Statistical Methods for the Neutrino Mass Hierarchy Determination

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Statistical Distribution

The two hierarchies are non-nested hypothesis, hence Wilks' theorem cannot be applied. This means that the $\Delta\chi^2$, defined as

$$\Delta\chi^2 = \chi^2_{IH} - \chi^2_{NH}$$

does not follow a one-degree-of-freedom χ^2 distribution and the number of σ's $n \neq \sqrt{\Delta\chi^2}$. Under certain conditions it instead follows a Gaussian distribution [1, 2, 3] with $\sigma = 2\sqrt{\overline{\Delta\chi^2}}$, where $\overline{\Delta\chi^2}$ is the expected $\Delta\chi^2$. These conditions seem to be satisfied in the case of reactor neutrino experiments, but not in the case of accelerator neutrino experiments.

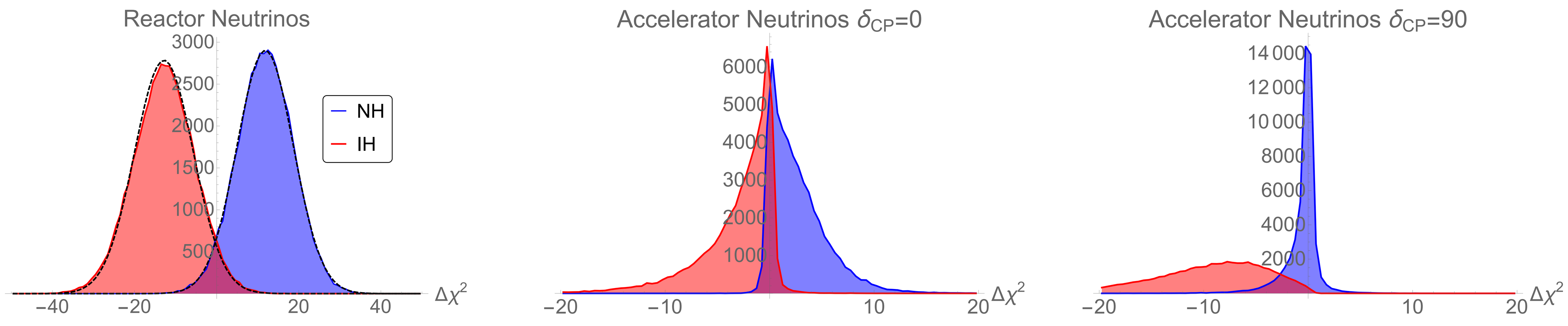


Figure 1: Left Panel: Pdf of $\Delta\chi^2$ in reactor neutrino experiments; the dashed curves are Gaussian fits. Central and right panels: Pdf of $\Delta\chi^2$ for accelerator neutrinos, using different values of δ_{CP} [4]

Additional Parameter

A possible solution for the non-nested problem is to introduce a new pull parameter, without physical meaning: this was proposed first in [5] for reactor neutrino experiments, writing

$$|\Delta m^2_{31}| = |\Delta m^2_{32}| + (2\eta - 1)|\Delta m^2_{21}|$$

$\eta = 1 \rightarrow$NH, $\eta = 0 \rightarrow$ IH. A more general approach, that can be used also with accelerator neutrinos, was suggested in [6], considering the linear combination

$$\eta f(E) + (1 - \eta) g(E)$$

where $f(E)$ and $g(E)$ are the spectra for normal and inverted hierarchy, respectively. In this way the problem is reduced to parameter fitting; $\Delta\chi^2$, which can be defined for both hierarchies, now follows a χ^2 distribution

$$\Delta\chi^2_{NH} = \chi^2_{\eta=1} - \chi^2_{\min} \qquad \Delta\chi^2_{IH} = \chi^2_{\eta=0} - \chi^2_{\min}$$

Laplace Method

In the Bayesian approach, if additional pull parameters $\boldsymbol{\theta}$ are present they must be **marginalized**, *i.e.*

$$\Pr(\mathbf{D}|MH) = \int \Pr(\mathbf{D}|MH, \boldsymbol{\theta})\pi(\boldsymbol{\theta})\mathrm{d}^n\boldsymbol{\theta}$$

while in the frequentist approach they are **minimized**, using the best fit value for $\boldsymbol{\theta}$.
When several pull parameters are present, marginalization requires multi-dimensional integrals. However, if the χ^2 is strongly peaked around the minimum, and Det(C) is the same for the two hierarchies (C=covariance matrix), using the Laplace method we can prove that

$$\Delta\chi^2_B = \Delta\chi^2_F$$

$\Delta\chi^2_B, \Delta\chi^2_F$ are the $\Delta\chi^2$ obtained marginalizing or minimizing over the pull parameters, respectively.

