“GRETINA/AUX Gamma Ray Tracking software”

The GT tracker

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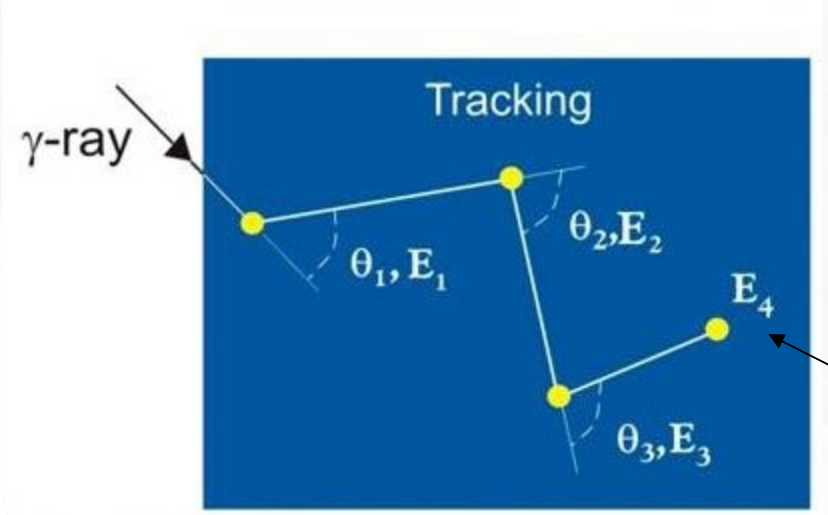
torben lauritsen, ANL

Tracking documentation

- Classical I-Y and Co NIM paper: NIM A 340 (1999) 69-83
- Other papers: NIM A 615 (2010) 188, NIM A 550 (2005) 379, NIM A 533 (2004) 454, NIM A 437 (1999) 538, etc
- ‘tracking package’ documentation @ http://www.phy.anl.gov/gretina/GT_aux.pdf
- I-Y has introduction on tracking in this document as well

Tracking example:



Have four Interaction points
(i.e., three Compton scatterings)

For each point:

Find observed scattering angle
+ know interaction energy

(assume total photo absorption)

Theoretically we know:

$$E'_\gamma = \frac{0.511}{1 + \frac{0.511}{E_\gamma} - cos(\theta)}$$

Create Figure Of Merit

$$FOM = \frac{\sqrt{(\sum_i (\theta_i^{theo} - \theta_i^{obs})^2)}}{n_{interactions}}$$

trackMain

- Not going to discuss the tracking principles more here
- ...just how to ***use*** the tracking program, trackMain, in the offline mode
- BTW: the tracking task also rotates the interaction points into world coordinates from the crystal coordinates
- ----------
- As usual: there is a ***chat file*** with commands and comments; *go trough the main items*...

How to get the track ware

- wget http:/www.phy.anl.gov/gretina/gt_bgs_track/tar.tgz
- tar -zxvf tar.tgz
- Read README

instructions

- mkdir bin_Linux_i386
- Make clean, make
- Follow steps in ‘go’ file (modify where needed)
-

