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ALGEBRAICALLY INVISIBLE SELECTION: FECUNDITY-VIABILITY REGIMES ACTING ON EVOLUTION ALGEBRAS

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Abstract. An evolution algebra encodes uniparental inheritance: its natural basis indexes genotypes and its structure constants a_{ij} record the rate at which a parent of type i produces offspring of type j . The classical genetic algebra literature excludes selection from its scope; this paper appears to give the first treatment of selection inside the algebra. A selection regime is a pair (u, v) of positive weights acting on parental fecundity and offspring viability, deforming the algebra into the principal isotope with structure matrix $\text{diag}(u)M\text{diag}(v)$. We prove that, modulo regimes acting trivially, the selected algebra is isomorphic to the original precisely when $u_i v_i^2$ is constant across genotypes, the exponent reflecting the quadratic character of uniparental reproduction. We compute the moduli space on a fixed digraph, identify the cycle monomials of the bipartite support graph — cross ratios $a_{ij}a_{kl}/(a_{il}a_{kj})$ in the generic case — as the exact invariants of arbitrary selection, and obtain a doubly stochastic normal form through an essentially unique balancing regime. Non-degenerate selection preserves all graph-determined structure but not non-basic ideals; lethal selection creates evolutionarily closed genotype classes. A three-genotype drug-resistance pathway illustrates the results, including an invisible regime that reverses the population's long-run composition.

Keywords: evolution algebra; genetic algebra; natural selection; fecundity; viability; isotopy; ideal; matrix scaling; quasispecies.

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1. INTRODUCTION

Algebras have been used to describe inheritance since Etherington associated with a Mendelian population an algebra whose multiplication represents the fusion of gametes [1]. The resulting theory of baric, train and Bernstein algebras is surveyed by Reed [2], Wörz-Busekros [3] and Lyubich [4]. Tian's evolution algebras [5] address the complementary biological regime: a natural basis $e_1, \dots, e_n$ indexes genotypes, the relations $e_i e_j = 0$ for $i \neq j$ express that distinct genotypes do not combine, and $e_i^2 = \sum_j a_{ij} e_j$ records the offspring distribution of a parent of type i . The formalism thus models uniparental reproduction: asexual microbial lineages, organellar and mitochondrial inheritance, clonal propagation in plants, and the somatic evolution of tumour cell populations [6]. A substantial structure theory has developed, resting on the digraph Γ with an edge $i \rightarrow j$ whenever $a_{ij} \neq 0$: decomposition into irreducible components and their uniqueness [7], basic ideals as classification invariants [8], the correspondence between ideals and hereditary subsets of Γ [9], graph-theoretic criteria for nilpotency and the automorphism group scheme [10, 11], connections with Markov chains [12], and applications to concrete populations [13].

Selection is absent from this body of work, by an explicit boundary rather than an oversight: Lyubich, surveying algebraic methods in evolutionary genetics [14], wrote that equations embracing selection demand analytic methods and that for this reason the dynamics of selection lay outside his survey. The obstruction was technical, not conceptual: differential fitness destroys the baric weight homomorphism around which the classical theory is organized, so selection could not be accommodated without leaving that framework. Bernstein algebras axiomatize the Hardy–Weinberg law, that is, precisely the selectively neutral case; an evolution algebra is standardly read as describing inheritance without selective pressure [2, 5]; and the recent survey of Tian's programme [15] records six open problems, none concerning fitness. Where selection does appear in algebraically flavoured population genetics it appears dynamically, as a map on the simplex, not as a structure on the algebra: so in Lyubich's own later monograph [4], in the theory of quadratic stochastic operators [16] and their Volterra subclass, and in Eigen's quasispecies equation [17, 18, 6], whose governing matrix is a mutation matrix multiplied by

a diagonal matrix of fitnesses [19]. The present paper does not contest that $W = Q \text{diag}(f)$ factorization, which is standard biology.

The algebraic question, however, has not been addressed. If selection multiplies the structure constants of an inheritance algebra by weights, it moves the algebra within the class of evolution algebras supported on the same digraph. Which structural features move with it, and which are fixed? Equivalently: what can an observer who knows the isomorphism type of the inheritance algebra, but not the labelling of genotypes by absolute rates, learn about the selection acting on the population? The answer is complete and is given below.

Selection enters here as a deformation of the algebra itself. A *selection regime* is a pair (u, v) of positive weights, u_i scaling the fecundity of a parent of type i and v_j the viability of an offspring of type j , and it carries the algebra with structure matrix M to the principal isotope with structure matrix $\text{diag}(u)M\text{diag}(v)$. That selection should act by diagonal multiplication is not a convenience but the standard decomposition of fitness: a fecundity component attached to the parental genotype scales rows, a viability component attached to the offspring genotype scales columns, and their product is the expected contribution per parent. Isotopy is not foreign to genetic algebra: Gonshor introduced mutation through an isotope [20], Benavides, Mallol and Costa deformed train algebras isotopically [21], and Falcón, Falcón and Núñez encoded non-Mendelian mutation the same way [22]; on the biological side, the matrix $M\text{diag}(v)$ is Eigen's quasispecies matrix $Q\text{diag}(f)$ [17, 19]. What has not been examined is how such a deformation interacts with the structure theory of the algebra it deforms, and that interaction is governed by a single arithmetic fact. A change of natural basis $f_i = \lambda_i e_i$ transforms the structure constants by $a_{ij} \mapsto \lambda_i^2 a_{ij} \lambda_j^{-1}$ [23, 24, 11], the square arising because reproduction is encoded as a quadratic operation in a single parent. Comparing this rule with $u_i a_{ij} v_j$ shows, first, that every diagonal isomorphism leaves the same algebraic footprint as a selection regime (Theorem 4.3); and, second, that a regime returns the algebra to its own isomorphism class precisely when

$$u_i v_i^2 = \text{constant in } i$$

(Theorem 4.4). Selection is therefore algebraically undetectable exactly along a fecundity–viability trade-off with exponent two: a genotype twice as viable must be four times less fecund, and then no invariant of the inheritance algebra registers that selection occurred, although the

induced frequency dynamics, and with them the long-run composition of the population, may change completely. Within the evolution-algebra formalism the exponent is forced rather than fitted; its empirical standing is conditional on the adequacy of that formalism as a model of the population, a point taken up in Sections 3 and 9.

The remainder of the paper measures what selection can and cannot alter. Over the positive reals, the evolution algebras supported on a fixed digraph Γ form, modulo diagonal isomorphism, a vector space of dimension $|\mathcal{E}| - \text{rank } B_\Gamma$ for an explicit integer matrix B_Γ , with complete invariants the monomials in the structure constants obeying a local balance law: twice the outflow exponent equals the inflow exponent at every vertex (Theorem 5.1). On a directed cycle no such invariant survives, so the digraph is a complete invariant there (Corollary 5.2); this is the mechanism behind the isomorphism criteria obtained for graph and random-walk algebras in [24]. Adjoining selection enlarges the action to the full row-column scaling group, whose invariant theory is classical [25, 26, 27]: the alternating cycle monomials of the bipartite support graph, of which the cross ratios $a_{ij}a_{kl}/(a_{il}a_{kj})$ are the generic case, are exactly the features of an inheritance mechanism that no selective environment can alter (Theorem 5.4). Sinkhorn's theorem [28, 29, 30] furnishes each selection orbit with an essentially unique doubly stochastic representative, a normal form in which all main effects of productivity and survival have been normalized away (Theorem 6.1). On the ideal-theoretic side, a non-degenerate regime fixes the digraph and with it every graph-determined structure — basic ideals [8], hereditary classes [9], the optimal decomposition [7], simplicity — while an arbitrarily mild viability difference destroys non-basic ideals; lethal regimes create new evolutionarily closed genotype classes and can drive the algebra to nilpotency (Section 7). A three-genotype model of a two-step drug-resistance pathway illustrates the main statements, including the reversal of the population's long-run composition by an algebraically invisible regime (Section 8), and Section 9 discusses limitations and continuations.

Of the material below, the rescaling rule, the graph-determined invariants, the invariant theory of row-column scaling, Sinkhorn's theorem and the quasispecies factorization are quoted from the literature; the selection regime and the theorems on invisibility, moduli, selection-invariants, the balanced normal form, and the behaviour of ideals under selection and lethality are, to the

author's knowledge, new. The machinery of diagonal equivalence is itself classical, and the contribution claimed is its transfer to evolution algebras together with the biological reading that transfer supports. The computations reported in Section 8 were carried out symbolically and checked numerically.

2. PRELIMINARIES

We fix conventions here and assemble the definitions and known results on which the paper rests: evolution algebras and their natural bases, the associated digraph and its hereditary subsets, basic ideals, and the transformation rule for the structure constants under a diagonal change of natural basis. All of it is drawn from the literature; [5, 7, 8, 9] give systematic treatments.

