Protocol M: For Detection of Non-Generic Information Compression Interface in Human Autonomic Neurobiology

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1. Abstract

This protocol proposes an empirical test for the existence of a localized biological interface that performs **non-generic time-resolved information compression** distinguishable from standard neural processing.

The primary candidate interface is the **baroreflex-brainstem pathway**, with emphasis on the **Nucleus Tractus Solitarius (NTS)**. The central hypothesis is that this pathway may exhibit a compression profile – defined by entropy-rate reduction, irreversibility, energy-per-bit scaling consistent with irreversible compression, and structured output – that is statistically distinguishable from matched biological controls.

The protocol leverages established principles from:

- **Information theory** (Shannon entropy, entropy rate, mutual information),
- **Thermodynamics of computation** (Landauer-consistent scaling, not direct bound measurement),
- **Neurophysiology** (autonomic and sensory pathways),

and compares the candidate interface against a **tiered control set:**

1. spinal reflex arcs (primary automatic-response control),
2. non-NTS autonomic pathways (nearest physiological control),
3. visual processing cascade (generic biological compression baseline).

A positive result identifies a biologically real interface exhibiting a statistically distinguishable compression signature vector relative to controls. No claim is made that such an interface fully characterizes observer structure; rather, it establishes a measurable deviation from standard biological information processing.

This protocol tests for the existence of biological systems in which compression and invariant structure coexist under perturbation beyond the envelope of matched nonlinear dynamical controls.

II. Aim and Research Question

2.1 Aim

To determine whether a candidate autonomic neural interface exhibits a **time-resolved compression**

profile that is statistically distinguishable from matched biological controls.

2.2 Research Question

Does the mapping:

$\Pi : X(t) \rightarrow Y(t)$

implemented at the baroreflex-NTS interface exhibit:

- measurable entropy-rate reduction ($\Delta I\_rate > 0$),
- many-to-one, irreversible mapping,
- energy-per-bit scaling behavior consistent with irreversible compression,
- preservation of structured invariants under perturbation that are not reproducible in matched control systems (e.g., stable phase relationships, attractor geometry, or coupling structure),
- and geometric/temporal characteristics statistically distinguishable from control systems?

2.3 Minimal Claim

This protocol tests the existence of a **non-generic compression interface.**

Non-generic compression is operationally defined as compression that preserves invariant structure under perturbation, where such persistence exceeds that of matched nonlinear dynamical systems with equivalent dimensionality, approximate Lyapunov spectrum, and coupling topology under identical perturbation regimes.

It does **not** assume:

- a privileged interface exists,
- a complete theory of observer structure,
- or a fully specified target geometry.

Non-genericity is defined relative to a control class spanning representative biological compression archetypes (reflexive, autonomic, and hierarchical sensory systems), rather than an exhaustive enumeration of all possible systems.

Formally, invariant persistence must exceed the supremum over the matched control class.

If all measured compression signatures fall within the empirical control distribution bounds, the non-generic compression hypothesis is rejected.

All claims are therefore restricted to statistically detectable deviation from matched control systems at the level of the effective input-output interface, without requiring localization to a single anatomical substrate.

2.4 Structural Invariant Class (Definition)

Definition (Invariant-Preserving Compression):

A system $\Pi : X(t) \rightarrow Y(t)$ belongs to the class of invariant-preserving compression interfaces if there exists a non-trivial structural functional $\mathcal{I}$ such that:

$\mathcal{I}[Y(t)] - \mathcal{I}[X(t)] \leq \varepsilon\_inv$ under perturbation ε

where ε_inv is defined relative to the empirical control distribution simultaneously satisfying:

- $\Delta I\_rate > 0$ (irreversible information reduction),
- many-to-one mapping (loss of microstate detail),
- and non-random structured dependence $I(X; Y) > 0$.

Here, $\mathcal{I}$ may correspond to:

- phase-coupling structure (Φ),
- attractor topology,
- invariant ratios or geometric constraints,
- or other measurable structure-preserving features.

Generic compression systems do not, in general, preserve $\mathcal{I}$ under perturbation; instead, $\mathcal{I}$ degrades with increasing entropy or input disruption.

This defines a **positive class boundary** distinguishing invariant-preserving compression from generic biological compression.

This excludes systems in which apparent invariance arise from linear filtering, generic nonlinear transformations, or standard homeostatic control dynamics under matched perturbation conditions.

The primary invariant class used in this protocol is phase-structure coupling (Φ), treated as the principal invariant for hypothesis testing. Other invariants are considered secondary and supportive. Invariant preservation is evaluated within predefined tolerance bounds under matched perturbations, rather than exact equality. Invariant persistence must exceed that observed in matched control systems under identical perturbation. This requirement explicitly excludes invariance arising from criticality, synchronization artifacts, or generic nonlinear attractor dynamics matched in dimensionality and perturbation structure.

III. Background and Theoretical Basis

This section relies exclusively on **accepted scientific principles** and introduces operational definitions aligned with measurable biological time-series data.

3.1 Biological Signal Processing

Biological systems transform high-dimensional inputs into lower-dimensional neural representations:

$\Pi : X \rightarrow Y$ with $H(Y) < H(X)$

Examples include:

- sensory systems (vision, audition),
- autonomic regulation,
- reflex arcs.

These mappings are typically:

- nonlinear,
- many-to-one,
- constrained by channel capacity.