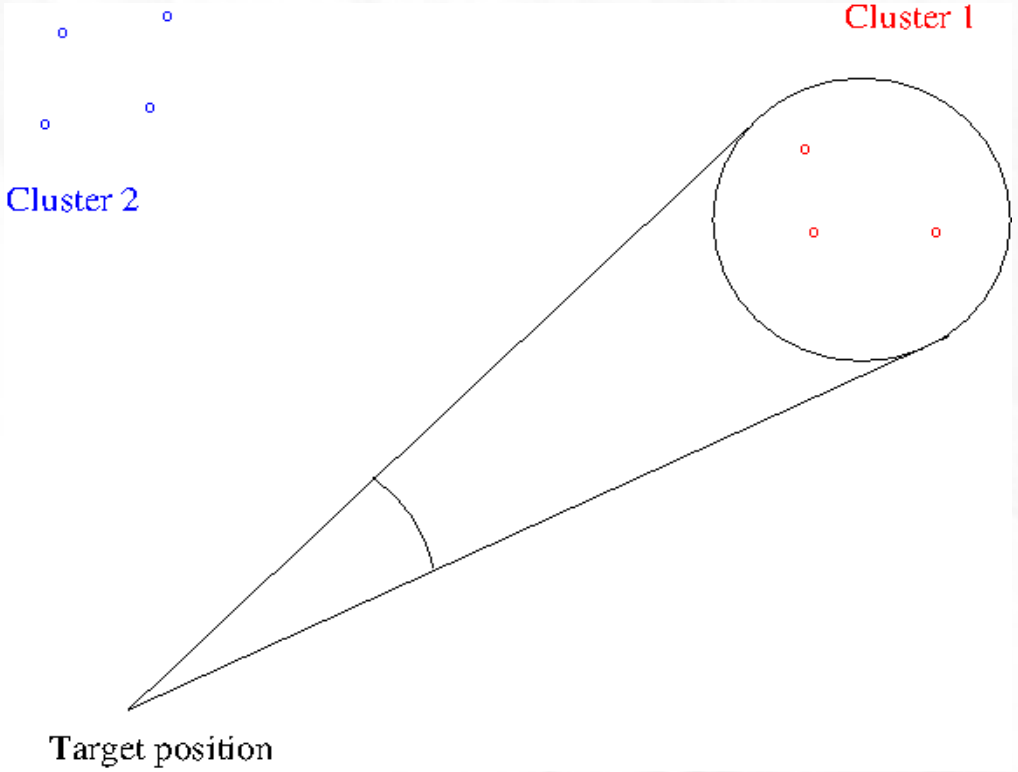
Starting point

- trackMain track.chat GTDATA/Global_mod.dat

Chat file

Coincidence data from combdata3

Clustering: first step in defining a 'gamma-ray hit'



Now we can talk about a Gamma ray hit! (-- or at least a candidate)

Simulations suggest a good clustering angle is about 5 degrees

```
#########################################################
# modify the  decomposition
# energies in the tracking
#########################################################

# use the CC FPGA energies or segment FPGA energies

useCCEnergy
;useSegEnergy


#####################
# clustering angle
#####################

#clustering angle (degrees) [aka 'alpha']
#not necessarily defined as in NIM paper!!

;clusterangle 21
clusterangle 22
#########################################################
# enabled detectors

enabled "1-130"
```

Cannot use the energies from decomposition task directly....

$$E_i = \frac{E_i}{\sum_i E_i} \times E_{CC}$$

```
#----------------
# --> specify the tracking strategies to use
# trackingstrategy <ndet> <option>
#  0: full tracking
#  1: [REMOVED] largest energy point (==first in E sort)
#  2: [REMOVED] random point
#  3: 'kickout', break @ first worse permutation
#  4: 'goodenough', break @ first OK FOM encountered
#  5: 'jump', specify jump option: g...t...

trackingstrategy 1 0
trackingstrategy 2 0
trackingstrategy 3 0

# use for full tracking (usually too costly CPU wise)
;trackingstrategy 4 0
;trackingstrategy 5 0
;trackingstrategy 6 0
;trackingstrategy 7 0
;trackingstrategy 8 0

# use for realistic realtime tracking
trackingstrategy 4 5 ggtt
trackingstrategy 5 5 ggttt
trackingstrategy 6 5 ggtttt
trackingstrategy 7 5 gggtttt
trackingstrategy 8 5 gggttttt
```

Not used

group tail

```
#-----------------------------------------------
# figure of merit cuts. In the trackingstrategy
# of 'goodenough', we bail if we get a FOM below
# the fomgoodenough value given. In the 'jump'
# trackingstrategy we jump to next group if the
# FOM is above the fomjump value given.

fomjump 1.0
fomgoodenough 1.0
```

```
#                       +-- number of datapoints following
#                        |    +-- set FOM to this value outside range
#                        |     |    +-- target to detector distance [cm]
#                        |     |    |
singlehitmaxdepth 22 1.9 18.5
0.000 0.59
0.050 0.59
0.060 0.65
0.080 0.82
0.100 1.04
0.150 1.7
0.200 2.31
0.300 3.15
0.400 3.72
0.500 4.15
0.600 4.53
0.800 5.17
1.000 5.74
1.250 6.38
1.500 6.94
2.000 7.84
3.000 9.01
4.000 9.66
5.000 10
6.000 10.16
8.000 10.17
10.00 10.01
# |       |
# |       +-- range (from surface of crystal) [cm]
#+-- energy [MeV]
# [data points for 0.0 and 16.3 must be there]
```

Mark with large FOM value

```
#########################################################
# FOM we assign to single hits
# so they can be on an equal playing
# field with multihits that have a finite FOM
#########################################################
```