Throughout, $\mathbb{K}$ is a field. All algebras are finite dimensional and commutative, and none is assumed associative. Statements phrased for *positive* regimes or positive structure constants are understood over $\mathbb{K} = \mathbb{R}$: this is the biologically relevant case, and it is where the square roots and logarithms used below are available. Sections 2–4 otherwise place no restriction on $\mathbb{K}$, while Sections 5 and 6 work over $\mathbb{R}$ throughout.

Definition 2.1 ([5]). An *evolution algebra* is a $\mathbb{K}$ -algebra $\mathcal{A}$ admitting a basis $\mathcal{B} = \{e_1, \dots, e_n\}$, called a *natural basis*, such that

$$e_i e_j = 0 \quad (i \neq j), \quad e_i^2 = \sum_{j=1}^n a_{ij} e_j.$$

The matrix $M_{\mathcal{B}} = (a_{ij})$, abbreviated to M when the basis is clear, is the *structure matrix* of $\mathcal{A}$ relative to $\mathcal{B}$, and $\Gamma = \Gamma(\mathcal{A}, \mathcal{B})$ is the digraph on $\{1, \dots, n\}$ with an edge $i \rightarrow j$ exactly when $a_{ij} \neq 0$. We write $\mathcal{E} = \mathcal{E}(\Gamma)$ for the edge set.

For $x = \sum_i x_i e_i$ and $y = \sum_i y_i e_i$ one has $xy = \sum_i x_i y_i e_i^2$, so the product is determined by $M_{\mathcal{B}}$. In the biological reading of [5, 13], the index set enumerates genotypes of a uniparentally reproducing population and a_{ij} is the rate, or the probability when rows are normalized, at which a parent of genotype i produces offspring of genotype j . The natural basis is therefore not a book-keeping choice but the biological one: its elements are the genotypes, and the theory privileges

it accordingly. Evolution algebras whose structure matrix is row stochastic are the Markov evolution algebras of [12]; the algebras arising in practice are nonnegative but rarely normalized, and no normalization is assumed here.

Alongside Γ we use its bipartite incidence graph $\beta(\Gamma)$: its vertices are a row copy and a column copy of $\{1, \dots, n\}$, and row i is joined to column j whenever $i \rightarrow j$ in Γ . Thus $\beta(\Gamma)$ has $|\mathcal{E}|$ edges, and it records which parent types feed which offspring types while forgetting the identification of the two index sets.

Two standard notions from the structure theory will be used. A subset $S \subseteq \{1, \dots, n\}$ is *hereditary* if, whenever $i \in S$ and $i \rightarrow j$, also $j \in S$; hereditary subsets are the genotype classes closed under inheritance, and by [9] they govern the ideal theory. An ideal I of $\mathcal{A}$ is *basic* relative to $\mathcal{B}$ if I is spanned by a subset of $\mathcal{B}$ [8]; the basic ideals relative to $\mathcal{B}$ are exactly the spans of hereditary subsets of $\Gamma(\mathcal{A}, \mathcal{B})$. The algebra is *non-degenerate* if $e_i^2 \neq 0$ for every i , and *perfect* if $\mathcal{A}^2 = \mathcal{A}$. For non-degenerate evolution algebras the decomposition into irreducible ideals exists and is unique [7], and for perfect algebras the digraph does not depend on the natural basis, by Lemma 2.3 below or by the results of [10].

The rescaling rule below underpins everything that follows. It appears in [23] as a step in the classification of low-dimensional evolution algebras and in [24] in the form incorporating a permutation, and it is encoded by the diagonal group scheme of [11].

Lemma 2.2 (rescaling rule; [23, 24, 11]). *Let $\mathcal{A}$ have natural basis $\mathcal{B} = \{e_i\}$ and structure matrix (a_{ij}) , and let $\lambda_1, \dots, \lambda_n \in \mathbb{K}^\times$. Then $\mathcal{B}^\lambda = \{f_i = \lambda_i e_i\}$ is again a natural basis, and the structure matrix relative to $\mathcal{B}^\lambda$ is*

$$a_{ij}^\lambda = \frac{\lambda_i^2}{\lambda_j} a_{ij}.$$

In particular $\Gamma(\mathcal{A}, \mathcal{B}^\lambda) = \Gamma(\mathcal{A}, \mathcal{B})$.

Proof. For $i \neq j$ we have $f_i f_j = \lambda_i \lambda_j e_i e_j = 0$, and

$$f_i^2 = \lambda_i^2 e_i^2 = \lambda_i^2 \sum_j a_{ij} e_j = \sum_j \lambda_i^2 a_{ij} \lambda_j^{-1} f_j.$$

The supports of (a_{ij}) and (a_{ij}^λ) coincide because multiplication by the nonzero scalars λ_i^2/λ_j does not alter whether an entry vanishes. $\square$

An isomorphism between evolution algebras is *diagonal* when it carries a fixed natural basis of the source to a rescaling of a fixed natural basis of the target, that is, when it acts as in Lemma 2.2. Composing with a permutation of the basis accounts for a relabelling of genotypes and is suppressed throughout; all statements below are made relative to a fixed labelling, and the results for the permuted case follow by taking orbits under the relevant subgroup of S_n . Whether diagonal isomorphisms exhaust all isomorphisms depends on the algebra, and the perfect case is settled by the following observation.

Lemma 2.3 (natural bases of a perfect algebra). *Let $\mathcal{A}$ be a perfect evolution algebra with natural basis $\mathcal{B} = \{e_1, \dots, e_n\}$. Then every natural basis of $\mathcal{A}$ has the form $\{c_1 e_{\sigma(1)}, \dots, c_n e_{\sigma(n)}\}$ with $c_i \in \mathbb{K}^\times$ and σ a permutation of $\{1, \dots, n\}$. Consequently every isomorphism between perfect evolution algebras is a rescaling as in Lemma 2.2 composed with a relabelling, and every perfect evolution algebra is non-degenerate.*

Proof. Since $\mathcal{A}^2$ is spanned by $e_1^2, \dots, e_n^2$, perfectness makes these n elements linearly independent. Let $\{f_1, \dots, f_n\}$ be a natural basis and write $f_i = \sum_k (f_i)_k e_k$. For $i \neq j$,

$$0 = f_i f_j = \sum_k (f_i)_k (f_j)_k e_k^2,$$

so independence of the e_k^2 forces $(f_i)_k (f_j)_k = 0$ for every k : the supports of $f_1, \dots, f_n$ are pairwise disjoint. Each f_i is nonzero, hence has nonempty support, and n pairwise disjoint nonempty subsets of an n -element set are singletons; thus $f_i = c_i e_{\sigma(i)}$. An isomorphism carries a natural basis to a natural basis, which gives the second assertion. If $e_i^2 = 0$ for some i then row i of $M_{\mathcal{B}}$ vanishes, $\mathcal{A}^2$ has dimension less than n , and $\mathcal{A}$ is not perfect; this is the third. $\square$

For degenerate algebras natural bases need not be related in this way and non-diagonal isomorphisms occur; Remark 4.2 bounds the consequences.

Three further field-theoretic assumptions enter at specific points. Proposition 3.2 uses square roots of the fecundities and carries that hypothesis explicitly; Corollary 5.2 uses that $2^r \neq 1$ in the field for the length r of a directed cycle, which holds in characteristic 0 but fails over finite fields, where the balance equations relax to congruences governed by the integers $2^r - 1$ (Remark 5.3); and Theorem 6.1 assumes positivity or total support, as stated there.

3. SELECTION AS A TWO-SIDED ISOTOPY

The central object of the paper, the selection regime, is introduced here. We establish its algebraic status as a principal isotope of the inheritance algebra and delimit its biological interpretation: the meaning of the two weight vectors, the justification for their multiplicative and separable action, and the extent to which arbitrary positive weightings correspond to realizable selective environments.

Reproduction contributes to the next generation through two multiplicatively independent channels. A parental genotype may produce more or fewer offspring, and an offspring genotype may survive to reproduce with higher or lower probability. In the discrete-generation model underlying an evolution algebra these are, respectively, a weighting of the rows and of the columns of the structure matrix.

