



# Cross-section extraction using template fitting in T2K cross-section measurements

Margherita Buizza Avanzini for the T2K collaboration





October 3rd 2023

# **Outline of the talk**

- 1. Measuring a neutrino cross section
- 2. Binned likelihood fitters as unfolding methods allowing complex analyses
- 3. What can we learn from the post fit informations: lots of diagnostics
- 4. From the post fit results to the cross section extractions



### What is a cross section?



# What is a cross section?



- Signal, to be defined considering the detector capabilities ⇒ final state topology
- Selected signal samples contain also some background ⇒ need of background samples
- Observables, to be chosen considering the detector capabilities (ND280 is tracking detector!) ⇒
  usually lepton and/or hadron kinematics
- Limit interaction model dependence of the efficiency correction ⇒ perform **2D** (or more) differential measurements, phase space restriction,... See more in S. Jenkins talk on thursday
- Cross section usually extracted as a function of the true variables ⇒ unfolding of detector effects

# What do we need to measure a cross section?

(taking as an example the Oxygen and Carbon CCOpi measurement from T2K)



Signal selections, that apply on the reconstructed events with an adequate choice of observables, for instance lepton kinematics



A Montecarlo prediction, that is the fundamental tool to:

- 1. have a first estimate of the background contamination and sample purity
- 2. move from the reco to the truth space (detector unfolding matrix and efficiency correction)
- 3. find the needed MC adjustments when compared to data



#### **Background selections**



data driven constraint of the background 5 remaining in the signal samples

Since your starting point is a Montecarlo prediction, you should take into account three main systematics sources that will affect it:

#### The neutrino flux prediction

In T2K, thanks to external experiment, we are able to quote the uncertainty on our flux predictions in bins of true neutrino energy



Since your starting point is a Montecarlo prediction, you should take into account three main systematics sources that will affect it:

#### The neutrino flux prediction

In T2K, thanks to external experiment, we are able to quote the uncertainty on our flux predictions in bins of true neutrino energy

#### The interaction model uncertainties

In T2K, we have a tool that allows to estimate the reweight to be applied to each event when we vary the value of specific parameters affecting the neutrino interaction predictions



Since your starting point is a Montecarlo prediction, you should take into account three main systematics sources that will affect it:

#### The neutrino flux prediction

In T2K, thanks to external experiment, we are able to quote the uncertainty on our flux predictions in bins of true neutrino energy

#### The interaction model uncertainties

In T2K, we have a tool that allows to estimate the reweight to be applied to each event when we vary the value of specific parameters affecting the neutrino interaction predictions

#### The detector effects

In T2K, a series of detector systematics are estimated by comparing reconstruction results between the MC and data. Uncertainties can be propagated to the MC predictions



from <u>O and C CCOpi</u> analysis

Since your starting point is a Montecarlo prediction, you should take into account three main systematics sources that will affect it:

#### The neutrino flux prediction

In T2K, thanks to external experiment, we are able to quote the uncertainty on our flux predictions in bins of true neutrino energy

#### The interaction model uncertainties

In T2K, we have a tool that allows to estimate the reweight to be applied to each event when we vary the value of specific parameters affecting the neutrino interaction predictions

#### The detector effects

In T2K, a series of detector systematics are estimated by comparing reconstruction results between the MC and data. Uncertainties can be propagated to the MC predictions

$$\frac{d\sigma}{dx_i dy_k} = \frac{N_{ik}^{signal}}{\varepsilon_{ik} \Phi N_{nucleons}^{FV}} \times \frac{1}{\Delta x_i \Delta y_k}$$

The effect of these uncertainties will propagate on several elements of the cross-section calculation

# What are the info contained in the reco bins?



We usually have several reconstructed signal samples as well as several reconstructed background samples

We usually bin reconstructed events in well reconstructable observables (like  $\cos\theta_{\mu}$  and/or  $p_{\mu}$ ), that are also the variable we could use to extract the cross section

In a reconstructed CC0 $\pi$  (cos $\theta_{\mu}$ ,  $p_{\mu}$ ) bin (j) we have N<sub>j</sub> reco events:



# What are the info contained in the reco bins?



We usually have several reconstructed signal samples as well as several reconstructed background samples

We usually bin reconstructed events in well reconstructable observables (like  $\cos\theta_{\mu}$  and/or  $p_{\mu}$ ), that are also the variable we could use to extract the cross section

In a reconstructed CC0 $\pi$  (cos $\theta_{\mu}$ ,  $p_{\mu}$ ) bin (j) we have N<sub>j</sub> reco events:

Reweight due to Num. of signal events Num. of background the systematics in the true bin i events in the true bin i according to the MC according to the MC effect **∧***T*signal bkg Mbkg signal  $W_i$ Reweight due to Smearing matrix to the systematics = what we want to extract move from the truth effect to the reco bins

Template parameters ARE the parameters of interest in our xsec analyses

They are **FREE** parameters that rescale the MC signal events (eventually corrected by some systematics) and thus they have the dominant effect (wrt the systematics parameters)

There is **one** template parameter **per truth signal bin** (in which you want to extract your cross section)

They thus apply on the MC truth space and on MC truth bins of signal events but they try to adjust the data/MC agreement in the reco space (the one that we really measure)

reco

true bins

effect

Data/MC correction, aka

template parameters



Reweight due to

the systematics

effect

Smearing matrix to

move from the truth

to the reco bins

Num. of reco events in the reco bin j and sample s



Num. of reco events in the reco bin j and sample s

Moving parameter c<sub>20</sub> ⇔ moving the signal content of truth bin 20 ⇔ moving the signal content of ALL the reco bins corresponding to true bin 20 ⇔ agreement with data is checked in the reco space

reco

true bins



Num of reco events in the reco bin j and sample s

#### Zoom on the template parameters from <u>O and C CCOpi</u> analysis





sample s



Smearing matrix for SIGNAL EVENTS (CC0pi on Oxvgen)

### Concretely :

i

- template parameters vary signal events in the truth space but this also affects the reco distributions where we can compare with real data (~ the unfolding matrix is recalculated at each iteration)
- template parameters are totally free ⇒ the unfolding process is totally unregularised (~ D'Agostini iterative unfolding with infinite num. of iterations)
- Regularisation can be introduced to smoothen the fit results ⇒ optional and checked to give results equivalent to the unregularised ones
- we work with a number of reconstructed bins much larger than the number of true bins ⇒ this limits the problem of "degenerate" solutions of the unfolding See also Lukas' talk from yesterday

\_Data/MC correction, aka template parameters Smearing matrix to move from the truth to the reco bins <sup>17</sup>

Moving parameter  $c_{14} \Leftrightarrow$  moving the signal content of truth bin  $16 \Leftrightarrow$ moving the signal content of ALL the reco bins corresponding to true bin 16 ⇔ agreement with data is checked in the reco space

Num. of reco events

in the reco bin j and

sample s

# **Cross section fitter**



Adjust the **unconstrained template pars in the truth space** to match the MC and data distributions in the reco space (especially in the signal samples)

Adjust the constrained nuisance parameters to match the MC and data distributions ⇒ propagation of systematics uncertainties Affect simultaneously the truth and the reco distributions ⇒ unfolding of the detector effects Simultaneously on signal and background samples ⇒ background subtraction

# T2K cross section fitter vs T2K model tuning



Adjust the unconstrained template pars in the truth space to match the MC and data distributions in the reco space (especially inthe signal samples)

Adjust the constrained nuisance parameters to match the MC and data distributions ⇒ propagation of systematics uncertainties Affect simultaneously the truth and the reco distributions ⇒ unfolding of the detector effects Simultaneously on signal and background samples ⇒ background subtraction

> Cross section likelihood fitter is a <u>complexification</u> of the likelihood fitter approach that we use to tune the flux and neutrino interaction models for the T2K oscillation analysis

> The MAIN difference consists in the presence of <u>template parameters</u> (~ free parameterisation of the SIGNAL cross section!) and of the <u>unfolding process</u>

# **Cross-section fitter**



Adjust the **unconstrained template pars in the truth space** to match the MC and data distributions in the reco space (especially in the signal samples)

