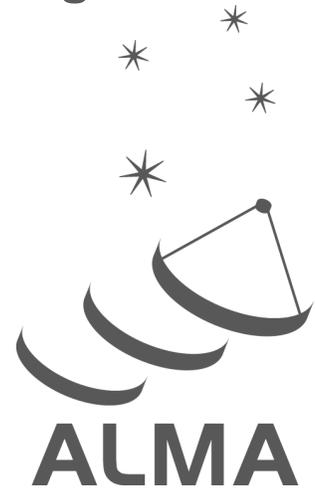


User Support:

# ALMA Science Pipeline User's Guide for Release 2020.1, CASA 6.1.1

## Interferometric and Single-Dish Processing



[www.almascience.org](http://www.almascience.org)

For further information or to comment on this document, please contact your regional Helpdesk through the ALMA User Portal at [www.almascience.org](http://www.almascience.org). Helpdesk tickets will be directed to the appropriate ALMA Regional Center at ESO, NAOJ or NRAO.

## Revision History:

---

Version	Date	Editors
3.13v1.0 CASA 4.5.1	January 2016	Pipeline Team
4.13v1.0 CASA 4.7.0	October 2016	Pipeline Team
4.13v2.0 CASA 4.7.2	July 2017	Pipeline Team
5.13v1.0 CASA 5.1.1	November 2017	Pipeline Team
6.13v1.0 CASA 5.4.0	October 2018	Pipeline Team
7.13v1.0 CASA 5.6.1	October 2019	Pipeline Team
7.13v2.0 CASA 6.1.1	October 2020	Pipeline Team

---

In publications, please refer to this document as:

**ALMA Pipeline Team, 2020, ALMA Science Pipeline User's Guide, ALMA Doc 7.13v2.0**



# Table of Contents:

Table of Contents: .....	1
<b>1 The ALMA Science Pipeline .....</b>	<b>4</b>
1.1 Purpose of this document .....	4
1.2 Pipeline Overview and nomenclature .....	4
<b>2 Quick Start .....</b>	<b>5</b>
<b>3 What's New in 2020.1 .....</b>	<b>6</b>
3.1 Major new capabilities .....	6
3.2 New features and improvements by weblog section and processing stage.....	6
3.3 Current Known Limitations of the 2020.1 Pipeline .....	15
<b>4 Pipeline Versions &amp; Documentation .....</b>	<b>18</b>
4.1 Obtaining the Pipeline .....	18
4.2 Pipeline-related Documentation .....	18
4.3 Pipeline & CASA Versions.....	18
4.4 Pipeline and CASA tasks.....	18
<b>5 Data Processing Files.....</b>	<b>20</b>
5.1 Archived scripts .....	20
5.2 Pipeline "Helper" text files.....	20
5.3 The Pipeline script to restore calibrated MSs: casa_piperestorescript.py .....	21
5.4 The Pipeline processing script: casa_pipescript.py .....	22
5.5 CASA equivalent commands file: casa_commands.log .....	26
<b>6 Modifying a Pipeline Run using casa_pipescript.py.....</b>	<b>27</b>
6.1 Pipeline re-processing considerations .....	27
6.2 Preparing to run casa_pipescript.py.....	27
6.3 Modifying Calibration Commands.....	28
6.4 Modifying IF Pipeline Imaging Commands.....	28
6.5 Manual imaging after running casa_pipescript.py .....	29
6.6 Manipulating the Pipeline Context.....	30
<b>7 Description of Pipeline "Helper" Text Files .....</b>	<b>32</b>
7.1 IF Pipeline: flux.csv .....	32
7.2 SD Pipeline: jyperk.csv .....	33
7.3 IF Pipeline: antennapos.csv.....	34
7.4 Both IF & SD Pipeline: uid*flagtemplate.txt and uid*flagstemplate.txt .....	35
7.5 IF Imaging Pipeline: uid*flagtargetstemplate.txt.....	36
7.6 IF Imaging Pipeline: cont.dat.....	36
<b>8 The Pipeline WebLog.....</b>	<b>38</b>
8.1 Overview .....	38
8.2 Navigation .....	40
8.3 Home Page .....	40
8.4 By Topic Summary Page.....	42
8.5 By Task Summary Page .....	42
8.6 Task Pages .....	45
8.7 WebLog Quality Assessment (QA) Scoring.....	49

<b>9</b>	<b>Interferometric pipeline tasks and “by task “weblog pages</b>	<b>56</b>
9.1	hifa_importdata	56
9.2	hifa_flagdata	56
9.3	hifa_fluxcalflag	56
9.4	hif_rawflagchans	58
9.5	hif_refant	59
9.6	h_tsyscal	59
9.7	hifa_tsysflag	59
9.8	hifa_antpos	62
9.9	hifa_wvrgcalflag	62
9.10	hif_lowgainflag	62
9.11	hif_setmodels	62
9.12	hifa_bandpassflag	63
9.13	hifa_bandpass	64
9.14	hifa_spwphaseup	64
9.15	hifa_gfluxscaleflag	64
9.16	hifa_polcalflag (polarization recipes only)	64
9.17	hifa_session_refant (polarization recipes only)	64
9.18	hifa_lock_refant (polarization recipes only)	65
9.19	hifa_gfluxscale	65
9.20	hifa_timegaincal	66
9.21	hifa_targetflag	66
9.22	hif_applycal	67
9.23	hif_makeimlist: Set-up parameters for calibrator images	68
9.24	hif_makeimages: calibrator images	68
9.25	hif_makeimlist: check source imaging	69
9.26	hif_makeimages: check source imaging and QA information	69
9.27	hifa_imageprecheck	71
9.28	hif_checkproductsizes: Mitigation to avoid overly long runs	73
9.29	hifa_exportdata	76
9.30	hif_mstransform	76
9.31	hifa_flagtargets	76
9.32	hif_makeimlist: Set-up parameters for target per-spw continuum imaging	76
9.33	hif_findcont	76
9.34	hif_uvcontfit	78
9.35	hif_uvcontsub	78
9.36	hif_makeimages: Make target per-spw continuum images	78
9.37	hif_makeimlist: Set-up parameters for target aggregate continuum images	81
9.38	hif_makeimages: Make target aggregate continuum images	81
9.39	hif_makeimlist: Set-up image parameters for target cube imaging	81
9.40	hif_makeimages: Make target cubes	82
9.41	hif_makeimlist: Set-up image parameters for representative bandwidth target cube	83
9.42	hif_makeimages: Make representative bandwidth target cube	83
9.43	hifa_exportdata	83
<b>10</b>	<b>Single Dish pipeline tasks and “by task “weblog pages</b>	<b>84</b>
10.1	hsd_importdata	84
10.2	hsd_flagdata	84
10.3	h_tsyscal	84

10.4	hsd_tsysflag.....	85
10.5	hsd_skycal .....	85
10.6	hsd_k2jycal.....	85
10.7	hsd_applycal.....	86
10.8	hsd_baseline.....	86
10.9	hsd_bflag.....	91
10.10	hsd_imaging .....	91
11	Per-channel imaging weights in cubes .....	94
11.1	Description of the perchanweightdensity parameter .....	94
11.2	Effect of perchanweightdensity on beam size and noise across a spectral window .....	95
11.3	perchanwt=True beam size compared to perchanwt=False and mfs beam sizes.....	101

# 1 The ALMA Science Pipeline

## 1.1 Purpose of this document

This document describes how to obtain the ALMA Pipeline, how to use it to calibrate and image ALMA interferometric (IF) and single-dish (SD) data, and a description of the Pipeline WebLog (collection of web pages with diagnostic information describing the pipeline run). Since interferometric and single-dish data are calibrated and imaged using different procedures and diagnostics, their recalibration procedures and WebLogs are described separately.

This document is applicable for the Cycle 7+ version (2020.1.0) of the ALMA Pipeline that is packaged with CASA 6.1.1 as “casa-6.1.1-10-pipeline-2020.1.0.36”, deployed for use in ALMA Operations in November 2020. This version is labeled as Pipeline Version 2020.1.0.36 CASA Version 6.1.1-10 in the WebLog.

## 1.2 Pipeline Overview and nomenclature

The ALMA Science Pipeline is used for the automated calibration and imaging of ALMA interferometric and single-dish data. ALMA Interferometric data refers to observations obtained with either the ALMA 12-m Array or 7-m Array, while single-dish data refers to observations obtained with the 12-m dishes of the ALMA Total Power Array.

The Pipeline consists of modular calibration and imaging tasks within the Common Astronomy Software Applications (CASA) data reduction package that are selected and put together in a specific order based on standard prescriptions or **recipes**. The ALMA pipeline recipes cover the processing requirements of ALMA “standard” interferometric and single-dish observing modes. Datasets resulting from ALMA “non-standard” observing modes are, as a rule, processed outside the pipeline, using manually modified CASA scripts. The standard and non-standard observing modes are defined in the Proposer’s Guide for each ALMA proposal cycle. The science pipeline is not yet commissioned for the combination of datasets obtained from different array components (separate IF array observations, or IF plus SD combinations).

The pipeline operates on a completed dataset that is comprised of all of the quality assured individual executions that result from completing a Scheduling Block (SB). An individual SB execution results in a dataset referred to as an **ASDM** (for ALMA Science Data Model), or **EB** (Execution block) and the collection of ASDMs (EBs) from a single SB are collected into a data structure called a Member Observing Unit Set (**MOUS**), which is the data unit that the pipeline operates on. The pipeline produces the following: calibration products for each ASDM (including calibration and flagging files and tables); imaging products (FITS images) made from all ASDMs (although not necessarily for all science targets); informative logs and scripts; and a **WebLog** consisting of a collection of webpages with diagnostic messages, tables, figures, and “Quality Assurance” (**QA**) scores. These products are reviewed as part of the ALMA Quality Assurance process, and, if satisfactory, are stored into the ALMA Science Archive. See the ALMA Technical Handbook for details on the ALMA data structures, quality assurance criteria, and archiving system.

The Pipeline is data-driven: i.e. the characteristics of each dataset drive the calibration and imaging strategy (the **Pipeline Heuristics**). During the Pipeline run, critical information (for

example, which calibration tables are used) are stored in the pipeline **Context**. Both the **Heuristics** and the **Context** are implemented as python classes.

In order to determine if the Pipeline was used in the processing of an ALMA dataset, please look at the WebLog or consult the README file in the data delivery package. Some projects may contain a mix of both manually and Pipeline-calibrated data.

## 2 Quick Start

- If you want to understand what data is in a downloaded package, and the steps and quality of how it was processed see, see **The Pipeline WebLog** (Sec. 8).
- If you want to restore the calibrated MS, run **scriptForPI.py** (Sec. 5.1) or **casa\_piperestorescript.py** (Sec. 5.3).
- If you want to see, edit, or rerun the pipeline task commands that were run, you want **casa\_pipescript.py** (Sec. 5.4).
- If you want to see the CASA task calls that were used, either look at the casa log linked at the bottom of each pipeline processing stage of the “By Task” section of the weblog, or see the full **casa\_commands.log** file (Sec. 5.5).

# 3 What's New in 2020.1

## 3.1 Major new capabilities

- Full-polarization data observed in sessions for polarization projects now can be processed through the IF calibration pipeline, including all regular flagging, bandpass, fluxscale, time-varying gain calibration. Quality assessment is performed on the calibration quality, and information on the parallactic angle is provided. The reference antenna is held fixed when solving for time-varying gains, so these pipeline-processed data can be subsequently processed with a manual script including the CASA polcal task.
- Multiple improvements to IF flagging are expected to address ~2/3 of the previously reported instances needing manual flags in operations.
- In particular, a new stage hifa\_targetflag will automatically flag egregious outliers on the science target for the first time.
- Use of the gfluxscale scale factors has been replaced by the average calibrated visibility amplitudes in plots, QA assessment, and reporting of secondary calibrator flux densities to the ALMA Source Catalog. This is expected to greatly decrease misinterpretation, make derived flux densities more robust, and aide in diagnosing hardware issues.
- IF findContinuum has been significantly improved for the case of broad lines and extended emission (e.g. CO)

## 3.2 New features and improvements by weblog section and processing stage.

- **hifa\_importdata** displays parallactic angle coverage if pol\* calibration intents are present, and reports a poor QA score if that angle coverage is less than 60deg.

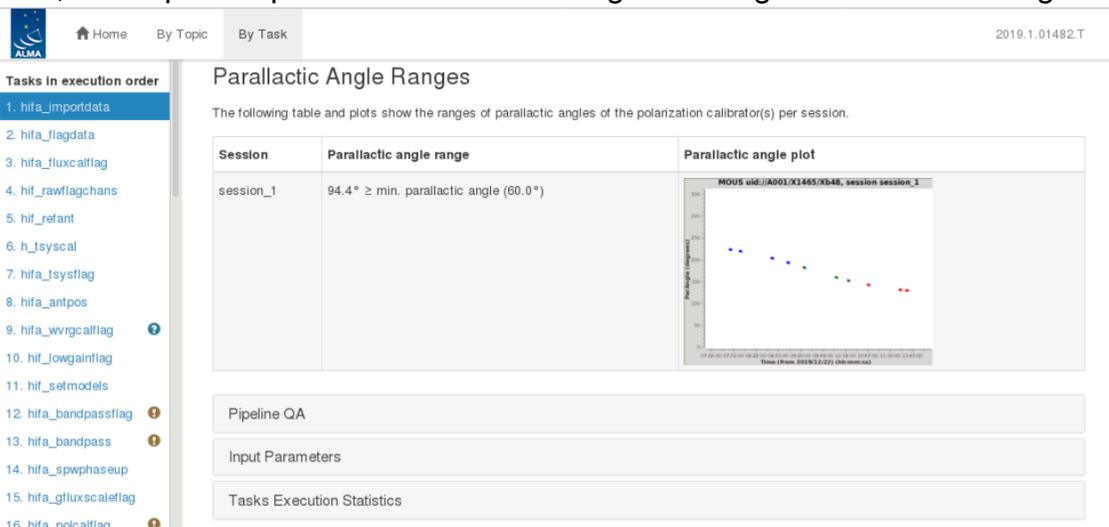


Figure 1: Parallactic angle coverage shown in hifa\_importdata weblog for a polarization project.

- **hifa\_polcalflag** (new stage in polarization recipes): flags bad data on the pol\* intents, similarly to hifa\_bandpassflag and hifa\_gfluxscaleflag:

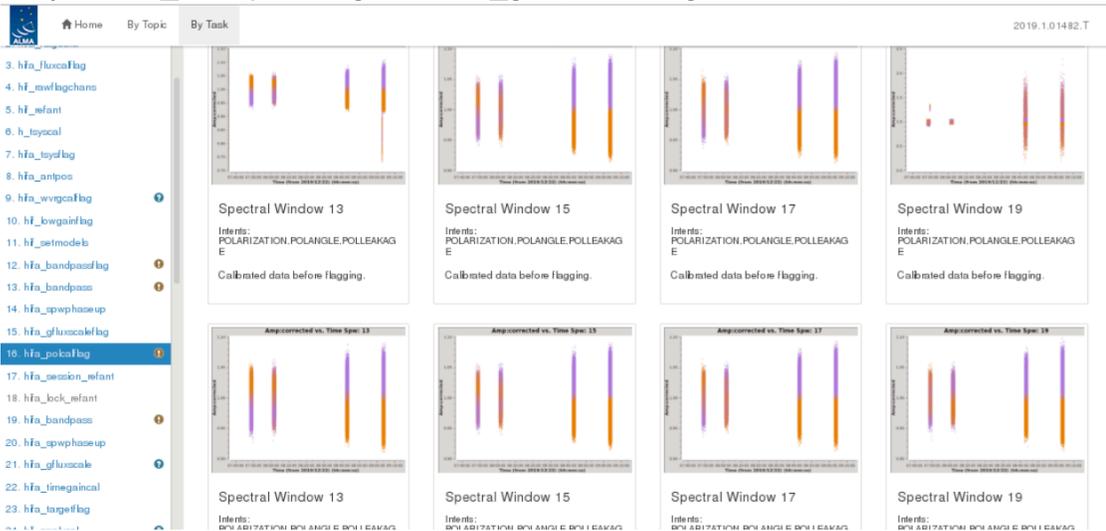


Figure 2: Flagging of the POL\* intent by hifa\_polcalflag

- **hifa\_session\_refant** (new stage in polarization recipes): determines the best common refant to use across executions of a session, as required for the casa polcal task later. Antennas are first ranked by the product of their per-EB ranking. It performs a gaincal 'int' 'p' on all PHASE intent scans for each EB starting with the highest ranking antenna as sole refant, and checks the resulting caltable to see if the refant ever changes. It chooses the first antenna that does not result in any change of refant. If none of the top 3 antennas qualify (which should be rare), then the antenna with the most solutions as refant is chosen, and a QA warning message is displayed with the number of phase outliers, where the word "outlier" means that the refant phase was non-zero, which indicates that another refant was chosen for some integrations. The total number of possible solutions is  $N_{EBs} * N_{spws} * N_{int} * N_{pol}$ .
- **hifa\_lock\_refant** (new stage in polarization recipes): refant is fixed for subsequent calibration, i.e. refantmode='strict' (rather than the gaincal default refantmode="flex" which allows gaincal to change the refant in the midst of heavily flagged scans). Subsequent calibration stages include a rerun of hifa\_bandpassflag and hifa\_spwphaseup to ensure that the bandpass and phase-offset calibration tables are created with the single fixed refant.

- **hifa\_flagdata**: edges of ACA spws of width  $\leq 1000$  MHz that are tuned too close to edge of the baseband are now flagged. These could cause noisy channels with deviant beamsizes.

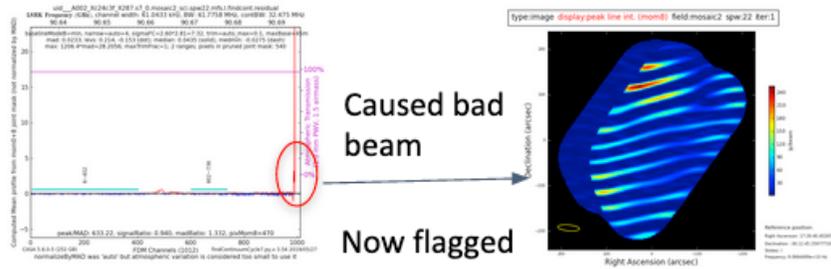


Figure 3: Unflagged edge channels used to cause bad edge channels in images.

- **correctedampflag (hifa\_gfluxscaleflag, and hifa\_polcalflag)**: For multi-scan calibrators (i.e. phase cals) when one polarization was flagged by the online flags but the other pol was not flagged, the data from the remaining polarization was not assessed. So if it contained any outliers, they would remain in the data and appear in hif\_applycal. Now both polarizations are flagged by the pipeline.
- **hifa\_timegaincal**: minsnr was raised from 2 to 3: the mismatch in the minsnr parameter between hifa\_bandpassflag/hifa\_polcalflag (minsnr=3) and hifa\_timegaincal (minsnr=2) was previously allowing some bad outlier visibilities to remain unflagged in the calibrated data – i.e., those that produce solutions with SNR between 2-3.
- **hifa\_targetflag (new stage)**:
  - Because science targets are generally not point sources, the flagging algorithm identifies outliers by examining statistics within successive overlapping uv bins, allowing it to adapt to arbitrary uv structure. By using a high threshold (12 sigma), nearly all cases of obvious outliers are now flagged with very limited flagging of good data. Sources with strong, resolved emission are more likely than others to have bad data go unflagged, particularly at short baselines.
  - The new stage does add processing time, particularly making the plots. So to save time, we only make the amp vs. time plots if flags are generated, and the amp vs. uv distance plots are made for only those spws that generated flags. Also, to avoid confusion in mosaics or single field surveys, these uv distance plots only show field IDs with new flags.

uid\_\_A002\_Xe64b7b\_X1be6d.ms

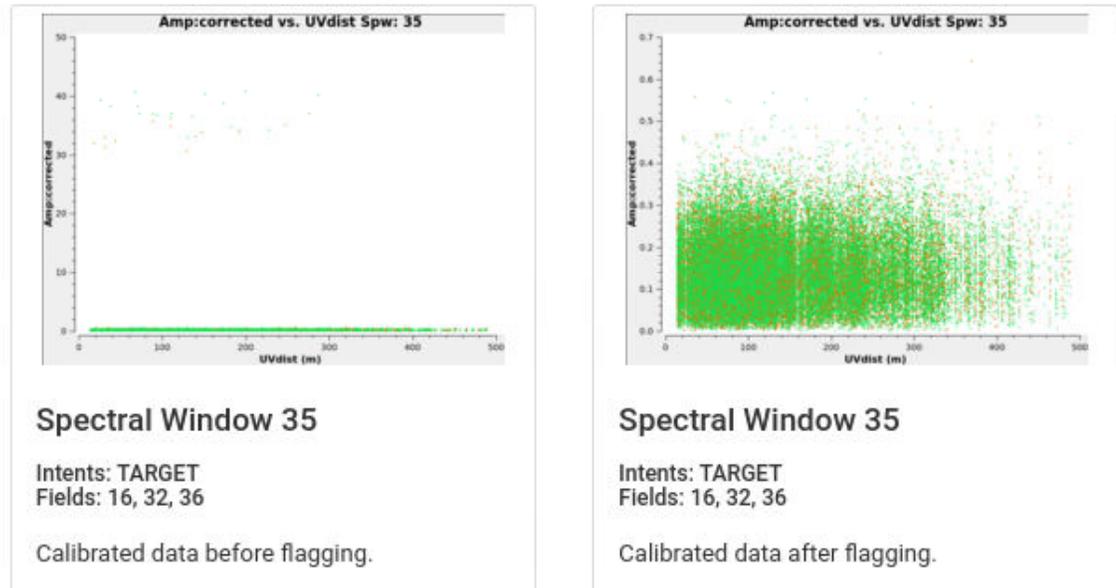


Figure 4: Example of target flagging.

- **hifa\_gfluxscale**: Mean visibility amplitudes of secondary calibrators are now plotted, used for QA, and reported in the AQUAreport, rather than the scaling factor derived by the fluxscale task:
  - The task **fluxscale** derives the correction factor needed to convert the observed mean gain amplitude of an absolute flux calibrator to its known flux, this correction factor is then transferred to the secondary calibrator(s) and their mean gain amplitude is then reported per spw. **The fluxscale derived mean gain amplitudes are commonly interpreted as the calibrator's actual flux density - however, it will only approach that if the S/N is high.** This is a natural consequence of the noise bias inherent when considering amplitude-only based flux densities, because it is a positive-definite quantity, excess noise can only push it upward. This is not a problem as long as the **corrected data** have correct and consistent (**complex-derived**) flux densities after correction. => **The best non-image estimate of the flux density (for an unresolved source at the phase center) is the mean of the complex data, not the amplitude-based mean gain.**
  - Previously, a plot of the fluxscale factors per spw were shown in **hifa\_gfluxscale**, and they sometimes yield alarming looking results, especially if the S/N varies from spw to spw (due to variable spw bandwidth, strong atmospheric lines, or even receiver performance), or if the S/N of a calibrator is uniformly low (too weak).
  - As of Pipeline2020, the vector average (i.e. complex) amplitude of the secondary calibrator's corrected visibilities are shown for each spw, we call this the "**calibrated visibility flux density**" or "mean visibility" for short. This plot should allow data reducers to more easily identify the small minority of cases in which a true issue requires attention. **Yellow QA Ratio of Sderived / Scatalogue messages are now more diagnostic of real issues.**
  - **The flux densities in the AQUAreport will now also be the calibrated visibility flux density.** This method is more robust, more consistent with what CalSurvey does, and will permit more reliable values from PI observations to be ingested into the Source Catalog.

- **hif\_applycal:**
  - QA message aggregation was corrected where outlier source/SPW/antennas combinations were sometimes inaccurate
  - clickable link to the cal library files is added to the Applied Calibrations table
- **hif\_makeimages (calibrators):** The peak flux in the hif\_makeimages stage is measured from the pb-corrected image and could sometimes come from another peak in the field and not reflect the correct calibrator flux. Now it is constrained to the inner 1/16, to capture the correct source, e.g. in the example in Figure 5 of a double calibrator.

```
type:image display:mean field:J1812-0648 spw:25 iter:1
```

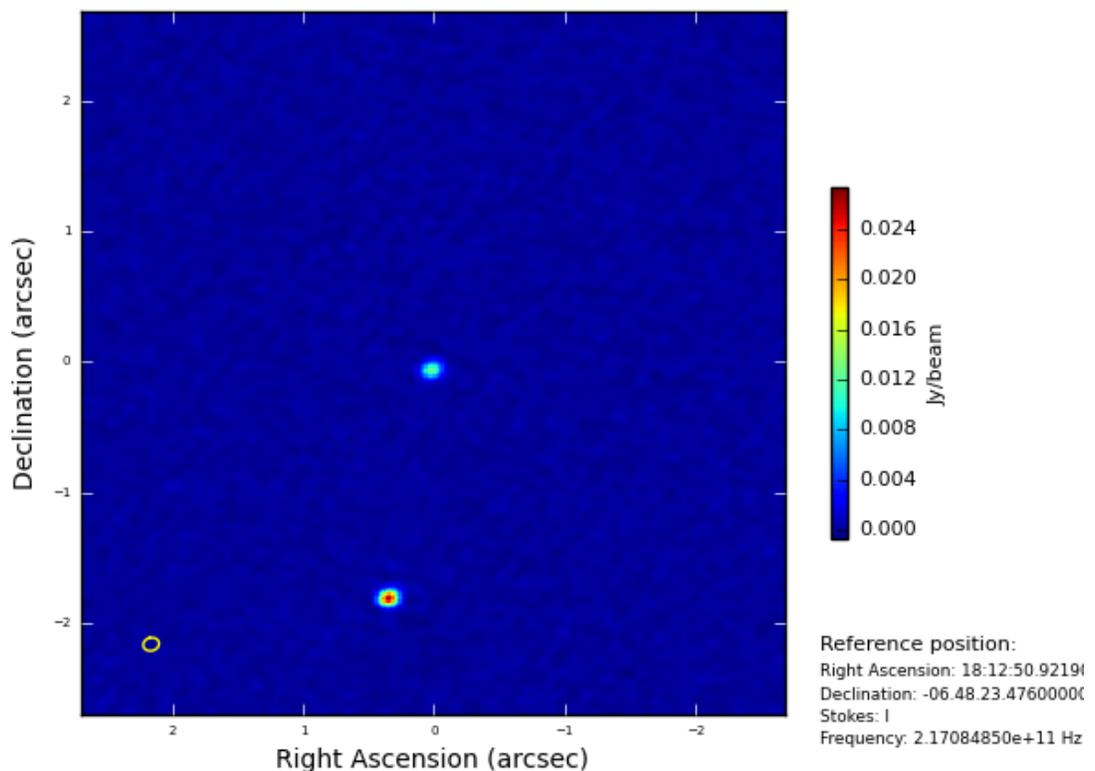


Figure 5: Double calibrator; previously the peak flux was reported as the off-center secondary peak, now it will be the central peak.

- **hifa\_imageprecheck:** beam calculations for unused values of robust (!=0.5) are now skipped for the ACA.
- **hifa\_findCont:**
  - Major new functionality has been added to findContinuum informed by months of PLWG research using the ALMAGAL large program data and the pipeline benchmark data. It is invoked on all FDM spws (and TDM spws from configurations <400m). Of the 21 reported cases of line contamination, 80% are now fixed by the new version.

- The initial set of channels found by the previous heuristics are used to construct mom8fc and mom0fc images, then the mom0fc is scaled and subtracted from the mom8fc to remove continuum sources (to zeroth order), creating a “momDiff” image. Residual emission in the momDiff then indicates line contamination, and the continuum frequency ranges are adjusted accordingly. See section 9.33 for details on the findContinuum logic reported in the plots, and Figure 6 for an example.
- In addition, Field anchors were added to the top of the weblog page.

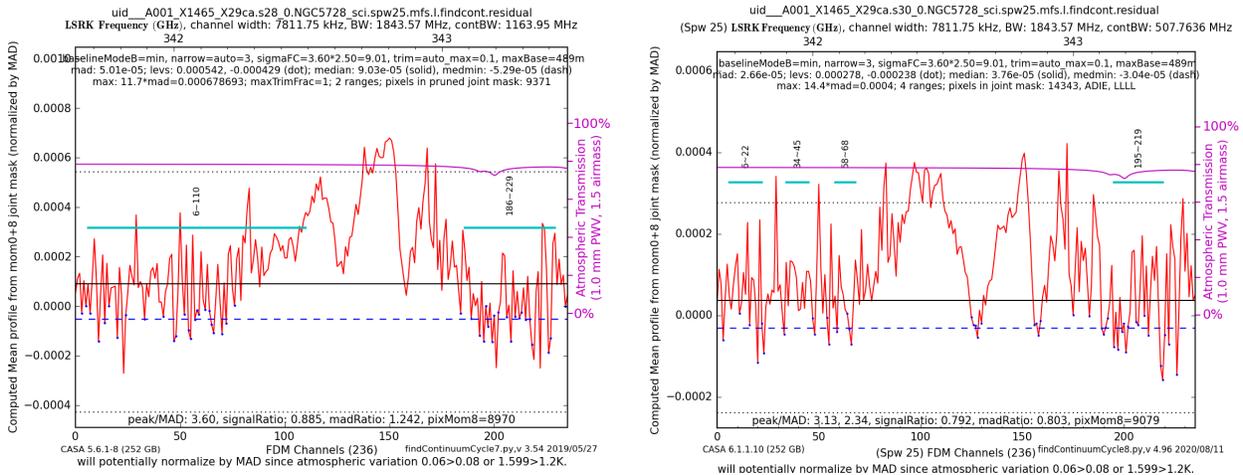


Figure 6: Improved findContinuum for wide line use case: Left: Cycle 7 pipeline, Right: 2020 pipeline.

### • hif\_makeimages

- Mosaics of fast-moving ephemeris sources should no longer have a small offset in their image center. The offsets were unlikely to be consequential, but are now fixed.
- auto-multithresh parameters were adjusted to more reliably include in the mask compact sources in extended arrays and diffuse emission in intermediate arrays (300-400m baselines). In Figure 7, the Cycle 7 mask is magenta, and the 2020.1 mask is white.

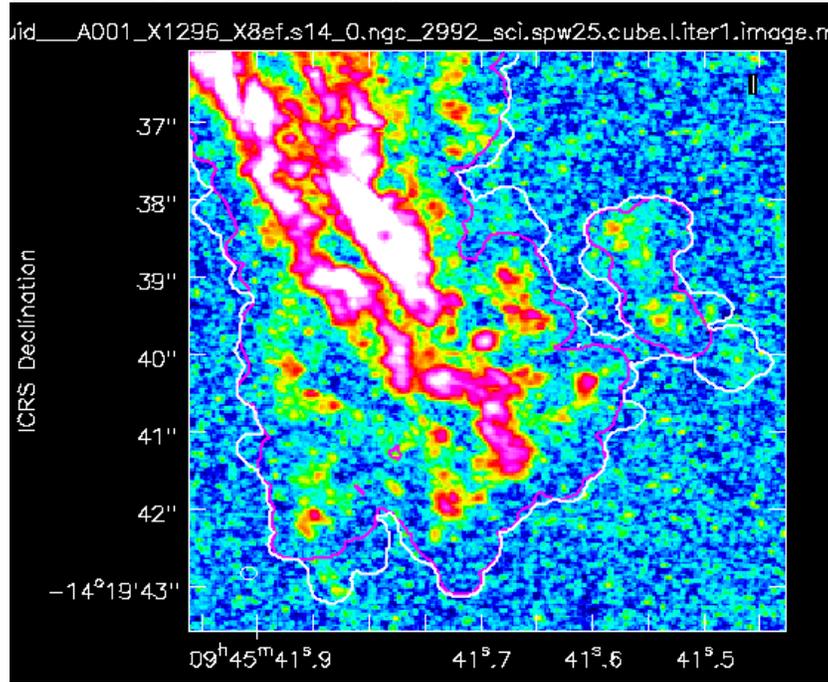


Figure 7: Improved automasking: Cycle 7 pipeline in magenta, 2020 pipeline in white.

- Weblog page has been rearranged into rows for clarity and to facilitate more rapid weblog review:

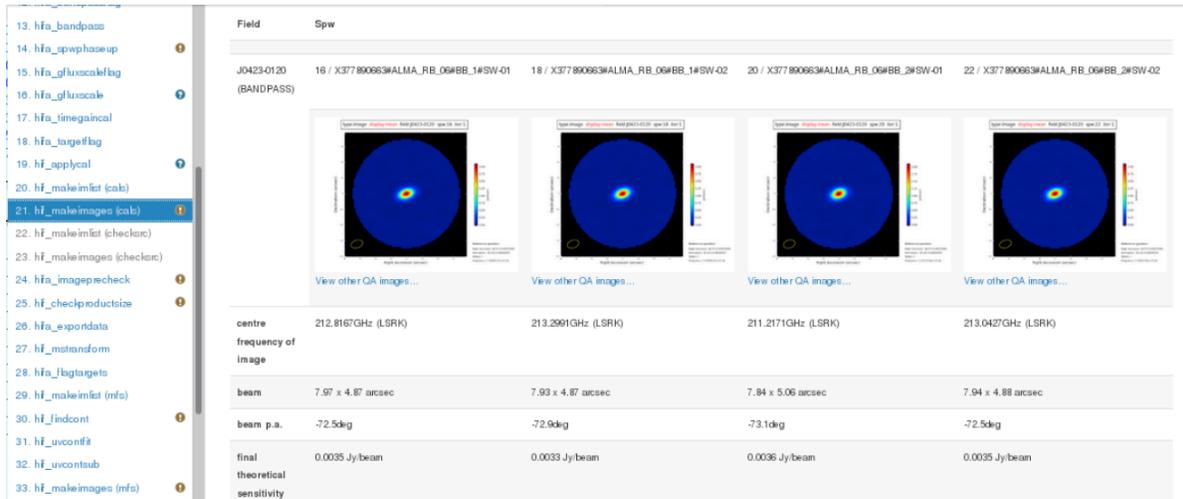


Figure 8: Column arrangement of makeimages weblog.

