

Spectrum Unfolding and Generic Reactor Antineutrino Spectrum Study at Daya Bay

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Introduction

A method of extracting a model-independent reactor antineutrino spectrum from measured inverse beta decay (IBD) events is developed and examined with Monte Carlo (MC) simulation. Multiple methods are investigated to obtain the antineutrino spectrum from the measured IBD prompt spectra. This antineutrino spectrum could be used to replace current models for predicting fluxes and energy spectra. A method to predict the antineutrino flux and spectrum for experiments of slightly different effective fission fractions is presented.

Spectrum Unfolding

Unfolding is to estimate the true spectrum $T(x)$ from a measured spectrum $M(y)$ and the detector response matrix $A(y,x)$ by correcting spectrum distortion due to detector effects, such as energy resolution.

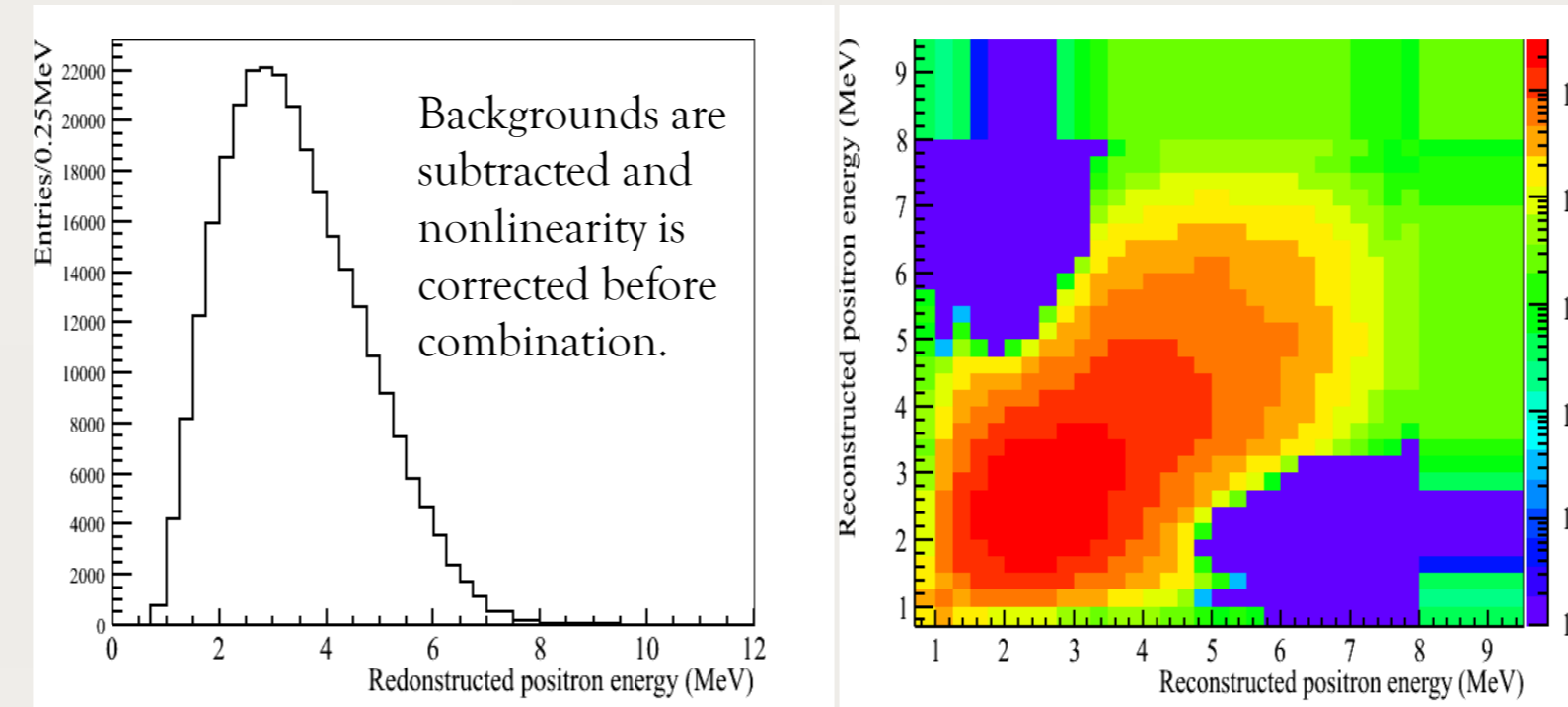
$$M(y) = \int A(y, x) T(x) dx.$$

Detector response matrix is usually obtained by MC.

Unfolding methods: Bayesian iterative method^[1], and Singular Value Decompositions (SVD)^[2] in RooUnfold^[3] framework.

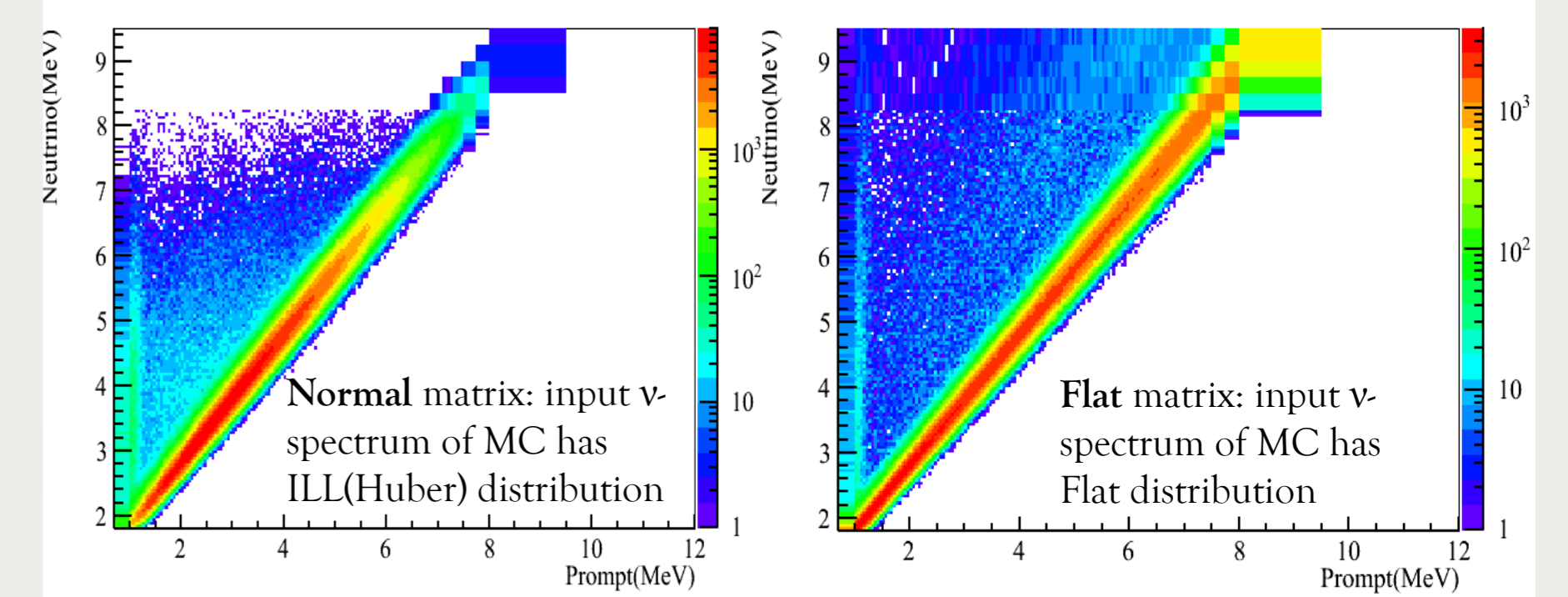
Input of Unfolding

Measured IBD prompt energy spectrum: three near site detectors are combined.