Adjust the constrained nuisance parameters to match the MC and data distributions ⇒ propagation of systematics uncertainties Affect simultaneously the truth and the reco distributions ⇒ unfolding of the detector effects Simultaneously on signal and background samples ⇒ background subtraction

By minimizing these two quantities with Minuit (Migrad/HESSE)

dominated by the effect of the template FREE parameters (for signal samples)

> encodes all our prior knowledge of the systematics parameters

$$2\ln(L^{\text{stat}}) = \sum_{s}^{\text{sub-samples reco bins}} 2\left(N_j^s - N_j^{s, \text{ obs}} + N_j^{s, \text{ obs}} \ln \frac{N_j^{s, \text{ obs}}}{N_j^s}\right)$$

$$-2\ln(L^{\text{syst}}) = \sum_{p} \left(\vec{p} - \vec{p}_{\text{prior}}\right) \left(V_{\text{cov}}^{\text{syst}}\right)^{-1} \left(\vec{p} - \vec{p}_{\text{prior}}\right)$$

NOTE: showing here the Poisson likelihood... but could also be in its Barlow-Beeston version NOTE 2: it is a binned likelihood fitter, but concretely parameters apply on an event-by-event basis

# **Cross-section fitter**



Adjust the **unconstrained template pars in the truth space** to match the MC and data distributions in the reco space (especially in the signal samples)

Adjust the constrained nuisance parameters to match the MC and data distributions ⇒ propagation of systematics uncertainties Affect simultaneously the truth and the reco distributions ⇒ unfolding of the detector effects Simultaneously on signal and background samples ⇒ background subtraction



# **Cross-section extraction**



### Fitter inputs: samples and template parameters



A typical example of input root file for the cross section likelihood fitter.

Per each event you need common information like: the neutrino type, the sample number, the true topology and reaction, the target type, the reco and truth kinematics variables, you are interested in,...

Here  $p_{\mu}$  and  $cos \theta_{\mu}$  are indicated as D1 and D2

Template parameters are introduced as weight parameters by simply defining the binning in truth variables that you want to use for the cross section extraction

### How we describe the FLUX and DETECTOR systematics

In both cases we have a series of weight (normalisation) parameters that can <u>gaussianly</u> move around their nominal value (1) according to a prior covariance matrix.

- Flux parameters are defined as one per bin of true neutrino energy (10 to 40 pars, depending on the analysis)
- Detector parameters are defined as one per reconstructed bin (~50 to ~1000 pars, depending on the analysis)





#### Example of flux correlation matrix

24

## How we describe the v INTERACTION systematics

Per each interaction parameter we construct so-called splines or response functions. They are usually, binned, i.e. they are constructed per reco or truth kinematics bin, per true neutrino interaction, per sample, per target nuclei. They encode the weight to be applied at each bin per each possible value of the parameter



Signal sample: mu in TPC True Bin 5 ( $0.6 < \cos\theta_{\mu} < 0.75, 0 < p_{\mu} < 0.35$ ) True interaction: CCQE Target: Oxygen



Once more, input covariance matrices encode the prior error of each parameter and the possible correlation between them

### Example of fitter outputs: fit parameter in an Asimov fit



T2K preliminary





Asimov fit (where MC prior = fake data) are a good way to test the overall fit machinery and the overall analysis sensitivity.

You expect:

- post fit parameter values to be identical to the prefit values
- post fit parameter errors to be ≤ the prefit errors

From the first on/off-axis CCOpi joint analysis

### Example of fitter outputs: fit parameters in a Fake data fit



T2K preliminary







Performing fake data studies is the way to answer:

- Is the fitter able to reproduce the fake data truth?
- Is my systematic model introducing enough freedom to the fitter to correctly adjust parameter values w/o biasing the signal results?

