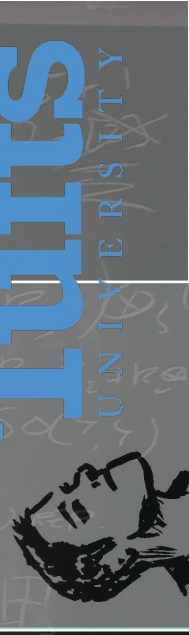
Unfolding at the LHC

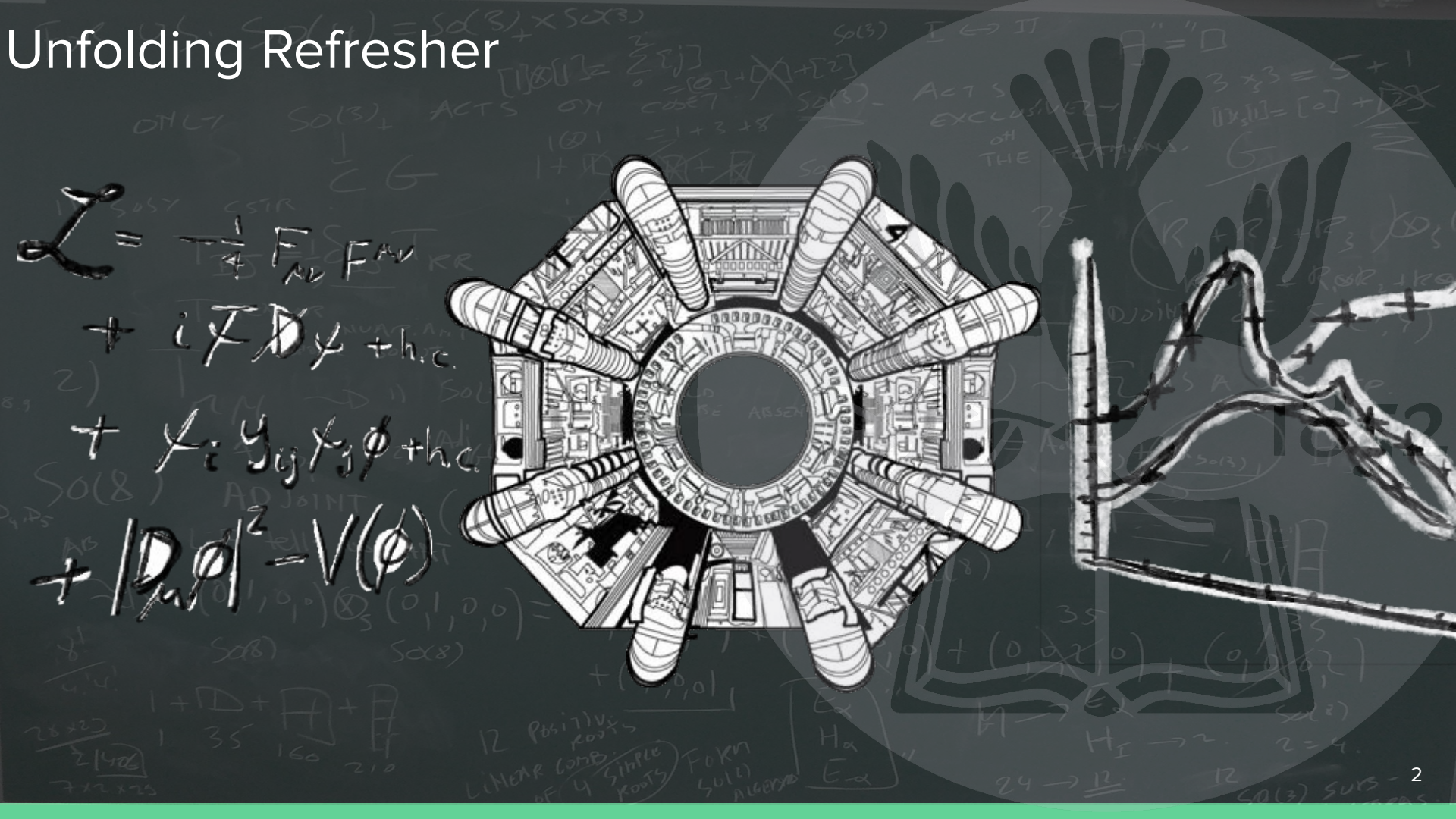
Vince Croft



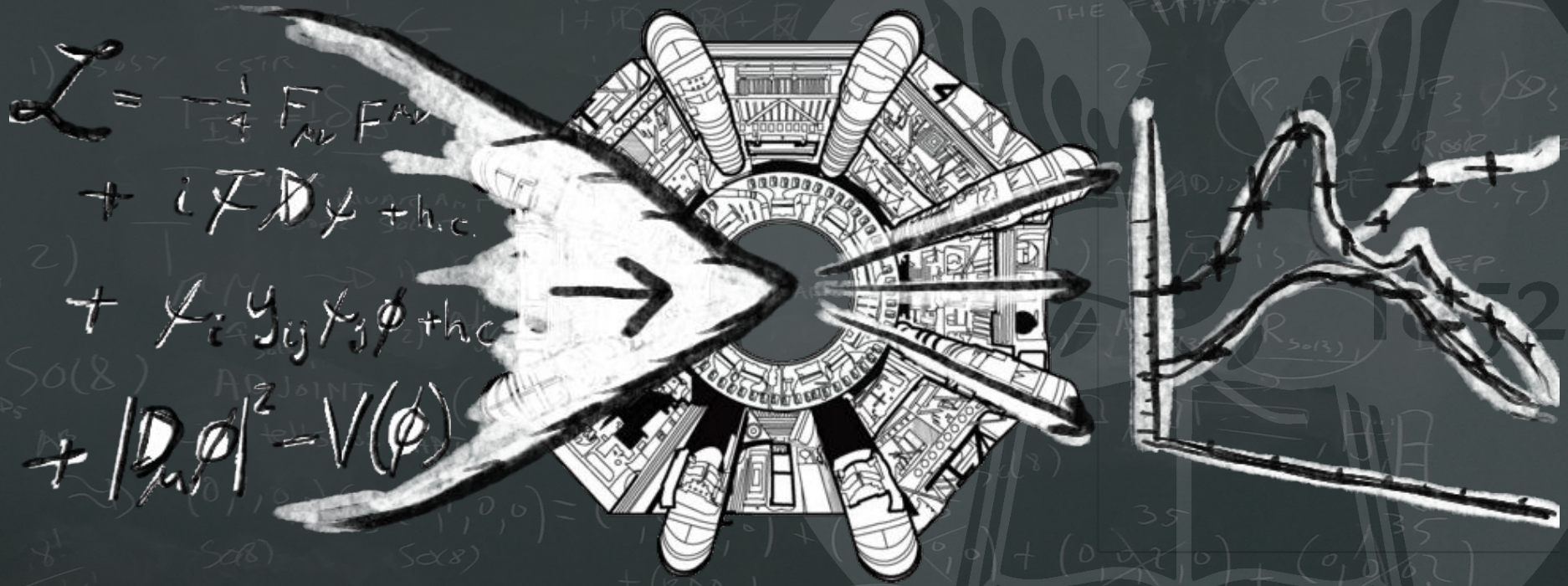
A review of unfolding at the LHC, including recent and future developments with RooUnfold

