

# Imaging Pipeline Reprocessing Tristan Ashton



# Introduction to the ALMA Pipeline

- Used to calibrated ALMA interferometric (IF) and single-dish (SD) data.
- Automated calibration and imaging
- Modular calibration and imaging tasks within CASA, put together based on standard prescriptions or recipes
- Produces a WebLog a collection of webpages with diagnostic messages, tables, figures and Quality Assurance (QA) scores
- User's guide and other useful documentation: <a href="https://almascience.nrao.edu/processing/science-pipeline">https://almascience.nrao.edu/processing/science-pipeline</a>





### **Outline**

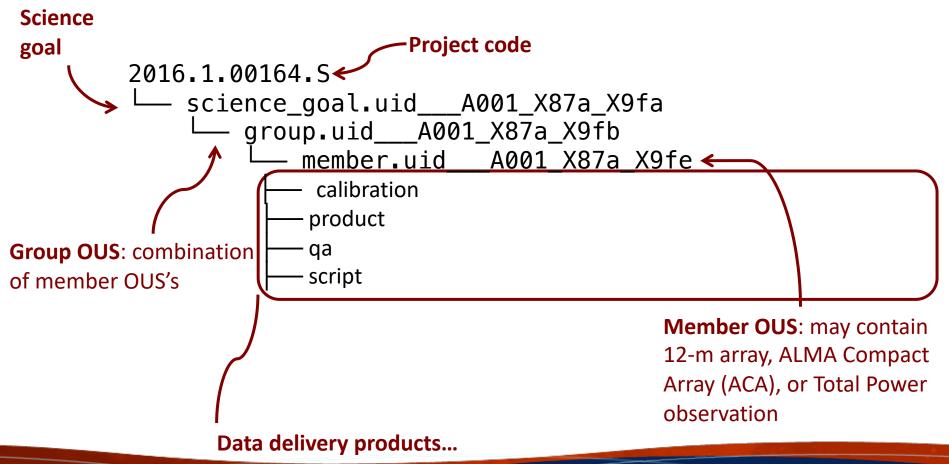
- Obtain the calibrated measurement set
  - scriptForPl.py
  - casa\_piperestorescript.py
  - SRDP
- How to re-run the calibration pipeline, if needed
  - casa pipescript.py
- How to run the imaging pipeline
  - https://casaguides.nrao.edu/index.php?title=ALMA Cycle 9 I maging Pipeline Reprocessing
  - scriptForReprocessing.py





# **QA2 Data Products Package: Directory Structure**

After untarring the processed data we have a directory tree:







# Restore calibrated measurement set scriptForPI.py

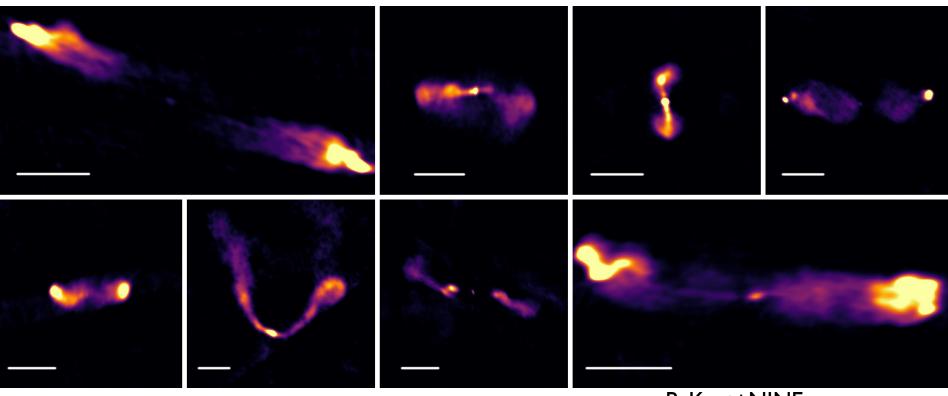
- cd into **script**/ directory
- Start the correct version of casa (casa --pipeline for PL tasks)
- Run scriptForPl.py: execfile('\*scriptForPl.py')
- https://help.almascience.org/index.php?/na/Knowledgebase/Article/View/267
- But if you do want to use a newer version of CASA, inspect the measurement set carefully to make sure flags were applied correctly.
- A few known issues are posted here:
  - https://help.almascience.org/index.php?/Knowledgebase/Article/View/379
  - https://help.almascience.org/index.php?/Knowledgebase/Article/View/395







