Comparing Generator Predictions to Data

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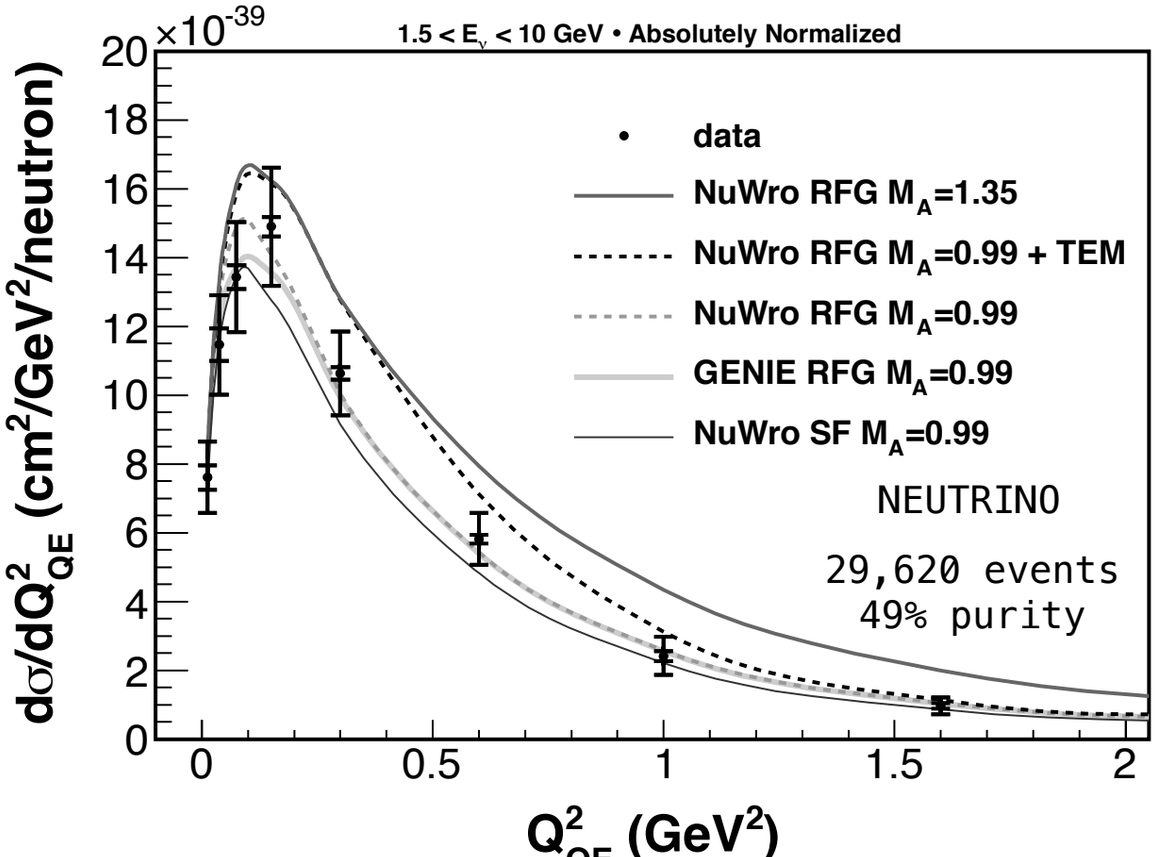
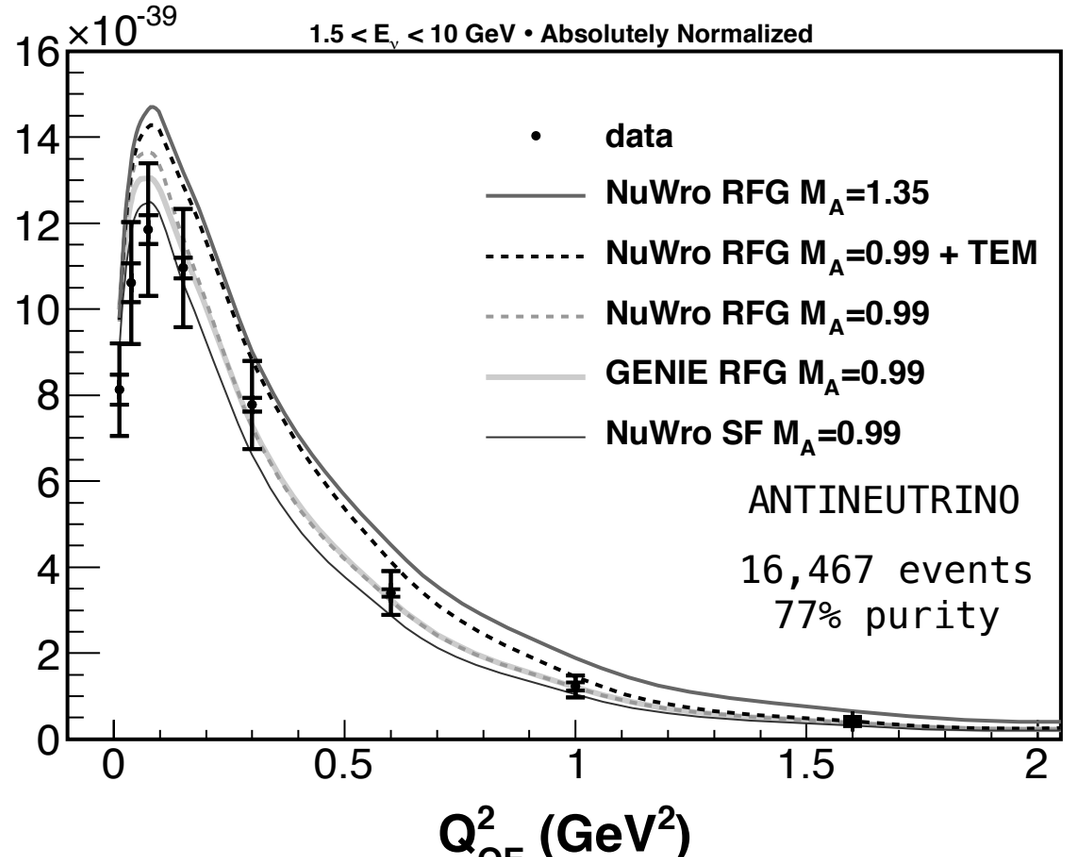
Fermilab


×10^-39
1.5 < E_ν < 10 GeV • Absolutely Normalized
data
NuWro RFG M_A=1.35
NuWro RFG M_A=0.99 + TEM
NuWro RFG M_A=0.99
GENIE RFG M_A=0.99
NuWro SF M_A=0.99
NEUTRINO
29,620 events
49% purity
dσ/dQ²_QE (cm²/GeV²/neutron)
Q²_QE (GeV²)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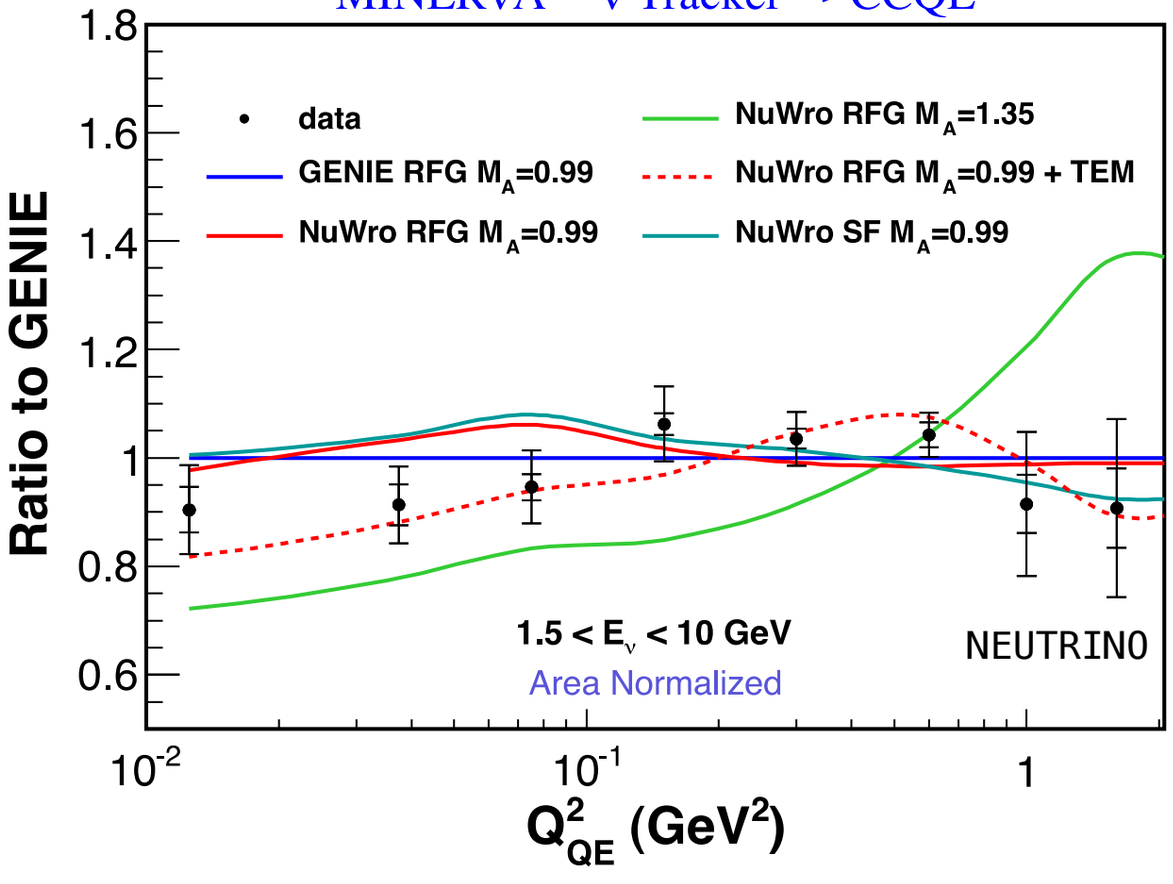
NuWro RFG M_A=0.99
GENIE RFG M_A=0.99
NuWro SF M_A=0.99
ANTINEUTRINO
16,467 events
77% purity
Q²_QE (GeV²)


