

Direct Sequence Laws under the Network Multispecies Coalescent

A genealogy equivalence, canonical coalescent-response behavior,
and finite determination with an epoch-complexity obstruction

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Abstract

We determine the exact population-level information in multilocus sequence alignments generated by a temporal species network under the independent-lineage Network Multispecies Coalescent (NMSC), without treating estimated gene trees or concordance factors as observed data. With known nonrecombining locus boundaries, contemporaneous labelled sampling, and one shared irreducible stationary reversible finite-state continuous-time Markov chain, the indexed family of length- L locus laws is equivalent to the stationary distribution, the trace-normalized substitution generator, and the mutation-scaled metric-genealogy law. The first step is a compact moment theorem for the random conditional site-pattern tensor. A determinant coordinate then recovers each realized additive gene-tree metric, while a continuum in the ancestral coalescence tail identifies the shared generator, including JC, K2P, K3P, and repeated-eigenvalue GTR strata.

We compile every finite temporal NMSC presentation into a finite typed continuous-time response system on partition-occupancy states. Its canonical reachable-observable residual behavior, denoted CCR, is coordinate independent, removes analytically invisible event times, and is unique up to typed linear isomorphism. Equality of CCR is equivalent to equality of normalized metric-genealogy laws. The minimal time-indexed realization has an intrinsic positive cone, but its finite analytic encoding does not supply a stochastic occupancy basis or an NMSC graph. Literal graph recovery is impossible on the strict physical domain: arbitrary sample-unary temporal funnels have identical response in every context. Species trees are nevertheless recovered pointwise with all exposed population rates. For one-reticulation presentations we give an exact finite port-response quotient and a graph theorem on the incidence-separated subclass; the reduced level-1 result additionally assumes scalar-separator faithfulness, and no unconditional level-1 or level-2 graph theorem is claimed.

The finite-locus hierarchy has two complementary conclusions. On every fixed finite union of compact semianalytic finite-presentation charts, one finite locus length determines the complete indexed family. The proof uses the Frisch–Siu Noetherian ring of analytic germs along a compact set and remains valid at coalescent–substitution resonances. No determining length can depend only on the number of sampled taxa, reticulations, alphabet size, and sampling design if demographic epoch count is unbounded. For every L we construct two strict two-taxon, zero-reticulation, known-JC demographic histories with identical laws through length L and different length- $(L + 1)$ laws. A Vandermonde Jacobian and the implicit-function theorem make the collision exact. We finally separate Borel inversion, finite proposed-model equivalence testing, moment approximation, and statistical consistency.

1 Introduction

Reticulate species histories are latent twice over in sequence data. The species network first generates a random metric gene genealogy through lineage transport, coalescence, and reticulation routing; the genealogy then generates an alignment through a substitution process. The observable object is therefore the direct alignment law after both layers have been integrated out. Replacing this law by estimated gene trees changes the statistical experiment and cannot establish direct-sequence identifiability.

Previous direct-sequence results establish generic unrooted species-tree recovery under broad reversible substitution models [1, 8], and logDet distances recover substantial level-1 network topology under an NMSC–GTR model [2]. At the gene-tree-summary layer, quartet distributions recover the tree of blobs and portions of level-1 or galled tree-child structure [3–5]. Full-likelihood introgression models also possess exact label-switching ambiguities, notably bidirectional introgression [16]. None of these facts by itself classifies the complete family of within-locus sequence laws.

Earlier work distinguishes displayed-tree sets from NMSC distributions and shows that distinguishability depends on sampling. Some networks remain indistinguishable even when gene-tree branch lengths are included [17]. Our sample-unary-funnel theorem proves contextual replacement for the complete metric-genealogy law under the sampling convention stated here. Metric-genealogy ambiguity itself is not new.

The present paper separates four questions that are often conflated:

1. What mixing measure is determined by all within-locus laws?
2. Can one invert a conditional sequence tensor to a realized metric genealogy and a shared substitution generator?
3. What finite object classifies the NMSC metric-genealogy behavior when literal network realization is nonunique?
4. Does one finite locus length suffice, and what complexity must its bound depend on?

The answer to the first two questions is a universal sequence–genealogy equivalence. The answer to the third is a finite typed linear behavior, CCR. The fourth has a positive compact finite-presentation theorem and a matching negative theorem showing that unbounded demographic epoch count cannot be omitted from any universal complexity bound.

1.1 Contributions and deliberate limits

The load-bearing positive theorem is pointwise, not merely generic. It covers any finite labelled temporal NMSC presentation in the strict domain and any irreducible stationary reversible generator. Repeated substitution eigenvalues are handled by matrix-semigroup arguments rather than spectral-coordinate division. The response theorem allows rectangular boundary maps and chronologically constrained timed words. The finite-order theorem is pointwise across resonances because the sequence map is treated by matrix-exponential analyticity, not by rational expressions that divide by rate differences.

Two limits are equally important. First, CCR is a canonical behavior rather than a canonical phylogenetic graph. Second, compact moment determinacy produces a mathematical inverse from the complete indexed hierarchy; it is not a finite-query algorithm. We prove graph recovery completely for sampled-complete species trees. The companion studies the strongly tree-child level-at-most-two graph inverse; none of its results is used here. Unknown stationary nonreversible generator recovery remains outside the theorem.

2 Model and observation objects

2.1 Temporal species-network presentations

Let X be a finite labelled taxon set, let S be a finite set of labelled sampled lineages, and fix a known surjection $\mathfrak{s} : S \rightarrow X$. A presentation on X has exactly the taxa in X as its labelled terminal populations; thus every graph leaf is sampled, possibly by several lineages. This sampled-complete convention is part of the literal graph object. Present time is 0. A *finite temporal NMSC presentation* consists of a finite rooted directed acyclic population graph with a time coordinate increasing backward in time, a finite event list

$$0 = t_0 < t_1 < \dots < t_J < \infty,$$

a finite set of extant population arcs in each open epoch (t_j, t_{j+1}) , a positive finite pairwise coalescence rate on every such arc, and an ancestral root population extending from t_J to infinity with positive finite rate. Tree boundaries transport lineages deterministically. At a binary reticulation, each lineage independently selects one of two parents with probability $\gamma \in (0, 1)$. All finite epoch durations are positive. Additional degree-two vertices are allowed only when they record a demographic rate change; their number is part of presentation complexity.

This formulation encompasses binary species networks, reticulation stacks, parallel temporal arcs, and finite piecewise-constant demography. Parameter-free degree-two subdivisions are presentations of the same process. A population subnetwork through which at most one sampled ancestral lineage can ever pass is not silently deleted; its exact invisibility is proved in [section 11](#).

2.2 Genealogy law

Backward in time, current gene lineages move deterministically at tree boundaries, route independently at reticulations, and coalesce pairwise on a common population arc according to Kingman's rate convention [12]. Loci are independent. Every site in one nonrecombining locus shares the same realized rooted metric genealogy G . Let

$$\mu_{N,\eta} \in \mathcal{P}(\mathcal{G}_S), \quad \eta = (\tau, \lambda, \gamma, \mathfrak{s}),$$

be the law on the standard Borel space of rooted labelled metric genealogies, including topology and coalescence times. Under the strict domain, merger times are distinct and avoid species-event times almost surely; contracted boundary trees are nevertheless included in $\mathcal{G}_S$ to make the space closed under limits.

2.3 Substitution model and scale

The alphabet has $2 \leq \kappa < \infty$ labelled states. A row generator Q satisfies $Q\mathbf{1} = 0$, $Q_{ab} \geq 0$ for $a \neq b$, is irreducible, and has a positive stationary row vector π . Zero off-diagonal entries are allowed; irreducibility requires the directed transition graph to be connected by directed paths. The principal theorem assumes reversibility,

$$D_\pi Q = Q^\top D_\pi, \quad D_\pi = \text{diag}(\pi).$$

Equivalently, the conductances $w_{ab} = \pi_a Q_{ab} = w_{ba} \geq 0$ have connected undirected support. They give analytic coordinates $Q_{ab} = w_{ab}/\pi_a$ with row sums determining the diagonal. Irreducibility, rather than positivity of each conductance, is sufficient for every sequence-genealogy argument

below. In particular, uniformization gives strictly positive transition probabilities at every positive time, and reversible symmetric similarity remains valid when some conductances vanish. Set

$$r(Q) = -\operatorname{tr} Q > 0, \quad Q_0 = Q/r(Q), \quad \operatorname{tr} Q_0 = -1,$$

and write mutation-scaled time and coalescence rates as

$$\bar{t} = r(Q)t, \quad \bar{\lambda} = \lambda/r(Q).$$

Changing the physical time unit by $c > 0$ acts as

$$(\tau, \lambda, Q) \mapsto (c\tau, \lambda/c, Q/c). \quad (1)$$

It leaves $Q\Delta t$ and $\lambda\Delta t$ invariant.

2.4 Direct indexed locus laws

For a realized genealogy G , let

$$V_Q(G) = (p_{Q,\pi}(a \mid G))_{a \in [\kappa]^S} \in \Delta_{d-1}, \quad d = \kappa^{|S|},$$

be its one-site conditional pattern vector, and let

$$\nu_\xi = (V_Q)_* \mu_{N,\eta}.$$

The observed population law of an ordered length- L nonrecombining-locus alignment is

$$\mathbb{P}_\xi^{(L)}(a_1, \dots, a_L) = \int_{\mathcal{G}_S} \prod_{\ell=1}^L p_{Q,\pi}(a_\ell \mid G) \, d\mu_{N,\eta}(G) = \int_{\Delta_{d-1}} \prod_{\ell=1}^L v_{a_\ell} \, d\nu_\xi(v). \quad (2)$$

The identifiability object is the indexed family $(\mathbb{P}^{(L)})_{L \geq 1}$. It is not an unordered set, an infinite observed locus, or a pooled single-site distribution.

3 Main classification theorem

Definition 3.1 (Principal model class). *For fixed $(X, S, \mathfrak{s})$, the principal class $\mathfrak{M}(X, S, \mathfrak{s}, \kappa)$ consists of finite temporal NMSC presentations as above, with contemporaneous labelled sampling, known nonrecombining locus boundaries, independent loci, independent lineage routing, positive finite rates and durations, inheritance probabilities in $(0, 1)$, and one shared irreducible stationary reversible κ -state generator. We assume $|S| \geq 2$.*

The finite response object used in the theorem is constructed in [section 8](#). Informally, it is the typed isomorphism class of the minimal future-response spaces of the normalized metric-genealogy density, together with the intrinsically visible event times.

Theorem 3.2 (Direct-sequence classification). *For $\xi, \xi' \in \mathfrak{M}(X, S, \mathfrak{s}, \kappa)$,*

$$\mathbb{P}_\xi^{(L)} = \mathbb{P}_{\xi'}^{(L)} \quad \text{for every } L \geq 1 \quad (3)$$

if and only if

$$\pi = \pi', \quad Q_0 = Q'_0, \quad \operatorname{CCR}(N, \bar{\tau}, \bar{\lambda}, \gamma; \mathfrak{s}) \cong \operatorname{CCR}(N', \bar{\tau}', \bar{\lambda}', \gamma'; \mathfrak{s}). \quad (4)$$

Equivalently, the indexed sequence family and the normalized triple

$$(\pi, Q_0, \bar{\mu}_{\text{metricGT}})$$

are connected by mutually inverse Borel maps on the principal model image. In physical units the universal scale ambiguity is (1). Beyond scale, equality is exactly equality of CCR behavior. This identifies the universal behavioral fiber; positive graph realizations are interpreted only on the species-tree, incidence-separated one-reticulation, and scalar-separator-faithful level-1 subclasses proved below.

Theorem 3.3 (Finite-locus hierarchy). *The following two statements hold.*

- (a) *Let K be a finite union of compact semianalytic normalized charts with fixed finite presentations, fixed sampling design, and a compact family of strict reversible generators. There exists a finite $L_*(K)$ such that for all $\xi, \xi' \in K$,*

$$\mathbb{P}_\xi^{(L_*(K))} = \mathbb{P}_{\xi'}^{(L_*(K))} \iff \mathbb{P}_\xi^{(L)} = \mathbb{P}_{\xi'}^{(L)} \text{ for every } L \geq 1.$$

The conclusion is pointwise, including repeated eigenvalues and rate resonances, but the proof is generally non-effective.

- (b) *There is no function $L_*(n, r, \kappa, \mathfrak{s})$ with this property when the number of finite demographic rate epochs is unbounded and omitted from the complexity argument. More precisely, for every $L \geq 1$ there are two strict two-taxon, zero-reticulation, known-normalized-JC models with the same sampling design and finite positive piecewise-constant demography such that their locus laws agree for $1 \leq \ell \leq L$ and disagree at $L + 1$.*

Theorem 3.4 (Graph content and sharp impossibility). *Global pointwise identifiability over the full strict temporal-network class fails through strict-interior collisions: replacing a sample-unary temporal funnel by another strict sample-unary funnel with the same temporal boundary produces the same metric-genealogy and direct sequence laws. In contrast:*

- (i) *on the sampled-complete species-tree class, the rooted labelled topology, divergence times, every exposed maximal constant-rate demographic epoch, and the ancestral-root rate are recovered pointwise in mutation units; an entire terminal demographic schedule is recovered exactly when at least two lineages are sampled from that terminal species;*
- (ii) *every one-reticulation presentation, including a zero-reticulation result of reduction, has a finite canonical port-response quotient encoded by all-partition prefix/suffix matrices at a law-defined common time; equality of these quotients is necessary and sufficient for normalized genealogy equivalence, and together with equality of the separately recovered π, Q_0 , for indexed-sequence equivalence;*
- (iii) *on the incidence-separated one-reticulation and scalar-separator-faithful, locally incidence-separated reduced level-1 subclasses, the graph ports and inheritance probability are recovered up to parent exchange $\gamma \leftrightarrow 1 - \gamma$ and the universal reductions; parent-corridor demography is recovered through its exact all-partition port-response fiber rather than a generally false linkage of hidden parent words.*

No unconditional level-1, strongly tree-child level-2, or general-network graph realization theorem is asserted.

