

Hydrogen as a Differential Test of the Holonomy Fraction

Excited Electron Record Cycles, Residual Shape Columns, Overconstrained Spectroscopy, Isotope and Antihydrogen Channels, and Machine-Checkable Post-Freeze Comparison Protocols

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Abstract

This paper is the fourth hydrogen manuscript and the fourteenth paper in the Dual-Time Theory (DTT) constants-and-hydrogen sequence. Papers 11–13 formulated hydrogen first as an alpha-free proton–electron temporal record resonance, then as a post-freeze gross-spectrum reconstruction, and finally as a post-freeze fine-structure and radiative-loop framework. The present paper turns hydrogen into a differential test bed for the holonomy-fraction program. The absolute low-energy boundary value is assigned upstream to a source-firewalled electron certificate,

$$\alpha_{\text{OS}}^{-1}(0) = 137 + H_e,$$

where the integer 137 is supplied by canonical complexification and the residual H_e is the finite-regulator determinant holonomy of the physical electron record cycle. Hydrogen spectroscopy is not permitted to choose this certificate, the electron connection, the cycle, the branch, or the low band. Instead, it tests whether the same record connection predicts state-dependent excited-cycle residuals after ordinary QED, recoil, reduced-mass, nuclear-size, hyperfine, and systematic effects have been removed.

For each hydrogenic level $a = (n, \ell, j, F, I, Z)$, we introduce a closed excited electron record cycle C_a , a low-band determinant holonomy H_a , and a residual relative to the selected reference state,

$$\eta_a := H_a - H_{1S}.$$

For a transition $i : a \rightarrow b$, the DTT shape is

$$S_i := \eta_b - \eta_a.$$

The empirical layer is formulated as a covariance-aware residual problem:

$$y_i = \nu_i^{\text{obs}} - \nu_i^{\text{QED}}(\alpha_{\text{DTT}}, R_p, \dots) - \nu_i^{\text{sys}} = \sum_A c_A S_A(i) + \epsilon_i,$$

where the columns S_A must be derived or predeclared before fitting. A model with one free amplitude per transition is explicitly rejected. The manuscript develops null, S-contact, spin-holonomy, high- ℓ Rydberg-suppressed, isotope-boundary, and antihydrogen orientation-sensitive pattern families; gives overconstraint, nuisance-projection, and decision-tree tests; defines a finite-regulator spectroscopy certificate; and supplies a machine-checkable nonphysical benchmark certificate and validator.

The strongest possible outcome is not merely agreement with one line. It is a pattern-level success: a small number of DTT-derived residual shape columns must explain many independent hydrogen, deuterium, Rydberg, and antihydrogen residuals without modifying the frozen electron certificate. If the data require line-by-line fitting, hidden use of α -dependent inputs, post-hoc branch selection, or transition-dependent amplitudes, the differential holonomy claim fails.

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1 Reader guide and role in the series

This manuscript is deliberately positioned after the papers that establish the upstream constants architecture and the post-freeze hydrogen framework. It is not a second derivation of the fine-structure constant. It is a differential spectroscopy protocol for testing whether the holonomy-fraction mechanism, once frozen, leaves a coherent state-dependent trace in bound-electron record cycles.

One-sentence purpose

Hydrogen spectroscopy is used here as a *test suite* for DTT residual shapes, not as an input source for α , $\hbar$, $c_\star$, the electron mass, or the ground-state electron holonomy certificate.

1.1 Series dependencies

The paper assumes the following upstream layers only in the status indicated.

Layer	Input used here	Not used here
Papers 1–2	dual-time records, projection metrology, bridge constants	numerical calibration of any constant
Paper 3	structural action–phase bridge $\Delta\theta = S/\hbar$	hydrogen spectroscopy as evidence for $\hbar$
Paper 4	additive record action and pre-quantum phase logic	a fitted action coefficient from spectra
Paper 6	local completion speed $c_\star$	SI numerical derivation of c
Paper 7	structural integer $N_3(10) = 137$	fractional residual $0.035999177\dots$
Papers 8–10	frozen electron holonomy certificate and coupling correspondence	any post-hoc tuning from hydrogen
Papers 11–13	alpha-free hydrogen geometry and post-freeze correction hierarchy	alpha-containing hydrogen formulas in the pre-freeze layer

1.2 Claim-status discipline

Item	Status		Comment
Absolute ground residual H_e	Upstream target	theorem	Computed, if at all, by the physical electron certificate of Paper 10. This paper does not tune it.
State cycles C_a	Theorem target / protocol		Must be derived from hydrogenic record geometry; preliminary columns may be used only as predeclared tests.
Shape columns $S_A(i)$	Conditional predictions	predictions	Valid only if fixed before data fitting and tied to record-cycle mechanisms.

Item	Status	Comment
Spectroscopy residuals y_i	Empirical comparison objects	Defined after standard QED and systematic corrections; not a replacement for bound-state QED.
Hydrogen tick formulas	Post-freeze tools only	Any formula containing α , R_∞ , a_0 , Lamb numerics, or Bohr velocity is quarantined before certificate freeze.
Successful prediction	Overconstrained pattern match	Requires more independent residuals than free DTT amplitudes.

1.3 Non-claims

This paper does not claim that the measured fine-structure constant is derived from hydrogen. It does not claim that the Lamb shift is derived without QED. It does not replace standard bound-state calculations. It does not use spectroscopy to select the branch of the electron determinant. It does not infer q_{rec} , $\hbar_\star$, cell volume, trace normalization, or low-band dimension from residual line fits.

Source firewall

Before the electron certificate is frozen, the following are forbidden as inputs to the holonomy construction: measured α , α^{-1} , electron anomaly a_e , quantum Hall constants, measured charge normalization, Rydberg data, Bohr velocity, Lamb-shift numerics, transition frequencies, and the inner-time tick $\Delta t_r = \alpha \hbar / (m_e c^2)$. After freeze, these quantities may enter only the empirical comparison layer.

Figure placeholder: Dependency graph for Paper 14

Show upstream theorem inputs on the left, the frozen electron certificate in the middle, and hydrogen/deuterium/Rydberg/antihydrogen comparison channels on the right. Red arrows should indicate forbidden backflow from spectroscopy to the certificate.

Label: dependency-graph

Figure 1: Dependency graph for Paper 14. Show upstream theorem inputs on the left, the frozen electron certificate in the middle, and hydrogen/deuterium/Rydberg/antihydrogen comparison channels on the right. Red arrows should indicate forbidden backflow from spectroscopy to the certificate.

2 The absolute residual and why differential tests matter

The holonomy-fraction program decomposes the low-energy on-shell inverse coupling as

$$\alpha_{\text{OS}}^{-1}(0) = 137 + H_e. \quad (1)$$

Here 137 is the structural integer produced by the projection-rigidity theorem, and H_e is the small branch of a determinant Wilson phase on the physical electron record cycle. The physical certificate

paper requires that H_e be obtained from a target-blind finite-regulator construction. This paper begins only after such a boundary value is fixed, or in a conservative mode after a reference boundary value is calibrated for test purposes.

The central empirical idea is simple. If the same DTT record connection also governs bound-electron excited cycles, then the absolute electron residual may not be the only trace. Excited states may carry small state-dependent differences

$$H_a - H_{1S}, \quad (2)$$

where a labels a hydrogenic record state. These differences are observable only through transition patterns after standard theory and systematics have been subtracted.

Definition 2.1 (Post-freeze boundary package). *A post-freeze boundary package is*

$$\mathfrak{A}_{\text{freeze}} = (H_e, \alpha_{\text{DTT,OS}}(0), \mathcal{C}_e, h_e, \mathfrak{q}_{\text{firewall}}, \mathfrak{q}_{\text{branch}}), \quad (3)$$

where $\mathcal{C}_e$ is the frozen electron certificate, h_e is its canonical hash, $\mathfrak{q}_{\text{firewall}}$ is the source-contamination report, and $\mathfrak{q}_{\text{branch}}$ records the pre-phase branch orientation. Hydrogen spectroscopy may read this package but may not alter it.

