

Frozen Locks: Neutrino Set, Neutrino Mass Rows & Water Rows (v2)

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Purpose

This note freezes three seed groups:

1. **Neutrino mixing (canonical set, v2)** — exact rational locks for the three angles and a CP phase.
2. **Neutrino mass rows (v1)** — a small-denominator rational for the mass-splitting ratio in normal ordering.
3. **Water rows (benchmark, v1)** — exact rational/identity anchors for solvent resonance and bioelectrochemistry knobs in EKTL/engine tests.

We report $\text{MDL}[\lceil p/q \rceil] = \lceil \log_2 p \rceil + \lceil \log_2 q \rceil$. Transcendentals (e.g. $\pi, \ln 2$) carry zero MDL charge in this program.

1 Frozen Neutrino Mixing Set (v2)

Canonical locks (as in the CKM/PMNS double-ledger):

$$\boxed{\sin^2 \theta_{12} = \frac{7}{23}, \quad \sin^2 \theta_{13} = \frac{2}{89}, \quad \sin^2 \theta_{23} = \frac{9}{16}, \quad \delta_{\text{PMNS}} = -\frac{\pi}{2}}$$

Derived, zero-cost consequences. First-row probabilities are exact rationals:

$$|U_{e1}|^2 = \frac{1392}{2047}, \quad |U_{e2}|^2 = \frac{609}{2047}, \quad |U_{e3}|^2 = \frac{2}{89}.$$

No extra parameters beyond the seeds above.

Audit Table (Neutrino Mixing)

#	Quantity	Exact value	p	q	MDL[[] p/q]	Status/Notes
N1	$\sin^2 \theta_{12}$	7/23	7	23	$3 + 5 = 8$ bits	FROZEN (v2)
N2	$\sin^2 \theta_{13}$	2/89	2	89	$1 + 7 = 8$ bits	FROZEN (v2)
N3	$\sin^2 \theta_{23}$	9/16	9	16	$4 + 4 = 8$ bits	FROZEN (v2)
N4	δ_{PMNS}	$-\pi/2$	–	–	0 bits	FROZEN (phase; transcendental)
D1	$ U_{e1} ^2$	1392/2047	1392	2047	$11 + 11 = 22$ bits	<i>Derived (0 model bits)</i>
D2	$ U_{e2} ^2$	609/2047	609	2047	$10 + 11 = 21$ bits	<i>Derived (0 model bits)</i>
D3	$ U_{e3} ^2$	2/89	2	89	$1 + 7 = 8$ bits	<i>Derived (0 model bits)</i>

MDL subtotal (Neutrino mixing seeds). MDL[[] mix = $8 + 8 + 8 + 0 = \boxed{24 \text{ bits}}$.

2 Frozen Neutrino Mass Rows (v1)

We freeze normal ordering and a compact rational for the *splitting ratio*; the absolute mass scale remains unfrozen (set by external priors, e.g. cosmology) to avoid unnecessary MDL.

Definition

Let

$$\Delta m_{21}^2 \equiv m_2^2 - m_1^2, \quad \Delta m_{31}^2 \equiv m_3^2 - m_1^2, \quad \text{NO: } \Delta m_{21}^2 > 0, \Delta m_{31}^2 > 0.$$

Frozen rational ratio (small denominator):

$$\boxed{R_{21/31} \equiv \frac{\Delta m_{21}^2}{\Delta m_{31}^2} = \frac{2}{65}}$$

This choice ($2/65 \approx 0.030769$) is a tight small-denominator fit to the standard-normal-ordering ratio and keeps the registry compact.

Audit Table (Neutrino Mass)

#	Quantity	Exact value	p	q	MDL[[] p/q]	Status/Notes
M0	Ordering	NO	–	–	0 bits	FROZEN (symbolic)
M1	$\Delta m_{21}^2 / \Delta m_{31}^2$	2/65	2	65	$1 + 6 = 7$ bits	FROZEN (v1)
B0	m_1^{bench}	1/1000 eV	1	1000	$0 + 10 = 10$ bits	<i>Benchmark only; non-parametric</i>

Consequences. Given any lightest mass m_1 , the spectrum is

$$m_2 = \sqrt{m_1^2 + \Delta m_{21}^2}, \quad m_3 = \sqrt{m_1^2 + \Delta m_{31}^2}, \quad \frac{\Delta m_{21}^2}{\Delta m_{31}^2} = \frac{2}{65}.$$

The laboratory observables

$$m_\beta = \sqrt{\sum_i |U_{ei}|^2 m_i^2}, \quad m_{\beta\beta} = \left| |U_{e1}|^2 m_1 + |U_{e2}|^2 m_2 e^{i\alpha_{21}} + |U_{e3}|^2 m_3 e^{i\alpha_{31}} \right|$$

are then fully determined by the mixing seeds (Sec. 1), this rational $R_{21/31}$, the lightest mass m_1 , and two Majorana phases $(\alpha_{21}, \alpha_{31})$ (no new seeds). A convenient non-parametric *benchmark* is $m_1 = 1 \text{ meV}$, for which one can print Σm_i , m_β , and the $m_{\beta\beta}$ envelope (min/max over phases) as in your one-cell script.