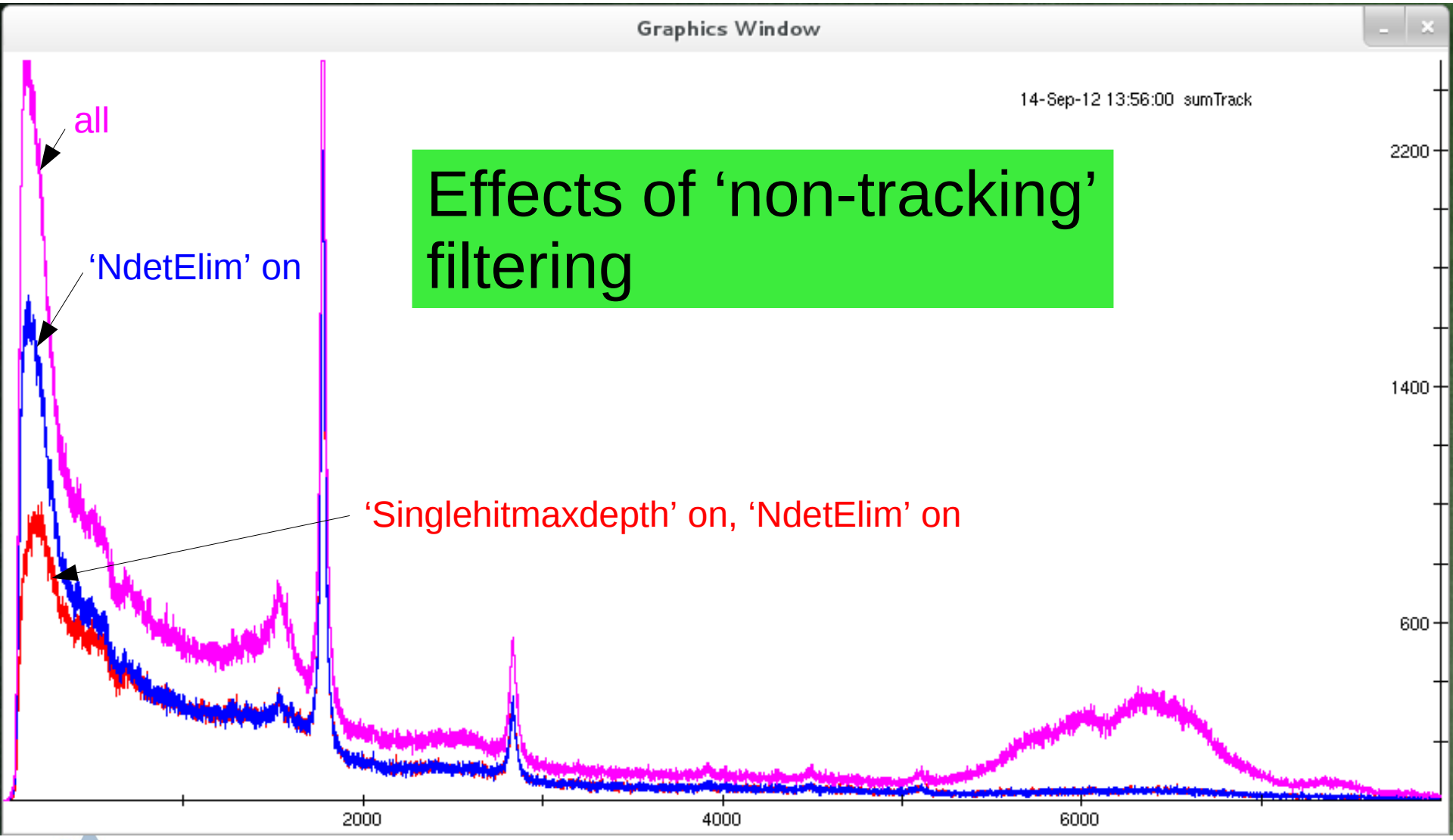
singlesfom 0.0

Matters for adding outlying single hits into clusters

```
#--------------------------------------
# ndet and associated energy range limits
#--------------------------------------

# for each number of sector hits (==ndet)
# we expect a certain energy range. Assign
# events outside these limits a FOM that
# excludes them from further analysis
#            +-- ndet value
#             |    +-- elo limits
#             |    |        +-- ehi limits
#             |    |        |   +-- assign this FOM value if outside
#             |    |        |   |
ndetElim 1   0.0   0.8 1.81
ndetElim 2   0.0   1.6 1.82
ndetElim 3   0.0   3.2 1.83
ndetElim 4   0.4   6.4 1.84
ndetElim 5   0.8  18.8 1.85
ndetElim 6   1.6  27.6 1.86
ndetElim 7   3.2  53.2 1.87
ndetElim 8   6.4  99.0 1.88
ndetElim 9  18.1  99.0 1.89
```

