

A_N Versus *Pt* Status Update
Pt Unfolding Closure Test

RBRC Meeting
2020-05-27
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- Unfolding concept
- Statistical fluctuations and migrations

One-dimensional pt case

- True transverse momentum
- Measured transverse momentum
- Response matrix
- Closure test using Monte Carlo

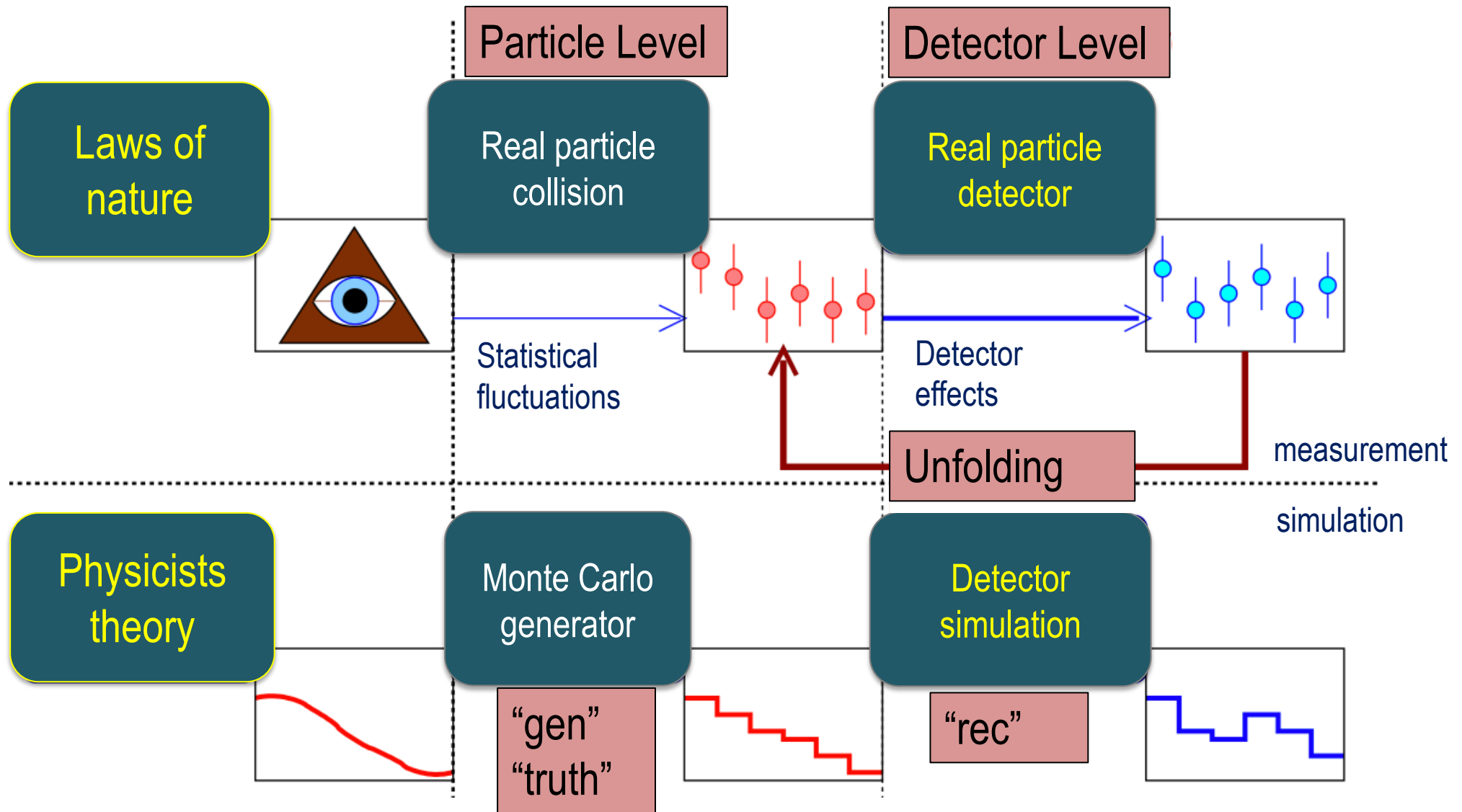
Two-dimensional pt in phi case

- True transverse momentum in phi
- Measured transverse momentum in phi
- Detector response matrix
- Closure test using Monte Carlo

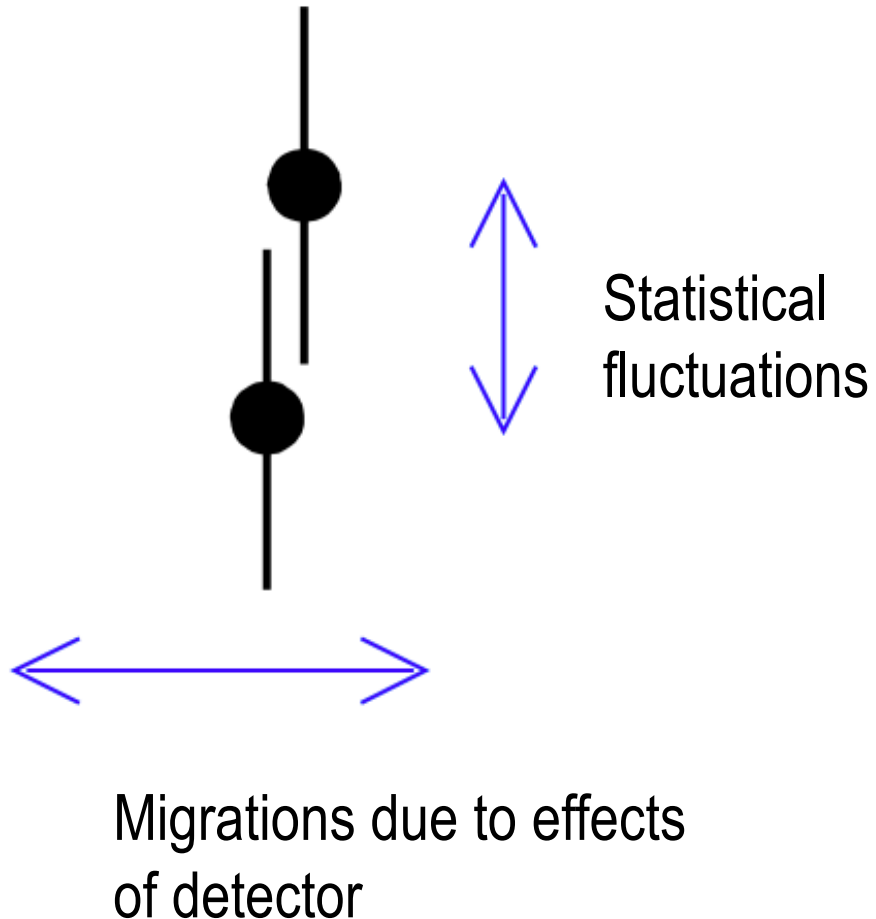
Conclusions

- Summary
- To-do-list

Unfolding overview – Unfolding concept



Unfolding overview – Statistical fluctuations and migrations due to detector effects