The remainder of the paper proves these statements. The technical supplement gives the complete timed-Hankel, breakpoint, analytic-germ, and collision-transversality details.

4 Indexed moment recovery

Theorem 4.1 (Multilocus moment theorem). *Let ν be a probability measure on the compact simplex Δ_{d-1} and let (2) define an indexed family of ordered categorical laws. Then:*

- (i) *a word $(a_1, \dots, a_L)$ records the mixed monomial moment $\int \prod_{\ell} v_{a_\ell} d\nu$;*
- (ii) *$\mathbb{P}^{(L)}$ determines every moment of total degree at most L by marginalizing trailing coordinates;*
- (iii) *the indexed family $(\mathbb{P}^{(L)})_{L \geq 1}$ determines ν uniquely, and ν determines the family.*

The statement retains repeated site patterns and is unchanged if sites are recorded as exchangeable counts rather than ordered words, provided multinomial multiplicities are retained.

Proof. Conditional independence of sites given $V = v$ gives (2). Summing the last $L - \ell$ coordinates multiplies the integrand by $(\sum_a v_a)^{L-\ell} = 1$, so all lower moments are recovered. If two measures agree on the indexed family, they agree on every coordinate monomial and hence every polynomial. Coordinate polynomials form a unital point-separating subalgebra of $C(\Delta_{d-1})$; Stone–Weierstrass makes them uniformly dense. Equality against all continuous functions and the Riesz representation theorem give equality of measures. The converse is immediate. $\square$

Proposition 4.2 (Measurability and marginalization). *Metric genealogy space is a finite disjoint union of labelled topology cones, glued along contracted-edge faces. The pruning map $G \mapsto V_Q(G)$ is continuous on each cone and Borel globally. Although coalescence times are unbounded, its image lies in the compact simplex. Summing character states outside a sampled subset commutes with products and integration, so the indexed law determines every sampled-subset law and mixing measure.*

Proof. Transition matrices are continuous functions of edge lengths and pruning uses finitely many sums and products. The topology-cone partition is finite for fixed S , proving Borel measurability. The marginalization assertion follows from applying the corresponding linear simplex map at every site. $\square$

5 From a conditional tensor to a metric genealogy

For a pair of sampled leaves i, j , let $J_{ij}(v)$ be the $\kappa \times \kappa$ marginal of a conditional tensor v . Let u_{ij} and w_{ij} be the two branch-time distances from their gene-tree MRCA to the leaves.

Lemma 5.1 (Pair determinant identity). *For every stationary finite-state CTMC, reversible or not,*

$$J_{ij} = e^{Q^\top u_{ij}} D_\pi e^{Q w_{ij}}, \quad \frac{\det J_{ij}}{\det D_\pi} = e^{(\text{tr } Q)(u_{ij} + w_{ij})}. \quad (5)$$

Hence $\det J_{ij} > 0$ at every finite genealogy and

$$\delta_{ij}(v) := -\log \det(D_\pi^{-1} J_{ij}(v)) = r(Q)(u_{ij} + w_{ij}). \quad (6)$$

Proof. Conditioning on the MRCA state gives the first identity. Since $\det e^{At} = e^{t \text{tr } A}$ and $\text{tr } Q^\top = \text{tr } Q$, taking determinants gives the second. Irreducibility and finite branch lengths make D_π and both exponentials nonsingular. $\square$

Theorem 5.2 (Conditional metric-genealogy inversion). *For $|S| \geq 2$, the map*

$$v = V_Q(G) \mapsto (\delta_{ij}(v))_{i,j \in S}$$

recovers the mutation-scaled canonical contracted unrooted metric genealogy. If samples are contemporaneous, its unique equidistant point restores the temporal root and every normalized coalescence time. The inverse from the set of valid conditional tensors to canonical rooted metric genealogies is Borel. For $|S| = 2$ the root is the midpoint of the single recovered edge.

Proof. By lemma 5.1, (δ_{ij}) is an additive tree metric. The Buneman four-point reconstruction recovers every positive split edge and its length; zero split lengths are contracted [7, 14]. On each region defined by strict four-point inequalities, the edge lengths are linear combinations of distance entries. Fixing a deterministic tie rule on equality faces therefore yields a Borel canonical reconstruction.

A contemporaneous rooted genealogy is ultrametric. Its root is the unique point equidistant from all leaves: choose a diameter pair and take its midpoint; ultrametricity forces every other leaf to the same radius. This remains valid after zero-edge contraction and specializes to the ordinary midpoint for two leaves. Vertex times follow from root-to-vertex distances. The construction uses finitely many inequalities and arithmetic operations on each stratum, so it is Borel. $\square$

The support of ν may contain the limiting independent pair matrix with determinant zero, corresponding to infinite pair distance. It receives no probability mass under a finite-rate NMSC. All inversions above are therefore almost sure: define the inverse on the positive-determinant valid-tensor set and extend it by one arbitrary fixed default genealogy on the null complement. The determinant-zero point is not a contracted finite genealogy.

6 Recovery of an unknown shared reversible generator

Lemma 6.1 (Ancestral support tail). *For every sampled pair in a strict finite NMSC, there is a finite time T_0 after which both surviving lineages occupy the ancestral root population. Conditional on survival to T_0 , their coalescence time has a positive exponential density on (T_0, ∞) . Consequently, the support of the pair-matrix pushforward contains a nondegenerate tail of the conditional pair curve.*

Proof. The finite population graph has a final ancestral population. Every routing history reaches it by $T_0 = t_J$, and survival through finitely many positive-duration epochs has positive probability. The root population has positive finite Kingman rate, so the additional waiting time has full support $(0, \infty)$. Continuity of the pair-matrix map transfers this interval to support. $\square$

Under reversibility, (5) simplifies to

$$J_{ij} = D_\pi e^{Q d_{ij}}, \quad d_{ij} = u_{ij} + w_{ij}. \quad (7)$$

Set $s = -\log \det(D_\pi^{-1} J) = r(Q)d$. Thus the observed tail is intrinsically parameterized as

$$M(s) = D_\pi^{-1} J = e^{Q_0 s}. \quad (8)$$

Theorem 6.2 (Shared reversible generator recovery). *The conditional-tensor mixing measure ν generated by the principal model determines π and $Q_0 = Q/(-\text{tr } Q)$ pointwise on the labelled alphabet. The result includes JC, K2P, K3P, and every repeated-eigenvalue reversible stratum.*

Proof. Every one-leaf marginal of every conditional tensor equals π , so π is read directly from ν . Pairwise marginalization gives the exact pair-matrix distribution and its support. By lemma 6.1,

that support contains an open tail of (8); the determinant gives the value of s at each matrix. Therefore the analytic graph $s \mapsto M(s)$ is known on an interval, and

$$Q_0 = M'(s)M(s)^{-1}.$$

This uses no eigenspace choice and is unchanged by repeated eigenvalues.

For an independent verification, choose two tail values $s_2 > s_1$. Reversibility makes Q_0 similar through $D_\pi^{1/2}$ to a real symmetric matrix with nonpositive eigenvalues. Hence

$$M(s_2)M(s_1)^{-1} = e^{Q_0(s_2-s_1)}$$

has positive real eigenvalues and its principal matrix logarithm is uniquely $Q_0(s_2 - s_1)$. Dividing by the observed determinant-coordinate difference gives Q_0 . A global state permutation is an ambiguity only if the observed alphabet itself is declared unlabelled. $\square$

Remark 6.3 (One conditional pair matrix already suffices). *Any positive-distance realized conditional pair matrix J in the recovered mixing law gives*

$$A = D_\pi^{-1}J = e^{sQ_0}, \quad s = -\log \det A = r(Q)d > 0, \quad Q_0 = \frac{\text{Log}(A)}{s}.$$

Here d is the total pair path length, twice the pair coalescence age for contemporaneous sampling. Reversible symmetric similarity gives positive spectrum for A , so its real principal logarithm is exactly sQ_0 , including repeated eigenvalues and irreducible zero-conductance faces. This observation concerns a conditional matrix recovered through the mixing measure, not the population-averaged pair matrix; the support-tail proof above also remains valid.

7 Universal direct sequence–genealogy equivalence

Let $\bar{\mu}$ be the pushforward of the physical metric-genealogy law after multiplying every genealogy length by $r(Q)$.

Theorem 7.1 (Sequence–genealogy equivalence). *On $\mathfrak{M}(X, S, \mathfrak{s}, \kappa)$,*

$$(\mathbb{P}_\xi^{(L)})_{L \geq 1} \iff \nu_\xi \iff (\pi, Q_0, \bar{\mu}_\xi). \quad (9)$$

The equivalence is pointwise and Borel.

Proof. The first equivalence is [theorem 4.1](#). The space $\mathcal{P}(\Delta_{d-1})$ of probability measures on the compact tensor simplex is compact metrizable in the weak topology. The full coordinate-moment map is continuous and injective by Stone–Weierstrass, hence is a homeomorphism onto its image. Thus the indexed sequence family recovers ν through an explicit Borel inverse, without a global image theorem.

One-leaf marginals recover π . For a sampled pair, push ν forward to its pair-matrix law. Its support is a closed subset of a finite-dimensional Euclidean space and the support map is Borel in the Effros structure. Strict ancestral coalescence supplies two positive-determinant support points with distinct determinant coordinates. A Borel pair is obtained by enumerating pairs of disjoint rational matrix boxes with separated determinant-coordinate closures, selecting the first pair that meets the support, and then using nested rational subboxes to select one support point from each. Order the selected matrices M_1, M_2 so that

$$s_2 = -\log \det(D_\pi^{-1}M_2) > s_1 = -\log \det(D_\pi^{-1}M_1).$$

Put $K_i = D_\pi^{-1} M_i$. The principal-logarithm formula from [theorem 6.2](#) gives

$$Q_0 = \frac{1}{s_2 - s_1} \text{Log}(K_2 K_1^{-1}),$$

and continuity of the principal logarithm on matrices with positive real spectrum makes this selector Borel. Apply the finite-stratum Borel tree reconstruction of [theorem 5.2](#) to ν -almost every tensor and push forward to obtain $\bar{\mu}$.

Conversely, pruning with (π, Q_0) on each normalized genealogy is Borel and gives ν ; (2) then gives every indexed law. These explicit constructions prove the claimed mutually inverse Borel maps. $\square$

Proposition 7.2 (Physical-unit conversion for a fixed normalized realization). *Fix one normalized physical realization $(N, \bar{\tau}, \bar{\lambda}, \gamma, Q_0, \pi, \mathfrak{s})$. Its remaining conversion between mutation units and physical time is exactly*

$$(\tau, \lambda, Q) \mapsto (c\tau, \lambda/c, Q/c), \quad c > 0.$$

If an external calibration fixes the substitution-rate scale or one nonzero physical interval, this action is removed. The complete observational fiber may additionally contain non-scale CCR-equivalent realizations, including sample-unary funnel replacements, parent-presentation changes, latent-role switches, and the qualified sister-triangle equivalences treated in the companion paper.

Proof. Write $Q = rQ_0$ within the fixed normalized realization. Physical genealogy times are the normalized times divided by r , and physical coalescence rates are $r\bar{\lambda}$. Replacing r by r/c gives precisely (1), and every positive choice of physical conversion scale arises this way. This argument compares physical-unit representations of the fixed normalized realization; it makes no assertion that all realizations of the same observable law share the same graph or normalized parameterization. $\square$

8 Finite typed NMSC response systems

We now compress the normalized metric-genealogy law without presuming a unique positive network realization.

8.1 Raw partition–occupancy realization

Fix an open population epoch e and a partition $\mathcal{P}$ of S into current gene-lineage blocks. Let $\Omega_{e,\mathcal{P}}$ be the finite set of allowable assignments of those blocks to population arcs present in epoch e . Define the row state space

$$H_{e,\mathcal{P}} = \mathbb{R}^{\Omega_{e,\mathcal{P}}}.$$

For $\omega \in \Omega_{e,\mathcal{P}}$, let $n_p(\omega)$ be the number of blocks assigned to population p . The no-merger generator is diagonal,

$$A_{e,\mathcal{P}}(\omega, \omega) = - \sum_p \binom{n_p(\omega)}{2} \bar{\lambda}_p. \quad (10)$$

If blocks $B, C \in \mathcal{P}$ occupy the same population p , the marked merger map

$$C_{e,\mathcal{P}}^{B,C} : H_{e,\mathcal{P}} \longrightarrow H_{e,\mathcal{P}/(B \sim C)}$$

has entry $\bar{\lambda}_p$ to the assignment obtained by replacing B, C by $B \cup C$; all other entries are zero. At a population boundary, a rectangular stochastic map transports assignments. A tree boundary is

deterministic. At a reticulation, each block routes independently, so an assignment of m blocks contributes a product $\gamma^k(1-\gamma)^{m-k}$. Simultaneous boundaries are represented by their chronological matrix product.

