

# SEISMIC UNIX

by  
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# 1. Reformat

`segypread tape=data.sgy | segyclean>data.su`

input

output

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## Trace Data viewing

□ We have two types of plotting seismic data:

□ **wiggle** view : traces are plotted as lines, with peaks and troughs.  
The peaks are filled with color – usually black- to make it easily distinguished.

□ Variable density – **image** - : use color scale to represent peaks and troughs .  
Might be colored or gray scale.

## 2. suxwigb

### Suxwigb < input [options] 2

- ❑ The command need an input , but no output file.
- ❑ Options include :
  - ❑ title : The name of the plot
  - ❑ label1 : label on axis 1 – y axis –
  - ❑ label2 : label on axis 2 – x axis –
  - ❑ other options can be found by typing : xwigb in the terminal

## 3. suximage

### Suximage < input [options] 3

- ❑ The command need an input , but no output file.
- ❑ Options include :
  - ❑ title : The name of the plot
  - ❑ label1 : label on axis 1 – y axis –
  - ❑ label2 : label on axis 2 – x axis –
  - ❑ cmap=rgb'n' : color map in Red-Green-Blue form , n is a no.
  - ❑ other options can be found by typing : ximage in the terminal

## 4.Data Selection

- ❑ If there are a lot of data we can Select some shots from the hole line by using the command:

❑ **suwind < (input file) key=ep min=1 max=6 > (output file)** 4

Where:

ep: energy source point number

- ❑ Then display the selected shots by using the Trace Data viewing commands

# QC Seismic Data

## Trace Header

Key	Definition
dt	sample interval in microseconds
ns	number of samples in this trace
ntr	number of traces
offset	offset
traci	trace sequence number within line
tracr	trace sequence number within reel (entire data set)
tracf	trace sequence number within field record (gather)
Sx /Gx	Source/receiver x location
cdp	Common mid point number
Fldr	Field record number – shot no.-



## **Surange < input [option] > output 5**

- ☐ The input is your seismic data file “.su”
- ☐ The output is a text file , also you may leave it with no output, values will be printed to your terminal
- ☐ Options :
  - ☐ Key=[header value]  
In case you want to look at one key header only
  - ☐ The output will be :
    - No. of traces
    - Header word [min value] [max value] (first-last)

## **Delete Header**

**SUSTRIP < INPUT FILE > OUTPUT FILE 6**

**THE OUTPUT DATA WILL BE WITH NO HEADER.**

# Set a New Header

- ❑ first step: Add ns (number of sample)

**suaddhead < input file ns= > output file** **7**

- ❑ input files: stripped file.
- ❑ ns: number of samples (1501).
- ❑ Then view the new trace header using:
  - ❑ **Surange < input.**

- ❑ Second step: Set one or more header word

**sushw < input file key=sx or gx (optional parameters) > output file** **8**

- ❑ The **sushw** command used to set new header words, using the stepping trace number in the calculations, this is very useful if a mistake was made when creating the header in the field.
- ❑ input file: the output file from the add ns step (first step).
- ❑ Optional parameters include:
  - ❑ key=,... header key word(s) to set
  - ❑ a=0,... value(s) on first trace
  - ❑ b=0,... increment(s) within group
  - ❑ c=0,... group increment(s)
  - ❑ d=0,... trace number shift(s)
  - ❑ j=0,... number of elements in group



```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sushw < addhead.su key=dt,sx,offset a=4000,6400,200 b=0,0,200
c=0,-100,0 j=0,32,32 > addhead1.su

processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sushw < addhead.su key=dt,sx,offset a=4000,6400,200 b=0,0,200
c=0,-100,0 j=0,32,32 > addhead1.su
[ ~/Desktop ] $ surange < addhead1.su
594 traces:
trac1      1 594 (1 - 594)
trid       1
offset     200 6400 (200 - 3600)
sx         4600 6400 (6400 - 4600)
ns         1501
dt         4000

Shot coordinate limits:
          North(6400,0) South(6400,0) East(6400,0) West(4600,0)

Midpoint coordinate limits:
          North(3200,0) South(3200,0) East(3200,0) West(2300,0)
[ ~/Desktop ] $
```

❑ Third step: change header word using one or two header word

**suchw < input file key1= key2= key3= a= b=... > output file**

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❑ The **suchw** command used to change or create new header words, based

on existing header word values  $\text{val}(\text{key1}) = (a + b * \text{val}(\text{key2}) + c * \text{val}(\text{key3})) / d$

❑ input file: the output file from the **Sushw** step (second step).

❑ Optional parameters include:

❑ key1= output,... header key word(s) to set

❑ Key2 and key3: input header key word(s)

❑ a=1,... overall shift(s)

❑ b=1,... scale(s) on first input key(s)

❑ c=1,... scale on second input key(s)

❑ d=2,... overall scale(s)





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```
[ ~/Desktop ] $ suchw < addhead1.su key1=gx key2=offset key3=sx b=1 c=1|suchw key1=cdp  
key2=gx key3=sx b=1 c=1 d=2 > addhead2.su
```

```
[ ~/Desktop ] $ surange < addhead2.su
```

594 traces:

```
trac1      1 594 (1 - 594)  
cdp        4700 9600 (6500 - 6400)  
trid       1  
offset     200 6400 (200 - 3600)  
sx         4600 6400 (6400 - 4600)  
gx         4800 12800 (6600 - 8200)  
ns         1501  
dt         4000
```

Shot coordinate limits:

North(6400,0) South(6400,0) East(6400,0) West(4600,0)

Receiver coordinate limits:

North(6600,0) South(6600,0) East(12800,0) West(4800,0)

Midpoint coordinate limits:

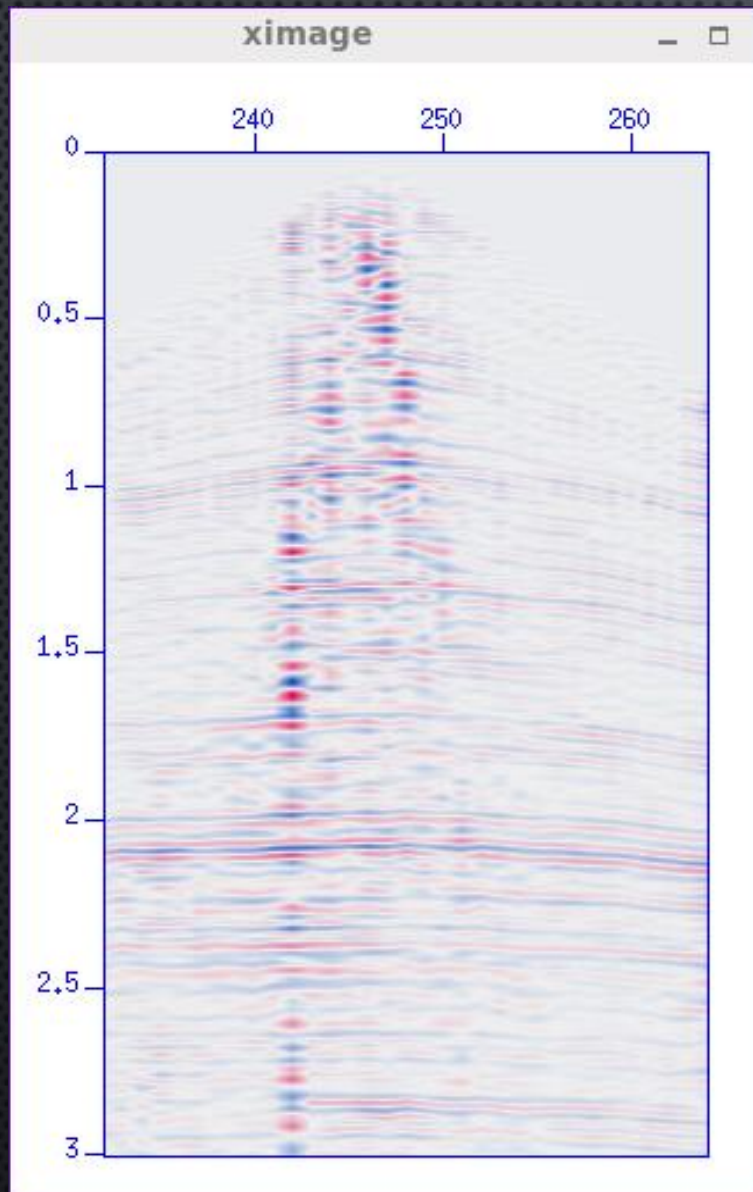
North(6500,0) South(6500,0) East(9600,0) West(4700,0)

```
[ ~/Desktop ] $
```

# GAIN

## sugain

- THE **SUGAIN** COMMAND IS USED TO PERFORM BOTH,  $T^2$  GAIN AND AGC, BY USING THE CORRECT OPTIONS.
- **TO APPLY  $T^2$  METHOD :**
  - **SUGAIN < INPUT TPOW=2 > OUTPUT** 10
  - TPOW = : YOU CAN CHANGE THE VALUE, IT DON'T HAVE TO BE 2 , YOU CAN TRY {1,1.5,2,2.5,3....}
- **TO APPLY AGC METHOD :**
  - **SUGAIN < INPUT AGC=1 WAGC=0.5 JON=1 > OUTPUT** 11
  - AGC=1 WILL TELL SUGAIN TO USE AGC.
  - WAGC= : SPECIFY THE WINDOW FOR AGC.



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File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < shot.8 tpow=2 > shotgain.8
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < shot.8 tpow=2 > shotgain.8
```

```
[ ~/Desktop ] $
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

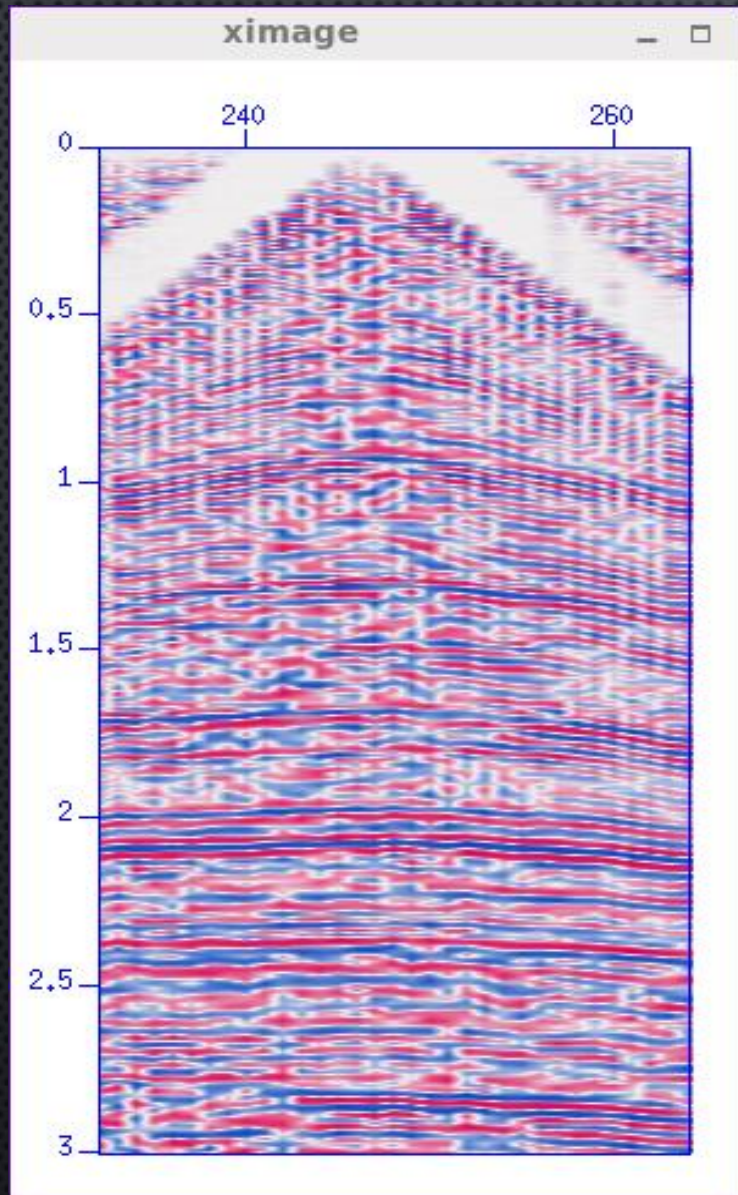
```
[ ~/Desktop ] $ sugain < shot.8 tpow=2 > shotgain.8
```

```
[ ~/Desktop ] $ suximage < shotgain.8 &
```

```
[1] 8238
```

```
[ ~/Desktop ] $
```





processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < shot.8 agc=1 wagc=.5 jon=1 > shotagc.8
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < shot.8 agc=1 wagc=.5 jon=1 > shotagc.8  
[ ~/Desktop ] $
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < shot.8 agc=1 wagc=.5 jon=1 > shotagc.8  
[ ~/Desktop ] $ suximage < shotagc.8 &  
[1] 8487  
[ ~/Desktop ] $
```

# AGC Script

❑ Used to run group of commands at the same time.

❑ Use **gedit (file name).txt** command to create the script file.

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❑ Write in the text file the following commands:

Sugain < input agc=1 wagg=.5 | suxwigb or suximage title=wagg .5 &

Sugain < input agc=1 wagg=1 | suxwigb or suximage title=wagg 1 &

Sugain < input agc=1 wagg=1.5 | suxwigb or suximage title=wagg 1.5 &

Sugain < input agc=1 wagg=2 | suxwigb or suximage title=wagg 2 &

❑ press save and exit the text file.

