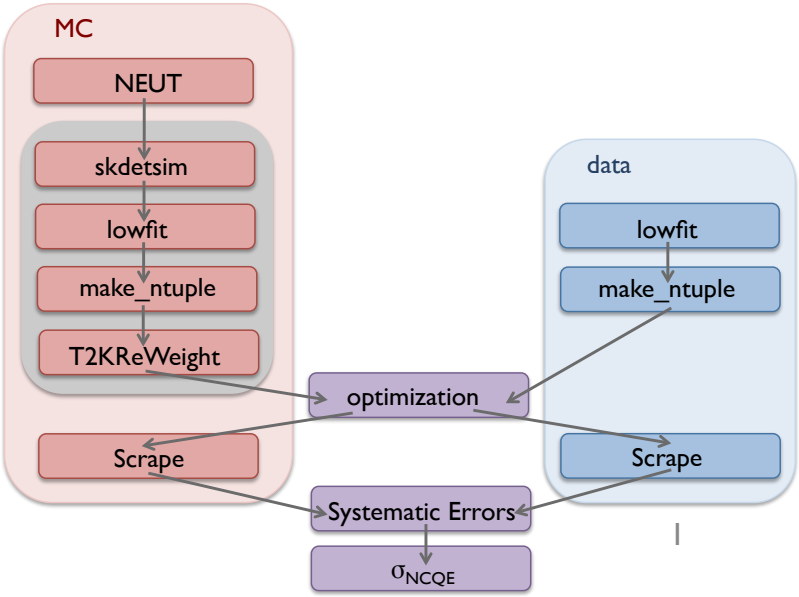
ncgamma analysis tools



Corina Nantais
group meeting
15 June 2017

MC lowfit

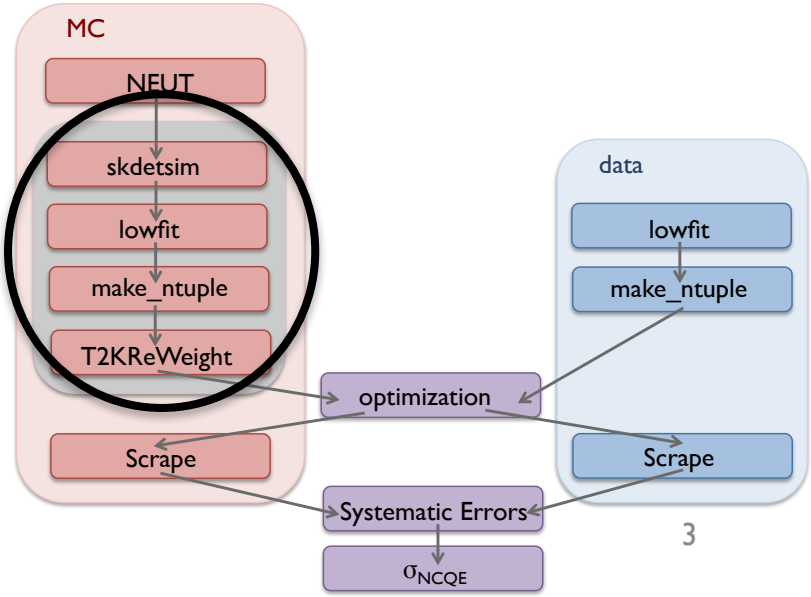
- Fukuda-san asked:
- Should we use …/ncgamma/lowfit/lowfit_t2k_mc
  or …/ncgamma/mc/lowfit/ (which has lowfit_sk4_zbs)

- Huang-san:
- …/ncgamma/lowfit/lowfit_t2k_mc was made by Alex and Huang-san.
  You should use this.
- …/ncgamma/mc/lowfit/ is for reference only, because it is old version

- Last time, I used …/ncgamma/mc/lowfit/lowfit_sk4_zbs
- Should I change ProcessNCEL_mc.sh to …/ncgamma/lowfit/lowfit_t2k_mc?

T2KReWeight during Processing MC

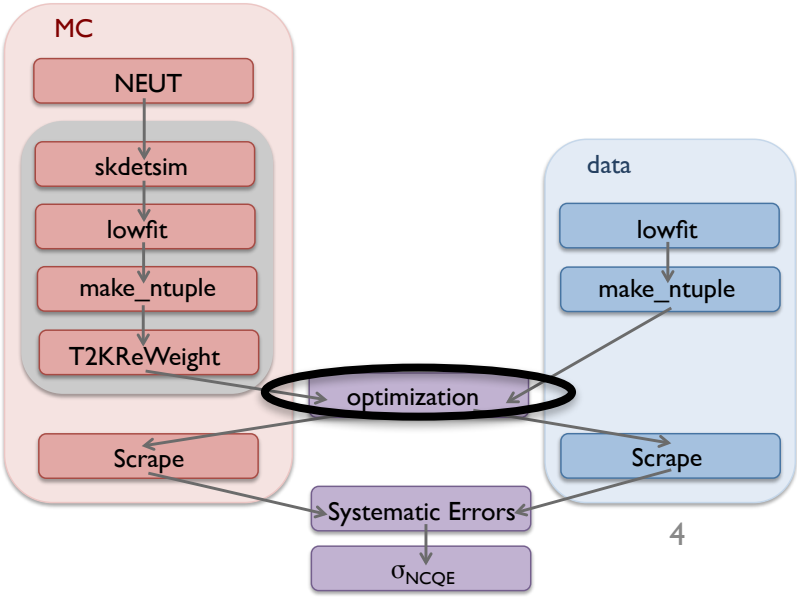
- last time, issue where T2KReWeight during Processing MC worked interactively, but not when submitting jobs
- keyboard mishap solved thanks to Hiro
- all T2KReWeight files generated successfully



