/dr13/apo/gcam/56741/ $GCAM_DATA/56741/
```

8.6. Running the MANGA pipeline

Before running the DRP, make sure to download the raw spectroscopic data and the guider data.

8.6.1. 2d Extraction

To run the pipeline, start IDL from any directory. There are many ways to run the pipeline, but the simplest is to reduce a single night of data for one plate using the mdrp_runmanga2d calling routine. To reduce, for example, the all-sky plate from MJD 56693, you would run

```
mdrp_runmanga2d,inop='56693',outop='56693',plate='7341',/full
```

Plate specifies the plate of the observations you are reducing. Inop is a string specifying the MJD of the input raw data directory. Outop is a string name that specifies the output location inside the redux folder, for the reduced files. It is customary to also use the MJD of the observations to keep things orderly. mdrp_runmanga2d.pro will automatically create the appropriate directory structure inside the redux folder at runtime, as well as set all required input path names for the rest of the pipeline. The output folder structure is created as $MANGA_SPECTRO_REDUX / mangadrp_version / [PLATE] / [MJD] / . In the above example, the output folder containing the reduced files is $MANGA_SPECTRO_REDUX/v1_5_4/7341/56693/. The keyword /full specifies to run the full reduction pipeline, as opposed to the quick DOS pipeline. This will (as of May 2014) reduce exposures through the entire 2d DRP; the outputs of this code are the mgFlat, mgArc, mgFrame, mgSFrame, mgFFrame, mgCFrame files, which contain the 2d row-extracted spectra.

8.6.2. 3d Cube Production

Once the 2d pipeline has been fully run for all MJD, the 3d pipeline can be called (for, e.g., plate 7443) by

```
mdrp _runmanga3d,'7443'
```

This will search the MJD subdirectories for mgCFrame-type files and use this to construct the per-IFU RSS and datacube files.

The 3d pipeline can also be run only for individual IFUs (or a subset of them) by specifying, e.g.,:

```
mdrp _runmanga3d,'7443',doifu='12703'
```

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