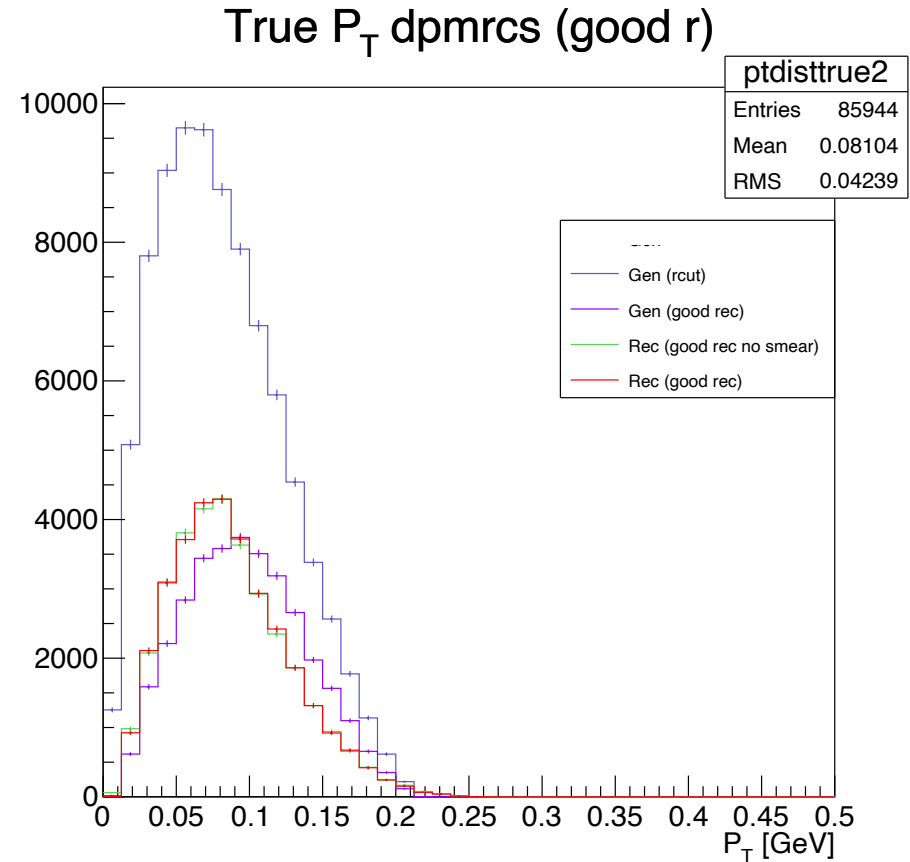
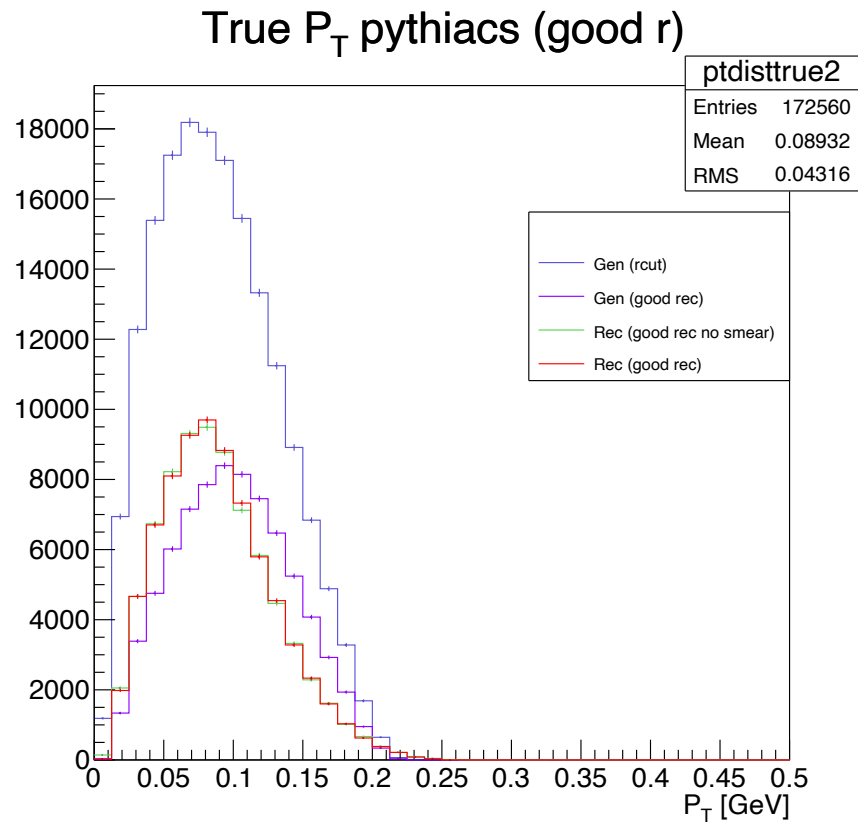
Unfolding:

- Is used to correct for migration effects in the presence of statistical fluctuations.

Result:

- Is an estimation of the “truth” distribution.
- Covariance matrix (statistical uncertainties)

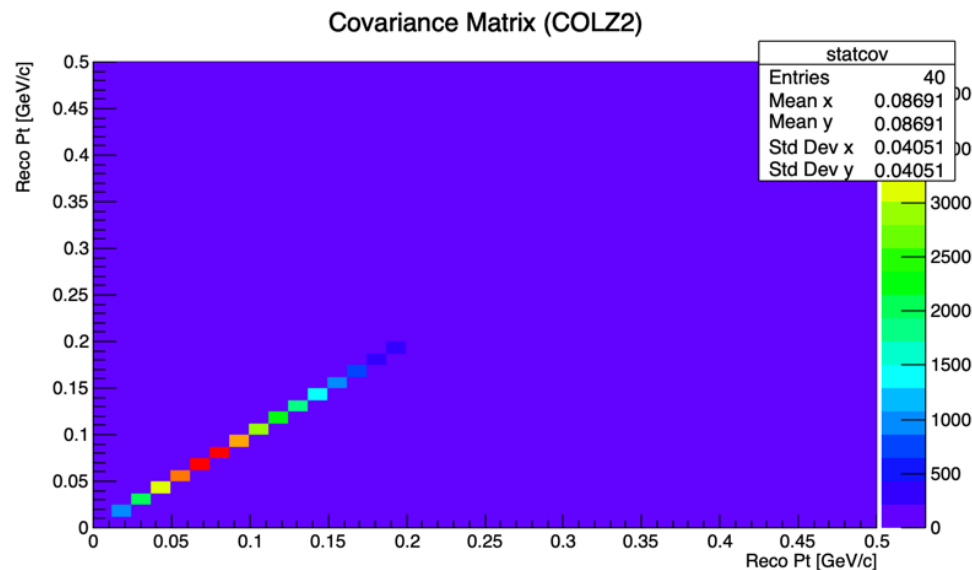
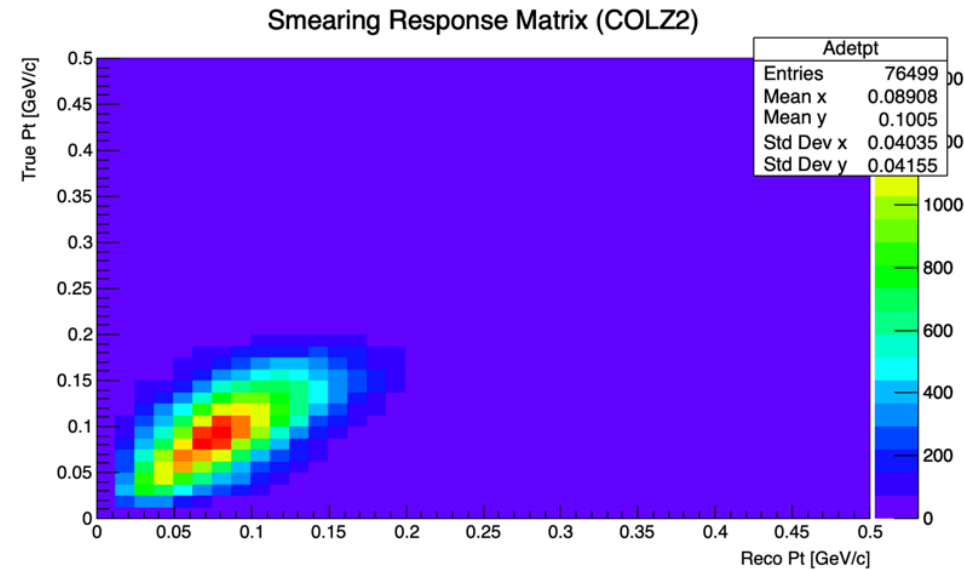
One-dimensional pt unfolding closure test – Unfolding inputs



$$P_{T(True)} = \sqrt{p_x * p_x + p_y * p_y} \quad \text{In magenta line labelled as Gen (good rec)}$$

$$P_{T(Reco)} = \frac{r E_{reco}}{IP} \quad \text{with } r = \sqrt{x_{ev} * x_{ev} + y_{ev} * y_{ev}} \text{ and } IP = 1800 \text{ cm (collision point to ZDC)}$$

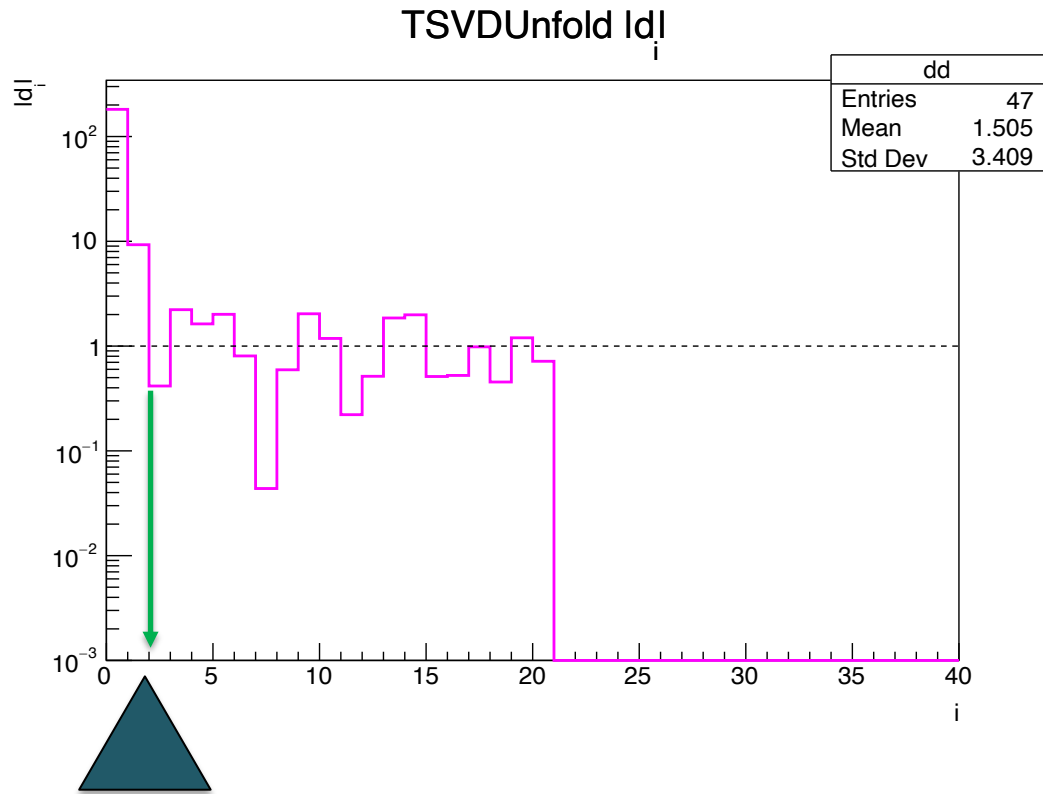
One-dimensional pt unfolding closure test – Unfolding inputs



- Detector smearing matrix from pythia Monte Carlo.
- It is correlation of the measured pt and the true pt distribution from red and purple lines in left panel of previous slide.
- Pythia detector response matrix is used to unfold dpmjet measured distribution in red on the right panel in previous slide.
- With statistical uncertainty, expect to reproduce dpmjet's truth pt distribution in purple line in right panel of previous slide.