These values have not been determined accurately yet

Effects of ‘non-tracking’ filtering



```
#############################################################
# methods for dealings with UNTRACKED (monster) clusters
#############################################################

#---------------
# enable reclustering for UNTRACKED (monster) clusters
# [method 1 of 2 to deal with those]
#                  +- 'kickout' FOM value
#                  |      +- threshold FOM for recluster
#                  |      |    +- ndet minimum for reclustering
#                  |      |    |  +- max number of reductions in alpha
#                  |      |    |  |   +- reduction factor for alpha
#                  |      |    |  |   |
;recluster1   0.01  0.1  3 10  0.90

#---------------
# enable splitting of clusters for UNTRACKED (monster) clusters
# [method 2 of 2 to deal with those]
#              +- 'kickout' FOM value
#              |   +- threshold FOM for splitting
#              |   |    +- ndet minimum for splitting
#              |   |    |  +- ndet maximum for splitting
#              |   |    |  |  +- max number of tries before giving up
#              |   |    |  |  |
#              |   |    |  |  |
;splitclusters1 0.01 0.6  3 16 100
```

```
#################################################
# methods for splitting already tracked clusters
# that don't look right
#################################################

#---------------
# enable reclustering for TRACKED clusters
#                 +- 'kickout' FOM value
#                 |       +- threshold FOM for recluster
#                 |       |   +- ndet minimum before trying to recluster
#                 |       |   |     +- max number of reductions in alpha
#                 |       |   |     |   +- reduction factor for alpha
#                 |       |   |     |   |
;recluster2  0.10  0.8 3   6  0.90

#---------------
# enable splitting of clusters
#                    +- 'kickout' FOM value
#                    |      +- threshold FOM for splitting
#                    |      |   +- ndet minimum for splitting
#                    |      |   |      +- ndet maximum for splitting
#                    |      |   |      |  +- max number of tries before giving up
#                    |      |   |      |  |      +- good enough improvement fraction
#                    |      |   |      |  |      |
;splitclusters2 0.10 0.7  3   16 200 0.4
```

```
#####################################################
# methods for combining already tracked clusters
# that don't look right
#####################################################

#----------------
# enable combination of clusters
#                       +- 'kickout' FOM value
#                        |      +- threshold FOM for combining
#                        |       |   +- ndet maximum for combining
#                        |       |   |      +- max distance for inclusion attempt
#                        |       |   |       |
;combineclusters 0.10 0.1  5    10

#########################################
# combine single hits (matchmaker)
#########################################

#                    +- 'kickout' FOM value
#                    |      +- max distance for inclusion attempt
#                    |       |
;matchmaker 0.10  10
```

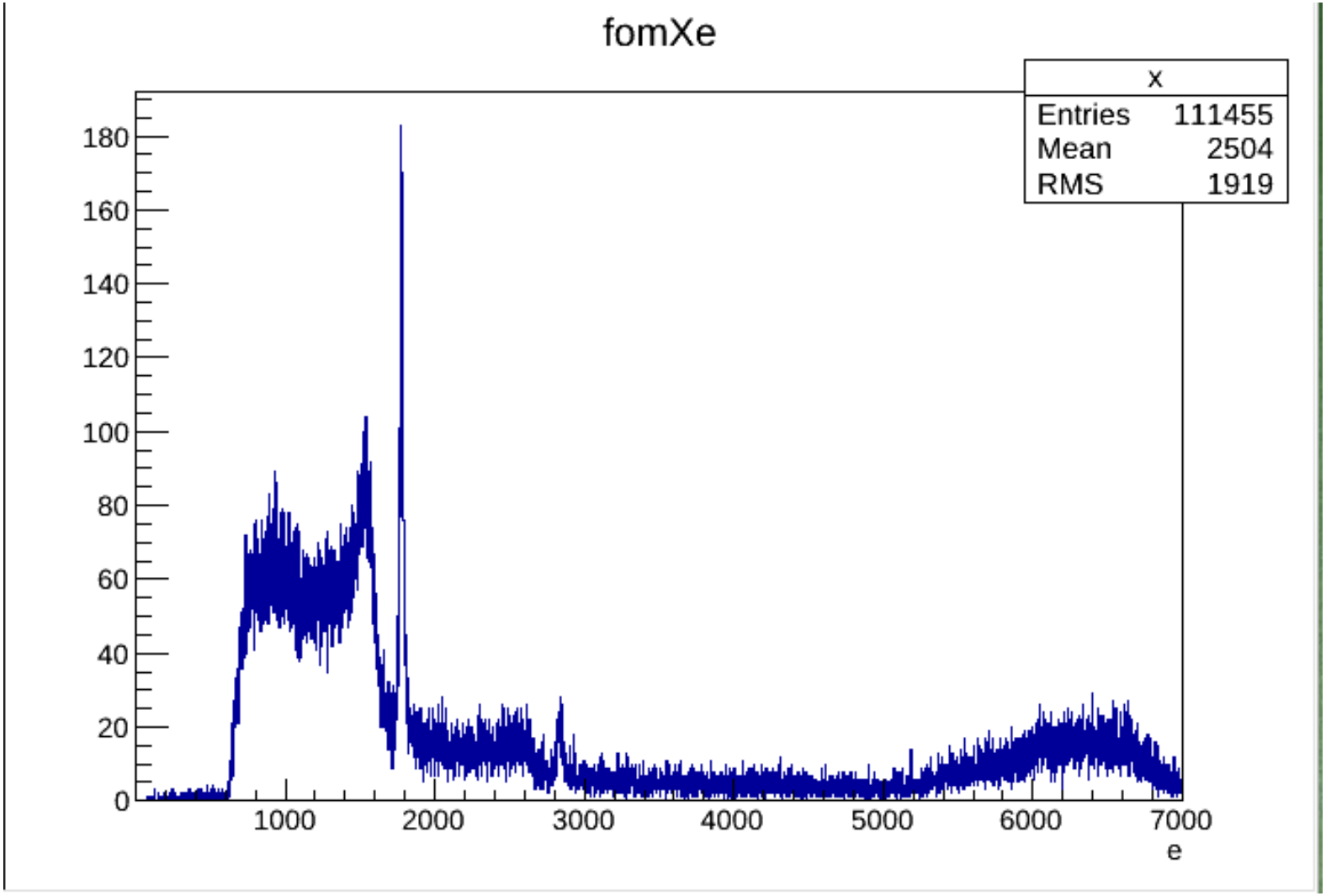
```
#----------------
# number of itterative loops (more than one
# is very CPU costly! and does not help much
# at the moment, could even hurt!)

itterations 1
```