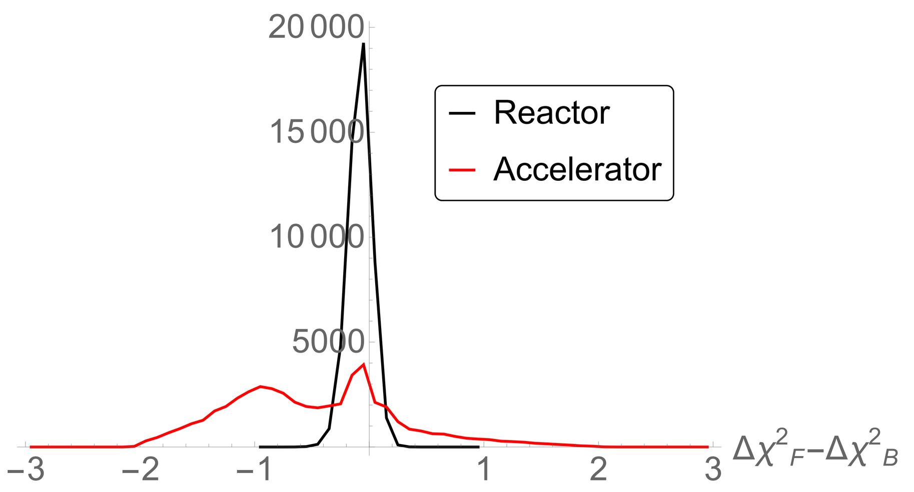


Figure 2: Difference between marginalization and minimization in accelerator and reactor neutrino experiments (simplified models with only one parameter)

Frequentist Approach

Hypothesis Test [3] We test the two hierarchies separately: before the experiment, we define two threshold $T_{c,NH}$ and $T_{c,IH}$; if $\Delta\chi^2 > T_{c,IH}$ the inverted hierarchy is rejected, if $\Delta\chi^2 < T_{c,NH}$ the normal hierarchy is rejected :

- The confidence level (CL) that can be achieved depends only on $T_{c,NH}$, $T_{c,IH}$, not on the actual result of the experiment (that determines only if such a CL is achieved or not) $\Rightarrow$ convenient to quantify the precision of future experiments
- It is possible to accept or reject both hierarchies at the same time
- To calculate CL we need to know the pdf of $\Delta\chi^2$; problems when it depends strongly on pull parameters

Possible definition of sensitivity (for the Gaussian, symmetric case, generalization is trivial):

- **Median Sensitivity**: $T_{c,NH(IH)} = -(+)\overline{\Delta\chi^2}$. $n = \sqrt{\overline{\Delta\chi^2}}$, power=0.5
- **Crossing Sensitivity**: $T_{c,NH} = T_{c,IH} = 0$, $n = \sqrt{\overline{\Delta\chi^2}}/2$, power=CL

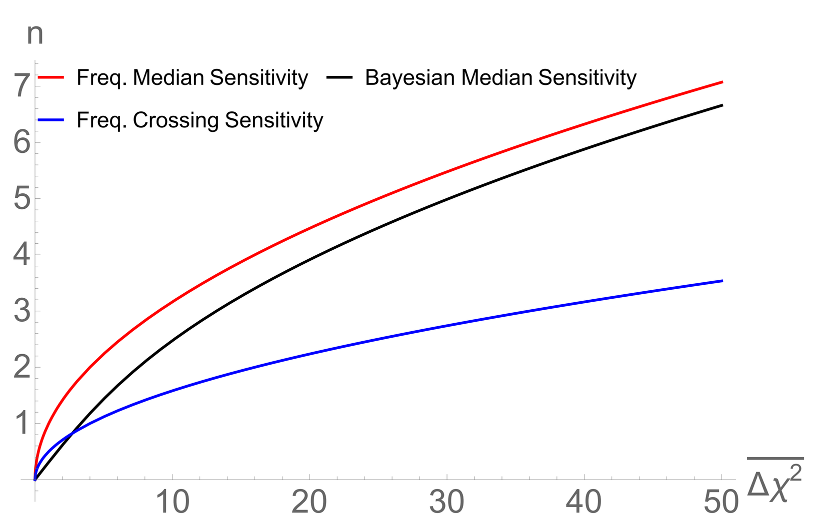
p-value Probability of getting a "more extreme" result than the one obtained from the experiment

$$\text{p-value} = \Pr(\Delta\chi^2 > (<)\Delta\chi^2_{obs}|IH(NH))$$

- Also relies on the knowledge of $\Delta\chi^2$'s pdf
- **Two** quantities must be considered: **both** the p-values for NH and IH. Ex: NH excluded at 5σ's, IH excluded at 1σ's or NH excluded at 5σ's, IH excluded at 5σ's
- p-value(NH)«1 does not necessarily implies IH

Bayesian Approach [2, 4]

- **Frequentist Approach** $\Rightarrow$ Pr(**D** | MH): probability of the data **D** given MH. Suppose we find p-value(NH)=0.0001: alone not enough to say NH is unlikely
- **Bayesian Approach** $\Rightarrow$ Pr(MH | **D**): probability that the hierarchy is normal (or inverted) given the data



Using Bayes theorem

$$\Pr(NH|\mathbf{D}) = \frac{\pi(NH)}{\pi(NH) + \pi(IH)K^{-1}}$$

Bayes Factor: $K = \dfrac{\Pr(\mathbf{D}|NH)}{\Pr(\mathbf{D}|IH)} = e^{-\Delta\chi^2/2}$

- Provide a single quantity $\rightarrow$ better quantify likelihood of NH vs. IH
- Depends upon the choice of priors! However very natural choice for MH: $\pi(NH) = \pi(IH) = 0.5$
- Bayesian and frequentist give **different (and complementary) information!**.
- More complete analysis by using both approaches

Conclusions

- Some results regarding the pdf of $\Delta\chi^2$, but not applicable to all cases
- Different approaches available: no "right" or "wrong" choices, but important to report the convention used
- Bayesian method gives only **one quantity**, *i.e.* Pr(MH | **D**), while frequentist gives the compatibility of **both** hierarchies with the data
- **Different** and **complementary** information: more accurate analysis reporting both

References

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