# **NRAO Science Ready Data Products**



B. Kent+NINE program

https://science.nrao.edu/srdp

https://data.nrao.edu





### What is the SRDP

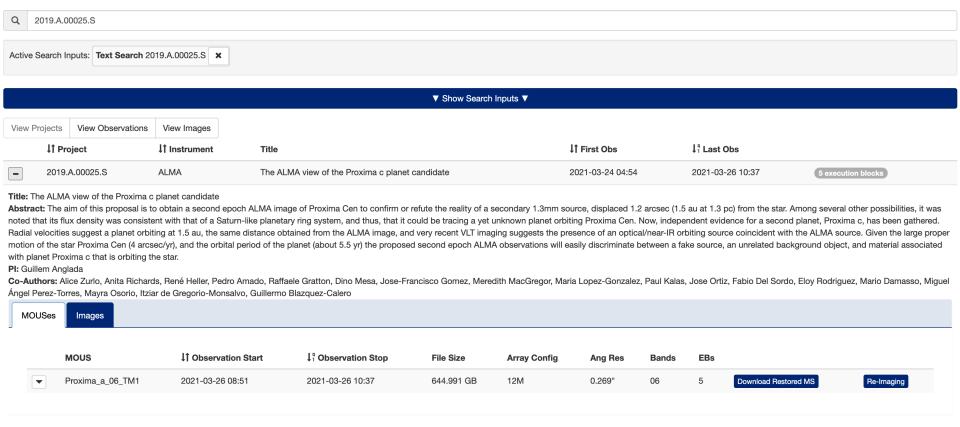
**Project?** 

- Data from modern radio interferometers such as the VLA and ALMA are both very large in terms of volume, and complicated in terms of what the data model allows.
- Significant barriers now exist for newcomers to data from these instruments, and even individuals with expertise find data processing very burdensome.
- This reduces the scientific output of these facilities rather than being limited by the technical capabilities of the instruments, scientists are limited by the logistics of data processing



### Calibrated MS from NRAO Archive

### data.nrao.edu



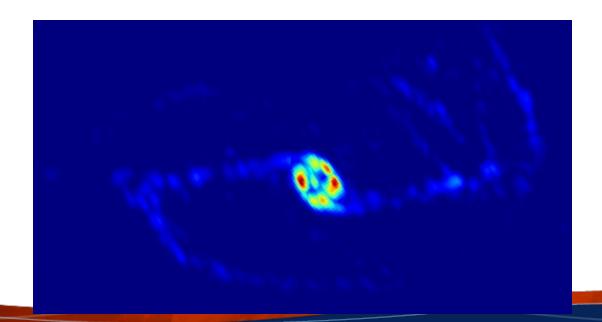






### **ALMA Imaging**

- Users can select their own imaging parameters via a web interface
- Pipeline software will apply the calibration to the raw data, then make the image per the users' request.
- Allows the user to image the part of the cube they want, at the resolution they need.





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  - casa\_pipescript.py
- How to run the imaging pipeline
  - https://casaguides.nrao.edu/index.php?title=ALMA\_Cycle\_9\_I maging\_Pipeline\_Reprocessing
  - scriptForReprocessing.py



# Re-running the pipeline using casa\_pipescript.py

- Needed if you want to:
  - Add flags
  - Update fluxes
  - Update baselines
  - Use a new version of pipeline
  - Add or remove ASDM
  - Change reference antennas

Please see the Pipeline User's Guide for examples!

https://almascience.nrao.edu/processing/science-pipeline





# Pipeline Helper text files

- flux.csv:
  - update the flux of calibrators.
- jyperk.csv:
  - SD pipeline to set the "Kelvin to Jansky" calibration factors which set the overall fluxscale of the data.
- antennapos.csv:
  - update the positions of the antenna elements
- uid\*flagtemplate.txt:
  - add additional CASA flagging commands
- uid\*flagtsystemplate.txt:
  - add additional CASA flagging commands that will be applied to the tsys
- uid\*flagtargetstemplate.txt:
  - add additional CASA flagging commands that will be applied to the data after the calibration tables are calculated, but before science target imaging is performed.
- cont.dat:
  - used to specify the continuum frequency ranges used for constructing the continuum images and creating the continuum-subtracted cubes.







# Re-running the calibration

https://almascience.nrao.edu/processing/science-pipeline

- Create rawdata/, working/, and products/ subdirectories
- Copy uid\*casa\_pipescript.py to casa\_pipescript.py in the working/ directory (edit to include PL steps you wish to repeat)
- Copy flux.csv, antennapos.csv (if present), and uid\*flagtemplate.py (one flagtemplate.py per execution, modify as needed) to the working/ directory
- Copy raw ASDMs (rename without suffix .asdm.sdm) to rawdata/ directory





# Re-running the calibration

https://almascience.nrao.edu/processing/science-pipeline

- In working/
- Modify the pipeline "helper" files
- Edit casa\_pipescript.py to only include the pipeline steps you
  wish to repeat (e.g. commenting out the findcont or imaging
  steps, which are very computationally expensive).
  - See the Pipeline User's Guide
- Start the version of CASA containing Pipeline using
  - casa --pipeline
- You are now ready to run the script by typing execfile('casa\_pipescript.py').



