



What we measure when we measure σ

Cross-section extraction techniques at T2K

Stephen Dolan

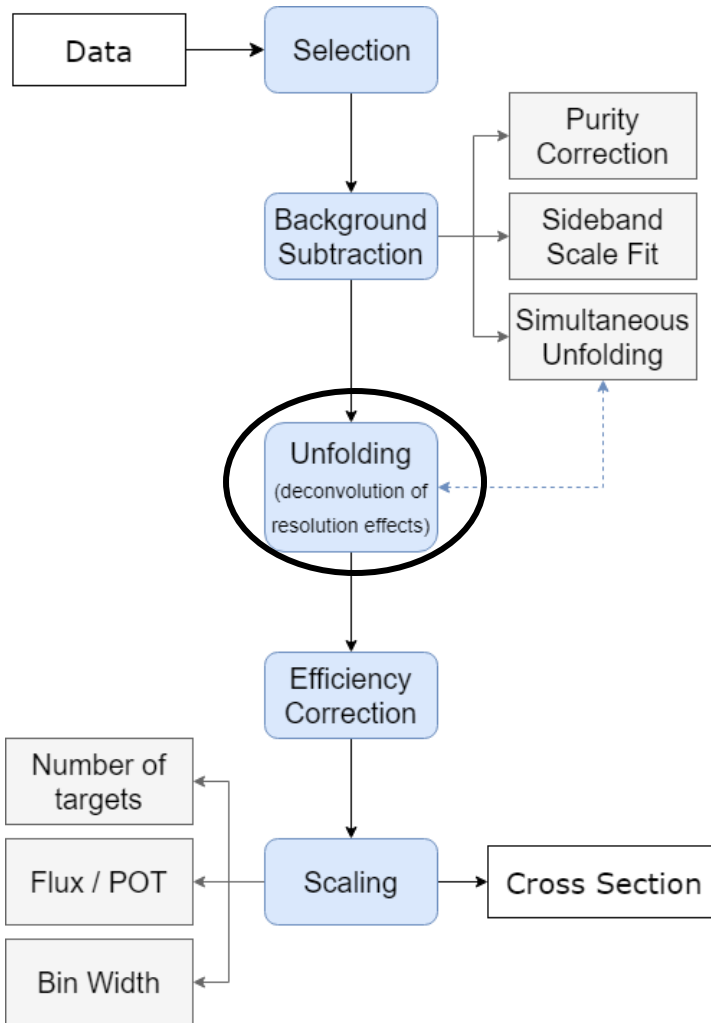
For the T2K Collaboration

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Unfolding

An over-simplified cross-section analysis



- Unfolding is a key part of cross-section analyses
- It is the process of deconvolving detector resolution effects from data
- (Almost) all recent results which can be compared to theory/generator predictions are unfolded
- Unfolding without care can bias your result

Unfolding

- Measure **selected** number of events in bins of a **reconstructed** quantity
Efficiency correct
- Want the **total** number of **signal events** in bins of a **true** quantity
Bkg subtract
- Unfolding

Assuming no background

Number of events in reco bin j

$$R_j = \sum_{\text{True Bins}, i} S_{ji} T_i$$

Number of events in true bin i

Smearing matrix

Number of events in true bin i

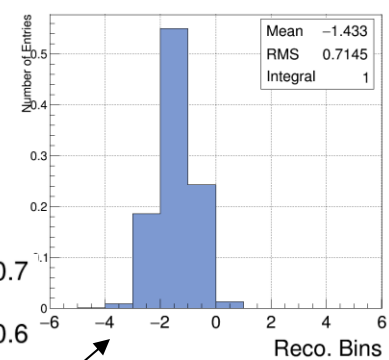
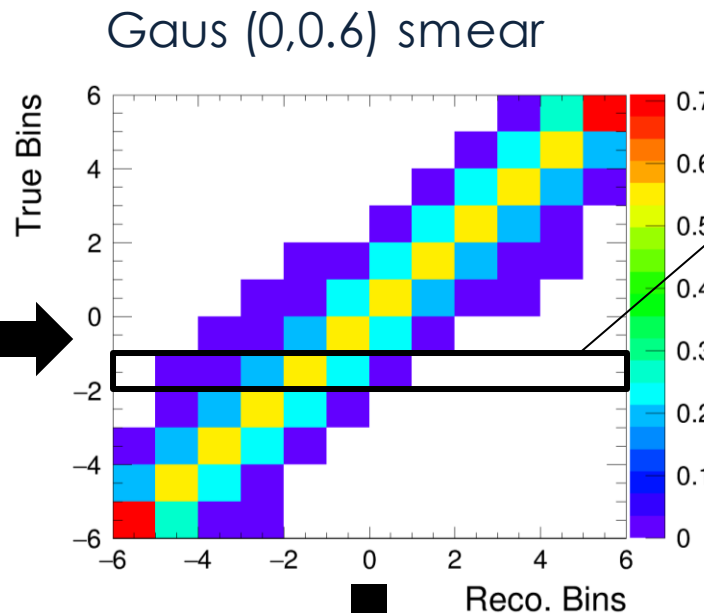
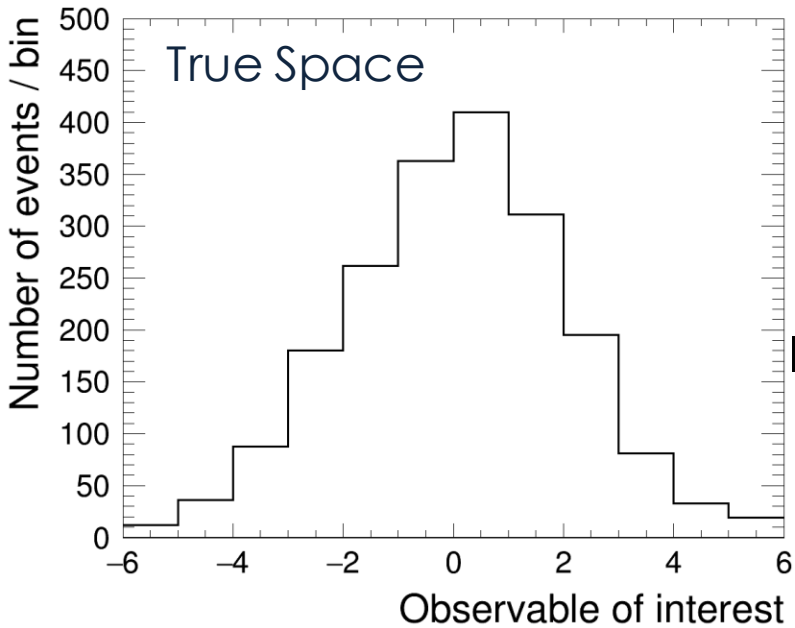
$$T_i = \sum_{\text{Reco Bins}, j} U_{ij} R_j$$

Number of events in reco bin j

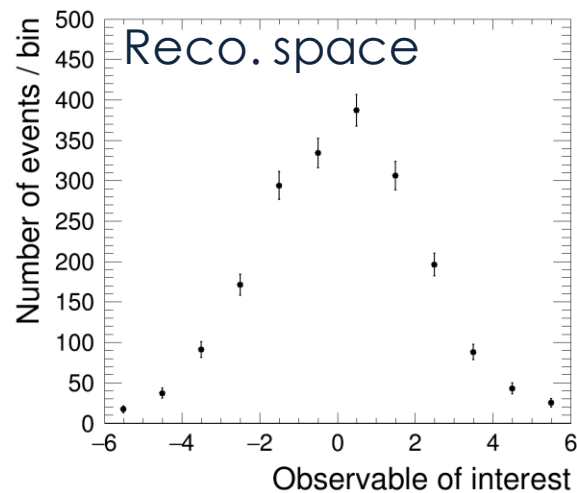
Unsmearing matrix

- Unfolding is finding U_{ij} from S_{ji} .
- Simplest method: use S_{ji}^{-1}

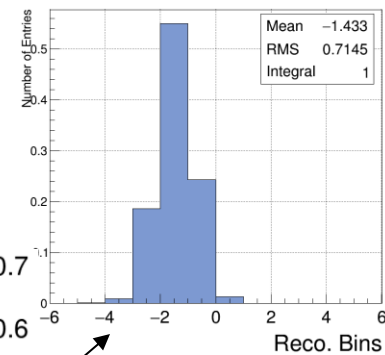
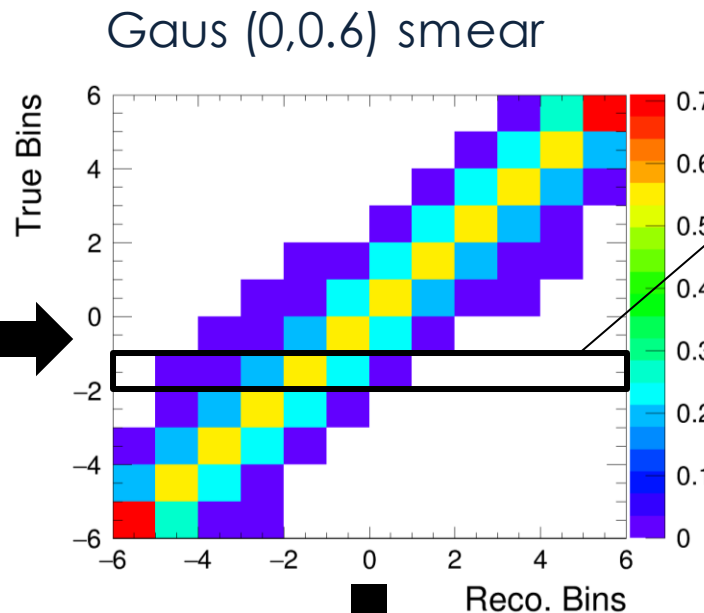
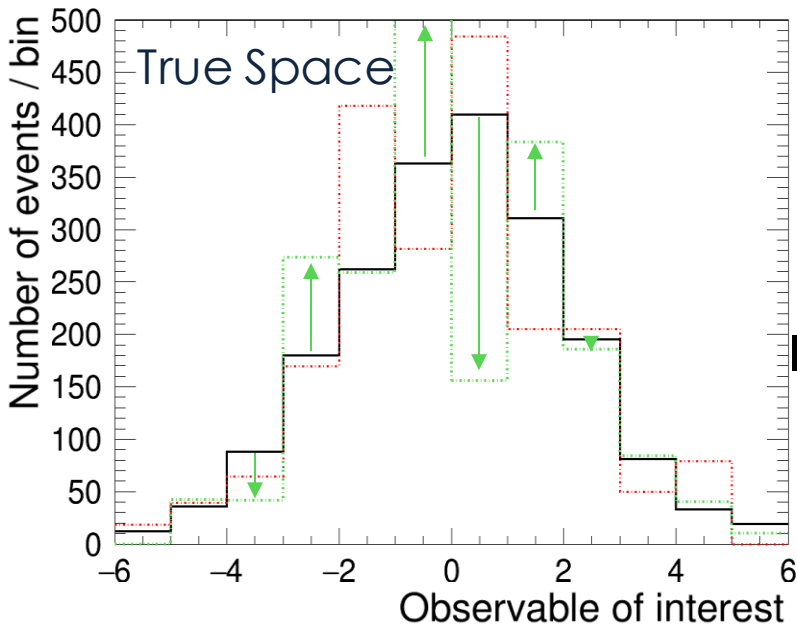
Toy example - smearing



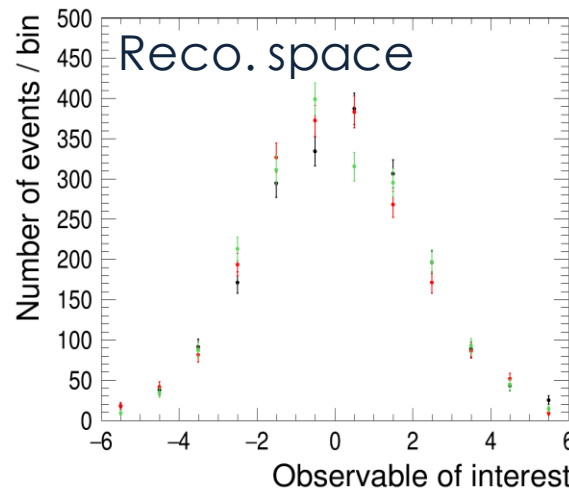
- 2000 events with bins of width 1.0 with a “resolution” of 0.6
- Quasi-realistic example



Toy example - smearing

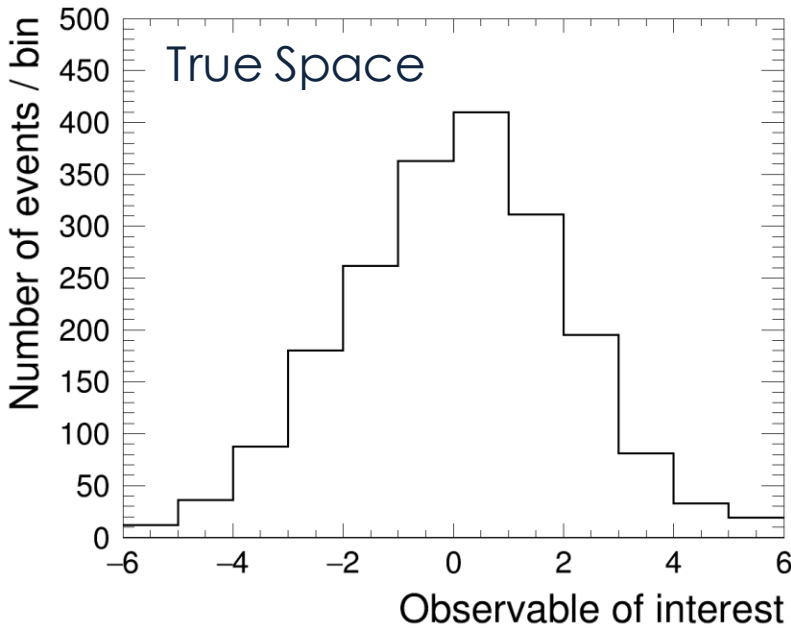


- Often free to move one bin down so long as we move the adjacent bins up to compensate*: see small changes in the reco. space
- True even with large variations
- Doesn't bode well for solving the inverse problem ...

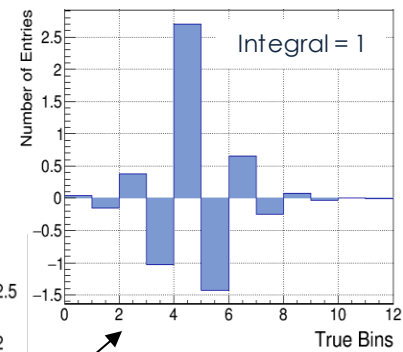
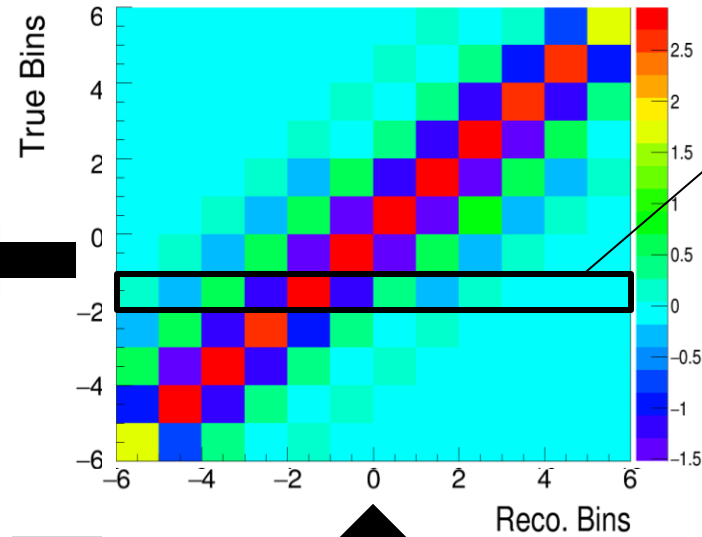


*This is intuitive: If you remove some events from a bin you can repopulate them with the "spill over" from the adjacent bins

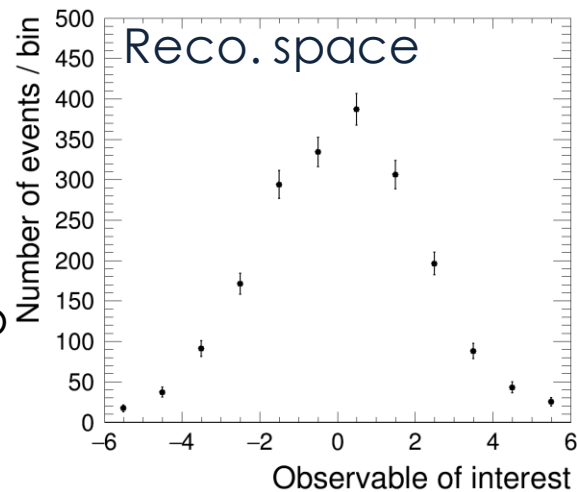
Toy example - unfolding



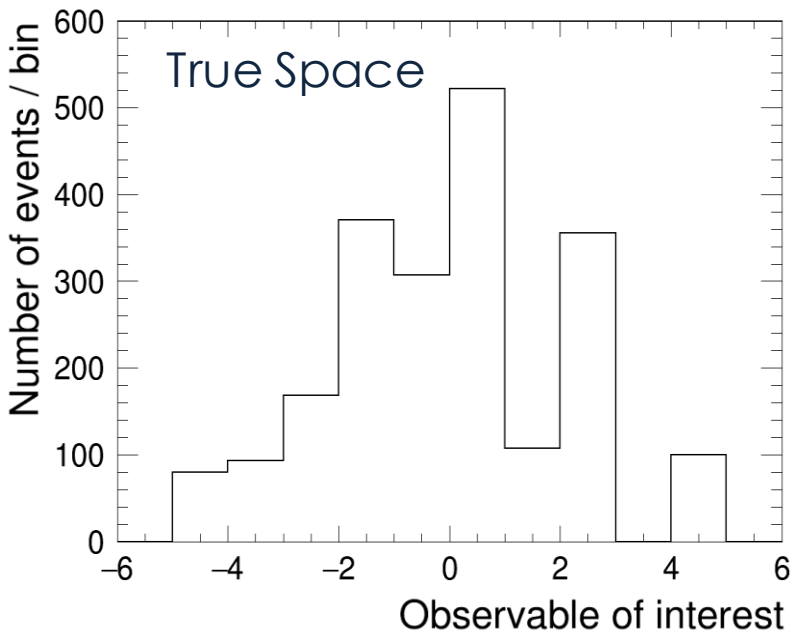
Inverse (Gaus (0,0.6) smear)



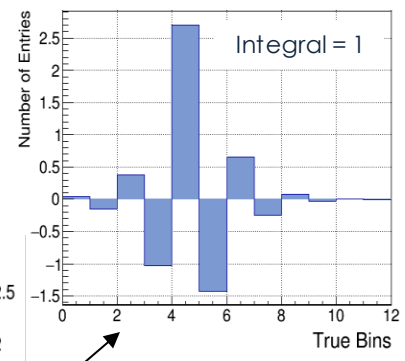
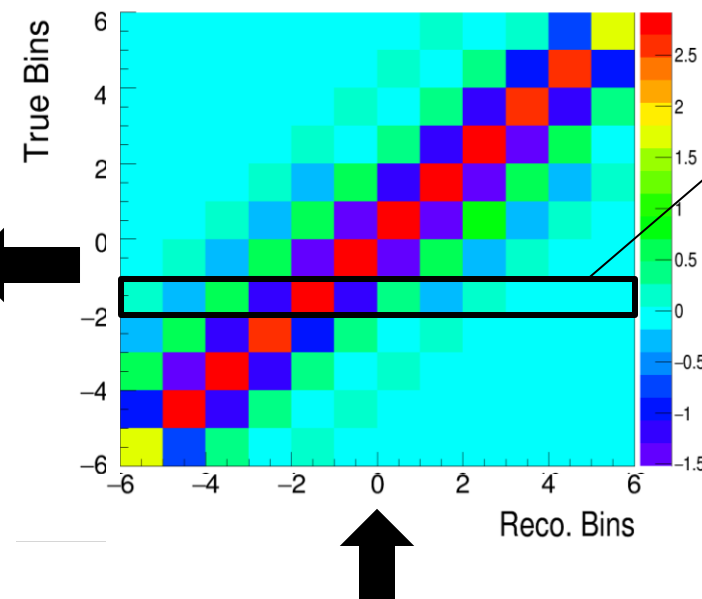
- So the inverse looks fine provided that:
 - Response in MC is exactly the same as the real response
 - The reco. MC sim. is identical to the real data ...



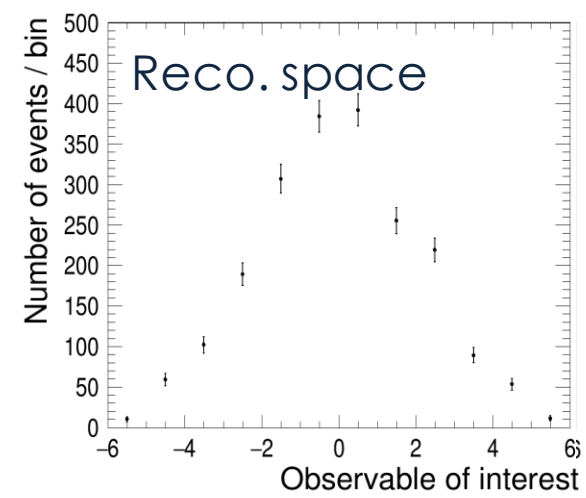
Toy example - unfolding



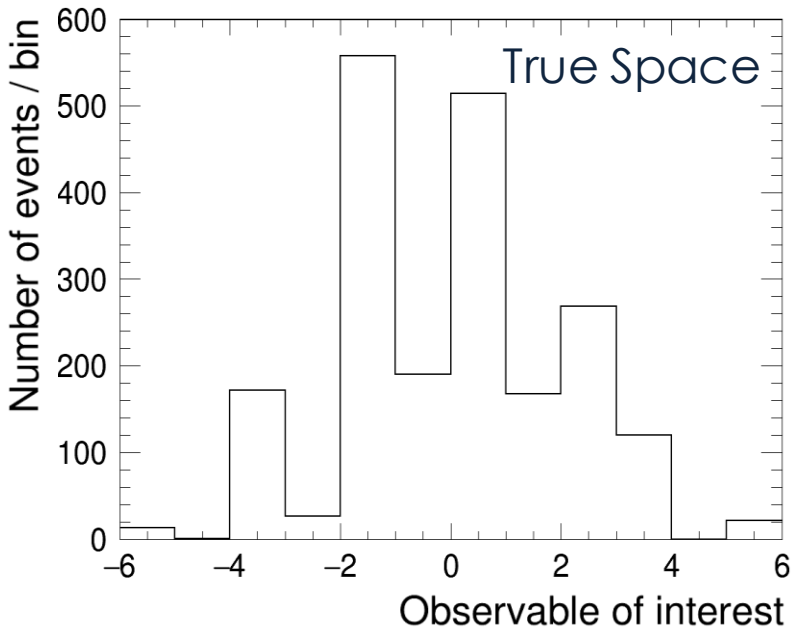
Inverse (Gaus (0,0.6) smear)



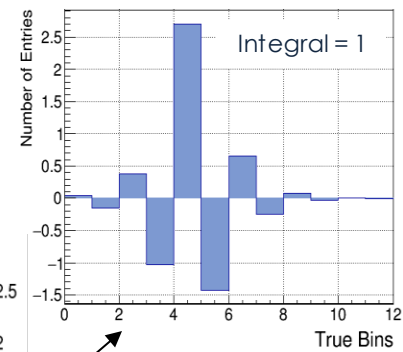
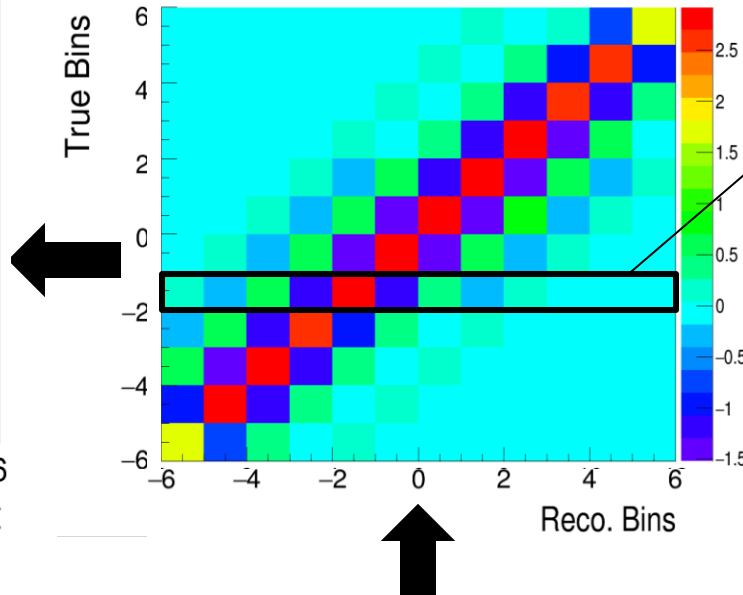
- Let's try a Poisson fluctuation of the reco. space!
- HUGE variation in the true space