For an admissible ranked labelled merger history $h = (m_1, \dots, m_{|S|-1})$ with absolute merger times $0 < s_1 < \dots < s_{|S|-1}$, insert every species event between consecutive merger times. Its density is the scalar matrix product

$$b_h(s_1, \dots, s_{|S|-1}) = \alpha E_0 C_{m_1} E_1 R_1 E_2 \dots C_{m_{|S|-1}} E_f \beta, \quad (11)$$

where each $E = e^{A\Delta}$, every C is a marked rectangular merger map, every R a rectangular population boundary, α is the sampled initial assignment, and $\beta = 1$ after the final merger. Only chronologically and type-compatible products are admissible.

Proposition 8.1 (Finite analytic response representation). *For fixed S and a finite presentation, there are finitely many types, marks, boundary maps, and ranked history chambers. Every density (11) is real analytic in the absolute merger times and strict physical parameters on each chamber. These densities, with their natural Lebesgue reference measures, determine the normalized metric-genealogy law.*

Proof. There are finitely many partitions of S , finitely many occupancy assignments, and finitely many ranked binary merger histories. Matrix exponentials are entire in their matrix entries and duration. Products with the finite boundary maps are analytic. Strict NMSC genealogies have no merger atoms at species-event times and no simultaneous mergers, so the law is the finite collection of these chamber densities. Conversely, integrating them over Borel subsets of the chambers reconstructs the law. $\square$

8.2 Timed residual behavior

A *timed prefix* is an admissible partial history ending at an interior time t with a specified epoch-partition type $q = (e, \mathcal{P})$. A *timed suffix* begins at the same (q, t) and completes the history. Concatenation pz is allowed only when all types, marks, and times match. Let $b(pz)$ be the corresponding scalar density.

Definition 8.2 (Future-response space). *For a prefix p ending at (q, t) , define its residual future function*

$$r_{p,t} : z \mapsto b(pz).$$

The canonical future-response space is

$$\mathcal{V}_{q,t} = \text{span}\{r_{p,t} : p \text{ ends at } (q, t)\}.$$

Every raw prefix reaches a row vector $x_p \in H_q$ and $r_{p,t}(z) = x_p \Phi(z) \beta$. Hence $\dim \mathcal{V}_{q,t} \leq \dim H_q$.

For an epoch-partition type q and an interior time t , let $R_q(t) \subseteq H_q$ be the span of all raw prefix row states reaching q at time t .

Lemma 8.3 (Analytic prefix-span saturation). *Let $t < t'$ lie in the same open epoch and let A_q be the no-mark generator for the fixed target type q . Then*

$$R_q(t') = R_q(t) e^{A_q(t'-t)}.$$

This includes prefixes whose last merger occurs in (t, t') .

Proof. Fix an admissible merger-mark pattern ending in type q , and let its free merger times range over an ordered open simplex. If s_k is its final merger time and $G(s)$ is the row immediately after that mark, write the row at target time u as

$$G(s)e^{A_q(u-s_k)} = H(s)e^{A_q u}, \quad H(s) := G(s)e^{-A_q s_k}.$$

If the last transition into q is instead a fixed boundary at time a , use $H(s) := G(s)e^{-A_q a}$; for an empty pattern the same formula has constant H . In every case H is an H_q -valued real-analytic map independent of the target time. The simplex cut out by requiring all current-epoch mergers to occur before t is a nonempty open subset of the corresponding simplex before t' whenever the pattern is admissible; mergers have no minimum holding time, and t, t' cross no population boundary.

Let $\ell \in H_q^*$ annihilate the values of H on the smaller simplex. The scalar analytic function ℓH vanishes on a nonempty open set, so it vanishes on the connected larger simplex. Thus the spans of the H -values are equal for this mark pattern. There are only finitely many admissible mark patterns leading to q ; intersecting their annihilators proves equality of their total spans. Multiplication by the genuinely common factors $e^{A_q t}$ and $e^{A_q t'}$ now gives

$$R_q(t') = R_q(t)e^{-A_q t}e^{A_q t'} = R_q(t)e^{A_q(t'-t)}.$$

Rectangular marked maps cause no difficulty because analyticity and the annihilator argument take place only in the fixed target space H_q . $\square$

Theorem 8.4 (Canonical minimal typed realization). *The future-response spaces have the following properties.*

- (i) *They are finite dimensional, reachable by construction, and observable because a future function is zero exactly when it vanishes on every suffix.*
- (ii) *No-mark extension, labelled merger, and population-boundary extension induce linear maps between the appropriate typed spaces.*
- (iii) *Inside one open epoch, no-mark transport between any two interior times is an isomorphism.*
- (iv) *For every finite raw realization, restricting each raw type to its reachable subspace and quotienting by its complete observational nullspace yields a realization canonically isomorphic to the future-response system.*
- (v) *Any two reachable-observable typed realizations of the same behavior are related by a unique typed linear isomorphism intertwining all flows, marks, boundaries, initial states, and terminal functionals.*

Proof. Finiteness was just proved. Prefix extension defines the typed operations and reachability. Observability is literal equality of future functions.

For interior transport, [lemma 8.3](#) proves surjectivity on raw reachable spans. For injectivity, suppose a reachable raw residual x becomes observationally zero after no-mark propagation from t to t' . Fix an entire admissible suffix mark pattern in the current epoch and everything after the next fixed boundary, if any. Its ordered merger times range over a connected open simplex, and the scalar response of x is jointly real analytic in all those times. The hypothesis makes it zero on the nonempty open sub-simplex on which every current-epoch mark occurs after t' . The multivariate identity theorem therefore makes it zero on the whole simplex, including the region with marks between t and t' . Mark-free suffixes are handled by the same one-variable flow argument. Taking the finite union over mark patterns shows that x was already observationally null at t . Hence no-mark transport is injective on the observational quotients and therefore an isomorphism.

Let $\mathcal{R}_q \subseteq H_q$ be the span of raw prefix states and

$$\mathcal{N}_q = \{x \in \mathcal{R}_q : x\Phi(z)\beta = 0 \text{ for every admissible suffix } z\}.$$

The map $x + \mathcal{N}_q \mapsto [z \mapsto x\Phi(z)\beta]$ is well defined, injective, and surjective onto $\mathcal{V}_q$. Operations preserve $\mathcal{N}_q$ and descend. This proves (iv).

For uniqueness, map the state reached by every prefix in the first minimal realization to the state reached by the same prefix in the second. If two linear combinations of prefix states agree in the first, their difference has zero response against every suffix; equality of behaviors and observability make the corresponding difference zero in the second. Thus the map is well defined and injective. Reachability makes it surjective. Its definition forces every intertwining relation and uniqueness. $\square$

This is a continuous-time typed version of the classical finite-Hankel principle for minimal linear representations [6, 10]. The proof verifies the hypotheses needed here, including constrained timed words and rectangular type changes.

Proposition 8.5 (Finite analytic encoding of the residual bundle). *The minimal realization is indexed by absolute time. For each raw epoch choose an interior anchor a , also in the final unbounded epoch. For each partition type q , no-mark transport identifies every interior fiber with $\mathcal{R}_q(a)/\mathcal{N}_q(a)$. In these coordinates no-mark transport is the identity, while a merger $q \rightarrow q'$ at time t is induced by*

$$e^{A_q(t-a)} C_{q,q'} e^{-A_{q'}(t-a)}.$$

Boundary maps and initial/terminal data are obtained by the corresponding anchor transports. Fixed quotient bases therefore give a finite encoding by raw matrices, exponential formulas, and finite linear maps. The time-dependent merger matrices need not be constant, even when all relevant fibers have dimension one.

Proof. Prefix-span saturation gives $\mathcal{R}_q(t) = \mathcal{R}_q(a)e^{A_q(t-a)}$. Null preservation and injectivity of interior transport give $\mathcal{N}_q(t) = \mathcal{N}_q(a)e^{A_q(t-a)}$. Conjugating the actual merger map at t gives the displayed formula, which consequently preserves the reachable and null subspaces needed to induce the quotient map. Its entries are analytic functions of t in fixed quotient bases. A boundary at h between anchors a_-, a_+ has the induced matrix

$$e^{A_-(h-a_-)} R_h e^{-A_+(h-a_+)}.$$

The same transport formulas apply to the finite initial endpoint and terminal functional. A finite anchor in the root epoch works for every finite t there; no evaluation at infinity is used. There are finitely many raw epochs, partition types, and matrices. This proves finite encodability without assuming autonomous generators on the fixed-time minimal spaces. $\square$

8.3 Intrinsic breakpoints and the definition of CCR

Definition 8.6 (Visible event time). *A temporal event time t_j is visible if at least one scalar ranked-history density fails to admit a real-analytic continuation through t_j after identifying its left and right history coordinates. Otherwise it is invisible.*

Proposition 8.7 (Finite breakpoint test). *For every pair of adjacent ranked-history chambers meeting along a face $s_j = h$, where h is the event under test, let f_-, f_+ be the analytic extensions of their raw scalar density formulas. Choose one point s^* of that open face. In coordinate s_i , let*

$n_{\epsilon,i}^-, n_{\epsilon,i}^+$ be the raw dimensions immediately before and after its merger in formula f_ϵ , for $\epsilon \in \{-, +\}$, and set

$$D_i = n_{-,i}^- n_{-,i}^+ + n_{+,i}^- n_{+,i}^+.$$

The event is invisible if and only if, for every such face pair,

$$\partial_1^{k_1} \cdots \partial_m^{k_m} (f_- - f_+)(s^*) = 0 \quad (0 \leq k_i < D_i).$$

This is a finite test. Its verdict is independent of hidden-state basis and raw event refinement; the displayed sufficient bound uses raw formula dimensions, not minimal fixed-time residual dimensions. Simultaneous boundaries compose.

Proof. Each raw formula is a finite matrix-exponential product and is entire in the merger coordinates. In coordinate s_i its variable factor is $e^{A^- s_i} C e^{-A^+ s_i}$, with constant factors absorbed on either side. Differentiation acts by the Sylvester operator $X \mapsto A^- X - X A^+$ on a matrix space of dimension $n^- n^+$. The direct sum of the two side operators has dimension D_i and gives a constant-coefficient derivative recurrence for $f_- - f_+$, uniformly in the other coordinates. Cayley–Hamilton, applied one coordinate at a time, determines all Taylor coefficients from the displayed mixed box. Its vanishing is therefore equivalent to equality of the analytic extensions. There are finitely many histories and chamber faces. Checking every open face glues the chamber formulas; their entire extensions also agree at intersections of faces. Thus the test is exactly scalar analytic continuation. This proves invariance of its verdict. Identity boundaries leave every scalar formula unchanged, and consecutive simultaneous boundary maps compose in chronological order. $\square$

Definition 8.8 (Canonical coalescent-response behavior). *The canonical coalescent-response behavior*

$$\text{CCR}(N, \bar{\eta}; \mathfrak{s})$$

is the typed linear-isomorphism class of the time-indexed reachable–observable future-response system, with its finite analytic encoding from [proposition 8.5](#), after all invisible event times have been removed and simultaneous visible boundaries have been composed. Removing an invisible boundary glues the analytic scalar behavior and its residual transports; it does not assert that the resulting interval is one constant-generator raw population epoch. The supplement proves this gluing directly from the continued Hankel kernels.

Theorem 8.9 (CCR equality theorem). *Two finite normalized NMSC presentations have isomorphic CCR if and only if their normalized metric-genealogy laws agree. CCR is finite and coordinate independent. Every residual fiber has the intrinsic closed, pointed, generating cone*

$$\mathcal{C}_{q,t} = \{f \in \mathcal{V}_{q,t} : f(z) \geq 0 \text{ for every compatible suffix } z\},$$

and legal prefix extensions preserve this family of cones. This construction does not provide a simplicial cone, stochastic occupancy basis in the minimal dimension, or NMSC network realization.

Proof. Refine the two finite event lists to their union. Equality of laws gives equality almost everywhere of the corresponding Radon–Nikodym densities on every common ranked-history chamber. Their difference is real analytic there, so almost-everywhere equality implies equality everywhere on the connected chamber. The systems therefore have identical residual future functions, visible breakpoints, and canonical operations. Conversely, a typed isomorphism preserves every complete prefix–suffix scalar pairing, so all common-chamber densities agree; [proposition 8.1](#) then gives equality of laws. Finiteness and uniqueness follow from [theorem 8.4](#) and [proposition 8.5](#). The

construction uses future functions in absolute time, so it is independent of coordinates. Each suffix evaluation is a linear functional, making the displayed cone closed and convex. If both f and $-f$ lie in it, all evaluations vanish, hence $f = 0$. Actual prefix residuals are nonnegative and span the fiber, so the cone is generating. Prefix extension evaluates f on suffixes beginning with that extension, proving preservation. These assertions concern a compatible cone family; they do not choose a simplicial cone or biological occupancy coordinates. $\square$

Combining [theorems 7.1](#) and [8.9](#) proves [theorem 3.2](#).

8.4 Finite equality testing for proposed exact systems

Proposition 8.10 (Chamberwise finite-jet criterion). *Suppose two proposed raw response systems are supplied over an exact domain in which the finitely many matrix exponentials used below and equality of their entries have a terminating zero test. Refine to the union of their event lists and take the signed difference. For each common ranked-history chamber c , choose one interior time vector s^c . If its j th merger changes a state space of dimension $d_{c,j}^-$ to one of dimension $d_{c,j}^+$ in the signed direct-sum realization, set*

$$D_{c,j} = d_{c,j}^- d_{c,j}^+.$$

The two behaviors are equal if and only if, for every c , the signed density f_c satisfies

$$\partial_1^{k_1} \dots \partial_m^{k_m} f_c(s^c) = 0 \quad (0 \leq k_j < D_{c,j}).$$

For a zero-dimensional chamber this means equality of its single scalar value. Hence proposed-model CCR equality has a finite exact test. The criterion is not the unrestricted closure of prefix states under generator powers: chronological chamber constraints remain part of the test.

