

## Project information

|                     |                                                                   |
|---------------------|-------------------------------------------------------------------|
| <b>Name</b>         | New Light in the Dark Heart of Cygnus A                           |
| <b>Code</b>         | 2018.1.01104.S                                                    |
| <b>PI</b>           | Daniel Perley                                                     |
| <b>Organization</b> | Astrophysics Research Institute, Liverpool John Moores University |
| <b>Co-Is</b>        | C. carilli, K. Nyland, R. Perley                                  |

## ObsUnitSet information

|                   |                               |
|-------------------|-------------------------------|
| <b>Name</b>       | Member OUS (Cygnus_A_Nucleus) |
| <b>QA2 Status</b> | 🟢SemiPass                     |

|                                                |                          |
|------------------------------------------------|--------------------------|
| <b>Member OUS Status ID</b>                    | uid://A001/X133d/X29fb   |
| <b>SchedBlock name</b>                         | Cygnus_A_a_07_TM1        |
| <b>SchedBlock UID</b>                          | uid://A001/X133d/X29f5   |
| <b>Array</b>                                   | TM1                      |
| <b>Mode</b>                                    | Standard [Long baseline] |
| <b>Band</b>                                    | ALMA_RB_07               |
| <b>Repr.Freq. (sky)</b>                        | 350.50 [GHz]             |
| <b>Spectral setup</b>                          | TDM                      |
| <b>Sources</b>                                 | Cygnus_A_Nucleus         |
| <b>Other SBs in this Group</b>                 |                          |
| <b>OUS (Member OUS Status ID in brackets):</b> |                          |
| <b>Execution count</b>                         | 0.80 of 1 expected       |

## Final QA2 comment

|                  |                               |
|------------------|-------------------------------|
| CASA Version     | 5.6.1-8 (environment)         |
| Pipeline Version | 42866M (Pipeline-CASA56-P1-B) |

Reduction mode: PL calibration and imaging.

Calibration issues: None.

Imaging issues: RMS is high than requested. angular resolution give a beam larger than requested. Since this is a C6 B grade project, this MOUS is delivered as QA2 semipass

General info for PL products: The continuum was identified by the pipeline although it is recommended that the PI do a more careful identification of the continuum. The continuum was subtracted from all the spectral windows. Self-calibration was not performed. All pipeline products only have a shallow clean, the PI may want to do a deeper clean to improve the images.

For additional information on the calibration and imaging pipeline products please see the Knowledgebase article: <https://help.almascience.org/index.php?/Knowledgebase/Article/View/375/>

## RMS and beam size at representative frequency

|                                           |                                            |                            |       |                             |        |
|-------------------------------------------|--------------------------------------------|----------------------------|-------|-----------------------------|--------|
| <b>Sensitivity goal</b>                   | 0.05000 [mJy] over bandwidth 7.50000 [GHz] |                            |       |                             |        |
| <b>Angular resolution goal</b>            | 0.06000 - 0.09000 [arcsec]                 |                            |       |                             |        |
| <b>Achieved RMS for desired bandwidth</b> | 0.40300 [mJy]                              | <b>for continuum</b>       |       | N/A                         |        |
| <b>Achieved synthesized</b>               |                                            |                            |       |                             |        |
| <b>Major axis (arcsec)</b>                | 0.125                                      | <b>Minor axis (arcsec)</b> | 0.058 | <b>Position angle (deg)</b> | -3.322 |

## Execution blocks summary

| EB                       | N Ant. | Start Time        | End Time          | ToS (sec) | Avg. Elev. (deg) | Trans. Elev. | Mean PWV (mm) | Phase RMS (deg) | Min BL (m) | Max BL (m) | AR (") | MRS (") | EF   |
|--------------------------|--------|-------------------|-------------------|-----------|------------------|--------------|---------------|-----------------|------------|------------|--------|---------|------|
| uid://A002/Xe0b441/X3621 | 47     | 2019-08-30 01:28: | 2019-08-30 02:28: | 3628      | 26.1             | 26.2         | 0.5           | 0.587           | 38.4       | 3637.7     | 0.1    | 1.1     | 0.80 |

## Pipeline executions

| CASA version | Pipeline version              | Report date         | Processing time |
|--------------|-------------------------------|---------------------|-----------------|
| 5.6.1-8      | 42866M (Pipeline-CASA56-P1-B) | 2019-10-15 23:55:11 | 3:43:01         |