3.2 Information-Theoretic Description

Uncertainty in a signal is given by Shannon entropy:

$H(X) = - \Sigma\, p(x) \log p(x)$

However, for continuous physiological time series, **information reduction is defined using entropy rate or conditional entropy**, not static entropy.

Define the entropy-rate reduction:

$\Delta I\_rate := H(X\_t \mid X\_(t - 1)\hat{}k) - H(Y\_t \mid Y\_(t-1)\hat{}m)$

where:

- X_t, Y_t are time-indexed signals,
- $X\_(t-1)\hat{}k, Y\_(t-1)\hat{}m$ denote embedded past states.

This formulation is:

- time aware,
- invariant under reparameterization of time series,
- and empirically estimable from physiological data.

Information retained between input and output is:

$I(X:Y)$

which captures **non-random structured dependence** between signals.

3.3 Irreversibility and Compression

Neural transformations are not invertible in general:

$X \leftarrow\!/\!- Y$

This reflects:

- lossy encoding,
- thresholding,
- feature extraction.

Irreversibility implies that multiple input states map to a single output state, producing:

- many-to-one compression,
- loss of microstate detail,
- and non-recoverable information.

3.4 Thermodynamic Constraint (Landauer-Consistent Scaling)

Any irreversible reduction of information is associated with a minimum thermodynamic cost:

$Q \geq k\_B\ T \ln 2 \cdot \Delta I\_\text{bits}$

This protocol does not attempt to directly measure the Landauer bound in biological systems. Instead, it tests whether candidate interfaces exhibit **relative energy-per-bit scaling behavior consistent with irreversible information processing.**

Define the energy-per-bit ratio:

R_Q := Q / ΔI_rate

The empirical question becomes whether:

- R_Q is non-uniform across systems,
- and whether the candidate interface exhibits distinct scaling relative to controls.

R_Q is explicitly excluded from primary hypothesis decision criteria and serves only as a comparative thermodynamic signature for exploratory analysis. R_Q is treated strictly as a comparative phenomenological scaling proxy and is not interpreted as a direct thermodynamic quantity or used as a primary decision variable.

3.5 Empirical Consequence

If a biological interface performs **non-generic, structured compression,** it should exhibit:

- measurable entropy-rate reduction ($\Delta I\_\text{rate} > 0$),
- measurable energy-per-bit scaling,
- structured (non-random) output exhibiting invariant features under perturbation that degrade or fail in matched control systems,
- and distinct temporal or geometric organization relative to matched controls.

IV. Hypothesis

4.1 Primary Hypothesis

There exists a candidate interface R_NTS such that:

$\Pi\_NTS : X\_cardio\ (t) \rightarrow Y\_NTS\ (t)$

satisfies:

A. Entropy-Rate Reduction

$\Delta I\_rate > 0$

B. Many-to-One Mapping

Distinct input states map to the same output state, consistent with lossy compression.

C. Irreversibility

The mapping is not invertible on the relevant physiological timescale, producing non-recoverable loss of microstate information.

D. Energy-Per-Bit Scaling

$R\_Q := Q\_NTS / \Delta I\_rate.NTS$

exhibits scaling behavior that is statistically distinguishable from matched control systems.

E. Structured Retention with Invariance

$I(X\_cardio;\ Y\_NTS) > 0$

retained features exhibit stability under controlled perturbations in a manner not reproducible within the control distribution,

F. Distinct Compression Signature

Define the compression signature vector:

$B = (\Delta I\_rate, R\_Q, I(X; Y), G\_dim, \Phi\_strength)$

The candidate interface satisfies:

$D(B\_NTS, D\_control) > \tau$

where:

- D is a statistical distance measure (e.g., KL divergence, Mahalanobis distance),
- $D\_control$ is the empirical distribution of control signatures,

- τ is a predefined threshold.

4.2 Null Hypothesis

$H\_0 : B\_\text{NTS} \in D\_\text{control}$

The NTS behaves as a generic biological compression interface.

4.3 Alternative Hypothesis

H_1: B_NTS $\notin$ D_control

The NTS exhibits a statistically distinguishable compression profile.

4.4 Interpretation Boundary

A positive result indicates:

A biologically real interface exhibiting a **non-generic compression signature** relative to matched controls.

It does **not** establish:

- a full theory of observer structure,
- uniqueness of the interface,
- or a complete causal mechanism beyond measured variables.

A negative result (failure to exceed threshold τ) constitutes rejection of the non-generic compression hypothesis at the tested site.

V. Candidate Interface

5.1 Primary Candidate: Baroreflex-NTS Pathway

The primary candidate interface is the **baroreflex afferent pathway terminating in the Nucleus Tractus Solitarius (NTS).**

This includes:

- arterial pressure sensing (aortic arch, carotid sinus),
- baroreceptor transduction,
- afferent transmission via cranial nerves,
- central integration in the NTS.

5.2 Anatomical Components

Key structures include:

- Baroreceptors – located in the aortic arch and carotid sinus
- Vagus nerve – carrying aortic afferent signals
- Glossopharyngeal nerve – carrying carotid afferent signals
- Nucleus tractus solitarius – as the primary convergence and integration site

5.3 Functional Characteristics

The pathway exhibits:

- continuous high-dimensional input (pressure waveform, derivatives, phase),
- multi-channel sensory convergence,
- nonlinear thresholding and encoding,
- strong coupling to physiological rhythms (cardiac, respiratory),
- known integration before redistribution to downstream autonomic outputs.