Proof. Fix a chamber and one absolute merger-time coordinate s_j , holding the other coordinates fixed. Around the corresponding marked map C_j , all dependence on s_j has the form

$$e^{A_j^- s_j} C_j e^{-A_j^+ s_j}$$

up to factors independent of s_j . After vectorization its derivatives are powers of the Sylvester operator

$$\mathcal{L}_j(X) = A_j^- X - X A_j^+$$

on a space of dimension $D_{c,j}$. Cayley–Hamilton therefore gives a constant-coefficient recurrence of order at most $D_{c,j}$ for the derivatives in s_j , uniformly in the other merger times. Applying these recurrences one coordinate at a time shows that the displayed finite box of mixed derivatives determines every Taylor coefficient at s^c . If the finite box vanishes, analyticity makes f_c zero near s^c , and the real-analytic identity theorem makes it zero on the connected chamber. The converse is immediate. There are finitely many refined ranked-history chambers, and their densities determine the law by [proposition 8.1](#). Every required derivative is a finite chronologically constrained matrix product, so the stated exact-domain assumption makes the test terminating; no bit-complexity claim is made for arbitrary black-box reals. $\square$

9 Coordinate invariance and ordered-simplex integration

Absolute merger times are the primary coordinates in [definition 8.8](#). The following calculation explains precisely why a complete gap spectrum is not canonical.

Within a fixed-duration epoch, let $u_0 + \dots + u_m = \Delta$. A term $ce^{-\langle \rho, u \rangle}$ satisfies

$$e^{-\langle \rho + a\mathbf{1}, u \rangle} = e^{-a\Delta} e^{-\langle \rho, u \rangle}.$$

Omitting gap u_j gives

$$ce^{-\langle \rho, u \rangle} = ce^{-\rho_j \Delta} \exp \left[- \sum_{i \neq j} (\rho_i - \rho_j) u_i \right]. \quad (12)$$

Thus only the exponent class modulo $\mathbb{R}\mathbf{1}$ is intrinsic. Choosing another omitted gap is an invertible affine change of the relative interior of the simplex, and pullback preserves all linear relations and residual spaces.

Nested coalescence integrations are governed by confluent divided differences, not products of one-dimensional integrals.

Theorem 9.1 (Ordered-simplex formula). *Use the convention*

$$f[a_0, \dots, a_m] = \frac{f[a_1, \dots, a_m] - f[a_0, \dots, a_{m-1}]}{a_m - a_0}$$

for distinct endpoints, with the usual Hermite confluent extension. Then

$$I_m(a_0, \dots, a_m; \Delta) := \int_{\substack{u_i \geq 0 \\ u_0 + \dots + u_m = \Delta}} e^{-\sum_i a_i u_i} du_0 \dots du_{m-1} = (-1)^m [a_0, \dots, a_m] e^{-\Delta x}. \quad (13)$$

In particular,

$$I_m(A, \dots, A; \Delta) = \frac{\Delta^m}{m!} e^{-A\Delta}.$$

For arbitrary multiplicities, I_m is a finite sum $\sum_j p_j(\Delta) e^{-\alpha_j \Delta}$ with $\deg p_j$ less than the multiplicity of α_j .

Proof. Put $u_i = \Delta t_i$. The Hermite–Genocchi formula gives

$$[a_0, \dots, a_m] f = \int_{\sum t_i = 1, t_i \geq 0} f^{(m)} \left(\sum_i t_i a_i \right) dt_0 \dots dt_{m-1}.$$

For $f(x) = e^{-\Delta x}$, $f^{(m)} = (-\Delta)^m e^{-\Delta x}$, and the Jacobian contributes Δ^m , proving (13). At a repeated node, a divided difference becomes the corresponding derivative divided by factorial, giving the full-resonance formula. Grouping arbitrary repeated nodes in the Hermite interpolation formula gives the stated exponential-polynomial form [9]. $\square$

No proof in this paper inverts $a_i - a_j$ on a locus where it can vanish. More generally, every fixed-presentation sequence coordinate is real analytic on a neighborhood of the strict parameter domain: scale each finite integration chamber to a fixed unit simplex, use the entire dependence of matrix exponentials on their entries, and differentiate under the integral. The infinite root epoch is an integral of a uniformly stable finite matrix semigroup and equals a stable inverse on the transient subspace. Repeated substitution eigenvalues, repeated hazards, and coalescent–substitution resonances therefore cause no singularity in the physical map.

10 Species-tree tomography

For two sampled lineages i, j in a species tree, let T_{ij} be their coalescence time and $S_{ij}(t) = \Pr(T_{ij} > t)$. Sampling consistency reduces their process to two lineages.

Lemma 10.1 (Pair survival response). *Let τ_{ij} be the time at which the two species paths first enter a common population. Then*

$$S_{ij}(t) = 1 \quad (t < \tau_{ij}), \quad -\frac{d}{dt} \log S_{ij}(t) = \lambda_{p(t)}$$

for almost every $t > \tau_{ij}$, where $p(t)$ is their common population arc. Every strict demographic breakpoint on that shared path appears as a hazard breakpoint.

Proof. Before τ_{ij} the lineages occupy distinct populations and cannot coalesce. Afterward, conditional survival over an interval is the exponential of minus the integrated pairwise Kingman rate. Taking the logarithmic derivative gives the result. $\square$

Theorem 10.2 (Complete species-tree inversion). *The normalized metric-genealogy law of a species tree identifies pointwise:*

- (i) *the rooted labelled species-tree topology and every divergence time;*
- (ii) *every actual demographic rate-change time and maximal constant-rate epoch on an internal population path exposed to two sampled ancestral lineages;*
- (iii) *the ancestral-root rate;*
- (iv) *the complete pendant demographic schedule for taxon x if and only if at least two lineages are sampled from x .*

The remaining quotients are parameter-free degree-two suppression, the complete pendant demographic schedule of every singleton-sampled taxon, and the physical scale action. Adjacent epochs with equal rates are one maximal epoch and do not define an observable breakpoint.

Proof. The support threshold of T_{ij} is τ_{ij} . The matrix (τ_{ij}) is the cophenetic ultrametric of the rooted species tree; its nested equal-threshold clusters recover the rooted labelled topology and divergence times. By lemma 10.1, the piecewise logarithmic hazards recover every common-population rate and demographic boundary. For an internal population edge, choose sampled descendants in two child clusters. Conditional on no earlier coalescence, both lineages occupy the edge with positive probability, so its hazard is exposed. The root rate is the eventual tail hazard.

With one lineage from terminal species x , no pair can coalesce anywhere on its pendant path, so every rate, rate-change time, and epoch subdivision on that path is absent from every genealogy density. With two sampled lineages from x , their pair process begins together at time zero and its complete piecewise logarithmic hazard recovers the pendant schedule. These arguments give both necessity and sufficiency. $\square$

The proof uses metric support and hazards, not the most probable topological gene tree, and is unaffected by anomaly zones.

11 Graph versus behavior

11.1 Strict universal graph impossibility

Definition 11.1 (Sample-unary temporal funnel). *A temporal subnetwork between boundary populations a at time t_a and b at time $t_b > t_a$ is sample-unary if every reachable sampled-lineage configuration contains at most one lineage in its interior and no sampled lineage can enter through an interior side population.*

Theorem 11.2 (Contextual funnel invisibility). *Replace a sample-unary funnel by any other finite strict two-terminal sample-unary temporal split-merge subnetwork with the same lower and upper boundary populations and times and no interior side contact with the surrounding context. Assign arbitrary positive finite population rates and inheritance probabilities in $(0, 1)$ internally. The normalized metric-genealogy law, CCR, and every direct locus law remain unchanged. The replacement is valid inside an arbitrary common surrounding context.*

Proof. At most one lineage traverses the funnel, so no Kingman merger can occur there and every internal population rate drops out. Temporal compatibility makes every traversing route take the same elapsed time $t_b - t_a$. Summing the probabilities of all independent routing histories gives one. Thus a present lineage enters at a and exits at b with the same time and state under every replacement. Conditioning on all external history before and after the funnel proves contextual equality. $\square$

This generalizes the obstruction mechanism but does not claim priority for the first funnel examples. Published bidirectional-introgression models provide additional full-likelihood role switches [16].

11.2 One-reticulation port-response quotient

For the graph statements below, a presentation is *reduced* when parameter-free degree-two vertices are suppressed, adjacent equal-rate epochs on an unchanged population are merged, simultaneous raw boundaries are composed, and every maximal sample-unary two-terminal corridor is contracted. A two-parent corridor from h to its first common reconvergence is *anchor free* when no sampled side lineage can enter either parent population or share a population with a routed one-block sector before that reconvergence. A *private side certificate* for parent P is a labelled lineage z and an open interval on which a child lineage routed to P has positive first-merger density with z , while the competing route has zero such density. An *ancestor-descendant contrast* is a sampled lineage on the directed interval between nested parents whose labelled merger-support onset differs between the two routes. Configurations with none of these certificates, including an unresolved bi-unary sister orientation, remain classified by reduced port behavior but are outside the incidence-level graph corollary.

Let T_μ be the finite set of visible event times of the normalized law, and set

$$a = a(\mu) = \begin{cases} \frac{1}{2} \min T_\mu, & T_\mu \neq \emptyset, \\ 1, & T_\mu = \emptyset. \end{cases}$$

This is a common intrinsic time for law-equal presentations. An invisible raw boundary at a is removed by analytic continuation; a supplied reticulation time is not retained as a distinguished interface.

For every labelled partition q of S , split complete histories at a . A prefix sector specifies a ranked merger pattern from the discrete partition to q and its merger-time intervals relative to $T_\mu \cup \{a\}$; a suffix sector specifies a ranked completion from q to one block and its corresponding intervals. Include zero-density sectors. The resulting domains are products of open prefix and suffix chambers, and

$$H_{q,a}(p, z) = b(pz)$$

is the actual unnormalized complete-history kernel. The suffix is empty when q has one block.

Proposition 11.3 (Finite intrinsic port encoding). *There are finite linearly independent prefix and suffix feature lists ϕ_q, ψ_q , and a unique finite coefficient matrix C_q , such that*

$$H_{q,a}(p, z) = \phi_q(p)C_q\psi_q(z). \quad (14)$$

Each feature is an absolute-time exponential monomial on one sector and zero on the others. Polynomial factors may be included in a general exponential-polynomial matrix encoding; the diagonal raw NMSC generators require only degree-zero polynomial factors. Distinct exponent vectors are combined before coefficients are recorded; features whose resulting coefficient rows or columns vanish are discarded. The sector domains, feature functions and matrices are determined by μ , and $\text{rank } H_{q,a} = \text{rank } C_q$.

Proof. Every raw complete density is a finite exponential polynomial. On a chamber defined by visible times, the finitely many raw formulas separated only by invisible faces have the same entire continuation. Indeed adjacent formulas agree on an open neighbourhood of the removed face, and the raw subdivision of the connected chamber has connected adjacency graph. Thus one exponential polynomial represents the whole intrinsic chamber. Split each exponent vector and polynomial monomial into its prefix and suffix coordinates and collect coefficients. Distinct exponential-polynomial features are linearly independent on an open chamber; features on different sectors have disjoint interiors. This proves uniqueness and the rank equality. There are finitely many partitions, ranked histories, sectors and raw terms. No assertion of a constant generator on an intrinsic interval is needed. $\square$

Definition 11.4 (Intrinsic one-reticulation port behavior). *The reduced port behavior $\mathfrak{B}$ consists of T_μ , $a(\mu)$, and the finite typed sector/feature/coefficient data in (14), up to reachable–observable interface isomorphism. Explicitly, a rank factorization $C_q = L_q R_q$ gives the lower feature map $\phi_q L_q$ and upper feature map $R_q \psi_q$; different minimal factorizations are identified by their unique intertwiner. A zero matrix has a zero-dimensional port. This construction also applies when sample-unity reduction removes the sole reticulation and leaves a species tree.*

Theorem 11.5 (Complete one-reticulation response classification). *Two presentations with at most one reticulation have equal normalized metric-genealogy laws if and only if their reduced port behaviors are related by typed reachable–observable isomorphisms. For fixed identified physical parent incidences, allowing all finite demographic words and event times to vary, the complete positive parameter fiber is equality of the intrinsic visible-time/sector records and the finite all-partition equations*

$$C_q(\theta) = C_q(\theta') \quad \text{for every labelled partition } q, \quad (15)$$

where absent features are padded by zero in the union of the two feature lists. Equivalently, the synchronized finite-jet equations of [proposition 8.10](#) compare all raw exterior and parent-word responses on their common refinement. This is a finite comparison for every pair of supplied finite presentations, including different word lengths.

When the incidences, h , and all demographic words are fixed and only inheritance varies, choose finite raw prefix-row and future-column bases A_q, D_q immediately below and above the sole routing boundary. They are independent of γ . The exact inheritance fiber is

$$A_q B_{h,q}(\gamma) D_q = A_q B_{h,q}(\gamma') D_q \quad \text{for every } q, \quad (16)$$

a finite polynomial system of degree at most $|S|$. Parent exchange sends γ to $1 - \gamma$. Inheritance is absent exactly when all these pairing matrices are constant in γ . Coincident one-block parent futures remove only the affine one-block witness; pair routing can still identify γ by [lemma 11.7](#). Distinct known one-block futures make γ unique up to exchange.