Definition 3.1. A *selection regime* on an evolution algebra $\mathcal{A}$ with natural basis $\mathcal{B}$ is a pair (u, v) with $u = (u_1, \dots, u_n) \in (\mathbb{K}^\times)^n$ and $v = (v_1, \dots, v_n) \in (\mathbb{K}^\times)^n$. The *selected algebra* $\mathcal{A}^{u,v}$ is the algebra on the same underlying space with natural basis $\mathcal{B}$ and structure matrix

$$M^{u,v} = \text{diag}(u) M_{\mathcal{B}} \text{diag}(v), \quad \text{that is} \quad a_{ij}^{u,v} = u_i a_{ij} v_j.$$

We call u the *fecundity* and v the *viability* component. A regime is *lethal* at j if $v_j = 0$, in which case the same formula is used with $v_j = 0$ allowed. A regime is *sterile* at i if $u_i = 0$, which annihilates the row of i as lethality annihilates the column of j . The two boundary cases are parallel, and Section 7 treats lethality for definiteness.

Writing $\circ$ for the product of $\mathcal{A}^{u,v}$, this reads $e_i \circ e_j = 0$ for $i \neq j$ and $e_i \circ e_i = u_i \sum_j v_j a_{ij} e_j$: the parent of type i contributes u_i times as much as before, and among its offspring those of type j are weighted by v_j .

The biological reading of the two weight vectors is as follows. The life cycle of a uniparental organism factors through two censuses: an adult of genotype i produces a brood whose size is governed by the fecundity of i , and each newborn of genotype j survives to the next reproductive census with a probability governed by the viability of j . Writing u_i for the ratio of the selected to the unselected expected brood size of genotype i , and v_j for the corresponding survival ratio of genotype j , the expected number of j -offspring at the next census per i -adult is $u_i a_{ij} v_j$, because

brood size and offspring survival act at different life stages on statistically independent events. The multiplicative and separable form of Definition 3.1 is thus the standard fecundity–viability decomposition of fitness, not a modelling convenience, and it is the same decomposition that produces Eigen’s quasispecies matrix $Q \text{diag}(f)$ (Remark 3.3 below).

Three caveats bound its scope. Selection that acts on the parent’s survival between broods, or that couples brood size to offspring genotype, does not factor as $u_i v_j$ and lies outside the family considered here; selection acts in nature on phenotypes, so u and v are genotype-level aggregates obtained by averaging over the genotype–phenotype map; and while any pair of positive vectors defines a regime mathematically, the regimes accessible to a real environment form a constrained subset, since fecundity and viability advantages are typically linked by physiological trade-offs [31]. The last of these matters for interpreting the invisibility theorem: the invisible family $u_i v_i^2 = \text{const}$ is itself a trade-off curve, so it is not an isolated corner of parameter space. Power-law trade-offs between offspring number and offspring survival arise naturally in allocation models, where a fixed reproductive budget is divided between producing offspring and provisioning them [31]; which exponent a given organism realizes is an empirical matter, and nothing below asserts that real trade-offs have exponent 2. The theorem singles out the exponent-2 member of the family as the algebraically cryptic one; a population on a linear trade-off $u_i v_i = \text{const}$, or on any other exponent, is visible. Nor is the result fragile against deviations: the displacement of the selected algebra from the original in the moduli coordinates of Section 5 depends linearly on $\log(u_i v_i^2)$, so regimes near the trade-off curve are near-invisible and detectability degrades continuously with the deviation. Finally, pleiotropic constraints restrict the biologically accessible pairs (u, v) to a submanifold of the full parameter space; since the results below are invariance statements over the full group of regimes, they remain valid on every such restriction, which can only shrink the set of realizable regimes.

Recall that an *isotope* of an algebra, in Albert’s sense, is the algebra obtained by composing the original product with fixed invertible linear maps, $x \circ y = T(S(x)S'(y))$; isotopy preserves the underlying space while deforming the multiplication, which is exactly the effect a selective environment has on an inheritance mechanism.

Proposition 3.2. $\mathcal{A}^{u,v}$ is an evolution algebra. If $\mathbb{K}$ contains a square root s_i of each u_i , then $\mathcal{A}^{u,v}$ is the principal isotope of $\mathcal{A}$ given by

$$x \circ y = T(S(x)S(y)), \quad S = \text{diag}(s_1, \dots, s_n), \quad T = \text{diag}(v_1, \dots, v_n),$$

where the product on the right is taken in $\mathcal{A}$. In particular $\mathcal{A}^{1,v}$ is the isotope $x \circ y = T(xy)$ of Gonshor's type [20], and $(u, v) \mapsto \mathcal{A}^{u,v}$ defines an action of the group $(\mathbb{K}^\times)^n \times (\mathbb{K}^\times)^n$ on the set of evolution algebras with natural basis $\mathcal{B}$.

Proof. The displayed relations are of the form required by Definition 2.1, so $\mathcal{A}^{u,v}$ is an evolution algebra. For the isotope statement, $S(x)S(y) = \sum_i s_i^2 x_i y_i e_i^2 = \sum_i u_i x_i y_i \sum_j a_{ij} e_j$, and applying T multiplies the coefficient of e_j by v_j , giving $\sum_i u_i x_i y_i \sum_j v_j a_{ij} e_j = x \circ y$. The action property is immediate from $\text{diag}(u')(\text{diag}(u)M\text{diag}(v))\text{diag}(v') = \text{diag}(u'u)M\text{diag}(vv')$. $\square$

Remark 3.3. Definition 3.1 is not a novel biological model. With $u = 1$ the matrix $M\text{diag}(v)$ is the quasispecies matrix of Eigen [17, 18], written $W = Q\text{diag}(f)$ in the standard normalization [19, 6], and viability selection acting diagonally on offspring types is textbook population genetics. The contribution lies in the algebraic question posed of it, and in the separation of the two channels: as Theorem 4.4 shows, u and v interact with the algebra through the single combination $u_i v_i^2$, so a formalism using only one of them cannot see the phenomenon described below.

Two subgroups of the group of selection regimes will be used repeatedly. Set

$$\mathcal{N} = \{(u, v) : u_i v_j = 1 \text{ for every edge } i \rightarrow j\}, \quad \mathcal{D} = \{(u, v) : u_i v_i^2 = c \text{ for some } c \in \mathbb{K}^\times\}.$$

Regimes in $\mathcal{N}$ leave every structure constant literally unchanged, so $\mathcal{A}^{u,v} = \mathcal{A}$ as algebras on the same basis; the cancellation $u_i v_j = 1$ is algebraic, not physical, and such regimes are invisible for this trivial reason, no isomorphism being involved. On the single-edge digraph $1 \rightarrow 2$, for instance, the regime $u = (2, 1)$, $v = (1, \frac{1}{2})$ doubles the fecundity of the parent while halving the viability of its offspring type, and the offspring flux $u_1 a_{12} v_2 = a_{12}$ is unchanged. We call the members of $\mathcal{D}$ *compensatory regimes*; they realize the fecundity–viability trade-off announced in the introduction. The group of regimes is abelian, and the two subgroups intersect nontrivially: the scalar regimes $(t\mathbf{1}, t^{-1}\mathbf{1})$ lie in $\mathcal{D} \cap \mathcal{N}$ for every t , so the factorization of an

invisible regime as a product of a trade-off regime and a trivially acting one, established in Theorem 4.4, is not unique.

4. WHICH SELECTION REGIMES ARE INVISIBLE

We now characterize the selection regimes that cannot be detected from the isomorphism type of the inheritance algebra. The characterization proceeds in two steps. Theorem 4.3 shows that every diagonal isomorphism produces the same change in the structure constants as a suitable regime, so that a certain family of regimes is invisible for structural reasons; Theorem 4.4 then proves that, up to regimes acting trivially, this family exhausts the invisible ones and is cut out by a single scalar equation per genotype.

Definition 4.1. A selection regime (u, v) is *invisible* for $\mathcal{A}$ if $\mathcal{A}^{u,v}$ is diagonally isomorphic to $\mathcal{A}$. The invisible regimes form a subgroup $\mathcal{I} = \mathcal{I}(\mathcal{A})$ of $(\mathbb{K}^\times)^n \times (\mathbb{K}^\times)^n$.

That $\mathcal{I}$ is a subgroup follows from Proposition 3.2 together with the fact that diagonal isomorphisms compose.

Remark 4.2 (scope of the definition). Invisibility is defined through diagonal isomorphism, the notion appropriate to a fixed genotype labelling, and its two biological readings have different ranges of validity. Since a diagonal isomorphism is in particular an isomorphism, every invisible regime produces an algebra abstractly isomorphic to the original; the implication *invisible* $\Rightarrow$ *undetectable by any algebraic invariant* therefore holds for every evolution algebra. The converse reading, *visible* $\Rightarrow$ *detectable*, requires that every isomorphism onto $\mathcal{A}$ be diagonal up to a genotype relabelling, which holds when $\mathcal{A}$ is perfect (Lemma 2.3) but fails in general: the nilpotent algebra with $e_1^2 = e_2$, $e_2^2 = 0$ admits the non-diagonal automorphisms $e_1 \mapsto \alpha e_1 + \beta e_2$, $e_2 \mapsto \alpha^2 e_2$ for every β , so for degenerate algebras the set of regimes undetectable by abstract isomorphism can strictly contain the group computed below. Theorem 4.4 characterizes $\mathcal{I}$ exactly in all cases; its reading as a detectability criterion is asserted only for perfect algebras, a class that includes every mechanism with invertible structure matrix, in particular the example of Section 8.