Covariance matrix includes: Systematic, statistical and background subtraction uncertainties

Detector response matrix: from Geant4 MC (4M events)/Toy-MC (10M events)

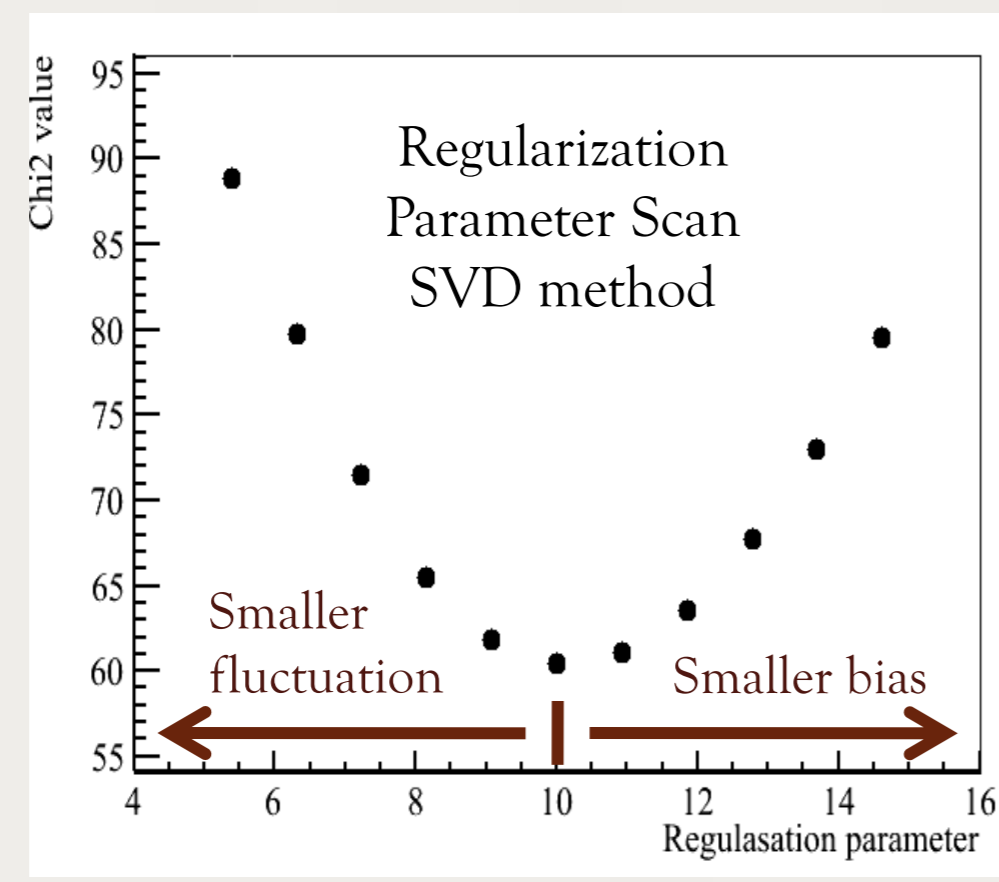


Detector response matrix includes: energy resolution, energy leakage. Nonlinearity and non-uniformity are corrected.

Regularization

Unfolding introduces bias and enhances fluctuations due to limited statistics of the measurement.

Regularization: Smooths unfolded spectrum. Balances bias and smoothness (right figure). Minimizes total errors between true and unfolded spectrum.



