A Topology-Driven Invariant Mass Kernel in Swirl–String Theory (SST): Reference Implementation and Benchmark Against Atomic and Molecular Masses

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Abstract

This manuscript documents a canonical reference implementation of the Swirl–String Theory (SST) invariant mass kernel, as encoded in `SST_Atom_Mass_Invariant.py`. The kernel maps a topological object T (specified by braid index b_T, Seifert genus g_T, component count n_T, and a dimensionless total ropelength $L_{\mathrm{tot}}(T)$) into an inertial mass $M(T)$ via a fixed, mode-independent functional. Three computation paths are supported: *canonical* (strict evaluation with fixed quark-geometry factors), *sector_norm* (single baryon-sector normalization fixed by the proton), and *exact_closure* (analytic closure in which the proton and neutron are matched exactly without modifying the kernel). A semi-empirical nuclear binding correction is used to map nucleon-level predictions to atomic masses. In the *exact_closure* mode (electron, proton, neutron exact by construction), the benchmark over elements H–U yields mean absolute percentage error $\approx 1.960\,00 \times 10^{-1}\,\%$ with maximum absolute error $\approx 1.840\,00\,\%$ for the fixed (Z, N) table used. A small molecule set (19 formulas) yields mean absolute percentage error $\approx 1.560\,00 \times 10^{-1}\,\%$.

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1 Scope and conventions

The goal is to present (i) the invariant kernel used in code, (ii) the calibration/closure steps that feed its geometric inputs, and (iii) a transparent benchmark against a fixed table of elemental (Z, N) choices and standard atomic weights (molar masses).

This document is a *methods + benchmark* paper: it does not attempt to derive the SST kernel from first principles beyond the canonical master equation assumption.

2 Canonical constants and reference values

Golden (hyperbolic): $\ln \phi = \operatorname{asinh}(0.5)$, hence $\phi = e^{\operatorname{asinh}(0.5)}$.
(Algebraic form $\phi = (1+\sqrt{5})/2$ is equivalent.)
The implementation uses the following constants (as literal numeric values in code):

$$\phi = \frac{1+\sqrt{5}}{2}, \tag{1}$$

$$\alpha \equiv \alpha_{\mathrm{fs}} = 7.297\,35 \times 10^{-3}, \tag{2}$$

$$c = 2.997\,92 \times 10^{8}\,\mathrm{m\,s^{-1}}, \tag{3}$$

$$\mathbf{v}_{\mho} = 1.093\,85 \times 10^{6}\,\mathrm{m\,s^{-1}}, \tag{4}$$

$$r_c = 1.408\,97 \times 10^{-15}\,\mathrm{m}, \tag{5}$$

$$\rho_{\mathrm{core}} = 3.893\,44 \times 10^{18}\,\mathrm{kg\,m^{-3}}, \tag{6}$$

$$N_A = 6.022\,14 \times 10^{23}\ \mathrm{mol^{-1}}. \tag{7}$$

Particle rest masses used for calibration and reporting are taken as fixed numerical targets in the code (electron, muon, tau, proton, neutron).

3 Invariant mass kernel

3.1 Energy density and effective volume

Define the characteristic kinetic energy density

$$u \;=\; \frac{1}{2}\,\rho_{\mathrm{core}}\,\mathbf{v}_{\mho}^{2}, \tag{8}$$

with units $\mathrm{J\,m^{-3}}$.

The code uses an effective volume proxy

$$V(T) \;=\; \pi\, r_c^{3}\, L_{\mathrm{tot}}(T), \tag{9}$$

where $L_{\mathrm{tot}}(T)$ is dimensionless.

3.2 Kernel definition

For each topological object T with invariants $(b_T, g_T, n_T, L_{\mathrm{tot}}(T))$, the invariant mass is

$$M(T) = \left(\frac{4}{\alpha}\right) b_T^{-3/2}\, \phi^{-g_T}\, n_T^{-1/\phi}\, \frac{u\,V(T)}{c^2}. \tag{10}$$

All factors preceding uV/c^2 are dimensionless; therefore the mapping is dimensionally consistent: uV is energy and division by c^2 yields mass.

