



Publishing Cross Sections at MINERvA



Noah Harvey Vaughan (*they/them*)

PhD Candidate, Oregon State University

NuXTract 2023

Wednesday October 6th, 2023

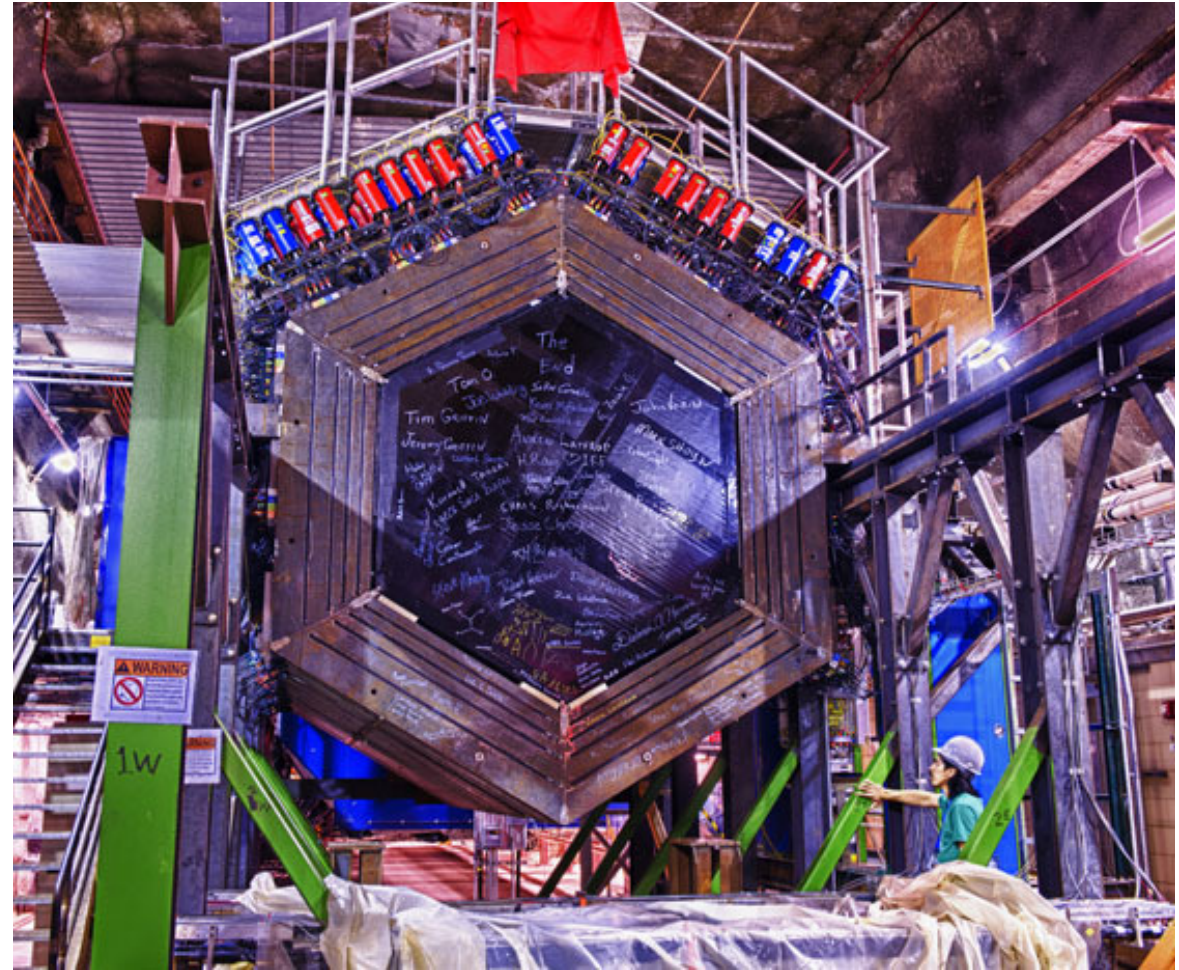


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Outline

MINERvA Cross Sections

- Overview of MINERvA
- MC tuning
- Background constraint
- Unfolding testing and process



MINERvA Experiment



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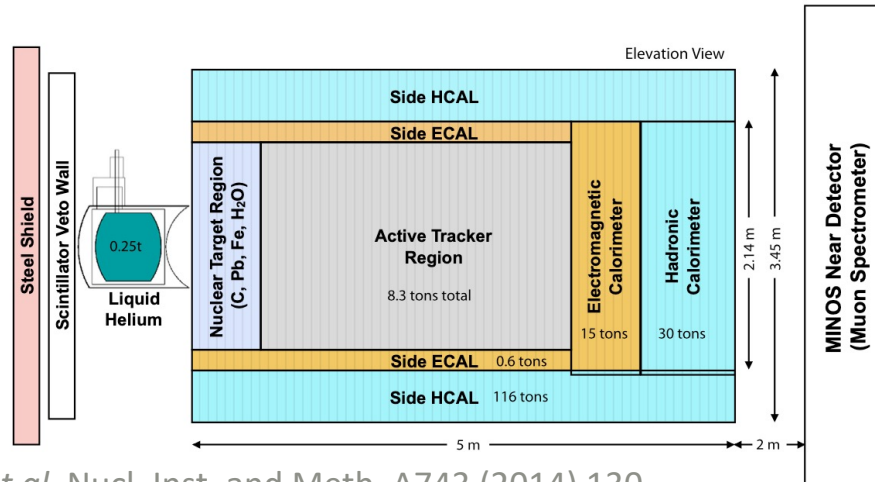
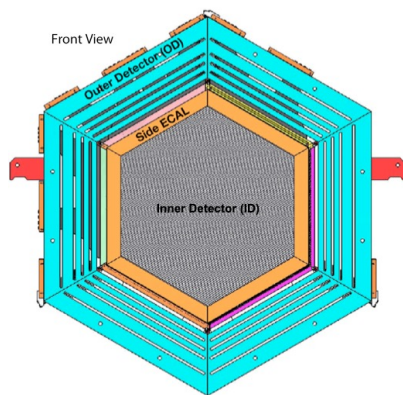
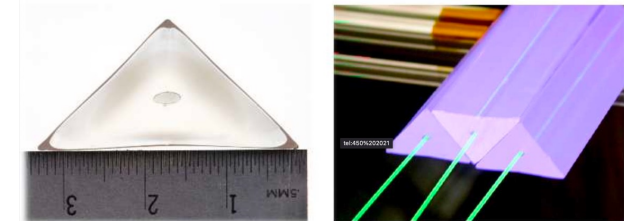
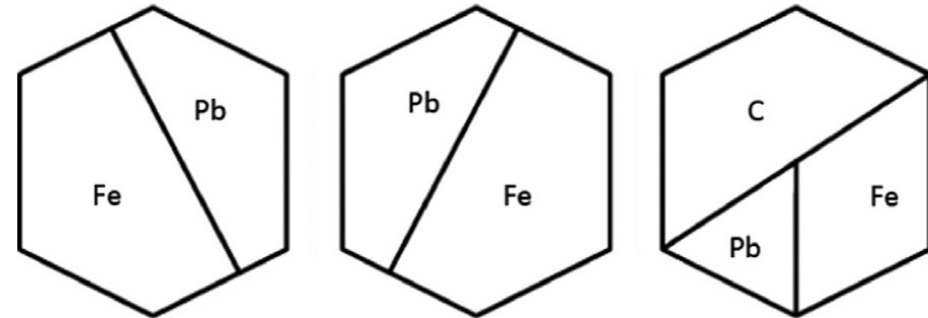
MINERvA Experiment

MINERvA
Experiment

MINERvA = **M**ain **I**njector
ExpeRiment on **v** (nu) **A** (atom)

- Dedicated x-section experiment at FNAL
- Data runs from 2009 – 2019:
 - NuMI LE POT: $4.0 \times 10^{20} \nu$, $1.7 \times 10^{20} \bar{\nu}$
 - NuMI ME POT: $\sim 3 \times \text{LE } \nu$, $\sim 7 \times \text{LE } \bar{\nu}$

Geometry of nuclear target planes

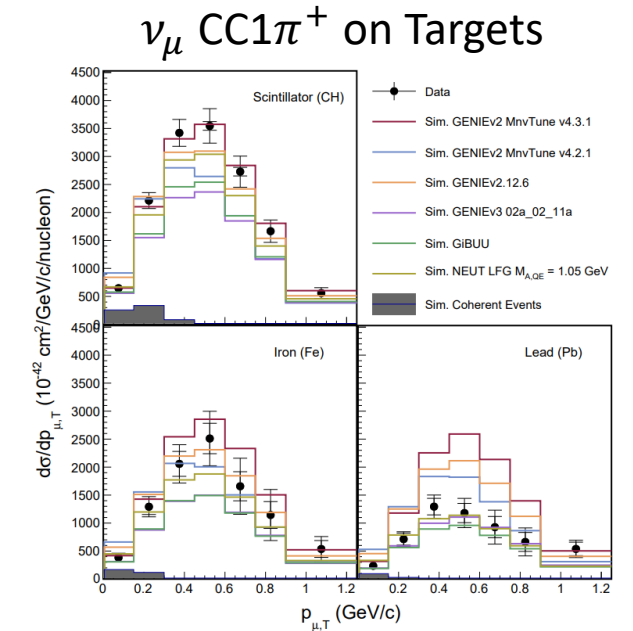
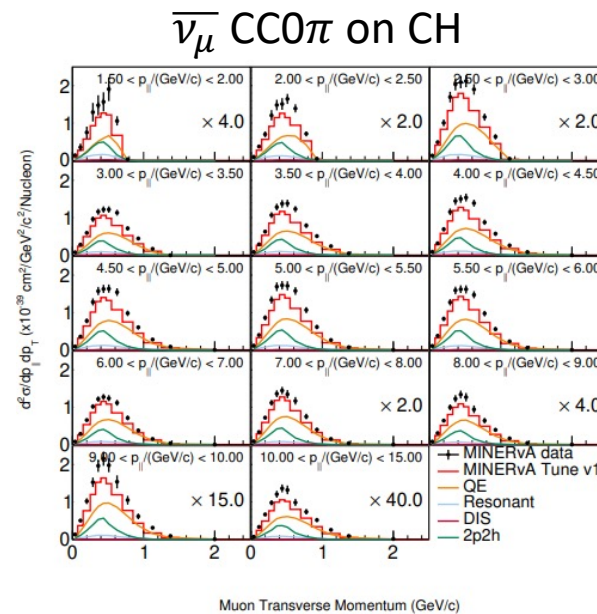
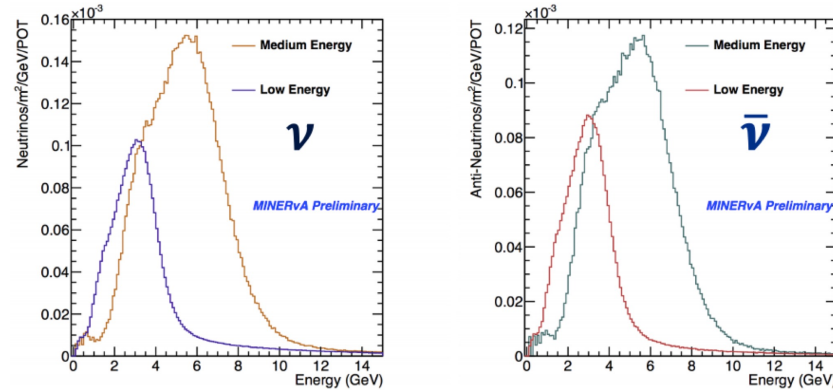