Monday 12 July 2021

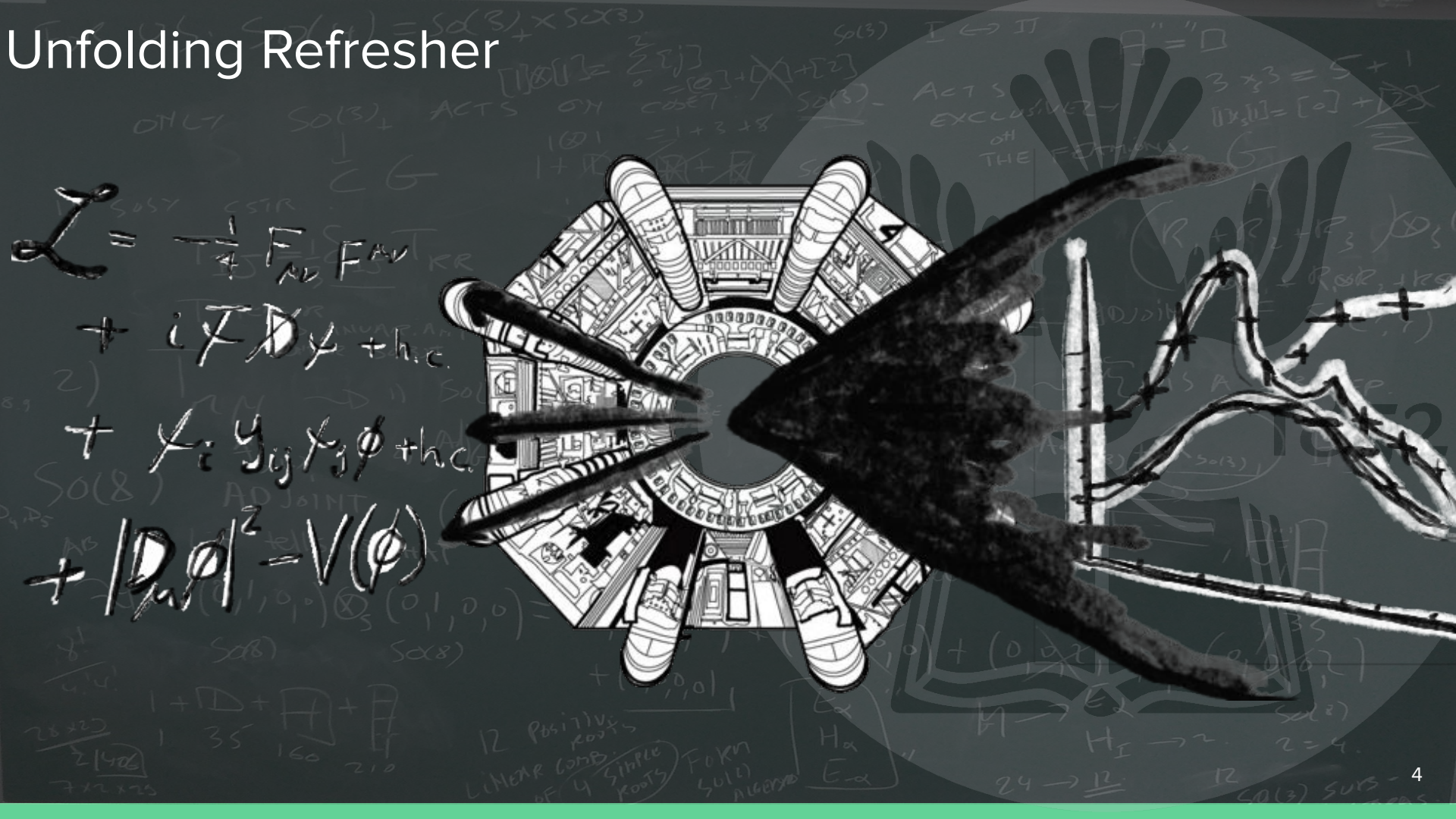
Unfolding Refresher



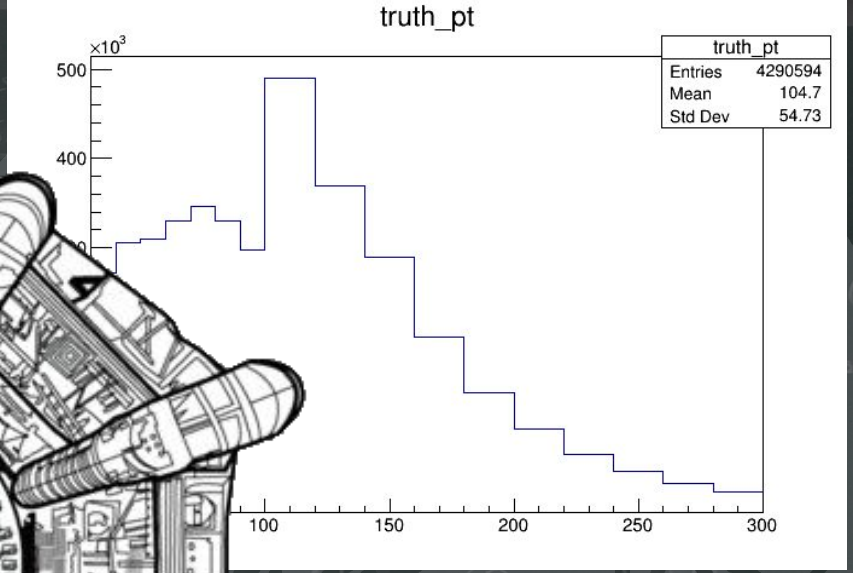
Unfolding Refresher

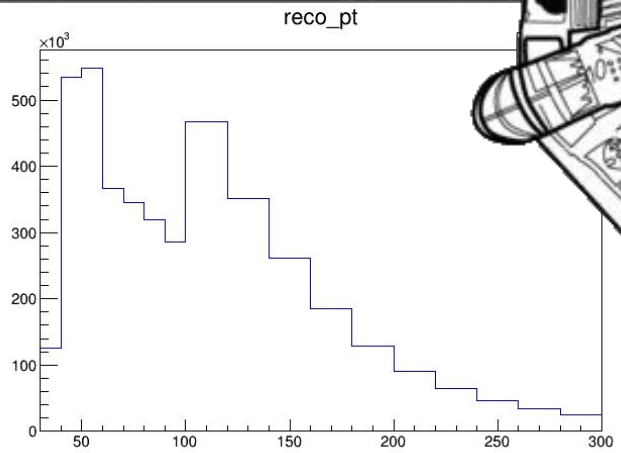


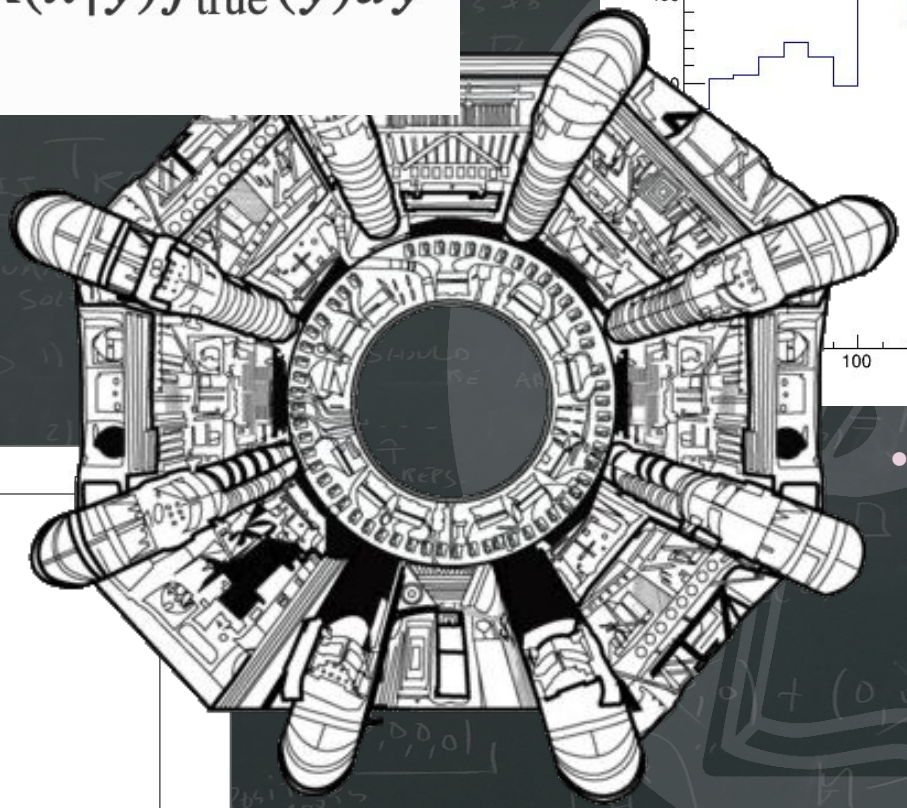
Unfolding Refresher