❑ activate your terminal and recall the text file using **chmod 776 (file name .txt)** command.

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❑ to run the commands in the text file use **./(file name.txt)** command.

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\*gain.txt (~/Desktop) - gedit

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Open Save Undo

\*gain.txt X

```
sugain < shot.8 agc=1 wagc=.5 | suximage title=wagc.5 &  
sugain < shot.8 agc=1 wagc=1 | suximage title=wagc1 &  
sugain < shot.8 agc=1 wagc=1.5 | suximage title=wagc1.5 &  
sugain < shot.8 agc=1 wagc=2 | suximage title=wagc2 &
```

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processing@localhost:~

File Edit View Search Terminal Help

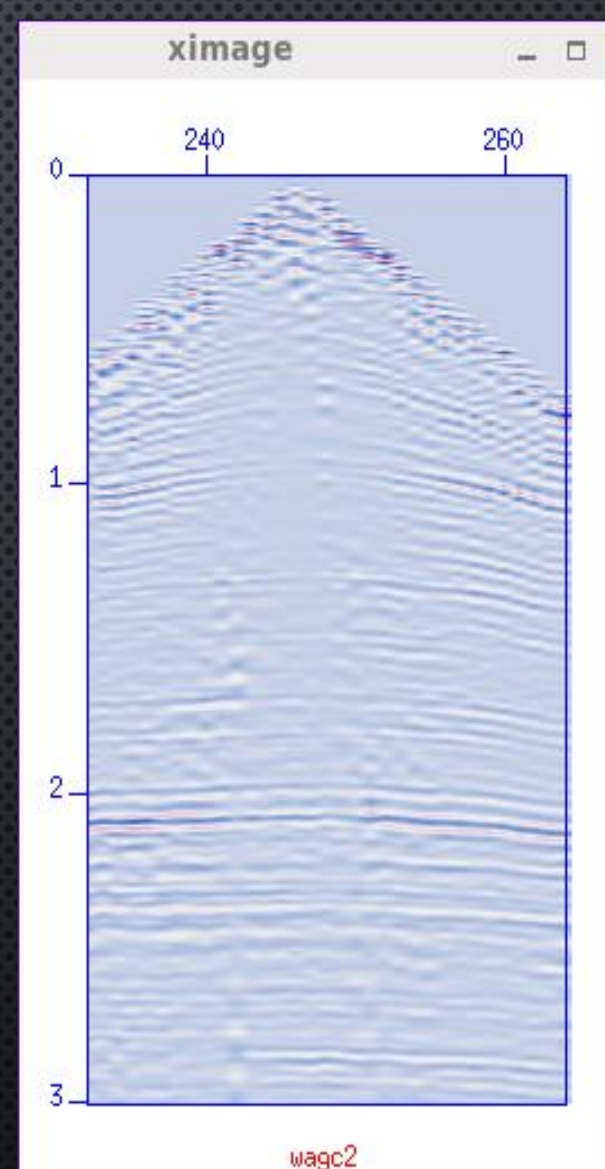
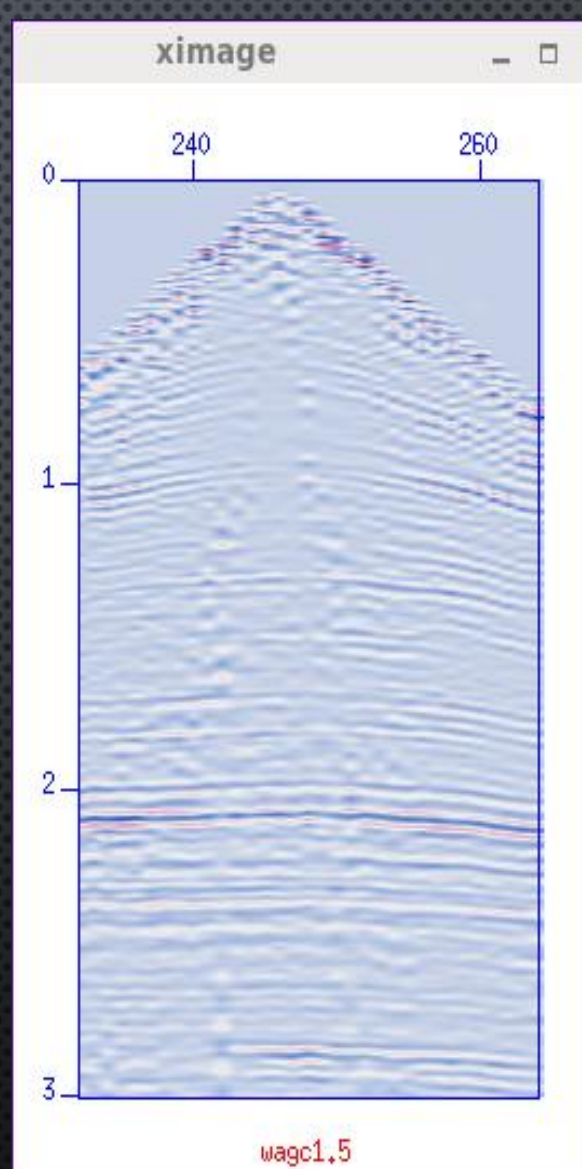
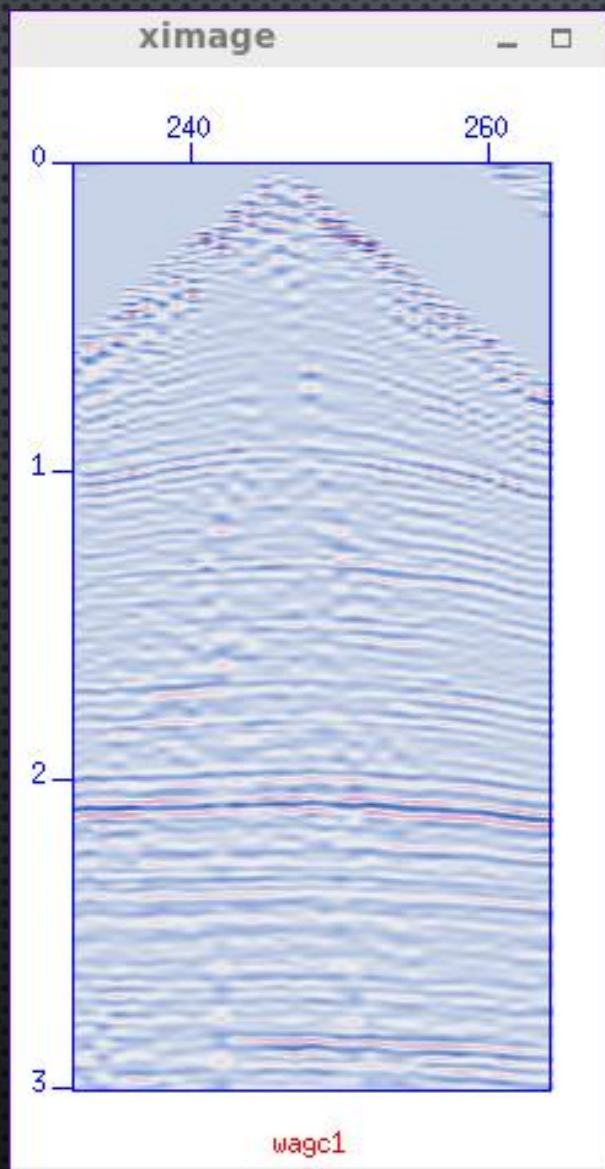
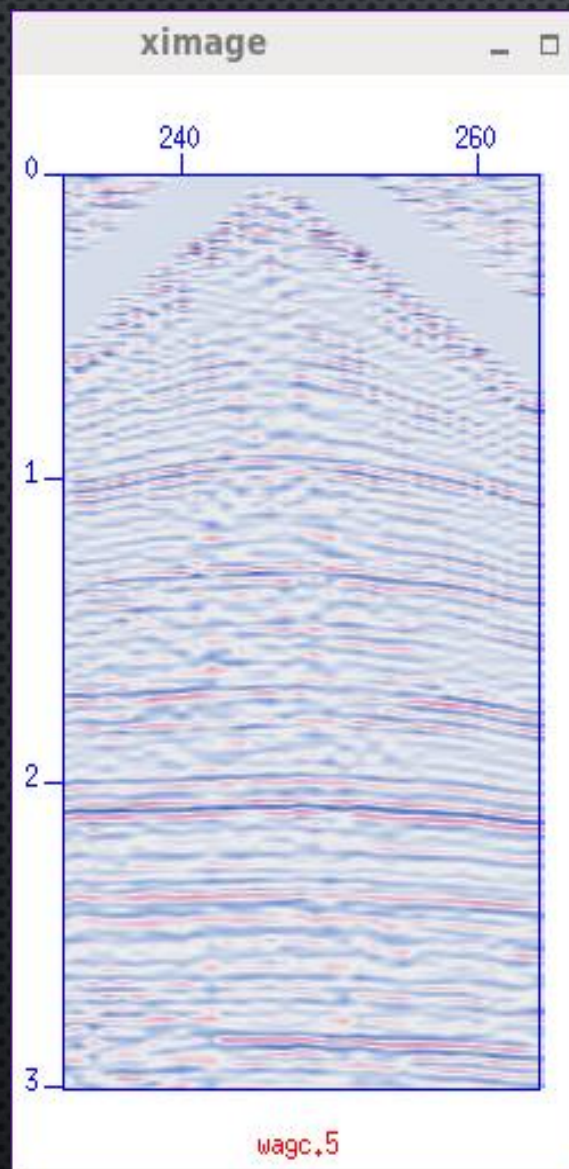
```
[ ~/Desktop ] $ gedit gain.txt
```

processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ gedit gain.txt  
[ ~/Desktop ] $ chmod 776 gain.txt  
[ ~/Desktop ] $ ./gain.txt
```


















## t^2 gain Script

- ❑ Used to run group of commands at the same time.
  - ❑ Use **gedit (file name).txt** command to create the script file.
  - ❑ Write in the text file the following commands:  
Sugain < input tpow=1 | suxwigg or suximage title=tpow 1 &  
Sugain < input tpow=1.5 | suxwigg or suximage title=tpow 1.5 &  
Sugain < input tpow=2 | suxwigg or suximage title=tpow 2 &  
Sugain < input tpow=2.5 | suxwigg or suximage title=tpow 2.5 &
  - ❑ press save and exit the text file.
  - ❑ activate your terminal and recall the text file using **chmod 776 (file name .txt)** command.
  - ❑ to run the commands in the text file use **./(file name.txt)** command.

 \*gain.txt (~/Desktop) - gedit


File Edit View Search Tools Documents Help

 Open  Save   Undo      

\*gain.txt X 1.txt X


