



Science & Technology Facilities Council
Rutherford Appleton Laboratory

RooUnfold developments

Tim Adye

Rutherford Appleton Laboratory



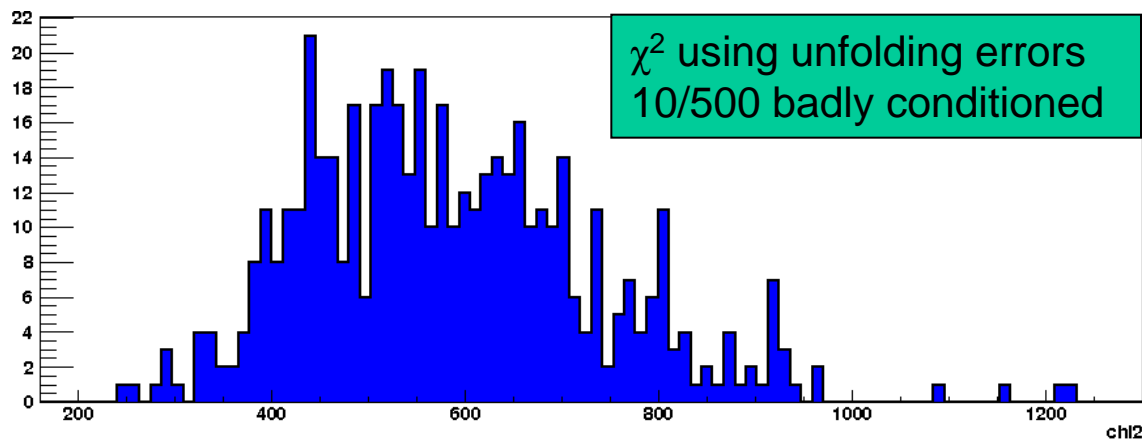
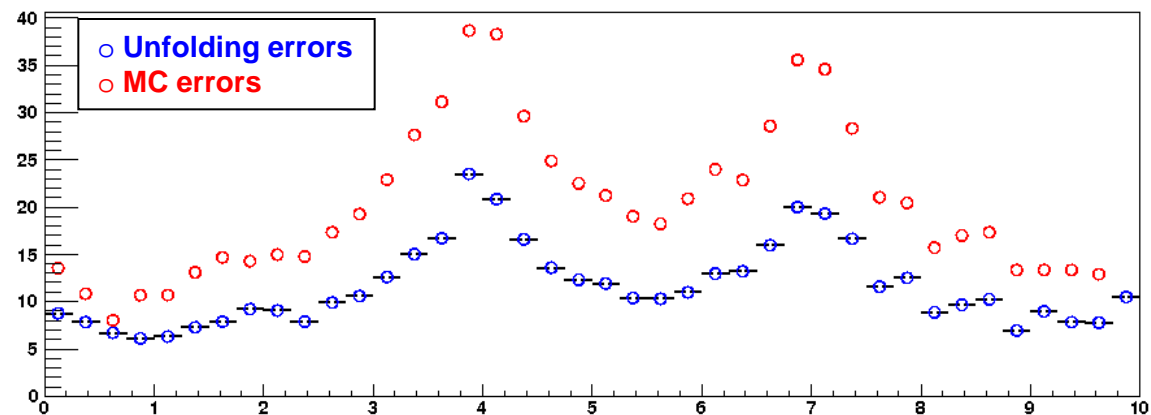
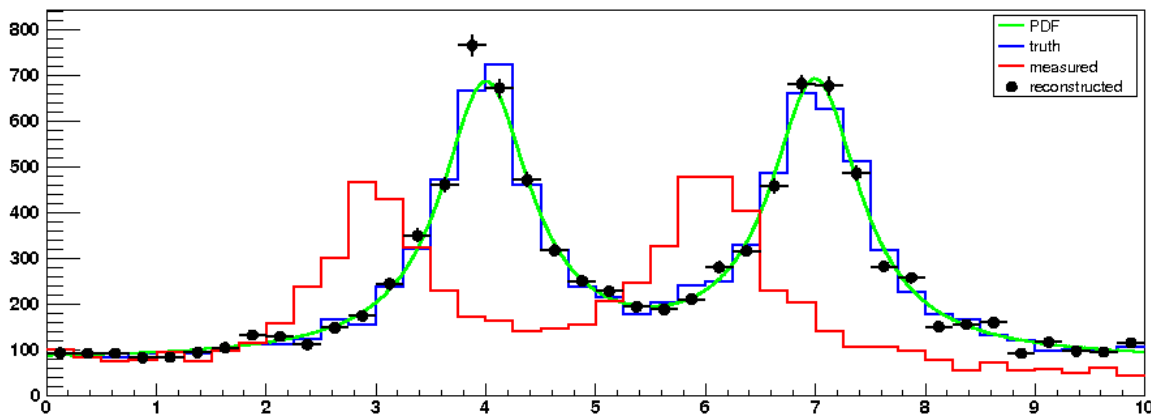
Unfolding Framework
Project Meeting
15th September 2010



