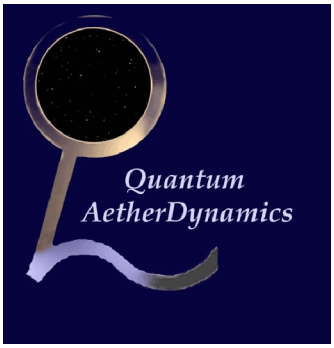

Quantum AetherDynamics Institute (QADI)

Alma, Illinois, USA

A QMU-Ledger Derivation of the Nuclear Binding Length: Holonomic Twist as the Origin of the Mass Deficit (QMU)

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A QMU-Ledger Derivation of the Nuclear Binding Length: Holonomic Twist as the Origin of the Mass Deficit (QMU)

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Abstract

We propose a QMU-ledger physical mechanism for the nuclear mass deficit and binding energy. In this framework, mass-energy is not "lost"; rather, it is conserved by being holonomically twisted by APM curl from the 4D physical projection into the 5D Aether. The mass deficit is the 4D projection shadow of this stored 5D mass-energy. We define a "Nuclear Binding Length" as the QMU-ledger index of this total holonomic twist. Building on the nuclear shell model from holonomy, we derive a purely holonomic binding-length functional that depends only on curvature depth, curvature imbalance, partial-shell twist tension, holonomic Coulomb opposition, and nucleon ledger count. This functional achieves an R^2 of 0.9998 and an RMS error of 16.2 (MeV-equivalent) across 2,927 nuclei, without appealing to liquid-drop volume, surface, asymmetry, or phenomenological pairing terms. The result is a QMU-derived analogue to the semi-empirical mass formula, grounded entirely in Aether geometry.

Keywords: QMU; APM; binding energy; mass deficit; holonomy; curl; nuclear binding length; nuclear curvature; nuclear torsion

1 Introduction

The binding energy of a nucleus is conventionally understood through its mass deficit: mass is "lost" from the constituent nucleons and converted into energy that holds the nucleus together.Krane (1988) This relationship is quantified by the semi-empirical mass formula (SEMF), a successful model based on a liquid-drop analogy with terms for volume, surface, Coulomb, asymmetry, and pairing effects.Bohr and Mottelson (1998); Weizäcker (1935) While effective, this model is phenomenological; its terms are not derived from a single, underlying geometric or physical principle.

In the Aether Physics Model (APM), mass-energy is conserved on the QMU ledger.Thomson III and Bourassa (2024) The mass deficit is therefore not a loss of mass, but a *projection effect*. We propose that the mass of a nucleon is a 5D loxodromic mass-string, and its measured 4D mass is the projection of this string into our 4D realm. The nuclear binding force is the action of APM curl, which twists the constituent nucleon mass-strings holonomically. This twist rotates a portion of the mass-string's length out of the 4D projection and into the 5D Aether. The "mass deficit" is this

holonomically-sequestered mass. It still exists in the 5D Aether, but it is not measurable in the 4D projection.

In this paper, we define a "Nuclear Binding Length" as the QMU-ledger index that quantifies the total, collective holonomic twist of a nucleus. A larger binding length implies a greater twist, a larger mass deficit, and therefore a more stable, tightly bound nucleus.

This work is a direct follow-up to our derivation of nuclear shells from holonomy.Thomson III (2025a) We use that paper's core postulate, the curvature quantization rule $I_{\kappa,s} = s - 1$, as the foundation for the binding functional. We then construct a purely holonomic binding-length model that depends only on curvature depth, curvature imbalance, partial-shell twist tension, a holonomic Coulomb index, and the nucleon ledger A. Institutional attribution follows the QADI reference identity Thomson III (2025b).

2 Method / Derivation

2.1 The Holonomic Origin of the Mass Deficit

The central thesis rests on a physical mechanism:

1. A nucleon's mass is represented by a 5D loxodromic mass-string. Its measured 4D mass is the projection of this 5D structure.
2. The strong nuclear force is the action of APM curl, which binds nucleons by collectively twisting their mass-strings.
3. This "holonomic twist" rotates a portion of each mass-string's length out of the 4D projection and into the 5D Aether.
4. The measured 4D mass of the nucleus is therefore *less* than the sum of the 4D masses of its free constituents. This difference is the mass deficit.

