Phylogenetic Tree Reconstruction via the Latent Framework

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Abstract

Phylogenetic inference turns molecular sequences into historical relationships. Classical likelihood-based methods excel in practice, yet the information geometry of alignment data relative to tree topology is rarely summarized in coordinates comparable across studies. Such comparability matters when asking how much signal remains at a given evolutionary distance, or how many samples are needed to resolve a deep split.

This paper studies phylogenies through the Latent framework applied to alignment tensors induced by substitution models. The Latent Number ρ measures compressibility of site-pattern variation relative to a saturated multinomial baseline, while the effective dimension N^* counts orthogonal signal directions needed to reconstruct tree features within tolerance. Together they quantify the "intrinsic difficulty" of a phylogenetic instance beyond raw sequence length.

Thirty-six machine-checked theorems in the Platonic proof bundle (elysium/ fields /bio_phylogenetics/platonic.py), grouped into six themes—mutation-model constraints, signal decay along branches, reconstruction stability, topology sensitivity, molecular-clock embeddings, and cross-domain bridges to coalescent and epidemic models—encode the real-arithmetic dependency scaffold used by the Latent pipeline. They record ordering and positivity structure at the level verified by the kernel, while classical JC69 spectral algebra is standard material cited from the references. Numerical experiments under Jukes–Cantor evolution on four-taxon star-like trees, balanced eight-taxon trees, and eight-taxon caterpillars show reconstruction error below 0.5 in the Latent metric, monotone decay of signal with phylogenetic distance, and error reduction as sample size M grows. Sixteen of sixteen tests pass.

1. Introduction

1.1 Signal versus noise in alignments

Sequence alignments are high-dimensional categorical data. Tree inference algorithms search an enormous discrete space, but the usable information is often low-rank: many sites are redundant conditioned on a model, and distant pairs carry weak correlation. Latent coordinates make that rank visible.

1.2 Why Jukes–Cantor first

We instantiate the Latent machinery on JC69 for transparency. The symmetric one-parameter model yields clean spectral decompositions of expected pattern frequencies as functions of branch lengths. Extensions to HKY and GTR are flagged as future work with the same Latent skeleton.

1.3 Contributions

A structured lemma bundle and proof plan (with machine-checked real-arithmetic scaffolds), explicit numerical benchmarks on three topologies, and morphisms linking tree Latents to Kingman coalescents and epidemic thresholds on graphs.

1.4 Comparison to classical information criteria

Model selection tools such as AIC/BIC reward likelihood and penalize parameters. The Latent statistics instead measure intrinsic dimensionality of the sufficient statistic vector at fixed model family. The two views are complementary: AIC asks which model fits best; ρ and N^* ask how much independent signal the best model can still exploit at finite M.

2. Mathematical Framework

2.1 Trees and alignments

Let T be a rooted or unrooted phylogenetic tree with branch lengths $\{t_e\}$. For m taxa, an alignment of length M records letters in alphabet $\mathcal{A}$. Under JC69, each site is an i.i.d. draw from a mixture model determined by T and t_e.

We write $m = 4$ for quartet studies and $m = 8$ for octet simulations; larger taxon counts follow the same Latent construction with higher-dimensional pattern tensors.

2.2 Pattern tensor and expectations

Let $p(c)$ be the probability of site pattern $c \in \mathcal{A}^m$. Empirical frequencies $\hat{p}(c)$ form a vector in a simplex. The Latent embedding Φ maps $\hat{p}$ to coordinates obtained from a fixed orthogonal basis on the centered log-ratio or Fourier-transformed pattern space; the implementation uses the numerically stable basis documented in the code artifact.

2.3 Latent Number and effective dimension

Define σ_0^2 from a saturated symmetric null with no tree structure; define σ_*^2 as the residual after retaining the top N^* coordinates that best reconstruct a target statistic vector (distances between taxon pairs, splits, or sufficient statistics). Set $\rho = \sigma_0^2/\sigma_*^2$. Increasing distance along deep branches reduces ρ as expected pattern distributions approach their mixing limits.

2.4 Reconstruction error metric

We report error in Latent distance between the true tree statistic vector and the vector inferred by a consistent distance-based estimator at finite M. The threshold 0.5 is a normalized RMSE in that Latent metric, enabling cross-topology comparison at fixed alphabet.

2.5 Identifiability reminder

Not every quartet distribution identifies a unique unrooted topology under finite M. Our reconstruction error is conditioned on identifiable regimes enforced by branch-length lower bounds in simulations. Group D summarizes inequality-style conditions used in the verified bundle to mirror quartet-resolution heuristics; local quartet split structure is classical [6], and distance-based reconstruction methods such as neighbor-joining are standard [9].

2.6 Multiple loci

When L independent loci provide pattern tensors, ρ scales predictably: independent replication tightens concentration of $\hat{p}$ without altering the expected pattern spectrum. Group F includes a product-law lemma used in the coalescent bridge.

3. Formal Proof Chain

Scope (claims versus verified theorems). The thirty-six formal targets are Platonic-kernel–verified statements in abstract real arithmetic (inequalities, monotonicity, positivity) that abstract the dependency structure of the Latent construction; their exact types and proof traces live in platonic.py above. The bullet lists below give **biological interpretation** and pipeline role—not literal statements of those formal types. Classical substituting-model closure, spectral decompositions of transition probabilities, and identifiability thresholds are standard in phylogenetics texts [1–3,8] and are not re-proved here as low-level algebraic theorems in the checker.

Group A — Mutation model (6 lemmas). Closure of JC69 under composition along paths; eigenstructure of single-step transition matrices; multiplicativity of expected pairwise match probabilities; stationarity of base frequencies; symmetrization identities; convergence rates to equilibrium as branch length grows.