$$f(x)_{\text{meas}} = \int R(x|y) f_{\text{true}}(y) dy$$



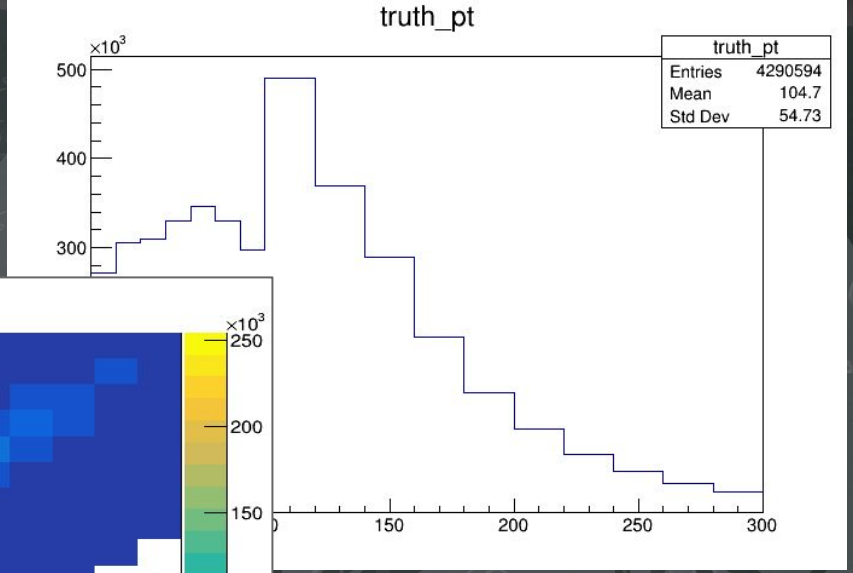


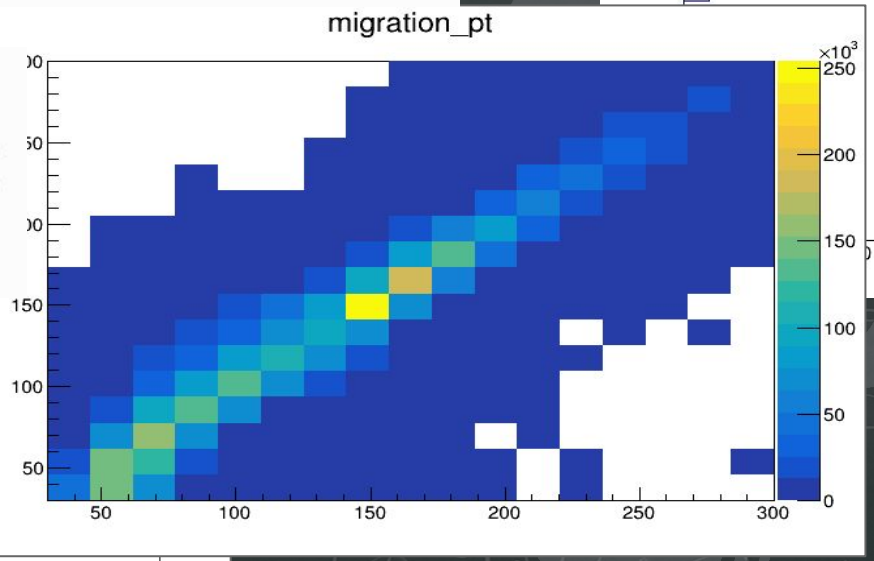


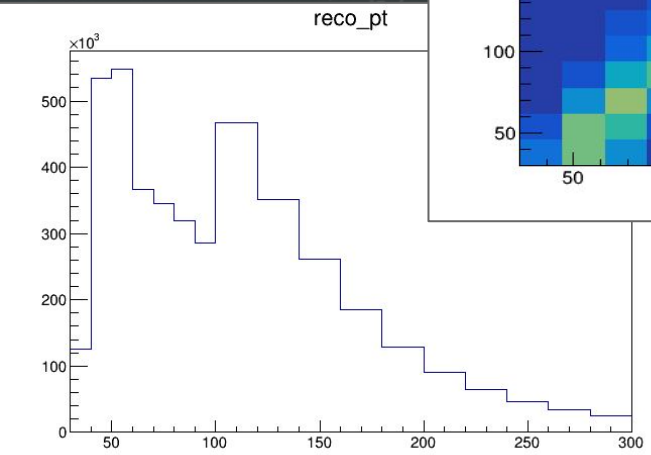
- How to approximate functions in thi problem?
  - Quadrature methods - Nystrom basis
  - Expansion methods - Galerkin

