The algorithm for the PWO calorimeter

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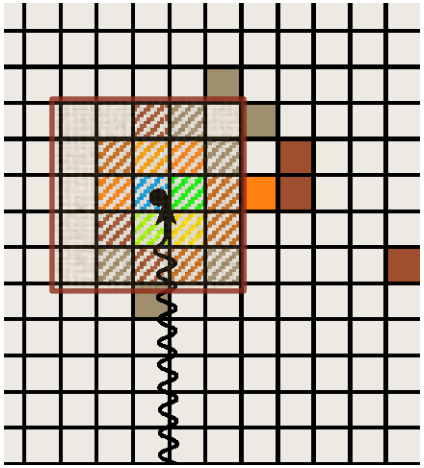
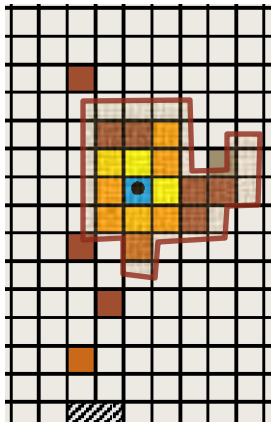
5x5 VS island

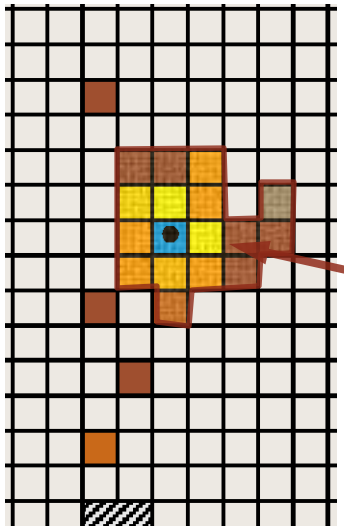
- 5x5 algorithm:
  - 1) Find maximum energy deposition cell
  - 2) declare all 5x5 area around belonging one hit
- Island algorithm:
  - 1) Find maximum energy deposition cell
  - 2) declare all simply connected area around as initial “raw” cluster
  - 3) try to split “raw” cluster into many hits





GAMS island algorithm

(what is inside, block-scheme
with original function names preserved)



data_pht
(prepare integer arrays for involved cells:
cell address: *100*row+column*,
cell energy: in *[10 MeV]* units

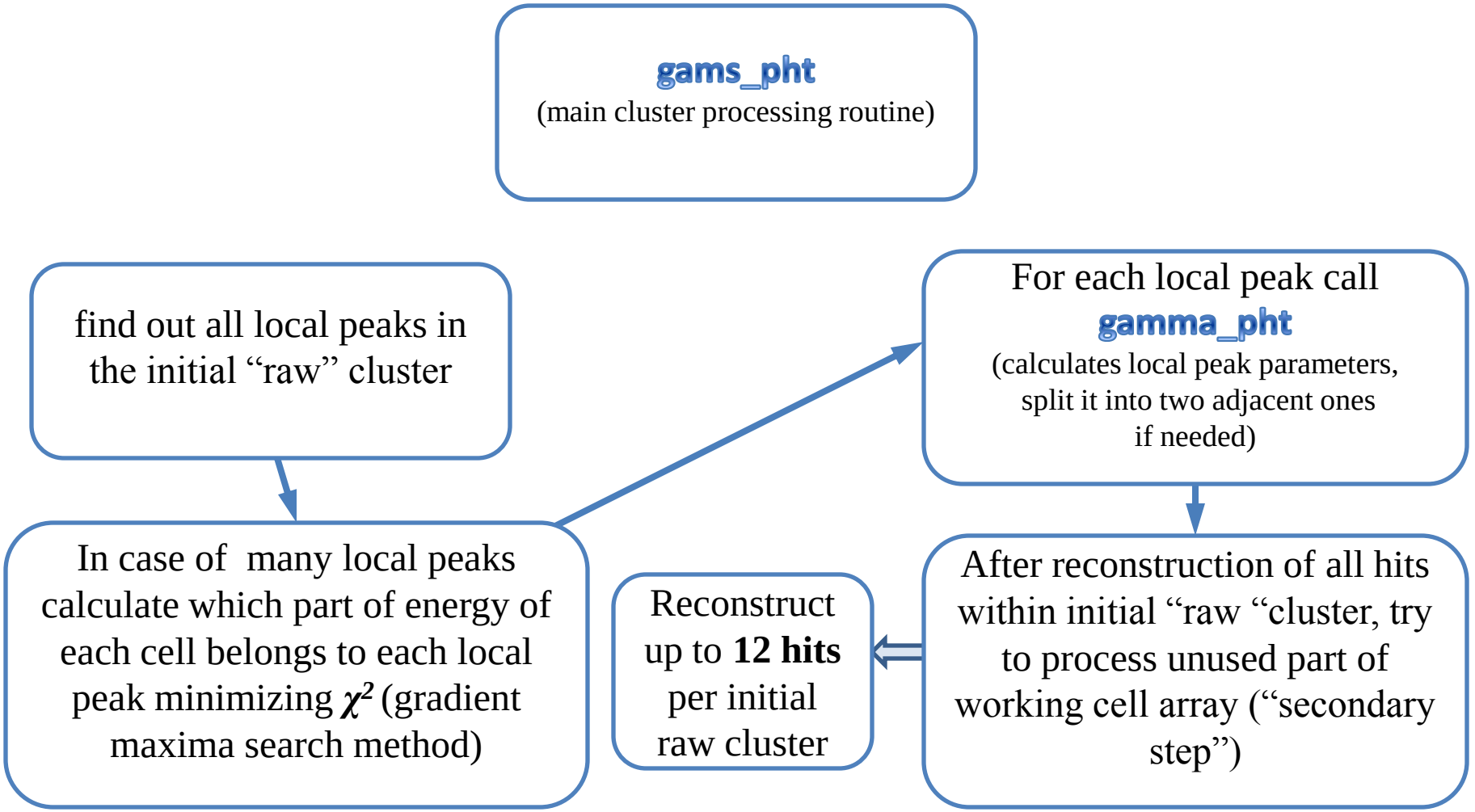
clus_pht
(initial cluster search as a simply connected cell areas)

order_pht
(sort cell energy array in increasing order)