Theorem Target 2.2 (Differential holonomy test target). *Given a frozen package $\mathfrak{A}_{\text{freeze}}$, DTT should derive a finite list of state-dependent residual shape columns $S_A(i)$ from hydrogenic record-cycle geometry. The data residual vector should lie in the span of these columns, within covariance, with fewer amplitudes than measured transitions.*

3 Hydrogenic record labels and excited closed cycles

3.1 State labels

A hydrogenic level is denoted

$$a = (X, Z, A, n, \ell, j, F, m_F, \chi), \quad (4)$$

where X names the system, such as H, D, muonium, positronium, or antihydrogen; Z and A encode the nuclear charge and isotope; (n, ℓ, j, F, m_F) are the usual spectroscopic labels; and χ stores external-field, trap, preparation, and extraction metadata. For most formulas this is shortened to

$$a = (n, \ell, j, F). \quad (5)$$

3.2 Closed excited electron record cycles

Definition 3.1 (Hydrogenic excited record cycle). *For each admissible state label a , a hydrogenic excited electron record cycle is a closed morphism*

$$C_a : C_a(0) \rightarrow C_a(1) = C_a(0) \quad (6)$$

inside the bound proton–electron reconstruction geometry, equipped with finite-regulator realizations

$$C_{a,r} \subset \mathcal{R}_{H,r}. \quad (7)$$

The cycle is not a classical orbit. It is the closed record of state reconstruction, phase locking, boundary matching, and electron-sector transport for the level a .

Definition 3.2 (State holonomy). *Let $\nabla_{\text{DTT},r}^e$ be the same lifted electron record connection used in the ground electron certificate, restricted or pulled back to the state cycle $C_{a,r}$. Let $P_{a,r}$ be the structurally selected low physical projector for that state. The finite-regulator state holonomy is*

$$H_{a,r} := \text{br}_a \frac{1}{2\pi} \text{Arg}_{P_{a,r} \mathcal{H}_{a,r}} \det V_{a,r}, \quad (8)$$

where $V_{a,r}$ is obtained by one of the admissible determinant routes: exact band invariance, polar-unitary compression, or moving determinant-line transport. If the limit exists,

$$H_a = \lim_{r \rightarrow \infty} H_{a,r}. \quad (9)$$

The ground reference must be specified with care. Hyperfine, isotope, and centroid conventions affect comparisons.

Definition 3.3 (Reference residual). *Let a_0 be the chosen reference state, typically the hyperfine centroid of hydrogen 1S after the extraction protocol has been declared. Define*

$$\eta_a := H_a - H_{a_0}. \quad (10)$$

For a transition $i : a \rightarrow b$, define the DTT transition shape

$$S_i := \eta_b - \eta_a. \quad (11)$$

Remark 3.4. *If every η_a vanishes, DTT still may provide the absolute boundary value of α , but hydrogen spectroscopy contains no additional differential holonomy signal. This null result is a legitimate outcome.*

4 Finite-regulator state-cycle certificate

4.1 Certificate object

A differential hydrogen test needs the analog of the electron certificate, but with state labels and spectroscopy metadata.

Definition 4.1 (Differential holonomy spectroscopy certificate). *A finite-regulator differential spectroscopy certificate is*

$$\mathcal{C}_r^{\text{spec}} = (\mathfrak{A}_{\text{freeze}}, \mathcal{D}_{H,r}^{\text{af}}, \mathcal{I}_{H,r}^{\text{post-freeze}}, \{a\}_{a \in \mathcal{A}_r}, \{C_{a,r}\}, \{P_{a,r}\}, \{U_{a,r}^{\text{amb}}\}, \{V_{a,r}\}, \{H_{a,r}\}, \{\eta_{a,r}\}, \{S_{i,r}\}, X_r, C_r, \mathbf{q}_r, h_r). \quad (12)$$

Here X_r is the predeclared shape design matrix, C_r is the covariance model for the residual vector, $\mathbf{q}_r$ stores firewall and no-backflow checks, and h_r is a canonical hash.

4.2 Regulator consistency

For a state-cycle family to be physically interpretable, it must not depend on a single arbitrary discretization. The regulator sequence must provide comparison maps

$$\Phi_{r \rightarrow r'} : \mathcal{R}_{H,r} \rightarrow \mathcal{R}_{H,r'} \quad (13)$$

that carry states, cycles, projectors, and low-band holonomies into one another up to controlled error.

Criterion 4.2 (State-cycle Cauchy criterion). *A family $\{H_{a,r}\}$ is regulator stable if for every declared state a ,*

$$|H_{a,r'} - H_{a,r}| \leq \varepsilon_{r,r'}^{\text{conn}} + \varepsilon_{r,r'}^{\text{band}} + \varepsilon_{r,r'}^{\text{det}} + \varepsilon_{r,r'}^{\text{branch}}, \quad (14)$$

with the right-hand side tending to zero along the declared regulator trajectory. The same must hold for $\eta_{a,r}$ and $S_{i,r}$.

4.3 No independent branch per level

Firewall Warning 4.3 (Branch coherence). *The branch map br_a may depend on a structural orientation theorem, but it may not be chosen independently for every transition. A branch rule that corrects signs after comparison with spectral residuals is a fit, not a prediction.*

Theorem Target 4.4 (Coherent branch theorem). *There exists a state-family orientation functional*

$$\mathcal{O}_{a,r}^{\text{spec}} = \mathcal{O}(C_{a,r}, P_{a,r}, J_r, \partial_r, \omega_r, \chi_a) \quad (15)$$

computed before $H_{a,r}$, and a fixed branch map $\text{br}(\mathcal{O}_{a,r}^{\text{spec}})$, such that all state residuals η_a are branch-coherent across the chosen spectroscopy family.

Figure placeholder: State-cycle family over hydrogenic labels

Depict a common electron record connection being pulled back to multiple closed cycles C_{1S} , C_{2S} , C_{nS} , C_{nD} , and high- ℓ Rydberg cycles. The same connection and branch convention feed all cycles.

Label: `state-cycle-family`

Figure 2: State-cycle family over hydrogenic labels. Depict a common electron record connection being pulled back to multiple closed cycles C_{1S} , C_{2S} , C_{nS} , C_{nD} , and high- ℓ Rydberg cycles. The same connection and branch convention feed all cycles.

5 From state holonomies to transition residuals

5.1 Residual equation

For a transition $i : a \rightarrow b$, write

$$\nu_i^{\text{obs}} = \nu_i^{\text{QED}}(\alpha_{\text{DTT}}, \Theta_{\text{nuc}}, \Theta_{\text{sys}}) + \delta\nu_i^{\text{DTT}} + \delta\nu_i^{\text{unmodelled}}. \quad (16)$$

Here ν_i^{QED} denotes the standard bound-state prediction including the chosen on-shell boundary value, reduced mass, recoil, finite-size, fine-structure, Lamb-shift, hyperfine, external-field, and known systematic corrections. The empirical residual is

$$y_i := \nu_i^{\text{obs}} - \nu_i^{\text{QED}}(\alpha_{\text{DTT}}, \hat{\Theta}_{\text{nuc}}, \hat{\Theta}_{\text{sys}}). \quad (17)$$

The DTT model is

$$y_i = \sum_{A=1}^p c_A S_A(i) + \epsilon_i, \quad (18)$$

where $S_A(i)$ are predeclared shape columns and c_A are amplitudes associated with independently derived mechanisms.

5.2 Sensitivity translation

If a small state-dependent reconstruction shift changes $N = \alpha^{-1}$ by S_i , then

$$\frac{\delta\alpha}{\alpha} \simeq -\frac{S_i}{N_{\text{eff}}}, \quad (19)$$

with $N_{\text{eff}} \simeq 137 + H_e$. For a transition with sensitivity coefficient

$$K_i := \frac{\partial \ln \nu_i}{\partial \ln \alpha}, \quad (20)$$

one obtains the linear comparison rule

$$\frac{\delta\nu_i^{\text{DTT}}}{\nu_i} \simeq -K_i \frac{S_i}{N_{\text{eff}}}. \quad (21)$$

This formula is not a substitute for bound-state QED. It is a bookkeeping map from an additive inverse-coupling residual to a small spectroscopic perturbation.

