

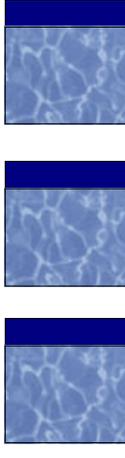
Issues of Unfolding

Workshop on Advanced Multivariate & Statistical Techniques

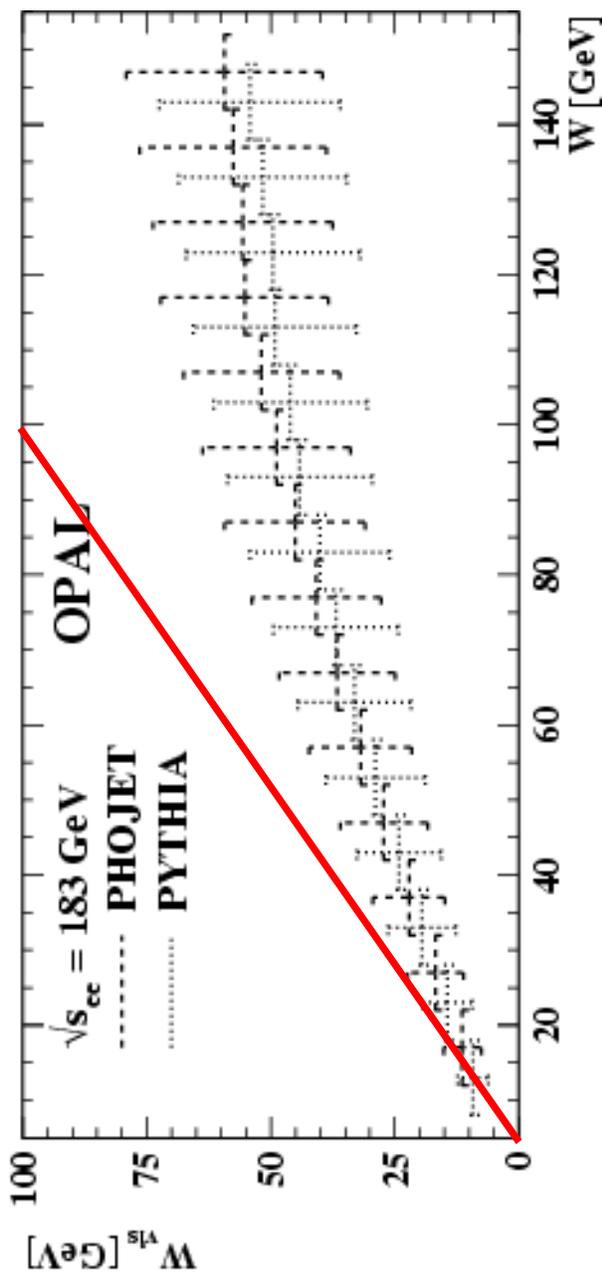
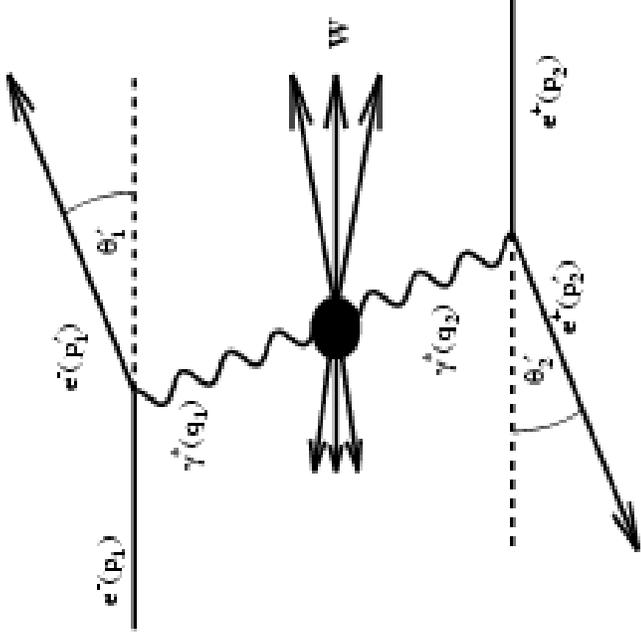
Fermilab, June 1, 2002

Stefan Söldner –Rembold (FNAL)