5.4 Rationale for Selection

The NTS is selected as the primary candidate due to :

1. **Convergence** – multiple physiological signals collapse into a central integration site.
2. **Continuous Analog Input** – unlike discrete sensory events, cardiovascular signals are continuous and dynamic.
3. **Known Nonlinearity –** thresholding, saturation, and integration are well documented.
4. **Physiological Centrality –** the system directly regulates core homeostatic processes.
5. **Testability –** inputs, outputs, and proxies are measurable in principle.
6. **Operational Tractability** – the NTS represents a high-convergence interface that is sufficiently characterized to allow estimation of entropy-rate reduction, energy-per-bit scaling, and structured output using existing or achievable measurement techniques.

5.5 Interpretation Constraint

The NTS is treated as a high-probability candidate interface due to convergence and measurability. This selection does not imply that it is the sole or primary site of non-generic compression within the broader biological system.

5.6 Secondary Candidate Class (Deferred)

Additional candidate regions remain open for future evaluation:

- sacral autonomic networks,
- cardiopelvic interactions,
- reproductive-autonomic interfaces.

These regions are not included in the present protocol due to lower immediate measurement tractability, but may be evaluated using the same invariant and signature-based framework in subsequent studies.

VI. Tiered Control Set

To distinguish non-generic compression from standard biological processing, the candidate interface is compared against a **tiered control set** using a shared compression signature representation.

6.1 Tier 1 – Spinal Reflex Control (Primary Control)

Mapping

$\Pi\_reflex : X\_sensory\ (t) \rightarrow Y\_motor/reflex\ (t)$

Characteristics

- rapid, automatic response,
- minimal central processing,
- direct sensory-to-motor transformation,
- known compression and irreversibility,
- limited abstraction or integration.

Purpose

Provides a baseline for **fast, automatic biological compression under minimal integrative load,** serving as the primary comparator for distinguishing non-generic compression signatures.

6.2 Tier 2 – Automatic Control (Nearest-Family Control)

Mapping

$\Pi\_auto : X\_visceral\ (t) \rightarrow Y\_auto\ (t)$

Characteristics

- physiological regulation,
- multi-signal integration,
- homeostatic control,
- similar substrate to NTS.

Purpose

Tests whether the candidate interface is statistically distinguishable within autonomic systems, not merely different from non-autonomic processing.

6.3 Tier 3 – Visual Compression Baseline

Mapping

$\Pi\_vis : X\_light\ (t) \rightarrow Y\_visual\ (t)$

Characteristics

- well-characterized compression cascade,
- strong dimensionality reduction,
- hierarchical processing,
- feature extraction and abstraction.

Purpose

Provides a baseline for **generic biological information compression, establishing a high-dimensional sensory compression reference.**

6.4 Control Principle

For each control system *j*, define the compression signature vector:

$B_j = (\Delta I\_rate.j, R\_Q.j, I\_j, G\_dim.j, \Phi\_strength.j)$

where:

- $\Delta I\_rate.j$ = entropy-rate reduction,
- $R\_Q.j = Q\_j / \Delta I\_rate.j$ = energy-per-bit ratio,
- $I\_j = I(X; Y)$ = mutual information,
- $G\_dim.j$ = geometric dimensionality metric,
- $\Phi\_strength.j$ = temporal/phase organization measure.

The control set is not assumed to exhaust all possible generic compression systems but is selected to span representative biological compression classes relative to the tested interface.

The control set is intended to provide representative coverage of primary biological compression regimes, not exhaustive coverage of all possible system classes.

6.5 Non-Genericity Criterion

The candidate interface is evaluated by comparing its signature vector to the empirical control distribution:

$D(B\_NTS, D\_control) > \tau$

where:

- D is a statistical distance measure (e.g., KL divergence, Mahalanobis distance),
- $D\_control$ is the distribution of control signatures across all tiers,
- τ is a predefined threshold.

The control set is selected to span primary classes of biological compression, including minimal reflex processing, autonomic integration, and high-dimensional sensory compression.

6.6 Normalization Requirement

All comparisons are performed under matched or normalized input complexity conditions, such that:

H_rate(X_candidate) ≈ H_rate(X_control)

or are adjusted using complexity normalization procedures.

Where necessary, additional normalization is applied to account for differences in timescale, noise structure, coupling strength, and sampling access across systems.
Where feasible, comparisons include synthetic nonlinear control systems matched for dimensionality, coupling structure, and input statistics, to test whether observed invariance exceeds known dynamical attractor behavior.

Where feasible, synthetic nonlinear control systems are constructed to match input statistics, dimensionality, and dynamical structure, ensuring that observed deviations cannot be attributed to generic nonlinear dynamics.

VI.X Synthetic Control Construction

Synthetic Control Construction

Synthetic control systems are constructed to match the candidate system along the following axes:

- embedding dimensionality
- entropy rate (within tolerance)
- power spectral density
- approximate Lyapunov spectrum
- nonlinear coupling topology and order

while explicitly lacking invariant-preserving structure by construction.

Non-generic classification requires that such matched systems fail to reproduce the observed compression signature vector under identical perturbation and normalization conditions.

VII. Variables and Measurement Definitions

7.1 Input State

$X(t) = (P(t), \dot{P}(t), \Phi_{cardiac}(t), \Phi_{resp}(t), ...)$

where:

- $P(t)$ = arterial pressure waveform,
- $\dot{P}(t)$ = rate of pressure change,
- $\Phi_{cardiac}(t)$ = cardiac phase,
- $\Phi_{resp}(t)$ = respiratory phase.