```
sugain < shot.8 tpow=1.5 | suximage title=tpow1.5 &  
sugain < shot.8 tpow=1.8 | suximage title=tpow1.8 &  
sugain < shot.8 tpow=2 | suximage title=tpow2 &  
sugain < shot.8 tpow=2.5 | suximage title=tpow2.5 &
```

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 processing@localhost:~

File Edit View Search Terminal Help

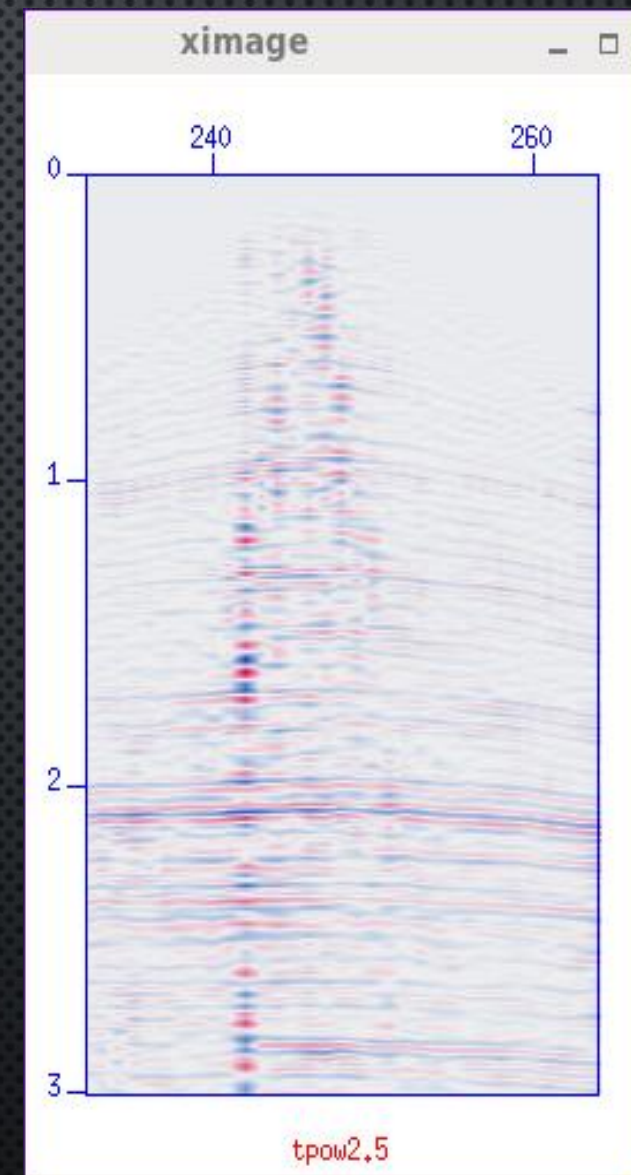
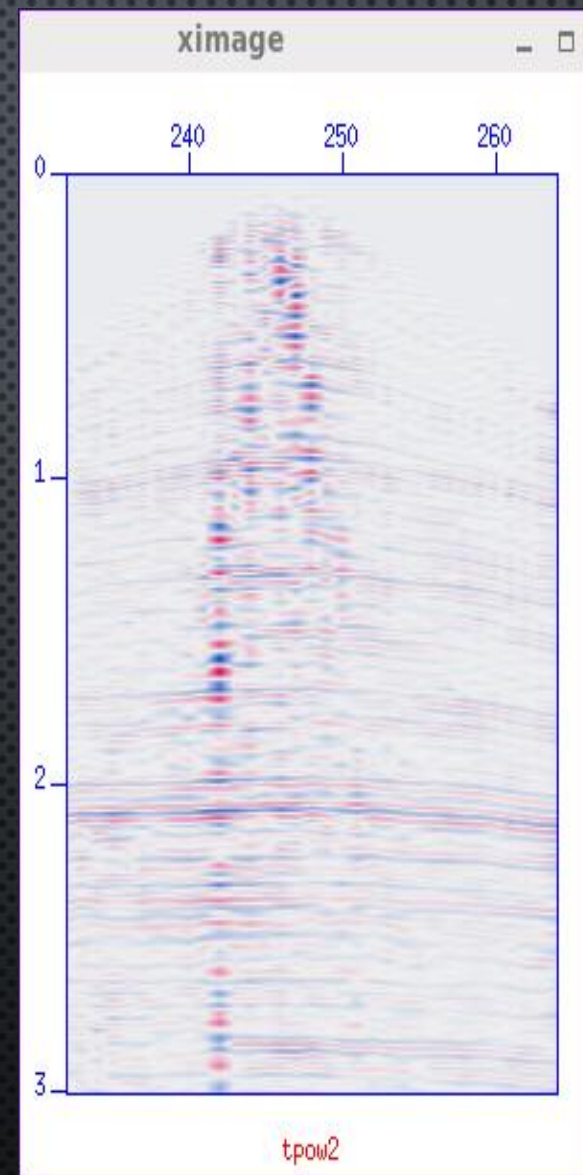
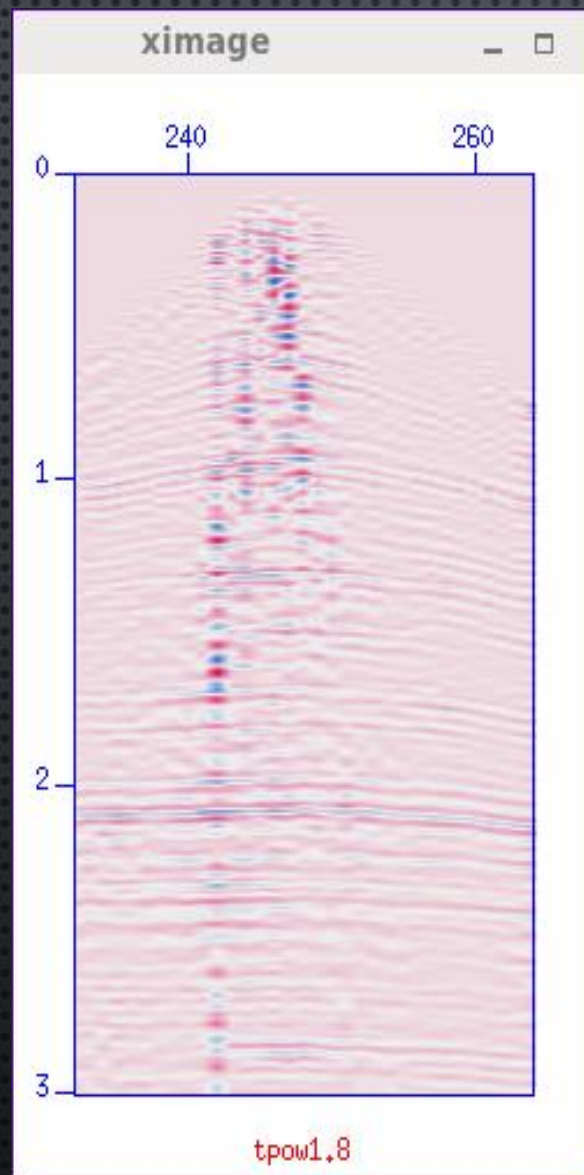
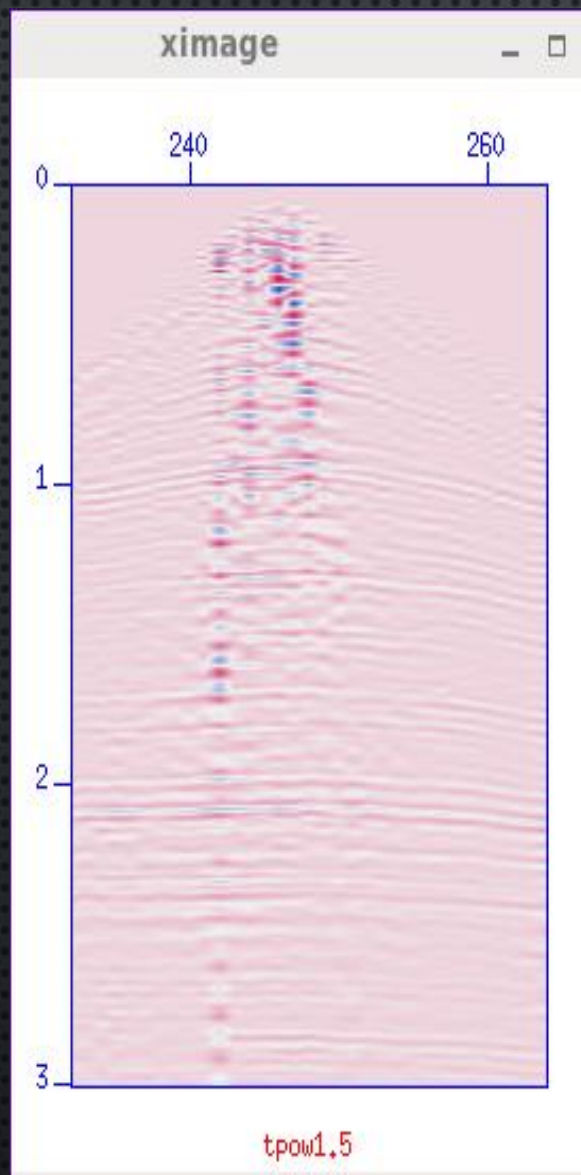
```
[ ~/Desktop ] $ gedit gain.txt
```

 processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ gedit gain.txt  
[ ~/Desktop ] $ chmod 776 gain.txt  
[ ~/Desktop ] $ ./gain.txt
```





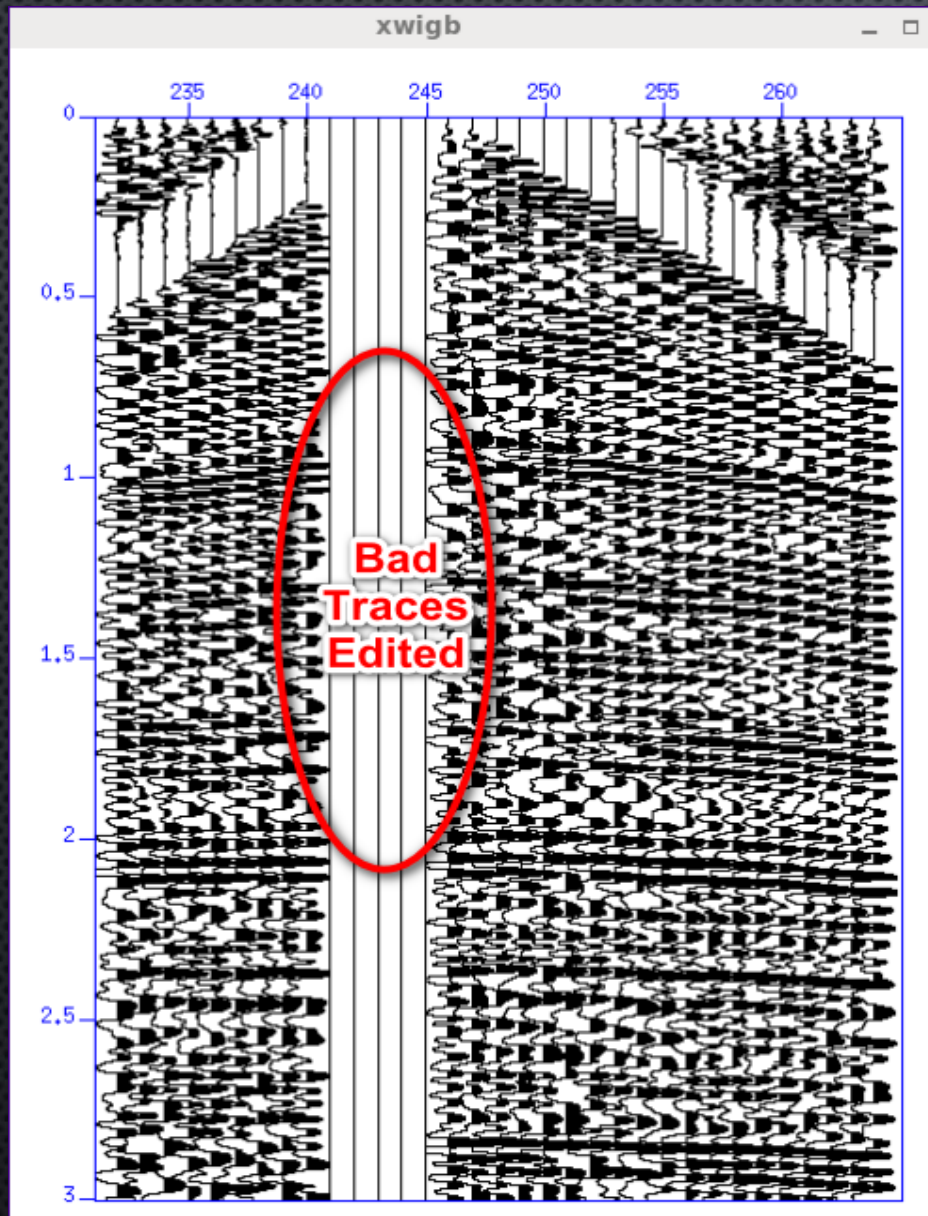
# Edit and Mute

## Edit

sukill < stdin > stdout min= count= 15

- ❑ **SUKILL:** zero out traces.
  - ❑ Stdin: standard input.
  - ❑ Stdout: standard output.
- ❑ parameters:
  - ❑ **Min= first trace to kill.**
  - ❑ **Count= number of traces to kill**





processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sukill < shotagc.8 min=10 count=5 | suxwigb perc=99 &
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sukill < shotagc.8 min=10 count=5 | suxwigb perc=99 &  
[1] 3758  
[ ~/Desktop ] $
```

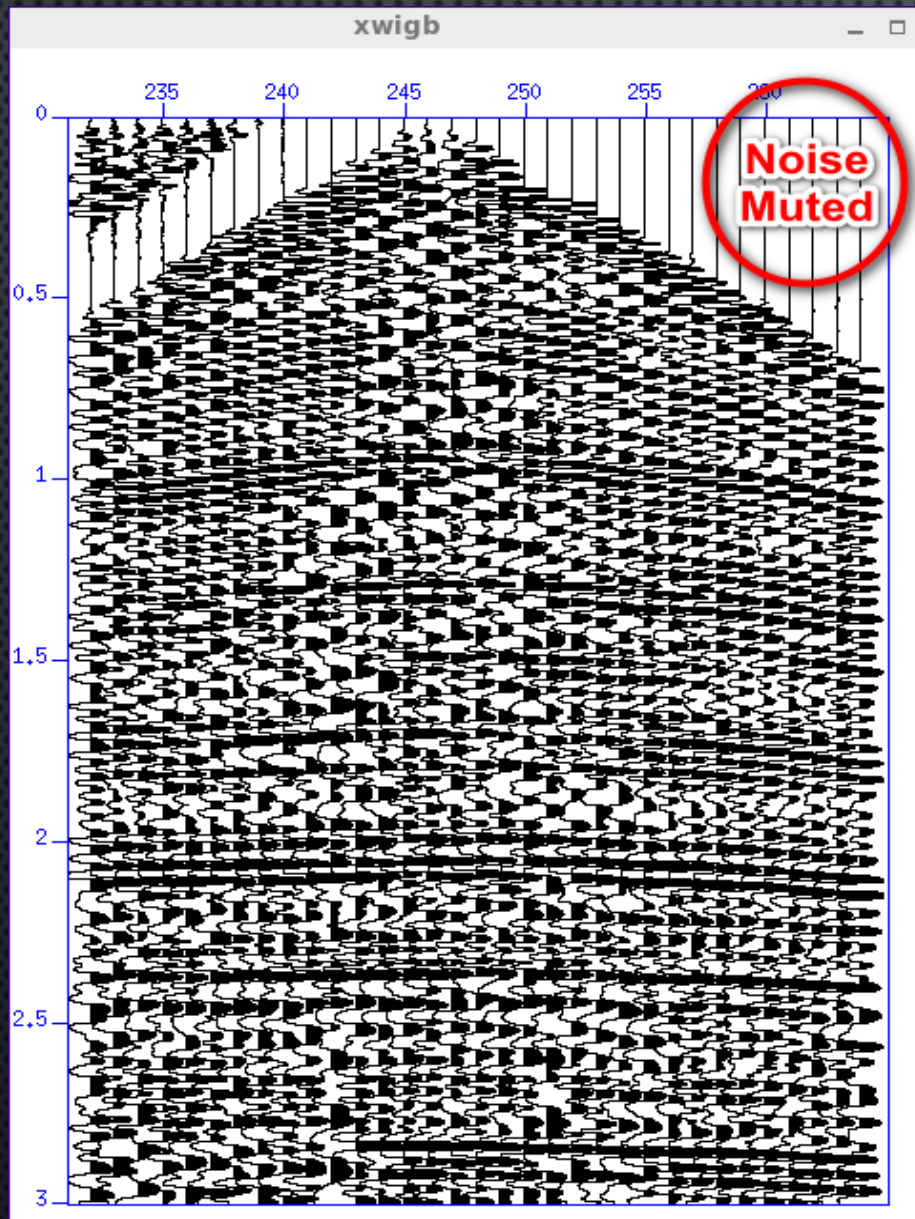


# Mute

sumute < stdin > stdout key= xmute= tmute=

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- ❑ **sumute**: zero out part of traces.
  - ❑ Stdin: standard input.
  - ❑ Stdout: standard output.
- ❑ parameters:
  - ❑ xmute= position values.
  - ❑ tmute= corresponding time values (sec).
  - ❑ key= header word (tracI,tracr).