5.3 Nuisance directions

Real spectra contain nuisance parameters: Rydberg constant conventions, proton radius, deuteron radius, reduced mass, recoil conventions, line-pulling, blackbody shifts, Zeeman/Stark shifts, hyperfine extraction, and theoretical truncation errors. Let θ_μ denote such parameters and define the nuisance matrix

$$Z_{i\mu} := \frac{\partial \nu_i^{\text{QED}}}{\partial \theta_\mu}. \quad (22)$$

A strong DTT test must compare X , the DTT shape matrix, against residual components not already absorbed by Z .

Definition 5.1 (Nuisance-projected residual). *Given covariance matrix C , define the C^{-1} -weighted projection onto the nuisance column space:*

$$P_Z = Z(Z^T C^{-1} Z)^{-1} Z^T C^{-1}. \quad (23)$$

The nuisance-projected residual and DTT design matrix are

$$y_\perp = (I - P_Z)y, \quad X_\perp = (I - P_Z)X. \quad (24)$$

Only $X_\perp$ carries independent DTT spectroscopic content.

6 Shape columns and physical mechanisms

A shape column must come from a mechanism. The following families are not final predictions unless their amplitudes and angular factors are derived from record-cycle geometry. They are the canonical test families for Paper 14.

6.1 Null column

The null model is

$$\eta_a = 0, \quad S_i = 0. \quad (25)$$

It states that the holonomy fraction is purely a boundary value and produces no state-dependent residue.

6.2 Universal state-independent shift

A universal shift $\eta_a = \eta_0$ is invisible in transitions:

$$S_i = \eta_0 - \eta_0 = 0. \quad (26)$$

It is therefore not an excited-state prediction. Any constant shift belongs to the boundary H_e , not to spectroscopy.

6.3 S-state contact column

If the differential residual is localized near the reconstruction core, S states dominate. The standard test column is

$$\eta_{nS}^{\text{contact}} = \beta_S n^{-3} + O(n^{-4}), \quad (27)$$

while high- ℓ states have suppressed contact support.

For a $2S \rightarrow nS$ transition,

$$S_{2S \rightarrow nS}^{\text{contact}} = \beta_S (n^{-3} - 2^{-3}) + O(n^{-4}). \quad (28)$$

The shape in n is independent of β_S . For $n = 8, 9, 10$, the unnormalized factors are

$$s_8 = 8^{-3} - 2^{-3} = -\frac{63}{512}, \quad (29)$$

$$s_9 = 9^{-3} - 2^{-3} = -\frac{721}{5832}, \quad (30)$$

$$s_{10} = 10^{-3} - 2^{-3} = -\frac{31}{250}. \quad (31)$$

Relative to the $2S \rightarrow 8S$ line, these are close to

$$1 : 1.00473 : 1.00775. \quad (32)$$

Thus $2S \rightarrow nS$ alone mainly constrains amplitude; discrimination improves when S lines are combined with D states, fine-structure intervals, high- ℓ Rydberg states, isotope shifts, and antihydrogen channels.

6.4 Spin-holonomy columns

If the residual is spinorial, define angular factors $\sigma_{\ell jF}$ from the spin-record connection. A typical column is

$$\eta_{n\ell jF}^{\text{spin}} = \beta_\ell n^{-3} \sigma_{\ell jF} + O(n^{-4}). \quad (33)$$

Fine-structure intervals then test differences

$$S_{n\ell,j \rightarrow j'}^{\text{spin}} = \beta_\ell n^{-3} (\sigma_{\ell j' F'} - \sigma_{\ell j F}) + O(n^{-4}). \quad (34)$$

The angular factors may not be fitted independently for every j . They must be derived from the DTT spin connection or predeclared by a finite set of representation-theoretic options.

6.5 High- ℓ Rydberg suppression

If the residual is core-local, circular and near-circular high- ℓ states suppress it:

$$\eta_{n,\ell=n-1}^{\text{core}} = o(n^{-3}). \quad (35)$$

If instead DTT predicts a global record-loop area term, one may obtain a different scaling,

$$\eta_{n\ell}^{\text{area}} = \beta_A A_{n\ell}^{\text{rec}}, \quad (36)$$

where $A_{n\ell}^{\text{rec}}$ is an alpha-free or post-freeze derived record-loop area invariant. High- n Rydberg data discriminate between core-local and global-loop mechanisms.

6.6 Nuclear-boundary and isotope columns

An electron-only residual predicts equality between hydrogen and deuterium after standard reduced-mass and nuclear-size corrections:

$$\eta_a^{\text{H}} - \eta_a^{\text{D}} = 0 \quad \text{after standard corrections.} \quad (37)$$

A nuclear-boundary coupling predicts instead

$$\eta_a^X = \eta_a^e + \gamma_N \Xi_N(X, a), \quad (38)$$

where Ξ_N must be a predeclared nuclear compactness, radius, boundary-action, or isotope record invariant.

6.7 Antihydrogen orientation columns

For antihydrogen $\bar{H}$, a conservative CPT-even holonomy gives

$$\eta_{\bar{H},a} = \eta_{H,a}. \quad (39)$$

An orientation-sensitive record cycle could give

$$\eta_{\bar{H},a} = -\eta_{H,a} \pmod{1}, \quad (40)$$

only if a charge-conjugation/orientation theorem derives this sign. Without that theorem, the sign-flip model is not the conservative DTT prediction.

6.8 Environmental and trap columns

Spectroscopy often occurs in fields, traps, beams, cavities, or material environments. A DTT environmental column must be defined using external record variables, for example

$$\eta_a^{\text{env}} = \beta_E (\Xi_E(a, \mathcal{E}) - \Xi_E(a, \mathcal{E}_0)). \quad (41)$$

This can be useful for laboratory tests of record stability, but it must not masquerade as a fundamental holonomy residual.

Figure placeholder: Residual shape-column families

A matrix-style figure showing rows as transitions and columns as null, S-contact, spin-holonomy, Rydberg-suppressed, isotope-boundary, and antihydrogen orientation shapes.

Label: `shape-columns`

Figure 3: Residual shape-column families. A matrix-style figure showing rows as transitions and columns as null, S-contact, spin-holonomy, Rydberg-suppressed, isotope-boundary, and antihydrogen orientation shapes.

7 Empirical channels

System	What it tests	DTT pattern to compare
Hydrogen $1S - 2S$	anchor transition, reference extraction, strongest line constraint	null state-dependence or baseline constraint; not a pre-freeze input
Hydrogen $2S - nS$, $n = 8, 9, 10$	S-state contact residual	shape $n^{-3} - 2^{-3}$; limited discrimination alone
Hydrogen $2S - nD$	noncontact excited cycles	suppressed contact term or spin/projective residual
Fine-structure intervals	spin holonomy and angular factors	approximate n^{-3} spin pattern at fixed ℓ
High- n Rydberg	asymptotic suppression vs global area	vanishing core-local residual or alternative scaling
H/D isotope shifts	electron-only vs nuclear-boundary coupling	common residual after nuclear corrections or predicted nuclear scaling
Muonium/positronium	lepton-sector vs nuclear-boundary separation	mass-ratio and annihilation/recoil complications must be isolated
Antihydrogen	CPT and cycle orientation	same sign if CPT-even; sign reversal only if derived

Table 3: Spectroscopic comparison channels for state-dependent holonomy residuals. The table is a test plan, not a data fit.