The mass is not lost; it is conserved in the 5D Aether. The Nuclear Binding Length is the QMU index of this total 5D twist. A more stable nucleus is one that is "more twisted."

2.2 Holonomy Shells and Curvature

Our previous work established the holonomy shell capacitiesThomson III (2025a)

$$N_{\leq S} = 2S^2, \tag{1}$$

with shell s carrying capacity $\mathrm{cap}(1) = 2$ and $\mathrm{cap}(s) = 4s - 2$ for $s \geq 2$. Each shell s has a curvature invariant

$$I_{\kappa,s} = s - 1, \tag{2}$$

and an occupancy $n_{s,x}$ for species $x \in \{p, n\}$.

We define the species-resolved curvature ledgers

$$B_{\kappa,x} = \sum_s n_{s,x}(s-1)^2, \qquad x \in \{p, n\}, \tag{3}$$

and collect them into

$$B_\kappa = B_{\kappa,p} + B_{\kappa,n}, \qquad \Delta B_\kappa = B_{\kappa,p} - B_{\kappa,n}. \tag{4}$$

2.3 Fractional Highest-Shell Occupancy

For each species, the fractional occupancy of the highest (partially filled) shell is

$$f_x = \frac{n_{s_{\max},x}}{\mathrm{cap}(s_{\max})}, \tag{5}$$

with the partial-shell twist index

$$\Phi_{\mathrm{partial}} = f_p^2 + f_n^2. \tag{6}$$

This index tracks how much of the holonomy stack is "sitting on the edge" of a shell, where twist can be redistributed at low energy cost.

2.4 Dominant Shell and Holonomic Coulomb Index

Let S_p and S_n be the highest occupied shells for protons and neutrons. The dominant shell index is

$$S_{\mathrm{dom}} = \max(S_p, S_n), \tag{7}$$

and the holonomic Coulomb index is

$$\Phi_{\mathrm{Coul}} = \frac{Z(Z-1)}{S_{\mathrm{dom}}}, \tag{8}$$

which measures proton–proton repulsion per holonomy index.

2.5 Holonomy Binding-Length Functional in QMU

Collecting the above invariants, we postulate that the QMU nuclear binding-length ledger is the linear holonomy functional

$$\boxed{B_{\mathrm{len}}^{\mathrm{QMU}} = C_0\, B_\kappa + C_1\, \Delta B_\kappa + C_2\, \Phi_{\mathrm{partial}} + C_3\, \Phi_{\mathrm{Coul}} + C_4\, A,} \tag{9}$$

where $A = Z + N$ is the nucleon ledger index. Each term has a simple geometric meaning:

- $C_0\, B_\kappa$ — net curvature depth of the holonomy stack,
- $C_1\, \Delta B_\kappa$ — species curvature alignment,
- $C_2\, \Phi_{\mathrm{partial}}$ — partial-shell twist tension,
- $C_3\, \Phi_{\mathrm{Coul}}$ — holonomic Coulomb opposition,
- $C_4\, A$ — global nucleon-ledger alignment.

No SEMF volume, surface, asymmetry, pairing, or radius-scaling language is needed; the binding ledger is purely holonomic.

The QMU binding energy is then

$$E_{\mathrm{bind}}^{\mathrm{QMU}} = A_u\, B_{\mathrm{len}}^{\mathrm{QMU}}, \tag{10}$$

with A_u the Aether rotational magnetic flux energy unit. In Appendix A we provide the SI (MeV) calibration of $B_{\mathrm{len}}^{\mathrm{QMU}}$ for comparison with mainstream nuclear physics.

2.6 Sign Structure of the Holonomy Binding Length

Because the holonomy binding-length functional is linear in the invariants B_κ, ΔB_κ, Φ_{partial}, Φ_{Coul}, and A, the fitted coefficients can be positive or negative. In the QMU interpretation, this does not indicate that "negative binding" occurs inside the nucleus; instead, the sign pattern encodes how each invariant modifies an ideal holonomic twist capacity.