```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sumute < shotagc.8 key=trac1 xmute=250,255,260 tmute=.2,.3,.5 |
suxwigb perc=99 &
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sumute < shotagc.8 key=trac1 xmute=250,255,260 tmute=.2,.3,.5 |
suxwigb perc=99 &
[1] 3918
[ ~/Desktop ] $
```



# suxgraph < infile [options] &

- ❑ Plot seismic files, using x axis as amplitude.
- ❑ [options] :
  - ❑ label1= : set the label of y axis.
  - ❑ label2= : set the label of x axis.
  - ❑ type= normal : plot key1 on x-axis instead of y-axis  
seismic : plot key1 on y-axis.
  - ❑ width= : set the width of the plot window
  - ❑ height= : set the height of plot window.
  - ❑ using suxgraph will plot all trace on top of each other, Best used to plot amplitude spectrum.

# FILTERING

## 1D FILTER

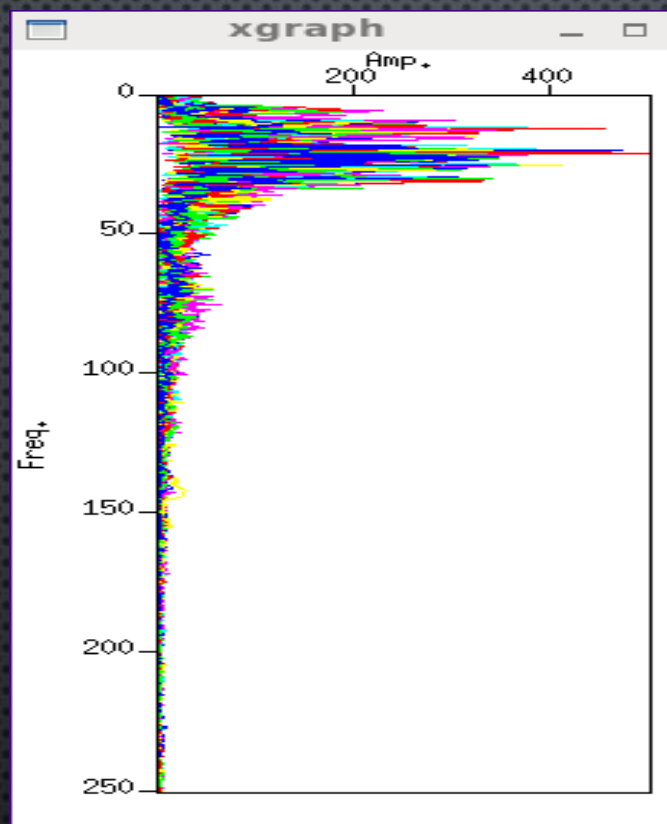
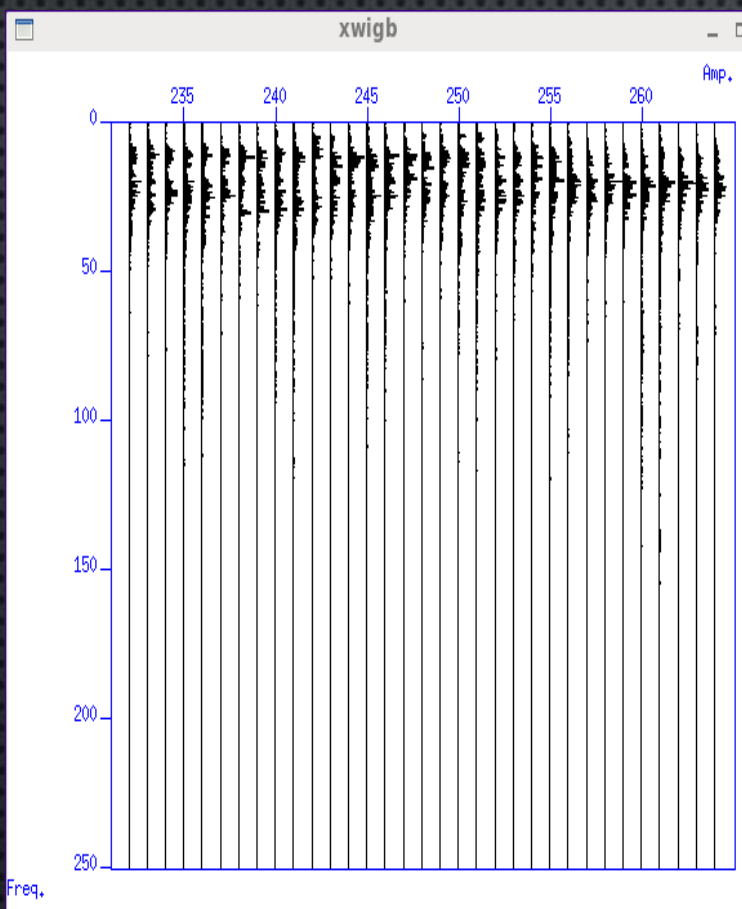
### PLOTTING AMPLITUDE SPECTRUM

- ❑ To calculate the amplitude spectrum we use 'suspecfx'
- ❑ No options ! Just specify the input
- ❑ usually we use suxgraph with suspecfx.

❑ `suspecfx < input | suxgraph &` 17

- ❑ If the input is more than one trace – complete shot – you will see the spectrum of the traces above each other.
- ❑ you can use suxwigb instead of suxgraph , in this case it will plot the spectrum of each trace separately.





```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suscepfx < shotagc.8 | suxgraph label1=Freq. label2=Amp. &
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suscepfx < shotagc.8 | suxgraph label1=Freq. label2=Amp. &
[1] 3953
[ ~/Desktop ] $
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suscepfx < shotagc.8 | suxwigb label1=Freq. label2=Amp. &
[1] 4022
[ ~/Desktop ] $
```

# Applying all types of filter

**□ `sfilter < infile [options] > outfile`**

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□ options :

□  $f=f_1, f_2, f_3, f_4$  : the four frequency corners.

□  $amps=a_1, a_2, a_3, a_4$  : amplitude corresponding to each frequency corner.

□  $amps=1, 1, 0, 0$  : low-pass filter

□  $amps=0, 0, 1, 1$  : high-pass filter

□  $amps=0, 1, 1, 0$  : Band-pass filter

□  $amps=1, 0, 0, 1$  : Band-reject filter

□ **Don't leave spaces around '=' , type '**amps**' not 'amp' , and '**f**' not 'F'**,

□ spelling mistake in the options will not give error , but the output will not be as you wish!



# Filter Script

- ❑ Used to run group of commands at the same time.
  - ❑ Use **gedit (file name).txt** command to create the script file.
  - ❑ Write in the text file the following commands:  
Sufilter < input f=10,20,30,50 amps=1,1,0,0 | suspecfx | suxgraph title=Low-pass &  
Sufilter < input f=10,20,30,50 amps=0,0,1,1 | suspecfx | suxgraph title=High-pass &  
Sufilter < input f=10,20,30,50 amps=0,1,1,0 | suspecfx | suxgraph title=Band-pass &  
Sufilter < input f=10,20,30,50 amps=1,0,0,1 | suspecfx | suxgraph title=Band-reject &
  - ❑ press save and exit the text file.
  - ❑ activate your terminal and recall the text file using **chmod 776 (file name .txt)** command.
  - ❑ to run the commands in the text file use **./(file name.txt)** command.

filter.txt (~/Desktop) - gedit

File Edit View Search Tools Documents Help

Open Save Undo

filter.txt