The input state is treated as a continuous, multi-channel time series suitable for entropy-rate estimation.

7.2 Output State (Operational Definition)

$Y(t)$ = neural or physiological representation downstream of NTS

Direct measurement of NTS output is generally not feasible in humans; therefore, output states are defined using a tiered measurement framework. All interpretations are conditioned on the fidelity of the selected output proxy, and consistency across measurement tiers (A-C) is required to support conclusions.

Accordingly, all positive claims require consistency across measurement tiers and are interpreted as conditional on proxy fidelity rather than direct neural observability.

Positive results require cross-tier consistency across at least two independent proxy classes with non-overlapping measurement pathways (e.g., neural vs physiological), ensuring that observed structure cannot be attributed to a single downstream aggregation channel.

Interpretations are restricted to features that remain stable across independently derived proxy classes, reducing the likelihood of artifact propagation through a single measurement pathway.

All claims are defined at the level of the effective interface as realized through observable outputs, rather than requiring isolation of a single anatomical locus. All claims are restricted to the effective input-output interface as realized through observable outputs, and do not require identification of an isolated anatomical substrate.

7.3 Measurement Tiers

Tier A – Direct / Invasive Measurement

- NTS electrophysiology (animal models),
- direct afferent neural recordings,
- microelectrode or optogenetic probes.

Provides highest fidelity estimation of $Y(t)$ and direct access to compression dynamics.

Tier B – Targeted Human Measurement (Primary Operational Tier)

- brainstem-focused fMRI or neuroimaging targeting NTS regions,
- autonomic output decomposition (e.g., vagal/sympathetic balance),
- evoked response paradigms linked to baroreflex activation.

Provides indirect but structured estimates of NTS activity suitable for comparative analysis.

Tier C – Indirect Physiological Proxies

- heart rate variability (HRV) decomposition,

- baroreflex sensitivity measures,
- cardiorespiratory phase coupling metrics.

Provides accessible, lower-resolution proxies of NTS-related processing.

Tier A (direct or animal-model measurements) is treated as the primary validation anchor where available, while Tier B and C measurements provide convergent but indirect evidence.

Observed structure must additionally satisfy directional dependence constraints (e.g., transfer entropy or Granger causality), confirming that measured outputs reflect input-driven transformation rather than global coupling artifacts.

7.4 Entropy-Rate Estimation

$\Delta I\_rate = H(X\_t \mid X(t - 1)^k) – H(Y\_t \mid Y\_(t – 1)^m)$

Estimated using:

- discretization + plug-in estimators,
- k-nearest neighbor (kNN) entropy-rate estimators,
- permutation entropy (robustness check).

All entropy-rate and invariant measurements must exceed surrogate baselines constructed via IAAFT phase-randomized controls and block-resampled surrogates preserving autocorrelation structure.

Failure to exceed surrogate baselines constitutes classification as generic.

Estimator Validity Constraints

Embedding dimensions (k, m) are selected using established methods (e.g., false nearest neighbors or information-theoretic criteria). Entropy-rate estimates are corrected for finite-sample bias (e.g., Miller-Madow or kNN bias correction) and are only accepted after convergence under increasing data length and stability across estimator classes. Estimates failing convergence or bias-stability criteria are excluded from analysis.

7.5 Energetic Measurement (Relative)

$R\_Q = Q / \Delta I\_rate$

where Q is approximated using:

- metabolic proxies (e.g., oxygen consumption, BOLD signal),
- autonomic energy expenditure markers,
- physiological workload indicators.

The goal is not absolute energy measurement, but relative energy-per-bit scaling across systems. Energy-per-bit estimates are treated as secondary indicators due to reliance on indirect physiology proxies and are not required for primary hypothesis acceptance. R_Q is used for relative scaling

comparison only and does not independently determine hypothesis acceptance or falsification.

7.6 Mutual Information

$I(X; Y)$

Estimated using:

- kNN mutual information estimators,
- Gaussian approximation (where appropriate),
- permutation-based significance testing.

Used to confirm non-random structured dependence between input and output.

7.7 Geometric Structure

G_dim

Estimated using:

- PCA / ICA (linear baseline),
- UMAP or diffusion maps (nonlinear structure),
- attractor reconstruction (e.g., Takens embedding where feasible).

Used to quantify dimensionality and stability of output representation.

7.8 Temporal / Phase Organization

$\Phi\_strength$

Measured via:

- phase-locking value (PLV),
- cross-spectral coherence,
- persistence of phase relationships across perturbations.

Captures structured temporal organization beyond simple signal correlation.

7.9 Normalization and Controls

All measurements are normalized for input complexity and sampling conditions, including:

- matched entropy-rate of input signals,
- consistent sampling frequency,
- controlled perturbation conditions.

VIII. Derived Quantities and Metrics

8.1 Entropy-Rate Reduction:

$\Delta I\_rate := H(X\_t \mid X\_(t - 1)\hat{}k) - H(Y\_t \mid Y\_(t - 1)\hat{}m)$

where $H(\cdot \mid \cdot \triangledown$denotes conditional entropy estimated from time-series embeddings.

Estimation procedures include:

- discretizaiton + plug-in estimators,
- k-nearest neighbor (kNN) entropy-rate estimators,
- permutation entropy (robustness check).

Primary test:

$\Delta I\_rate > 0$ with confidence interval excluding zero.

8.2 Mutual Information (Structured Dependence)

$I(X; Y)$

Estimated using:

- kNN estimators,
- Gaussian approximation (when appropriate),
- permutation-based null models.