- A clickable link has been added from the image display page to the tclean command used to create that image:

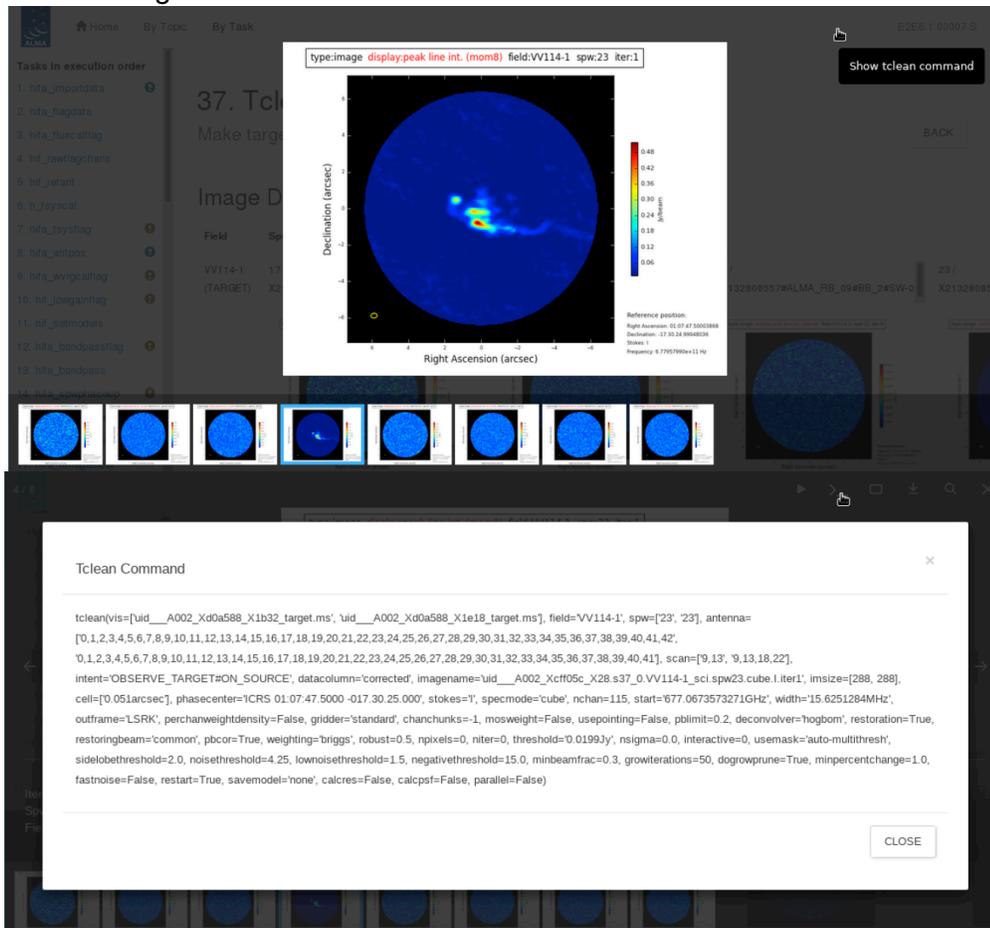
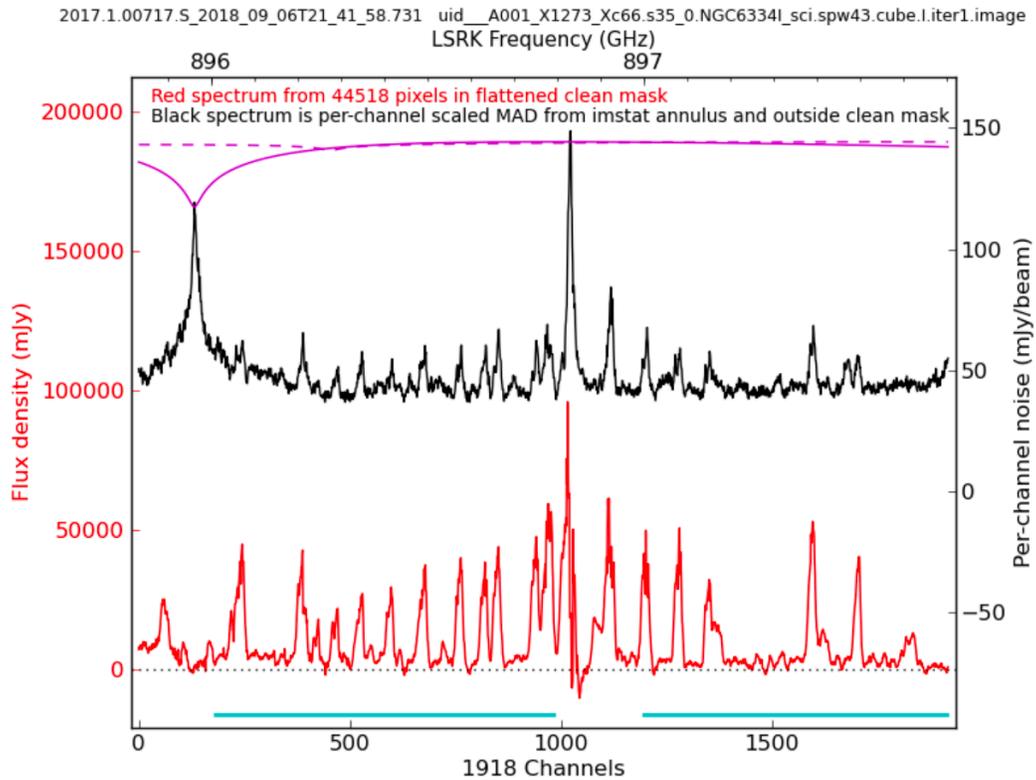


Figure 9: click on >\_ when viewing the png of an image product (top), to get a popup (bottom) containing the tclean command.

- **hif\_makeimages (cubes)**

- New QA calculation based on the line free moment 8 (peak intensity) “\_fc” image allows assessment of whether line-free channels are indeed line-free.
- Sometimes there is no simple way to denote continuum (a line forest), and sometimes the signal-to-noise is too low to determine whether the findCont selection is adequate, but the new QA metric will identify cases that merit manual examination.
- **In most cases, the cubes do not need to be re-generated**, because a small change in the continuum ranges will not have a significant effect on uvcontfit, but sometimes one may want to create a manual continuum image outside of the pipeline to avoid line contamination (the data reducer will do so if they deem it appropriate).



- **hsd\_importdata**
  - In Intent vs time and Field vs time plots, REFERENCE (OFF\_SOURCE) is explicitly distinguished as a TARGET intent
- **hsd\_skycal**
  - New plots of interval of OFF-source/interval of ON-source as a function of time for each MS, field, antenna, and SpW are displayed.
- **hsd\_baseline**
  - The baseline correction for the case that a large mask exists at the band edge is improved. When the masked channels at the band edge is larger than  $nchan/4$  and less than  $nchan/2$ , the fitting function switched to a 2<sup>nd</sup> order polynomial from cspline fitting. When the masked channels at the band edge is larger than  $nchan/2$ , the fitting function switched to a 1<sup>st</sup> order polynomial.
- **hsd\_imaging**
  - New heuristics in hsd\_imaging detect line contamination at the OFF position and/or ATM features and give a warning. A mask is created of pixels that have signal to noise ratio <10%. Then, the averaged spectrum from the masked pixels is calculated. If the negative peak of the average spectrum is less than – 4 times standard deviation, the pipeline gives a warning that “Absorption feature is detected in the emission-free area. Please check calibration result in detail.”
  - The theoretical RMS taking into account the flagging fraction is calculated and listed in the Image Sensitivity table as well as the observed RMS
- **hsd\_imaging**
  - The weight cube fits files corresponding to image fits files are produced in “products” directory. The extension is “.weight.fits”.

- **All stages:** More stringent security in most web browsers in 2020 broke the weblog when displayed using a file:// URL. The weblog now contains instructions for what users can do if they encounter this error, including a new local html server embedded in the pipeline that users can access through CASA. Instead of “failure to load” error messages, users will now see the page in Figure 10:

The screenshot shows a web browser interface with a navigation menu on the left and a main content area. The main content area displays an error message: "Error: cannot load content". Below the error message, there is a section titled "Solutions" with a "Recommended: use h\_webLog()" section. This section includes instructions on how to view the weblog locally or via HTTP from inside a CASA session. A terminal window shows the output of the `h_webLog()` command, which includes information about the pipeline mode, the location of the weblog files, and the status of the HTTP server. Below the terminal output, there is a section titled "Alternative: lower browser security" with instructions for Firefox, Safari, and Chrome.

**Tasks in execution order**

1. hifa\_importdata
2. hifa\_flagdata
3. hifa\_fluxcallflag
4. hif\_rawflagchans
5. hif\_refant
6. h\_tsyscal
7. hifa\_tsysflag

## Error: cannot load content

Browser security prevents the weblog from displaying the requested content.

Viewing the web log locally is not possible with your web browser security settings. To view the web log you must serve the web log via HTTP by using `h_webLog` from inside a CASA session, or relax your web browser security.

### Solutions

**Recommended: use `h_webLog()`**

From inside a CASA session, navigate to the root of the unstarred weblog directory, e.g., `pipeline-procedure.hifa_calimage`, and run `h_webLog`. This command will serve the web log via HTTP and launch a browser connecting to the web log. The web log URL is also printed to the CASA logger, should you need to navigate to the web log manually. The URL to access is highlighted in the example CASA logger output below.

```
CASA <S>: h_webLog()
2020-07-30 12:57:20 INFO h_weblog:::casa #####
2020-07-30 12:57:20 INFO h_weblog:::casa #### Begin Task: h_weblog ####
2020-07-30 12:57:20 INFO h_weblog:::casa h_weblog( pipelinemode='automatic', relpath='' )
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Found weblogs at:
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa+ main/pipeline-procedure_hifa_calimage/html/t1-1.html
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Using existing HTTP server at 127.0.0.1 port 30000 ...
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Opening http://127.0.0.1:30000/main/pipeline-procedure_hifa_calimage/html/t1-1.html
2020-07-30 12:57:20 INFO h_weblog:::casa Result h_weblog: None
2020-07-30 12:57:20 INFO h_weblog:::casa Task h_weblog complete. Start time: 2020-07-30 08:57:19.880720 End time: 2020-07-30 08:57:20.064263
2020-07-30 12:57:20 INFO h_weblog:::casa #### End Task: h_weblog ####
2020-07-30 12:57:20 INFO h_weblog:::casa #####
```

For security, the web log HTTP server is only accessible from the same computer as the CASA session. To view the web log from another computer, forward the port using SSH. For example, to access the web log hosted on a remote machine called `remotepc`, where the CASA log reports the web log is available at port 30000, execute:

```
ssh -L 30000:localhost:30000 remotepc
```

### Alternative: lower browser security

These modification lowers your browser security and should be reverted after viewing the weblog!

**Firefox**

Navigate to `about:config` and search for the `privacy.file_unique_origin` preference. Change the preference value to false.

**Safari**

Open Safari preferences, navigate to *Advanced* tab and check the *Show Develop in menu bar* option. From the new *Develop* menu option now visible at the top of the screen, select *Disable Local File Restriction*.

**Chrome**

The `--disable-web-security` and `--user-data-dir` command line arguments must be passed to Chrome via the command line. For example, on MacOS start Chrome like this:

```
/Applications/Chrome.app/Contents/MacOS/Chrome --disable-web-security --user-data-dir~/tmp
```

Figure 10: Page displayed when intra-weblog javascript is blocked by browser security.

### 3.3 Current Known Limitations of the 2020.1 Pipeline

The current **Known limitations** of the 2020.1 pipeline include:

- The pipeline is commissioned only for ALMA “standard mode” observations, as defined in the Proposers Guide for the latest cycle, subject to the additional restrictions listed next:

- All raw data (ASDMs) run through the pipeline must have complete and properly formatted binary and metadata. This is not always the case for ASDMs from earlier ALMA cycles. In particular:
  - The SD pipeline can only be run on data from Cycle 3 or later.
  - The IF pipeline will not work with ALMA Cycle 0 data, nor with some Cycle 1 – 2 data.
- Manually calibrated data from Cycles 1 – 3 are likely to have problems if run through the pipeline.
- The raw data (ASDMs) run through the pipeline should have a “quality assurance level 0” (QA0) assessment of “QA0 Pass”. Running the pipeline on non-quality assured data (“QA0 SemiPass” or “QA0 Fail”) is not expected to give sound results and may fail.
- The pipeline assumes that it has access to all of the available RAM on the node where it is run. If other processes use significant amounts of this RAM, the pipeline may fail.
- Unfortunately a late-discovered CASA bug prevents all parameters from being listed for pipeline and CASA tasks when “inp” is typed. Setting those parameters and typing “go”, using the tasks in functional form e.g. “hifa\_bandpass(pipelinemode='automatic’) at the command line and in scripts, as well as using the tasks in a PPR, all work correctly – it is merely an issue with listing the parameters to the terminal. Users are encouraged to consult the inline “help taskname”, and the Science Pipeline Reference Manual available on the science portal, for the complete list of parameters of each task.

**Additional limitations of the Interferometric Pipeline are:**

- While the IF pipeline calibration and flagging tasks do include low signal-to-noise heuristics, they will produce poor results if the calibrators are too weak.
- In order to increase delivery rates of data to PIs, the archived imaging products may be binned in frequency, limited in the imaged field of view, and/or restricted to a subset of sources (See Sec. 9.28). Users can make the missing products by making small modifications to the scripts that are archived with the data.
- The frequency ranges for interferometric continuum identification and subtraction are done in an automated manner that works well over a very broad range of observing modes and source properties. In some cases (e.g. hot core line emission, noisy broadband continuum), it is expected that better results can be obtained by more careful examination of individual sources and/or spectral windows. If the data are heavily binned in frequency before this task is run, the results may be compromised. The user can edit **cont.dat** (Sec. 7.6) and rerun sections of the imaging pipeline to obtain their own continuum subtracted visibilities and new line images.
- The IF PL imaging steps use the “effective channel bandwidth” from the raw data file to calculate the theoretical image sensitivity and hence clean thresholds. This information is not correctly entered for ALMA data from Cycles 2 and earlier; as a result, the clean thresholds will be higher than intended when such data is run through the imaging pipeline.

- The pipeline does not include science target self-calibration. Therefore, the pipeline imaging products of bright sources will be dynamic range limited.
- The interferometric imaging pipeline commands should work with measurement sets calibrated outside the pipeline, but this has not been tested extensively and may have as-yet undetermined failure modes.

**Additional limitations of the Single-dish Pipeline are:**

- The frequency ranges for single dish line identification and spectral baseline subtraction are done in an automated manner that has been optimized to detect moderate channel width (wider than 100 channels) emission lines at the center of a spectral window. It is expected that better results can be obtained by more careful examination of individual sources and/or spectral windows. The following cases are most strongly affected:
  - Narrow emission lines (less than 100 channels), especially in TDM mode.
  - Emission at the edge of a spectral window.
  - Cubes with a “forest” of emission lines.
- The SD pipeline imaging results may be unusable if there is emission in the “off” position and/or if the atmospheric line features still remain in the calibrated data. However, as described above, new diagnostic plots will aide in clearly identifying this situation for DRs.
- The number and total size of all ASDMs run through the SD pipeline cannot exceed limits set by the server specification (e.g. 50GB raw data for 64GB RAM).
- If `hsd_baseline` is run manually to subtract the baseline in an individual spw, `hsd_blflag` and `hsd_imaging` should be run before proceeding to subtract the baseline from the next spw. Otherwise, `hsd_baseline` will overwrite the baseline solutions for the previous spws.
- Observed RMS tends to be larger than theoretical RMS. There are two possible reasons to explain this trend. One is that the ATM and ripple features remain in the final image. The second one is that the pixels located at the map edge are included in the measurement of the observed RMS.
- Strong emission is flagged in `hsd_blflag`. In some cases, emission components at some channels (i.e. wing component) are not identified as the line. This increases the RMS at corresponding channels. Essentially, improving the line identification algorithm is required to fix this issue. In operation, this issue can be avoided by changing the threshold of `blflag` manually.

A list of pipeline “known issues” that arise after the publication date of this document is maintained on the ALMA Science Portal at <http://almascience.org/processing/> . This list will be updated as issues are discovered during the cycle.

## 4 Pipeline Versions & Documentation

### 4.1 Obtaining the Pipeline

A link to the CASA+pipeline package is available, along with installation instructions and supporting documentation, from the **Science Pipeline** section of the **ALMA Science Portal** at <http://www.almascience.org> (under the “Processing” tab, or directly at <http://almascience.org/processing/>). If any issues are encountered with CASA installation, please contact the ALMA Helpdesk via the link on the ALMA Science Portal.

The pipeline tasks become available by starting up CASA using the command:

```
% casa --pipeline
```

Or to run CASA with pipeline tasks using MPI (multi-core parallelization):

```
% mpicasa -n 8 casa --pipeline
```

### 4.2 Pipeline-related Documentation

The User documentation currently relating to the Pipeline is also available from the Science Pipeline section of the Science Portal referenced above. This includes:

- **ALMA Science Pipeline User’s Guide:** This document.
- **ALMA Science Pipeline Reference Manual:** Description of individual Pipeline tasks.

Examples of common re-imaging modifications to the IF pipeline script are given at: [https://casaguides.nrao.edu/index.php/ALMA\\_Imaging\\_Pipeline\\_Reprocessing](https://casaguides.nrao.edu/index.php/ALMA_Imaging_Pipeline_Reprocessing).

In addition, Chapters 10, 11, and 13 of the **ALMA Technical Handbook** provide more information in calibration in general, how Quality Assurance is performed, and how data is archived.

### 4.3 Pipeline & CASA Versions

The pipeline heuristic tasks have a specific version number, and are bundled with a specific version of CASA. These versions are reported in the README file that is archived with the pipeline data products, and are also reported on the Home page of the WebLog for each pipeline-processed dataset (see Figure 19 for an example).

In general, the version of Pipeline+CASA used in ALMA Operations to calibrate and image the archived data will be the same as the publicly posted pipeline version available from the “Obtaining CASA” page, but they can be slightly different (e.g. for bugs that have an operational workaround but which are fixed in the posted public version). There is a “**Pipeline Version Tracker**” available from the Science Portal at <http://almascience.org/processing/>, which lists the versions of CASA+Pipeline used in ALMA Operations as well as the versions which should be used for any restoring or reprocessing of the data from the same cycle (as described elsewhere in this document).

### 4.4 Pipeline and CASA tasks

The pipeline heuristics are written as special CASA tasks, where they appear with a `hif_` or `hifa_` (for interferometric) or `hsd_` (for single-dish) prefix. They can be viewed and executed within CASA in exactly the same way as other CASA tasks (if one has launched CASA with “--pipeline”). For example, one can view the possible inputs for the task `hifa_importdata`

by typing `inp hifa_importdata`. (There is a known issue that some parameters of some tasks do not show up in CASA 6.\* versions. If one sets the parameter, the task runs correctly, one simply can't see the set value with 'inp'. This will hopefully be fixed in future CASA versions.) To see all the tasks available in CASA, type `taskhelp`. The pipeline heuristics use CASA tasks wherever possible to perform the data reduction or imaging. E.g. the pipeline bandpass calibration & flagging task `hifa_bandpassflag` calls the CASA bandpass task, and the interferometric imaging task `hif_makeimages` calls the CASA imaging task `tclean`.

The standard pipeline processing recipes are deterministic and should always give the same result for the same data. However, the CASA pipeline tasks are designed to be highly flexible, so that they can have the default inputs over-ridden with user-specified values, or be added, subtracted, or rearranged to produce alternative processing recipes. This enables a manual "mix and match" mode for data reduction and imaging that combines standard CASA pipeline tasks with other CASA commands or python code to produce scripts that are better tuned to the idiosyncrasies of a specific dataset. The exact pipeline commands that will reproduce the standard recipe are delivered with each dataset, in a script called **member.<mous\_uid>.<recipe>.casa\_pipescript.py** (see Sec. 5.4 below). One could edit and add to that script to implement "mixed mode" processing.

Some common "manual mode" modifications are presented in the Sec. 6 below. A complete list of the variables for each pipeline task is given in the ALMA Science Pipeline Reference Manual.

CASA pipeline tasks operate like other CASA tasks. In particular, the scope of variables follow CASA rules. This means that when CASA pipeline tasks are called with no arguments, they will assume any previously defined variables used by the task, whereas calling the same task with at least one argument will not. For example, typing the commands `"refant='DA45'; hifa_gfluxscale();"` will use the antenna named 'DA45' as the reference antenna, whereas typing `"refant='DA45'; hifa_gfluxscale(pipelinemode='interactive');"` will result in the pipeline picking a reference antenna according to its default heuristics.

This document, along with the Pipeline Reference Manual, describe key aspects of the CASA pipeline tasks. Important changes to other CASA tasks are documented in the Release Notes for the corresponding CASA release, available from the CASA page at [https://casa.nrao.edu/casa\\_obtaining.shtml](https://casa.nrao.edu/casa_obtaining.shtml).

## 5 Data Processing Files

### 5.1 Archived scripts

There are several scripts that are archived with ALMA data deliveries. These are described in the document **ALMA QA2 Data Products** (sometimes cycle-specific) available from ALMA Science Portal under the “Processing” tab (or directly at <https://almascience.nrao.edu/processing/> ). The particular scripts for a specific dataset should also be described in the QA2 report archived with the data products. This report will vary based on how the data were processed (pipeline calibrated + imaged; pipeline calibrated & manually imaged; manually calibrated + pipeline imaged, manually calibrated + manually imaged).

The scripts produced by the pipeline are archived with the data and have file names like **member.<mous\_uid>.<recipe>.casa\_pipescript.py** and **member.<mous\_uid>.<recipe>.casa\_piperestorescript.py**. The former includes all pipeline processing commands that were run on the data, and is more fully described below. The latter “restores” the data, which means that rather than re-running the pipeline calibration commands, it uses previously derived calibration and flagging tables and applies them directly to the raw data, producing a calibrated measurement set. This is much quicker and requires less computing resources than re-running the pipeline calibration commands. However, expert users should be aware that if the latter, faster method it used, then the state of the measurement sets are not exactly the same as in a complete run (e.g. the model of the calibrators will not be set).

Every delivery package also includes a master script with a file name like **member.<mous\_uid>.scriptForPI.py**, that will reproduce the calibrated data regardless of how it was processed. This script is not created by the pipeline, but instead by the data packaging software so that it is produced for both pipeline and manually reduced data. For pipeline calibrated data, it will simply invoke the pipeline-produced **casa\_piperestorescript.py** or **casa\_pipescript.py** scripts mentioned above.

**Using scriptForPI.py is the recommended and fastest method of obtaining calibrated ALMA data from the delivery.** However, one can also run the pipeline **casa\_piperestorescript.py** using the steps in Sec. 5.3. To *change* the calibration results, one would re-run the commands in **casa\_pipescript.py** after making modifications, as described in Sec. 6

### 5.2 Pipeline “Helper” text files

Both the IF and SD pipeline use a number of text files that, if present, will affect the pipeline results (e.g. by applying manually identified flags or by updating calibrator fluxes or antenna positions before calculating the calibration tables). These files are particularly useful for users to over-ride the default pipeline behavior when re-running the pipeline at home, as more fully described in Sec. 6 below. They include the following:

- **flux.csv**: This file is used by the IF pipeline to update the flux of calibrators. The flux of the calibrator with the “AMPLITUDE” intent will affect the overall flux scale of the data. If this file is not present where the pipeline is run, the pipeline will attempt to contact the ALMA source catalog for previously recorded flux densities, and if that doesn’t succeed, the fluxes in the ASDM(s) will be used, representing the best flux

estimate at the time the SB was executed. If no flux value appears in either the flux.csv file or the ASDM, a flux of 1.0 Jy is adopted.

- **jyperk.csv**: This file is used by the SD pipeline to set the “Kelvin to Jansky” calibration factors which set the overall fluxscale of the data. If it is not present where the pipeline is run, then a conversion factor of unity is assumed.
- **antennapos.csv**: This file is used by the IF pipeline to update the positions of the antenna elements. If it is not present where the pipeline is run, the positions in the ASDM(s) will be used.
- **uid\*flagtemplate.txt**: This file is used to add additional CASA flagging commands that will be applied to the data before the calibration tables are calculated.
- **uid\*flagssystemplate.txt**: This file is used to add additional CASA flagging commands that will be applied to the tsys spws before the calibration tables are calculated.
- **uid\*flagtargetstemplate.txt**: This file is used to 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**: This file is used to specify the continuum frequency ranges used for constructing the continuum images and creating the continuum-subtracted cubes. This particular file is described in more detail below and in the reimaging casaguide [https://casaguides.nrao.edu/index.php/ALMA\\_Imaging\\_Pipeline\\_Reprocessing](https://casaguides.nrao.edu/index.php/ALMA_Imaging_Pipeline_Reprocessing).

The format of each of these files is given in Sec. 7.

### 5.3 The Pipeline script to restore calibrated MSs: **casa\_piperestorescript.py**

To restore data calibrated by the pipeline, one can either run **scriptForPI.py** as described in **ALMA QA2 Data Products** document available from ALMA Science Portal under the “Processing” tab (or directly at <https://almascience.org/processing>), or one can run the pipeline-provided **casa\_piperestorescript.py** script:

- Create **rawdata/**, **working/**, and **products/** subdirectories.
- Download the raw ASDMs from the archive and put them in **rawdata/**. Make sure the naming of the raw ALMA data is consistent with those provided in the script (e.g. if the data ends in **.asdm.sdm** then rename to not have this suffix).
- Copy or move **\*manifest.xml**, **\*caltables.tgz**, **\*flagversions.tgz**, and **\*calapply.txt** to **products/**.
- Copy **uid\*casa\_piperestorescript.py** to **casa\_piperestorescript.py** to **working/**.
- In **working/**, start `casa -pipeline`, and `execfile("casa_piperestorescript.py")`.

#### 5.3.1 Results from running the SD **casa\_piperestorescript.py**

- A calibrated MS for each ASDM with a name like **"\*.ms"**. Note that the baseline subtraction is not done for the restored calibrated MS.

Running the script through `hsd_baseline` command will additionally create:

- A calibrated, baseline subtracted MS for each ASDM with a name like `"*ms_bl"`. The pipeline "automatic" mode reproduces the baseline subtraction. If instead the user may want to set the mask ranges to be used for baseline subtraction, CASA task `sdbaseline()` is recommended to use. In such case, please be aware of that WebLog is not generated for CASA tasks. If the baseline subtraction is done with the CASA task `sdbaseline()`, any further Pipeline tasks cannot be used.

Running the script through `hsd_blflag` command will result in:

- flagging based on the baseline rms for each ASDM. The `hsd_blflag` command has to be run after `hsd_baseline` at least once. In the standard operation, `hsd_baseline` and `hsd_blflag` are repeated twice to improve the quality of baseline detection.

Running the script through `hsd_imaging` command will additionally create:

- native resolution images per spectral window, antenna, and source.

## 5.4 The Pipeline processing script: `casa_pipescript.py`

### 5.4.1 Format of `casa_pipescript.py`

The complete set of pipeline commands are given in the script `casa_pipescript.py`. This is a python script that includes all tasks and parameter values, in the correct sequence, that were used for the pipeline run. A typical `casa_pipescript.py` script for a SD Pipeline run (including both calibration+imaging steps) is shown in Figure 11, while a typical IF pipeline script including both pipeline calibration and imaging steps is shown in Figure 12.

For data that were both calibrated and imaged in the pipeline (including all SD data run through the pipeline), the `casa_pipescript.py` file will include both the calibration and imaging pipeline commands. For IF data that were calibrated in the pipeline but imaged outside of the pipeline, the `casa_pipescript.py` file will only include the IF calibration pipeline commands (up to the line `"# Start of pipeline imaging commands"` line), and the archived data will include a separate `scriptForImaging.py` script containing the manual (CASA) imaging commands. If instead the IF data were manually calibrated and pipeline imaged, the `scriptForPI.py` would include the manual (CASA) calibration commands, and the IF pipeline imaging commands (those following the line `"# Start of pipeline imaging commands"` line in Figure 5) would be included in a separate `scriptForImaging.py` script.

```
__rethrow_casa_exceptions=True
h_init()
hsd_importdata(vis = ['uid__A002_X877e41_X452'])
hsd_flagdata(pipelinemode='automatic') ## Uses *flagtemplate.txt
h_tsyscal(pipelinemode='automatic')
hsd_tsysflag(pipelinemode='automatic')
hsd_skycal(pipelinemode='automatic')
hsd_k2jycal(pipelinemode='automatic') ## Uses jyperk.csv
hsd_applycal(pipelinemode='automatic')
hsd_baseline(pipelinemode='automatic')
hsd_blflag(pipelinemode='automatic')
hsd_baseline(pipelinemode='automatic')
hsd_blflag(pipelinemode='automatic')
hsd_imaging(pipelinemode='automatic')
h_save()
```

**Figure 11: Example of the Single Dish Pipeline calibration + imaging script casa\_pipescript.py. The “##” comment line identifies the pipeline command that uses one of the pipeline “helper” text files described in Sec. 5.2.**

```

__rethrow_casa_exceptions = True
context=h_init()
try:
    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_bandpass(pipelinemode="automatic")
    hifa_spwphaseup(pipelinemode="automatic")
    hifa_gfluxscaleflag(pipelinemode="automatic")
    hifa_gfluxscale(pipelinemode="automatic")
    hifa_timegaincal(pipelinemode="automatic")
    hifa_targetflag(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()

```

Figure 12: Example of a non-polarization IF Pipeline casa\_pipescript.py script for a dataset that was run through the Pipeline for both calibration and imaging. The “##” comment lines identify the pipeline commands that uses one of the pipeline “helper” text files described in Sec. 5.2

The tasks names, order, and parameter values in the **casa\_pipescript.py** script reflect the processing recipe used for each individual delivery. Additionally, the `pipelinemode` parameter is set to “automatic” for each task. In this mode, the task takes the default settings for each tasks and only a limited number of parameters are exposed for editing by a user. Setting the pipeline mode to “interactive” will usually enable the values of a larger number of parameters to be changed. To see the variables available in the pipeline “automatic” mode, type “`pipelinemode='automatic'; inp <task_name>`” at the CASA command line. To see the variables available in the pipeline “interactive” mode, type “`pipelinemode='interactive'; inp <task_name>`”. See the **ALMA Science Pipeline Reference Manual** for more details, and Sec. 6 below for examples of modified pipeline re-runs.

### 5.4.2 Results from running the single dish casa\_pipescript.py

Running the script will create:

- A calibrated, baseline subtracted MS for each ASDM with a name like `uid__A00X_XXXX_XXX.ms_bl`.
- Baseline subtracted image cubes of the the science targets in \*.image format (1 per spectral window, all antennas combined, at the native correlator frequency spacing).
- A **pipeline-\*/html** directory containing
  - The Pipeline WebLog (see Sec. 8).
  - The **casa\_commands.log** file (see Sec. 5.5).

### 5.4.3 Results from running the interferometric casa\_pipescript.py

Running the script through the first `hif_makeimages` command (calibrator imaging) will create:

- A calibrated MS for each ASDM with a name like `uid__A00X_XXXX_XXX.ms`. This ms includes both calibrator and science data and all spectral windows, with the raw data in the DATA column, and the calibrated continuum + line data in the CORRECTED column.
- Continuum images of the bandpass, phase, and (if present) check source calibrators (1 per spectral window, in \*.image format). To view a \*.image file e.g. use `casaviewer image_file_name`.
- A **pipeline-\*/html** directory containing:
  - The Pipeline WebLog (see Sec. 8).
  - The `casa_commands.log` file (see Sec. 5.5).

Running the script through `hif_mstransform` command will additionally create:

- A calibrated MS for each ASDM containing only science target data (only science targets and spectral windows), with a name like `uid__A00X_XXXX_XXX_target.ms`. This ms will have the raw data in the DATA column, and calibrated continuum + line data in the CORRECTED column.

Running the script through `hif_uvcontsub` command will result in:

- The science-target only MS (`uid__A00X_XXXX_XXX_target.ms`), now with the calibrated continuum + line data in the DATA column, and the calibrated continuum subtracted data in the CORRECTED column.

Running the script through the final `hif_makeimages` command (science target spectral line imaging) will additionally create:

- Per-spw continuum images, aggregate continuum images, and continuum subtracted image cubes of at least some science targets (the number of targets may be reduced either automatically – see Sec. 9.28 – or manually).

## 5.5 CASA equivalent commands file: `casa_commands.log`

The `casa_commands.log` file is written by the pipeline to provide a list of the equivalent CASA task commands (as opposed to Pipeline tasks) used by the Pipeline to process a dataset. While this log cannot be used to create a CASA reduction script that is identical to the Pipeline processing, it provides executable CASA commands with the parameter settings used by the pipeline. The log is commented to indicate which Pipeline stage the tasks were called from and why. The imaging commands given in this file can be easily modified to produce new imaging products with more finely tuned inputs (e.g. interactive masks and deeper cleaning thresholds).

## 6 Modifying a Pipeline Run using `casa_pipescript.py`

### 6.1 Pipeline re-processing considerations

As a rule, it does not make sense to rerun the `casa_pipescript.py` exactly as delivered, since this will merely reproduce the calibrated measurement set (which for IF Pipeline calibrated data is much more easily generated using `scriptForPI.py` or `casa_piperestorescript.py` to “restore” the calibration, as described in Sec. 5.1 above) and/or already-delivered products. Instead, it is likely that the user may want to redo the calibration after some modifications or produced modified imaging products. This section describes a few of the more common calibration and imaging changes for both the IF and SD Pipeline tasks. See the **ALMA Science Pipeline Reference Manual** for more complete details on the pipeline tasks and their inputs.

Re-running the pipeline can be very resource-intensive, both from a compute-time and disk-space perspective. For the compute time, an idea of how long the pipeline took when can be inferred from the WebLog (using the **Execution Duration** shown on the top of the “Home” page of the WebLog – see Figure 19, or the **Task Execution Statistics** that are listed for each task in the “By Task” part of the WebLog – see e.g. Figure 22. Those times, however, reflect the run times using the ALMA Operations processing clusters, which have 64 – 256 GB RAM, and likely use parallel processing (multi-core) for imaging. Concerning disk space, to re-run SD or IF pipeline calibration, it is advisable to have a system with at least 8 GB RAM, and 50 – 75 GB free disk space per ASDM. To re-run the IF imaging pipeline, it is advisable to have a system with  $\geq 64$  GB RAM, and the available disk space needs to be 10 – 100 times the expected size of the final imaging products.

The above resource requirements for the IF imaging pipeline are rather daunting. However, in practice, it is unlikely that the imaging pipeline commands would need to be rerun in their entirety. It would be much quicker and demand much less computing resources to only image the sources and or spectral windows (spw) or channels of interest, at an appropriate spectral resolution. This can be done by finding the corresponding `tclean()` command in the provided `casa_commands.log` file, modifying it as desired, and running it in CASA. These commands work on the measurement set created by the pipeline `hif_mstransform()` command, so that part of the imaging script would need to be run first.

Please contact ALMA via the Helpdesk if assistance is needed with data reprocessing.

### 6.2 Preparing to run `casa_pipescript.py`

The following steps describe how to modify and re-run the Pipeline, starting from the products and directory structure created after downloading the data:

- Create `rawdata/`, `working/`, and `products/` subdirectories
- Copy `uid*casa_pipescript.py` to `casa_pipescript.py` in the `working/` directory.
- To re-run IF calibration: copy `flux.csv`, `antennapos.csv` (if present), and `uid*flagtemplate.txt` to the `working/` directory (there will be one `flagtemplate.py` file per EB). Depending on the delivery method, `flux.csv` and `antennapos.csv` are likely to be found in `uid*auxproducts.tgz` which will need to be unzipped.
- To re-run IF imaging also:

Copy **uid\*flagtargetstemplate.txt** to the **working/** directory (note there is one per ASDM).

Copy **cont.dat** (there will only be one per MOUS) to the **working/** directory.

- To re-run SD calibration & imaging: copy **jyperk.csv** and **uid\*flagtemplate.txt** to the **working/** directory (there will be one file per ASDM).

In the **rawdata** directory:

- Make sure the naming of the raw ALMA data is consistent with those provided in the script (e.g. if the data ends in **.asdm.sdm** then move to names which do not have this suffix).
- Modify the pipeline “helper” files as desired (e.g. editing the **\*flagtemplate.txt** file to add any additional flags – see Sec. 7 for other options).
- 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).
- Start the version of CASA containing Pipeline using `casapy --pipeline`

You are now ready to run the script by typing `execfile('casa_pipescript.py')`. Alternatively, you can sequentially execute individual commands from **casa\_pipescript.py**, stopping at any point to run other CASA commands (plotms, etc).

**Note that to re-run the Pipeline multiple times, it is recommended to start each time from a clean working directory containing only CASA “helper” text files and the casa\_pipescript.py script.**

### 6.3 Modifying Calibration Commands

The pipeline calibration commands can be modified to produce different results.

For instance, problematic datasets (ASDMs) can be excluded from the processing by editing the “vis=” and “session=” lists in `hifa_importdata` or `hsd_importdata` tasks in the **casa\_pipescript.py** script.

As a second example, a user-specified prioritized reference antenna list can be specified via the “refant” variable in calibration tasks, over-riding the pipeline reference antenna heuristics, by switching to `pipelinemode='interactive'` and passing the desired refant list. E.g.

```
hifa_bandpass(pipelinemode="interactive", refant='DV06,DV07')
```

See the Pipeline Reference Manual for more options.

Another use case is to keep the default pipeline commands, but to change the values in the Pipeline “helper” text files to e.g. change the flux scaling, or update antenna positions (see Sec. 7 for details). The new values will be used when the relevant `hif_` commands are run.

### 6.4 Modifying IF Pipeline Imaging Commands

The pipeline imaging commands can be modified to produce different products. Typical reasons for re-imaging include:

- Imaging improvements to be gained from interactively editing an emission specific clean mask and cleaning more deeply. The pipeline generates a clean mask automatically (see Sec. 9.36 for specifics). Cases with moderate to strong emission (or absorption) can benefit from deeper clean with additional interactive clean masking, with the most affected property being the integrated flux density.
- Non-optimal continuum ranges. The pipeline uses heuristics that attempt to identify continuum channels over a very broad range of science target line properties. Particularly for strong line forests (hot-cores) and occasionally for TDM continuum projects the pipeline ranges can be non-optimal – too much in the first case and too little in the second.