Bias Estimation with Blinding Tests

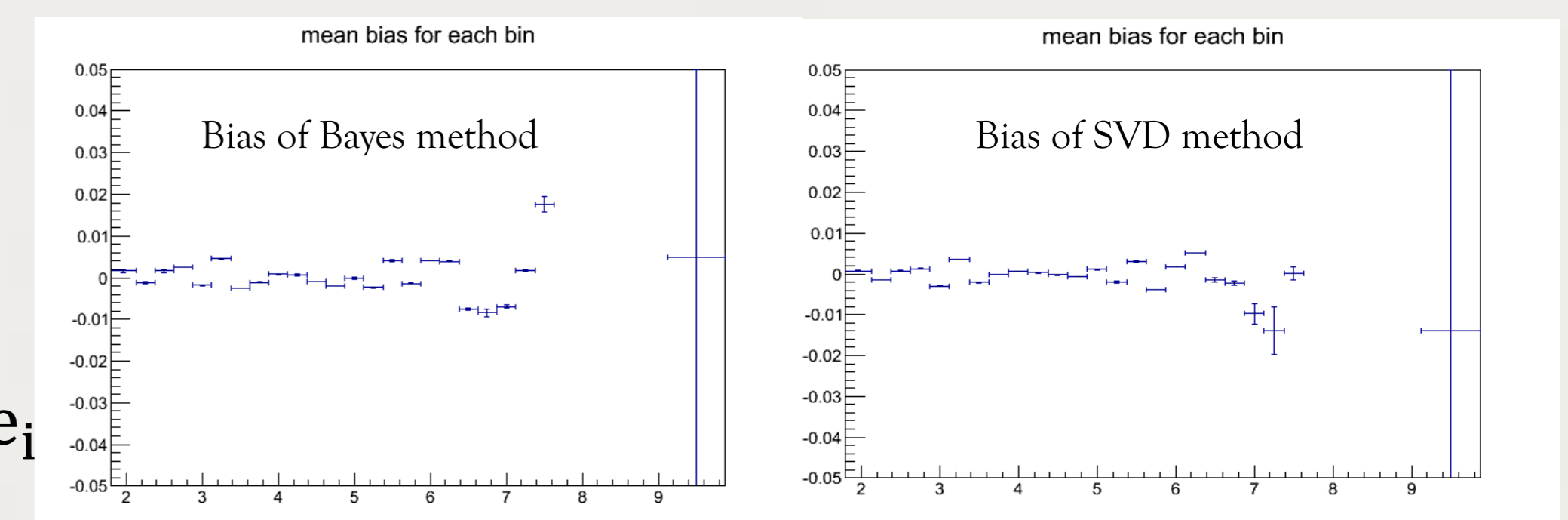
Toy-MC is used in blinding tests to estimate bias from unfolding.

10,000 “measured” spectra are generated including detector effects and statistical fluctuations and then unfolded with both Bayesian and SVD methods.

Mean of bin-by-bin bias is within 1% when using both Bayesian and SVD methods.

Bin-by-bin biases are determined by the differences between the N true and unfolded spectra:

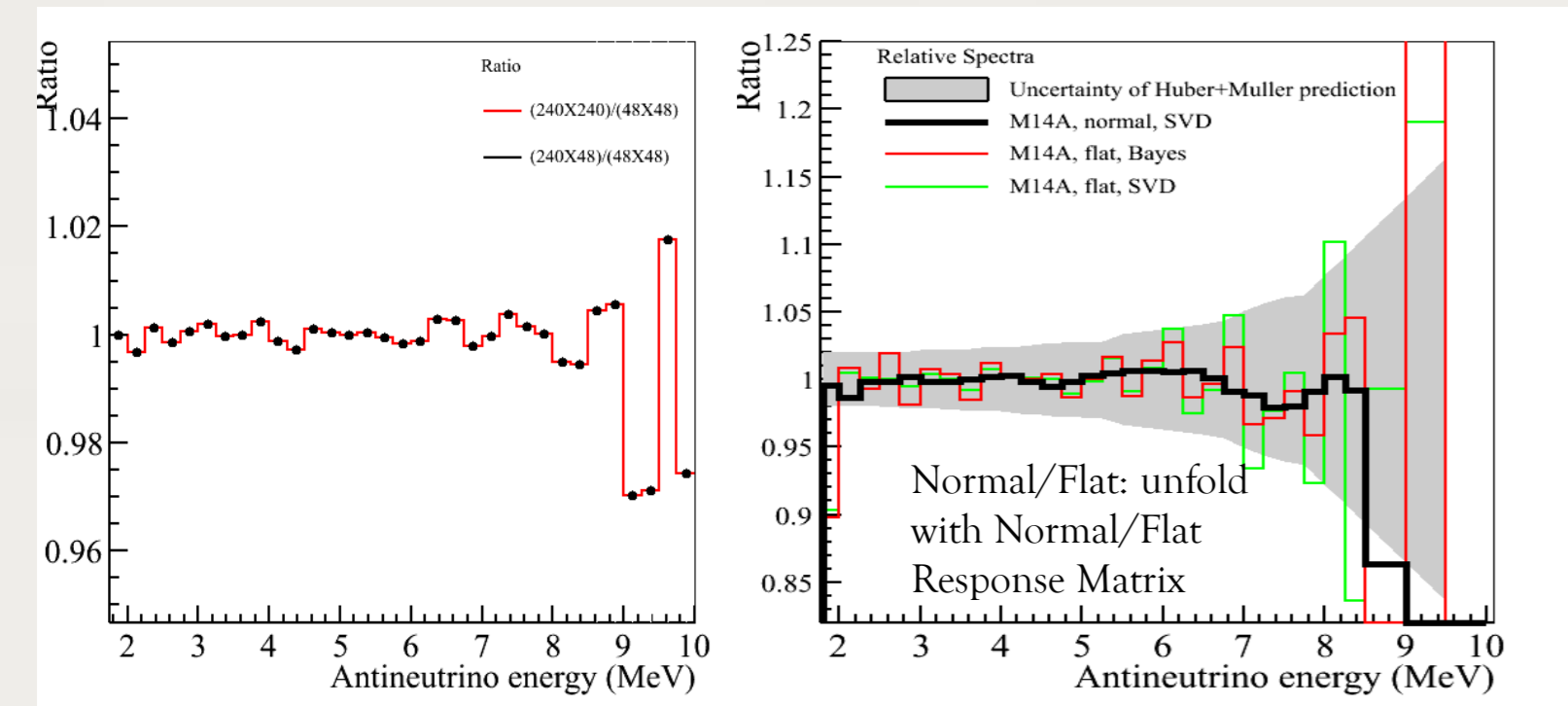
$$\text{Bias} = \frac{1}{N} \sum_i^N (\text{Unfolded}_i - \text{True}_i) / \text{True}_i$$