To do list

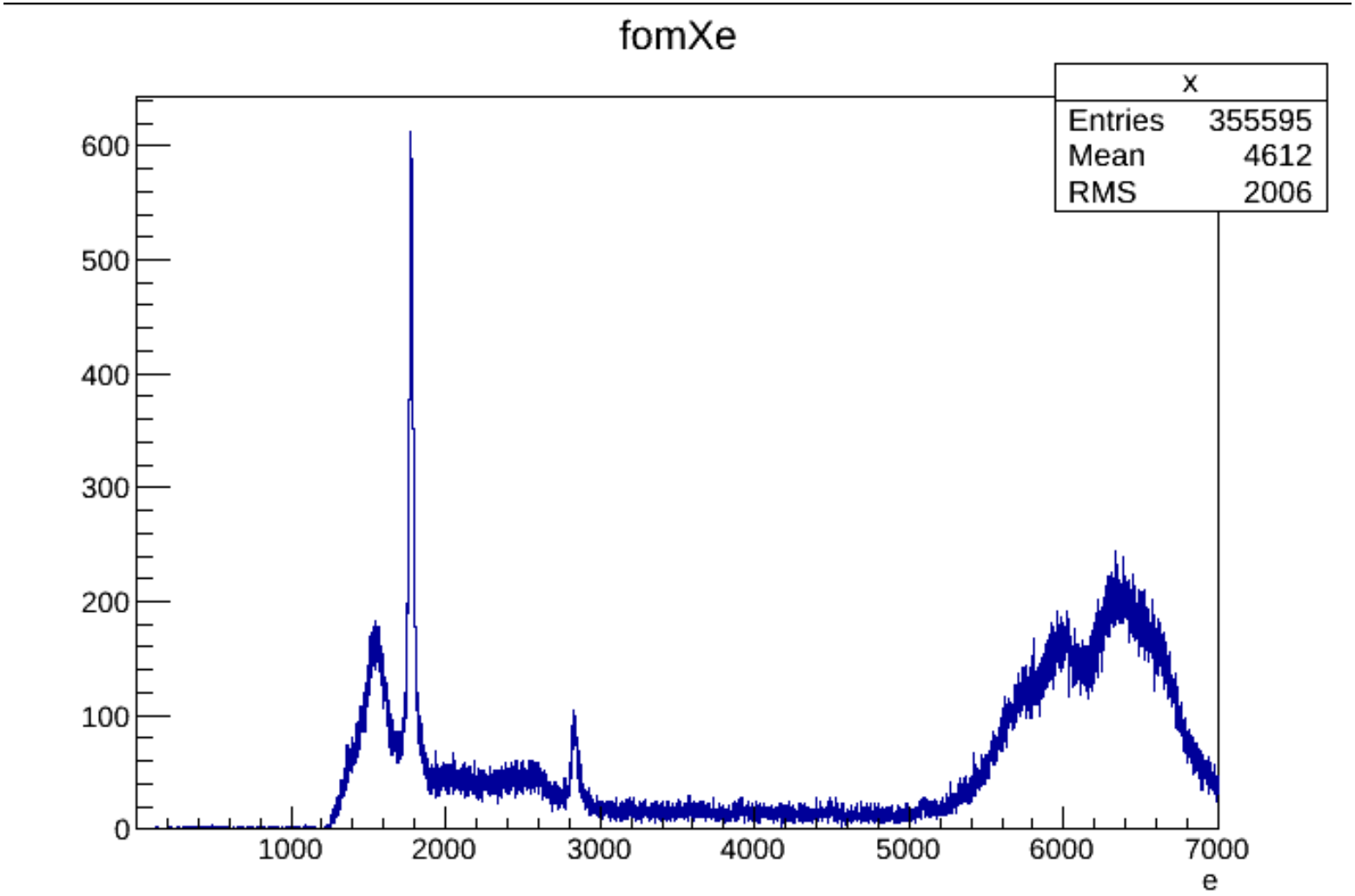
- Write tracked data out in standard gebData format (timestamp??, does it matter?)
- Backward compatibility to old data formats
- Add zlib compression? (we do at dgs, gain a factor of ~2)
- Add pair creation in tracking
- use uncertainty information in tracking
- Decomposition task should send best and second best fit so we could try them in the tracking
- **More simulations? (hits across crystals, not necessarily right next to one another), getting GEANT simulation data from AGATA**
- **Expand ctkana**