10-year-old analogy (one sentence). Think of u as how "packed" the motion-energy is in a material, and $V(T)$ as how much of that packed region the string-shape occupies; more packed energy times more occupied volume means more mass.

4 Topology-to-geometry assembly and computation paths

4.1 Lepton calibration

A base topology for each lepton is specified as:

$$\text{electron base:} \quad (b, g, n) = (2, 1, 1), \tag{11}$$

$$\text{muon base:} \quad (b, g, n) = (5, 2, 1), \tag{12}$$

$$\text{tau base:} \quad (b, g, n) = (7, 3, 1). \tag{13}$$

Given a target mass M_{target} and fixed (b, g, n), the code solves for the required ropelength by rearranging (10):

$$L_{\text{tot}}(T) = \frac{M_{\text{target}} c^2}{\left(\frac{4}{\alpha}\right) b^{-3/2} \phi^{-g} n^{-1/\phi}\ u\ \pi r_c^3}. \tag{14}$$

This step makes each listed lepton mass exact for its chosen base topology (it is a calibration, not a prediction).

4.2 Baryon-sector ropelength mapping

The baryon sector uses fixed $(b, g, n) = (3, 2, 3)$ and constructs baryon ropelengths from two geometric factors (s_u, s_d) via

$$L_{\text{tot}}(p) = \lambda_b\, (2\pi^2 \kappa_R)\, (2s_u + s_d), \tag{15}$$

$$L_{\text{tot}}(n) = \lambda_b\, (2\pi^2 \kappa_R)\, (s_u + 2s_d), \tag{16}$$

with $\kappa_R \approx 2$ (default $\kappa_R = 2$ in code).

Modes.

- **canonical:** (s_u, s_d) fixed by constants (hyperbolic-volume assignments external to this script); $\lambda_b = 1$.
- **sector_norm:** (s_u, s_d) fixed as in canonical; λ_b chosen so the proton mass is exact.
- **exact_closure (default):** (s_u, s_d) solved analytically so that *both* proton and neutron are exact with $\lambda_b = 1$.

4.3 Analytic closure used in `exact_closure`

Let $A(b, g, n)$ denote the kernel prefactor multiplying L_{tot}:

$$A(b, g, n) = \left(\frac{4}{\alpha}\right) b^{-3/2} \phi^{-g} n^{-1/\phi}\ \frac{u\, \pi r_c^3}{c^2}. \tag{17}$$

Define $S \equiv 2\pi^2 \kappa_R$ and $K \equiv A(3, 2, 3)\, S$. Then

$$M_p = K(2s_u + s_d), \tag{18}$$

$$M_n = K(s_u + 2s_d). \tag{19}$$

Solving yields

$$s_u = \frac{2M_p - M_n}{3K}, \tag{20}$$

$$s_d = \frac{M_p}{K} - 2s_u. \tag{21}$$

This is the exact algebra implemented by `fit_quark_geom_factors_for_baryons`.

5 From nucleons to atoms and molecules

5.1 Atomic mass assembly and binding correction

For a chosen nuclide (Z, N) with $A = Z + N$, the script constructs

$$M_{\text{sum}}(Z, N) = Z\, M_p^{\text{pred}} + N\, M_n^{\text{pred}} + Z\, M_e^{\text{pred}}. \tag{22}$$

It then subtracts a semi-empirical mass defect (binding energy divided by c^2),

$$M_{\text{atom}}^{\text{pred}}(Z, N) = M_{\text{sum}}(Z, N) - \Delta m(Z, N), \tag{23}$$

where $\Delta m(Z, N)$ is computed via the semi-empirical mass formula (SEMF)

$$B(Z, N) = a_v A - a_s A^{2/3} - a_c \frac{Z(Z-1)}{A^{1/3}} - a_a \frac{(N-Z)^2}{A} + \delta(A, Z)\, a_p A^{-1/2}, \tag{24}$$

$$\Delta m(Z, N) = \frac{B(Z, N)}{c^2}. \tag{25}$$

The code uses a MeV→kg conversion factor to implement Δm directly in kilograms. Coefficients are fixed in the script:

$$(a_v, a_s, a_c, a_a, a_p) = (15.75, 17.8, 0.711, 23.7, 11.18)\ \text{MeV}.$$

5.2 Molecules

Chemical binding energies are neglected (eV scale). A molecular mass prediction is the sum of predicted atomic masses of constituents:

$$M_{\text{mol}}^{\text{pred}}(\text{formula}) = \sum_i \nu_i\, M_{\text{atom}}^{\text{pred}}(Z_i, N_i), \tag{26}$$

where ν_i are stoichiometric coefficients.