```
sufilter < shotagc.8 f=10,20,30,50 amps=1,1,0,0 | suscepfx | suxgraph title=Low-pass &  
sufilter < shotagc.8 f=10,20,30,50 amps=0,0,1,1 | suscepfx | suxgraph title=High-pass &  
sufilter < shotagc.8 f=10,20,30,50 amps=0,1,1,0 | suscepfx | suxgraph title=Band-pass &  
sufilter < shotagc.8 f=10,20,30,50 amps=1,0,0,1 | suscepfx | suxgraph title=Band-reject &
```

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processing@localhost:~/

File Edit View Search Terminal Help

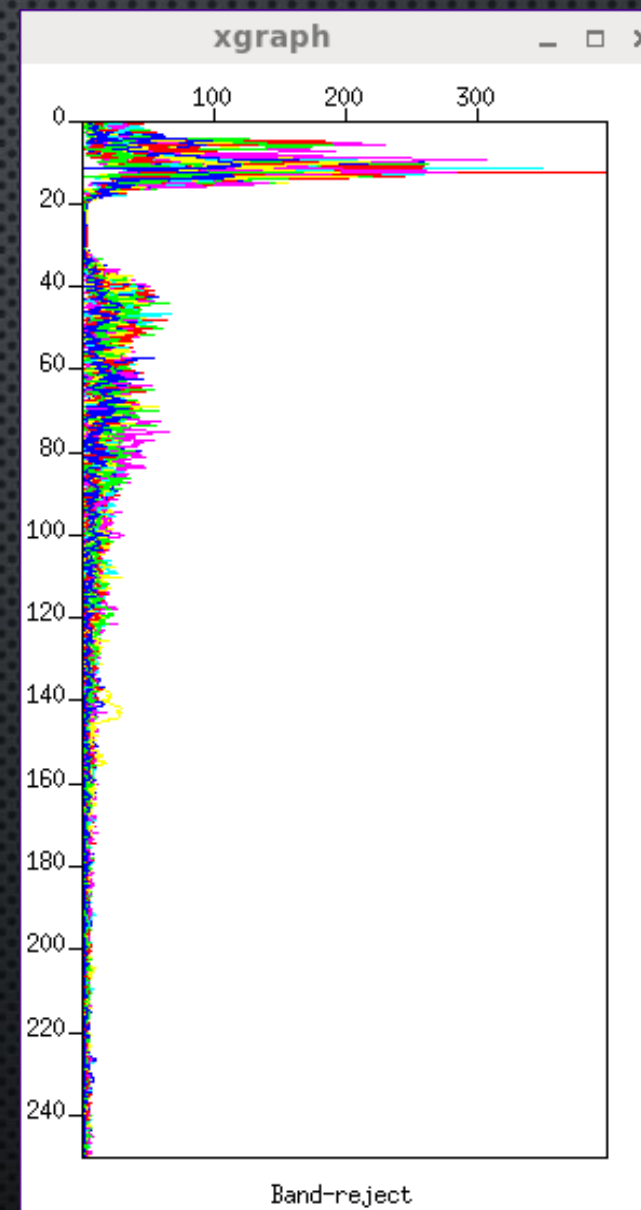
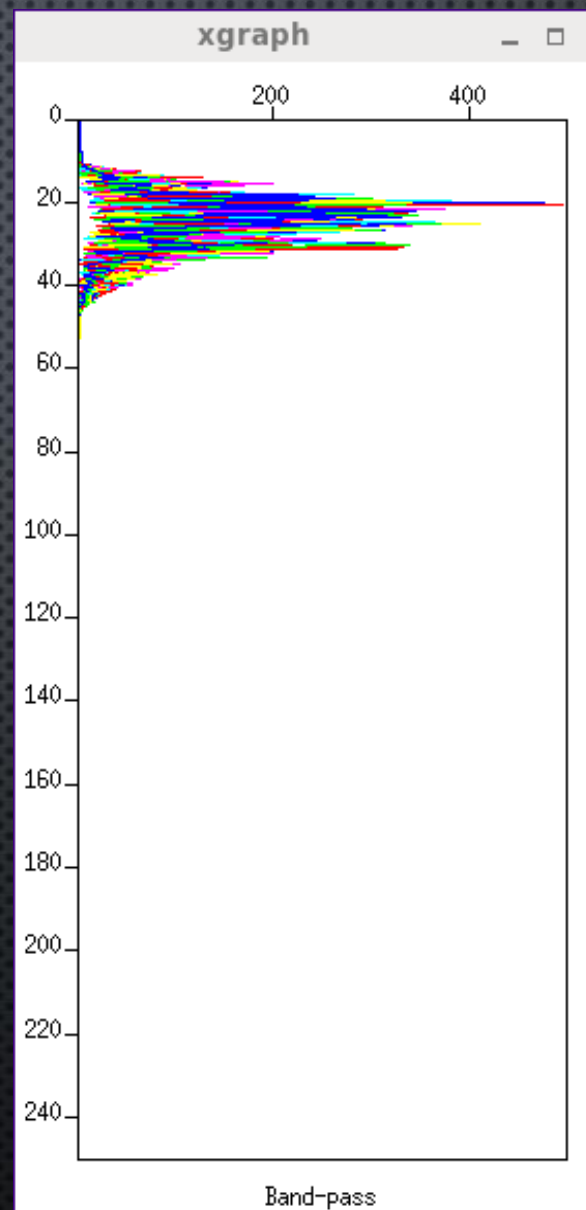
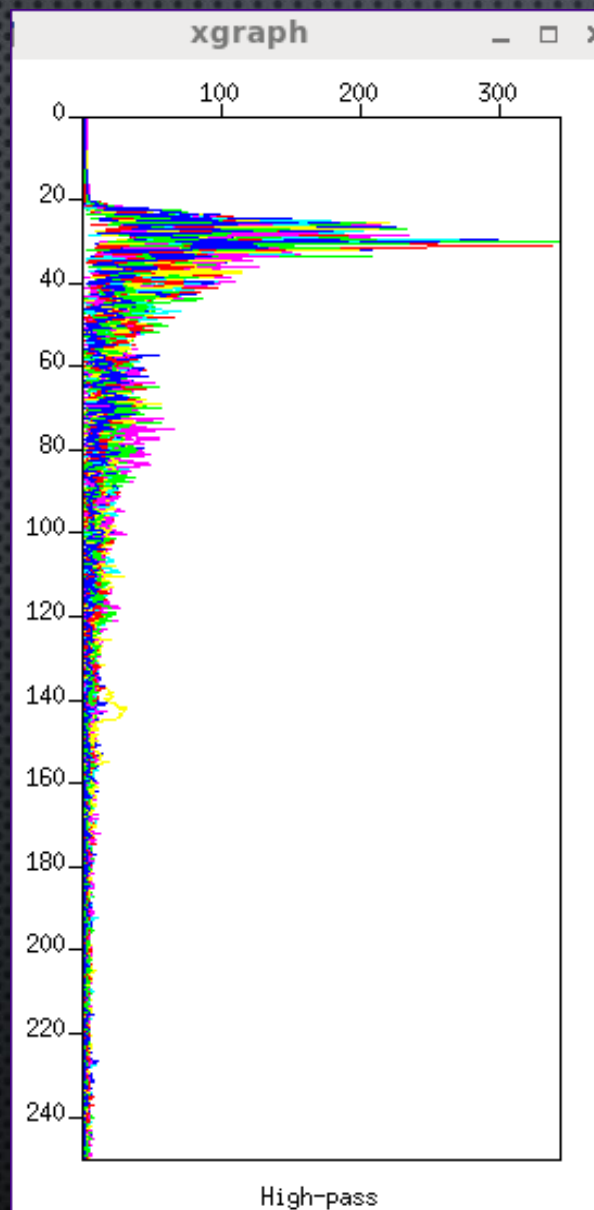
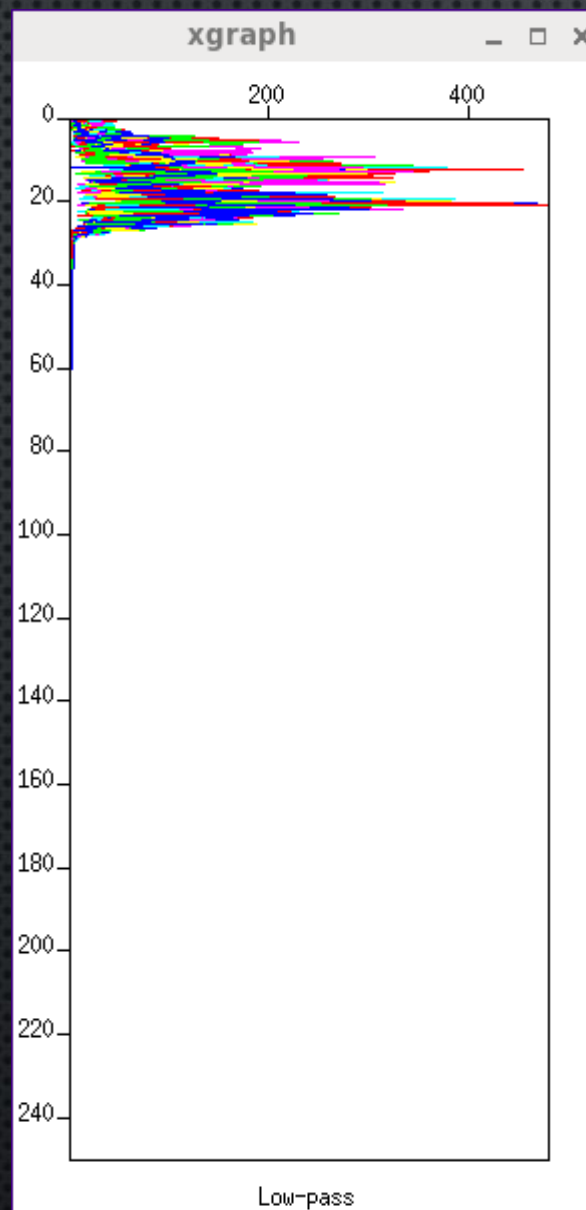
```
[ ~/Desktop ] $ gedit filter.txt
```

processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ gedit filter.txt  
[ ~/Desktop ] $ chmod 776 filter.txt  
[ ~/Desktop ] $ ./filter.txt
```





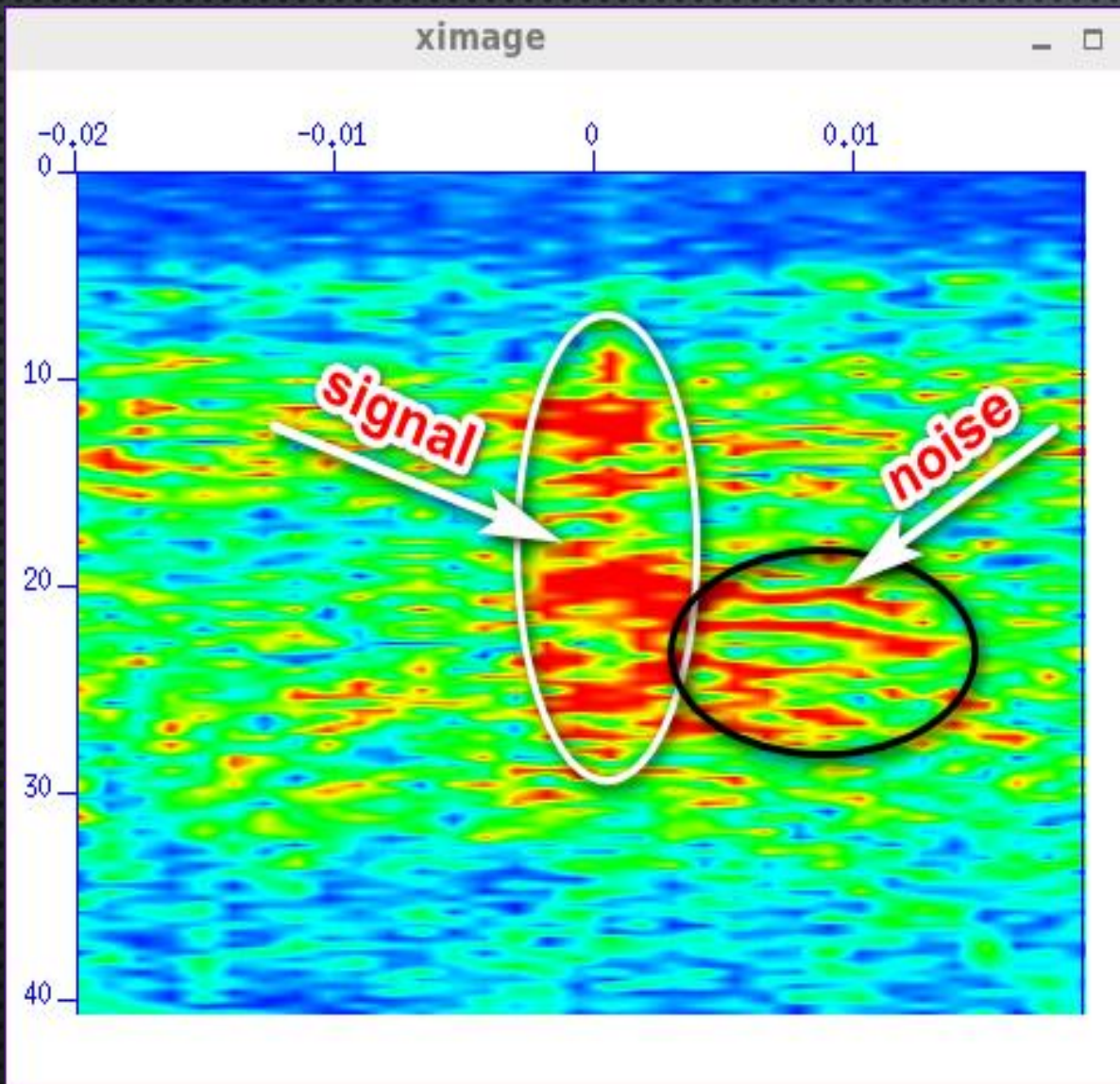
# F-K Filter (Velocity Filter)

**Suspecfk < input dx= dt= > output**

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- ❑ **suspecfk**: transfer command from time domain into frequency domain (F-K domain).
- ❑ **dx**: geophone interval **25**
- ❑ **dt**: sample rate. **0.002**
- ❑ Then display the F-K domain by **suximage** command





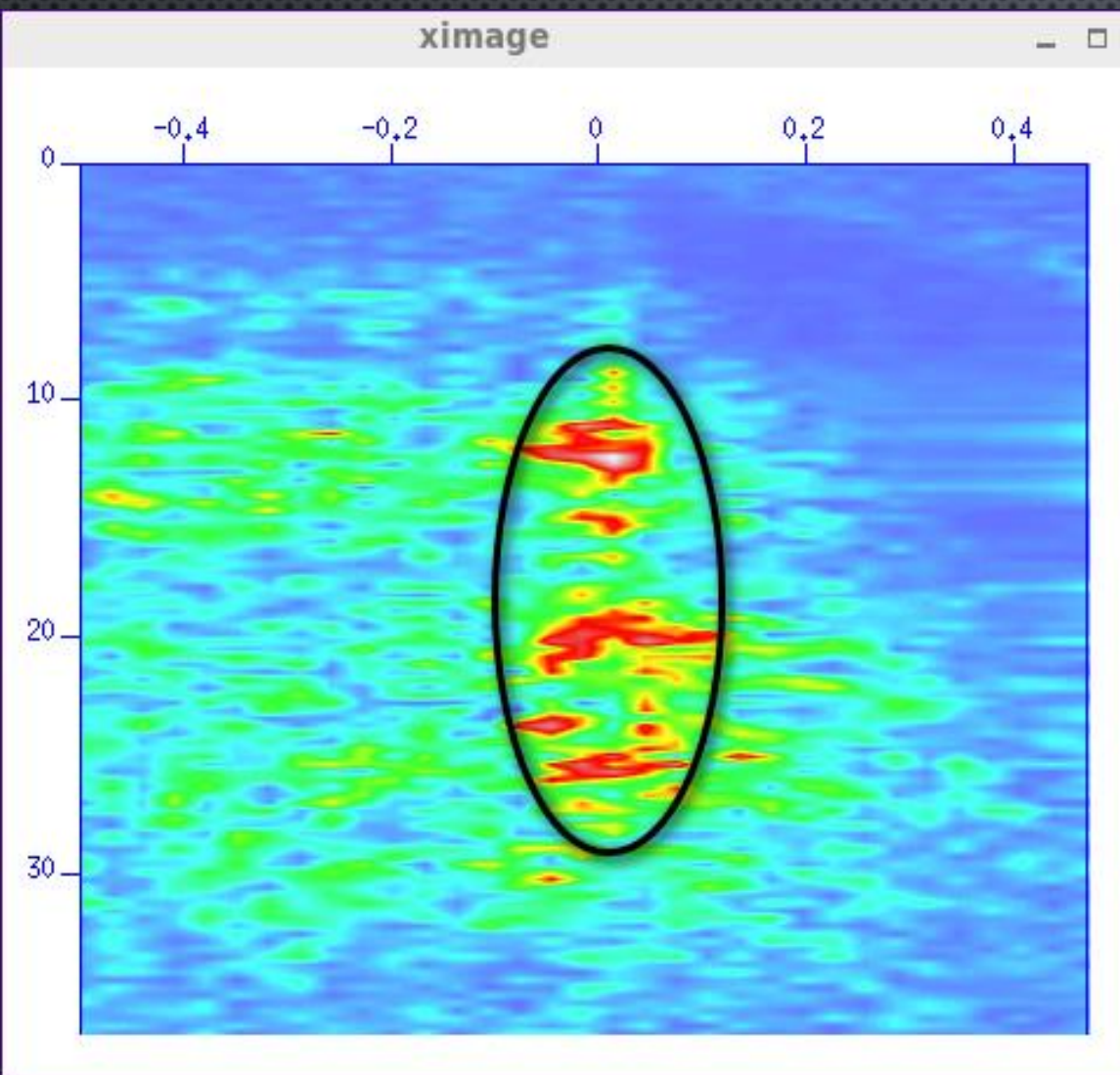
```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suspectfk < shotagc.8 dx=25 dt=.002 | suximage perc=99 &
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suspectfk < shotagc.8 dx=25 dt=.002 | suximage perc=99 &
[1] 6623
[ ~/Desktop ] $
```

# SUDIPFILT < INPUT DX= DT= SLOPES= AMPS= | SUSPECFK | SUXIMAGE & 20

- ❑ **sudipfilt**: to execute the F-K filter step to mute unwanted noises.
- ❑ dx: geophone interval
- ❑ dt: sample rate.
- ❑ slopes: slopes of noises (1/v).
- ❑ amps:
  - ❑ 1: signal.
  - ❑ 0: noise.