Optimization

- Need both data and MC to get the cut parameter. Data uses off-timing for background. Optimize cut criteria 4.0-6.5 MeV for 0.5 MeV width bin. See README.txt

- currently using old beamweights
- …/ncgamma/SystematicErrors/beamweights/
- already copied over from when I did SelectNCGamma_data.py and SelectNCGamma.py
- change to 13a flux next



Calcmc.py

- Calcmc.py takes in MC ntuples
- Specify T2K Run
- Output is root file in hist/ and txt files in dat/

Calcmc.py

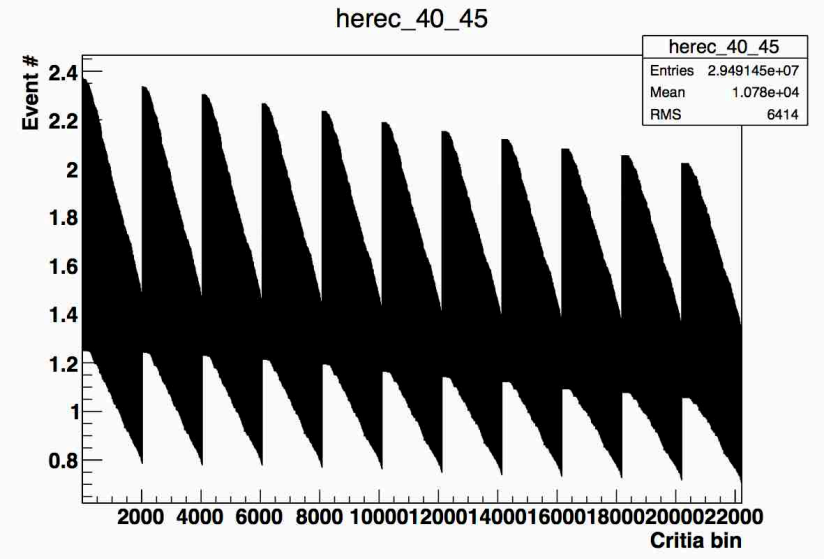
```
/home/cnantais/usr4/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.097.root tree:h1 entries=1234567890
/home/cnantais/usr4/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.098.root tree:h1 entries=1234567890
/home/cnantais/usr4/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.099.root tree:h1 entries=1234567890
Begin processing 100 nue files
Error in <TFile::ReadBuffer>: error reading all requested bytes from file /home/cnantais/usr4/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root, got 63 of 300
Error in <TFile::Init>: cannot read directory info of file /home/cnantais/usr4/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root
/home/cnantais/usr4/lemc/lentuple/lentp_numubar.ncgamma_flux11a_neut532.000.root tree:h1 entries=1234567890
/home/cnantais/usr4/lemc/lentuple/lentp_numubar.ncgamma_flux11a_neut532.000.root tree:h1 entries=1234567890
/home/cnantais/usr4/lemc/lentuple/lentp_numubar.ncgamma_flux11a_neut532.001.root tree:h1 entries=1234567890
```

That file is only 63 B, instead of ~100 kB?

calmcRun4.root

- scp T2K/NCgamma/May2017/optimization/calmcRun4.root

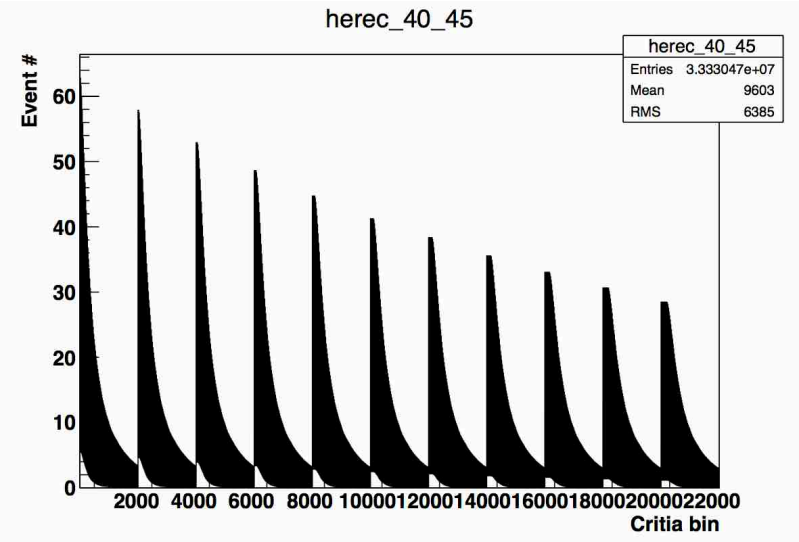
```
[root [1] .ls
 TFile**         calmcRun4.root
  TFile*         calmcRun4.root
   KEY: TH1D     herec_40_45;1   herec_40_45
   KEY: TH1D     herec_45_50;1   herec_45_50
   KEY: TH1D     herec_50_55;1   herec_50_55
   KEY: TH1D     herec_55_60;1   herec_55_60
   KEY: TH1D     herec_60_65;1   herec_60_65
```



I don't get it?

Calcoffbeam.py

- Calcoffbeam.py takes in data ntuples
- Uses off-beam events (-500, -5) us
- Specify T2K Run
- Output is root file in hist/ and txt files in dat/



I don't get it?