Primary test:

$I(X; Y) > I\_null$ (statistically significant above shuffled baseline)

8.3 Energy-Per-Bit Scaling

$R\_Q = Q / \Delta I\_rate$

where Q is derived from metabolic or physiological proxies.

Comparative metric:

$\Delta R\_Q = R\_Q.NTS - R\_Q.control$

Primary test:

$\Delta R\_Q \neq 0$ with statistically significant deviation from control distribution

8.4 Geometric Structure

G_dim = effective dimensionality of Y(t)

Estimated using:

- PCA / ICA (linear dimensionality),
- UMAP / diffusion maps (nonlinear embedding),
- attractor reconstruction (Takens embedding, where feasible).

Derived metrics include:

- intrinsic dimensionality,
- manifold stability across time,
- trajectory consistency under perturbation.

Primary test:

G_dim.NTS is statistically distinguishable from G_dim.control

Non-generic compression may manifest as reduced or reorganized effective dimensionality relative to control systems, reflecting structured constraint or coordinated dynamics not present in generic processing.

8.5 Temporal / Phase Organization

Φ_strength

Measured via:

- phase-locking value (PLV),
- cross-spectral coherence,
- persistence of phase relationships under perturbation.

Primary test:

Φ_NTS > Φ_control (or otherwise statistically distinguishable)

For primary hypothesis testing, Φ is operationalized using phase-locking value (PLV) as the canonical estimator, with coherence-based measures treated as secondary robustness checks.

The primary test is not elevated phase coupling magnitude, but persistence of phase structure under controlled perturbation relative to matched control systems.

Define phase persistence under perturbation as:

ΔΦ_decay := Φ_baseline – Φ_perturbed

The primary discriminator is the rate and magnitude of Φ degradation under controlled perturbation relative to matched control systems, rather than absolute Φ magnitude.

The primary invariant test is comparative:

$\Delta\Phi\_decay.NTS < \Delta\Phi\_decay.control$

evaluated across matched perturbation amplitudes and surrogate-preserving phase-randomized controls.

Directionality and Control Requirement

Valid phase-invariance results require:

1. confirmation of directional dependence (e.g., transfer entropy or Granger causality demonstrating $X \rightarrow Y$),
2. persistence under phase-scrambled surrogate controls, and
3. failure of matched oscillator, filtering, or coupled-phase synthetic systems to reproduce the observed phase stability.

Phase structure alone, without these conditions, is not sufficient to establish invariant-preserving compression.

8.6 Invariant Class (Operational Definition)

A system exhibits one instance of $\mathcal{I}$ (phase-structure invariant) if the coupling structure $\Phi(X,Y)$ remains stable under entropy-increasing perturbations of the input signal, i.e.,

$\Phi(X,Y)\_perturbed \approx \Phi(X,Y)\_baseline$

within the statistical bounds defined by control distributions.

Invariant features must exhibit degradation under identical perturbations in matched control systems, establishing comparative rather than absolute invariance.

8.7 Compression Signature Vector

$B = (\Delta I\_rate, R\_Q, I(X; Y), G\_dim, \Phi\_strength)$

Each system produces a single vector B_j, enabling direct comparison across systems.

8.8 Multivariate Distance Metric *D*

To quantify deviation of the candidate compression signature vector B_NTS from the control distribution, we define a primary multivariate distance metric based on the Mahalanobis distance:

$D\_M(B\_NTS, D\_control) := \sqrt{[(B\_NTS - \mu\_control)^T \Sigma\_control^{-1}(B\_NTS - \mu\_control)]}$

where $\mu\_control$ and $\Sigma\_control$ are the mean vector and covariance matrix of the control distribution $D\_control$.

To ensure numerical stability and robustness under finite sample conditions, $\Sigma\_control$ is estimated using shrinkage covariance methods (e.g., Ledoit-Wolf regularization).

Decision Rule

The primary non-genericity test is defined as:

$D_M(B_{NTS}, D_{control}) > \tau$

where τ is the 95^{th} percentile of the empirical control distance distribution, computed under identical preprocessing, normalization, and estimation procedures.

Robustness Constraints

Distributional Agreement Requirement

Classification as non-generic require agreement between Mahalanobis distance and at least one distributional distance metric (e.g., Wasserstein distance). If Mahalanobis distance indicates non-genericity while distributional metrics do not, the result is considered inconclusive and does not satisfy the primary decision criterion.

A valid classification as non-generic requires:

1. **Stability under covariance regularization.** The inequality $D_M > \tau$ must hold under reasonable variations in covariance estimation (e.g., shrinkage intensity).
2. **Consistency under resampling.** The result must persist under bootstrap or block-resampled control distributions.

Secondary Distance Measures (Robustness Only)

Synthetic Control Exclusion Condition

Non-generic classification additionally requires that synthetic nonlinear systems matched in embedding dimension, approximate Lyapunov spectrum, power spectral density, and coupling topology fail to reproduce the observed compression signature vector. Reproduction under these matched conditions results in classification as generic.

Alternative distance measures are used exclusively for robustness verification and do not determine primary hypothesis acceptance:

- **Wasserstein distance** is used to verify robustness under non-Gaussian control distributions.
- **KL divergence** may be used as an auxiliary diagnostic where density estimation is reliable.

A valid result requires that these secondary measures do not contradict the classification obtained via Mahalanobis distance.