### Spectral Windows

| Transition              | Central Frequency (sky, GHz) | Bandwidth (GHz) | N of channels |
|-------------------------|------------------------------|-----------------|---------------|
| Single_Continuum (SW-1) | 336.521                      | 2.000           | 128           |
| Single_Continuum (SW-1) | 338.416                      | 2.000           | 128           |
| Single_Continuum (SW-1) | 348.521                      | 2.000           | 128           |
| Single_Continuum (SW-1) | 350.479                      | 2.000           | 128           |

### Instructions

#### INTERFEROMETRY INSTRUCTIONS OVERVIEW

[Introduction](#)  
[Data Delivery Contents](#)  
[Interferometric Calibration and Imaging Regeneration](#)  
[How to Restore the Calibrated MeasurementSet for Your Data](#)  
[Primary Beam Correction](#)

#####

#### INTRODUCTION

-----

ALMA currently provides data products for each member observation unit set (MOUS), corresponding to one or more executions of a single scheduling block (SB). In all cases except for polarization projects, each execution is independently calibrated, and then all executions are imaged together. The following text describes the contents of this data package. Further details and updates can be found in the ALMA Knowledge Base (KB) articles indicated throughout this document.

#####

#### DATA DELIVERY CONTENTS

-----

Each data package tarball expands to contain a single member\_ouss\_id directory. This directory contains the following directories: calibration, script, qa, log, product.

- For pipeline-calibrated products, the details of what calibration and flagging was performed, many diagnostic plots, and quality assessment is located in the weblog, found in 'qa/'. It should be unzipped and viewed in a web browser. For manually calibrated products, several text files and png images are provided, which can be used in conjunction with the scriptForCalibration.py described below to understand how the data were calibrated. 'qa/' also contains a "QA2 report" which compares the requested image rms to the achieved value.

- 'product/' contains fits files of selected image products. Typically not every image is created (every spectral window for every source), but sufficient images are provided to indicate the quality of the calibration and images. As with calibration, if the products were created by the imaging pipeline, a detailed comprehensive explanation of what images were created, how continuum was subtracted, and the quality of the processing is contained in the pipeline weblog in 'qa/'. If images were created manually, please refer to the scriptForImaging.py described below for details of the

process.

- 'script/' contains the scripts to
    - calibrate raw visibilities: casa\_pipescript.py in the case of pipeline calibration, and scriptForCalibration.py in the case of manual calibration.
    - restore calibrated visibilities without fully rerunning the pipeline: casa\_piperestorescript.py
    - To restore calibrated visibilities, a wrapper script is provided "scriptForPI.py" that works for either pipeline or manually calibrated data. See the section "How to restore the calibrated MeasurementSet (MS) for your data" further below.
    - create images: casa\_pipescript.py in the case of pipeline imaging, and scriptForImagingPrep.py and scriptForImaging.py in the case of manual imaging.
    - In case the calibration was done by the automated pipeline, you will also see the Pipeline Processing Request File (PPR).
- (Note: the ALMA archive may prepend the script names with the MOUS UID.)
- 'calibration/' contains the files needed for calibration starting from the initial ASDM files to the fully calibrated data.
  - 'log' contains the CASA log files.

For more information see the ALMA QA2 Data Products document, the ALMA Technical Handbook (in particular chapter 11 on the QA2 pass criteria), and the relevant Call for Proposals for this Cycle, which are available for download from the ALMA Science Portal at

<http://almascience.org/documents-and-tools>

#####

## INTERFEROMETRIC CALIBRATION AND IMAGING REGENERATION

-----

This section concerns ALMA interferometric (12m Array and ACA) data. The ALMA KB article "How to Restore the Calibrated MeasurementSet (MS) for your Data" at <https://help.almascience.org/index.php?Knowledgebase/Article/View/399> will contain an up-to-date version of the procedures described below.

### How to Restore the Calibrated MeasurementSet (MS) for your Data

-----

Calibration is the first step of processing interferometric data. Many users will want to recreate the calibrated measurement set and then perform the second step (imaging) using their own scripts, or by modifying an imaging script provided with the data.

In order to obtain your calibrated data, you first need to obtain the raw data in ASDM format from the request handler. If you downloaded and untarred all available files for this delivery as described in the notification email, then you will already see (in addition to the directories shown in the tree listing above) a directory "raw" containing your raw data in subdirectories named "uid\*.asdm.sdm" and no further action is necessary. If you do not have a raw directory, you will need to download and untar the tar balls of the raw data belonging to this delivery. If you untar the raw data tarballs in the same directory that you untarred the tarball of the products then they should appear in the "raw" directory in your "member\_ouss\_..." directory.