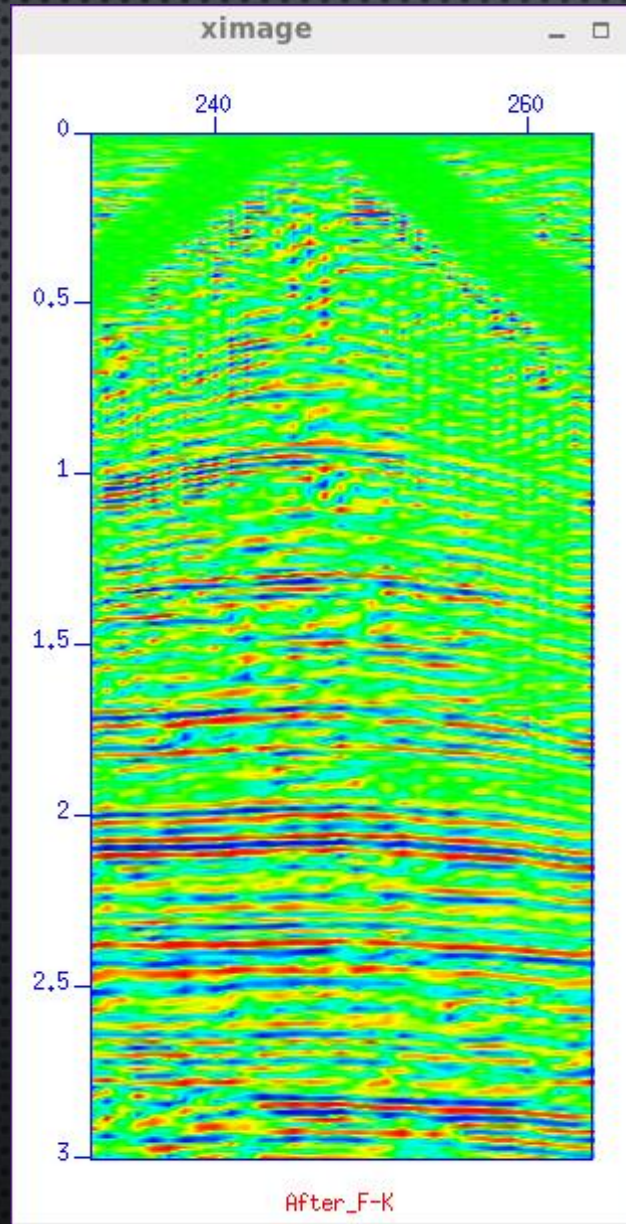
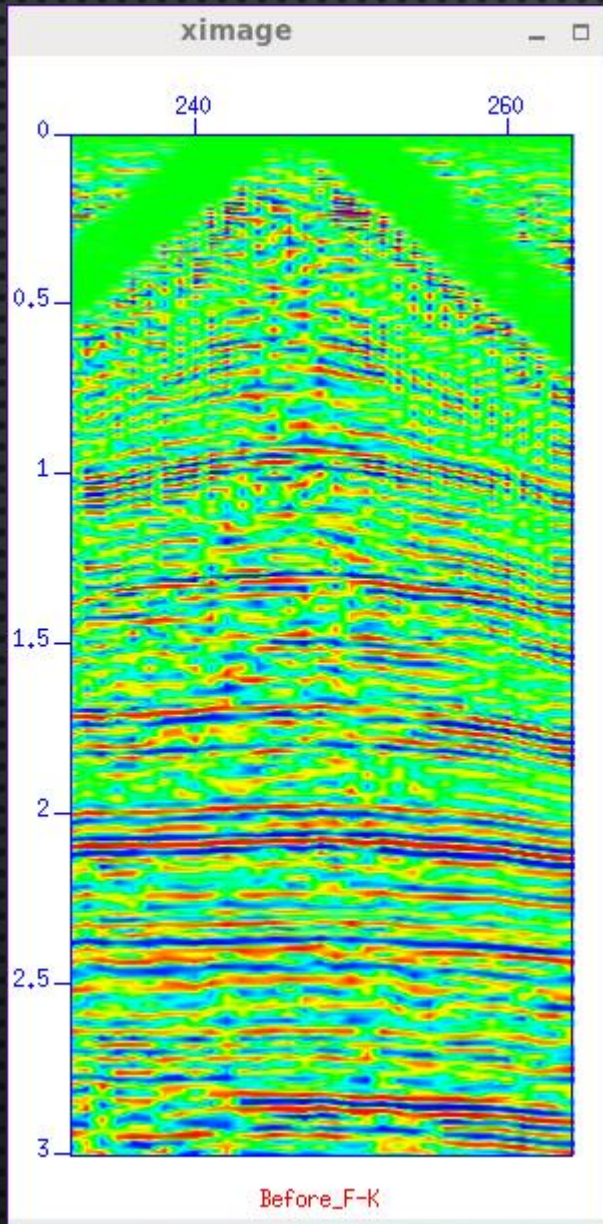




```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sudipfilt < shotagc.8 dx=25 dt=.002 slopes=0,.001,.002,.003,.004
amps=1,0,0,0,1 | suspectfk | suximage &
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sudipfilt < shotagc.8 dx=25 d=.002 d2=1 slopes=0,.001,.002,.003,
.004 amps=1,0,0,0,1 | suspectfk | suximage &
[1] 9766
[ ~/Desktop ] $
suspectfk: tr.d2 not set, assuming d2=1.0
```





```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sudipfilt < shotagc.8 dx=25 d=.002 d2=1 slopes=0,.001,.002,.003,
.004 amps=1,0,0,0,1 > FK.su
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suximage < shotagc.8 perc=99 title=Before_F-K &
[1] 10268
[ ~/Desktop ] $ suximage < FK.su perc=99 title=After_F-K &
[2] 10293
[ ~/Desktop ] $
```



# RESAMPLING

❑ THE DATA IS RESAMPLED FROM THE CURRENT SAMPLE INTERVAL TO A COARSER SAMPLE INTERVAL TO REDUCE THE RUN TIME OF THE PROCESSING STEPS.

❑ IF SAMPLE INTERVAL IS 2 MS (.002 S):

$$dt = \frac{1}{2f(Nyq)}$$

❑ THEN  $2DT * FN = 1$ , THEN  $2*0.002 FN = 1$ , THEN  $FN = 250 \text{ HZ}$ .

❑ IF ANY WAVE HAS FREQUENCY HIGHER THAN  $FN$  IT MAY ALIASED AND GIVE FALSE RESULTS.

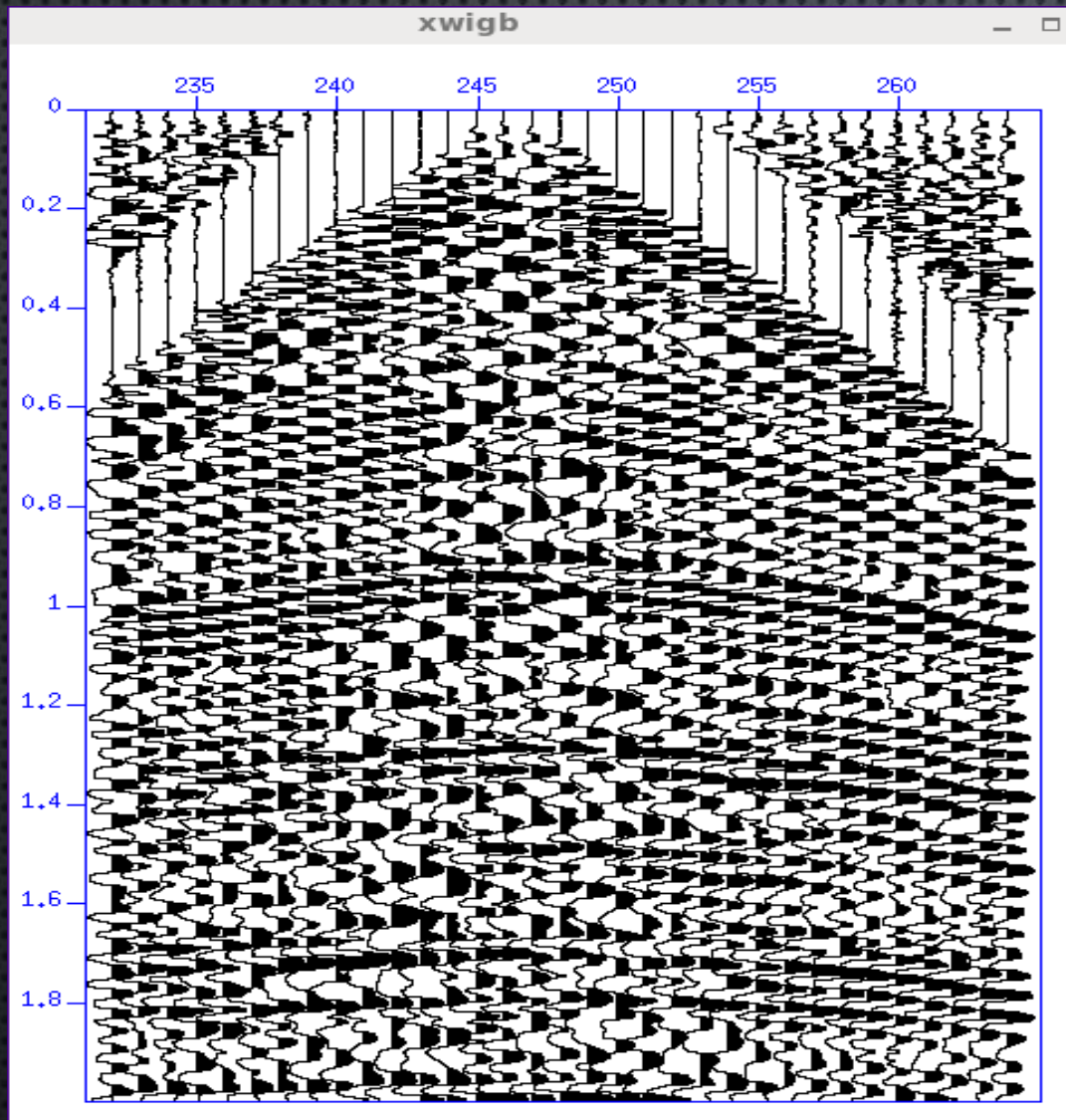
❑ SO WE PERFORM ANTIALIASING FILTER BEFORE RESAMPLING (LOW PASS FILTER).

SUFILTER < INPUT F= AMPS= | SURESAMP NT= DT= > OUTPUT

21

❑ NT: NO. OF SAMPLES PER TIME ON OUTPUT.