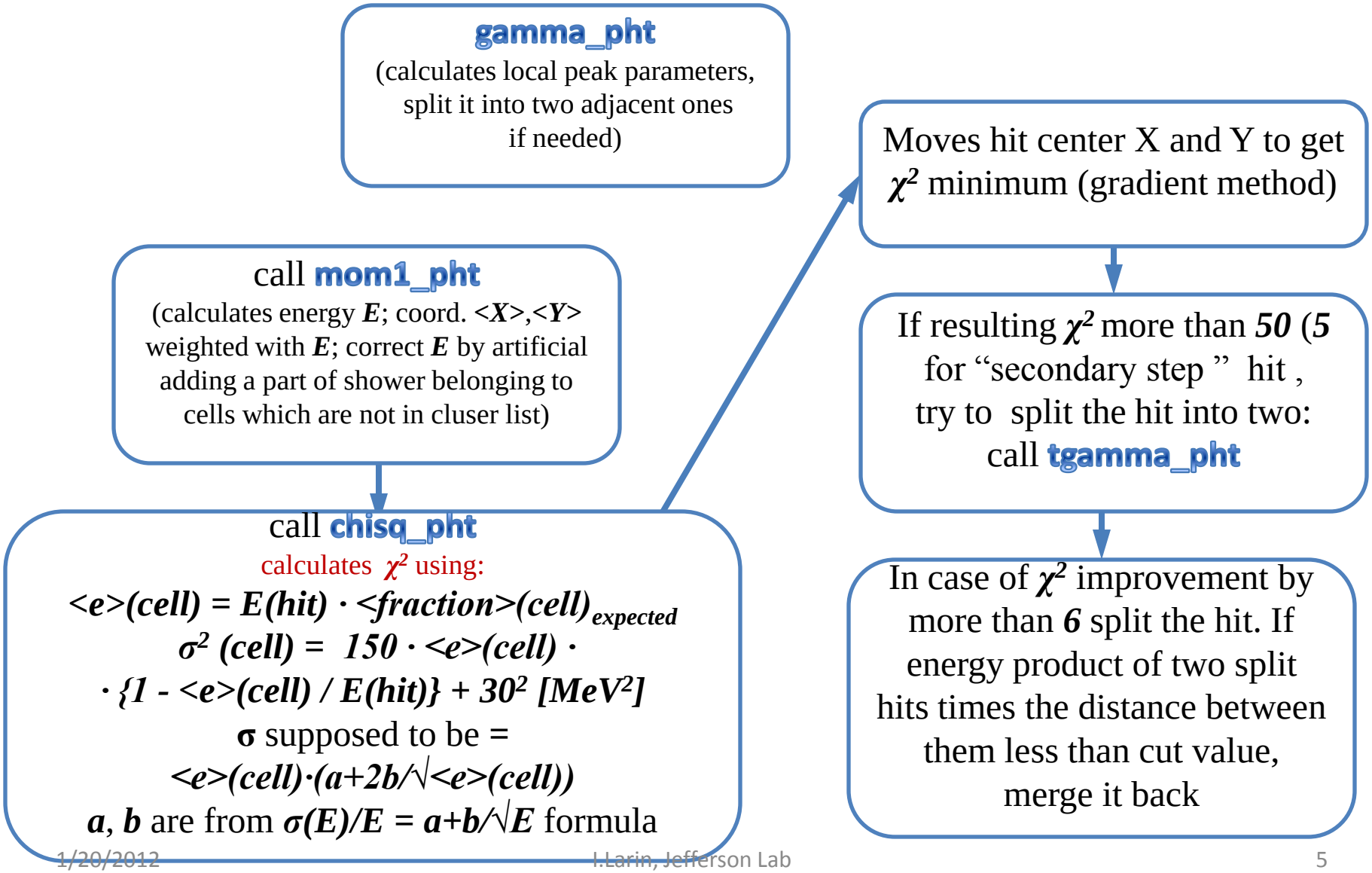
loop over initial "raw" clusters:
call **gams_pht** for each one

out_pht
(cut off low energy clusters)

GAMS island algorithm (continued)