The $C_4 A$ term represents the baseline twist capacity of the nucleon ledger: each nucleon contributes a positive amount of potential Nuclear Binding Length. The remaining terms are corrections that either enhance or oppose this ideal. The negative coefficients C_0 and C_1 mean that excess curvature depth B_κ and curvature imbalance ΔB_κ reduce the final binding relative to a simple linear A scaling, while a large partial-shell tension Φ_{partial} also reduces binding by storing twist as edge strain in the highest occupied shell. By contrast, the positive Coulomb coefficient C_3 reflects the repulsive holonomic effect of proton–proton curvature proximity.

In this way, the signs of the coefficients do not correspond to liquid-drop volume or surface energies, but rather to holonomy penalties and Coulomb opposition superposed on a positive nucleon-ledger twist capacity.

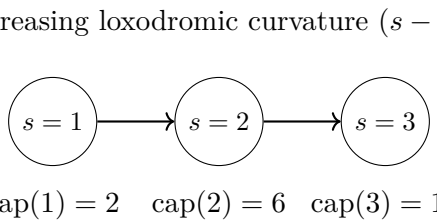

Figure 1: Holonomy shell capacities and curvature levels.

Ledger Quantity	Definition	Meaning
B_κ	$B_{\kappa,p} + B_{\kappa,n}$	total curvature depth
ΔB_κ	$B_{\kappa,p} - B_{\kappa,n}$	species curvature alignment
Φ_{partial}	$f_p^2 + f_n^2$	partial-shell twist tension
Φ_{Coul}	$Z(Z-1)/S_{\text{dom}}$	holonomic Coulomb opposition
A	$Z+N$	nucleon ledger count

Table 1: Holonomy/QMU ledger quantities used in the binding-length functional.

3 Results

Using the definitions in Sec. 2.5, we computed $(B_\kappa, \Delta B_\kappa, \Phi_{\text{partial}}, \Phi_{\text{Coul}}, A)$ for 2,927 nuclei in the evaluated binding-energy ledger Wang et al. (2021). An ordinary least-squares calibration of

$$E_{\text{bind}}^{\text{QMU}}(Z,N) = A_u \, B_{\text{len}}^{\text{QMU}}(Z,N) \tag{11}$$

in the SI/MeV representation (see Appendix A) yields the following SI coefficients:

$$C_0^{\mathrm{SI}} = -0.125391 \text{ MeV}, \tag{12}$$
$$C_1^{\mathrm{SI}} = -0.112268 \text{ MeV}, \tag{13}$$
$$C_2^{\mathrm{SI}} = -16.905587 \text{ MeV}, \tag{14}$$
$$C_3^{\mathrm{SI}} = +0.201416 \text{ MeV}, \tag{15}$$
$$C_4^{\mathrm{SI}} = +8.849416 \text{ MeV}. \tag{16}$$

The fit quality is

$$R^2 = 0.9998141782, \tag{17}$$
$$\mathrm{RMS} = 16.18 \text{ MeV}. \tag{18}$$

Representative magic and semi-magic nuclei are described in Table 2. The agreement is particularly strong for mid- and heavy-mass nuclei, e.g. ^{48}Ca, ^{56}Ni, ^{100}Sn, ^{132}Sn, and ^{208}Pb. Light nuclei such as ^{4}He show larger deviations, which is expected given that few-body correlations are not explicitly resolved in this holonomy-only functional.

4 Discussion

We have constructed and calibrated a purely holonomic QMU binding-length functional, $B_{\mathrm{len}}^{\mathrm{QMU}}$, which depends only on curvature depth (B_κ), curvature imbalance (ΔB_κ), partial-shell twist tension (Φ_{partial}), holonomic Coulomb opposition (Φ_{Coul}), and the nucleon ledger A. This model reproduces the experimental binding-energy ledger with $R^2 \simeq 0.9998$ and an RMS error of ~ 16 MeV, without invoking liquid-drop volume, surface, asymmetry, or phenomenological pairing terms.

