Study of the accuracy of reactor antineutrino spectrum reconstruction

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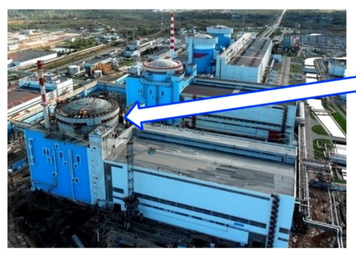
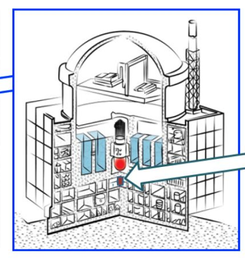
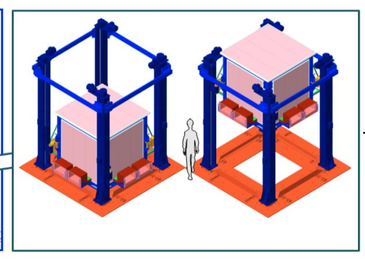
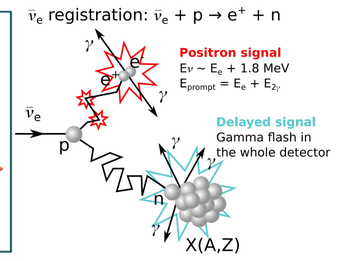
Experimental setup

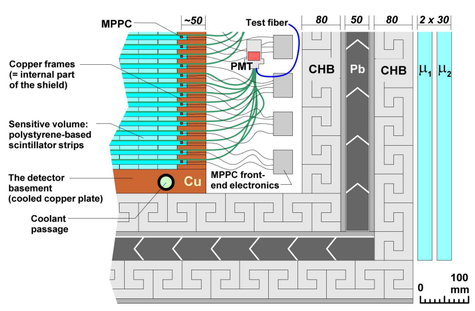
- DANSS – Detector of reactor AntiNeutrino based on Solid-state Scintillator
- Location: Kalinin Nuclear Power Plant, 3 GW commercial reactor, 5 10^{13} ν cm^{-2} s^{-1}, 50 m w.e. overburden
- 10.9 -12.9 m from the reactor core center, movement online
- Multilayer Cu (5 cm) + CHB (8 cm) + Pb (5 cm) + CHB (8 cm) passive shielding
- Two-layer muon μ-veto on 5 sides
- 2500 scintillator strips with Gd containing coating for neutron capture
- Light collection with 3 WLS fibers
- Central fibers are read out with individual SiPMs
- The electron antineutrinos are detected via the inverse beta decay (IBD) reaction

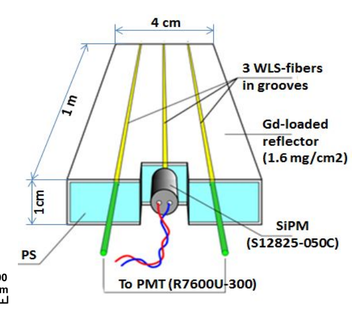


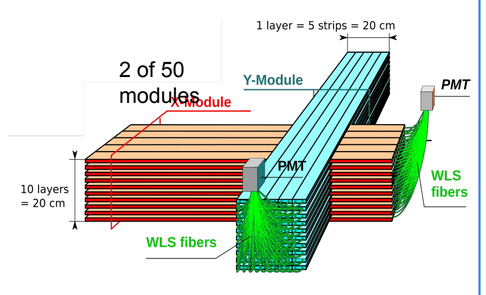












Motivation

A number of experiments see a discrepancy between the measured neutrino spectrum and the predicted one (Daya Bay, PROSPECT, STEREO, RENO)
The unfolding procedure eliminates detector effects.
This allows:

- Compare measurements with theoretical predictions
- Compare experiments with different responses
- Get input to a subsequent analysis

The problem of unfolding

Objective is to estimate true distribution from measurement, distorted by:

- detector effects
- statistical fluctuations

$$S(E_p) = \int S(E_{\bar{\nu}_e}) R(E_{\bar{\nu}_e}, E_p) \mathrm{d}E_{\bar{\nu}_e}$$

