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Version : 2.0

2 ant IA POCKET BEAMFORMER

Note : This colour : used for Main titles.
This colour : used for sub/sub-sub titles.
This colour : used for command lines.
This colour : used for the response from the ROACH or PC.
This colour : used for procedure writeup/information/note.

[CTRL_PC] : 192.168.4.68
[USER_CTRL_PC] : gmrt
[CTRL_PC_PASS] : gmrttifr
[PYTHON_DIR] : /home/gmrt/

1. Power ON and instrument settings :

(a) Power on Distribution boards , AC distribution boards in the RACK
(verify : PC , ethernet swithces & ROACH Units are powered ON).
(b) Now Switch ON the instruments and do the following settings -
(i) Signal generator settings as CLOCK to F engine ROACH boards : Freq = 600MHz , Power = 0dbm, Set “Mod to OFF and RF to ON”
(c) Power “ON” the ROACH boards by pressing the switch at front panel. All Roach boards will boot through NFS (Network File System) on control PC {192.168.4.68}.

2. Interconnections :

1. Connect the clock signal available at top of the rack to ROACH unit clk_i input of iADC.
2. Either connect 32MHz or Broadband analog signals or Noise Source through 200 MHz LPF, Total Power over BW between -14dbm to -17dbm to iADC's inputs.

3. Initialization :

Follow these steps to initialize the ROACH board and load the design :

```
ssh -X gmrt@192.168.4.68
gmrt@ctrlpoco$ cd ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/python_scripts/
#Do the following changes according to your requirements in the script.
python_scripts$ vim ./pobe_incoh_2k.py
my_corr.write_int("acc_cntrl_int_time",512)
#int. time for Beamformer-IA (1024 for 600MHz clock & 512 for 400MHz clock).
my_corr.write_int("Input_mux",0)
#use 1 for digital noise and 0 for analog noise(ADC input). Change the Input_mux to 0 for ADC input.
python_scripts$ ./pobe_incoh_2k.py
```

4. Check packets :

gmrt@ctrlpoco$ cd ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/python_scripts/

python_scripts$ sudo wireshark

To check whether packets are reaching the PC from ROACH. "The Wireshark Network Analyzer" window opens !
Select Capture/Interfaces in the Menu. Another window "Wireshark: Capture Interfaces" opens!
Observe at Packets and Packets/sec. Counts here shows packets are being received (0 for no packets received).
Select File/Quit to exit !

5. Dump packets using Gulp :

Set the number of packets to be captured.
gmrt@ctrlpoco:$ cd /data/Gulp/

gmrt@ctrlpoco:/data/Gulp$ vim gulp.c
int num_packets = -1; /* number of packets to capture change to -1 to capture till ctrl+c* or any number to capture those many packets/
gmrt@ctrlpoco:/data/Gulp$ sudo make
This needs to be done only if gulp.c is modified.

gmrt@ctrlpoco$ cd ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/python_scripts

python_scripts$ sudo /data/Gulp/gulp -i eth2 > ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz_14122012.dat
This runs the gulp from /data/Gulp area and dumps the data packets being received in the area /home/gmrt/ BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/

6. Depacketize the dumped data using c program :

gmrt@ctrlpoco$ cd /home/gmrt/BeamForm_test/Cambodge/Depacketisation_Scripts/c_files/
vim file_fast.c #edit as per your requirement explained below.

fprintf(ha,"%u\n",v);
// remove comment to make the o/p ASCII file plotable by GNUPLOT IMH/KDB.

fwrite(&v,sizeof(v),1,ha);
// remove comment to make the o/p BINARY file plotable by PMON IMH/KDB.

To create exe file after changes ;
2antenna$ gcc -o file_fast.o file_fast.c

Usage : ./file_fast.o <Dump_filename> <OUTPUT_filename> <Packet_size> <Scaling_factor>

This Depacketizes the *.data file in to *.out file with packet_size of 2k and scaling factor of 1k.

2antenna$ ./file_fast.o ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz/150mhz_14122012.dat1 ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz/150mhz_14122012.out 2048 1024

2antenna$ /home/gmrt/BeamForm_test/URG/file_fast.o ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz/150mhz_14122012.dat1 ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz/150mhz_14122012.out 2048 1024

7. Plot the Depacketized OUTPUT_file using GNUPLOT.

gmrt@ctrlpoco:$ cd ~/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/python_scripts

python_scripts$ gnuplot

gnuplot> plot "/home/gmrt/BeamForm_test/Cambodge/PoBe_Incoherent/2antenna/150mhz_14122012.out1" w l

In this data we have fed 150mhz , so the tone appears in the channel 384 {(512/200)*150}.
No extra peak appears in the spectrum.