- Outline:
- 1) Motivation
 - 2) What is unfolding ?
 - 3) Methods
 - a) Inversion
 - b) Blobel unfolding (RUN)
 - c) SVD unfolding (GURU)
 - d) D'Agostini unfolding (Bayes)
 - e) Max. Entropy unfolding
 - 4) A few comparisons
 - 5) A comment about bin – by –bin 'unfolding'
 - 5) Summary



Motivation

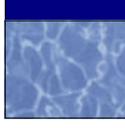
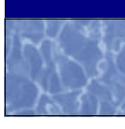


To unfold the measured distribution, we have to take into account the following effects:

- background
- limited acceptance (e.g. geometric losses)
- limited experimental resolution (smearing)
- statistical fluctuations and separating them from 'real' data properties

$$g(\vec{y}) = \int A(\vec{y}, \vec{x}) f(\vec{x}) dx + b(\vec{y})$$

$$\vec{g} = A \vec{f} + \vec{b}$$



$$\vec{g} = A \vec{f} + \vec{b}$$

$$A_{ji} = \frac{n_{ij}^{gen}}{n_i} \leq 1$$

$$\vec{f} = A^{-1} (\vec{g} - \vec{b})$$

ϵ : migration probability

$$\begin{pmatrix} g_1 \\ g_2 \end{pmatrix} = \begin{pmatrix} 1-\epsilon & \epsilon \\ \epsilon & 1-\epsilon \end{pmatrix} \begin{pmatrix} f_1 \\ f_2 \end{pmatrix}$$

$$A^{-1} = \frac{1}{1-2\epsilon} \begin{pmatrix} 1-\epsilon & -\epsilon \\ -\epsilon & 1-\epsilon \end{pmatrix}$$

$$V_f = \frac{1}{(1-2\epsilon)^2} \begin{pmatrix} (1-\epsilon)^2 g_1 + \epsilon^2 g_2 & -\epsilon(1-\epsilon)(g_1 + g_2) \\ -\epsilon(1-\epsilon)(g_1 + g_2) & (1-\epsilon)^2 g_2 + \epsilon^2 g_1 \end{pmatrix}$$

$$\epsilon = 0 \rightarrow \vec{g} = \vec{f}$$

$$\epsilon = 0.5 \rightarrow A^{-1} \text{ singular}$$

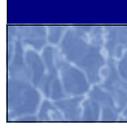
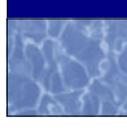
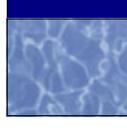
Example:

$$\epsilon = 0.4$$

$$g_1 = 100 \pm 10, g_2 = 81 \pm 9$$

$$f_1 = 138 \pm 35, f_2 = 43 \pm 33$$

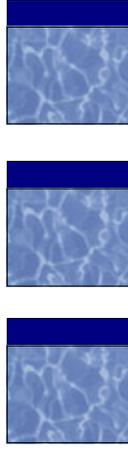
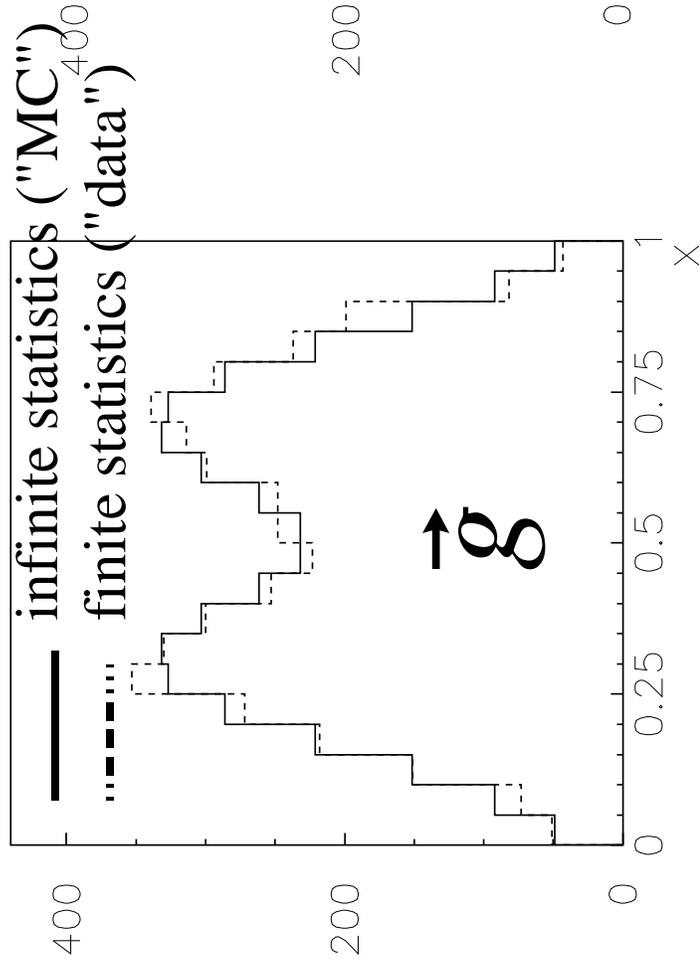
$$\rho = -0.92$$