Aliaga, et al. Nucl. Inst. and Meth. A743 (2014) 130



Cross section publication history

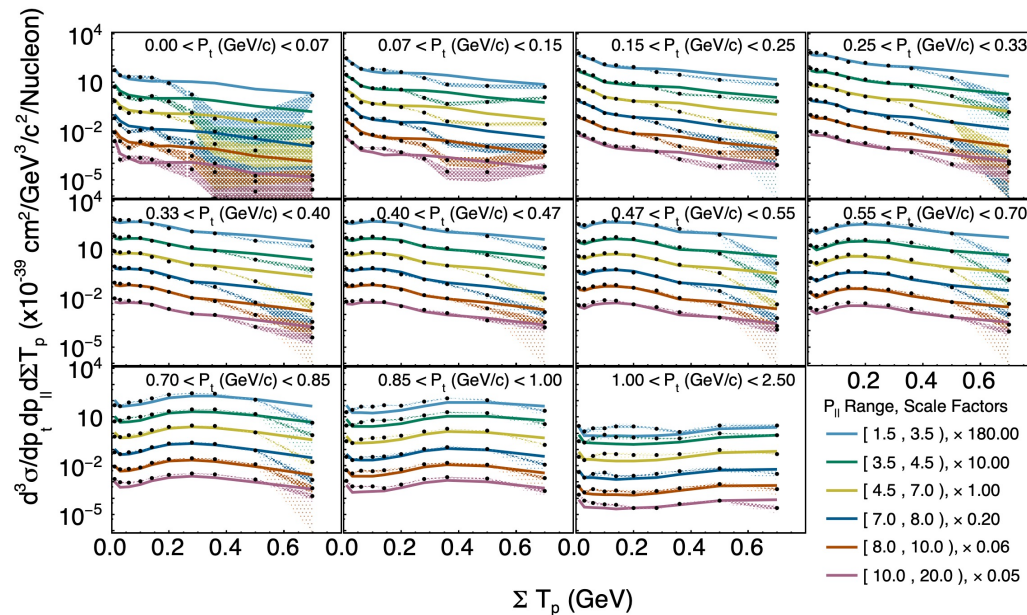
- LE: 32 published; ME: 12 published, more in progress
- Processes studied:
 - QElike, π production, 2p2h
 - DIS
 - Coherent
- Comparison of targets



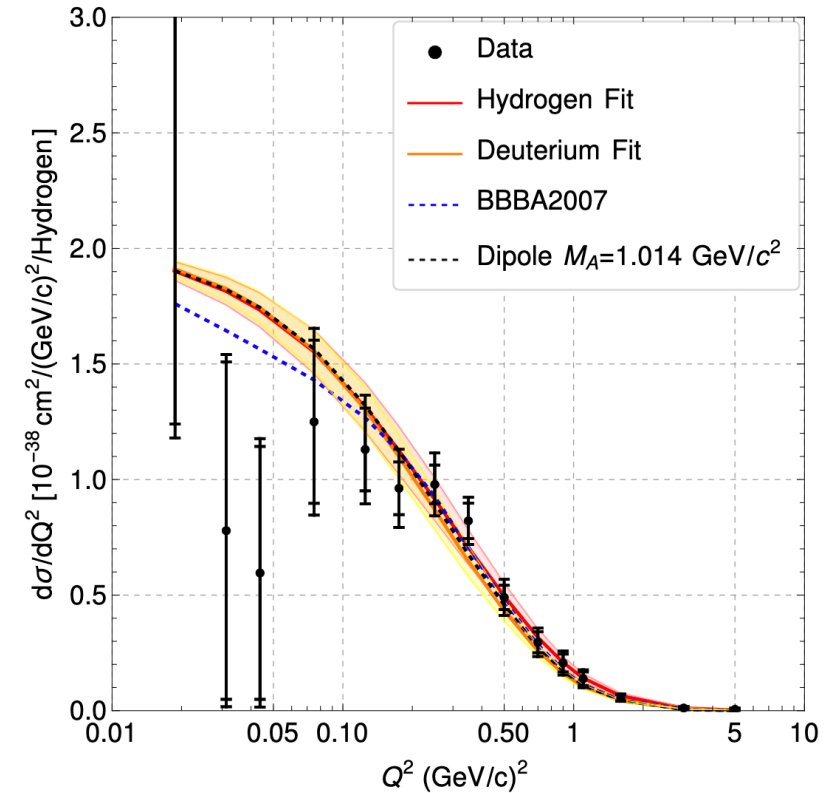
Cross section publication history

More difficult stuff too...

- 1.3 M events in first 3D ν_μ CCQElike
- Highly exclusive ($\sim 5k$ events) Hydrogen x-sec



ΣT_p (GeV)
D. Ruterbories, Phys.Rev.Lett. 129 (2022)



T. Cai, Nature 614, 48-53 (2023)



Extracting a Cross-section

Steps analyzers take for most cross-sections at MINERvA



Extraction process

Cross Section
Extraction

Somewhat simplistically, analyzers start by:

- Choosing a process(es) they want to study (inclusively or exclusively)
- Creating a truth level signal definition of this process
- Choosing reconstruction cuts to select events in the data, reconstructed MC
- Cuts and sig def chosen to maintain compatibility with preexisting measurements



Extraction process

Somewhat simplistically, analyzers start by:

- Choosing a process(es) they want to study (inclusively or exclusively)
- Creating a truth level signal definition of this process
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For variable x in truth bins i with reconstruction bins α :

$$\left(\frac{d\sigma}{dx}\right)_i = \frac{\sum_{\alpha} U_i^{\alpha} (N_{data,\alpha} - N_{data,\alpha}^{bkg})}{\epsilon_i(\Phi T)(\Delta x_i)}$$



Higher Dimensions

2D: For variables x, y , in truth bins i, j with reconstruction bins α, β :

$$\left(\frac{d^2\sigma}{dx dy} \right)_{ij} = \frac{\sum_{\alpha\beta} U_{ij}^{\alpha\beta} \left(N_{data, \alpha\beta} - N_{data, \alpha\beta}^{bkg} \right)}{\epsilon_{ij}(\Phi T)(\Delta x_i \Delta y_j)}$$

3D: For variables x, y, z in truth bins i, j, k with reconstruction bins α, β, γ :

$$\left(\frac{d^3\sigma}{dx dy dz} \right)_{ijk} = \frac{\sum_{\alpha\beta\gamma} U_{ijk}^{\alpha\beta\gamma} \left(N_{data, \alpha\beta\gamma} - N_{data, \alpha\beta\gamma}^{bkg} \right)}{\epsilon_{ijk}(\Phi T)(\Delta x_i \Delta y_j \Delta z_k)}$$



Ingredients

Cross Section Extraction

For variable x in truth bins i with reconstruction bins α :

$$\left(\frac{d\sigma}{dx}\right)_i = \frac{\sum_{\alpha} U_i^{\alpha} (N_{data,\alpha} - N_{data,\alpha}^{bkg})}{\epsilon_i(\Phi T)(\Delta x_i)}$$

Background Subtraction



Ingredients

Cross Section Extraction

For variable x in truth bins i with reconstruction bins α :

$$\left(\frac{d\sigma}{dx}\right)_i = \frac{\sum_{\alpha} U_i^{\alpha} (N_{data,\alpha} - N_{data,\alpha}^{bkg})}{\epsilon_i(\Phi T)(\Delta x_i)}$$

Background Subtraction

Unfolding



Ingredients

Cross Section Extraction

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Background Subtraction

Unfolding

Efficiency & Acceptance Correction



Ingredients

Cross Section Extraction

For variable x in truth bins i with reconstruction bins α :

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Flux & Target Normalization



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Cross Section Extraction

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Bin Width Normalization



Ingredients

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Background Subtraction

Unfolding

Efficiency & Acceptance Correction

Flux & Target Normalization

Bin Width Normalization



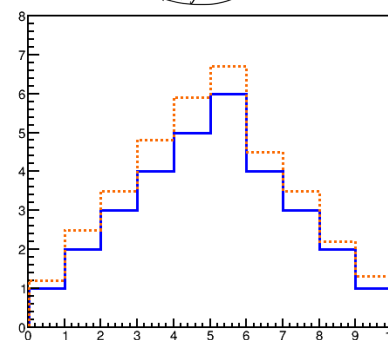
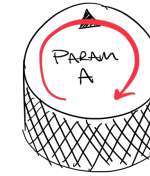
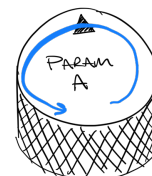
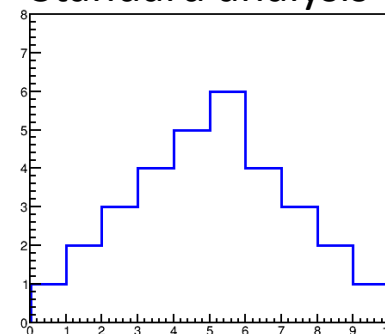
Note on MINERvA Systematics