Other science goal driven reprocessing needs may include:

- Desire to use wide image channels in the imaging stage to increase the S/N of cubes.
- Desire to use a different Briggs Robust image weighting than the default of robust=0.5 (smaller robust = smaller beam, poorer S/N; larger robust = larger beam, better S/N).
- Desire to uv-taper images to increase the S/N for extended emission.
- Desire to use different continuum frequency ranges than determined by the pipeline, by modifying the cont.dat file (Sec. 7.6).

Some re-imaging examples are given in a “CASA Guide” at [https://casaguides.nrao.edu/index.php/ALMA\\_Imaging\\_Pipeline\\_Reprocessing](https://casaguides.nrao.edu/index.php/ALMA_Imaging_Pipeline_Reprocessing). There you will find examples of the following:

- Making aggregate continuum image with all channels of all spectral windows.
- Redoing continuum subtractions with user-derived continuum ranges.
- Making a cube of subset of sources, spectral windows, with a different robust weight and channel binning factor.

Of particular note is that the `hifa_importdata()` command has a parameter `asimaging`, which is used to import measurement sets that, like the `_target.ms` created by the pipeline, have calibrated line+continuum data in the `DATA` column, and continuum-subtracted line data in the `CORRECTED` column. Subsequent `hif_makeimages` calls will default to using `DATA` for `ms` imaging and `CORRECTED` for cube imaging.

## 6.5 Manual imaging after running `casa_pipescript.py`

### 6.5.1 SD Data

After calibration with the script `casa_pipescript.py`, it is possible to re-image using the CASA Single Dish task, `sdimaging`, with user-defined parameters. As mentioned earlier, the Single Dish Pipeline creates a calibrated MS with a filename extension of “\*.ms\_bl” for each ASDM. The `sdimaging` command will make images of all MS that are specified in the `infile` parameter. For other parameters in `sdimaging`, refer to the `*casa_commands.log` file.

Note that the images included in the delivery package have the native frequency resolution and a cell size of one-ninth of the beam size, as recommended in the SD “CASA Guide”

([https://casaguides.nrao.edu/index.php/M100\\_Band3\\_SingleDish](https://casaguides.nrao.edu/index.php/M100_Band3_SingleDish)). If you want to change the frequency resolution and cell size, we recommend that you import the delivered FITS data cubes into CASA and regrid them using the CASA task `imregrid`.

It is also possible to revise the baseline subtraction using your preferred mask range instead of the pipeline-defined range. We recommend doing this on the images using the CASA tasks `imcontsub` or `sdbaseline` during your own manual calibration (refer to the CASA Guides).

## 6.5.2 IF Data

For IF data that are pipeline calibrated but *manually* imaged, the imaging commands will be included in a separate **scriptForImaging.py** script, containing all the CASA commands used to create the delivered products. In order to use this imaging script after using **casa\_pipescript.py** to recalibrate, the science spectral windows must first be “split” out from the calibrated measurement sets and the measurement sets output with a `.split.cal` suffix. To perform the split, in CASA e.g.:

```
split('uid__A002_X89252c_X852.ms',  
      outputvis='uid__A002_X89252c_X852.ms.split.cal',  
      spw='17,19,21,23')
```

The science spectral windows are specified in the Pipeline WebLog (Home > Observation Summary > Measurement Set Name > Spectral Setup, in the ID column) or can be determined using the CASA task `listobs` e.g.

`listobs('uid__A002_X89252c_X852.ms')`, where the results will be reported in the CASA logger.

If the pipeline-calibrated data is restored using **scriptForPI.py**, that script will perform the split command for the user

If a script named **scriptForFluxCalibration.py** is present in the script directory, this must also be executed prior to running **scriptForImaging.py**.

## 6.6 Manipulating the Pipeline Context

It is recommended to always run the Pipeline using python scripts. New Pipeline runs/scripts need to be initialized using `h_init` in order to create an empty pipeline **context**.

If the script is modified to only run a subset of the pipeline tasks, the **context** should be saved after the last task by using `h_save`. To resume the run, use `h_resume` to load the saved **context** before executing any pipeline tasks. See the **ALMA Science Pipeline Reference Manual** for more information.

To use the Pipeline to calibrate a dataset but to e.g. insert a different bandpass table into the processing, the following procedure should be followed:

- Run the pipeline until the end of the bandpass table creation task `hifa_bandpass`.
- View the calibration tables that Pipeline will use with `h_show_calstate`.
- Export the calibration tables Pipeline uses to a file on disk using `h_export_calstate`.
- Edit the calstate file to replace the name of the Pipeline-created bandpass table with the one it is wanted to use instead.

- Import the edited calstate file back to the **context** using `h_import_calstate` and resume the processing.

## 7 Description of Pipeline “Helper” Text Files

As mentioned in Sec. 5.2, both the IF and SD pipeline use a number of text files that are read by various pipeline tasks (as indicated by comments `##` in Figure 11 and 12), and which affect the pipeline results (e.g. by applying manually identified flags or by updating calibrator fluxes or antenna positions before calculating the calibration tables). These files are particularly useful for users to over-ride the default pipeline behavior when re-running the pipeline at home, as described in the following section. Below we describe all of the currently available control files, identifying whether they are used by the IF pipeline, SD pipeline, or both in the subsection heading.

### 7.1 `flux.csv` (IF Pipeline)

From Cycle 4 onward, the fluxes of standard ALMA quasar calibrators at the observed frequencies for each spw are written into the ASDM, using extrapolated values calculated from entries in the ALMA Source Catalog available at the time of observation. These fluxes are sometimes updated subsequently (thereby bracketing the observation in time), allowing for more accurate interpolated fluxes to be used for the absolute flux calibration.

Since the pipeline is usually run days to weeks after an observation is completed, better flux densities are often available at that time, so the pipeline `hifa_importdata` task does the following:

If `dbservice=True`, an online observatory database is queried and the best flux densities for the time and frequency of the observation are interpolated, overriding values in the ASDM.

If the `flux.csv` text file exists in the working directory, any values therein, for example as retrieved by `analysisUtils::getALMAFluxCsv()`, will in turn override results from the online database.

If no flux density is available in ASDM, `dbservice`, or `flux.csv`, a flux of 1Jy will be assumed.

After evaluating this sequence of preferred sources, the flux densities for each source and spw are written into the `flux.csv` text file. Note that even if all values are taken from `flux.csv`, they will be written back to `flux.csv`, so the file’s modification date will be updated.

The new flux value of the flux calibrator (the source with `intent=AMPLITUDE`) is then used in the subsequent `hif_setmodels` task. Values for the other calibrator intents (`BANDPASS`, `PHASE`, `CHECK`) are also updated, but these values are only shown for comparison against the values derived from the pipeline calibration calibration (both are shown in a table in the `hifa_gfluxscale` stage of the WebLog – see Sec. 9.19).

The format of the `flux.csv` file is shown in Figure 13 below. It contains one row for every spw of every calibrator (intents of `AMPLITUDE`, `BANDPASS`, `PHASE` or `CHECK`) in every ASDM in the MOUS. This file can be edited by users and the pipeline re-run in order to scale the fluxes of each ASDMs to a different value for the `AMPLITUDE` calibrator. Changing the values of other calibrators will not have an effect on the calibration.

```

ms,field,spw,I,Q,U,V,spix,comment

uid___A002_Xd0adbe_Xd5a.ms,0,25,0.8818,0.0,0.0,0.0,-0.750167691515,"# field=J1550+0527
intents=AMPLITUDE,ATMOSPHERE,BANDPASS,POINTING,WVR origin=DB age=4 queried_at=2018-09-14 20:47:41 UTC # +-
0.0849Jy, freq=109.517GHz, spec_index=-0.750+-0.168, Band3/7_separation=0 days, spixAge=-14 days, Band3age=5
days, setjy parameters for field 0 (J1550+0527): spix=-0.7502, reffreq='109.5167GHz',
fluxdensity=[0.881754,0,0,0], au.getALMAFluxcsv v1.4207 executed on 2018-09-14 21:27:01 UT"

uid___A002_Xd0adbe_Xd5a.ms,0,27,0.8926,0.0,0.0,0.0,-0.750167691515,"# field=J1550+0527
intents=AMPLITUDE,ATMOSPHERE,BANDPASS,POINTING,WVR origin=DB age=4 queried_at=2018-09-14 20:47:42 UTC # +-
0.0868Jy, freq=107.746GHz"

uid___A002_Xd0adbe_Xd5a.ms,0,29,0.9630,0.0,0.0,0.0,-0.750167691515,"# field=J1550+0527
intents=AMPLITUDE,ATMOSPHERE,BANDPASS,POINTING,WVR origin=DB age=4 queried_at=2018-09-14 20:47:42 UTC # +-
0.1032Jy, freq=97.383GHz"

uid___A002_Xd0adbe_Xd5a.ms,0,31,0.9767,0.0,0.0,0.0,-0.750167691515,"# field=J1550+0527
intents=AMPLITUDE,ATMOSPHERE,BANDPASS,POINTING,WVR origin=DB age=4 queried_at=2018-09-14 20:47:43 UTC # +-
0.1061Jy, freq=95.563GHz"

uid___A002_Xd0adbe_Xd5a.ms,1,25,0.1435,0.0,0.0,0.0,-0.577110147696,"# field=J1458+0416
intents=ATMOSPHERE,PHASE,WVR origin=Source.xml age=N/A queried_at=N/A # +-0.0076Jy, freq=109.517GHz,
spec_index=-0.577+-0.121, Band3/7_separation=0 days, spixAge=+4 days, Band3age=4 days, setjy parameters for
field 1 (J1458+0416): spix=-0.5771, reffreq='109.5167GHz', fluxdensity=[0.143542,0,0,0]"

uid___A002_Xd0adbe_Xd5a.ms,1,27,0.1449,0.0,0.0,0.0,-0.577110147696,"# field=J1458+0416
intents=ATMOSPHERE,PHASE,WVR origin=Source.xml age=N/A queried_at=N/A # +-0.0077Jy, freq=107.746GHz"

```

**Figure 13: Example of a flux.csv file used by the interferometric pipeline (one per MOUS) – blank lines added here for readability.**

The original flux.csv file written by the pipeline upon the initial run of the hif\_importdata task, starts out with "origin=Source.xml" as part of the comment on all lines. Lines updated with the online database will have "origin=DB".

## 7.2 jyperk.csv (SD pipeline)

ALMA single-dish observations do not include observations of absolute amplitude calibrators. Instead, the observatory conducts regular observations of standard single-dish calibrators and stores them in an observatory database. When the single-dish pipeline is run, ALMA staff run commands outside the pipeline to extract the best value of these "Kelvin to Jansky" calibration factors, based on the observing date, frequency, T<sub>sys</sub>, and source elevation. The appropriate values are written into a the **jyperk.csv** text file that is read and applied when the hsd\_k2jyca1 task is run.

The format of the **jyperk.csv** file is shown in Figure 14 below. It contains one row for every spw in every ASDM in the MOUS. This file can be edited by users and the pipeline re-run in order to scale the fluxes of each ASDM to a different value.

```

MS,Antenna,Spwid,Polarization,Factor
uid___A002_Xb1d975_Xf65.ms,PM02,17,I,43.785
uid___A002_Xb1d975_Xf65.ms,PM02,19,I,43.782
uid___A002_Xb1d975_Xf65.ms,PM02,21,I,43.664
uid___A002_Xb1d975_Xf65.ms,PM02,23,I,43.63
uid___A002_Xb1d975_Xf65.ms,PM02,25,I,43.638
uid___A002_Xb1d975_Xf65.ms,PM02,27,I,43.64
uid___A002_Xb1d975_Xf65.ms,PM02,29,I,43.641
uid___A002_Xb1d975_Xf65.ms,PM04,17,I,43.785
uid___A002_Xb1d975_Xf65.ms,PM04,19,I,43.782
uid___A002_Xb1d975_Xf65.ms,PM04,21,I,43.664
uid___A002_Xb1d975_Xf65.ms,PM04,23,I,43.63
uid___A002_Xb1d975_Xf65.ms,PM04,25,I,43.638
uid___A002_Xb1d975_Xf65.ms,PM04,27,I,43.64
uid___A002_Xb1d975_Xf65.ms,PM04,29,I,43.641
uid___A002_Xb1cc39_X1e46.ms,PM02,17,I,43.782
uid___A002_Xb1cc39_X1e46.ms,PM02,19,I,43.778
uid___A002_Xb1cc39_X1e46.ms,PM02,21,I,43.661
uid___A002_Xb1cc39_X1e46.ms,PM02,23,I,43.627
uid___A002_Xb1cc39_X1e46.ms,PM02,25,I,43.635
uid___A002_Xb1cc39_X1e46.ms,PM02,27,I,43.636
uid___A002_Xb1cc39_X1e46.ms,PM02,29,I,43.638
uid___A002_Xb1cc39_X1e46.ms,PM04,17,I,43.782
uid___A002_Xb1cc39_X1e46.ms,PM04,19,I,43.778
uid___A002_Xb1cc39_X1e46.ms,PM04,21,I,43.661
uid___A002_Xb1cc39_X1e46.ms,PM04,23,I,43.627
uid___A002_Xb1cc39_X1e46.ms,PM04,25,I,43.635
uid___A002_Xb1cc39_X1e46.ms,PM04,27,I,43.636
uid___A002_Xb1cc39_X1e46.ms,PM04,29,I,43.638

```

Figure 14: Example of a `jyperk.csv` file used by the single-dish pipeline (one per MOUS)

### 7.3 antennapos.csv (IF pipeline)

The position of every antenna in an interferometric observation must be known in order to properly transfer the calibration from the phase calibrator to the science targets. If these positions have errors, it will lead to phase errors in the imaging of the science target (increasing with telescope position error and separation between the phase calibrator and science target).

The antenna positions are calculated by special observatory observations taken outside of PI science observing, and the positions stored in an observatory database. This database is queried at the time of an SB execution, and the appropriate antenna positions are written into the ASDM. These positions are sometimes updated subsequently, especially if the observation happened close to an array reconfiguration or if an array element was recently moved.

Since the pipeline is usually run days to weeks after an observation, ALMA staff run commands outside of the pipeline to get the best-available antenna positions at the time the pipeline is run. These are written into the `antennapos.csv` text file, which is then read in by the pipeline `hifa_antpos` task (if it exists in the directory where the pipeline is run) and used to over-ride the values in the ASDM.

The format of the `antennapos.csv` file is shown in Figure 15 below. It contains one row for every antenna in every ASDM in the MOUS. This file can be edited by users and the pipeline re-run in order to correct antenna position errors.

```

name,antenna,xoff,yoff,zoff,comment
uid___A002_Xbb63ba_X18b0.ms,DA42,1.27536e-04,-3.54105e-04,-2.38014e-04,
uid___A002_Xbb63ba_X18b0.ms,DA46,1.98098e-04,-5.34528e-04,-3.65393e-04,
uid___A002_Xbb63ba_X18b0.ms,DA49,1.69321e-04,-2.81896e-04,-1.76309e-04,
uid___A002_Xbb63ba_X18b0.ms,DA52,-4.06882e-05,3.45109e-04,3.15047e-04,
uid___A002_Xbb63ba_X18b0.ms,DA62,-1.79249e-04,2.50696e-04,7.12701e-05,
uid___A002_Xbb63ba_X18b0.ms,DV03,-3.92453e-04,2.85912e-04,3.14499e-04,
uid___A002_Xbb63ba_X18b0.ms,DV08,-2.76083e-04,7.41071e-04,1.87197e-04,
uid___A002_Xbb63ba_X18b0.ms,DV14,-5.41156e-05,2.61746e-04,3.44329e-04,
uid___A002_Xbb63ba_X18b0.ms,DV15,-1.21313e-04,3.67910e-04,1.49062e-04,
uid___A002_Xbb63ba_X18b0.ms,DV23,1.73257e-04,1.36402e-04,-1.23099e-04,
uid___A002_Xbb63ba_X18b0.ms,DV25,3.12879e-03,-5.08802e-03,-2.87630e-03,
uid___A002_Xbb63ba_X18b0.ms,PM03,1.78948e-04,-5.00918e-04,-2.14580e-04,
uid___A002_Xbb63ba_X1626.ms,DA42,1.27536e-04,-3.54105e-04,-2.38014e-04,
uid___A002_Xbb63ba_X1626.ms,DA46,1.98098e-04,-5.34528e-04,-3.65393e-04,
uid___A002_Xbb63ba_X1626.ms,DA49,1.69321e-04,-2.81896e-04,-1.76309e-04,
uid___A002_Xbb63ba_X1626.ms,DA52,-4.06882e-05,3.45109e-04,3.15047e-04,
...

```

Figure 15: Example of a `antennapos.csv` file used by the interferometric pipeline (one per MOUS); the offset units are in meters. Corrections that are comparable, or larger than the observing wavelength are consequential.

## 7.4 `uid*flagtemplate.txt` & `uid*flagssystemtemplate.txt` (both pipelines)

The pipeline flagging heuristics may prove inadequate, and users may wish to add additional flagging commands to exclude these data from the calibration. These manually-identified flags can be introduced to any Pipeline reduction by editing the `uid*flagtemplate.txt` files that are provided with the archived pipeline products and rerunning the pipeline calibration steps. There should be one file for every MS that needs additional flagging, with a name matching the MS uid. The flag commands can be any valid CASA `flagdata` command. For interferometric data, use the `<AntID>` syntax to flag only cross-correlation data for `<AntID>`, while for single dish data use the `"<AntID>&&*"` syntax to flag both cross- and auto-correlation data for `<AntID>`, and the `"<AntID>&&&"` syntax to flag auto-correlation data for `<AntID>`. Examples of the syntax to use in editing these files are given at the top of the files `uid*flagtemplate.txt` (see Figure 16).

These flag files will be picked up by the `hifa_flagdata/hsd_flagdata` tasks which are run before the calibration tasks, therefore excluding the manually identified data from being used to generate the calibration tables.

Since the `tsys` spectra are calculated from a different ASDM subtable, any commands that the user desires to flag the `tsys` spectral windows have to be applied differently by the pipeline, so have to be put into the separate `flagssystemtemplate.txt` file. The flagging syntax is the same, only that those commands should refer to `tsys` spectral windows in particular.

```

# User flagging commands file for the calibration pipeline
#
# Examples
# Note: Do not put spaces inside the reason string !
#
# mode='manual' antenna='DV02;DV03&DA51' spw='22,24:150~175' reason='QA2:applycal_amplitude_frequency'
#
# mode='manual' spw='22' field='1' timerange='2018/02/10/00:01:01.0959~2018/02/10/00:01:01.0961'
reason='QA2:timegaincal_phase_time'
#
# TP flagging: The 'other' option is intended for bad TP pointing
# mode='manual' antenna='PM01&&PM01' reason='QA2:other_bad_pointing'
#
# Tsys flagging:
# mode='manual' antenna='DV02;DV03&DA51' spw='22,24' reason='QA2:tsysflag_tsys_frequency'
#
mode='manual' timerange='2016/12/05/03:55:30.1440' reason='QA2:applycal_outlier_amp'
mode='manual' antenna='PM02&&&' reason='PRTSIR2995'

```

Figure 16: Example of a `uid*flagtemplate.txt` file used by both the interferometric and single-dish pipeline (one per ASDM)

## 7.5 `uid*flagtargetstemplate.txt` (IF imaging pipeline)

Users should examine the science data (e.g. using the CASA task `plotms`, or examining at the MS using the CASA viewer). If bad data are found, flagging commands can be added to the `uid*flagtargetstemplate.txt` files that are provided with the archived pipeline products to exclude these data from subsequent imaging. There should be one file for every MS that needs additional flagging, with a name matching the MS uid. As for the `uid*flagtemplate.txt` files, the flag commands can be any valid CASA `flagdata` command. If these files are found in the directory where the pipeline is run, they will be picked up by the `hifa_flagtargets` task and applied to the data before science target imaging.

## 7.6 `cont.dat` (IF imaging pipeline)

The pipeline-identified continuum frequency ranges, in LSRK units, for each spectral window of each source are entered into a file called `cont.dat` that is delivered with the pipeline products. This file lists the LSRK frequency ranges that were used to make the per-spw and aggregate continuum images, and for fitting and subtracting the continuum for the image cubes. When this file is in the directory where the pipeline is (re)run, the pipeline will use these entries directly instead of using its own heuristics (via the `hif_findcont` task) to determine them. Therefore, a user can edit this file (or create their own) in order to use a different continuum range. Alternatively, a user-defined file name can be passed as an argument to the `hif_makeimlist` task. An example `cont.dat` file is shown in Figure 17.

```

Field: G09_0850-0019
SpectralWindow: 17
NONE

SpectralWindow: 19
337.659971874~339.253995016GHz LSRK

SpectralWindow: 21

SpectralWindow: 25
349.755169752~351.067897111GHz LSRK
351.271057297~351.380451244GHz LSRK

```

Figure 17: Example of a `cont.dat` file used by the interferometric pipeline (one per MOUS). This example is for an MOUS that has 5 spectral windows; the entry for spw 21 is empty and spw 23 is omitted, which will result in the `hif_findcont` command determining the frequency ranges for these spectral windows.

The behavior of `hif_findcont` and the subsequent continuum subtraction and continuum and line imaging commands is as follows:

- If the `spw` line in `cont.dat` is followed by one or more frequency ranges, `hif_findcont` will not run its heuristics on the `spw`. The task `hif_uvcontfit` will use these frequency ranges to fit and subtract the continuum from this `spw`. Subsequent continuum images will include only these frequency ranges for this `spw`, and the `spw` line cubes will be made from the continuum subtracted data.
- If the `spw` line is followed by a line containing “NONE”, `hif_findcont` will not run its heuristics on the `spw` (if the delivered **cont.dat** file contains `spw` entries with “NONE”, this indicates that the `hif_findcont` task failed to find any continuum frequency ranges). The task `hif_uvcontfit` will skip fitting this `spw`. Subsequent continuum images will include the full frequency range for this `spw` (logging a warning), and the `spw` line cubes will have had no continuum subtraction performed.
- If a `spw` is not followed by a frequency range or is missing from **cont.dat** when `hif_findcont` is run, then it will try to find the frequency ranges, and these will be used to make subsequent continuum images, and for continuum subtraction.

## 8 The Pipeline WebLog

This section gives an overview of the Pipeline WebLog, which is a collection of webpages with diagnostic messages, tables, figures, and “Quality Assurance” (QA) scores. It is reviewed, along with the pipeline calibration and imaging products, as part of the ALMA Quality Assurance process, but also provides important information to investigators on how the pipeline calibration and imaging steps went.

The section describes common elements to the single dish and interferometric Pipeline WebLogs. Subsequent sections present descriptions of the SD- or IF- specific “By Task” part of the WebLog.

### 8.1 Overview

The WebLog is a set of html pages that give a summary of how the calibration of ALMA data proceeded, of the imaging products, and provides diagnostic plots and Quality Assurance (QA) scores. The WebLog will be in the **qa** directory of an ALMA delivery. To view the WebLog, untar and unzip the file using e.g. **tar zxvf \*weblog.tgz** . This will provide a **pipeline\*/html** directory containing the WebLog, which can be viewed using a web browser e.g. **firefox index.html**.

#### [Note about browser security \[new 2020\]:](#)

Most modern browsers now prevent javascript when using a file:// URL (e.g. viewing a weblog on a local directory). The page below should appear, which describes the mitigation options. One can either use a localhost web server that is now delivered with CASA+Pipeline2020, or one can adjust the security settings in the browser.

ALMA Home By Topic By Task Project Code N/A

**Tasks in execution order**

1. hifa\_importdata
2. hifa\_flagdata
3. hifa\_fluxcallflag
4. hif\_rawflagchans
5. hif\_refant
6. h\_tsyscal
7. hifa\_tsysflag

## Error: cannot load content

Browser security prevents the weblog from displaying the requested content.

Viewing the web log locally is not possible with your web browser security settings. To view the web log you must serve the web log via HTTP by using `h_weblog` from inside a CASA session, or relax your web browser security.

### Solutions

**Recommended: use `h_weblog()`**

From inside a CASA session, navigate to the root of the untarred weblog directory, e.g., `pipeline-procedure_hifa_calimage`, and run `h_weblog`. This command will serve the web log via HTTP and launch a browser connecting to the web log. The web log URL is also printed to the CASA logger, should you need to navigate to the web log manually. The URL to access is highlighted in the example CASA logger output below.

```
CASA -<S>: h_weblog()
2020-07-30 12:57:20 INFO h_weblog:::casa #####
2020-07-30 12:57:20 INFO h_weblog:::casa #### Begin Task: h_weblog #####
2020-07-30 12:57:20 INFO h_weblog:::casa h_weblog( pipelinemode='automatic', relpath='' )
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Found weblogs at:
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa+ main/pipeline-procedure_hifa_calimage/html/t1-1.html
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Using existing HTTP server at 127.0.0.1 port 30000 ...
2020-07-30 12:57:20 INFO h_weblog::pipeline::casa Opening http://127.0.0.1:30000/main/pipeline-procedure_hifa_calimage/html/t1-1.html
2020-07-30 12:57:20 INFO h_weblog:::casa Result h_weblog: None
2020-07-30 12:57:20 INFO h_weblog:::casa Task h_weblog complete. Start time: 2020-07-30 08:57:19.880720 End time: 2020-07-30 08:57:20.064263
2020-07-30 12:57:20 INFO h_weblog:::casa #### End Task: h_weblog #####
2020-07-30 12:57:20 INFO h_weblog:::casa #####
```

For security, the web log HTTP server is only accessible from the same computer as the CASA session. To view the web log from another computer, forward the port using SSH. For example, to access the web log hosted on a remote machine called `remotepc`, where the CASA log reports the web log is available at port 30000, execute:

```
ssh -L 30000:localhost:30000 remotepc
```

### Alternative: lower browser security

These modification lowers your browser security and should be reverted after viewing the weblog!

#### Firefox

Navigate to `about:config` and search for the `privacy.file_unique_origin` preference. Change the preference value to false.

#### Safari

Open Safari preferences, navigate to `Advanced` tab and check the `Show Develop in menu bar` option. From the new `Develop` menu option now visible at the top of the screen, select `Disable Local File Restriction`.

#### Chrome

The `--disable-web-security` and `--user-data-dir` command line arguments must be passed to Chrome via the command line. For example, on MacOS start Chrome like this:

```
/Applications/Chrome.app/Contents/MacOS/Chrome --disable-web-security --user-data-dir~/tmp
```

The WebLog provides both an overview of datasets and details of each each pipeline processing. Therefore most calibration pages of the WebLog will first give a single “representative” view, with further links to a more detailed view of all the plots associated with that calibration step. Some of these (those produced by the CASA tasks `plotms` and `plotbandpass`) will have a “Plot command” link that provides the CASA command to reproduce the plot (see Figure 18). When viewing image products, a similar link will provide the `tclean` command that produced the image. For some stages, the detailed plots can be

### WebLog Quick Tips

- Any text written in blue, including headings, is a link to further information.
- To go straight to viewing calibrated science target visibilities, go to **By Task > hif\_applycal** and scroll down to the bottom.
- Histograms can have selector boxes drawn on them using the mouse.
- The CASA commands for re-creating many of the WebLog plots are provided.

filtered by a combination of outlier, antenna and spectral window criteria. Where histograms are displayed, in modern web browsers it is possible to draw boxes on multiple histograms to select the plots associated with those data points. All pipeline stages are assigned a QA score to give an “at a glance” indication of any trouble points.

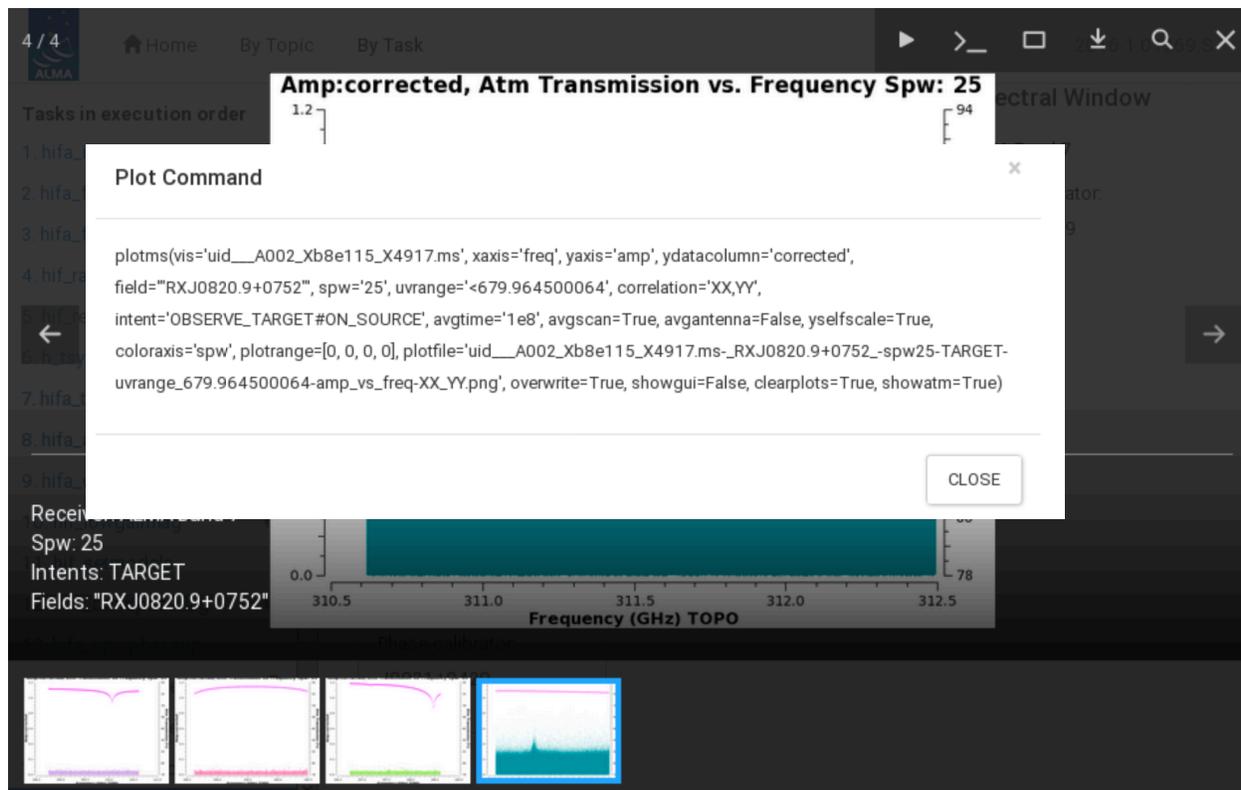


Figure 18: Example of WebLog plot with a "Plot command" link (>) that provides the CASA command for reproducing the plot.

## 8.2 Navigation

To navigate the main pages of the WebLog, click on items given in the bar at the top of the WebLog home page. Also use the **Back** button provided at the upper right on some of the WebLog sub-pages. Avoid using “back/previous page” on your web browser (although this can work on modern browsers). Throughout the WebLog, links are denoted by text written in blue and it is usually possible to click on thumbnail plots to enlarge them.

## 8.3 Home Page

The first page in the WebLog gives an overview of the observations (proposal code, data codes, PI, observation start and end time), a pipeline execution summary (pipeline & CASA versions, link to the current pipeline documentation, pipeline run date and duration), and an **Observation Summary** table. Clicking on the “environment” link next to the CASA version will open a popup detailing hardware and software used, and number of cores if MPI; see Figure 20). Clicking on the bar at the top of the home page (see Figure 19) enables navigation to **By Topic** or **By Task**.

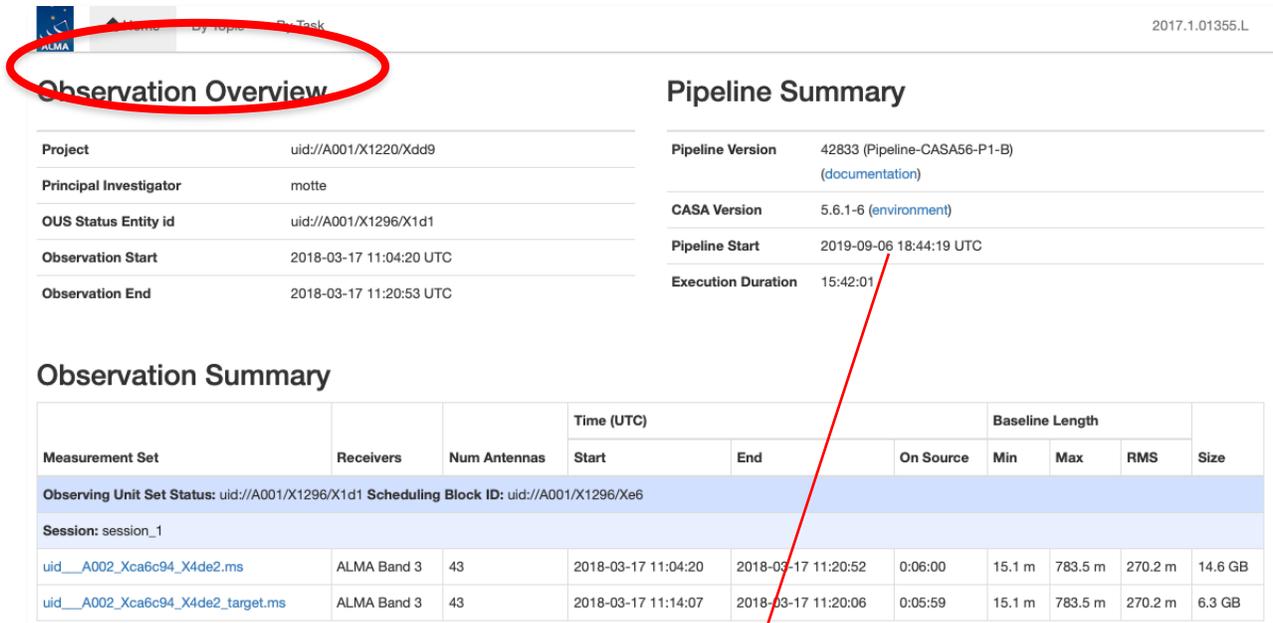


Figure 19: WebLog Home Page. The Navigation Bar is circled in red.

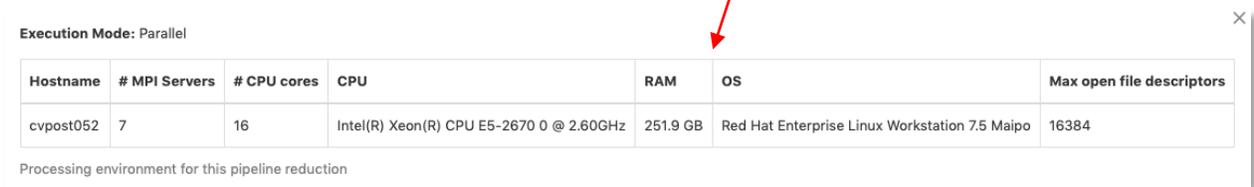


Figure 20: Processing Environment popup window

The **Observation Summary** table lists all the measurement sets included in the pipeline processing, grouped by observing “sessions”. Each measurement set is calibrated independently by the pipeline. For data that have been run through the imaging stages of the pipeline, two MS will be listed – the original one including all data and spectral windows, and a target.ms containing only calibrated science target data. The table provides a quick overview of the ALMA receiver band used, the number of antennas, the start/end date and time, the time spent on source, the array minimum and maximum baseline length, the rms baseline length and the size of that measurement set. To view the observational setup of each measurement set in more detail, click on the name of it to go to its overview page.

### 8.3.1 Measurement set Overview pages

Clicking on the measurement set name in the **Observational Summary** table brings up the **Measurement set Overview page** (Figure 21). Each measurement set **Overview** page has a number of tables: **Observation Execution Time**, **Spatial Setup (includes mosaic pointings)**, **Antenna Setup**, **Spectral Setup** and **Sky Setup (includes elevation vs. time plot)**. For more information on the tables titled in blue text, click on these links. There are additionally links to **Weather**, **PWV**, **Scans** and **Telescope Pointings** (in the case of Single Dish observations) information. Two thumbnail plots, which can be enlarged by clicking on them, show the observation structure either as **Field Source Intent vs Time** or **Field Source ID vs Time**. To view the CASA listobs output from the observation, click on **Listobs Output**.



