



RADPYC2026

NUMERICAL ANALYSIS OF INVERSE SEESAW MODELS AND LEPTON FLAVOR VIOLATION PROCESSES

Aurora Pontón
Gallardo Rodríguez

Advisors:

Dr. Gerardo Hernández
Tomé
Dr. Roberto Noriega
Papaqui

OVERVIEW

| | |
|--|-----------|
| Motivation | 3 |
| Low Scale Seesaw Model | 9 |
| Numerical Analysis Using Bio-Inspired Algorithms | 13 |
| Results and Conclusions | 14 |
| Perspectives | 17 |

HOW DO NEUTRINOS OBTAIN MASS?

- This question arises because neutrino oscillation experiments have shown that neutrinos change flavor as they propagate, which is only possible if they have mass.
- However, in its original formulation, the Standard Model (SM) describes neutrinos as strictly massless particles.

$$-\mathcal{L}_Y = (Y_u)_{ij} \bar{Q}_{L_i} u_{R_j} \Phi + (\tilde{Y}_d)_{ij} \bar{Q}_{L_i} d_{R_j} \Phi + (Y_e)_{ij} \bar{L}_{L_i} e_{R_j} \Phi + \text{h.c.}$$

This is because no right fields are incorporated for neutrinos.

- Therefore, it is necessary to extend the SM introducing new fields or a new mechanism to generate small neutrino masses.

LEPTON FLAVOR VIOLATION (LFV)

- An important point to highlight is that **if neutrinos are massive, then LFV processes are allowed.**

How significant are these effects?

- In the SM, leptons come in three generations, each associated with a conserved lepton flavor number +1, while their antiparticles have -1.

| GENERATION | CHARGED LEPTON | NEUTRINO |
|------------|----------------|------------|
| 1st | e | ν_e |
| 2nd | μ | ν_μ |
| 3rd | τ | ν_τ |

Allowed Process



conserves number and leptonic flavor

Forbidden Process



conserves total lepton number but violates lepton flavor

THE SEESAW MECHANISM

- If right hand fields for neutrinos are allowed then the Seesaw mechanism provide a natural explanation for the smallness of neutrino masses.

$$\mathcal{M}_\nu = \begin{pmatrix} 0 & M_D \\ M_D^T & M_R \end{pmatrix}$$

where M_D is the Dirac mass matrix, and M_R is the Majorana mass matrix for the sterile neutrinos.

- The light neutrino masses arise from their mixing with new heavy states.
- The observed light neutrino masses m_ν are naturally suppressed by the presence of a high mass scale M associated with sterile neutrinos.

$$m_\nu \sim \frac{m_D^2}{M}$$

The heavier the sterile neutrinos are, the lighter the active neutrinos we observe.

THE SEESAW MECHANISM (HIGH SCALE)

- Main drawback: **extremely high mass scale**

In order to explain light neutrino masses of

$$m_\nu \sim 0.1 \text{ eV}$$

with a Dirac mass term of the electroweak scale,

$$m_D \sim 100 \text{ GeV}$$

the Type-I seesaw mechanism predicts a heavy mass scale

$$M_R \sim \frac{m_D^2}{m_\nu} \sim 10^{23} \text{ eV}$$

- Far beyond experimental reach:
current particle accelerators operate at energies of the order of the TeV scale.
- Decoupling of heavy states: effects of new heavy particles are strongly suppressed at low energies. For example, LFV processes.
- **Is there a similar small-scale mechanism?**

LOW-SCALE SEESAW MODELS (LSSM)

- LSSM can generate potentially observable signals:

$$\mu \rightarrow e\gamma, \mu \rightarrow 3e, \mu - eC$$

- These processes are currently being explored by:
 - MEG II, Mu3e, Mu2e, COMET, and PRISM