8 Covariance-aware overconstraint tests

8.1 Design matrix

Let M transitions be measured and let p DTT shape columns be predeclared. Define

$$X_{iA} = S_A(i), \quad i = 1, \dots, M, \quad A = 1, \dots, p. \quad (42)$$

The residual model is

$$y = Xc + \epsilon, \quad \text{Cov}(\epsilon) = C. \quad (43)$$

The generalized least-squares estimator is

$$\hat{c} = (X^T C^{-1} X)^{-1} X^T C^{-1} y. \quad (44)$$

The goodness-of-fit statistic is

$$\chi^2 = (y - X\hat{c})^T C^{-1} (y - X\hat{c}), \quad \nu_{\text{dof}} = M - p. \quad (45)$$

Criterion 8.1 (Overconstraint). *A differential holonomy test is minimally overconstrained if*

$$M - p \geq 2. \quad (46)$$

It is strongly overconstrained if the same column set succeeds across at least three distinct channel classes, for example S-state, D-state or fine-structure, isotope, and antihydrogen/Rydberg channels.

8.2 Column-rank discipline

A fit with $p = M$ is interpolation, not prediction. A fit with nearly collinear columns is weak even if $p < M$. Define the weighted Gram matrix

$$G = X^T C^{-1} X. \quad (47)$$

The effective column rank is the number of singular values of $C^{-1/2}X$ above a predeclared threshold. The model is empirically meaningful only if

$$\text{rank}_{\text{eff}}(X) < M - 1. \quad (48)$$

8.3 Nested model tests

The null model $X = 0$, S-contact model, S+spin model, S+spin+isotope model, and orientation-sensitive model should be nested only when their mechanisms are nested. Adding a column because a residual remains is not allowed. The acceptable logic is:

1. derive or predeclare a mechanism;
2. compute its shape column;
3. fit only its amplitude, if the amplitude is not already derived;
4. reject the mechanism if the residual vector does not lie in its column space.

Theorem 8.2 (No line-by-line fitting). *Suppose a model assigns an independent amplitude c_i to every transition i , so that $X = I_M$. Then the model is not a differential DTT prediction, because every residual vector lies in its column space. Such a model is rejected by the overconstraint criterion.*

Proof. With $X = I_M$, one obtains $\hat{c} = y$ and $\chi^2 = 0$ for any residual vector. The model has no excluded residual patterns and hence no predictive content. $\square$

9 Decision tree for empirical comparison

Protocol 9.1 (Post-freeze comparison protocol). *The spectroscopy comparison must be performed in the following order.*

- E1. Freeze the electron certificate or declare the conservative calibration mode.*
- E2. Fix the QED scheme, preferably the low-energy on-shell boundary convention plus a declared bound-state theory package.*
- E3. Select transitions, extraction conventions, and covariance matrix before inspecting DTT fit quality.*
- E4. Declare the DTT shape families: null, S-contact, spin-holonomy, high- ℓ suppressed, isotope-boundary, orientation-sensitive, or environmental.*
- E5. Project out ordinary nuisance directions such as Rydberg, proton radius, nuclear radius, and systematic parameters.*
- E6. Fit or bound only the small number of amplitudes attached to predeclared mechanisms.*
- E7. Reject any model requiring a separate amplitude or branch choice for each transition.*
- E8. Translate final residual bounds into additive inverse-coupling units ΔN .*
- E9. Archive the full comparison certificate with data hashes, theory-version hashes, covariance, shape columns, amplitudes, and residual diagnostics.*

**Figure placeholder: Decision tree for
differential holonomy spectroscopy**

A flow chart from frozen electron certificate to QED residuals, nuisance projection, predeclared shape matrix, overconstraint test, and accept/reject outcomes.

Label: `decision-tree`

Figure 4: Decision tree for differential holonomy spectroscopy. A flow chart from frozen electron certificate to QED residuals, nuisance projection, predeclared shape matrix, overconstraint test, and accept/reject outcomes.

10 Conservative mode before the physical electron certificate is completed

If the physical electron certificate has not yet been populated, a conservative mode may still test differential residuals. In that mode one treats the reference boundary value as calibrated:

$$\alpha_{\text{ref}}^{-1} = 137 + 0.035999177\dots, \quad (49)$$

while forbidding any claim that the absolute value has been derived. Predictive content then lives only in differences

$$\Delta N(x; x_0) = \delta N(x) - \delta N(x_0). \quad (50)$$

For a fixed-kinematics bound

$$\left| \frac{\Delta\alpha}{\alpha} \right| < \epsilon, \quad (51)$$

one obtains

$$|\Delta N| \lesssim N_{\text{eff}}\epsilon \simeq 137\epsilon. \quad (52)$$

Bound on $ \Delta\alpha/\alpha $	Corresponding bound on $ \Delta N $
10^{-9}	1.37×10^{-7}
10^{-12}	1.37×10^{-10}
10^{-15}	1.37×10^{-13}
10^{-18}	1.37×10^{-16}

Table 4: Approximate translation between fractional coupling constraints and additive reconstruction-residual constraints.

Conservative mode is useful for designing experiments and ruling out large residual patterns. It is not evidence that the absolute holonomy has been computed.

11 State families in detail

11.1 S-state program

The S-state program begins with $1S - 2S$ as an anchor and uses $2S - nS$ transitions to test contact-like state dependence. Because $n = 8, 9, 10$ shapes are close, the S program should be paired with at least one non-S or high- ℓ channel.

The basic S-contact design column for transition $2S \rightarrow nS$ is

$$X_{2S \rightarrow nS}^{(S)} = n^{-3} - 2^{-3}. \quad (53)$$

A refined column may include finite-size or relativistic envelope corrections,

$$X_{2S \rightarrow nS}^{(S, \text{ref})} = n^{-3}(1 + a_1/n + a_2/n^2) - 2^{-3}(1 + a_1/2 + a_2/4), \quad (54)$$

but the coefficients a_1, a_2 must come from a DTT calculation or from a declared standard-theory expansion, not from residual fitting.

11.2 D-state and noncontact program

D states suppress core contact. If S-state residuals appear but $2S \rightarrow nD$ residuals do not, that supports a core-local mechanism. If D-state residuals appear with a shape not reducible to nuclear-size or QED uncertainties, that suggests a spin/projective or global-loop column.

11.3 Fine-structure intervals

Fine-structure intervals are especially useful because many gross-energy nuisance directions cancel. A spin-holonomy column should be tested against intervals such as

$$nP_{3/2} - nP_{1/2}, \quad nD_{5/2} - nD_{3/2}, \quad (55)$$

with approximate n^{-3} scaling if the residual is short-range and spinorial.

11.4 High- n Rydberg tests

High- ℓ circular states provide a decisive asymptotic channel. A core-local DTT residual should vanish faster than n^{-3} , whereas a global loop-area mechanism may scale with a record-loop invariant. The Rydberg program should therefore include both circular/near-circular states and lower- ℓ reference states when possible.

11.5 Isotope tests

Hydrogen/deuterium comparisons are powerful because an electron-only residual should be common after standard reduced-mass and nuclear-size corrections. A nuclear-boundary DTT column must specify its isotope variable in advance:

$$\Xi_N \in \{R_N^2, \mu_H/m_e, I(I+1), \text{nuclear record compactness}, \dots\}. \quad (56)$$

A model that chooses Ξ_N after seeing isotope residuals is not predictive.

11.6 Muonium and positronium

Muonium has no nuclear size at the proton level but has a heavier positive lepton. Positronium has equal masses and annihilation channels. These systems are valuable for separating nuclear-boundary mechanisms from lepton-sector mechanisms, but they require dedicated QED treatment and must not be folded into hydrogen fits without a separate covariance and theory-error ledger.

11.7 Antihydrogen

Antihydrogen tests orientation. The conservative expectation is CPT-even unless a DTT orientation theorem gives a sign flip. Therefore the decision tree is:

1. Test CPT-even residual equality.
2. If deviation appears, verify standard systematics and QED extraction.
3. Only then test whether the deviation matches a prederived orientation-sensitive column.

12 Finite-regulator derivation of shape columns

The strongest version of Paper 14 is not phenomenological. It derives the shape columns S_A from finite record geometry.