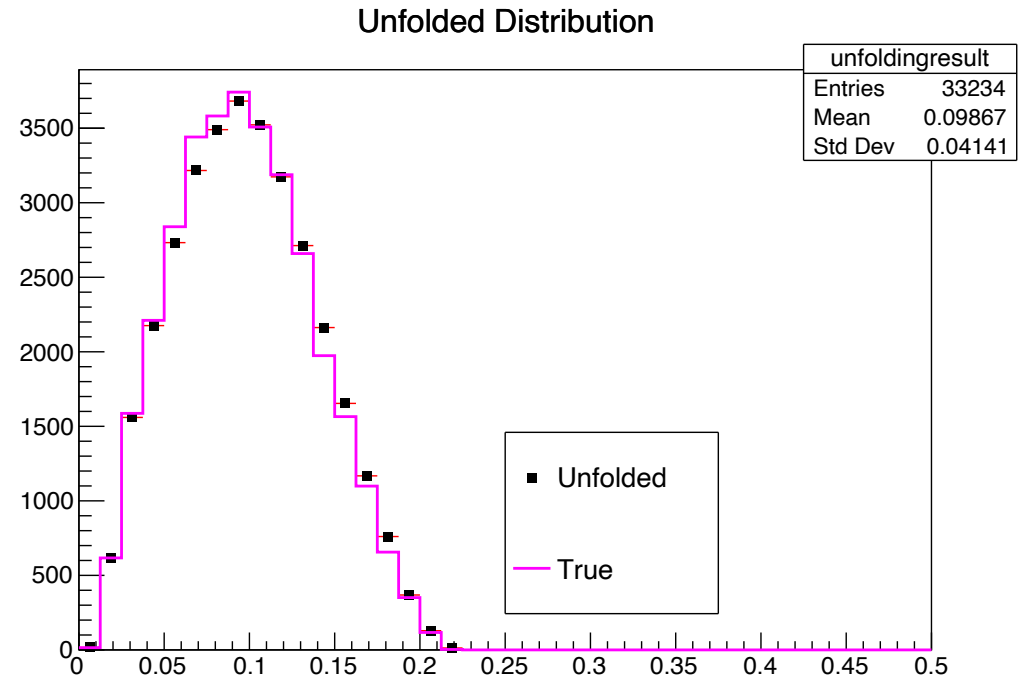
- Input covariance matrix obtained from the square of the errors of the measured pt (red line) distribution from dpmjet Monte Carlo sample in right panel of previous slide.

One-dimensional pt unfolding closure test



Unfolded the measured pt distribution using regularization parameter = 2

Parameter = 2 gives the best minimum curvature = 0.000007 and maybe chosen as optimum value.

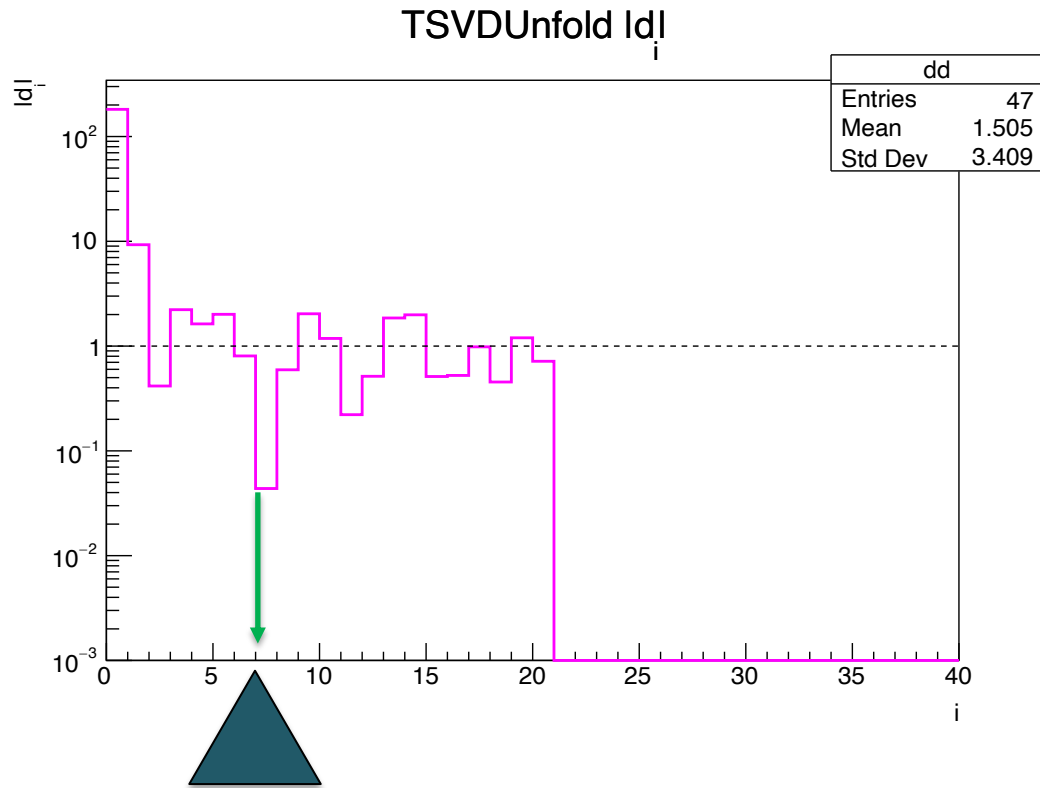


Magenta line: True distribution from dpmjet MC.

Solid black boxes: Unfolded distribution.

Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

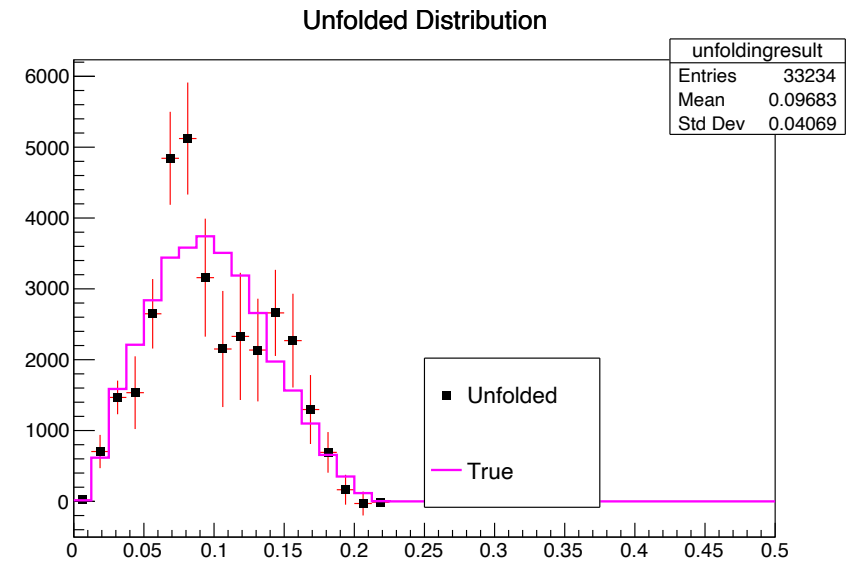
One-dimensional pt unfolding closure test



Unfolded the measured pt distribution using regularization parameter = 7

Regularization parameter = 7 gives a large minimum curvature = 0.343233.

Best minimum curvature should be almost zero.



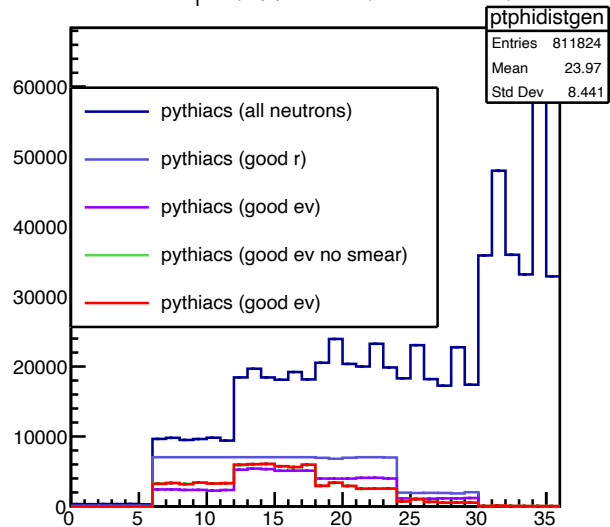
Magenta line: True distribution from dpmjet MC.

Solid black boxes: Unfolded distribution.

