

Giant Metre-wave Radio Telescope (GMRT)

NCRA-TIFR

The GMRT Beam Monitor (GBMon ver2)

Standard Operating Procedure

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GBMon monitors the current state of beam-former data recording using the GMRT. This tool can be effectively used even by external users to monitor the data quality. Initial tests found that GBMon can run parallelly with the GMRT observations without hampering the data recording.

This SOP document explains the various available options to run GBMon for each of the selected beam. Provided that each selected beam is set to IA or PA mode with "Total Intensity" selected at interferometer acquisition.

GBMon can be run via the terminal or a GUI and a remote user can view GBMon's plot output on a web interface. GBMon can be used to monitor multiple beams simultaneously; for each beam, GBMon needs to be launched separately. The following steps need to be repeated for each beam. The product files, png images, and log files are generated at `/common-h10/gpuuser/gbmon/`.

Steps to follow before running GBMon

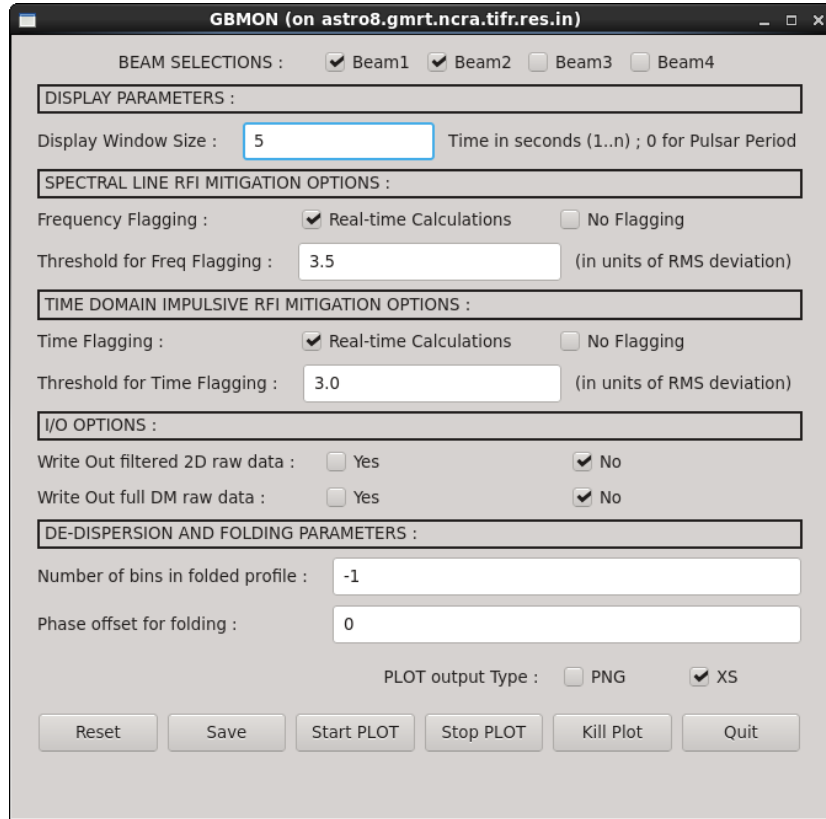
1. Log in as `cmcuser@192.168.70.2` machine on a terminal/konsole.
2. check that the following commands are already given into the "MNCScriptManager" either manually or by launching of automatically generated setup file for the pulsar observations as provided by GTAC or TEST observer. relevant beam information can be set using the following commands with their valid values accordingly.
 - (a) `set_gwb_beam`
 - (b) `set_gwb_beam_disk`
 - (c) `associate_gwb_beam`

Help to above commands can be seen using `"?"`.

GBMon via the GUI

GBMon can be run via a GUI. The GUIs for each beam are independent, and these can be run simultaneously without affecting each other. Follow these steps:

1. Log into the astro8 machine [ssh -X observer@astro8].
2. Depending on the desired beam, enter the command `gbmon_gui_beam<no.>`. This will open the GUI window, which looks like the following-



Example of GUI entries for GBMon

3. At the top "BEAM SELECTIONS" shows the beams that are currently acquiring data. This will be preset as per real-time beam parameters selections from TGC. This is just for information and it DOES NOT indicate the beams on which GBMon is running. That is determined by the number of beams at an instance while launching the GUI.
4. Here is a description of the parameters that the user can set-
 - Display window size: the duration of time considered for each plot window. This value is preset to 5 seconds. Enter 0 to set this parameter to the pulsar period.
 - Frequency Flagging: Real-time narrow band flagging ON or OFF (No flagging).
 - Threshold for frequency flagging: value in units of RMS deviation.
 - Time Flagging: Real-time wide band flagging ON or OFF (No flagging).
 - Threshold for time flagging: value in units of RMS deviation.
 - Write Out filtered 2D raw data: Yes or No.
 - Write Out Full-DM raw data: Yes or No.

- Number of bins in folded profile (-1 for native resolution).
- Phase offset for folding.
- Plot Output Type: ‘PNG’ saves the GPTool plots as images that can be viewed on the web interface (see below). ‘XS’ generates plots on the current desktop terminal/workspace. Only one option can be selected at a time.

5. Here is a description of the 6 buttons at the bottom of the GUI-

- Reset - Resets the changed parameters to default values.
- Save - Saves the parameters selection on GUI.
- Start Plot - Start GBMon for the beam mentioned in the GUI launch command (and not for all the beams selected in the ‘beam selections’). It will open a terminal window that will print GBMon run status.
- Stop Plot - currently disabled.
- Kill Plot - Kills the GBMon run of the current beam (abruptly).
- Quit - quit the interface.

