Electron energy resolution correction in the ATLAS LAr Electromagnetic Calorimeter

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ATLAS - IJCLab

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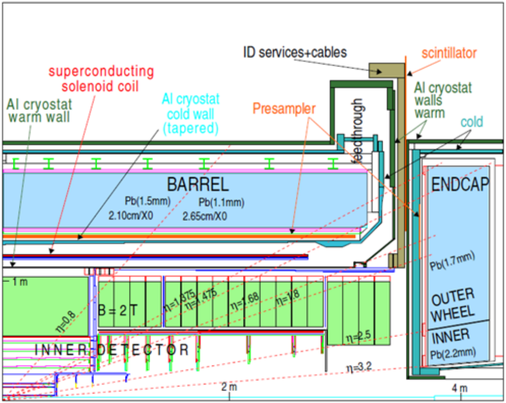
The LAr Electromagnetic Calorimeter of the ATLAS experiment



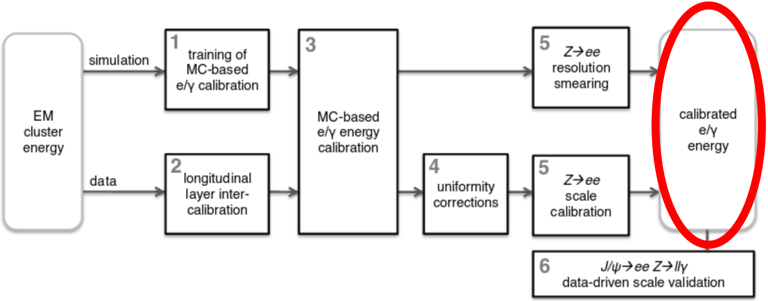
Proper calibration of the calorimeter (both on the Data and MC sides) is vital for precision measurements, such as:

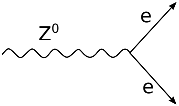
- W-boson mass
- Higgs boson mass

$\Rightarrow$ continuous efforts to improve it

LAr calorimeter e/γ calibration chain: based on $Z \to ee$ sub-samples

The study shown here is done at the level of the step highlighted with the red circle.





$$m_Z = 91.1876 \pm 0.0021 \text{ GeV}$$

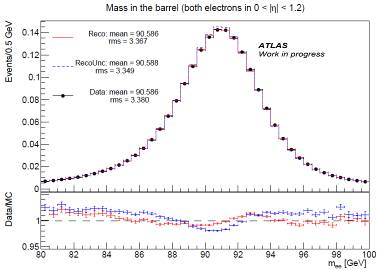
$$\Gamma_Z = 2.4952 \pm 0.0023 \text{ GeV}$$

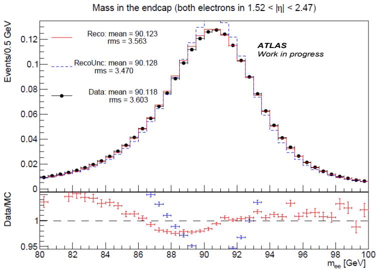
electrons are described by their $[E,\, p^{\mathrm{T}},\, \eta,\, \phi]$

$$\text{Reminder}: m_{ee}^2 = 2E_1E_2(1-\cos\theta_{12}) = 2p_1^{\mathrm{T}}p_2^{\mathrm{T}}\left(\cosh(\eta_1-\eta_2) - cos(\phi_1-\phi_2)\right)$$

$$\text{where} \qquad p^{\mathrm{T}} = \frac{E}{\cosh\eta}$$

Mass line shape discrepancy (2018 $Z \to ee$ Data/MC)





Reco: Latest official calibrated MC / RecoUnc: MC without calibration

Seeking to understand better the difference between Data and MC

Method proposed by USTC group: event-by-event MC electron energy resolution correction

$$\Delta = E_{reco} - E_{truth} \to \Delta' = E'_{reco} - E_{truth}$$

$$E'_{reco} = E_{truth} + \Delta'$$

$$\text{where} \quad \Delta' = f(\Delta) \qquad \to \text{e.g. } \Delta' = p_0\Delta + p_1\Delta^2 + p_2$$

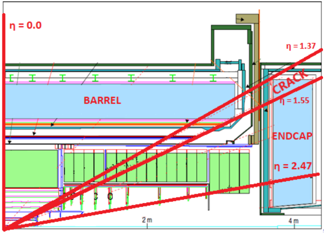
(Initial USTC study here.)

Energy resolution correction

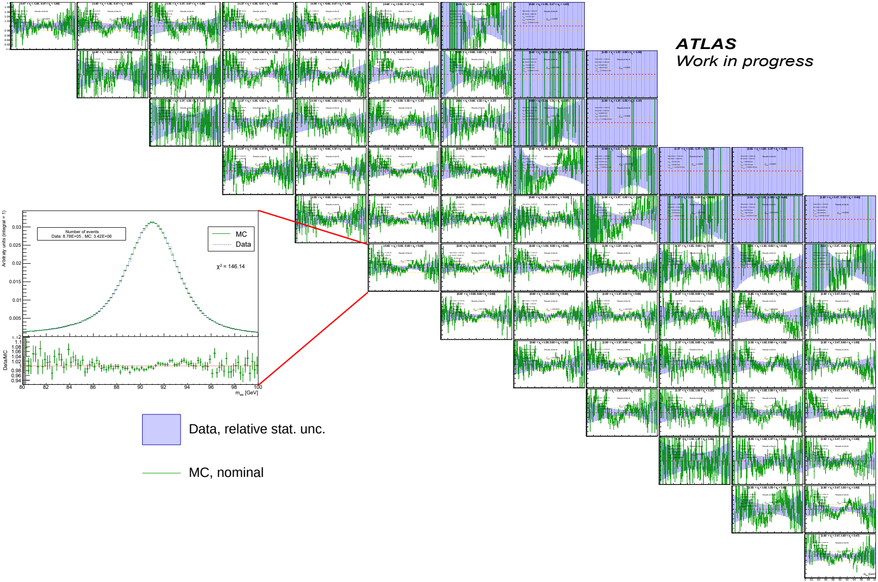
- Best Δ' parameters sought with Minuit2.
- Minimizing the shape difference between the Data and MC mass distributions.
- The most simple form of the correction looks like $\Delta' = f(\Delta) = p_0\Delta + p_1\Delta^2 + p_2$
- η-binning defined as: $\{0.0, 0.6, 1.0, 1.37, 1.55, 1.82, 2.47\}$ (positive and negative)

  e.g. η-bin 1 $= -2.47 < \eta < -1.82$

  η-bin 7 $= 0.0 < \eta < 0.6$
- $Z \to ee$ gives two electrons (each with their own η and energy)
  - study done in a 2-D grid defined by $[\eta_1, \eta_2]$
- N.B. 12 regions in $\eta \to$ 12 sets of parameters $\vec{p_\eta} = (p_0, p_1, p_2, ..)$
- The current study is done on top of the latest official calibration