Definition 12.1 (State-family constructor). *A state-family constructor is a map*

$$\text{HydSpec}_r : (\mathcal{D}_{H,r}^{\text{af}}, \mathfrak{A}_{\text{freeze}}, \chi_{\text{ext}}) \longmapsto \{C_{a,r}, P_{a,r}, V_{a,r}, H_{a,r}\}_{a \in A_r}. \quad (57)$$

It is admissible only if it is functorial under regulator refinement and under relabeling of equivalent record presentations.

Theorem Target 12.2 (Shape derivation theorem). *For each mechanism A , the finite-regulator constructor should produce a limit*

$$S_A(i) = \lim_{r \rightarrow \infty} (\eta_{b,r}^{(A)} - \eta_{a,r}^{(A)}) \quad (58)$$

for every transition $i : a \rightarrow b$, with a regulator error estimate and no reference to measured line residuals.

12.1 Locality and support

A common route to n^{-3} is contact support. In ordinary hydrogenic language, S-state contact densities scale like $|\psi_{nS}(0)|^2 \sim n^{-3}$. In DTT language this should become a statement about record-envelope support near the proton–electron reconstruction core:

$$\eta_a^{\text{contact}} \propto \langle P_a, \Pi_{\text{core}} P_a \rangle_{\text{rec}}. \quad (59)$$

The DTT proof should not rely on a literal orbit; it should derive the projected envelope scaling from the record geometry and the post-freeze Coulomb envelope.

12.2 Spin and angular support

A spin-holonomy column arises from the spinorial part of the lifted connection,

$$\nabla_{\text{DTT}}^e = \nabla^{\text{scalar}} + \nabla^{\text{spin}} + \nabla^{\text{boundary}} + \dots. \quad (60)$$

The angular factor $\sigma_{\ell j F}$ should be computed by tracing ∇^{spin} over the low-band projector, not by fitting intervals.

12.3 Rydberg asymptotics

For high- ℓ Rydberg cycles the electron record support avoids the core. A core-local residual should satisfy

$$\left| \eta_{n,\ell=n-1}^{\text{core}} \right| \leq C n^{-3-\delta} \quad (61)$$

for some $\delta > 0$, or an even stronger exponential/circular-state suppression depending on the envelope class. A global record-loop residual should instead supply a separate asymptotic law.

13 Compatibility with QED and bound-state theory

DTT residual spectroscopy is an overlay on top of standard QED calculations, not a replacement. The order of operations is:

$$\begin{array}{c}
 \text{frozen } \alpha_{\text{DTT,OS}}(0) \\
 \downarrow \\
 \text{QED running and bound-state scheme} \\
 \downarrow \\
 \nu_i^{\text{QED}}(\alpha_{\text{DTT}}, \theta_{\text{nuc}}, \theta_{\text{sys}}) \\
 \downarrow \\
 \text{DTT differential residual columns } S_A(i) \\
 \downarrow \\
 \text{covariance-aware comparison.}
 \end{array} \tag{62}$$

Firewall Warning 13.1 (Do not double count). *A DTT residual column may not reproduce a correction already included in ν_i^{QED} unless the paper explicitly reassigns that correction and removes it from the baseline. In default mode, fine structure, Lamb shift, recoil, reduced mass, finite nuclear size, and hyperfine corrections remain in the standard baseline.*

14 The residual certificate format

14.1 Required fields

The spectroscopy certificate must contain:

1. frozen electron certificate hash and boundary value;
2. list of transition labels and extraction conventions;
3. observed frequencies or residual inputs, with references and covariance;
4. QED/bound-state theory version and parameter ledger;
5. nuisance parameter matrix and projection rule;
6. DTT shape-column definitions and mechanism labels;
7. statement whether each amplitude is derived, bounded, or fitted;
8. fit result, covariance, χ^2 , degrees of freedom, and residual diagnostics;
9. source-firewall scan;
10. canonical serialization hash.

14.2 Minimal JSON sketch

Listing 1: Schematic spectroscopy residual certificate.

```

{
  "certificate_type": "dtc_hydrogen_differential_holonomy_v1",
  "paper": "Paper 14",
  "mode": "post_freeze_or_conservative",
  "electron_certificate_hash": "sha256:...",

```

```

"forbidden_prefreeze_sources_present": false,
"transitions": ["2S-8S", "2S-9S", "2S-10S", "2S-8D", "nP_fs", "H-D", "Rydberg", "antiH
"],
"covariance": "diagonal_or_full_matrix_hash",
"shape_columns": ["S_contact", "spin_holonomy", "isotope_boundary"],
"number_of_transitions": 8,
"number_of_shape_columns": 3,
"overconstraint": true,
"line_by_line_fit": false,
"chi2": "computed_by_validator",
"dof": "computed_by_validator",
"canonical_hash": "sha256:..."
}

```

15 Toy finite example

The package associated with this paper contains a nonphysical toy certificate. The toy uses eight synthetic residual entries and three predeclared columns. It demonstrates the validator logic only; it is not a hydrogen data analysis.

The toy model uses:

$$y_i = c_S X_{iS} + c_{\text{spin}} X_{i\text{spin}} + c_N X_{iN} + \epsilon_i, \quad (63)$$

with fixed coefficients and small residual noise. The validator checks:

$$M - p \geq 2, \quad (64)$$

that no forbidden pre-freeze source tokens appear, that no line-by-line amplitudes are used, and that the generalized least-squares residual is compatible with the declared covariance.

Toy status

The toy certificate proves only that the certificate machinery and overconstraint validator are executable. It does not analyze real hydrogen data and does not certify a physical DTT residual.

16 What counts as success or failure

16.1 Success modes

A nontrivial success could be:

1. the frozen ground-state holonomy gives the low-energy boundary value, and all excited-state residuals are consistent with zero;
2. a state-dependent coefficient such as β_S is derived once from record geometry and multiple S and non-S lines follow the predicted shape;
3. S, D, fine-structure, and high- ℓ Rydberg states show the predicted angular-momentum hierarchy;
4. H/D and H/anti-H comparisons follow a derived electron-only, nuclear-boundary, or orientation-sensitive rule;

5. null results bound $|\eta_a|$ at a level that constrains DTT record geometry.

16.2 Failure modes

The differential program fails if:

1. the electron certificate is modified after spectroscopy comparison;
2. α -dependent hydrogen formulas enter the pre-freeze holonomy construction;
3. every transition is assigned its own free amplitude;
4. the branch is selected per line;
5. the residual column is indistinguishable from a nuisance parameter direction;
6. the predicted Rydberg or isotope asymptotics are contradicted by overconstrained data;
7. standard QED/theory/systematic uncertainties absorb the claimed signal.

17 Publication roadmap for real-data use

A future real-data Paper 14 should be organized as follows:

1. publish the frozen electron certificate or declare conservative calibration mode;
2. publish the exact transition list and extraction conventions;
3. publish the QED baseline code/version and parameter covariance;
4. publish DTT shape columns before fitting;
5. run nuisance projection and overconstraint tests;
6. archive machine-readable residual certificate;
7. state success/failure without changing the upstream certificate.

Figure placeholder: Real-data package structure

Show four machine-readable layers: frozen alpha certificate, spectroscopy data/covariance, standard-theory baseline, DTT residual-shape certificate.

Label: `real-data-package`

Figure 5: Real-data package structure. Show four machine-readable layers: frozen alpha certificate, spectroscopy data/covariance, standard-theory baseline, DTT residual-shape certificate.

18 Baseline construction and extraction conventions

The most common failure mode of a residual-spectroscopy paper is to compare theory and experiment without specifying what has already been removed. Paper 14 therefore treats the baseline itself as part of the certificate. A transition residual is meaningful only relative to a declared theoretical and experimental extraction pipeline.

18.1 Hyperfine centroids

For a level with hyperfine components F , the centroid convention must be declared before comparison. A generic centroid has the form

$$\nu_{nlj}^{\text{cent}} = \frac{\sum_F w_F \nu_{nljF}}{\sum_F w_F}, \quad w_F \in \{2F+1, w_F^{\text{exp}}, w_F^{\text{protocol}}\}. \quad (65)$$

The weights may reflect statistical multiplicity, experimental line extraction, or a DTT record-envelope convention, but the choice cannot be changed after inspecting residuals.