Proof. Equal laws have the same visible times and anchor. Analyticity upgrades almost-everywhere density equality to equality on every common chamber, so their kernels and unique coefficient matrices coincide. Minimal rank factorizations give the typed intertwiners. Conversely, every complete history outside the zero-probability boundary set has a unique split at a , including histories with every merger on one side. Preserving all pairings in (14) therefore preserves every density and hence the entire law. This also proves (15), including its exterior demographic scope; [proposition 8.10](#) gives the stated equivalent synchronized finite system.

For the inheritance specialization, no routing occurs below or above the sole boundary, so A_q, D_q do not depend on γ . Independent choices make every raw entry of $B_{h,q}$ polynomial of degree at most the number of blocks, at most $|S|$. Every complete pairing is a linear combination of the finite basis pairings, and conversely, proving (16). This polynomial claim is made before a possibly parameter-dependent minimal basis is chosen. Equality of $\gamma u + (1 - \gamma)v$ and $\gamma' u + (1 - \gamma')v$ for fixed known $u \neq v$ forces $\gamma = \gamma'$. $\square$

Remark 11.6 (Why the common time is necessary). Take arcs $R \rightarrow U, V$, two parallel arcs $U \rightarrow H$, and $H \rightarrow x, V \rightarrow y, z$. With rates one, inheritance $1/2$, and ages $(\tau(R), \tau(U), \tau(V)) = (5, 4, 2) \log 2$, the choices $\tau(H) = \log 2$ and $3 \log 2$ give the same complete law: the x corridor carries one lineage until U . Yet the raw-cut type $q = \{\{y, z\}, \{x\}\}$ has reachable-observable dimensions zero and one, since the later prefix merger probability is $1 - e^{-\log 2} = 1/2$. Deleting only the symbol h cannot identify these interfaces. Relocating a cut must repartition complete histories across all intervening marked strips: $b(pwz)$ becomes $H_{q,t}(p, wz)$ or $H_{q',t'}(pw, z)$ according to the cut. This finite coefficient rearrangement allows different q -dimensions. The supplement gives the explicit tree and retained-reticulation regressions.

Lemma 11.7 (Pair-exposed inheritance germ). Suppose two labelled child lineages can survive separately to h . On the first boundary-free parent interval, conditional on that survival, their no-merger response is

$$S(u) = 2\gamma(1 - \gamma) + \gamma^2 e^{-\lambda_1 u} + (1 - \gamma)^2 e^{-\lambda_2 u}, \quad u > 0, \quad (17)$$

with $\lambda_1, \lambda_2 > 0$. This germ identifies $\{\gamma, 1 - \gamma\}$, including when $\lambda_1 = \lambda_2$, and makes h visible against the single child-population semigroup below it.

Proof. The two lineages choose different parents with probability $2\gamma(1 - \gamma)$ and then cannot merge on this interval; the two same-parent assignments give the exponential terms. Uniqueness of positive finite exponential sums recovers the mass $r = 2\gamma(1 - \gamma)$ at exponent zero, so

$$\{\gamma, 1 - \gamma\} = \left\{ \frac{1 - \sqrt{1 - 2r}}{2}, \frac{1 + \sqrt{1 - 2r}}{2} \right\}.$$

If the positive exponents coalesce, their combined coefficient $1 - r$ gives the same result. The nonzero constant component prevents this analytic germ from being a single positive-rate exponential, proving visibility. $\square$

Lemma 11.8 (Finite law-defined child decoder). *For each pair of sampled labels i, j , its survival function has, on a boundary-free one-sided neighborhood of a cut t , the frozen form*

$$S_{ij}(t + u) = p_0 + \sum_{k=1}^r w_k e^{-\lambda_k u}, \quad w_k, \lambda_k > 0,$$

where the positive rates are distinct after equal atoms are combined. On the left, derivatives at t mean the local analytic extension evaluated at the boundary; no frozen physical evolution beyond its epoch is asserted. Put

$$m_k = (-1)^k S_{ij}^{(k)}(t), \quad H_r = (m_{a+b+2})_{0 \leq a, b < r}, \quad v_r = (m_{a+1})_{0 \leq a < r}.$$

The unnormalized mass $q_{ij}(t)$ of an unmerged co-occupied pair is the law-defined finite-jet expression

$$q_{ij}(t) = v_r^\top H_r^{-1} v_r. \quad (18)$$

The positive-atom count is certified by H_r positive definite and $\det H_{r+1} = 0$; count zero is certified by $m_1 = 0$, in which case $q_{ij} = 0$.

In a reduced one-reticulation presentation with at least two sampled descendants below its reticulation, the unique negative-jump time of these scalar functions is its routing time h . The graph of pairs with $q_{ij}(h+) - q_{ij}(h-) < 0$ is exactly the complete graph on its sampled child cluster C .

Proof. In a frozen population epoch an unmerged pair either occupies distinct populations and cannot merge, or occupies one population with a positive constant rate. The displayed positive exponential mixture follows after summing its actual route assignments; it concerns current occupancy, not an observed historical route. With $V_{ak} = \lambda_k^a$,

$$H_r = V \operatorname{diag}(w_k \lambda_k^2) V^\top, \quad v_r = V(w_k \lambda_k)_k.$$

The Vandermonde matrix is invertible, proving (18) and the moment-rank certificate. An extra distinct positive atom would make H_{r+1} positive definite, so its zero determinant certifies the exact count. Only finitely many one-sided derivatives are required.

Every surviving pair in C occupies the child population immediately below the sole reticulation. Its co-occupancy jump is

$$q_{ij}(h+) - q_{ij}(h-) = -2\gamma(1 - \gamma)S_{ij}(h) < 0.$$

A pair outside this clique cannot lose co-occupancy there. Tree transport, including a multifurcation, gives only nonnegative jumps; demographic changes give none. An unrelated simultaneous tree event cannot involve the two lineages in the reticulation's child population and so cannot cancel a negative clique entry. Positive temporal arcs rule out an uncomposed zero-time tree-reticulation chain. With only one reticulation there is no other negative routing event. This proves a common decoder independently of the choice of finite manifest and without requiring distinct ages for unrelated events. $\square$

Definition 11.9 (Incidence separation). *A finite scalar child certificate for (C, h) is a manifest for the decoder of lemma 11.8: for every labelled pair it records the two one-sided positive-atom counts at h , verifies the corresponding finite shifted-Hankel positivity and singularity predicates, and verifies that the negative co-occupancy jump support is precisely the complete graph on C , with $|C| \geq 2$. Count-zero pairs use the $m_1 = 0$ predicate. These are scalar finite-jet conditions involving no hidden occupancy state. Every pair-exposed one-reticulation presentation admits such a finite manifest, including equal positive rates, multifurcations, and unrelated simultaneous event ages.*

A reduced one-reticulation presentation is incidence separated when it has this certificate for its child cluster and time and each parent incidence is additionally certified by at least one of: a private side certificate, an ancestor–descendant contrast, or the two unordered sides of an anchor-free pair-exposed child marginal as in lemma 11.7. Every remaining parameter ambiguity is compared through the exact all-partition equation (15), not through an unnamed graph move.

A singleton child’s raw routing time is not identified by a coincident event elsewhere: it can move inside the positive interval below its fixed parental contacts while its outlet times, route weights, and complete law stay unchanged. It remains covered by the universal intrinsic port-response theorem, but cannot satisfy a child-time identification certificate. This separates the behavioral classification from the qualified incidence conclusion.

Definition 11.10 (CCR-balanced suffix exchange). *Let t be a cut at which a type-compatible operator σ_t exchanges two physical parent continuations. It is CCR-balanced if, for every labelled cut partition q ,*

$$r(\sigma_t - I)o = 0 \quad \text{for all actual reachable rows } r \in \mathcal{R}_{t,q} \text{ and future columns } o \in \mathcal{O}_{t,q}. \quad (19)$$

Replacing the two continuation suffixes at t preserves the complete marked-history law if and only if (19) holds.

The final assertion is immediate by cutting every complete density at t : equality after the proposed switch is exactly the vanishing of all displayed prefix–suffix pairings. It is basis independent and tests actual reachable mixtures, not latent parent basis vectors.

Proposition 11.11 (Strict posterior-balance collision). *There are two strict, sampled-complete, reduced one-reticulation presentations with the same rooted incidence graph, reticulation time, and inheritance probability, but different parent-corridor demographic words and identical complete metric-genealogy laws. They are not related by global parent exchange or the universal presentation reductions.*

Proof. Take $X = \{A, B\}$ and sampled lineages $x, y \mapsto A, z \mapsto B$. Let x, y reach a reticulation at h , let the two parent corridors have no sampled side contact before reconverging, and let z join only above that reconvergence. Put $\gamma = 1/3$. On a first parent chamber of length $\log 4$, use rates 1, 2. On a second positive chamber use rates (3, 4) in N and (4, 3) in N' , with every other time and rate common and positive. Conditional on x, y surviving to h , the first-chamber survival is

$$S_1(u) = \frac{4}{9} + \frac{1}{9}e^{-u} + \frac{4}{9}e^{-2u}.$$

At its upper boundary the same-parent survivor weights balance:

$$\frac{1}{9}e^{-\log 4} = \frac{4}{9}e^{-2\log 4} = \frac{1}{36}.$$

Consequently both second-chamber survivals equal

$$S_2(v) = \frac{4}{9} + \frac{1}{36}e^{-3v} + \frac{1}{36}e^{-4v},$$

and $-S'_2(v)$ gives the same marked merger density. Once x, y merge, one block traverses the anchor-free remainder and its parent role is unobservable; if they remain split, both enter the same population at reconvergence. The common surrounding process, including z , therefore composes with the same complete local kernel. Yet the parent rate words are

$$\{(1, 3), (2, 4)\} \quad \text{and} \quad \{(1, 4), (2, 3)\},$$

which neither the identity nor a global parent swap matches. All durations, rates, and inheritance probabilities are strict. This is (19) with equal two-block posterior weights. $\square$

For an anchor-free corridor carrying at most two child blocks, write the two same-route survivor weights at a chamber boundary as

$$w_1 = \gamma^2 e^{-A_1(t)}, \quad w_2 = (1 - \gamma)^2 e^{-A_2(t)}.$$

If $w_1 \neq w_2$, the weights link the unordered exponential atoms across that boundary. If $w_1 = w_2$, exchanging the two complete continuation words is CCR-balanced. For arbitrary higher-block interfaces, no claim is made that permutations exhaust every positive solution of (15); the finite all-partition equation is the exact fiber.

Corollary 11.12 (One-reticulation graph content). *For any two incidence-separated presentations with isomorphic CCR, the labelled downstream cluster, h , unordered parent-incidence pair, and $\{\gamma, 1 - \gamma\}$ agree. Species-tree inversion identifies every exposed exterior tree parameter. Parent-corridor demography is compared through the exact reduced port behavior and equation (15), which includes CCR-balanced suffix exchanges such as proposition 11.11; raw parent-word linkage is not claimed.*

Proof. The finite scalar child certificate and lemma 11.8 recover the same C and h from an equal law, independently of the supplied manifest. A private side cell locates its labelled parent incidence by its support onset; its first exponential hazard gives the adjacent rate and its normalized coefficient gives the route weight. A sampled intervening path orders nested parents by unequal support thresholds. With no side anchor, lemma 11.7 identifies the unordered inheritance weights, while its constant split component and the later disappearance of that component locate the two endpoints of the unique reduced anchor-free cycle. The exterior pieces follow from theorem 10.2. What remains is precisely the actual all-partition port behavior of theorem 11.5; proposition 11.11 proves why it cannot generally be replaced by linked latent parent schedules. $\square$

11.3 Reduced level-1 gluing

For a labelled cluster $C \subseteq S$, an interior cut t , and a labelled partition q of C at t , let $\mathcal{P}_{C,t,q}$ be the admissible timed C -prefix histories ending at (t, q) , with complementary lower lineages integrated under their common law, and let $\mathcal{Z}_{C,t,q}$ be the compatible full continuations. Define the scalar cut kernel from the common-chamber Radon–Nikodym density by

$$H_{C,t,q}(p, z) = b(pz).$$

For a suffix cylinder $A \subseteq \mathcal{Z}_{C,t,q}$ write

$$H_{C,t,q}(p, A) = \int_A b(pz) \, dz, \quad \mathbf{1}_{C,t,q} = \mathcal{Z}_{C,t,q}.$$

All quantities in this subsection are therefore functions of the marked-history law, not of an occupancy presentation.

Lemma 11.13 (Canonical continuation at a scalar cut). *Suppose $H_{C,t,q}$ is nonzero and rank one. Then*

$$\alpha_{C,t,q}(p) := H_{C,t,q}(p, \mathbf{1}_{C,t,q}), \quad \beta_{C,t,q}(A) := \frac{H_{C,t,q}(p, A)}{\alpha_{C,t,q}(p)}$$

are well defined on positive prefix rows, $\beta_{C,t,q}$ is independent of p , and $\beta_{C,t,q}(\mathbf{1}_{C,t,q}) = 1$. They are the unique positive rank-one factors with this normalization. Conversely, independence of the displayed ratio from p is equivalent to rank one. Hence α and β are invariants of the scalar law and remove the reciprocal row-column gauge.