### Re-running the pipeline using casa\_pipescript.py

https://almascience.nrao.edu/processing/science-pipeline

```
rethrow casa exceptions = True
context=h init()
    hifa importdata(dbservice=False,
     vis=['uid___A002_X877e41_X452'], session=['session_1'])
                                            ## Uses flux.csv
    hifa flagdata(pipelinemode="automatic")##Uses *flagtemplate.txt
    hifa fluxcalflag(pipelinemode="automatic")
    hif rawflagchans(pipelinemode="automatic")
    hif refant(pipelinemode="automatic")
    h tsyscal(pipelinemode="automatic")
    hifa tsysflag(pipelinemode="automatic")
    hifa antpos(pipelinemode="automatic") ## Uses antennapos.csv
    hifa wvrgcalflag(pipelinemode="automatic")
    hif lowgainflag(pipelinemode="automatic")
    hif setmodels(pipelinemode="automatic")
    hifa_bandpassflag(pipelinemode="automatic")
    hifa spwphaseup(pipelinemode="automatic")
    hifa gfluxscaleflag(pipelinemode="automatic")
    hifa qfluxscale(pipelinemode="automatic")
    hifa_timegaincal(pipelinemode="automatic")
    hif applycal(pipelinemode="automatic")
    hif makeimlist(intent='PHASE, BANDPASS, AMPLITUDE')
    hif makeimages(pipelinemode="automatic")
    hif makeimlist(per eb=True, intent='CHECK')
    hif makeimages(pipelinemode="automatic")
   hifa_imageprecheck(pipelinemode="automatic")
   hif checkproductsize(maxproductsize=350.0, maxcubesize=40.0,
maxcubelimit=60.0)
    hifa_exportdata(pipelinemode="automatic")
# Start of pipeline imaging commands
    hif mstransform(pipelinemode="automatic")
    hifa_flagtargets(pipelinemode="automatic")
                                ## Uses *flagtargetstemplate.txt
    hif makeimlist(specmode='mfs')
                                            ## Uses cont.dat
    hif_findcont(pipelinemode="automatic") ## Modifies cont.dat
    hif uvcontfit(pipelinemode="automatic") ## Uses cont.dat
    hif uvcontsub(pipelinemode="automatic")
    hif_makeimages(pipelinemode="automatic")## Uses cont.dat
    hif makeimlist(specmode='cont')
                                            ## Uses cont.dat
    hif makeimages(pipelinemode="automatic")## Uses cont.dat
    hif makeimlist(specmode='cube')
                                            ## Uses cont.dat
    hif makeimages(pipelinemode="automatic")## Uses cont.dat
    hif makeimlist(specmode='refBW')
                                            ## Uses cont.dat
    hif makeimages(pipelinemode="automatic")## Uses cont.dat
finally:
    h save()
```

Calibration tasks; ## indicates the use of pipeline helper files

Imaging tasks; ## indicates the use of pipeline helper files





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  - SRDP
- How to re-run the calibration pipeline, if needed
  - casa\_pipescript.py
- How to run the imaging pipeline
  - https://casaguides.nrao.edu/index.php?title=ALMA\_Cycle
     9\_Imaging\_Pipeline\_Reprocessing
  - scriptForReprocessing.py





# Pipeline Image Reprocessing

- Pipeline images are quality assessed but may not be science ready
  - All sources/spws may not be imaged (image mitigation to avoid long PL runs)
  - Change continuum selection
  - Change weighting, channel width, automasking, etc.
    - SRDP re-imaging can handle many of these situations!
- For pipeline calibrated data, see
   <a href="https://casaguides.nrao.edu/index.php/ALMA\_lmaging\_Pipeline\_Reprocessing">https://casaguides.nrao.edu/index.php/ALMA\_lmaging\_Pipeline\_Reprocessing</a>
- For manually calibrated data, see <a href="https://casaguides.nrao.edu/index.php?title=ALMA\_Imaging\_Pipeline\_Reprocessing\_for\_Manually\_Calibrated\_Data">https://casaguides.nrao.edu/index.php?title=ALMA\_Imaging\_Pipeline\_Reprocessing\_for\_Manually\_Calibrated\_Data</a>

### Restore Calibration and Prepare for Re-imaging

- Move to directory with calibrated data
- Copy the uid\*flagtargetstemplate.txt and cont.dat from the calibration directory (if you have one)
- Make your changes, either to helper files or casa\_pipescript.py
- Start casa --pipeline
- execfile('casa\_pipescript.py')