5.3 Reference conversion from molar mass

For each table entry with molar mass M_{mol} (g/mol), the script uses

$$M_{\text{ref}} = \frac{M_{\text{mol}} \times 10^{-3}}{N_A} \quad [\text{kg}], \tag{27}$$

to obtain a per-entity reference mass.

6 Results (from the provided run)

This section records the numerical outcomes printed by the script for the run corresponding to *exact_closure* (the observed command-line mode string in the log is non-canonical but triggers the exact-closure branch in the current implementation).

6.1 Fitted/derived geometric quantities

With $\kappa_R = 2$,

$$S = 2\pi^2 \kappa_R = 3.947\,84 \times 10^{1}, \tag{28}$$

$$A(3,2,3) = 4.653\,60 \times 10^{-30}, \tag{29}$$

$$K = A(3,2,3)\, S = 1.837\,17 \times 10^{-28}. \tag{30}$$

Exact-closure geometric factors (dimensionless):

$$s_u = 3.030\,60, \tag{31}$$

$$s_d = 3.043\,15, \tag{32}$$

$$\lambda_b = 1. \tag{33}$$

Calibrated ropelengths (dimensionless):

$$L_{\mathrm{tot}}(e) = 3.339\,63 \times 10^{-2}, \tag{34}$$

$$L_{\mathrm{tot}}(\mu) = 4.416\,51 \times 10^{1}, \tag{35}$$

$$L_{\mathrm{tot}}(\tau) = 1.990\,71 \times 10^{3}, \tag{36}$$

$$L_{\mathrm{tot}}(p) = 3.594\,25 \times 10^{2}, \tag{37}$$

$$L_{\mathrm{tot}}(n) = 3.599\,21 \times 10^{2}. \tag{38}$$

Reported ratios:

$$\frac{L_\mu}{L_e} \approx 1.322\,46 \times 10^{3}, \tag{39}$$

$$\frac{L_\tau}{L_\mu} \approx 4.507\,43 \times 10^{1}. \tag{40}$$

6.2 Benchmark summary statistics

Define percentage error as

$$\varepsilon = 100\% \times \frac{M^{\mathrm{pred}} - M^{\mathrm{ref}}}{M^{\mathrm{ref}}}.$$

For the elements table (92 entries, H–U) in *exact_closure*:

$$\mathrm{MAE}(|\varepsilon|) \approx 1.960\,00 \times 10^{-1}\,\%, \tag{41}$$

$$\mathrm{median}(|\varepsilon|) \approx 6.900\,00 \times 10^{-2}\,\%, \tag{42}$$

$$\mathrm{RMSE}(|\varepsilon|) \approx 3.740\,00 \times 10^{-1}\,\%, \tag{43}$$

$$\max|\varepsilon| \approx 1.840\,00\,\%, \tag{44}$$

$$\mathrm{p95}(|\varepsilon|) \approx 8.080\,00 \times 10^{-1}\,\%. \tag{45}$$

For the molecules table (19 entries):

$$\mathrm{MAE}(|\varepsilon|) \approx 1.560\,00 \times 10^{-1}\,\%, \tag{46}$$

$$\mathrm{median}(|\varepsilon|) \approx 3.860\,00 \times 10^{-2}\,\%, \tag{47}$$

$$\max|\varepsilon| \approx 1.330\,00\,\%. \tag{48}$$

6.3 Selected examples

Table 1 lists representative entries (exact_closure).

Table 1: Selected benchmark entries in *exact_closure*.