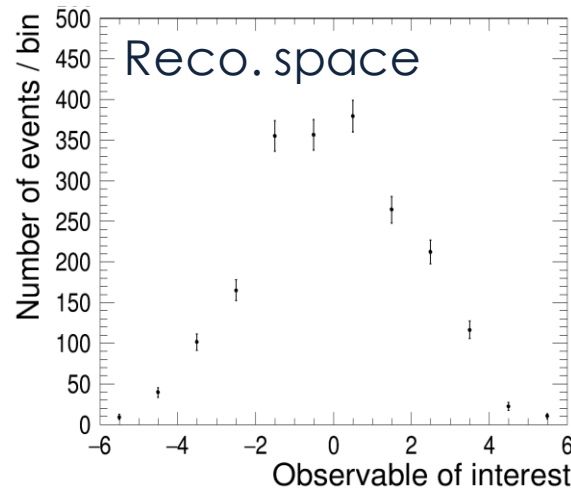
Toy example - unfolding



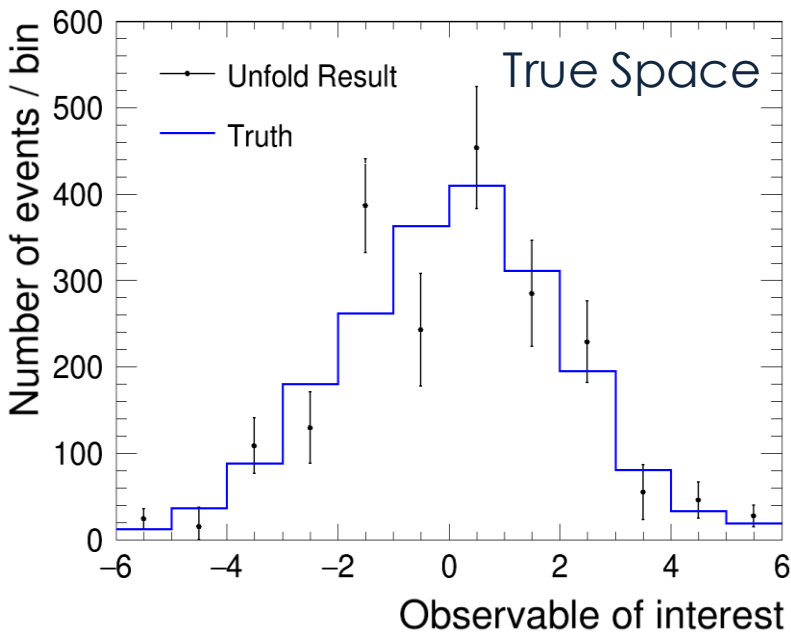
Inverse (Gaus (0,0.6) smear)



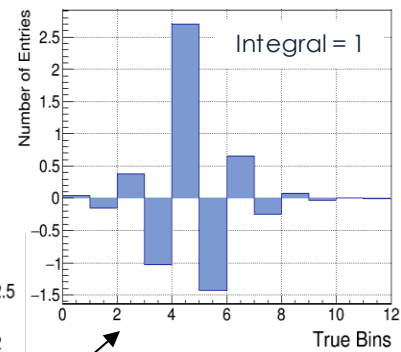
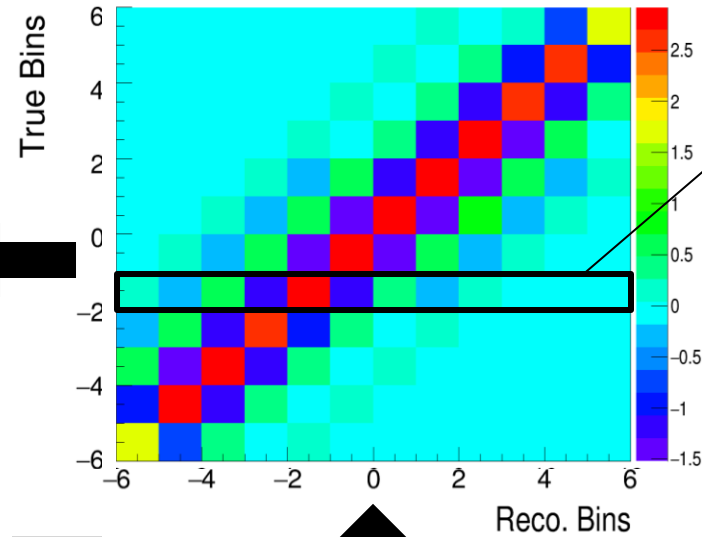
- Let's try another fluctuation
- Same thing ...



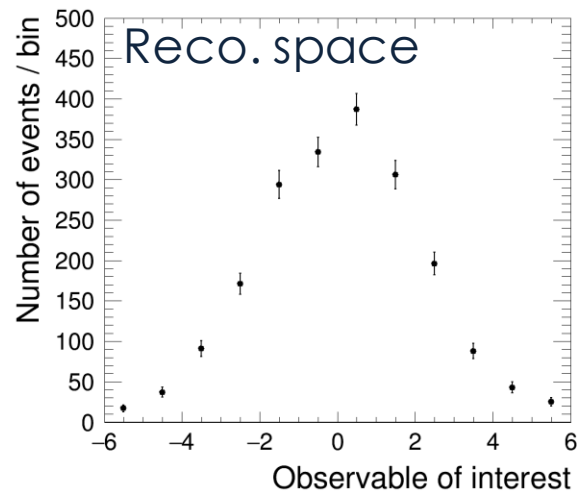
Toy example - unfolding



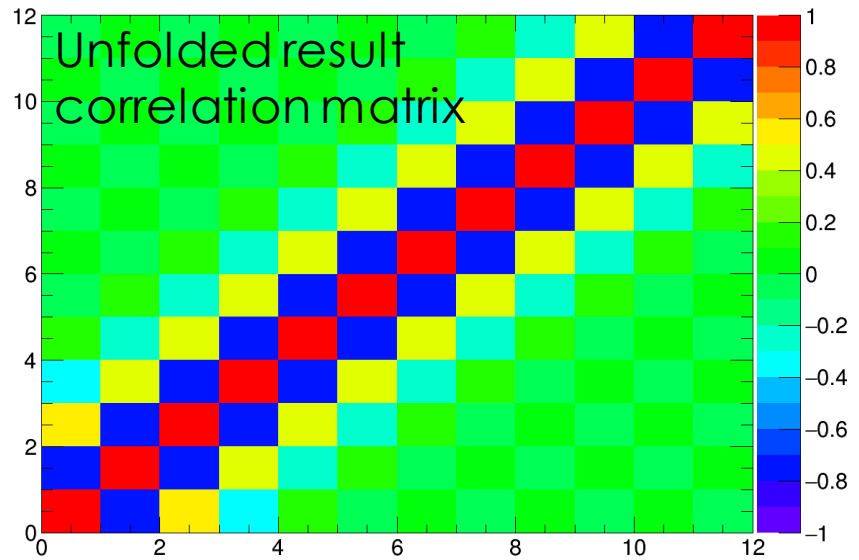
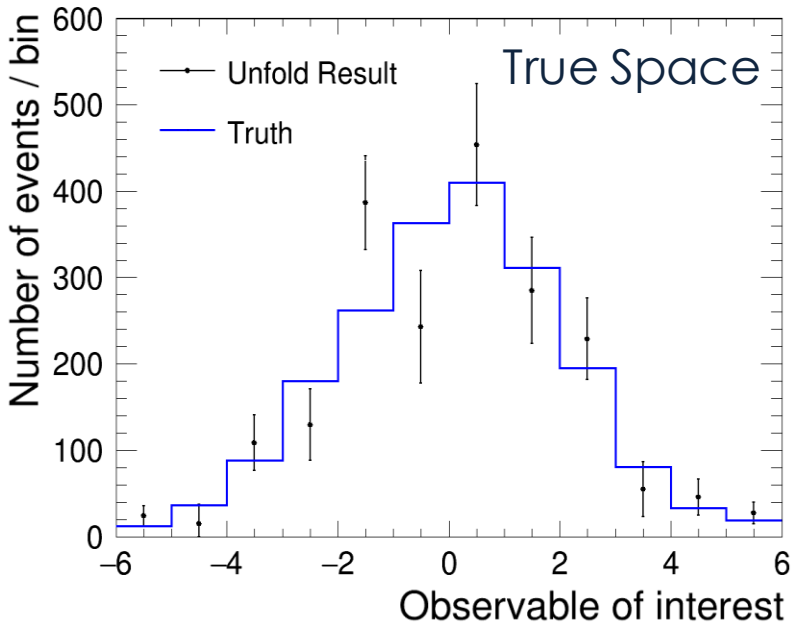
Inverse (Gaus (0,0.6) smear)



- Many fluctuations allow us to build a result with errors
- In most realistic circumstances we get a result which oscillates around the truth
- It doesn't look great

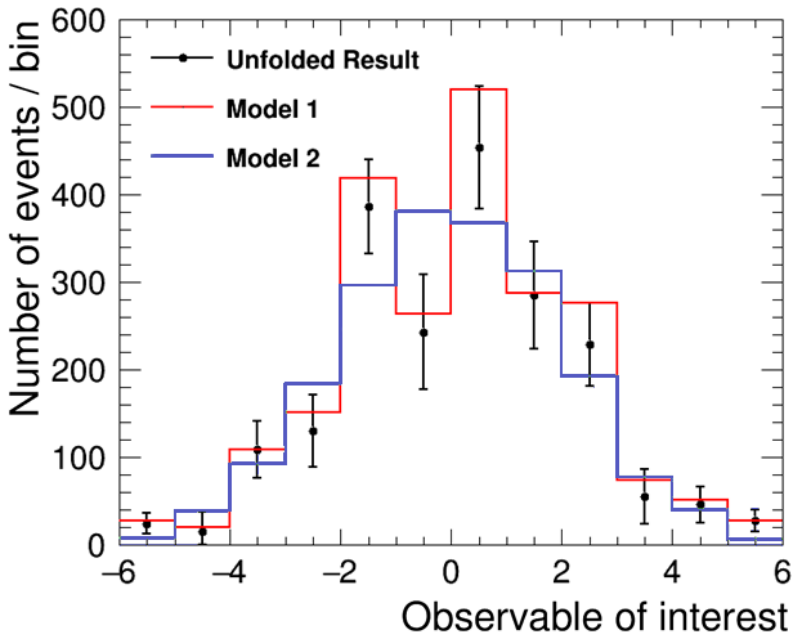


Toy example



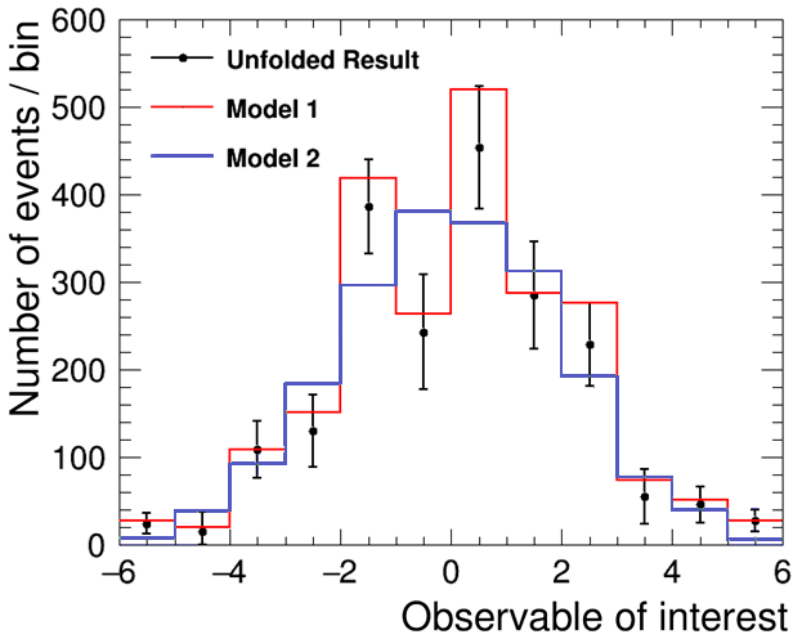
- This result is the *unregularised result*, but is it correct?
- From the correlation matrix we can see that the oscillatory behaviour is accompanied by large bin-to-bin anti-correlations.
- In this case, actually find that the $\frac{\chi^2}{NDOF} = 0.44$, pretty good!
- In fact, if we want to minimise bias this is probably the best thing we can do

The unregularised result



- Although the result is absolutely correct, it can be almost meaningless without the accompanying covariance matrix.
- Can you judge which of the models on the left fits the result best?

The unregularised result



$$\chi_1^2 / DOF = 2.7 \rightarrow p = 0.0013$$

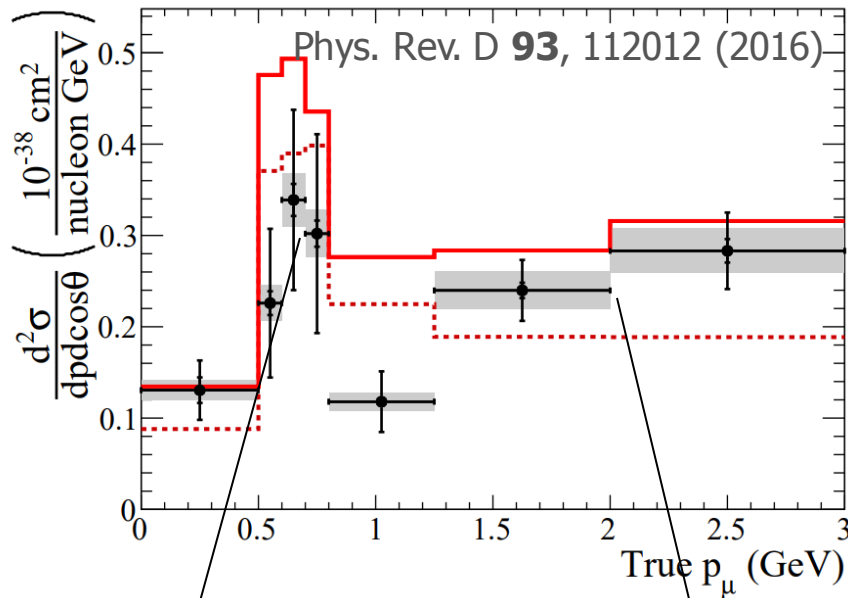
$$\chi_2^2 / DOF = 1.2 \rightarrow p = 0.25$$

- Although the result is absolutely correct, it can be almost meaningless without the accompanying covariance matrix.
- Can you judge which of the models on the left fits the result best?
- Even when we have the covariance matrix “chi-by-eye” is not very reliable ...

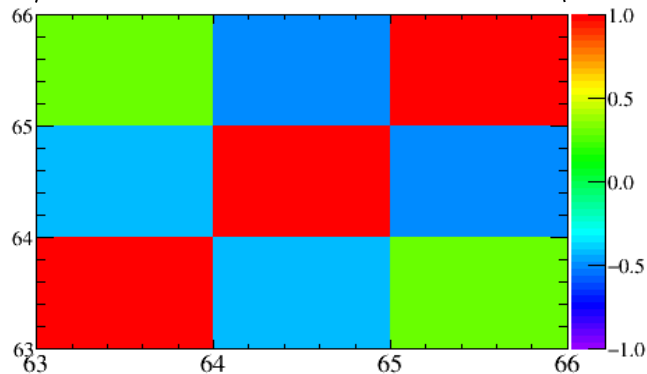
- The unregularised result is **ideal for calculating χ^2** , but potentially very misleading for “by-eye” comparisons.

Case study: $CC0\pi$ analysis

$0.98 < \text{true } \cos\theta_\mu < 1.00$



- Our *unregularised* ND280 $\nu_\mu CC0\pi$ analysis shows a dip in the momentum distribution for forward going muons at about 1 GeV
- This had some physicists excited, there has been some discussion about what this large “dip” could be.
- But in reality the **large anti-correlations** between the pertinent bins make this result compatible with no dip.
- The “dip” may just be a statistical effect from the unregularised unfolding



Stat. correlation matrix for these three bins

The case for regularisation

Unregularised results with large anti-correlations are the best option for making χ^2 comparisons, but:

- *We might want to have an idea of the result's shape or to compare the model in a specific region of phase-space*
- *We can't accurately estimate the χ^2 from a plot in a paper or conference*
- *Not enough result comparison papers / talks calculate χ^2 ...*

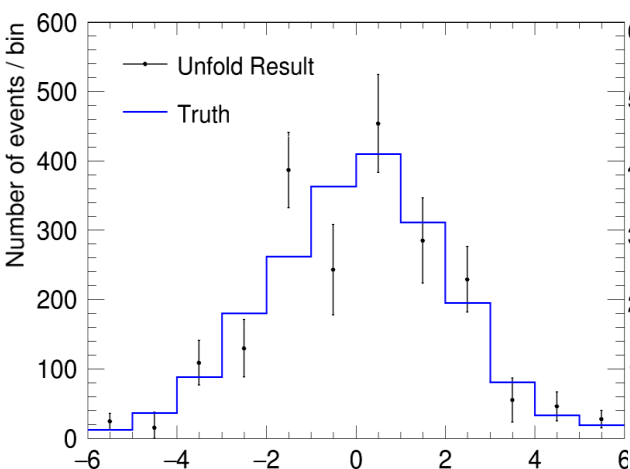
Perhaps producing a result which can be better interpreted by eye could be useful too ...

Can we just re-bin it?

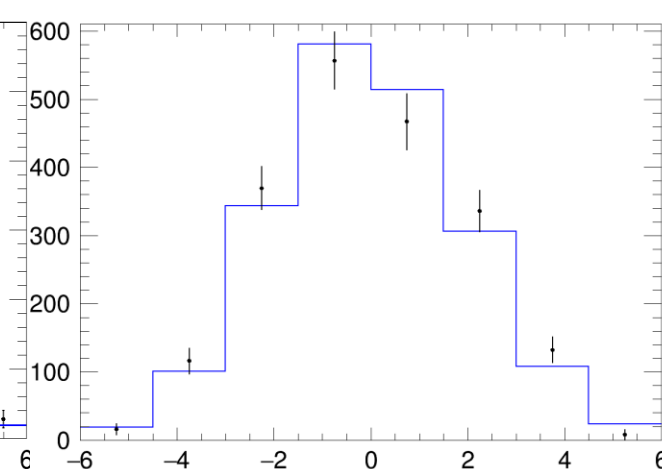
The oscillatory unfolded results are caused by a combination of:

- *Fine binning compared to the detector resolution*
- *Large statistical uncertainty in the reco. data*

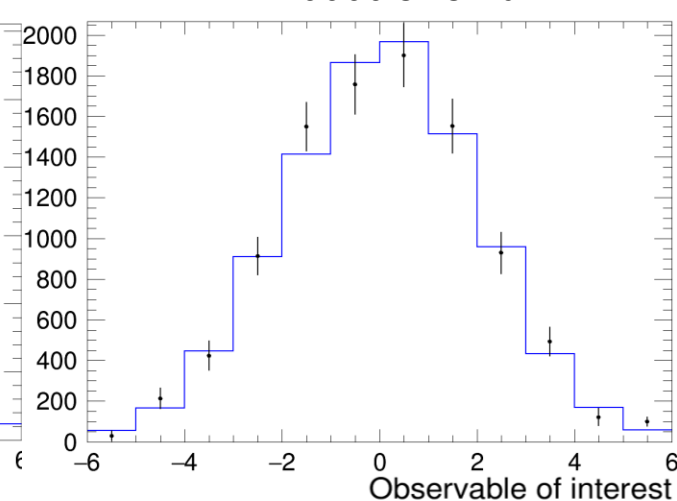
Gaus (0,0.6) smear
1.0 bin width
2000 events



Gaus (0,0.6) smear
1.5 bin width
2000 events



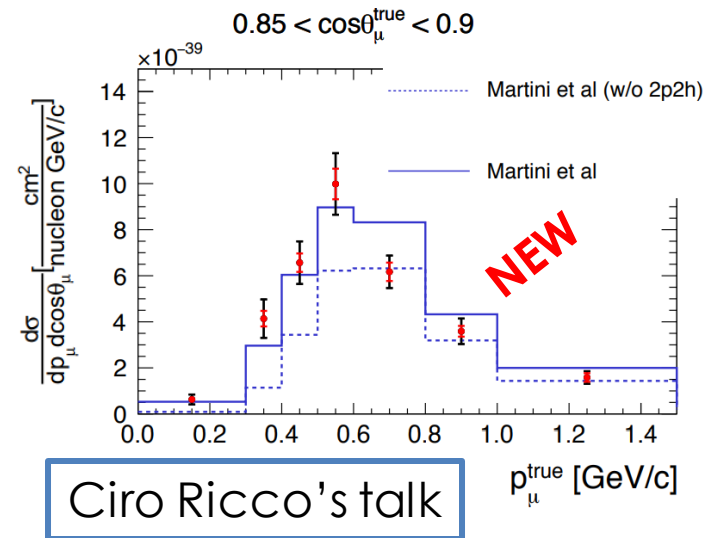
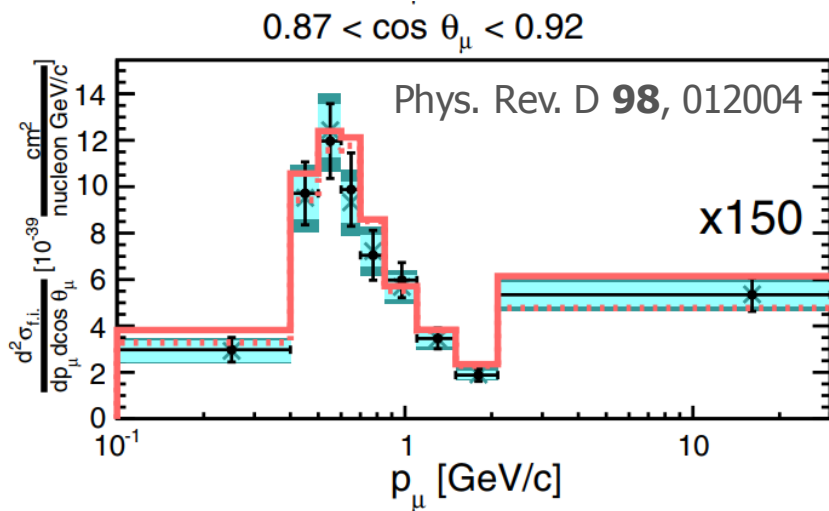
Gaus (0,0.6) smear
1.0 bins
10000 events



Can we just widen our bins until we get a smooth result?

Can we just re-bin it?