Cross Section Extraction

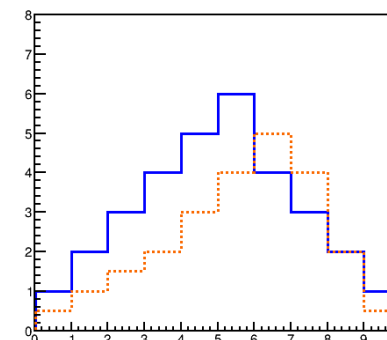
MINERvA handles systematics through MnvHND's, inherited THND

- Central value universe: CVUniverse, stored as ROOT histogram
- *Systematic universes* (error bands): shifts and migrations on CVUniverse
- Typically, a $\pm 1\sigma$ shift on some parameter
- More detail on data preservation talk

Standard analysis



Shift parameter one way



Shift parameter the other way



MINERvA Models and Tunes

Brief overview of empirical and physics tunes on MINERvA simulation



Making and using MnvTunes

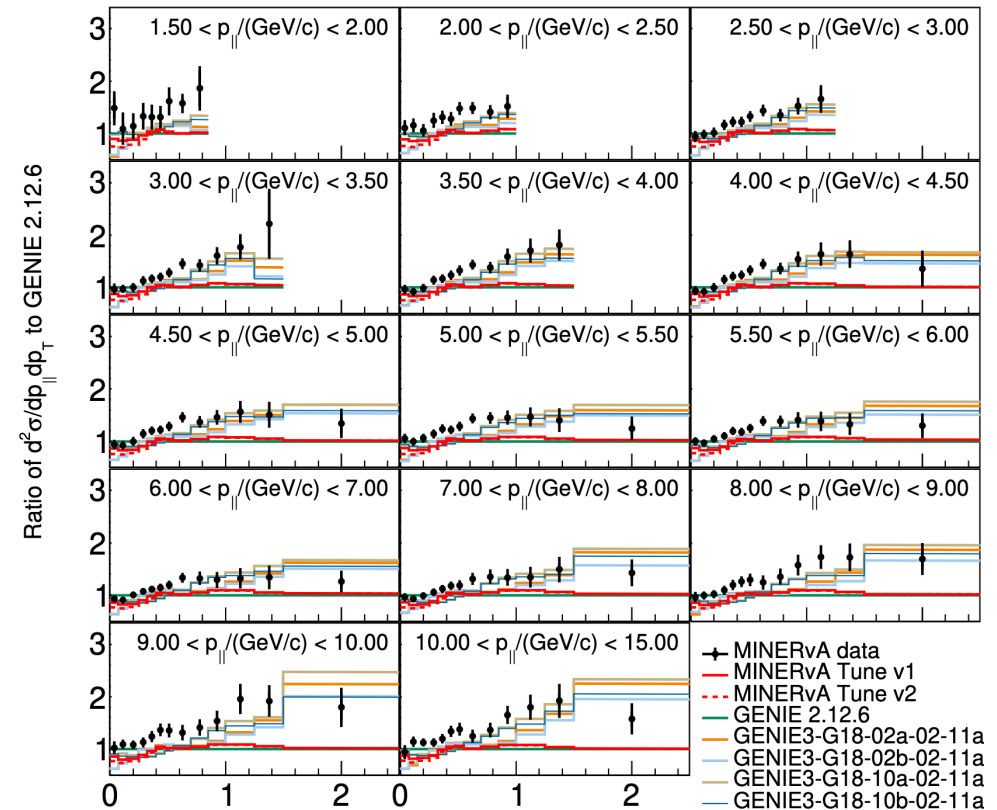
MnvTune

MINERvA creates tunes on simulation from measurements

- Base simulation GENIE 2.12.6
- Theory/physics based if not included in generator
- Based off MINERvA measurements and other experiments

Using MnvTunes

- Applied as weights, event-by-event
- Analyzers choose appropriate tune for unfolding, analysis



A. Bashyal, Phys.Rev.D 108 (2023)



Constraining the Background

How analyzers constrain the background using the simulated sample

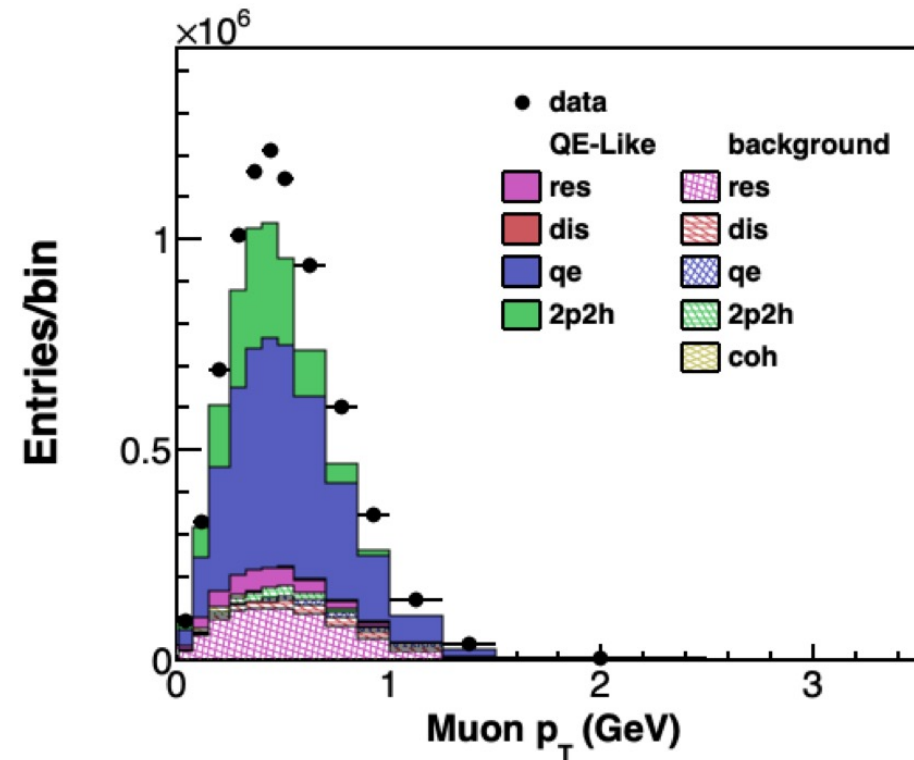


General idea

Background Constraint

Selected data contaminated with background events

- Can use simulation (with *truth* info) to inform removal
- Directly subtracting MC background introduces model dependence
- Use data driven methods to constrain the background instead



A. Bashyal, Fermilab JETP, 10 March 2023

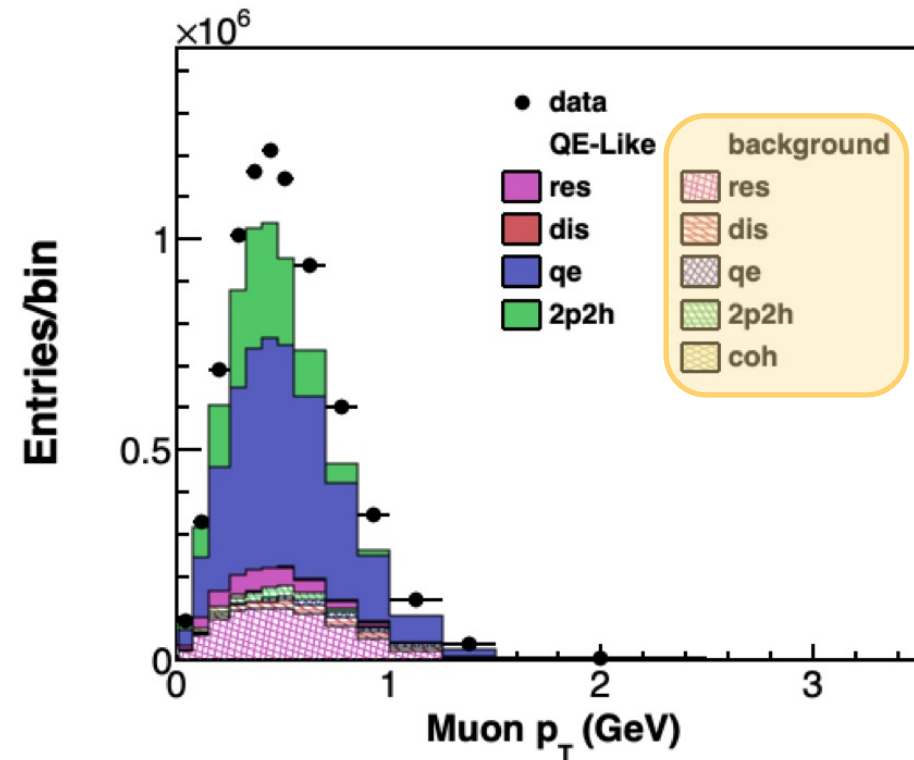


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A. Bashyal, Fermilab JETP, 10 March 2023



Sidebands

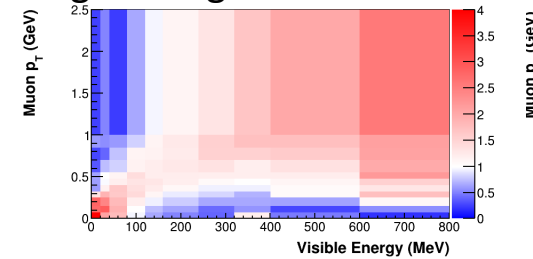
Background Constraint

General idea:

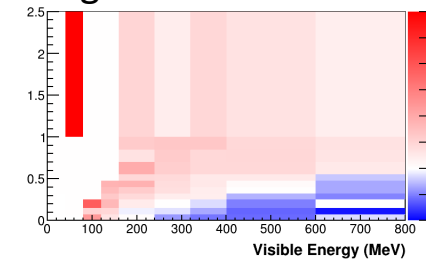
1. Choose a signal sample, sidebands that select for main backgrounds
2. Fit background distributions to data
3. Use fits to tune predicted backgrounds in signal sample