Criterion 18.1 (Centroid discipline). *If a DTT shape column is claimed to be independent of hyperfine structure, the same centroid convention must be used across the reference transition, excited transition, isotope comparison, and antihydrogen comparison. If the column is hyperfine-sensitive, the hyperfine dependence must be included explicitly as η_{nljF} , not hidden in a data reduction choice.*

18.2 Reference constants and nuisance parameters

The baseline prediction may depend on a parameter vector

$$\Theta_{\text{base}} = (\alpha_{\text{DTT}}, R_{\infty}, R_p, R_d, m_e/m_p, m_e/m_d, \dots). \quad (66)$$

Some of these are fixed by the upstream DTT package, some by external metrology, and some are profiled nuisance parameters. The certificate must state which is which.

Quantity	Default role in Paper 14	Firewall comment
α_{DTT}	frozen upstream boundary value	cannot be inferred from hydrogen residuals in strong mode
R_{∞}	derived/post-freeze baseline parameter	may be profiled only in conservative spectroscopy mode
R_p, R_d	nuclear-size nuisance parameters	cannot be used to absorb arbitrary DTT columns
Mass ratios	external or later DTT inputs	must carry covariance if measured values are used
External-field parameters	experimental nuisance directions	must be included in Z if correlated with residuals

Table 5: Baseline parameter roles for differential holonomy spectroscopy.

18.3 Theory error and truncation covariance

Bound-state theory contains truncation uncertainty. It should not be added as an unstructured diagonal padding whenever a residual is inconvenient. Instead, theory uncertainty should be represented by a declared covariance contribution

$$C = C_{\text{exp}} + C_{\text{th}} + C_{\text{sys}} + C_{\text{ext}}. \quad (67)$$

If the same uncalculated term affects several transitions, C_{th} should contain correlations. A strong DTT residual must survive these correlations.

Firewall Warning 18.2 (Theory-error backfitting). *Increasing theory uncertainties after seeing that a DTT column fails is equivalent to post-hoc model selection. It is not permitted in the strong comparison protocol.*

19 Identifiability, profiling, and residual geometry

19.1 Profiled nuisance fit

A practical comparison may fit DTT amplitudes and nuisance parameters simultaneously:

$$y = Xc + Z\delta\theta + \epsilon. \quad (68)$$

The joint estimator is

$$\begin{pmatrix} \hat{c} \\ \hat{\delta\theta} \end{pmatrix} = (W^T C^{-1} W)^{-1} W^T C^{-1} y, \quad W = (X \ Z). \quad (69)$$

However, a DTT column is identifiable only through the component of X orthogonal to Z . If

$$(I - P_Z)X_A \approx 0, \quad (70)$$

then column A cannot be tested by the selected data set.

19.2 Residual angle

Define the weighted angle between a DTT column x and the nuisance space $\text{span}(Z)$ by

$$\sin^2 \phi_Z(x) = \frac{x^T (I - P_Z)^T C^{-1} (I - P_Z) x}{x^T C^{-1} x}. \quad (71)$$

A robust spectroscopy set should satisfy

$$\sin \phi_Z(X_A) > \phi_{\min} \quad (72)$$

for every claimed DTT column. This criterion prevents confusing a DTT residual with a small shift in R_∞ , proton radius, or an external-field calibration.

19.3 Prediction power

For a proposed experimental set, define the Fisher matrix for DTT amplitudes after nuisance projection:

$$F_X = X_\perp^T C^{-1} X_\perp. \quad (73)$$

The determinant $\det F_X$, or the smallest eigenvalue of F_X , measures how well the transition set separates the declared columns. This gives a principled way to design a hydrogen/Rydberg/isotope/antihydrogen program.

Criterion 19.1 (Experimental design criterion). *A transition set is DTT-discriminating if F_X is full rank, $M - p \geq 2$, and every column has nonzero nuisance-projected norm. Among such sets, prefer those maximizing the smallest eigenvalue of F_X subject to experimental feasibility.*

20 Full residual-model taxonomy

This section lists residual-model classes in increasing strength. The class must be declared before data fitting.

20.1 Class 0: boundary-only model

$$\mathcal{M}_0 : \quad \eta_a = 0 \quad \forall a. \quad (74)$$

This is the most conservative model. It says the holonomy fraction fixes only the low-energy boundary coupling. Hydrogen tests standard QED with α_{DTT} , but no extra excited-state residual exists.

20.2 Class 1: one-column contact model

$$\mathcal{M}_1 : \quad \eta_a = c_S \mathbf{1}_{\ell=0} n^{-3}. \quad (75)$$

This is testable mainly with S/non-S contrasts.

20.3 Class 2: contact plus spin

$$\mathcal{M}_2 : \quad \eta_a = c_S \mathbf{1}_{\ell=0} n^{-3} + c_{\text{sp}} n^{-3} \sigma_{\ell j F}. \quad (76)$$

This requires fine-structure intervals or resolved j, F data.

20.4 Class 3: contact plus spin plus isotope boundary

$$\mathcal{M}_3 : \quad \eta_a = c_S S_a + c_{\text{sp}} P_a + c_N \Xi_N(X, a). \quad (77)$$

This requires both H/D or other isotope channels and non-isotope transitions.

20.5 Class 4: orientation-sensitive antimatter model

$$\mathcal{M}_4 : \quad \eta_{\bar{H},a} = \epsilon_C \eta_{H,a}, \quad \epsilon_C \in \{+1, -1\}. \quad (78)$$

The value $\epsilon_C = -1$ is allowed only if a DTT charge-conjugation orientation theorem supplies it before comparison.

20.6 Class 5: derived finite-regulator model

The strongest model has no phenomenological shape ansatz. Instead,

$$\eta_a = \lim_{r \rightarrow \infty} \left[\text{br}_a \frac{1}{2\pi} \text{Arg det } V_{a,r} - \text{br}_{a_0} \frac{1}{2\pi} \text{Arg det } V_{a_0,r} \right]. \quad (79)$$

Then the shape matrix X is generated by a constructor and shipped as a certificate. This is the long-term target of the paper.

21 Isotope, antimatter, and lepton-family decision tables

21.1 H/D decision table

Observed pattern	Interpretation	Next check
H and D agree after standard corrections	electron-only or null residual	test S/non-S and Rydberg channels
D differs with nuclear-radius scaling	nuclear-boundary column possible	verify radius covariance and isotope-shift systematics
D differs with reduced-mass scaling	mass-ratio or recoil nuisance possible	test muonium/positronium separation
D differs line-by-line	likely systematics or failed model	reject unless a derived column predicts it

Table 6: Hydrogen/deuterium isotope decision table.

21.2 Antihydrogen decision table

Observed pattern	Interpretation	Next check
$\eta_{\bar{H}} = \eta_H$	CPT-even holonomy supported	improve precision and test more states
$\eta_{\bar{H}} = -\eta_H$ with derived branch theorem	orientation-sensitive cycle supported	verify branch theorem and trap systematics
$\eta_{\bar{H}}$ differs without a derived theorem	not a DTT prediction yet	treat as anomaly/systematic or new theorem target
State-dependent mismatch	high-risk region	requires resolved state-cycle construction

Table 7: Antihydrogen orientation decision table.

21.3 Muonium and positronium decision table

System	DTT use	Caution
Muonium	separates lepton-positive core from nuclear finite-size effects	strong recoil and mass-ratio dependence
Positronium	tests equal-mass lepton pair and annihilation sectors	annihilation and QED theory errors dominate many channels
Hydrogen-like ions	tests Z -scaling of record columns	high- Z QED and nuclear effects must be controlled

Table 8: Lepton-family and ion-system roles.