In a likelihood fitter you can check that the parameters in the fit move towards the expected values

For instance, in this example the fake data is obtained by modifying the signal cross section w.r.t. the nominal values:

- CCOpi off-axis x 0.8
- CCOpi on-axis x 1.2

 $\Rightarrow$  this is exactly what the post fit template pars values reproduce 27

### Example of fitter outputs: number of events is reco space and postfit -2InL ( $\chi^2$ )

Just a subset of reco samples



A series of diagnostics of the results:

- Checking the agreement in the reco space (num of events per bin)
- quoting the value of the total -2InL ( $\chi^2$ )
- quoting the value of the  $\chi^2$  per sample  $\Rightarrow$  this is a way to verify if there is a particularly problematic sample

## Additional fit diagnostic: p-value

So-called "coverage studies" are realized by performing a series of fits on a series of fake data (FD) distributions. FD are obtained by simultaneously:

- statistically varying the content of each reconstructed bin (Poisson, bin-to-bin independent)
- throwing all the systematics parameters based on their prior values and errors

You then construct the  $\chi^2$  curve using the postfit value of the -2lnL of each fit. This gives you:

- the effective number of degrees of freedom (~N<sub>bin</sub> N<sub>Template pars</sub>)
- the possibility to quote the p-value once you perform the fit on real data (is the analysis model compatible with the data fit?)



### Post fit correlation and covariance matrix

From an ongoing O/C CCOpi joint analysis



In addition to the post fit parameters values and errors, the fit also provide the post fit **covariance and correlation matrices** that encode the covariances and correlations among all the parameters.

This is a fundamental ingredient that we need to move from the "postfit space" to the "cross-section space"

# The cross-section extraction and the error propagation: the concept



Post fit errors, covariances and values of each parameter are the fundamental ingredients to calculate the value of the cross section in each true bin and estimate the corresponding error. This is done throwing toys starting from the post fit covariance matrix and parameter values: at each toy a new set of template+nuisance parameters is estimated by gaussianly varying the best fit value of each parameter according to the post fit covariance matrix

Per each toy, all the quantities entering in the cross-section calculation are recalculated and used to estimate the cross-section value in each bin. Over a big number of toys, the cross section in each bin is estimated as the mean (or the value obtained at the best fit), while its corresponding error is the RMS of the distribution



Ongoing CH/water CCOpi joint analyses

### Extracting the cross section: fake data



### Extracting the cross section: real data



### **XSEC** covariance matrices



The other fundamental ingredient you need to provide in order to safely compare your xsec results with model predictions

### **Final remarks**

Template fitting is used in T2K for cross section extraction since ~ 8 years, including a series of joint analyses, and will continue to be the reference unfolding method

This is an unfolding method allowing a series of useful **diagnostic** about the correctness of your results

In the years, we refined and **optimized a series of techniques:** coverage studies, error propagation, data release

Same for the fitter itself: we started with a software (manual) sharing between collaborators, moving then to the <u>Super-xsLLHFitter</u> and recently to <u>GUNDAM</u>, an open source tool that encodes all the features (+ many others!) of the T2K cross section fitter and of the T2K near detector fitter used for the oscillation analysis *See L. Munteanu's talk tomorrow* 

See next talk (N. Latham) for additional details on T2K template fitters for xsec!



### Systematics error contributions

from the joint on/off-axis analysis



#### from the joint O/C analysis



# How we describe the FLUX systematics

Taking as an example used inputs for the ongoing water and CH CCOpi analysis of T2K

Uncertainty on the flux can affect:

- the shape of the spectrum, i.e. the number of events per bin (numerator in the xsec)
- The total integrated flux (denominator in the xsec)



#### Input flux covariance matrix (v\_i in v\_i beam)

In T2K (cross-section) analyses, flux systematics are implemented as weight parameters that affect the true events depending on the neutrino energy and according to a prior covariance matrix provided by the beam experts

# How we describe the DETECTOR systematics

Taking as an example used inputs for the published O and C CCOpi analysis of T2K

In a similar way as for the flux, we provide a prior covariance matrix, by taking into account the event rate change in each reco bin and sample when varying all the detector systematics together.