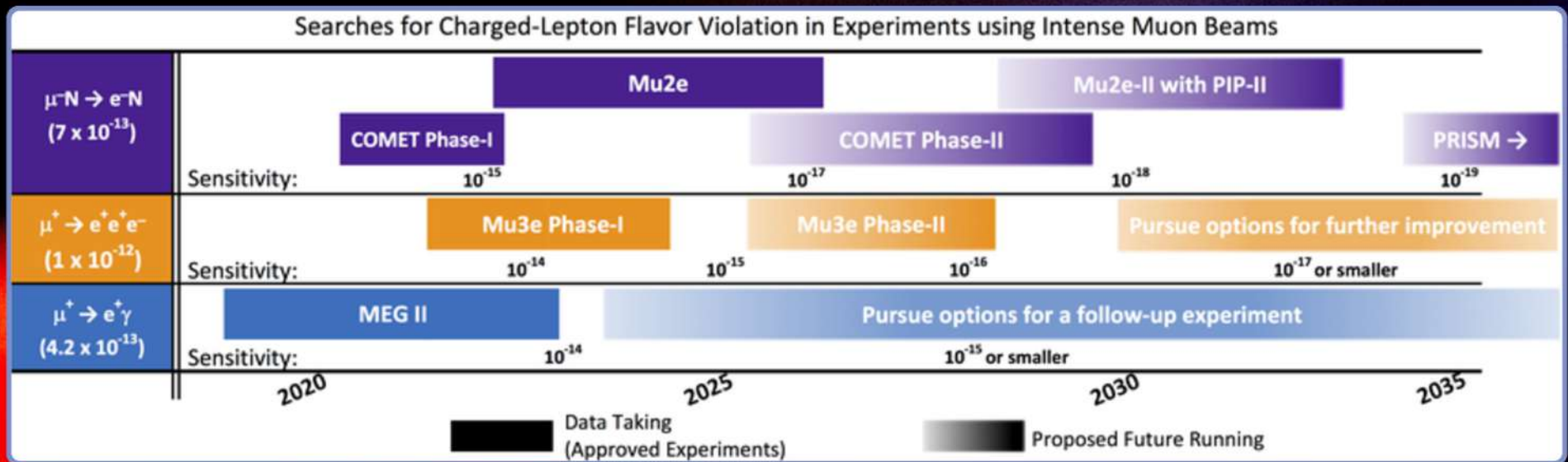


Figure 1: Current and projected sensitivities for muon-based LFV experiments [1].

LOW-SCALE SEESAW MODELS (LSSM)

- The full neutral lepton mass matrix in the LSSM takes the form

$$\mathcal{M}_N = \begin{pmatrix} 0 & M_D^T & M_L^T \\ M_D & 0 & M \\ M_L & M^T & \mu \end{pmatrix},$$

where M_D is a Dirac mass matrix, M is the heavy neutrino mass matrix, M_L and μ are lepton-number violating terms.

LINEAR [2]

$$\mu = 0$$

Small neutrino masses generated by a tiny M_L parameter.

Framework applicable

INVERSE [3]

$$M_L = 0$$

Small neutrino masses generated by a tiny μ parameter.

Focus of this work

[2] Forero, Morisi, Tórtola et al., JHEP 09 (2011).

[3] Gonzalez-Garcia & Valle, Phys. Lett. B 216 (1989).

INVERSE SEESAW MODEL

- We begin our analysis with the *inverse seesaw model*, where the smallness of the lepton number violating parameter μ naturally explains the lightness of active neutrino masses
- The mass matrix takes the 9×9 block form shown here, which describes a total of 6 heavy neutrino states

$$M_{9 \times 9}^{\text{ISS}} = \begin{pmatrix} \mathbf{0}_{3 \times 3} & M_{D_{3 \times 3}} & \mathbf{0}_{3 \times 3} \\ M_{D_{3 \times 3}}^T & \mathbf{0}_{3 \times 3} & M_{3 \times 3} \\ \mathbf{0}_{3 \times 3} & M_{3 \times 3}^T & \mu_{3 \times 3} \end{pmatrix}.$$