# **CASA** imaging pipeline script

## Without calibration steps!

```
import glob as glob
 __rethrow_casa_exceptions = True
 context = h_init()
#Ine Tollowing context.set_state() statements are setting ancillary information and indeed not
context.set_state('ProjectSummary', 'proposal_code', 'E2E6.1.00092.S')
context.set_state('ProjectSummary', 'piname', 'unknown')
context.set_state('ProjectSummary', 'proposal_title', 'unknown')
context.set_state('ProjectStructure', 'ous_part_id', 'X118955135')
context.set_state('ProjectStructure', 'ous_title', 'Undefined')
context.set_state('ProjectStructure', 'ppr_file', '../working/PPR_uid__A002_Xd0adbd_X56.xml')
context.set_state('ProjectStructure', 'ps_entity_id', 'uid://A002/Xd0adbd/X51')
context.set_state('ProjectStructure', 'ous_entity_id', 'uid://A002/Xd0adbd/X4d')
context.set_state('ProjectStructure', 'ous_entity_id', 'uid://A002/Xd0adbd/X55')
 #The following context.set state() statements are setting ancillary information and indeed not really necessary for imaging.
 context.set_state('ProjectStructure', 'ousstatus_entity_id', 'uid://A002/Xd0adbd/X55')
## Delete uid*_target.ms and flagversions if it exists
 os.svstem('rm -rf uid* target.ms')
 os.system('rm -rf uid* target.ms.flagversions')
MyVis=glob.glob('*.ms')
try:
       hifa_importdata(vis=MyVis,dbservice=False)
       hif mstransform(pipelinemode="automatic")
       hifa flagtargets(pipelinemode="automatic")
       hifa_imageprecheck(pipelinemode="automatic")
       hif_checkproductsize(maxproductsize=350.0, maxcubesize=40.0, maxcubelimit=60.0)
       hif makeimlist(specmode='mfs')
       hif findcont(pipelinemode="automatic")
       hif_uvcontfit(pipelinemode="automatic")
       hif_uvcontsub(pipelinemode="automatic")
       hif makeimages(pipelinemode="automatic")
       hif_makeimlist(specmode='cont')
       hif_makeimages(pipelinemode="automatic")
       hif makeimlist(specmode='cube')
       hif makeimages(pipelinemode="automatic")
       hif makeimlist(specmode='repBW')
       hif_makeimages(pipelinemode="automatic")
       hifa exportdata(imaging products only=True)
 finally:
       h save()
```

#### Goals From OT:

Representative Target: G353.41

Representative Frequency: 93.1787 GHz (SPW 25)

Bandwidth for Sensitivity: 2000 MHz

Min / Max Acceptable Resolution: 0.760 arcsec / 1.14 arcsec Maximum expected beam axial ratio (from OT): Not available

Goal PI sensitivity: Not available Single Continuum: False

#### Estimated Synthesized Beam and Sensitivities for the Representative Target/Frequency

Estimates are given for four possible values of the tolean robust weighting parameter: robust = 0.0, +0.5 (default), +1.0, and +2.0. If the "Min / Max Acceptable Resolution" is available (>=Cycle 5 12-m Array data), the robust value closest to the default (+0.5) that predicts a beam area (defined as simply major x minor) that is in the range of the PI requested beam areas according to the table row for repBW (Bandwidth for Sensitivity) is chosen. If none of these robust values predict a beam area that is in range, robust=+2.0 is chosen if the predicted beam area is too small, and robust=0.0 is chosen if the predicted beam area is too large. The chosen robust value is highlighted in green and used for all science target imaging. In addition to an estimate for the repBW, an estimate for the aggregate continuum bandwidth (aggBW) is also given assuming NO line contamination but accounting for spw frequency overlap. If the Bandwidth for Sensitivity (repBW) is > the bandwidth of the spw containing the representative frequency (repSPW), then the beam is predicted using all spws, otherwise the beam is predicted for the repSPW alone. A message appears on the "By Task" view if a non-default value of robust (i.e., not +0.5) is chosen. Additionally, if the predicted beam is not within the PI requested range using one of the four robust values, Warning messages appear on this page.

These estimates should always be considered as the BEST CASE SCENARIO. These estimates account for Tsys, the observed uv-coverage, and prior flagging. The estimates DO NOT account for (1) subsequent science target flagging; (2) loss of continuum bandwidth due to the hif\_findcont process (i.e. removal of lines and other spectral features from the data used to image the continuum); (3) Issues that affect the image quality like (a) poor match of uv-coverage to image complexity; (b) dynamic range effects; (c) calibration deficiencies (poor phase transfer, residual baseline based effects, residual antenna position errors, etc.). It is also important to note that both the repBW and aggBW beam calculations are intrinsically multi-frequency synthesis continuum calculations, using the relevant spws as described above. The synthesized beam for a single channel in a cube will typically be larger and can be significantly larger depending on the details of uv-coverage and channel width.