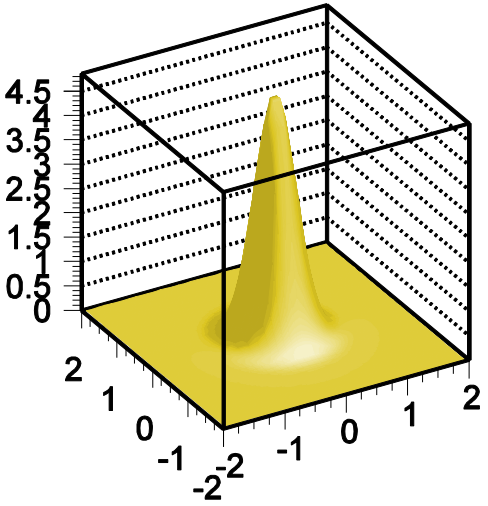


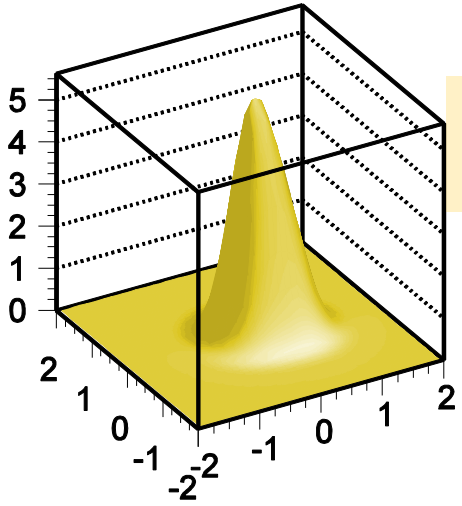
GAMS island algorithm (continued)



Cluster overlapping: different cases

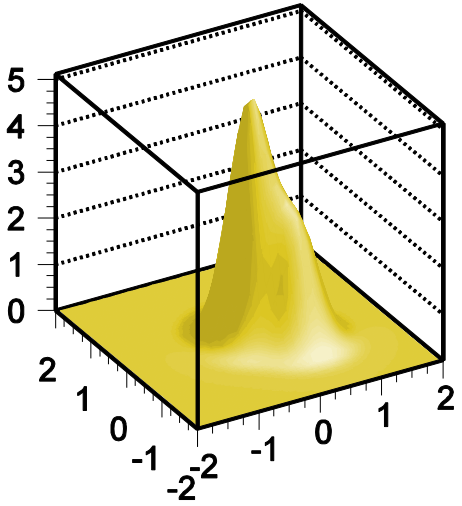
Single cluster

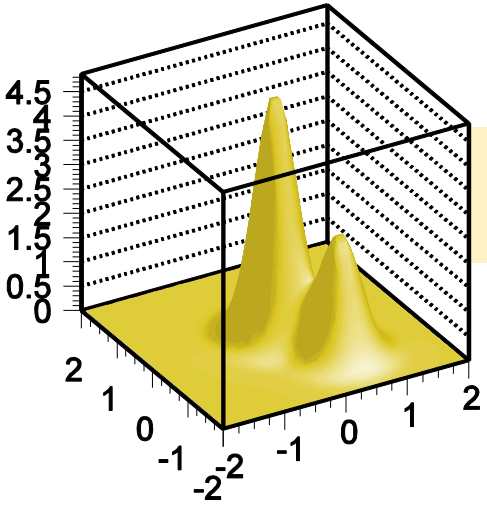




Two clusters can not be distinguished

Two clusters do not produce two maxima but can be distinguished



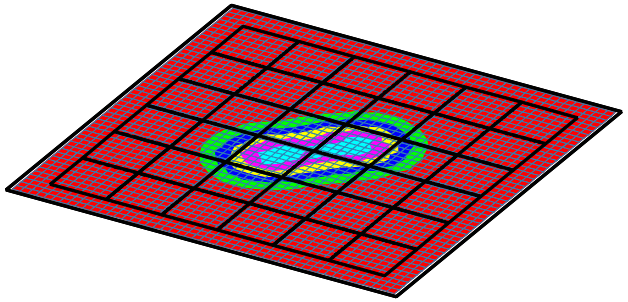


Two clusters produce two maxima

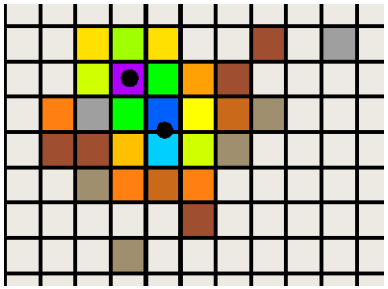
Cluster overlapping cases

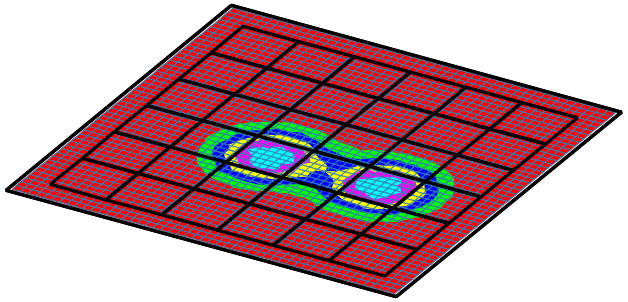
Shower density

Cluster pattern

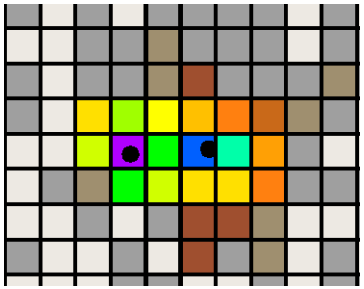


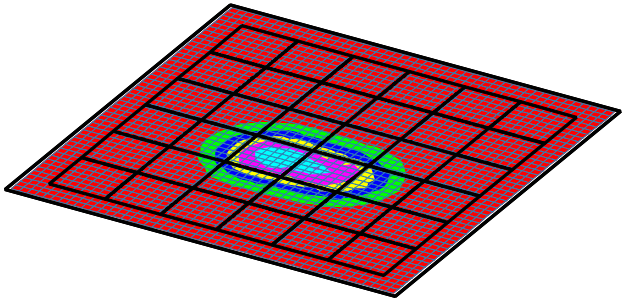
second maximum:
Corner to corner:
dist. = √2 cells