Proof. Write a positive rank-one factorization as $H(p, A) = a(p)c(A)$. Integrating over all completions gives $\alpha(p) = a(p)c(\mathbf{1})$, so the displayed ratio is $c(A)/c(\mathbf{1})$ and is independent of p . Its total mass is one. This fixes the reciprocal factorization gauge, proving uniqueness. Conversely, $H(p, A) = \alpha(p)\beta(A)$ is rank one. $\square$

For $s < t$, let $\omega = ((e_1, u_1), \dots, (e_m, u_m))$ be a labelled binary C -merger word: $s < u_1 < \dots < u_m < t$, e_j is the specified pair of current blocks merged at u_j , no other C -merger occurs on (s, t) , and $q \cdot \omega = q'$ is the terminal partition. Put $u_0 = s$ and $u_{m+1} = t$. For a positive finite piecewise-constant pair-rate word λ define

$$\mathbf{K}_{\lambda;s,t}(q, \omega) = \left(\prod_{j=1}^m \lambda(u_j) \right) \exp \left\{ - \sum_{j=0}^m \binom{|q| - j}{2} \int_{u_j}^{u_{j+1}} \lambda(v) \, dv \right\}. \quad (20)$$

The empty word is included. This is the density of the specified labelled Kingman word, not the density summed over target pairs.

Definition 11.14 (Law-scalar continuation component). *Fix $2 \leq |C| \leq |S|$. An open interval J is law scalar for C if:*

- (S1) *for every $t \in J$, no marked history with a $C-S \setminus C$ merger below t has positive support; this condition is vacuous for $C = S$;*
- (S2) *for every $t \in J$ and every feasible labelled partition q of C , $H_{C,t,q}$ is nonzero and rank one, with the canonical factors of [lemma 11.13](#);*
- (S3) *there is a positive finite piecewise-constant rate word λ_J on J such that, for every $s < t$ in J , every feasible (q, ω, q') , and every compatible suffix cylinder A at (t, q') ,*

$$\beta_{C,s,q}(\omega A) = \mathbf{K}_{\lambda_J;s,t}(q, \omega) \beta_{C,t,q'}(A). \quad (21)$$

Here a feasible starting partition has a positive prefix row. All label-compatible merger words from that partition are tested, including words with zero observed density; feasibility does not discard such words. If their terminal kernel vanishes, the test fails: the positive Kingman word has positive

total continuation mass. A complete scalar-separator component is a maximal connected law-scalar interval J with nonempty interior. It is recorded as

$$P = (C, J, a, b, \lambda_P, (\alpha_{C,t,q}, \beta_{C,t,q})_{t \in J,q}), \quad (a, b) = (\inf J, \sup J),$$

and its canonical law key is the entire record, denoted $\kappa_\mu(P)$. Distinct intervals with the same cluster remain distinct records. The unique unbounded component, denoted Ω , is the ancestral-root record and has cluster S ; finite full- S components are retained too. A proper cluster has finite upper endpoint because it eventually has supported cross-mergers in the root population. The labelled terminal atoms are A_x with their known sampling blocks $S_x = \mathfrak{s}^{-1}(x)$, not separate species leaves for samples in one taxon. No unexposed singleton demographic word is inserted. [Lemma 11.16](#) justifies the asserted root convention.

Lemma 11.15 (Observable boundary composition and maximality). *Let $J_- = (a, d)$ and $J_+ = (d, b)$ be law-scalar intervals for the same C . They belong to one complete component if and only if their rate words concatenate to a positive finite piecewise-constant λ and (21) holds for every spanning choice $s < d < t$, including the empty word and every labelled target-pair word. It is enough to check such choices in one two-sided neighborhood of d . An unequal rate jump may therefore lie in one component, while adjacent equal rates form one maximal epoch. The criterion mentions no raw boundary, population name, or physical port.*

Every finite endpoint of a complete component is law determined: attempted extension either creates a supported cross-merger history, a nonzero 2×2 rank minor, or failure of a spanning cocycle on a labelled merger word and suffix cylinder. Isolated rank-one resonances do not create components.

Proof. On the non-unary support, the ratio of a specified-pair merger density to the corresponding no-merger density recovers λ almost everywhere, so the rate word is unique. If the spanning identities hold near d , split any merger word at d and apply the two within-interval cocycles; the Kingman factors multiply, proving the identity for every $s < d < t$. The converse is immediate from restriction. If a measure identity fails, a cylinder fails because the marked cylinders generate the continuation sigma-field. Finite presentations have finitely many analytic strata, so nonextendability has one of the stated finite support, minor, or cylinder witnesses. All tests use H , α , and β only. $\square$

A physical population bridge satisfies the continuation cocycle by the strong Markov property and its Kingman generator. This includes every demographic rate change. Conversely, a raw routing boundary is glued only if its complete labelled continuation law is exactly scalar; no observation in μ can then justify retaining it as a separator.

The *rooted bridge/blob tree* contracts each nontrivial level-1 blob to a vertex, retains ordinary branching vertices and terminal taxa, and suppresses demographic degree-two subdivisions while retaining their bridge rate words. Unary nontrivial blobs are retained. The ancestral root corridor lies above the top vertex; singleton terminal corridors retain their incidence without unexposed demographic words. Ordinary branching vertices are allowed zero temporal span, and attachments to one blob can occur at different ages.

Call a reduced level-1 presentation *scalar-separator faithful* when its non-unary proper-cluster bridge corridors are in incidence-preserving bijection with the corresponding maximal law-scalar components and their finite endpoints are the adjacent component or terminal boundaries. This is the proper-cluster graph-domain hypothesis, imposed separately on each presentation, not an ingredient in κ_μ . Full- S corridors obey the same correspondence without an additional hypothesis

by the next lemma. Call it *locally incidence separated* when every blob response conditioned at its incident canonical law ports satisfies the preceding incidence certificates.

Lemma 11.16 (Full-sample corridors and the root record). *In a strict sampled-complete level-1 presentation, the complete law-scalar components for $C = S$ are precisely its maximal full- S physical bridge corridors. There is exactly one unbounded component Ω . Adding these records imposes no further faithfulness restriction.*

Proof. A full- S bridge has the Kingman cocycle by the Markov property. Conversely, choose a cut in a full- S scalar interval away from every raw boundary and scalar-rate breakpoint, and condition on the positive prefix with no sample merger. On a sufficiently short following interval, (S3) gives the complete marked Kingman law. Freeze the raw population configuration and rates there. Its probability of complete coalescence by elapsed time u is an entire matrix-exponential function, equal for small $u > 0$ to the Kingman completion probability. The identity theorem extends equality to every $u > 0$, so its limit is one. Any posterior occupancy assignment using two populations would remain split forever in the frozen process and give a positive deficit. Thus every reachable no-merger assignment is co-occupied.

Strict independent routing and positive finite survival make the support of route assignments a product over sampled labels. With at least two labels, that product is entirely co-occupied only when every label has the same singleton accessible-population set. The common arc is a bridge: inside a nontrivial level-1 cycle, a sampled descendant of its reticulation has positive routes on both temporally overlapping arms, contradicting singleton accessibility. Maximality and the spanning-cocycle rule now identify exactly the full- S corridors. The eventual root population supplies an unbounded one; two distinct maximal intervals cannot both be unbounded. This frozen continuation is an exact identifiability argument, not a stable extrapolation procedure. $\square$

Lemma 11.17 (Occurrence order reconstructs incidence). *For distinct complete records write $P \prec Q$ when*

$$C_P \subsetneq C_Q \quad \text{or} \quad (C_P = C_Q \text{ and } b_P \leq a_Q),$$

and write $A_x \prec P$ exactly when $S_x \subseteq C_P$. Distinct terminal atoms are incomparable. On the scalar-separator-faithful class this is the physical corridor-ancestry order, with unique maximum Ω .

Make a vertex v_P for every record and join each nonmaximal record or atom to its unique least older record. Identify A_x with v_P when its cover is P , $a_P = 0$, and $C_P = S_x$. The resulting rooted tree $\mathcal{T}_\mu$ is the bridge/blob tree. At each nonterminal v_P , the upper incident port is P ; its lower incident list is exactly the records and singleton terminal atoms immediately below P . These lists are determined before any local response is extracted.

Proof. By faithfulness and lemma 11.16, records correspond to non-unary physical corridors. In the physical rooted tree, intersecting corridor clusters lie on one ancestor chain: otherwise their disjoint descendant subtrees would have disjoint nonempty sampled clusters. Strict inclusion gives that chain's direction. Equal clusters can repeat, but their distinct nonempty temporal intervals are ordered, and the younger corridor ends no later than the older one begins. This proves exactly the displayed order, including terminal atoms. All older corridors above any object lie on one finite chain ending at Ω , so the least older record is unique.

Associate P to the younger vertex of its corridor. Every retained nonterminal vertex has at least two sampled descendants: branching gives two sampled branches, while a unary blob with only one descendant sample was a contracted sample-unary funnel. Thus each such vertex has its non-unary upper record; the top uses Ω . A multisampled terminal also has a pendant record, whereas a singleton terminal is its atom. Any retained vertex intervening between two corridors

therefore supplies an intermediate record. Conversely an intermediate record lies on that path. Covers are consequently exactly adjacent physical vertices. The sole redundant atom link is the specified zero-time link to its own multisampled terminal record. This proves the incidence formula.

No positive gap is required at an ordinary tree vertex: lower endpoints can meet at $b_Q = a_P$. Same-cluster pieces meeting across a scalar degree-two boundary have already concatenated by [lemma 11.15](#). A positive-duration unary gall instead lies between distinct ordered occurrences. Disjoint branches can overlap in time or have simultaneous events; their disjoint clusters keep them incomparable. $\square$

For example, an anchor-free gall with child cluster $C = \{x, y\}$ routes at $\log 2$, reconverges at $2 \log 2$, and meets an outside lineage at $3 \log 2$. Its distinct records include

$$(C, (0, \log 2)) \quad \text{and} \quad (C, (2 \log 2, 3 \log 2)).$$

The occurrence order retains the intervening unary blob. Arbitrarily many nested galls produce an ordered chain of repeated clusters, including full- S chains above all sampled taxa. A set-valued cluster Hasse diagram would erase these vertices.

Lemma 11.18 (Private-side fixed-cut certificate). *Let child labels x, y route independently at time h , and let a private label z occupy parent population P of rate $\lambda > 0$. Take $C = \{x, y, z\} \subsetneq S$ and an outside label $w \in S \setminus C$. Fix $t = h + D$ before the next boundary of P , choose $0 < u_1 < u_2 < D$, and then choose $\delta > 0$ so that $t + \delta$ precedes the next relevant population or demographic boundary and the parent reconvergence. Let p_u be the observed prefix density in which xz is the first merger at $h + u$ and no second merger occurs before the common cut t ; every p_u ends in $q = \{\{x, z\}, \{y\}\}$. In the co-occupied sector the two q -blocks remain together in P at rate λ throughout $[t, t + \delta]$; in the split sector they cannot meet there. Marginalize w over all its compatible future histories (its common factor cancels from the minor), and let z_M, z_S specify, respectively, merger and survival of the two q -blocks over that interval. With*

$$a(u) = \gamma(1 - \gamma)\lambda e^{-\lambda u}, \quad c(u) = \gamma^2 \lambda e^{-\lambda D - 2\lambda u},$$

the four scalar density entries are

$$H(p_u, z_M) = c(u)(1 - e^{-\lambda \delta}), \quad H(p_u, z_S) = a(u) + c(u)e^{-\lambda \delta}.$$

Their 2×2 determinant is

$$(1 - e^{-\lambda \delta})(c(u_1)a(u_2) - c(u_2)a(u_1)) > 0.$$

Thus this concrete nonbridge cut violates (S2) using actual rows at one fixed cut.

Proof. The split assignment contributes $a(u)$ and cannot realize z_M . The co-occupied three-block assignment contributes $c(u)$; after the first merger it realizes z_M with probability $1 - e^{-\lambda \delta}$ and z_S with probability $e^{-\lambda \delta}$. Since $c(u)/a(u)$ is a positive constant times $e^{-\lambda u}$, the determinant is positive for $u_1 < u_2$. $\square$

This lemma proves that a nontrivial (S2) witness is realizable, and positive early cross-merger support gives further sufficient certificates against many nonbridge cuts. These examples are not asserted to exhaust arbitrary level-1 presentations; exhaustion is exactly the scalar-separator-faithful hypothesis. Anchor-free factorization may instead persist to the true reconvergence component, while wholly one-block corridors are removed by reduction.

Lemma 11.19 (Canonical port matching and gluing). *The family $\mathcal{P}_\mu^{\text{sep}}$, its complete keys, and the tree $\mathcal{T}_\mu$ with every incident list $\mathbf{P}_v$ are determined by μ , equivalently by CCR. Cut at the incident ports of a vertex recovered by lemma 11.17. All-completions normalization of this joint multi-cut kernel gives a canonical typed local response $\mathfrak{L}_\mu(v)$ whose synthetic ports retain their individual keys. The collection of these keyed local responses has at most one global behavioral assembly.*

Proof. Equality of laws gives equality of every H , hence of the normalized factors, cocycle tests, maximal intervals, endpoints, keys, and reconstructed incident lists. Choose interior cuts in the records on such a list, and time zero at a known terminal atom. Singleton pendant transport contributes no demographic factor; ordinary tree vertices permit a zero-span deterministic local response. The lower incident clusters partition the upper cluster in the one recovered tree. Positivity supplies a joint positive no-merger entry cylinder at every feasible tuple of incident partitions. Let $H_{\mathbf{P}_v}(\mathbf{p}, A)$ be the scalar kernel obtained by making those law-specified cuts in the original law. The Markov property of the faithful bridge decomposition makes it rank one between the joint lower histories and the conditioned local response. Normalize it directly by

$$\alpha_{\mathbf{P}_v}(\mathbf{p}) = H_{\mathbf{P}_v}(\mathbf{p}, \mathbf{1}), \quad \beta_{\mathbf{P}_v}(A) = \frac{H_{\mathbf{P}_v}(\mathbf{p}, A)}{\alpha_{\mathbf{P}_v}(\mathbf{p})}.$$

This is a joint law normalization; no product of separately marginalized entry factors is assumed. Integrating nonlocal continuations against $\beta_{\mathbf{P}_v}(\mathbf{1}) = 1$ recovers $\mathfrak{L}_\mu(v)$ without choosing a latent port basis.