22 Acceptance theorem for Paper 14

Theorem Target 22.1 (Differential holonomy acceptance theorem). *A Paper 14 differential holonomy claim is accepted for a transition family $\mathcal{T}$ only if all of the following hold:*

1. *the upstream boundary package $\mathfrak{A}_{\text{freeze}}$ is frozen or conservative mode is declared;*
2. *the spectroscopy source firewall passes;*
3. *the QED/bound-state baseline and covariance are fixed before DTT fitting;*
4. *the DTT shape matrix X is derived or predeclared before comparison;*
5. *X remains identifiable after nuisance projection;*
6. *$M - p \geq 2$, with effective column rank below $M - 1$;*
7. *the residual vector lies in $\text{span}(X_{\perp})$ within covariance;*
8. *the same model succeeds across independent channel classes, or a null result yields a declared bound;*
9. *no line-by-line amplitudes, branch changes, or post-hoc shape columns are introduced.*

Failure of any item downgrades the result to exploratory phenomenology or rejects the claimed residual.

23 Pseudocode for a complete comparison

Listing 2: Pseudocode for a Paper 14 comparison.

```
load frozen_alpha_certificate
assert source_firewall_passed(frozen_alpha_certificate)

load spectroscopy_dataset
load qed_baseline_model
load covariance_matrix
load predeclared_dtt_shape_columns

assert no_forbidden_prefreeze_sources(spectroscopy_dataset.metadata)
assert not line_by_line_shape(predeclared_dtt_shape_columns)

y = observed_frequencies - qed_baseline_model(frozen_alpha_certificate, nuisance_defaults
)
Z = nuisance_jacobian(qed_baseline_model)
Pz = weighted_projector(Z, covariance_matrix)

X_perp = (I - Pz) @ shape_matrix
y_perp = (I - Pz) @ y
assert rank_effective(X_perp) == number_of_columns
assert len(y) - number_of_columns >= 2

fit = generalized_least_squares(y_perp, X_perp, covariance_matrix)
report chi2, dof, amplitudes, amplitude_covariance, residual_diagnostics
serialize certificate
hash certificate
compare conclusions without modifying upstream electron certificate
```

24 Extended figure placeholders

Figure placeholder: Nuisance-projection geometry

Draw the residual vector, the nuisance space $\text{span}(Z)$, the DTT shape space $\text{span}(X)$, and the projected residual $y_{\perp}$. The figure should show why a column parallel to nuisance directions is not testable.

Label: `nuisance-geometry`

Figure 6: Nuisance-projection geometry. Draw the residual vector, the nuisance space $\text{span}(Z)$, the DTT shape space $\text{span}(X)$, and the projected residual $y_{\perp}$. The figure should show why a column parallel to nuisance directions is not testable.

Figure placeholder: Isotope and antihydrogen decision map

Display H, D, muonium, positronium, and antihydrogen as separate branches. Label electron-only, nuclear-boundary, lepton-family, and orientation-sensitive residual paths.

Label: `isotope-antihydrogen-map`

Figure 7: Isotope and antihydrogen decision map. Display H, D, muonium, positronium, and antihydrogen as separate branches. Label electron-only, nuclear-boundary, lepton-family, and orientation-sensitive residual paths.

Figure placeholder: Experimental design via Fisher matrix

Show candidate transitions as rows added to a matrix. The determinant or smallest eigenvalue of the nuisance-projected Fisher matrix increases when independent channels are added.

Label: `experimental-design`

Figure 8: Experimental design via Fisher matrix. Show candidate transitions as rows added to a matrix. The determinant or smallest eigenvalue of the nuisance-projected Fisher matrix increases when independent channels are added.

A Notation ledger

Symbol	Meaning
H_e	ground electron determinant holonomy residual from the frozen electron certificate

$a = (n, \ell, j, F)$	shortened hydrogenic state label
C_a	closed excited electron record cycle associated with state a
H_a	determinant holonomy on state cycle C_a
η_a	state residual relative to reference a_0 , usually $1S$ centroid
S_i	transition residual shape $\eta_b - \eta_a$ for $i : a \rightarrow b$
y_i	empirical residual after standard theory and known systematics
X_{iA}	design matrix of predeclared DTT shape columns
C	covariance matrix for residuals
Z	nuisance-parameter design matrix
P_Z	weighted projection onto nuisance directions
N_{eff}	effective inverse-coupling scale, approximately $137 + H_e$

B Source-role ledger

Source class	Allowed role	Forbidden role
Holonomy certificate	supplies frozen H_e , branch, and connection	cannot be changed after spectroscopy
Canonical 137 theorem	supplies flat integer 137	cannot supply excited residuals by itself
Alpha-free hydrogen geometry	supplies state-cycle ontology and orientation language	cannot determine α by spectrum fitting
Post-freeze	supply baseline formulas after	cannot be pre-freeze inputs to
Bohr/fine/Lamb	constants are fixed	electron holonomy
pers		
Spectroscopy data	tests residual shapes	cannot choose q_{rec} , $\hbar_*$, branch, low band, or electron cycle

C Certificate schema checklist

1. Does the certificate identify post-freeze or conservative mode?
2. Is the electron certificate hash recorded?
3. Are transition labels and extraction conventions fixed?
4. Is the covariance matrix supplied or referenced by hash?
5. Are QED baseline version and nuisance parameters declared?
6. Are DTT shape columns predeclared?
7. Is $M - p \geq 2$?
8. Are line-by-line amplitudes absent?
9. Has the source firewall scan passed?
10. Is the final certificate serialized and hashed?

D Referee stress tests

Objection	Response in this manuscript
Is hydrogen being used to derive α ?	No. Hydrogen is post-freeze. The electron certificate supplies α ; hydrogen tests residual patterns.
Is this just fitting residuals?	The overconstraint rule rejects line-by-line fitting and requires predeclared shape columns.
Does it replace QED?	No. Standard QED/bound-state theory supplies the baseline. DTT is a residual overlay or null test.
Can the branch be chosen per transition?	No. Branch coherence is a theorem target and must be computed before phase readout.
What if all residuals vanish?	That is a legitimate result: DTT may only set the boundary value and predict no excited-state difference.
What if isotope residuals appear?	They must match a predeclared nuclear-boundary column or be attributed to standard nuclear/systematic effects.
What if antihydrogen differs?	A sign flip requires a derived orientation theorem; otherwise CPT-even equality is the conservative prediction.

E Figure plan

1. Dependency graph for Papers 8–14.
2. State-cycle family over (n, ℓ, j, F) .
3. Shape-column matrix.
4. Nuisance projection geometry.
5. Decision tree for post-freeze comparison.
6. Isotope and antihydrogen branch map.
7. Machine-readable certificate flow.

F Detailed derivation of the inverse-coupling sensitivity map

This appendix records the calculation behind the comparison equation used in the main text. It is included so that the spectroscopy layer can be audited without appealing to informal proportionality arguments.

Let a transition frequency be written as a downstream bound-state observable

$$\nu_i = \nu_i(N, \boldsymbol{\lambda}), \quad N = \alpha^{-1}, \quad (80)$$

where N is the inverse boundary coupling supplied by the frozen DTT certificate and $\boldsymbol{\lambda}$ denotes ordinary nuisance parameters such as reduced mass, nuclear radii, recoil conventions, finite-size parameters, and external-field corrections. The conventional sensitivity coefficient is

$$K_i = \frac{\partial \ln \nu_i}{\partial \ln \alpha} = -\frac{\partial \ln \nu_i}{\partial \ln N}. \quad (81)$$

For a small transition-specific inverse-coupling residual S_i , the change in N is $N \mapsto N + S_i$. Hence

$$\delta \ln \nu_i = \frac{\partial \ln \nu_i}{\partial \ln N} \frac{S_i}{N} + O(S_i^2) \quad (82)$$

$$= -K_i \frac{S_i}{N} + O(S_i^2). \quad (83)$$

Multiplying by ν_i gives

$$\delta \nu_i^{\text{DTT}} = -\nu_i K_i \frac{S_i}{N_{\text{eff}}} + O(S_i^2). \quad (84)$$

This is the origin of the inverse-coupling design column used in the paper.