SPARES

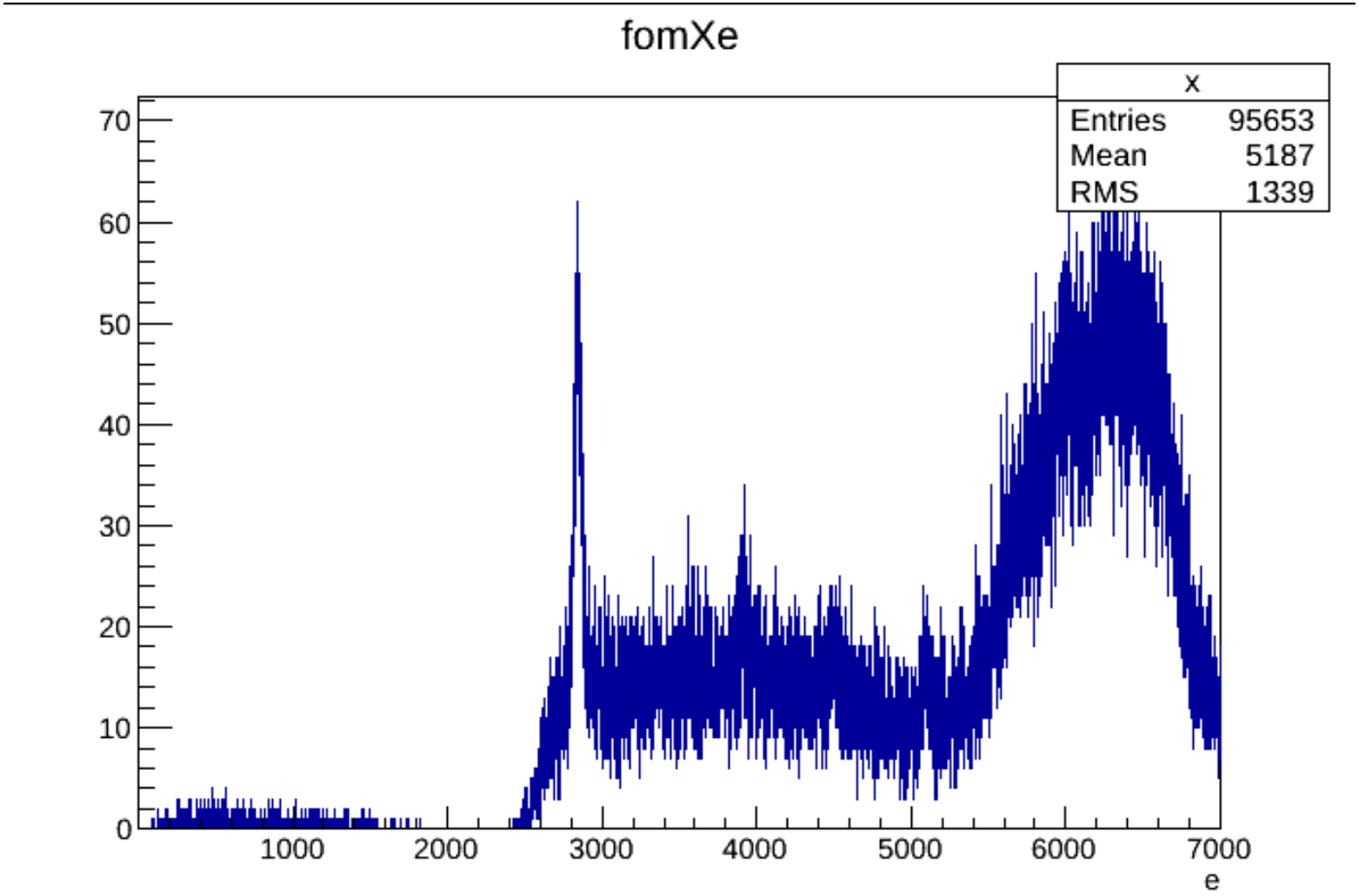
ndetElim 1 0.0 0.8 1.81



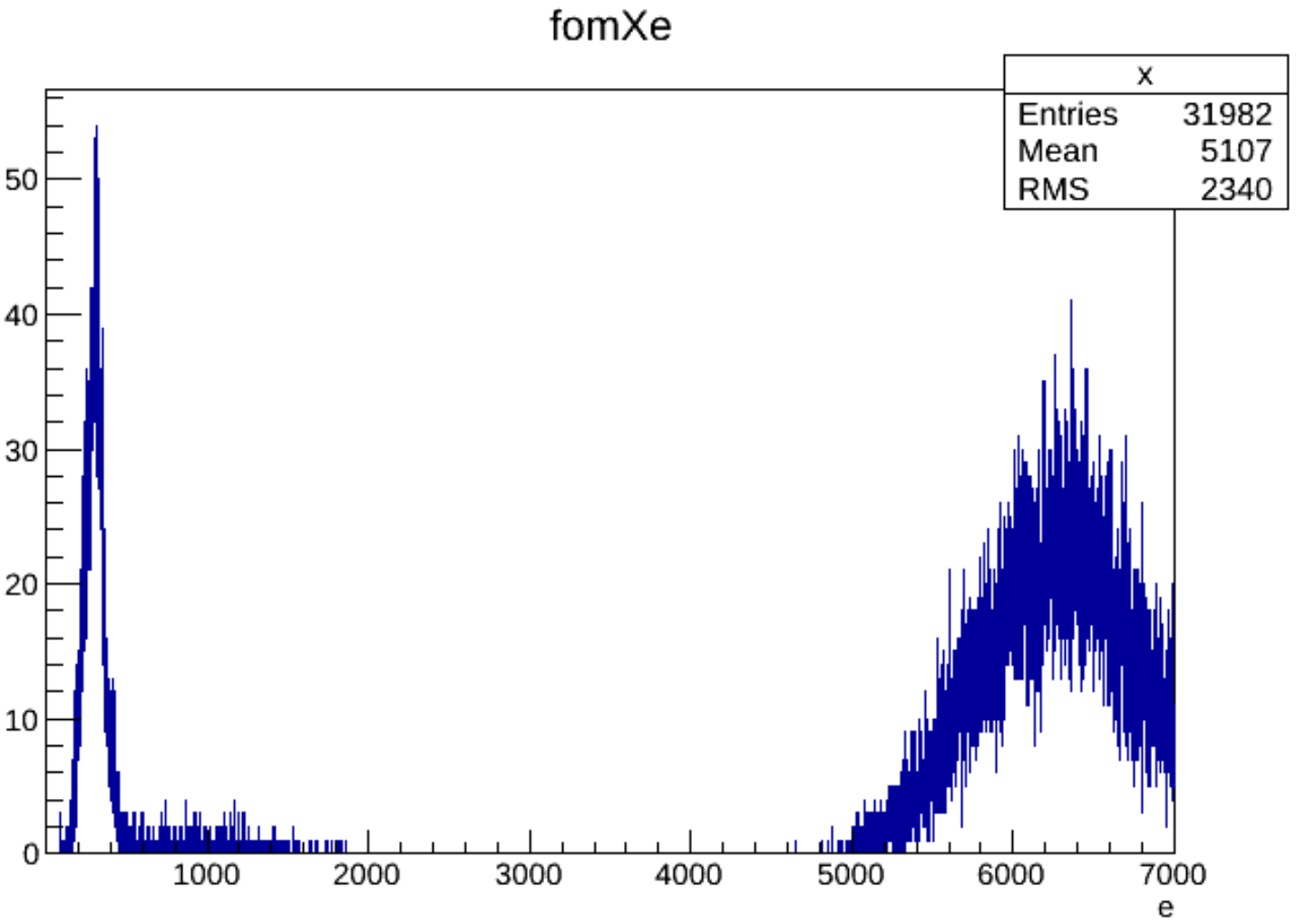