$$f(x)_{\text{meas}} = \int R(x|y) f_{\text{true}}(y) dy$$

$$\nu = R\mu$$





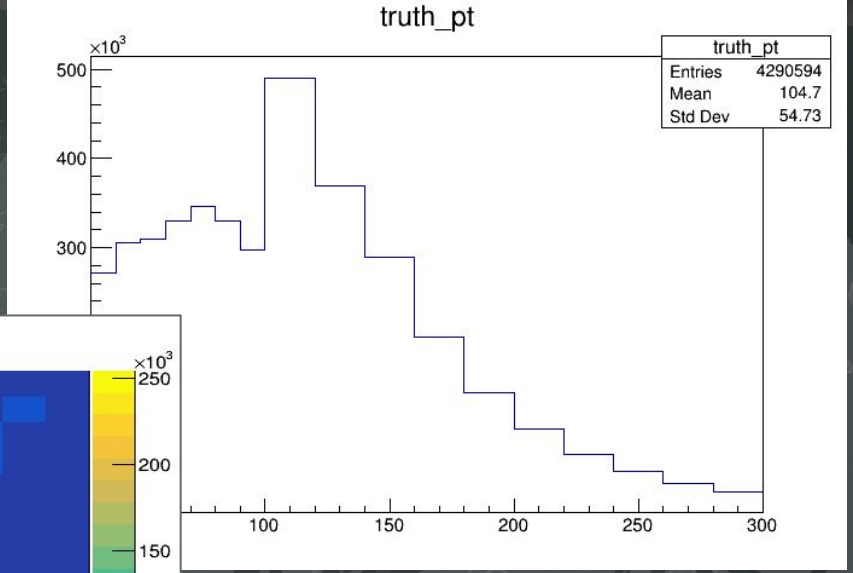


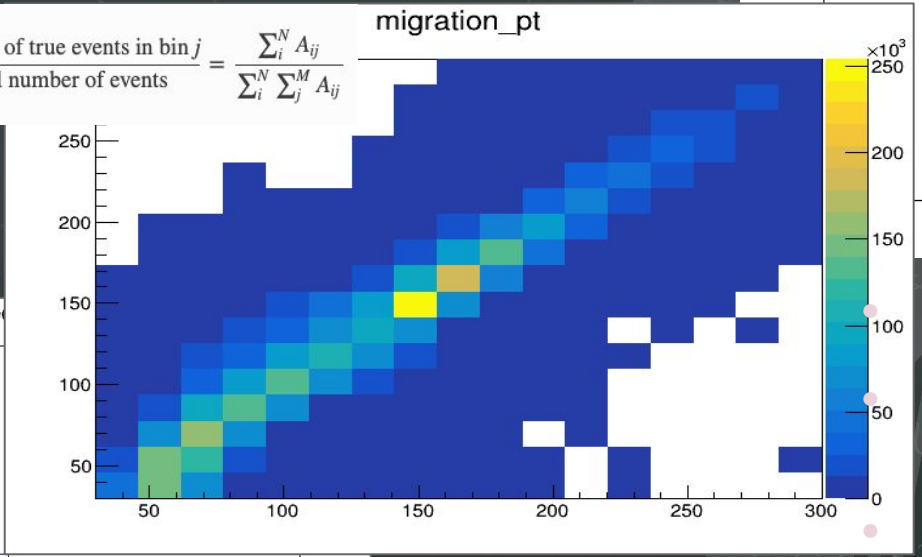
- Approximate effect of systematics in a non-parametric way
- Allows for linear algebra to be used in lieu of numerical solutions

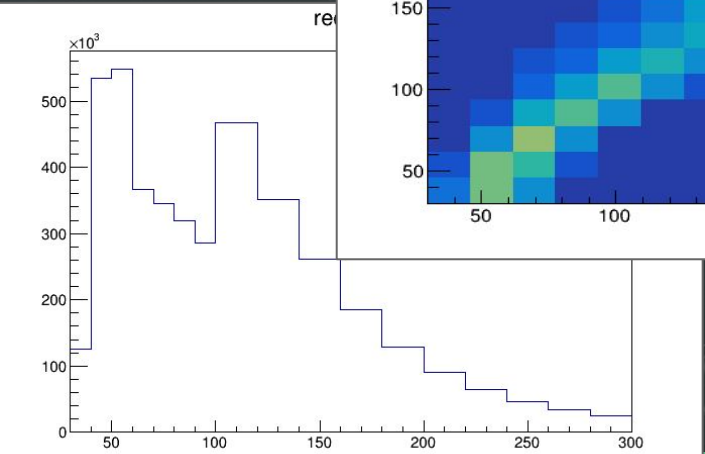
Unfolding Refresher

- Take 2d response truth⇔reco to create mapping
- Detector smearing leads to inconsistencies
- Regularisation away from the Maximum Likelihood solution reduces dependencies on such statistical artifacts.

$$P(\text{true value in bin } j) = \frac{\text{Number of true events in bin } j}{\text{Total number of events}} = \frac{\sum_i^N A_{ij}}{\sum_i^N \sum_j^M A_{ij}}$$







the response R can be formulated as a ratio of probabilities such that truth*Response = reco
If the bins match the response is square therefore

- Truth = Resonse^{-1}Reco

This inversion is not always exact.

- This inversion is equivalent to maximising logL(truth) = ∫logP(data;reco)