Figure 21: Measurement Set Overview Page. Click on the table headings in blue for more information about each.

## 8.4 By Topic Summary Page

The **By Topic** summary page provides an overview of all **Warnings and Errors** triggered, a Quality Assessment overview in **Tasks by Topic** and **Flagging Summaries** for the processing.

## 8.5 By Task Summary Page

The **By Task** summary page (Figure 22) gives a list of all the pipeline stages performed on the dataset. It is not displayed per measurement set as the Pipeline performs each step on every measurement set sequentially before proceeding to the next step; e.g. it will import and register all measurement sets with the Pipeline before proceeding to perform the ALMA deterministic flagging step on each measurement set. The name of each step on the By Task page is a link to more information.

On the right hand side of the page are colored bars and scores that indicate how well the Pipeline processing of that stage went. Green bars should indicate a fairly problem-free dataset, while blue or red bars indicate less than perfect QA scores. Encircled symbols to the left of each task name ("?", "!" or "x"), indicate that there are informative QA messages on the subtask pages. The messages in the stages with a "?" appear in the expandable "Pipeline

QA" section of the task weblog page (Figure 24), while those with a "!" or "x" appear at the top. Stages with a "!" symbol next to them can indicate either poor QA scores (QA Score progress bar on the Task Summaries page will be yellow with a short descriptive text) or informative "warnings", which are important messages about the stage execution but which are not thought to indicate a quality issue with the data (the QA Score progress bar on the Task Summaries page will be green, e.g. the hifa\_tsysflag and hif\_lowgainflag stages in Figure 22).

## Task Summaries

Task	QA Score	Duration
1. <a href="#">hifa_importdata</a> : Register measurement sets with the pipeline	1.00	0:04:00
2. <a href="#">hifa_flagdata</a> : ALMA deterministic flagging	1.00	0:20:34
3. <a href="#">hifa_fluxcalflag</a> : Flag spectral features in solar system flux calibrators	1.00	0:00:03
4. <a href="#">hif_rawflagchans</a> : Flag channels in raw data	1.00	0:04:01
5. <a href="#">hif_refant</a> : Select reference antennas	1.00	0:00:19
6. <a href="#">h_tsyscal</a> : Calculate Tsys calibration	1.00	0:04:36
7. <a href="#">hifa_tsysflag</a> : Flag Tsys calibration	0.98	0:05:56
8. <a href="#">hifa_antpos</a> : Correct for antenna position offsets	Nonzero antenna position offsets  0.90	0:00:07
9. <a href="#">hifa_wvrgcalflag</a> : Calculate and flag WVR calibration	1.00	0:07:31
10. <a href="#">hif_lowgainflag</a> : Flag antennas with low gain	1.00	0:12:08
11. <a href="#">hif_setmodels</a> : Set calibrator model visibilities	1.00	0:04:13
12. <a href="#">hifa_bandpassflag</a> : Phase-up bandpass calibration and flagging	1.00	0:54:47
13. <a href="#">hifa_spwphaseup</a> : Spw phase offsets calibration	1.00	0:02:39
14. <a href="#">hifa_gfluxscaleflag</a> : Phased-up flux scale calibration + flagging	1.00	0:10:19
29. <a href="#">hif_uvconfit</a> : UV continuum fitting	1.00	0:13:50
30. <a href="#">hif_uvcontsub</a> : UV continuum subtraction	1.00	0:00:59
31. <a href="#">hif_makeimages</a> : Make target per-spw continuum images	1.00	0:26:32
32. <a href="#">hif_makeimlist</a> : Set-up parameters for target aggregate continuum imaging	1.00	0:00:24
33. <a href="#">hif_makeimages</a> : Make target aggregate continuum images	1.00	0:34:01
34. <a href="#">hif_makeimlist</a> : Set-up parameters for target cube imaging	1.00	0:00:24
35. <a href="#">hif_makeimages</a> : Make target cubes	1.00	8:49:16
36. <a href="#">hif_makeimlist</a> : Set-up parameters for representative bandwidth target cube imaging	No clean targets expected  N/A	0:00:18
37. <a href="#">hif_makeimages</a> : Make representative bandwidth target cube	Nothing to image  N/A	0:00:08
38. <a href="#">hifa_exportdata</a> : Prepare pipeline data products for export	1.00	0:22:38
<b>CASA logs and scripts</b>		
<ul style="list-style-type: none"> <li>• <a href="#">View, view in new tab or download casa-20190906-184353.log</a> (12.3 MB)</li> <li>• <a href="#">View, view in new tab or download casa-20190906-230242.log</a> (73.2 MB)</li> <li>• <a href="#">View, view in new tab or download casa_commands.log</a> (288.7 KB)</li> <li>• <a href="#">View, view in new tab or download casa_pipescript.py</a> (2.5 KB)</li> <li>• <a href="#">View, view in new tab or download casa_piperestorescript.py</a> (165 bytes)</li> <li>• <a href="#">View, view in new tab or download PPR_uid__A001_X1296_X1d2.xml</a> (11.7 KB)</li> </ul>		

Figure 22: By Task summary view. The page has been truncated so both the top and bottom can be seen. Each pipeline stage is listed, along with its QA score (colored bars to the right), computing run-time for each stage, and links to the CASA logs and scripts.

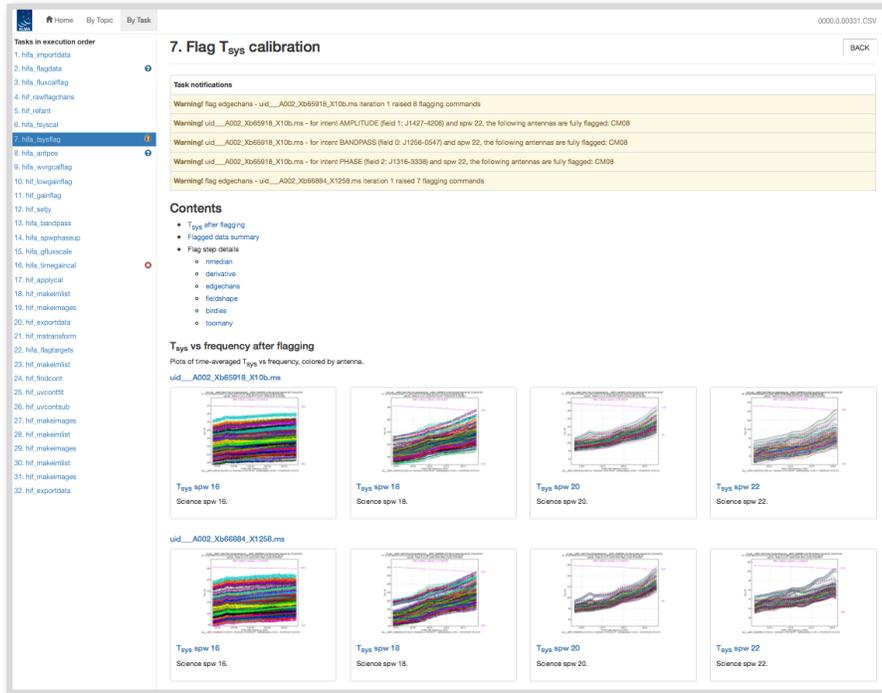
### 8.5.1 CASA logs and scripts

At the bottom of the **By Task** summary page are links to the CASA logs and supporting files and scripts. These include the complete CASA log file produced during the pipeline run, the

pipeline restoration scripts described in Sec. 5.1: `casa_pipelinescript.py` and `casa_piperestorescript.py`, and the `casa_commands.log` file described in Sec. 5.5.

## 8.6 Task Pages

Each task has its own summary page that is accessed by clicking on the task name on the **By Task** summary page or in the left navigation menu from other pages. The task pages provide the outcome, or the representative outcome, of each Pipeline task executed. **For a fast assessment of the calibration results, go straight to the applycal page.** At the top of the page will be any Task Notification (see Figure 23). These provide informative messages or warnings generated from the QA scoring and should be reviewed carefully.



**Figure 23:** `hifa_tsysflag` task page, showing the task notifications at the top, and diagnostic plots (Tsys for each spw grouped by MS). Further down on the page are flagging summary tables. To see the sub-page for this task, click on the measurement set name in blue above each set of plots. This will take you to a page of detailed plots for individual MS/antenna/spectral windows (see Figure 25 for an example).

At the bottom of each task page are expandable sections for **Pipeline QA**, **Input Parameters** and **Task Execution Statistics**, and links to the CASA log commands for the specific task. An example is given in Figure 24.

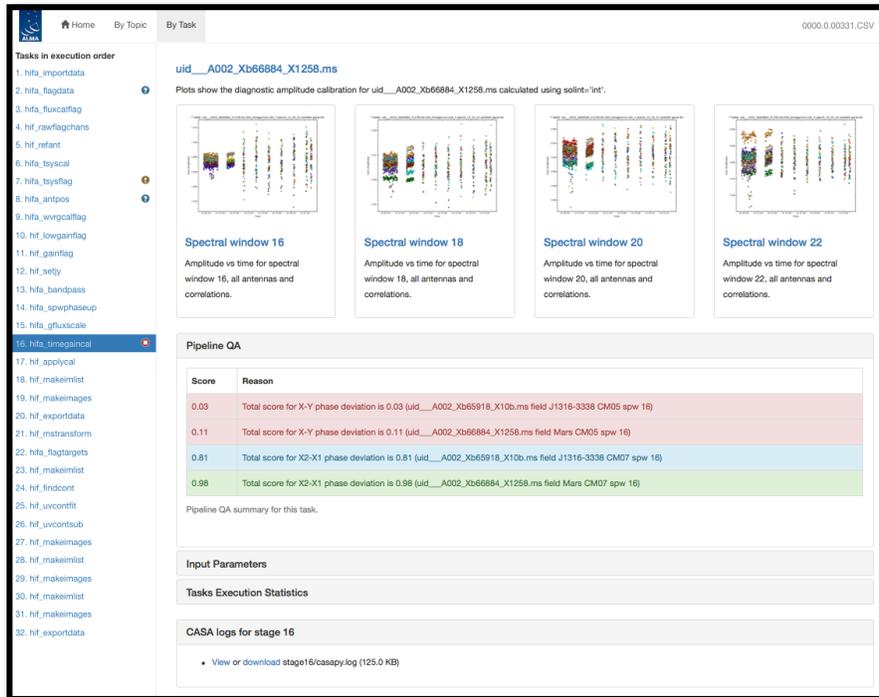
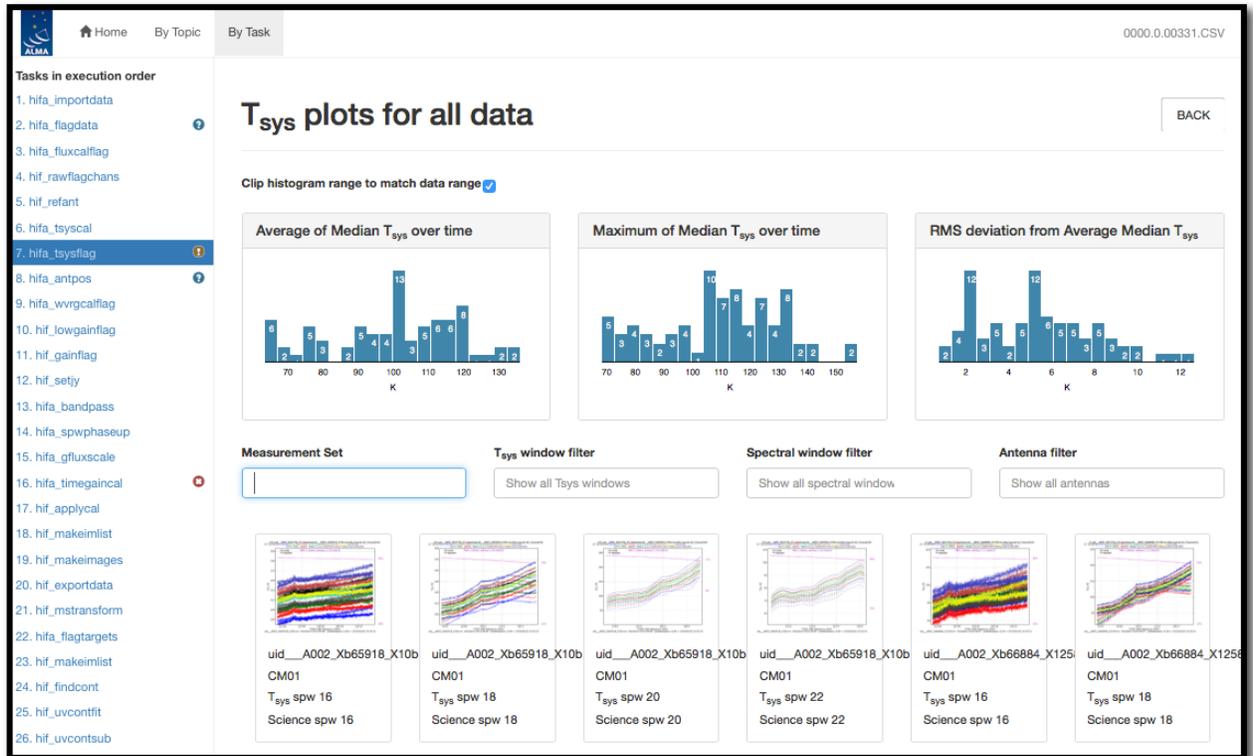


Figure 24: Bottom of the hifa\_timegaincal page, showing the expanded Pipeline QA section, as well as the expandable sections for Input Parameters, Task Execution Statistics and link to the CASA logs for this stage.

### 8.6.1 Task sub-pages and plot filtering

Most sub-pages have further links in order to access a more detailed view of the outcome of each task. These links are often labelled by the measurement set name. Some of these plots can be filtered by entering one or more MS, antenna, or spectral window in the appropriate box. Still others have histograms of various metrics that can be selected using the cursor in a drop-and-drag sense to outline a range of histogram values and displays the plots for the MS/antenna/spw combinations that are responsible for those histogram values. An example of these subpages and plot filtering is given in Figure 25 – Figure 27 below, using the **By Task > hifa\_tsysflag: Flag Tsys calibration** pages.



**Figure 25: Unfiltered view of the hifa\_tsysflag sub-page. The page is arrived at by clicking on the measurement set link from the hifa\_tsysflag task page (Figure 23). Only the first row of plots are shown; many more appear below (one for each MS, antenna, spw combination). This page has histograms of three metric scores based on the median Tsys that can also be used to filter the plots that are displayed.**

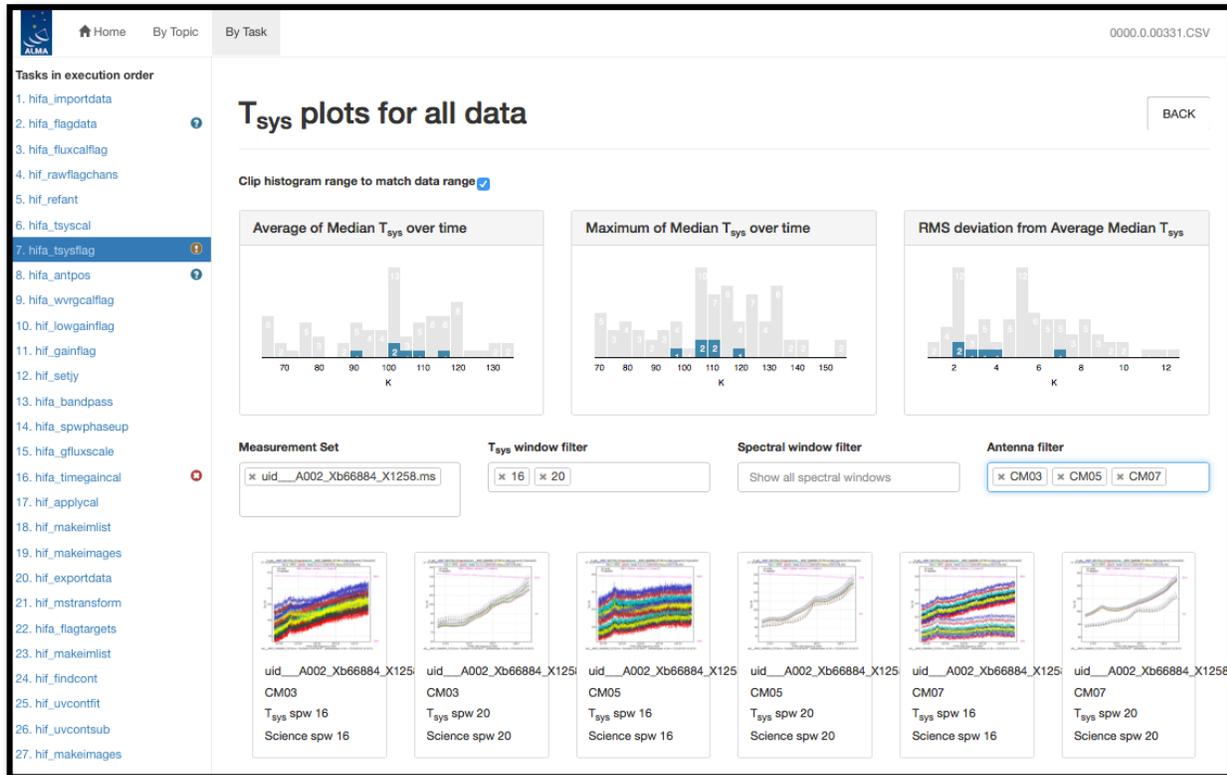


Figure 26: Same as Figure 25, but with a specific MS, Tsys window, and antenna filter set. The corresponding plots are displayed below, and their metric scores are shown by blue shading in the histogram plots.

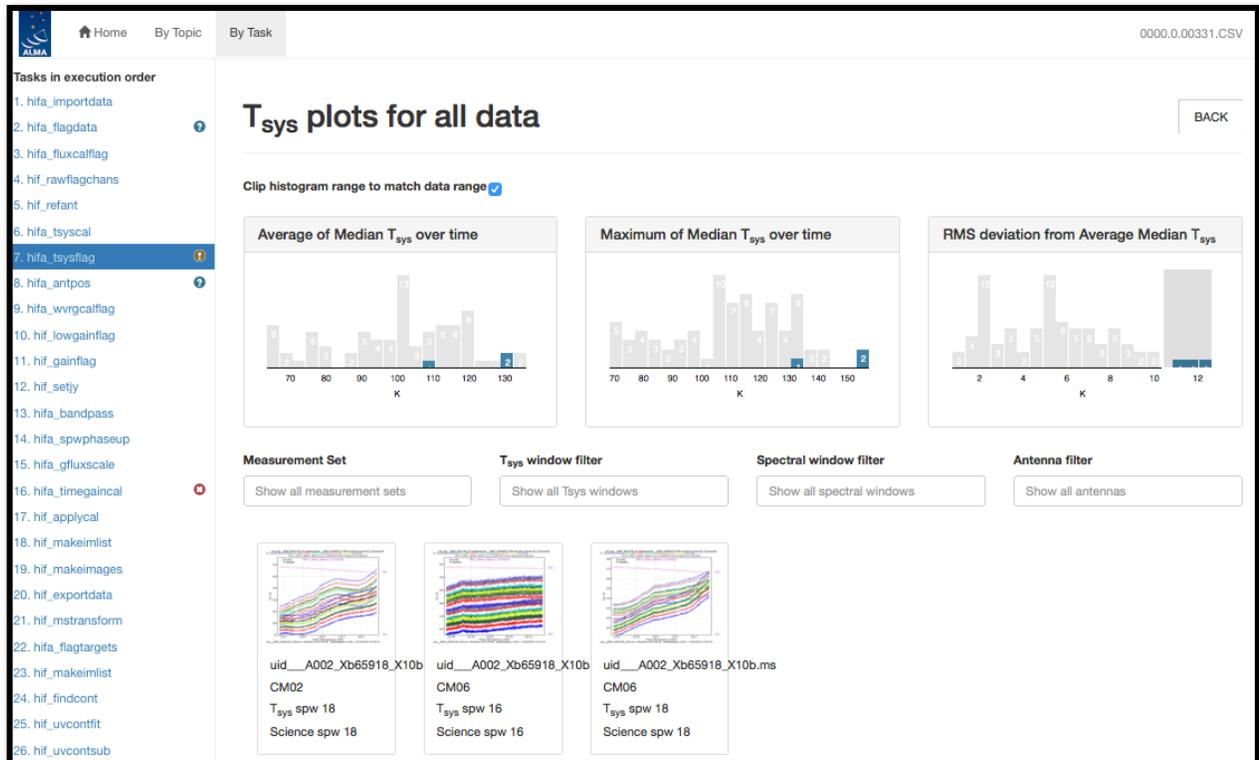


Figure 27: Same as Figure 25, but filtering to the plot of interest by using the mouse to draw a grey box on the highest histogram values in the RMS deviation from Average Median Tsys histogram plot (upper right). To clear the grey box filters on the histograms, click on any white space in the histograms.

## 8.7 WebLog Quality Assessment (QA) Scoring

Pipeline tasks have scores associated with them in order to quantify the quality of the dataset and the calibration. These scores are designed to inform data inspection as part of the ALMA quality insurance or "QA2" process. When scores are calculated per ASDM, the QA score is taken as the lowest of the per-ASDM scores. The scores are between 0.0 and 1.0 and are colorized according to the following table:

Score	Color	Meaning
0.90-1.00	Green	No issues identified
0.66-0.90	Blue	no serious issues identified, but a note has been added
0.33-0.66	Yellow	QA warning triggered; carefully inspect the results for this stage
0.00-0.33	Red	Serious issue; may not meet quality standards

The individual QA scores (1 per QA heuristic per ASDM) and associated messages appear in the expandable "Pipeline QA" section of the task weblog page (Figure 24). Yellow and Red QA scores and their associated messages will be repeated at the top of page.

### 8.7.1 Interferometric Pipeline QA Scores

Pipeline Task	Pipeline QA Scoring Metric	Score
<b>hifa_importdata</b>	Check that the required calibrators are present	1.0 all present
		0.1 subtracted for missing bandpass or flux calibrator
		1.0 subtracted for missing phase calibrator or Tsys calibration
		0.5 subtracted for existing processing history
<b>hifa_flagdata</b>	Percentage of incremental flagging	<p>For the following flag types: 'online', 'shadow', 'qa0', 'before' and 'applycal':</p> <p>Score is 0 if flag fraction is <math>\geq 50\%</math>            Score is 1 if flag fraction is <math>\leq 5\%</math>            Score is linearly interpolated between 0 and 1 for fractions between 60% and 5%.</p> <p>The percentages are accumulated for each flagging type. For example, 13.0% data flagged yields:  <math>1 - (0.130 - 0.05) / (0.60 - 0.05) = 0.85</math></p>

<b>hifa_fluxcalflag</b>	Percentage of incremental flagging	Additional 0%-5% flagging: score=1.0; flagging 5%-50% => 1.0...0.5; >50%: score=0.0. If there are mapped spws as a result of flagging, the score for that ms gets set to 0.66.
<b>hif_rawflagchans</b>	Percentage of data flagged due to deviant channels in rawdata	0% flagged: score=1.0; 100% flagged: score=0.0
<b>hif_refant</b>	Ability to choose a refant	1.0 if suitable reference antenna is found
<b>h_tsyscal</b>	Ability to calculate tsys calibration tables	1.0 if all SPWs mapped to Tsys window
<b>hifa_tsysflag</b>	Percentage of incremental flagging	Additional 0%-5% flagging: score=1.0; flagging 5%-50% => 1.0...0.5; >50%: score=0.0
<b>hifa_antpos</b>	If antenna positional corrections were applied	1.0 if no corrections needed; 0.9 if one or more antennas were corrected.
<b>hifa_wvrgcalflag</b>	Check phase RMS improvement	0.0 if RMS(without WVR)/RMS(with WVR) < 1, 0.5 – 1.0 for ratios between 1 and 2, and 1.0 for ratios > 2
<b>hif_lowgainflag</b>	Percentage of incremental flagging	Additional 0%-5% flagging: score=1.0; flagging 5%-50% => 1.0...0.5; >50%: score=0.0
<b>hifa_bandpassflag</b>	Percentage of incremental flagging	For each intent, a linear score representing the fraction of unflagged data that got newly flagged. I.e., if 60% was previously flagged, and among remaining 40%, half got flagged (such that total flagging is now 80%), then the score for this intent would be 0.5.
<b>hifa_bandpass</b>	Judge phase and amplitude solution flatness per antenna, spectral window and polarization	two algorithms: Wiener entropy and derivative deviation, and signal-to-noise ratio (scores: Wiener entropy: error function with 1-sigma deviation of 0.001 from 1.0; derivative deviation: error function with 1-sigma deviation of 0.03 for the outlier fraction; signal-to-noise ratio: error function with 1-sigma deviation of 1.0 for the signal-to-noise ratio)

<b>hifa_spwphaseup</b>	Fraction of spectral windows without phase solutions transferred from other windows	Score is the fraction of spectral windows for which phase solutions are unmapped to expected number of spectral windows
<b>hifa_gfluxscaleflag</b>	Percentage of incremental flagging	First calculate the newly flagged fraction per intent, then it combines the scores from all intents by multiplying them; i.e., if it evaluated AMPLITUDE and PHASE, and it got a score of 0.6 and 0.2 for those respectively, then the total score would be $0.6 \times 0.2 = 0.12$
<b>hifa_polcalflag (polarization recipe only)</b>	Percentage of incremental flagging	For POL* intents, a linear score representing the fraction of unflagged data that got newly flagged. I.e., if 60% was previously flagged, and among remaining 40%, half got flagged (such that total flagging is now 80%), then the score for this intent would be 0.5.
<b>hifa_session_refant (pol recipe only)</b>	Ability to determine a refant	1.0 if suitable reference antenna is found
<b>hifa_gfluxscale</b>	SNR of fitted flux values	Fitted flux values with SNR < 5.0 are assigned a score of 0.0, SNR > 20.0 a score of 1.0, and a linearly scaled value in between. If there are missing derived fluxes, then the ratio of the number of derived values to the number of spws is computed, and if this is lower than the SNR score, it supercedes the score for that ms. An additional score assesses consistency of the derived flux densities in different spws – it is known that for low-SNR (e.g. narrow) spws, the gfluxscale derived flux density can be systematically biased high. $r\_SPW = (\text{derived flux for SPW}) / (\text{catalog flux for SPW})$ , $K\_SPW = r\_spw / r\_max\_snr\_spw$ . $Q\_total = \text{Max}( 1 - K\_spw )$ . The QA score scales from 1.0 for $Q\_total=0$ , to a score of 0.75 if $Q\_total=20\%$ , and further lower QA scores for larger $Q\_total$ .

<b>hifa_timegaincal</b>	No QA score	Always set = 1.0
<b>hifa_targetflag</b>	Percentage of incremental flagging	For TARGET intents, a linear score representing the fraction of unflagged data that got newly flagged. I.e., if 60% was previously flagged, and among remaining 40%, half got flagged (such that total flagging is now 80%), then the score for this intent would be 0.5.
<b>hif_applycal</b>	Percentage of incremental flagging; Determine if corrected Amp/Phase vs. Freq of any antenna differs from mean for all antennas.	Additional 0%-5% flagging: score=1.0; flagging 5%-50% => 1.0...0.5, >50%: score=0.0. This QA score calculation is restricted to scans matching the 'TARGET' intent if present. If no 'TARGET' intent data is present, a warning is raised, and the QA score calculation reverts to using scans for any available intent. Corrected Amplitude/Phase-vs-Frequency: QA score =0.9 if linear fit for any antenna, calculated on a per-scan, per-polarization basis, differs significantly from the mean fit for all antennas.
<b>hif_makeimlist</b>	Determine if expected targets/spw will be imaged	1.0 when all objects with desired intent appear in list for all science spw
<b>hif_makeimages (non-checksource calibrators &amp; science targets)</b>	Determine if noise is close to theoretical	Ratio of sensitivity measured in non-pbcor image in a 0.3 – 0.2 PB annulus compared to the “dynamic range correction factor” times the theoretical noise (see Sec. 9.24 & Sec. 9.36 for the DR correction factors). Score=1 when ratio is 1 or lower Score=0 when ratio is 5 or higher For cubes: score based on peak emission in line-free mom8 image (see Sec. 9.40) compared to the median noise in the cube. The score is an erf function between 0.33 and 0.9 based on the fraction of the image that is above the threshold of median + 5*(median channel noise).
<b>hif_makeimages (Checksources)</b>	Determine if phase transfer worked for	Geometric mean of following two scores:

	checksource, by checking for decorrelation and positional shift	Score1=1.0 – abs[(catalog position – fitted position)/beam size] Score2=1.0-abs[gfluxscale flux – fitted image flux)/gfluxscale flux] Score2 is an indicator of significant decorrelation, although the score may be low for other reasons, including low calibrator S/N.
<b>hifa_exportdata</b>	Check that Pipeline products have been exported	1.0 when files successfully exported
<b>hifa_imageprecheck</b>	For the representative target & spw check that a robust parameter between 0 – 2 can meet the PI requested angular resolution (AR)	0.5 if no representative target / frequency is found. If the PI's desired AR is found in the ASDM, a QA score is assigned as follows: 1.0: PI's AR achieved in both axes with robust=0.5 0.85: PI's AR achieved in both axes with a different robust 0.5: At least one axis is out of range, but the beam area is still within the PI's range 0.25: not even the beam area can be brought within the PI's desired range by changing robust.
<b>hif_checkproductsize</b>	Check whether target cubes need to be made with non-default parameters or fewer targets imaged in order to keep the image or total product sizes within set limits	0.5 if the products had to be imaged with non-default parameters (larger cells, wider channels, smaller FOV, fewer targets or spw). 0.25 if the images cannot be made without exceeding the set limits.
<b>hif_mstransform</b>	Check that proper files were created	1.0 when target.ms files successfully created; otherwise 0.0
<b>hifa_flagtargets</b>	Determine if any target flags were applied	1.0 when no flagging commands applied
<b>hif_findcont</b>	Determine if continuum could be identified for all spw	1.0 if continuum frequency ranges found for all spw. If not, the score is the number of spws with ranges divided by the number of expected spws.

<b>hif_uvcontfit</b>	Determine if continuum could be fit	1.0 if continuum fit table created
<b>hif_uvcontsub</b>	Determine if continuum could be subtracted	Always set = 1.0

### 8.7.2 Single-Dish Pipeline QA scores

Pipeline Task	Pipeline QA Scoring Metric	Score
<b>hsd_importdata</b>	Check that the required calibrators are present	1.0 ATMOSPHERE intents are present
		0.5 subtracted for existing processing history
		0.5 subtracted for existing model data
		1.0 one continuous observing session
		1.0 all source coordinate are present
<b>hsd_flagdata</b>	Percentage of incremental flagging	<p>0 &lt; score &lt; 1 == 60% &lt; fraction flagged &lt; 5%" (for 'online', 'shadow', 'qa0', 'before' and 'applycal')</p> <p>where "0 &lt; score &lt; 1 == HIGH% &lt; fraction flagged &lt; LOW%" means</p> <ul style="list-style-type: none"> <li>• Score is 0 if flag fraction &gt;= HIGH%</li> <li>• Score is 1 if flag fraction &lt;= LOW%</li> </ul> <p>Score is linearly interpolated between 0 and 1 for fractions between HIGH% and LOW%</p>
<b>hsd_skycal</b>	Check elevation difference between ON and OFF	<p>Score is 1.0 if elevation difference between ON and OFF is &lt;= 3 degree</p> <p>Score is 0.8 if elevation difference between ON and OFF is &gt; 3 degree</p>
<b>hsd_k2jycal</b> <sup>1</sup>	Check that all Kelvin-to-Jy conversion factors are provided	<p>1.0 if Kelvin-to-Jy conversion factor present</p> <p>0.0 Missing Kelvin-to-Jy conversion factor for some data</p>
<b>hsd_applycal</b>	Percentage of incremental flagging	<p>Additional 0%-5% flagging: score=1.0; flagging 5%-50% =&gt; 1.0...0.5, &gt;50%: score=0.0. QA score calculation is restricted to scans matching the 'TARGET' intent if present. If no</p>

<sup>1</sup> After the database starts, score is changed following, 1.0 if Kelvin-to-Jy conversion factor successfully acquired from Database, 0.8 if Kelvin-to-Jy conversion factor presents but not acquired from Database, and 0.0 Missing Kelvin-to-Jy conversion factor for some data

		'TARGET' intent data is present, a warning is raised, and the QA score calculation reverts to using scans for any available intent.
<b>hsd_baseline</b>	Check that one or more than one emission line is detected by line-finder.	1.0 there is more than one emission line detected in at least one spw.
		0.0 No line is detected in all spw.
<b>hsd_bflag</b>	Percentage of incremental flagging per source per spw.	Additional 0%-5% flagging: score=1.0; flagging 5%-50% => 1.0...0.5, >50%: score=0.0
<b>hsd_imaging</b>	Determine if observed area is not masked.	1.0 if no pixel masked 0.5 if any of the pixels in the pointing area masked 0.0 if 10% of the pixels in the pointing area masked Score is linearly interpolated between 0 and 0.5 for fractions between HIGH% and LOW%
<b>hsd_exportdata</b>	Check that Pipeline products have been exported	1.0 when files successfully exported

## 9 Interferometric pipeline tasks and “by task” weblog pages

This section describes navigation of the Task sub-pages for each Interferometric Pipeline task starting from the “By Task” tab. For a detailed description of task inputs and parameters, refer to **ALMA Science Pipeline Reference Manual**.

Note that stages that don’t perform any actions are in grey font in the “by task” weblog navigation sidebar, such as `hifa_wvrgcalflag` for 7m data with no WVRs, or `hifa_makeimages` (rep BW cube) when no representative/user bandwidth cube is required.

### 9.1 `hifa_importdata`

In this task, ASDMs are imported into measurement sets, Binary Data Flags are applied, and some properties of those MSs are calculated. The WebLog page shows a summary of imported MSs, and flux densities of calibrators. Flux densities are read from the Source table of the ASDM, which is recorded by the online system at the time of observation by interpolating in frequency the recent measurements in the calibrator catalog (see Appendix C of the ALMA Technical Handbook). The “new” ALMA source catalog is queried, and if that returns sensible values, the ASDM values are replaced with the query values. This allows observatory measurements performed after the science observation to be used to obtain a better estimate of the calibrator flux density. The flux densities for each calibrator in each science spw in each MS are written to the file `flux.csv` in the `calibration/` subdirectory of a data delivery package. The values in this file can be edited before continuing with the pipeline execution if you first use the `importonly` option of `epr.executepr`.

If a POL\* intent is present, the parallactic angle coverage of each polarization session is shown graphically, and reported quantitatively.

### 9.2 `hifa_flagdata`

In this task, the online (XML format) flags, which includes the QA0 flags for antenna pointing calibration failures, are applied along with the rest of the deterministic flagging reasons (unwanted intents, autocorrelations, shadowed antennas, and TDM edge channels). The WebLog page shows the percentage of flagged data per MS. The “Before Task” column contains only the effect of the Binary Data Flags (BDF) applied during `hifa_importdata`. The additional flags are applied in the order of columns shown in the table. The percentage in each column reflects the additional amount of data flagged when applying this flag reason. The QA score for this stage is based on `BDF+QA0+online+template+shadow` flagging.

### 9.3 `hifa_fluxcalflag`

The WebLog shows any flagging or `spwmap` that was required. If the flux calibrator is a solar system object, known lines in the object (e.g. CO in Titan’s atmosphere) are flagged by this task. If more than 75% of a given spw is flagged on the flux calibrator for this reason, then a `spwmap` is calculated to transfer the flux scale from another spw. The WebLog shows if any flagging or `spwmap` was required.