Calcoffbeam.py

these files are 0.5 kB instead of ~10 MB
maybe it's ok?

```
/home/cnantais/usr4/lowedata/ntuple//data.lowfit.71243.merge.root tree:h1 entries=1234567890
/home/cnantais/usr4/lowedata/ntuple//data.lowfit.71244.merge.root tree:h1 entries=1234567890
/home/cnantais/usr4/lowedata/ntuple//data.lowfit.71245.merge.root tree:h1 entries=1234567890
Begin processing 328 data files
Error in <TChain::LoadTree>: Cannot find tree with name h1 in file /home/cnantais/usr4/lowedata/ntuple//data.lowfit.70620.merge.root
Error in <TChain::LoadTree>: Cannot find tree with name h1 in file /home/cnantais/usr4/lowedata/ntuple//data.lowfit.70628.merge.root
Error in <TChain::LoadTree>: Cannot find tree with name h1 in file /home/cnantais/usr4/lowedata/ntuple//data.lowfit.70635.merge.root
Error in <TChain::LoadTree>: Cannot find tree with name h1 in file /home/cnantais/usr4/lowedata/ntuple//data.lowfit.70636.merge.root
```

fom_3para.py

- fom_3para.py determines optimized cuts
- Specify T2K run
- Results will printed to screen

fitpara.C

- root –l
- .L fitpara.C
- fitpara("fomRun4_3parahist.root")

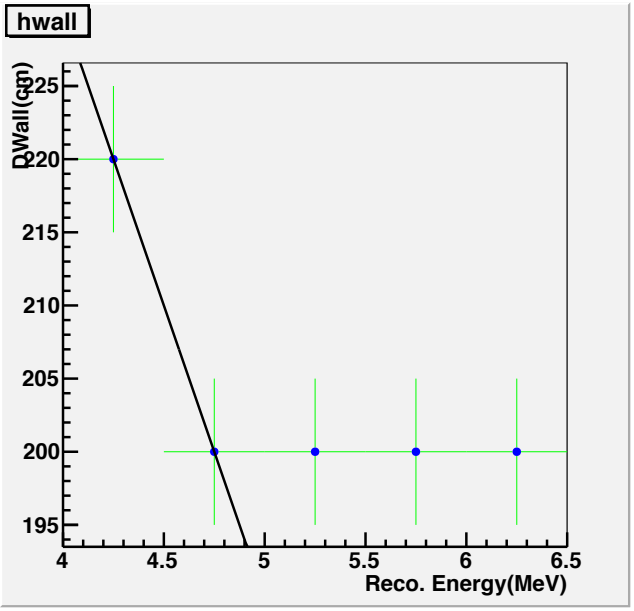
```
root [1] fitpara("fomRun4_3parahist.root")
Error in <TGClient::TGClient>: can't open display "10.30.4.27:0.0", switching to batch mode...
 In case you run from a remote ssh session, reconnect with ssh -Y
Info in <TCanvas::Print>: .pdf file fit.pdf has been created

****************************************
Minimizer is Linear
Chi2                      =   4.6101e-21
NDf                       =            0
p0                        =          390   +/-   63.7377
p1                        =          -40   +/-   14.1421
Info in <TCanvas::Print>: Current canvas added to .pdf file fit.pdf
fitlow4fitup6.5

****************************************
Minimizer is Linear
Chi2                      =        635.2
NDf                       =            3
p0                        =         1935   +/-   16.7519
p1                        =         -284   +/-   3.16228
Info in <TCanvas::Print>: Current canvas added to .pdf file fit.pdf

****************************************
Minimizer is Linear
Chi2                      =         26.8
NDf                       =            3
p0                        =       0.4465   +/-   0.0167519
p1                        =        -0.05   +/-   0.00316228
Info in <TCanvas::Print>: Current canvas added to .pdf file fit.pdf
Info in <TCanvas::Print>: Current canvas added to .pdf file fit.pdf
(int)0
root [2]
```

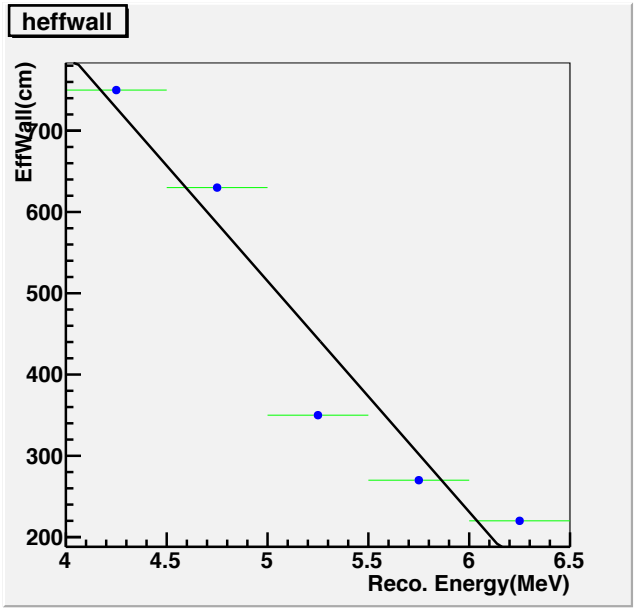
TN-244

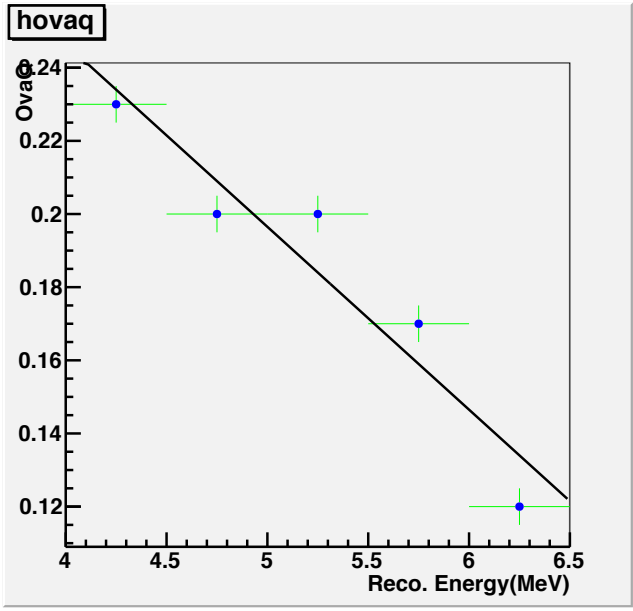
cut criteria	dwall $\geq$ 200	effwall $\geq$ 200	ovaQ
p_0	200.	2200	0.4095
p_1	0.	-328.0	-0.046

a bit different, maybe ok

fit.pdf


hwall
RWall(cm)
225
220
215
210
205
200
195
4
4.5
5
5.5
6
6.5
Reco. Energy(MeV)


heffwall
EffWall(cm)
700
600
500
400
300
200
4
4.5
5
5.5
6
6.5
Reco. Energy(MeV)


hovaq
Ovaq
0.24
0.22
0.2
0.18
0.16
0.14
0.12
4
4.5
5
5.5
6
6.5
Reco. Energy(MeV)