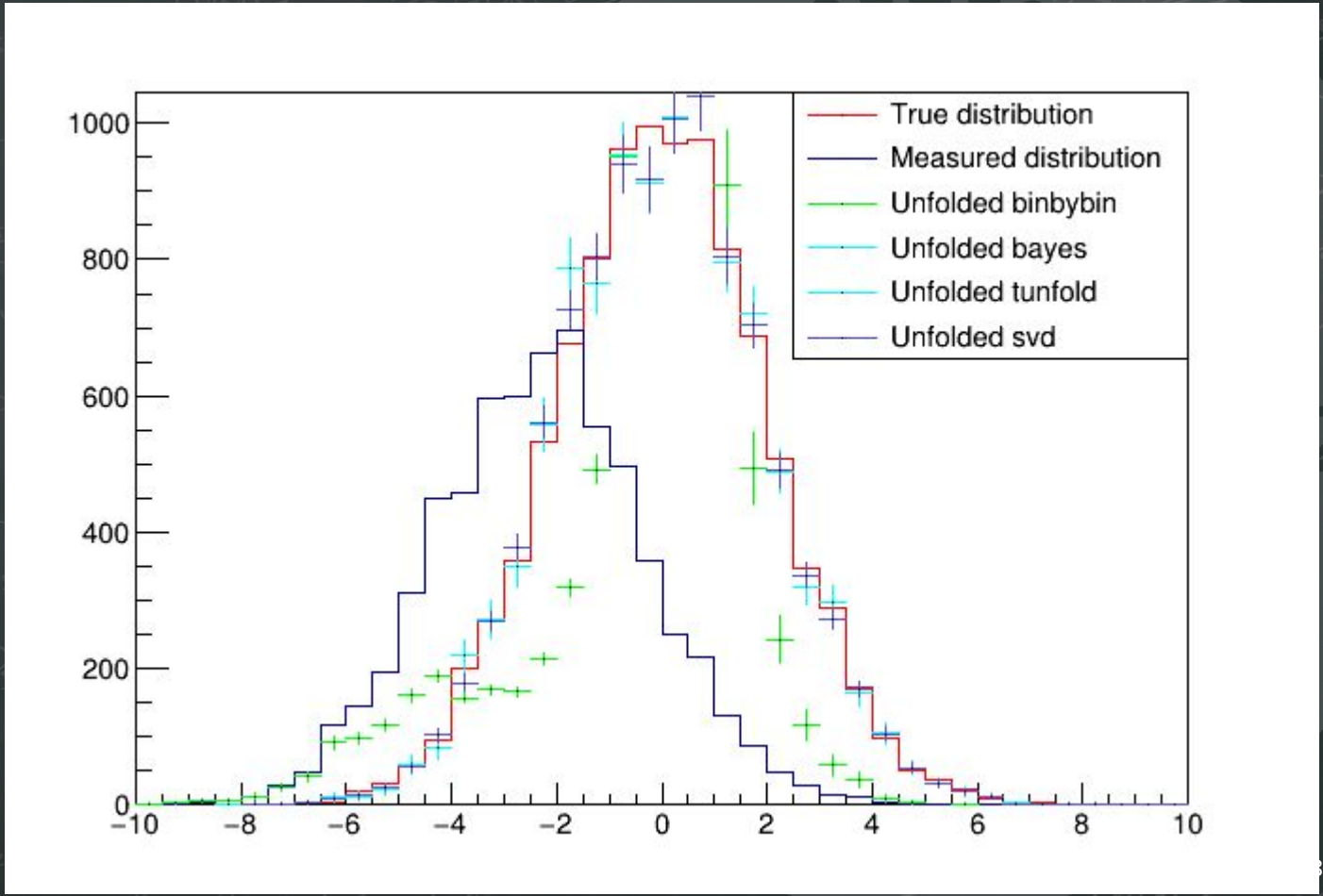
Unfolding Methods

- Common interface to multiple methods
- Each with different error propagation
- Each with different responses to distributions