Matrix inversion works if

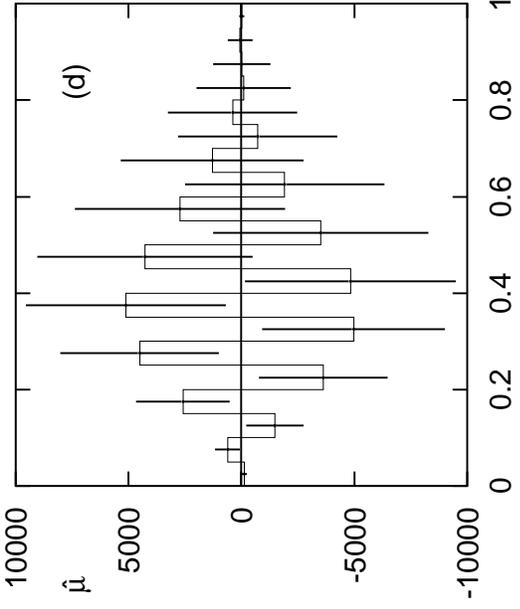
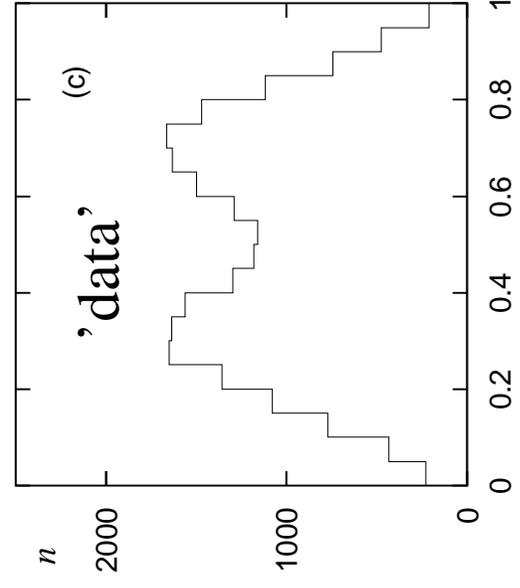
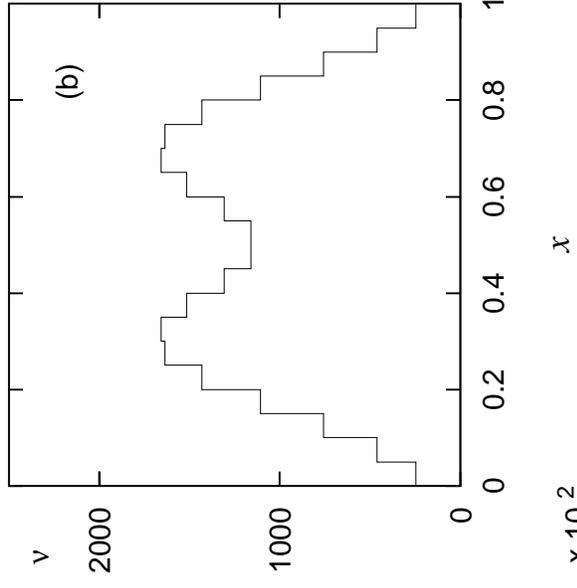
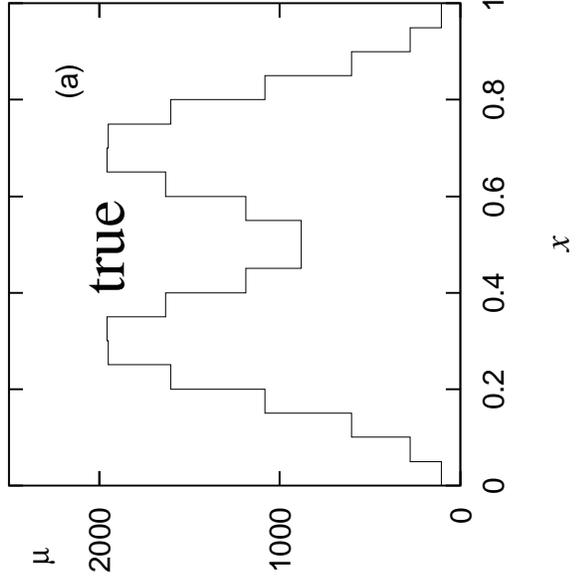
- number of bins are small (here 2)
- migrations are small
(i.e. bin size is (much) larger than resolution)