Most analyzers use this method, but fitting & tuning methods vary

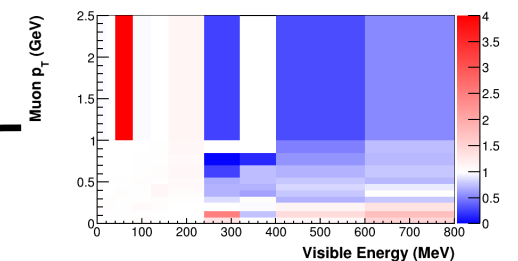
Single charged π Scale Factors



Single π^0 Scale Factors



Multi- π Scale Factors



D. Ruterbories, Phys.Rev.Lett. 129 (2022)



Sidebands

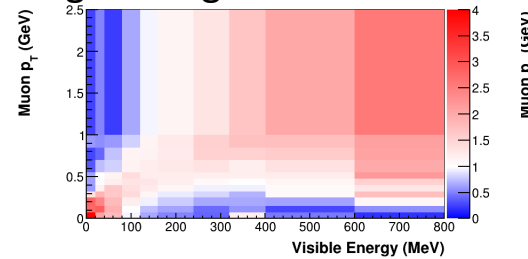
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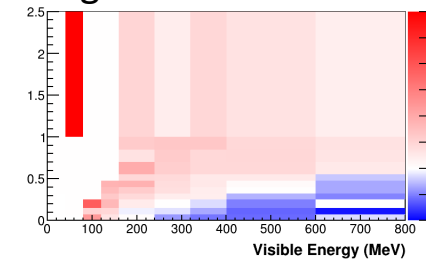
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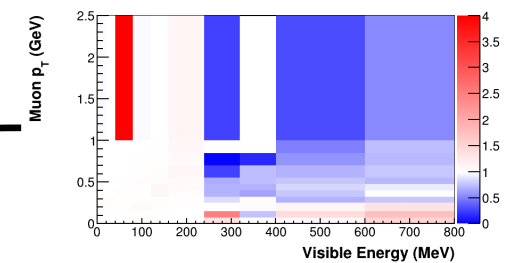
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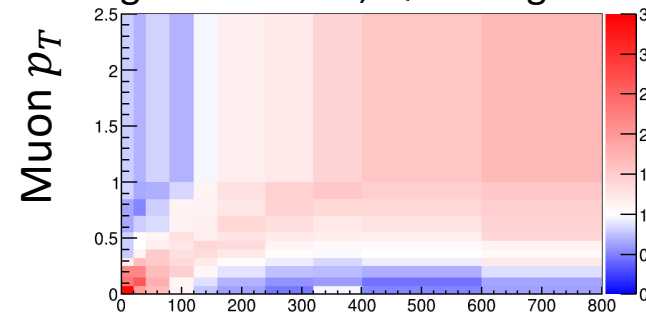
Single π^0 Scale Factors



Multi- π Scale Factors



Background Scales, QEl-like Signal Region



D. Ruterbories, Phys.Rev.Lett. 129 (2022)



Unfolding

How analyzers do unfolding in MINERvA using the D'Agostini method



Smearing in Reconstruction

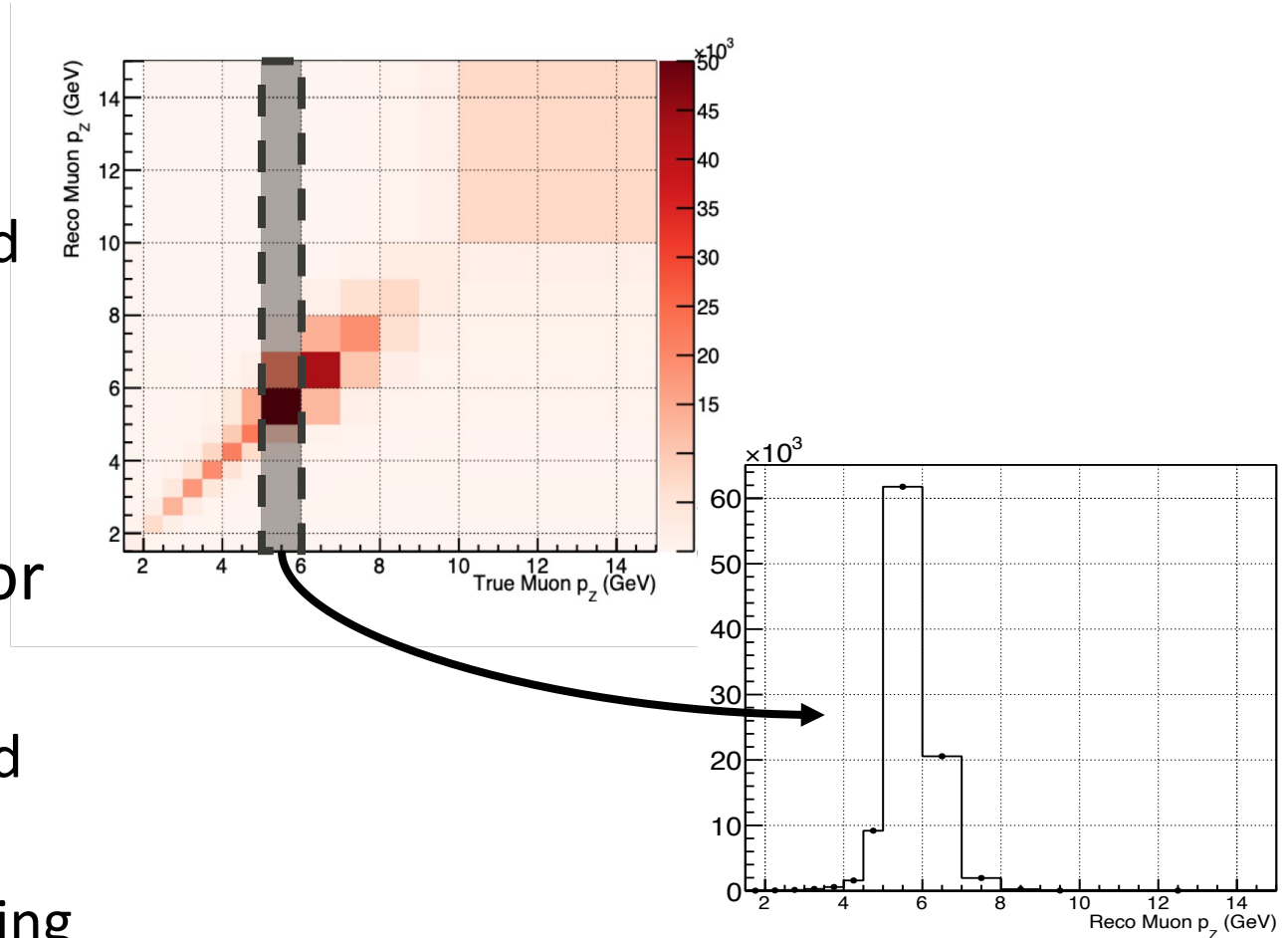
Unfolding

Data is in reconstructed bins

- “Smearing” of events \Rightarrow measured different than *true* value
- Detector resolution and reco algorithms sources of smearing

Unsmear reconstructed data for detector-independent result

- Use simulation, has both *truth* and *reco* information
- Migration matrix describes smearing from *truth* \rightarrow *reconstruction*



A. Bashyal, Fermilab JETP, 10 March 2023



D'Agostini Unfolding

Unfolding

A method of iterative “Bayesian” unfolding, outlined [here](#) and [here](#)

- Distributions unfolded binwise
- Regularized by number of iterations
- Multidimensional unfolding
- Implemented in RooUnfold

$$\lambda_j^{(k+1)} = \frac{\lambda_j^{(k)}}{\sum_{i=1}^N U_{ij}} \sum_{i=1}^N \frac{U_{ij} y_i}{\sum_{l=1}^p U_{il} \lambda_l^{(k)}}$$

- k is number of iterations
- $\lambda^{(0)}$ is initial truth distribution
- U is response
- y is smeared data



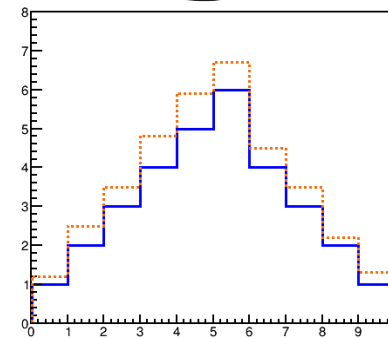
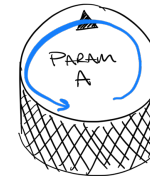
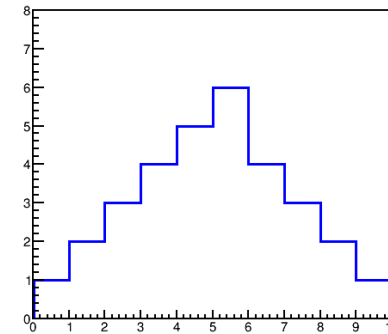
D'Agostini Unfolding

Unfolding

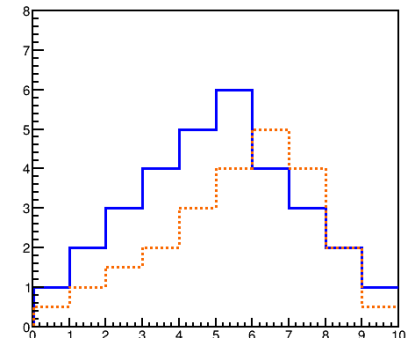
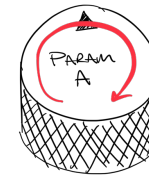
Implementation in MINERvA:

- RooUnfold based, extended to UnfoldUtils to handle *systematic universes*
- Square migration matrices typical, but non-square possible and explored
- Unfolds each *systematic universe* individually
- Unfolding uncertainties calculated from *central value universe*