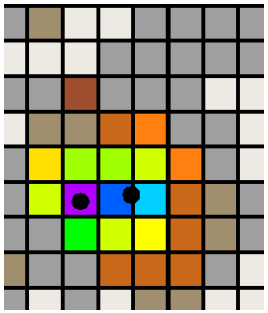


second maximum:
Side to side:
dist. = 2 cells





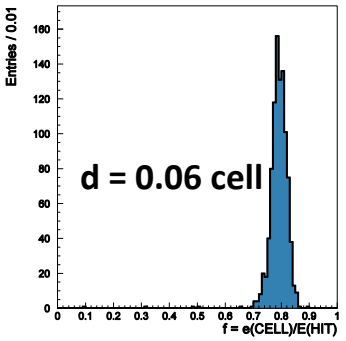
No second maximum

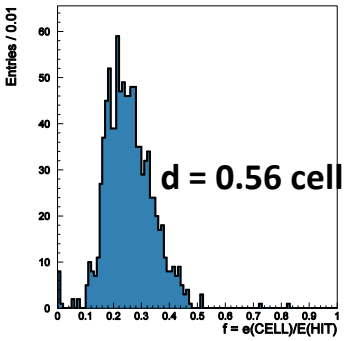


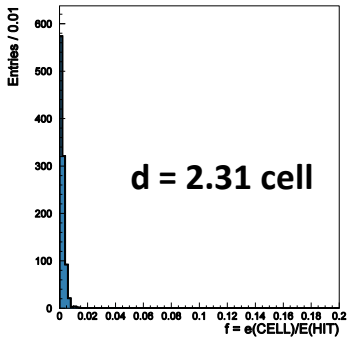
Things to be improved:

- cluster elements (which cells belong to which hit) are not stored
- Missed channels (cells with zero signal) are not participating in χ^2 calculation
- Only rough estimation of σ for χ^2 calculation
- χ^2 calculation assumes Gaussian distribution of energy deposition in cells. Real distributions are not Gaussian, log-likelihood needs to be implemented

Electron scan data for total energy fraction deposited in cell as a function of ***d*** - distance between hit point and cell center:







- There are a lot of hardcoded constants - the code is difficult for transferring

What is inside

- ***"Phot_cell"*** function: expected mean energy fraction of total energy deposited in the cell as a function of the distance between hit point and cell center
- Its sigma

Transverse shower profile:

- Integrated energy function:

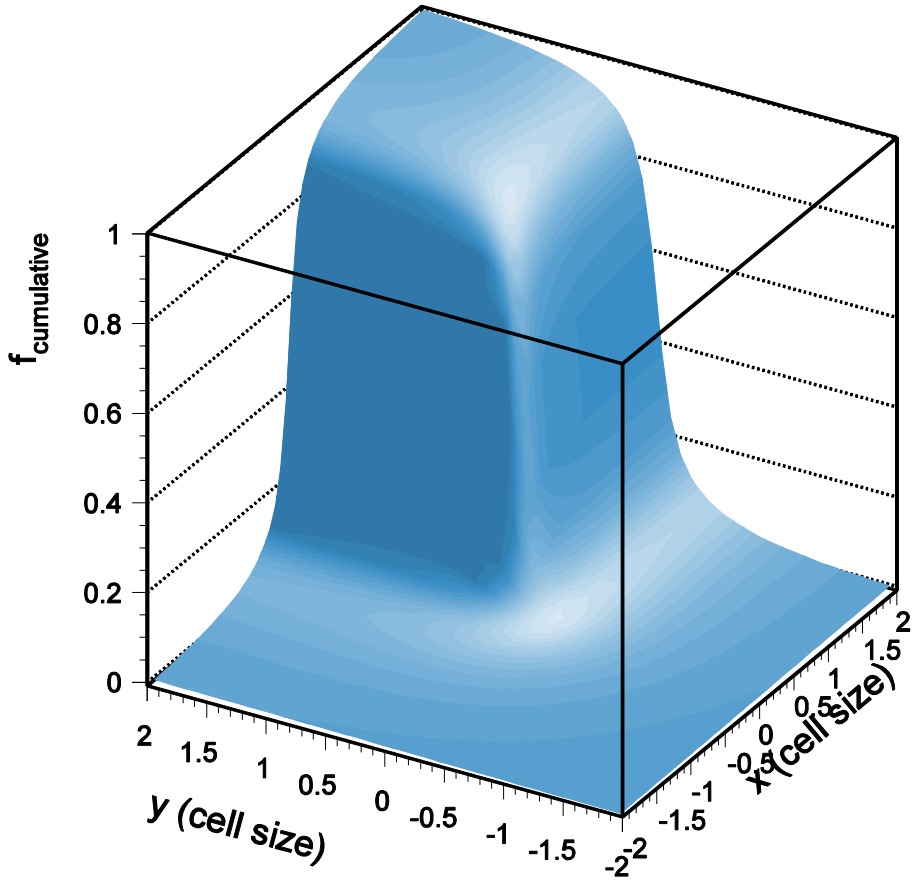
$$F(x,y) \equiv \frac{E_{\text{int}}(x,y)}{E_{tot}} = \int_{-\infty}^{x} dx' \int_{-\infty}^{y} dy' \ \rho(x',y')$$