- **Yes!** Many of T2K's recent results do this (see Ciro's & Dan's talks)
- This is largely unbiased unfolding where the **resolution of the detector is clearly shown by the width of the bins**
- Potential issues*:
 - Bin widths optimised on MC, not on data
 - Coarser binning can give greater model dependencies



* Although these could be mitigated by first extracting a result in fine bins and then combining adjacent bins until the result is smooth

Tikhonov regularisation

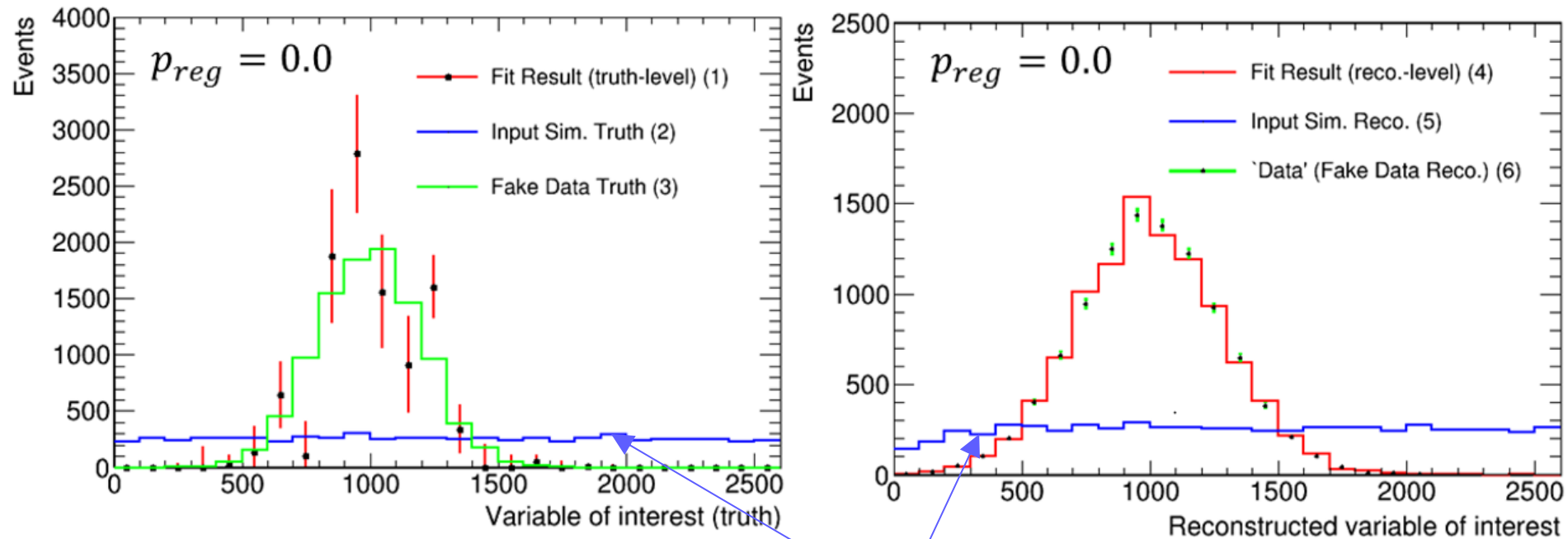
- Rather than combining bins completely, another option is to **loosely tie them together** with a penalty term (to be used in the likelihood fitting method of cross-section extraction – see backups)

$$\chi_{reg}^2 = p_{reg} \sum_i (bin_i - bin_{i-1})^2$$

(this is just one potential penalty term, others are possible depending on how exactly you want to smooth your result)

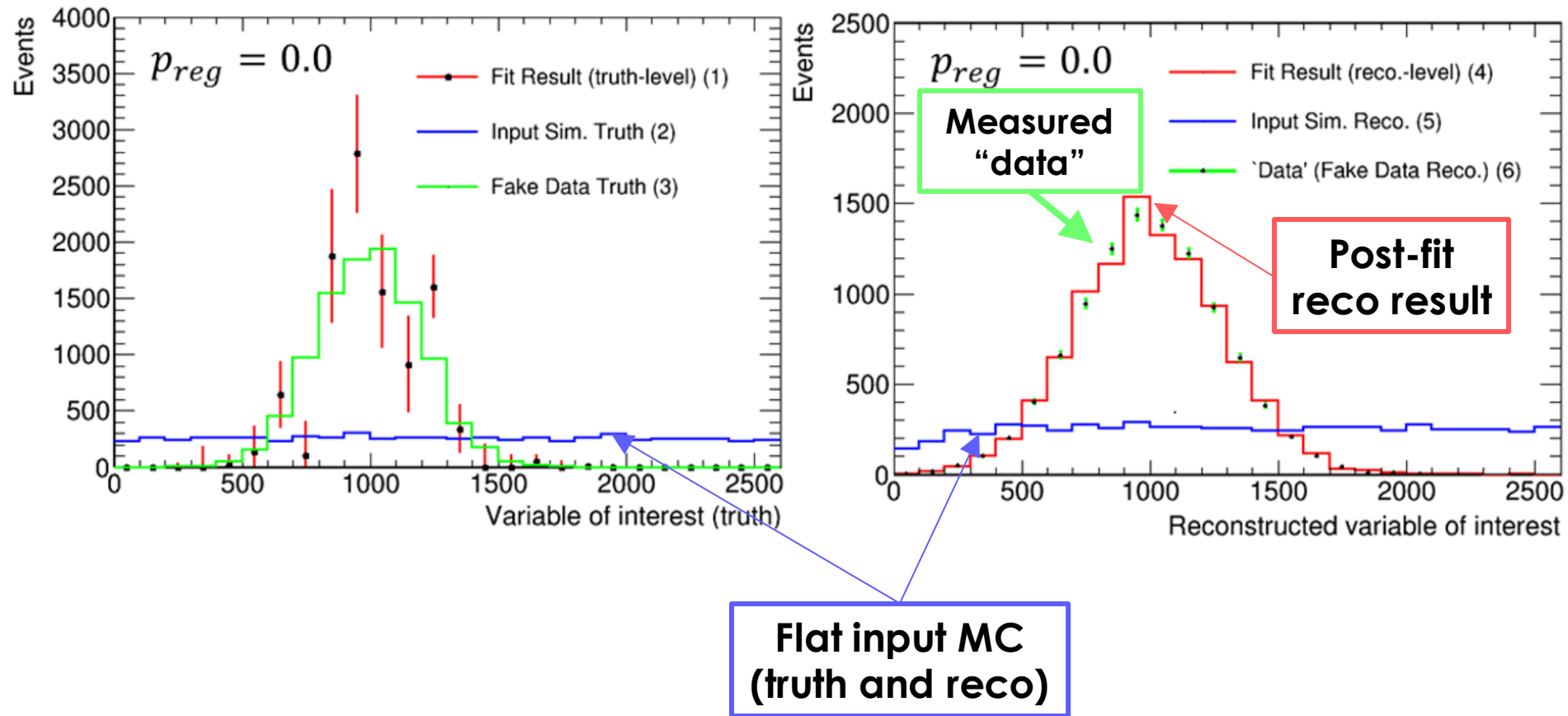
- If p_{reg} is very large then this is equivalent to combining bins
- The inclusion of a penalty term means that the result moves away from the maximum likelihood solution and is therefore **at least a little biased**.
- How can we choose p_{reg} to give us a result we can better compare to by-eye but avoid excessive bias?

The role of regularisation

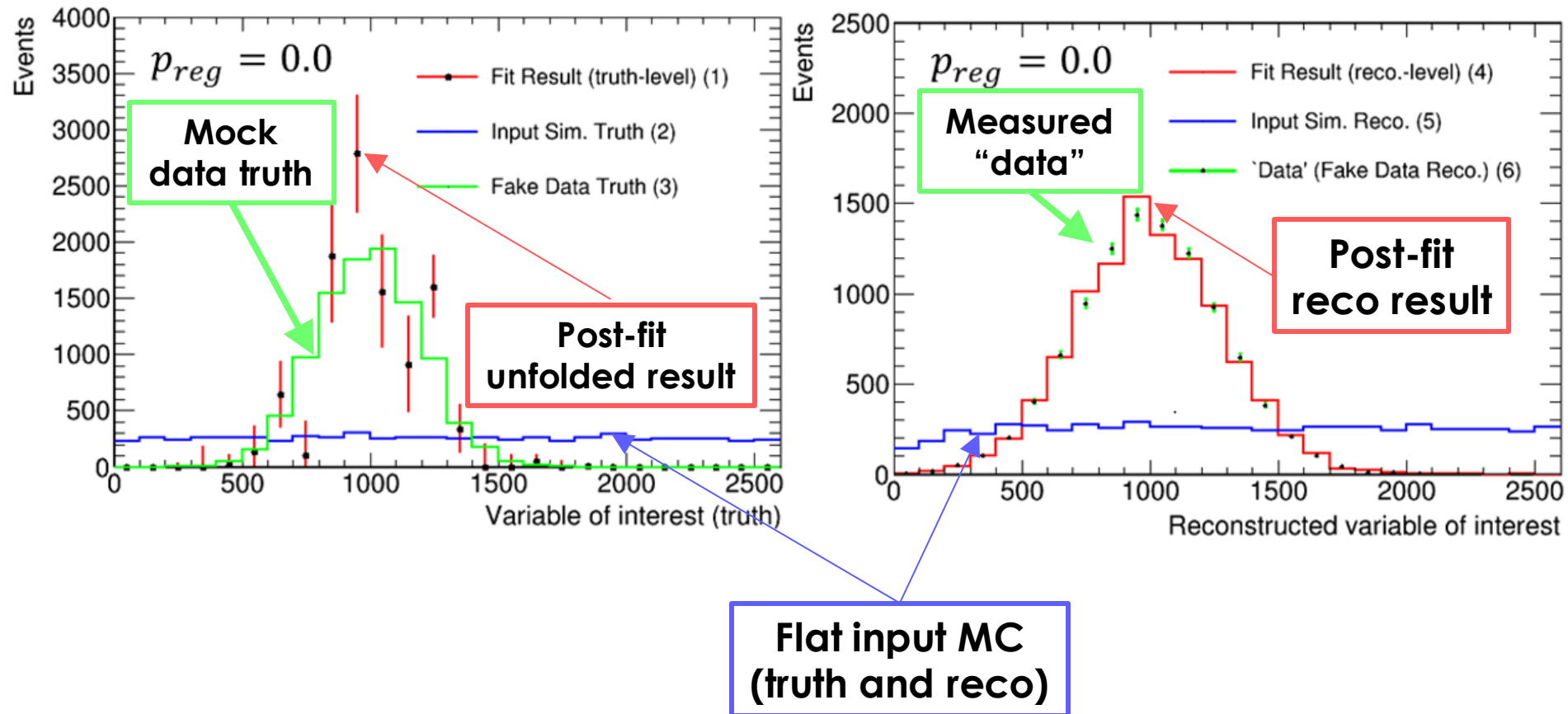


Flat input MC
(truth and reco)

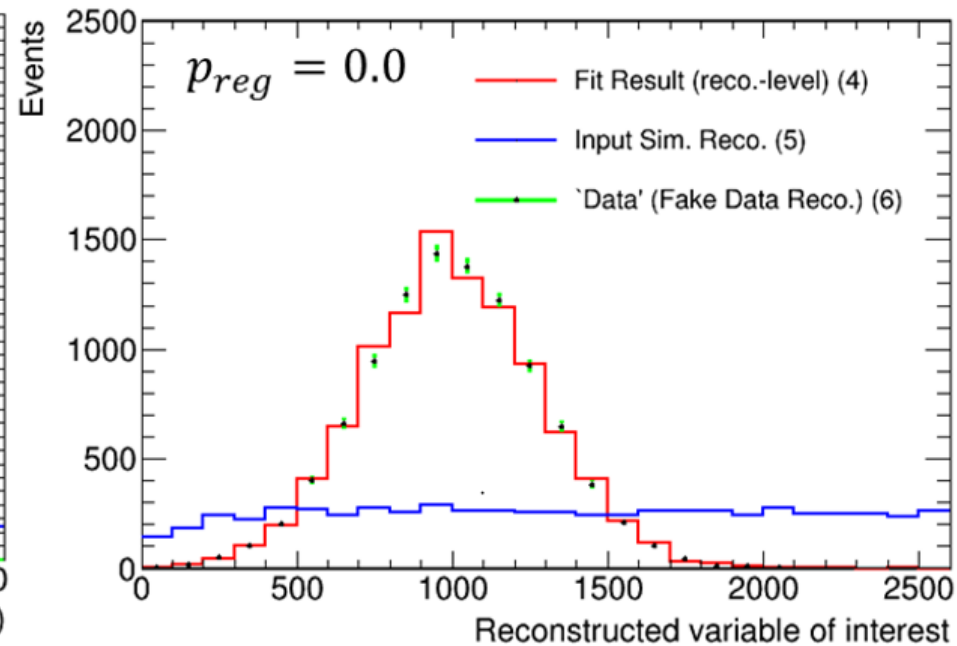
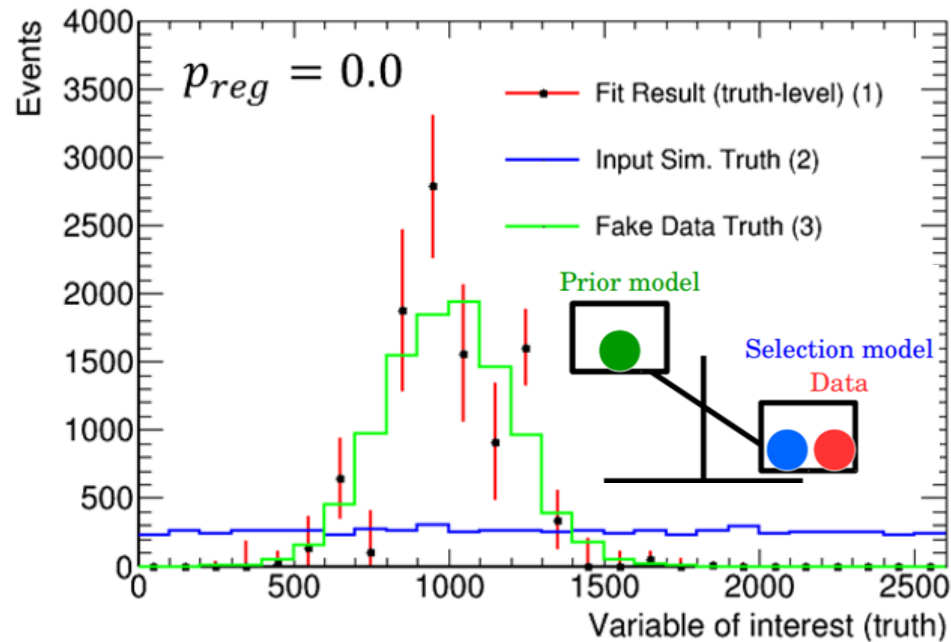
The role of regularisation



The role of regularisation

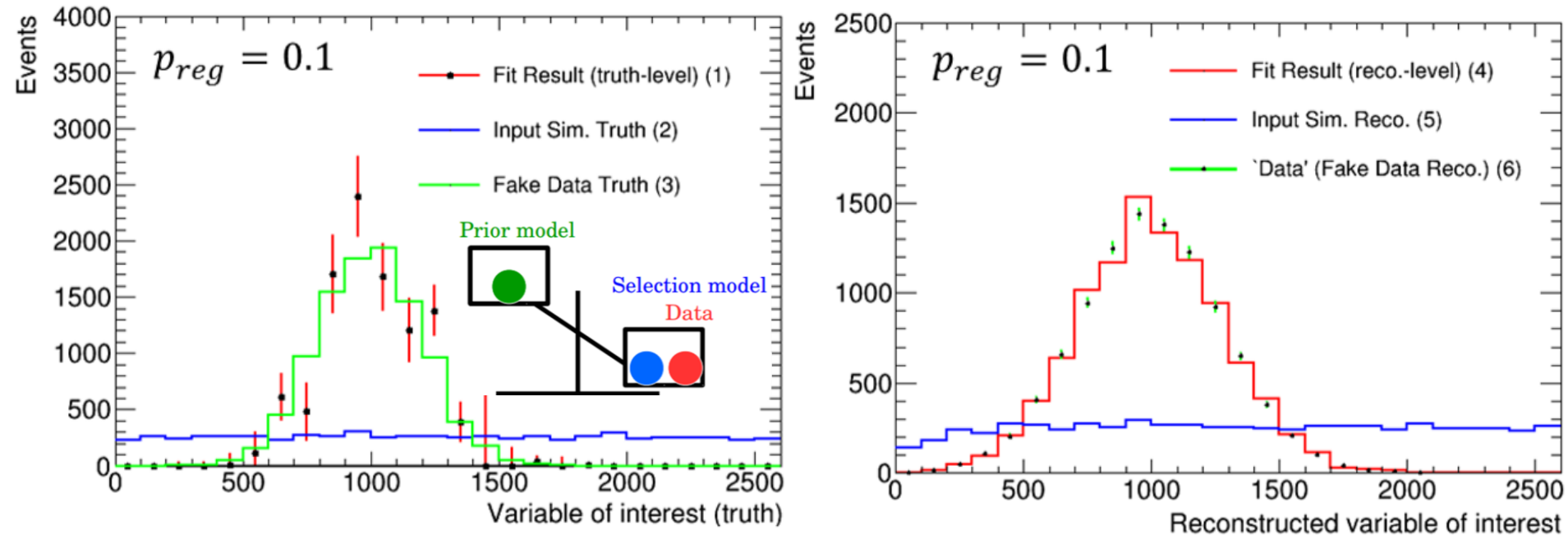


The role of regularisation



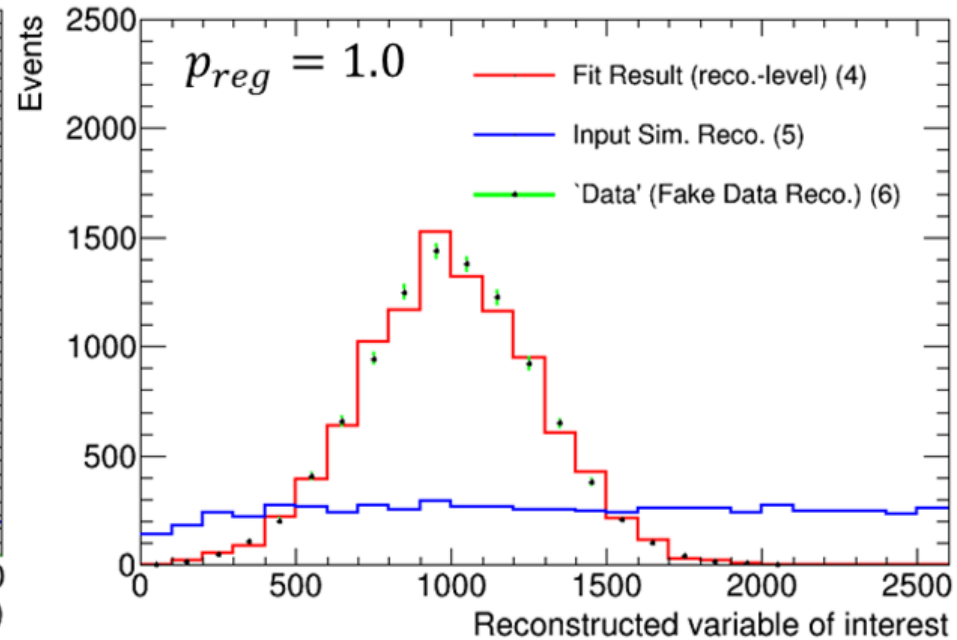
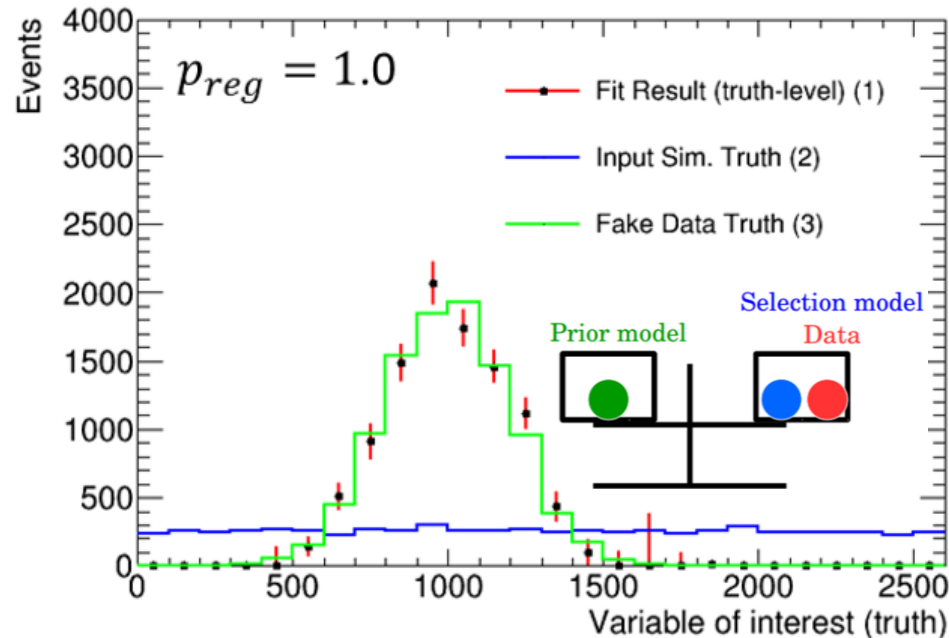
Read p_{reg} as regularisation strength

The role of regularisation



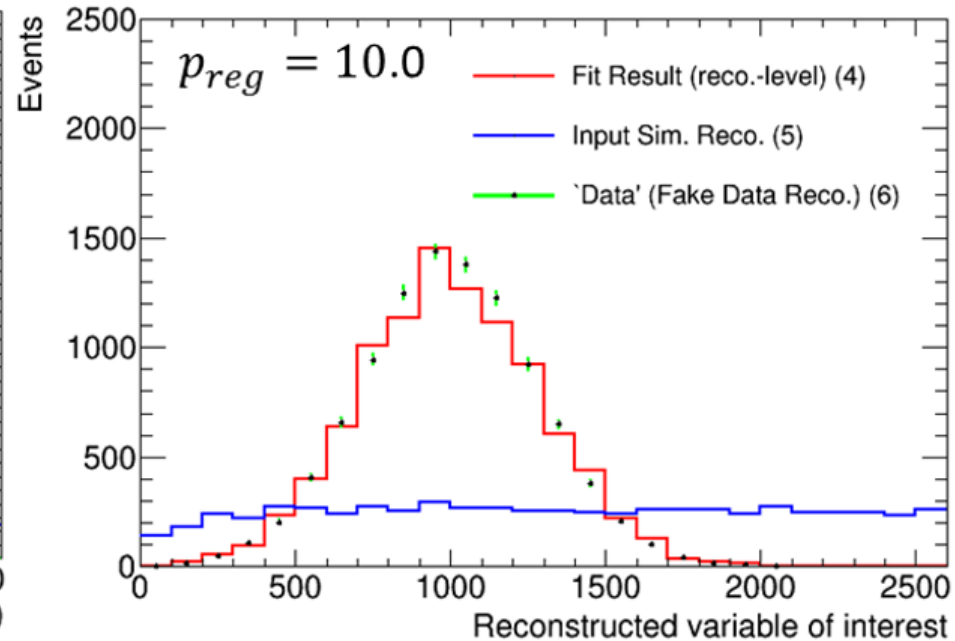
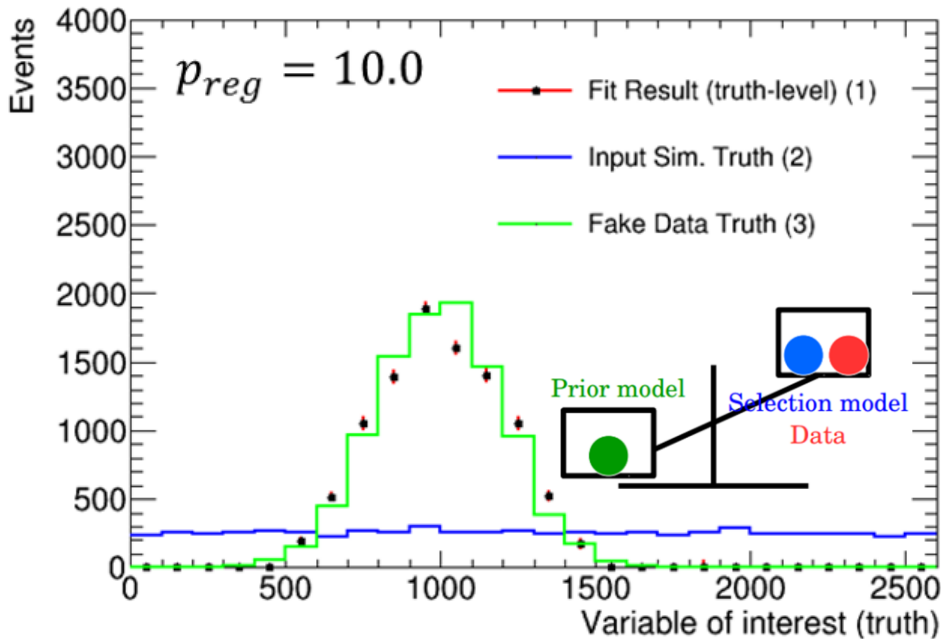
Read p_{reg} as regularisation strength