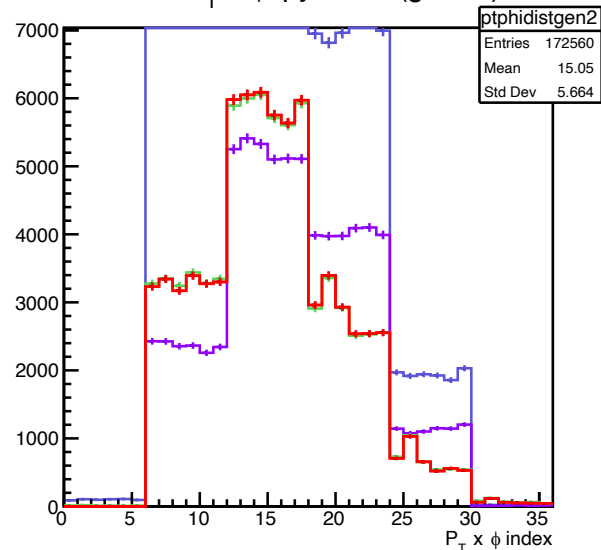
Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

Two-dimensional pt unfolding closure test – Unfolding inputs

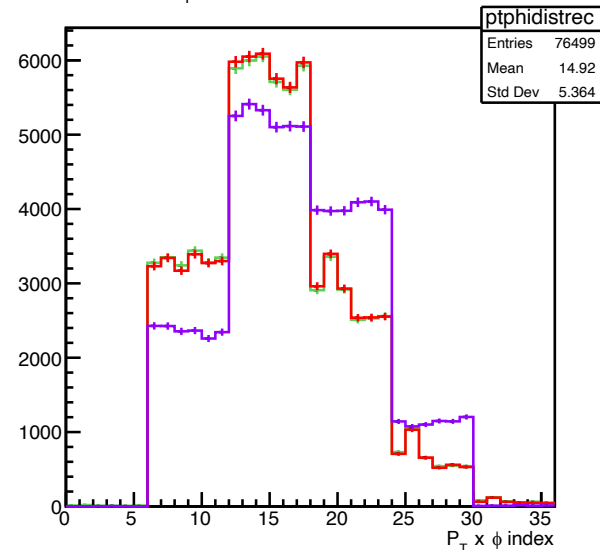
True $P_T \times \phi$ pythiacs (all neutrons)



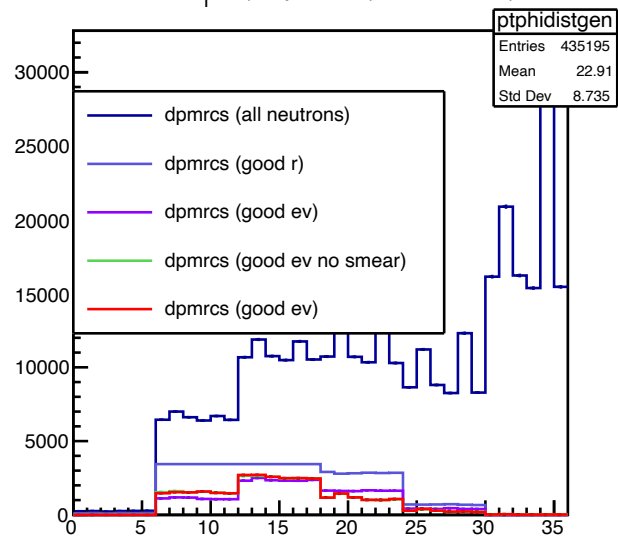
True $P_T \times \phi$ pythiacs (good r)



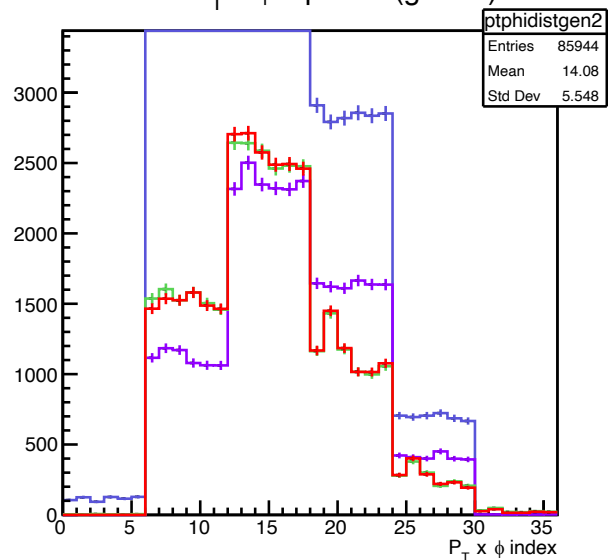
Reco $P_T \times \phi$ pythiacs (good ev no smear)



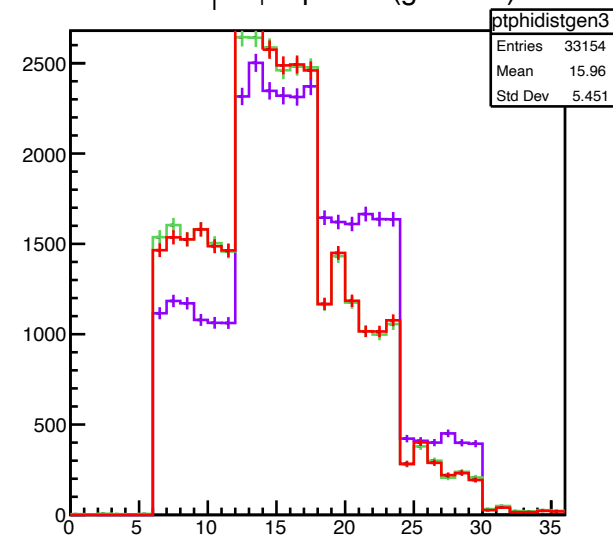
True $P_T \times \phi$ dpmrcs (all neutrons)



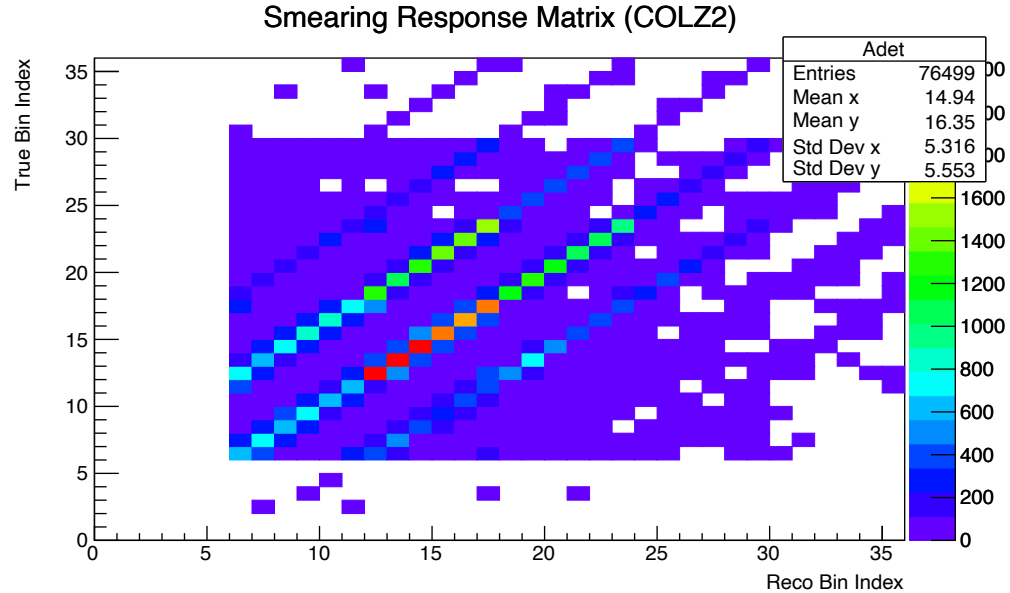
True $P_T \times \phi$ dpmrcs (good r)



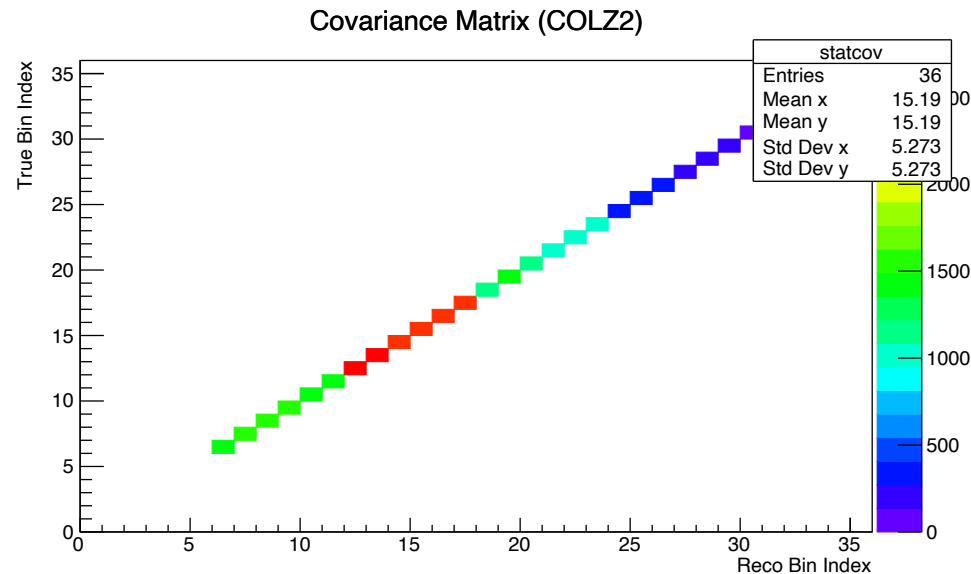
True $P_T \times \phi$ dpmrcs (good ev)



