

# GEM Commissioning Plan

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## 1 Purpose

The focus of this document is to plan to full procedure for the BigBite GEM commissioning with beam at the start of the GMn experiment in the SBS run program. The commissioning of the GEMs is essential for optics reconstruction. The successful commissioning of the GEMs implies an understanding of the internal alignment of the GEMs and an optimal gain setting with known efficiency.

## 2 Commissioning Tasks

### 2.1 HV scan

With the beam on at 5 uA on the single foil C target, all GEM layers should be turned on. The trigger should use the GMn1 configuration. GEM layers 1, 3, and 5 will be varied individually in voltage according to Table 1. GEM layers 2 and 4 will be varied individually in voltage according to Table 2.

Table 1: HV scan in UV and back tracker layers

Voltage	Expected Current [ $\mu$ A]
3720**	759.09
3697**	754.55
3653**	745.45
3608**	736.36
3564	727.27
3519	718.18
3475	709.09
3430	700.00
3385	690.91

Table 2: HV scan in XY (INFN) layers

Voltage	Expected Current [ $\mu$ A]	Trip Current [ $\mu$ A]
4150**	105.3	106.5
4100**	104.0	105
4075**	103.4	104.5
4050**	102.7	104
4025**	102.13	104
4000	101.5	102.5
3950	100.2	102
3900	98.9	100
3800		97.5

The expected current for the INFN GEMs is an average for all the chambers. There will be some variances per chamber around this value, but all should remain well under the trip limit. Additionally, the “\*\*” in

Tables 1 and 2 indicates an HV value that will be skipped unless it is later determined that we go back and find the efficiency at that voltage.

The trip level for UVa GEMs will always be set to **780  $\mu$ A**. The procedure for the HV scan is described:

1. Set the INFN GEMs to 4kV and the UVa GEMs to 3564 V.
2. Vary each layer individually according to the relevant table.
3. Run Andrew’s GUI analysis and record the efficiencies per layer
  1. From **a-onl**
  2. Type “gosbs”
  3. Run **panguin -r runnum -f bb\_gem\_for\_shiftcrew.cfg**
4. Plot the efficiencies per layer vs the voltage. Use the numbers generated by Fig. 1.
5. If the efficiency curve shows we are not in the plateau, then we may increase in 25 V increments.

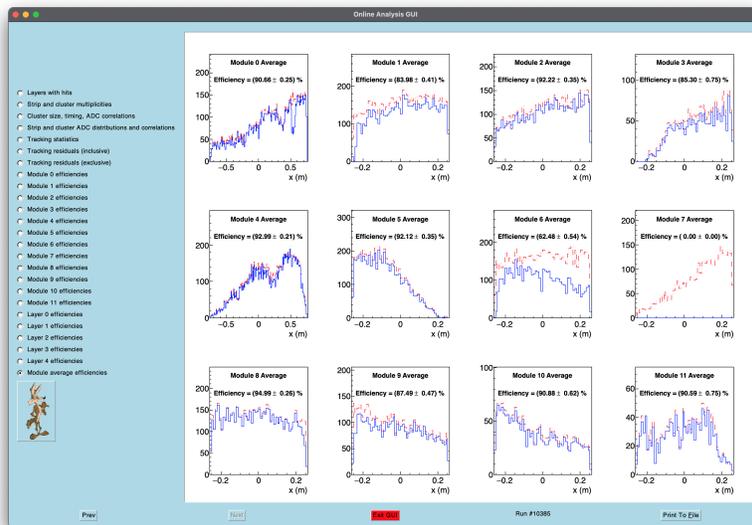


Figure 1: GUI used to record efficiency numbers. Note that Module 0 is Layer 1 UV, and Module 4 is Layer 3 UV. Modules 1-3 correspond to J0 (bot-mid-top) and Modules 5-7 correspond to J2 (bot-mid-top). Modules 8-11 correspond to the backtracker from top to bottom.

## 2.2 Replaying

To replay EVIO files:

1. log into aonlX under the a-onl account.
2. `cd $HOME/sbs/GEM_replay`
3. Execute a command with the following format: `./run_BBGEM.sh runnum seg_start seg_num prefix event_begin event_end pedestal_mode`
  - “runnum” is the CODA run number
  - seg\_start is the first evio file segment to analyze
  - seg\_num is the number of file segments to analyze
  - “prefix” is used to generate the EVIO file name. (Example values of “prefix” under the current CODA setup are “bbgem” or “e1209019\_trigtest”)

- event\_begin and event\_ means analyze starting and ending at these events
- pedestal\_mode is set to 0/1 (off/on) which disables tracking and triggers generation of pedestal diagnostic histograms and output text files for use in DAQ configuration and analyzer database

For example to replay a pedestal run execute:

```
./run.BBGEM.sh runnum 0 1 prefix 0 5000 1
```

The database used for the replay is located at /adaqfs/home/a-onl/sbs/sbs\_devel/SBS-replay/DB/db.bb.gem.dat. This contains the definitions of all the module alignments, pedestal files, and more. If any changes are made it must be recorded here.

## 2.3 Alignment

With the single carbon foil target and sieve installed, ramp BB magnet to off. Ask for a stable beam current of 1  $\mu$ A.

1. Log into a-onl@aonlX. The relevant script is at: \$SBS\_REPLAY/scripts/gems/GEM\_align.C
2. Replay the run using the GEMs-only replay.  
Replay should produce a file as **GEM\_alignment\_info\_bb.gem\_runXXXXX.txt**. This file contains the GEM position and angle information that the replay used (read from database) in the format the alignment script wants.
3. Setup the config file  
-In \$SBS\_REPLAY/scripts/gems there are files called “configalign\_bbgem\_XXX.txt” where XXX is a run number. Copy one of these files, and replace XXX with the run number you want to use for the alignment.  
-Copy-paste the information from “GEM\_alignment\_info...” produced by the replay into the alignment config file you want to use. This ensures that the starting positions and angles for the alignment match the ones used by the replay.  
-You may also need to tweak the global cut used to select tracks for the alignment. The chi2 cut and number of tracks cut and track number of hits cut might need to be adjusted depending on the quality of the initial alignment. For now, include a cut **bb.gem.track.nhits>=4**.  
-Put the list of root files to be included in the alignment at the top of the file before the keyword “endlist”.
4. **.L gems/GEM\_align.C+**
5. **GEM\_align(“configfilename.txt”);**  
This will start the alignment process. You will get many output files including:  
-**GEM\_align\_results\_bb.gem.root** where you can see the quality of the results before replaying.  
-**newGEMalignment.txt** contains the alignment results in the format needed for the alignment script itself (units are meters, radians).  
-**db\_align\_bb.gem.dat** contains the alignment results in the format expected by the analyzer database. This should be copy-pasted into the database. Note that the analyzer expects angles in degrees.