MINERνA • ν Tracker → CCQE
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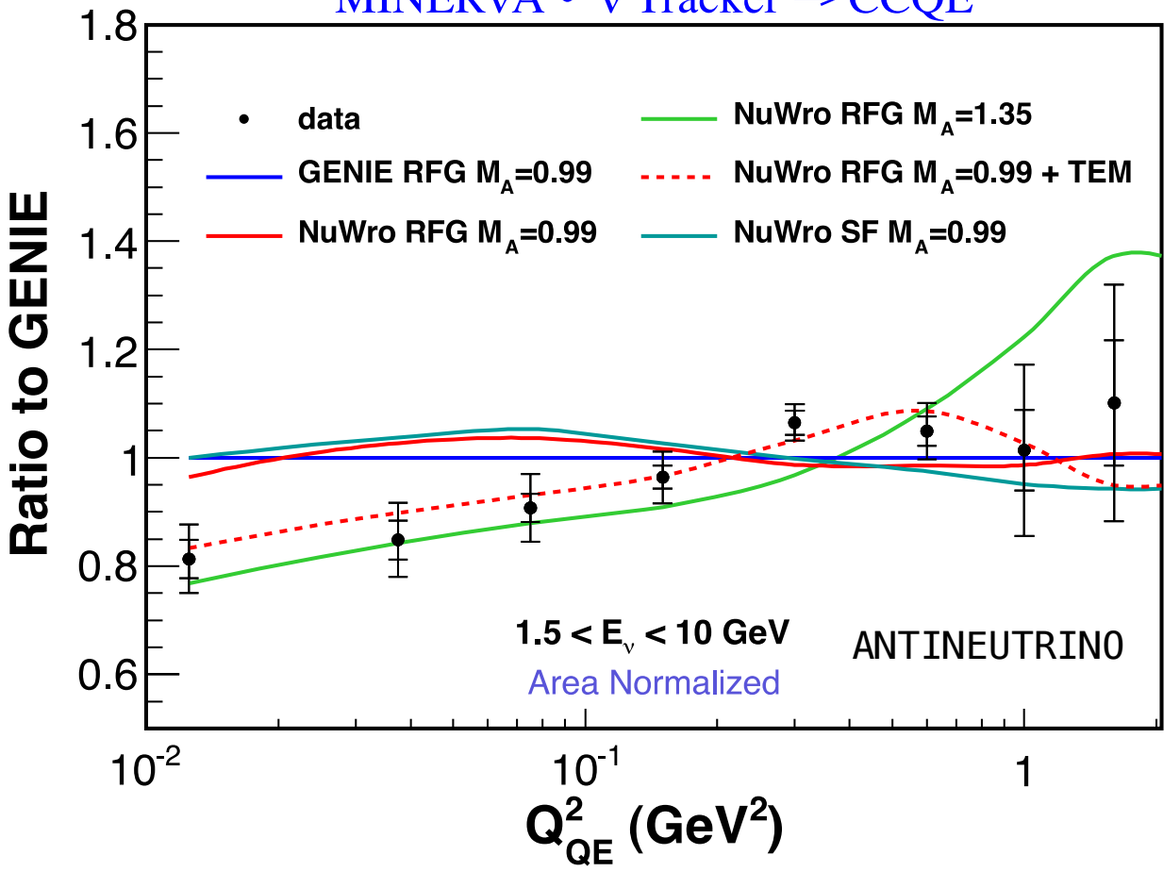
NuWro RFG M_A=0.99 + TEM
NuWro SF M_A=0.99
1.5 < E_ν < 10 GeV
Area Normalized
NEUTRINO
Ratio to GENIE
Q²_QE (GeV²)


MINERνA • ν̄ Tracker → CCQE
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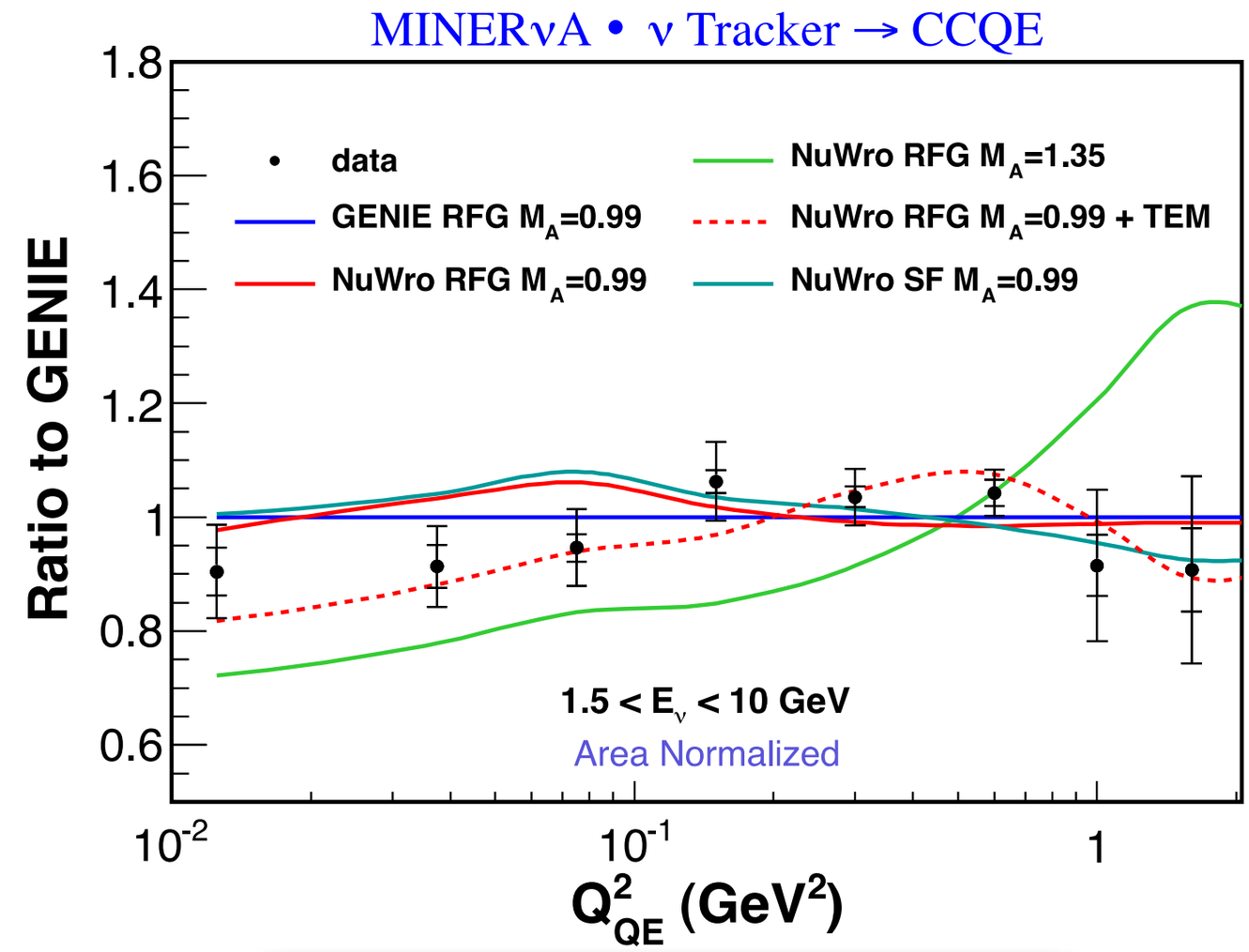
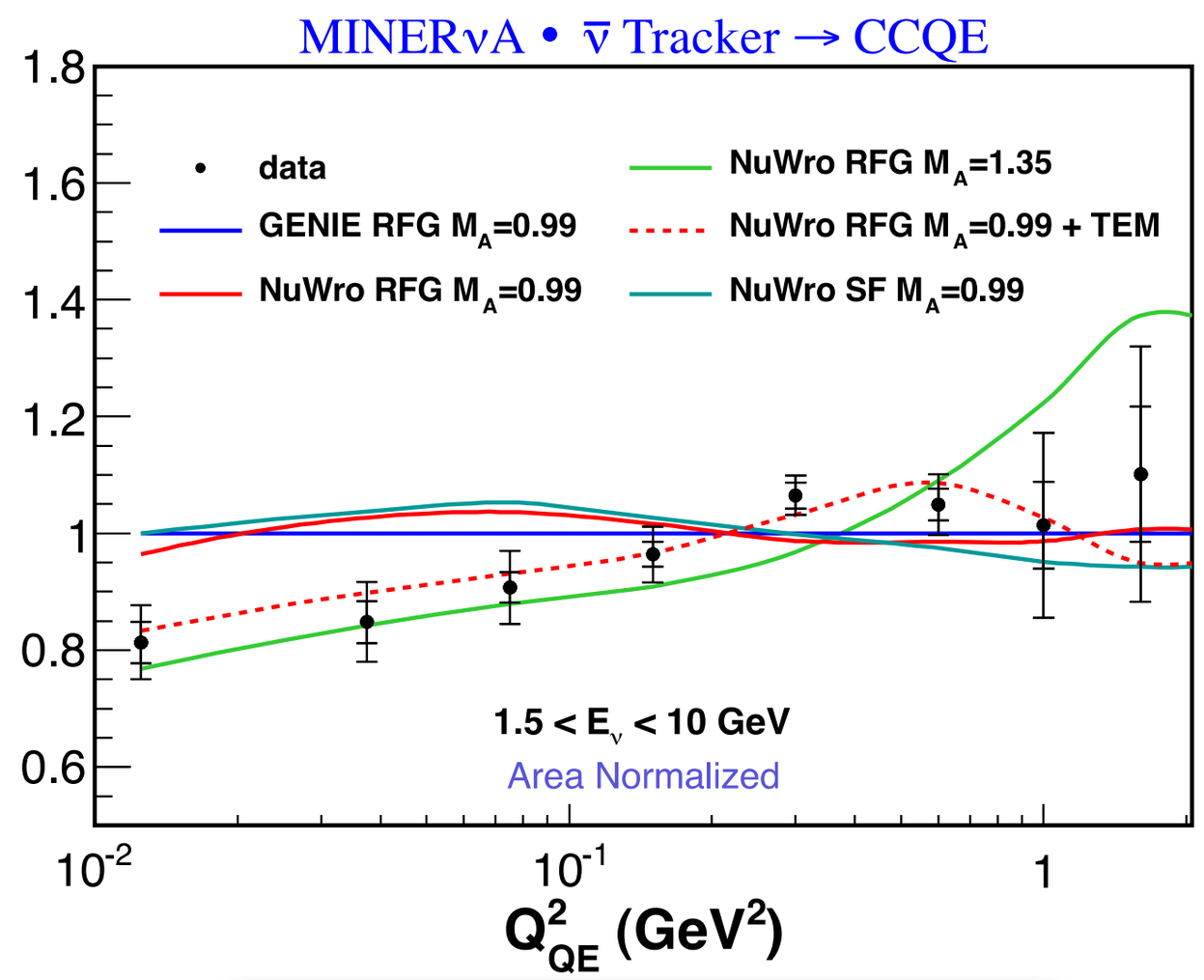
1.5 < E_ν < 10 GeV
Area Normalized
ANTINEUTRINO
Ratio to GENIE
Q²_QE (GeV²)