- Each with different regularisation parameters.

How to pick a method?

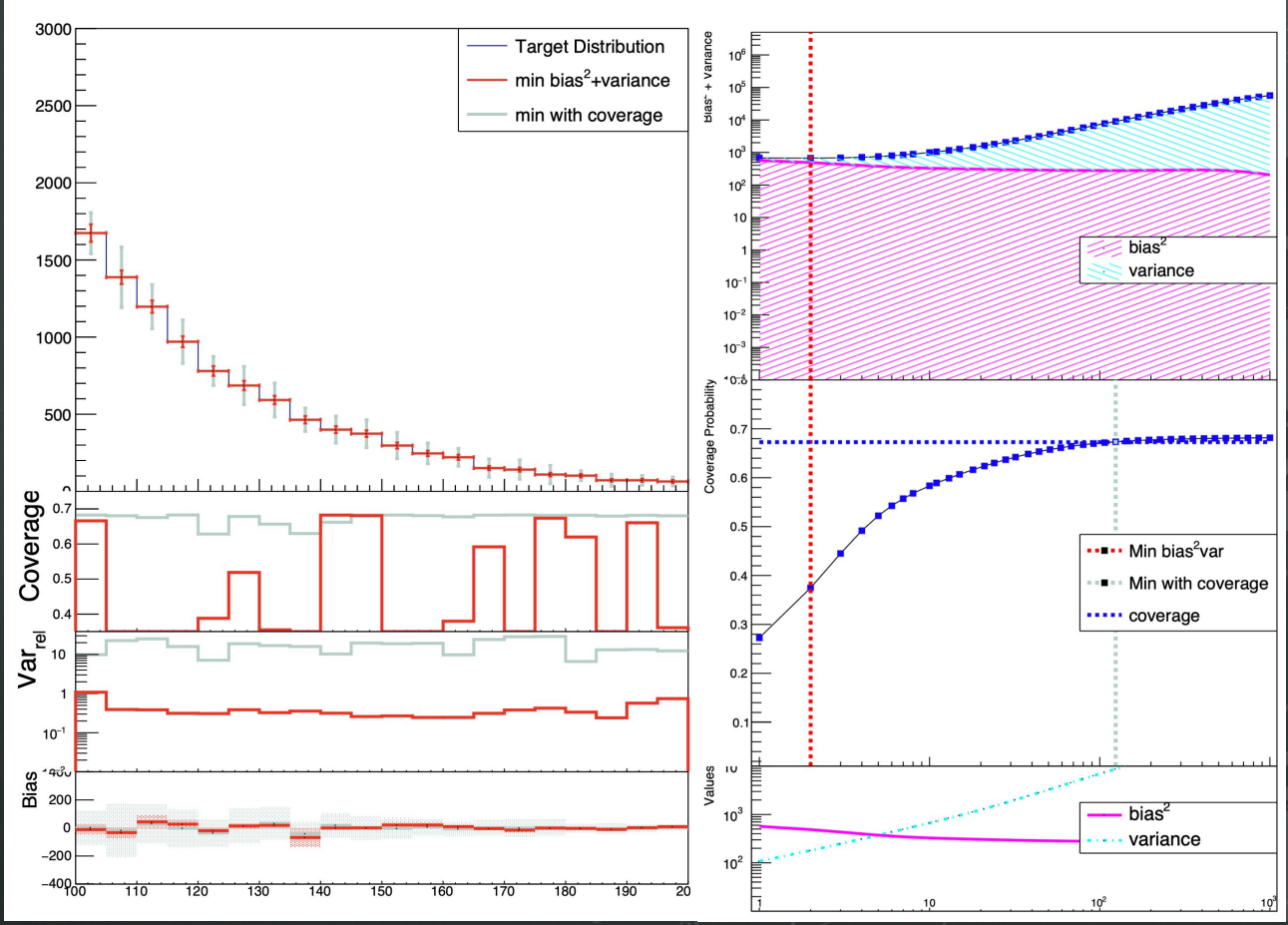
How to choose a regularisation?