If two keyed assemblies first differed in one local marked cylinder, attach to it the common positive joint entry cylinder at its lower incident keys and the all-completions columns at its upper keys, and integrate all disjoint modules over their normalized completions. Joint rank one and (21) make every attached factor common and positive, so the resulting global marked-cylinder densities would differ. Thus disjoint blobs cannot compensate. Matching and reattachment use $\kappa_\mu(P)$ only. $\square$

Theorem 11.20 (Scalar-separated level-1 quotient). *For any two reduced scalar-separator-faithful, locally incidence-separated level-1 presentations with isomorphic CCR, the rooted bridge/blob trees, local parent incidences, and inheritance probabilities agree modulo independent parent exchange. Their global assemblies of reduced local port behaviors agree. Raw demographic gluing is compared only through the all-partition fibers (15), including every applicable CCR-balanced suffix exchange and any other positive solution, together with the universal reductions and physical scale gauge.*

Proof. Isomorphic CCRs give the same marked-history law and hence the same canonical port records. Lemmas 11.16 and 11.17 reconstruct their common rooted bridge/blob tree and every incident port list, retaining repeated clusters and the full- S root sector. Only then does lemma 11.19 extract each local keyed response without deleting samples.

For this local application, a synthetic port retains every block of its arriving partition as a separate labelled lineage, together with its port key and entry time. Strict finite survival makes the all-singleton entry tuple feasible with positive probability. Fix that tuple and take each pair's own restriction of the normalized keyed local response. A block entering later can be kept in its own isolated placeholder until its known entry time; such an entry can only increase co-occupancy. Every child-entry block is already present below the component's sole reticulation, so lemma 11.8 recovers its negative child clique and routing time exactly as in the one-reticulation case. The retained keys convert the clique into child-port incidence, and the same local law supplies the stated parent certificates. Thus the use of corollary 11.12 does not collapse a multi-lineage port to one lineage or assume that certificates survive deletion of an attached module.

Local incidence separation and [corollary 11.12](#) recover the local parent incidences and inheritance weights modulo independent parent exchange. The gluing lemma reattaches them uniquely at the behavioral level. Equation (15) and [proposition 11.11](#) give exactly the retained demographic quotient. $\square$

No unconditional level-1 theorem is advertised. Sample-unary galls, unresolved sister cases, non-faithful scalar separators, and positive all-partition port fibers remain explicit parts of the observable quotient. Existing quartet-level classifications have their own, coarser ambiguity mechanisms and cannot be transferred to CCR without proof [4].

12 The finite-locus hierarchy

12.1 Compact finite-presentation determination

Definition 12.1 (Compact normalized presentation chart). *A chart K_i is a compact semianalytic subset of the strict normalized parameter domain of one fixed raw presentation and event ordering. It has finitely many topology and demographic epochs, bounded normalized event times, positive rates bounded above and away from zero, inheritance probabilities bounded away from 0 and 1, and a compact semianalytic family of irreducible stationary reversible generators with trace -1 . A compact finite-presentation class is a finite disjoint union $K = \bigsqcup_i K_i$.*

The substitution family may meet zero-conductance faces while remaining irreducible. In the conductance coordinates of [section 2](#), allow signed conductances on a small ambient neighborhood, retaining positive π and nonzero trace-normalization denominator. This gives an analytic extension of the finite-time formulas. At every physical point, ancestral transient matrices are invertible because positive root coalescence causes absorption; their inverses remain analytic on a neighborhood. Compactness gives the needed ambient neighborhoods of each chart pair. Thus the analyticity hypothesis does not impose positivity on every substitution off-diagonal entry.

For a length- L word a , let

$$f_{L,a}(\theta, \theta') = \mathbb{P}_\theta^{(L)}(a) - \mathbb{P}_{\theta'}^{(L)}(a).$$

By the analyticity argument after [theorem 9.1](#), every $f_{L,a}$ is real analytic on a neighborhood of each compact chart pair.

Theorem 12.2 (Compact finite separation). *Every compact finite-presentation class K has a finite determining length $L_*(K)$.*

Proof. Fix an ordered chart pair $C = K_i \times K_j$. Let $\mathcal{A}(C)$ be the ring of germs along C of real-analytic functions defined on neighborhoods of C . The ambient chart-pair manifold is a coherent real-analytic space, and C is compact semianalytic. Frisch’s compact-semianalytic theorem [11, Theorem I.9], in the explicit real-analytic criterion of Siu [15, Theorem 2 and the final Remark concerning statement (1)], therefore makes $\mathcal{A}(C)$ Noetherian. The supplement checks these hypotheses directly, including finite connectedness via semianalytic triangulation. Let $I \subseteq \mathcal{A}(C)$ be the ideal generated by all sequence-coordinate differences $f_{L,a}$. Noetherianity gives finitely many generators. Because I is generated by the displayed family, a finite subset of the actual $f_{L,a}$ already generates it: expand finite ideal generators as finite combinations of the original family and collect all family elements used.

Let L_{ij} be the largest length in that finite subset. If two points of C have equal length- L_{ij} laws, marginalization gives equality for every selected shorter coordinate. Every other difference

germ is a finite analytic combination of the selected differences on some neighborhood of the entire compact set C , hence vanishes at the pair. Thus all indexed laws agree. The converse is trivial. There are finitely many ordered chart pairs; take $L_*(K) = \max_{i,j} L_{ij}$. $\square$

This proof is global along the compact set. It does not rely on an unsafe intersection of infinitely many shrinking local neighborhoods. It gives no practical numerical bound and makes no statement about a fixed presentation over an unrestricted noncompact parameter domain.

12.2 Exact arbitrarily-high-order JC collisions

Consider two taxa, one sampled lineage per taxon, a positive divergence time τ , no reticulation, and known trace-normalized JC. Let $T = \tau + Y$ be the pair coalescence time. For a fixed positive JC decay constant β , set

$$X = e^{-\beta T} \in (0, 1).$$

A specified diagonal and off-diagonal pair pattern have conditional probabilities

$$d(X) = \frac{1 + 3X}{16}, \quad o(X) = \frac{1 - X}{16}. \quad (22)$$

Consequently every length- L pair-alignment word has conditional probability polynomial in X of degree at most L .

Lemma 12.3 (JC moment equivalence). *The length- L pair-alignment law is determined by $m_k = \mathbb{E}[X^k]$, $0 \leq k \leq L$. Conversely the collection of length- L word probabilities determines these moments. If two laws agree through m_L and differ at m_{L+1} , their length- $(L+1)$ laws differ.*

Proof. Products of the affine functions in (22) have degree at most L . Conversely $X = 4(d - o)$, so products and linear combinations of pair-pattern indicators recover every power through degree L . The all-diagonal word $d(X)^{L+1}$ has nonzero coefficient $(3/16)^{L+1}$ on X^{L+1} , proving the last assertion after lower moments cancel. $\square$

We now realize enough moment directions by strict demography. Fix $0 < a_1 < \dots < a_m$, $\lambda_0 > 0$, and for small $\theta \in \mathbb{R}^m$ set the ancestral pair hazard, measured from divergence, to

$$\lambda_\theta(t) = \lambda_0 + \sum_{j=1}^m \theta_j \mathbf{1}_{\{t \geq a_j\}}. \quad (23)$$

All cumulative rates are positive in a neighborhood of 0. The survival function is

$$S_\theta(t) = \exp \left[-\lambda_0 t - \sum_j \theta_j (t - a_j)_+ \right].$$

For $s > 0$, integration by parts gives

$$L_\theta(s) = \mathbb{E}[e^{-sY}] = 1 - s \int_0^\infty e^{-st} S_\theta(t) dt,$$

and differentiation at 0 yields

$$\left. \frac{\partial L_\theta(s)}{\partial \theta_j} \right|_0 = \frac{s}{(s + \lambda_0)^2} e^{-(s + \lambda_0)a_j}. \quad (24)$$

Theorem 12.4 (Arbitrary-order strict collision). *For every $L \geq 1$, there are two distinct strict finite-epoch demographic models of the form (23) whose direct locus laws agree for all lengths $1, \dots, L$ and differ at length $L + 1$.*

Proof. Take $m = L + 1$ and $s_k = k\beta$. Since $m_k(\theta) = e^{-s_k\tau} L_\theta(s_k)$, the Jacobian of $(m_1, \dots, m_m)$ at 0 has entries (24) times $e^{-s_k\tau}$. After removing nonzero row and column factors, its core is

$$(e^{-k\beta a_j})_{k,j=1}^m = (x_j^k)_{k,j=1}^m, \quad x_j = e^{-\beta a_j}.$$

Its determinant is

$$\left(\prod_j x_j \right) \prod_{i < j} (x_j - x_i) \neq 0.$$

Thus the first L moment map has rank L , while the map including m_{L+1} has rank $L+1$. The implicit-function theorem gives a one-dimensional real-analytic level manifold of $(m_1, \dots, m_L)$ through 0. The differential of m_{L+1} is nonzero on its tangent line, so m_{L+1} is nonconstant there. Parameterize the level curve analytically as $c(u)$ with $c(0) = 0$. Its tangent vector has no zero coordinate, since deleting any column of the first L Vandermonde rows leaves an invertible $L \times L$ generalized Vandermonde matrix. Every coordinate of $c(u)$ therefore has a nonzero linear term and is nonzero for all sufficiently small $u \neq 0$. Choose two sufficiently close such points with different m_{L+1} values. All cumulative rates in (23) remain positive, all intervals $a_{j+1} - a_j$ remain positive, and the terminal hazard is finite and positive. The moment equalities are exact by construction. [Lemma 12.3](#) transfers them to the locus laws. $\square$

Since $n = 2$, $r = 0$, $\kappa = 4$, and the sampling design remain fixed while only the number of demographic epochs grows, [theorem 12.4](#) proves part (b) of [theorem 3.3](#). It does not refute the compact theorem or assert failure of a global bound for a fixed presentation size on an unrestricted noncompact domain.

13 Reconstruction and statistical consequences

13.1 Four different senses of reconstruction

The complete indexed moment sequence identifies ν but does not by itself provide a finite-query terminating algorithm. We distinguish:

1. the Borel inverse of [theorem 7.1](#), whose input is the complete indexed population law;
2. finite exact equality testing for two proposed raw systems, given by [proposition 8.10](#);
3. finite reconstruction on a specified compact class once a sufficient $L_*(K)$ is known;
4. numerical approximation from finitely many empirical moments.

Proposition 13.1 (Truncated moment approximation). *Let ν be a probability measure on Δ_{d-1} and let $\mathcal{C}_L$ be the set of probability measures matching all its mixed moments through degree L . In the bounded-Lipschitz (equivalently weak) metric,*

$$\sup_{\rho \in \mathcal{C}_L} d_{\text{BL}}(\rho, \nu) \longrightarrow 0.$$

Proof. The probability-measure space on the compact simplex is compact metrizable. The sets $\mathcal{C}_L$ are nonempty, nested, and closed. Their intersection is $\{\nu\}$ by [theorem 4.1](#). If the displayed convergence failed, choose $\rho_L \in \mathcal{C}_L$ a fixed distance away and extract a weakly convergent subsequence. Every fixed moment eventually matches, so the limit lies in the intersection, a contradiction. $\square$

13.2 Fixed-length consistency on compact classes

Let K be a compact finite-presentation class and $L_* = L_*(K)$. The finite alignment alphabet has size $D = d^{L_*}$. Let $F_{L_*} : K \rightarrow \Delta_{D-1}$ be the direct law map and let $Y = F_{L_*}(K)$.

Theorem 13.2 (Fixed-length quotient consistency). *From independent length- L_* loci generated at $\theta_0 \in K$, let $\hat{P}_K$ be the empirical full-alignment distribution and choose*

$$\hat{y}_K \in \arg \min_{y \in Y} \|\hat{P}_K - y\|_1.$$

Then $\hat{y}_K \rightarrow F_{L_*}(\theta_0)$ almost surely. Thus the exact sequence-equivalence/CCR quotient is strongly consistently estimated. Raw parameter consistency is asserted only when a chosen representative is unique and the local inverse is continuous.

Proof. Continuity of matrix exponentials and finite integrations makes Y compact. The strong law gives $\hat{P}_K \rightarrow F_{L_*}(\theta_0)$. Since the true point lies in Y , the triangle inequality bounds the minimizer's error by twice the empirical error. [Theorem 12.2](#) identifies the image point with the full sequence quotient. $\square$

13.3 Increasing-order designs

For all-length classes without a supplied determining length, use the product metric

$$d_\infty(P, Q) = \sum_{\ell \geq 1} 2^{-\ell} \|P^{(\ell)} - Q^{(\ell)}\|_1.$$

Write

$$d_{\leq L}(P, Q) = \sum_{\ell=1}^L 2^{-\ell} \|P^{(\ell)} - Q^{(\ell)}\|_1$$

for its truncation. Below, δ_K is this truncated distance between the empirical marginal vector and the true vector through order L_K ; marginalization is an ℓ^1 contraction. If K independent loci all have known length $L_K \rightarrow \infty$, their prefixes estimate every order $\ell \leq L_K$. A sufficient growth condition for simultaneous empirical control is

$$\frac{d^{L_K}}{K} \rightarrow 0. \tag{25}$$

Alternatively, one may receive separate independent samples at every retained length.