The main problem are the statistical fluctuations present in all data sets (the following example is taken from G.Cowan's talk at the Durham meeting)



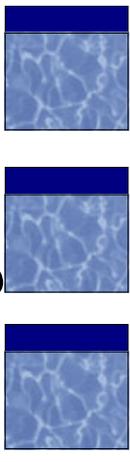


infinite statistics (exp. value)



Statistical fluctuations and real fine structure can not be distinguished

Stefan Söldner–Rembold, FNAL, 6/1/2002



Blobel Unfolding (RUN)

Code: <http://www.desy.de/~blobel/wwwrunf.html>

Documentation: The RUN manual, OPAL Technical Note 361

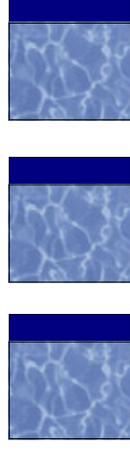
Method: – Minimize the negative sum of the Log –Likelihoods to observe the given number of entries in a bin

$$-\log L(\vec{g}, \vec{f}, A) + \tau C(\vec{f})$$

- C(f) is a regularisation parameter given by the 2nd derivative (curvature) of the solution (Thikhonov)
- Final result is expressed through a weighing function:

$$f(x) = f_{mult} f_{MC}(x)$$

- which is parametrised by a smooth function (B – splines)
- parameters: τ (nrdf) and number of knots (B – spline)
- RUN suggests number of bins (keep correlations small)



SVD Unfolding (GURU)

Code: <http://www.hep.man.ac.uk/~vato>

Documentation: A.Höcker, V.Kartvelishvili, NIM A372 (1996) 469

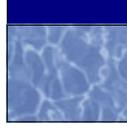
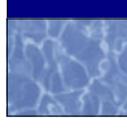
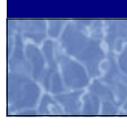
Method: – χ^2 Minimisation

$$\vec{f} = A^{-1} (\vec{g} - \vec{b})$$

$$\chi^2 = (A \vec{f} - (\vec{g} - \vec{b}))^T V_g^{-1} (A \vec{f} - (\vec{g} - \vec{b}))$$

- The problem is solved by
- Singular Value Decomposition (SVD)
- Regularisation is obtained by replacing χ^2

$$\chi^2 \rightarrow \chi^2 + \tau C(\vec{f})$$



D'Agostini Unfolding

Code: http://www-zeus.roma1.infn.it/~agostini/bayes_distr.txt

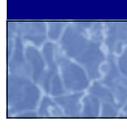
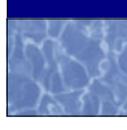
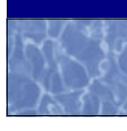
Documentation: G. D'Agostini, NIM A362 (1995) 487

Method: – iterative procedure based on Bayes' theorem

$$P(C_i/E_j) = \frac{P(E_j/C_i)P(C_i)}{\sum_k P(E_j/C_k)P(C_k)}$$

$$P(E_j/C_i) = A_{ji}$$

- take MC distribution for initial distribution $P^0(C_i)$
- and iterate until a χ^2 cut-off is reached
- regularisation is obtained by smoothing $P^n(C_i)$



Maximum Entropy Method

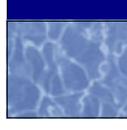
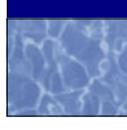
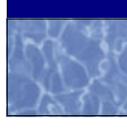
Code: glen.cowan@cern.ch