Neutrino (Left), Antineutrino (Right)





Neutrino

NuWro Model	RFG	RFG +TEM	RFG	SF
M_A (GeV/c^2)	0.99	0.99	1.35	0.99
Rate χ^2/d.o.f.	3.5	2.4	3.7	2.8
Shape χ^2/d.o.f.	4.1	1.7	2.1	3.8

Antineutrino

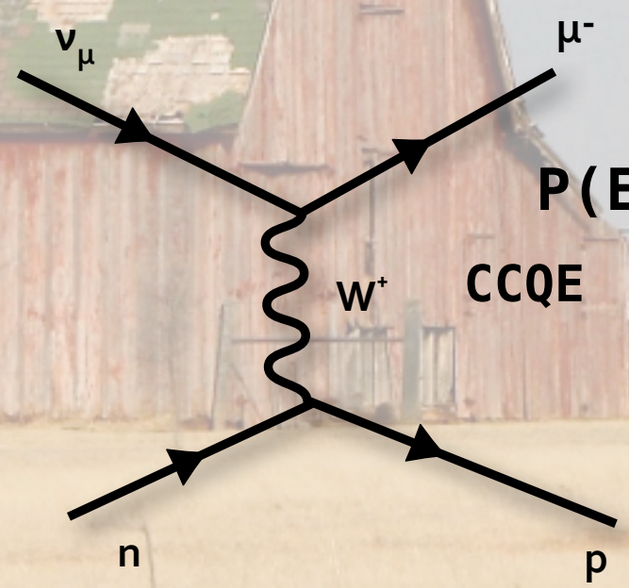
NuWro Model	RFG	RFG +TEM	RFG	SF
M_A (GeV)	0.99	0.99	1.35	0.99
Rate χ^2/d.o.f.	2.64	1.06	2.90	2.14
Shape χ^2/d.o.f.	2.90	0.66	1.73	2.99

Overview

- What is a cross section?
  - How do you measure one?
    - Normalization
    - Target Considerations
    - Signal Definition
    - Detector Effects & Unfolding
    - MC Validation

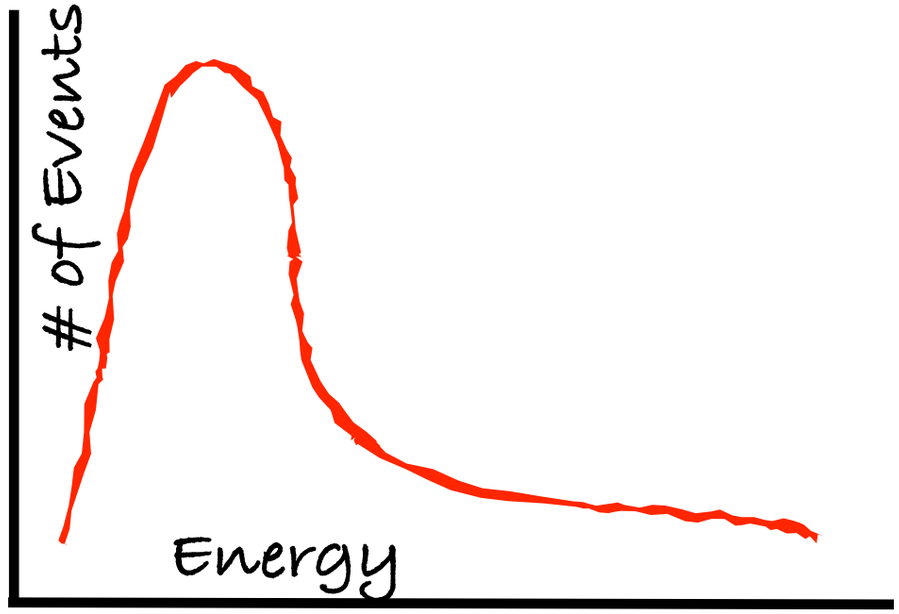
Cross Section

- Essentially, the cross section is a measure of the likelihood of a particular reaction.



- "[T]he most commonly calculated quantities in quantum field theory are scattering cross sections." *–Peskin & Schroder, p. 4*

How Do You Measure a Cross-Section?



- Suppose after years of toil, your experiment measures the above event rate as a function of energy.
- How do we make it useful to the community?
- The measurement above is a convolution of flux, cross-section, and detector acceptance effects.

How Do You Measure a Cross-Section?

- Detectors measure dN/dX_r, where X_r is a reconstructed physical parameter (e.g., final state lepton energy).
- It is hard enough to measure dN/dX_r, but you can't even publish it! You need to extract $d\sigma/dX_r$.
  - Remove detector acceptance & bias effects (X_r to X_t).
  - Flux-Folded (flux integrated - divide by the average flux).
    - You must also publish your flux in this case! You are not comparing the same distributions when studying $d\sigma/dX_r$ integrated over two different fluxes!
  - Flux-Unfolded ($\sigma(E)$ with corrections for each energy bin).

$$\left(\frac{d\sigma}{dX}\right)_i = \frac{1}{T\Phi} \times \frac{1}{dX_i} \times \frac{\sum_j U_{ij}\left(d_j - b_j\right)}{\epsilon_i}$$

- Flux-folded: For each *bin* in your measurement, i:
  - T = number of scattering targets (nucleons, atoms, etc.)
  - Φ = Integrated flux.
  - dX_i = The bin width.
  - U_{ij} = The Unfolding Matrix – Transform measured variables to “true” variables. For each bin i, you must sum over all the contributing measured bins, j.
  - d_j = The measured distribution in data.
  - b_j = The background estimate.
  - ε_i = The efficiency (acceptance) of the detector for that bin.

$$\left(\frac{d\sigma}{dX}\right)_i = \frac{1}{T} \times \frac{1}{\Phi_i \times dE_i} \times \frac{\sum_j U_{ij}\left(d_j - b_j\right)}{\epsilon_i}$$

- Flux-unfolded: For each *bin* in your measurement, i:
  - T = number of scattering targets (nucleons, atoms, etc.)
  - Φ_i = Integrated flux in the bin.
  - dE_i = The bin width.
  - U_{ij} = The Unfolding Matrix – Transform measured variables to “true” variables. For each bin i, you must sum over all the contributing measured bins, j.
  - d_j = The measured distribution in data.
  - b_j = The background estimate.
  - ε_i = The efficiency (acceptance) of the detector for that bin.