8. Plot the Depacketized OUTPUT_file using pmon.

NOTE : DO NOT USE PMON on GSB cluster while GMRT OBSERVATIONS AND / OR SOFTWARE TESTING RELATED WORKS ARE GOING ON. IT MIGHT CREATE PROBLEMS LIKE BUFFER LOSS.

Step 1 : For using PMON utility you need to first install PMON software in your machine or you can login to machine in which PMON is already installed.

In GMRT, PMON is installed on machine gsbm3.

a] open a terminal and type following command :
ssh -X gsbuser@gsbm3
b] enter the password : gmrt.123

Step 2 : Create your own directory in the below mentioned area to store your data.

a] type following command :
cd /mnt/b/gsbuser/

b] mkdir <dir_name>

Step 3 : To use PMON at least 3 files must be present in your current directory namely,

i] pmon.in
ii] raw.hdr
iii] file that contains the actual data that you want to dedisperse
e.g. PulsarB1133+16.raw

A] pmon.in :

This file is divided into two parts using ':' to left of which you need to enter specifications. The R.H.S part just describes what you have to enter. You don't modify this R.H.S part. This file can be edited according to your specifications.

e.g. : vi pmon.in

```
2.62144,591.0,200.0,+1          : Sample Interval (millisec), Center Freq (MHz), BW (MHz) & Sideband flag
                                  (+1/-1).
512,2,90          : Total # of Freq Channels, Start & Stop Freq Ch #s to use.
512               : Reference Ch # for De-dispersion.
1.0,0.1           : Time Interval per plot, Time Interval between updates (both in secs).
2.5               : Time Interval for Fold/Spectral updates (in secs).
0,0,0.0           : Start Block # , Total # of Blocks and fraction of blocks to be skipped (give  0,0,0.0 for
                    doing entire file).
B1133+16          : Source name with or without J/j/B/b prefixed.(This gets ignored if name passed at
                    command line)
60,12,12          : N_Span (min), N_Coeff, Max_HA for the Polynomial coefficients in the polyco.dat.
-1                : DM (pc/cm^3) for de-dispersion: For acquiring DM using Catalogue give  a # <  0.0
-1                : period  (millisec) for folding: For acquiring period using Catalogue give a #  <= 0.0
1.0,1.0           : Expansion factor for time plot, Expansion factor for folded profile.
0.0,0.0           : Phase offset for markers & Initial Phase Offset for folding (in units of true sample).
0.0,0.0           : Zoom-in: Start & Stop Xaxis Fraction for profile/spectrum plots(use 0,0 for full range).
0                 : Domain of Folding : Time(0) / Freq(1).
4,4               : # of Polarization added in the GAC data, # of integration in the DSP.
2                 : # of Bad Bands: If its 'N' then list the start & stop chan # for each band in next N lines.
1,4               : Start Chan # , Stop Chan # for Bad Band 1.
253,256           : Start Chan # , Stop Chan # for Bad Band 2.
```

B] raw.hdr :

This file must be edited according to your timing specifications. This file contains date and time of your data recording. If required copy the *.hdr file as raw.hdr.

e.g. vi raw.hdr

#Start time and date
IST Time: 11:50:25.178647040 -> here enter time as precise as possible.
Date: 21:09:2011 -> here enter date
#Start ACQ SEQ NO = 12621 -> keep as it is.

C] File containing data to be dedispersed :

Copy your file containing data to dedispersed e.g PulsarB1133+16.raw in your directory.

Case i] if your original data file is present in same machine where pmon is installed use following command :

mv /dir1/dir2/filename /mnt/b/gsbuser/yourdir/filename

in above command you enter the actual directory names and file names

case ii] if your original data file is present in other machine use following command :

scp username@ipaddress :/dir1/dir2/filename /mnt/b/gsbuser/yourdir/filename

Step 4 :

Now type :

pmon -f filename -s sourcename

e.g. pmon -f PulsarB1133+16.raw -s B1133+16

after ' : ' type following command and press 'enter'
/xs

You will see the profile in PGPLOT window which will consist of 4 subplots:

1] chart record of dedispersed data -- time vs signal amplitude.

2] Bandshape -- frequency vs bandshape amplitude.

3] Folded profile (cumulative)v -- pulse phase vs profile amplitude.

4] Folded profile (current) -- pulse phase vs profile amplitude.

Ctrl + c will stop this pmon plot. This will create a file profile.dat. This is best profile file which can be plotted using gnuplot.