Optimization

- Enter optimization fit results:
- .../ncgamma/Processing/Sel.py
- .../ncgamma/Processing/SelectNCGamma_data.py
- .../ncgamma/Processing/SelectNCGamma.py
- .../ncgamma/SelectionFigures/Sel.py

- (really, just keep previous Run 4 optimized cuts for now)

- Each Run optimized separately

Scrape

- The ntuples produced are not quite ready to be used in the systematic error analysis yet. For this you need to create a “Scraped” ntuple.
- This will be a single file containing all the events (MC or data) and only the minimum number of variables to run the analysis.
- This is where the cuts are applied.

runscrape.csh

- 5 for data, do these for sure
- 3 for mc, do I do these?

ScrapeLE.py and Scrapper.py

- ./runscrape.csh
- problem with OrderedDict
  (even though Hayato-san said he installed ordereddict 1.1?)

```
~/ncgamma/Processing@sukap001[590]_% ./runscrape.csh
Traceback (most recent call last):
  File "ScrapeLE.py", line 7, in <module>
    from OrderedDict import OrderedDict
ImportError: No module named OrderedDict
Traceback (most recent call last):
  File "ScrapeLE.py", line 7, in <module>
    from OrderedDict import OrderedDict
ImportError: No module named OrderedDict
Traceback (most recent call last):
  File "ScrapeLE.py", line 7, in <module>
    from OrderedDict import OrderedDict
ImportError: No module named OrderedDict
Traceback (most recent call last):
  File "ScrapeLE.py", line 7, in <module>
    from OrderedDict import OrderedDict
ImportError: No module named OrderedDict
Traceback (most recent call last):
  File "ScrapeLE.py", line 7, in <module>
    from OrderedDict import OrderedDict
ImportError: No module named OrderedDict
~/ncgamma/Processing@sukap001[591]_%
```

ScrapeLE.py and Scrapper.py

- go back to my work around

```
import os
from ROOT import TChain, TTree, TH1, TFile, TArrayF
from glob import glob
from collections import defaultdict
#from OrderedDict import OrderedDict
import numpy as n
import progressbar as pb

import collections

#class SterileScrapper:
class Scrapper:
    runs = ["1","2","3","4"] #,"3b","3c"]
    #runs = ["1","2","3","4","5"] #,"3b","3c"]
    mcmode = True
    fluxtunes = defaultdict(dict)
    groupedFiles = defaultdict(list)
    friendFiles = False
    storeWeights = False
    trees = {}
    scales = {}
    #treevars = OrderedDict()
    treevars = collections.OrderedDict()
    batch = True
```

Scrapper.py

Scrape

- ./runscrape.csh
- error with mc nue 85, is it ok otherwise?

```
32000 / 34089
33000 / 34089
34000 / 34089

Traceback (most recent call last):
  File "ScrapeLE.py", line 215, in <module>
    for mctree, fileType in scrape.Loop(specialFriend = timingFriend):
  File "/home/cnantais/ncgamma/Processing/Scrapper.py", line 183, in Loop
    friendTree.Add(self.friendFiles[infile])
KeyError: '/disk01/usr4/cnantais/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root'
~/ncgamma/Processing@sukap001[597]_%
```

friend trees

- "no friend trees given"
- but files are there? is this ok?

also problem with mc nue 86?

```
4418000 / 4420848
4419000 / 4420848
4420000 / 4420848

Getting flux weights from ~/ncgamma/SystematicErrors/beamweights/
Weight file not found for /disk01/usr4/cnantais/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root but found before
Weight file found for /disk01/usr4/cnantais/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.086.root but not before
Friend files found in /disk01/usr4/cnantais/lemc/weights_postfit_banff/xsec_prefit/
Creating branch erec/D
Creating branch pnu/D
Creating branch inu/I
Creating branch mode/I
```

Scrape output

- 4 were created:
- ncgamma.data.ontiming.root
- ncgamma.data.ontiming.nosel.root
- ncgamma.data.offtiming.nosel.root
- ncgamma.data.widetiming.nosel.root

- but not:
- xsec_prefit.ankowski.nosel
- is that ok?

- Dec 2015 has 5 data + 3 mc

- definitely can't do the niwg one, because no weights from T2KReWeight

SelectionPlots

- SelectionPlots.py takes in those root files and makes histograms for things like reconstructed energy, Cherenkov angle, dwall, effwall, and ovaq.
- Specify T2K Run

SelectionPlots.py

- asking for 4, but I'm missing xsec_prefit.ankowski.nosel
- what do I do?

```
#scrapedir = os.path.expandvars("$HOME/ana/T2K/ncgamma/Scraped/2014Oct")
#scrapedir = os.path.expandvars("$HOME/usr3/plot/2014Nov/")
scrapedir = os.path.expandvars("/home/cnantais/ncgamma/Processing/")
files = { "ontime"  : join(scrapedir,"ncgamma.data.ontiming.nosel.root"),
          "offtime" : join(scrapedir,"ncgamma.data.offtiming.nosel.root"),
          "widetime": join(scrapedir,"ncgamma.data.widetiming.nosel.root"),
          "mc"      : join(scrapedir,"ncgamma.xsec_prefit.ankowski.nosel.root")
```