Open in SWAN



RooFitUnfold

- A common framework of metrics for Unfolding performance across methods and parameters
- Statistical Modelling with RooFit



- Improved variance calculations
- Input pdfs (not just histograms)
- Statistical coverage
- Internal bias calculation

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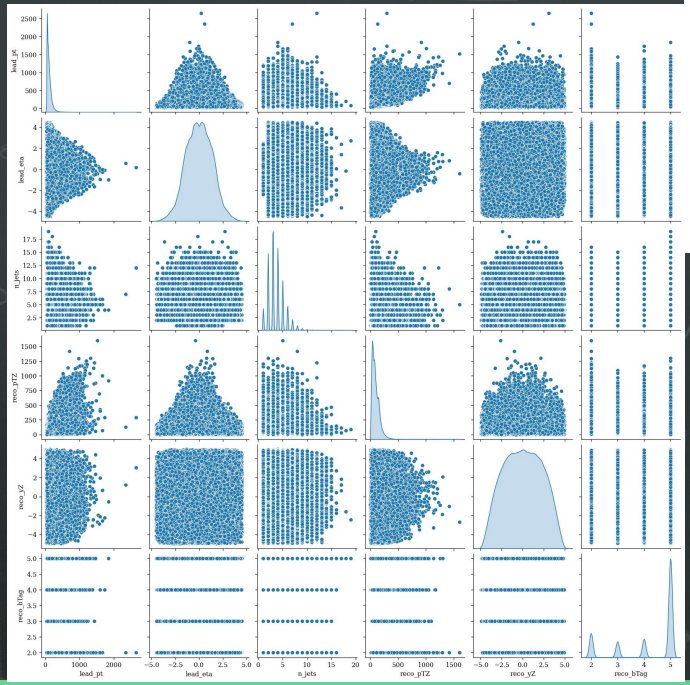
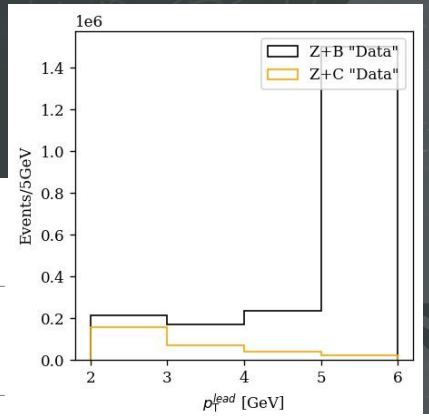
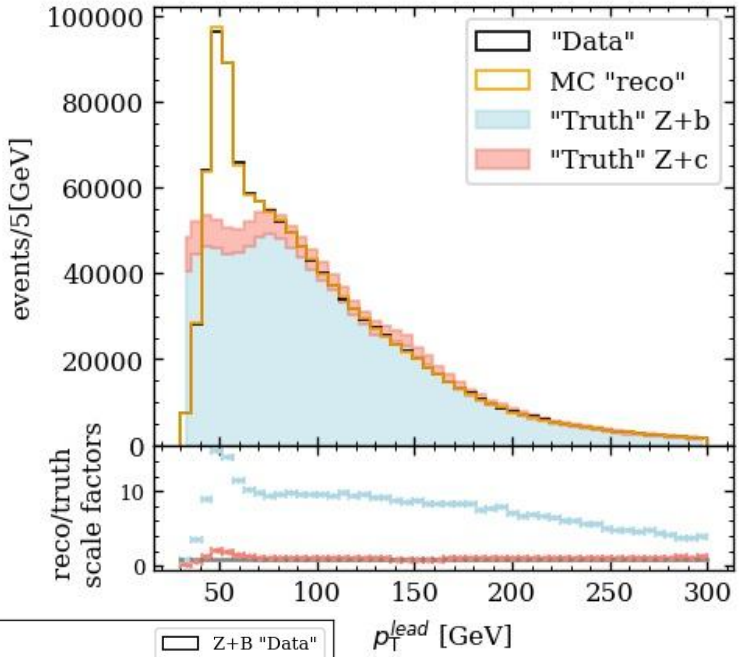
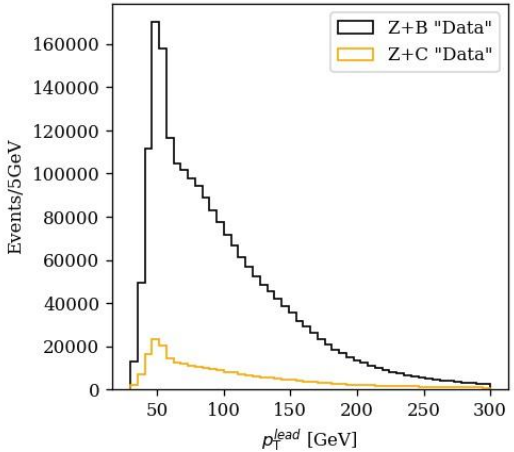
https://arxiv.org/abs/1910.14654

Problem has lots of correlated Information - Why not include it?

