

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 $L_{\text{tot}}(T)$) 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): $\ln \phi = \text{asinh}(0.5)$, hence $\phi = e^{\text{asinh}(0.5)}$.

(*Algebraic form $\phi = (1 + \sqrt{5})/2$ is equivalent.*)

The implementation uses the following constants (as literal numeric values in code):

$$\phi = \frac{1 + \sqrt{5}}{2}, \quad (1)$$

$$\alpha \equiv \alpha_{\text{fs}} = 7.29735 \times 10^{-3}, \quad (2)$$

$$c = 2.99792 \times 10^8 \text{ m s}^{-1}, \quad (3)$$

$$\mathbf{v}_o = 1.09385 \times 10^6 \text{ m s}^{-1}, \quad (4)$$

$$r_c = 1.40897 \times 10^{-15} \text{ m}, \quad (5)$$

$$\rho_{\text{core}} = 3.89344 \times 10^{18} \text{ kg m}^{-3}, \quad (6)$$

$$N_A = 6.02214 \times 10^{23} \text{ mol}^{-1}. \quad (7)$$

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

$$u = \frac{1}{2} \rho_{\text{core}} \mathbf{v}_o^2, \quad (8)$$

with units J m^{-3} .

The code uses an effective volume proxy

$$V(T) = \pi r_c^3 L_{\text{tot}}(T), \quad (9)$$

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

3.2 Kernel definition

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

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

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:

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

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

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

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

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

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

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

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

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} :

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

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

$$M_p = K(2s_u + s_d), \quad (18)$$

$$M_n = K(s_u + 2s_d). \quad (19)$$

Solving yields

$$s_u = \frac{2M_p - M_n}{3K}, \quad (20)$$

$$s_d = \frac{M_p}{K} - 2s_u. \quad (21)$$

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

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

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

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

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

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

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

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:

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

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

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

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 $\kappa_R = 2$,

$$S = 2\pi^2 \kappa_R = 3.94784 \times 10^1, \quad (28)$$

$$A(3, 2, 3) = 4.65360 \times 10^{-30}, \quad (29)$$

$$K = A(3, 2, 3) S = 1.83717 \times 10^{-28}. \quad (30)$$

Exact-closure geometric factors (dimensionless):

$$s_u = 3.03060, \quad (31)$$

$$s_d = 3.04315, \quad (32)$$

$$\lambda_b = 1. \quad (33)$$

Calibrated ropelengths (dimensionless):

$$L_{\text{tot}}(e) = 3.33963 \times 10^{-2}, \quad (34)$$

$$L_{\text{tot}}(\mu) = 4.41651 \times 10^1, \quad (35)$$

$$L_{\text{tot}}(\tau) = 1.99071 \times 10^3, \quad (36)$$

$$L_{\text{tot}}(p) = 3.59425 \times 10^2, \quad (37)$$

$$L_{\text{tot}}(n) = 3.59921 \times 10^2. \quad (38)$$

Reported ratios:

$$\frac{L_\mu}{L_e} \approx 1.32246 \times 10^3, \quad (39)$$

$$\frac{L_\tau}{L_\mu} \approx 4.50743 \times 10^1. \quad (40)$$

6.2 Benchmark summary statistics

Define percentage error as

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

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

$$\text{MAE}(|\varepsilon|) \approx 1.96000 \times 10^{-1}\%, \quad (41)$$

$$\text{median}(|\varepsilon|) \approx 6.90000 \times 10^{-2}\%, \quad (42)$$

$$\text{RMSE}(|\varepsilon|) \approx 3.74000 \times 10^{-1}\%, \quad (43)$$

$$\max |\varepsilon| \approx 1.84000\%, \quad (44)$$

$$\text{p95}(|\varepsilon|) \approx 8.08000 \times 10^{-1}\%. \quad (45)$$

For the molecules table (19 entries):

$$\text{MAE}(|\varepsilon|) \approx 1.56000 \times 10^{-1}\%, \quad (46)$$

$$\text{median}(|\varepsilon|) \approx 3.86000 \times 10^{-2}\%, \quad (47)$$

$$\max |\varepsilon| \approx 1.33000\%. \quad (48)$$

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
$\text{C}_8\text{H}_{10}\text{N}_4\text{O}_2$	$3.224\ 60 \times 10^{-25}$	$3.223\ 41 \times 10^{-25}$	-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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