Central Value



Param A universe 1



Param A universe 2



D'Agostini Unfolding

Unfolding

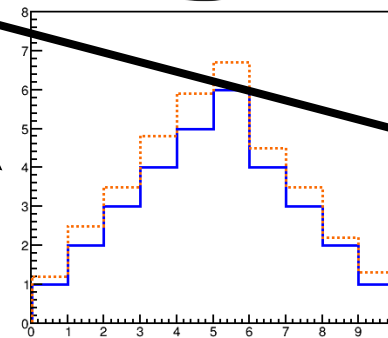
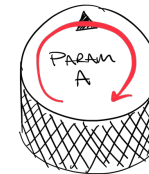
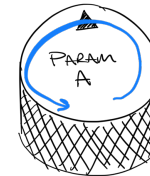
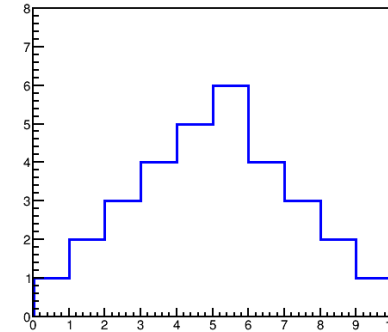
Implementation in MINERvA:

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- Squared non-linearities
- Unfolds each *systematic universe* individually
- Unfolding uncertainties calculated from *central value universe*

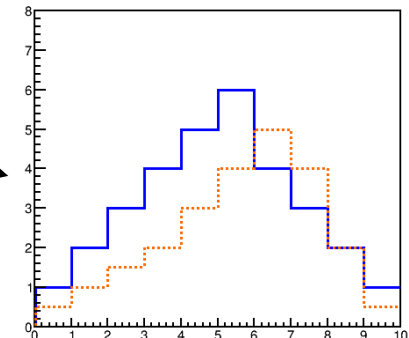
Unfold each of these

but

Central Value



Param A universe 1



Param A universe 2



Unfolding Studies

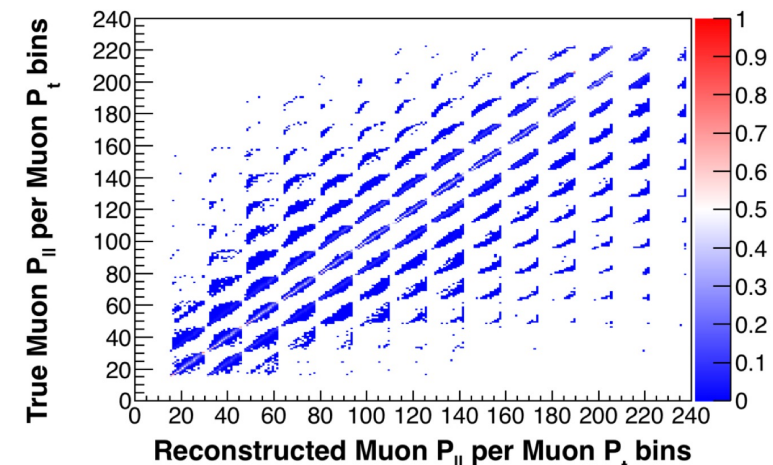
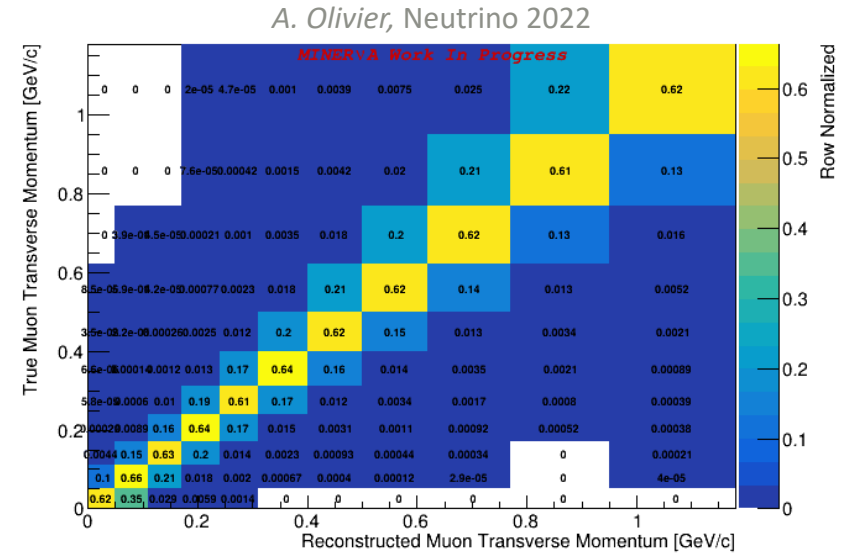
Unfolding

Each analyzer does unfolding studies

- Check behavior of migration matrix
- Ensure full consideration of unfolding uncertainties, closure tests
- Optimize number of iterations

What can be changed to fix issues?

- Adjust binning to reduce correlation, off-diagonal migration matrix
- Introduce new systematics to parameterize some cause of smearing
- Try new physics models to better match data