RooUnfold version 1.0.2 improvements

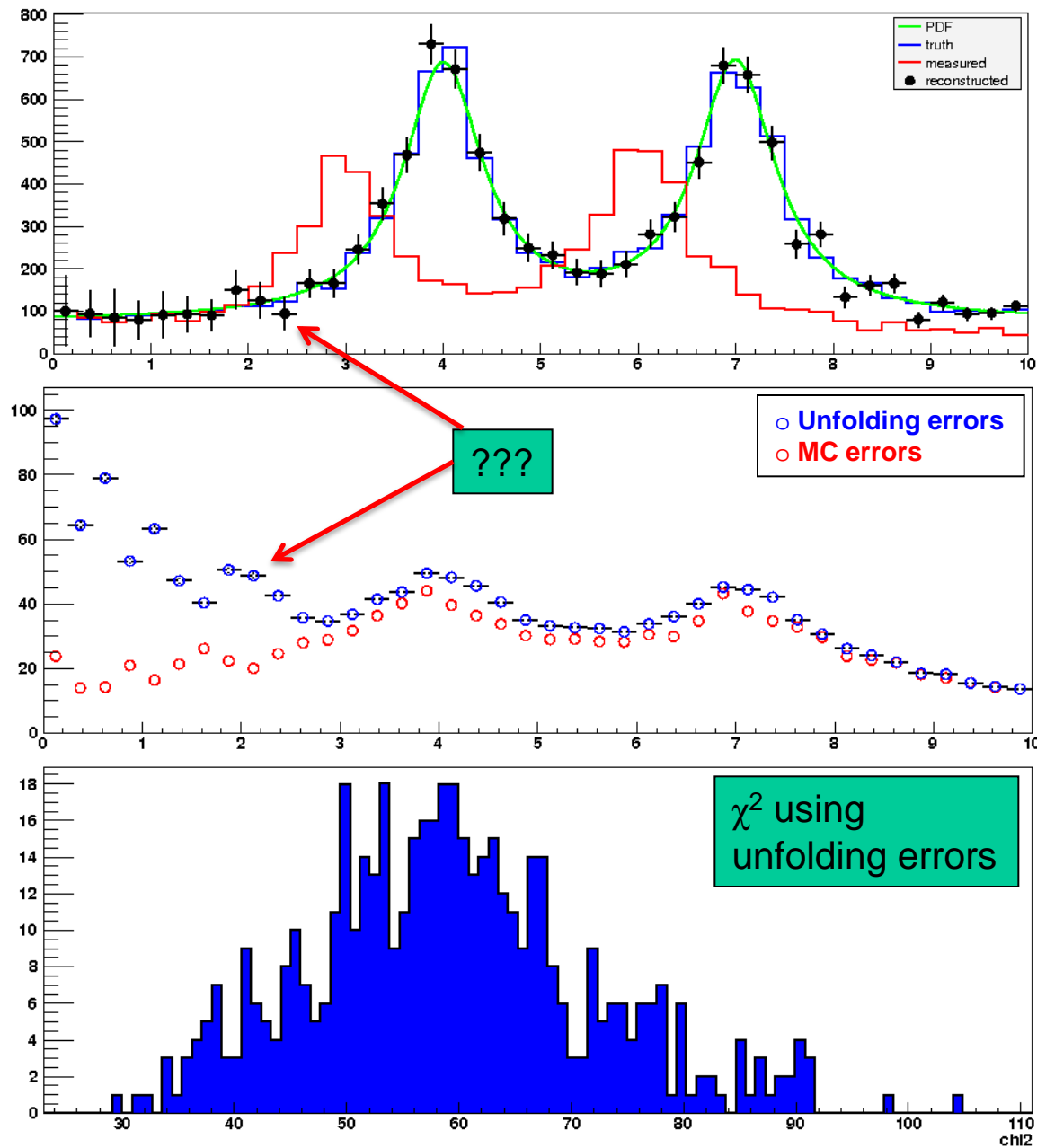
- A simple (though not yet fully-featured) interface to TUnfold
 - Handles 0-, 1-, 2-order polynomial regularisation for 2D and 3D distributions
- Unregularised matrix inversion method (eg. for comparison)
- Unfolding errors for all algorithms can be calculated using MC toys: can switch between
 - bin-by-bin errors (fastest),
 - full covariance matrix from the propagation of errors in the unfolding, or
 - covariance matrix from MC toys (slow)
- Regularisation parameter and errors test procedures
- An option to include the histogram underflow and overflow bins in the unfolding
 - Currently just for 1D histograms
- New convenience methods
 - generic constructors (`New(alg), Clone()`)
 - χ^2 calculation
 - vector accessors
- Class documentation