- Parameterized shape *(Lednev's parameterization)*:

$$F(x,y) = \frac{1}{2\pi} \sum_i a_i \cdot f_{cumulative}(\frac{x}{b_i}, \frac{y}{b_i}); \textit{normalization}: \sum_i a_i = 1$$

$$f_{cumulative}(u,v) = \text{Arctg}\frac{u+v}{1-uv} + \text{Arctg}\frac{uv}{\sqrt{1+u^2+v^2}}$$

PWO cumulative function (electron scan data fit)

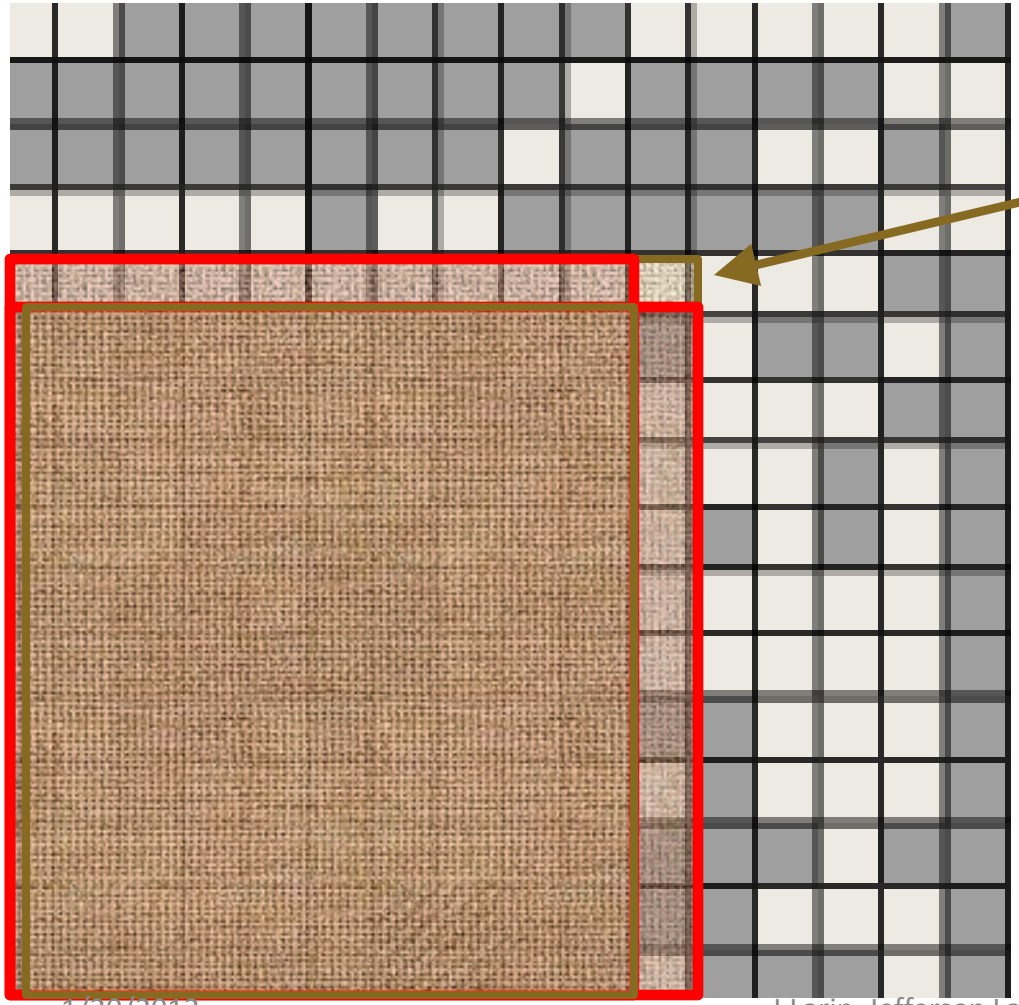


Examples of set of constants obtained from the PWO electron scan data fit:

a1	0.815636	0.91497
b1	0.0887125	0.105129
a2	-0.78113	-0.068324
b2	1.06357	894.971
a3	0.965494	0.153355
b3	0.729796	0.541627

Usually a2<0

Calculating cell energy from cumulative function difference:



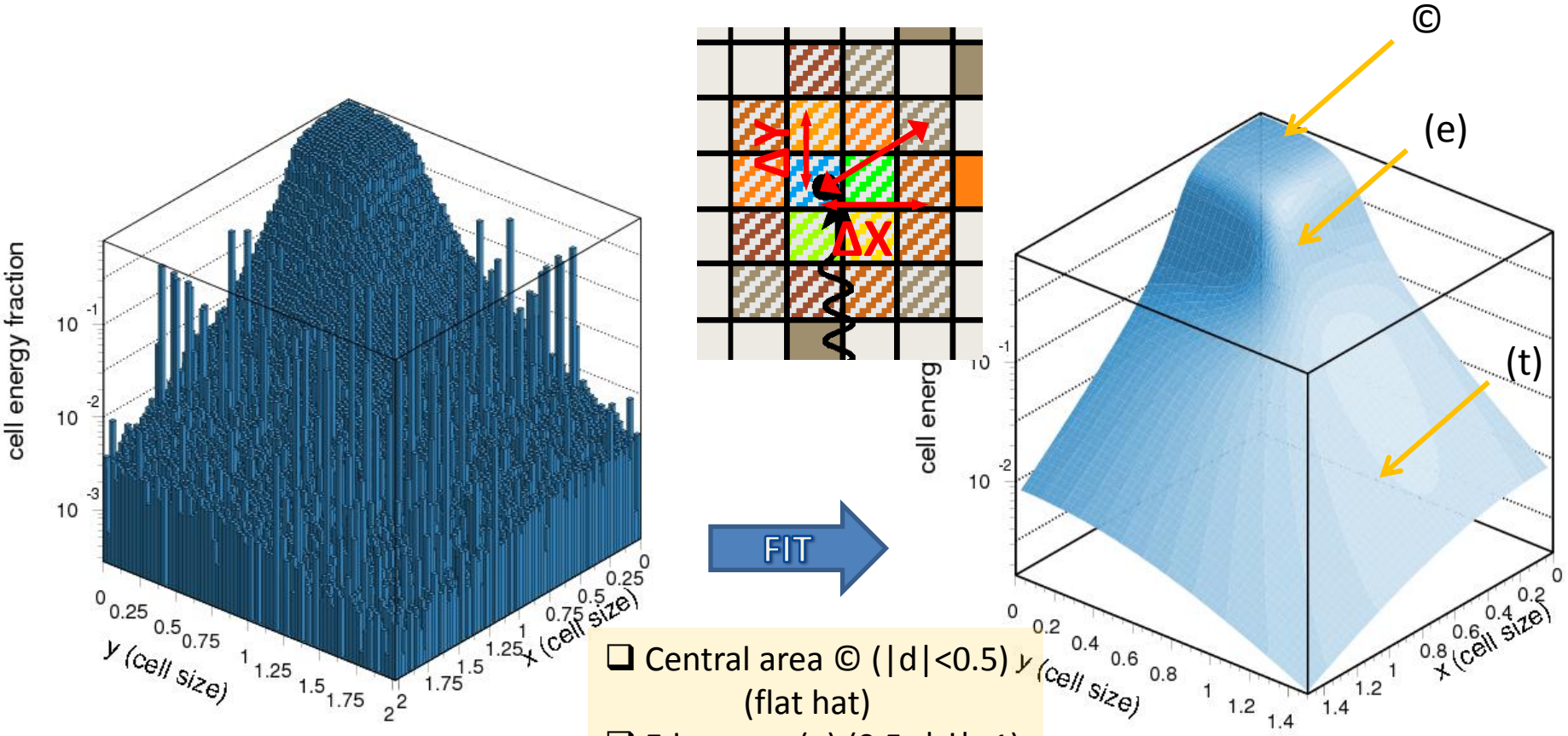
$$f_{cell} = F(x_{cell} + \frac{1}{2} l_{cell}, y_{cell} + \frac{1}{2} l_{cell}) +$$

$$+ F(x_{cell} - \frac{1}{2} l_{cell}, y_{cell} - \frac{1}{2} l_{cell}) -$$

$$- F(x_{cell} + \frac{1}{2} l_{cell}, y_{cell} - \frac{1}{2} l_{cell}) -$$

$$- F(x_{cell} - \frac{1}{2} l_{cell}, y_{cell} + \frac{1}{2} l_{cell})$$

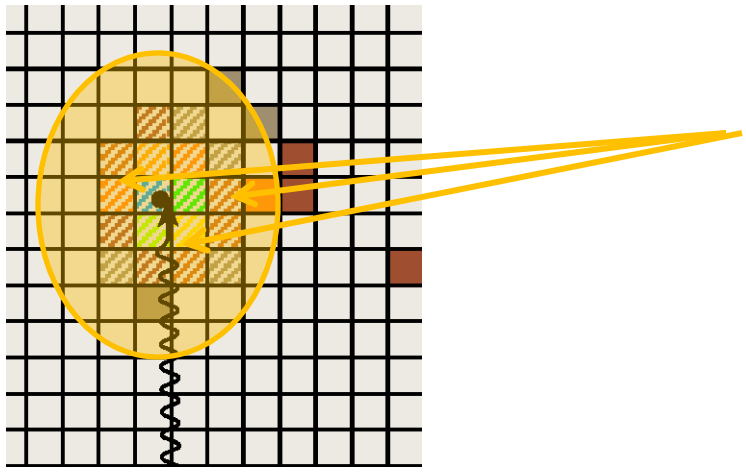
Cell energy fraction VS distance between hit point and cell center: electron scan data (E_e≈4GeV) and it's fit



- Central area © (|d|<0.5) (flat hat)
- Edge area (e) (0.5<|d|<1) (high gradient value)
- Tail area (t) (|d|>1) (exponential decreasing)

Monte-Carlo implementation:

- Function of cell energy fraction and its sigma can be used for "fast" Monte-Carlo simulations w/o real shower propagation. This allows to save 3-4 order of magnitude of simulation time

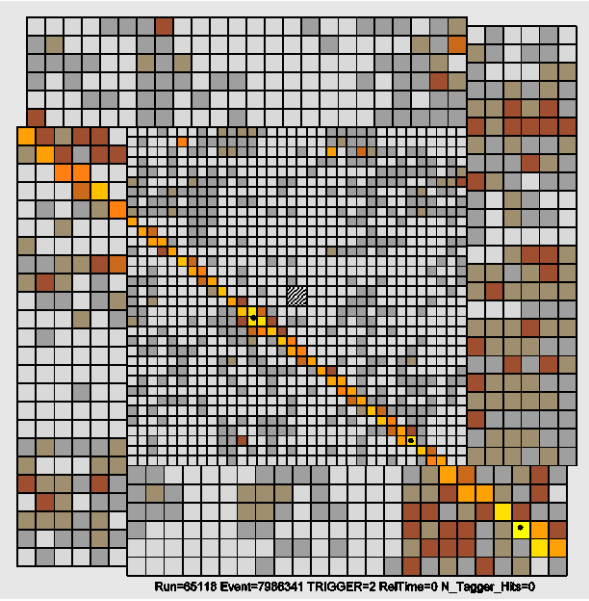


$$< E_{cell} > = E_{hit} \cdot f_{cell}$$

Other Monte-Carlo options:

- Real shower propagation:
  - 4-5 order of magnitude more CPU time
  - but cluster shape closer to real, in particular for irregular areas like holes, shielded cells, corners
- Photon (and hadronic) shower libraries:
  - Shape of cluster closer to reality
  - needs some work to create
  - operates with relatively large files and takes relatively large program memory
  - In case if hit momentum is not perpendicular to calorimeter surface needs excessive library volume and still very approximate
  - Probably good solution for hadronic part where resolution is not critical

Non γ-e particles:

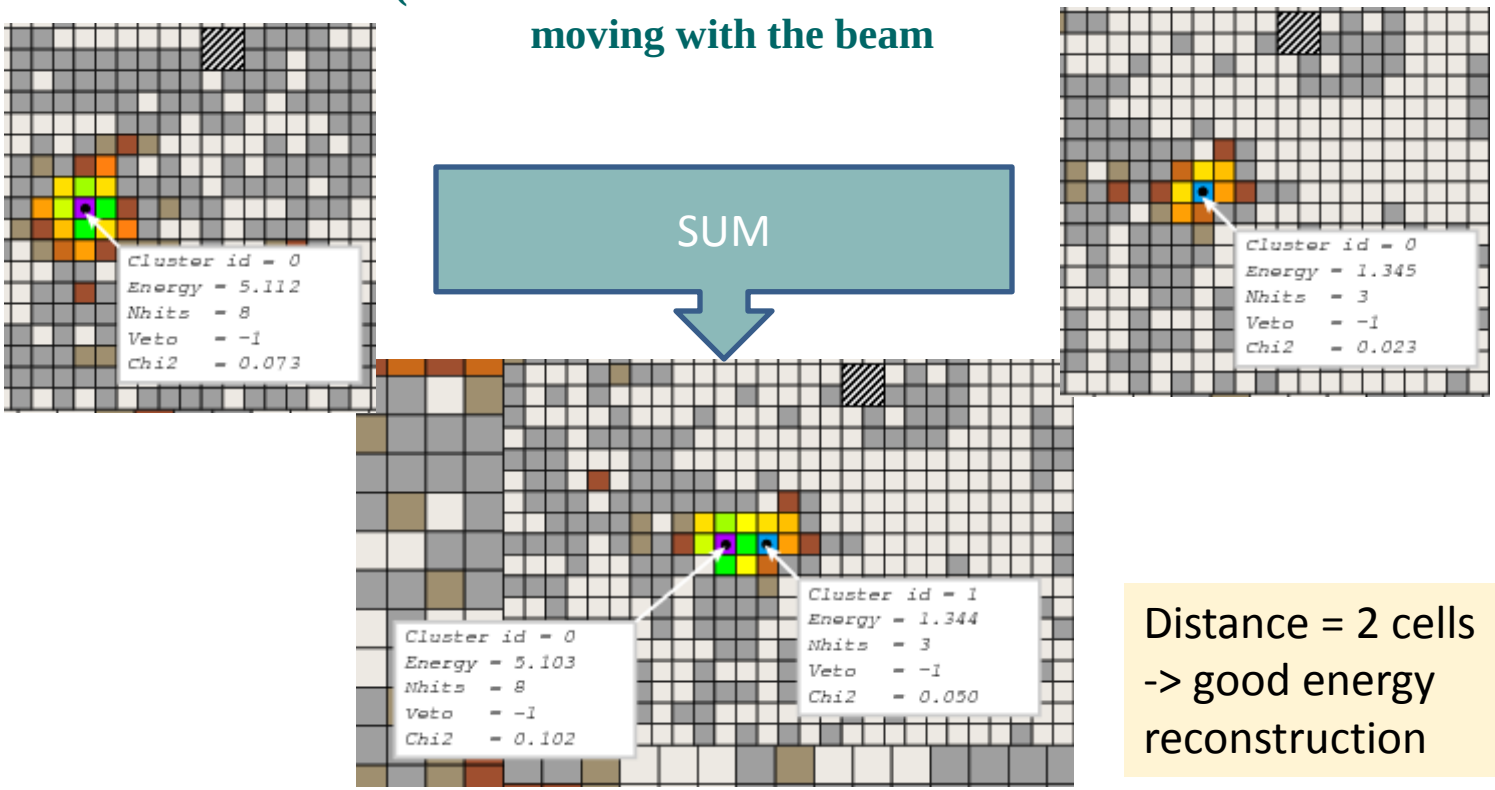


- MIPs (2 parameters: mean & sigma)

- Neutral hadrons (*neutrons* and K_L)
- Charged hadrons (= MIP + Neutral hadron),
- π^+, π^-, p give probably different showers at low energies
- Important notice: *E-M calorimeter could be used for identification of hadrons to reject background in decays reconstruction like* $\eta \rightarrow \pi^+ \pi^- \gamma$ *(was successfully implemented in SELEX experiment at Fermilab)*