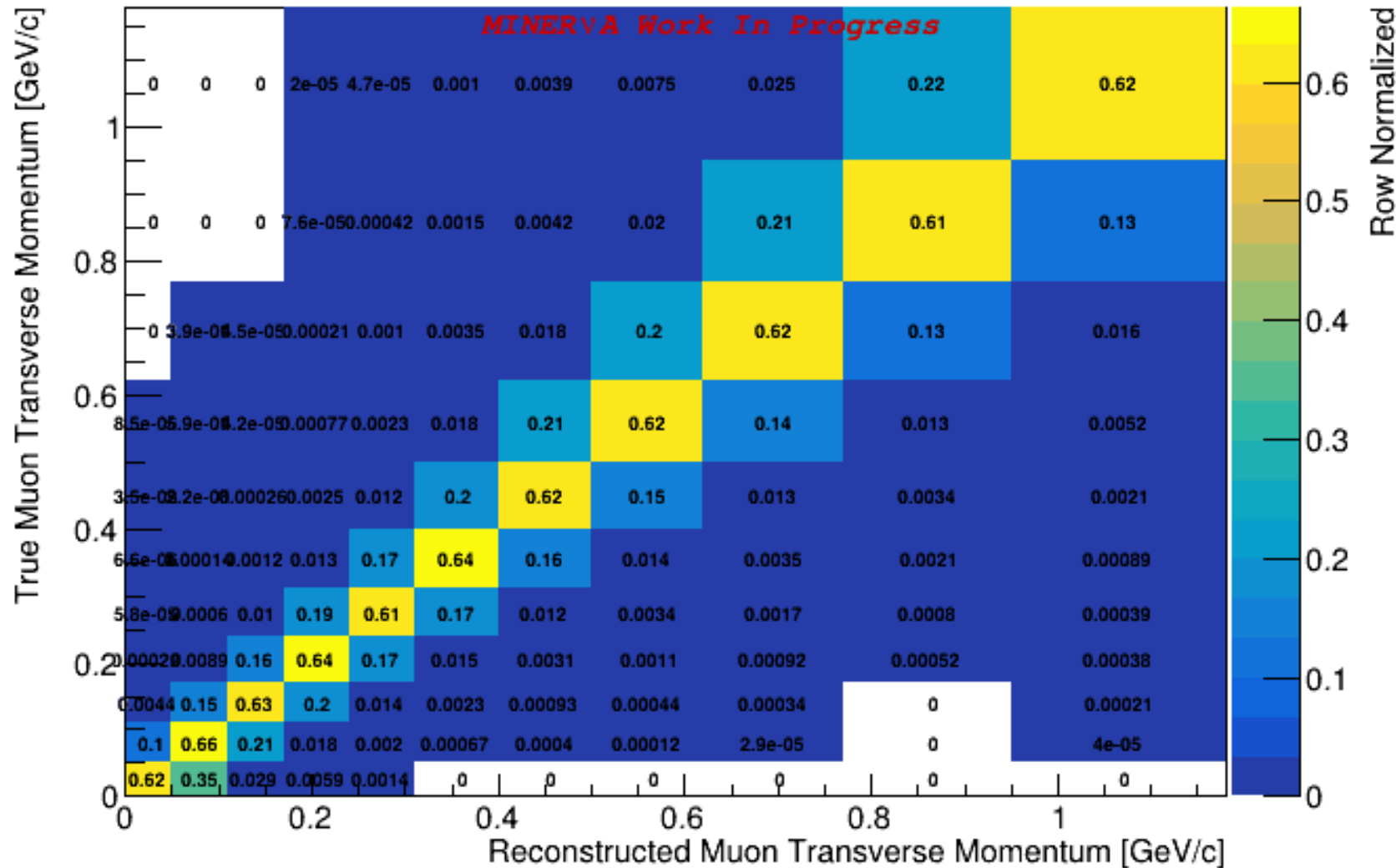


A. Bashyal, Fermilab JETP, 10 March 2023



Migration Matrix 1D

Unfolding

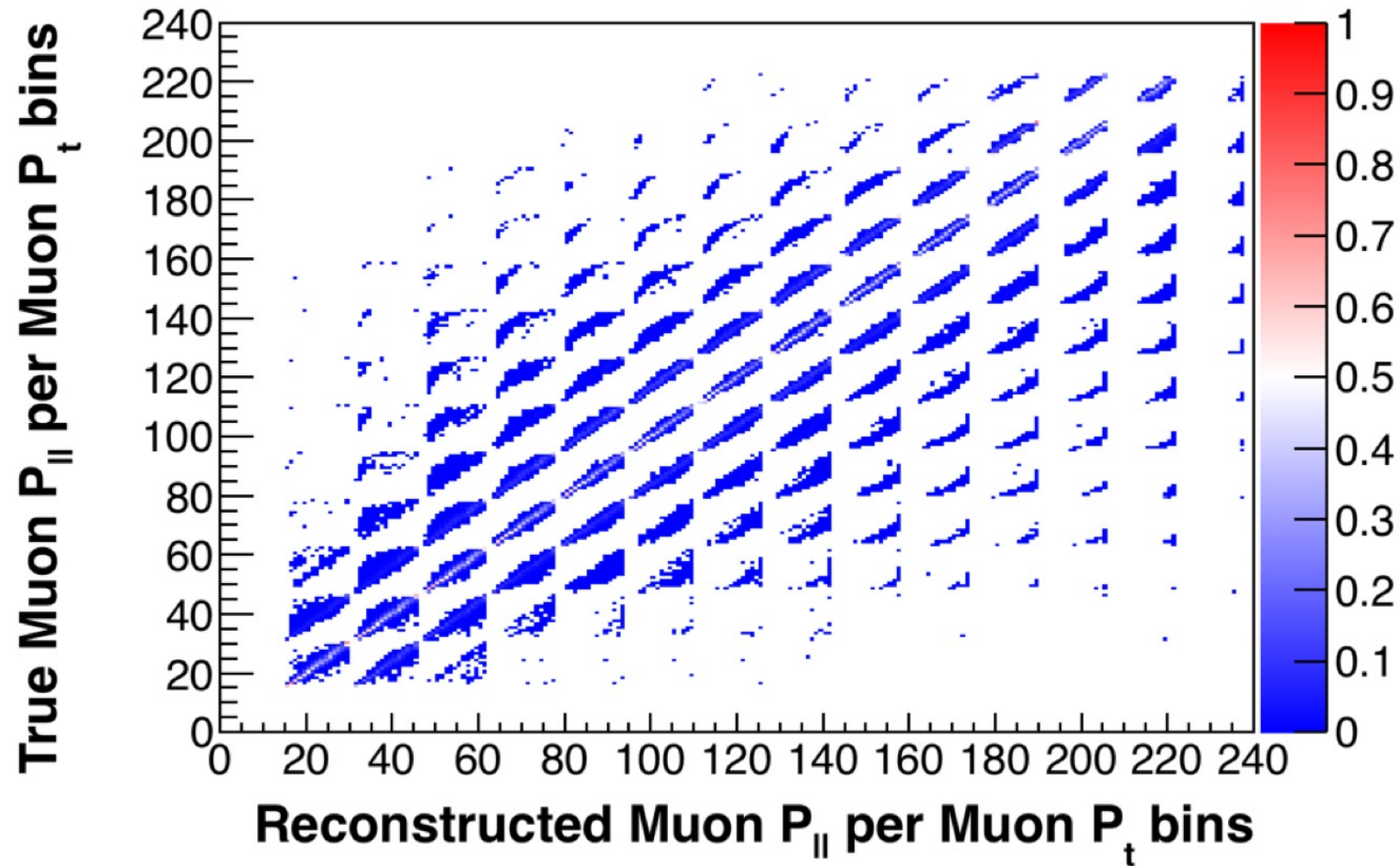


A. Olivier, Neutrino 2022



Migration Matrix 2D

Unfolding



TransWarp for unfolding studies

Unfolding

Analyzers use “TransWarp” macro to test unfolding:

- 5 histograms as inputs:
 - *Migration matrix*
 - *Reco & True MC*
 - *Reco & True fake data as specified number of statistical universes of random Poisson throws on MC*



Using TransWarp

Unfolding

Conditions when filling:

- All hist data exposure equivalent, typically POT scaled
- Sometimes single model for all hist
- Sometimes different models for *fake data* and *migration matrix*

Often comparing an unfolded distribution to a true distribution

$$\chi^2 = \sum_{\alpha\beta} (\hat{\lambda}^{(k)} - \lambda)_\beta V_{\beta\alpha}^{-1} (\hat{\lambda}^{(k)} - \lambda)_\alpha$$

- λ is true kinematic
- $\hat{\lambda}^{(k)}$ is unfolded kinematic after k iterations
- V is unfolding covariance matrix

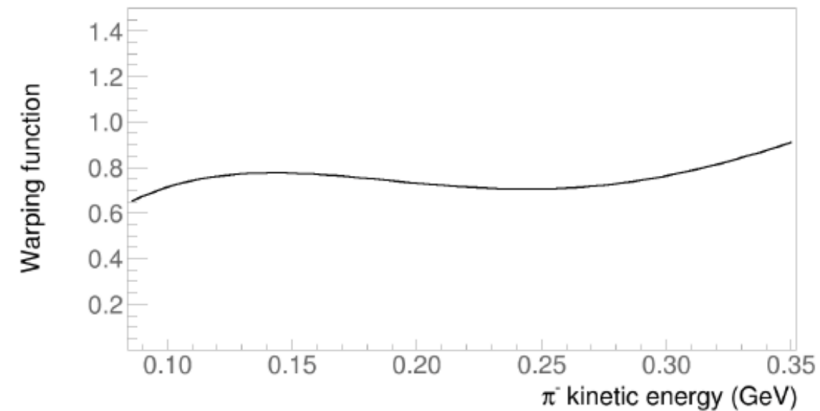
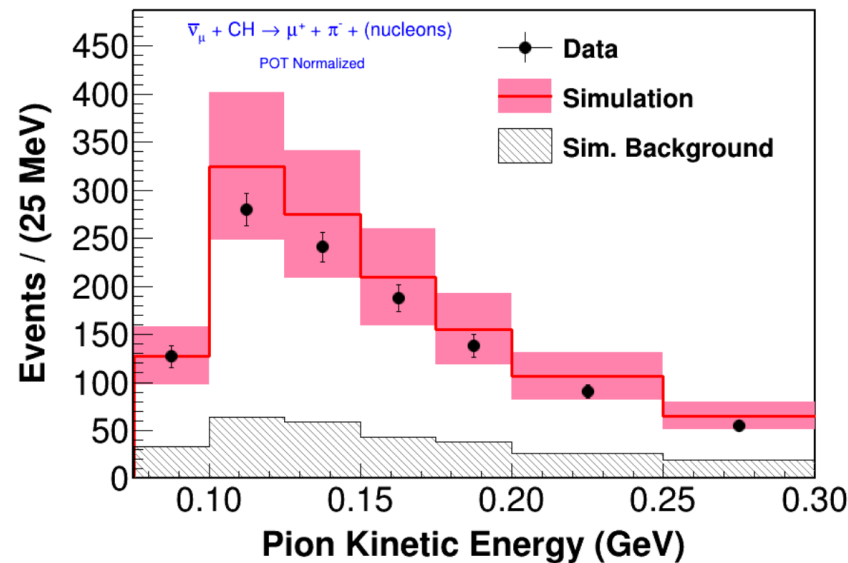


“Warping” to Determine N_{iter}

Unfolding

1. Options to fill *fake data*:

- Different physics model than *migration matrix* (e.g., *MnvTune v1* vs *v2*)
- Same model, weighted by some function from a data/MC ratio fit (“warp”)
- Same model, up- or down-scaling (“CV scaling”)



P. Rodrigues, PhySTAT, 24 Jan 2019

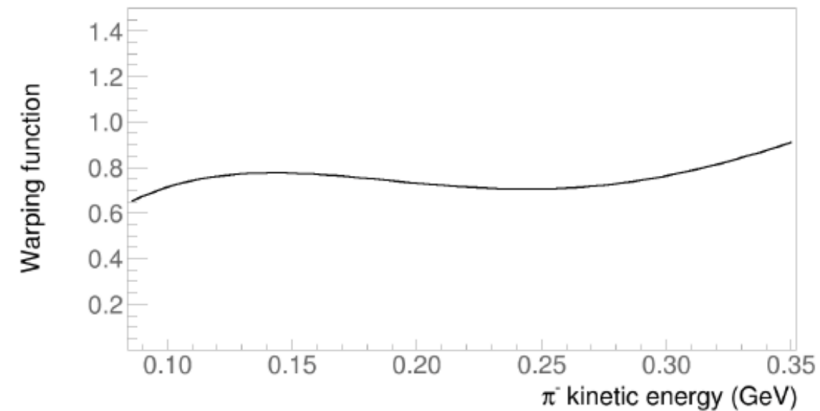
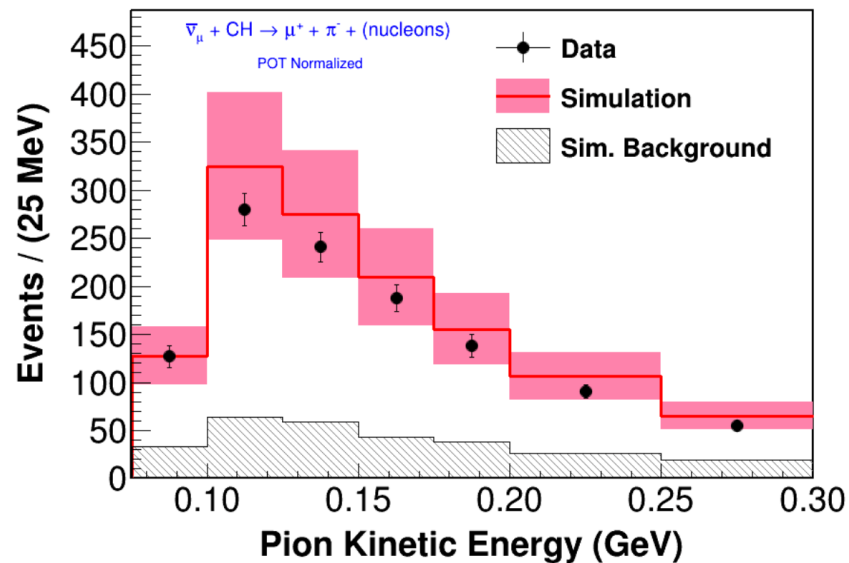