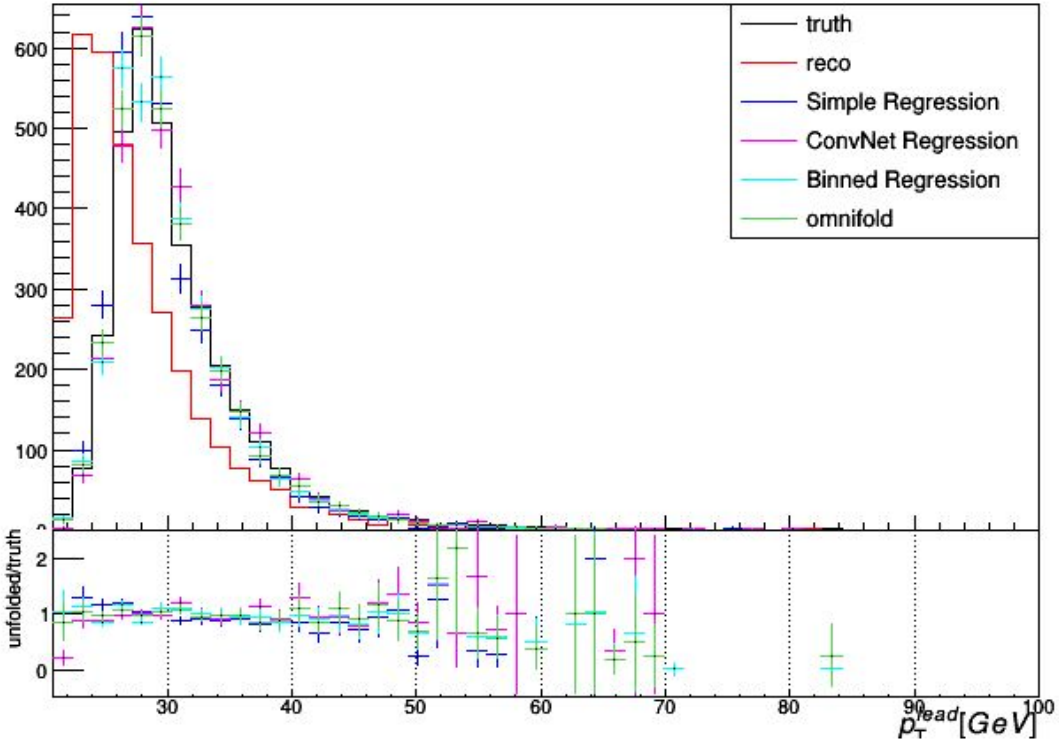






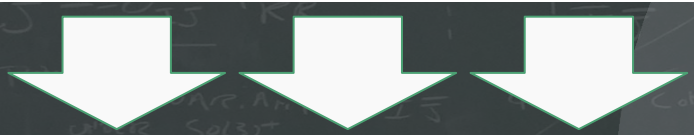


Lots of possibilities!



Common Interface!

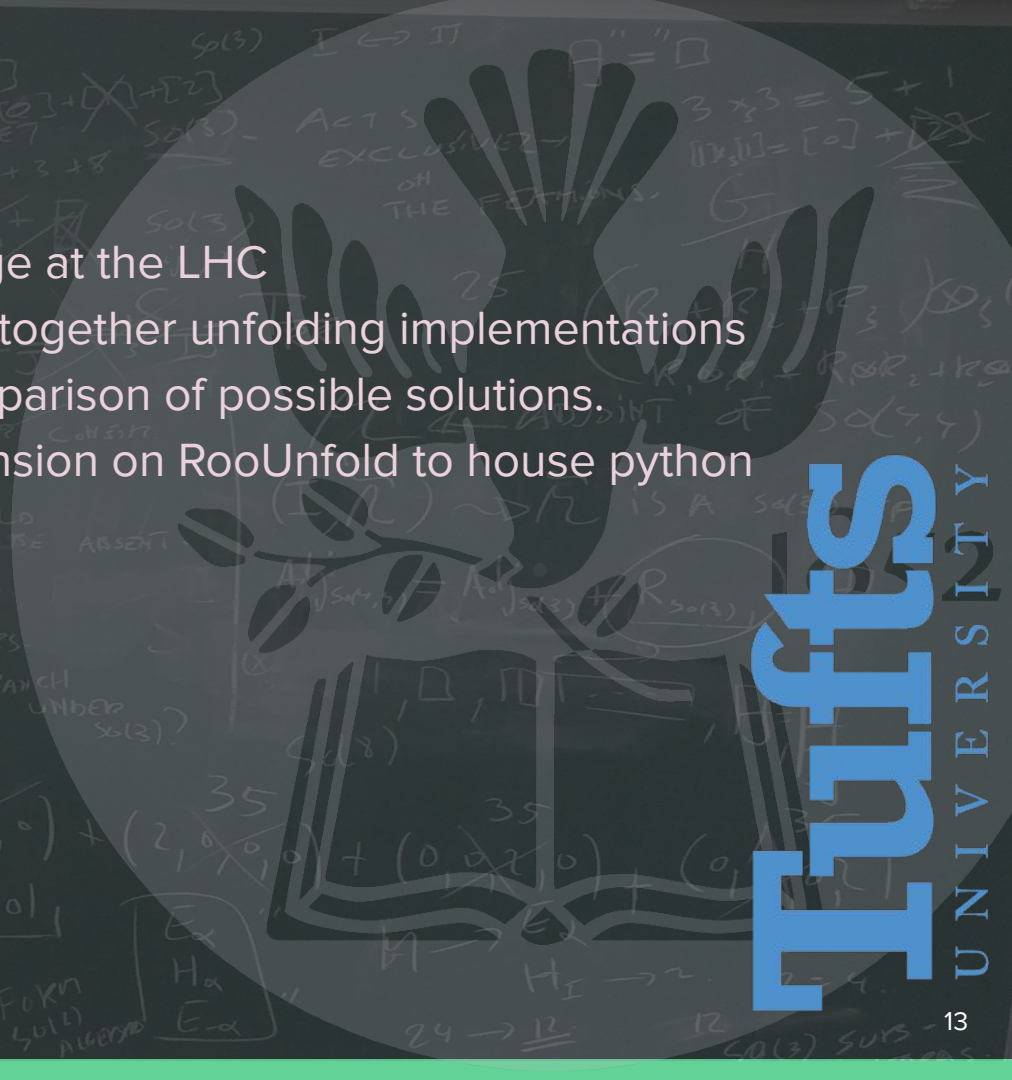
```
In [1]: import ROOT
        response = ROOT.RooUnfoldResponse(reco,truth,migration)
        unfold = ROOT.RooUnfoldBayes(response, data)
        unfolded_hist = unfold.Hunfold()
```



```
In [2]: import RooUnfoldML
        response = RooUnfoldML.RooUnfoldMLResponse(reco,truth)
        h_dnn = RooUnfoldML.RooUnfoldBinnedRegression(response,data)
        unfolded_hist = h_dnn.Hunfold()
```

Easy to use

- Will Ship as a lightweight extension to RooUnfold
- Optional extra flag on compilation
- Minimal Dependencies
- Meaningful default settings

Summary

- Unfolding is seeing increased usage at the LHC
- RooUnfold is a good way to group together unfolding implementations
- RooFitUnfold allows statistical comparison of possible solutions.
- RooUnfoldML is a lightweight extension on RooUnfold to house python based ML unfolding solutions