A useful bound follows immediately. If a transition residual is bounded by $|\delta \nu_i| \leq \sigma_i$, then

$$|S_i| \lesssim \frac{N_{\text{eff}} \sigma_i}{|K_i| \nu_i} \quad (85)$$

when $K_i \neq 0$. This bound is meaningful only after the standard-theory uncertainty and covariance have been included; otherwise it can understate the true residual allowance.

G Shape-column construction templates

A shape column is admissible only when it is the output of a declared mechanism. The following templates are included to help future authors produce machine-readable columns before fitting.

G.1 Contact-support template

Input data:

1. state list $a \in \mathcal{S}$;
2. support functional $\rho_{\text{core}}(a)$ computed from the record envelope;
3. reference state g ;
4. transition list $i : a \rightarrow b$.

Output:

$$S_i^{\text{contact}} = (\rho_{\text{core}}(b) - \rho_{\text{core}}(g)) - (\rho_{\text{core}}(a) - \rho_{\text{core}}(g)). \quad (86)$$

For a simple hydrogenic proxy, $\rho_{\text{core}}(nS) \propto n^{-3}$ and $\rho_{\text{core}}(n\ell) = 0$ for $\ell \neq 0$. In a strong DTT application, the proxy must be replaced by the finite-regulator record density computed from $P_{a,r}$.

G.2 Angular-holonomy template

Input data:

1. record angular orientation functional $\mathcal{J}(a)$;
2. branch orientation $\mathcal{O}_a$;
3. suppression envelope $u_{n\ell}$.

Output:

$$\eta_a^{\text{ang}} = \beta_{\text{ang}} u_{n\ell} \mathcal{J}(a) \mathcal{O}_a. \quad (87)$$

A common preliminary proxy is $\mathcal{J}(a) = \sigma_{\ell j}$, but the strong theorem must derive $\mathcal{J}$ from the transported determinant line.

G.3 Isotope-boundary template

Input data:

1. isotope descriptor Ξ_X ;
2. state-support descriptor $\mathbf{f}_a$;
3. transition map $i : a \rightarrow b$.

Output:

$$S_i^{\text{iso}} = \Xi_X(\mathbf{f}_b - \mathbf{f}_a). \quad (88)$$

This template is allowed only if Ξ_X is declared independently of the transition residuals being fit.

H State-cycle constructor pseudocode

Input :

```
frozen electron certificate hash h_e
alpha-free hydrogen record datum D_H_r
state label a=(X,n,ell,j,F,mF,zeta,chi)
regulator level r
```

Algorithm:

1. verify h_e and load the frozen DTT connection class
2. construct the neutral hydrogen record complex $R_{H,r}$
3. identify the preparation/support subcomplex for state a
4. construct the closed state record cycle $C_{a,r}$
5. build the comparison surface $\Sigma_{a,r}$ if available
6. build the physical state bundle $E_{a,r}^{\text{phys}}$
7. compute the mixed operator $K_{a,r}^{\text{mix}}$
8. isolate the low physical projector $P_{a,r}$
9. check the certificate gap $m_{a,\text{cert}(r)} > 0$
10. compute ambient holonomy $U_{a,r}^{\text{amb}}$
11. choose exact, polar, or moving-det-line determinant route
12. evaluate pre-phase orientation $O_{a,r}$
13. only then compute $H_{a,r}$
14. serialize the state-cycle datum and record its hash

Output:

```
state-cycle certificate S_{a,r}
```

The pseudocode is deliberately more restrictive than a normal phenomenological model. It prevents a future analysis from silently changing the record cycle when the residual data are inconvenient.

I Data-release template for a real Paper 14

A future real-data version should include a machine-readable directory with the following structure.

```
paper14_real_data_release/
  README.md
  frozen_electron_certificate/
    certificate.json
    validation_output.txt
    sha256.txt
  state_cycle_constructor/
    source_or_schema_reference.txt
    hash.txt
  standard_theory_backend/
    backend_version.txt
    nuisance_parameters.json
    covariance_policy.json
  transitions/
    states.csv
    transitions.csv
    extraction_conventions.md
  residuals/
    observed_minus_theory.csv
    covariance_matrix.csv
  dtt_shapes/
    shape_columns.csv
    shape_column_ledger.json
    shape_hash.txt
  analysis/
    fit_script.py
    fit_output.json
    leave_one_channel_out.json
    null_model_report.json
  firewall/
    contamination_scan.txt
    no_backflow_attestation.txt
```

The most important feature is that the files in `frozen_electron_certificate/`, `state_cycle_constructor/`, `standard_theory_backend/`, and `dtt_shapes/` must be committed before the residual vector is used for fitting.

J Antihydrogen and conjugation protocol

Antihydrogen is not merely another isotope. It tests whether the record-orientation functional behaves correctly under conjugation. Let $\mathcal{C}$ denote the conjugation operation on the relevant record data. A conservative CPT-even theorem target is

$$H_{\mathcal{C}a} = H_a, \quad \eta_{\mathcal{C}a} = \eta_a. \quad (89)$$

An orientation-odd theorem target is

$$H_{\mathcal{C}a} = H_g - \eta_a, \quad \eta_{\mathcal{C}a} = -\eta_a, \quad (90)$$

for the relevant differential piece. The second option is much stronger and must be derived from the DTT branch-orientation theorem, not inferred from a difference between hydrogen and antihydrogen measurements.

A real antihydrogen comparison must report:

1. whether the analyzed quantity is CPT-even or orientation-odd in the DTT ledger;
2. whether hyperfine centroids or resolved hyperfine components are used;
3. how magnetic-field and trap effects enter the covariance matrix;
4. whether the same shape column predicts both hydrogen and antihydrogen results.

K Null-result bounds in additive reconstruction units

Because DTT uses the additive inverse-coupling variable $N = \alpha^{-1}$, bounds should be reported both as frequency residuals and as reconstruction-residual bounds. For a single transition,

$$|S_i|_{95} \approx \frac{N_{\text{eff}}}{|K_i|} \frac{|y_i|_{95}}{\nu_i}. \quad (91)$$

For a shape column $S_i = cX_i$, the covariance-aware bound is

$$\sigma_c^2 = (X^T C^{-1} X)^{-1} \quad (92)$$

for a one-column model. For multiple columns, the diagonal of $(X^T C^{-1} X)^{-1}$ gives the profiled covariance of the amplitudes when nuisance directions have already been projected out.

A useful reporting table is:

Channel	frequency bound	equivalent bound	$ S $	dominant covariance source
$1S - 2S$	placeholder	placeholder		standard constants/systematics
$2S - nS$	placeholder	placeholder		line correlation and QED back-end
Rydberg	placeholder	placeholder		field shifts and state preparation
Antihydrogen	placeholder	placeholder		trap and magnetic-field modeling

L Extended figure placeholders

References

- [1] M. Haj Yousef, *Projection Metrology in Dual-Time Theory: A Framework for Emergent Physical Constants*, draft manuscript, 2026.

Figure placeholder: Contact-column geometry

Show high support near the record core for S states and suppressed support for high angular momentum states.

Label: `contact-column-geometry`

Figure 9: Contact-column geometry. Show high support near the record core for S states and suppressed support for high angular momentum states.

Figure placeholder: Antihydrogen conjugation test

Show hydrogen and antihydrogen state cycles related by orientation reversal, with CPT-even and orientation-odd residual options.

Label: `conjugation-test`

Figure 10: Antihydrogen conjugation test. Show hydrogen and antihydrogen state cycles related by orientation reversal, with CPT-even and orientation-odd residual options.

Figure placeholder: Nuisance projection

Show residual vector decomposition into standard-theory nuisance directions, DTT shape directions, and orthogonal unexplained residual directions.

Label: `nuisance-projection`

Figure 11: Nuisance projection. Show residual vector decomposition into standard-theory nuisance directions, DTT shape directions, and orthogonal unexplained residual directions.

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