Theorem 4.3. *Let $\lambda \in (\mathbb{K}^\times)^n$ and let $\mathcal{B}^\lambda$ be the rescaled natural basis of Lemma 2.2. Then the selection regime*

$$u_i = \lambda_i^2, \quad v_j = \lambda_j^{-1}$$

satisfies $M^{u,v} = M_{\mathcal{B}^\lambda}$. Hence every diagonal isomorphism of $\mathcal{A}$ has the same effect on the structure constants as a selection regime, and $\mathcal{D} \subseteq \mathcal{I}$: every regime with $u_i v_i^2$ constant is invisible.

Proof. With $u_i = \lambda_i^2$ and $v_j = \lambda_j^{-1}$ we get $a_{ij}^{u,v} = \lambda_i^2 a_{ij} \lambda_j^{-1} = a_{ij}^\lambda$ by Lemma 2.2, so $\mathcal{A}^{u,v}$ has the same structure matrix as $\mathcal{A}$ written in the basis $\mathcal{B}^\lambda$, hence is diagonally isomorphic to $\mathcal{A}$. These regimes satisfy $u_i v_i^2 = \lambda_i^2 \lambda_i^{-2} = 1$.

For a general member of $\mathcal{D}$, suppose $u_i v_i^2 = c$ for all i . Put $\lambda_i = v_i^{-1}$, so that $u_i = c v_i^{-2} = c \lambda_i^2$ and $v_j = \lambda_j^{-1}$. Then

$$a_{ij}^{u,v} = u_i a_{ij} v_j = c \lambda_i^2 a_{ij} \lambda_j^{-1} = c a_{ij}^\lambda.$$

The uniform factor c is itself a rescaling: taking $\mu_i = c$ for all i in Lemma 2.2 gives $a_{ij}^\mu = c^2 a_{ij} c^{-1} = c a_{ij}$. Hence $M^{u,v}$ is obtained from $M_{\mathcal{B}}$ by the rescaling λ followed by the rescaling μ , and $\mathcal{A}^{u,v} \cong \mathcal{A}$. $\square$

Before proceeding to the converse, we interpret Theorem 4.3. A relabelling of an inheritance algebra by rescaled basis vectors is a mathematical convention, while selection is a physical intervention, and the theorem does not identify the two; what it asserts is that their effects on the structure constants coincide. A basis rescaling by λ leaves the same algebraic footprint as a selective pressure multiplying the fecundity of genotype i by λ_i^2 and the viability of genotype j by λ_j^{-1} . Consequently no algebraic invariant can separate the two, the isomorphism class of an inheritance algebra is unchanged by a genuinely nontrivial family of selective pressures, and the next theorem shows that this family is all there is.

The scope of the word *invisible* should be fixed here, since it is easily overread. It refers to the isomorphism class of the inheritance algebra and to nothing else. An observer who has measured the absolute rates a_{ij} in a fixed genotype labelling, before and after the environment changed, sees an invisible regime immediately: every entry of the structure matrix has moved.

What such an observer cannot do is recover the regime from any quantity that survives a rescaling of the natural basis — from the structural description of the mechanism rather than from its calibrated rates. The theorems below therefore bound what is inferable from the algebra, not what is measurable in a laboratory.

Theorem 4.4 (invisibility). *Let $\mathcal{A}$ be an evolution algebra with natural basis $\mathcal{B}$, structure matrix M and digraph Γ . Then*

$$\mathcal{I}(\mathcal{A}) = \mathcal{D} \cdot \mathcal{N}.$$

That is, a selection regime is invisible if and only if it differs, by a regime acting trivially on the structure constants, from one satisfying $u_i v_i^2 = \text{const}$. If moreover $\mathcal{N}$ is trivial modulo the scalar family $\{(t, t^{-1})\}$, which happens exactly when $\beta(\Gamma)$ is connected and meets every index, then

$$(u, v) \in \mathcal{I}(\mathcal{A}) \iff u_i v_i^2 \text{ is independent of } i.$$

Proof. The inclusion $\mathcal{D} \cdot \mathcal{N} \subseteq \mathcal{I}$ holds by Theorem 4.3 and because $\mathcal{N}$ acts trivially, $\mathcal{I}$ being a group.

For the reverse inclusion, suppose $(u, v) \in \mathcal{I}$. By Definition 4.1 this means that $\mathcal{A}^{u,v}$ is diagonally isomorphic to $\mathcal{A}$, so the isomorphism sends $e_i \mapsto \lambda_i e_i$ for some $\lambda \in (\mathbb{K}^\times)^n$ and the two structure matrices agree entrywise in the basis $\mathcal{B}$: $a_{ij}^{u,v} = a_{ij}^\lambda$ for all i, j . No non-diagonal isomorphism enters, and none is claimed to; Remark 4.2 records what changes if abstract isomorphism is used instead. Comparing entries on the support and cancelling the nonzero a_{ij} ,

$$(1) \quad u_i v_j = \frac{\lambda_i^2}{\lambda_j} \quad \text{for every edge } i \rightarrow j.$$

Define $u'_i = \lambda_i^2$ and $v'_j = \lambda_j^{-1}$; then $(u', v') \in \mathcal{D}$, since $u'_i (v'_i)^2 = 1$. Put $(u'', v'') = (u, v)(u', v')^{-1}$, that is $u''_i = u_i \lambda_i^{-2}$ and $v''_j = v_j \lambda_j$. By (1), for every edge $i \rightarrow j$,

$$u''_i v''_j = u_i \lambda_i^{-2} v_j \lambda_j = \frac{\lambda_i^2}{\lambda_j} \cdot \lambda_i^{-2} \lambda_j = 1,$$

so $(u'', v'') \in \mathcal{N}$ and $(u, v) = (u', v')(u'', v'') \in \mathcal{D} \cdot \mathcal{N}$.

For the last statement, recall the bipartite graph $\beta(\Gamma)$ of Section 2. A pair (u, v) lies in $\mathcal{N}$ precisely when $\log u_i + \log v_j = 0$ along every edge of $\beta(\Gamma)$, and the solution space of this

system has dimension equal to the number of connected components of $\beta(\Gamma)$ together with the isolated indices. If $\beta(\Gamma)$ is connected and touches every index, the solutions are exactly $u_i = t$, $v_j = t^{-1}$; such a pair lies in $\mathcal{D}$, since $u_i v_i^2 = t \cdot t^{-2} = t^{-1}$ is constant. Hence $\mathcal{S} = \mathcal{D}$ in that case, and membership in $\mathcal{D}$ is the stated condition. $\square$

Remark 4.5. The exponent 2 in $u_i v_i^2$ is not a free parameter within the formalism. It is inherited from Lemma 2.2, where the square appears because e_i^2 is a product of the basis vector with itself: uniparental reproduction is encoded as a quadratic operation applied to a single parent, so rescaling the parent scales its offspring output twice over while rescaling the offspring type scales it once. The condition is, for the same reason, model-dependent: it is a property of the evolution-algebra encoding of inheritance, and a different encoding yields a different exponent. For a Mendelian algebra, where the product $e_i e_j$ is bilinear in two distinct parents, the corresponding computation gives $\lambda_i \lambda_j \lambda_k^{-1}$; the invisible regimes of sexual inheritance are therefore governed by a different trade-off.

Corollary 4.6. *Let $\mathbb{K} = \mathbb{R}$, let $\mathcal{A}$ be perfect with positive structure constants, so that by Lemma 2.3 diagonal and abstract isomorphism coincide up to genotype relabelling, and let (u, v) be a positive selection regime with $\mathcal{N}$ as small as in Theorem 4.4. The isomorphism type of the inheritance algebra records the regime if and only if the quantity $u_i v_i^2$ is not constant across genotypes. In particular, pure viability selection ($u = 1$) is detectable unless all v_i agree, and pure fecundity selection ($v = 1$) is detectable unless all u_i agree; but a regime combining the two along the curve $u_i v_i^2 = \text{const}$ is undetectable no matter how strong it is.*

Proof. Immediate from Theorem 4.4: with $u = 1$ the condition reads v_i^2 constant, and over $\mathbb{R}_{>0}$ this forces v constant; with $v = 1$ it reads u_i constant. $\square$

The section closes with the relation between algebraic invisibility and the induced dynamics. Uniparental reproduction induces linear frequency dynamics: the selected mechanism updates a composition vector p by $p \mapsto pM^{u,v}$, followed by normalization. Call a positive regime (u, v) *dynamically equivalent to neutrality* for $\mathcal{A}$ if there exist $w \in \mathbb{R}_{>0}^n$ and $c > 0$ with

$$\text{diag}(w)^{-1} M^{u,v} \text{diag}(w) = cM,$$

in which case $q(t) = p(t) \text{diag}(w)$ evolves under the selected mechanism exactly as the unselected composition does, up to the overall factor c removed by normalization: the selected trajectories are the unselected ones seen through a fixed reweighting of genotype counts.