The role of regularisation



Read p_{reg} as regularisation strength

The role of regularisation

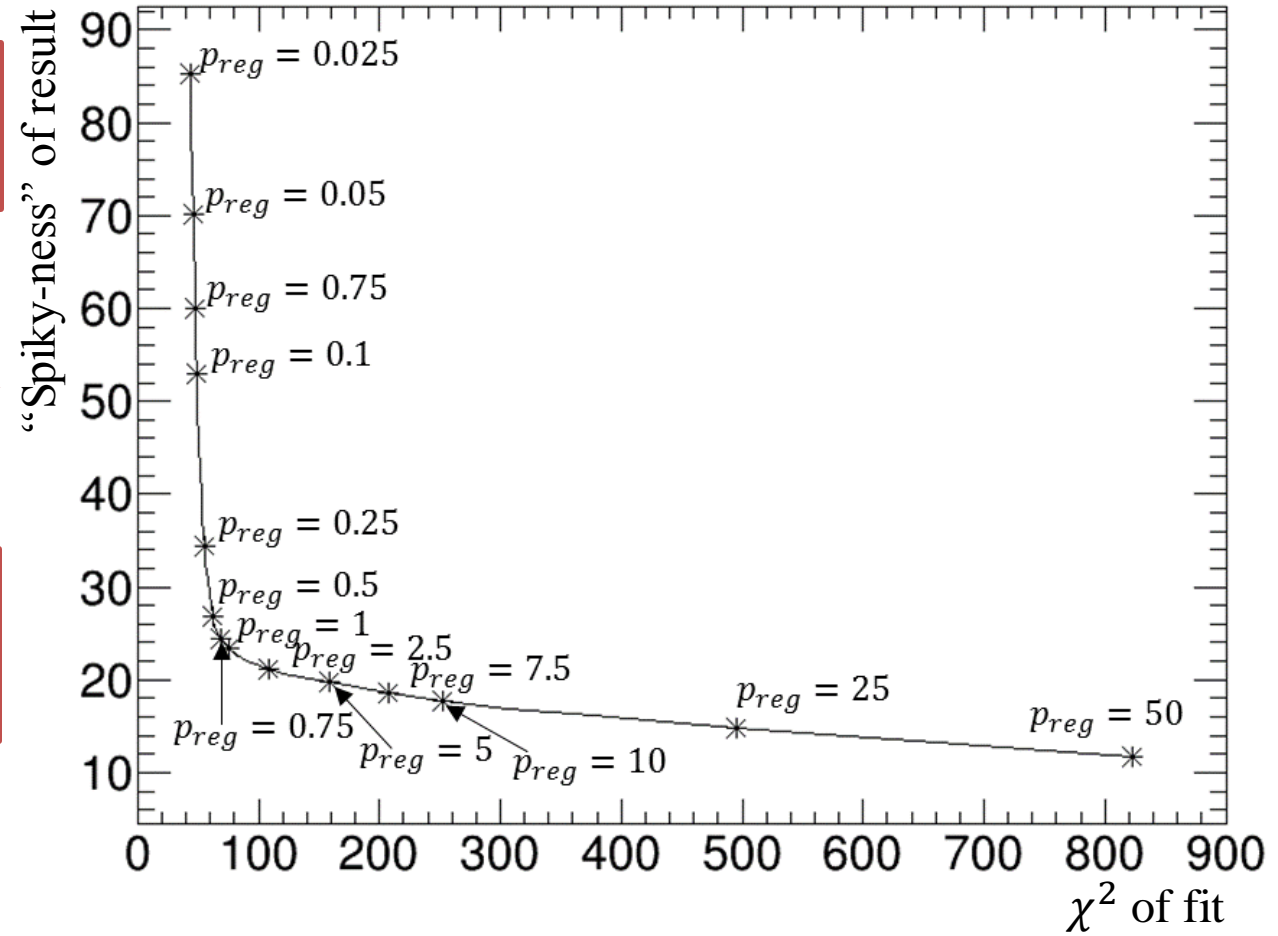


Read p_{reg} as regularisation strength

Regularisation optimisation: The L-curve

$$\sum_i (bin_i - bin_{i-1})^2 = \frac{\chi_{reg}^2}{p_{reg}}$$

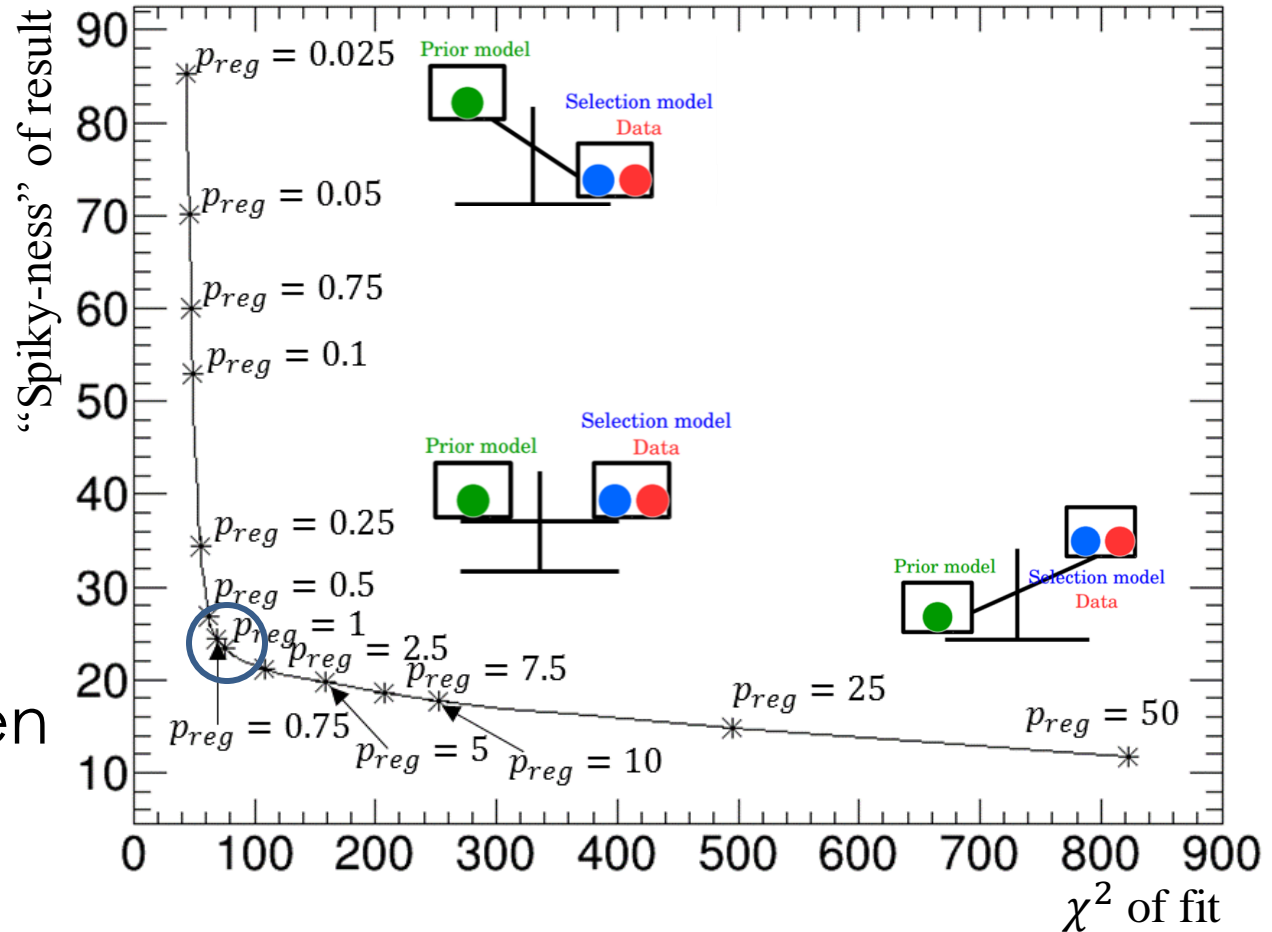
The quantity we want to minimise with our regularisation



This is a measure of bias – basically the deviation from the unregularised result

Regularisation optimisation: The L-curve

- Balance regulation with bias by **choosing the “kink” in the curve**
- **L-curve can be formed on real data** – data driven regularisation



- Well established statistical method to **select the smoothest of many almost degenerate solutions:**

<http://epubs.siam.org/doi/abs/10.1137/1034115>

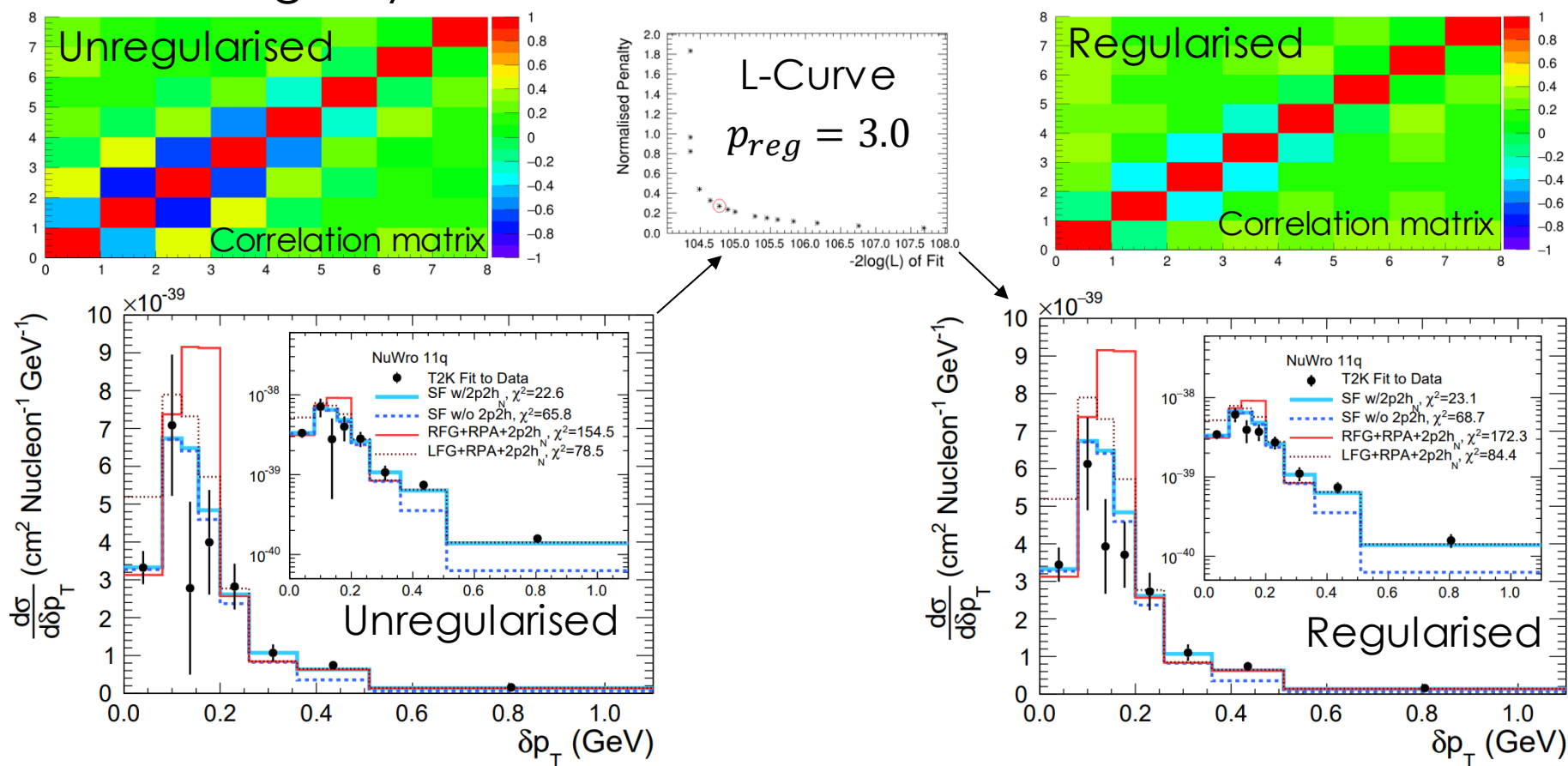
<http://epubs.siam.org/doi/abs/10.1137/0914086>

<http://arxiv.org/pdf/1205.6201v4.pdf> - use in TUnfold

Case study: $CC0\pi$ in δp_T

- Measure $CC0\pi$ +protons cross section in missing transverse momentum (δp_T)
- Unregularised best for χ^2 , regularised best for actually showing anywhere

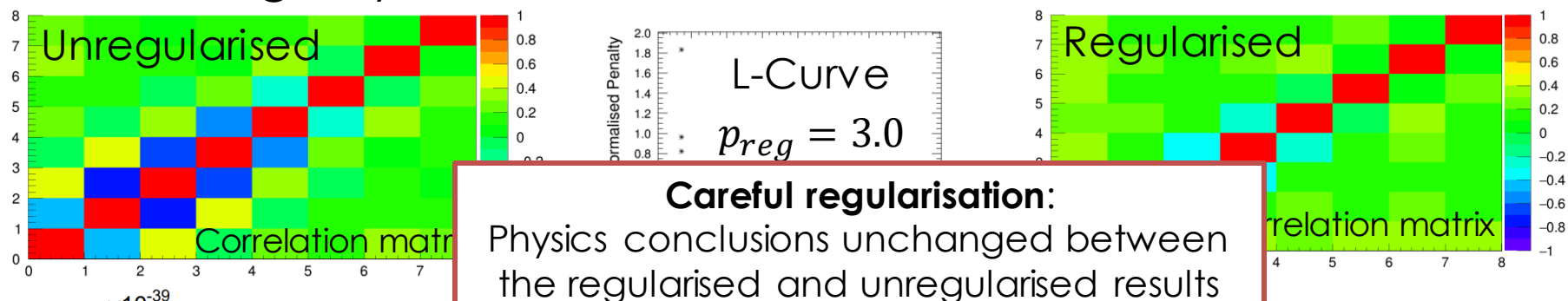
Phys. Rev. D **98**, 032003 (2018)



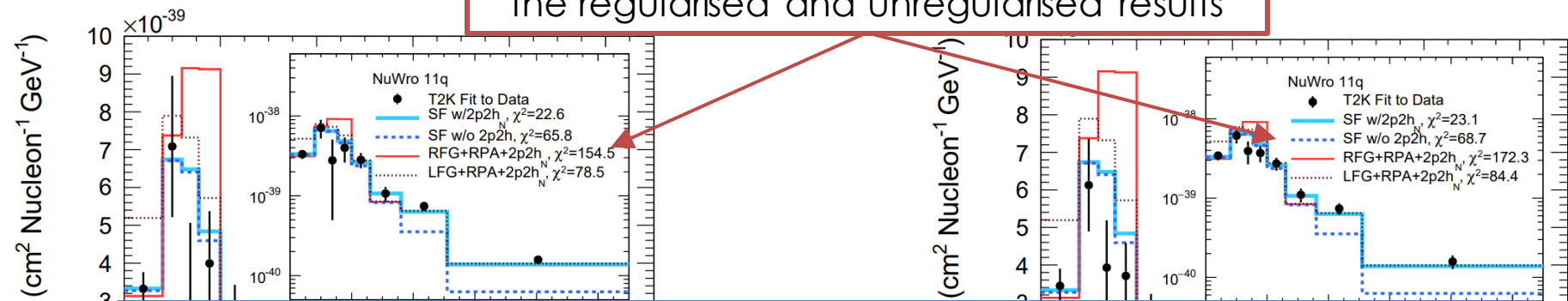
Case study: $CC0\pi$ in δp_T

- Measure $CC0\pi$ +protons cross section in missing transverse momentum (δp_T)
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Phys. Rev. D **98**, 032003 (2018)



Careful regularisation:
Physics conclusions unchanged between the regularised and unregularised results

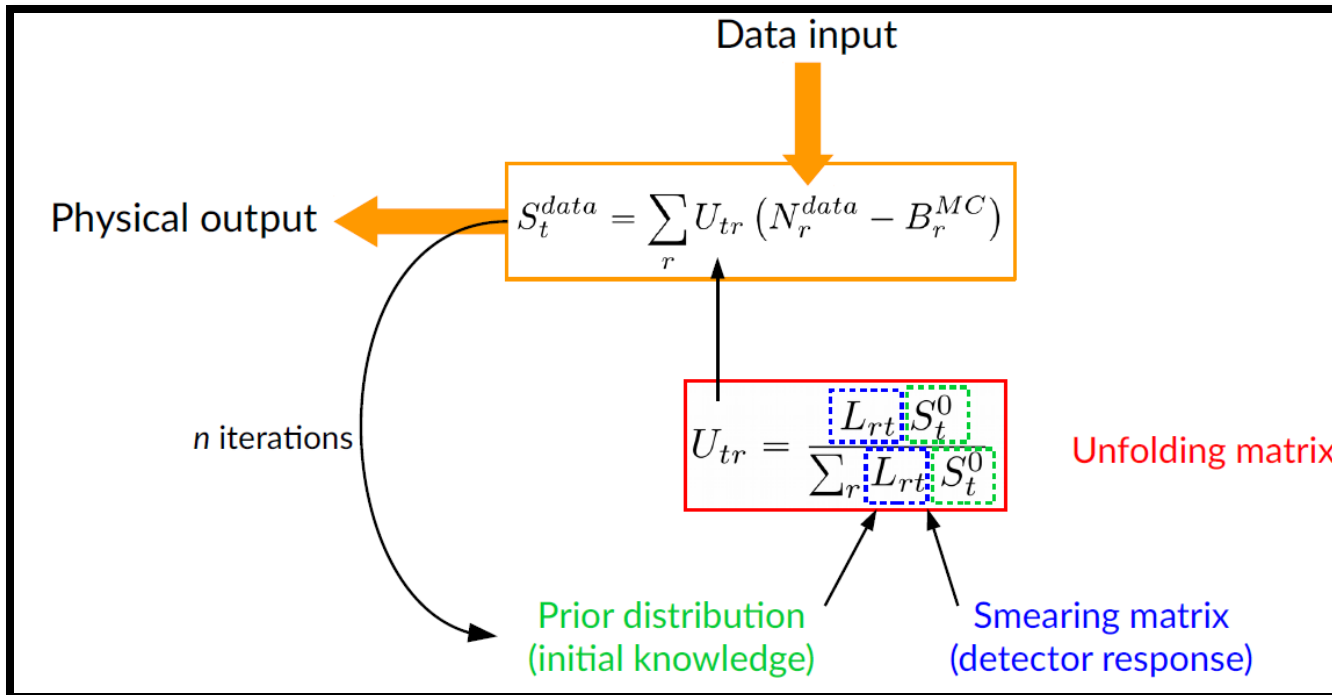


- **CAUTION:** here we can see that whilst the unregularised result has reduced correlations, interpreting a goodness of fit by eye is still challenging.
- **You still need a covariance for a regularised result!**

D'Agostini's method

*Although this method uses Bayes' theorem, **it is not a Bayesian technique** (in fact it's equivalent to the widely-used "Expectation-maximisation algorithm") [M.Kuusela]

- Using Bayes' theorem* to form unsmearing matrix:

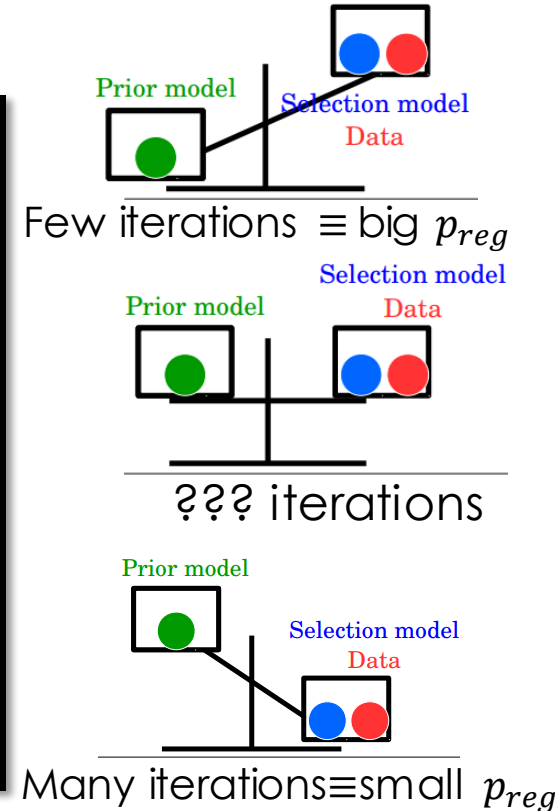
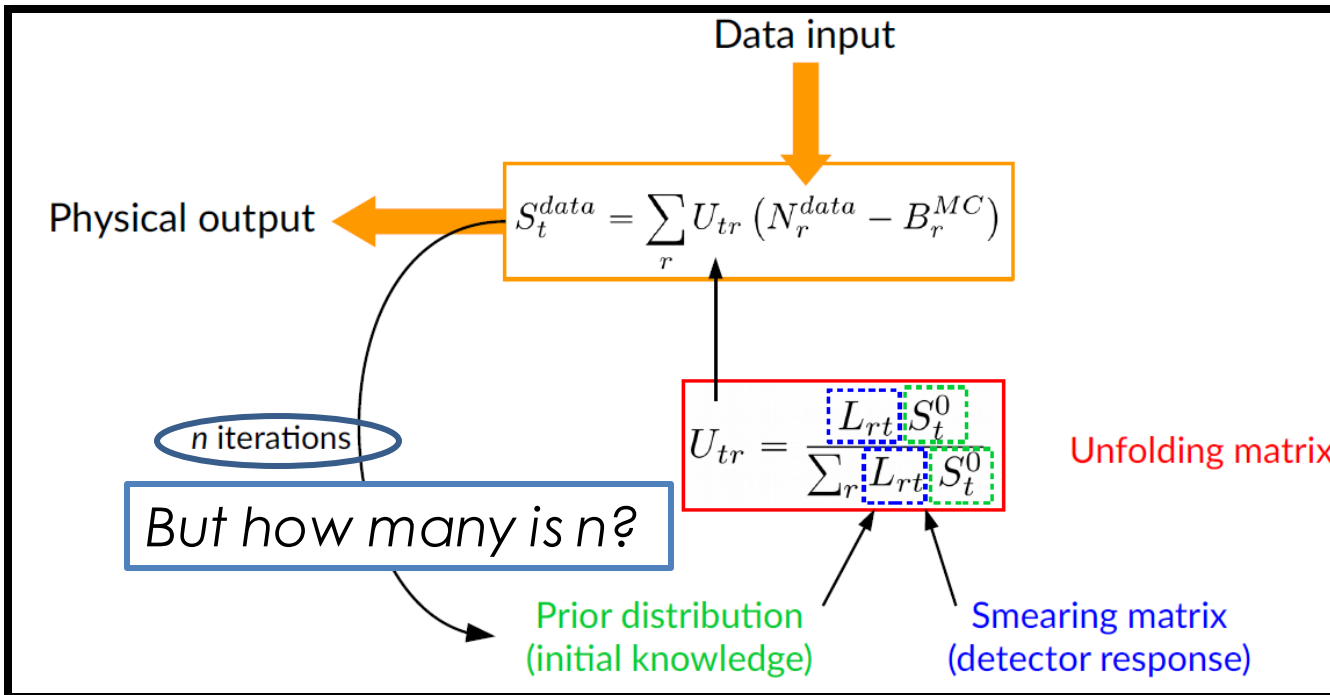


- Most commonly used method (MINERvA, MiniBooNE, T2K)
- If **prior** formed from MC - **model dependence is explicit**
- Mitigate by updating **prior** with unfolded result and iterating
- Many iterations** (typically hundreds / thousands) → **unregularised result**

D'Agostini's method

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- Using Bayes' theorem* to form unsmearing matrix:

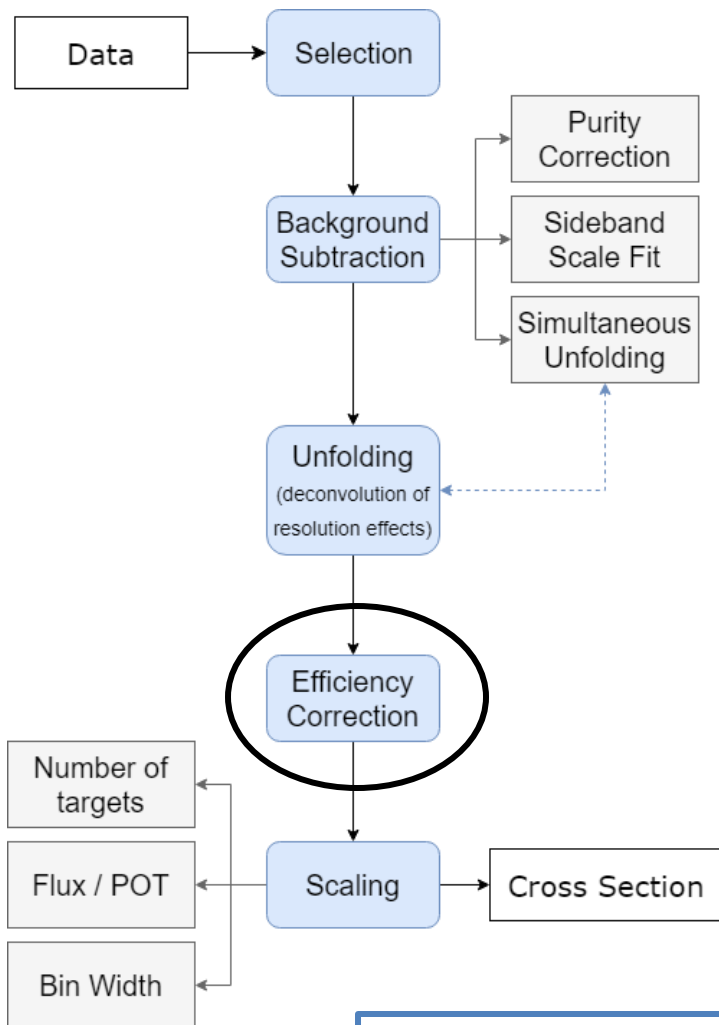


- Changing the number of iterations can change physics conclusions**
- Typically select number of iterations **based on mock-data** studies
- If real data looks different, can select "wrong" number (toy example in backups)
- Benjamin** will show this with a real analysis, presents a **data-driven** alternative

See talk from Benjamin Quilain

Efficiency corrections

An over-simplified xsec analysis

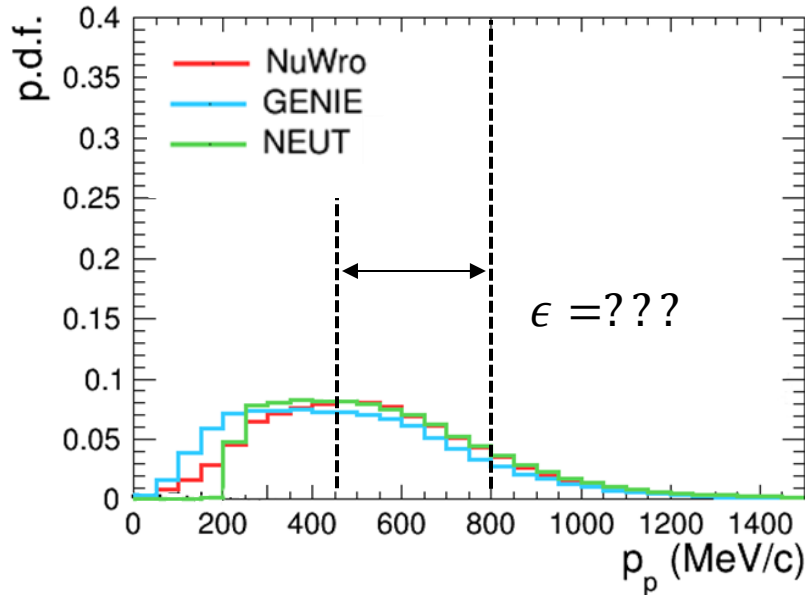


- After unfolding we have the a measure of the true number of *selected* signal events
- To get to a cross section, we need to correct for our detectors acceptance
- It's also easy to add bias here ...
- Not entirely separate from unfolding
 - Unfolding in too few variables can give bias here

For more details: arXiv 1805.07378 (TENSIONS Workshop 2016)

Toy example

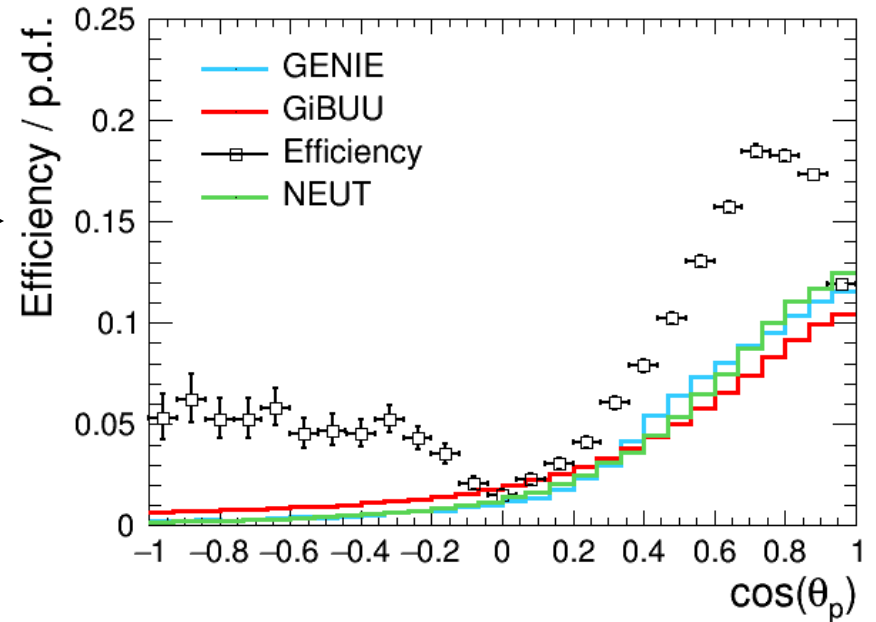
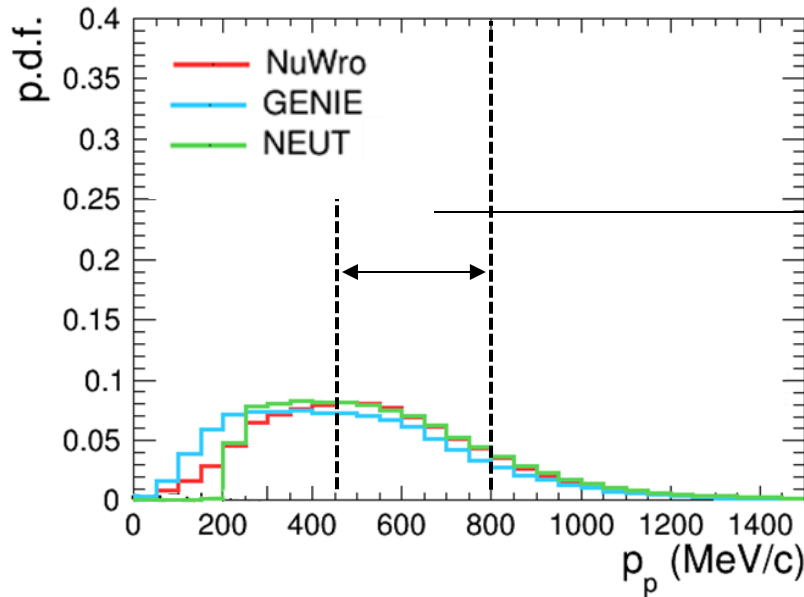
- I want to measure a cross section in some range of proton momentum



- But my detection efficiency depends on both proton momentum and angle (and on other particles, but let's focus on the angle for the moment!)
- I can't know the efficiency (ϵ) without knowing the distribution of proton angle within the bin

Toy example

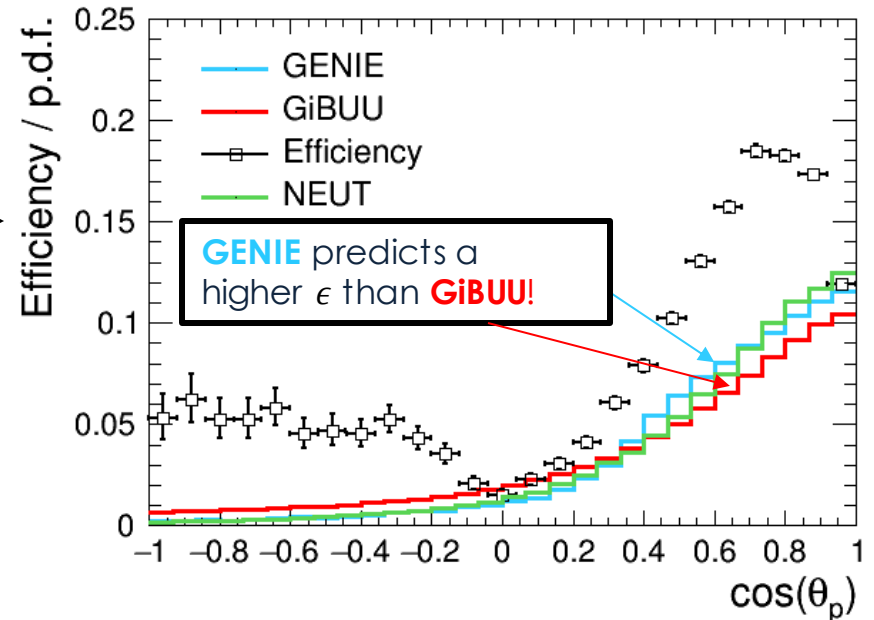
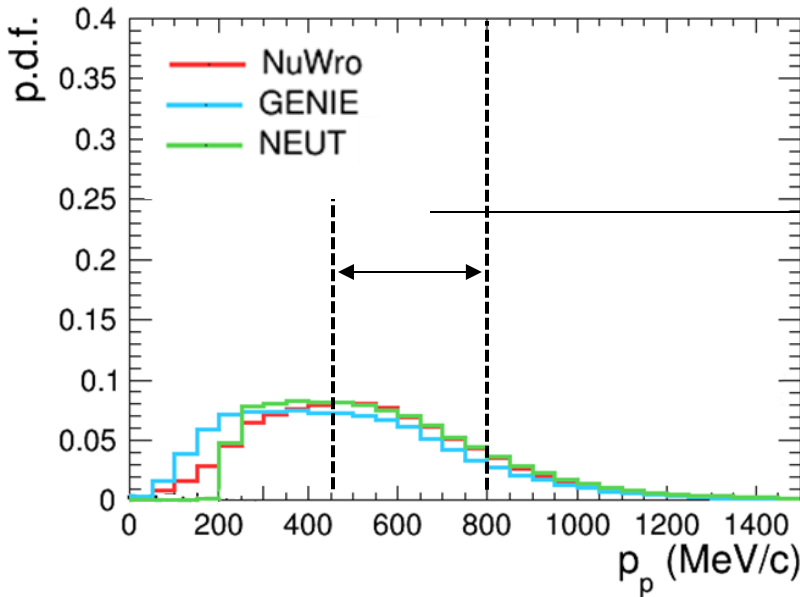
- I want to measure a cross section in some range of proton momentum



- The efficiency in the momentum bin is a convolution of the efficiency **and the predicted cross section**

Toy example

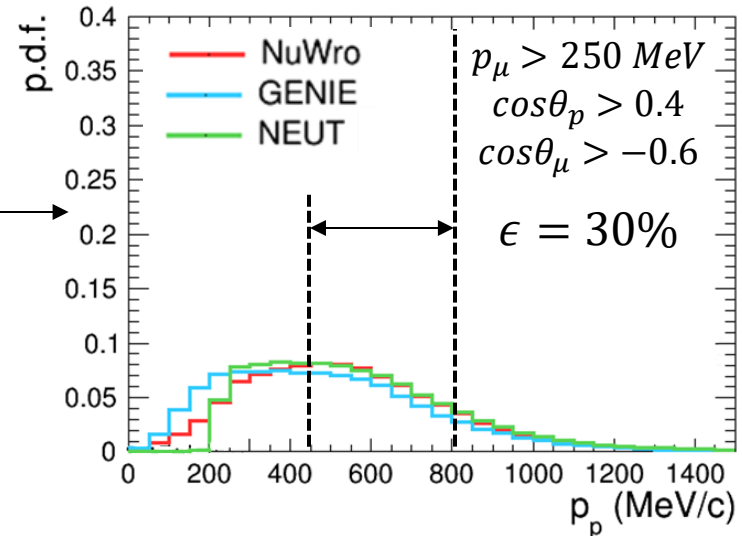
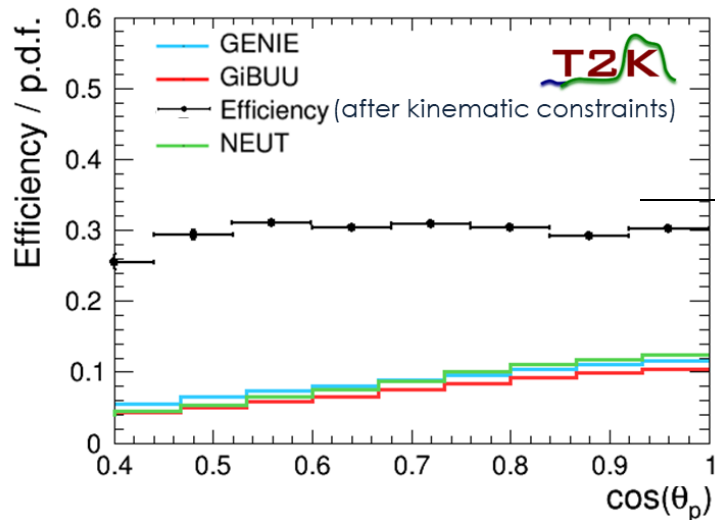
- I want to measure a cross section in some range of proton momentum



- The efficiency in the momentum bin is a convolution of the efficiency **and the predicted cross section**
- Compared to GiBUU, GENIE predicts a higher cross section **in the high efficiency region** → GENIE predicts a higher (~5-10%) efficiency
- Efficiency depends on the input model** → Bias

Kinematic constraints

- Placing kinematic constraints on outgoing particles ($p_{\mu,p}, \theta_{\mu,p}$) can leave us with a relatively flat efficiency in a specific region of $\cos \theta_p$



- In this case the shape of the input model doesn't alter the efficiency → **model independent correction!**
- T2K analyses try to ensure integration only over flat-efficiencies in observables where simulations have poor predictive power (Example in backups)

Summary

- Unfolding / efficiency correcting without bias is hard – but our analyses have some innovative ways to mitigate the problem
- All methods (not just on T2K) give results with some correlations
 - χ^2 (or similar) is usually essential to validate physics conclusions

Unregularised Result

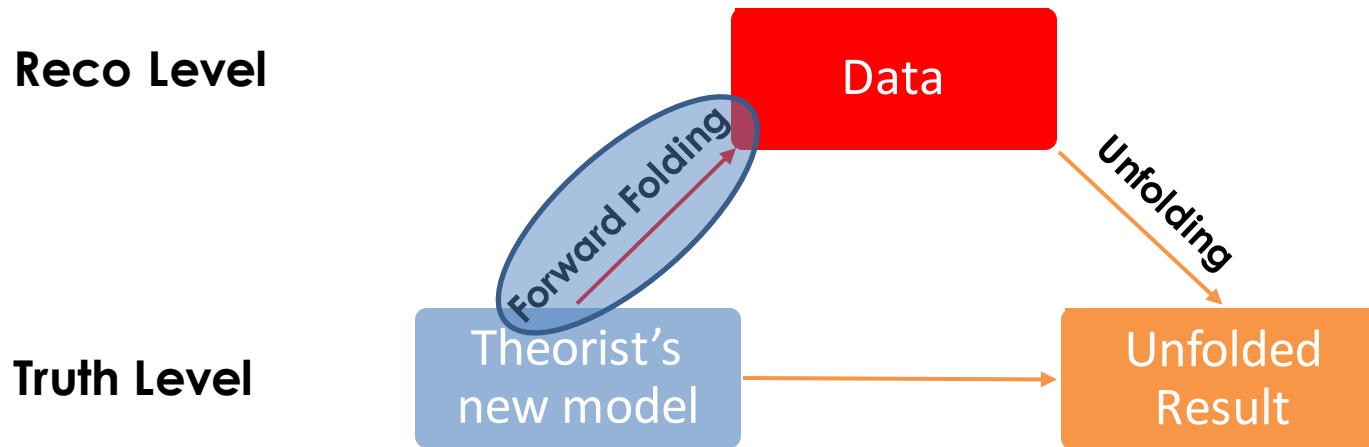
- ✓ Gives correct χ^2 with no unfolding bias
- X Potentially useless for anything other than χ^2 without corresponding covariance, and even then we can't trust “chi-by-eye”
- Useful part of data release and as a reference to check bias of regularised results

Regularisation

- ✓ Smoother results, easier to interpret
- X Adds at least some bias – worse for getting reliable χ^2
- Not easy to choose a regularisation strength that suits data based on MC
→ Use **data-driven** methods

Just don't unfold!

- Producing an *unfolded* result that can be interpreted by-eye with is **hard**! But maybe there's another way ...



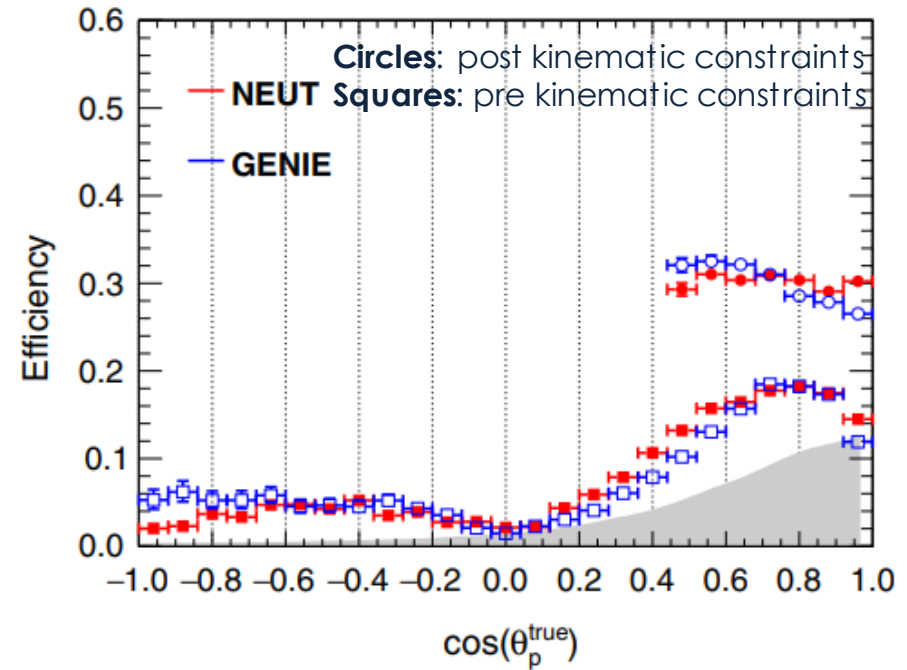
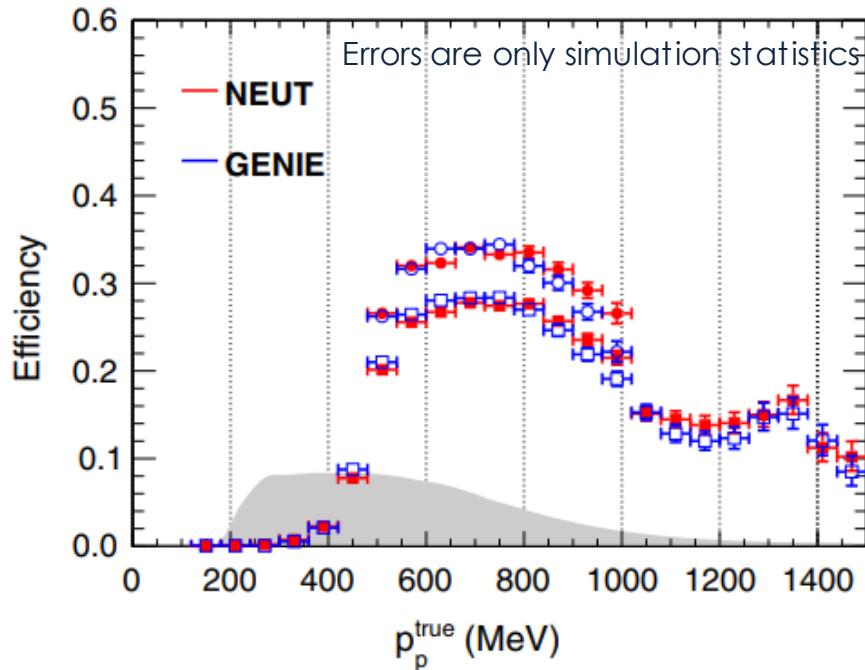
Sounds easy!
Right, Lukas...?

Thank you for listening

Efficiency correction example

Phys. Rev. D **98**, 032003

- Measuring δp_T relies on integrating the efficiency over $p_{\mu,p}, \theta_{\mu,p}$
- We set kinematic constraints in each to keep efficiency relatively flat, especially in regions of phase space where models have low predictive power (proton kinematics)
- Still not perfect, ideally should efficiency correct in all relevant kinematics



D'Agostini's method

**Although this method uses Bayes' theorem, it is not a Bayesian technique (in fact it's equivalent to the widely-used "Expectation-maximisation algorithm") [M.Kuusela]*

- Using Bayes' theorem* to form unsmearing matrix:

$$U_{ij} = \frac{P_{rel}(r_j|t_i) P_0(t_i)}{\sum_{i=1}^{N_t} P(r_j|t_i) P_0(t_i)}$$

Labels in diagram: Smearing Matrix, MC Prior, Unsmearing Matrix

$$P(r_j|t_i) = N_{ij}^{MC} / T_i^{MC}$$

$$P_{rel}(r_j|t_i) = \frac{P(r_j|t_i)}{\sum_{j=1}^{N_r} N_{ij}^{MC} / T_i^{MC}}$$

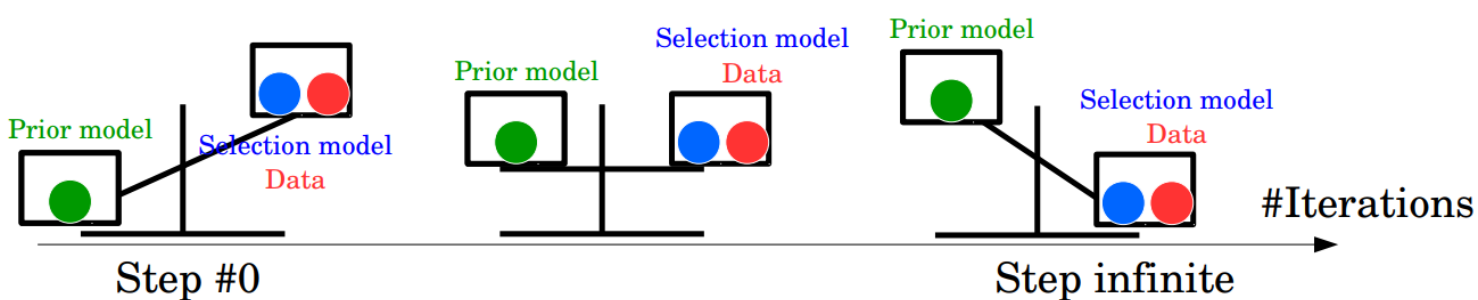
$$P_0(t_i) = \frac{T_i^{Prior}}{\sum_{i=1}^{N_t} T_i^{Prior}}$$

N_{ij} - number of events in true bin i and reco bin j

T_i - number of events in true bin i

r_j/t_i - reco/true bin j/i

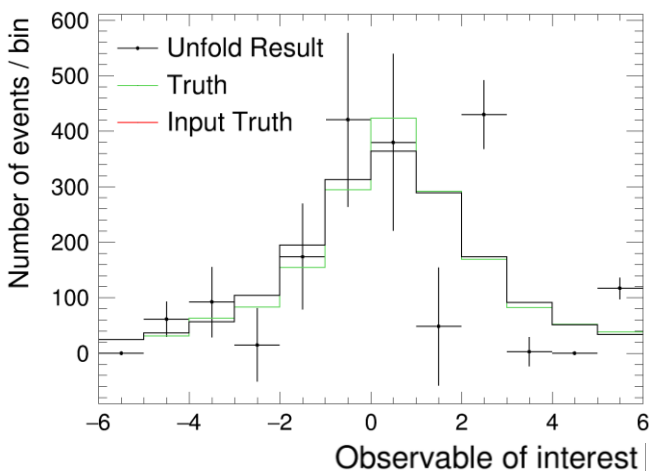
- Most commonly used method (MINERvA, MiniBooNE, T2K)
- If prior formed from MC (as it typically is), **model dependence is explicit**
- Mitigate by updating prior with unfolded result and iterating
- Many iterations** (typically many hundreds / thousands) → **unregularised result**



But typically this is not provided for D'Agostini-based analyses ...