Grid on $[\eta_1, \eta_2]$ of nominal Data/MC mass lineshape ratios



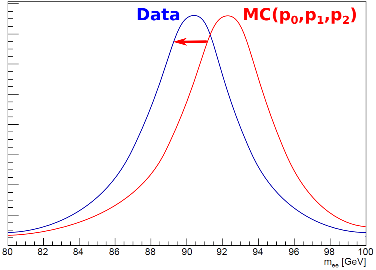
Bin-by-bin event migration and the χ^2 curve problem

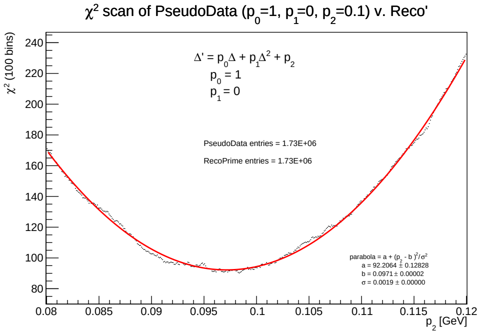
Problem with the χ^2 curve

Let

$$\chi^2 = \sum_{i}^{n\ \text{bins}} \frac{\left(\text{bin}^{\text{MC}}{}_i - \text{bin}^{\text{DATA}}{}_i\right)^2}{\sigma^2_{\text{MC},i} + \sigma^2_{\text{DATA},i}}$$

→ the χ^2 is computed between mass histograms (i.e. finite number of bins)
→ change in Δ' parameters = migration of events from one bin to another
→ MC' histogram does not transform continuously as a function of p_0, p_1, etc.
→ χ^2 curve is not continuous!
↳ (opposite from traditional cases, which compare hist. v. pdf)





(this plot was obtained by doing a manual scan on p_2 and fitting a parabola, not reliable for many parameters)

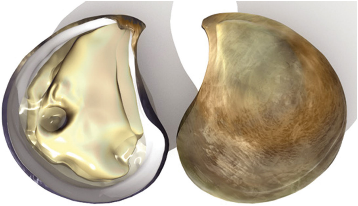
Problem with the oyster i.e. χ^2 curve

Bin-to-bin χ^2

European (Ostrea Edulis)

- Not particular flavourful
- Bumpy shell (not-so-nice edges)
- Can get stuck when shucking/minimizing

Ideal (desired) scenario



American (Crassostrea virginica)

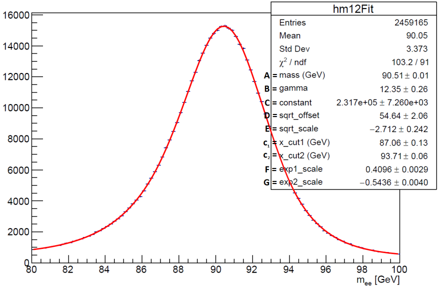
- Très bon
- Smooth surface
- Easy to minimize

TREATMENT TO MIGRATION: Fit a function (PDF) on the MC' histogram, and use it to predict the corresponding MC' value at each bin ($\int_{\text{bin}} f(x)dx/\text{bin}$). Since there is correlation between bins and propagated errors from the fit, the χ^2 looks like

$$\chi^2 = d^{\mathrm{T}} V^{-1} d.$$

$\Rightarrow$ Example of Breit-Wigner core with exponential tails fitted on MC:

$$f(x) = \begin{cases} 80 < x < c_1 : & e^{F(x-P)} + R \\ c_1 < x < c_2 : & \dfrac{C}{(x-A)^2 + B} + E(x-D)^2 \\ c_2 < x < 100 : & e^{G(x-Q)} + S \end{cases}$$



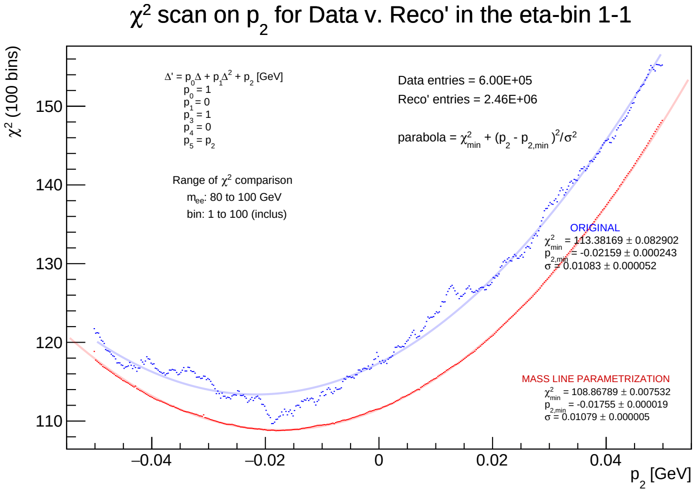
c_1 and c_2 are the transition nodes, their values are also fitted

R and S assure continuity of the function
P and Q assure continuity of the derivative

$\rightarrow$ in total, the function depends on 9 free parameters: A, B, C, D, E, F, G, c_1, c_2

χ^2 scan on p_2, using the mass line profiling. NO MORE FLUCTUATIONS

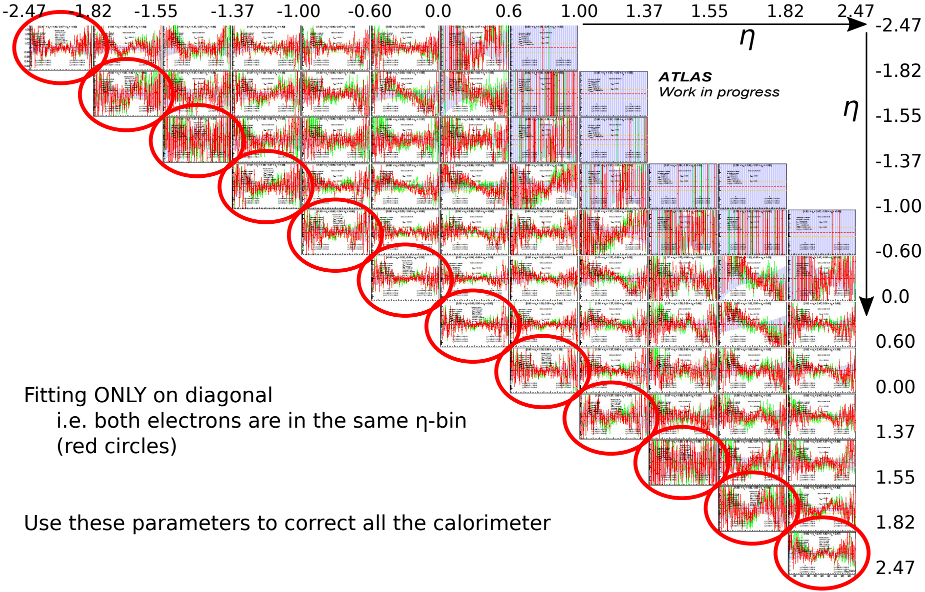
- Blue: χ^2 between 2 histograms
- Red: χ^2 between a histogram and the fit of the other one



For the following results, MINUIT "sees" only the red curve.