robust	uvtaper	Synthesized Beam	Cell	Beam Ratio	Bandwidth	BW Mode	Effective Sensitivity
0.0	0	1.16 x 0.996 arcsec @ 79.2 deg	0.2 x 0.2 arcsec	1.16	2000 MHz	repBW	0.000157 Jy/beam
0.0	0	1.16 x 0.996 arcsec @ 79.2 deg	0.2 x 0.2 arcsec	1.16	2930 MHz	aggBW	0.000129 Jy/beam
0.5	0	1.25 x 1.08 arcsec @ 79.1 deg	0.22 x 0.22 arcsec	1.16	2000 MHz	repBW	0.000124 Jy/beam
0.5	0	1.25 x 1.08 arcsec @ 79.1 deg	0.22 x 0.22 arcsec	1.16	2930 MHz	aggBW	0.000102 Jy/beam
1.0	0	1.37 x 1.20 arcsec @ 78.6 deg	0.24 x 0.24 arcsec	1.14	2000 MHz	repBW	0.000115 Jy/beam
1.0	0	1.37 x 1.20 arcsec @ 78.6 deg	0.24 x 0.24 arcsec	1.14	2930 MHz	aggBW	9.53e-05 Jy/beam
2.0	0	1.43 x 1.25 arcsec @ 77.2 deg	0.25 x 0.25 arcsec	1.14	2000 MHz	repBW	0.000115 Jy/beam
2.0	0	1.43 x 1.25 arcsec @ 77.2 deg	0.25 x 0.25 arcsec	1.14	2930 MHz	aggBW	9.49e-05 Jy/beam

#### Pipeline QA

Score	Reason				
0.85	Predicted non-default robust=0.0 beam is within the PI requested range				





### **Example Cases for Imaging Pipeline changes**

- Aggregate continuum Images with all channels
- Revise continuum ranges
- Remake cubes for a subset of spw and fields with channel binning, new robust, and uv-taper
- All Examples in CASA Guide:

https://casaguides.nrao.edu/index.php?title=ALMA\_Cycle\_8\_Imaging Pipeline Reprocessing

# Aggregate Continuum Image With All Channels

```
## Edit the USER SET INPUTS section below and then execute
## this script (note it must be in the 'calibrated/working' directory.
import glob as glob
rethrow_casa_exceptions = True
pipelinemode='automatic'
context = h init()
## USER SET INPUTS
## Select a title for the weblog
context project summary proposal code='NEW AGGREGATE CONT'
## Delete uid*_target.ms and flagversions if it exists
os.system('rm -rf uid*_target.ms')
os.system('rm -rf uid* target.ms.flagversions')
Change name so pipeline does not
## Move cont.dat to another name if it exists
                                                  pick up the file. All unflagged
os.system('mv cont.dat original.cont.dat'
## Make a list of all uv-datasets appended with *.ms
                                                  channels will be used in
MvVis=alob_alob('*.ms')
                                                  continuum image.
   ## Load the *.ms files into the pipeline
   hifa_importdata(vis=MyVis,dbservice=False,pipelinemode=pipelinemode)
   ## Split off the science target data into its own ms (called
   ## *target.ms) and apply science target specific flags
                                                             No findcont step to
   hif_mstransform(pipelinemode=pipelinemode)
   hifa flagtargets(pipelinemode=pipelinemode)
                                                             make new cont.dat!
   ## calculate the synthesized beam and estimate the sensitivity
   ## for the aggregate bandwidth and representative bandwidth
   ## for three values of the robust parameter.
   hifa_imageprecheck(pipelinemode="automatic")
   ## check the imaging product size and adjust the relevent
   ## imaging parameters (channel binning, cell size and image size)
   ## User can comment this out if they don't want size mitigation.
   hif checkproductsize(maxproductsize=350.0, maxcubesize=40.0, maxcubelimit=60.0)
   ## Skip the continuum subtraction steps and make an aggregate
   ## continuum image with all unflagged channels (file named
   ## cont.dat should NOT be present in directory).
   hif_makeimlist(specmode='cont',pipelinemode=pipelinemode)
   hif_makeimages(pipelinemode=pipelinemode)
   ## Export new images to fits format if desired.
   hifa exportdata(pipelinemode=pipelinemode)
finally:
```

h save()

## **Revise Continuum Range**

See Section 7.6 of Pipeline User's guide for more cont.dat

Edit or create a cont.dat file in the working directory

#### 31. Find Continuum

Field	Spw	Continuum Frequency Range Start End Frame		Status	Average spectrum	
GM_Aur	25	260.13811 GHz	260.14079 GHz	LSRK	NEW	out_ability 12465, 71541-51, 500 Aur. on ourly on 1 the district reduction of the control 113 Aur. on our 125 Aur. on our 125 Aur. on our 113 Aur. our
		260.14250 GHz	260.14397 GHz			10 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C
		260.14726 GHz	260.14812 GHz			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
		260.14971 GHz	260.15276 GHz			Source A state of the state of
		260.15691 GHz	260.15874 GHz			GEALT PRINCIPAL N.S. S.L.S. opportunis 6.95. respilator, 1.106, pointure-1.110  OBALLY OFFI SON THE BOOK OFFI SON THE
		260.16009 GHz	260.16070 GHz			
		260.16241 GHz	260.16631 GHz			
		260.16876 GHz	260.17633 GHz			
		260.17816 GHz	260.18146 GHz			
		260.18304 GHz	260.18402 GHz			
		260.18683 GHz	260.18976 GHz			
		260.19367 GHz	260.19635 GHz			
		260.19867 GHz	260.19989 GHz			
		260.20563 GHz	260.20881 GHz			