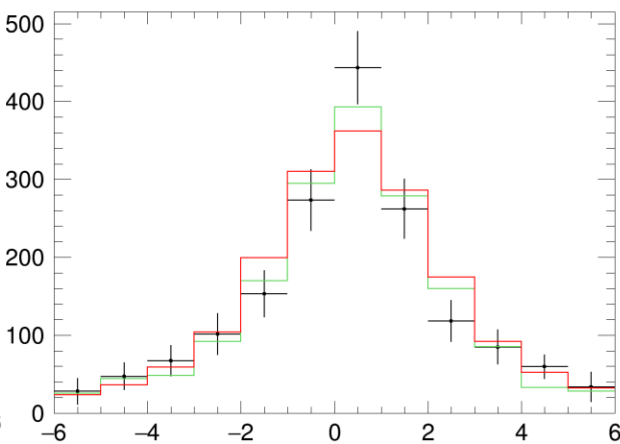
How many iterations? – Choose via MC

Gaus (0.1,1.0) smear, 1.0 bin width, 2000 events, Truth is a BW(0.4,3.0), Input is a BW(0.3,2.5)



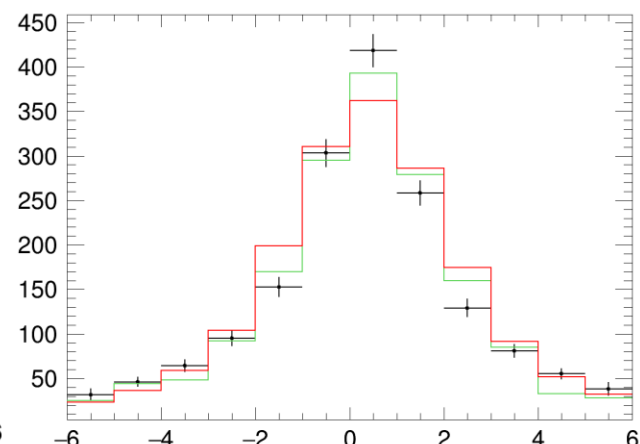
500 iterations (~unreg)

$$\chi^2_{truth} = 12, \chi^2_{input} = 26$$



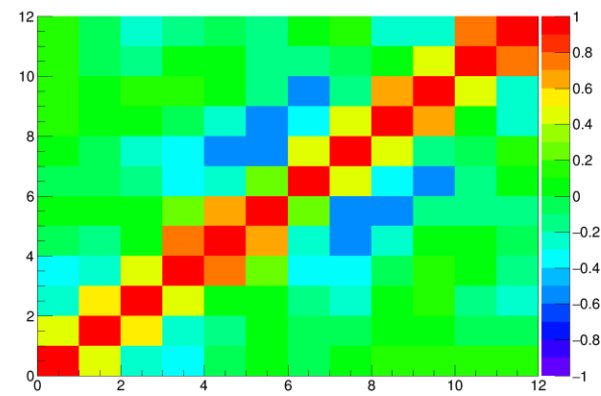
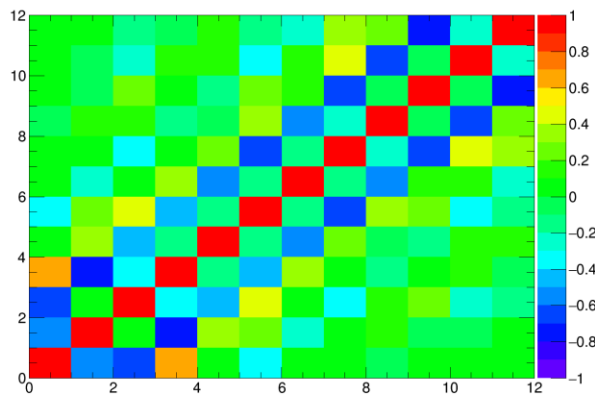
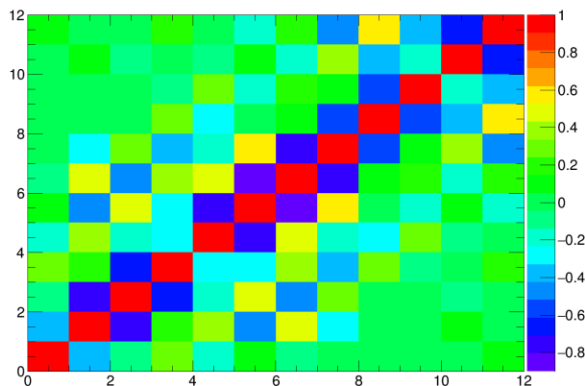
50 iterations

$$\chi^2_{truth} = 18, \chi^2_{input} = 27$$



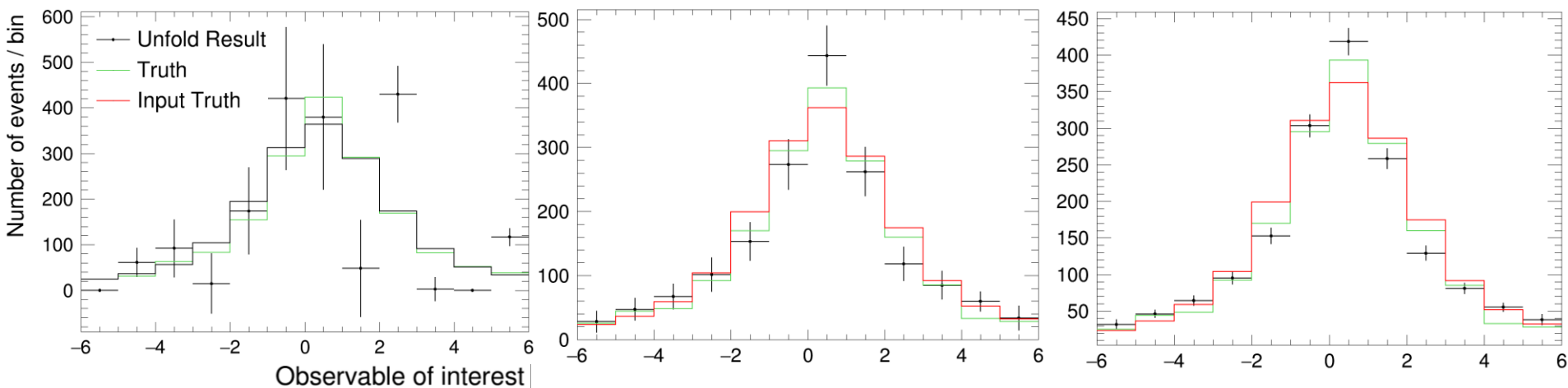
4 iterations

$$\chi^2_{truth} = 299, \chi^2_{input} = 212$$



How many iterations? – Choose via MC

Gaus (0.1,1.0) smear, 1.0 bin width, 2000 events, Truth is a BW(0.4,3.0), Input is a BW(0.3,2.5)



500 iterations (~unreg)

$$\chi^2_{truth} = 12, \chi^2_{input} = 26$$

50 iterations

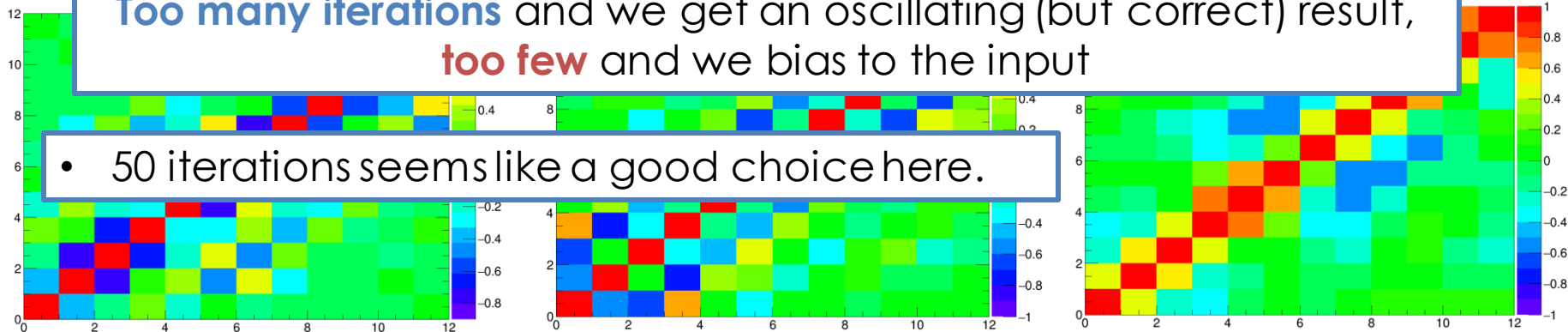
$$\chi^2_{truth} = 18, \chi^2_{input} = 27$$

4 iterations

$$\chi^2_{truth} = 299, \chi^2_{input} = 212$$

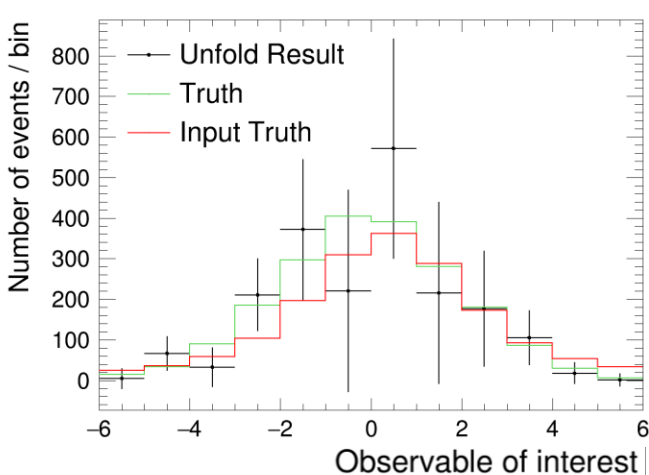
Too many iterations and we get an oscillating (but correct) result,
too few and we bias to the input

- 50 iterations seems like a good choice here.



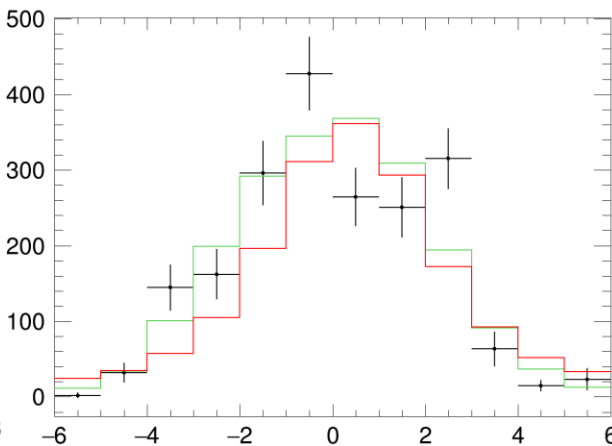
How many iterations? – Choose via MC

Gaus (0.1, 1.0) smear, 1.0 bin width, 2000 events, Truth is a Gaus(0, 2.0), Input is a BW(0.3, 2.5)



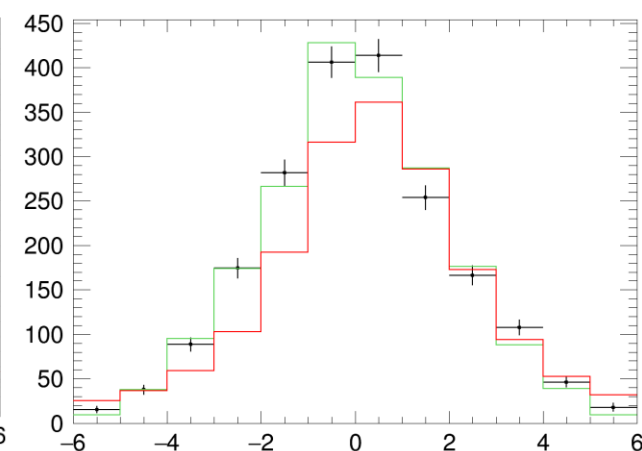
2000 iterations (~unreg)

$$\chi^2_{truth} = 2.9, \chi^2_{input} = 134$$



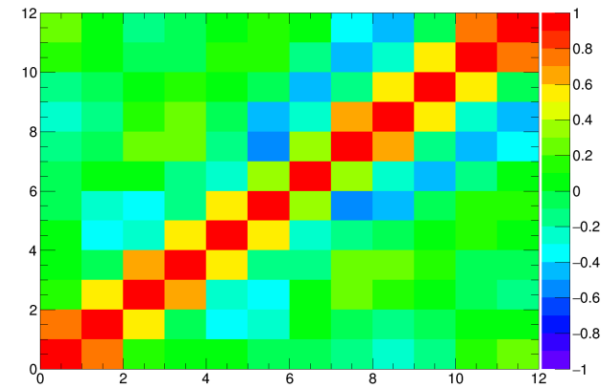
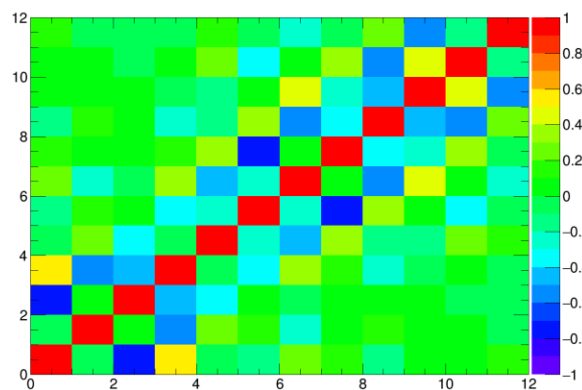
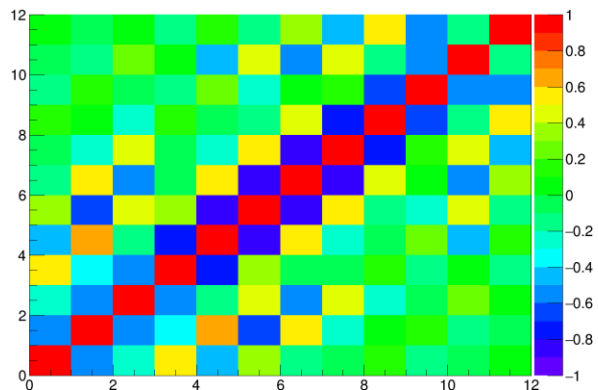
50 iterations

$$\chi^2_{truth} = 32, \chi^2_{input} = 254$$



4 iterations

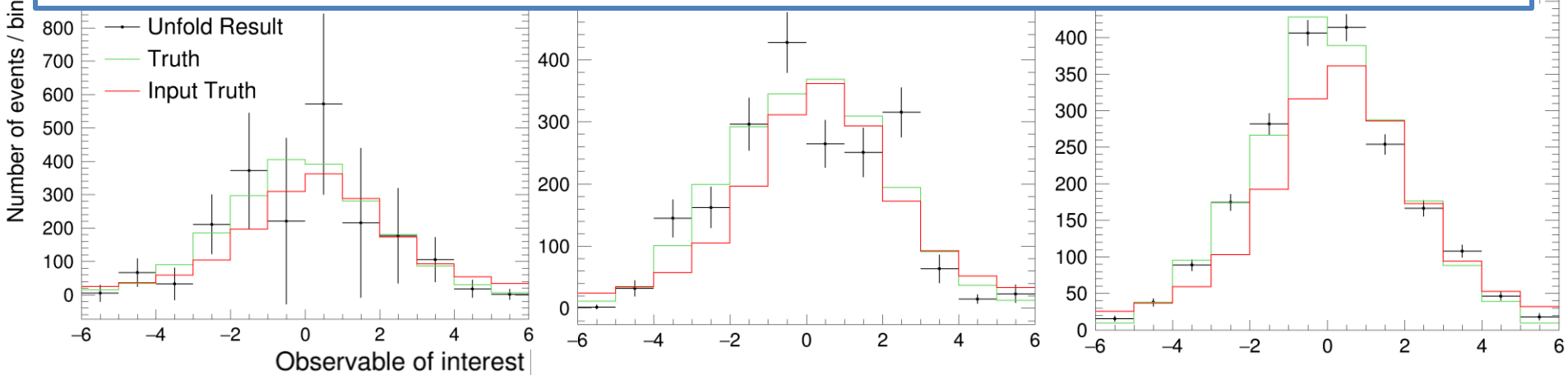
$$\chi^2_{truth} = 9606, \chi^2_{input} = 1568$$



How many iterations? – Choose via MC

Gaus (0.1,1.0) smear, 1.0 bin width, 2000 events, Truth is a Gaus(0,2.0), Input is a BW(0.3,2.5)

A (small) change to the modelled truth and 50 iterations doesn't seem so good!



2000 iterations (~unreg)

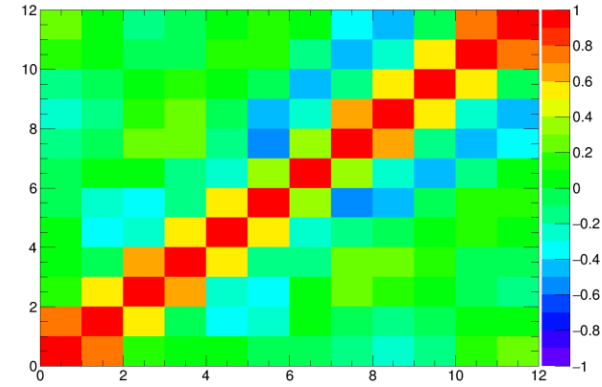
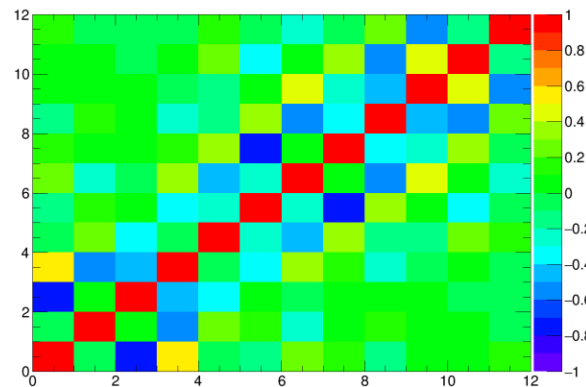
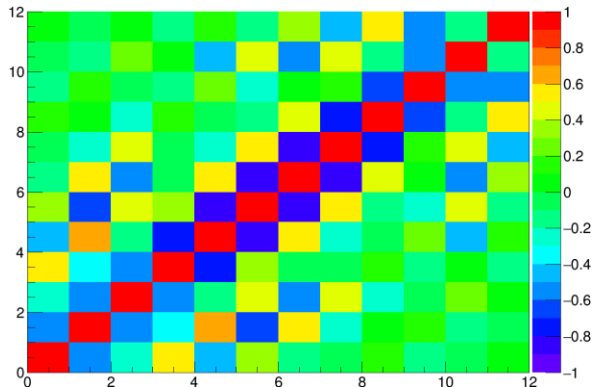
$$\chi^2_{truth} = 2.9, \chi^2_{input} = 134$$

50 iterations

$$\chi^2_{truth} = 32, \chi^2_{input} = 254$$

4 iterations

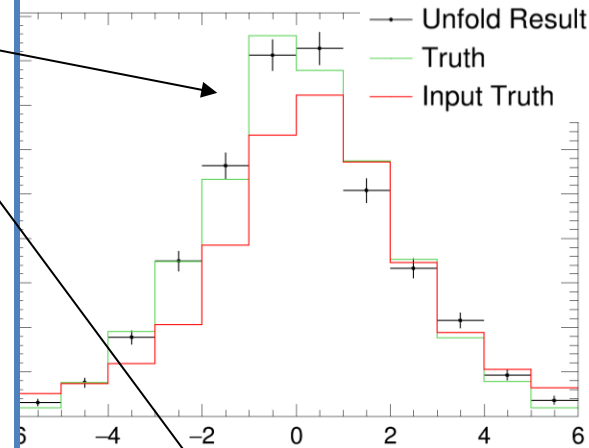
$$\chi^2_{truth} = 9606, \chi^2_{input} = 1568$$



How many iterations? – Choose via MC

Gaus (0.1, 1.0) smear, 1.0 bin width, 2000 events, Truth is a Gaus(0, 2.0), Input is a BW(0.3, 2.5)

- Too few iterations can give a result which *looks okay but is actually biased to the shape of the input*
- Adjacent bins are correlated, even though we binned close to our detector resolution
- Early termination of D'Agostini can give unrealistically small errors



First test for this: **Check that the χ^2 preference in model comparisons is similar to the unregularised results**

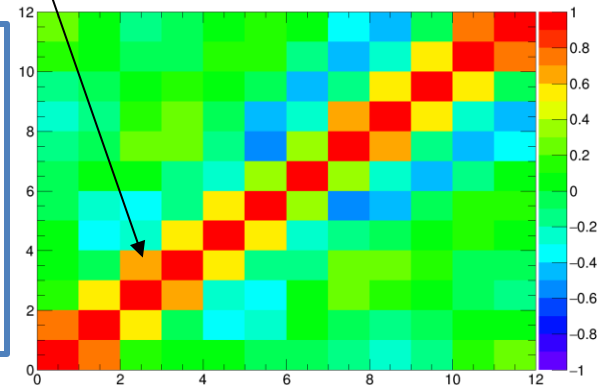
2000 iterations (~unreg)
 $\chi^2_{truth} = 2.9, \chi^2_{input} = 134$

50 iterations
 $\chi^2_{truth} = 32, \chi^2_{input} = 254$

4 iterations
 $\chi^2_{truth} = 9606, \chi^2_{input} = 1568$



- **Changing the number of iterations can change physics conclusions**
- **MC-driven** methods of optimising the number of iterations (esp. without the above test) are dangerous → can easily get a biased result if the prior used was far from the truth.



How many iterations? – Choose via data

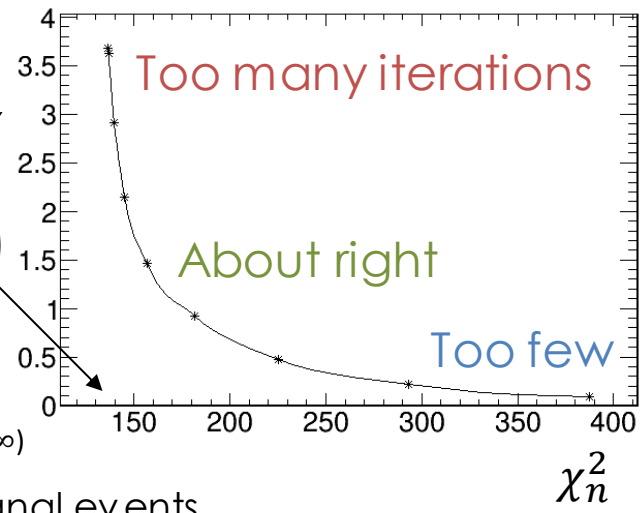
- To mitigate this issue two recent T2K analyses utilising D'Agostini's method employ a **data-driven** regularisation

- Similar approach to L-Curve:
 - Balance the impact of the smoothing (Y)
 - With the distance to the unregularised result (X)

$$\chi_n^2 = \sum_{bin\ i,j} (N_i^n - N_i^\infty)(Cov^n)^{-1}(N_j^n - N_j^\infty)$$

(Use some suitably large number in place of ∞)

n – num. iterations Cov – covariance matrix N – num. unfolded signal events



Case Study: On-axis CC1 π measurement

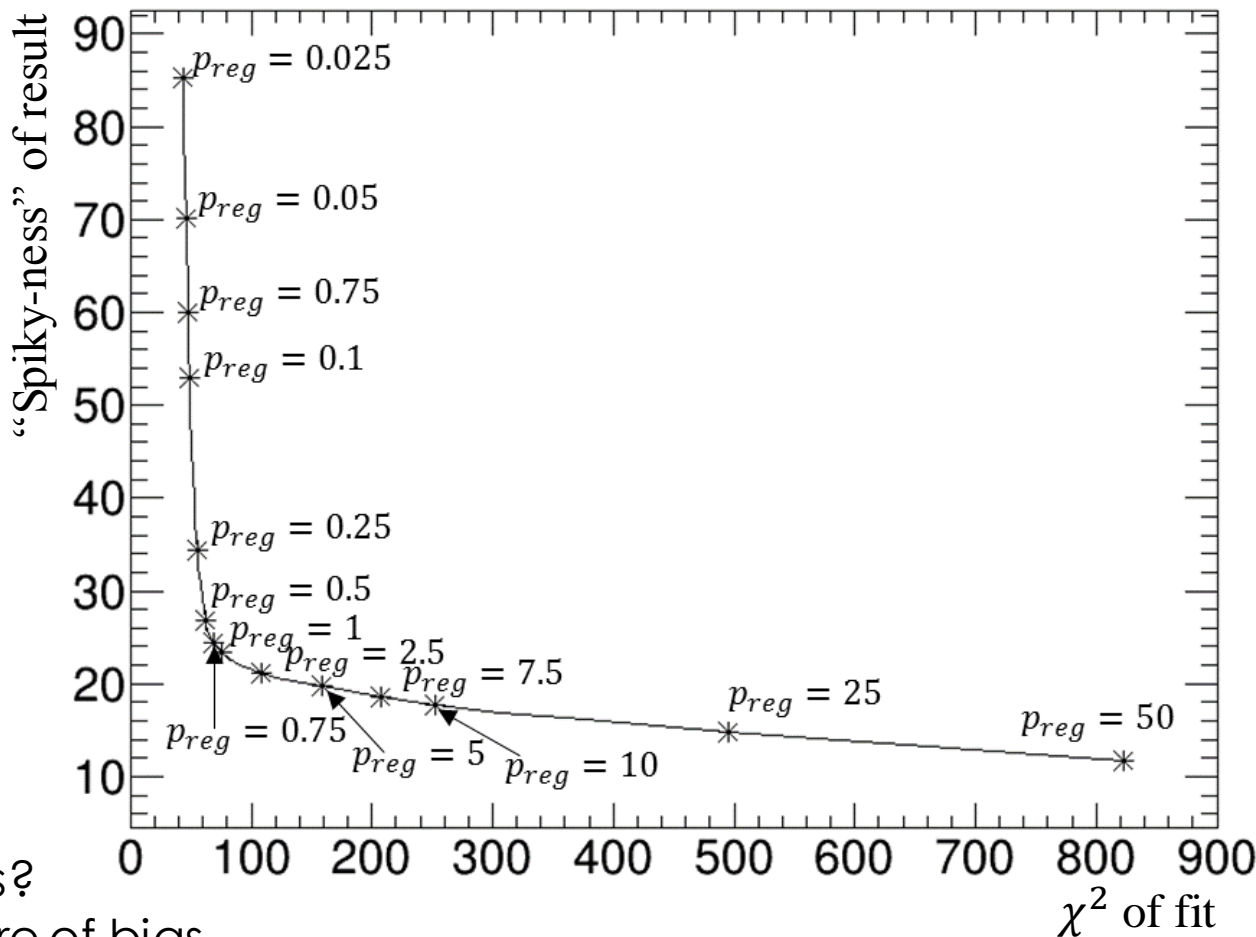
- Number of iterations chosen via fake data: **3 – 7**
- Number of interactions chosen via data: **16**

See talk from Benjamin Quilain

What if my L-curve isn't L-shaped?