In Mars, Venus, Titan and Neptune, 12CO is flagged in all ALMA bands. In Mars, Venus, and Titan, 13CO is also flagged. In Titan, HCN, H13CN and HC15N are also flagged, as is

HCN  $v_2=1$ . Finally, in Titan CH<sub>3</sub>CN is flagged up through Band 8. The frequency width that is flagged is based on published spectra of 1 or 2 transitions of the species. For other transitions, this frequency width is scaled to maintain consistent velocity widths. Also, because the flags are applied in topocentric frame, the final width that is flagged is further broadened by the maximum relative velocity between the object and the geocenter (computed over the next decade). A detailed list of topocentric frequency ranges flagged is given in the following table:

<b>Mars</b>	CO: [115.204, 115.338], [230.404, 230.672], [345.595, 345.997], [460.773, 461.309], [691.071, 691.875], [806.184, 807.120], [921.265, 922.335]  13CO: [110.190, 110.212], [220.377, 220.421], [330.555, 330.621], [440.721, 440.809], [661.001, 661.133], [771.108, 771.260], [881.196, 881.370]
<b>Venus</b>	CO: [115.206, 115.337], [230.407, 230.669], [345.600, 345.992], [460.779, 461.303], [691.081, 691.865], [806.194, 807.110], [921.277, 922.323]  13CO: [110.192, 110.210], [220.380, 220.418], [330.560, 330.616], [440.727, 440.803], [661.011, 661.123], [771.118, 771.250], [881.208, 881.358]
<b>Titan</b>	CO: [114.92, 115.67], [229.49, 231.74], [343.82, 347.62], [458.29, 463.80], [687.75, 694.66], [803.46, 809.85]  13CO: [110.18, 110.22], [220.28, 220.52], [330.36, 330.82], [440.42, 441.15], [660.60, 661.53], [770.65, 771.72], [880.73, 881.82]  HCN: [88.45, 88.81], [176.73, 177.80], [264.96, 266.81], [353.29, 355.72], [441.74, 444.52], [618.45, 622.16], [707.01, 710.74], [795.56, 799.31], [883.82, 887.86]  HC15N: [86.04, 86.07], [172.05, 172.16], [258.04, 258.27], [430.02, 430.45], [601.95, 602.60], [773.88, 774.64], [859.84, 860.62]  H13CN: [86.33, 86.35], [172.63, 172.73], [258.91, 259.11], [431.44, 431.88], [603.98, 604.56], [776.48, 777.16], [862.72, 863.42]  HCN $v_2=1$ : [177.192, 177.286], [178.088, 178.184], [265.782, 265.924], [267.128, 267.270], [354.365, 354.555], [356.161, 356.351], [442.942, 443.178], [445.184, 445.422], [620.058, 620.390], [623.197, 623.529], [708.596, 708.974], [712.182, 712.562], [797.117, 797.543], [801.149, 801.577], [885.619, 886.091], [890.096, 890.572]  CH <sub>3</sub> CN: [91.938, 92.008], [110.304, 110.409], [128.659, 128.809],

	[147.039,147.209], [165.415,165.608], [183.792,184.006], [202.168,202.403], [220.543,220.798], [238.916,239.194], [257.289,257.587], [275.660,275.980], [294.030,294.371], [312.399,312.761], [330.766,331.149], [349.205,349.534], [367.572,367.920], [385.938,386.303], [404.301,404.683], [422.735,423.062], [441.098,441.440], [459.459,459.814], [477.881,478.186], [496.239,496.557]
<b>Neptune</b>	CO: [113.99,116.51], [226.98,234.52], [339.97,351.54], [454.95,467.55], [685.93,696.57], [802.92,810.58]

## 9.4 hif\_rawflagchans

This task was designed to detect severe baseline-based anomalies prior to performing antenna-based calibration. These bad data are often due to hardware problems during the observation. Outlier channels and outlier baselines are detected in the uncalibrated visibilities of the bandpass calibrator.

The WebLog page links to the images of the values used for flagging. Any flagged data are shown on the plots along with a summary of all flagging performed in this task. The following two rules are used to evaluate the need for flagging:

### 1) "bad quadrant" matrix flagging rule:

This starts with the "baseline" vs. "channel" flagging view. In this view, some data points may already be flagged, e.g. due to an earlier pipeline stage.

First, outliers are identified as those data points in the flagging view whose value deviates from the median value of all non-flagged data points by a threshold factor times the median absolute deviation (MAD) of the values of all non-flagged data points, where the threshold is 'fbq\_hilo\_limit' (default: 8.0).

In formula:  $flagging\ mask = (data - median(all\ non\ flagged\ data)) > (MAD(all\ non\ flagged\ data) * fbq\_hilo\_limit)$

Next, the flagging view is considered as split up in 4 quadrants of channels (since some problems manifest in only one or more quadrants), and each antenna is evaluated separately as follows:

- a) Select baselines belonging to antenna and select channels belonging to quadrant.
- b) Determine number of newly found outlier datapoints within selection.
- c) Determine number of originally unflagged datapoints within selection.
- d) Determine fraction of "number of newly found outliers" over "number of originally unflagged datapoints".
- e) If the latter fraction exceeds the fraction threshold 'fbq\_antenna\_frac\_limit' (default: 0.2), then a flagging command is generated that will flag all channels within the evaluated quadrant for the evaluated antenna.
- f) Otherwise, no action is taken (i.e. the newly found outlier datapoints are not individually flagged by this rule),

Next, the flagging view is still considered as split up in 4 quadrants of channels, and each baseline is evaluated separately, as follows:

- a) Select baseline and select channels belonging to quadrant.

- b) Determine number of newly found outlier datapoints within selection.
- c) Determine number of originally unflagged datapoints within selection.
- d) Determine fraction of "number of newly found outliers" over "number of originally unflagged datapoints".
- e) If the latter fraction exceeds the fraction threshold 'fbq\_baseline\_frac\_limit' (default: 1.0), then a flagging command is generated that will flag all channels within the evaluated quadrant for the evaluated baseline.
- f) Otherwise, no action is taken (i.e. the newly found outlier datapoints are not individually flagged by this rule).

## 2) "outlier" matrix flagging rule:

Data points in the flagging view are identified as outliers if their value deviates from the median value of all non-flagged data points by a threshold factor times the median absolute deviation of the values of all non-flagged data points, where the threshold is 'fhl\_limit' (default: 20.0).

$$\text{In formula: } \text{flagging mask} = (\text{data} - \text{median}(\text{all non-flagged data})) > (\text{MAD}(\text{all non-flagged data}) * \text{fhl\_limit})$$

Flagging commands are generated for each of the identified outlier data points.

If the number of data points in the flagging view are smaller than the minimum sample 'fhl\_minsample' (default: 5), then no flagging is attempted.

## 9.5 hif\_refant

An ordered list of preferred reference antennas is calculated, with preference given to central array location and low flagging fraction through the following score:

$$\text{Refant score} = [1 - (\text{normalized distance from center})] + [1 - (\text{normalized fraction of good data})]$$

The WebLog page shows that list, and the score for each antenna can be found in the casa log for this stage.

## 9.6 h\_tsyscal

System temperature (Tsys) as a function of frequency is calculated from the atmospheric calibration scan data by the online system at the time of observation. These spectra are imported to a table of the MS during `hifa_importdata`. In `hifa_tsyscal`, these spectra are copied into a CASA calibration table by the `gencal` task, which flags channels with zero or negative Tsys. The WebLog shows the mapping of Tsys spectral windows to science spectral windows, and plots Tsys before flagging. Mapping is often necessary because in data from Cycles 0-5, Tsys can only be measured in TDM windows on the 64-station baseline correlator.

## 9.7 hifa\_tsysflag

This task flags the Tsys cal table created by the `hifa_tsyscal` pipeline task. Erroneous Tsys measurements of several different kinds are detected, including anomalously high Tsys over an entire spectral window, spikes or "birdies" in Tsys, and discrepant "shape" or Tsys as a function of frequency. Details are provided in the WebLog for each kind of flagging

performed, and all of the Tsys spectra are plotted again. In these plots, all of the anomalies should be gone.

Tsysflag provides six separate flagging metrics, where each metric creates its own flagging view and has its own corresponding flagging rule(s). In the current standard pipeline, all six metrics are active, and evaluated in the order set by the parameter "metric\_order" (default: 'nmedian, derivative, edgechans, fieldshape, birdies, toomany').

### 1) Metric 1: "nmedian"

A separate view is generated for each polarisation and each spw. Each view is a matrix with axes "time" vs. "antenna". Each point in the matrix is the median value of the Tsys spectrum for that antenna/time.

The views are evaluated against the "nmedian" matrix flagging rule, where data points are identified as outliers if their value is larger than a threshold-factor \* median of all non-flagged data points, where the threshold is 'fnm\_limit' (default: 2.0).

Individual sources are evaluated separately with the default setting of fnm\_byfield=True; this is to prevent elevation differences between targets from causing unnecessary flags (mostly affects high frequencies).

Flagging commands are generated for each of the identified outlier data points.

### 2) Metric 2: "derivative"

A separate view is generated for each polarisation and each spw. Each view is a matrix with axes "time" vs. "antenna". Each point in the matrix is calculated as follows:

- calculate "valid\_data" as the channel-to-channel difference in Tsys for that antenna/timestamp (for unflagged channels)
- calculate  $median(abs(valid\_data - median(valid\_data))) * 100.0$

The views are evaluated against the "max abs" matrix flagging rule, where data points are identified as outliers if their absolute value exceeds the threshold "fd\_max\_limit" (default: 5).

Flagging commands are generated for each of the identified outlier data points.

### 3) Metric 3: "edgechans"

A separate view is generated for each spw and each of these intents: ATMOSPHERE, BANDPASS, and AMPLITUDE. Each view contains a "median" Tsys spectrum where for each channel the value is calculated as the median value of all selected (spw,intent) Tsys spectra in that channel (this combines data from all antennas together).

The views are evaluated against the "edges" vector flagging rule, which flags all channels from the outmost edges (first and last channel) until the first channel for which the channel-to-channel difference first falls below a threshold times the median channel-to-channel difference, where the threshold is "fe\_edge\_limit" (default: 3.0).

A single flagging command is generated for all channels newly identified as "edge channels".

### 4) Metric 4: "fieldshape"

A separate view is generated for each spw and each polarization. Each view is a matrix with axes "time" vs. "antenna". Each point in the matrix is a measure of the difference of the Tsys spectrum for that time/antenna from the median of all Tsys spectra for that antenna/spw in the "reference" fields that belong to the reference intent specified by "ff\_refintent" (default: "BANDPASS").

The exact fieldshape value is calculated as:  $100 * \text{mean}(\text{abs}(\text{normalized tsys} - \text{reference normalized tsys}))$ , where a 'normalized' array is defined as: "array / median(array)"

The views are evaluated against the "max abs" matrix flagging rule, where data points are identified as outliers if their absolute value exceeds the threshold "ff\_max\_limit" (default: 5).

## 5) Metric 5: "birdies"

A separate view is generated for each spw and each antenna. Each view contains a "difference" Tsys spectrum calculated as:

*"channel-by-channel median of Tsys spectra for antenna within spw" - "channel-by-channel median of Tsys spectra for all antennas within spw".*

The views are evaluated against the "sharps" vector flagging rule, which flags each view in two passes:

- a. flag all channels whose absolute difference in value to the following channel exceeds a threshold "fb\_sharps\_limit" (default: 0.05).
- b. around each newly flagged channel, flag neighboring channels until their channel-to-channel difference falls below 2 times the median channel-to-channel difference (this is intended to flag the wings of sharp features).

A single flagging command is generated for all channels newly identified as "birdies".

## 6) Metric 6: "toomany"

A separate view is generated for each polarisation and each spw. Each view is a matrix with axes "time" vs. "antenna". Each point in the matrix is the median value of the Tsys spectrum for that antenna/time. (This is the same as for "nmedian" metric).

The views are evaluated against two separate flagging rules:

- a. "tmf" (too many flags): This evaluates each timestamp one-by-one, flagging an entire timestamp when the fraction of flagged antennas within this timestamp exceeds the threshold "tmf1\_limit" (default: 0.666). Flagging commands are generated per timestamp.
- b. "tmef" (too many entirely flagged): This evaluates all timestamps at once, flagging all antennas for all timestamps within current view (spw, pol) when the fraction of antennas that are entirely flagged in all timestamps exceeds the threshold "tmef1\_limit" (default: 0.666). Flagging commands are generated for each data point in the view that is newly flagged.

## 9.8 hifa\_antpos

Sometimes the antenna positions were refined after the science data were recorded. If such refinements have been located, they are applied in this task. The corrections are listed in the WebLog, and the data are corrected via a calibration table.

## 9.9 hifa\_wvrgcalflag

Water Vapor Radiometer (WVR) power measurements are converted into a phase correction table that can be applied to the science data. The phase rms during observation of the bandpass calibrator, with and without the WVR correction, is used 1) to detect poorly performing WVR units on individual antennas, and 2) to determine if the WVR correction helps overall.

The WebLog shows the effects of the phase correction in several ways, if any antennas' WVR data are flagged (the required phase correction is then interpolated from nearby antennas), and also prints a warning if the correction is deemed not helpful enough to apply at all.

In hifa\_wvrgcalflag, a QA score is produced for each measurement set of an OUS. The QA score is zero if the RMS improvement ratio is less than 1.0, and 1 if it is greater than 2.0. If it is between 1.0 and 2.0, the score will be linearly scaled to be in the range of 0.5 to 1.0. Thus, a ratio of 1.08 will produce a QA score of 0.54. The final score is the lowest score from all ms. If the ratio for any ms is below 1.32, then a QA notification is also generated for it at the top of the hifa\_wvrgcalflag page.

## 9.10 hif\_lowgainflag

Antennas with persistently discrepant amplitude gains are detected and flagged. The WebLog links to grayscale images of the relative gain of each antenna calculated using the observation of the bandpass calibrator, and shows if any antennas are flagged.

This task first creates a bandpass caltable, then a gain phase caltable, and finally a gain amplitude caltable. This final gain amplitude caltable is used to identify antennas with outlier gains, for each spw. Flagging commands for outlier antennas (per spw) are applied to the entire MS.

A separate view is created for spw. Each view is a matrix with axes "time" vs. "antenna". Each point in the matrix is the absolute gain amplitude for that antenna/timestamp.

The views are evaluated against the "nmedian" matrix flagging rule, where data points are identified as outliers if:

- a. Their value is smaller than a threshold-factor \* median of all non-flagged data points, where the threshold is 'fnm\_lo\_limit' (default: 0.7), or
- b. Their value is larger than a threshold-factor \* median of all non-flagged data points, where the threshold is 'fnm\_hi\_limit' (default: 1.3).

Flagging commands are generated for each of the identified outlier data points.

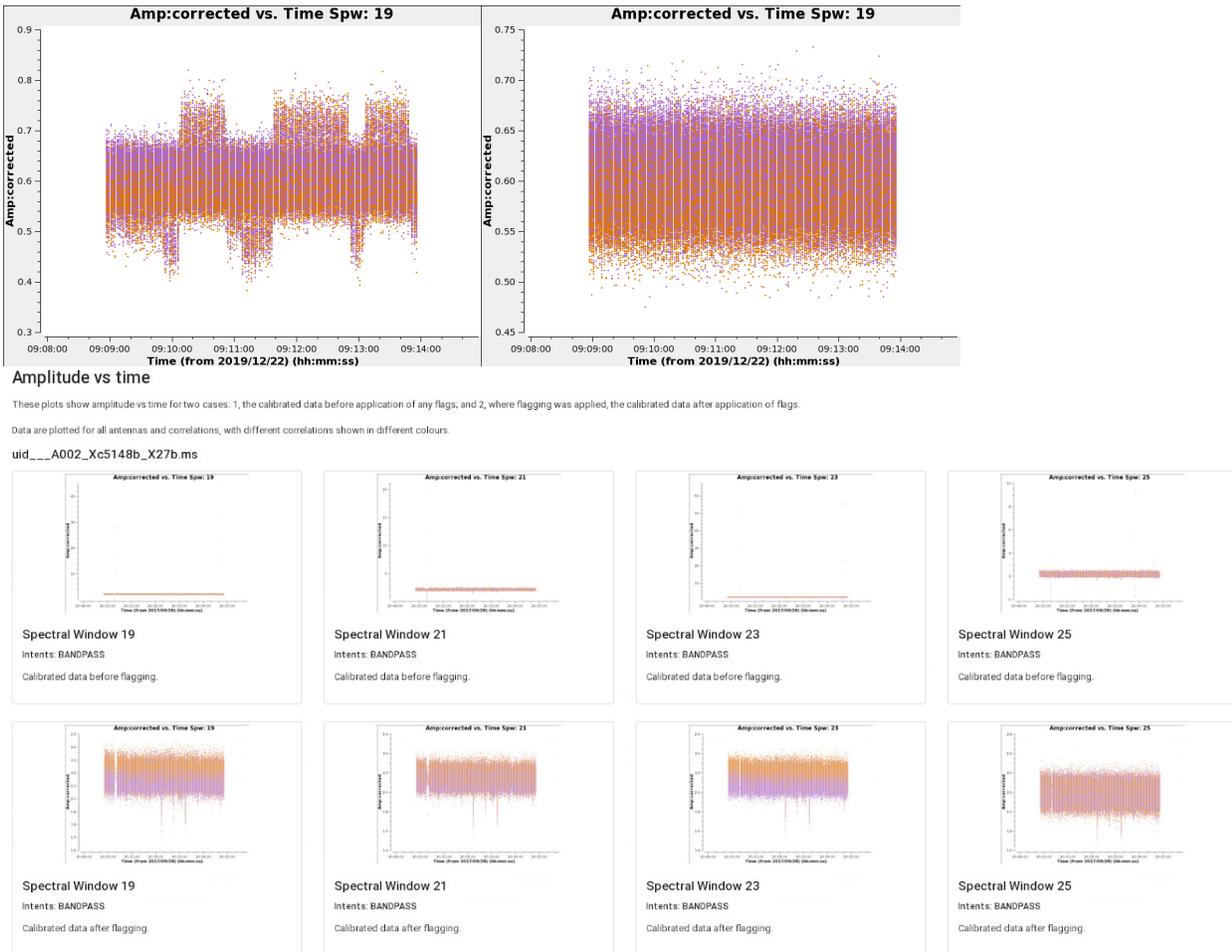
## 9.11 hif\_setmodels

The model flux density of the amplitude calibrator is set, either from an internal CASA model (solar system objects), or the results of observatory calibrator monitoring (quasars) which

ultimately appear in the file flux.csv (see `hifa_importdata`). These flux densities are listed on the WebLog page, along with plots of the amplitude calibrator as a function of uv distance (which is useful to assess resolved solar system objects). If the bandpass calibrator is distinct from the amplitude calibrator and is a frequently monitored quasar, its model is also set at this stage.

## 9.12 hifa\_bandpassflag

After calculating an initial bandpass solution, flagging is performed by comparing the scalar difference between the amplitudes of the calibrated visibilities and the model for the bandpass calibrator (Figure 28). If flags are found, the bandpass phase-up and bandpass calibration tables are recomputed.



**Figure 28: bandpass flag removing outlier amplitudes – before and after flagging**

Note about flagging summary table: the “before” flagging fraction in `hifa_bandpassflag` may differ from the “after” flagging fraction in `hifa_flagdata`, because `hifa_bandpassflag`'s "before" summary is done on an MS that has temporarily already had some caltables applied (and thus some flagging already propagated). This is done because the before/after summary in `hifa_bandpassflag` is intended to clearly show how much new flagging is done by `hifa_bandpassflag`.

### 9.13 hifa\_bandpass

In this task, the bandpass calibrator is self-calibrated (phase only is first calibrated on as short a time interval as allowed by signal-to-noise, listed on the WebLog page). The antenna-based bandpass phase and amplitude solution is then calculated using a S/N-dependent frequency interval, also listed on the WebLog page. Finally, the WebLog page links to plots of all of the bandpass solutions, with the atmospheric transmission curve overlaid.

### 9.14 hifa\_spwphaseup

The relative phase offsets between spectral windows are determined for each antenna using the observation of the bandpass calibrator. (The offset is assumed to be constant in time during each execution.) If narrow spectral windows are present, a mapping is determined so that the calculated phase calibration as a function of time can be subsequently transferred (during subsequent gaincal and applycal tasks) from wider, higher S/N spectral windows to the narrow ones. If any such reference spwmaps are required, then they are listed on the WebLog page. The assumption of constant phase offsets vs. time is tested downstream in hif\_timegaincal by solving for new time-based phase solutions per spw with the spwphaseup table (and associated mapping) applied. If the signal-to-noise is sufficiently poor, all spws are combined for subsequent calculation of time-varying gains, and a warning is printed here to indicate that combination has occurred.

### 9.15 hifa\_gfluxscaleflag

As with hifa\_bandpassflag, outliers in the the calibrated visibilities of the flux, phase, and check source calibrators are flagged before a final fluxscale is calculated. The weblog shows the before and after flagging plots as a function of time and of uv distance.

### 9.16 hifa\_polcalflag (polarization recipes only)

As with hifa\_bandpassflag, outliers in the the calibrated visibilities of the polarization calibrators are flagged. The weblog shows the before and after flagging plots as a function of time and of uv distance.

### 9.17 hifa\_session\_refant (polarization recipes only)

A single reference antenna is selected for each entire *session* (for ALMA polarization observations, this is often 2-3 EBs). Antennas are first ranked by the product of their per-EB ranking (based on flag fraction and central location in the array, as in hifa\_refant). The task next performs a gaincal 'int' 'p' on all PHASE intent scans for each EB starting with the highest ranking antenna as sole refant, and checks the resulting caltable to see if the refant ever changes. It chooses the first antenna that does not result in any change of refant. If none of the top 3 antennas qualify (which should be rare), then the antenna with the most solutions as refant is chosen, and a message is displayed with the number of phase outliers, where the word "outlier" is where phase outlier means that the refant phase was non-zero, which indicates that another refant was chosen for some integrations. The total number of possible solutions is  $N\_EBs * N\_spws * N\_int * N\_pol$ .

## 9.18 hifa\_lock\_refant (polarization recipes only)

Sets the refant to a single antenna and refantmode="fixed" for all subsequent calibration tasks. This can be "unlocked" with the hifa\_unlock\_refant task, but that is not needed in the standard polcalibration or polcalimage recipes.

Note that in polcal and polcalimage recipes, hifa\_bandpass and hifa\_spwphaseup are called a second time following the locking of the refant, to ensure that the bandpass and spw-offsets cal tables are using that fixed refant.

## 9.19 hifa\_gfluxscale

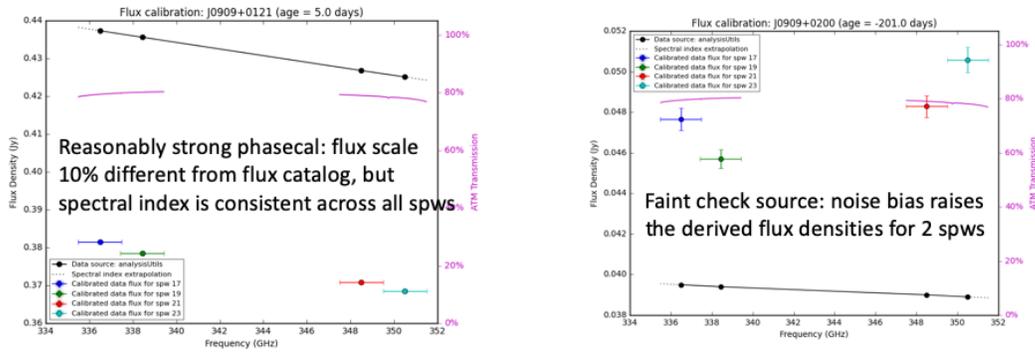
In this task, the absolute flux scale is transferred from the amplitude calibrator to the other calibrators and ultimately to the science target (via the phase calibrator). A phase-only self-calibration is performed on all calibrators prior to this flux calculation.

The WebLog for this stage lists the derived flux densities (measured by the vector averaged calibrated visibility amplitude) of the non-amplitude calibrators (usually phase and bandpass calibrators), along with the flux values extracted from the ALMA Source Catalog. Plots of amplitude as a function of uv distance are shown, and if the absolute flux calibrator is resolved (decreasing flux with increasing uv distance, usually only the case for solar system objects), only data on short baselines are used to calculate the flux densities of the secondary calibrators. Any such uv limits are listed in the table at the top of the WebLog page. Blank entries mean that all UV ranges and/or all antennas were used, which will be the case for quasars.

Antennas Used for Flux Scaling		
The following antennas were used for flux scaling, entries for unresolved flux calibrators are blank		
Measurement Set	UV Range	Antennas
uid__A002_Xa25bbf_X6823.ms	<319.210m	
uid__A002_Xa216e2_X1e58.ms	<318.242m	
uid__A002_X9ec9e7_X1804.ms	<322.242m	
uid__A002_X88063e_X1f1.ms		
uid__A002_X87f18c_Xd0.ms	<32.306m	CM01, CM02, CM10, CM05, CM12, CM09, CM11, CM03

Figure 29: uv ranges for fluxscale table.

Derived flux density vs catalog flux density plots are shown for non-amplitude calibrators (see Figure 30). Faint sources can have systematically elevated gfluxscale derived flux densities in low SNR spws. The pipeline also calculates a QA metric to detect such spw-spw discrepancies (see QA Table in section 8.7.1), and gives an informational statement (blue) if the spw-spw variation is greater than 10%.



1.00	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0121 (PHASE,WVR) spw 17 in vid___A002_X01033_X0091.ms differs by 1% from the ratio for the highest SNR spw (19)
1.00	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0121 (PHASE,WVR) spw 21 in vid___A002_X01033_X0091.ms differs by 2% from the ratio for the highest SNR spw (19)
1.00	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0121 (PHASE,WVR) spw 23 in vid___A002_X01033_X0091.ms differs by 3% from the ratio for the highest SNR spw (19)
1.00	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0200 (CHECK,WVR) spw 17 in vid___A002_X01033_X0091.ms differs by 4% from the ratio for the highest SNR spw (19)
1.00	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0200 (CHECK,WVR) spw 21 in vid___A002_X01033_X0091.ms differs by 6% from the ratio for the highest SNR spw (19)

Score	Reason
0.75	Ratio of $S_{\text{band}}/S_{\text{catalog}}$ for J0909+0200 (CHECK,WVR) spw 23 in vid___A002_X01033_X0091.ms differs by 11% from the ratio for the highest SNR spw (19)

Pipeline QA summary for this task.

**Figure 30: Examples of the plot comparing derived flux densities to source catalog flux densities, and associated QA messages (in the QA section at the bottom of the gfluxscale web page)**

## 9.20 hifa\_timegaincal

In this task, gain as a function of time is calculated from observations of the phase calibrator. The WebLog page shows plots of this gain, both on a scan timescale (as will be interpolated to the science target), and on an integration timescale (useful for assessing weather and calibration quality). An additional plot is also provided that helps to assess time variations of the spw to spw offsets as a function of time, in optimal cases the scatter about zero should be small.

## 9.21 hifa\_targetflag

Because science targets are generally not point sources, the flagging algorithm needs to be more clever than bandpassflag, gfluxscaleflag, and polcalflag. The algorithm identifies outliers by examining statistics within successive overlapping radial uv bins, allowing it to adapt to arbitrary uv structure.

The new stage does add processing time, particularly making the plots. So to save time, we only make the amp vs. time plots if flags are generated, and the amp vs. uv distance plots are made for only those spws that generated flags. Also, to avoid confusion in mosaics or single field surveys, these uv distance plots only show field IDs with new flags.

uid\_\_A002\_Xe64b7b\_X1be6d.ms

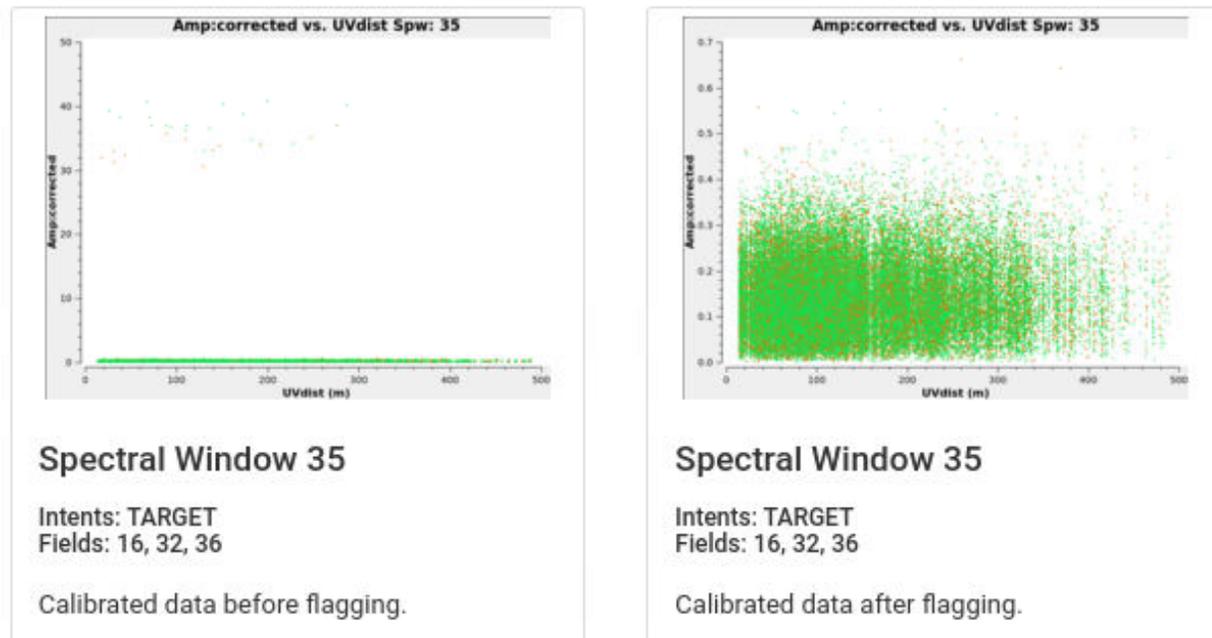


Figure 31: Example flagging of high outliers in target visibilities.

## 9.22 hif\_applycal

In this task, all previously calculated calibration tables are applied to the science data. Any failed calibration solutions, and flagged Tsys scans, will result in flagging of actual science data in this stage, so the WebLog shows a summary of that additional flagging, and high flagging will result in a low QA score.

The WebLog page also includes many useful plots of the calibrated data as a function of time and frequency. To reduce the number of plots and processing time to create them, plots of targets only include the representative target, and for mosaics, only the brightest field.

Outliers in these plots can indicate remaining bad data. To help identify these, a QA score is calculate based on the corrected Amplitude-vs-Frequency and Phase-vs-Frequency plots for each calibrator (which are produced for each measurementset and spw). This score is based on fitting a linear function to the corrected data for each antenna, and seeing if the slope or offset of that fit differs significantly from a similar fit to the calibrated data of all antennas. These fits are done on a per-scan, per-polarization basis. If any antenna is found to have a significant difference, the QA score for this stage is set to 0.9 (blue color), and details of the deviant antennas are reported in the expandable “Pipeline QA” table at the bottom of the page. It is important to note that not all reported outliers are (1) visible in the corresponding applycal plots (which are averaged over all scans and polarizations), or (2) consequential to the final products (since the mean calibration solutions are still robust and adequate to calibrate the final data). However, if problems with the calibration are subsequently found, these messages provide clues on where to look for problems. For data that are delivered as QA2 Pass, one can assume that the ALMA data reviewers have checked these messages and concluded that the overall calibration is not significantly compromised.

Finally, a plot of the uv coverage (original and after all calibration flags are applied) is provided for the representative Source and spw.

### 9.23 hif\_makeimlist: Set-up parameters for calibrator images

This stage determines image parameters (image size, cell size, etc) to be used in the subsequent hif\_makeimages stage, and reports them on the WebLog page (See Figure 32). The “specmode” can be mfs for per-spw continuum multi-frequency synthesis images, “cont” for mfs continuum images of several spectral windows, or “cube” for spectral cubes. The first time the task is run is in preparation for making per-spw mfs images of the calibrators.

field	intent	spw	phasecenter	cell	imsize	imagename	specmode	start	width	nbin	nchan	uvrange
J1256-0547	BANDPASS	16	ICRS 12:56:11.1670 -005.47.21.525	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1256-0547_bp.spw16.mfs	mfs			-1	-1	
J1256-0547	BANDPASS	18	ICRS 12:56:11.1670 -005.47.21.525	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1256-0547_bp.spw18.mfs	mfs			-1	-1	
J1256-0547	BANDPASS	20	ICRS 12:56:11.1670 -005.47.21.525	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1256-0547_bp.spw20.mfs	mfs			-1	-1	
J1256-0547	BANDPASS	22	ICRS 12:56:11.1670 -005.47.21.525	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1256-0547_bp.spw22.mfs	mfs			-1	-1	
J1316-3338	PHASE	16	ICRS 13:16:07.9859 -033.38.59.173	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1316-3338_ph.spw16.mfs	mfs			-1	-1	
J1316-3338	PHASE	18	ICRS 13:16:07.9859 -033.38.59.173	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1316-3338_ph.spw18.mfs	mfs			-1	-1	
J1316-3338	PHASE	20	ICRS 13:16:07.9859 -033.38.59.173	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1316-3338_ph.spw20.mfs	mfs			-1	-1	
J1316-3338	PHASE	22	ICRS 13:16:07.9859 -033.38.59.173	[2.5arcsec]	[60, 60]	uid__A002_Xb5270a_X1c.sSTAGENUMBER.J1316-3338_ph.spw22.mfs	mfs			-1	-1	

Figure 32: Example of the WebLog for the hif\_makeimlist stage. This example is for setting up the parameters for calibrator per-spw multi-frequency synthesis (mfs) continuum images.

### 9.24 hif\_makeimages: calibrator images

This stage actually creates the images requested by the most recent hif\_makeimlist. The first time it is run is to create per-spw mfs continuum images of the calibrators, using briggs weighting with robust=0.5.

Calibrator images are cleaned to a threshold of 2 x (predicted rms noise) x (dynamic range correction factor). The dynamic range (DR) correction factor accounts for the fact that targets with a high dynamic range will have larger imaging artifacts, which should not be cleaned. The artifacts are worse for poorer UV coverage, so different dynamic range corrections factors are adopted for 12-m Array and 7-m Array observations according to the following tables:

Calibrator Dynamic Range	12-m Array DR correction factor
≤ 1000	1
1000 – 3000	DR/1000
≥ 3000	DR/3000

Calibrator Dynamic Range	7-m Array DR correction factor – 1EB
≤ 200	1
≥ 200	DR/200

See the description in Sec. 9.36 for more information and examples of the `hif_makeimages` stage. Low QA scores for non-Check source calibrators may indicate the need for additional flagging and/or significant decoherence.

### **9.25 `hif_makeimlist`: check source imaging**

Prepare to create check source images, one per EB.