MDL subtotal (Neutrino mass seeds). MDL[] mass = $0 + 7 = \boxed{7 \text{ bits}}$. (If an absolute anchor like $\Delta m_{31}^2 = 2453/10^6 \text{ eV}^2$ were ever frozen, it would add ≈ 32 bits; we leave it unfrozen here.)

3 Frozen Water Rows (Benchmark v1)

Instrument-facing anchors for solvent resonance and bioelectrochemical checks in EKTL/engine experiments. Exact rationals (or identities) keep MDL minimal while enabling reproducible tests.

Solvent Resonance Anchors

Primary dielectric relaxation (*Debye*) and a hydration tail; frequency drives are rational multiples of the center.

$$\tau_D = \frac{83}{10} \text{ ps}, \quad \tau_H = 1 \text{ ns}, \quad \mathcal{R} = \{\frac{1}{2}, 1, 2, 3\}$$

Angular resonance $\omega_0 = 1/\tau$, drive set $\omega = r \omega_0$ with $r \in \mathcal{R}$; linear frequency $f_0 = \omega_0/(2\pi)$ is allowed (explicit 2π costs zero MDL).

Bioelectrochemical Benchmarks

Reference membrane potential and pH gradient for Nernst gates; simple rationals/integers.

$$\Delta\psi_{\text{ref}} = \frac{3}{20} \text{ V } (= 150 \text{ mV}), \quad \Delta\text{pH}_{\text{ref}} = 1$$

At temperature T , the dimensionless proton chemical potential is

$$\ln a = \frac{q_e \Delta\psi}{k_B T} + (\ln 10) \Delta\text{pH}, \quad \text{bit-normalized gate: } \ln a / \ln 2.$$

Any fitted small rational approximation to $\ln a / \ln 2$ should be recorded as a separate *derived* line (no new seeds).

Audit Table (Water)

#	Quantity	Exact value	p	q	MDL[] p/q	Status/Notes
W1	τ_D/ps	83/10	83	10	$7 + 4 = 11$ bits	FROZEN (Debye center)
W2	τ_H/ns	1/1	1	1	$0 + 0 = 0$ bits	FROZEN (hydration center)
W3	r_1 (drive ratio)	1/2	1	2	$0 + 1 = 1$ bits	FROZEN
W4	r_2	1	1	1	$0 + 0 = 0$ bits	FROZEN
W5	r_3	2	2	1	$1 + 0 = 1$ bits	FROZEN
W6	r_4	3	3	1	$2 + 0 = 2$ bits	FROZEN
B1	$\Delta\psi_{\text{ref}}$ (V)	3/20	3	20	$2 + 5 = 7$ bits	FROZEN
B2	$\Delta\text{pH}_{\text{ref}}$	1	1	1	$0 + 0 = 0$ bits	FROZEN

MDL subtotal (Water seeds). MDL[] water = $11 + 0 + 1 + 0 + 1 + 2 + 7 + 0 = \boxed{22 \text{ bits}}$.

4 Seed MDL Totals (this document)

MDL[] mix = 24 bits, MDL[] mass = 7 bits, MDL[] water = 22 bits

$$\Rightarrow \boxed{\text{MDL[] seeds, total} = 53 \text{ bits.}}$$

For baseline comparison: encoding neutrino mixing (4 floats), a splitting ratio (1 float), and water anchors (8 floats) with 64-bit reals would cost $(4 + 1 + 8) \times 64 = 832$ bits. Thus these freezes yield a conservative net saving of $832 - 53 = \boxed{779 \text{ bits}}$ before counting any derived observables (which cost 0 model bits under this program).

5 Freeze Checklist & Provenance

- **Versioning.** This file is *Frozen v2 (mix), v1 (mass), v1 (water)*. Replacements should increment version tags and list superseded row IDs.
- **Scope.** Mass ordering and the ratio $R_{21/31}$ are frozen; the absolute mass scale remains unfrozen (external prior). If you later freeze an absolute anchor (e.g. Δm_{31}^2 as a rational), add it here with a new row.
- **Benchmark link.** The non-parametric $m_1 = 1 \text{ meV}$ benchmark corresponds to your one-cell neutrino script; it does not add MDL.
- **Water provenance.** Debye $\sim 8.3 \text{ ps}$, hydration $\sim 1 \text{ ns}$; drive ratios $\{1/2, 1, 2, 3\}$; bioelectric knobs $\Delta\psi \approx 150 \text{ mV}$, $\Delta\text{pH} = 1$.