Is the condition on the Y-axis reasonable?

- If the form of the penalty pushes the result somewhere that is incompatible with the no regularisation case, the drop on the y-axis can be limited to very small values of p_{reg}



How did you form the x-axis?

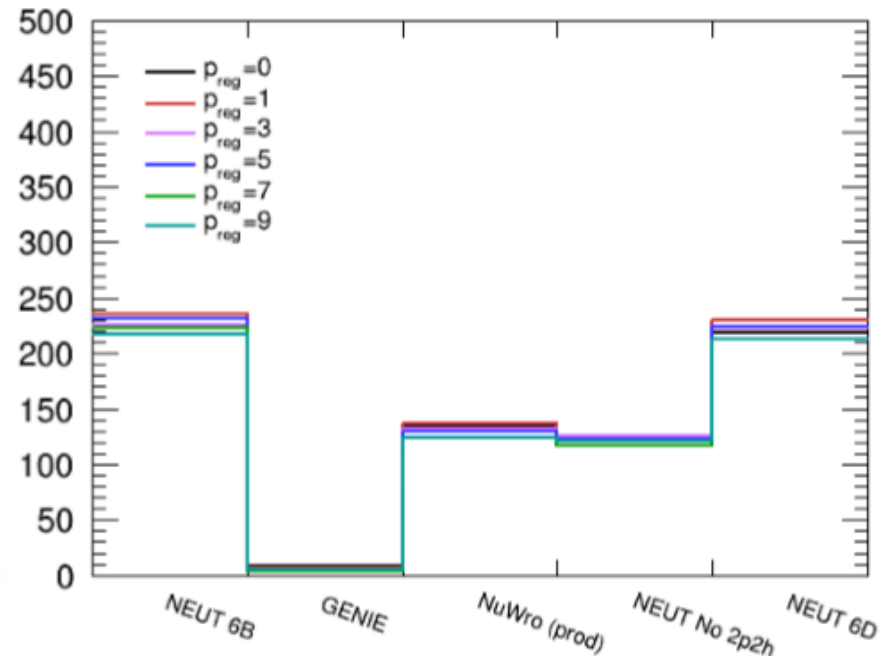
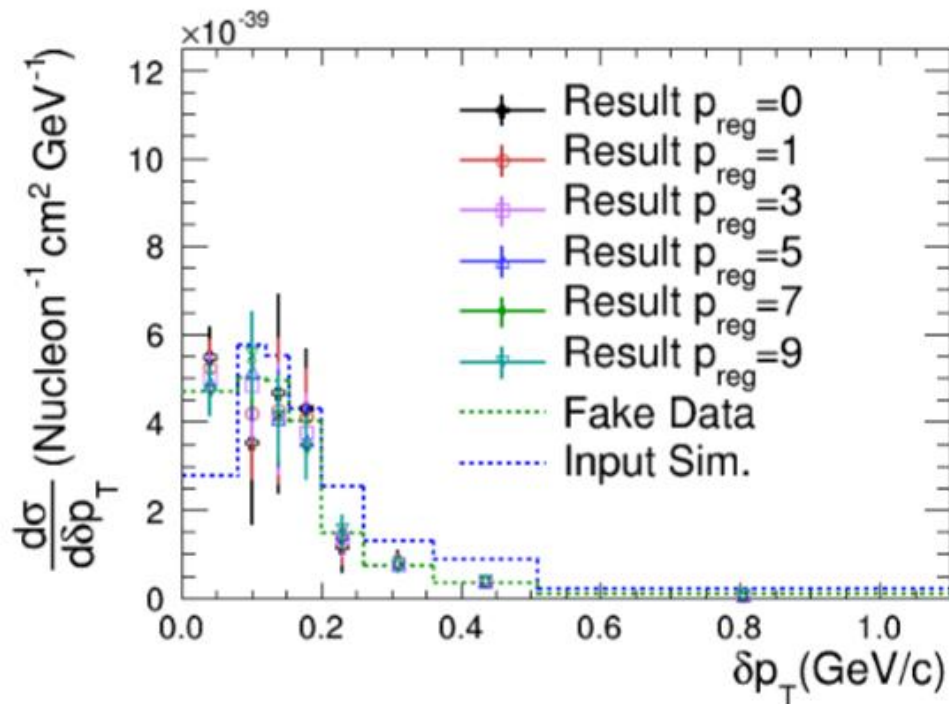
- This needs to be a measure of bias.

What is the first value on the x-axis?

- How does this compare with the x-axis value of the unregularised result? If they're very different consider smaller p_{reg}

Aesthetic regularisation

- A result with a carefully chosen regularisation strength shouldn't significantly alter the physics conclusions with respect to the unregularised case – it's just aesthetic.



Unregularised result as a reference for regularised result bias

TABLE IX. The full and shape-only χ^2 comparisons to the δp_T result with nominal and no regularization. The table is ordered by the size of the no-regularization shape-only χ^2 . More details of these models can be found in Sec. IVA.

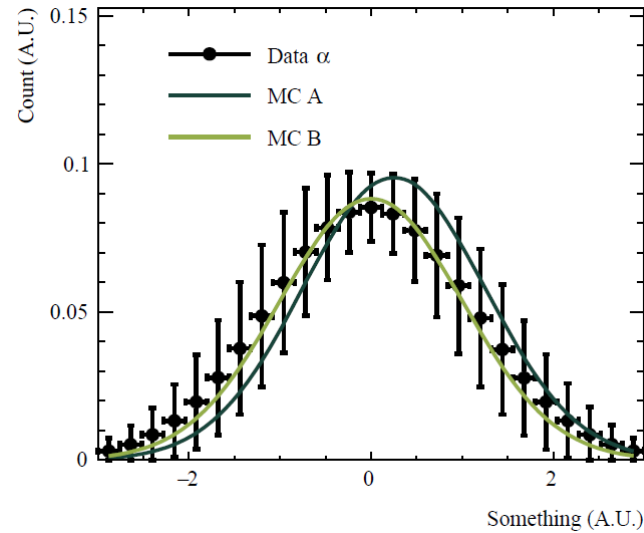
Generator	Full		Shape Only	
	No Reg.	Nom. Reg.	No Reg.	Nom. Reg.
NEUT 5.4.0 (LFG _N + 2p2h _N)	31.6	30.4	3.38	2.60
NEUT 5.3.2.2 (SF + 2p2h _N + 2 × FSI)	15.9	14.8	11.0	10.1
NEUT 5.3.2.2 (SF + 2p2h _N)	31.9	30.3	16.6	15.5
NuWro 11q (SF + 2p2h _N)	22.6	23.1	16.8	15.6
NuWro 11q (LFG + 2p2h _N)	81.5	81.7	39.0	15.6
NuWro 11q (LFG + RPA + 2p2h _N)	78.5	84.4	39.9	36.3
NEUT 5.3.2.2 (SF + 2p2h _N + No FSI)	114	112	42.9	41.4
GENIE 2.12.4 (RFG + 2p2h _E)	92.9	92.4	47.9	47.7
NuWro 11q (SF w/o 2p2h)	65.8	68.7	55.4	54.8
NEUT 5.3.2.2 (SF w/o 2p2h)	93.3	91.5	61.2	59.6
GiBUU 2016 (LFG + 2p2h _G)	77.0	78.9	66.1	59.6
NuWro 11q (RFG + 2p2h _N)	150	155	67.2	69.0
NuWro 11q (RFG + RPA + 2p2h _N)	155	172	68.6	70.4
GENIE 2.12.4 (RFG w/o 2p2h)	94.6	97.8	74.1	76.2

- These numbers are very similar → No change of physics conclusions from regularisation. Important test.

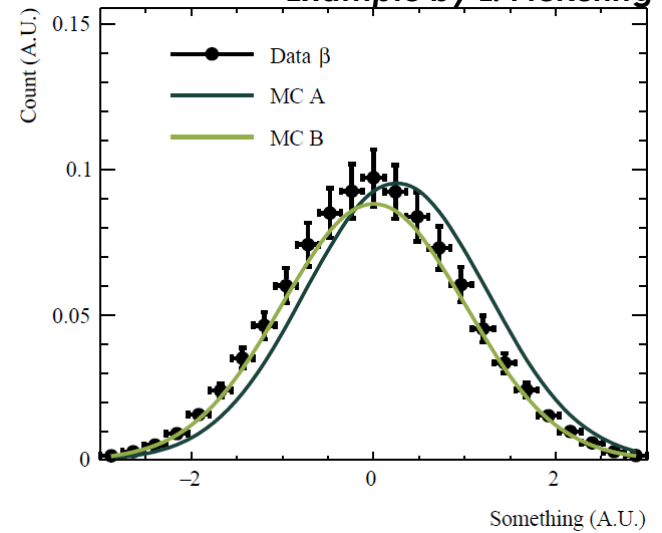
Phys. Rev. D **98**, 032003

Do I really need a covariance?

Guess which MC fits
each data better
better?



Example by L. Pickering

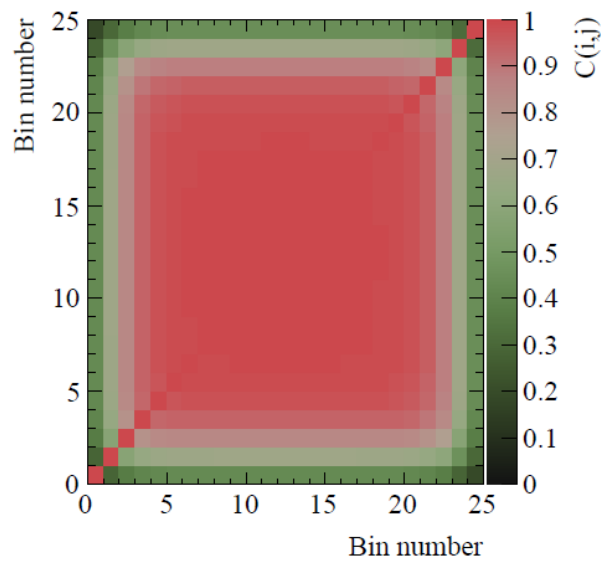
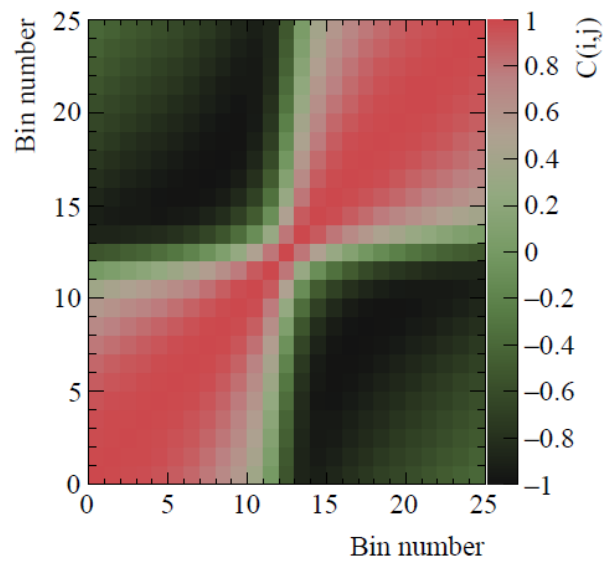
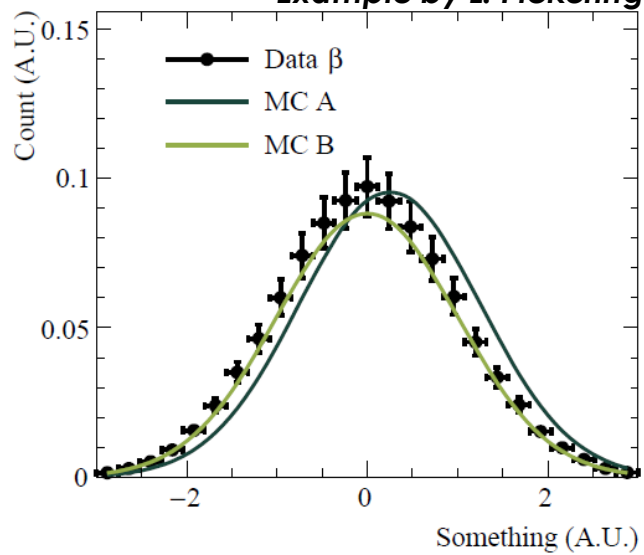
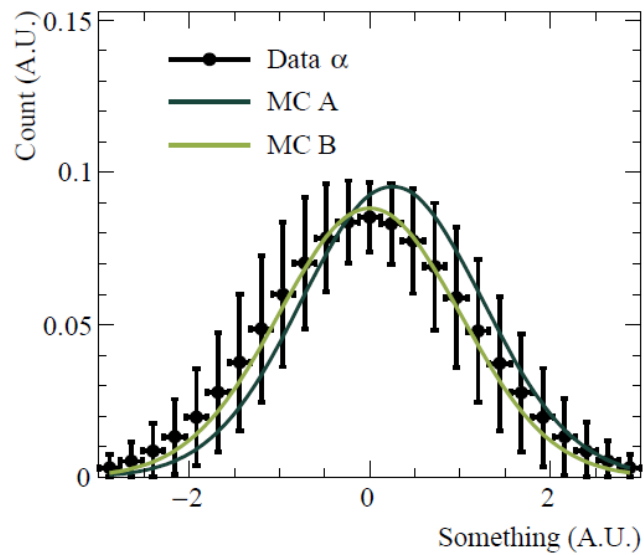


Do I really need a covariance?

Example by L. Pickering

How about now?

Can you do chi-by-eye?

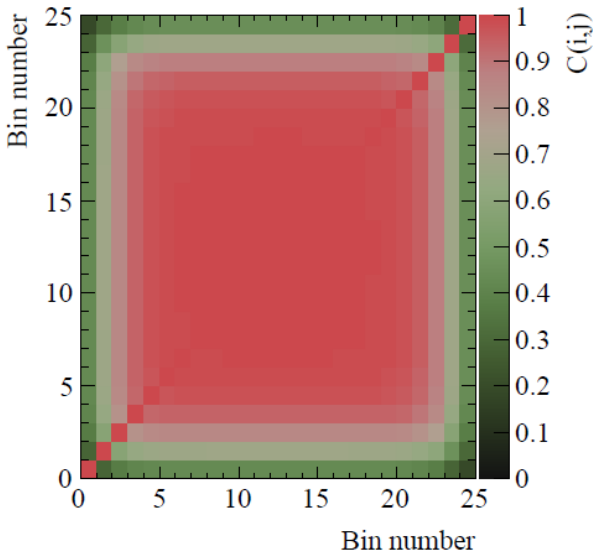
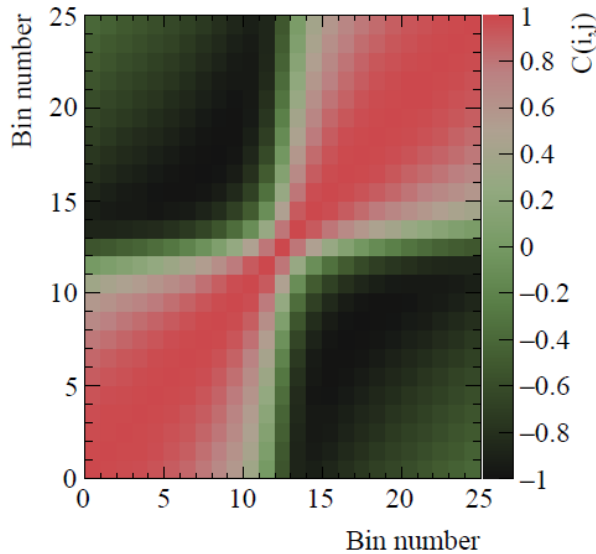
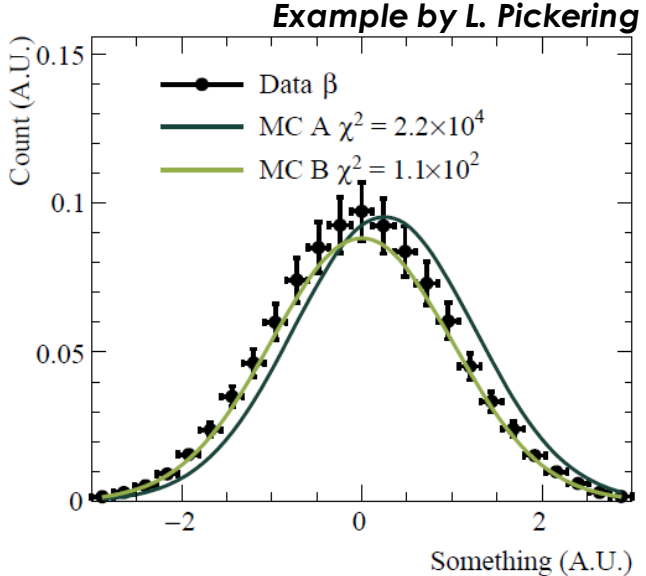
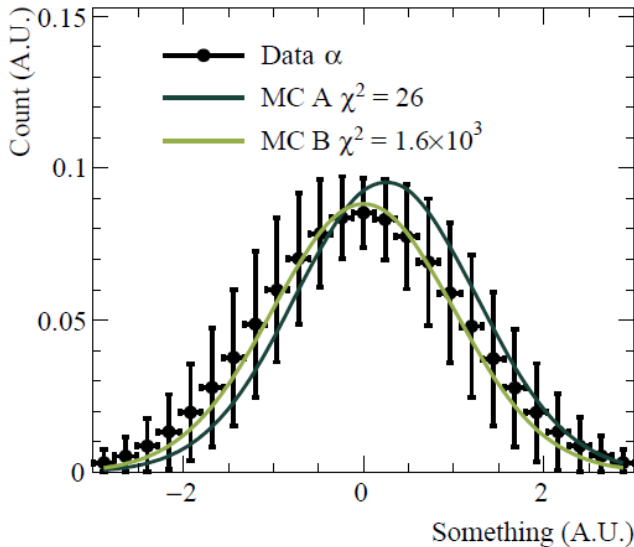


Chi-by-eye?

Interpreting any result-simulation comparison without a covariance matrix and a goodness of fit is dangerous.

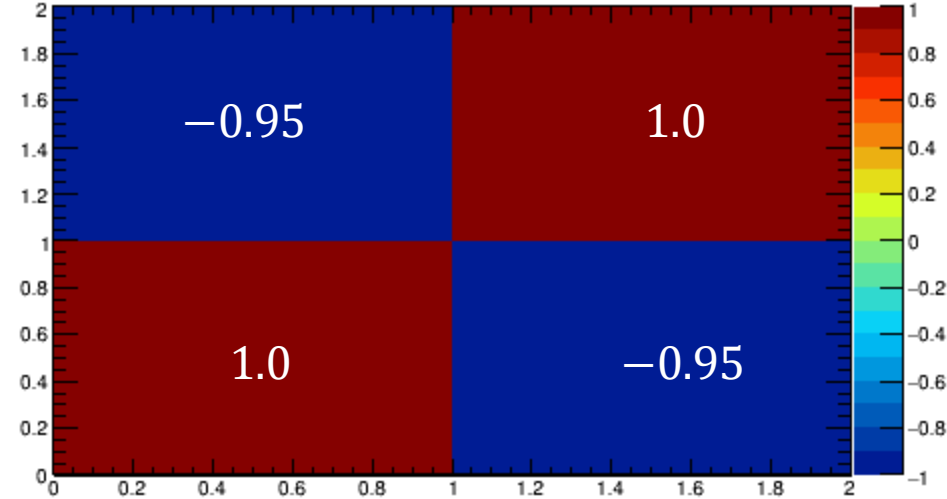
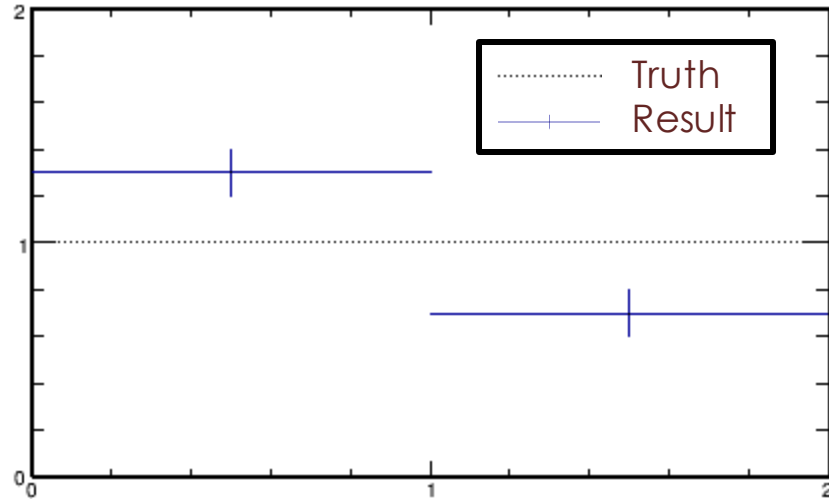
If you really must, then the regularised result is better, but may still be misleading.

If you make a conclusion by eye, check the χ^2 tell the same story.



But the result looks awful!?