### **9.26 `hif_makeimages`: check source imaging and QA information**

After creating images, the pipeline calculates and shows a table of check source fitting results per spw, and per EB:

- Check source position offset from catalogue position in mas and synthesized beams, warning level  $> 0.15 * \text{synthesizedBeam}$
- Fitted [Peak Intensity / Flux Density] Ratio can help to assess decorrelation AND presence of resolved emission, warning level  $< 0.8$
- [Fitted / gfluxscale] Flux Density Ratio, warning level  $< 0.8$
- Warning also given if S/N of fitted or gfluxscale flux densities are low  $< 20$
- The images themselves which are per EB / spw are located below the table, and except for being per EB are unchanged
- Check source imaging uses the dynamic range modifiers in Section 9.36

# 21. Tclean/MakelImages

Make check source images

BACK

**Task notifications**

- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 33: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.52 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.68, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 35: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.48 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.66, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 37: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.53, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 39: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.43, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 41: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.47 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.66, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 43: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.37 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.70, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 45: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.60 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.64, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 47: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.52 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.60, however, the S/N of the gfluxscale measurement is low

## Check Source Fit Results

EB	Field	Virtual SPW	Bandwidth (GHz)	Position offset (mas)	Position offset (synth beam)	Fitted Flux Density (mJy)	Image S/N	Fitted [Peak Intensity / Flux Density] Ratio	gfluxscale Derived Flux	gfluxscale S/N	[Fitted / gfluxscale] Flux Density Ratio
uid__A002_Xcb8a93_Xc096	J1717-3342	33	1.875	12.57 +/- 3.96	0.07 +/- 0.022	159 +/- 7	38.97	0.68	303.10 +/- 63.10	4.80	0.52
		35	1.875	9.43 +/- 4.33	0.05 +/- 0.024	155 +/- 8	36.05	0.66	322.21 +/- 74.18	4.34	0.48
		37	1.875	10.99 +/- 3.39	0.06 +/- 0.019	161 +/- 7	42.68	0.71	303.43 +/- 62.83	4.83	0.53
		39	1.875	10.84 +/- 4.10	0.06 +/- 0.024	153 +/- 8	34.39	0.71	351.88 +/- 106.68	3.30	0.43
		41	1.875	5.46 +/- 4.25	0.03 +/- 0.023	150 +/- 7	37.66	0.66	320.33 +/- 96.82	3.31	0.47
		43	1.875	12.77 +/- 5.21	0.07 +/- 0.029	145 +/- 9	28.63	0.70	387.40 +/- 120.59	3.21	0.37
		45	1.875	10.82 +/- 3.96	0.06 +/- 0.022	172 +/- 7	39.51	0.64	284.74 +/- 24.12	11.80	0.60
		47	1.875	6.90 +/- 4.49	0.04 +/- 0.025	164 +/- 8	37.54	0.60	315.26 +/- 93.88	3.36	0.52

# 21. Tclean/MakelImages

Make check source images

BACK

**Task notifications**

- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 33: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.52 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.68, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 35: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.48 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.66, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 37: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.53, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 39: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.43, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 41: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.47 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.66, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 43: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.37 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.70, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 45: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.60 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.64, however, the S/N of the gfluxscale measurement is low
- QA uid\_\_A002\_Xcb8a93\_Xc096 field J1717-3342 spwid 47: has a low [Fitted / gfluxscale] Flux Density Ratio of 0.52 and a low Fitted [Peak Intensity / Flux Density] Ratio of 0.60, however, the S/N of the gfluxscale measurement is low

## Check Source Fit Results

EB	Field	Virtual SPW	Bandwidth (GHz)	Position offset (mas)	Position offset (synth beam)	Fitted Flux Density (mJy)	Image S/N	Fitted [Peak Intensity / Flux Density] Ratio	gfluxscale Derived Flux	gfluxscale S/N	[Fitted / gfluxscale] Flux Density Ratio
uid__A002_Xcb8a93_Xc096	J1717-3342	33	1.875	12.57 +/- 3.96	0.07 +/- 0.022	159 +/- 7	38.97	0.68	303.10 +/- 63.10	4.80	0.52
		35	1.875	9.43 +/- 4.33	0.05 +/- 0.024	155 +/- 8	36.05	0.66	322.21 +/- 74.18	4.34	0.48
		37	1.875	10.99 +/- 3.39	0.06 +/- 0.019	161 +/- 7	42.68	0.71	303.43 +/- 62.83	4.83	0.53
		39	1.875	10.84 +/- 4.10	0.06 +/- 0.024	153 +/- 8	34.39	0.71	351.88 +/- 106.68	3.30	0.43
		41	1.875	5.46 +/- 4.25	0.03 +/- 0.023	150 +/- 7	37.66	0.66	320.33 +/- 96.82	3.31	0.47
		43	1.875	12.77 +/- 5.21	0.07 +/- 0.029	145 +/- 9	28.63	0.70	387.40 +/- 120.59	3.21	0.37
		45	1.875	10.82 +/- 3.96	0.06 +/- 0.022	172 +/- 7	39.51	0.64	284.74 +/- 24.12	11.80	0.60
		47	1.875	6.90 +/- 4.49	0.04 +/- 0.025	164 +/- 8	37.54	0.60	315.26 +/- 93.88	3.36	0.52

Figure 33: Check source imaging diagnostic table

## 9.27 hifa\_imageprecheck

The representative source and spw containing the representative frequency selected by the PI in the OT are used to calculate the synthesized beam and to make sensitivity estimates for the aggregate bandwidth and representative bandwidth for several values of the robust parameter. This information is reported in the hifa\_imageprecheck weblog, including a table like the example shown in Figure 34. If no representative target/frequency information is available, it defaults to the first target and center of first spw in the data (i.e. pre-Cycle 5 data does not have this information available).

The best Briggs weighting “robust” parameter in the range<sup>2</sup> of 0.0 – 2.0 that best matches the PI’s requested angular resolution is chosen automatically:

- The robust values are considered in order: +0.5, +1.0, 0.0, +2.0.
- If one value has a predicted beam with both axes within the PI desired range, that robust is used. If that robust is not the default 0.5, a warning is printed.
- If no robust produces a beam with both axes within range, the robust that produces a predicted beam area closest to the mean of the PI’s range is chosen.
- If no robust can produce a beam area within the PI’s range, the robust that produces a predicted beam area closest to the mean of the PI’s range is used, a red QA score is assigned, and an error message is printed at the top of the webpage.

The chosen robust is used for all subsequent target images.

For the ACA only robust=0.5 is considered.

Note: the cell and imsize chosen in this and the following stage is stored in the pipeline context so that all product images (mfs, cubes) have the same cell and imsize. If these stages are run with non-default intent/source selections, slightly different cell and imsize may naturally result.

---

<sup>2</sup> Smaller robust values are not considered, since they result in images with poorer imaging characteristics (higher noise, more spectral noise curvature – see Sec. 11– and a compromised ability to recover extended emission), especially for mosaics or when the uv coverage is sparse.

## 22. Image Pre-Check

BACK

### 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 tclean 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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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	<input type="checkbox"/>	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

Pipeline QA summary for this task.

## 22. Image Pre-Check

BACK

**Task notifications**

**Warning!** Predicted non-default robust=1.0 beam is within the PI requested range

**Goals From OT:**  
 Representative Target: ngc\_2992  
 Representative Frequency: 228.8683 GHz (SPW 25)  
 Bandwidth for Sensitivity: 22.9 MHz (rounded to nearest integer #channels (12), repBW = 23.44 MHz)  
 Min / Max Acceptable Resolution: 0.152 arcsec / 0.252 arcsec  
 Goal PI sensitivity: Not available  
 Single Continuum: False

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

Estimates are given for five possible values of the clean robust weighting parameter: robust = -0.5, 0.0, +0.5 (default), +1.0, and +2.0. If the "Min / Max Acceptable Resolution" is available ( $\geq$  Cycle 5 12m-array data), the robust value closest to the default (+0.5) that predicts a beam that is in range of the PI request (for both axes) according to the table row for repBW (Bandwidth for Sensitivity) is chosen. If no robust value predicts a beam that is in range, the robust is chosen that yields the lowest "%Diff from mean AR" value for the repBW (Bandwidth for Sensitivity) rows. The "%Diff from mean AR" is defined as the percent difference between the predicted beam area and the beam area of the geometric mean (mean AR) of the PI requested range. When the "Min / Max Acceptable Resolution" is not available (or = 0.0 / 0.0), robust=+0.5 is used. 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 five 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.)

robust	uvtaper	Synthesized Beam	%Diff from mean AR	cell	bandwidth	bwmode	Effective Sensitivity
-0.5		0.161 x 0.0955 arcsec @ -83.3 deg	-59.9%	0.019 x 0.019 arcsec	23.44 MHz	repBW	0.000596 Jy/beam
-0.5		0.157 x 0.0937 arcsec @ -83.5 deg	-61.6%	0.019 x 0.019 arcsec	7500 MHz	aggBW	3.44e-05 Jy/beam
0.0		0.165 x 0.103 arcsec @ -85.0 deg	-55.7%	0.021 x 0.021 arcsec	23.44 MHz	repBW	0.000426 Jy/beam
0.0		0.161 x 0.101 arcsec @ -85.1 deg	-57.6%	0.02 x 0.02 arcsec	7500 MHz	aggBW	2.47e-05 Jy/beam
0.5		0.181 x 0.126 arcsec @ -88.0 deg	-40.5%	0.025 x 0.025 arcsec	23.44 MHz	repBW	0.000329 Jy/beam
0.5		0.177 x 0.122 arcsec @ -88.0 deg	-43.7%	0.024 x 0.024 arcsec	7500 MHz	aggBW	1.91e-05 Jy/beam
1.0		0.207 x 0.158 arcsec @ 87.6 deg	-14.7%	0.032 x 0.032 arcsec	23.44 MHz	repBW	0.000293 Jy/beam
1.0		0.203 x 0.154 arcsec @ 87.5 deg	-18.5%	0.031 x 0.031 arcsec	7500 MHz	aggBW	1.71e-05 Jy/beam
2.0		0.221 x 0.173 arcsec @ 85.3 deg	-0.3%	0.035 x 0.035 arcsec	23.44 MHz	repBW	0.000289 Jy/beam
2.0		0.218 x 0.170 arcsec @ 85.8 deg	-3.4%	0.034 x 0.034 arcsec	7500 MHz	aggBW	1.68e-05 Jy/beam

**Figure 34: example imageprecheck page, showing the "Goals from the OT" including the PI desired sensitivity. The table shows the sensitivity and predicted beam for a range of robust values. The pipeline then choses the best robust value (see text).**

### 9.28 hif\_checkproductsizes: Mitigation to avoid overly long runs

This function will modify the characteristics of the imaging products in order to decrease their size, thereby decreasing the time needed to make them so that data can be delivered to PI's more expediently. Figure 35 shows an example weblog page for a mitigated dataset.

## 23. Check Product Size BACK

---

**Task notifications**

**QA Size had to be mitigated (nbins,field)**

**Warning!** Could not translate spw name SW-1 to ID. Trying frequency matching heuristics.

Allowed maximum cube size: 40 GB  
 Allowed cube size limit: 60 GB  
 Predicted maximum cube size: 58 GB  
 Mitigated maximum cube size: 29 GB  
 Allowed product size: 350 GB  
 Initial predicted product size: 1.86e+03 GB  
 Predicted product size after cube size mitigation: 232 GB  
 Mitigated product size: 232 GB

Size mitigation parameters for subsequent hif\_makeimlist calls

nbins	hm_imsize	hm_cell	field	spw
25:2,31:2,27:2,29:2	default	default	"569314"	default

**Pipeline QA**

**Input Parameters**

**Tasks Execution Statistics**

**CASA logs for stage 23**

- [View or download stage23/casapy.log \(276.9 KB\)](#)

**Figure 35: Screenshot of new hif\_checkproductsize stage of IF Pipeline. In this example, the cubes for spw25 had to be binned by a factor of 2, and the FOV was limited to the 0.5 response point of the primary beam in order to get the products below the default thresholds. Before the mitigation the maximum cube would have been 96GB; after the mitigation, it is predicted to be 21.7 GB.**

Datasets that have been mitigated will have imaging products with different characteristics than those that have not been mitigated. Full imaging products can be recreated by users, using the tclean commands that are in the casa\_commands.log file, or by calling the appropriate hif\_makeimlist, hif\_makeimages with the defaults (which will make full imaging products without mitigations – be aware that this could take many days to complete).

The mitigations are done in a priority order, with the mitigation halted once the predicted sizes fall below the thresholds. The default limits are:

- maxcubesize: 40 GB
- maxcubelimit: 60 GB
- maxproductsize: 350 GB

The pipeline recipe explicitly encodes these values so it can be easily changed universally for all pipeline runs. The casa\_pipescript.py (Figure 12) also encodes these values explicitly, so they can be easily changed on a per-MOUS basis, and the pipeline re-run using the modified file.

The size calculations (in GB) are based on the following:

$$\text{mfssize} = 4. * \text{nx} * \text{ny} / 1\text{e}9$$

cubysize = 4. \* nx \* ny \* nchan / nbin / 1e9

productsize = 2.0 \* (mfssize + cubysize)

The mitigation cascade is as follows:

Step 1: If cubysize > maxcubysize, for each spw that exceeds maxcubysize:

- a. If (nchan == 3840) or (nchan in (1920, 960, 480)) AND online channel averaging was NOT already performed, set nbin=2.
- b. If still too large, then calculate the Gaussian primary beam (PB) response level at which the largest cube size of all targets is equal to the maximum allowed cube size. The cube sizes are initially calculated at primary beam power level PB=0.2. For an image of width d, the response level at the edge will be  $PB = \exp(-d^2 \ln(2)/FWHM^2)$ , the image size is proportional to  $d^2 \propto -\ln(PB)$ , and the required power level to create an image of size = maxcubysize is:

$PB\_mitigation = \exp(\ln(0.2) * maxcubysize / current\_cubysize)$

- i. Then account for imsize padding:  $PB\_mitigation = 1.02 * PB\_mitigation$
- ii. Then limit the size reduction to PB=0.7:  $PB\_mitigation = \min(PB\_mitigation, 0.7)$
- iii. Then round to 2 significant digits:  $PB\_mitigation = \text{round}(PB\_mitigation, 2)$

NOTES: this mitigation cannot be applied to mosaics, only single fields, and the same mitigated FoV is used for all science target image products.

- c. If still too large, change the pixels per beam (cell size) from 5 to 3.
- d. If still too large, *stop with error*, the largest size cube(s) cannot be mitigated.

Step 2: If productsize > maxproductsize

- a. If the number of science targets (single fields or mosaics) is greater than 1, reduce the number of targets to be imaged until productsize < maxproductsize. The representative target is always retained.
- b. If productsize still too large, repeat steps 1a, 1b, and 1c, recalculating productsize each time.
- c. If productsize is still large, *stop with error*, the productsize cannot be mitigated.

Step 3: For projects with large cubes that can be mitigated, restrict the number of large cubes that will be cleaned:

- a. If there are cubes with sizes greater than  $0.5 * maxcubelimit$ , limit the number of large cubes to be cleaned to 1. The spw encompassing the representative frequency shall always be among the cubes retained.

Step 4: For projects that have many science targets, limit the number to be imaged to 30, the representative target is always retained in the list.

When the cube or product size cannot be mitigated, the following warning will appear at the top of the hif\_checkproductsize stage:

“QA Maximum cube size cannot be mitigated”

and then the pipeline will stop in the first `hif_makeimlist` that creates cubes with the message: “Error! Size mitigation had failed. Will not create any clean targets.”

In the example shown in Figure 35, the initial data products were estimated to include a cube that would be 96 GB. This triggered two mitigations: spectral window 25 was binned by a factor of 2, and the FOV was restricted to the 0.5 response point of the Primary Beam. This was sufficient to get the cube size down to 21.7 GB, so the mitigation cascade stopped. The total product size after the cube mitigation is 52.1 GB, so products for all sources could be made.

### 9.29 `hifa_exportdata`

Calibration tables, calibrator images (exported in fits format), and other products are moved from the pipeline `/working` to the `/products` directory.

***NOTE: The subsequent stages are only present if the imaging pipeline was run.***

### 9.30 `hif_mstransform`

For each execution, calibrated visibilities for the science target(s) are split to a new MS with “target.ms” in the name, as listed on the front WebLog page.

### 9.31 `hifa_flagtargets`

Flagging of the science target data, if determined to be necessary by an observatory scientist, is performed as listed in the `*flagtargetstemplate.txt` files linked to the WebLog page. The WebLog also shows a summary table of any flagging performed.

### 9.32 `hif_makeimlist`: Set-up parameters for target per-spw continuum imaging

Imaging parameters are determined and listed for creation of per-spw mfs continuum images of each science target. This run of `hif_makeimlist` also controls the parameters used to create the dirty cubes used by the `hif_findcont` stage, including any channel binning (listed in the “nbins” column of the `hif_makeimlist` table).

### 9.33 `hif_findcont`

In this task, dirty image cubes are created for each spectral window of each science target. The cubes are made at the native channel resolution unless the `nbins` parameter was used in the preceding `hif_makeimlist` stage, and use `robust=1` Briggs weighting for optimal line sensitivity, even if a different `robust` had been chosen in `hifa_imageprecheck` to match the PI requested angular resolution.

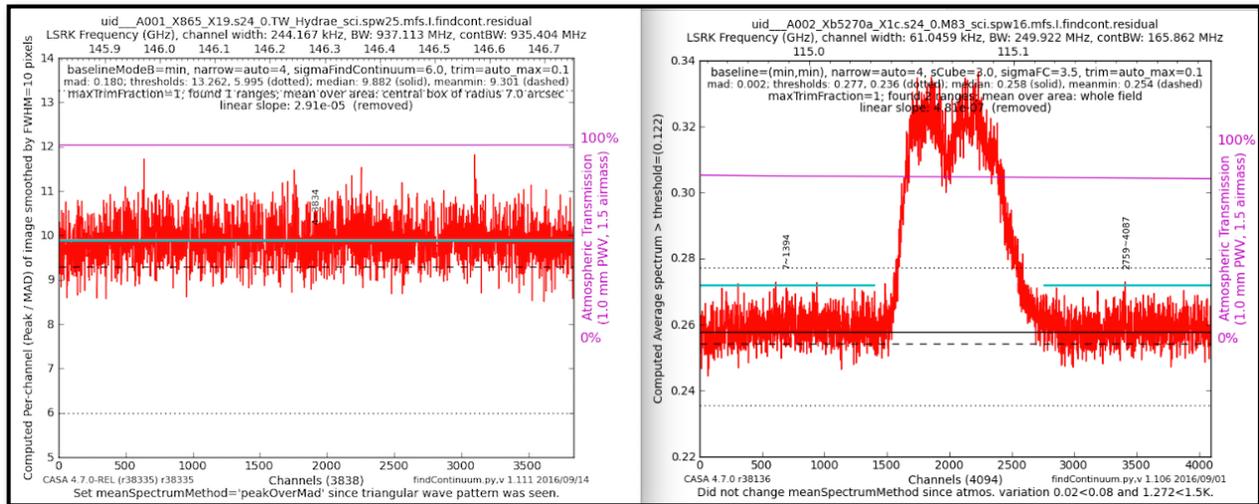
The pipeline then generates and evaluates the mean spectrum of a masked region of the dirty line+cont image constructed from `moment0` and `moment8` (peak) images.

- If fewer than 4 pixels of contiguous emission are found after pruning, the whole field at the >30% primary beam level is used.

- In either case, what is displayed really is a spectrum of the source (created by the ia tool). (see examples in Figure 36).

The mask threshold is based on imstat robust statistics (chauvenet MAD). The mask image can be viewed if necessary in the working directory (\*.joint.mask2 if present, otherwise \*.joint.mask).

Frequency ranges are calculated that are the least likely to contain any line emission or absorption, and these are listed in the LSRK frame on the WebLog page, as well as being indicated by the cyan colored horizontal line(s) on the spectra.



**Figure 36: Two examples of `hif_findcont` plots, one with the entire window identified as continuum (left), and another with two identified continuum regions (right; identified continuum indicated by cyan lines).**

The initial set of channels found by the previous heuristics are used to construct `mom8fc` and `mom0fc` images, then the `mom0fc` is scaled and subtracted from the `mom8fc` to remove continuum sources (to zeroth order), creating a “`momDiff`” image. Residual emission in the `momDiff` then indicates line contamination.

In order to eliminate the excess, two possible paths can be followed:

- “Amend Mask” Path (Code starts with A)
- “Only Extra Mask” Path (Code starts with E)

Two paths are needed, because growing the size of the mask (Amend) can be beneficial in some cases, while negative in others (due to dilution effects). Only Extra works best in the latter case. Note: The mask shown in the `hif_findcont` weblog is the original mask, not the amended/extra mask.

The logic path followed is indicated by a letter code in the legend along with a 4-letter improvement code (L=Lower, S=Same, H=Higher) on stats of the `momDiff` image (Peak, PeakOutsideMask, Sum, ScaledMADOutsideMask). If either of the first two codes are H(igher) the channel selection is “reverted” to its original state.

If the logic code is “S, SSSS”, it means the spectrum was assessed but no changes were deemed necessary by the new heuristics. If the logic code is blank, “PR”

or “P#”, then it was excluded from consideration, including mom8fc images with a large fraction of negative pixels and strong emission pixels (P#), high dynamic range continuum use cases (PR), and long baseline (>400m) TDM cases (blank), all of which are dominated by false positives that result in unnecessary processing, and a generally undesirable decrease in continuum bandwidth.

If no lines ranges are found, then the corresponding continuum-subtracted cube will not be subsequently cleaned (in order to save processing time).

The continuum frequency ranges are also printed to a file called “cont.dat”. If this file already exists before `hif_findcont` is executed, then it will first examine the contents. For any spw that already has frequency ranges defined in this file, it will not perform the analysis described above in favor of the a priori ranges. For spws not listed in a pre-existing file, it will analyze them as normal and update the file. In either case, the file `cont.dat` is used by the subsequent `hif_uvcontfit` and `hif_makeimages` stages.

### 9.34 `hif_uvcontfit`

The previously determined continuum frequency ranges as shown in the **cont.dat** file are used to fit the continuum of each visibility. The fit is performed for each spw independently using a `fitorder=1`, and a calibration table is used to store the resulting fits called “uvcont.tbl”. The WebLog for this stage reports the continuum ranges from `hif_findcont` in LSRK but translated to the topocentric (TOPO) frame for each MS.

### 9.35 `hif_uvcontsub`

The `hif_uvcontfit` calibration table is applied to the data. **After this step, the original continuum + line emission is contained in the DATA column of the MS, while the continuum subtracted data are written to the CORRECTED column.**

### 9.36 `hif_makeimages`: Make target per-spw continuum images

Cleaned continuum images are created for each spectral window, each science target, using the continuum frequency ranges determined from `hif_findcont` (as written in the `cont.dat` file) and the robust selected from the `hifa_imageprecheck` stage and any mitigation triggered by the `hif_checkproductsizes` stage.

The pipeline uses the `tclean` auto-masking method “auto-multithresh” in all `hif_makeimages` stages. This algorithm is intended to mimic what an experienced user would do when manually masking images while interactively cleaning. The parameters `sidelobethreshold` and `noisethreshold` control the masking of the image. The `sidelobethreshold` indicates the minimum sidelobe level that should be masked, while the `noisethreshold` indicates the minimum signal-to-noise value that should be masked. The threshold used for masking is the greater of the two values calculated for each minor cycle based on the rms noise and sidelobe levels in the current residual image. Due to a feature that “prunes” small (< `minbeamfrac`) noise-like automask regions real emission can have all mask regions “pruned” resulting in no clean mask for very compact, typically high S/N emission or absorption. For continuum imaging stages, `tclean` is run again but falling back to a clean mask that is simply a fraction of the primary beam (0.3 .pb if no mitigation of the field of view has occurred). To save time this is not done for cube imaging stages.

The pipeline tclean automask parameters vary as a function of imaging type, and the 75th percentile baseline length, b75. These differences are needed because, for example, the smaller 12m-array configurations tend to have better uv-coverage and psfs than more extended configurations. The parameter fastnoise=True calculates the noise via a simple median absolute deviation, which is fast, but may overestimate the noise in cases where the field is filled with emission. Fastnoise=False uses the Chauvenet method to estimate the noise, which may be more accurate in this case, but it is slower.

<b>Automask parameter</b>	<b>7m-array</b>	<b>12m-array b75 &lt; 300 m</b>	<b>12m-array b75 = 300 m – 400m</b>	<b>2m-array b75 &gt;400 m</b>
noisethreshold	5.0	4.25	5.0	5.0
sidelobethreshold	1.25	2.0	2.0	2.5
lownoisethreshold	2.0	1.5	1.5	1.5
minbeamfrac	0.1	0.3	0.3	0.3
negativethreshold	0.0	0.0 (continuum)/15.0 (line)	0.0 (continuum)/7.0 (line)	0.0 (continuum)/7.0 (line)
fastnoise	False	False	False	True

Images are cleaned to a threshold of 2 x (predicted rms noise) x (dynamic range correction factor). The dynamic range correction factor accounts for the fact that sources with a high dynamic range will have larger imaging artifacts, which should not be cleaned. The artifacts are worse for poorer UV coverage, so different dynamic range (DR) corrections factors are adopted for 12-m Array and 7-m Array observations, for science targets according to the following tables:

<b>Source Dynamic Range</b>	<b>12-m Array DR correction factor</b>
≤ 20	1
20 – 50	1.5
50 – 100	2
100 – 150	2.5
≥ 150	max (2.5, DR/150)

<b>Source Dynamic Range</b>	<b>7-m Array DR correction factor – 1EB</b>	<b>7-m Array DR correction factor – 2 or more EBs</b>
≤ 4	1	1
4 – 10	1.5	1.5
10 – 20	2	2
20 – 30	2.5	2.5
30 – 55	max (2.5, DR/30)	2.5
55 – 75		3.0
≥ 75		max (3.5, DR/55)

The resulting non-primary beam corrected images are displayed on the WebLog page. For each image, the properties are shown next to the associated image png (see Figure 37). In particular, the following are reported: the center frequency, beam parameters (major and minor FWHM resolution & position angle), theoretical sensitivity, cleaning threshold, dynamic range of the dirty image (image peak to theoretical noise) and corresponding DR correction

factor, the non-pbcor image rms (the noise measured in the non-primary beam corrected image over an annulus between the 0.3 to 0.2 response point of the primary beam, or a smaller analogous annulus if field of view mitigation has occurred), image max /min of the primary beam corrected image, fractional bandwidth, aggregate bandwidth, and the image QA score (meant to indicate how close the measured noise is to the theoretical noise, considering also the DR correction factor – see Sec. 8.7.1).

### 33. Tclean/MakeImages

Make target per-spw continuum images BACK

---

#### Image Details

##### Fields

- 04191+1523 (TARGET)
- 04287+1801 (TARGET)
- 04288+1802 (TARGET)
- HH\_30 (TARGET)
- IRAM04191 (TARGET)

Field	Spw			
04191+1523 (TARGET)	16 / X1527843298#ALMA_RB_07#BB_1#SW-0	18 / X1527843298#ALMA_RB_07#BB_1#SW-0	20 / X1527843298#ALMA_RB_07#BB_2#SW-0	22 / X1527843298#ALMA_RB_07#BB_3#SW-0

[View other QA images...](#)

[View other QA images...](#)

[View other QA images...](#)

[View other QA images...](#)

<b>centre frequency of image</b>	329.3312GHz (LSRK)	330.5892GHz (LSRK)	328.2968GHz (LSRK)	339.5162GHz (LSRK)
<b>beam</b>	4.72 x 3.47 arcsec	4.67 x 3.46 arcsec	4.68 x 3.55 arcsec	4.52 x 3.48 arcsec
<b>beam p.a.</b>	-77.9deg	-79.2deg	-76.8deg	-81.2deg
<b>final theoretical sensitivity</b>	0.003 Jy/beam	0.0029 Jy/beam	0.0015 Jy/beam	0.0026 Jy/beam
<b>cleaning threshold</b>	0.018 Jy/beam Dirty DR: 46 DR correction: 3	0.018 Jy/beam Dirty DR: 53 DR correction: 3	0.01 Jy/beam Dirty DR: 1e+02 DR correction: 3.5	0.015 Jy/beam Dirty DR: 60 DR correction: 3

Figure 37: Example of `hif_makeimages` stage for per-spw continuum images. Clicking on the thumbnail will enlarge the image. Clicking the “View other QA images” link will bring up the detailed image page (Figure 38).

The “View Other QA Images” links for each image show the primary beam corrected image, residual, clean mask (red area), dirty image, primary beam, psf, and clean model (Figure 38).

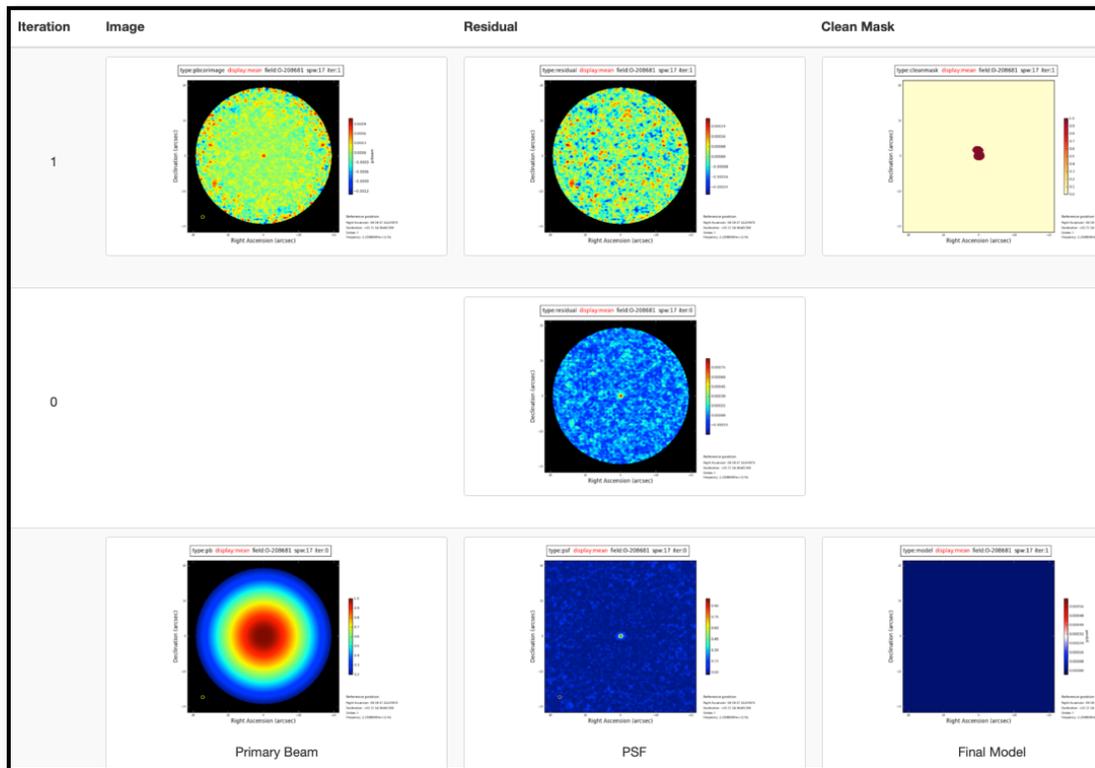


Figure 38: Details page that is displayed after clicking on the “View other QA images” link on the `hif_makeimages` WebLog page.

### 9.37 `hif_makeimlist`: Set-up parameters for target aggregate continuum images

Imaging parameters are calculated and listed for creation of an aggregate (all spectral windows combined) continuum image (`specmode='cont'`) of each science target and the robust selected from the `hifa_imageprecheck` stage and any mitigation triggered by the `hif_checkproductsizes` stage.

### 9.38 `hif_makeimages`: Make target aggregate continuum images

A cleaned aggregate continuum image of each science target is formed from the `hif_findcont` channels (as listed in the `cont.dat` file) is created. The aggregate continuum image(s) are made with `nterms=2` if the fractional bandwidth is  $\geq 10\%$  (only currently possible for ALMA Bands 3 and 4 data). Automasking and cleaning as in Sec. 9.36.

The resulting non-primary beam corrected images are displayed on the WebLog page. The “View Other QA Images” links show the primary beam corrected image, psf, clean model, dirty image, and residual image (Figure 38).

### 9.39 `hif_makeimlist`: Set-up image parameters for target cube imaging

Parameters are calculated and listed for creation of spectral cube images of each continuum-subtracted spectral window of each science target. The cube parameters use the robust selected from the `hifa_imageprecheck` stage and any mitigation triggered by the `hif_checkproductsizes` stage.

## 9.40 hif\_makeimages: Make target cubes

Cleaned continuum-subtracted cubes are created for each science target and spectral window at the native channel resolution (unless channel binning has been selected using `nbins` in the preceding `hif_makeimlist`) from the CORRECTED column. Cubes are made in the radio LSRK frequency frame. Only channels that have not been designated as continuum channels are cleaned. Automasking and cleaning as in Sec. 9.36.

The WebLog page displays non-primary beam corrected peak intensity images for each cube (“moment 8”) along with properties of the cubes (see Figure 39). The information is similar to that described in Sec. 9.36 for continuum images, except that the noise is the median rms over all channels (still measured in a 0.3 – 0.2 PB annulus), and instead of fractional and aggregate bandwidth the “channel” information is given as the number of channels imaged times the channel width. Recall that if no online or `nbins` (pipeline option) channel averaging is done, the velocity resolution will be twice the channel width.

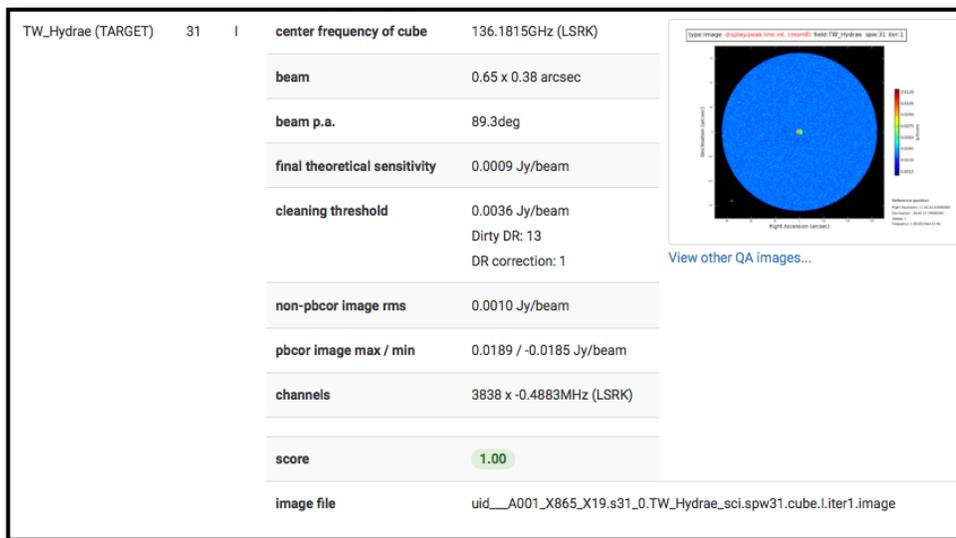


Figure 39: Example of `hif_makeimages` WebLog page for image cubes – scrolled down slightly from Figure 37, to show the full list of displayed values.

In addition to the “View other QA images” for continuum images demonstrated in Sec. 9.36, additional plots are included for continuum subtracted cubes: an integrated intensity (“moment 0”) and peak intensity (“moment 8”) image using the `hif_findcont` continuum frequency ranges (labeled “Line-free Moment 0 / 8”; see Figure 40), and spectra of the signal (red) and noise (black) extracted over the masked area of the cube. The line-free Moment images should be noise-like if the continuum subtraction worked well. This is evaluated through a QA score based on the peak emission of the line-free `mom8` compared to the median of the channel noise.

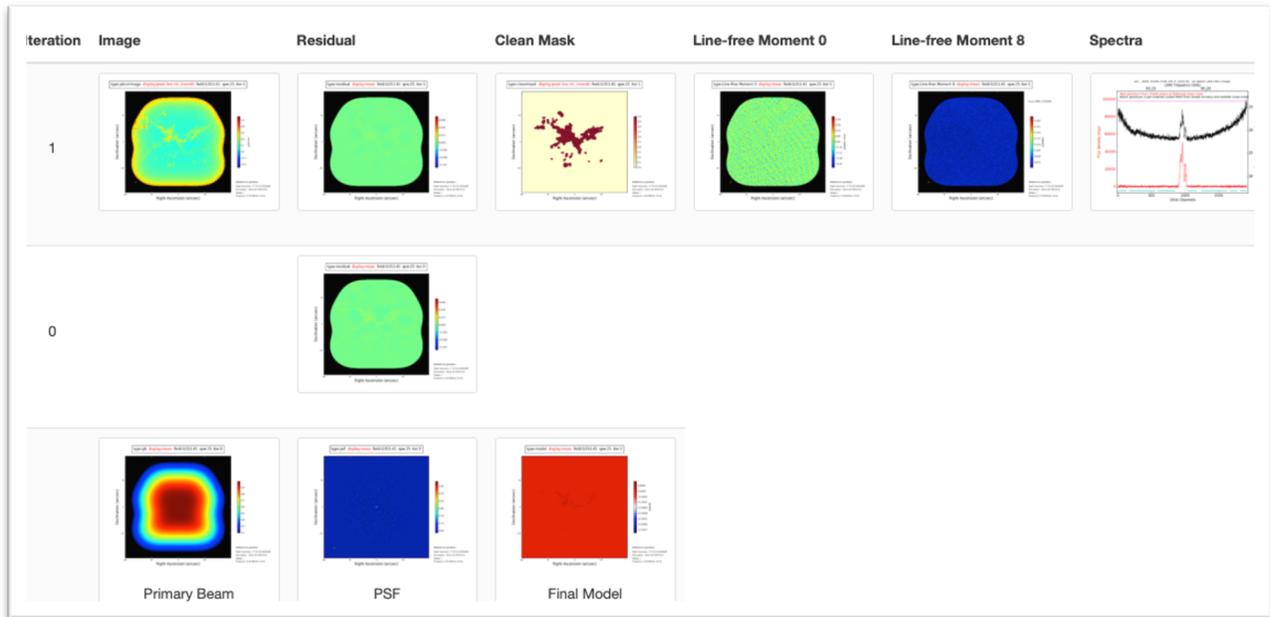


Figure 40: Example of an image cube details page including the line-free moment 0 and moment 8 images.