Documentation: K.Affholderbach, G.Cowan, J.Phys.G24 (1998) 457

Method: – Minimize the negative sum of the log – likelihoods
(see Blobel) but use different regularisation

$$-\log L + f_{tot} H(\vec{f})$$

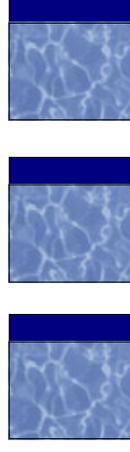
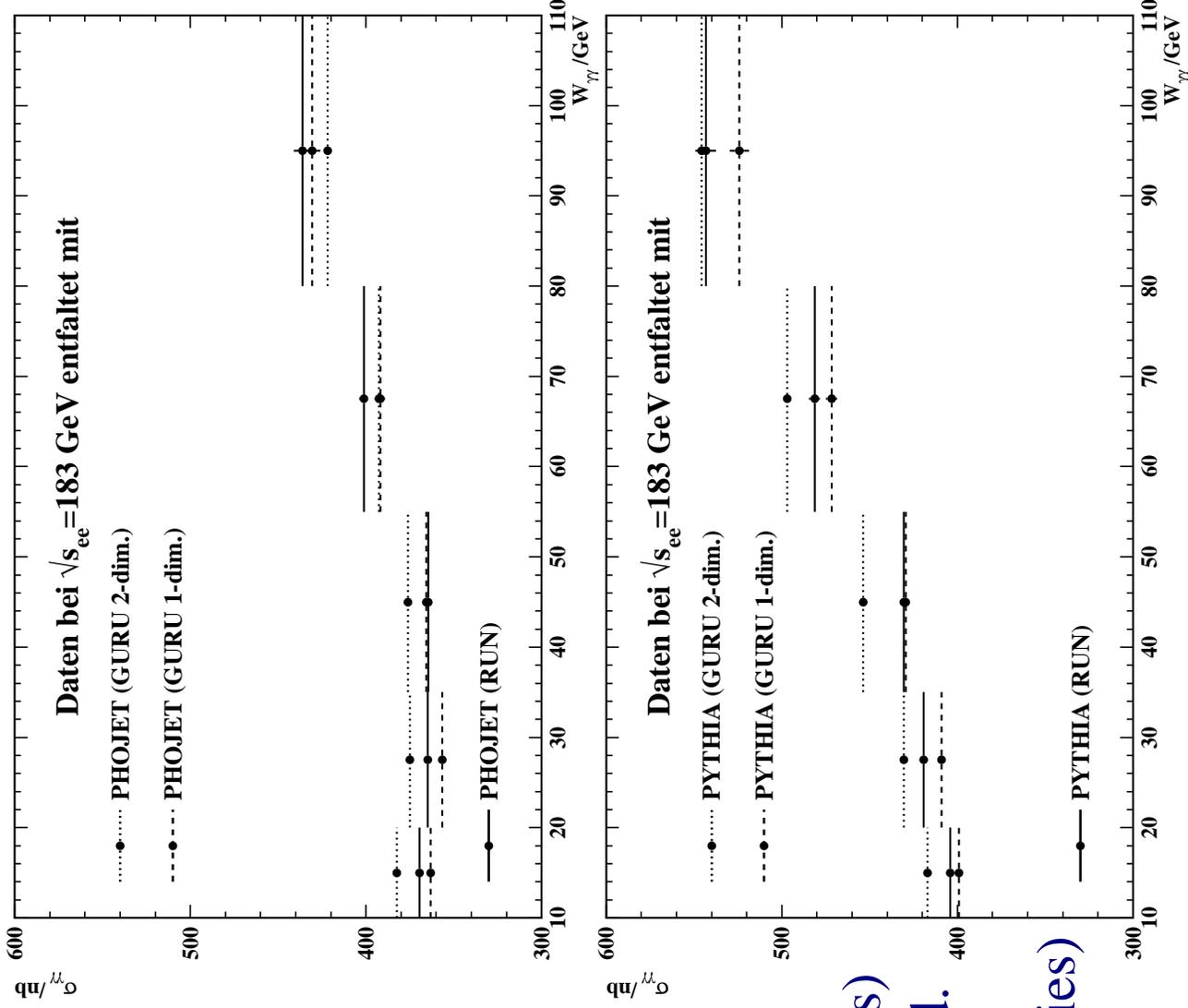
- H is the Shannon Entropy
- Regularisation does not depend on bin position
(no edge effects)