❑ DT: SAMPLE INTERVAL ON OUTPUT (IN SEC.).



```
processing@localhost:~/Desktop  
File Edit View Search Terminal Help  
[ ~/Desktop ] $ sufilter < shotagc.8 f=120,125 amps=1,0 | suresamp  
nt=500 dt=.004 | suxwigb perc=99 &
```

```
processing@localhost:~/Desktop  
File Edit View Search Terminal Help  
[ ~/Desktop ] $ sufilter < shotagc.8 f=120,125 amps=1,0 | suresamp  
nt=500 dt=.004 | suxwigb perc=99 &  
[1] 2704  
[ ~/Desktop ] $
```



# Normal Move Out

SORT, VELOCITY ANALYSIS AND NMO CORRECTION

## NMO CORRECTION

❖ To apply NMO Correction

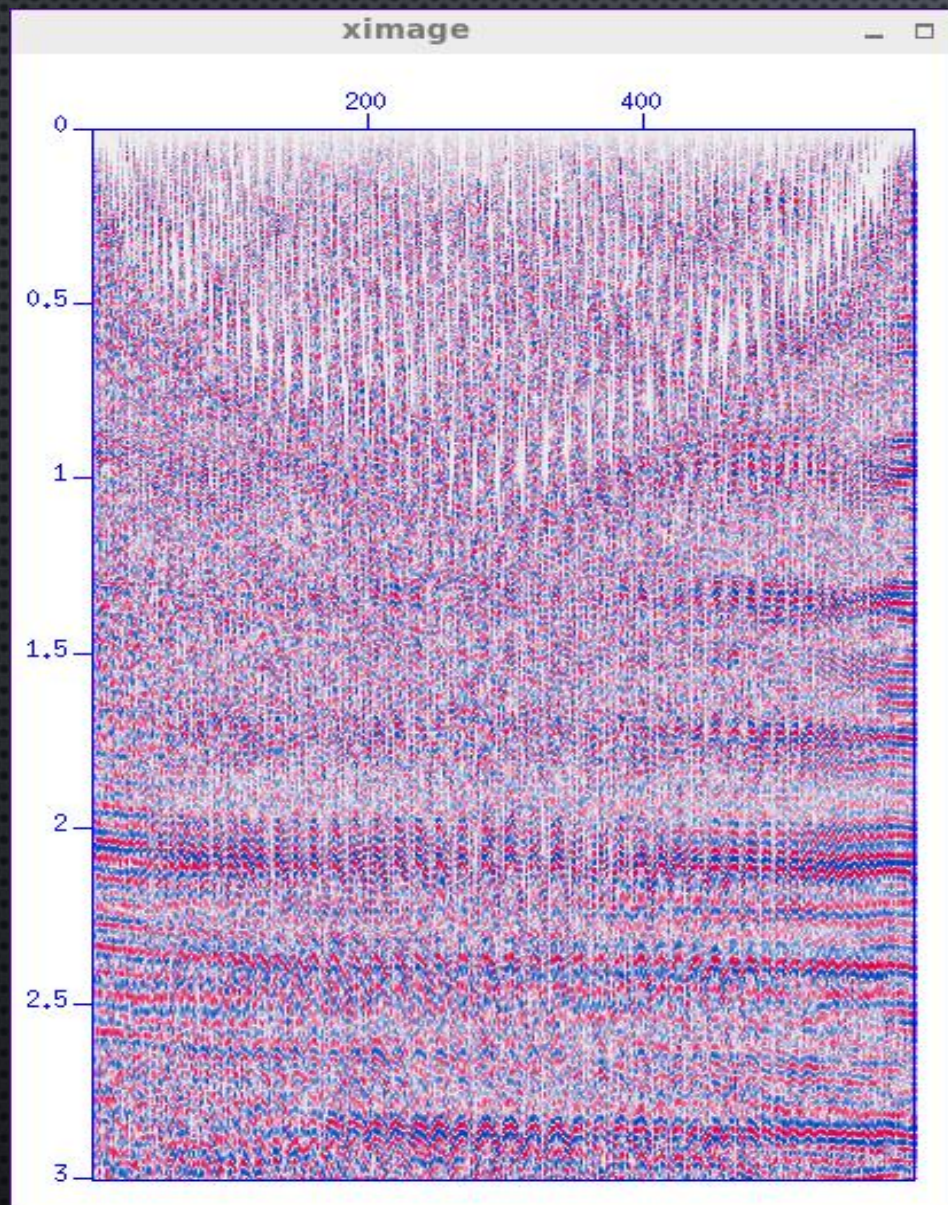
- I. **Sorting** the shot gathered data into common mid-point gathers (CMP).
- II. Picking appropriate stacking velocities (**velocity analysis**).
- III. Apply **NMO Correction** step.

# I. Sorting

**susort < input cdp > output**

- ❑ Susort: sorting command
- ❑ Don't Write "key", write the header word directly (fldr, cdp, tracf, offset, CMP,...).
- ❑ Don't use it with pipe lines – not recommended .
- ❑ If no key is specified then by default the data will be sorted to CMP domain





processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < data.su agc=1 wagc=.5 jon=1 > dataagc.su  
[ ~/Desktop ] $ susort < dataagc.su cdp > data.cdp  
[ ~/Desktop ] $
```



processing@localhost:~/Desktop

File Edit View Search Terminal Help

```
[ ~/Desktop ] $ sugain < data.su agc=1 wagc=.5 jon=1 > dataagc.su  
[ ~/Desktop ] $ susort < dataagc.su cdp > data.cdp  
[ ~/Desktop ] $ suximage < data.cdp perc=99 &  
[1] 3676  
[ ~/Desktop ] $
```



# VELOCITY ANALYSIS

- ❑ **THE AIM OF THE VELOCITY ANALYSIS IS TO FIND THE VELOCITY, THAT FLATTENS A REFLECTION HYPERBOLA, WHICH RETURNS THE BEST RESULT WHEN STACKING IS APPLIED.**
- ❑ THERE ARE DIFFERENT WAYS TO DETERMINE THE VELOCITY
  - ❑ (t2-x2) ANALYSIS.
  - ❑ CONSTANT VELOCITY PANELS (CVP).
  - ❑ CONSTANT VELOCITY STACKS (CVS).
  - ❑ ANALYSIS OF VELOCITY SPECTRA.
- ❑ FOR ALL METHODS, SELECTED CMP GATHERS ARE USED.



Seismic\_Unix/src/demos/Velocity\_Analysis/Traditional >>> **copy** Velan

```
Velan X
#!/bin/sh
# Velocity analyses for the cmp gathers
# Authors: Dave Hale, Jack K. Cohen, with modifications by John Stockwell
# NOTE: Comment lines preceeding user input start with ##
#set -x

## Set parameters
velpanel=nodedata      # gained and deconvolved seismic data,
                        # sorted in cdp's
vpicks=stkvel.pl       # output file of vnmo= and tnmo= values
normpow=0              # see selfdoc for suvelan
slowness=0             # see selfdoc for suvelan
cdpfirst=1             # minimum cdp value in data
cdplast=3500           # maximum cdp value in data
cdpmin=1500            # minimum cdp value used in velocity analysis
cdpmax=3500            # maximum cdp value used in velocity analysis
dcdp=500              # change in cdp for velocity scans
fold=12               # only have 12 shots, otherwise would be
                        # 64/2=32 for dsx=dgx, or maximum number
                        # of traces per cdp gather
dxcdp=50              # distance between successive midpoints
                        # in full datas set

## Set velocity sampling and band pass filters
nv=128                # number of velocities in scan
dv=75.0               # velocity sampling interval in scan
fv=4000.0             # first velocity in scan
nout=501              # ns in data

## Set interpolation type
interpolation=akima    # choices are linear, spline, akima, mono
```

Velan1 X

## ## Set parameters

```
velpanel=data_sorted.su # gained and deconvolved seismic data,
                        # sorted in cdp's
vpicks=stkvel.p1        # output file of vnmo= and tnmo= values
normpow=0               # see selfdoc for suvelan
slowness=0              # see selfdoc for suvelan
cdpfirst=202            # minimum cdp value in data
cdplast=266             # maximum cdp value in data
cdpmin=230              # minimum cdp value used in velocity analysis
cdpmax=250              # maximum cdp value used in velocity analysis
dcdp=10                 # change in cdp for velocity scans
fold=12                 # only have 12 shots, otherwise would be
                        # 64/2=32 for dsx=dgx, or maximum number
                        # of traces per cdp gather
dxcdp=50                # distance between successive midpoints
                        # in full datas set
```

## ## Set velocity sampling and band pass filters

```
nv=51                  # number of velocities in scan
dv=200                 # velocity sampling interval in scan
fv=5000                # first velocity in scan
nout=1501              # ns in data
```

## ## Set interpolation type

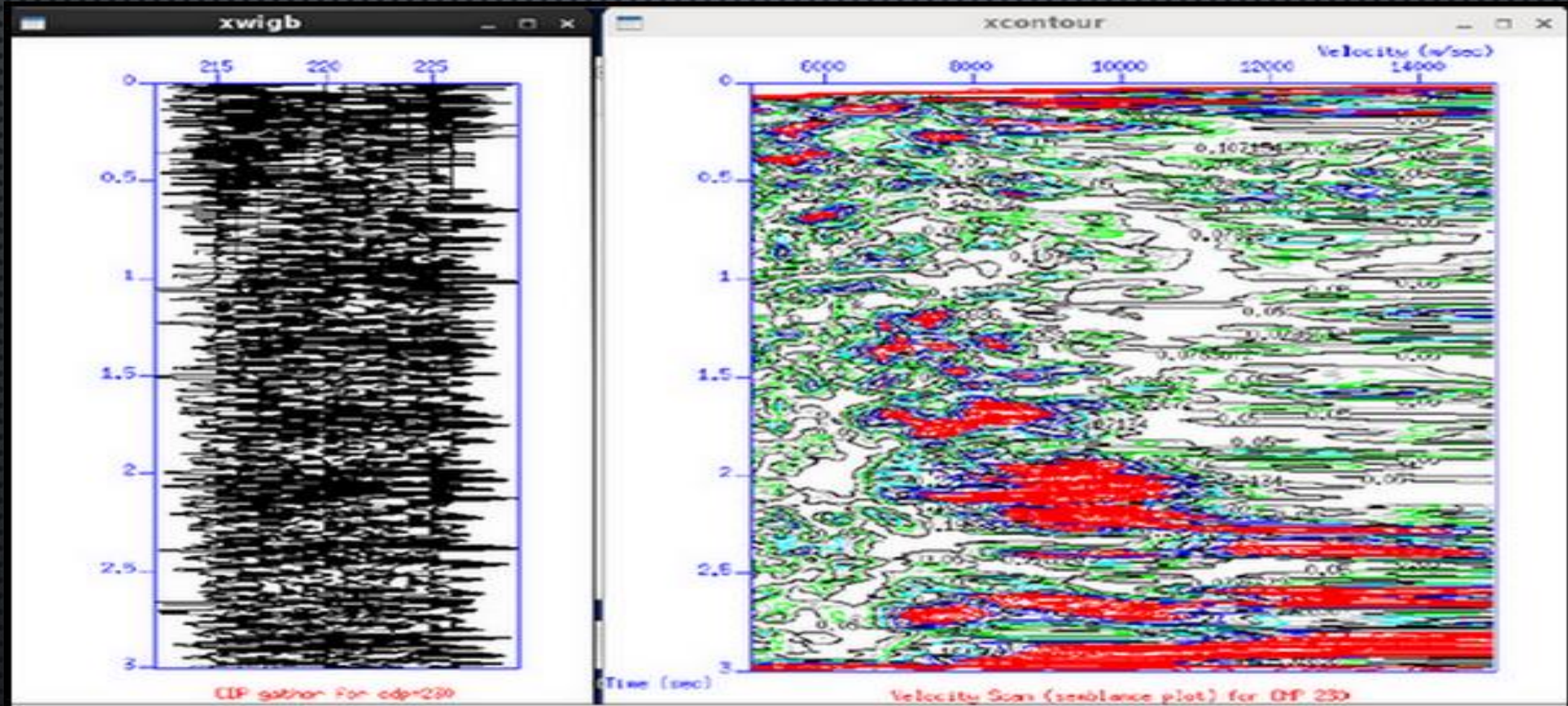
```
interpolation=akima    # choices are linear, spline, akima, mono
```

## ## set filter values