Proposition 4.7 (transversality of the two notions of triviality). *Let $\mathbb{K} = \mathbb{R}$, let the structure constants be positive, and let Γ have a loop at every vertex, that is, let every genotype produce own-type offspring at a positive rate. Then:*

- (i) *a positive regime (u, v) is dynamically equivalent to neutrality if and only if $u_i v_i$ is constant in i ;*
- (ii) *if moreover Γ is weakly connected, a regime is both invisible and dynamically equivalent to neutrality if and only if u and v are constant vectors.*

Algebraic invisibility is governed by $u_i v_i^2$ and dynamical neutrality by $u_i v_i$; away from uniform regimes the two loci are disjoint, so invisible regimes are dynamically active and dynamically neutral regimes are algebraically visible.

Proof. (i) If $u_i v_i = c$ for all i , take $w = u$: then $(\text{diag}(w)^{-1} M^{u,v} \text{diag}(w))_{ij} = w_i^{-1} u_i a_{ij} v_j w_j = a_{ij} u_j v_j = c a_{ij}$. Conversely, the loop at i gives $w_i^{-1} u_i a_{ii} v_i w_i = u_i v_i a_{ii} = c a_{ii}$ with $a_{ii} \neq 0$, so $u_i v_i = c$.

(ii) Loops place every index in the support, and weak connectivity of Γ makes $\beta(\Gamma)$ connected, so by Theorem 4.4 invisibility reads $u_i v_i^2 = c_2$; combined with $u_i v_i = c_1$ from (i) this gives $v_i = c_2/c_1$ and $u_i = c_1^2/c_2$ for every i . Conversely uniform regimes satisfy both conditions. $\square$

A regime may therefore be invisible and still consequential. The two notions of triviality are cut out by trade-off curves of different exponents, 2 for the algebra and 1 for the dynamics, and they meet only in the uniform regimes that rescale the whole population at once. The exponent gap is again that of Remark 4.5: the algebra is quadratic in the parent, while the frequency flow is linear in the composition.

5. MODULI AND INVARIANTS

The invisibility theorem describes when two selected algebras coincide up to isomorphism; this section quantifies the complementary question of how many distinct algebras a given inheritance digraph supports and which functions of the structure constants separate them. We compute the space of diagonal isomorphism classes, exhibit a complete system of monomial invariants, and then enlarge the group action by selection to determine the invariants that survive every selective environment.

We fix the digraph and examine the degrees of freedom of the structure constants. From here on $\mathbb{K} = \mathbb{R}$ and all structure constants on the support are positive, so that logarithms may be taken; rates are positive, and the restriction removes the root-extraction and torsion phenomena that complicate a general field.

Let Γ be a digraph on $\{1, \dots, n\}$ with edge set $\mathcal{E}$, $|\mathcal{E}| = m$. Write $\text{EA}(\Gamma)$ for the set of evolution algebras with natural basis $e_1, \dots, e_n$ whose structure matrix has support exactly $\mathcal{E}$ and positive entries there; identifying an algebra with its vector of structure constants, $\text{EA}(\Gamma) \cong \mathbb{R}_{>0}^{\mathcal{E}}$. Define the linear map

$$B_\Gamma : \mathbb{R}^n \longrightarrow \mathbb{R}^{\mathcal{E}}, \quad (B_\Gamma x)_{ij} = 2x_i - x_j \quad (i \rightarrow j).$$

Taking logarithms turns the rescaling rule of Lemma 2.2 into the affine action $\log a \mapsto \log a + B_\Gamma x$, with $x_i = \log \lambda_i$.

Theorem 5.1 (moduli of inheritance algebras on a fixed digraph). *Let $\mathcal{A}, \mathcal{A}' \in \text{EA}(\Gamma)$ have structure constants a, a' . Then:*

- (i) *$\mathcal{A}$ and $\mathcal{A}'$ are diagonally isomorphic if and only if $\log a' - \log a \in \text{Im } B_\Gamma$. The set of diagonal isomorphism classes is therefore a real vector space of dimension*

$$\dim \text{EA}(\Gamma) / \sim = m - \text{rank } B_\Gamma.$$

- (ii) *$\ker B_\Gamma = \{x \in \mathbb{R}^n : x_j = 2x_i \text{ whenever } i \rightarrow j\}$, so $\text{rank } B_\Gamma = n - \dim \ker B_\Gamma$.*

- (iii) *A function $\prod_{(i,j) \in \mathcal{E}} a_{ij}^{\kappa_{ij}}$ with $\kappa \in \mathbb{Z}^{\mathcal{E}}$ is a diagonal isomorphism invariant if and only if*

$$(2) \quad 2 \sum_{j: v \rightarrow j} \kappa_{vj} = \sum_{i: i \rightarrow v} \kappa_{iv} \quad \text{for every vertex } v.$$

The solutions of (2) form a lattice of rank $m - \text{rank } B_\Gamma$, and the associated monomials are a complete system of invariants: $\mathcal{A}$ and $\mathcal{A}'$ are diagonally isomorphic if and only if every such monomial takes the same value on both.

Proof. (i) By Lemma 2.2, $\mathcal{A}'$ is obtained from $\mathcal{A}$ by the rescaling λ exactly when $a'_{ij} = \lambda_i^2 a_{ij} \lambda_j^{-1}$ for all edges, that is, taking logarithms and $x_i = \log \lambda_i$, when $\log a' - \log a = B_\Gamma x$. Since λ ranges over $\mathbb{R}_{>0}^n$ and x over $\mathbb{R}^n$, the action is by translations by the subspace $\text{Im } B_\Gamma$, the orbit of $\log a$ is the coset $\log a + \text{Im } B_\Gamma$, and the orbit space is the quotient vector space $\mathbb{R}^{\mathcal{E}} / \text{Im } B_\Gamma$, of dimension $m - \text{rank } B_\Gamma$.

(ii) $B_\Gamma x = 0$ says $2x_i - x_j = 0$ for every edge $i \rightarrow j$, which is the stated condition; the rank-nullity theorem gives the second claim.

(iii) Under the rescaling λ , each factor $a_{vj}^{\kappa_{vj}}$ acquires $\lambda_v^{2\kappa_{vj}}$ and each factor $a_{iv}^{\kappa_{iv}}$ acquires $\lambda_v^{-\kappa_{iv}}$, so the monomial $\prod a_{ij}^{\kappa_{ij}}$ is multiplied by $\prod_v \lambda_v^{t_v}$ with $t_v = 2\sum_{j:v \rightarrow j} \kappa_{vj} - \sum_{i:i \rightarrow v} \kappa_{iv}$; invariance for all λ is $t_v = 0$ for all v , which is (2). Equivalently, the monomial has logarithm $\langle \kappa, \log a \rangle$, constant on cosets of $\text{Im } B_\Gamma$ exactly when $B_\Gamma^\top \kappa = 0$, and the v -th coordinate of $B_\Gamma^\top \kappa$ is t_v . The space of linear functionals constant on the orbits is $(\text{Im } B_\Gamma)^\perp = \ker B_\Gamma^\top$, of dimension $m - \text{rank } B_\Gamma$, and it is spanned by integer vectors because B_Γ has integer entries. Completeness follows from (i): since $\text{Im } B_\Gamma = (\ker B_\Gamma^\top)^\perp$, the condition $\log a' - \log a \in \text{Im } B_\Gamma$ is equivalent to $\langle \kappa, \log a' \rangle = \langle \kappa, \log a \rangle$ for every $\kappa \in \ker B_\Gamma^\top$, and integer κ suffice because they span. $\square$

In (2) the left sum runs over the edges leaving v and the right sum over the edges entering it, a loop at v occurring in both. The condition is thus a local balance law: at every genotype, twice the total exponent carried by the outgoing rates must equal the total exponent carried by the incoming rates. The factor 2 is again the trace of the quadratic reproduction, and it makes the lattice markedly smaller than the corresponding lattice for ordinary weighted digraphs, where the balance is one-to-one and cycles supply invariants freely.

