# Investigating the efficacy of Novel Statistical Methods in Neutrino Oscillation Analysis

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# Why does this new statistical test think they have what it takes to go all the way?

•Multivariate analysis (multiple measurements made on each experimental unit) plays a key role in our understanding of neutrino oscillations as it is used to test the compatibility of experimental and simulated data.

processing

time

•Since neutrinos are very difficult to detect, we have limited events and so the phase space in the multidimensions is sparsely populated [1]. Despite this, the compatibility is still often tested by binning the data and computing a test statistic called the **Pearson's**  $\chi^2$  [2].

Too many bins with low occupancy reducing significance of discrepancy between data sets

**Too few bins** that fine structure is hidden.

•Binning data always results in a loss of information and an unsatisfactory compromise must be made between too many and too few bins.

•For these reasons, it's expected that methods that don't involve binning can perform better, specifically the "point to point dissimilarity method".

## What are the tests we are comparing?

## In the red corner - Point to Point Dissimilarity Test

$$T = \frac{1}{n_d(n_d - 1)} \sum_{i,j \ge 1}^{n_d} \psi(|\mathbf{x}_i^d - \mathbf{x}_j^d|) + \frac{1}{n_{mc}(n_{mc} - 1)} \sum_{i,j \ge 1}^{n_{mc}} \psi(|\mathbf{x}_i^{mc} - \mathbf{x}_j^{mc}|) - \frac{1}{n_d n_{mc}} \sum_{i,j \ge 1}^{n_{mc}} \psi(|\mathbf{x}_i^d - \mathbf{x}_j^{mc}|)$$

Where the scripts d and mc refer to actual and MC simulated data, n refers to number of data events, and x is the event position vector [3].

- Based on the distance between a point and every other data and Monte-Carlo point.
- No loss of information can slow the computing process down.
- Uncommonly used technique, not much literature on best usage.

## Kernel Function $\psi(|x_i-x_j|)$ :

The kernel function is effectively a weighting function acting on every pair on points, we will be investigating:

- How 4D space can be rescaled to give all dimensions equal potential in affecting the value of T
- Whether the Kernel function would be more effective taking in 4 variables rather than a simple "distance" variable.

# In the blue corner - The Chi-Squared Test

$$\chi^2 = \sum_{i}^{n_b} \frac{(O_i - E_i)^2}{E_i}$$

Where  $n_b$  is the number of bins,  $O_i$  is the observed and  $E_i$  is the expected number of data events in the  $i^{th}$  bin [2].

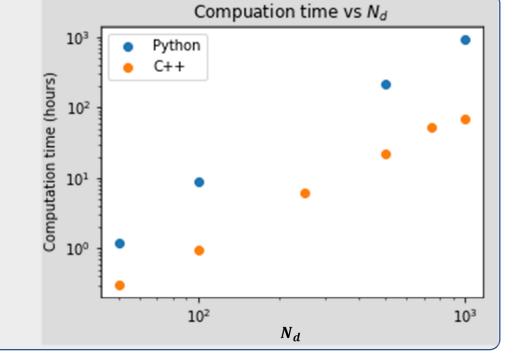
- Smaller  $\chi^2$  values mean greater agreement
- Has to be used on binned data since it tests the number of occurrences at a value/range
  - Loss of information due to binning of points causing large variations in the binned data [4].

Loss of information due to binning of data

## Reducing the processing time

#### Python vs C++

- Python is much slower since it uses an interpreter and also determines the data type at run time.
- Python code can easily be converted into Cython code by specifying the data types, which generates C++ optimised code [5].



#### How are we going to compare the tests?

## p-value distributions

The agreement between the data sets is quantified by the test statistics of  $\chi^2$  and T. These measure different things and so we want to use them to form a mutual quantity we can compare them on: the distribution of p-values.

The p-value quantifies the significance of any discrepancy between the data and the probability density function (p.d.f. - defines a probability for a discrete random variable). This is defined for a test statistic S as the probability of finding an S-value corresponding to lesser agreement than the observed S-value:  $p = \int_{S}^{\infty} g_{f_0}(S) dS$ 

 $g_{f_0}(S)$  corresponds to the p.d.f. of the test statistic when both the actual and MC data come from the same parent p.d.f. [6].

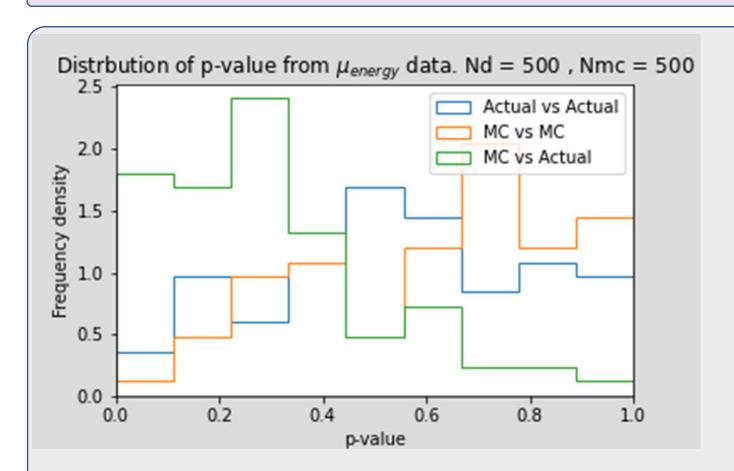
## **Permutation test** [7]

- 1. Combine both the actual and MC simulated data sets into a pool of size  $N_d + N_{mc}$ .
- 2. Randomly draw a sample of size  $N_d$  and temporarily label this "actual data", label the remaining "MC simulated" data.
- 3. Calculate the corresponding T known as  $T_1$ .
- 4. Repeat this n times to obtain  $T_{perm} = \{T_1, T_2, \dots, T_{N_{perm}}\}$
- 5. The p-value can then be estimated using:

$$p \approx |T_{perm} > T|/|T_{perm}|$$

- The p.d.f. of a  $\chi^2$  distribution with  $n_b$  degrees of freedom is well documented (and dependent on the data set) meaning the p calculation is straightforward.
- The p.d.f. of the 'point to point dissimilarity function' is dependent on the data, and is not well known meaning p must be estimated using the permutation test.

# What are the results of the comparison?



Distributions of p-values were plotted (like the one on the LH side), and the rejection power at 95% confidence interval calculated.

## The point to Point Dissimilarity test shown to be superior to the $\chi^2$ test:

This is a very powerful goodness of fit tool. It showed excellent rejection power for  $N_d \ge 1,000$ , and was superior to  $\chi^2$  for all  $N_d$  tested. The downsides include: not being as easy to understand conceptually as the  $\chi^2$  test and slow computation time. However the latter can be greatly reduced by using Cython (or straight C++ code).

#### Rejection power at 95% confidence interval $N_d$ 12% 3%

100

83% 33% 500 67% 1,000 100%

#### Ideas for further study:

- Analyse other "non binning tests" such as: the distance to nearest neighbour test, the local density test.
- Investigate using different definitions of distance between two points, that is, use values of  $p \neq 2$  in the Minkowski distance (generalised distance) [8]:  $D(X,Y) = (\sum_{i=1}^{n} |x_i - y_i|^p)^{1/p}$ .

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