ndetElim 2 0.0 1.6 1.82



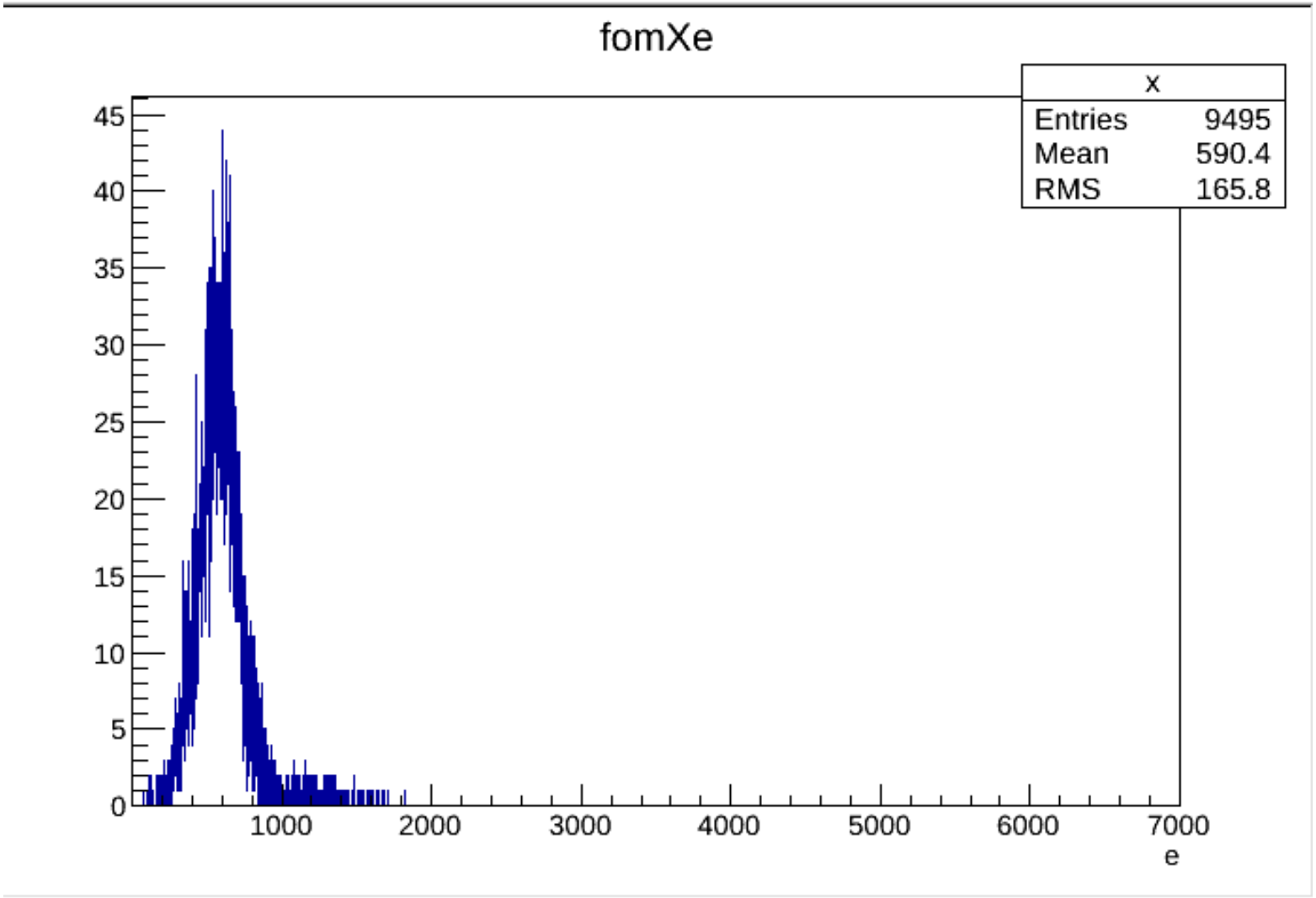
ndetElim 3 0.0 3.2 1.83



ndetElim 4 0.4 6.4 1.84



ndetElim 5 0.8 18.8 1.85



singlehitmaxdepth 23 1.9 18.5
0.000 0.59
0.050 0.59
.
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