Normalization

- GENIE does not use "raw" interaction probabilities to compute interactions.
  - Otherwise, we would have to generate billions or even trillions of neutrinos, and walk them through the geometry, in order to generate one event.
    - This would be a very inefficient use of CPU.
- Instead, we compute the maximum density-weighted path-length through the detector geometry and scale interaction probabilities so that path has an interaction probability of 1.

Normalization

- We need to carefully track "exposure."
  - (Our flux models, of course, are not perfect, but we need to use them in a self-consistent manner.)
- This is managed by the flux driver. Beyond the scope of this lecture.

Targets

- Typically, you will provide as input to GENIE an XML spline file that contains GENIE cross sections as a function of energy for various reaction channels.

- When comparing to a real detector, it is important to keep in mind that the fiducial volume used for analysis will likely contain a mix of elements.

- For example, the MINERvA detector has a scintillator tracker, which is often referred to as a "carbon" target. However, the scintillator chemical formula looks more like C_8H_8. Furthermore there is glue, tape, reflective paint, etc., adding titanium, oxygen, silicon, etc. in trace amounts.

- Because vertex precision is not at the atomic level, event rates measured in the bulk reflect all these materials.

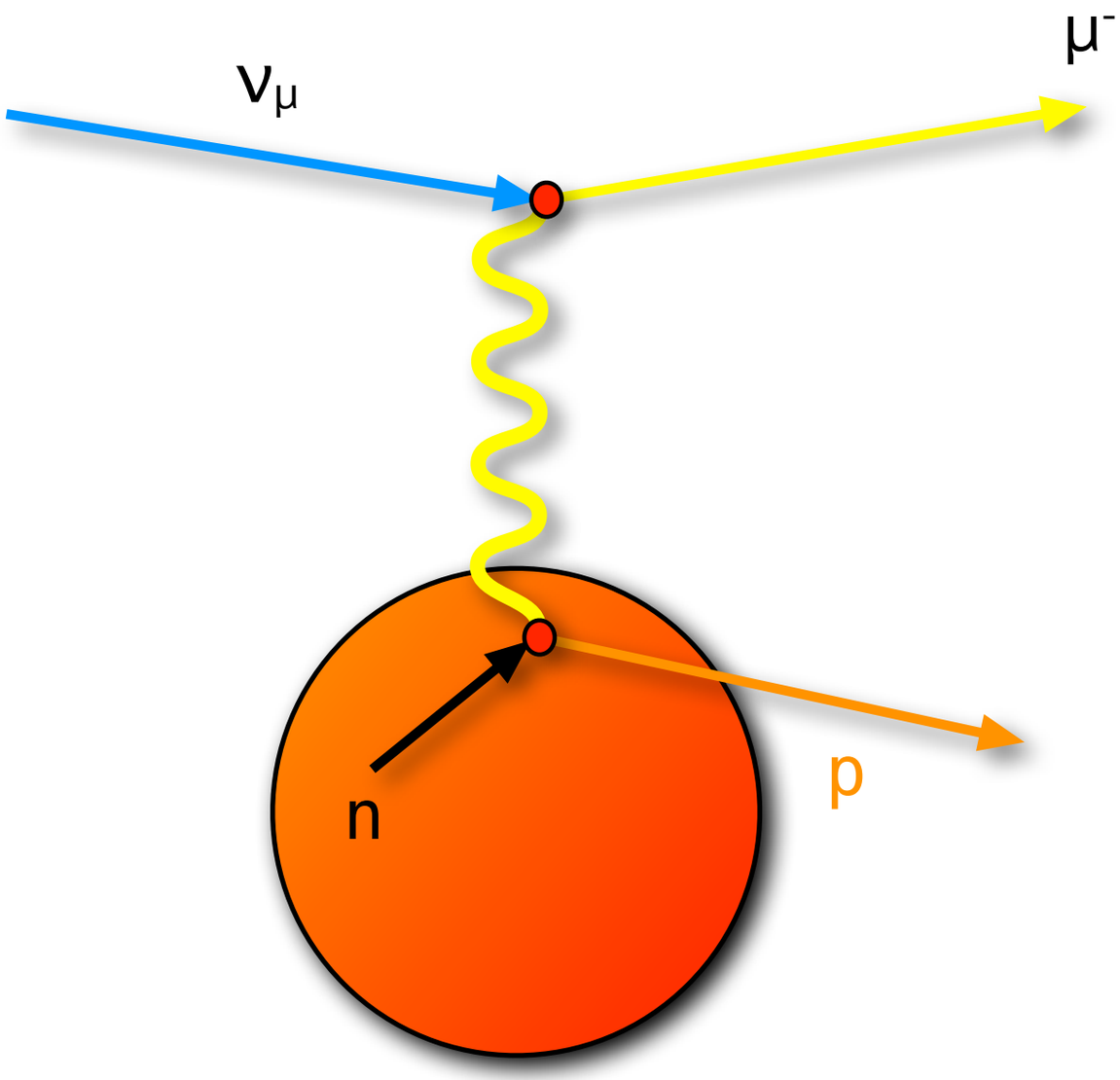
Targets

- Experiments often report cross-sections per:
  - Isoscalar nucleon (sum of protons and neutrons)
  - Atom (e.g. per ^{12}C, etc.)
  - Per proton / neutron (e.g. for anti-nu / nu CCQE)
- Reporting per nucleon makes scaling simpler (recall that cross-sections scale ~linearly with the number of nucleons).

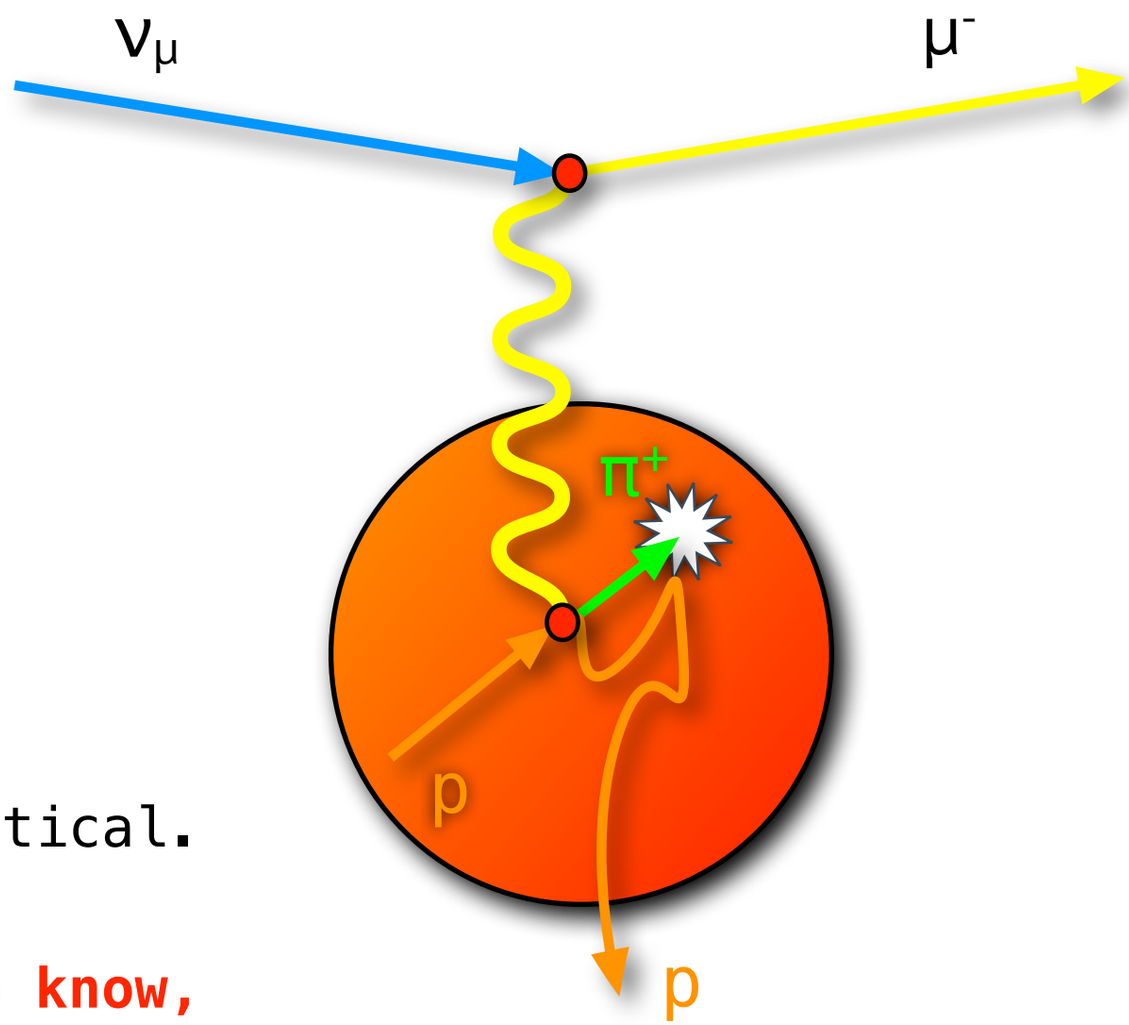
Signal Definition

- In reality we do not measure CCQE, Resonance, DIS, etc.
- We see a muon and a heavily ionizing hadron with a common origin and a couple of very soft hits in the vicinity of the vertex.
- What was the mechanism?
- There are several possible channels, and different aspects of the physics compete to produce the final state we observe.
- We have to do a probability-weighted integral over the all possibilities.
  - This is why the event generator is so important!