Applying GAMS island algorithm to PWO calorimeter (PrimEx2)

Mixing two events from the snake scan (one cluster is constant and another is moving with the beam



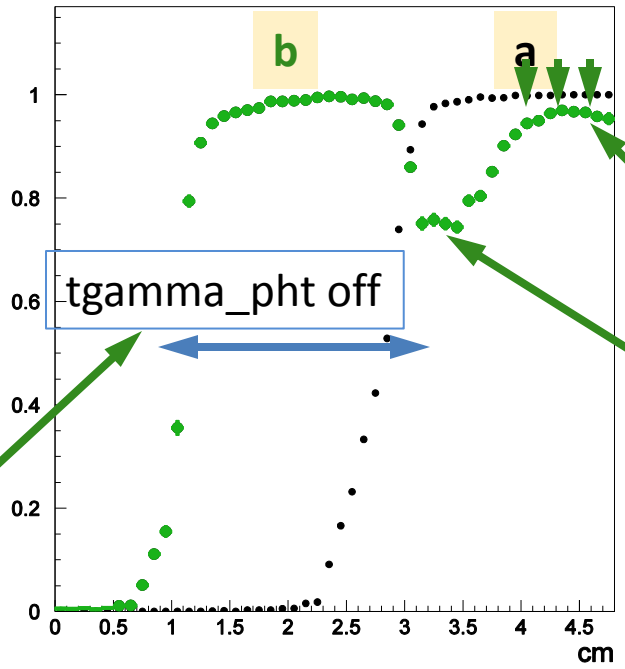
Distance = 2 cells
-> good energy reconstruction

Applying GAMS island algorithm to PWO calorimeter: probability to separate two clusters as a function of distance between hit points

First cluster: “permanent” with energy 5.1GeV,
second (“moving”) with energy 1…5 GeV;
Events with artificial split counted as missed

Curve a – GAMS cut settings

Curve b – changed cut settings



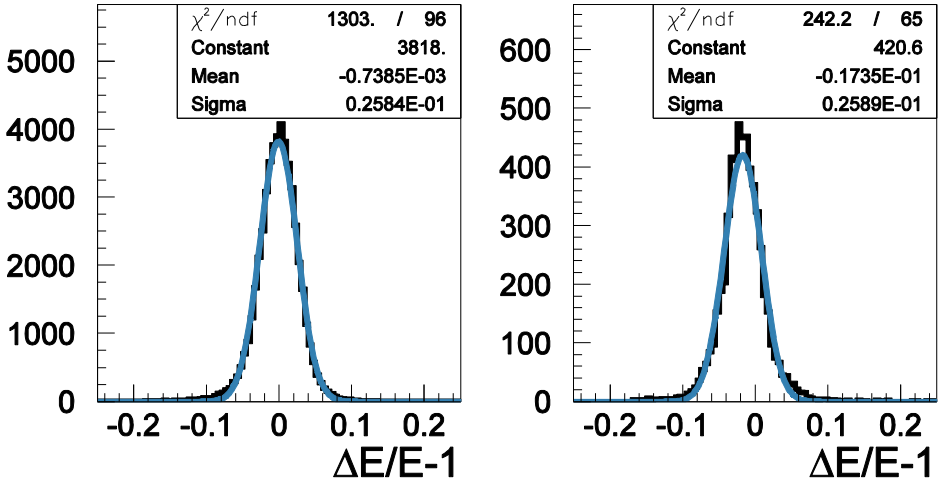
Decreasing due to artificial split

“transition” zone

No energy dependence for ***d***

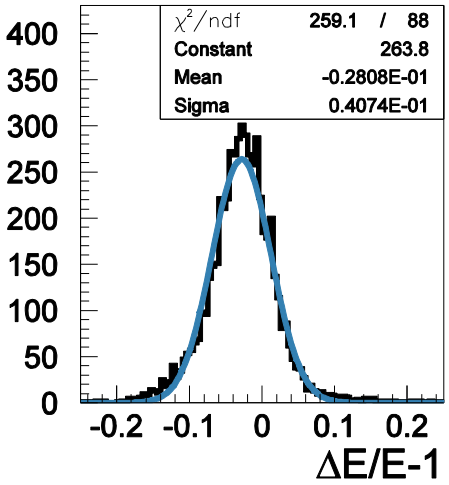
Energy resolution:

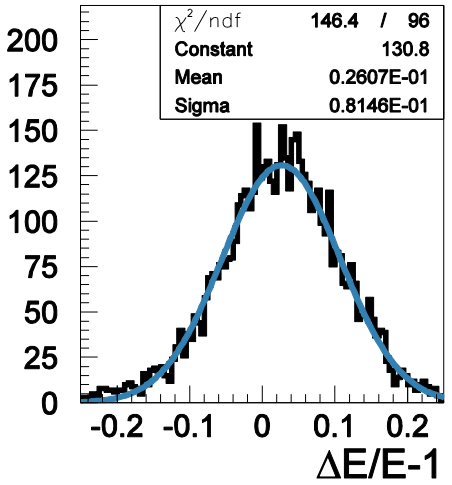
Original reconstruction (no mixing)
σ = 2.6%



d= 4.3cm … 4.7cm
σ = 2.6%

d= 2.3cm … 2.7cm
σ = 4.1%





d= 1.3cm … 1.7cm
σ = 8.1%

- Separation threshold should be selected to not disturb clusters much
- GAMS used separation threshold to distinguish pi0s
- Algorithm tune up is in progress