SelectionPlots.py

- python SelectionPlots.py
- does this need PyROOT?

```
~/ncgamma/SelectionFigures@sukap001[615]_% python SelectionPlots.py
Traceback (most recent call last):
  File "SelectionPlots.py", line 119, in <module>
    gStyle.SetErrorX(0.001)
NameError: name 'gStyle' is not defined
~/ncgamma/SelectionFigures@sukap001[616]_%
```

maybe I need a logon file?
what is PYTHONSTARTUP?

```
import os, sys
if sys.argv[0] and "PYTHONSTARTUP" in os.environ:
    execfile(os.environ['PYTHONSTARTUP'])
#from SterileSel import *
from Sel import *
from os.path import join
from HandyFuncs import pbloop, VerticalRange, GetHists
import cPickle as pickle
from array import array
```

- try copying rootlogon.py from SystematicErrors/ to SelectionFigures/
- nope, same

Check nue 85

- detsim/ too small (44K and 52M instead of 216K and ~80M for hbk and zbs)
- lowfit/ size 0 for nue 49, 85, 93 (small nue 30, 41, 57, 76, 98, nmb 19)
- lentuple/ small (63 B instead of ~120 KB, others were a bit small)
- flux_prefit/ missing
- xsec_prefit/ missing

SelectNCGamma.py

- meanwhile, moving on

- python SelectNCGamma.py –o ncgammamcRun4.root /disk/…/lemc/lentuple/lentp_nu*.root
- <1 min

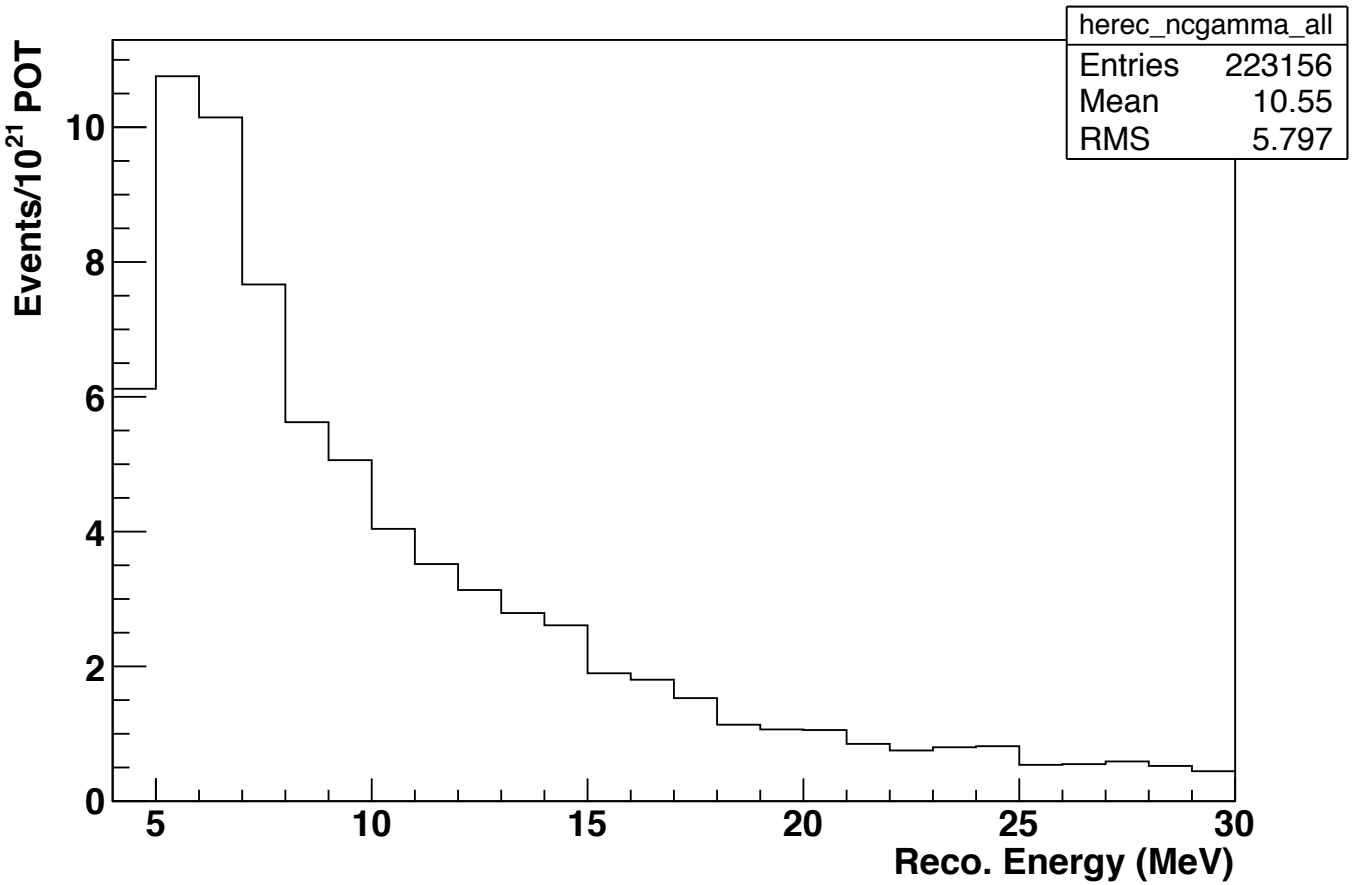
- almost immediately, error with 85
- is it ok?