Unfolded Spectrum and Covariance Matrix

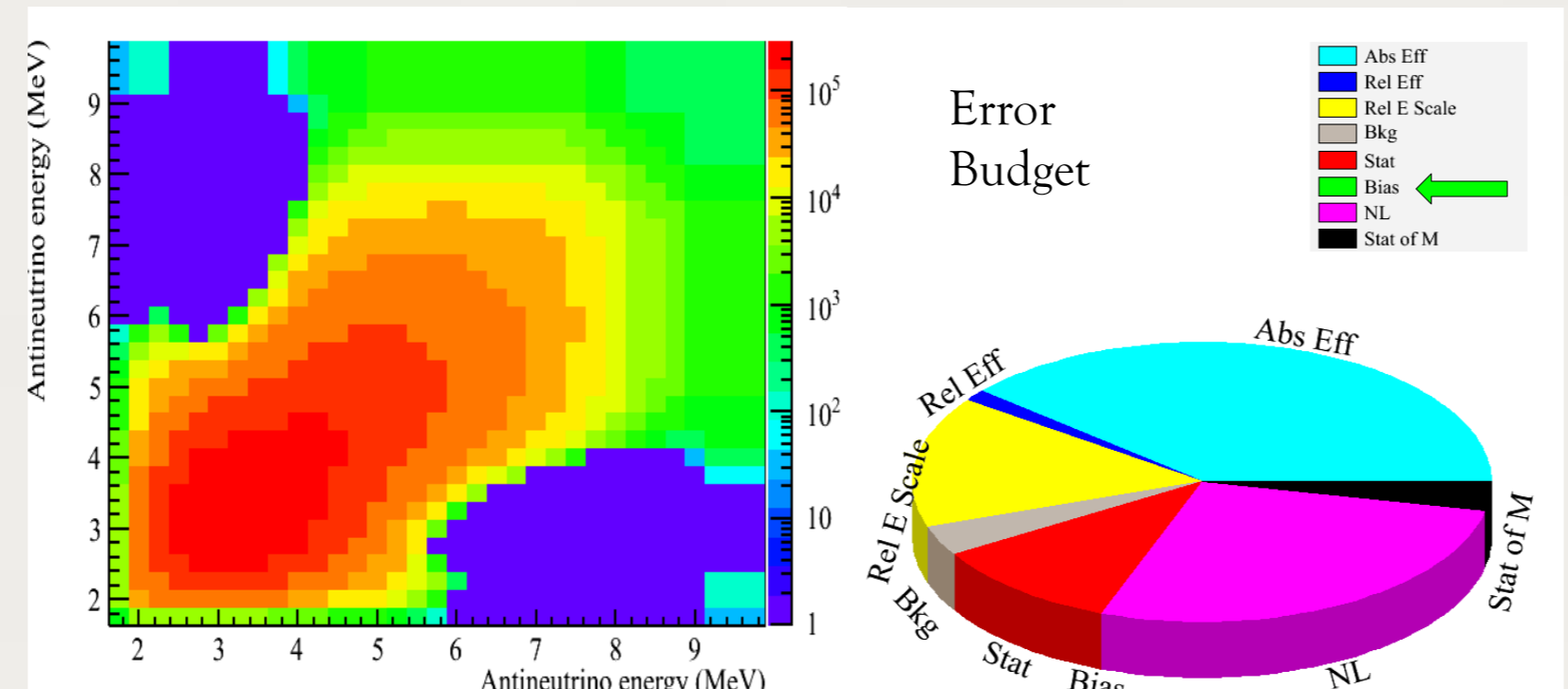
Antineutrino spectrum from unfolding measured IBD prompt spectrum.

Unfolded spectra with different binning (left), and by different methods/matrices (right) are consistent.



Covariance Matrix is propagated by unfolding program, and validated with Toy-MC method in blinding tests.

Unfolded covariance matrix keeps the same structure. Bias is negligible.