Unfolding of binned (discrete) distributions, where bin-to-bin migrations are described by a matrix equation:

$$\mu_i = \sum A_{ij} x_j + b_i$$

μ_i : expected measurement in bin i given the truth x
A_{ij} : probability of truth bin j to reconstruct in bin i
x_j : truth in bin j
b_i : background in bin i

$A_{ij} = \frac{N_{ij}^{\mathrm{MCreco,MCtruth}}}{N_j^{\mathrm{MCtruth}}}$ is calculated from MC

SVD approach to data unfolding

The problem can be formulated as minimizing the functional:

$$\chi^2(x) = (Ax - y)^{\mathrm{T}} V_y^{-1} (Ax - y)$$

Singular Value Decomposition:

$$A = U \Sigma V^{\mathrm{T}} = \sum_{i=1}^{n} u_i \sigma_i v_i^{\mathrm{T}}$$

Pseudoinverse:

$$A^{\#} = V \Sigma^{-1} U^{\mathrm{T}}$$

The naive solution is bad due to small singular values and fluctuations in the positron spectrum

$$x = (V \Sigma^{-1} U^{\mathrm{T}}) y = \sum_{j=1}^{n} \frac{1}{\sigma_j} c_j v_j, \text{ where } \quad c_j = y^{\mathrm{T}} u_j$$

Therefore, we add a regularization term and apply the SVD decomposition to the corresponding system.
Here: matrix C allows to write down the curvature of the solution, parameter tau is responsible for the strength of regularization.

$$\chi^2(x) = (Ax - y)^{\mathrm{T}} V_y^{-1} (Ax - y) + \tau (Cx)^{\mathrm{T}} Cx$$

$$C = \begin{pmatrix} -1+\xi & 1 & 0 & 0 & \dots & & \\ 1 & -2+\xi & 1 & 0 & \dots & & \\ 0 & 1 & -2+\xi & 1 & \dots & & \\ & \dots & & & \dots & & \\ & \dots & & & 1 & -2+\xi & 1 \\ & \dots & & & & 1 & -1+\xi \end{pmatrix}$$

Systematic uncertainties evaluation

Sources:

- Energy shifting
- Energy scaling
- Energy resolution
- Background
- Initial antineutrino spectrum model

$$V_{ij}^{\mathrm{sys}} = \frac{1}{N^{\mathrm{expts}}} \sum^{N^{\mathrm{expts}}} (N_i^{\mathrm{ran}} - N_i^{\mathrm{nom}})(N_j^{\mathrm{ran}} - N_j^{\mathrm{nom}})$$

N^{expts} is the number of toy MC samples
N^{ran} is the random (fluctuated) predicted number of events at the prompt energy bin i,
N^{nom} is nominal number of events in bin i.

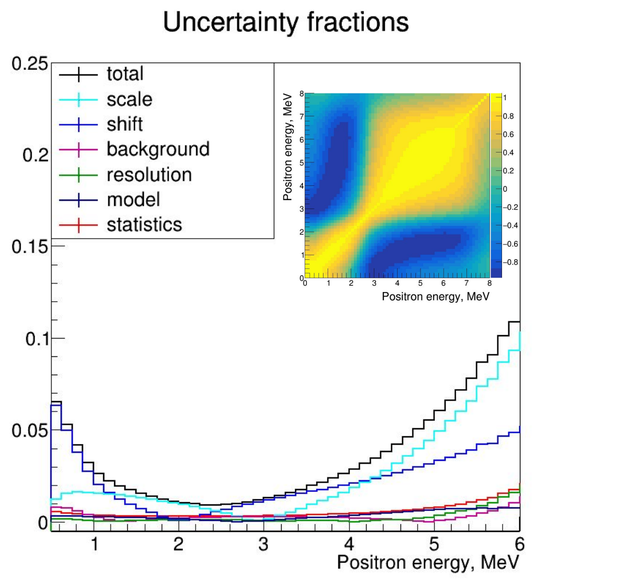
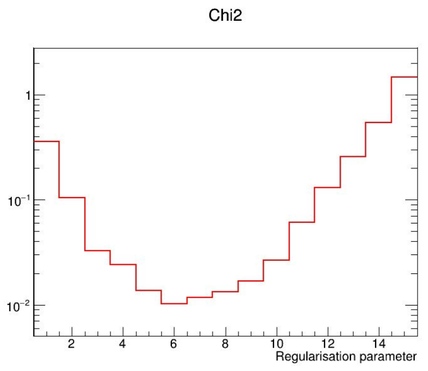


Fig.: The fractional size of the diagonal elements of the covariance matrix, $\sqrt{V_{ii}}/N_i^{pred}$, for each component in each prompt energy bin. Inset: the elements of the correlation matrix, $V_{ij}/\sqrt{V_{ii}V_{jj}}$ for the total uncertainty.