Corollary 5.2. *Let Γ be a directed cycle on n vertices, $1 \rightarrow 2 \rightarrow \dots \rightarrow n \rightarrow 1$. Then $\ker B_\Gamma = 0$, $\text{rank } B_\Gamma = n = m$, and $\text{EA}(\Gamma)$ consists of a single diagonal isomorphism class: any two evolution algebras with positive structure constants supported on a directed cycle are isomorphic. The digraph serves as a complete invariant for this class of algebras.*

Proof. An element of $\ker B_\Gamma$ satisfies $x_{t+1} = 2x_t$ cyclically, hence $x_1 = 2^n x_1$, hence $x_1 = 0$ since $2^n \neq 1$ in $\mathbb{R}$; the same applies to every coordinate, so $\ker B_\Gamma = 0$ and $\text{rank } B_\Gamma = n$. As $m = n$, Theorem 5.1(i) gives a moduli space of dimension 0; since the orbit space is a vector space, it is a point. The same computation shows (2) forces $\kappa_t = 2\kappa_{t+1}$ around the cycle, hence $\kappa = 0$: no nonconstant invariant exists. $\square$

Corollary 5.2 is the general mechanism behind the case analyses in the literature comparing the evolution algebra of a graph with that of the associated random walk, where the two algebras differ by a row scaling and are found to be isomorphic exactly under degree conditions [24]: whenever the relevant part of the digraph is cyclic, the scaling can always be absorbed.

Remark 5.3 (structure of the balance lattice). Two small digraphs display the arithmetic of (2). A loop at v enters the balance at v twice through the outflow sum and once through the inflow sum, hence with net coefficient one. For the digraph with loops at two vertices and a connecting edge $0 \rightarrow 1$, the balance equations $\kappa_{00} + 2\kappa_{01} = 0$ and $\kappa_{11} - \kappa_{01} = 0$ give the rank-one lattice generated by $(\kappa_{00}, \kappa_{01}, \kappa_{11}) = (-2, 1, 1)$, hence the single invariant $a_{01}a_{11}/a_{00}^2$. For the 2-cycle $0 \rightarrow 1 \rightarrow 0$ the equations $\kappa_{10} = 2\kappa_{01}$ and $\kappa_{01} = 2\kappa_{10}$ force $3\kappa_{01} = 0$, so over $\mathbb{R}$ only $\kappa = 0$, in accordance with Corollary 5.2.

The balance law (2) is an equality rather than a congruence only because $\mathbb{R}_{>0}$ is torsion free. Over an arbitrary field, $\prod_e a_e^{\kappa_e}$ is invariant precisely when $\prod_v \lambda_v^{t_v} = 1$ for every $\lambda \in (\mathbb{K}^\times)^n$, with t_v as in the proof of Theorem 5.1; if $\mathbb{K}^\times$ has finite exponent N , which for $\mathbb{K} = \mathbb{F}_q$ means $N = q - 1$, this weakens to the congruences $t_v \equiv 0 \pmod{N}$, and monomials that are not invariant over $\mathbb{R}$ become invariant. On the 2-cycle over $\mathbb{F}_4$, for instance, $a_{01}a_{10}^2$ has $t = (0, 3)$ and is invariant, the rescaling multiplying it by $\lambda_1^3 = 1$. The integers governing this are the $2^r - 1$ attached to cycles of length r — here $2^2 - 1 = 3$ — the same integers that control the diagonal group scheme of [11]. The invariant theory of this section is thus characteristic-dependent over finite fields, a case not treated here.

We now adjoin selection. In logarithmic coordinates a regime (u, v) acts by $\log a_{ij} \mapsto \log a_{ij} + p_i + q_j$ with $p = \log u$, $q = \log v$, that is by the linear map

$$C_\Gamma : \mathbb{R}^n \oplus \mathbb{R}^n \longrightarrow \mathbb{R}^{\mathcal{E}}, \quad (C_\Gamma(p, q))_{ij} = p_i + q_j$$

(mnemonically, B_Γ for the basis-change action, C_Γ for the combined row–column scaling). Theorem 4.3 says precisely that $\text{Im } B_\Gamma \subseteq \text{Im } C_\Gamma$, since $2x_i - x_j = p_i + q_j$ with $p = 2x$, $q = -x$.

Theorem 5.4 (what selection cannot change). *Let Γ be a digraph and $\mathcal{A}, \mathcal{A}' \in \text{EA}(\Gamma)$.*

- (i) *The group generated by the selection regimes and the diagonal isomorphisms acts on $\text{EA}(\Gamma)$ through C_Γ alone, and $\text{rank } C_\Gamma = 2n - c(\Gamma)$, where $c(\Gamma)$ is the number of connected components of the bipartite graph $\beta(\Gamma)$, isolated indices counted as components.*
- (ii) *The space of functions on $\text{EA}(\Gamma)$ invariant under all selection regimes and all diagonal isomorphisms has dimension*

$$m - 2n + c(\Gamma) = b_1(\beta(\Gamma)) \geq 0,$$

the cyclomatic number of the bipartite support graph, that is, its number of edges minus its number of vertices plus its number of connected components; in particular the dimension vanishes exactly when $\beta(\Gamma)$ is a forest. The space is spanned by the logarithms of the cycle monomials $\rho_\gamma = \prod_{e \in \gamma} a_e^{\pm 1}$, one for each cycle γ of $\beta(\Gamma)$ with exponents alternating in sign along γ . The 4-cycles of $\beta(\Gamma)$ are the quadruples $i \rightarrow j, i \rightarrow l, k \rightarrow j, k \rightarrow l$ of edges of Γ , whose monomials are the cross ratios

$$\rho_{ij,kl} = \frac{a_{ij} a_{kl}}{a_{il} a_{kj}};$$

when Γ has full support the cross ratios alone span, while for sparse supports longer alternating cycles contribute invariants not expressible through cross ratios.

- (iii) *Consequently $\mathcal{A}'$ can be obtained from $\mathcal{A}$ by some selection regime if and only if $\mathcal{A}$ and $\mathcal{A}'$ have the same values of all cycle monomials — of all cross ratios, in the full-support case; and no selection regime, of any strength, alters any ρ_γ .*

Proof. (i) By Theorem 4.3, $\text{Im } B_\Gamma \subseteq \text{Im } C_\Gamma$, so the group generated by the two actions has image $\text{Im } C_\Gamma$. For the rank, $C_\Gamma(p, q) = 0$ means $p_i + q_j = 0$ along every edge of $\beta(\Gamma)$; on a connected component of $\beta(\Gamma)$ this determines all values from any one of them, giving one degree of freedom per component, and an index touched by no edge is free as well. Hence $\dim \ker C_\Gamma = c(\Gamma)$ and $\text{rank } C_\Gamma = 2n - c(\Gamma)$.

(ii) The invariants are $\ker C_\Gamma^\top$, of dimension $m - \text{rank } C_\Gamma = m - 2n + c(\Gamma)$, and $C_\Gamma^\top$ is the unsigned vertex–edge incidence matrix of $\beta(\Gamma)$: the condition $C_\Gamma^\top \kappa = 0$ reads $\sum_{j:i \rightarrow j} \kappa_{ij} = 0$ for every i and $\sum_{i:i \rightarrow j} \kappa_{ij} = 0$ for every j . For a graph with $2n$ vertices, m edges and c components the unsigned incidence matrix has rank $2n - c$ when every component is bipartite, so the kernel has dimension $m - 2n + c(\Gamma)$, the cyclomatic number, and is spanned by the vectors supported on cycles with entries alternating ± 1 along the cycle — the alternation is consistent because every cycle of a bipartite graph is even. A 4-cycle of $\beta(\Gamma)$ visits row vertices i, k and column vertices j, l , and its alternating vector is the exponent pattern of $\rho_{ij,kl}$; for full support the 4-cycles span the cycle space of the complete bipartite graph $K_{n,n}$, since already the $(n-1)^2$ quadruples $\rho_{1j,i1}$ with $i, j \geq 2$ are independent and the cycle space has dimension $n^2 - 2n + 1$; this recovers the classical description of the invariants of diagonal equivalence in the analysis of contingency tables [25, 26], developed further in iterative scaling and log-linear analysis [32, 33] and treated systematically for patterns and circuits by Engel and Schneider [27, 34].