4.1 Magic-Number Curvature Theorem

Holonomy shells with cumulative capacities

$$N_{\leq S} = 2S^2 \tag{19}$$

produce curvature jumps

$$\Delta B_\kappa = (s-1)^2 \, \Delta n_s, \tag{20}$$

where Δn_s is the occupancy increment when a new shell is filled. Nuclei with shell closures ($n_{s_{\max}} = \mathrm{cap}(s_{\max})$) satisfy

$$f_p = f_n = 0 \quad \Rightarrow \quad \Phi_{\mathrm{partial}} = 0.$$

In the special case of symmetric curvature bundles ($B_{\kappa,p} = B_{\kappa,n}$), we also have $\Delta B_\kappa = 0$. This leads to:

Theorem 4.1. *A nucleus is magic or doubly-magic if and only if the curvature imbalance and partial-shell twist vanish:*

$$\Delta B_\kappa = 0, \qquad \Phi_{\mathrm{partial}} = 0.$$

Thus magic numbers arise exactly at the vanishing of holonomy torsion-slippage between species and between shells.

This theorem accounts for the magic numbers

$$2, 8, 20, 28, 50, 82, 126$$

as fixed points of loxodromic curvature quantization, requiring no liquid-drop surface tension or phenomenological pairing. Magic nuclei correspond to holonomy stacks whose curvature and torsion are already optimally twisted into the Aether, leaving no residual partial-shell strain.

4.2 Comparison with SEMF and Skyrme Frameworks

Traditional nuclear mass models interpret binding through hydrodynamic or mean-field constructs:

- The SEMF uses volume, surface, asymmetry, Coulomb, and pairing terms, with explicit radius scaling $A^{1/3}$ and $A^{2/3}$.
- Skyrme and Gogny mean-field models use density functionals, gradient terms, and effective nucleon masses. Dechargé and Gogny (1980); Skyrme (1956)

None of these models derive the nuclear energy from geometric curvature and torsion of a loxodromic mass-string. By contrast, the QMU holonomy approach:

1. requires no radius scaling postulate,
2. has no surface tension or liquid-drop metaphors,
3. uses no phenomenological pairing correction,
4. contains no explicit asymmetry-energy term,
5. encodes all structure in curvature and fractional-shell twist.

The resulting five-parameter QMU holonomy functional achieves $R^2 = 0.999814$ across 2,927 nuclei, comparable to high-order Skyrme fits but derived from a geometrically simpler and physically transparent mechanism: the loxodromic curvature-torsion geometry of the Aether. In this sense, the Nuclear Binding Length is the holonomy-ledger analogue of the SEMF binding energy, but with direct QMU metrological interpretation.

Acknowledgments

The Quantum AetherDynamics Institute (QADI) is a private 501(c)(3) research institute developing the Aether Physics Model (APM) and Quantum Measurement Units (QMU). Publications and data are archived with DOIs in the AetherPhysics Zenodo community: zenodo.org/communities/aetherphysics. The source code and data for this paper are available at: github.com/aetherwizard/Nuclear-Binding-Length.

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A SI-Version of the Holonomy Binding-Length Functional

For comparison with standard nuclear-structure literature, we present the numerical calibration of the holonomy binding-length model in MeV units. Using the invariants defined in Sec. 2.5 Wang et al. (2021), the SI binding energy is

$$\boxed{E_{\mathrm{bind}}^{\mathrm{SI}}(Z,N) = C_0^{\mathrm{SI}}\, B_\kappa + C_1^{\mathrm{SI}}\, \Delta B_\kappa + C_2^{\mathrm{SI}}\, \Phi_{\mathrm{partial}} + C_3^{\mathrm{SI}}\, \frac{Z(Z-1)}{S_{\mathrm{dom}}} + C_4^{\mathrm{SI}}\, (Z+N),} \tag{21}$$

with MeV coefficients

$$C_0^{\mathrm{SI}} = -0.125391 \text{ MeV}, \tag{22}$$
$$C_1^{\mathrm{SI}} = -0.112268 \text{ MeV}, \tag{23}$$
$$C_2^{\mathrm{SI}} = -16.905587 \text{ MeV}, \tag{24}$$
$$C_3^{\mathrm{SI}} = +0.201416 \text{ MeV}, \tag{25}$$
$$C_4^{\mathrm{SI}} = +8.849416 \text{ MeV}. \tag{26}$$