Problem with diagonal fits

Initial methodology: Fit on diagonal bins only



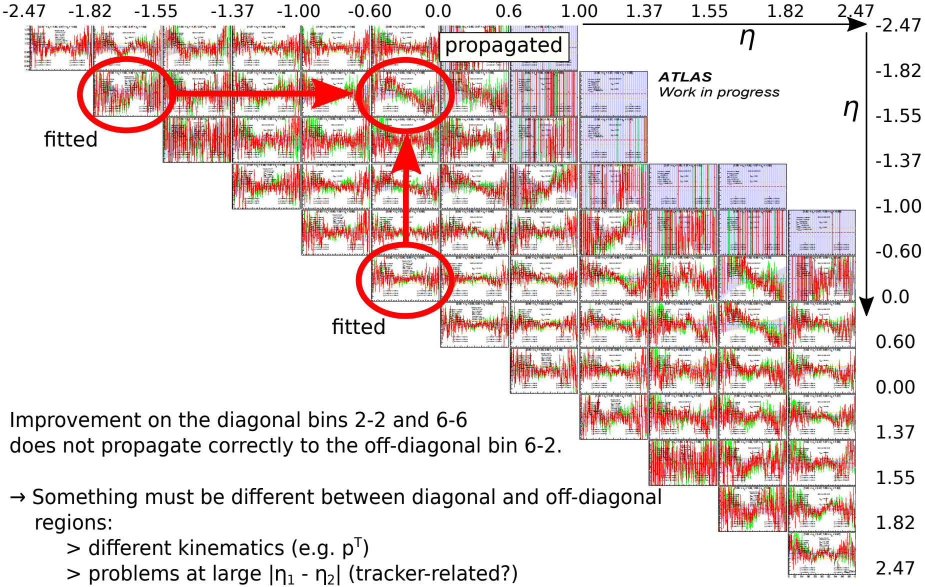
Fitting ONLY on diagonal

i.e. both electrons are in the same η-bin

(red circles)

Use these parameters to correct all the calorimeter

Initial methodology: Fit on diagonal bins only



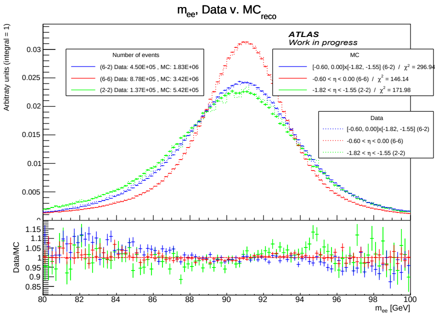
Improvement on the diagonal bins 2-2 and 6-6 does not propagate correctly to the off-diagonal bin 6-2.

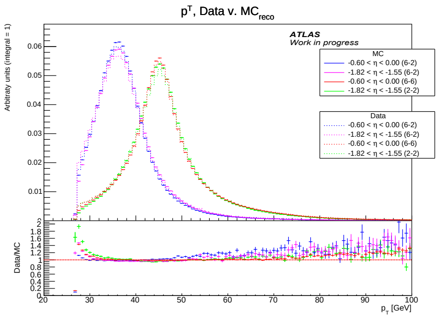
→ Something must be different between diagonal and off-diagonal regions:

> different kinematics (e.g. p^T)

> problems at large $|\eta_1 - \eta_2|$ (tracker-related?)

Inspection of kinematics (η-bin 2-2, 6-6, and 6-2)





Clearly there are different kinematics across different regions.

In particular, comparing diagonal v. off-diagonal η-bins:

- Several checks were done for the tracker
  $\rightarrow$ No important contribution to the mass disagreement
- Different p^{T} distributions $\rightarrow \vec{p}_\eta = \vec{p}(\eta, p^{\mathrm{T}})$

Back to the calibration

Parametrizations of the resolution correction

Looking for the “magic” parametrization that improves all (or most) of the η-bins

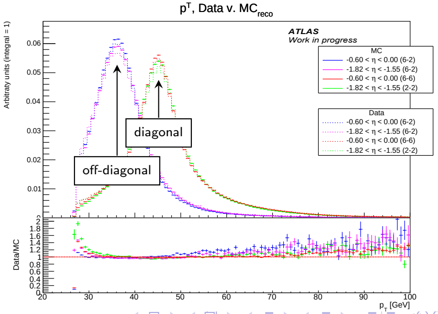
As shown before, it is very likely that there is a p^{T} dependence.

Let us concentrate on two equivalent parametrizations (and build up from there):

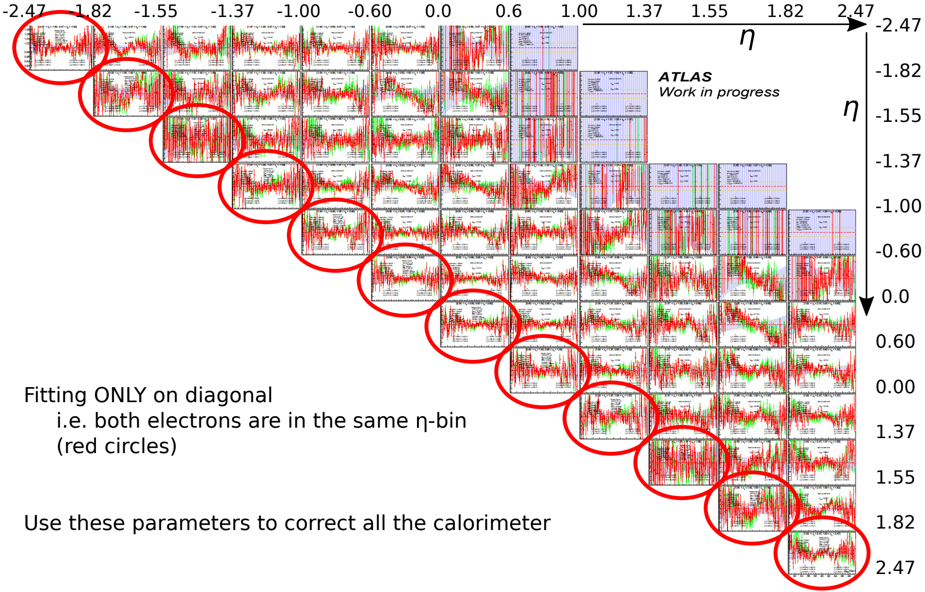
- $\Delta' = p_0\Delta + p_1\Delta^2 + p_2$
- $\Delta' = \left(p_0 + p_3(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta + \left(p_1 + p_4(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta^2 + \left(p_2 + p_5(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)$

Why -45 GeV?