#### 9.41 `hif_makeimlist`: Set-up image parameters for representative bandwidth target cube

If the PI requested spectral resolution (bandwidth for sensitivity) is at least 4x larger than the correlator channel width, then in addition to cubes created at that correlator width, the representative source and spw are imaged at the PI's requested resolution, in this and the next stage.

#### 9.42 `hif_makeimages`: Make representative bandwidth target cube

If the PI requested bandwidth for sensitivity (representative bandwidth) is significantly coarser ( $> 4x$ ) than the native correlator channel width, an additional cube is created at the PI's bandwidth (note: this stage is always created even if it is not populated).

#### 9.43 `hifa_exportdata`

Science target images are converted to FITS format and copied to the `/products` subdirectory as well as the `cont.dat` file from the `hif_findcont` stage. This stage is run in operations, but is not included in the `casa_pipescript.py` script.

# 10 Single Dish pipeline tasks and “by task “weblog pages

This section describes navigation of the Task sub-pages for each Single Dish Pipeline task starting from the “By Task” tab. For a detailed description of parameters for each task, refer to the **ALMA Science Pipeline Reference Manual**.

## 10.1 hsd\_importdata

The WebLog for `hsd_importdata` task shows the summary of imported MSs, grouping of spws to be reduced as a group, and spw matching between Tsys and science spws. This task also generates figures of Telescope Pointings, which are available in the MS Summary page (i.e. from the Home page, click the MS name, and then click on “Telescope Pointing”). There are two types of plots that can be found containing full information on all pointings and just on-source pointings (Figure 41). In these plots, the red circle indicates the beam size of the antennas and its location is the starting position of the raster scan. The Red (small) dot indicates the last position of the raster. The green line represents the antenna slewing motion, and in the right panel of Figure 41 the green line going to/from the red dot indicates that the antenna goes to the last scan and returns to the OFF position. The grey dots indicate flagged data. `hsd_importdata` generates pointing pattern plots with ephemeris correction in addition to the plots without correction if target is moving source.

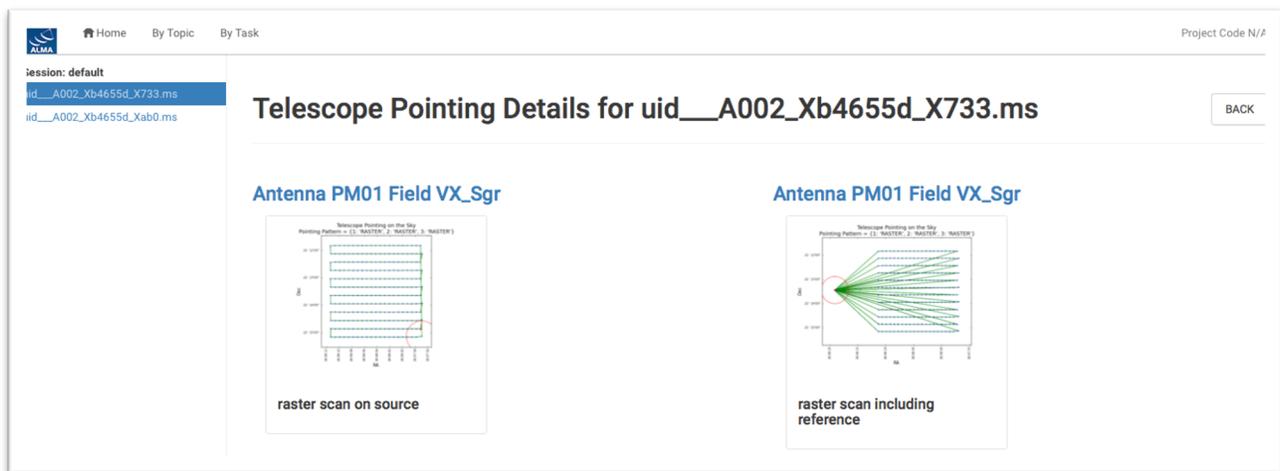


Figure 41: The detailed page of Telescope Pointing in the MS summary page.

## 10.2 hsd\_flagdata

The WebLog for the `hsd_flagdata` task shows the summary of flagged data percentage per MS due to binary data and online flagging, manually inserted file (**\*flagtemplate.txt**), shadowing, unwanted intents, and edge channels. Note that the value in the “Before Task” column corresponds to the percentage of flagged data by binary data flagging (BDF).

## 10.3 h\_tsyscal

This page shows the associations of Tsys and science spectral windows to be used for Tsys (amplitude-scale) calibration, and also shows the original Tsys spectra per spectral window.

## 10.4 hsd\_tsysflag

This page shows the flagged Tsys spectra per spectral window after heuristic flagging is applied.

## 10.5 hsd\_skycal

The WebLog shows the integrated OFF spectra per spw and per source. The y-axis is the direct output from the correlator, which means the values are dominated by signals from both the atmosphere and receivers (Figure 42). The different colors indicate different scans (times). The magenta lines indicate the atmospheric transmission at each frequency.

The time-averaged plots of the OFF spectra are also shown in this page for the purpose of assessing the time variability of the spectra. The different colors here indicate different spws. Note that the OFF spectrum is not averaged over the spectral windows yet, but it will be in the future.

The coordinates of the OFF position can be confirmed in the Reference Coordinates table.

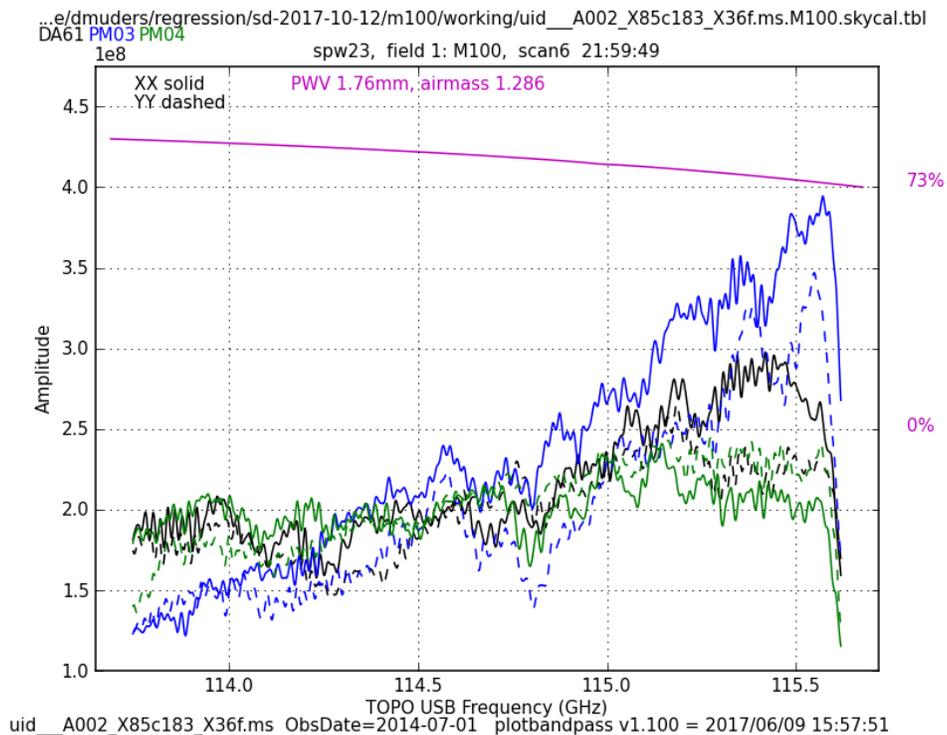


Figure 42: An example of OFF spectrum

In addition, amplitude versus time plots for the OFF\_SOURCE data and elevation difference between ON\_SOURCE and OFF\_SOURCE data plots are shown in this page.

## 10.6 hsd\_k2jycal

This page shows the list of Kelvin-to-Jansky conversion factors that Pipeline has read from a file "jyperk.csv", which shall contain the factors per spw, per antenna, and per polarization.

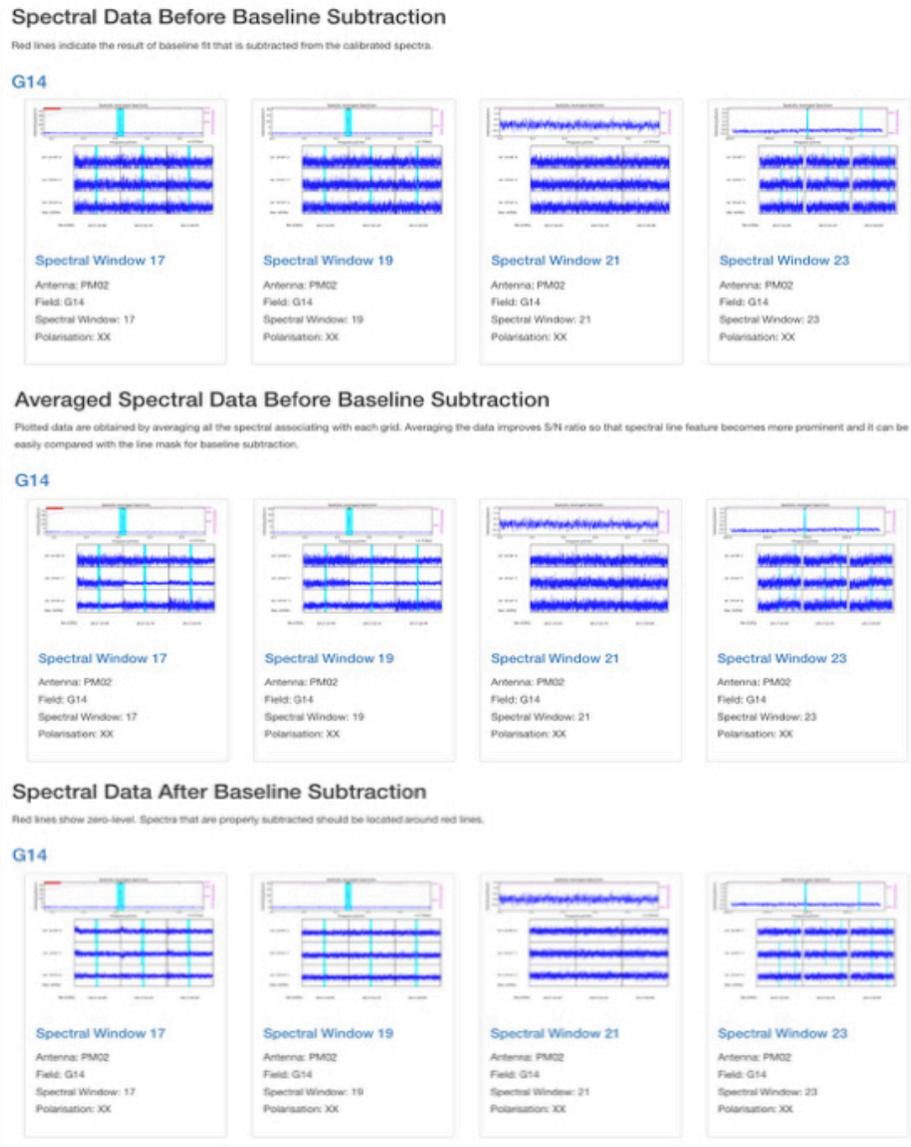
## 10.7 hsd\_applycal

This page shows a list of the calibrated MSs with the name of the applied Tsys, Sky and amplitude calibration (Kelvin-to-Jansky conversion) tables, and also shows the integrated spectra after calibration.

## 10.8 hsd\_baseline

### Spectral data before/after baseline subtraction

The `hsd_baseline` page of the WebLog shows the three grids of spectra per source: the one on the top and in the bottom correspond to the spectra before and after the baseline subtraction, respectively. The one in the middle is obtained by averaging all the spectra associated with each grid (see Figure 43). Averaging the data improves the S/N ratio making the spectral line features more prominent, which makes it easier to compare them with the line mask for baseline subtraction (see below). These plots, which appear just after clicking the `hsd_baseline` link of the WebLog, show a representative spectral grid of each spw. Normally they correspond to the spectral grid of a certain antenna. The spectral grids are shown in R.A./Decl. coordinates. Each small panel shows **one** representative spectrum per grid cell (which sometimes we call “sparse profile map”). The red (horizontal) line over-plotted on the spectrum indicates the fitted function to be used for baseline subtraction for spectral data before baseline subtraction, while the zero-level for spectral data after baseline subtraction.



**Figure 43** An example of the summary page of hsd\_baseline.

On the top panel of each spectral grid, a spatially integrated spectrum per ASDM, antenna, spw and polarization is shown. The magenta lines indicate the atmospheric transmission at each frequency. The cyan filled regions indicate the mask channels containing emission line that are identified in the entire map, and red thick bars indicate the channels masked by a “deviation mask” algorithm, designed to exclude atmospheric lines and lines at the band edge from the baseline fit.

Detailed plots of the spectra can be seen in the detail pages, which can be opened by clicking the “Spectral Window” link below the grid of spectra in the summary page. In the detail pages the spectral maps of all the antennas are shown. In the upper part of the detail pages there are boxes that can be used to set filters to plot spectral maps by antenna, field, spectral window and polarization.

## R.A. vs Dec. plots

There are four different plots per spw, i.e. “clustering\_detection”, “clustering\_validation”, “clustering\_smoothing”, and “clustering\_final”. The number of plots in each figure is the same as that of the candidate line components. The “cluster\_detection” plot (Figure 44a) shows the grid cells having emission line exceeding the threshold. In the plot, yellow grid cells show a region where there is a single time-domain group with detected emission lines. Cyan squares indicate grid cells where there are more than one time-domain groups with detected emission lines.

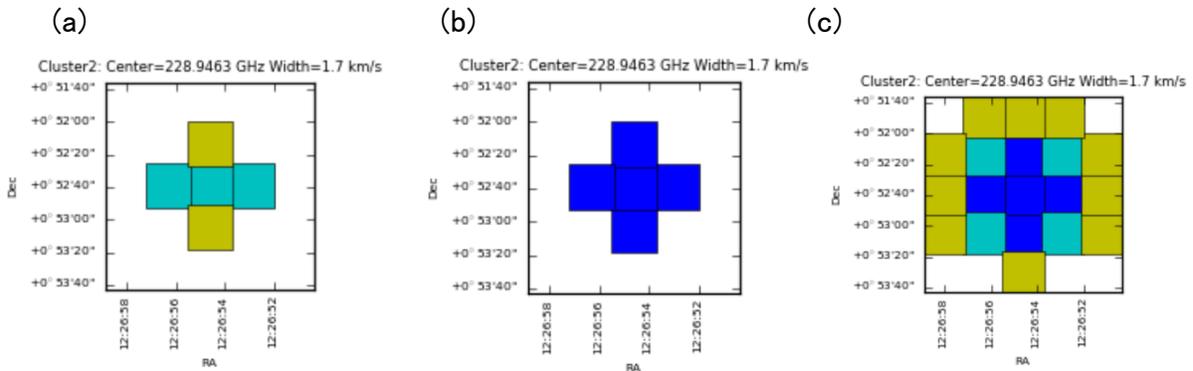


Figure 44 Examples of (a) clustering\_detection, (b) clustering\_validation, and (c)clustering\_smoothing.

After line detection, the algorithm calculates how many spectra containing emission lines are included in the grid cell in order to judge whether the grid cell possibly contains true emission lines. At this line detection validation step, the ratio of the number of spectra having detected emission lines (defined as “Nmember”) per grid cell and the number of total spectra belonging to the grid cell (“Nspectra”) is calculated. The “clustering\_validation” plot (Figure 44b) shows this ratio for each grid cell, i.e., the grid cell is marked as:

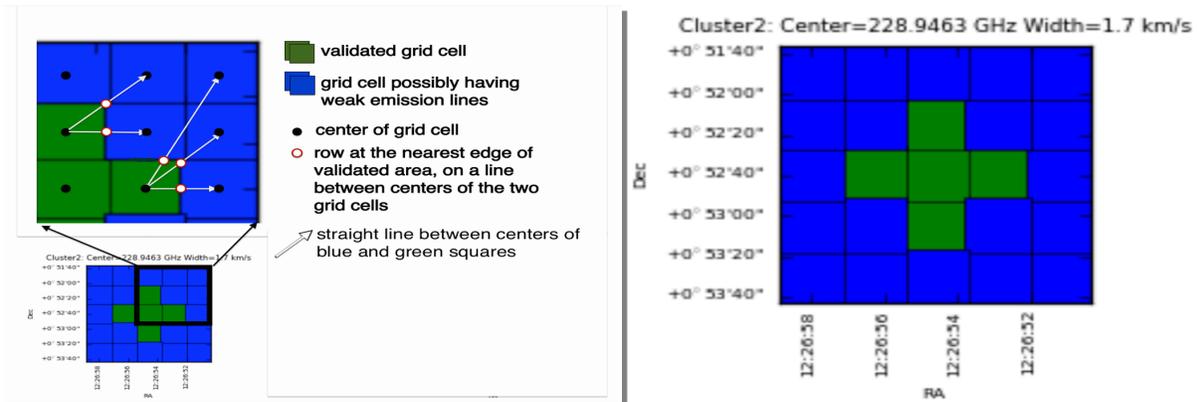
- “Validated” if  $N_{member}/N_{spectra} > 0.5$  (Blue squares in Figure 44b)
- “Marginally validated” if  $N_{member}/N_{spectra} > 0.3$  (Cyan squares)
- “Questionable” if  $N_{member}/N_{spectra} > 0.2$  (Yellow squares)

After the validation step, the grid containing the  $N_{member}/N_{spectra}$  rate per grid cell is smoothed by a Gaussian-like grid function. This is to eliminate the isolated grid cells having a single emission line candidate while enhancing the grid cells with detected emission line in neighboring grid cells.

Figure 44c shows an example of “clustering\_smoothing”. Blue squares represent the grid cells with points exceeding the defined threshold, i.e., the grid cells having promising detections of emission lines that are also found in the neighboring grid cells. Cyan and yellow squares are the grid cells with points slightly below the threshold (Border), or lower than the threshold (Questionable).

(a)

(b)



**Figure 45 (a)** An example of how the mask range is calculated. In the blue squares, the mask channel range is the range obtained at the nearest edge of any validated area by interpolating mask channel ranges in the valid grid cells (white-filled red circle). **(b)** An example of clustering\_final.

As a final step, the mask region for each grid cell is determined. In the validated area after the validation and the smoothing steps (blue squares in Figure 44c or green squares in Figure 45), mask channel ranges are calculated over the spatial domain by inter/extrapolating the mask ranges of the integrated spectra in the validated cells, and over each single non-integrated spectrum. The mask channel range is determined and used in baseline subtraction in the green and blue squares of Figure 45a. An example of “clustering\_final” is shown in Figure 45b.

### Line Center vs. Line Width plot

This plot shows the extent of each identified emission line candidate on the parameter space of the line width versus the line center<sup>3</sup>. The small dots indicate spectra containing identified emission line. The red ovals show each clustering region with a size of the cluster radius.

### Number of Clusters vs. Score plot

This plot shows the number of clusters and corresponding scores based on the cluster size determined from the “line width” v.s. “line center” plot using clustering analysis (K-means algorithm)<sup>4</sup>. The scoring is empirically defined so that the score gets better (smaller) when the cluster size is smaller, the number of clusters is smaller, and the number of outliers is fewer than those of other clusters. The users will know which number of clusters is more plausible by searching for the number of clusters with a lower score. This plot is basically for developers.

### Fitting order determination

Pipeline performs baseline fitting using a cubic spline that connects an empirically defined number of segments of each spectrum.

<sup>3</sup> Starting with the Cycle 7 pipeline, hierarchy algorithm is adopted instead of kmean. The hierarchy algorithm tends to identify larger number of clusters with smaller radius compared with kmean. Please keep in mind this property when Cycle 7 results are compared with prior Cycles.

<sup>4</sup> Starting with the Cycle 7 pipeline, hierarchy algorithm is adopted instead of kmean so the current plots are the dummy.

In a first step, the spectra are grouped in space and time domains. Pipeline groups the spectra that were observed close in time and position with respect to each other. Subsequently, Pipeline analyzes each (emission-masked) spectrum through Fast Fourier Transform (FFT) to obtain the power spectra. Note that input for the discrete Fourier Transform is (spectrum-average)\*flag, where “flag” is set to zero for the emission-masked channels, while set to 1 for other channels. The power spectra of all integrations in a group are summed together and divided by its average value (averaging over frequency channels). Based on the peak value of the normalized Fourier spectra ( $P_{FFT}$ ), the number of segments for cubic spline fitting ( $N_{segment}$ ) is defined empirically:

- If  $1 < P_{FFT} < 3$ , then  $N_{segment} = 3$ ,
- If  $3 \leq P_{FFT} < 5$ , then  $N_{segment} = 4$ ,
- If  $5 \leq P_{FFT} < 10$ , then  $N_{segment} = 5$ ,
- If  $P_{FFT} \geq 10$ , then  $N_{segment} = F_{FFT} \times 2 + 1$ , where  $F_{FFT}$  is the frequency corresponding to the peak  $P_{FFT}$ .

In a second step, in order to take into account the proportion of masked channels, the obtained  $N_{segment}$  is newly defined as  $N_{segment} \times (N_{ch} - N(mask)) / N_{ch}$ , where  $N_{ch}$  is the number of spectral channel and  $N(mask)$  is the number of channels masked. Note that unmasked channels are equally divided into segments, i.e., number of unmasked channels is same for all segments. Finally, the Pipeline performs the baseline fitting and baseline subtraction using cubic splines, which are third order polynomial that meet the boundary condition at the joint between the segments.

### Mask range determination

When baseline fitting is performed, the emission channel range is masked out. The mask range is determined by following equation:

$$mask = \{(maxW - width) \times (2 \times minW + 10) + (width - minW) \times maxW\} / (maxW - minW)$$

where  $minW$  is minimum channel width,  $maxW$  is maximum channel width,  $width$  is channel width where the emission is above a threshold with at least five adjacent channels (see Figure 32). The  $minW$  and  $maxW$  are empirically determined and set to 2 and 500, respectively. Finally, the range of central channelmask divided by 2 will be masked out. In this definition, the relatively narrow channel width will have slightly larger mask range. For example, if  $width = 5$  channels, the mask range will be 8 channels at the central channel. For  $width = 500$  channels, the mask range will be 250 channels at the central channel.

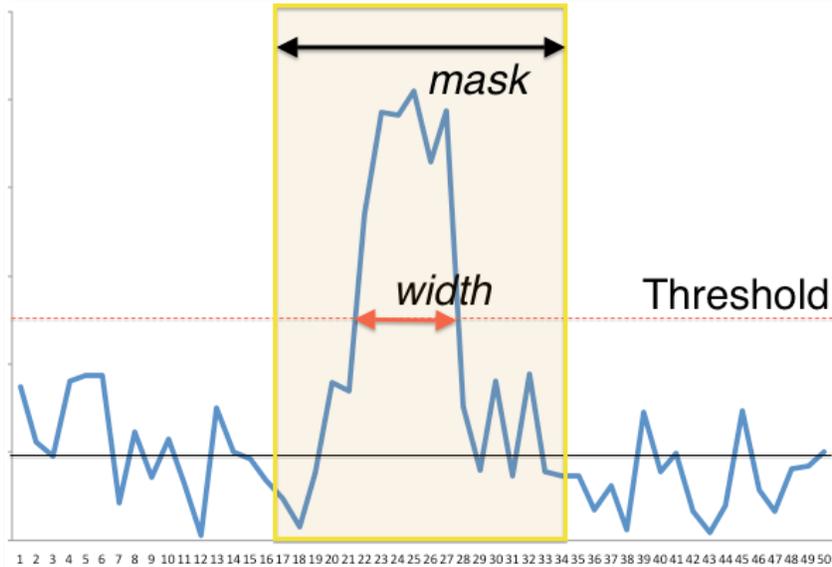


Figure 46: An example of spectrum with Pipeline defined mask range. “Width” corresponds to the number of channels where the emission is above the threshold.

## 10.9 hsd\_bflag

The WebLog shows the list of flagged data percentage using five criteria that are explained in the ALMA Pipeline Reference Manual. When you click on “details”, you will get the detailed figures to evaluate these criteria as a function of rows (one row corresponds to a spectrum for one integration). The flagged and unflagged data are shown in red and blue, respectively.

## 10.10 hsd\_imaging

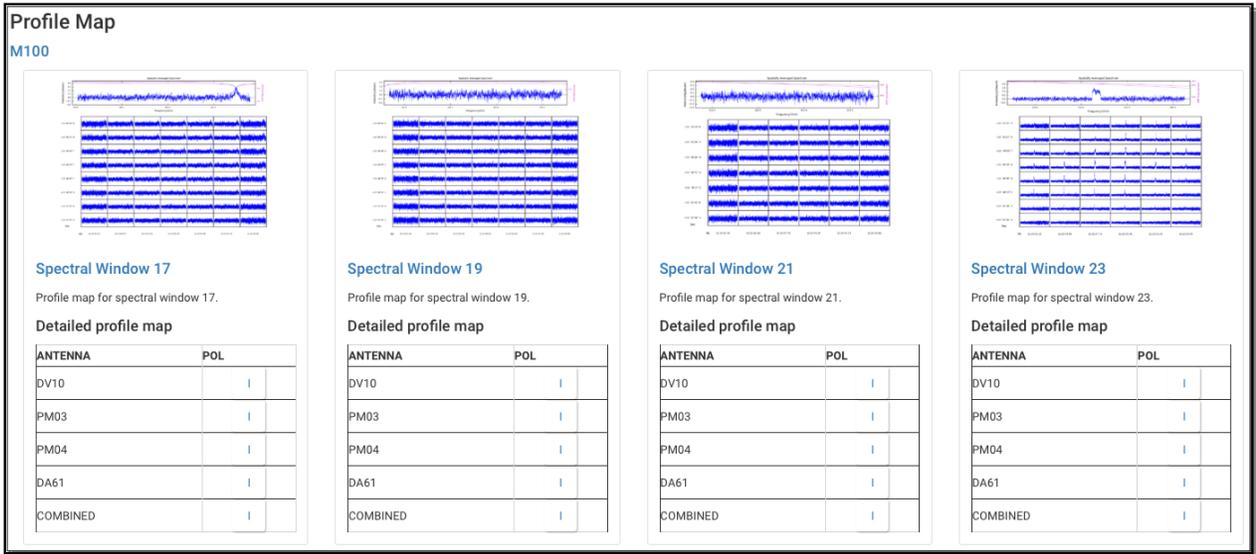
### Image Sensitivity Table

The achieved sensitivity for the final cubes per Spw and Source as well as the theoretical RMS taken into account the flagging fraction are shown in the table. For the cube of representative Spw, the sensitivity is calculated with the PI's requested bandwidth, while for the other Spws the sensitivities are measured with the native resolution.

### Profile Map

Figure 47 shows the top of the summary page. Three types of profile maps are available in the WebLog: 1) The simplified profile map of the combined image per spw at the top, 2) a simplified profile map per antenna, and 3) a detailed profile map. In the simplified profile map, the magenta lines indicate the atmospheric transmission at each frequency. One transmission profile is plotted for each ASDM processed. To access the simplified profile map per antenna, click the corresponding “Spectral Window”. Each spectrum of the simplified profile maps (either 1. or 2.) corresponds to an averaged spectrum in an area of  $\frac{1}{8}$  of the image size (imsize), so that the total number of spectra in the profile map is 8 times 8. If the number of pixels (along x- or y-axis) is less than eight, it shows all spectrum per pixel. To see the detailed profile maps, click the icon with a symbol of polarization in the polarization column (see Figure 47). Each bin of the profile map is equivalent to a pixel, but with an

interval of three cells. Due to the limitation of the allowed number of plots per page (max 5 x 5 plots per page), the rest of the plots are displayed in other pages.



**Figure 47** An example of the profile map.

## Channel Map

The number of channel maps per spw corresponds to the number of emission lines that have been identified by the clustering analysis. In each channel map (see Figure 48), the top-middle plot shows the identified emission line and the determined line width (bracketed by two red vertical lines), overplotted on the averaged flux spectrum (in Jy) as a function of frequency (in GHz).

The top-left plot shows the zoom-up view of the identified emission line, but with velocity axis. The vertical axis is the averaged flux in Jy and the horizontal axis is in units of km/s. The (center) velocity of 0 km/s corresponds to the central frequency of the spectral range where line emission was detected, while the velocity range is equivalent to the masked region where the emission line was identified. The line velocity width is gridded into 15 bins, which are shown as red vertical lines. The top-right plot shows the total integrated intensity map (in Jy/beam km/s) over the all channels in the spw. Finally, the channel maps within the velocity range of the identified emission line are shown in the panel at the bottom. Each channel plot corresponds to a bin in the top-left plot.

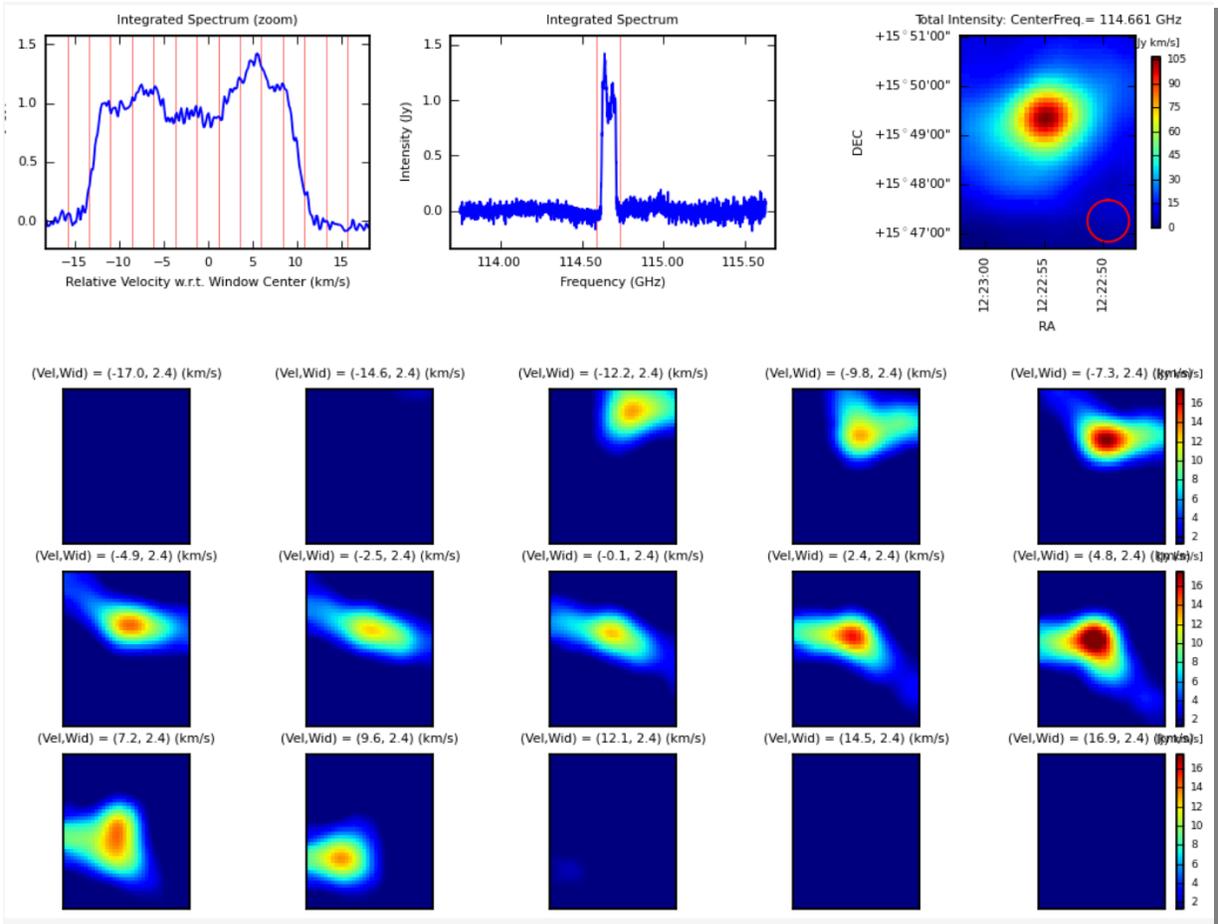


Figure 48 An example of channel map.

The **Baseline RMS Map** is created using the baseline RMS stored in the baseline tables. The baseline RMS is calculated by `hsc_baseline` using emission free channels.

The **Integrated Intensity Map** for each spw is generated using `immoments` task with all the available channel range.

The **contamination plot** contains three plots of Peak SN map, mask map, and masked-averaged spectrum. The open circle in Peak SN map indicate the peak SN position. Mask map indicate the pixels that have a lower 10% SN ratio values. In masked-averaged spectrum, the spectrum in red indicates the spectrum averaged over the masked pixels, while the spectrum in grey indicates the spectrum at the peak SN position. If the negative peak of the masked-averaged spectrum is less than  $-4 * \text{std}$ , the pipeline gives a warning.

# 11 Per-channel imaging weights in cubes

Since CASA 5.6, the calculation of imaging weights can now be performed either per-channel or for all channels, according to the `tclean` parameter `perchanweightdensity`. This can have significant effects on the image produced. Users should be aware of these effects when creating new images, either using pipeline tasks or with `tclean`.

- The `tclean` `perchanweightdensity` parameter was effectively `False` in the Cycle 6 pipeline and CASA 5.4 and all prior versions of CASA and pipeline (the parameter did not exist prior to CASA 5.5.0).
- As of CASA 5.6.0 (i.e. the version used for ALMA Cycle 7 data reduction), `perchanweightdensity = True` is the default in `tclean`.
- ALMA has decided that the Cy7 and 2020.1 Imaging Pipelines will create cubes with `perchanweightdensity = False` (consistent with all previous version of the imaging PL), but is likely to change to use `perchanweightdensity = True` in Cycle 8.

## 11.1 Description of the `perchanweightdensity` parameter

Briggs imaging weights are calculated based on the density of visibilities in each uv grid cell:

$$w_i = \frac{\omega_i}{1+W_k f^2}$$

where

$w_i$  is the image weight for a given visibility point  $i$ ;

$\omega_i$  is the visibility weight of baseline  $i$ ;

$W_k = \frac{\sum_{cell=k} \omega_k}{\sum_i \omega_i}$  is the weight density of a given cell  $k$  (with  $\omega_k$  the weight of a uv point that falls in cell  $k$ ).

$$f^2 = \frac{(5 \times 10^{-R})^2}{\frac{\sum_k W_k^2}{\sum_i \omega_i}}$$

$R$  is the robust sub-parameter.

$$w_i = \frac{\omega_i}{1+W_k f^2}$$

where

$w_i$  is the image weight for a given visibility point  $i$ ;

$\omega_i$  is the visibility weight of baseline  $i$ ;

$W_k = \frac{\sum_{cell=k} \omega_k}{\sum_i \omega_i}$  is the weight density of a given cell  $k$  (with  $\omega_k$  the weight of a uv point that falls in cell  $k$ ).

$$f^2 = \frac{(5 \times 10^{-R})^2}{\frac{\sum_k W_k^2}{\sum_i \omega_i}}$$

R is the robust sub-parameter.

Recall that natural imaging weights  $w_i$  are 1.0, and it is by assigning image weight  $w_i < 1.0$  to shorter baselines that Briggs weighting can form a smaller synthesized beam.

For a given robust value R, fewer (u,v) points in a given cell (lower weight density  $W_k$ ) will result in larger imaging weights (closer to 1, i.e. closer to natural), and a larger synthesized beam.