(iii) The orbit of $\log a$ under $\text{Im } C_\Gamma$ is the coset $\log a + \text{Im } C_\Gamma$, and two points lie in the same coset if and only if all functionals in $(\text{Im } C_\Gamma)^\perp$ agree on them, which by (ii) is the equality of all cycle monomials. Invariance under a regime (u, v) is also immediate by direct substitution: along an alternating cycle each u_i and each v_j appears once with exponent $+1$ and once with exponent -1 . $\square$

Theorem 5.4 answers the question posed in the introduction: selection can carry an inheritance algebra to any member of its cycle-monomial class and to no algebra outside it. The invariance of the cross ratios themselves is classical scaling theory [25, 26, 27]; the contribution of the theorem is the identification of the combined isomorphism-plus-selection action with the full scaling group on $\text{EA}(\Gamma)$, the extension to arbitrary supports through the cycle space of $\beta(\Gamma)$, and the resulting biological reading. The cross ratio $\rho_{ij,kl}$ compares how two parental genotypes i, k divide their output between two offspring genotypes j, l ; it is a measure of the interaction between parent and offspring type, purged of all main effects, and it is a property of the inheritance mechanism itself rather than of the selective environment. Whatever fitnesses are imposed, these interaction terms persist. Their number is fixed by the topology of the mechanism: those whose bipartite support graph is a forest carry no selection-invariant at all, so any

two positive inheritance algebras on such a digraph are related by a selection regime, and the capacity of a mechanism to record selection grows with the cycle structure of its support.

Example 5.5 (cyclic phase variation). Longer alternating cycles occur in real mechanisms. Consider a lineage cycling through three heritable states, as in bacterial phase or antigenic variation: each genotype breeds true at a fidelity a_{ii} and switches one step around the cycle at a rate $a_{i,i+1}$ (indices modulo 3), giving the six edges $1 \rightarrow 1$, $1 \rightarrow 2$, $2 \rightarrow 2$, $2 \rightarrow 3$, $3 \rightarrow 3$, $3 \rightarrow 1$. The bipartite support graph is a single 6-cycle without chords, so $b_1 = 6 - 6 + 1 = 1$ and the mechanism carries exactly one selection-invariant; but no quadruple of Theorem 5.4(ii) exists in this support, and the invariant is the 6-cycle monomial

$$\frac{a_{11} a_{22} a_{33}}{a_{12} a_{23} a_{31}},$$

the ratio of total fidelity to total switching around the cycle. Under any regime (u, v) both numerator and denominator are multiplied by $u_1 u_2 u_3 v_1 v_2 v_3$, so the quantity is invariant; no environment can change the balance of persistence against cycling, although any individual rate can be driven anywhere.

6. THE BALANCED NORMAL FORM

The classification of Section 5 describes the selection orbits on $\text{EA}(\Gamma)$ implicitly, through the cross ratios that separate them. This section makes the description explicit by producing, within each orbit of positive algebras, a canonical representative: a selection regime, unique in the appropriate sense, under which the structure matrix becomes doubly stochastic. The existence and uniqueness rest on the classical scaling theorems of Sinkhorn and of Brualdi, Parter and Schneider, and the biological status of the resulting normal form is discussed after the proof.

Theorem 6.1 (balancing selection regime). *Let $\mathcal{A}$ be an evolution algebra whose structure matrix M has all entries positive. Then there is a selection regime (u, v) , with u, v positive, such that the structure matrix of $\mathcal{A}^{u,v}$ is doubly stochastic:*

$$\sum_j a_{ij}^{u,v} = 1 \text{ for every } i, \quad \sum_i a_{ij}^{u,v} = 1 \text{ for every } j.$$

The regime is unique up to the substitution $(u, v) \mapsto (tu, t^{-1}v)$, $t > 0$; the doubly stochastic matrix itself is unique outright, the scalar ambiguity residing only in the factors, and it is a canonical representative of the selection orbit of $\mathcal{A}$: two positive inheritance algebras are related by a selection regime if and only if they have the same balanced form. For M merely nonnegative the same conclusion holds provided M has total support, and the scaling factors are unique up to a positive scalar on each fully indecomposable block.

Proof. Existence and uniqueness of positive diagonal matrices D_1, D_2 with D_1MD_2 doubly stochastic, and the uniqueness of D_1, D_2 up to reciprocal scalars, are Sinkhorn's theorem for positive M [28] and the theorem of Sinkhorn and Knopp [29] in the nonnegative case with total support; see also Brualdi, Parter and Schneider [30] for the version with prescribed row and column sums, and [35] for the classification of nonnegative matrices under diagonal equivalence. Setting $u = \text{diag}(D_1)$ and $v = \text{diag}(D_2)$, the structure matrix of $\mathcal{A}^{u,v}$ is D_1MD_2 , which proves existence. Two algebras are in the same selection orbit exactly when their structure matrices are diagonally equivalent, and by uniqueness the doubly stochastic representative of the orbit is well defined, whence the last assertion. $\square$

The biological status of the balanced form should be stated precisely. It is not a state the population evolves toward, and it is relative to the chosen natural basis, hence to the chosen resolution of genotypes; it is a canonical representative, in the spirit of a normal form, whose role is comparative. Two inheritance mechanisms measured in different laboratories under different, possibly unknown, selective environments are selection-equivalent if and only if their balanced forms coincide, so the balanced form is the description of the mechanism with all main effects of parental productivity and offspring survivability normalized away — a selectively neutralized version of the data. What remains in it is exactly the interaction structure, which by Theorem 5.4 is the selection-invariant content; in the 2×2 case of Section 8 the balanced form displays the single invariant as a canonical mutation rate. The balanced form is not in general reachable by a change of natural basis: row stochasticity alone imposes n conditions and double stochasticity $2n - 1$, against the n parameters available in Lemma 2.2. The extra n parameters of selection are what make the normalization possible, which is another way of seeing that selection is a strictly larger group action than isomorphism. In practice the balanced form is computed by the

Sinkhorn–Knopp iteration, which alternately normalizes row and column sums and converges for every matrix with total support [29]. The balancing pair (u, v) is a normalization device and need not be an environment any organism could experience; the constraints of Section 3 apply to it as to any other regime, and the normal form is useful because it is canonical, not because it is realizable.

7. IDEALS, HEREDITARY CLASSES AND LETHALITY

We turn to the action of selection on the ideal structure of the inheritance algebra, where the dichotomy between what selection fixes and what it moves is sharpest. Proposition 7.1 shows that a non-degenerate regime preserves every graph-determined invariant; Proposition 7.2 shows that this preservation does not extend to non-basic ideals; and Proposition 7.3 analyses the boundary case of lethal regimes, which alter the digraph itself.

Proposition 7.1. *Let (u, v) be a selection regime with all u_i, v_j nonzero. Then $\Gamma(\mathcal{A}^{u,v}, \mathcal{B}) = \Gamma(\mathcal{A}, \mathcal{B})$. Consequently $\mathcal{A}$ and $\mathcal{A}^{u,v}$ have the same basic ideals relative to $\mathcal{B}$, the same hereditary and hereditary saturated subsets, the same lattice of graph-determined ideals in the sense of [9], and $\mathcal{A}^{u,v}$ is non-degenerate, perfect, irreducible or simple exactly when $\mathcal{A}$ is. The optimal decomposition of [7] into irreducible components has the same index set for both.*

Proof. $a_{ij}^{u,v} = u_i a_{ij} v_j$ vanishes if and only if a_{ij} does, so the digraphs coincide. Basic ideals relative to $\mathcal{B}$ are the spans of hereditary subsets [8], hereditary and hereditary saturated subsets are defined from the digraph, and the correspondence of [9] between ideals and hereditary subsets is a statement about the digraph; non-degeneracy is the condition that no row of the structure matrix vanishes, perfectness that the structure matrix is invertible, which is preserved since $\det(\text{diag}(u)M \text{diag}(v)) = \det(M) \prod_i u_i \prod_j v_j \neq 0$ if and only if $\det M \neq 0$; irreducibility and simplicity are characterized graph-theoretically in [7, 9]. $\square$

Proposition 7.2. *Non-basic ideals are not preserved. Let $\mathcal{A}$ have natural basis e_1, e_2 and $e_1^2 = e_2^2 = e_1 + e_2$, and let $I = \mathbb{K}(e_1 + e_2)$. Then $I = \mathcal{A}^2$ is an ideal of $\mathcal{A}$, but for the pure viability regime $u = (1, 1)$, $v = (1, \alpha)$ with $\alpha \neq 1$, the subspace I is not an ideal of $\mathcal{A}^{1,v}$.*

Proof. In $\mathcal{A}$, $(e_1 + e_2)e_1 = e_1^2 = e_1 + e_2 \in I$ and likewise $(e_1 + e_2)e_2 \in I$, so I is an ideal. In $\mathcal{A}^{1,v}$ the structure matrix is $\begin{pmatrix} 1 & \alpha \\ 1 & \alpha \end{pmatrix}$, so $(e_1 + e_2) \circ e_1 = e_1 \circ e_1 = e_1 + \alpha e_2$, which lies in I only if $\alpha = 1$. $\square$

The degeneracy of the example is not incidental: non-basic ideals arise only through numerical coincidences among structure constants. The ideal I of Proposition 7.2 exists because the two rows of the structure matrix happen to be equal, a coincidence with no counterpart in the digraph, and an arbitrarily small viability difference between the two genotypes destroys it. The genotype classes that survive every selective environment are exactly the hereditary ones, that is, the classes closed under inheritance. This is a structural argument for the primacy of basic ideals in the classification programme of [8]: they are the ideals with selective meaning.