Object	Actual mass (kg)	Predicted mass (kg)	ε (%)
H	$1.673\,56 \times 10^{-27}$	$1.673\,53 \times 10^{-27}$	$-1.480\,00$
He	$6.646\,48 \times 10^{-27}$	$6.656\,20 \times 10^{-27}$	$1.460\,00$
C	$1.994\,47 \times 10^{-26}$	$1.993\,10 \times 10^{-26}$	$-6.880\,00$
O	$2.656\,70 \times 10^{-26}$	$2.656\,31 \times 10^{-26}$	$-1.450\,00$
Fe	$9.273\,28 \times 10^{-26}$	$9.287\,66 \times 10^{-26}$	$1.550\,00$
Au	$3.270\,76 \times 10^{-25}$	$3.270\,62 \times 10^{-25}$	$-4.350\,00$
U	$3.952\,58 \times 10^{-25}$	$3.952\,69 \times 10^{-25}$	$2.850\,00$
H_2O	$2.991\,46 \times 10^{-26}$	$2.991\,02 \times 10^{-26}$	$-1.480\,00$
CO_2	$7.308\,03 \times 10^{-26}$	$7.305\,73 \times 10^{-26}$	$-3.160\,00$
$C_8H_{10}N_4O_2$	$3.224\,60 \times 10^{-25}$	$3.223\,41 \times 10^{-25}$	$-3.690\,00$

Table 2: Largest absolute percentage errors in *exact_closure* for the fixed (Z, N) table used by the script.

Object	Actual mass (kg)	Predicted mass (kg)	ε (%)
B	$1.795\,04 \times 10^{-26}$	$1.828\,06 \times 10^{-26}$	$1.839\,00$
Cl	$5.886\,61 \times 10^{-26}$	$5.806\,22 \times 10^{-26}$	$-1.366\,00$
Mg	$4.035\,94 \times 10^{-26}$	$3.982\,56 \times 10^{-26}$	$-1.323\,00$
Li	$1.152\,41 \times 10^{-26}$	$1.164\,99 \times 10^{-26}$	$1.091\,00$
Ne	$3.350\,97 \times 10^{-26}$	$3.319\,44 \times 10^{-26}$	$-9.410\,00$
HCl	$6.054\,33 \times 10^{-26}$	$5.973\,57 \times 10^{-26}$	$-1.334\,00$
NaCl	$9.704\,19 \times 10^{-26}$	$9.623\,19 \times 10^{-26}$	$-8.350\,00$

6.4 Largest deviations in the fixed table

Table 2 lists the largest absolute errors over the element and molecule sets.

7 Interpretation and limitations

(1) Table mismatch: isotopes vs standard atomic weights. The element table fixes a single (Z, N) per element, while the "actual" mass is computed from a standard molar mass (often an isotopic average). A strict test should compare against isotope-specific atomic masses (e.g., AME tables) for the chosen (Z, N).

(2) Nuclear binding model is semi-empirical. The SEMF step (24) is a phenomenological correction. The reported accuracy for atoms therefore reflects the combined effect of (i) exact nucleon calibration in *exact_closure*, and (ii) an empirical nuclear binding proxy.

(3) Leptons beyond the electron are not predicted in this implementation. Muon and tau ropelengths are solved from their measured masses via (14); they should be treated as calibrations unless an independent SST rule for lepton L_{tot} is introduced.

(4) Mode-handling robustness. In the current code, any unrecognized `mode` string falls through to the *exact_closure* branch. For publication-quality reproducibility, the CLI should validate mode strings and fail loudly on invalid values.

8 Falsifiable checks enabled by this kernel

Even within this script's structure, two immediate falsifiers can be stated:

- **Canonical baryons:** Fix (s_u, s_d) from hyperbolic-volume assignments and set $\lambda_b = 1$. The resulting proton/neutron residuals become a direct test of the Canon mapping (independent of the exact-closure fit).
- **Isotope-resolved benchmark:** Replace standard atomic weights with isotope masses for the script's chosen (Z, N) (or update (Z, N) to match dominant isotopes) and re-evaluate error statistics.

9 Reproducibility

The script writes `SST_Invariant_Mass_Results_{mode}.csv` and optionally a cross-mode comparison CSV. For non-interactive environments, the optional prompt should be disabled or guarded by `sys.stdin.isatty()`.

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