Field: GM\_Aur

SpectralWindow: 25

260.1381059540~260.1407923828GHz LSRK 260.1425019284~260.1439672532GHz LSRK 260.1472642340~260.1481190068GHz LSRK 260.1497064420~260.1527592020GHz LSRK 260.1569109556~260.1587426116GHz LSRK 260.1600858260~260.1606963780GHz LSRK 260.1624059236~260.1663134564GHz LSRK 260.1687556644~260.1763265092GHz LSRK 260.1781581652~260.1814551460GHz LSRK 260.1830425812~260.1840194644GHz LSRK 260.1868280036~260.1897586532GHz LSRK 260.1936661860~260.1963526148GHz LSRK 260.1986727124~260.1998938164GHz LSRK 260.1986727124~260.1998938164GHz LSRK





### **Revise Continuum Range**

```
## USER SET INPUTS
## Select a title for the weblog
context.project_summary.proposal_code = 'NEW CONTSUB'
## Delete uid*_target.ms and flagversions if it exists
os.system('rm -rf uid* target.ms')
os.system('rm -rf uid*_target.ms.flagversions')
## Select spw(s) that have new cont.dat parameters
## If all spws have changed use MySpw=''
MySpw='17'
## Make a list of all uv-datasets appended with *.ms
MyVis=glob('*.ms')
try:
   ## Load the *.ms files into the pipeline
   hifa_importdata(vis=MyVis,dbservice=False,pipelinemode=pipelinemode)
   ## Split off the science target data into its own ms (called
   ## *target.ms) and apply science target specific flags
   hif mstransform(pipelinemode=pipelinemode)
   hifa flagtargets(pipelinemode=pipelinemode)
   ## Fit and subtract the continuum using revised cont.dat for all spws
   hif_makeimlist(specmode='mfs',spw=MySpw)
                                          Will use new cont.dat in uvcontsub
   hif uvcontfit(pipelinemode=pipelinemode)
   hif_uvcontsub(pipelinemode=pipelinemode)
   hif_makeimages(pipelinemode=pipelinemode)
   ## calculate the synthesized beam and estimate the sensitivity
   ## for the aggregate bandwidth and representative bandwidth
   ## for three values of the robust parameter.
   hifa imageprecheck(pipelinemode=pipelinemode)
   ## check the imaging product size and adjust the relevent
   ## imaging parameters (channel binning, cell size and image size)
   ## User can comment this out if they don't want size mitigation.
   hif_checkproductsize(maxproductsize=350.0, maxcubesize=40.0, maxcubelimit=60.0)
   ## Make new aggregate cont
                                                           Will make Continuum images
   hif_makeimlist(specmode='cont',pipelinemode=pipelinemode)
   hif_makeimages(pipelinemode=pipelinemode)
                                                           using cont.dat selection
   ## Make new continuum subtracted cube for revised spw(s)
   hif_makeimlist(specmode='cube',spw=MySpw,pipelinemode=pipelinemode)
   hif makeimages(pipelinemode=pipelinemode)
   ## Export new images to fits format if desired.
   hifa_exportdata(pipelinemode=pipelinemode)
```

### Remake cubes with select spw, bins, fields, robust

## Select a title for the weblog context.project\_summary.proposal\_code = 'SUBSET CUBE IMAGING' ## Delete uid\*\_target.ms and flagversions if it exists os.system('rm -rf uid\* target.ms') os.system('rm -rf uid\*\_target.ms.flagversions') Select spw(s) to image and channel binning for each spcified ## MySpw. All spws listed in MySpw must have a corresponding MyNbins ## entry, even if it is 1 for no binning. MySpw='17,23' MyNbins='17:8,23:2' ## Select subset of sources to image by field name. ## To select all fields, set MyFields=' MyFields='CoolSource1,CoolSource2' ## Select Briggs Robust factor for data weighting (affects angular ## resolution of images) MyRobust=1.5 ## Make a list of all uv-datasets appended with \*.ms MyVis=qlob.qlob('\*.ms') ## Load the \*.ms files into the pipeline hifa\_importdata(vis=MyVis, dbservice=False, pipelinemode=pipelinemode) ## Split off the science target data into its own ms (called ## \*target.ms) and apply science target specific flags ## In this example we split off all science targets and science ## spws, however hif\_mstransform could also contain the spw and field ## selections hif\_mstransform(pipelinemode=pipelinemode) hifa\_flagtargets(pipelinemode=pipelinemode) ## Fit and subtract the continuum using existing cont.dat ## for selected spws and fields only. hif\_makeimlist(specmode='mfs') hif\_uvcontfit(spw=MySpw,field=MyFields,pipelinemode=pipelinemode) hif\_uvcontsub(spw=MySpw,field=MyFields,pipelinemode=pipelinemode) hif makeimages(pipelinemode=pipelinemode) ## calculate the synthesized beam and estimate the sensitivity ## for the aggregate bandwidth and representative bandwidth