Detector parameters act as weight parameters on each event depending on its reconstructed bin and samples and according to the input covariance matrix



# **Cross-section extraction**



Adjust the **unconstrained template pars in the truth space** to match the MC and data distributions in the reco space (especially in the signal samples)

Adjust the constrained nuisance parameters to match the MC and data distributions ⇒ propagation of systematics uncertainties Affect simultaneously the truth and the reco distributions ⇒ unfolding of the detector effects Simultaneously on signal and background samples ⇒ background subtraction

By minimizing these two quantities with Minuit (Migrad/HESSE)

$$\begin{array}{l} \begin{array}{l} \mbox{dominated by the effect of the} \\ \mbox{template FREE parameters} \end{array} = 2\ln(L^{\rm stat}) = \sum_{s}^{\rm sub-samples reco bins} 2\left(N_{j}^{s} - N_{j}^{s, \, obs} + N_{j}^{s, \, obs} \ln \frac{N_{j}^{s, \, obs}}{N_{j}^{s}}\right) \\ \mbox{encodes all our prior knowledge} \\ \mbox{of the systematics parameters} \end{array} = 2\ln(L^{\rm syst}) = \sum_{p} \left(\vec{p} - \vec{p}_{\rm prior}\right) \left(V_{\rm cov}^{\rm syst}\right)^{-1} \left(\vec{p} - \vec{p}_{\rm prior}\right) \\ \mbox{Optional regularisation term that helps to} \\ \mbox{smoothen anticorrelation between nearby ci} \end{array} = \left[ -2\ln\mathcal{L}_{reg} = \lambda \sum_{j}^{N-1} (c_{i} - c_{i+1})^{2} \right] \text{see backup} \qquad 42 \end{array}$$

# Regularisation

Known effect of the unfolding procedure: when the binning is fine wrt detector resolution, many combinations of true bins lead to the same set of reconstructed bins. The unfolded results appear to fluctuate around the truth, cursing a typical "zig-zaging" between near-by bins

Introduce penalty terms in the likelihood to avoid too big bin-to-bin "oscillations". Can indeed bias the final result towards the input model  $\Rightarrow$  L-curve method to decide the "strenght" of the regularisation by balancing between the obtained smoothness against the introduced bias.







# The effect of the regularisation



→ O regularised results

- O unregularised results



# Regularisation

Regularised and un-regularised results perfectly compatible

however regularised results are less zig-zaging and in principle easier to interpret "by-eye"

Anyway a proper estimation of the data/model agreement still needs the use of the post fit covariance matrix

In other word, applying a resularisaiton corresponds to select a subset of degenerate models without large fluctuations between neighboring bins. The penalty term enforces this extra constraint based on the assumption that the large fluctuations are unphysical, but this may also bias the results as a whole. The full, unreguarized result is best, but regularization can be used to choose the exact fit point used in published plots, since any of the degenerate results in the set are essentially equivalent even if they have small differences in the chisq.

# **Covariance and correlation matrices**



# From the reco to the truth space

#### **Reco space**

Truth space



# The binned likelihood fitter

Then we perform a binned likelihood fit where we try to minimize:

$$\begin{split} \chi^{2} &= \chi^{2}_{stat} + \chi^{2}_{syst} + \chi^{2}_{reg, p} + \chi^{2}_{reg, \theta} \\ &= \sum_{j}^{reco\,bins} 2(N_{j}^{MC} - N_{j}^{obs} + N_{j}^{obs}\ln\frac{N_{j}^{obs}}{N_{j}}) + \chi^{2}_{syst} + \chi^{2}_{reg, p} + \chi^{2}_{reg, \theta}, \end{split}$$

#### Key features of the fitter

- Unconstrained fit (or template) parameters that estimate the signal in each bin ⇒ minimize the model dependence!
- Detector, flux and theoretical interaction parameters included as **nuisance parameters** ⇒ reduce the systematics!
- Data-driven regularization ⇒ minimize the anti-correlation between adjacent bins (optional)!

### **Cross section extraction**



### The Barlow-Beeston likelihood

$$-2\ln\mathcal{L}_{stat} = \chi_{stat}^2 = \sum_j^{\text{bins}} 2\left(\beta_j N_j^{\text{exp}} - N_j^{\text{obs}} + N_j^{\text{obs}} \ln\frac{N_j^{\text{obs}}}{\beta_j N_j^{\text{exp}}} + \frac{(\beta_j - 1)^2}{2\sigma_j^2}\right)$$

# From the reco to the truth space