Signal Definition



Interactions take place in dense nuclear matter. (Otherwise, your experiment takes 100 years.)



Final State Interactions (FSI) are critical.

$$E_{visible} \neq E_\nu$$

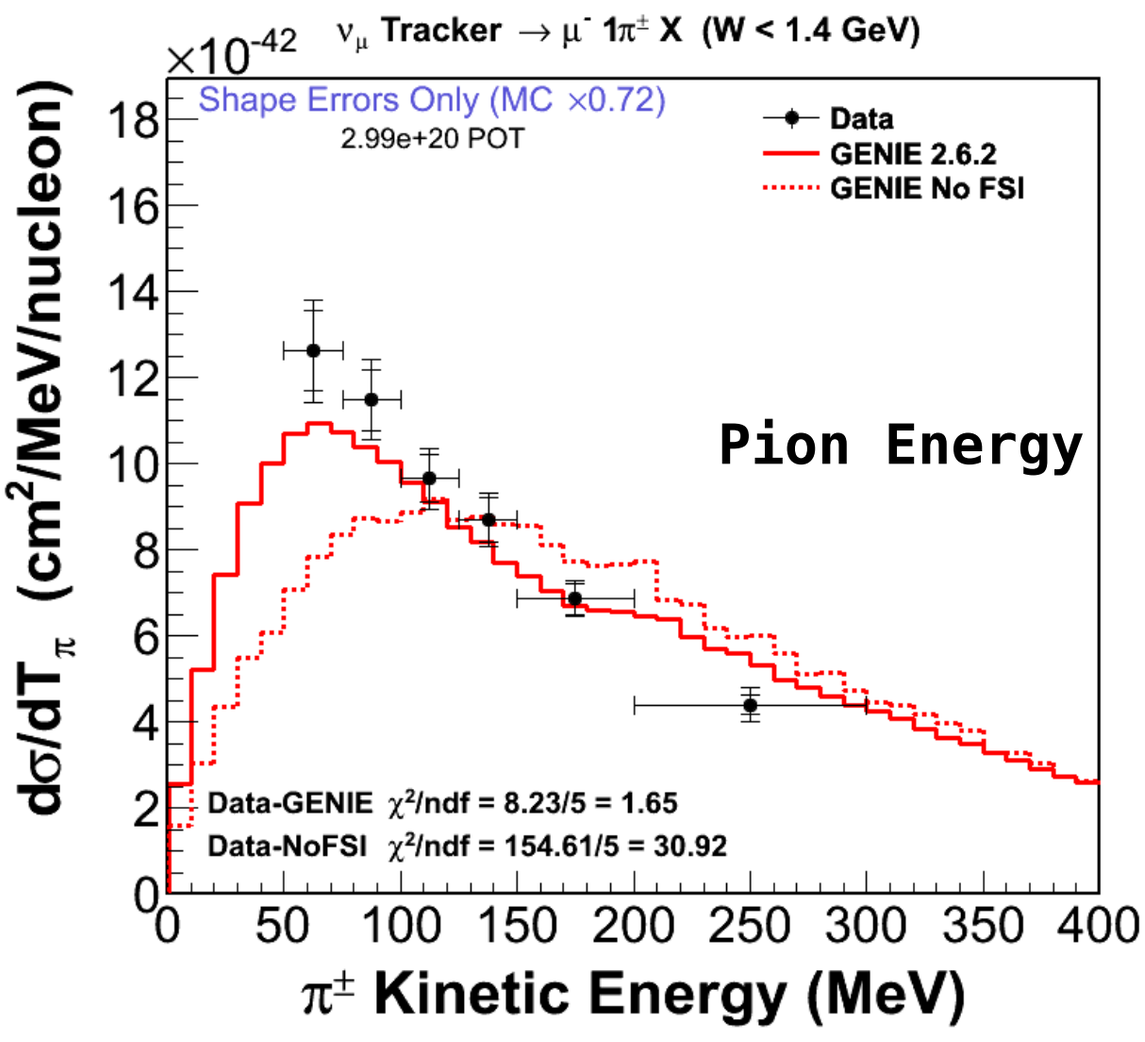
Not a calibration problem! You need to know, "what are the physics?"

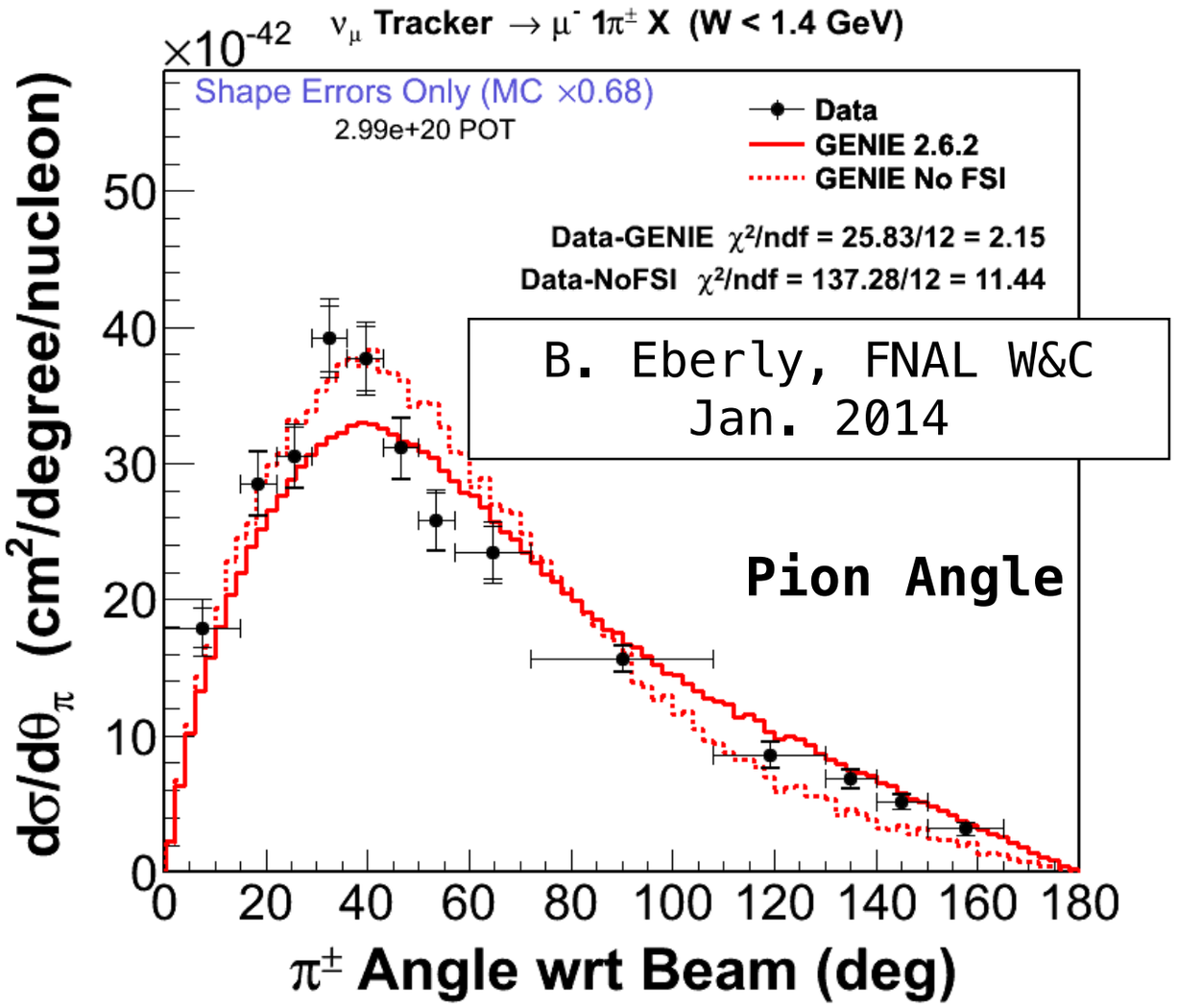
Model-Independent Measurements

- "Exclusive" signal definitions are useful, but it often makes sense to define your measurements ipurely in terms of observables.

$$\nu_\mu \mathrm{CH} \to \mu^- \pi^+ \mathrm{X}$$

$$\nu_\mu \mathrm{A} \to \mu^- \pi^+ \mathrm{A}$$





Unfolding

- Detectors smear and bias “true” kinematic information in the process of measuring an event.
- We need to correct for these effects to make results useful to theorists.
  - We can supply smearing functions so a reader may convolute their model with our detector response and see if their prediction matches data.
  - Or we can remove smearing effects so theoretical calculations may be directly compared to experimental results.
- Try to unfold observables! Unfolding model-dependent, derived quantities is less useful.
  - For example, in CCQE, don't unfold Q^2; unfold muon kinematics and calculate Q^2, etc.