For the next step, you will need the right version of CASA to be installed. Please find the line starting with "CASA version used for reduction:" in your QA2 report or README. The version indicated there is what you need to use for running the scriptForPI.

Once the raw data is in place, cd into directory "script", start

```
casa --pipeline
```

and type

```
execfile('scriptForPI.py')
```

(For more information on the execution of the pipeline please refer to the ALMA Science Pipeline User's Guide available at <http://almascience.org/documents-and-tools/pipeline-documentation-archive>)

Running the scriptForPI will result in one or more calibrated measurement sets (MSs) ready for imaging. You can use the uid\_\*.ms directly, keeping in mind that the calibrated data is stored in the CORRECTED data column, and all sources (including calibrators) are in the MS. If you want to run the imaging pipeline, you should run it from this point, without changing the uid\_\*.ms.

(Notes: [i] the ALMA archive may prepend the script name with the MOUS UID as in member.uid\_\_Axxx\_Xxxx\_Xxxx.scriptForPI.py . You will need to use the prepended name in those cases. [ii] For some versions, CASA is released without pipeline. If your CASA version is not one with the ALMA pipeline included, the "--pipeline" switch is not available. Check in the "script" directory of your delivery package to see if it contains a file named "PPR\*.xml". If there is no such file, you will be able to run the calibration without the pipeline.)

## Imaging

-----

If the data were imaged with the pipeline, many details of what images were created, how and why, are contained in the pipeline weblog. Each "task" of the pipeline weblog corresponds to a pipeline "hif\_" or "hifa\_" task which the user can run manually to reproduce what the pipeline did, optionally changing parameters. The full sequence of such tasks run by the pipeline is contained in "scripts/casa\_pipescript.py", which could be run to completely reproduce all pipeline processing. Alternatively, the calibrated measurement set produced above can be used as the basis for running only the imaging tasks in the pipeline. See [https://casaguides.nrao.edu/index.php/ALMA\\_Cycle\\_5\\_Imaging\\_Pipeline\\_Reprocessing](https://casaguides.nrao.edu/index.php/ALMA_Cycle_5_Imaging_Pipeline_Reprocessing) for details.

Each imaging section of the weblog also links to the CASA commands that were used by the pipeline these form a good initial template which users can modify to manually image the data with different parameters.

If the data were manually imaged, one should refer to script/scriptForImaging.py which contains the CASA commands that were used to create the image products from the calibrated MS. The "scriptForImaging.py" may partially be interactive (for masking) and should be executed by copy and paste.

## Options

-----

1) If you want to force scriptForPI.py to split out the science SPWs, you need to edit or create the file \*scriptForImaging.py (the ALMA archive might have prepended the name by the MOUS UID) and put at least one line into it that does not contain a "#" (the Python comment character). The scriptForPI will then regard this as a non-trivial imaging script and proceed with the splitting.

2) The scriptForPI will usually run the casa\_piperestorescript, which applies the calibration tables to the raw MS, restoring a calibrated MS. If this is not available (as can be the case for manually-calibrated datasets), the scriptForPI will instead run the entire calibration script on the raw ASDM. You can force the execution of the casa\_pipescript.py, which reruns the entire calibration pipeline, instead of the casa\_piperestorescript.py (which only restores the existing calibration) by moving the casa\_piperestorescript.py out of the script directory. Rerunning the pipeline can be useful if you want to tweak its parameters. Otherwise the restore is faster.

3) The scriptForPI offers some global variables for your convenience. You can find an explanation in this Knowledgebase Article: <https://help.almascience.org/index.php?/Knowledgebase/Article/View/380/>

#####

## PRIMARY BEAM CORRECTION

-----

The images included in delivery are corrected for the primary beam (PB) response, i.e. the dependence of the instrument's sensitivity on direction within the field of view.

For each image, two files are being delivered:

- a) the PB-corrected image (file name ending in ".pbcor.fits")
- b) the image of the PB which was used in the correction (ending in ".flux.fits")

The image noise was measured in the uncorrected image.

The corrected image (a) was then obtained by dividing the uncorrected image by the PB image (b). The

uncorrected image can be recovered using the CASA task `impbcor` in mode "m":

```
impbcor(imagename='image.pbcor.fits', pbimage='image.flux.fits', mode='m', outfile='image.recovered')
```

See also the ALMA KB article "Where is the Primary Beam Correction

Information in my Delivered Data" at

<https://help.almascience.org/index.php?/Knowledgebase/Article/View/398> for any updates to this procedure.

#####