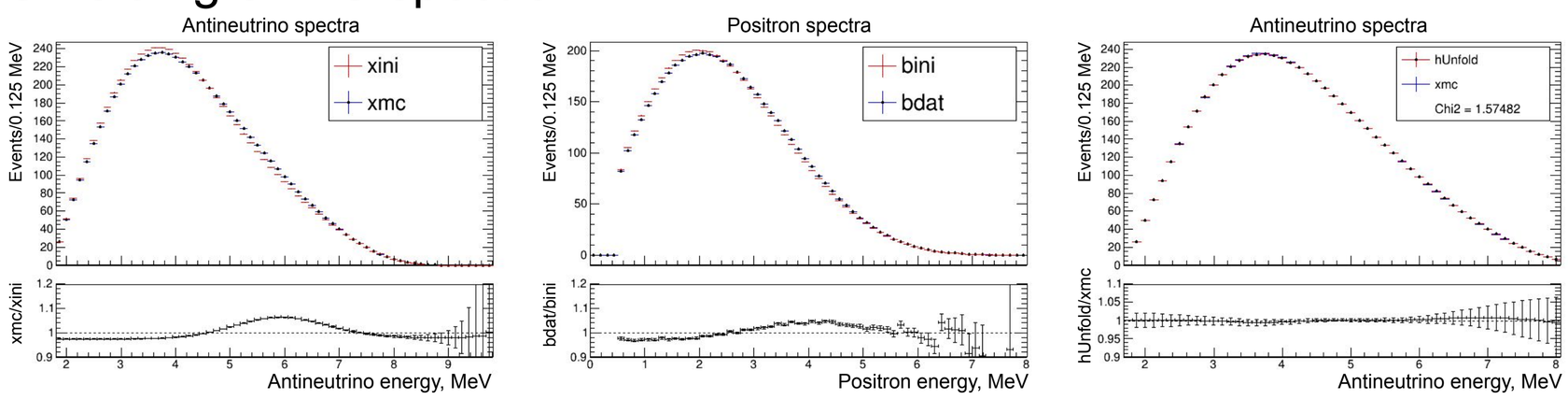
Choosing regularization

A k value scan for x_{unfold} was carried out during unfolding to find the minimum χ^2.

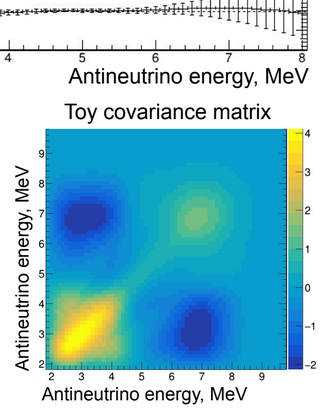
$$\chi^2 = \sum_{i=1}^{n} \frac{(x_{\mathrm{true}}^i - x_{\mathrm{unfold}}^i)^2}{V_x^{ii}}$$



Unfolding of MC spectra



xini(bini): prior distribution of antineutrinos (positrons) (passed to the algorithm for prescaling)
xmc: true distribution to be reconstructed (bump at 5.5 MeV added, this inspired by Daya Bay's unfolding result)
bdat: "measured" positron spectrum for true xmc antineutrino spectrum (with statistical fluctuations and detector effects)
hUnfold: unfolded spectrum of antineutrinos



Discussion

- Unfolding of the Monte-Carlo spectra using SVD decomposition gives a good estimate of the true spectra and allows to reconstruct the bump.
- However, due to the regularization term, bias towards the prior distribution is possible.
- By generating samples and scanning the Chi2 curve, it is possible to estimate the optimal regularization parameter.
- A study of systematics showed that the greatest contribution is made by energy shift and scaling.