Two-dimensional pt unfolding closure test – Unfolding inputs

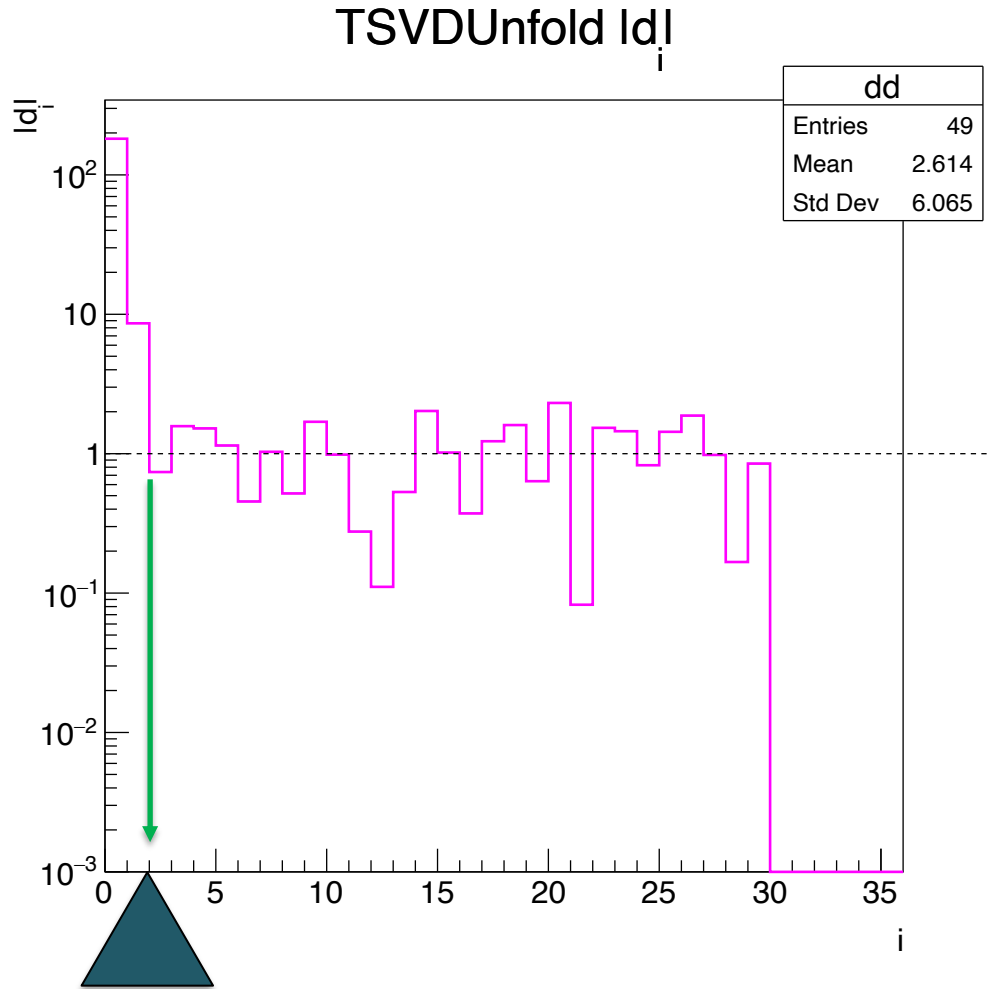


- Correlation matrix between true and measured pt in phi distributions.
- Two variables are being used here: pt and azimuth (phi)

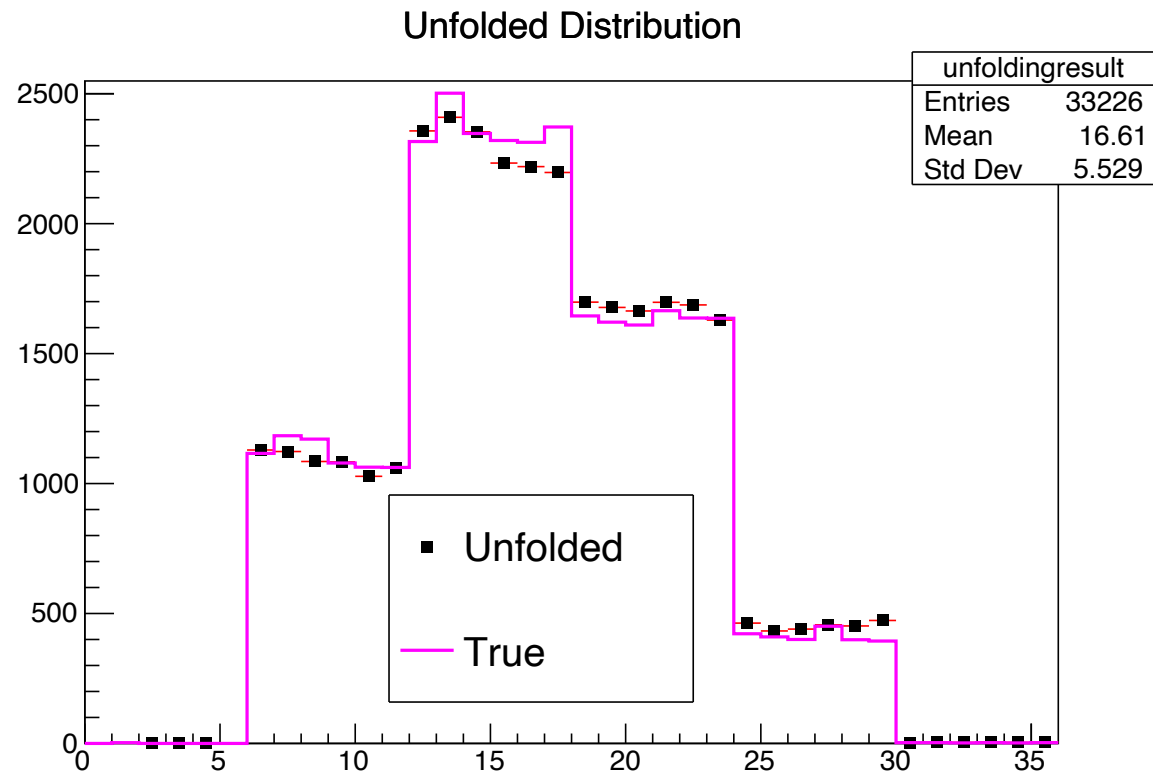


- Input covariance matrix obtained from the square of the errors of the measured pt distribution from dpmjet Monte Carlo sample.

Two-dimensional pt unfolding closure test – Regularization parameter = 2



Unfolded the measured pt distribution using regularization parameter = 2
Minimum curvature = 0.000002

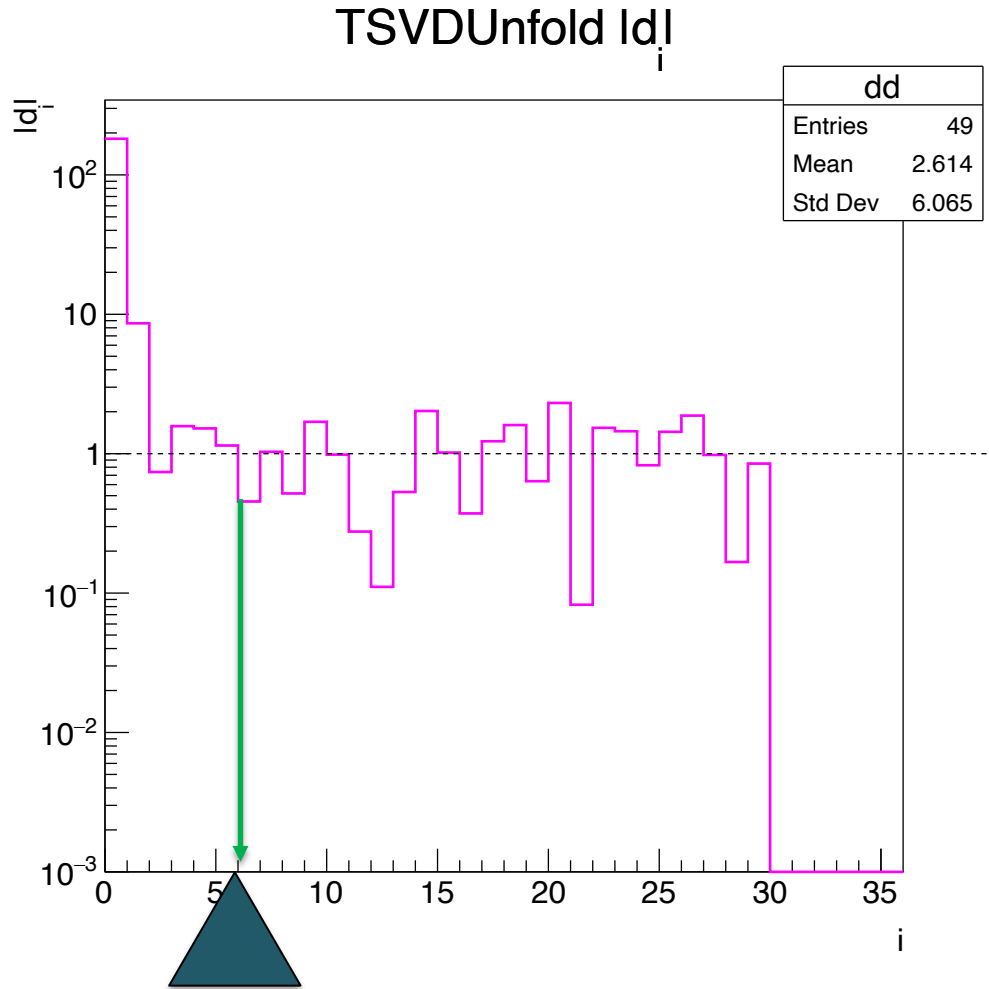


Magenta line: True distribution from dpmjet MC.