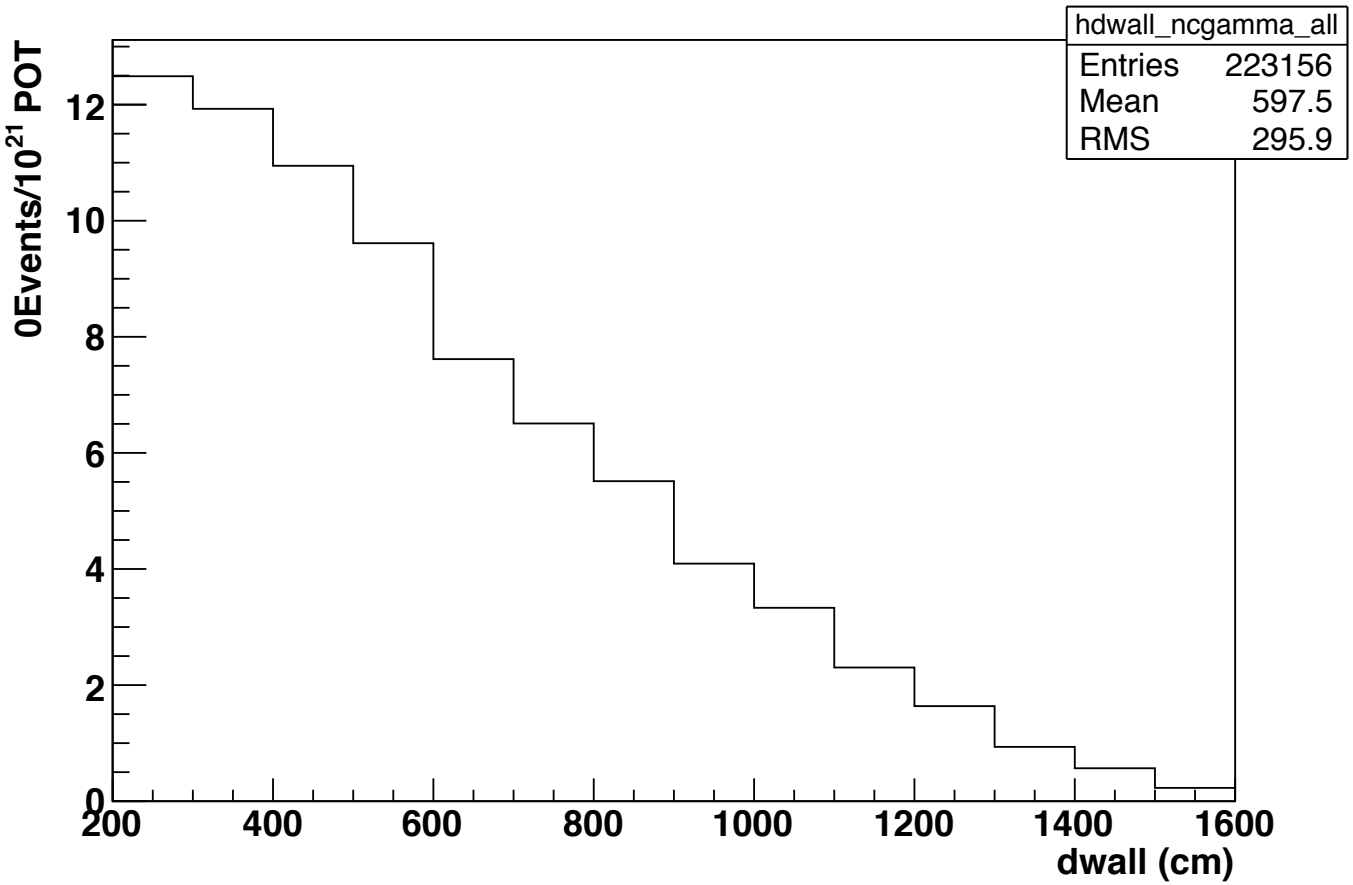
```
~/ncgamma/Processing@sukap001[622]_% python SelectNCGamma.py -o ncgammamcRun4.root /disk01/usr4/cnantais/lemc/lentuple/lentp_nu*.root
Begin processing 100 numu files
Begin processing 100 nue files
Error in <TFile::ReadBuffer>: error reading all requested bytes from file /disk01/usr4/cnantais/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root, got 63 of 300
Error in <TFile::Init>: cannot read directory info of file /disk01/usr4/cnantais/lemc/lentuple/lentp_nue.ncgamma_flux11a_neut532.085.root
Begin processing 100 numubar files
```