Unfolding

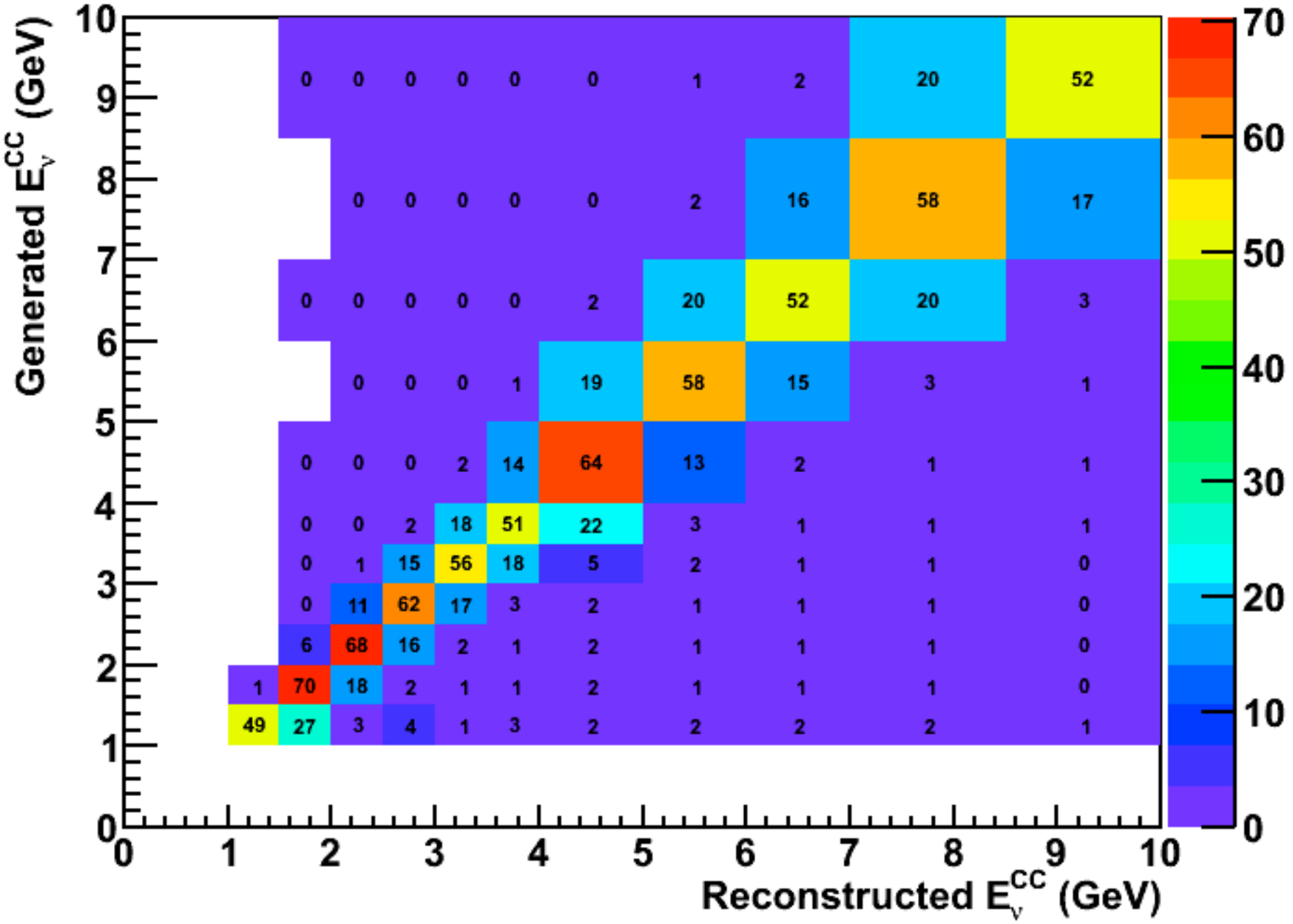
- “Matrix Inversion”: Find the matrix in MC that rotates “true” information (not necessarily generator level – avoid model dependence!) into reconstructed information. Very sensitive to binning and fluctuations & the matrix is not always invertible.

- “Regularization”: Local smoothing function to remove (statistical) fluctuations. Occasionally eats your physics!

- “Forward Iterators”: Build a smearing function and tune it until it transforms “true” information into reconstructed information.

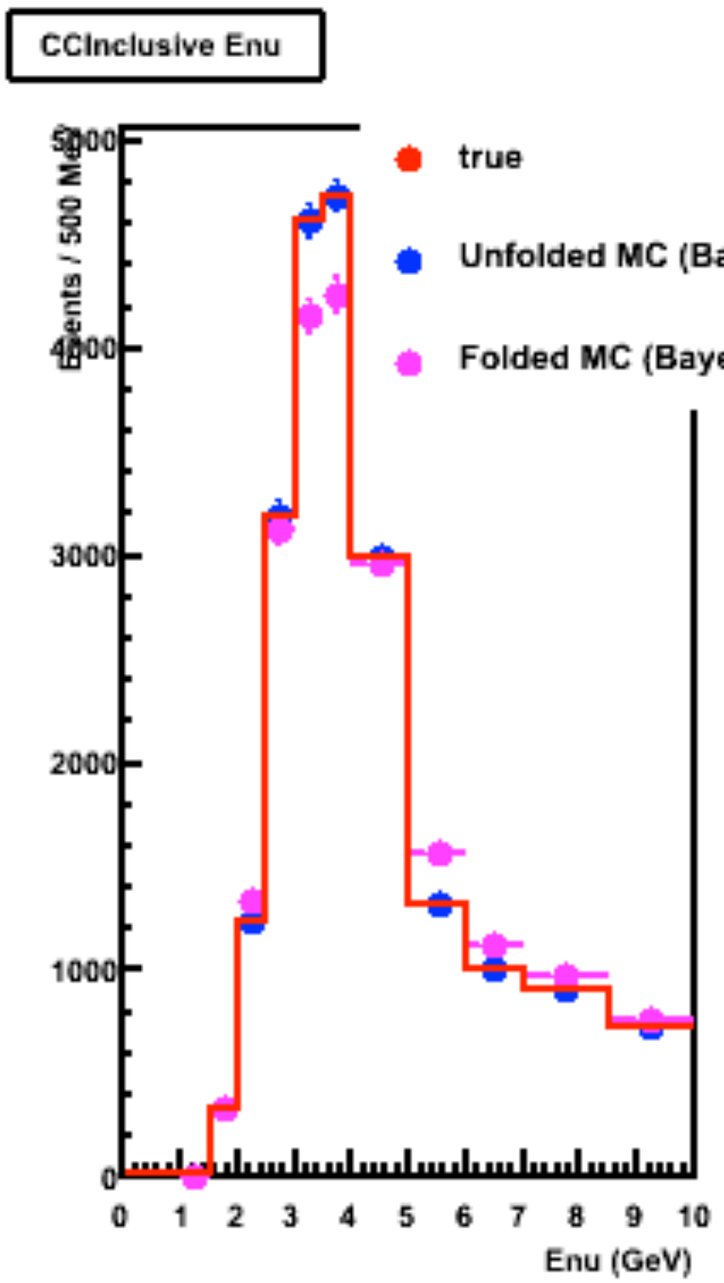
- "Iterative Bayes' Theorem": The most popular. Use a repeated application of Bayes' theorem to invert the response matrix, with regularization achieved by stopping iteration before reaching the "true" (but fluctuating) inverse.

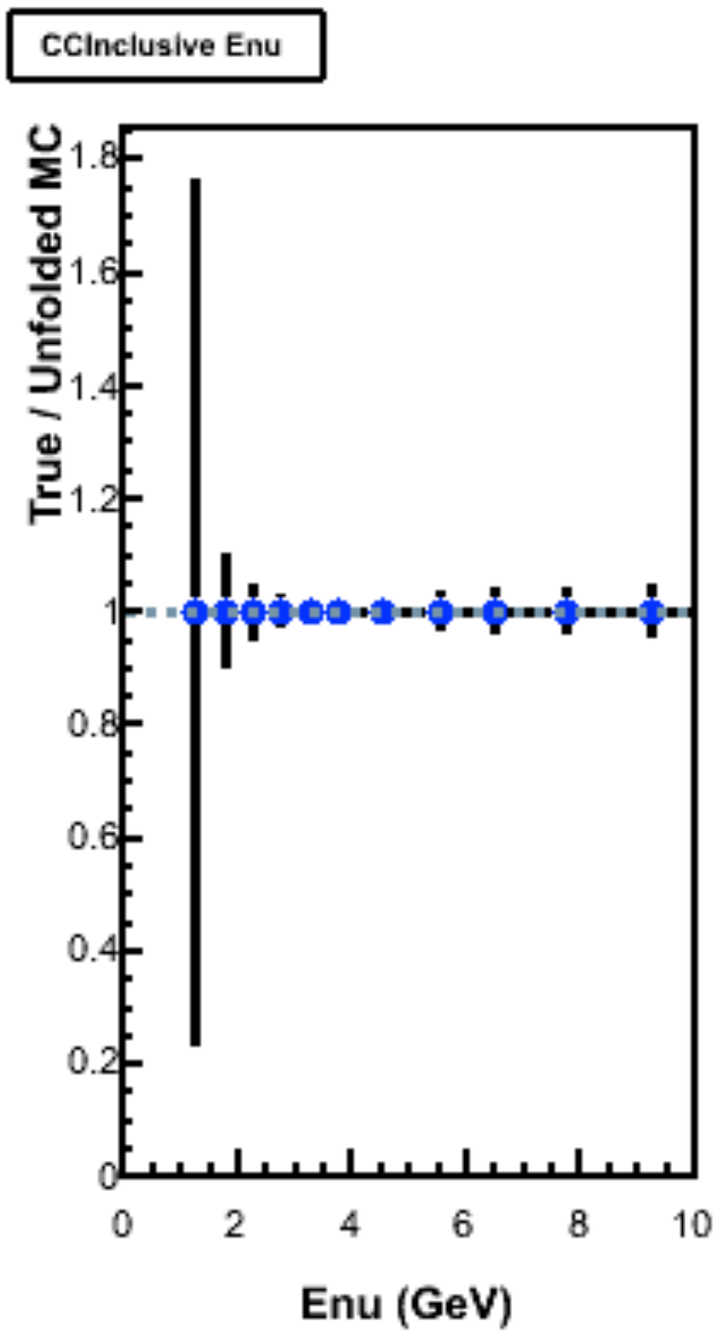
Example: Unfolding Neutrino Energy in MINERvA