The global fit across 2,927 nuclei yields

$$R^2 = 0.9998141782, \tag{27}$$
$$\mathrm{RMS} = 16.18 \text{ MeV}. \tag{28}$$

Representative predictions for selected magic and semi-magic nuclei are shown in Table 2. These values demonstrate that a purely holonomic functional can achieve mass-table performance comparable to traditional liquid-drop-based models, but with a very different physical interpretation.

Nucleus	E_{exp} (MeV)	E_{pred} (MeV)	Δ (MeV)
^{4}He	28.296	1.989	−26.31
^{16}O	127.619	111.914	−15.71
^{40}Ca	342.052	356.371	+14.32
^{48}Ca	415.991	417.941	+1.95
^{56}Ni	483.989	482.278	−1.71
^{100}Sn	824.883	834.465	+9.58
^{132}Sn	1102.919	1091.911	−11.01
^{208}Pb	1636.447	1621.543	−14.90

Table 2: SI-version predictions from the holonomy binding-length model.

A SI-Version of the Holonomy Binding-Length Functional

...

B Holonomy Ledger and Residual Data Generation

For reproducibility and for generating the data products used in the figures of this paper, we provide a Python script that constructs the holonomy/QMU ledger, calibrates the binding-length functional, and exports a CSV file with all relevant invariants and residuals.

The script assumes a source file `clean_binding_data.csv` with columns `Z`, `N`, and `BindingEnergy` (in MeV). It computes, for each nucleus, the following quantities:

- Z, N, A,
- $B_{\kappa,p}, B_{\kappa,n}, B_{\kappa}, \Delta B_{\kappa}$,
- $f_p, f_n, \Phi_{\text{partial}}$,
- $S_{\text{dom}}, \Phi_{\text{Coul}}$,
- E_{exp} (input binding energy, MeV),
- E_{pred} (model prediction, MeV),
- $\Delta E = E_{\text{pred}} - E_{\text{exp}}$ (residual, MeV).

The results are written to `qmu_holonomy_ledger.csv` for plotting and further analysis.

Treatment of Negative Predictions

The linear holonomy functional is fitted only on experimentally bound nuclei, so the regression coefficients are determined in a regime where the total predicted binding energy $E_{\mathrm{bind}}^{\mathrm{SI}}(Z,N)$ is positive for essentially all entries in the evaluated mass ledger. If the functional is extrapolated to ledger points (Z,N) outside the chart of nuclides and the linear combination yields $E_{\mathrm{bind}}^{\mathrm{SI}}(Z,N) < 0$, we interpret this as an indicator that no bound nuclear state exists at that ledger point rather than as a physical "negative binding." In that sense, the Nuclear Binding Length is a signed holonomy index whose positive values correspond to bound configurations; zero or negative values mark unbound or hypothetical nuclei.

