# Unfolding: available methods, points to consider

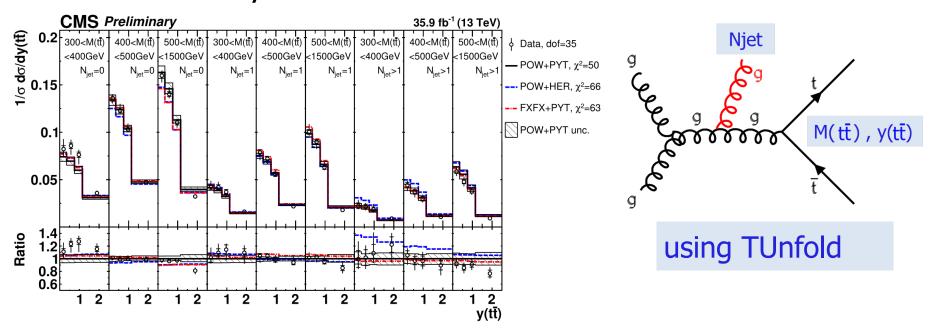
CMS annual TOP PAG meeting 21 Nov 2019, DESY

Olaf Behnke (DESY)

Tip: recent overview talk on unfolding methods in HEP by M. Kuusela

## Introduction

• Measured already 3D tt xsecs with 2016 data: TOP-18-004, 1904.05237



### Today:

### Least squares TUnfold

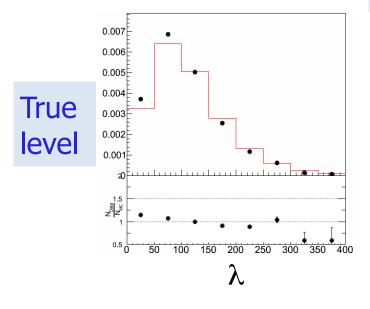
http://www.desy.de/~sschmitt/tunfold.html http://iopscience.iop.org/1748-0221/7/10/T10003/