Interpretation

Under this formulation, non-genericity is established only when the candidate system lies outside the empirical control manifold in a statistically robust, covariance-aware sense, and this deviation persists across estimation and distributional assumptions.

All primary conclusions are therefore contingent on deviation from both empirical biological controls and explicitly constructed matched nonlinear synthetic systems.

8.9 Statistical Testing Framework

All primary metrics are evaluated using:

- bootstrap confidence intervals,
- permutation-based null distributions,
- effect size estimation (e.g., Cohen's d, multivariate distance).

Multiple metrics must jointly support deviation from control distributions to satisfy the hypothesis.

8.10 Robustness and Cross-Validation

Results are validated by:

- comparing multiple entropy estimators,
- repeating across perturbation conditions,
- testing stability across measurement tiers (A-C),
- verifying invariance under resampling and noise injection.

IX. Experimental Design

9.1 Overview

The experiment design evaluates whether the candidate interface exhibits a non-generic compression signature by:

- applying controlled perturbations to input signals,
- measuring resulting changes in output structure,
- computing the compression signature vector *B,*
- and comparing results against the empirical control distribution.

All analysis steps, thresholds, and inclusion criteria are defined prior to data analysis to prevent post-hoc adaptation.

9.2 Input Perturbation Strategy

Controlled perturbations are applied to $X(t)$ to test:

- robustness of entropy-rate reduction,
- stability of retained structure,
- sensitivity of energy-per-bit scaling,
- persistence of geometric and temporal organization.

9.3 Perturbation Classes

A. Input Complexity Modulation

Manipulate entropy-rate of input signals via:

- controlled variation in pressure waveform variability,
- introduction of structured vs random fluctuations,
- modulation of signal predictability.

Expected effect:

- measurable changes in ΔI_rate,
- corresponding scaling behavior in R_Q

B. Phase Disruption

Disrupt temporal structure by:

- altering cardiac-respiratory coupling,
- introducing phase jitter or desynchronization.

Expected effect:

- reduction in $\Phi\_strength$,
- potential disruption of structured invariants.

C. Signal Noise Injection

Introduce controlled noise into input signals:

- additive white or colored noise,
- structured noise with known statistical properties.

Expected effect:

- changes in entropy-rate estimates,
- degradation of mutual information $I(X; Y)$,
- potential breakdown of geometric stability.

D. Physiological Perturbations

Apply controlled physiological challenges:

- othostatic tilt (baroreflex activation),
- breathing pattern modulation,
- pharmacological modulation (where feasible).

Expected effect:

- measurable changes across all signature components (Δ*I*_rate, *R_Q, I, G*_dim, Φ),
- differential response relative to control systems.

9.4 Measurement Sequence

For each experimental condition:

1. Acquire baseline input and output time series.
2. Apply perturbation.
3. Record resulting signals across measurement tiers.
4. Compute derived metrics:
   - Δ*I*_rate,
   - *R_Q,*
   - *I(X; Y),*
   - *G*_dim,
   - Φ_strength.
5. Construct compression signature vector *B*.

9.5 Control Comparison Protocol

For each control system *j*:

- repeat identical perturbation conditions,
- compute corresponding signature vector *B_j*,
- build empirical distribution *D*_control.

Primary comparison:

D(B_NTS, *D*_control)

9.6 Statistical Evaluation

All comparisons are evaluated using:

- bootstrap confidence intervals,
- permutation-based null testing,
- multivariate distance thresholds,
- effect size estimation.

Decision rule:

$D > \tau$ ß non-generic compression signature detected

9.7 Replication and Robustness

Results must be consistent across:

- multiple perturbation types,

- multiple subjects or trials,
- multiple measurement tiers,
- multiple estimation methods.

9.8 Experimental Constraints

- input signals must be normalized for entropy-rate
- sampling conditions must be consistent,
- noise levels must be controlled and documented,
- perturbations must remain within physiological safety limits.

X. Pass Criteria

A candidate interface is considered to exhibit a **non-generic compression signature** if the following criteria are satisfied.

10.1 Entropy-Rate Reduction

$\Delta I\_rate > 0$

with:

- confidence interval excluding zero,
- consistency across perturbation conditions
- and agreement across estimation methods.

10.2 Structured Dependence

$I(X; Y) > I\_null$

where:

- I_null is computed from permutation or shuffled baseline,
- significance is established via null distribution testing,
- and results are replicable across trials.

10.3 Energy-Per-Bit Scaling

$R\_Q.NTS \neq R\_Q.control$

such that:

- difference exceeds predefined threshold τ_R_Q,
- effect size is non-trivial,
- and deviation is stable across perturbations.

Failure or instability of R_Q does not invalidate the primary hypothesis if other criteria are satisfied.

10.4 Geometric Distinction

G_dim.NTS is statistically distinguishable from G_dim.control

with:

- consistent dimensionality difference,
- stable manifold structure under perturbation,
- and reproducible embedding results across methods.

10.5 Temporal Organization

Φ_NTS is statistically distinguishable from Φ_control

such that:

- phase-locking or coherence metrics are statistically distinguishable,
- and temporal structure persists under perturbation.

10.6 Compression Signature Criterion (Primary Decision Rule)

Let:

B_NTS = (ΔI_rate, R_Q, I(X; Y), G_dim, Φ_strength)

The candidate passes if:

D(B_NTS, *D*_control) > τ

where:

- *D* is a multivariate distance measure,
- *D*_control is the empirical distribution of control signatures,
- τ is a predefined threshold,
- and the result is statistically significant under permutation testing.