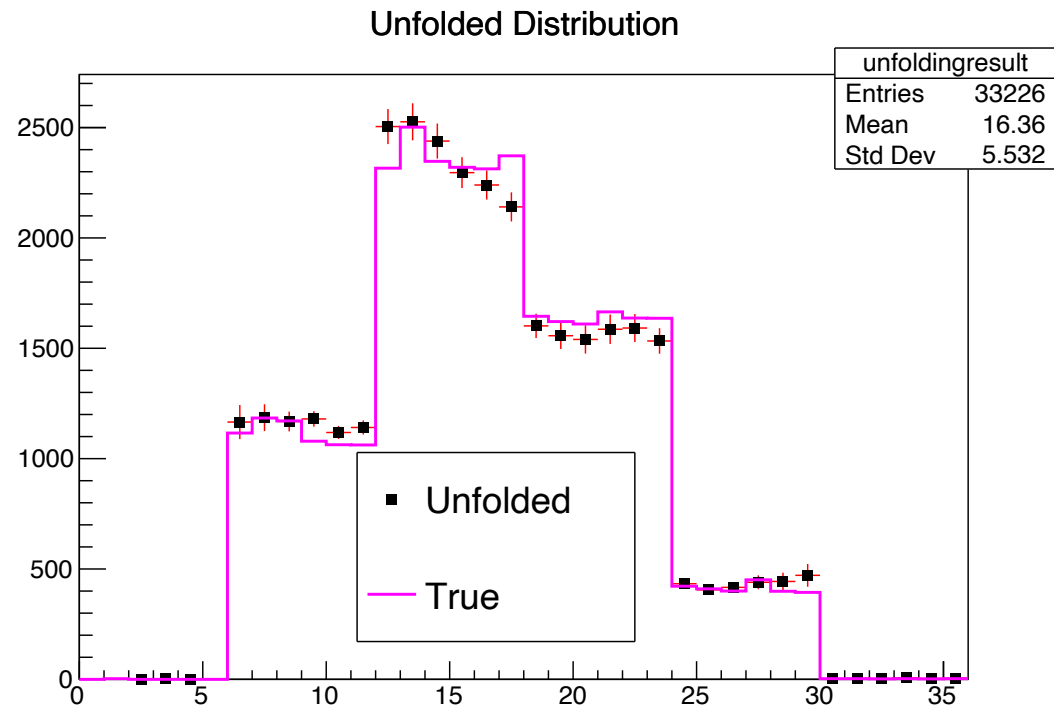
Solid black boxes: Unfolded distribution.

Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

Two-dimensional pt unfolding closure test – Regularization parameter = 6



Unfolded the measured pt distribution using regularization parameter = 6
Minimum curvature = 0.000331

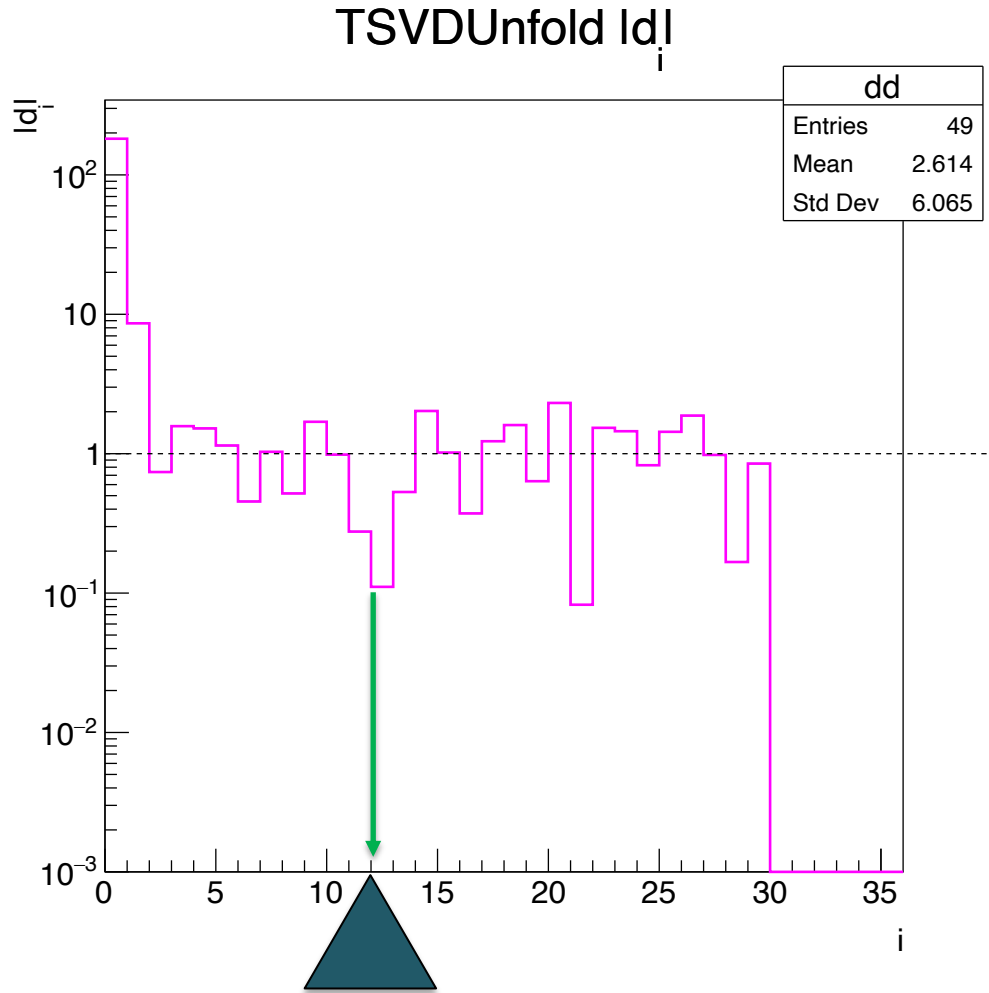


Magenta line: True distribution from dpmjet MC.

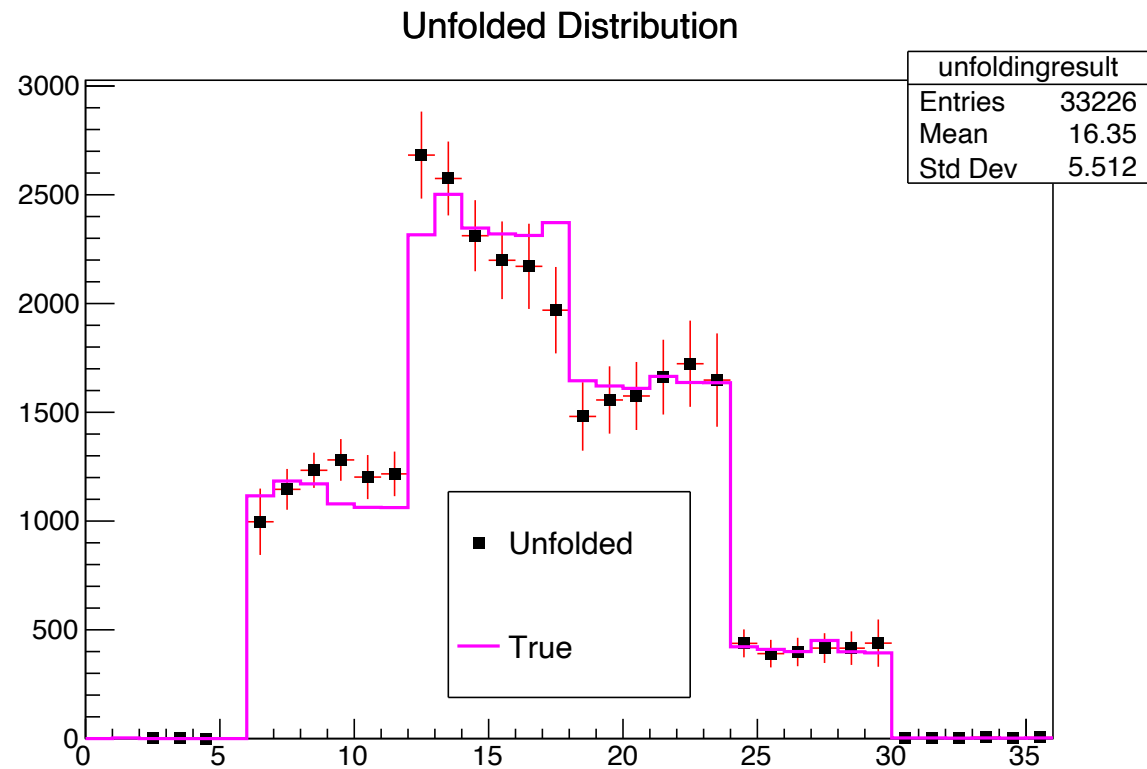
Solid black boxes: Unfolded distribution.

Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

Two-dimensional pt unfolding closure test – Regularization parameter = 12



Unfolded the measured pt distribution using regularization parameter = 12
Minimum curvature = 0.009416

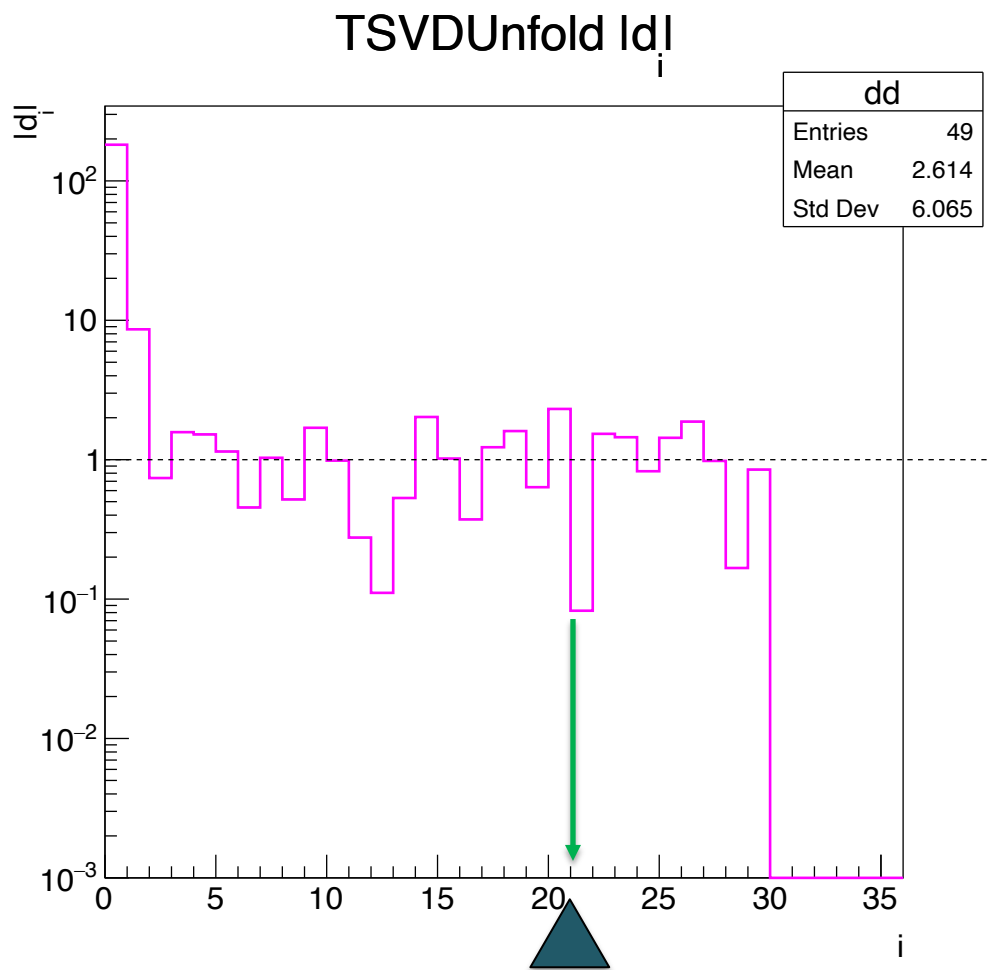


Magenta line: True distribution from dpmjet MC.

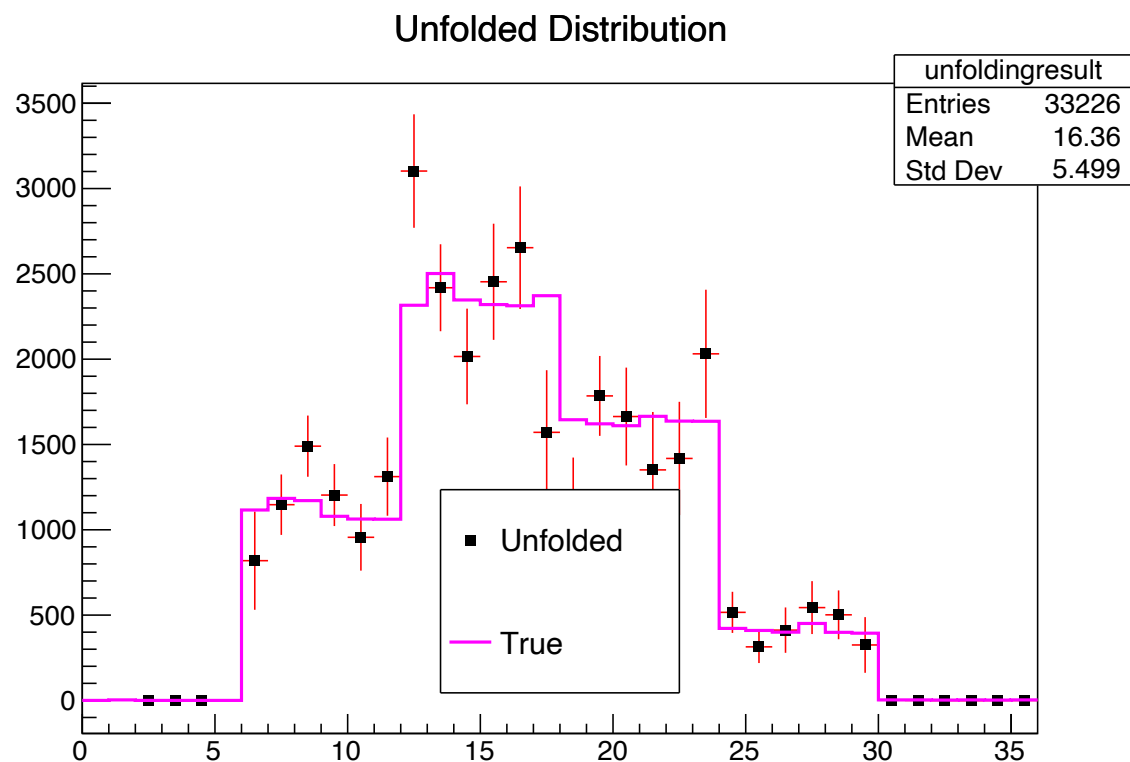
Solid black boxes: Unfolded distribution.

Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

Two-dimensional pt unfolding closure test – Regularization parameter = 21



Unfolded the measured pt distribution using regularization parameter = 21
Minimum curvature = 0.583



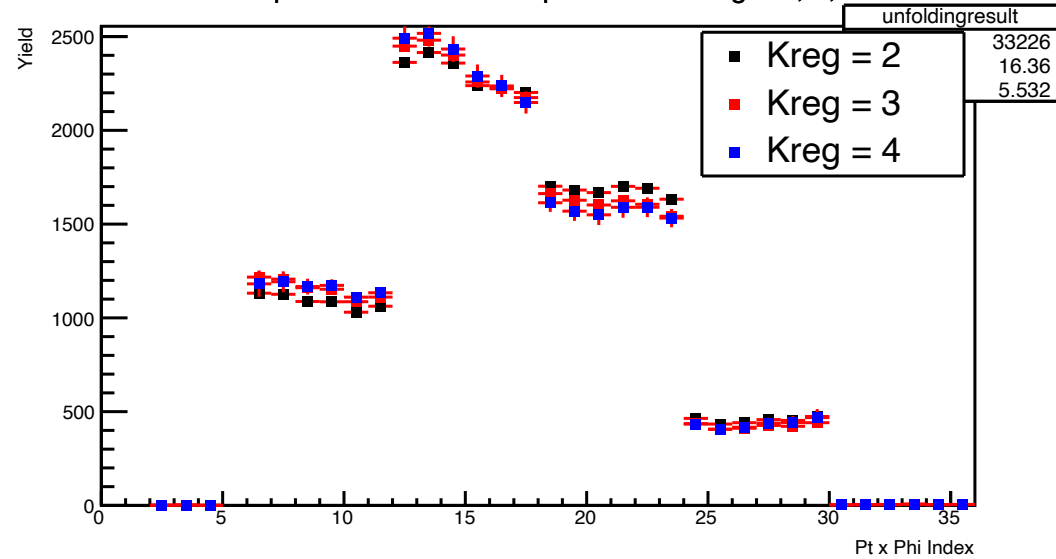
Magenta line: True distribution from dpmjet MC.

Solid black boxes: Unfolded distribution.