As of now, since the ‘Stop Plot’ button is disabled, the user can stop GBMon by clicking on the xterminal window of the desired beam (opened after clicking on Start Plot) and pressing Ctrl+C. After this, click on ‘Kill Plot’. This brings the GUI back to its original state, ready to be used again. Please note that directly clicking on the Kill Plot button will abruptly stop GBMon and the saved directory and some files will not be saved correctly.

GBMon via terminal

Follow the given steps to run GBMon via terminal:

Method 1

To start GBMon on Beam host machines, log on to the terminal, and run the commands locally.

1. Log into one of the beam host machines, GWBH7, GWBH8, GWBH9 or GWBH10.
2. Edit the file `gptool.in.beam<no.>` in `/common-h10/gpuuser/gbmon/` where `beam<no.>` corresponds to the current host machine. The following parameters in this file need NOT be changed since they are read from the GMRT systems or the ATNF pulsar catalog: `beam mode`, `polarization mode`, `frequency band`, `bandwidth`, `sideband`, `number of channels`, `sampling interval`, `pulsar period` and `DM`. Rest of the parameters in `gptool.in` can be changed as per the need.
3. Run the command: `python /common-h10/gpuuser/pulsar/packages/gbmon_tests/gbmon.py`. This will launch GBMon in the beam corresponding to the current host machine.

Step 3 can be done from any directory in any of the beam host machines. At any time during GBMon's run, the user can interrupt using **Ctrl+C**. At the end of each GPTool run after pressing **Ctrl+C** (GBMon may keep running) the output and log files generated by GBMon will be saved in a suitable directory in `/common-h10/gpuuser/gbmon/`, identified by the date, timestamps, observation/gtac code and the beam number in that order.

e.g. `22feb2022_1834_1835_TST2523_beam1`.

Method 2

Using this user can start GBMon remotely using the command terminal on `cmcuser@192.168.70.2` (TGC Host machine). Note that, this method runs commands in the background and STDOUT/STDERR are logged on individual beam hosts. Log files can be visible at:

`/common-h10/gpuuser/gbmon/gbmon_stdout_beam<num>_<PROJ>_ddmmmyyyy.log`

1. Log in as `cmcuser@192.168.70.2` machine on a terminal/konsole.
2. In the command terminal enter the command `gbmon_tgc`, this will start the GBMon for each of the selected IA/PA modes on each individual beam host simultaneously.
3. Output of the command will be directly visible on the web interface, as mentioned below.
Webpage: <https://www.gmrt.ncra.tifr.res.in/~astrosupp/gbmon/psr.html>
4. This command runs GBMon for preset default values and also takes in the required real-time parameters from the shared memory of the GWB.

Using the web interface

Once GBMon is run from either the terminal or from the GUI (in any beam), the user can remotely monitor GBMon's live output plots, as well as replay past GBMon runs using the web interface. To see a given run of GPTool on the web interface, follow the given steps:

1. Open the webpage: <https://www.gmrt.ncra.tifr.res.in/~astrosupp/gbmon/psr.html>
2. Click on 'select profile'.
3. (i) To view older runs of GBMon, select the item in the list with the appropriate timestamps, gtac code, and beam number. Then click on the 'Start' button to play the GBMon plots from the start.
(ii) To view the current live run of GBMon, click on 'refresh', then select '`realtime_beam<number>`' for a particular beam. Then click on the 'Live' button to view the real-time display of GBMon. Other buttons on the webpage can be used to navigate between the individual plot frames as desired.

Note: The web interface shows only those GPTool runs for which the `gptool.in` parameter 'pg-plot display device type' is set to '`/png`'. This can be done either by editing `gptool.in_beam<no.>` (if GBMon is being run via terminal) or by using the GUI.

Another way to see png images without the web interface

If GBMon is run with the ‘/png’ parameter then the live images can be seen through the terminal without the web interface. Knowing the beam number, follow these steps:

1. Log in to one of the beam host machines: GWBH7, GWBH8, GWBH9 or GWBH10.
2. Enter the following command:

```
python /common-h10/gpuuser/pulsar/packages/gbmon_tests/gbmon_png_viewer  
/common-h10/gpuuser/gbmon/realtime.beam<number>
```

This will show the live png images being created. Users cant view saved png images of previous GBMon runs through this.

GBMON output files and logs

GBMon generates the files and directories for each relevant beam in the following formats on the beam host machine at /common-h10/gpuuser/gbmon/

1. `ddmmyyyy_hhmm.PRJCODE.beam<no>`: Directory containing o/p files and directories for each gbmon process. This directory is created while the pulsar scan is running.
2. `ddmmyyyy_hhmm1_hhmm2.PRJCODE.beam<no>` : Directory containing o/p files and directories for each gbmon process. This directory is created after the completion of the pulsar scan. Here, hhmm1 refers to the start time and hhmm2 refers to the stop time of the scan.
3. `gbmon_stdout.beam<no>.PRJCODE.ddmmyyyy.log` : Text file containing STDOUT/STDERR for each gbmon process when run from a remote host (e.g. TGC Machine).
4. `gbmon.log_ddmmyyyy_hh:mm`: Text file containing STDOUT for each gbmon process when run using local beam host or GBMon GUI from astro8.

Scope for control room user and remote user

Before GBMon can be run in any way, the user (through the telescope operators) needs to set up data acquisition for the desired source with the correct parameters. For a user in the control room, GBMon can be run at full capacity via either terminal or the GUI as explained above. In the ‘xs’ mode, the plots will be displayed on the current desktop while in the ‘png’ mode, the user can open the web interface to see the plots (or use the ‘gbmon_png_viewer’ as explained above).

For a remote user, however, it is only possible to see the GBMon plots via the web interface. The user can’t launch GBMon or control it. Hence GBMon has to be run with the ‘png’ option by the operators, and then the remote user can follow the steps mentioned in ‘GBMon via the web interface’.