Different channels are located in different cells in uv-space because of the frequency difference (Figure 49). This is the basis of multi-frequency-synthesis (mfs) continuum imaging which takes advantage of this property to increase the *effective* uv-coverage. In CASA 5.5, the “perchanwt” parameter determines whether the imaging weights are calculated using only the (u,v) points for each channel of interest (perchanwt=True, new option), or using the points corresponding to all channels in the spw (perchanwt=False) similar to an mfs continuum image:

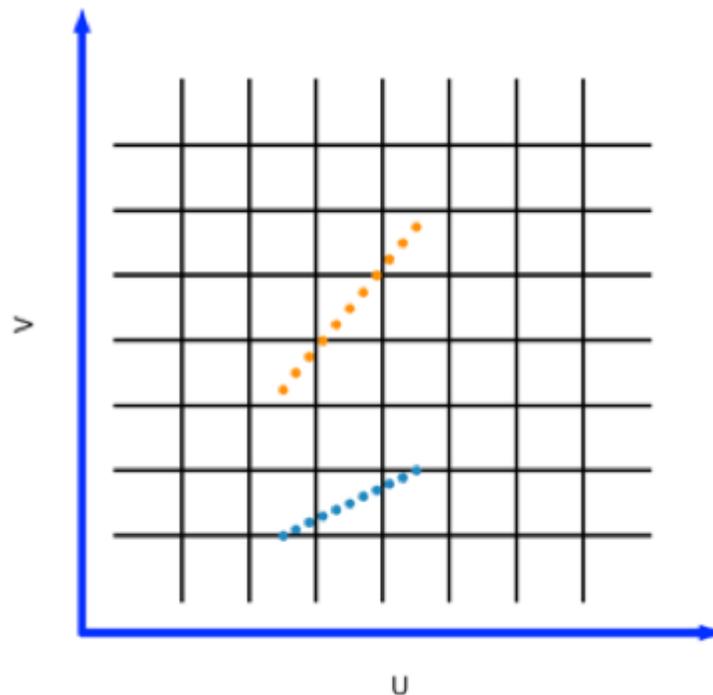


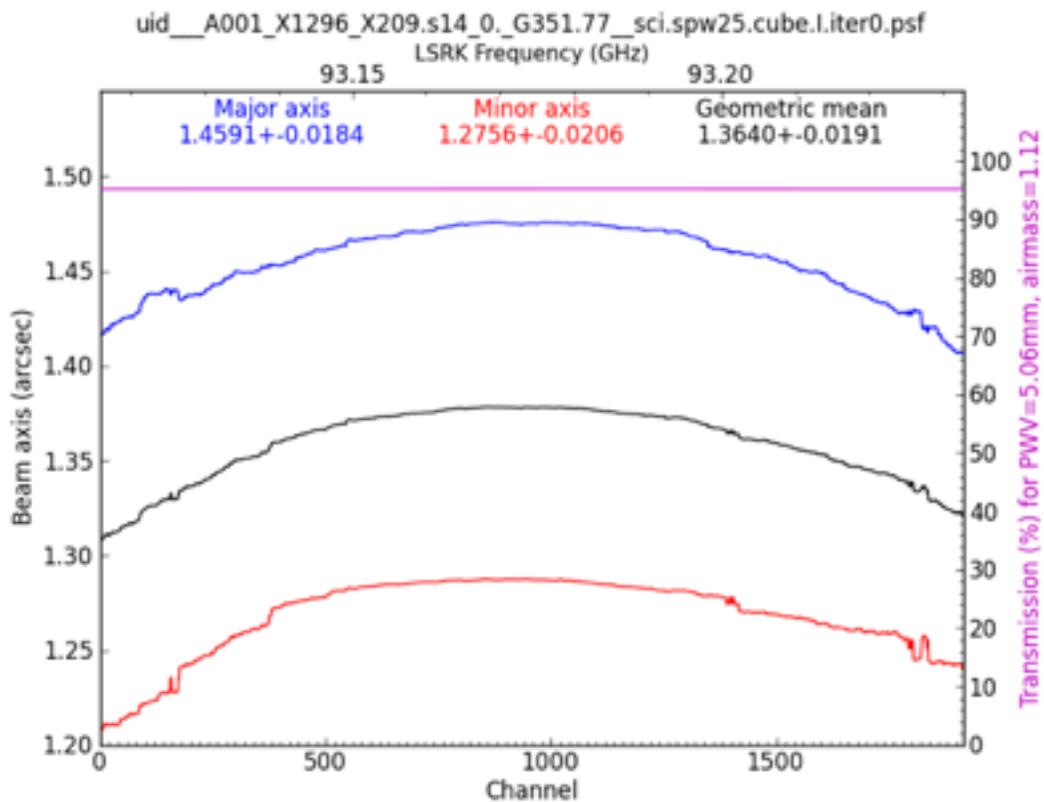
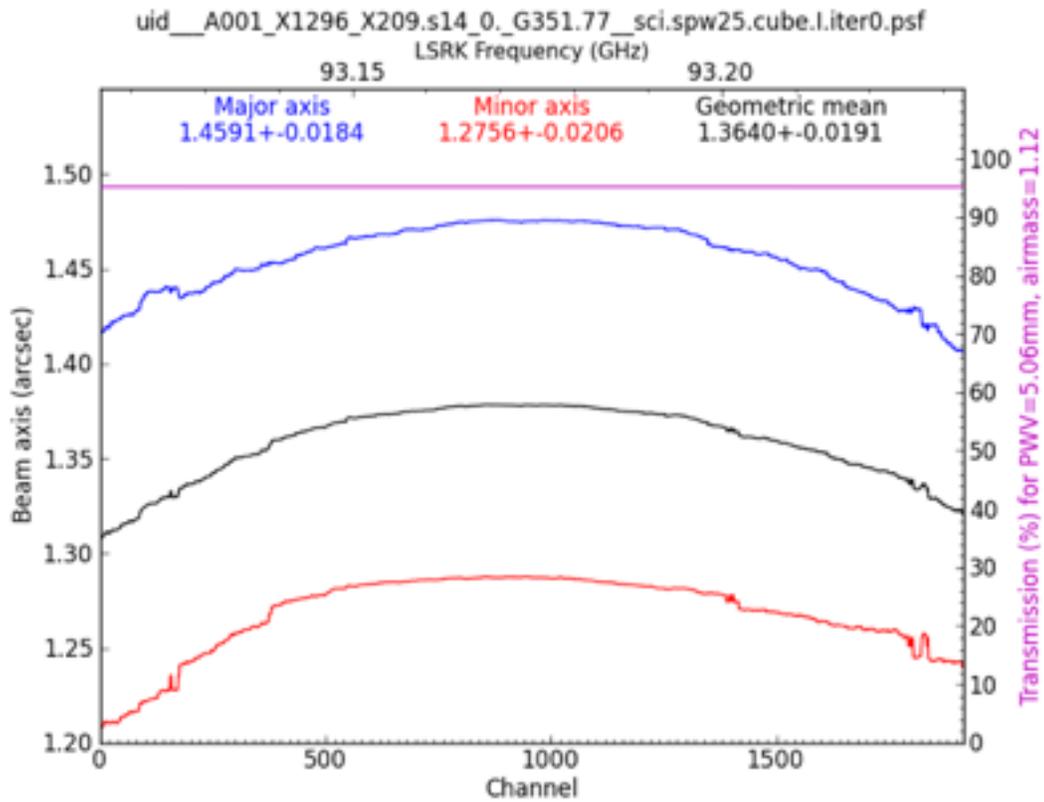
Figure 49: one integration, two different baselines, showing the uv points corresponding to different channels of the spw.

## 11.2 Effect of perchanweightdensity on beam size and noise across a spectral window

Perchanweightdensity=True produces nearly uniform beam size and noise across the spectral window regardless of the robust value. For natural weighting (robust = 2) perchanwt doesn't affect the result.

If all channels' (u,v) locations are used in the weight calculation (perchanweightdensity = False), then the beam is systematically smaller, but the noise is systematically higher at the edges of a spectral window. The centers of the spws statistically fall in more heavily populated uv cells, and thus get different imaging weights than the edges of spws. This effect is worsened by using more uniform values of the robust parameter (see Figure 52).

Note that the curvature shown in Figure 50 is not immediately apparent (except in the rms noise per channel) in ALMA image products, because the final image cubes are restored with the "commonbeam", i.e. the beam that is large enough to encompass all per-plane beams.



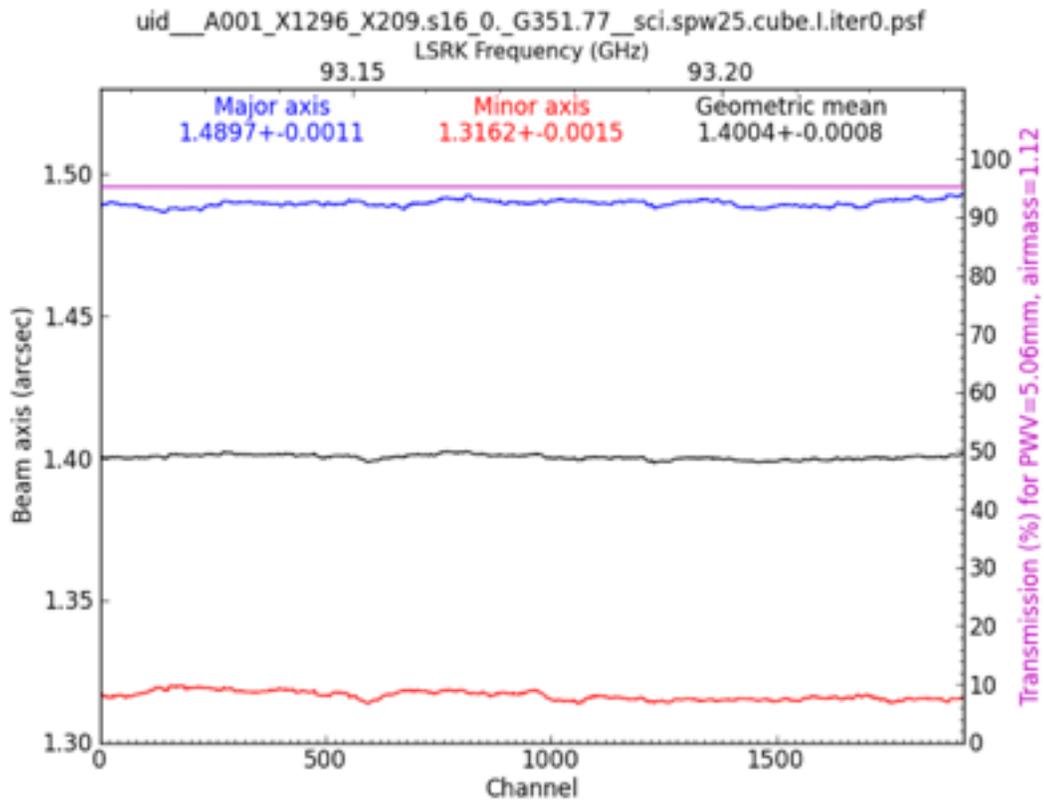
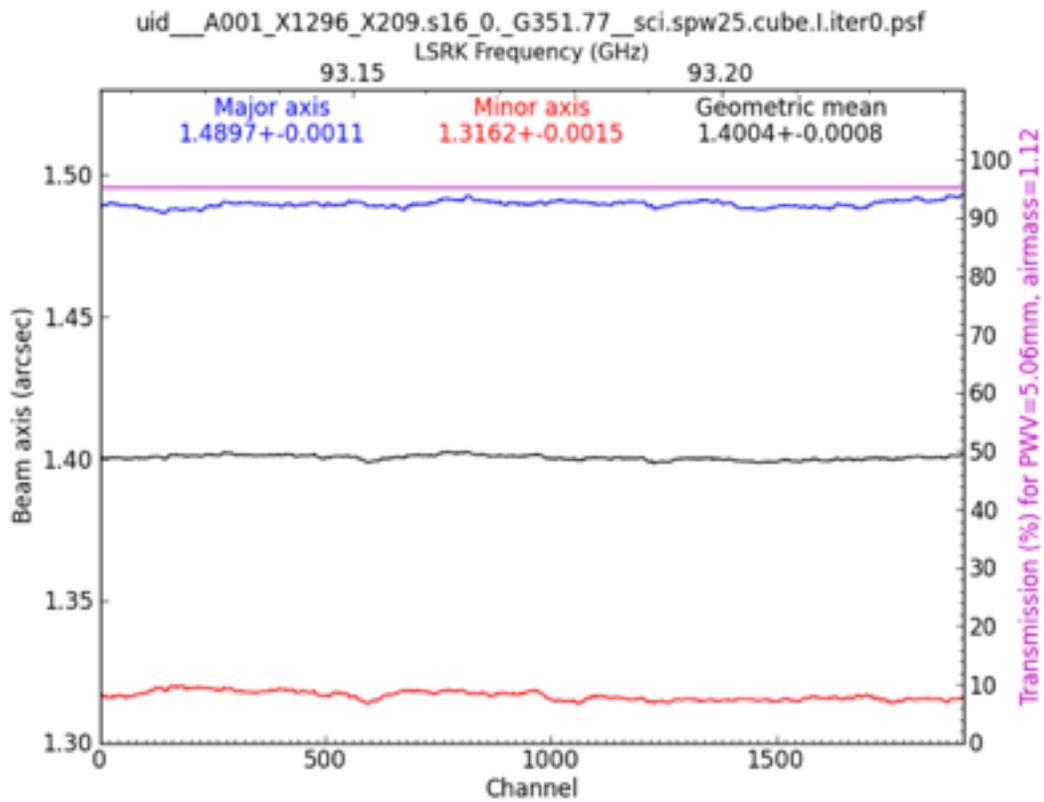
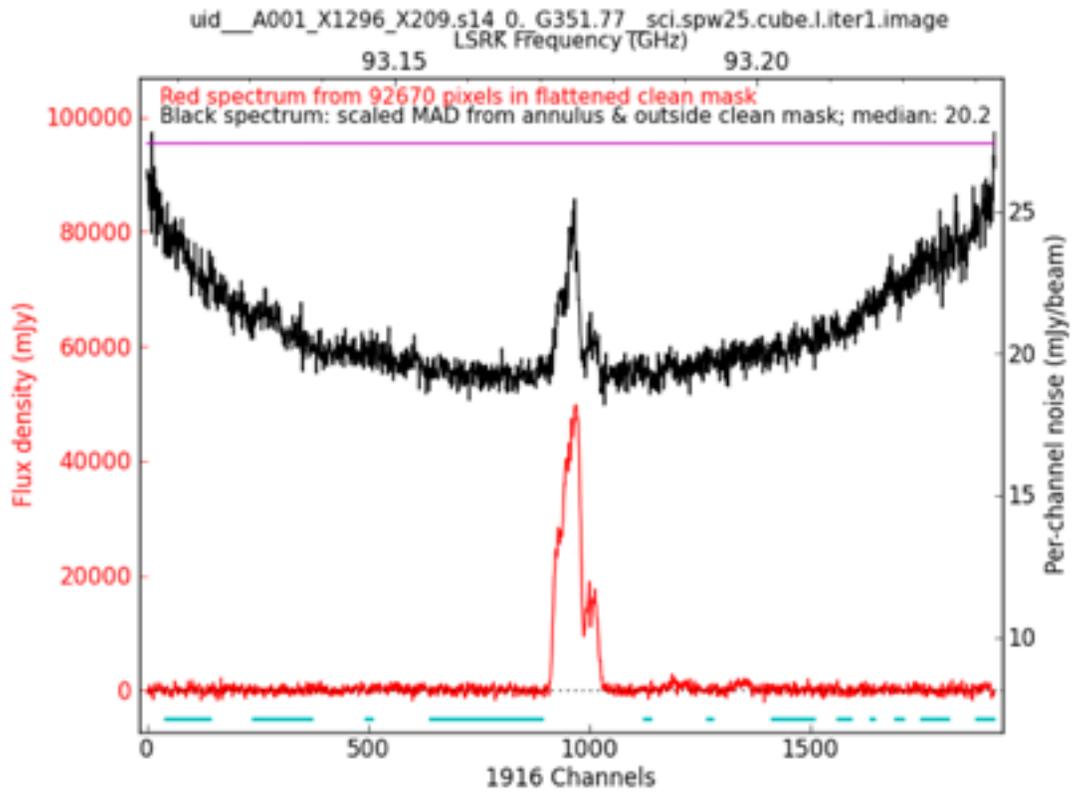
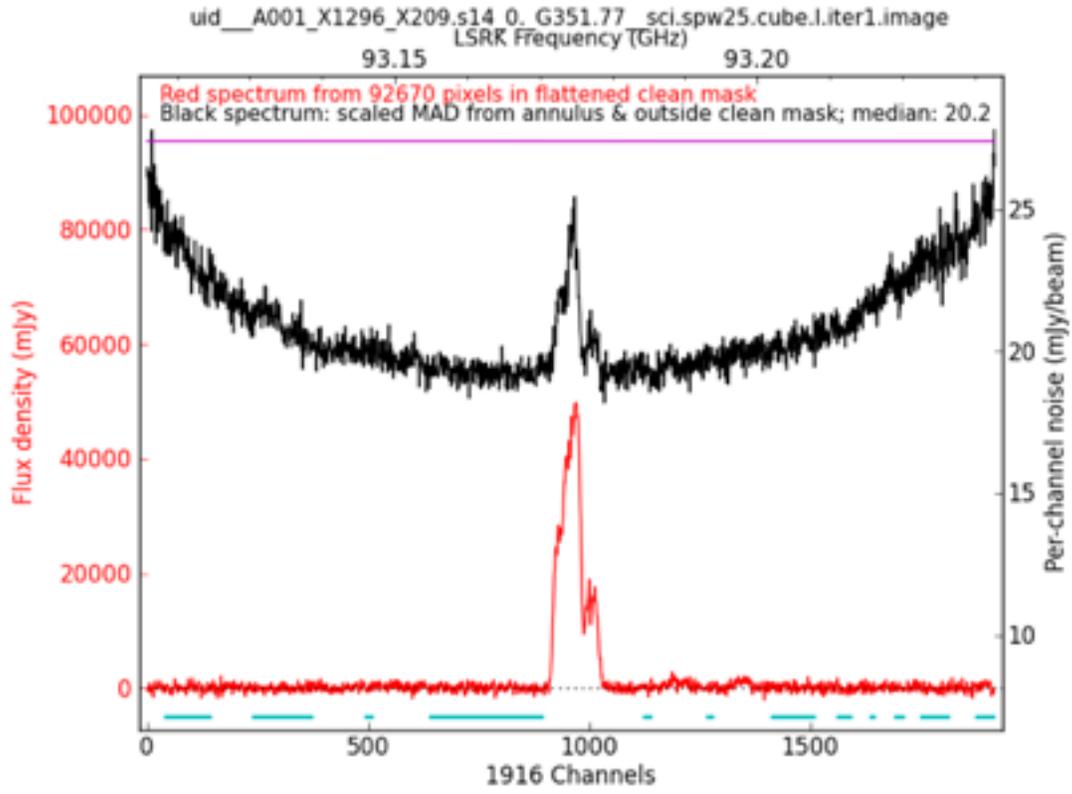


Figure 50: per-channel beams for a spectral window; perchanwt=False (left), and perchanwt=True (right)





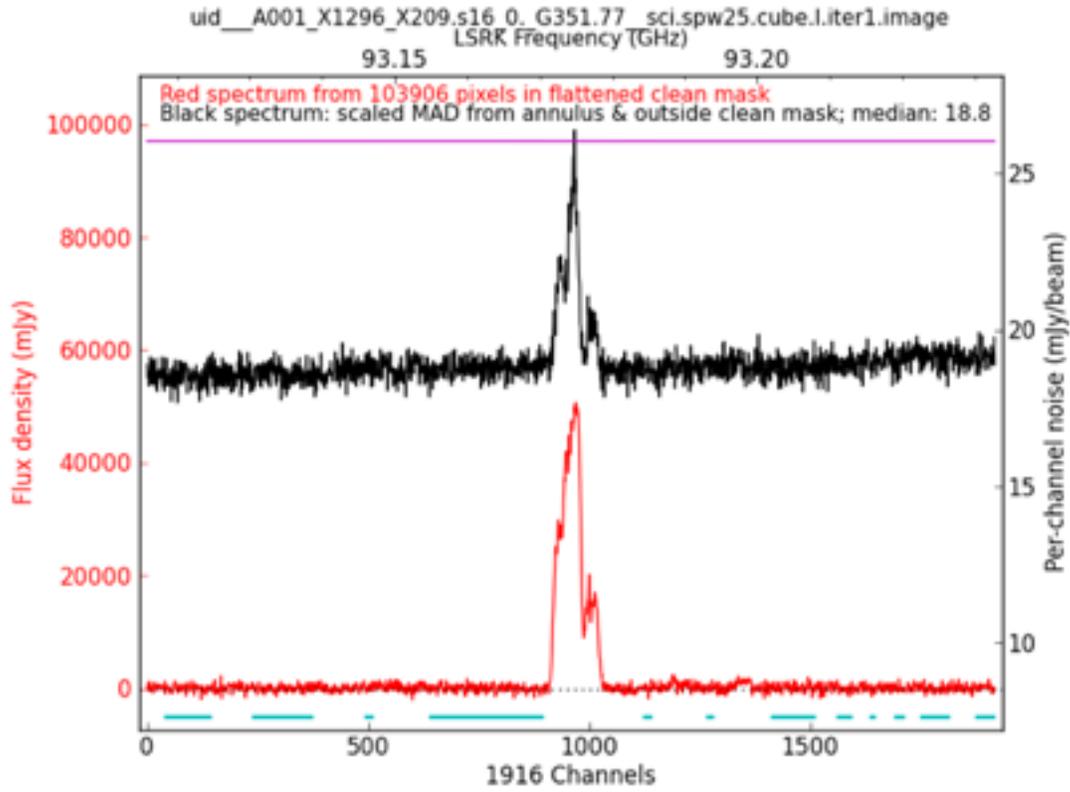
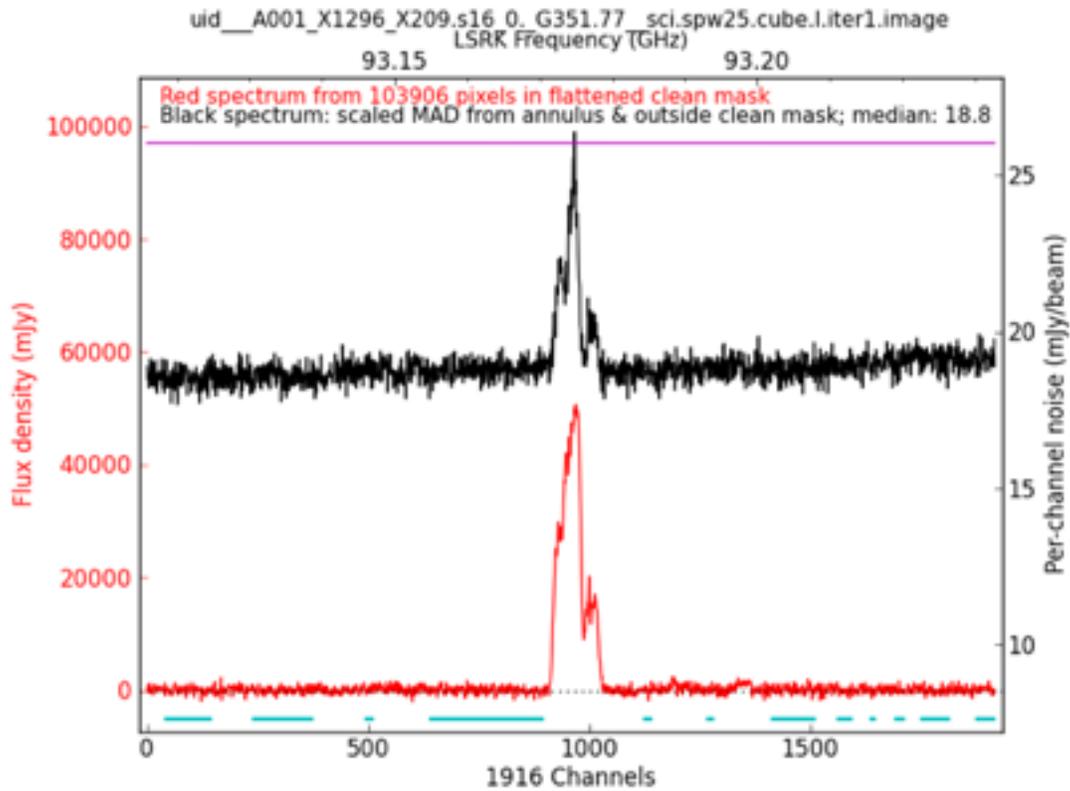


Figure 51: corresponding noise per channel of the same spw, with perchanwt=False (left), and perchanwt=True (right).



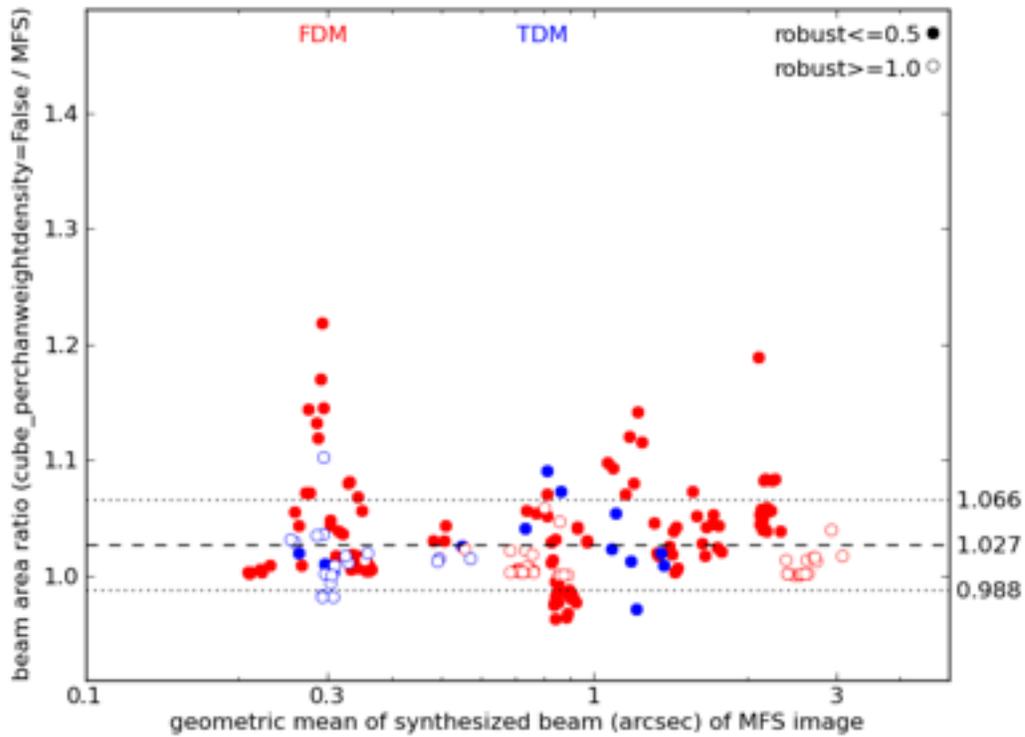
### 11.3 perchanwt=True beam size compared to perchanwt=False and mfs beam sizes

An mfs image of a given spectral window will use the (u,v) points corresponding to all channels to calculate image weights. Weights are calculated similarly for perchanweightdensity=False cubes. By contrast, **perchanweightdensity=True cube beamsizes are systematically larger than the corresponding mfs beamsizes for any value of robust < 2.0**, since only the smaller number of (u,v) points in one channel are used to calculate weights.

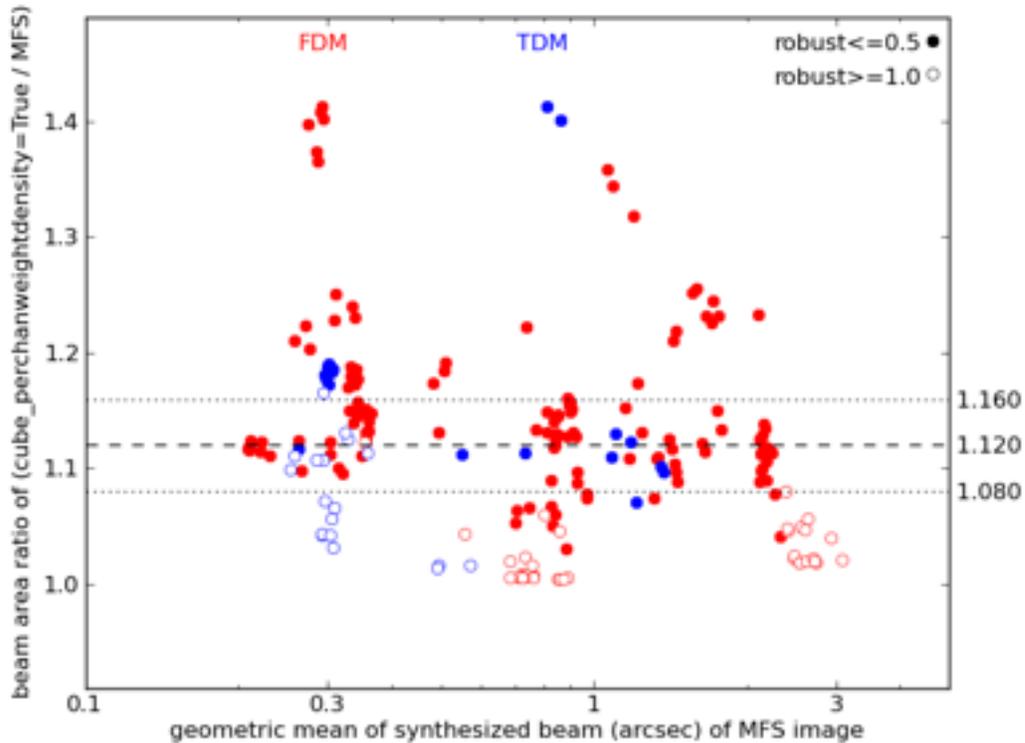
For the PLWG benchmark suite of datasets, selected to span ALMA parameter space, we have calculated cube (perchanwt=True, False) and mfs beam areas and rms in CASA 5.6 (**Error! Reference source not found.**). These plots distinguish between robust  $\leq 0.5$  (more uniform) and  $\geq 1.0$  (more natural).

It is also notable that using a more uniform robust for the cube compared to mfs cannot fix the situation. By its nature, perchanweightdensity=True has less dynamic range in the beam than perchanweightdensity=False with different choices of Briggs weighting, because fewer (u,v) points are available with which to adjust imaging weights.

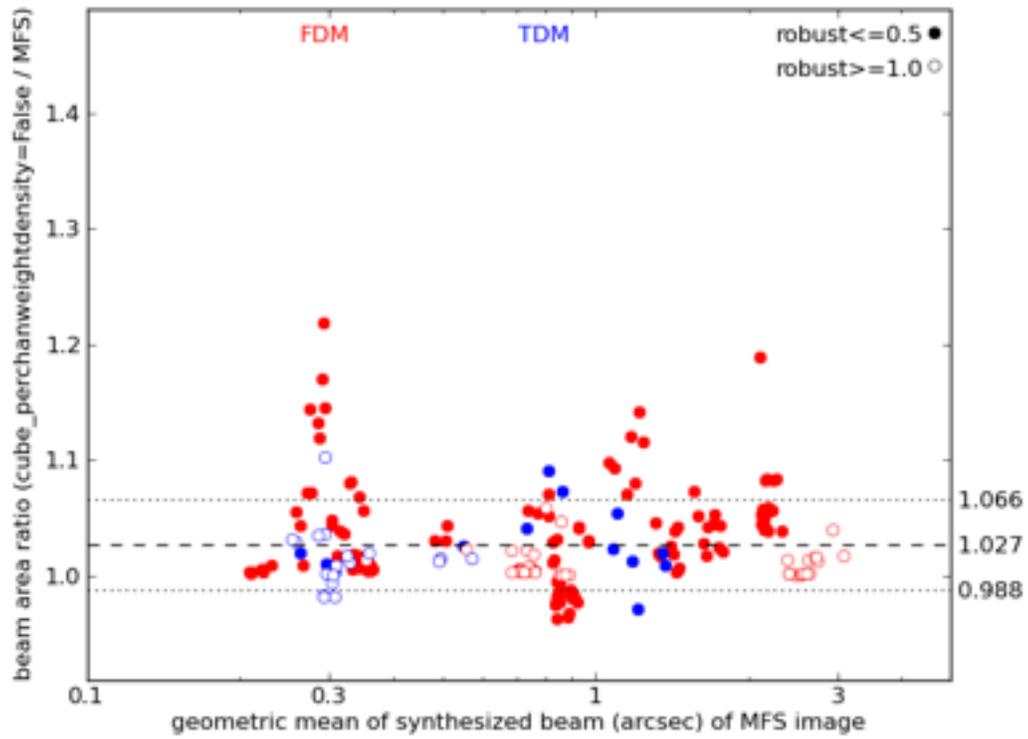
geo. mean beam ratio vs. mean MFS beam for 221 cubes from 12m array



beam area ratio vs. mean MFS beam for 221 cubes from 12m array



geo. mean beam ratio vs. mean MFS beam for 221 cubes from 12m array



beam area ratio vs. mean MFS beam for 221 cubes from 12m array

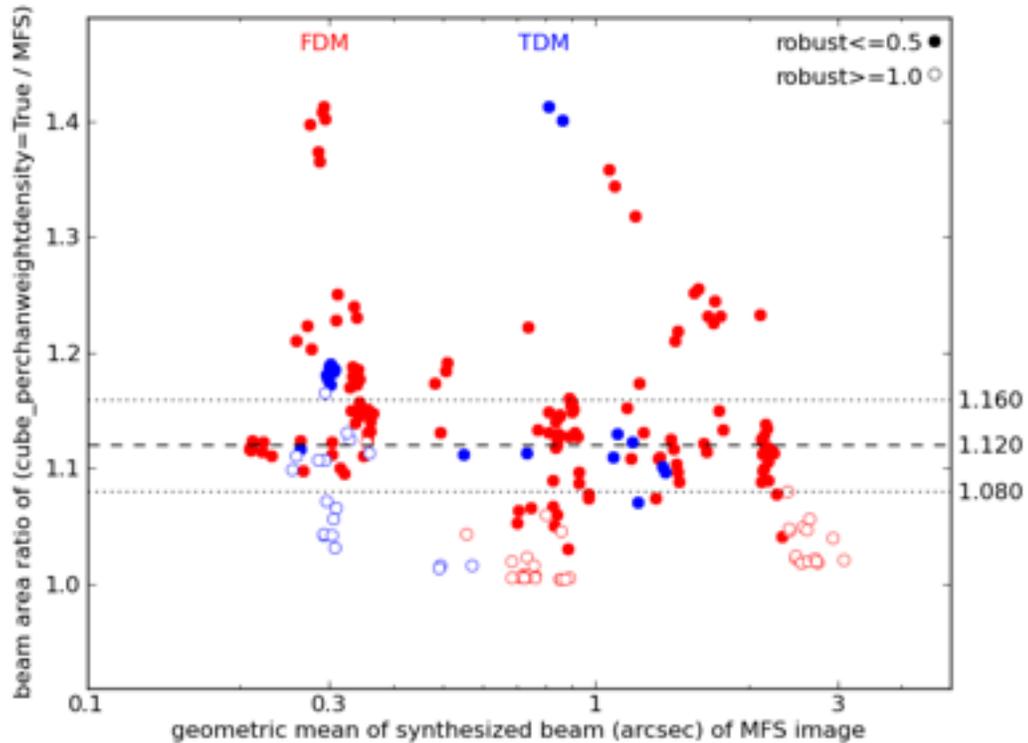


Figure 52: ratio of cube to mfs beam linear size with perchanwt=False, and perchanwt=True



The Atacama Large Millimeter/submillimeter Array (ALMA), an international astronomy facility, is a partnership of the European Organization for Astronomical Research in the Southern Hemisphere (ESO), the U.S. National Science Foundation (NSF) and the National Institutes of Natural Sciences (NINS) of Japan in cooperation with the Republic of Chile. ALMA is funded by ESO on behalf of its Member States, by NSF in cooperation with the National Research Council of Canada (NRC) and the National Science Council of Taiwan (NSC) and by NINS in cooperation with the Academia Sinica (AS) in Taiwan and the Korea Astronomy and Space Science Institute (KASI).

ALMA construction and operations are led by ESO on behalf of its Member States; by the National Radio Astronomy Observatory (NRAO), managed by Associated Universities, Inc. (AUI), on behalf of North America; and by the National Astronomical Observatory of Japan (NAOJ) on behalf of East Asia. The Joint ALMA Observatory (JAO) provides the unified leadership and management of the construction, commissioning and operation of ALMA.