```
f=15|,20,50,60         # bandwidth of data to pass
amps=0,1,1,0           # don't change
```

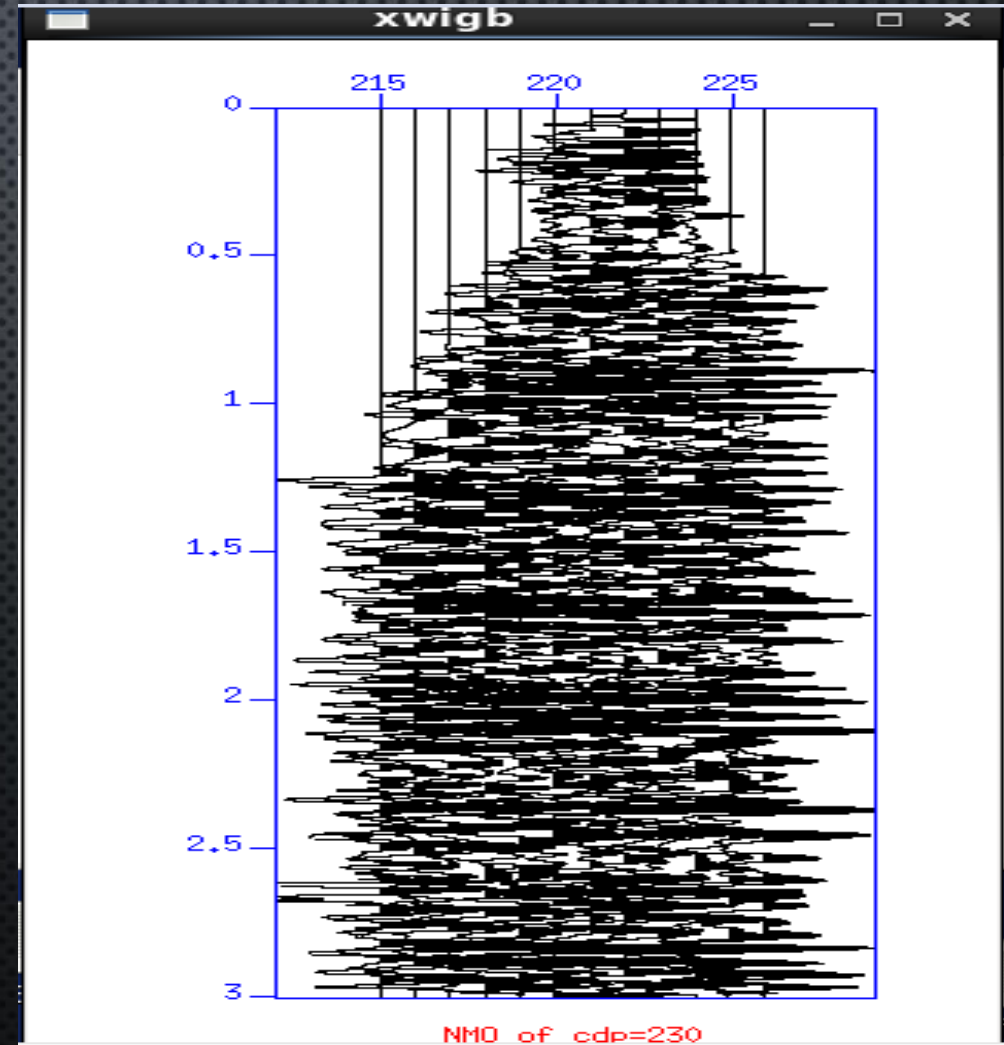
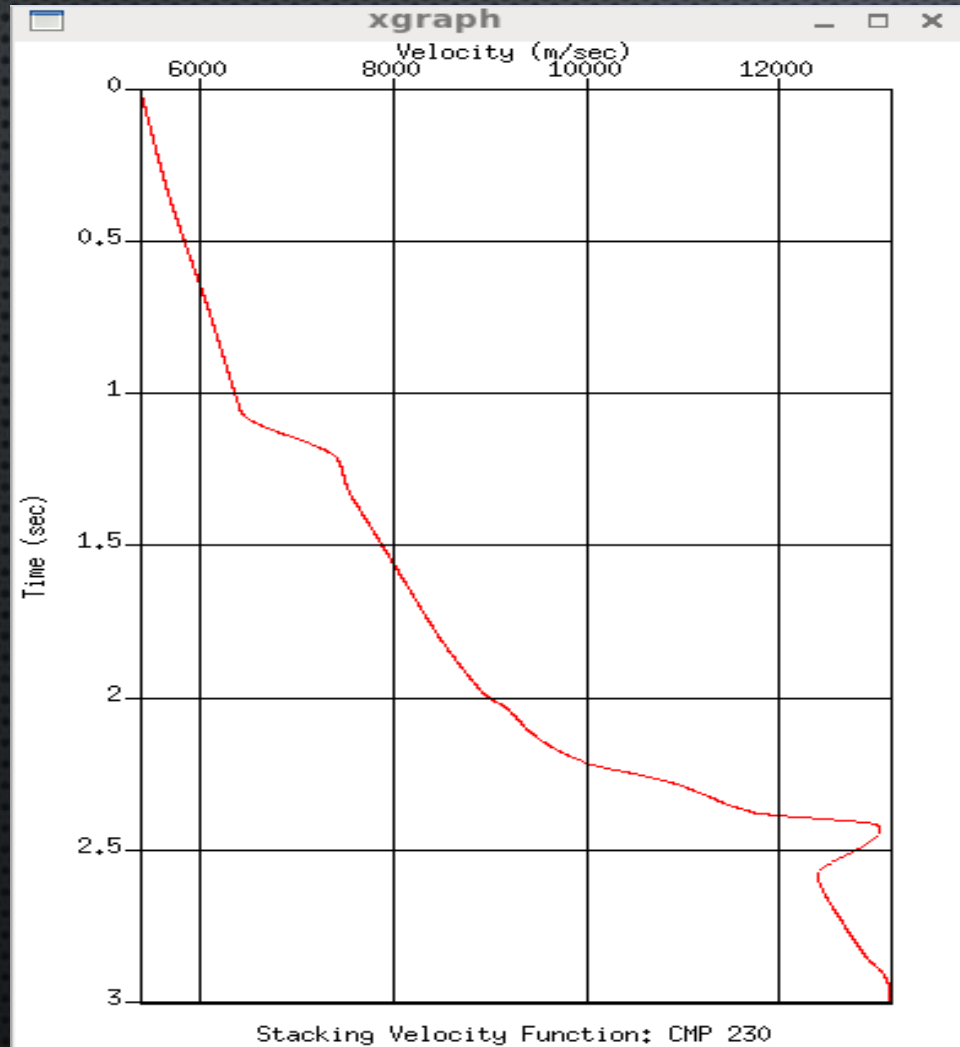


- ❑ xwigb displays the CMP gather and xcontour displays the semblance plot Activate xcontour image, pick the red anomalies “high semblance”, press “S” When you finish your picking, press q& close xwigb





- Look at the given Stacking velocity function then close it and go to your terminal and press enter to see your cdp after applying the NMO correction, investigate it then decide whether to accept it or repeat your picking Activate xwigb display then press ok to close it and go to your terminal and press ok





# NMO CORRECTION

**sunmo < input (options) > output**

❑ Two ways to input velocity to sunmo operation :

❑ First use tnmo, vnmo pairs :

sunmo < input tnmo=t<sub>1</sub>,t<sub>2</sub>,t<sub>3</sub> vnmo=v<sub>1</sub>,v<sub>2</sub>,v<sub>3</sub> > output

Note : use t/v pairs according to no. of hyperbolas.

for each tnmo there should be vnmo.

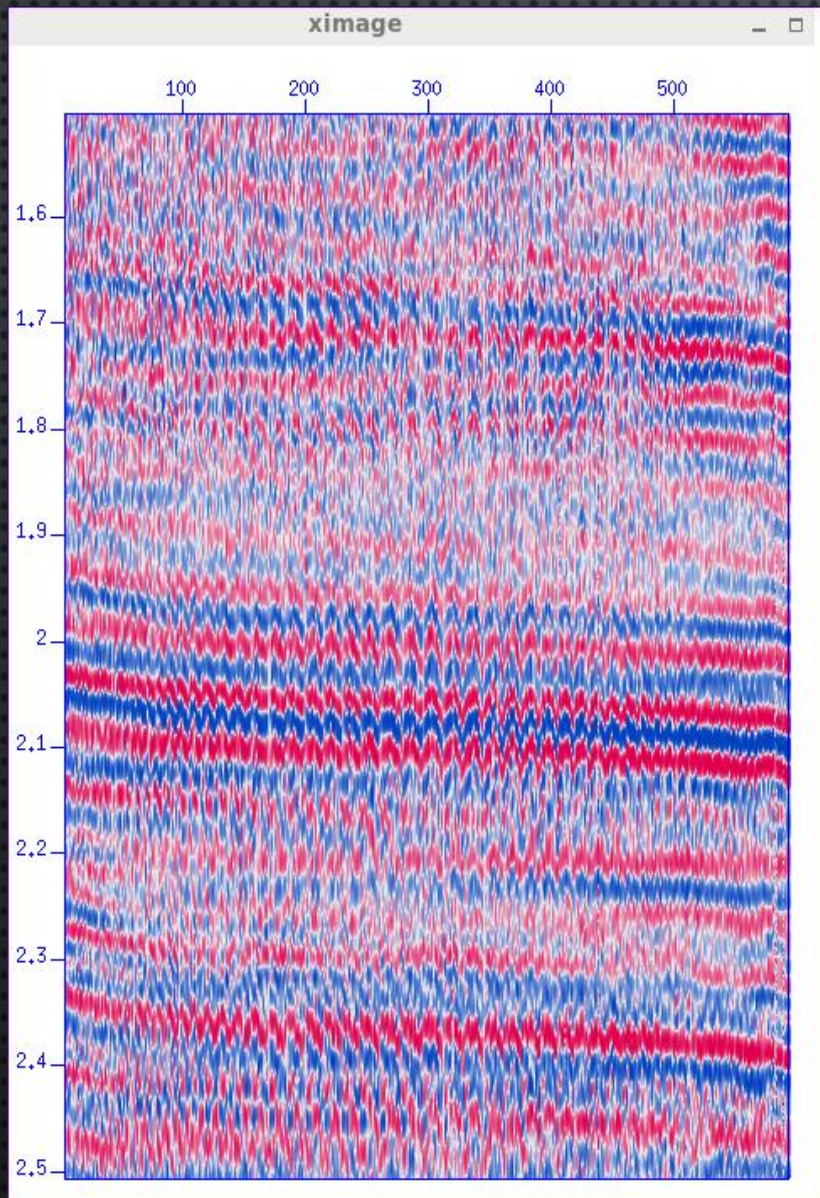
tnmo should be increasing.

❑ Second if you have velocity file:

sunmo < input par=velocity file > output

Note : Don't type " velocity file " use the name of the velocity file given.





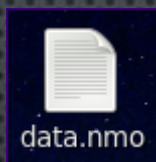
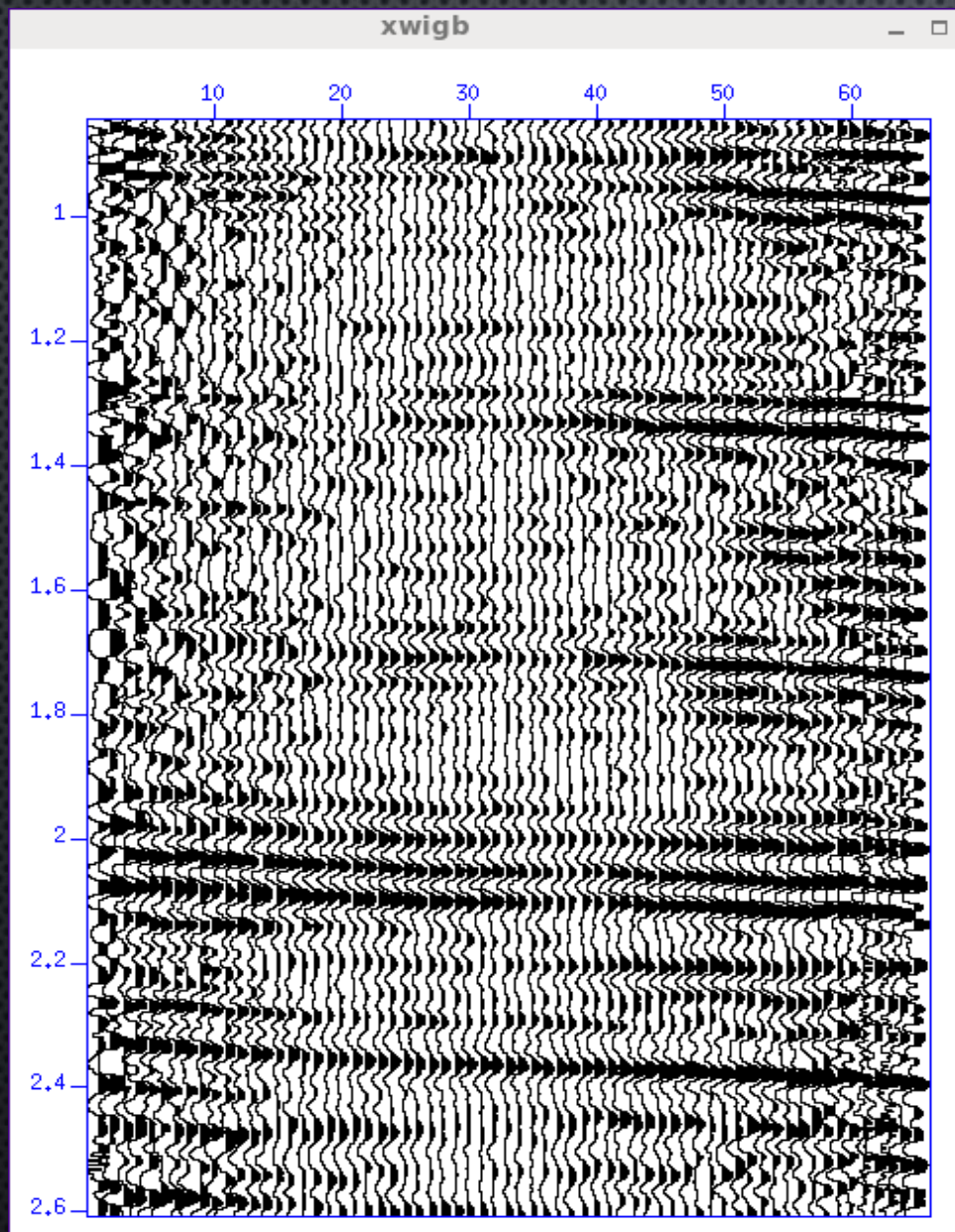
```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ suximage < data.cdp perc=99 &
[1] 4987
[ ~/Desktop ] $
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sunmo < data.cdp par=nmo | suximage perc=99 &
[1] 5046
[ ~/Desktop ] $
```



## Stack ( $\text{sustack} < \text{input} > \text{output}$ )

- ❑ After **NMO is applied**, we stack the data.
- ❑ As a result the amplitude of the reflection event will increase ( Amplitudes stack together )
- ❑ Random noise will stack out, its amplitude decrease, as seen from them snapshot



```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sunmo < data.cdp par=nmo > data.nmo
[ ~/Desktop ] $
```

```
processing@localhost:~/Desktop
File Edit View Search Terminal Help
[ ~/Desktop ] $ sunmo < data.cdp par=nmo > data.nmo
[ ~/Desktop ] $ sustack < data.nmo | suximage perc=99 &
[1] 5281
[ ~/Desktop ] $
```