The threshold τ is defined as the 95^{th} percentile of the empirical control distribution *D*_control, such that values exceeding this threshold are considered statistically significant deviations from control behavior. Statistical significance is additionally confirmed via permutation testing, ensuring that observed deviations exceed those expected under randomized input-output mappings.

Threshold stability is validated using cross-validation and out-of-sample evaluation, and conclusions must remain consistent under resampling and covariance-regularization procedures.

Mahalanobis distance is used as the primary multivariate distance metric due to its suitability for finite-sample, covariance-aware comparisons. Alternative metrics (e.g., KL divergence, Wasserstein distance) are used as robustness checks.

10.7 Robustness Requirement

All criteria must be satisfied under:

- multiple perturbation conditions,
- multiple measurement tiers (A-C),
- and multiple estimation methods.

10.8 Minimum Acceptance Condition

A positive result requires:

- satisfaction of compression signature criterion (10.6),
- and at least **two independent supporting metrics** among Sections 10.1 – 10.5.

The primary distance criterion must exceed τ with a non-trivial effect size relative to control variance, ensuring that significance is not driven by marginal deviations across multiple weakly contributing dimensions.

The multivariate distance criterion must exceed threshold τ with a non-trivial effect size relative to control variance, ensuring that significance is not driven by marginal deviations across multiple weakly contributing dimensions.

XI. Failure Conditions

Global Falsifier:

If matched synthetic or biological control systems reproduce the observed compression signature vector B under identical perturbation and normalization conditions, the non-generic compression hypothesis is rejected.

The hypothesis is considered **not supported** if any of the following conditions are met.

11.1 Absence of Entropy-Rate Reduction

$\Delta I\_rate \leq 0$

or:

- confidence interval includes zero,
- results are inconsistent across perturbations or estimators.

11.2 Absence of Structured Dependence

$I(X: Y) \leq I\_null$

such that:

- mutual information is indistinguishable from shuffled baseline,
- no stable structure is retained between input and output.

11.3 Lack of Distinct Energy-Per-Bit Scaling

$R\_Q.NTS \approx R\_Q.control$

such that:

- differences fall within control distribution bounds,
- or observed variation is attributable to noise or measurement error.

11.4 Absence of Geometric or Temporal Distinction

$G\_dim.NTS \approx G\_dim.control$ and $\Phi.NTS \approx \Phi.control$

with:

- no consistent dimensionality or structure differences,
- no persistent phase or temporal organization under perturbation.

11.5 Failure of Compression Signature Criterion

$D(B.NTS, D\_control) \leq \tau$

such that:

- the candidate signature lies within the empirical control distribution,
- or fails to exceed predefined threshold under statistical testing.

11.6 Instability or Non-Robustness

Results fail if:

- effects are not reproducible across perturbation conditions,
- results vary significantly across measurement tiers or estimators,
- or structure is not preserved under controlled variation.

11.7 Global Falsifier

If all measured compression signatures fall within the empirical control distribution bounds, the non-generic compression hypothesis is rejected at the tested interface.

11.8 Interpretation Constraint

Negative results are not reinterpreted as latent or undetected success. They constitute a valid rejection of the hypothesis at the tested site under the defined conditions.

11.9 Generic Failure Signature

Generic biological compression systems are expected to exhibit:

- rapid degradation of phase structure (Φ) under perturbation,
- loss of geometric stability (G_dim),
- and convergence toward control-aligned covariance structure.

This degradation profile defines the expected failure signature of generic systems and serves as a baseline comparator for identifying non-generic behavior. Matched synthetic nonlinear systems exhibiting equivalent persistence under identical perturbations are classified within this generic failure class.

11.10 Structural Falsifier Condition

The hypothesis is structurally falsified if:

- invariant structure persists under surrogate or randomized input that destroys input structure, or
- synthetic nonlinear systems matched in dimensionality and input statistics reproduce the observed compression signature vector B.

In such cases, observed effects are attributed to generic dynamical or statistical artifacts rather than a distinct compression interface.

Reproduction of the compression signature vector under matched synthetic nonlinear systems constitutes a definitive falsification, independent of biological control comparisons.

XII. Interpretation and Limits

12.1 Interpretation of Positive Result

A positive result indicates:

the existence of a biological interface exhibiting a non-generic compression signature, defined by entropy-rate reduction, structured dependence, energy-per-bit scaling behavior, and statistically distinguishable geometric and temporal organization relative to matched controls. The combined metrics capture not only compression but structured retention and organization under constraint, which may reflect higher-order coherence in the transformation process.

Such a result establishes:

- the presence of a measurable deviation from generic biological compression,
- a localized or distributed interface consistent with irreversible information processing,
- and a repeatable empirical signature across controlled perturbations.

The measured signature reflects not only compression but structured transformation under constraint, including retention of invariant relationships across perturbations.

This result is descriptive, not explanatory, and does not by itself establish underlying mechanisms beyond measured variables.

Operationally, a positive result identifies a transformation that reduces entropy while preserving structured dependence under perturbation, and whose stability properties are not reproducible by matched biological or synthetic control systems.

Detectability is constrained by a joint envelope of spectral visibility, measurement resolution, and statistical distinguishability from matched control distributions.

12.2 Interpretation of Negative Result

A negative result indicates:

the absence of a detectable non-generic compression signature at the tested interface under the defined experimental conditions.

This implies:

- the candidate interface behaves as a generic biological compression system,
- or that any non-generic structure is below detection threshold given current measurement resolution.