Error analysis for Bayesian algorithm

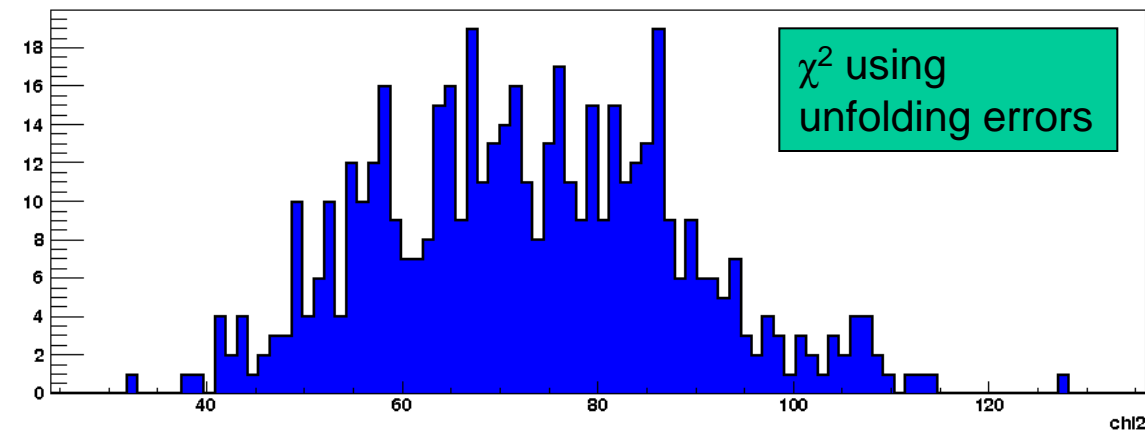
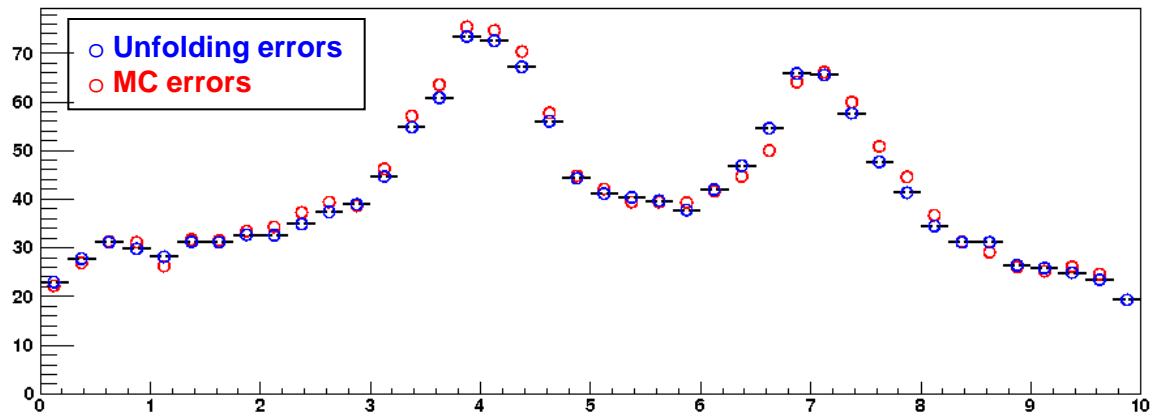
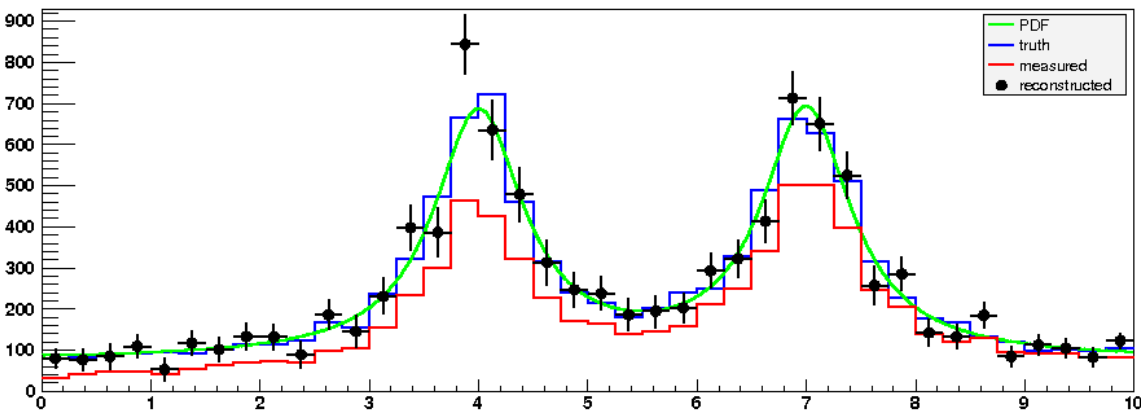


Error propagation in SVD
method would be even
worse – if we hadn't used
the MC errors all along

TUnfold



Unregularised matrix inversion



Does not work with large bin migrations, so here we test with no systematic bias

$$\chi^2$$

- Covariance matrix is often nearly singular or poorly conditioned
 - Is there a better way to calculate χ^2 ?
 - SVD helps, but still gives occasional problems (crazy χ^2)
- In any case, χ^2 is not a good figure of merit when testing unfolding
 - can improve χ^2 by relaxing regularisation → smaller errors, but larger residualsbut still useful to show, since its meaning is well-known
- What is a better objective figure of merit?