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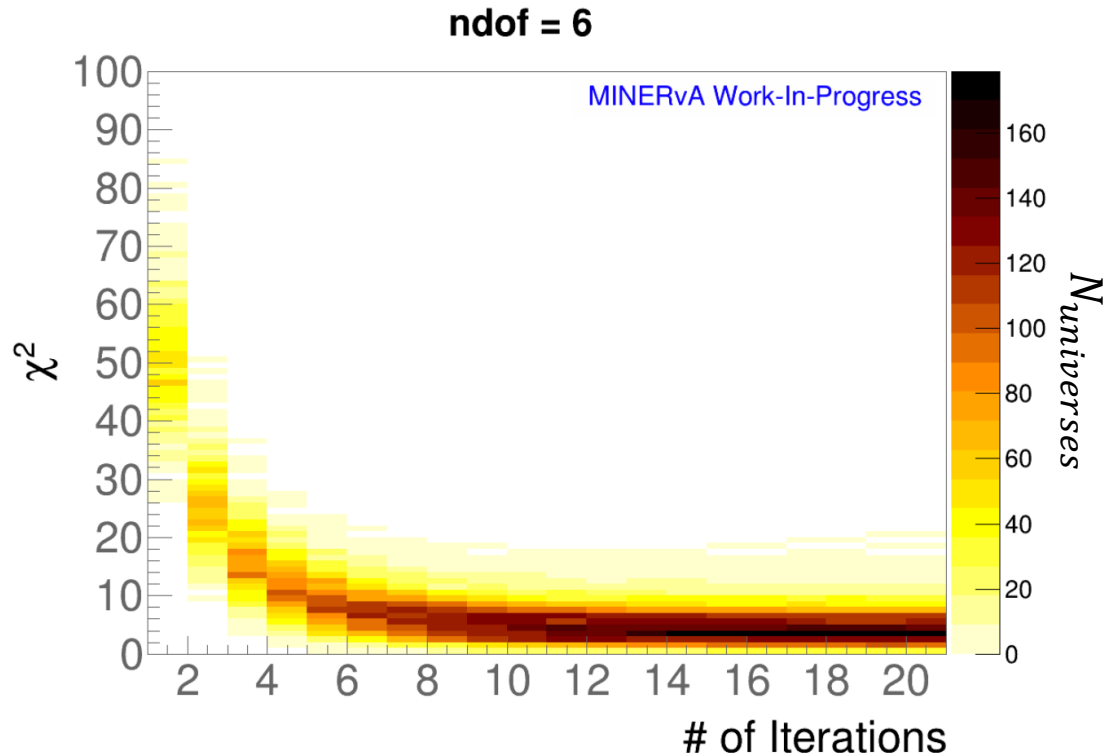


“Warping” to Determine N_{iter}

Unfolding

Continued...

2. Check χ^2 of *unfolded fake data* compared to *true fake data* vs. N_{iter}
 - All *statistical universes*, median, average
 - See minimum N_{iter} where χ^2 is minimized and stable



P. Rodrigues, PhySTAT 2019



Closing



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MINERvA Cross sections

Closing

MINERvA uses its dedicated design to extract many cross sections

- MINERvA produces results that help improve generators for the next generation of neutrino physics
 - *MnvTunes* inform how generators can improve to better match observation
- Analyzers expected to use methods that are well tested
 - Signal definition set as standards
 - Flexibility in constraining the background
 - Robust testing and implementation of D'Agostini unfolding



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Acknowledgements



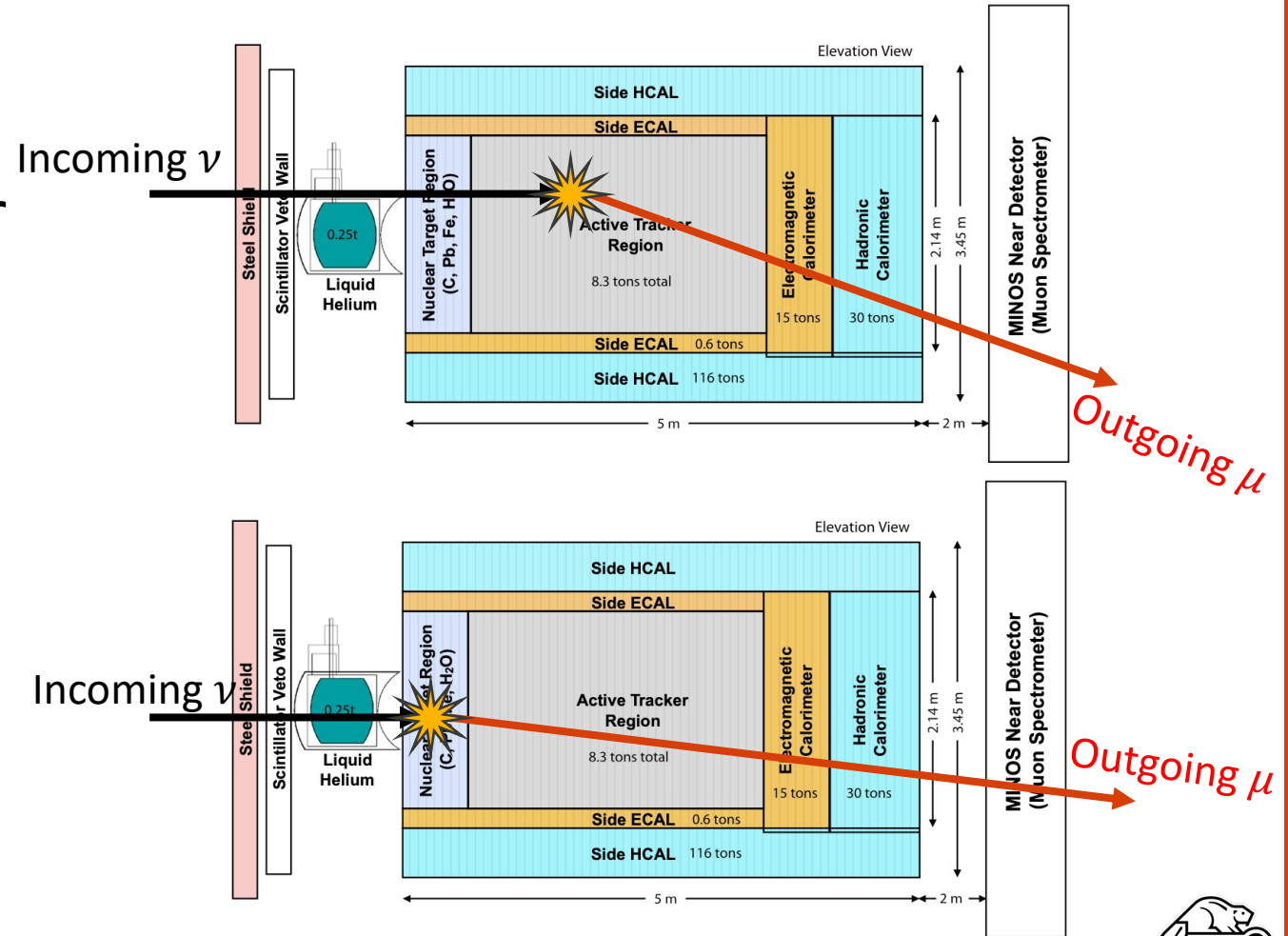
U.S. DEPARTMENT OF
ENERGY



Common reconstruction cuts

Backup: Cross Section Extraction

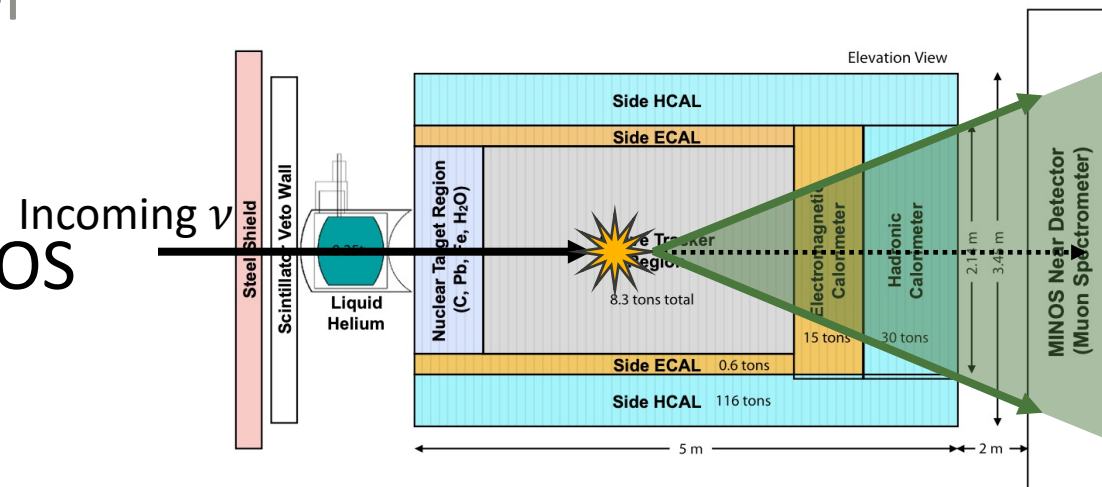
- Event vertex location, whether tracker or targets analysis



Common reconstruction cuts

Backup: Cross
Section Extraction

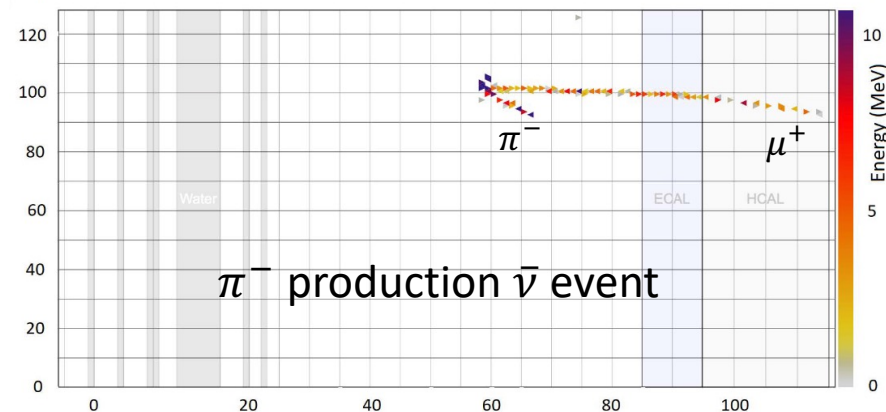
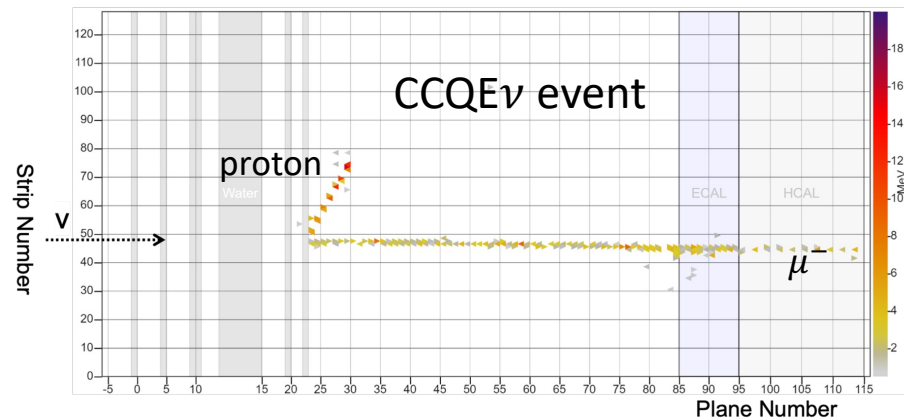
- Event vertex location, whether tracker or targets analysis
- Cuts on outgoing μ angle to ensure reconstruction in MINOS (momentum & helicity)