If there was no width of the Z, $p^{\mathrm{T}}_{Z} \approx 0$ and no resolution effects, at first order, the p^{T} for diagonal bins (e.g. 2-2 and 6-6) would be around $\frac{m_Z}{2} \approx 45$ GeV



Fit on diagonal bins: evidently not enough



Fitting ONLY on diagonal

i.e. both electrons are in the same η-bin

(red circles)

Use these parameters to correct all the calorimeter

SemiGlobal fits: correction methodology

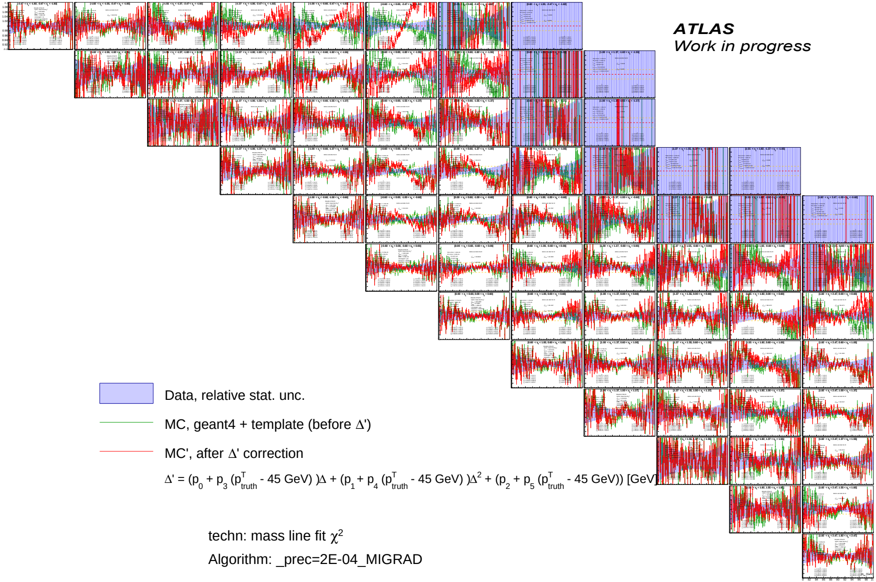
The fit must include (several) off-diagonal bins to sample multiple E^{T} regions.

Can define a multi-η-bin χ^2 as the sum of the individual bins:

$$\chi^2_{\text{total}} = \chi^2_{\eta\text{-}2\text{-}2} + \chi^2_{\eta\text{-}3\text{-}2} + \chi^2_{\eta\text{-}4\text{-}2} + \ldots$$

Each of the 12 sets of parameters $\vec{p}_\eta$ are fitted independently.
Iterations are done to take into account inter-η-region correlations.

SemiGlobal fits: results on the grid



Data, relative stat. unc.

MC, geant4 + template (before Δ')

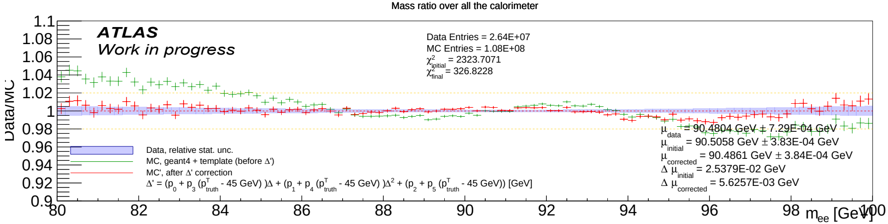
MC', after Δ' correction

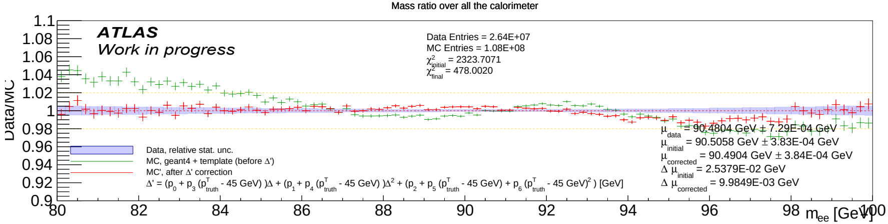
$\Delta' = (p_0 + p_3\,(p^T_{truth} - 45\text{ GeV}))\Delta + (p_1 + p_4\,(p^T_{truth} - 45\text{ GeV}))\Delta^2 + (p_2 + p_5\,(p^T_{truth} - 45\text{ GeV}))$ [GeV]

techn: mass line fit χ^2

Algorithm: _prec=2E-04_MIGRAD

Comparing the results of two different Δ' definitions, with first (top) and second (bottom) order p^{T} dependence.





Final notes

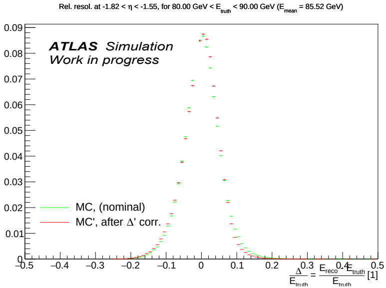
- Tracker effects were discarded as the source of the mass line discrepancy.
- Diagonal and off-diagonal bins have different kinematics, and this must be taken into consideration in the fit.
- Including explicit linear p^{T} dependency improves considerably the Data/MC agreement.
- Fitting on a single bin at a time is not enough. Several must be used for a wider sampling of the phase-space.
- Different sets of parameters cannot be uncorrelated among them
  $\rightarrow$ iterative SemiGlobal fits are promising

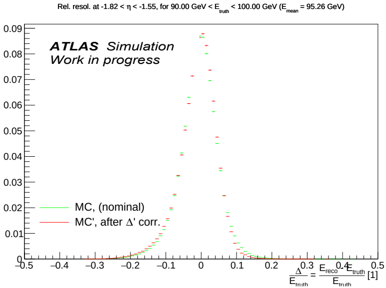
Backup

Effect of Δ' correction on the energy resolution

Examples of resolution shape deformation achieved with the Δ' correction.

- Green: nominal
- Red: after Δ' correction (for some $p_0, p_1, \ldots$ value)





Both plots show the relative energy resolution in the $-1.82 < \eta < -1.55$ region, for a couple of energy ranges ($80\ \mathrm{GeV} < E_{\mathrm{truth}} < 90\ \mathrm{GeV}$ and $90\ \mathrm{GeV} < E_{\mathrm{truth}} < 100\ \mathrm{GeV}$)

Δ' allows for asymmetric corrections: larger tail on the left, smaller one on the right, and position of the maximum gets slightly shifted to the right

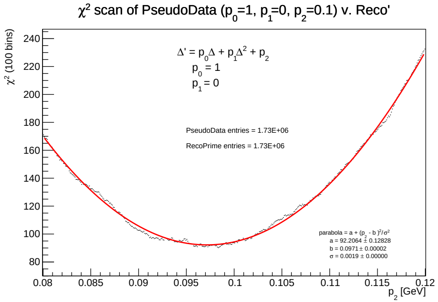
Problem with the χ^2 curve

Let

$$\chi^2 = \sum_{i}^{n\ \text{bins}} \frac{\left(\text{bin}^{\text{MC}}{}_i - \text{bin}^{\text{DATA}}{}_i\right)^2}{\sigma^2_{\text{MC},i} + \sigma^2_{\text{DATA},i}}$$

$\rightarrow$ the χ^2 is computed between histograms (i.e. finite number of bins)
$\rightarrow$ change in Δ' parameters = migration of events from one bin to another
$\rightarrow$ MC' histogram does not transform continuously as a function of p_0, p_1, etc.
$\rightarrow$ χ^2 curve is not continuous!