- Consider a two bin result:



$$pull_i = \frac{N_{fit} - N_{true}}{Error}$$

$$\left. \begin{aligned} pull_0 &= 3 \\ pull_1 &= 3 \end{aligned} \right\} \text{Fairly awful pull}$$

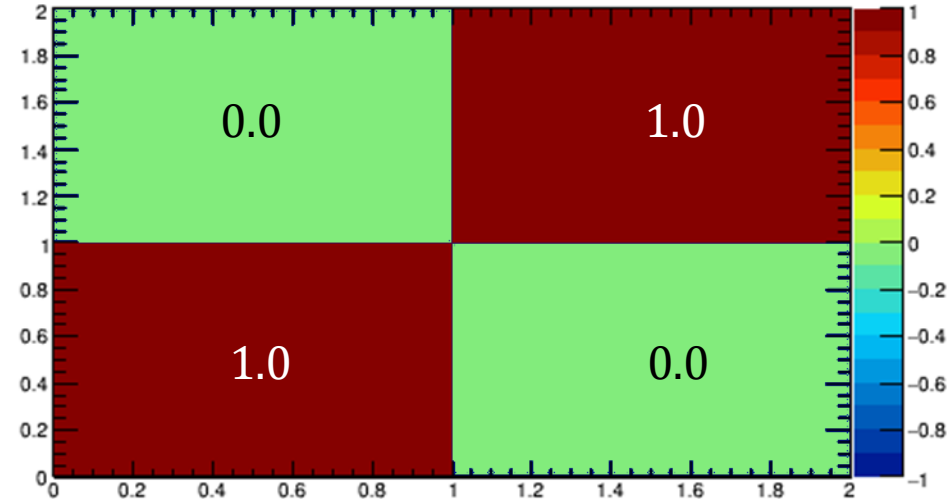
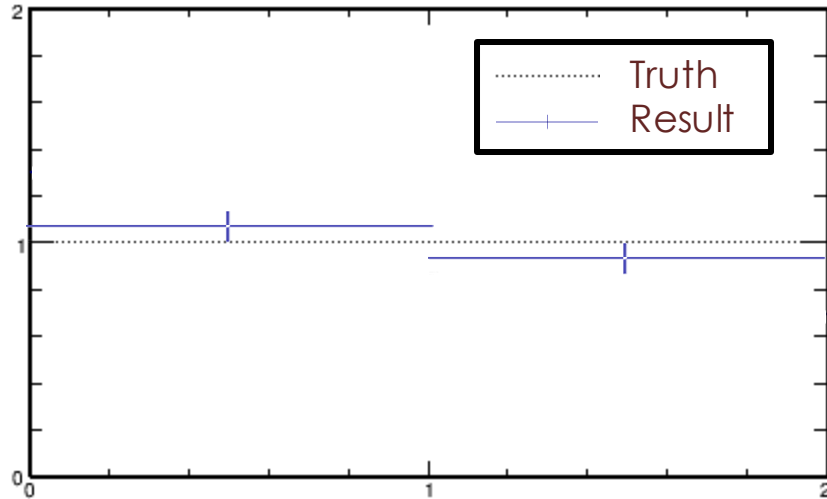
$$\chi^2 = (\overline{N_{fit}} - \overline{N_{true}})(V_{cov})^{-1}(\overline{N_{fit}} - \overline{N_{true}})$$

$$\chi^2 = 1.69 \} \text{Good } \chi^2$$

- Need to see the correlation matrix to tell whether the result is good or not.

But the result looks awful!?

- Consider a two bin result:



$$pull_i = \frac{N_{fit} - N_{true}}{Error}$$

$$\left. \begin{aligned} pull_0 &= 1 \\ pull_1 &= 1 \end{aligned} \right\} \text{Better pull}$$

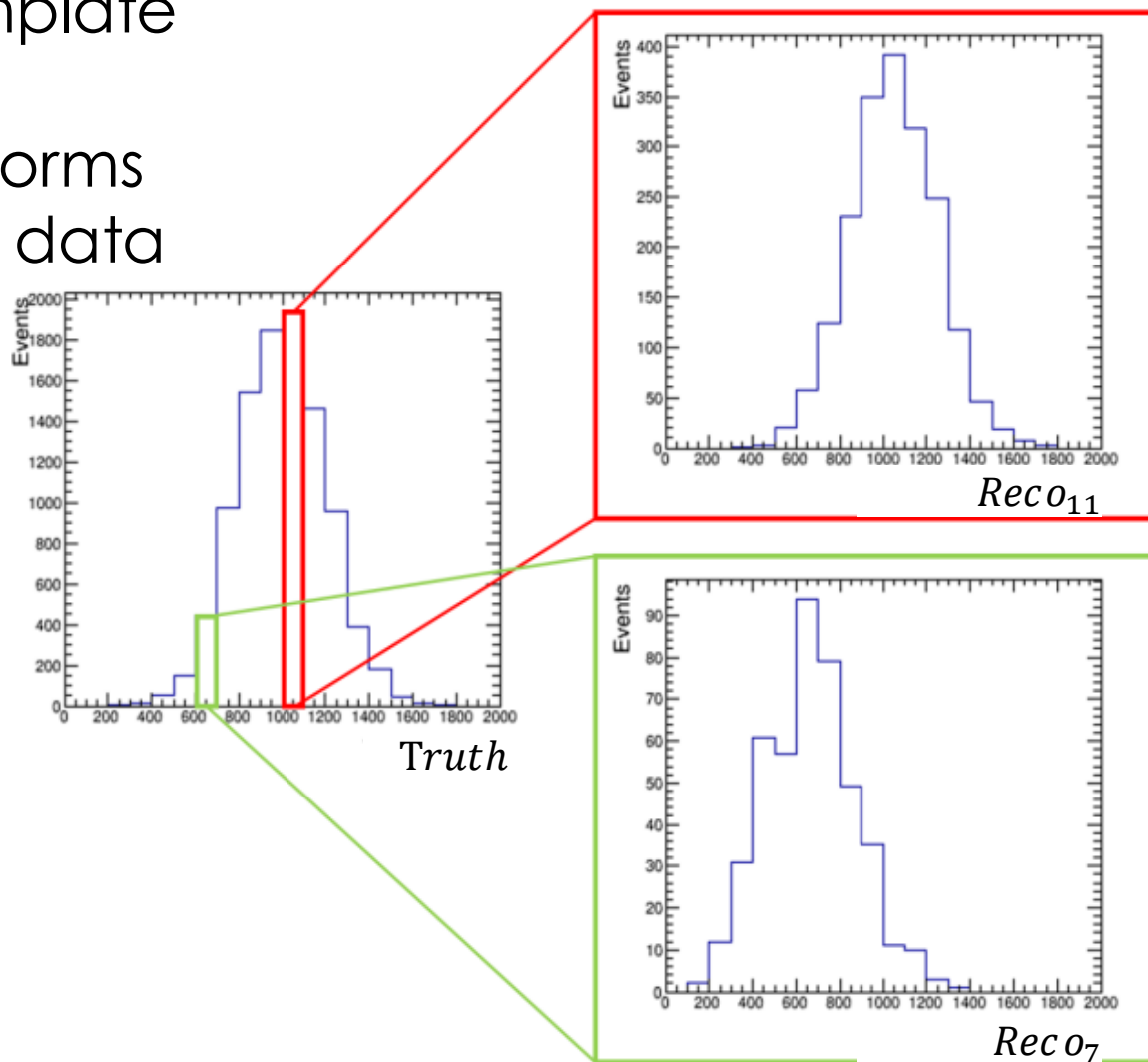
$$\chi^2 = (\overline{N_{fit}} - \overline{N_{true}})(V_{cov})^{-1}(\overline{N_{fit}} - \overline{N_{true}})$$

$$\chi^2 = 2.0 \} \text{Worse } \chi^2$$

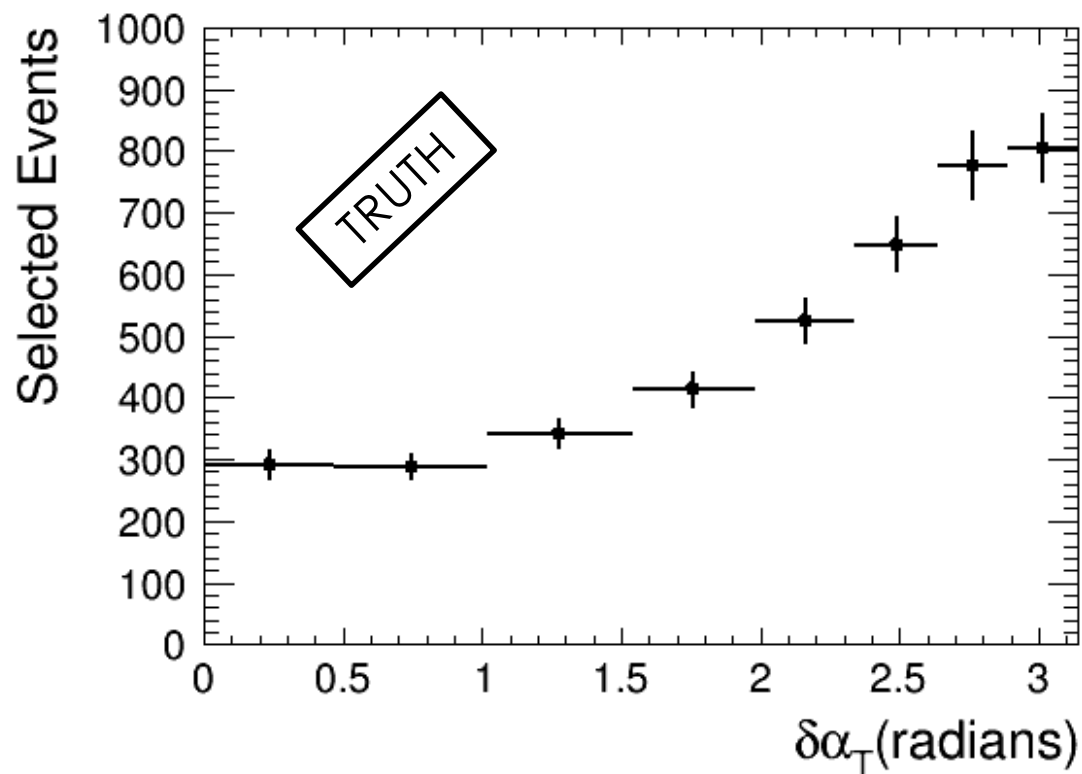
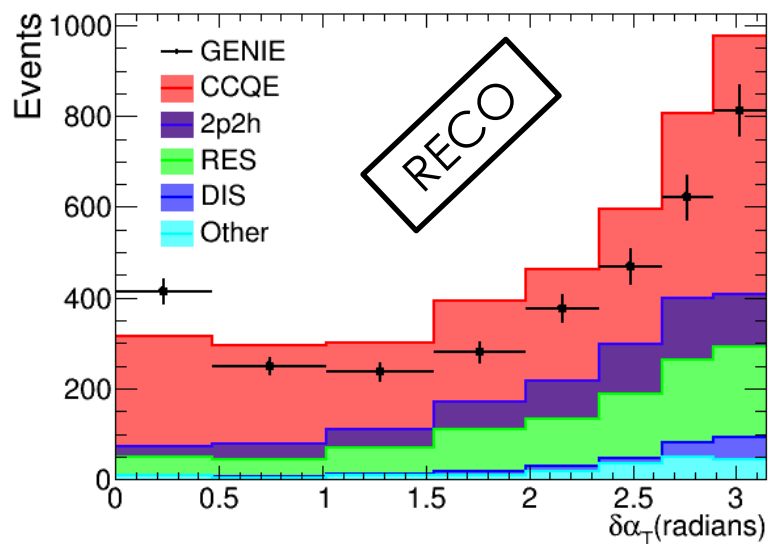
- Pulls/bin-to-bin bias doesn't tell the whole story

Unfolding at T2K: likelihood fitting

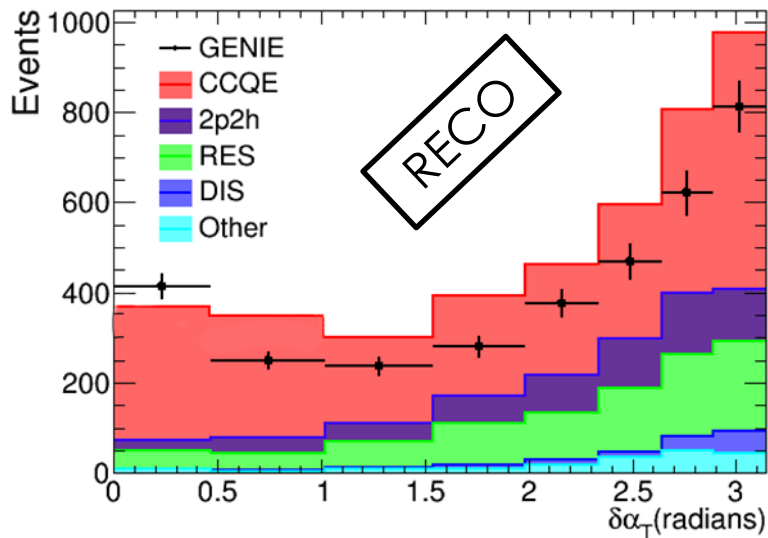
- True bin \rightarrow Reco. template
- Vary MC template norms (c_i) and compare to data
- Maximise Poisson likelihood + syst. penalty term (using max. gradient decent)



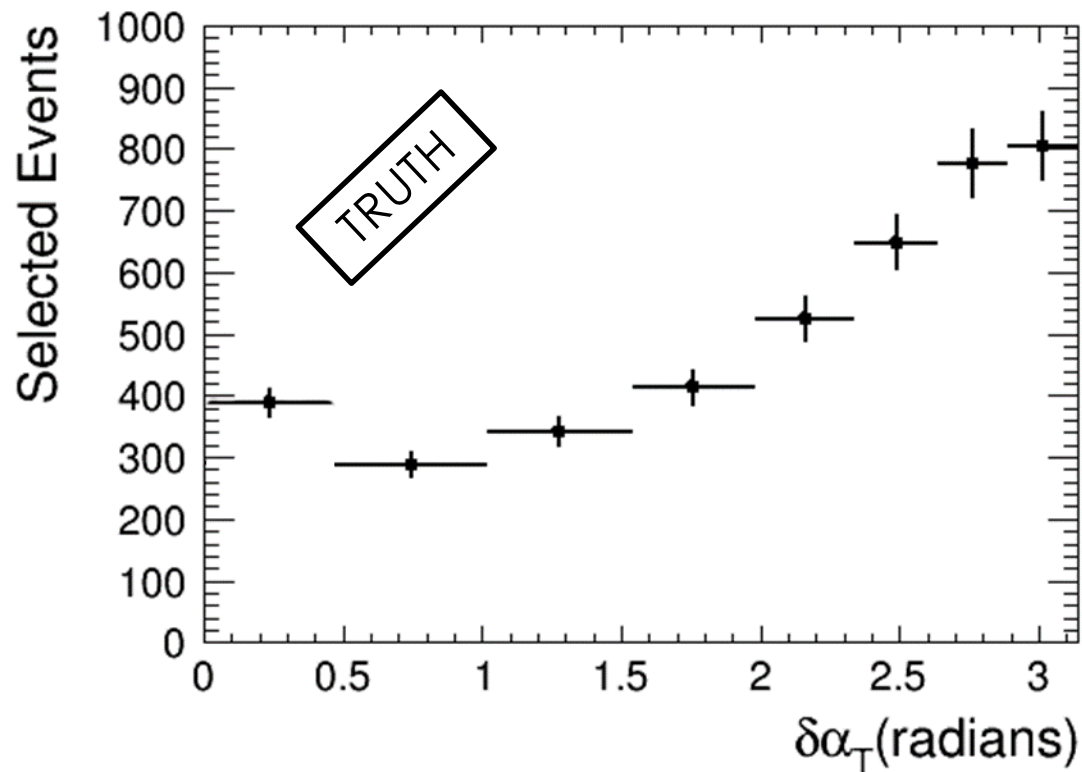
How does it work?



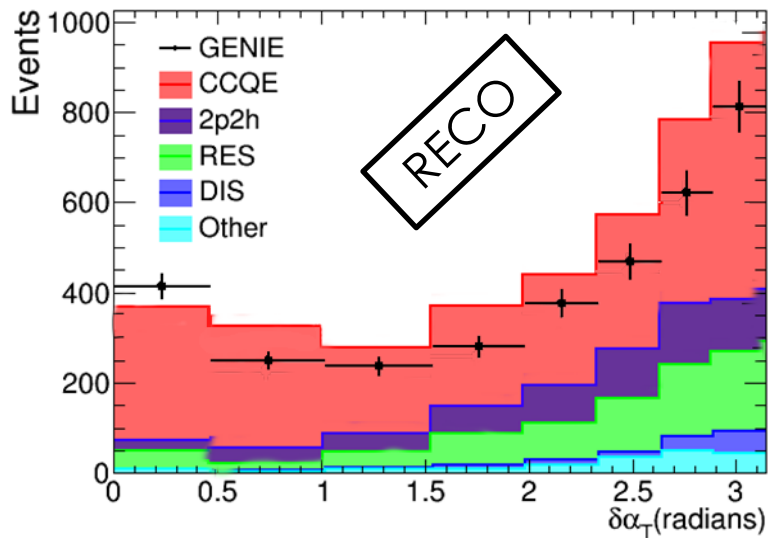
How does it work?



- Scale template weights

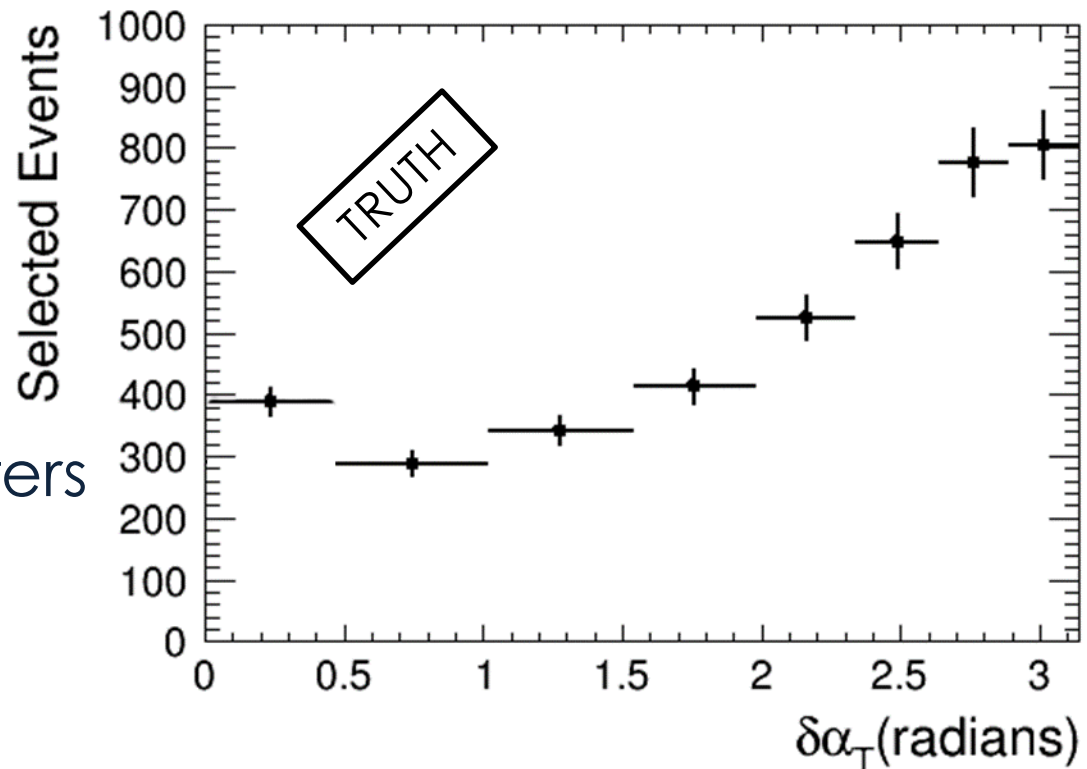


How does it work?

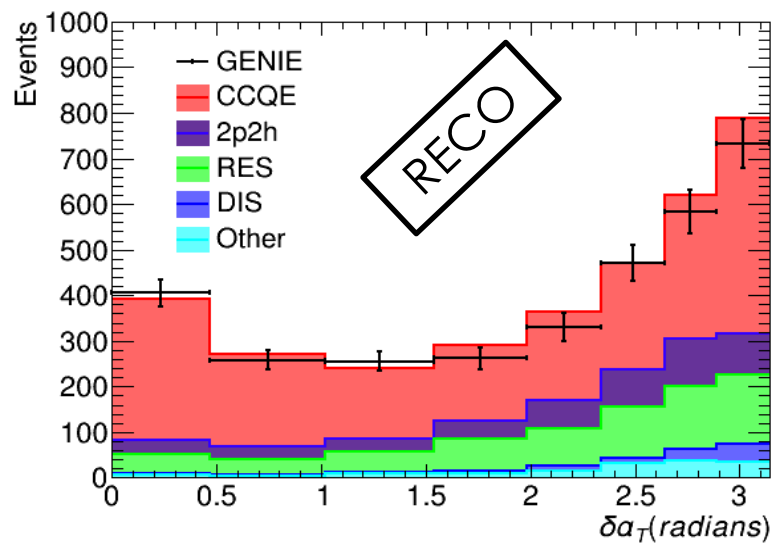


- Overall can alter:
 - Template weights
 - BG Model parameters
 - Flux
 - Detector response

- Alter background systematic parameters
- These should ideally be constrainable by control regions

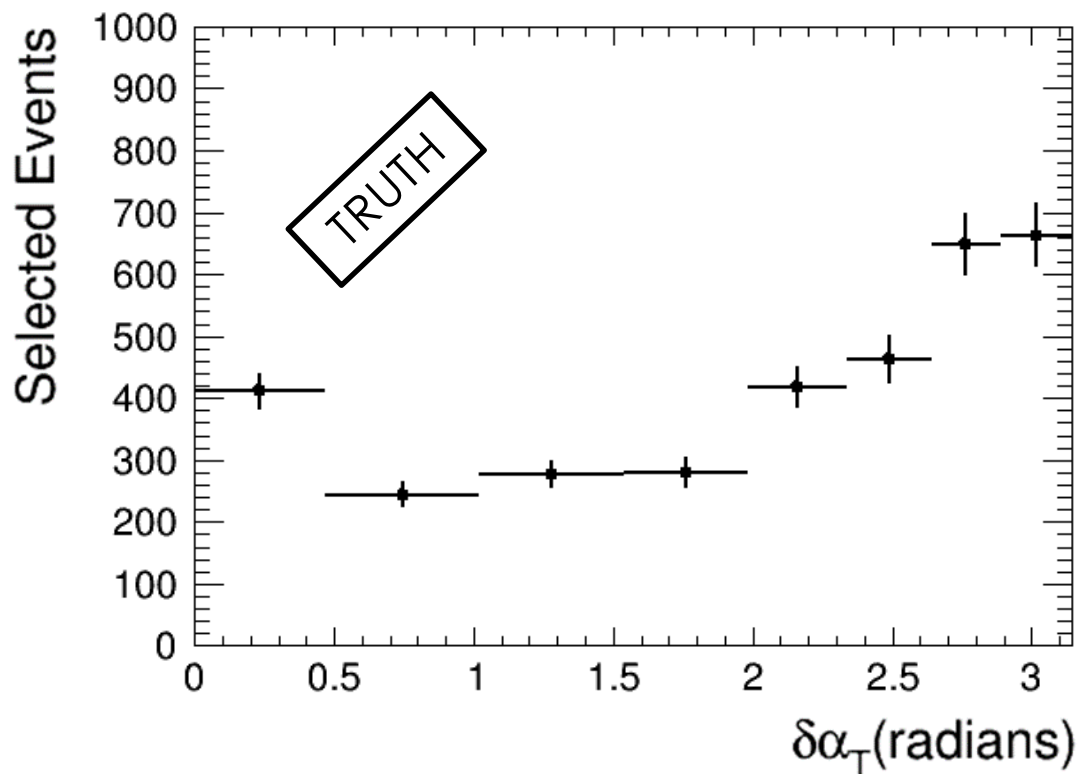


How does it work?



- Maximise likelihood / minimise $-2 \ln(L) \approx \chi^2$

- Keep iterating to maximize the likelihood



Regularisation in the likelihood fitter

- The best fit parameters are those that minimise the following:

$$\chi^2 = \chi_{stat}^2(\textit{fit goodness}) + \chi_{syst}^2(\textit{penalty}) + \chi_{reg}^2$$

$$\chi_{stat}^2 = \sum_j^{recobins} 2(N_j^{MC} - N_j^{obs} + N_j^{obs} \ln \frac{N_j^{obs}}{N_j^{MC}})$$

$$\chi_{syst}^2 = (\vec{a}^{syst} - \vec{a}_{prior}^{syst})(V_{cov}^{syst})^{-1}(\vec{a}^{syst} - \vec{a}_{prior}^{syst})$$

- With an optional regularisation term (other terms are possible, exact choice of term is beyond the scope of this talk):

$$\chi_{reg}^2 = p_{reg} \sum_i (c_i - c_{i-1})^2 = p_{reg} (\mathbf{c} - \mathbf{c}_{prior}) V_{cov}^{reg} (\mathbf{c} - \mathbf{c}_{prior})$$