## Don't need to run this task if you will use a different robust value anyway.

## for three values of the robust parameter.

h\_save()

## hifa\_imageprecheck(pipelinemode=pipelinemode)

## check the imaging product size and adjust the relevent ## imaging parameters (channel binning, cell size and image size) ## User can comment this out if they don't want size mitigation.

Include parameters in task calls

**Set parameters** 

Check Pipeline Reference Manual for parameters of pipeline tasks!

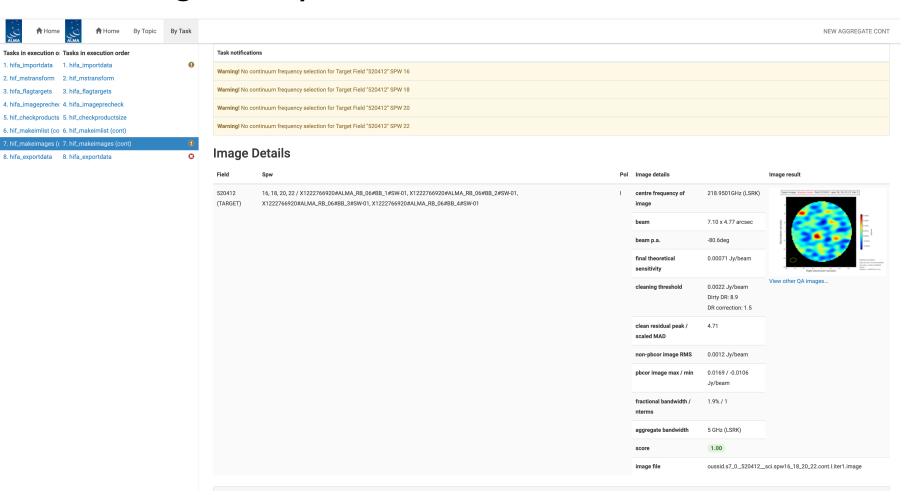
hif\_checkproductsize(maxproductsize=350.0, maxcubesize=40.0, maxcubelimit=60.0)

## Make new continuum subtracted cube for selected spw(s) and fields
hif\_makeimlist(specmode='cube',spw=MySpw,nbins=MyNbins,field=MyFields,robust=MyRobust, pipelinemode=pipelinemode)
hif\_makeimages(pipelinemode=pipelinemode)

## Export new images to fits format if desired.
hifa\_exportdata(pipelinemode=pipelinemode)

# Imaging pipeline reprocessing

A weblog is always created!







### **Outline**

- Obtain the calibrated measurement set
  - scriptForPI.py
  - casa piperestorescript.py
  - SRDP
- How to re-run the calibration pipeline, if needed
  - casa pipescript.py
- How to run the imaging pipeline
  - https://casaguides.nrao.edu/index.php?title=ALMA Cycle 9 I maging Pipeline Reprocessing
  - scriptForReprocessing.py