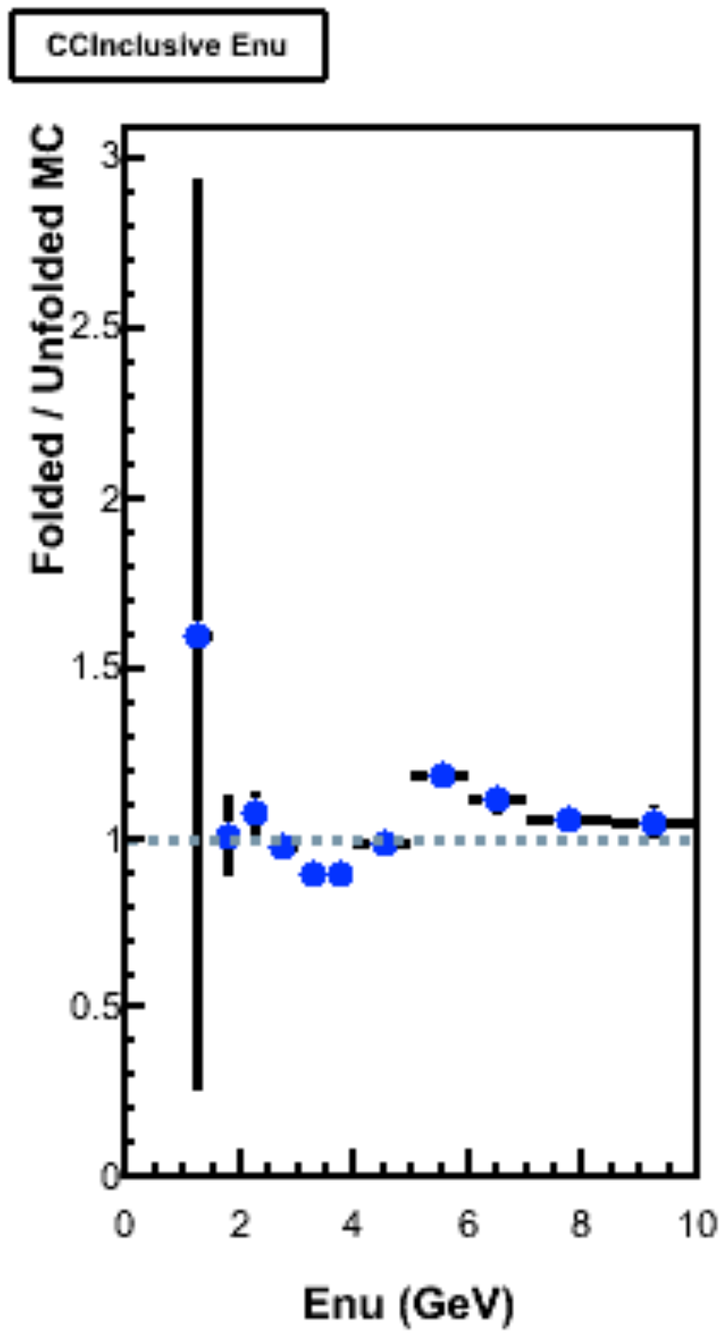


CC Inclusive Energy Transfer Matrix (computed via the iterative Bayesian Method).