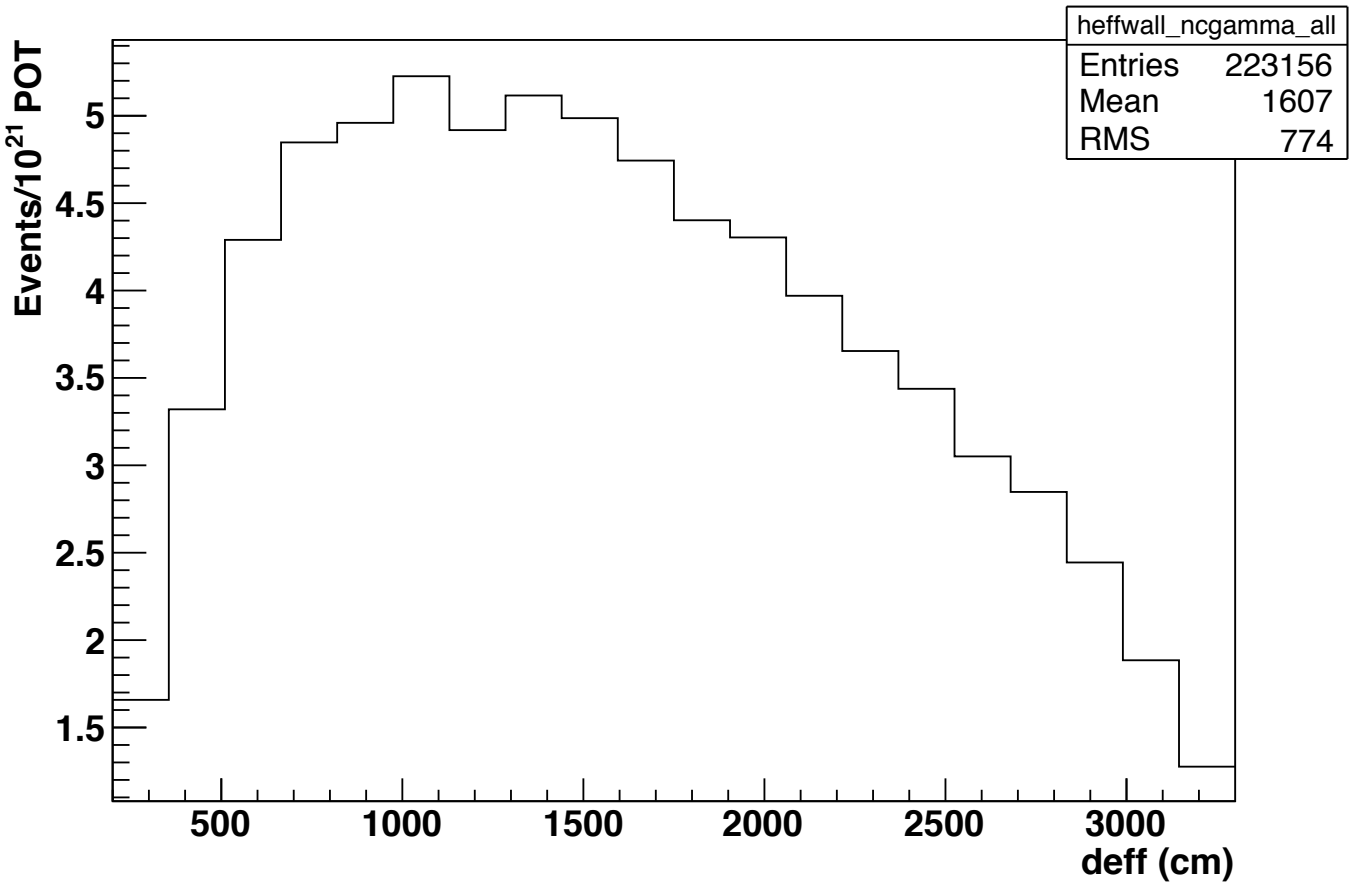
ncgammamcRun4.root

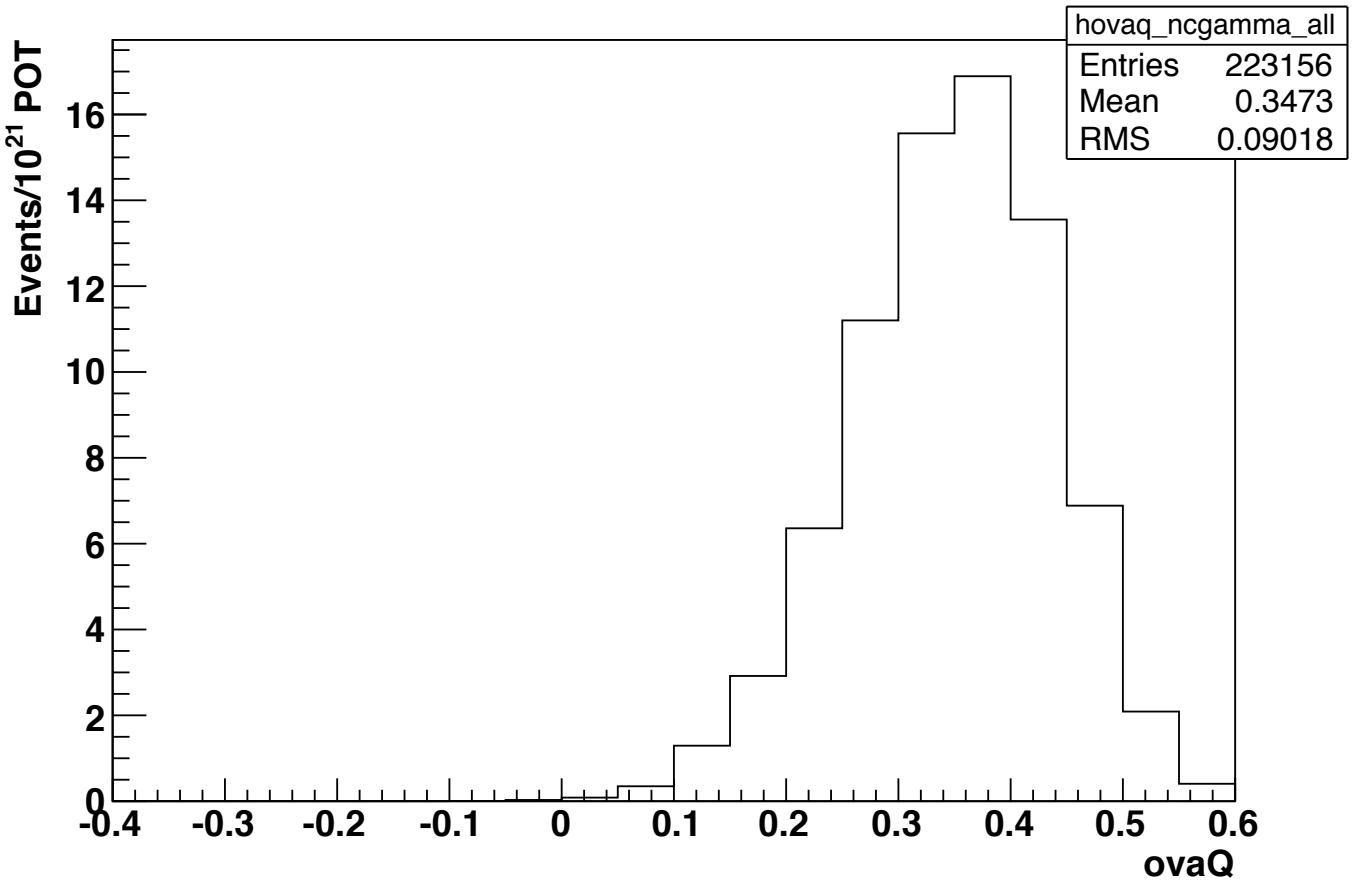
- henu, herec, hdwall, heffwall, hovaq
- nosel, ncgamma
- all, ccnqe, ncother, ccqe, ccnue, others, osc, signal