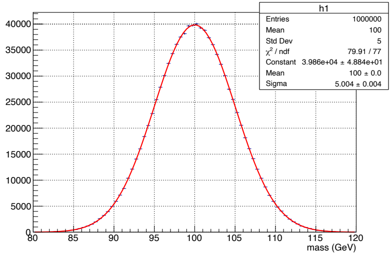
↳ (oposite from traditional cases, which compare hist. v. pdf)



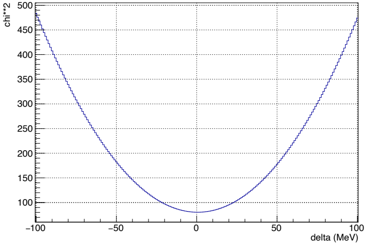
(this plot was obtained by doing a manual scan on p_2 and fitting a parabola, not reliable for many parameters)

Migration problem has been reproduced by Guillaume in a simplified case (shown bellow)

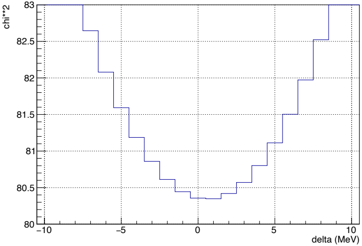
1 experiment
10**6 events   gaussian mean=100, sigma=5



Compute chi**2 from binned histogram data + analytic pdf
vs shift of mean (fixing sigma)

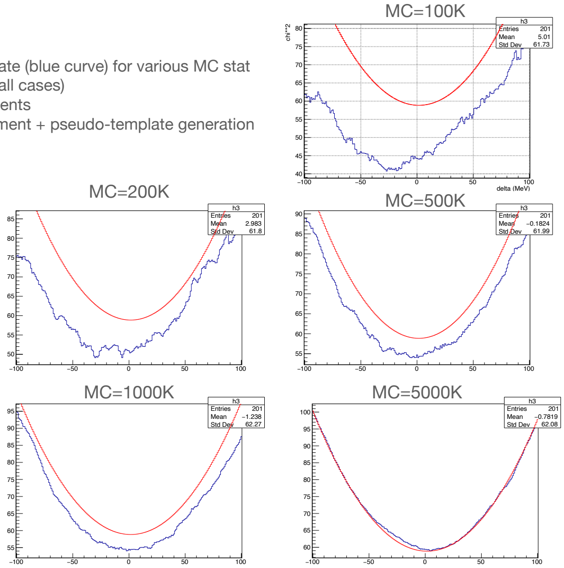


Zoom of chi**2 (1 MeV bins)
=> deltaChi**2=1 gives +-5 MeV which is the correct number



Migration problem has been reproduced by Guillaume in a simplified case (shown bellow)

Compute chi**2 with MC template (blue curve) for various MC stat
(red=analytical chi**2 same for all cases)
Pseudo data is always 100K events
Plot are for one pseudo-experiment + pseudo-template generation



Why is the migration a problem?

- χ^2 is not smooth $\rightarrow$ multiple (infinite) local minima!

  $\rightarrow$ impossibly to find the correct one with numerical methods
- Actual minimum of the "parabola" is not well defined!

  $\rightarrow$ completely dependent on the size of the sample

  $\rightarrow$ consistent with the non-migration case only in the infinitely large sample limit
- MINUIT is expecting to receive a well behaved (smooth) χ^2 function. Many of its functionalities are dependant on precise knowledge of the first and second derivatives, so the shape of the curve is problematic. For instance, MIGRAD easily fails due to gradient mis-estimation.

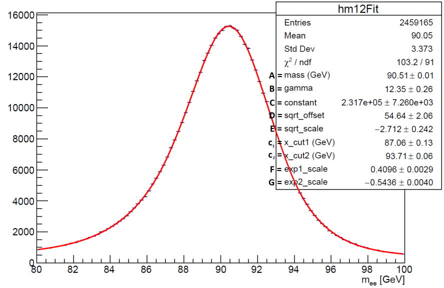
Getting rid of the migration: profiling the mass lineshape

TREATMENT TO MIGRATION: Fit a function (PDF) on the MC' histogram, and use it to predict the corresponding MC' value at each bin ($\int_{\text{bin}} f(x)dx/\text{bin}$). Since there is correlation between bins and propagated errors from the fit, the χ^2 looks like

$$\chi^2 = d^{\mathrm{T}} V^{-1} d.$$

$\Rightarrow$ Example of Breit-Wigner-like core with exponential tails fitted on MC:

$$f(x) = \begin{cases} 80 < x < c_1 : & e^{F(x-P)} + R \\ c_1 < x < c_2 : & \dfrac{C}{(x-A)^2 + B} + E(x-D)^2 \\ c_2 < x < 100 : & e^{G(x-Q)} + S \end{cases}$$



c_1 and c_2 are the transition nodes, their values are also fitted

R and S assure continuity of the function
P and Q assure continuity of the derivative

$\rightarrow$ in total, the function depends on 9 free parameters: A, B, C, D, E, F, G, c_1, c_2

Getting rid of the migration: profiling the mass lineshape: continuity

Fit function: Breit-Wigner core with exponential tails

$$f(x) = \begin{cases} 80 < x < c_1 : & exp1(x) = e^{F(x-P)} + R \\ c_1 < x < c_2 : & BW(x) = \dfrac{C}{(x-A)^2 + B} + E(x-D)^2 \\ c_2 < x < 100 : & exp2(x) = e^{G(x-Q)} + S \end{cases}$$

Node continuity conditions @ c_1 (analogous @ c_2):
Continuity of the derivative:

$$\left.\frac{\mathrm{d}\ BW(x)}{\mathrm{d}x}\right|_{x=c_1} = \left.\frac{\mathrm{d}\ exp1(x)}{\mathrm{d}x}\right|_{x=c_1} = Fe^{F(x-P)}|_{x=c_1}$$

$$\Rightarrow \quad P = \frac{-1}{F} \ln\left(\left.\frac{\mathrm{d}\ BW(x)}{\mathrm{d}x}\right|_{x=c_1} \times \frac{1}{F} \right) + c_1$$

Continuity of the function:

$$BW(x)\big|_{x=c_1} = exp1(x)\big|_{x=c_1} = e^{F(c_1-P)} + R$$

$$\Rightarrow \quad R = BW(x)\big|_{x=c_1} - e^{F(c_1-P)}$$

From the fitted mass line, the content of the bin k is predicted with

$$\mathrm{bin^{MC}}_k = \overline{f(x)}\Big|_{x_k} = \left(\int_{x_k-0.5\mathrm{binwidth}}^{x_k+0.5\mathrm{binwidth}} f(x)\mathrm{d}x\right)/\mathrm{binwidth}$$

Renaming the parameters of the function f as $\vec{a} = (a_1, ..., a_n)$ s.t. $f = f(x; \vec{a})$,