Theorem 13.3 (Increasing-order quotient consistency). *On a nested sequence of compact normalized finite-presentation sieves whose union contains the true finite model, a minimum-distance estimator in the truncated product metric is strongly consistent for the indexed sequence-law point, provided the sieve index and L_K grow slowly enough that empirical error and optimization error vanish, for example under (25). Through [theorem 3.2](#), this is consistency for the CCR equivalence class in the observable quotient topology induced by d_∞ .*

Proof. The standard bound $\mathbb{E}\|\hat{P}_K - P_K\|_1 \leq \sqrt{d^{L_K}/K}$ follows from Cauchy–Schwarz. The ℓ^1 error changes by at most $2/K$ when one locus is replaced, so McDiarmid's inequality and Borel–Cantelli control its deviation from the expectation. Equation (25) therefore gives an almost-sure retained-law error $\delta_K \rightarrow 0$. Once the nested sieve contains the true finite model, an ε_K -approximate minimizer $\hat{y}_K$ satisfies directly

$$d_{\leq L_K}(\hat{y}_K, P_0) \leq 2\delta_K + \varepsilon_K,$$

because the true law P_0 is an available competitor. The omitted product-metric tail is at most 2^{-L_K+1} , so

$$d_\infty(\hat{y}_K, P_0) \leq 2\delta_K + \varepsilon_K + 2^{-L_K+1} \longrightarrow 0.$$

Compactness is used only to obtain exact minimizers on each active sieve; no precompactness of their increasing union is required. $\square$

14 Parameter fibers and sampling exposure

Let θ be the normalized genealogy and substitution parameter vector for one raw presentation, and let B_θ denote its complete scalar genealogy response behavior. The identifiable coordinates π, Q_0 are included separately when defining a sequence-equivalence fiber.

Theorem 14.1 (Exact local fiber and infinitesimal observability). *Work in a sufficiently small fixed event-order analytic chart through θ . Choose fixed absolute evaluation points in every reference reduced chamber, avoiding all raw boundaries, and shrink the neighborhood so their raw chamber assignments remain fixed. Form a finite analytic response map F whose coordinates are (a) π, Q_0 , (b) the raw times corresponding to the reference intrinsic visible events, (c) chamber jets at the fixed points with a uniform signed-pair bound from [proposition 8.10](#), and (d) the left–right invisibility jets for each reference-invisible raw event from [proposition 8.7](#). Use order bounds large enough also for first variations: $4n_i^- n_i^+$ suffices in (c), where n_i^-, n_i^+ are the raw merger dimensions in the chamber containing the selected point, and $2D_i$ suffices in (d), with all orders strictly below the indicated bound in each coordinate. The supplement gives the augmented-operator proof. The level set of F itself enforces persistence of the reference visibility pattern; this pattern need not be assumed of every parameter in the neighborhood. For a direction v , the following are equivalent:*

- (i) *the variations of π, Q_0 , every intrinsic visible event time, and every scalar chamber germ of B_θ vanish, including both extensions at reference-invisible boundaries;*
- (ii) *every first parameter derivative of every coordinate of F vanishes;*
- (iii) *v belongs to the linearized tangent space of the local sequence-equivalence fiber, namely $\ker DF_\theta$.*

The exact local sequence-equivalence fiber is the finite real-analytic set $X = F^{-1}(F(\theta))$. The equations fixing π, Q_0 keep substitution coordinates physical even if the ambient analytic chart permits signed conductances. Let I be the local analytic ideal generated by all the coordinate equations, with all their analytic combinations included, and let $\text{in } I$ be its associated-graded initial ideal. Its real arc tangent cone is

$$C_{\text{arc}}(X, \theta) = \{v : \text{some analytic arc } \theta(t) = \theta + t^m v + o(t^m) \text{ lies in } X\}.$$

Real-analytic curve selection supplies these arc directions, and

$$C_{\text{arc}}(X, \theta) \subseteq V_{\mathbb{R}}(\text{in } I) \subseteq \ker DF_\theta.$$

The first inclusion can be strict over $\mathbb{R}$; after complexification, $V_{\mathbb{C}}(\text{in } I)$ is the usual analytic tangent cone. At a regular constant-rank point all real tangent directions equal $\ker DF_\theta$, and the local fiber dimension is its nullity. An event time is globally invisible exactly when every reduced scalar response analytically continues across it.

Proof. The finite invisibility equations enforce analytic gluing at every reference-invisible event by [proposition 8.7](#). The visible-time equations align the remaining chambers. Equality of the fixed-point jets then gives equality of every reduced chamber density by the signed-pair recurrences of

proposition 8.10; conversely equal behavior gives each of these equations. Including π, Q_0 and applying the bridge proves the exact level-set assertion.

For derivatives, an operator $\mathcal{L}(\theta)$ on a d -dimensional matrix space has its first variation represented by the $2d$ -dimensional block operator

$$\begin{pmatrix} \mathcal{L} & \dot{\mathcal{L}} \\ 0 & \mathcal{L} \end{pmatrix}.$$

The product rule also differentiates constant factors, which lie in the same base/first-variation space. Thus the stated enlarged mixed boxes determine all scalar first-variation germs. For invisible-face jets evaluated at a moving face, the chain-rule terms from its moving evaluation point vanish at the reference parameter because the entire signed side difference is zero there. Visible times have separate coordinates. This proves (i) $\Leftrightarrow$ (ii), and (iii) is the definition of the linearized equation kernel. The leading term of every arc in the level set annihilates every initial form of its full equation ideal; its linear forms give the second inclusion. Real-analytic curve selection, complex analytic tangent-cone theory, and the constant-rank theorem give the remaining statements. The final assertion is the scalar definition and finite test of visible breakpoints. $\square$

This criterion separates global influence from first-order sensitivity. A rate can influence data only through a reachable state with at least two blocks in its population and an observable continuation. An inheritance parameter can influence data only if at least one reachable routed configuration has parent assignments with distinct future responses. Either condition is globally sufficient when it makes the corresponding reduced analytic response nonconstant. Its derivative at a particular parameter is nonzero only when the first derivative of that response is nonzero there; symmetric routing points can be first-order singular even when the parameter is locally identifiable by higher-order terms. The global fiber may nevertheless include parent exchange, bidirectional-introgression role switches, the scale gauge, unary-funnel topology changes, or singular nonlinear CCR collisions.

15 Extensions and boundaries

Proposition 15.1 (Finite routing kernels). *Replace independent reticulation routing by any specified finite stochastic kernel on incoming block configurations, including common inheritance, finite correlated inheritance, or a finite latent reticulation state. For fixed kernels the moment, determinant, shared-generator, raw response, minimal-realization, compact finite-order, and consistency theorems remain valid after replacing the boundary matrices. Parameterized kernels give the same pointwise bridge and response equivalence; the analytic finite-order and local fiber theorems require their entries to extend real analytically on the stated parameter charts, and compact minimum-distance results require the corresponding continuity. The resulting CCR, and any separately proved graph interpretation, are convention specific.*

Proof. The sequence-genealogy bridge uses the same common positive-rate ancestral population and is independent of the earlier finite routing convention. The pointwise response proof needs finite boundary matrices; time analyticity holds for any fixed such matrices. Parameter analyticity and continuity enter only in the stated parameterized results. Different kernels generally produce different multilineage routing correlations, so no identifiability statement is transferred between conventions. $\square$

Proposition 15.2 (Serial calibration). *With known serial sampling dates, the determinant still recovers the additive normalized gene-tree metric. Root restoration becomes a dated-tree problem.*

If at least two distinct sampling dates are fixed in physical units and the dated root is identifiable, their normalized root-to-tip distance difference identifies $r(Q)$ and breaks the global scale action. If all dates are shifted and scaled only up to an unknown affine time unit, the corresponding time-unit gauge remains.

Proof. For leaves i, j sampled at known dates, root-to-tip physical path differences equal the date difference. The normalized additive metric multiplies these differences by $r(Q)$. A nonzero known date difference therefore determines the multiplier. $\square$

The determinant part of the bridge also holds for stationary nonreversible Q . What fails is (7): pair matrices trace a two-sided product rather than one observed semigroup. Higher-order conditional tensors may identify Q_0 up to time reversal or a smaller quotient, but a complete theorem is not proved here. A separate companion manuscript [13] studies the graph inverse problem for positive raw strongly tree-child presentations of level at most two. No result from that companion is used in the proofs of this paper.

Unknown locus boundaries and within-locus recombination change (2). Pooled sites retain only $\mathbb{E}[V]$. Site- or locus-rate mixtures can confound mutation scale and genealogy time unless a finite parametric family is specified. These models are outside the principal classification.

16 Information hierarchy and literature comparison

Observation object	Exact retained information	Principal loss or result
Pooled single sites	$\mathbb{E}[V]$	All nonlinear within-locus moments are lost.
Fixed length L	Moments of V through degree L	Finite on compact charts; no epoch-uniform order.
All indexed lengths	Full ν	Equivalent to $(\pi, Q_0, \bar{\mu}_{\text{metricGT}})$.
Metric genealogies	Ranked topology and all coalescence times	Equivalent to finite CCR, not necessarily a graph.
Topological gene trees	Topology probabilities	Metric thresholds and hazards lost.
Quartet or quintet CFs	Low-taxon topology marginals	Higher routing correlations and metric data lost.

The direct species-tree and logDet results cited above use pooled expectations or distances, while the present bridge uses the entire within-locus dependence. The tree-of-blobs and level-1/galled results from concordance factors concern coarser projections [3–5]. The funnel theorem is an arbitrary-context formulation of an obstruction type already visible in metric-genealogy work; it is not presented as the first funnel phenomenon. Bidirectional-introgression role switching is attributed to Yang and Flouri [16]. Classical Hankel minimality, divided differences, and compact analytic Noetherianity are used as mathematical infrastructure rather than claimed as inventions [9–11, 15].

17 Discussion

The positive scientific object is not an estimated gene-tree distribution. The complete indexed alignment law first recovers a compact mixing measure of conditional phylogenetic tensors. Determinants and a shared semigroup then recover the normalized metric-genealogy law. Only after this direct bridge is established do we ask what species history generated that law.

The universal inverse problem does not have a graph-valued answer. CCR is the finite canonical observable behavior. This is stronger than merely naming equality of distributions: it provides finite typed state spaces, analytic flows, marks, boundaries, an intrinsic breakpoint set, minimality, and a finite proposed-model equality criterion. It is weaker than a canonical positive network realization, and the distinction is unavoidable.

The finite-locus result is also genuinely two-sided. A fixed compact finite presentation is finitely separated because its analytic coordinate ideal along the compact parameter-pair set is Noetherian. Yet a bound that ignores demographic complexity is impossible even for two taxa and known JC. The collision theorem exposes why: finite locus length samples only finitely many Laplace moments, while each additional demographic epoch supplies another independent moment direction.

Further graph interpretation can compare two positive raw presentations through their common response, without requiring a positive realization theorem for every abstract CCR. The companion manuscript investigates this problem for the strongly tree-child level-at-most-two class. A separate substitution extension is recovery of an unknown stationary nonreversible generator from higher-order conditional tensors.

18 Conclusion

For the principal direct-sequence NMSC model,

$$(\mathbb{P}_\xi^{(L)})_{L \geq 1} \iff (\pi, Q_0, \bar{\mu}_{\text{metricGT}}) \iff (\pi, Q_0, \text{CCR}).$$

This is the exact all-length observational quotient. Species trees admit a unique graph interpretation with precisely exposed demographic parameters. One-reticulation systems admit an exact finite port quotient; on the incidence-separated subclass the child cluster, parent incidences, and inheritance weight are recovered, while corridor demography remains in the all-partition port fiber. Unrestricted literal networks do not admit unique graph recovery. Finite locus length suffices on every fixed compact semianalytic finite-presentation class, but no order can ignore unbounded demographic epoch count.

A Notation and theorem dependencies

Symbol	Meaning
S	labelled sampled-lineage set
N, η	temporal population presentation and NMSC parameters
Q, π	substitution generator and stationary distribution
$r(Q), Q_0$	– $\text{tr } Q$ and trace-normalized generator
G, μ	rooted metric genealogy and its NMSC law
$V_Q(G), \nu$	conditional site-pattern vector and its mixing law
$\mathbb{P}^{(L)}$	indexed direct law of a length- L locus
$\bar{\mu}$	metric-genealogy law in mutation-scaled time
$H_{e, \mathcal{P}}$	raw partition–occupancy row space
A, C, R	no-merger generator, marked merger map, boundary/routing map
$\mathcal{V}_{q, t}$	canonical future-response space
CCR	canonical coalescent-response behavior

The logical chain is

$$\text{moments} \Rightarrow \nu \Rightarrow (\pi, Q_0, \bar{\mu}) \Rightarrow \text{CCR},$$

with graph inversion and finite-order theorems branching afterward. The technical supplement supplies expanded proofs of measurability, timed-Hankel reduction, breakpoint jets, the compact-germ theorem’s application, and the implicit-function collision.

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