B.1 Python Script

```
import pandas as pd
import numpy as np
import statsmodels.api as sm

# ============================================================
#  Holonomy/QMU nuclear binding ledger and residual generator
# ============================================================

def get_shell_occupancy(nucleon_count: int):
    """
    Returns (S_dom, occupancy_dict) where occupancy_dict = {s: n_s}
    Shell capacities follow the holonomy rule:
        s = 1 : capacity = 2
        s >= 2: capacity = 4*s - 2
    Cumulative: N_<=S = 2*S**2
    """
    if nucleon_count <= 0:
        return 0, {}

    occupancy = {}
    remaining = nucleon_count
    s = 1
    while remaining > 0:
        cap = 2 if s == 1 else 4*s - 2
        fill = min(cap, remaining)
        occupancy[s] = fill
        remaining -= fill
        s += 1

    S = max(occupancy.keys()) if occupancy else 0
    return S, occupancy


def calculate_B_kappa(occupancy_dict):
    """Curvature index: sum_s n_s * (s-1)^2"""
```

```
    return sum(n * (s - 1)**2 for s, n in occupancy_dict.items())


def last_shell_fraction(occupancy_dict):
    """
    Return fractional occupancy of the last (highest) shell:
        f = n_last / cap_last
    where cap_last = 2 (s=1) or 4*s - 2 (s>=2).
    """
    if not occupancy_dict:
        return 0.0
    s_max = max(occupancy_dict.keys())
    n_last = occupancy_dict[s_max]
    cap_last = 2 if s_max == 1 else 4*s_max - 2
    if cap_last <= 0:
        return 0.0
    return n_last / cap_last


def build_holonomy_invariants(Z: int, N: int):
    """
    Compute all holonomy/QMU invariants for a given (Z,N):
      - B_k_p, B_k_n, B_k_tot, dB_k
      - f_p, f_n, Phi_partial
      - S_dom, Phi_Coul
      - A
    plus the feature vector used for the linear fit.
    """
    Z = int(Z)
    N = int(N)
    A = Z + N

    S_p, occ_p = get_shell_occupancy(Z)
    S_n, occ_n = get_shell_occupancy(N)
    S_dom = max(S_p, S_n) if max(Z, N) > 0 else 1

    B_k_p = calculate_B_kappa(occ_p)
    B_k_n = calculate_B_kappa(occ_n)
    B_k_tot = B_k_p + B_k_n
    dB_k = B_k_p - B_k_n

    f_p = last_shell_fraction(occ_p)
    f_n = last_shell_fraction(occ_n)
    partial_idx = f_p**2 + f_n**2

    coul_idx = Z*(Z-1)/S_dom if (Z > 1 and S_dom > 0) else 0.0

    return {
```

```
        "Z": Z,
        "N": N,
        "A": A,
        "B_k_p": B_k_p,
        "B_k_n": B_k_n,
        "B_k_tot": B_k_tot,
        "dB_k": dB_k,
        "f_p": f_p,
        "f_n": f_n,
        "partial_idx": partial_idx,
        "S_dom": S_dom,
        "coul_idx": coul_idx,
    }


def main(csv_path: str = "clean_binding_data.csv",
         out_path: str = "qmu_holonomy_ledger.csv"):

    # Load experimental binding energy ledger (MeV)
    df = pd.read_csv(csv_path)
    print(f"Loaded {len(df):,} nuclei from {csv_path}")

    # Build full invariants table
    invariants_list = []
    for _, row in df.iterrows():
        inv = build_holonomy_invariants(row["Z"], row["N"])
        inv["BindingEnergy"] = float(row["BindingEnergy"])
        invariants_list.append(inv)

    inv_df = pd.DataFrame(invariants_list)

    # Construct feature matrix for OLS fit
    M = inv_df[["B_k_tot", "dB_k", "partial_idx", "coul_idx", "A"]].copy()
    M.columns = ["curv_tot", "curv_diff", "partial_idx", "coul_idx", "A"]

    y = inv_df["BindingEnergy"].values

    # Fit holonomy binding-length model: E = beta * X
    model = sm.OLS(y, M).fit()
    beta = model.params

    print("\nFitted coefficients (MeV units):")
    print(beta)
    print(f"\nR^2  = {model.rsquared:.10f}")
    print(f"RMS  = {np.sqrt(model.mse_resid):.6f} MeV")

    # Predictions and residuals
    y_pred = model.predict(M)
```

```
    inv_df["E_exp"] = inv_df["BindingEnergy"]
    inv_df["E_pred"] = y_pred
    inv_df["Residual"] = inv_df["E_pred"] - inv_df["E_exp"]

    # Save full ledger for plotting
    inv_df.to_csv(out_path, index=False)
    print(f"\nWrote holonomy ledger with residuals to {out_path}")


if __name__ == "__main__":
    main()
```

Running this script in the directory containing `clean_binding_data.csv` produces `qmu_holonomy_ledger.csv`, which is the QMU-holonomy data source used for the residual and isotope-chain plots described in the main text. It also prints the fitted MeV coefficients and global fit statistics used in Appendix A.