the hierarchy among the mass scales is assumed to be

$$|\mu| \ll |M_D| \ll |M|.$$

NEUTRINO MASS MATRIX DIAGONALIZATION

- The neutrino mass matrix can be diagonalized using different methods. In this work, we consider two approaches. As a first step, we adopt the **block matrix diagonalization method (BMDM)** [4].
- This consists of constructing a unitary matrix U_ν such that

$$(U_\nu)^T M U_\nu = M_{\text{diag}}, \quad M_{\text{diag}} = \begin{pmatrix} m_\nu^{\text{diag}} & 0 \\ 0 & M_N^{\text{diag}} \end{pmatrix},$$

where the light and heavy neutrino states are separated perturbatively.

- This method is used as a reference to validate the numerical diagonalization procedures discussed later.

NEUTRINO MASS MATRIX DIAGONALIZATION

- The second approach consists of diagonalizing the full matrix exactly via its eigenvalues and eigenvectors, constructing a unitary matrix U such that:

$$U^\dagger M U = \text{diag}(m_1, m_2, \dots, m_n).$$

- This procedure provides an **exact diagonalization** of the full square mass matrix, including all mixings between light and heavy states.

The numerical analysis is carried out using three complementary approaches to explore the parameter space

| DIAGONALIZATION METHOD | EXPLORATION STRATEGY |
|------------------------|------------------------------|
| Block diagonalization | Random scan |
| Full diagonalization | Random scan |
| Full diagonalization | Bio-inspired algorithms (BA) |

PARAMETRIZATION

- Following the reference [5], the matrices M and μ are assumed to be diagonal:

$$M = v_M \text{diag}(1 + \epsilon_{11}^m, 1 + \epsilon_{22}^m, 1 + \epsilon_{33}^m),$$

$$\mu = v_\mu \text{diag}(1 + \epsilon_{11}^\mu, 1 + \epsilon_{22}^\mu, 1 + \epsilon_{33}^\mu).$$

- The key difference lies in the construction of the Dirac mass matrix:

Garnica et al. (2023)

M_D is constructed using the Casas-Ibarra parametrization [6]:

$$M_D = U_{\text{PMNS}} \sqrt{m_\nu^{\text{diag}}} R^T \sqrt{\mu^{-1}} M^T.$$

With U_{PMNS} : leptonic mixing matrix, m_ν^{diag} : light neutrino mass matrix, R : complex orthogonal matrix (θ, ϕ, ψ) .

This work

M_D is a fully general complex matrix

$$(M_D)_{ij} = m_{ij} + i \tilde{m}_{ij},$$

with $i, j = 1, 2, 3$.

[5] Garnica, Peinado & Hernández-Tomé, Phys. Rev. D 108 (2023).

[6] Casas & Ibarra, Nucl. Phys. B 618 (2001) 171.

PARAMETER SPACE

For the first two numerical approaches, the analysis is performed using **17 free parameters**, which define the scanned parameter space:

| PARAMETER | RANGE |
|---|---|
| $\epsilon_{11}^{\mu}, \epsilon_{22}^{\mu}, \epsilon_{33}^{\mu}$ | $[-0.5, 0.5]$ |
| $\epsilon_{11}^M, \epsilon_{22}^M, \epsilon_{33}^M$ | $[-0.5, 0.5]$ |
| θ, ϕ, ψ | $[0, 2\pi]$ |
| δ_{CP} | $[0, 2\pi]$ |
| $\sin^2 \theta_{12}$ | $[0.271, 0.369]$ |
| $\sin^2 \theta_{23}$ | $[0.434, 0.610]$ |
| $\sin^2 \theta_{13}$ | $[0.02000, 0.02405]$ |
| v_{μ} | $[1, 1000]\text{eV}$ |
| m_1 | $[0, 0.12/3]\text{eV}$ |
| m_2 | $\left[\sqrt{6.94 \times 10^{-5} + m_1^2}, \sqrt{8.14 \times 10^{-5} + m_1^2} \right] \text{eV}$ |
| m_3 | $\left[\sqrt{2.47 \times 10^{-3} + m_1^2}, \sqrt{2.63 \times 10^{-3} + m_1^2} \right] \text{eV}$ |