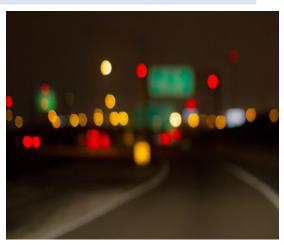
Max. Likelihood Combine tool

https://cms-analysis.github.io/HiggsAnalysis-CombinedLimit

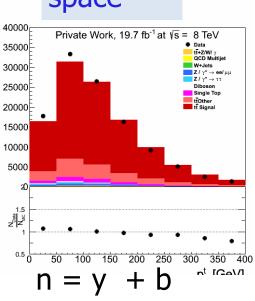
## Unfolding of $\lambda$

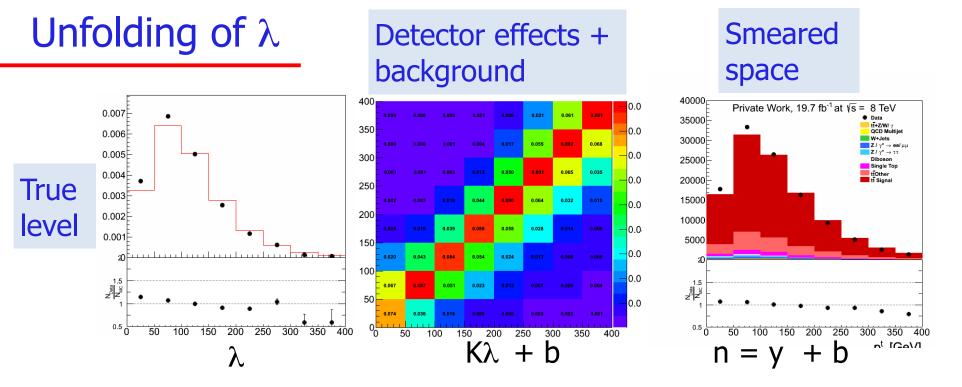


## Detector effects + background



## Smeared space



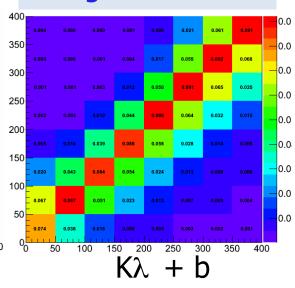


• Unfolding means estimating  $\lambda$  from n,  $\rightarrow \hat{\lambda}$ 

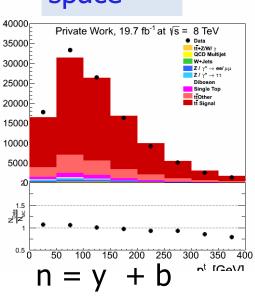
## Unfolding of $\lambda$

#### 

## Detector effects + background



## Smeared space



• Unfolding means estimating  $\lambda$  from n,  $\rightarrow \hat{\lambda}$ 

#### **TUnfold**

$$\chi^2 = [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]^t \mathbf{V_y}^{-1} [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]$$

#### **Combine**

$$L \sim \prod_{j-bins} Poiss[n_j | (\mathbf{K}\lambda)_j + b_j]$$

$$\tilde{\chi}^2 = -2 \ln L(\lambda)$$

## **Speed**

#### **TUnfold**

$$\chi^2 = [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]^t \mathbf{V_y}^{-1} [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]$$

Min. 
$$\chi^2$$
:  $d\chi^2/d\lambda^t=0$ 

$$\Rightarrow \hat{\boldsymbol{\lambda}} = (\mathbf{K^t} \mathbf{V_y^{-1}} \mathbf{K})^{-1} \mathbf{V_y^{-1}} \mathbf{K^t} \mathbf{y}$$

## Requires inversion of Hesse matrix:

$$(\mathbf{K^t}\mathbf{V_y^{-1}}\mathbf{K})^{-1} = V_{\hat{\lambda}}$$

#### Combine

$$L \sim \prod_{j-bins} Poiss[n_j|(\mathbf{K}\lambda)_j + b_j]$$

$$\tilde{\chi}^2 = -2\ln L(\lambda)$$

Numerical minimisation with Minuit  $\rightarrow$  need thousands of calculations of  $\tilde{\chi}^2$  for varying values of unfolded vector  $\lambda$ 



1:0

## **Precision**

#### **TUnfold**

$$\chi^2 = [\mathbf{y} - \mathbf{K}\lambda]^t \mathbf{V_y}^{-1} [\mathbf{y} - \mathbf{K}\lambda]$$

## Used Neyman $\chi^2$ has kown normalisation bias:

 $\#\text{events}_{\text{fitted}} = \#\text{events}_{\text{observed}} - \chi^2_{\text{min}}$ 

## TUnfold remedy: Area Constraint option

$$\chi^2 \to \chi^2 + \gamma(\sum_i (y_i - \sum_j K_{ij}\lambda_j))$$

Lagrange multiplier

Combine

#### Poisson based likelihood yields

#events\_fitted = #events\_observed



## **Data Combination**

#### **TUnfold**

### Combine run II data i=16, '17 and '18

## Uncorrelated yield vectors yi:

$$\chi^2 = \sum_{i} [\mathbf{y_i} - \mathbf{K_i} \boldsymbol{\lambda}]^t \, \mathbf{V_{y_i}}^{-1} \left[ \mathbf{y_i} - \mathbf{K_i} \boldsymbol{\lambda} \right]$$

## Correlated yield vectors yi.:

$$oldsymbol{y} = \left(egin{array}{c} oldsymbol{y}^{16} \ oldsymbol{y}^{17} \ oldsymbol{y}^{18} \end{array}
ight) \mathrm{V_y} = \left(egin{array}{c} V^{16,16} & V^{16,17} & V^{16,18} \ V^{16,17} & V^{17,17} & V^{17,18} \ V^{16,18} & V^{17,18} & V^{18,18} \end{array}
ight) \mathrm{K} = \left(egin{array}{c} K^{16} \ K^{17} \ K^{18} \end{array}
ight)$$

Min. 
$$\chi^2 = [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]^t \mathbf{V_y}^{-1} [\mathbf{y} - \mathbf{K} \boldsymbol{\lambda}]$$