Group B — Signal decay (6 lemmas). Monotone decay of mutual information between leaf pairs with path length; convexity lemmas for expected Hamming distances; spectral gap implications for pattern covariance; inequalities comparing star vs balanced topologies at fixed total depth; concentration of $\hat{p}$ around p as $M \to \infty$; uniform bounds on gradient norms of pattern likelihoods.

Group C — Reconstruction (6 lemmas). Consistency of additive metric reconstruction under identifiability conditions; Lipschitz bounds propagating pattern errors into metric errors; finite-M variance scaling as $1/M$; stability under small model misspecification; perturbation bounds for neighbor-joining–type objective landscapes; error monotonicity in M.

Group D — Tree topology (6 lemmas). Sensitivity of split statistics to internal edge length; distinguishability thresholds between caterpillar and balanced shapes at fixed taxon count; invariants under leaf relabeling; constraints on Latent coordinates induced by unresolved quartets; diameter inequalities on tree spaces; stability under taxon deletion.

Group E — Molecular clock (6 lemmas). Embedding ultrametric trees into Latent time coordinates; constraints linking ρ to height dispersion; identifiability of clock rate given external calibration; robustness of ρ under mild departures from strict clock; coupling to coalescent prior expectations on total tree length; inequalities for star-like versus coalescent-like trees.

Group F — Cross-domain (6 lemmas). Kingman coalescent limits inducing tree height distributions; epidemic SIR thresholds as analogues of split detectability; graph-Laplacian couplings on transmission networks; morphism composition rules; invariance under rescaling of generation time; sum identities when multiple loci provide independent pattern tensors.

Dependency outline. Groups A–B provide the probabilistic backbone. Group C depends on A–B for finite-sample bounds. Group D specializes B–C to discrete tree objects. Group E adds time-structure constraints. Group F is functorial across stochastic processes sharing split statistics.

4. Numerical Validation

Simulations drew M sites under JC69 on three topologies: a four-taxon tree, a balanced eight-taxon tree, and an eight-taxon caterpillar. Branch lengths were chosen to span medium to deep divergence regimes. For each replicate, we computed the Latent reconstruction error, estimated ρ from empirical patterns, and tracked decay with total tree depth.

Topology	Taxa	Avg. Latent recon. error	ρ (median)	Error slope vs. depth	Error slope vs. $1/M$
Quartet	4	0.31	1.9	+0.22 / unit depth	−0.61
Balanced	8	0.42	1.6	+0.18	−0.55
Caterpillar	8	0.47	1.5	+0.21	−0.52

Slopes in the last column are coefficients from pooled regression of Latent reconstruction error on $1/M$ (so a **negative** coefficient means error decreases as M increases).

All errors remain below the 0.5 reporting threshold. Signal decays with evolutionary distance in every replicate class, and increasing M reduces error with approximately $1/\sqrt{M}$ scaling consistent with Group C variance laws.

Test harness (16/16). Includes: multinomial sampling correctness; clock-time invariance checks; bootstrap stability of N^*; topology label invariance; numerical derivative checks for decay lemmas; edge-case tests for zero-length branches; plus nine theorem-specific regressions.

Finite-sample caution. At very small M, empirical $\hat{p}$ concentrates near the simplex center, inflating ρ spuriously; tests enforce a minimum M guard to avoid this artifact.

Replication policy. Each table entry aggregates at least 500 simulation replicates at $M \in \{200, 500, 1000\}$; reported slopes use pooled regression with heteroskedasticity-robust standard errors for comparability across topologies.

5. Cross-Domain Connections

Coalescent theory. Gene trees are random draws from coalescent models; Latent expectations over tree ensembles yield ρ distributions useful for experimental design (how many loci?).

Epidemic spreading. Transmission trees share split-statistic structure with phylogenies. Threshold lemmas in Group F connect detectability of deep splits to epidemic R_0 regimes on networks, enabling shared tooling between phylodynamics and the Latent calculus.

6. Discussion

Phylogenetic inference benefits from two Latent numbers: one (ρ) captures how compressible the alignment is under a model, the other (N^*) captures how many directions carry tree signal at finite M. Together they explain why balanced trees may be easier than caterpillars at equal taxon count: deeper internal symmetry changes the spectrum of pattern covariances.

Limitations: JC69 is simplistic; real data violate i.i.d. sites and stationarity. The Latent embedding choice matters; we document ours for reproducibility.

Future work will port the same pipeline to HKY/GTR, codon models, and partitioned alignments, and will couple ρ to Bayesian posterior contraction rates.

Non-claims. We do not benchmark maximum-likelihood software runtime or declare new inference algorithms; the contribution is geometric characterization plus proofs.

Design guidance. When ρ is low for a dataset, adding sites helps more than model tweaks; when N^* is already small, richer substitution models may yield diminishing returns—exactly the regime where model selection should be conservative.

Teaching note. Quartet puzzling becomes a linear algebra exercise in Latent coordinates: incompatible quartet signals occupy nearly orthogonal subspaces when branch lengths are well-separated, which is one way to visualize why some splits are statistically stubborn.

Software boundary. Reference implementations use pure NumPy for reproducibility; no GPU acceleration is assumed or required. Performance engineering is orthogonal to the Latent claims.

Ethics. Simulations use synthetic sequences only; no human or pathogen genomic data appear.

Audit trail. Random seeds, branch-length grids, and M schedules are archived alongside the validation module for third-party replay.

During the preparation of this work the author used large language models to assist with manuscript drafting and organization. The author reviewed and edited the content and takes full responsibility for the publication.

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