F. Wackerle
 OPAL PhD Thesis
 (Freiburg 1999)

Results published
 in EPJC14 (2000) 199

Unfolding methods
 have been applied
 to other problems in
 particle physics
 (e.g. τ spectral functions)
 but still not widely used.
 (tricky case: multiplicities)



Test of Unfolding Methods

OPAL
EPJC18 (2000) 15

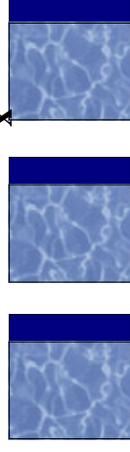
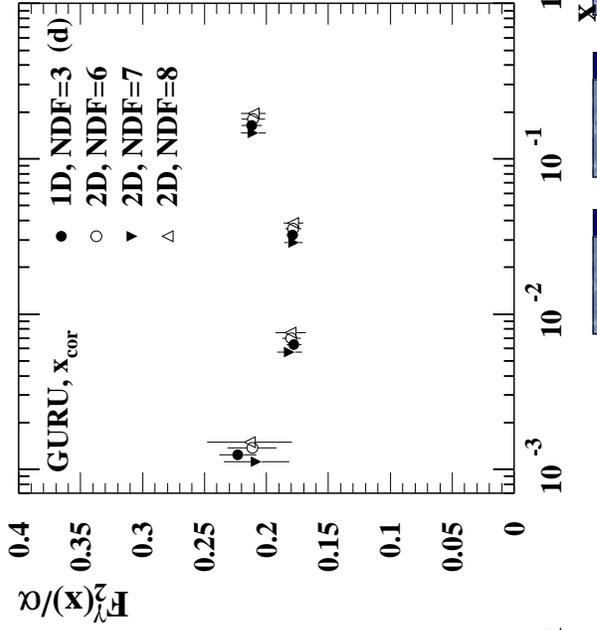
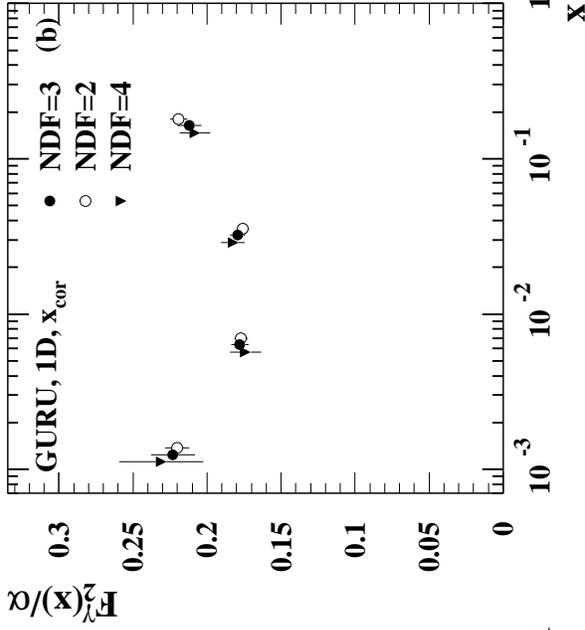
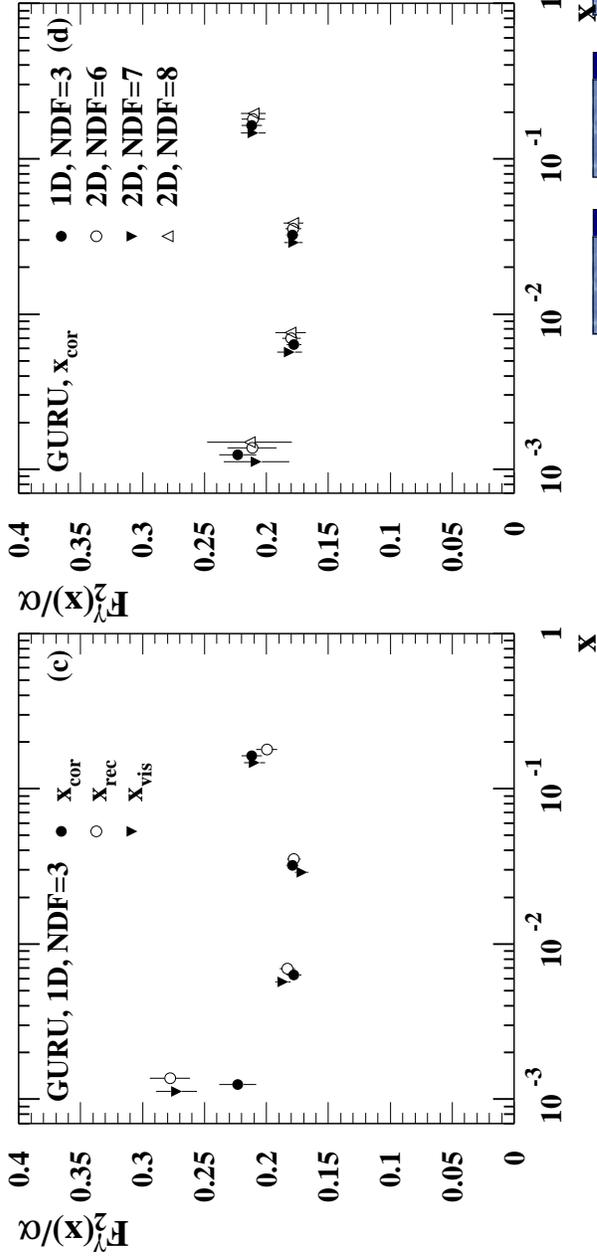
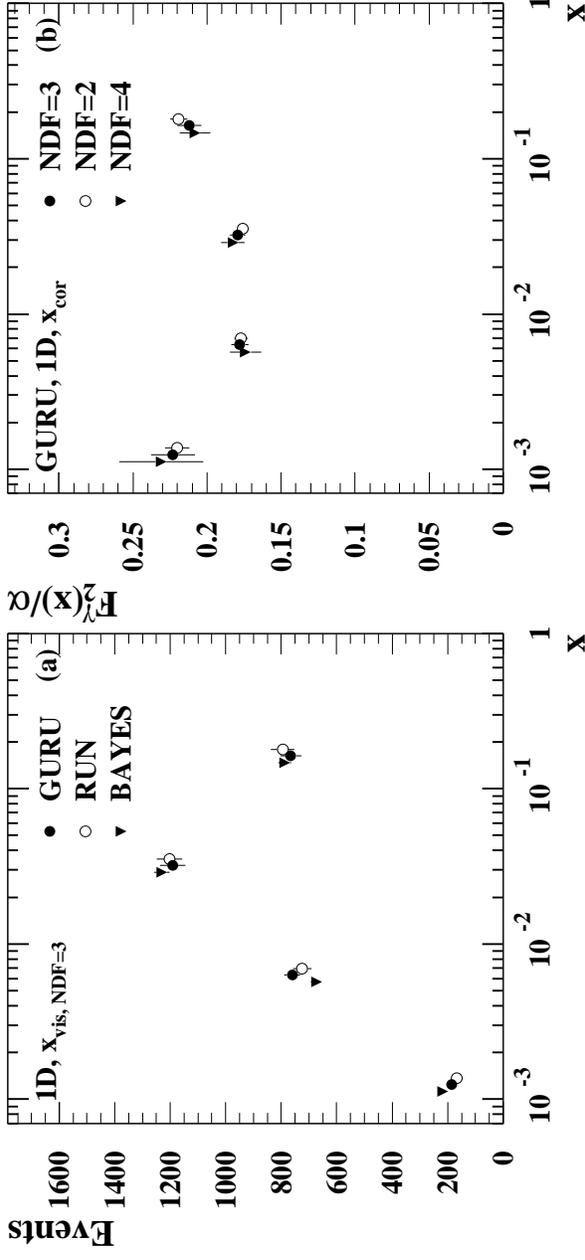
Similar problem:

Photon Structure
Function:

$$F_2^\gamma(x, Q^2)$$

$$x = \frac{Q^2}{Q^2 + W^2}$$

Q² is well measured
W² is badly measured

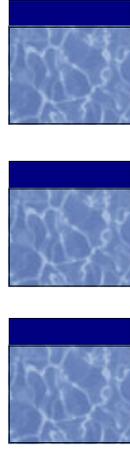
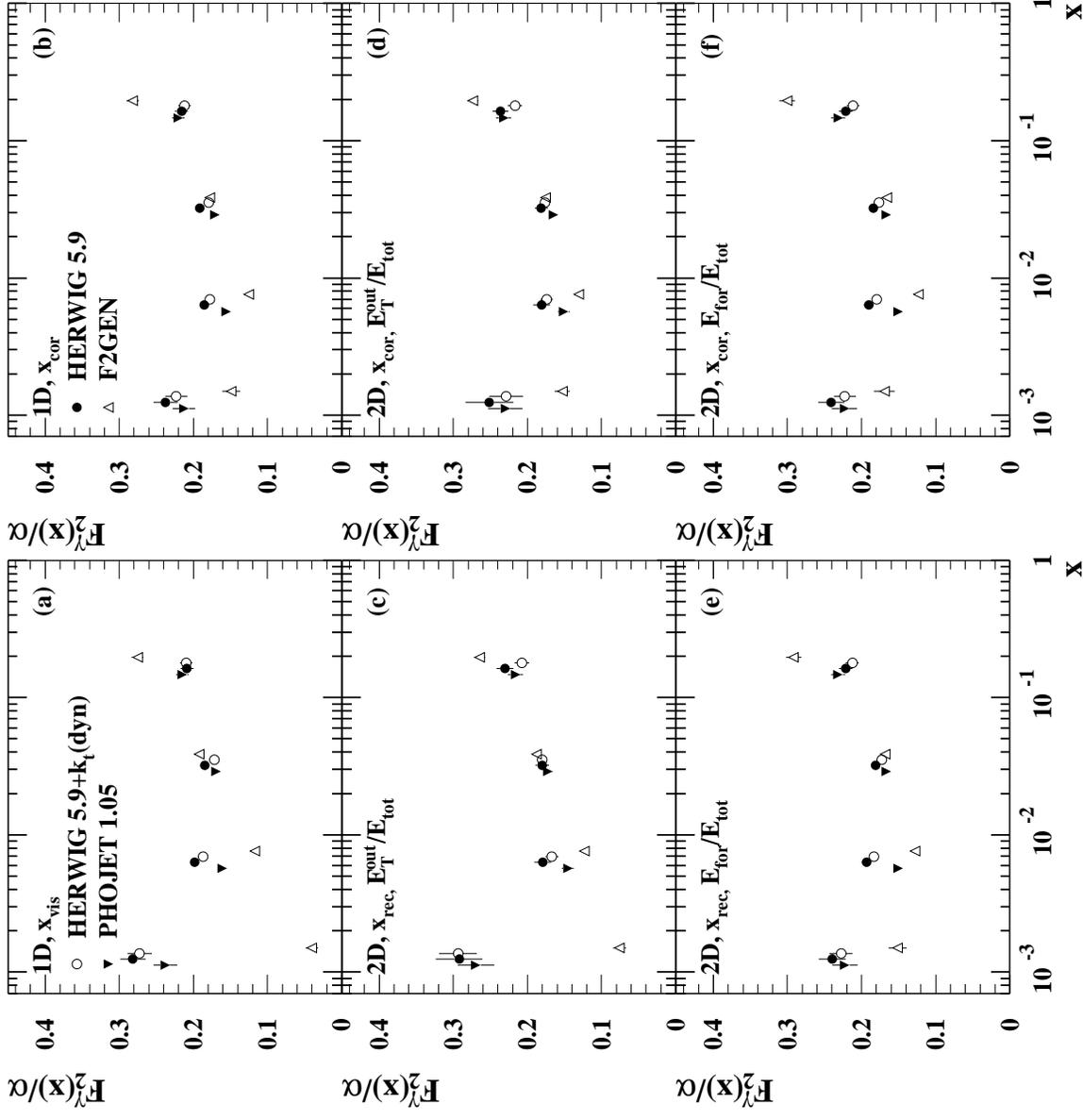


Two – Dimensional Unfolding

2–d unfolding
improves results
(smaller spread)

Still, good MC
description of data
is vital

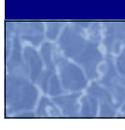
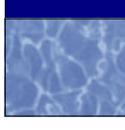
(in all distributions,
not only for the
unfolded quantities)



A comment about bin –by – bin unfolding

In special cases the results obtained using bin–by–bin ‘unfolding’ are close to a full regularised unfolding:

- migration matrix is diagonal
- MC and data agree well
- resolution effects are much smaller than bin size (migration small)
- $\langle x_{meas} \rangle \approx x_{true}$ transform if necessary, otherwise matrix is not diagonal
- correlations of the errors are ignored



Summary

- ❑ Regularised unfolding is necessary to take into account finite statistics, acceptance and resolution effects.
- ❑ Use all available information (e.g. 2d unfolding)
- ❑ Several methods used in HEP (GURU, RUN, BAYES, MaxEnt)