Example: Unfolding Neutrino Energy in MINERvA

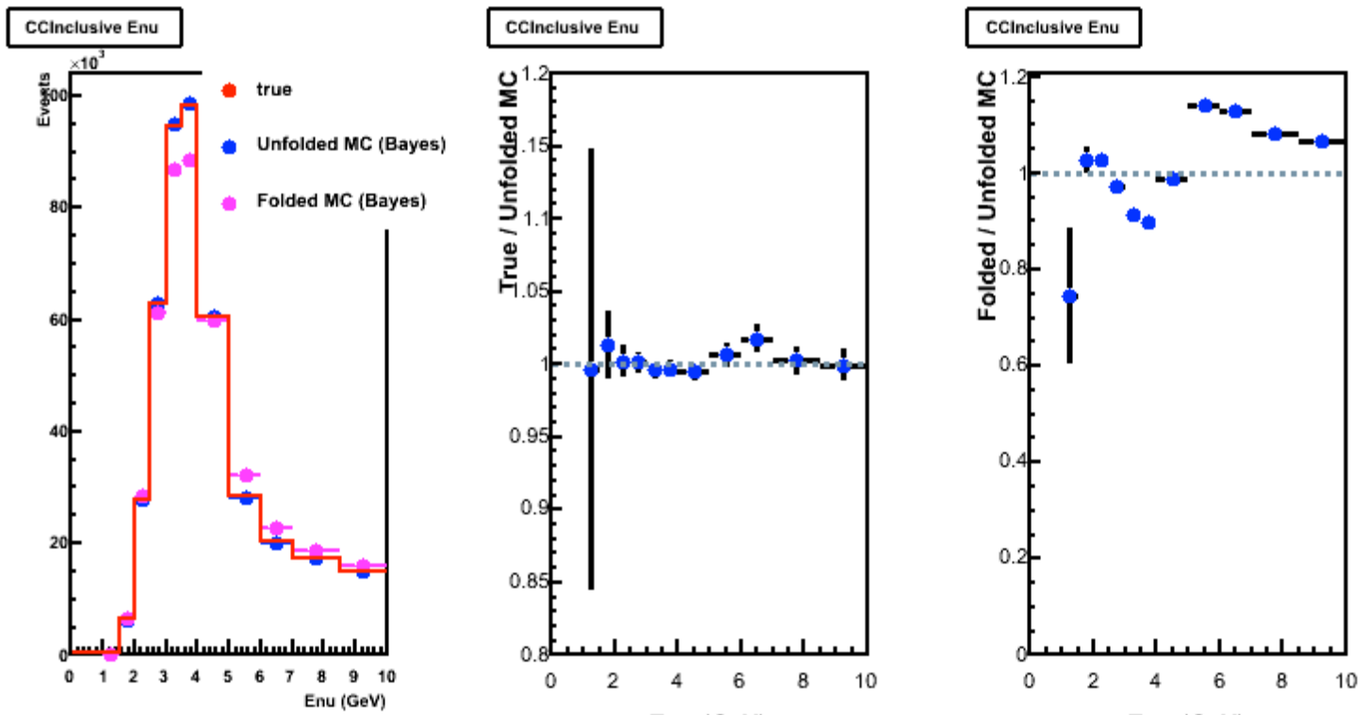




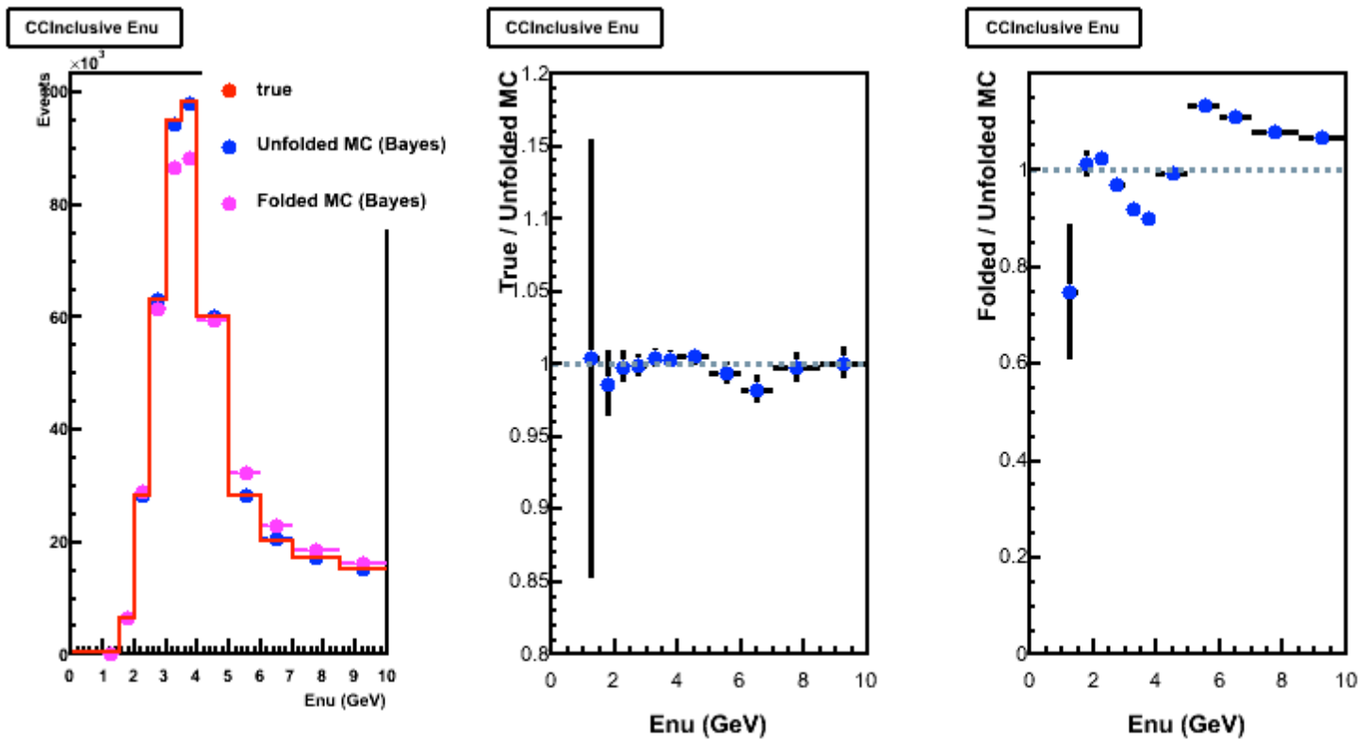


Example: Unfolding Neutrino Energy in MINERvA

- Unfold the first half of the data using a transfer matrix built from the second half.



- Then, unfold the second half with a transfer matrix built form the first half.



Unfolding

- **RooUnfold: arXiv 1105.1160 (2011)**
- **Nucl. Instrum. Meth. A 362, 487 (1995)**
  - This is the most popular...*
    - Nucl. Instrum. Meth. A 372, 469 (1996) [hep-ph/9509307]
    - S. Schmitt, arXiv 1205.6201.
    - Statistical Data Analysis by Glen Cowan.
      - http://www.pp.rhul.ac.uk/~cowan/sda/

*D'Agostini has a great webpage: http://www.roma1.infn.it/~dagos/prob+stat.html

MC Validation

- It is hard to do a simple exercise for comparing data to generator predictions.
- Fortunately, GENIE comes packaged with a lot of data and applications that compute the appropriate sample for comparison and comparison codes.
- Study these apps to understand the generator performance and to help think about how to compare data and simulation.

MC Validation

- Many levels of "validation."
  - Does it compile? Run one event? One million events? Is energy conserved? Is unitarity respected? Do predictions agree with known data?
- Every experiment/group MUST validate their installation of GENIE.
  - Not so easy to do. We're working on tools to automate the process.
  - At the very least, users should run some of the validation applications.

MC Validation

```
$ ls -1 $GENIE/src/validation

attic

eA

EvScan

Hadronization

Intranuke

MCx

Merenyi

NuXSec

StructFunc
```

Available apps.

MC Validation

```
$ ls -1 $GENIE/bin/gvld_*

gvld_e_hadro_atten

gvld_e_qel_xsec

gvld_e_res_xsec

gvld_hadronz_test

gvld_merenyi_test

gvld_sample_comp

gvld_sample_scan

gvld_sf

gvld_sf_sum_rule_test

gvld_xsec_comp
```

Available apps.

MC Validation

```
$ ls -1 $GENIE/src/scripts/production/batch

bulk_submit.pl

README

run_t2k_superk_production.sh

submit_eA_hadron_attenuation_validation_mc_jobs.pl

submit_eA_xsec_calc_jobs.pl

submit_eA_xsec_validation_mc_jobs.pl

submit_hadronization_validation_mc_jobs.pl

submit_intranuke_validation_mc_jobs.pl

submit_km3net_xsec_calc_jobs.pl

...
```

Code to run the apps. Ignore the "batch" aspects (unless you have a PBS queue, etc.). Just fish out commands to run the validation apps.

MC Validation

- Example:
  - git clone https://github.com/GENIEMC/HadronizationVald.git
  - Must have gxspl-vA-v2.8.0.xml in $XSECSPLINEDIR

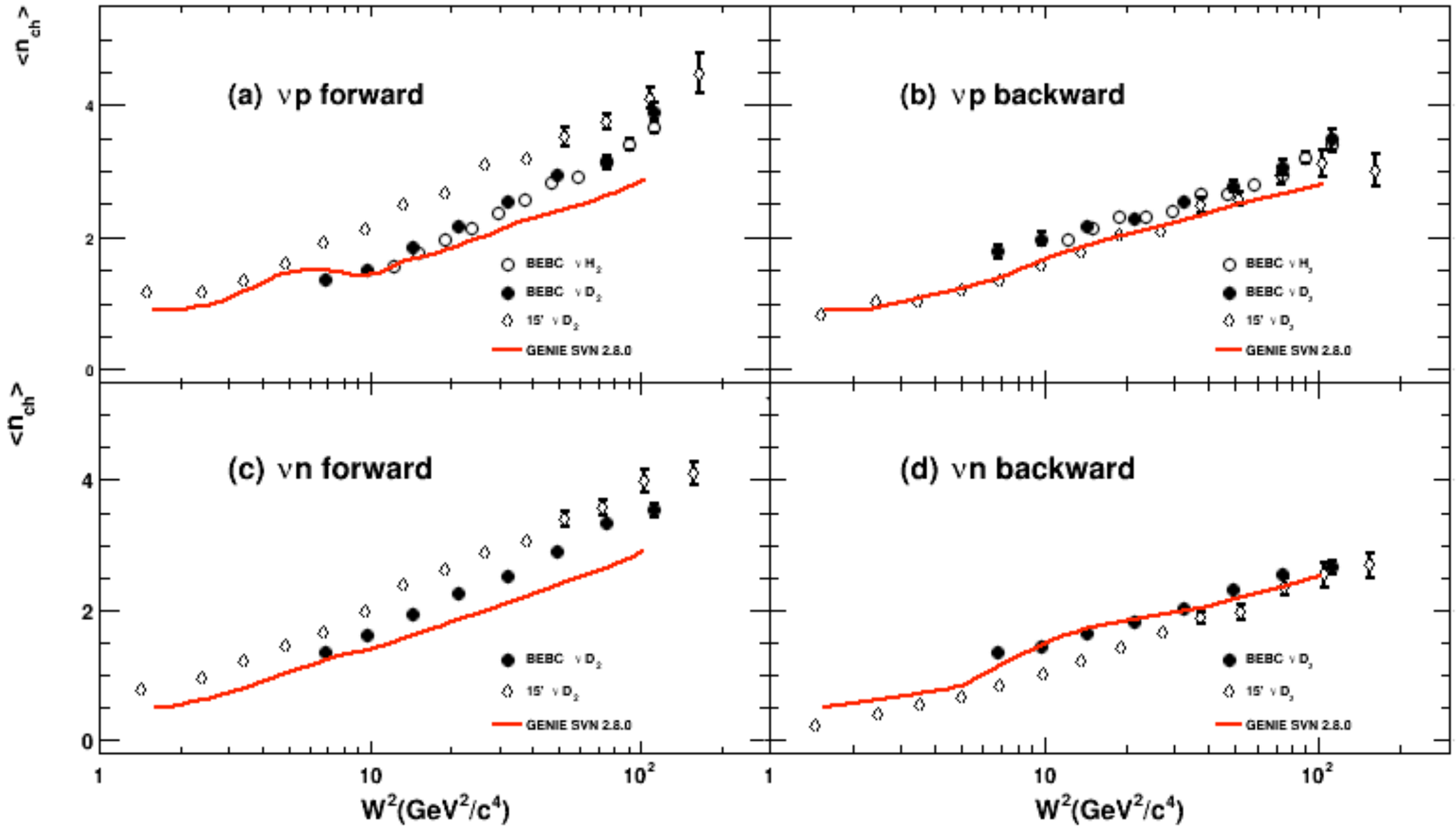
```
$ time nice ./gen_samples <N events>
```

- 30,000 events (about the minimum to get reasonable plots) takes about 20 minutes.

```
$ ./run_validation.sh
```

- Inspect the scripts to see how to make the required samples and run the validation app.
- Try to run `gvld_xsec_comp`.

MC Validation



Thanks!

Back-up

A Note on Jargon

- To some people, "final state interactions" mean interactions with the target that affect the final state (e.g., target structure can change the final state lepton momentum).

- To other people, "final state interactions" mean subsequent interactions of the particles produced at the hard scattering vertex with the nuclear medium, and they are usually referring to hadrons only (leptons are less effected on the way out).

  - Some people are very fired up about using one or the other.

- This situation is confusing and we need to fix it. In this talk I mean the *latter* – interactions in the nuclear medium by particles produced at the vertex after the neutrino interaction.