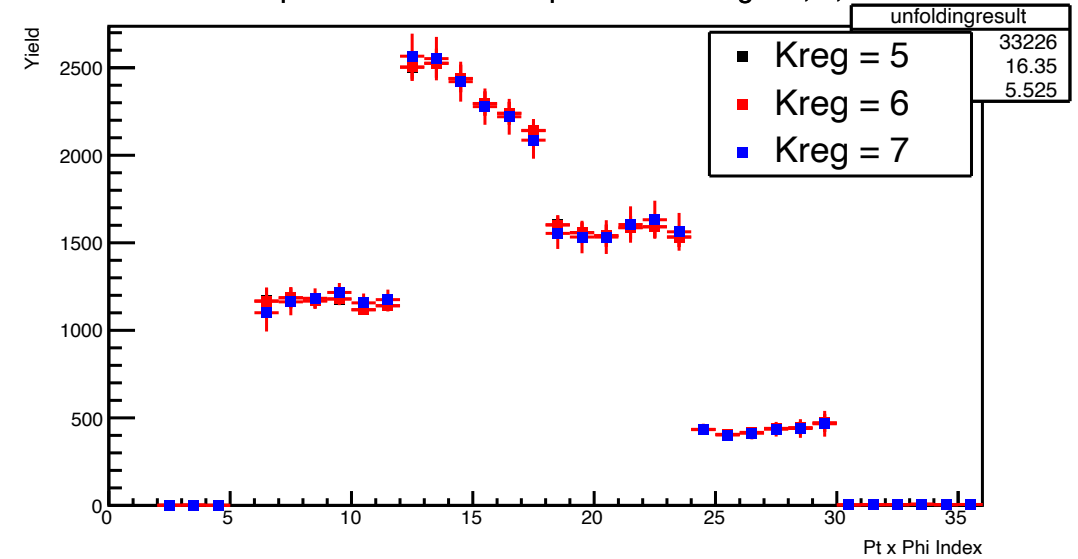
Unfolded distribution has been scaled to match the statistics between dpmjet and pythia.

Two-dimensional pt unfolding closure test – All possible parameter comparison

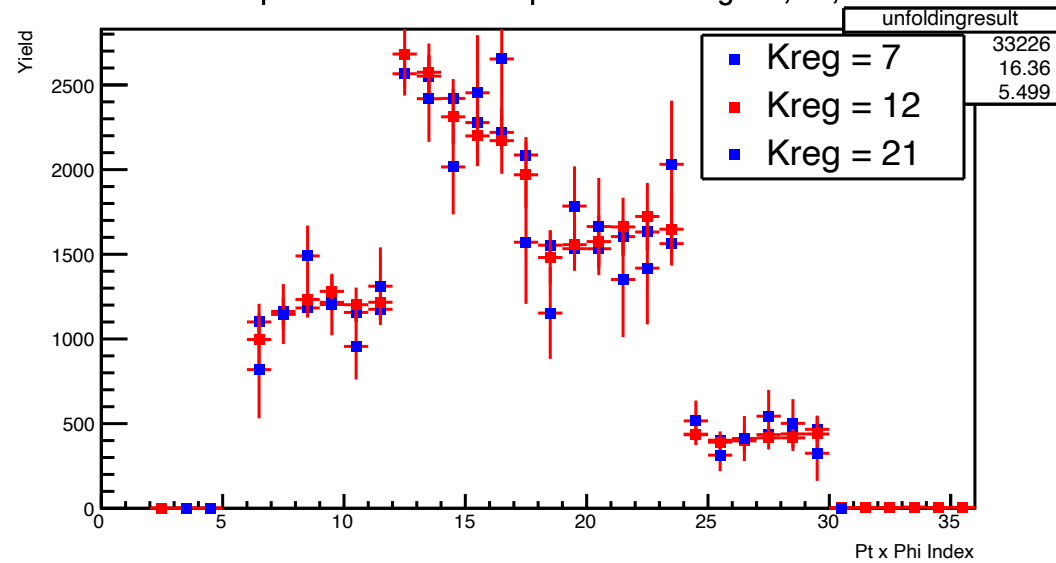
Comparison of unfolded spectra with kreg = 2, 3, 4



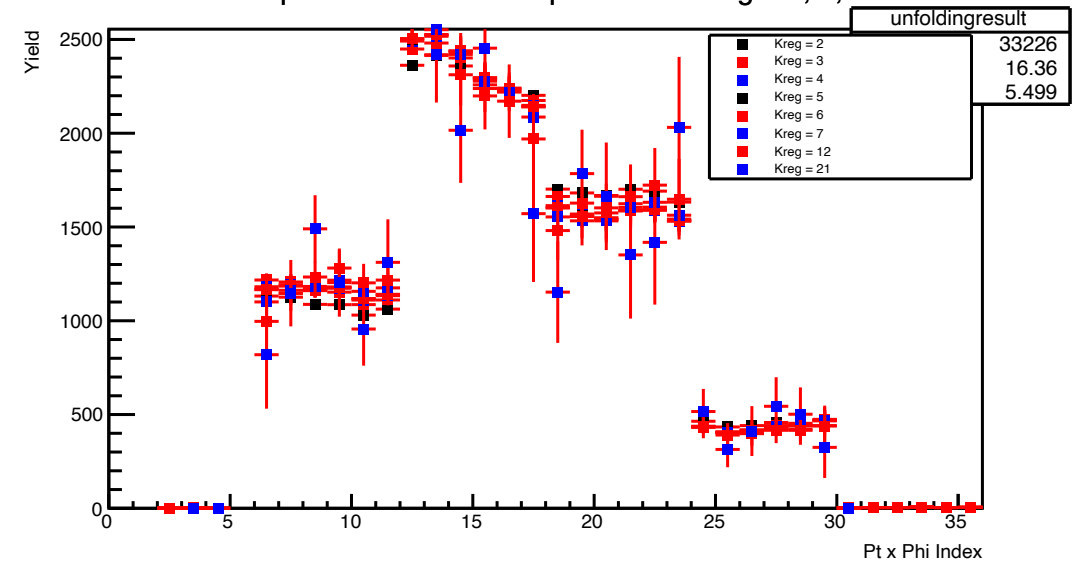
Comparison of unfolded spectra with kreg = 5, 6, 7



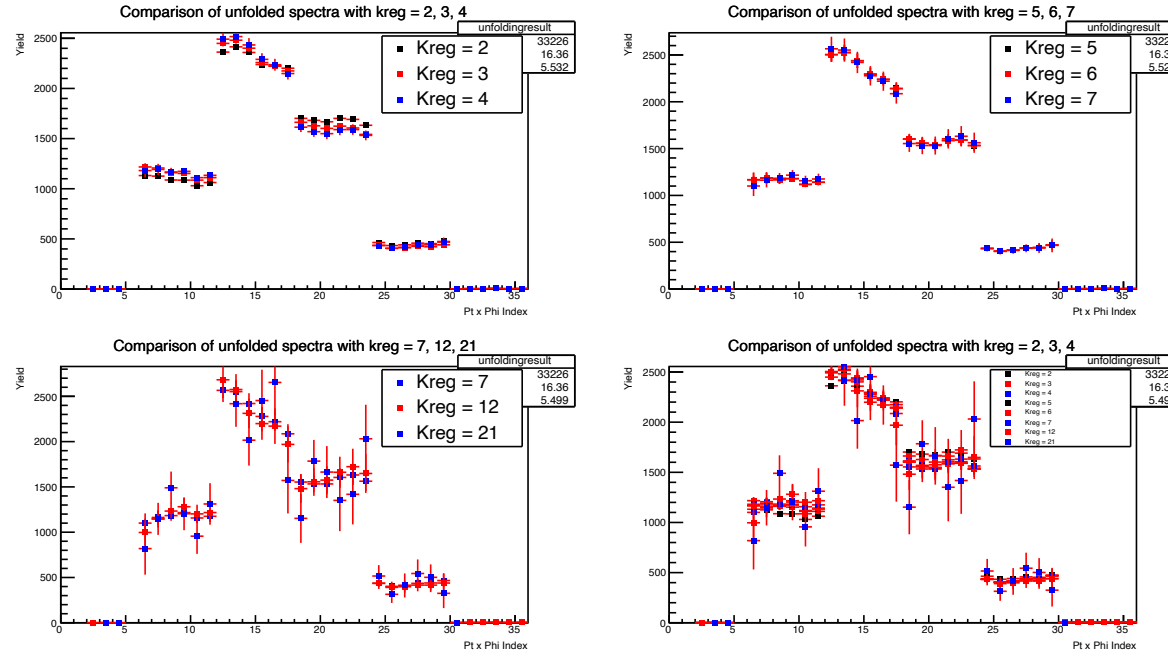
Comparison of unfolded spectra with kreg = 7, 12, 21



Comparison of unfolded spectra with kreg = 2, 3, 4



Two-dimensional pt unfolding closure test – All possible parameter comparison



Regularization parameter, Kreg	Minimum curvature value determines best optimum regularization parameter, the closer the value to zero the better
2	0.000002 (best value)
3	0.000010
4	0.000201
5	0.000307
6	0.000331
7	0.009416
12	0.009416
21	0.583000

Summary

- Calculated measured pt distributions using acceptance cut calculated from average weighted x and y position variables (x_{ev} and y_{ev}), having no spikes.
- The $x[ipart]$ and $y[ipart]$ position variables still show some spikes even after applying the the number of $smd > 1$ cut condition. Not used in this unfolding cross-check.
- Closure test seems to work well at small regularization parameter = 2 than at larger regularization parameter = 7 where it fails for the 1D case with increased statistical fluctuations.
- Similar trend for the 2D case. Lower values of regularization seem to agree better.
- Need to optimize unfolding code to work in PHENIX rcas computing machine. This closure test result is obtained using code compiled on local PC so far.

To do list (Schedule)

Period	Task
May 27 ~ May 30	<ul style="list-style-type: none">▪ Resolve problems in the unfolding that will arise.
June 1 ~ June 7	<ul style="list-style-type: none">▪ Unfolding and generation of asymmetries from unpolarized Monte Carlo samples.▪ Study of the asymmetry weights by trying various functional forms for the true p_T dependence of asymmetries.
June 8 ~ June 14	<ul style="list-style-type: none">▪ Optimization of weight to mimic the actual p_T dependence of pp data.