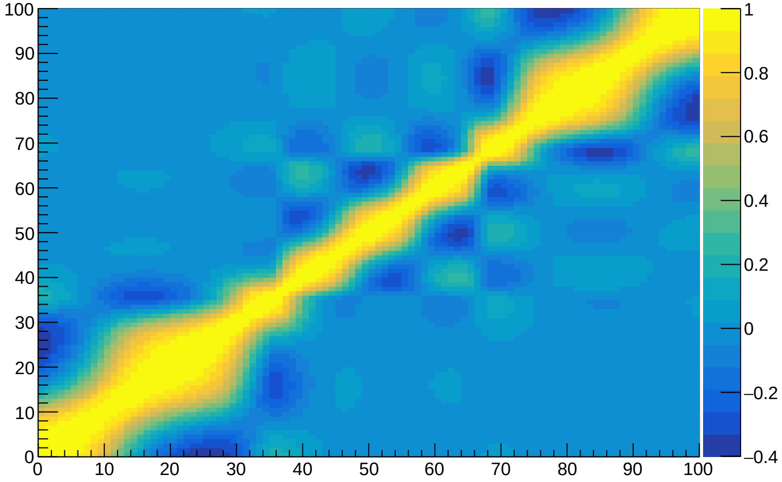
$$\mathrm{d}f\Big|_{x_k} = \sum_i \overline{\frac{\partial f}{\partial a_i}}\Big|_{x_k} \mathrm{d}a_i$$

The covariance between two bins, k and l, looks as

$$\begin{aligned}
\mathrm{cov^{MC}}(x_k, x_l) = V^{\mathrm{MC}}_{k,l} &= \langle \mathrm{d}f\Big|_{x_k}, \mathrm{d}f\Big|_{x_l} \rangle \\
&= \langle \sum_i \overline{\frac{\partial f}{\partial a_i}}\Big|_{x_k} \mathrm{d}a_i, \sum_j \overline{\frac{\partial f}{\partial a_j}}\Big|_{x_l} \mathrm{d}a_j \rangle \\
&= \sum_{i,j} \overline{\frac{\partial f}{\partial a_i}}\Big|_{x_k} \overline{\frac{\partial f}{\partial a_j}}\Big|_{x_l} \sigma_i \sigma_j \rho_{ij}
\end{aligned}$$

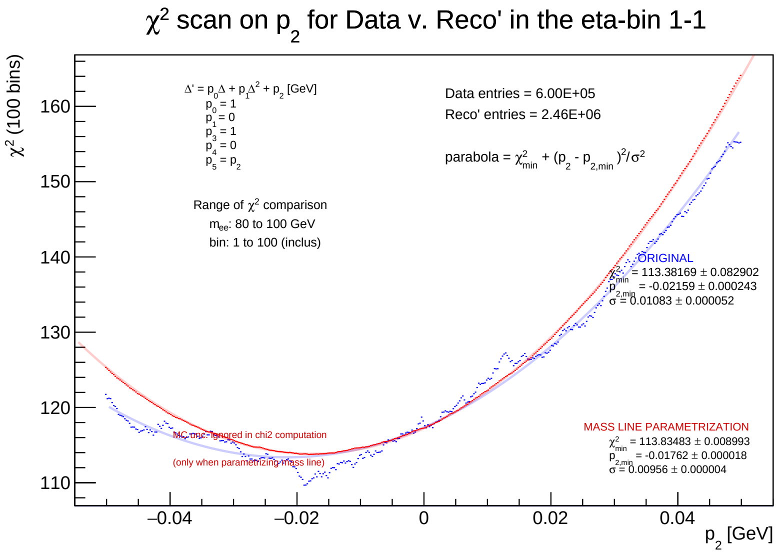
where σ_i and σ_j are the fit errors for the parameters of f, ρ_{ij} their respective correlation, and $\overline{\frac{\partial f}{\partial a_i}}\Big|_{x_k}$ the average value of the gradient in the bin k.

Getting rid of the migration: profiling the mass lineshape: correlation matrix



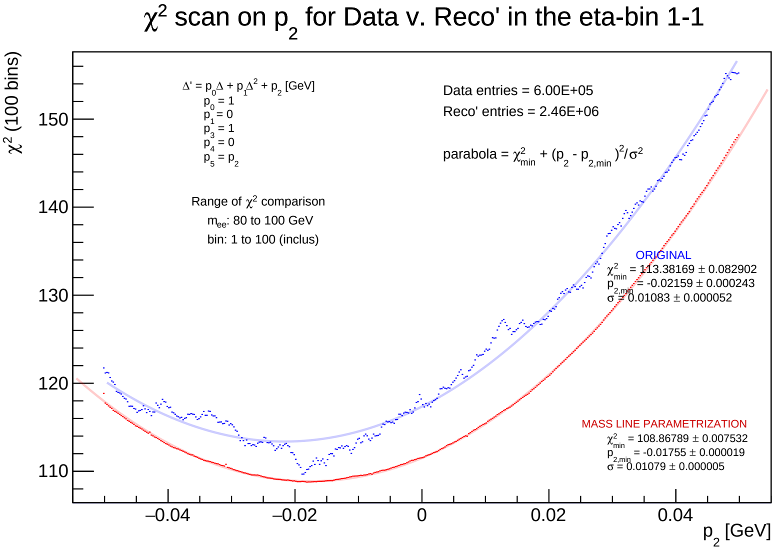
Example of the correlation matrix between bins C^{MC}, obtained for the η-bin 1-1, with $p_0 = 1.0$, $p_1 = 0.0$, $p_2 = 0.0$

χ^2 scan on p_2, using the mass line profiling. NO MORE FLUCTUATION



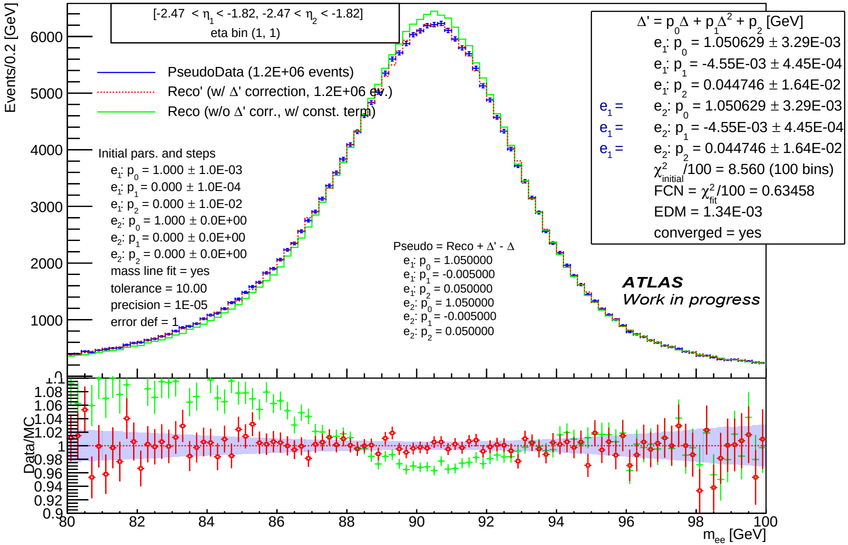
χ^2 computed by ignoring the propagated MC uncertainty

χ^2 scan on p_2, using the mass line profiling. NO MORE FLUCTUATION



χ^2 computed by INCLUDING the propagated MC uncertainty (covariance matrix)

Mass line profiling: CLOSURE test on PseudoData



Parametrizations of the resolution correction

Several Δ' definitions have been tested:

- A: $\Delta' = f(\Delta) = p_0\Delta + p_1\Delta^2 + p_2$
- B: $\Delta' = p_0\Delta + p_1\Delta^2 + p_2 + p_3\Delta^3$
- D: $\Delta' = p_0\Delta + p_1\Delta^2 + p_2 + p_3 \cdot p^{\mathrm{T}}_{\mathrm{reco}}$
- E: $\Delta' = p_0\Delta + p_1\Delta^2 + p_2 + p_3 \cdot E_{\mathrm{reco}}$
- F: $\Delta' = p_0(\Delta + p_2) + p_1(\Delta + p_2)^2$
- G: $\Delta' = \left(p_0(\Delta + p_2) + p_1(\Delta + p_2)^2\right)(1 + p_3) + p_3 \cdot E_{\mathrm{truth}}$
- H: $\Delta' = \begin{cases} p_0\Delta + p_1\Delta^2 + p_2 & \text{if } \Delta > 0 \\ p_3\Delta + p_4\Delta^2 + p_2 & \text{if } \Delta < 0 \end{cases}$
- J: $\Delta' = p_0\Delta + p_1\Delta^2 + p_2 + p_3 \cosh\eta$
- K: $\Delta' = p_0\Delta + p_1(p^{\mathrm{T}}_{\mathrm{reco}} - p^{\mathrm{T}}_{\mathrm{truth}}) + p_2(p^{\mathrm{T}}_{\mathrm{reco}} - p^{\mathrm{T}}_{\mathrm{truth}})^2 + p_3$
- L: $\Delta' = \left(p_0 + p_3(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta + \left(p_1 + p_4(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta^2 + \left(p_2 + p_5(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)$
- M: $\Delta' = p_0\Delta + p_1\Delta^2 + p_2 + p_3 \cdot p^{\mathrm{T}}_{\mathrm{truth}}$
- N: $\Delta' = \left(p_0 + p_3(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta + \left(p_1 + p_4(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})\right)\Delta^2 + \left(p_2 + p_5(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV}) + p_6(p^{\mathrm{T}}_{\mathrm{truth}} - 45\ \mathrm{GeV})^2\right)$

SemiGlobal fits: Correction methodology

Let us concentrate on a particular set of parameters, e.g. $\vec{p}_{\eta\text{-}2}$ for region $[-1.82, -1.55]$

Several bins will use this set of parameters: 2-1, 2-2, 3-2, 4-2, 5-2, 6-2, ...

POSSIBILITY: to constrain every region's $\vec{p}_{\eta\text{-}i}$ independently (i.e. one set at a time, leaving the rest fixed) using the whole calorimeter (which we will call SemiGlobal fit)

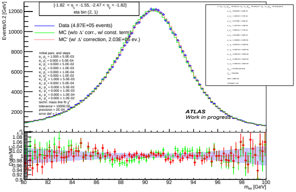
BUT the mass computation uses two electrons
$\rightarrow$ **Strong correlation among the $\vec{p}_{\eta\text{-}i}$ of different regions, which can't be neglected**

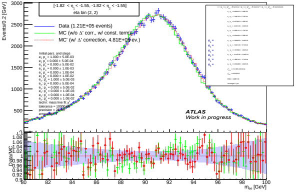
SO ITERATIONS MUST BE DONE:

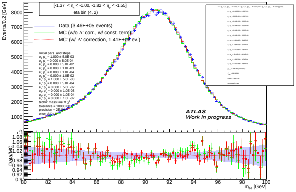
1. Set the initial value of all sets of parameters to their default value i.e. $p_0 = 1.0$ and $p_1 = p_2 = ... = 0.0$
2. Do a first SemiGlobal fit for each set of parameters i.e. 12 independent fits
3. Set the latest fitted parameters as new initial values for all regions
    - Which is equivalent to "correct" the calorimeter with these
    - This will give an improvement in the diagonal and degradation everywhere else
4. Re-do the 12 independent SemiGlobal fits
5. Repeat from step 3 until all parameters stabilize (about 20 iterations required)

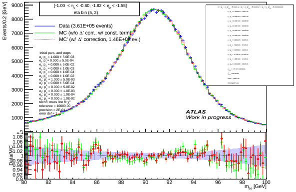
Correction methodology 2. SemiGlobal fits (for $\vec{p}_{\eta\text{-}2}$) (iteration 0)

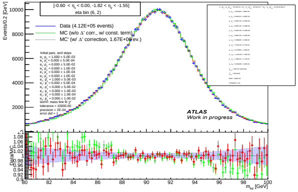
(these five regions were used simultaneously to minimize $\vec{p}_{\eta\text{-}2}$ alone





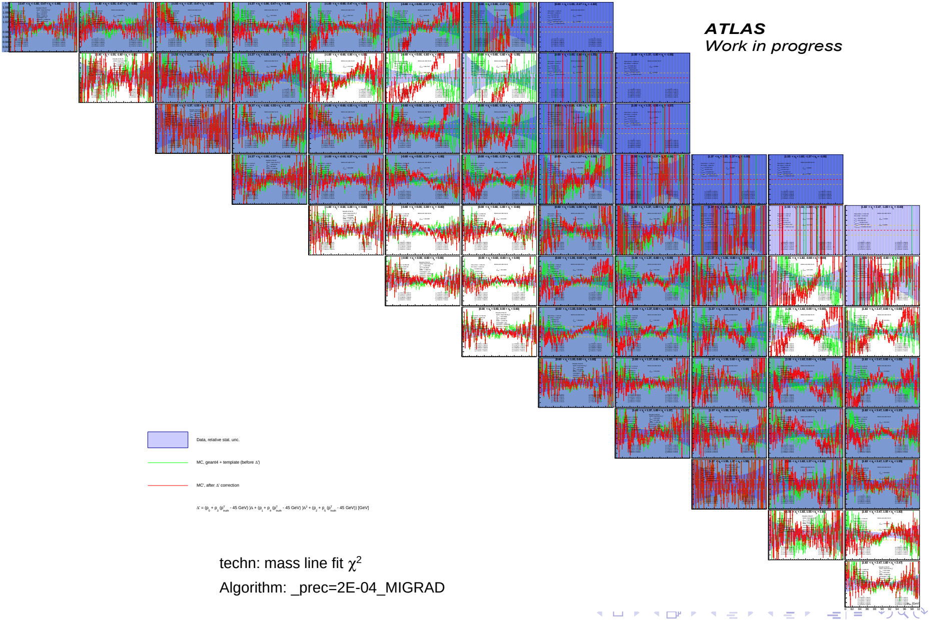




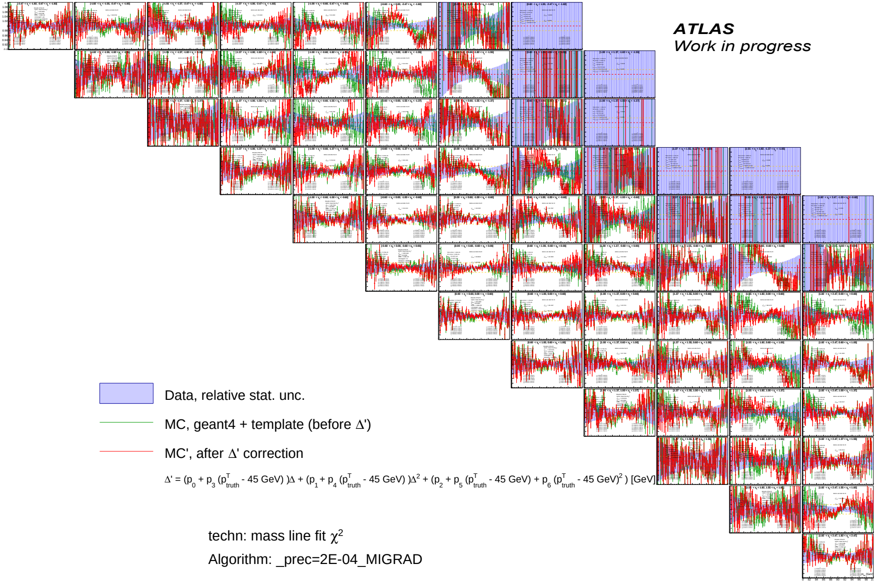


Improvement in every region when fitting a single set of parameters
(i.e. correcting only one electron at a time)