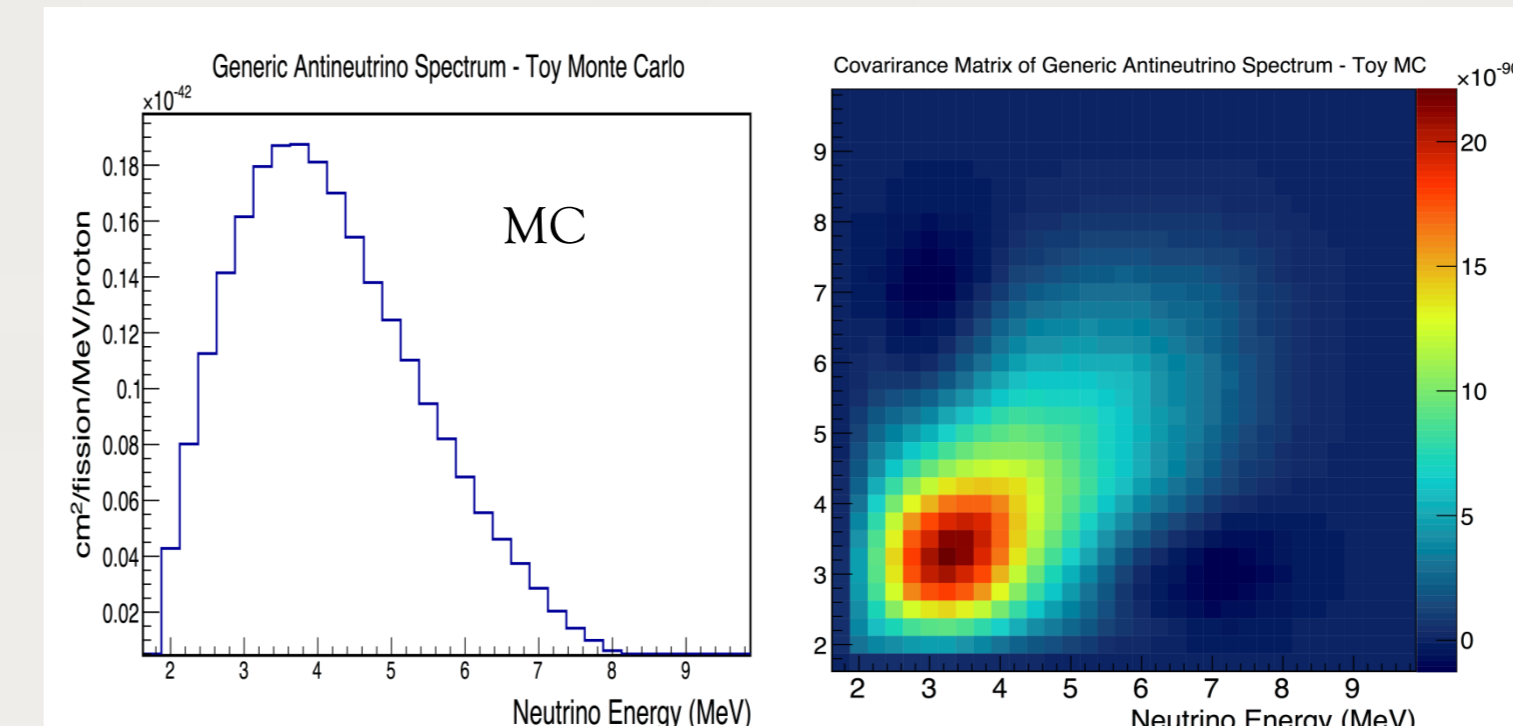


Generic Spectrum Extraction

1. Generate three test prompt spectra by MC for each near site detector. Combine them into one.

$$S_{generic}(E_\nu) = \frac{S_{unfolded}(E_\nu)}{P_{eff_sur}(E_\nu) \cdot N_p \cdot F_{total}}$$

2. Unfold it into an antineutrino spectrum $S_{unfolded}$.
3. Remove oscillation effect P_{eff_sur} and normalize the unfolded spectrum (proton number N_p , fission number F_{total}) into unit spectrum $S_{generic}$, which includes cross-section.



Prediction with Generic Spectrum

For any reactor experiments that have similar effective fission fractions as those of Daya Bay, the predicted antineutrino spectrum S_X is:

$$S_X = S_{DYB} + \sum_i (\alpha_X^i - \alpha_{DYB}^i) S_{ILL}$$

Where S_{DYB} is the generic spectrum from Daya Bay; α_{DYB} are fission fractions from Daya Bay; α_X are fission fractions of experiment X; $S_{ILL/Huber}$ are isotope spectra from ILL/Huber model.

Summary

Different unfolding methods, which are examined with toy MC and tested with measured IBD prompt spectra, yield consistent results. A method of extracting a generic spectrum from measured IBD spectra is developed. This antineutrino spectrum could be used for predicting antineutrino fluxes and spectra for other experiments.

References:

- [1]. G. D'Agostini, Nucl.Instrum.Meth. A362 (1995) 487-498.
- [2]. Höcker and Kartvelishvili, Nucl.Instrum.Meth.A372:469-481,1996.
- [3]. <http://hepunix.rl.ac.uk/~adye/software/unfold/RooUnfold.html>