



## What can I do with my NA added value data products?

Tristan Ashton - 2023-07-07 - Archive & Data Retrieval

The added-value delivery structure is designed to be fully compatible with use of ALMA Pipeline tasks and facilitate comparison with your delivered ALMA calibration + imaging pipeline weblog during analysis of the data and any reprocessing you choose to do. A number of workflows are supported in the new delivery format:

- You can proceed with your scientific analysis starting with the `uid*targets.ms` files and supply them to CASA tasks such as `tclean`, `uvcontsub`, or `gaincal` as a list (`vis=['MS1.ms', 'MS2.ms', etc]`). Examining the casa commands for each stage of the delivered ALMA calibration + imaging weblog will give examples of this (e.g. you can get the `tclean` command for any image that was made by clicking within the relevant `hif_makeimages()` stage).

- You can use `scriptForReprocessing.py` to restore the continuum subtracted data, re-image the data in the ALMA pipeline using new imaging parameters, or view the weblog (see below for usage). Here you can also easily modify `cont.dat` and rerun the continuum subtraction and/or imaging with a different continuum selection.

- You can generate the old style `calibrated_final.ms` either using `scriptForReprocessing.py`, or by hand via `concat()`. If you use `scriptForReprocessing.py`, there is also an option to generate an analogous `calibrated_final_line.ms`.

### #### scriptForReprocessing.py OVERVIEW ####

`scriptForReprocessing.py` is intended to be a convenient wrapper for many of the ALMA pipeline functions that users may wish to use on their NA delivered value-added products. See the ALMA Pipeline Users Guide and Reference Manual for a full description of the ALMA pipeline: <https://almascience.nrao.edu/processing/science-pipeline>

The script can be launched via CASA with any version of CASA that includes the ALMA

pipeline. See the above link for a mapping of ALMA Cycle, CASA version, and Pipeline version. Thus it should be launched as:

```
$ casa --pipeline -c scriptForReprocessing.py [options]
```

optional arguments:

<code>-h, --help</code>	show this help message and exit
<code>--contsub</code>	Fit and subtract continuum using the channel ranges from the local <code>cont.dat</code> file. Generates new <code>*uvcont.tbl</code> tables in <code>working_reprocess/</code> directory and <code>uid*targets_line.ms</code> in <code>measurement_sets/</code>
<code>--contsub_fast</code>	Continuum subtract data via <code>uvcontsub</code> and the local <code>*uvcont.tbl</code> files, but only using the CASA commands rather than pipeline calls (faster). Generates <code>uid*targets_line.ms</code> in <code>measurement_sets/</code>
<code>--image [IMAGE]</code>	Run the imaging pipeline and place images in the specified directory (default='images'). NOTE: unless <code>cont.dat</code> or the imaging options in this script are modified, the images produced will be identical to those on the ALMA Science Archive
<code>--cleanup</code>	Remove <code>working_reprocess/</code> directory and log files after any other options are executed. WARNING: removes weblogs inside of <code>working_reprocess/</code>
<code>--weblog [WEBLOG]</code>	Launches a browser to view weblog after other tasks are run. By default ('latest'), displays the latest weblog generated locally. Other options are to use the specific pipeline folder name (e.g. 'pipeline-20221010T192458')
<code>--calibrated_final</code>	Concatenate <code>uid*targets.ms</code> to produce <code>calibrated_final.ms</code> in <code>measurement_sets/</code>
<code>--calibrated_final_line</code>	Concatenate <code>uid*targets_line.ms</code> (if they exist) to produce <code>calibrated_final_line.ms</code> in <code>measurement_sets/</code>



```

may result in very large disk usage. Consider
# adjusting other mitigation
parameter first, or manually selecting the target/spw
# combinations you want.

# for all values below, see Pipeline Users Guide and Reference Manual for detailed
descriptions:
# https://almascience.nrao.edu/processing/science-pipeline
#
# any parameters not selected here can be edited manually in relevant section of the script
below
maxproductsize = 350. # for mitigation; in GB
maxcubeseize = 40. # for mitigation; in GB
maxcubelimit = 60. # for mitigation; in GB

field = None # String specifying fields to be imaged;
default is all (pending mitigation)
# Example: '3C279, M82'

phasecenter = None # Direction measure or field id of the image
center. The default phase center is
# set to the mean of the field
directions of all fields that are to be image together.
# Examples: 'ICRS
13:05:27.2780 -049.28.04.458', "TRACKFIELD" (for ephemeris)
spw = None # Spw(s) to image; default is all spws
# Example: '17, 23'

uvrange = None # Select a set of uv ranges to image; default
is all
# Examples: '0~1000klambda',
['0~100klambda', '300~1000klambda']
hm_imsz = None # Image x and y size in pixels or PB level;
default is automatically determined
# Examples: '0.3pb', [120, 120]

hm_cell = None # Image cell size; default is automatically
determined
# Examples: '3ppb', ['0.5arcsec',
'0.5arcsec']
nbins = None # Channel binning factor for each spw;
default is none
#
Format: 'spw1:nb1,spw2:nb2,...' with optional wildcards: '*:nb'
# Examples: '9:2,11:4,13:2,15:8',
':2'

```

robust = None  
automatically determined

# Robust value to image with; default is

# Example: 0.5

uvtaper = None

# Uvtaper to apply to data; default is none

# Example: ['1arcsec']

Tags  
delivery  
qa2