Correction methodology 2. SemiGlobal fits (iteration 0)

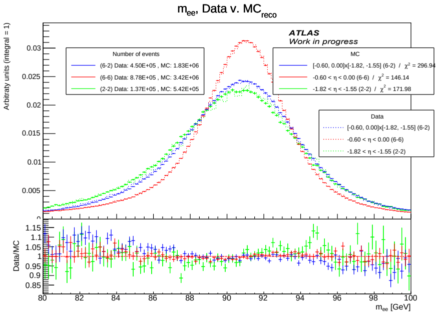


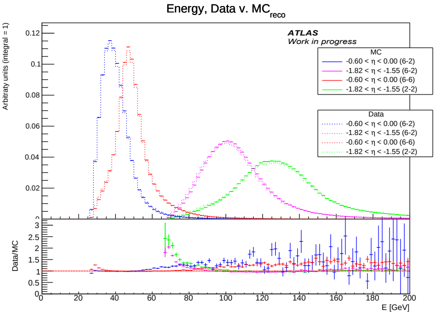
Correction methodology 2. SemiGlobal (20 iterations)

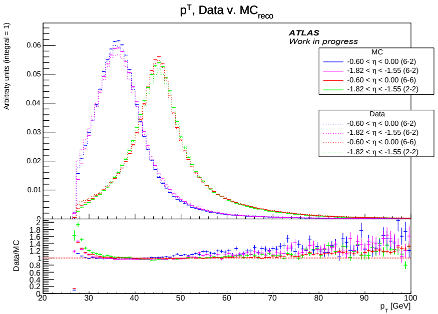


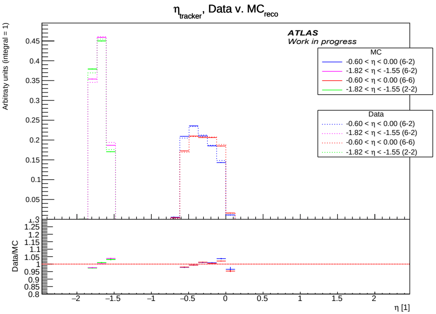
Inspecting kinematics in each region

Inspection of kinematics (η-bin 2-2, 6-6, and 6-2)









Inspection of kinematics (η-bin 6-2)

Clearly there are different kinematics across different regions.

In particular, comparing diagonal v. off-diagonal η-bins:

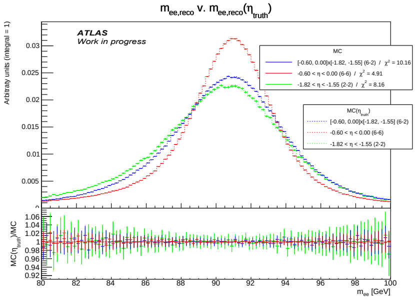
- Different $|\eta_1 - \eta_2|$ distributions $\rightarrow$ Tracker issues?
  - Check the effect of the resolution of angular quantities (η and ϕ)
  - Match Data/MC angular distributions via event reweighting, and check the effect on the mass distributions

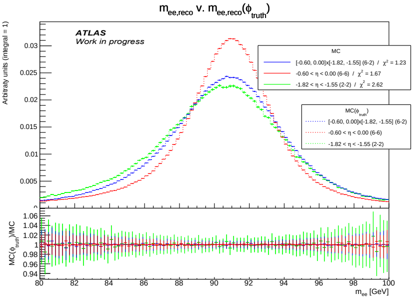
  TRACKER EFFECTS WHERE INSPECTED, AND RULED OUT

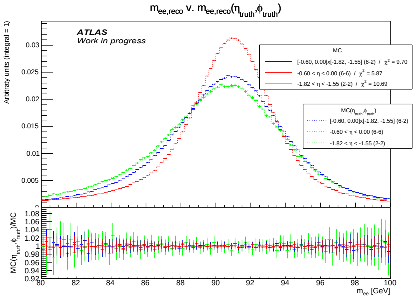
- Different p^{T} distributions $\rightarrow \vec{p}_\eta = \vec{p}(\eta, p^{\mathrm{T}})$

Ruling out effects from the tracker (η and ϕ)

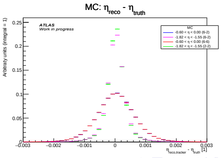
MC: nominal v. truth angle (i.e. effect of MC tracker resolution)

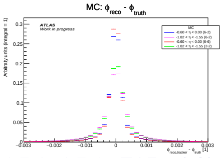






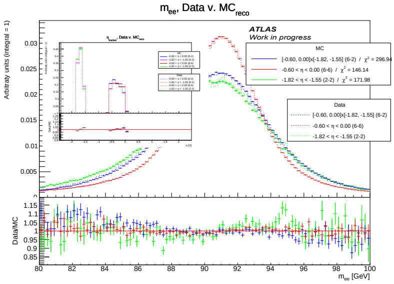
The MC resolution for $\eta_{tracker}$ and $\phi_{tracker}$ (bellow) also look healthy





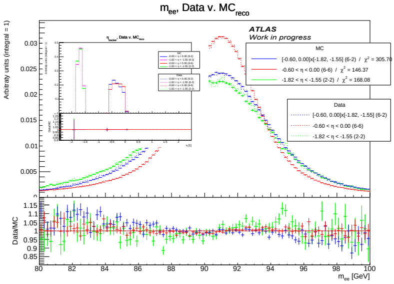
Reweighting η MC distribution to Data

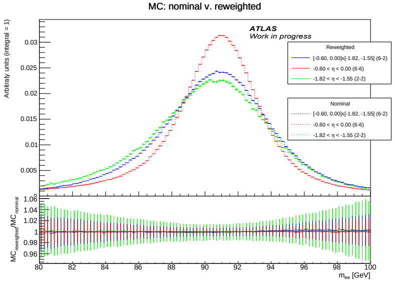
Before reweight



$\Rightarrow$

After reweight





Reweighting the distribution of η has no noticeable impact on the mass distribution.

The tracker is not the main culprit

No clear influence of the tracker on the mass discrepancy

$\rightarrow$ Or at least not enough to explain the currently observed differences

The difference must come primarily from the energy measurement (i.e. the calorimeter)

(as expected, but it is good to rule out a major influence from the tracker)