Negative results constrain candidate realizations of the hypothesis and reduce the viable search space.

12.3 Scope of Inference

This protocol does **not** establish:

- a complete theory of observer structure,
- uniqueness of the tested interface,
- or causal mechanisms beyond measured variables.

The protocol tests for the presence or absence of a specific class of measurable compression behavior, not its ultimate origin or interpretation.

12.4 Measurement Limitations

Results are subject to:

- limitations in signal resolution,
- indirect measurement of neural states (especially in human subjects),
- estimator bias in entropy and mutual information calculations,
- and constraints of physiological perturbation methods.

All conclusions are condition on the fidelity and validity of measurement procedures.

12.5 Statistical Interpretation Constraint

Statistical methods are employed strictly as detection and comparison tools, and do not imply that the underlying biological or informational processes are inherently statistical in nature.

12.6 Generalization Limits

Findings obtained at the candidate interface:

- may not generalize to all biological systems,
- may reflect properties specific to the tested pathway,
- and require independent validation across systems and conditions.

Some biological systems (e.g., visual processing pathways) may exhibit partial invariant structure under perturbation. The present protocol therefore detects relative, not absolute, non-genericity, conditioned on the chosen control set.

12.7 Framework Boundary

This protocol establishes a test for the presence of a non-generic compression interface. It does not assume or require any broader theoretical framework for its validity.

Appendix A – Information-Theoretic Rationale

A.1 Shannon Framework

Signal uncertainty:

$H(X) = - \Sigma\, p(x) \log p(x)$

Biological processing reduces uncertainty:

$H(Y) < H(X)$

A.2 Compression Mapping

$\Pi : X \rightarrow Y$

with:

- many-to-one mapping
- loss of microstate detail

A.3 Mutual Information

$I(X ; Y)$

captures preserved structure.

A.4 Landauer Constraint

$Q \geq k\_B\ T \ln 2 \cdot \Delta I$

Irreversible compression implies:

- physical cost
- measurable energy dissipation

A.5 Experimental Implication

If a biological system performs non-generic compression, it should exhibit:

- measurable ΔI
- measurable Q
- structured output
- detectable deviation from controls

A.6 Protocol Justification

This protocol tests:

Whether any biological interface exhibits a compression profile that deviates from standard neural processing.

No additional assumptions are required.

Final Statement

This protocol isolates a minimal, testable claim grounded in established physics and information theory: that biological systems may exhibit compression interfaces distinguishable from generic processing. It provides a structured method to detect such interfaces without requiring prior commitment to broader theoretical interpretations.

Appendix B. Detectability Constraints and Failure Modes

The following considerations do not alter the empirical protocol or decision criteria defined above. They provide a framework for interpreting negative or weak detection outcomes in terms of structured viability and measurement constraints. These constructs are strictly post hoc interpretive tools and are not used to modify hypothesis evaluation, threshold criteria, or experimental conclusions.

B.1 Notation Consistency Bridge

To avoid overload and preserve interpretability:

- $I(X; Y)$ = mutual information only

- $\mathcal{I}$_inv [·] = structural invariant functional
- I_spec = spectral rigidity index
- Δ_spec = effective spectral gap
- Φ = phase-structure metric (as defined in protocol)

These quantities are not required for protocol execution but support interpretation of structural stability.

B.2 Continuity-Residue Architecture

Detection is constrained by the ability of the system to realize and maintain structured continuity under perturbation.

We define a downstream architecture:

ρ_Ψ, τ_Ψ → $\mathcal{T}$_min → Q_real → ΔQ_def → R → $\mathcal{P}$*(R; I)* → J_cand

This separates:

- structural realizability ($\mathcal{T}$_min)
- realizable support (Q_real)
- continuity deficit (ΔQ_def)
- residual burden (R)
- persistence ($\mathcal{P}$)
- accumulated residue (J_cand)

This layer does not introduce new measurements, but provides interpretation of structural degradation.

B.3 J_null Identification Boundary

Persistent, accumulated, non-dischargeable unrealized continuity burden is identified as:

J_cand → J_null

This defines a failure mode in which structure cannot be stably realized despite underlying system dynamics.

B.4 Spectral Bridge (Protocol-Compatible Interpretation)

Accumulated residue impacts structural stability via spectral degradation:

J_null ↑ ß Δ_spec.eff ↓, I_spec.eff ↓ ß reduced stability of $\mathcal{I}$_inv

Operationally, this should appear as:

- reduced Φ-stability
- less stable G_dim
- more fragile compression signatures under perturbation

B.5 Spectral Collapse Threshold

There exists a critical threshold:

J_crit^{spec}

such that:

- below threshold → invariant-preserving compression is stable
- near threshold → fragile
- above threshold → unstable under perturbation

Even if:

$I(X; Y) > 0$

This formally separates:

existence of structure from **detectability of structure**

B.6 Detectability Envelope

Detection requires simultaneous satisfaction of:

- existence of invariant-preserving structure
- sufficient spectral viability
- statistical distinguishability from controls

Thus:

Detectability is jointly constrained by structure, spectral stability, and statistical resolution.

B.7 Interpretation of Negative Results (Extended)

Negative experimental results may arise from:

1. absence of invariant-preserving compression, or
2. presence of such compression outside the detectability envelope due to:
   - spectral collapse
   - residual burden accumulation
   - measurement resolution limits

This does not alter falsification criteria, but clarifies interpretation.