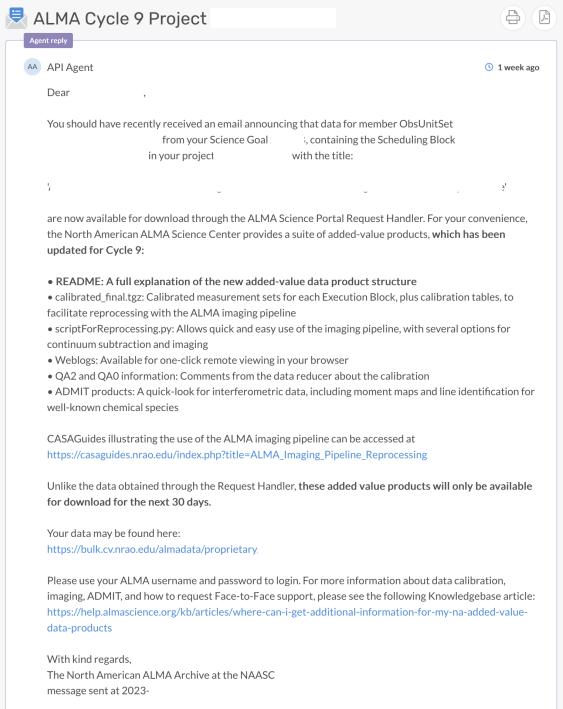






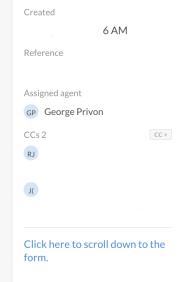
## scriptFo

- IncludeCycle \$
- calibrat









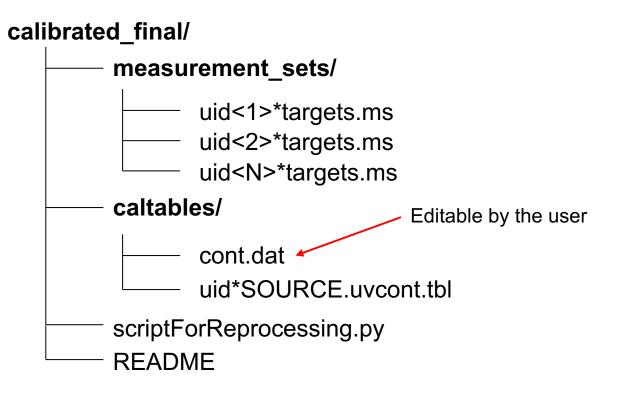
Department

Cycle 9 Observing Programs

**Ticket Properties** 

(NA)

# calibrated\_final.tgz





## Reproduce Pipeline Images

- By default, identical images to those seen in the original weblog are produced
- cd to calibrated\_final/
- Run casa --pipeline
  - execfile('scriptForReprocessing.py [flags]')
- Or: casa --pipeline -c scriptForReprocessing.py [flags]





# Script flags

-h, --help show this help message and exit --contsub Fit and subtract continuum using the channel ranges from the local cont.dat file. Generates new \*uvcont.tbl tables in working reprocess/ directory and uid\*targets\_line.ms in measurement\_sets/ Continuum subtract data via uvcontsub and the local \*uvcont.tbl files, but --contsub fast only using the CASA commands rather than pipeline calls (faster). Generates uid\*targets\_line.ms in measurement\_sets/ --image [IMAGE] Run the imaging pipeline and place images in the specified directory (default='images'). NOTE: unless cont.dat or the imaging options in this script are modified, the images produced will be identical to those on the ALMA Science Archive Remove working\_reprocess/ directory and log files after any other options --cleanup are executed. WARNING: removes weblogs inside of working\_reprocess/ --weblog [WEBLOG] 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') --calibrated final Concatenate uid\*targets.ms to produce calibrated\_final.ms in measurement sets/ --calibrated\_final\_line Concatenate uid\*targets\_line.ms (if they exist) to produce calibrated\_final\_line.ms in measurement\_sets/





### Imaging with different parameters

make\_mfs\_images = True make\_cont\_images = True make\_cube\_images = True make\_repBW\_images = True mitigate = True # generate mfs (per spw) images # generate aggregate continuum images

# generate cube images

# generate images corresponding to the requested representative bandwidth # run hif\_checkproductsize() and mitigate created products if necessary.

# Set to false if you want all spws and all targets imaged at full resolution.

# WARNING: turning off mitigation 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 maxcubesize = 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\_imsize = 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 # Robust value to image with; default is automatically determined

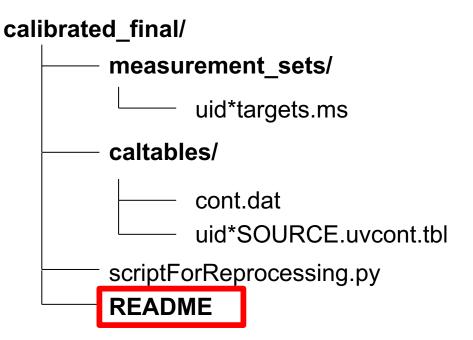
# Example: 0.5

uvtaper = None # Uvtaper to apply to data; default is none

# Example: ['1arcsec']



## calibrated\_final.tgz



https://help.almascience.org/kb/articles/where-can-i-get-additional-information-for-my-na-added-value-data-products

https://help.almascience.org/kb/articles/what-can-i-do-with-my-na-added-value-data-products





#### Historical Articles (25)

- Why are flux scaling and restoring beam calculations in the tas...
- Why must I justify data rates higher than 40 MB/s in my Cycle ...
- OT will not start due to a security exception

TA Tristan Ashton Published: Jul 6, 2023

- What is a Cycle 7 Solar data issue I should be aware of?
- I heard that images generated with CASA<5.1.1 are affected by ...</p>



#### Archive & Data Retrieval (32)

- How do I obtain a file of calibrated visibilities ("measurement s...
- How are ALMA data products packaged?
- Can I download individual data products or images?
- Can I search for a list of sources at the same time?
- Is it possible to resume interrupted downloads?

View all articles in Historical Articles >

View all articles in Archive & Data Retrieval >

Where can I get additional information for my NA added value data products?

AL Andrew Lipnicky Published: Jan 22, 2019

What are the current QA2 requirements?

Sw Sarah Wood Published: Nov 19, 2019

How can I solve this astroquery problem?

Published: May 27, 2021

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



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