PARAMETERS WITH BA

For this approach, the analysis is performed using **25 free parameters:**

| PARAMETER | RANGE |
|---|----------------------------------|
| $\epsilon_{11}^{\mu}, \epsilon_{22}^{\mu}, \epsilon_{33}^{\mu}$ | $[-0.5, 0.5]$ |
| $\epsilon_{11}^M, \epsilon_{22}^M, \epsilon_{33}^M$ | $[-0.5, 0.5]$ |
| v_{μ} | $[100, 1000]\text{eV}$ |
| m_{ij}^R, m_{ij}^I | $[5 \text{ MeV}, 5 \text{ GeV}]$ |

PRELIMINARY RESULTS

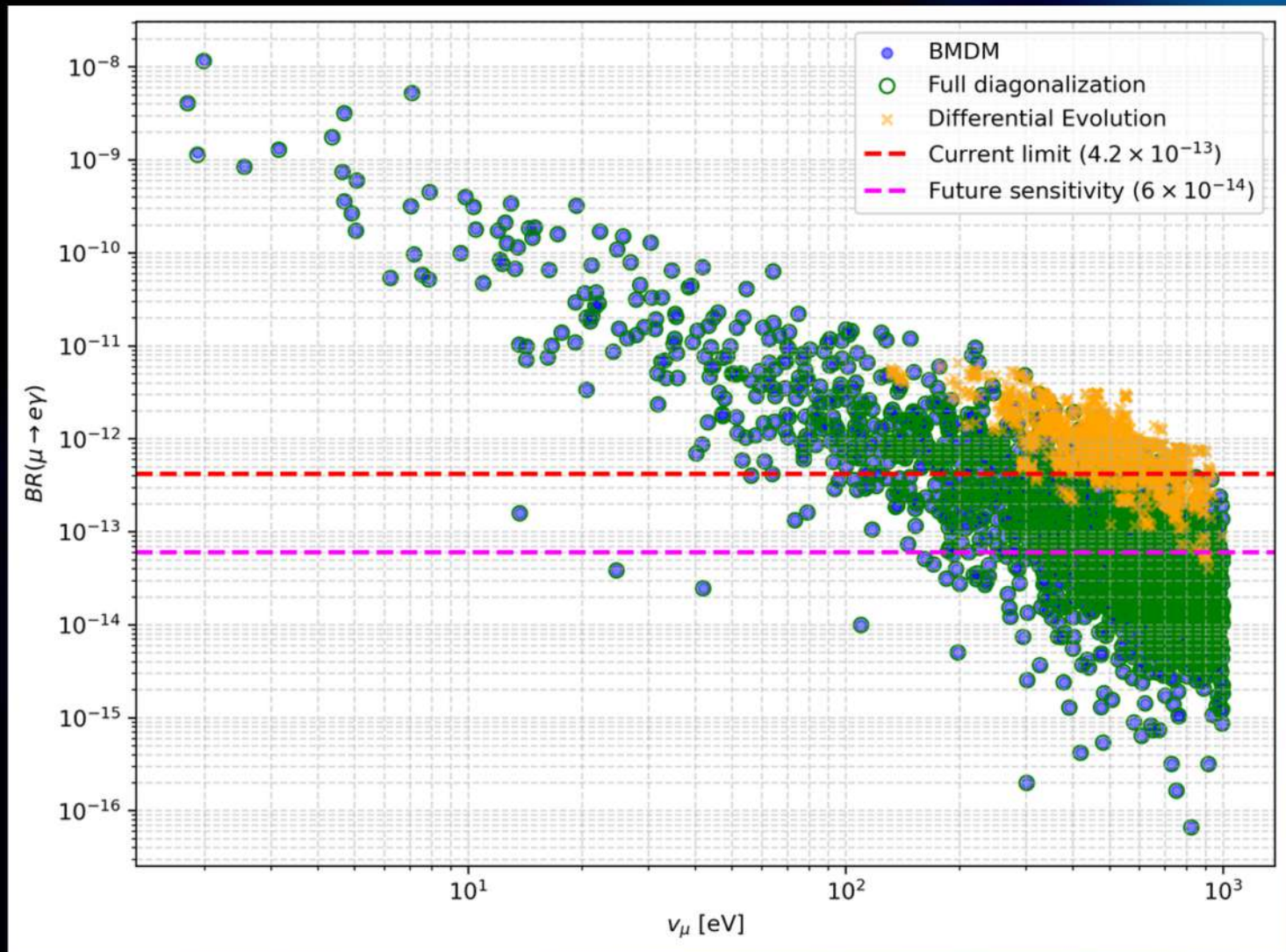


Figure 2: $BR(\mu \rightarrow e\gamma)$ vs ν_μ for three complementary approaches: block diagonalization (random scan), full diagonalization (random scan), and full diagonalization (BA).

PERSPECTIVES

- Implement constraints from $\mu \rightarrow 3e$ and $\mu - eC$.
- Apply the framework to other low-scale seesaw parametrizations.
- Extend the bio-inspired analysis to the Linear Seesaw Model.
- Include τ lepton flavor violating channels ($\tau \rightarrow e\gamma$, $\tau \rightarrow \mu\gamma$, $\tau \rightarrow 3\ell$)

Thank you!

BR($\mu \rightarrow e\gamma$)

The branching ratio is given by [7]:

$$\text{BR}(\mu \rightarrow e\gamma) = \frac{12\pi^2\alpha}{G_F^2 m_\mu^4} |F_M^\gamma(0)|^2$$

where the dipole form factor is

$$F_M^\gamma(0) = \frac{\alpha_W}{8\pi M_W^2} \frac{m_\mu}{2} \sum_i B_{\mu i}^* B_{ei} f_M^\gamma(x_i)$$

with $x_i = m_{\chi_i}^2/M_W^2$, $f_M^\gamma(x)$ the loop function, and B the mixing matrix.

BMDM

The full mass matrix is diagonalized perturbatively by constructing a block unitary matrix [4]:

$$U_\nu = \begin{pmatrix} V_1 & 0 \\ 0 & V_2 \end{pmatrix}$$

where $V_1 = U_{\text{PMNS}}$ and

$$V_2 = \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -i \\ 1 & i \end{pmatrix}.$$

The resulting block-diagonal mass matrix is:

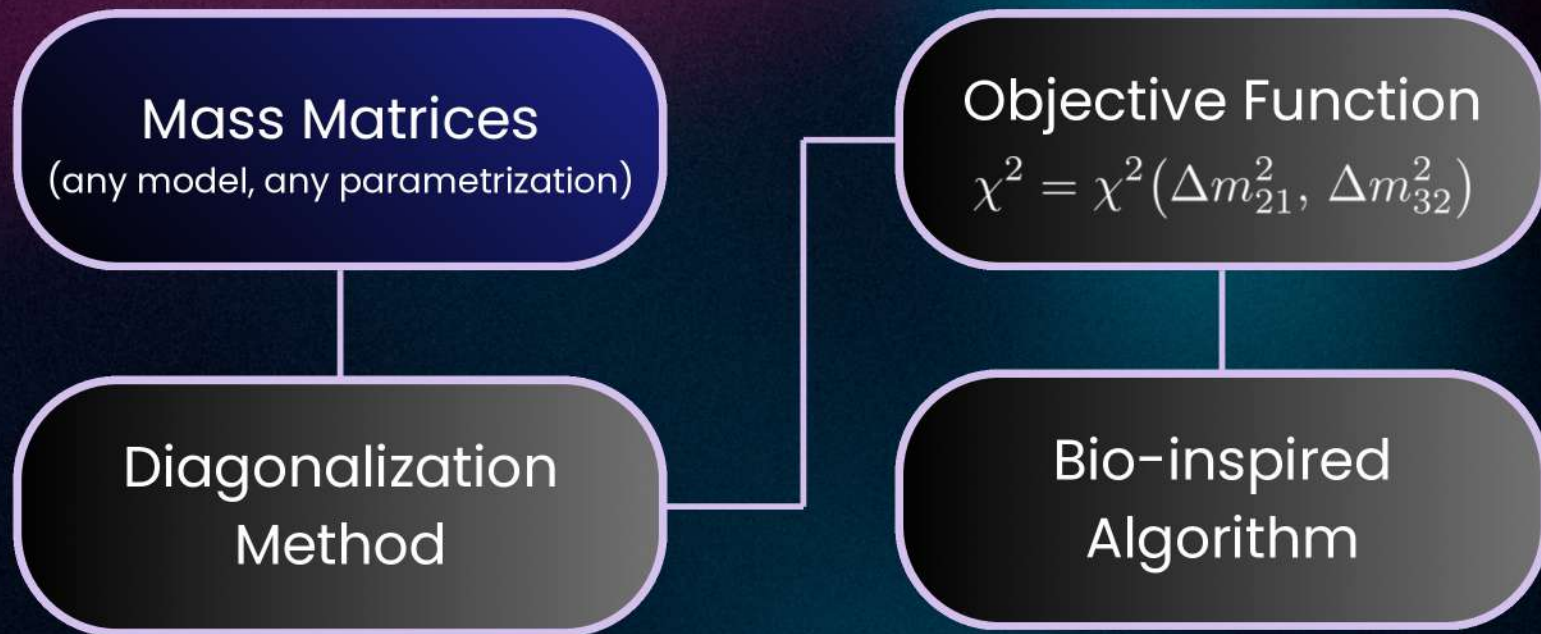
$$M_{\text{diag}} = \begin{pmatrix} m_\nu^{\text{diag}} & 0 \\ 0 & M_N^{\text{diag}} \end{pmatrix},$$

The mixing matrix is constructed as $B = (B_L \ B_H)$, where:

$$\begin{aligned} B_L &= (1 - \eta) U_{\text{PMNS}}, & \eta &= \frac{1}{2} M_D^* (M^*)^{-T} M^{-1} M_D^\dagger \\ B_H &= M_D^* (M^\dagger)^{-1} V_2 \end{aligned}$$

FRAMEWORK ARCHITECTURE

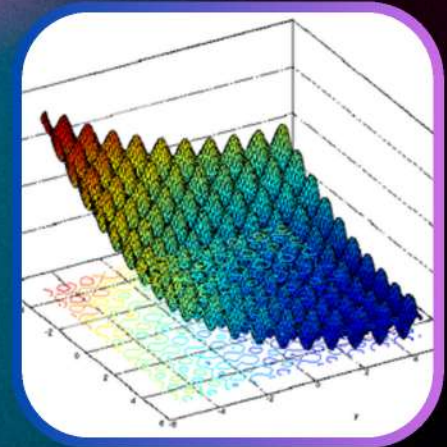
Our code is built following a modular library philosophy, allowing the same methodology to be applied to any seesaw model and any parametrization without rewriting from scratch.



BIO-INSPIRED OPTIMIZATION ALGORITHMS

Why use them?

- Well-suited for non-linear optimization problems.
- Efficient exploration of high-dimensional parameter spaces.
- Robust against noisy functions and multiple local minima.



How do they work? – Differential Evolution

- This algorithm evolves a population of candidate solutions through mutation, crossover, and selection, mimicking natural evolutionary processes. DE iterates until the population converges to the optimal region.
- The fitness function is a χ^2 built from the neutrino mass squared differences:

$$\chi^2 = \frac{1}{2} \left[\left(\frac{\Delta m_{21}^2 - \Delta m_{21, \text{exp}}^2}{\sigma_{21}} \right)^2 + \left(\frac{\Delta m_{32}^2 - \Delta m_{32, \text{exp}}^2}{\sigma_{32}} \right)^2 \right]$$

DIFFERENTIAL EVOLUTION