#### Combine

### Poisson counts n<sup>i</sup><sub>i</sub>:

$$\chi^2 = \sum_{i} [\mathbf{y_i} - \mathbf{K_i} \boldsymbol{\lambda}]^t \mathbf{V_{y_i}}^{-1} [\mathbf{y_i} - \mathbf{K_i} \boldsymbol{\lambda}] \quad L \sim \prod_{i} \prod_{j-bins} Poiss[n_j^i | (\mathbf{K^i} \boldsymbol{\lambda})_j + b_j^i]$$

$$\tilde{\chi}^2 = -2\ln L(\lambda)$$

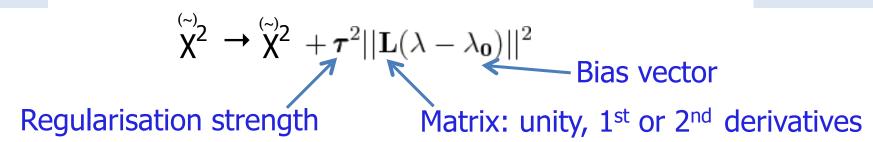


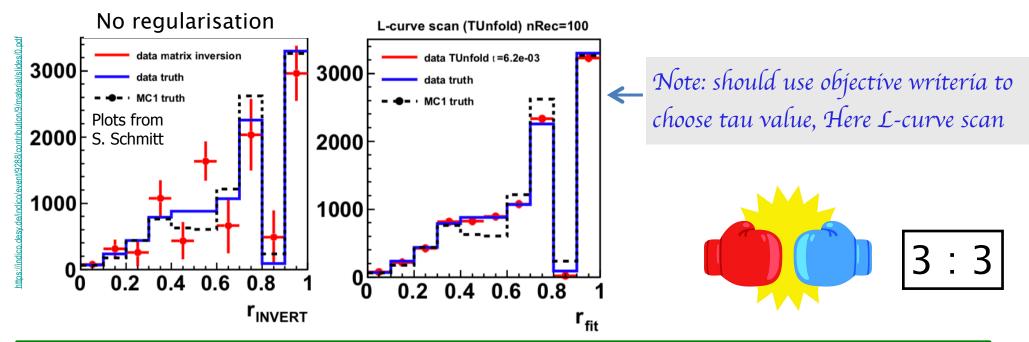
## Regularisation

**TUnfold** 

### Tikhonov regularisation:

Combine





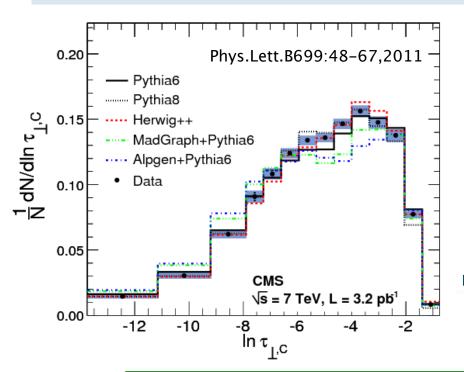
How can we make sure the constraint towards Bias vector (typically nominal signal MC prediction) is not too strong? → bottomline test

## **Bottomline test**

Idea: Comparing theory models to unfolded data should NOT be more discriminative than comparing folded theories to detector data

 $\rightarrow$  assess with data-model  $\chi^2$  tests at both levels (stat. uncert. only)

### Hadronic event shape analysis example with SVD unfolding



Material from talk M. Weber, PHYSTAT 2011

MC Generator	$\chi^2$ values between	$\chi^2$ values between
	data and smeared mc	unfolded data and Gen mc
PYTHIA6	421	398
HERWIG++	211	200
MADGRAPH	2590	2570
ALPGEN	3860	3860

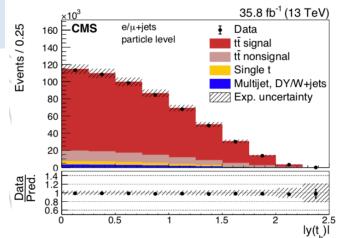
Chi2 order is the same before and after unfolding, values are similar