Common reconstruction cuts

Backup: Cross
Section Extraction

- Event vertex location, whether tracker or targets analysis
- Cuts on outgoing μ angle to ensure reconstruction in MINOS (momentum & helicity)
- Final state particles/event topologies



Summary of MnvTune vX.Y.Z

Backup:
MnvTune

X	Description	Z	Description
1	Original tune: Valencia RPA on QE (RFG), reduce non-RES π , low-recoil fit from LE to Valencia 2p2h	1	π and proton elastic FSI bug fix
2	Same as 1, w/ Stowell low- Q_{QE}^2 π suppression		
3	Same as 1, w/ SuSA 2p2h, enhanced Bodek-Ritchie tail in Valencia QE, 25 MeV removal on E_{avail} in π events w/ FS protons		
4	Same as 1, w/ π bubble chamber fit, CCNormRes scaled 1.15, MaRES set to 0.9, full MaRES and CCNormRes correlations		
Y	Description		
1	Normalization on coherent π production based on E_π		
2	Normalization on coherent π production based on E_π and θ_π		
3	Additional Low- Q_{QE}^2 π suppression, normalization on coherent π production based on E_π		
4	Replace dipole form of axial formfactor of QE with z-expansion from Meyer et al.		
5	Replace QE RFG nuclear model with NuWro SF		

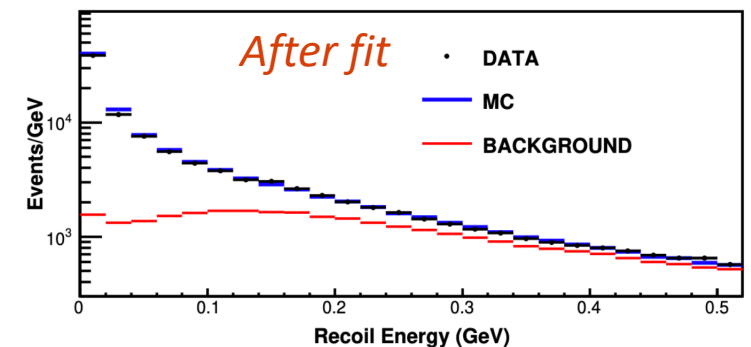
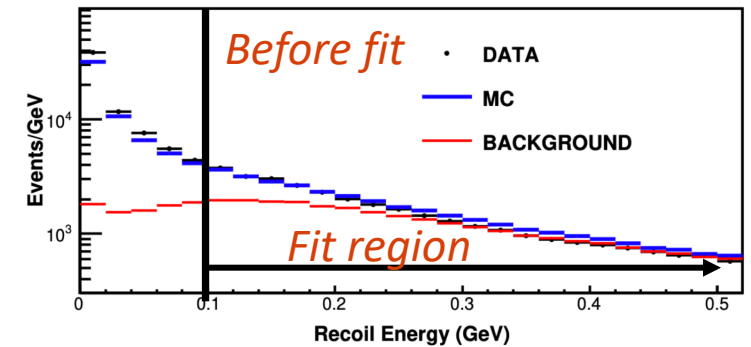
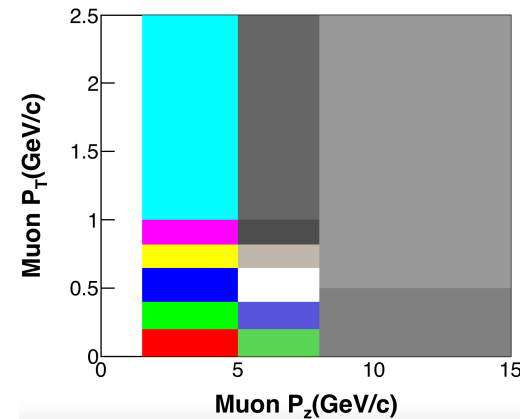
Tunes with a "0" or missing number indicate no tune from that list:
e.g., *MnvTune v1*, *MnvTune v1.0.1*



Other methods

Published 2D CCQE-like $\bar{\nu}_\mu$:

- Fit modified signal sample
- Treat background holistically (“QElike not”)
- LE: Fit full *recoil* spectrum
- ME: Fit only in background rich, high *recoil* (>100 MeV) region



A. Bashyal, Fermilab JETP, 10 March 2023



Closure tests

Backup:
Unfolding

1. Fill *fake data & migration matrix*, using same model
2. Compare *unfolded fake data to true fake data*,
 - Ratio vs. N_{iter} for un-thrown *statistical universe*, should be 1
 - χ^2 vs. N_{iter} of all *statistical universes* & their average, should be stable



Additional Stat Uncertainty

Backup:
Unfolding

Stat uncertainty for $N_{iter} > 1$ missing in some implementations

- Greatly underpredicts uncertainty without this
- Enhancement applied as scale, studies must be done to find scale factor
- Scale factor is typically similar between similar analyses

$$\frac{\partial \hat{n}(C_i)}{\partial n(E_j)} = M_{ij} + \sum_{k=1}^{n_E} M_{ik} n(E_k) \left(\frac{1}{n_0(C_i)} \frac{\partial n_0(C_i)}{\partial n(E_j)} - \sum_{l=1}^{n_C} \frac{\epsilon_l}{n_0(C_l)} \frac{\partial n_0(C_l)}{\partial n(E_j)} M_{lk} \right)$$

[T. Adye, arXiv:1105.1160 \[physics.data-an\]](https://arxiv.org/abs/1105.1160)



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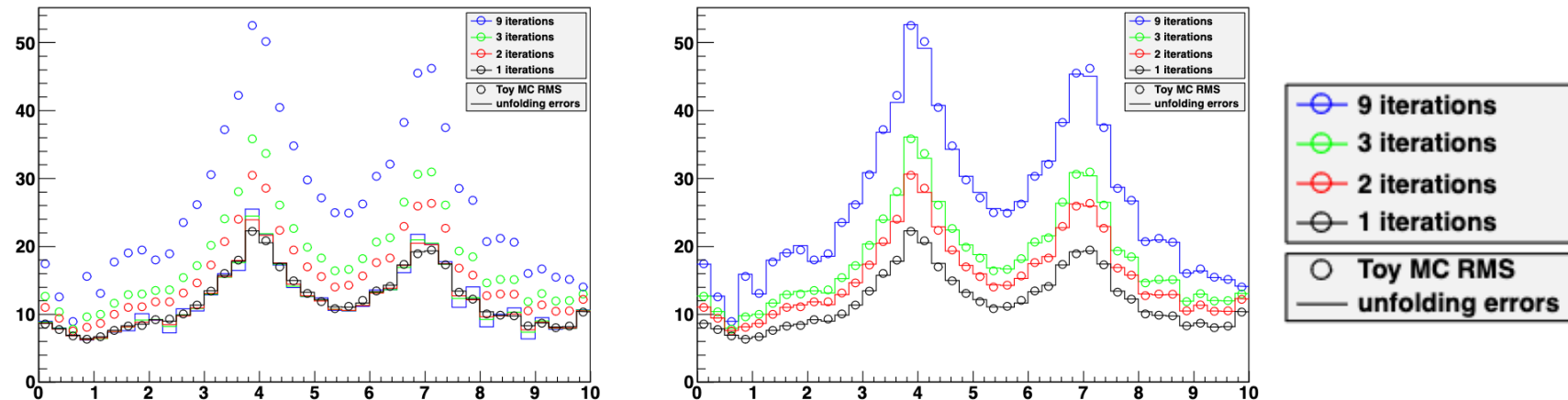


Fig. 5: Bayesian unfolding errors (lines) compared to toy MC RMS (points) for 1, 2, 3, and 9 iterations on the Fig. 2 test. The left-hand plot shows the errors using D’Agostini’s original method, ignoring any dependence on previous iterations (only the M_{ij} term in Eq. (3)). The right-hand plot shows the full error propagation.

[T. Auye, arXiv:1105.1160 \[physics.data-an\]](https://arxiv.org/abs/1105.1160)



Finding Stat Uncertainty Scale

Backup:
Unfolding

Analyzers can use the TransWarp macro here too:

1. Fill *fake data* and *migration matrix* using a single model
2. Check average χ^2 vs. N_{iter} for different *MC sample sizes*
 - Typically, change scale in integer steps 1 - 10, inc. the normal data exposure POT scale
 - Check how far χ^2 lines for each MC scale gets to $\chi^2 / ndf = 1$
3. Determine and save *uncertainty scale* to bring average $\chi^2 = ndf$
4. Scale unfolding covariance & error using the *uncertainty scale*, and run closure test
 - Ratio of *unfolded fake data* to *true fake data* should be unchanged
 - χ^2 vs. N_{iter} of all *statistical universes* will shift down slightly, remain stable



Other things to look for

Backup:
Unfolding

Other things to check to find issues (e.g., overly aggressive fake data)

- Migration matrices for *fake data*, the CV, ratios between migration matrices
- Warping weight vs. *true & reco* distributions
- *True fake data*, unfolded fake data *statistical universes*, average *unfolded fake data*
- Ratio of average *unfolded fake data* to *true fake data*



Upcoming results...

Closing

Quasielastic

- ν 3D transverse kinematic imbalance
- $\bar{\nu}$ 3D simultaneous leptonic & hadronic measurement
- $\nu/\bar{\nu}$ ratios
- Neutron tagging

Low hadronic recoil

- Interactions with 2+ neutrons
- ν_e & $\bar{\nu}_e$
- Charged π 's

Inelastic

- Several DIS results
- SIS results
- Interactions on Helium