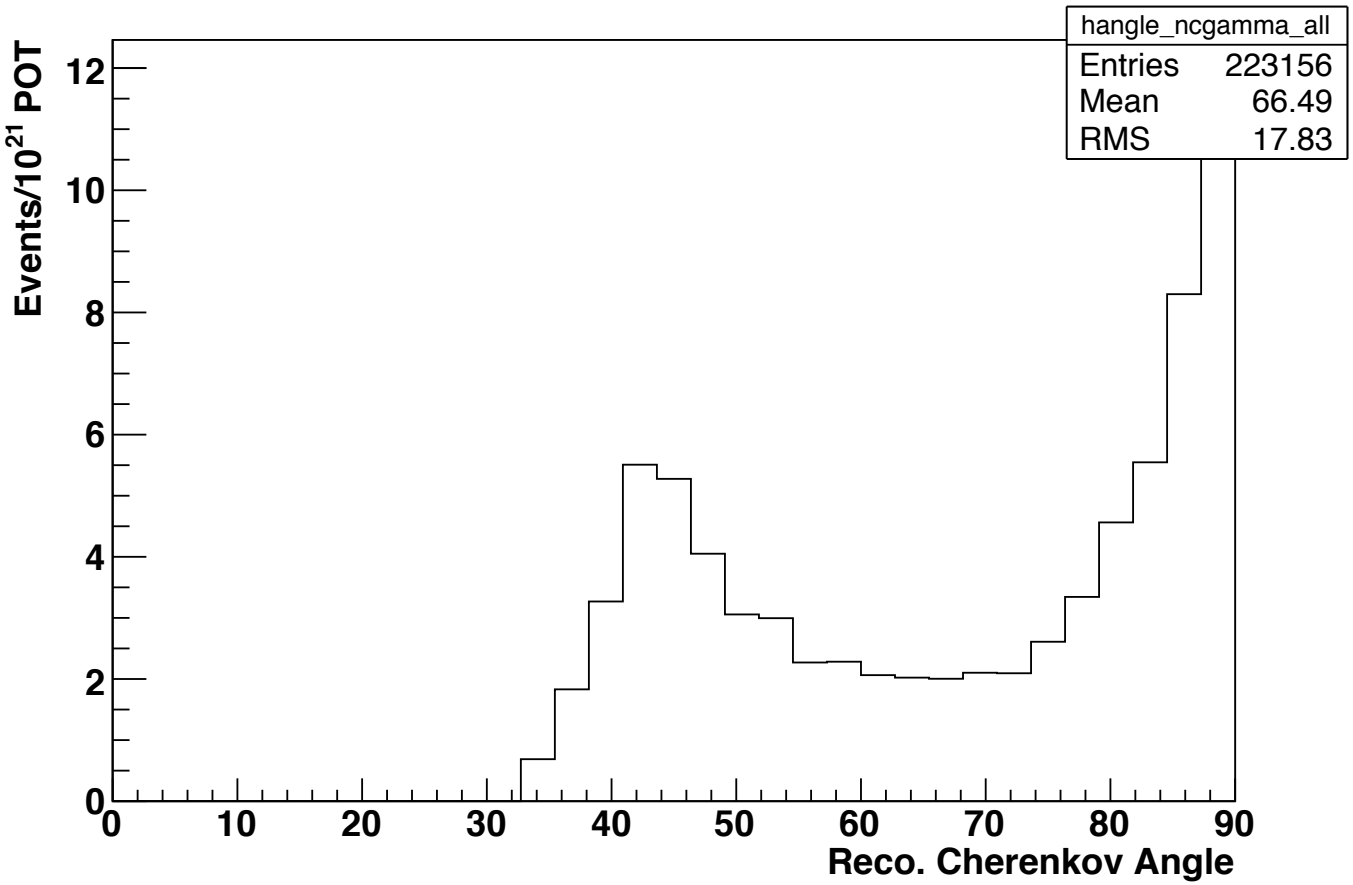
- I'm guessing the plot I'm used to is *_ncgamma_all


herec_ncgamma_all
Entries 223156
Mean 10.55
RMS 5.797
Events/10^21 POT
0
2
4
6
8
10
5
10
15
20
25
30
Reco. Energy (MeV)


hdwall_ncgamma_all
Entries 223156
Mean 597.5
RMS 295.9
0Events/10^21 POT
0
2
4
6
8
10
12
200
400
600
800
1000
1200
1400
1600
dwall (cm)


heffwall_ncgamma_all
Entries 223156
Mean 1607
RMS 774
Events/10^21 POT
5
4.5
4
3.5
3
2.5
2
1.5
500
1000
1500
2000
2500
3000
deff (cm)


hovaq_ncgamma_all
Entries 223156
Mean 0.3473
RMS 0.09018
Events/10^21 POT
0
2
4
6
8
10
12
14
16
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
0.3
0.4
0.5
0.6
ovaQ


hangle_ncgamma_all
Entries 223156
Mean 66.49
RMS 17.83
Events/10^21 POT
0
2
4
6
8
10
12
0
10
20
30
40
50
60
70
80
90
Reco. Cherenkov Angle