No sign of too strong regularisation in this example







-CMS

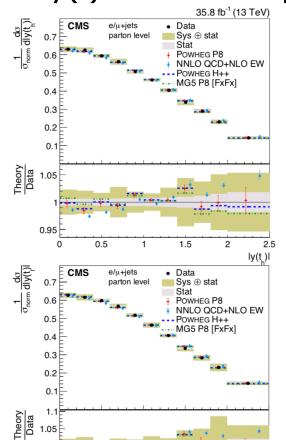
20

e/µ+jets

0.5

parton level

## y(t) unfolded to parton level



0.5

1.5

ly(t)l

Need ~ 5 iterations to have  $\chi^2_{data-models}$ similar at both levels

Need ~ 50 iterations to have  $\chi^2_{data-models}$ similar at both levels

→ Number of needed iterations depend on bin-size/resolution

35.8 fb<sup>-1</sup> (13 TeV)

Multijet, DY/W+jets Exp. uncertainty

Data

tt signal

Single t

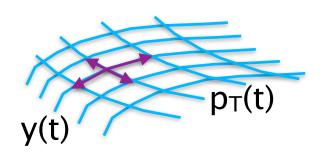
tt nonsignal

→ Don't use blindly RooUnfold D'Agostini unfolding default of 4 iterations

## Multi-differential cross section capabilities

#### **TUnfold**

- Automated mapping of multi-D input to internal 1D vectors
- Multi-D Tikhonov regularisation



#### Combine

• Multi-D unfolding performed e.g. in HIG-17-025,  $H \rightarrow \gamma \gamma$ 

$$\frac{d^2\sigma}{dp_T^{\gamma\gamma}\,d_{Njet}}$$

w/o regularisation

• So far max. total number of unfolded bins o(15)



4:3

## Background treatment

#### **TUnfold**

- User can supply for each background source:
  - bin-wise contribution + uncertainty
  - global normalisation factor + uncertainty
- → TUnfold subtract backgrounds and propagate errors

#### Combine

 Signals and backgrounds can be constrained from additional event categories, e.g. fitting to myy spectrum





Hig-17-025

## Systematic uncertainties

#### **TUnfold**

#### Combine

- Signal detector correction systematics → varied response matrices
- Nominal matrix K, ±1σ variations for source m: K<sub>m+</sub>, K<sub>m-</sub>
- Unfold with  $K_{m+} \rightarrow cross\ section$  variation  $\delta \hat{\lambda}_{\mathbf{m}_{+}}$
- TUnfold user has to perform all variations for all sources m and add to covariance matrix of λ



• Nuisance par  $\theta_m$ , morph  $K(\theta_m)$  from  $K_{m-}$ , K and  $K_{m+}$ 

$$L \sim \prod_{j-bins} Poiss[n_j|(K(\theta)\lambda)_j + b_j]$$
  
 $L \to L \cdot Pdfs(\theta)$ 

• Perform profile likelihood fit, data can also constrain  $\theta$ 





## MC Statistical uncertainties

**TUnfold** 

Combine

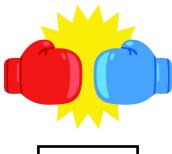
Statistical uncertainties of the response matrix K are:

ullet Error propagated to  $V_{\hat{\pmb{\lambda}}}$ 

 Barlow Beeston lite for each element of K,→ nuisance parameter with gaussian PDF

John Conway, arXiv1103.0354







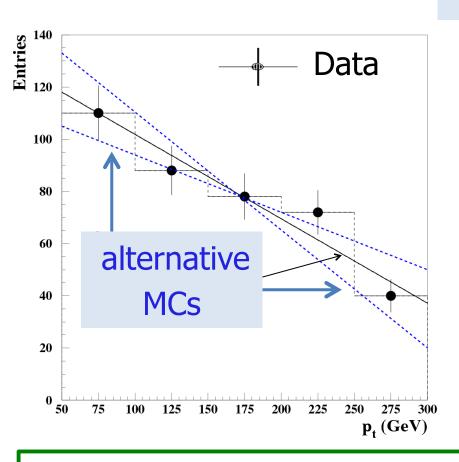


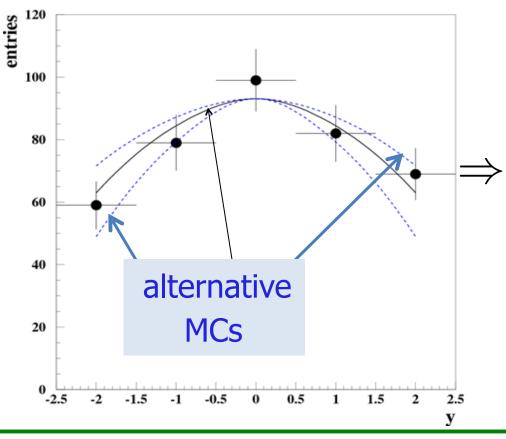
shutterstock.com • 305688461

## Model systematics

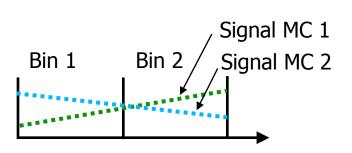
## MC generators model physics imperfectly

systematics of response matrix





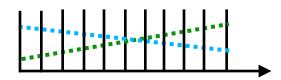
- $\rightarrow$  Recommend simultaneous multi-D unfolding of p<sub>T</sub>, y and other distributions and *projecting* results to 1D spectra of p<sub>T</sub>, y, etc.
- → Reduces model systematics (assumptions on the distribution of the variables integrated over)



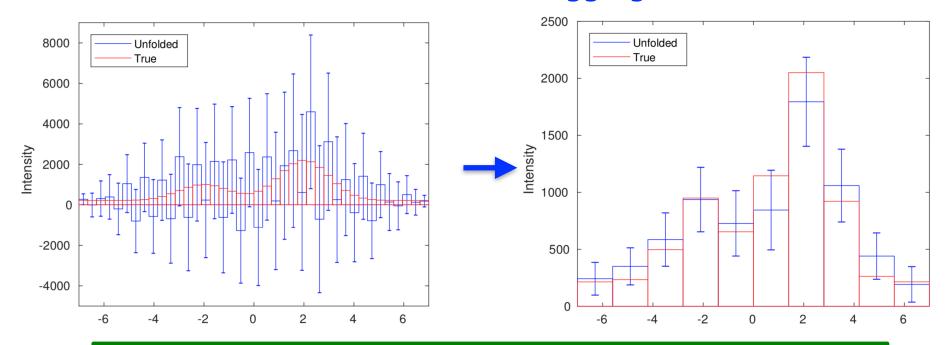
Different distributions within bins

- → Different response matrices
- → Model Systematics

Reduced effects within smaller bins



• Idea: unfold with fine bins and then aggregate results in wide bins



→ Improved modelling systematics, as detailed in talk https://indico.desy.de/indico/event/22731/session/5/contribution/24/material/slides/0.pdf

## **Summary**

#### TUnfold ideal for analyses:

- high statistics
- low background
- Multi-differential dσ
- Example: Top-pair dσ

#### Combine ideal for analyses:

- Any statistics, data can constrain background and systematics
- First dσ for low statistics, small s/b
- High precision measurements
- Example: dσ for single Top, Higgs

#### Not discussed tool:

SVD similar than TUnfold but less flexible



Unfolding is not a simple black box: requires thoughts and checks on optimal choices for binning, regularisation, systematics, needed MC statistics, and many other things

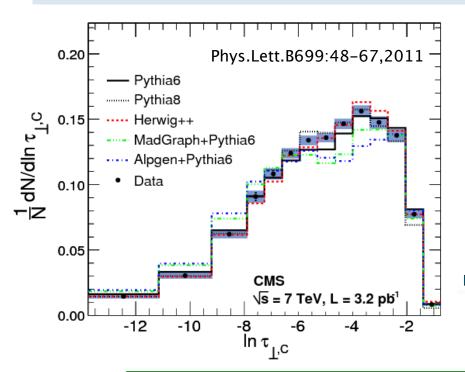
## Backup slides

## **Bottomline test**

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