Lethality behaves differently, because it is not an invertible regime: it lies outside the group of Section 3, the rescaling rule does not apply to it, and the results of Sections 4–6 do not extend to it. The following proposition treats it directly.

Proposition 7.3. *Let $L \subseteq \{1, \dots, n\}$ be nonempty and let (u, v) be lethal on L : $v_j = 0$ for $j \in L$ and all other entries of u, v nonzero. Write $\Gamma' = \Gamma(\mathcal{A}^{u,v}, \mathcal{B})$. Then:*

- (i) $\mathcal{A}^{u,v}$ is an evolution algebra with natural basis $\mathcal{B}$, and Γ' is obtained from $\Gamma = \Gamma(\mathcal{A}, \mathcal{B})$ by deleting every edge whose head lies in L . Each $j \in L$ becomes a vertex without incoming edges.
- (ii) $\mathcal{A}^{u,v}$ is degenerate if and only if some parent's entire offspring support is lethal, that is, some row i of M has $\{j : a_{ij} \neq 0\} \subseteq L$; in that case $e_i \circ e_i = 0$, and the uniqueness statement for the optimal decomposition of [7], which requires non-degeneracy, no longer applies.
- (iii) The hereditary subsets of Γ' are exactly the sets S such that every Γ -edge $i \rightarrow j$ with $i \in S$ has $j \in S \cup L$. In particular every hereditary subset of Γ is hereditary in Γ' , and the new basic ideals of $\mathcal{A}^{u,v}$ are the spans of those S that are Γ' -hereditary but not Γ -hereditary: the genotype classes whose only escape routes led to lethal types. Lethal selection therefore creates evolutionarily closed genotype classes, and never destroys one.

(iv) *If the deletion of the edges into L leaves Γ' without directed cycles, then $\mathcal{A}^{u,v}$ is nilpotent, by the cycle criterion of [10], and the extinction it encodes is dynamical as well as algebraic: the structure matrix $M^{u,v}$ is then nilpotent, so in the linear, density-independent reading of the rates the unnormalized abundance vector $p(0)(M^{u,v})^t$ vanishes for $t \geq n$ and the population is extinct after at most n generations. Lethal selection aimed at every self-replacing cycle of the mechanism thus drives both the algebra and the population to extinction.*

Proof. (i) The relations $e_i \circ e_j = 0$ ($i \neq j$) and $e_i \circ e_i = u_i \sum_k v_k a_{ik} e_k$ are again of the form of Definition 2.1; Definition 2.1 does not require the squares to be nonzero. The entry $a_{ik}^{u,v} = u_i a_{ik} v_k$ vanishes for $k \in L$ and is nonzero exactly when a_{ik} is, for $k \notin L$; this is the stated edge deletion.

(ii) $e_i \circ e_i = 0$ if and only if $a_{ik} v_k = 0$ for all k , which given the support of v means $a_{ik} = 0$ for all $k \notin L$. The uniqueness theorem for the optimal decomposition in [7] is stated for non-degenerate algebras.

(iii) S is hereditary in Γ' when no Γ' -edge leaves S . The Γ' -edges are the Γ -edges with head outside L , so the condition is that every Γ -edge from S has head in $S \cup L$. If S is Γ -hereditary the condition holds with L unused; the difference set is as described, and basic ideals are spans of hereditary subsets [8].

(iv) By [10] a finite-dimensional evolution algebra whose digraph has no directed cycles is nilpotent; a lethal set meeting every cycle removes all cycles, since each vertex of a cycle is the head of one of its edges. For the dynamical statement, order the vertices topologically with respect to Γ' ; the matrix $M^{u,v}$ is then strictly triangular, hence $(M^{u,v})^n = 0$. $\square$

The sterile case is parallel. For a sterile set L' , that is $u_i = 0$ for $i \in L'$, every edge with tail in L' is deleted, each $\{i\}$ with $i \in L'$ becomes hereditary, and the analogue of (iii) reads that S is hereditary in the new digraph precisely when every Γ -edge $i \rightarrow j$ with $i \in S \setminus L'$ has $j \in S$.

8. A THREE-GENOTYPE RESISTANCE PATHWAY

This section illustrates the main results on a single inheritance mechanism, computing in turn its moduli, its invisible and visible regimes, the induced frequency dynamics, its selection-invariant, its balanced form, and its ideal structure under lethality. Consider an asexual haploid

lineage with three genotypes arranged as in the classical two-step pathway to drug resistance: 1 the susceptible wild type, 2 a first-step mutant, 3 the fully resistant double mutant, which has lost the ability to revert. Let μ be the forward mutation probability per replication and ν the back-mutation probability from 2 to 1. The inheritance algebra $\mathcal{A}$ has natural basis e_1, e_2, e_3 and structure matrix

$$M = \begin{pmatrix} 1-\mu & \mu & 0 \\ \nu & 1-\mu-\nu & \mu \\ 0 & 0 & 1 \end{pmatrix}, \quad \mu = 0.02, \nu = 0.01.$$

The digraph has the six edges $1 \rightarrow 1$, $1 \rightarrow 2$, $2 \rightarrow 1$, $2 \rightarrow 2$, $2 \rightarrow 3$, $3 \rightarrow 3$ (Figure 1, left), so $n = 3$ and $m = 6$. Since $\det M = 0.9504 \neq 0$ the algebra is perfect, so by Remark 4.2 diagonal and abstract isomorphism coincide here up to genotype relabelling and every detectability statement below is unconditional; and since Γ is weakly connected with a loop at every vertex, both the sharp form of Theorem 4.4 and Proposition 4.7 apply.

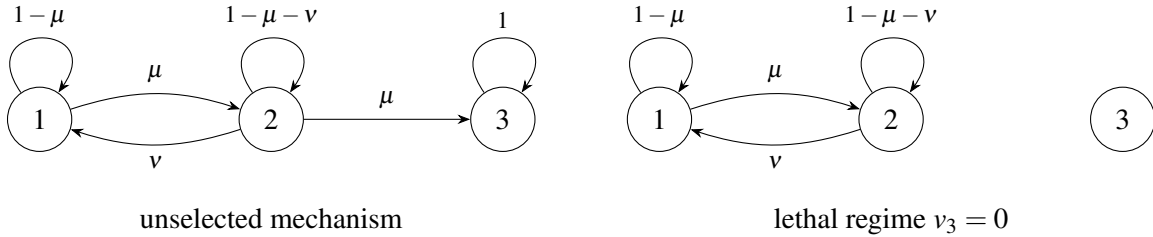


FIGURE 1. The three-genotype resistance pathway. Left: the digraph of the inheritance mechanism, with loops recording replication fidelity. Right: the digraph after a regime lethal to the resistant type, which deletes every edge into genotype 3; the susceptible pair $\{1, 2\}$ becomes hereditary, hence an evolutionarily closed class (Proposition 7.3).

Moduli. Here $\ker B_\Gamma = 0$: the loops force $x_j = 2x_j$, hence $x = 0$ at every vertex carrying a loop, and the remaining relations then vanish. Thus $\text{rank } B_\Gamma = 3$ and by Theorem 5.1 the diagonal isomorphism classes of positive inheritance algebras on this digraph form a space of dimension $6 - 3 = 3$. The mechanism therefore has three genuinely structural degrees of freedom; the remaining three of its six rates are absorbed by relabelling.

Invisible selection. The bipartite graph $\beta(\Gamma)$ is connected and touches every index, so $\dim \ker C_\Gamma = 1$ and Theorem 4.4 applies in its sharp form: a regime is invisible if and only if $u_i v_i^2$ is constant. The invisible regimes form a group of dimension $\dim \ker C_\Gamma + \text{rank } B_\Gamma = 1 + 3 = 4$ inside the six-dimensional group of all regimes. Concretely, take the viabilities $v = (1, 2, 4)$, so that the first-step mutant survives twice and the resistant type four times as well as the wild type, and the compensating fecundities $u = (1, \frac{1}{4}, \frac{1}{16})$ required by the trade-off. The sixteenfold fecundity cost is chosen to keep the arithmetic transparent rather than for realism; any milder pair on the same curve is equally invisible, with a correspondingly milder effect on the dynamics. Then

$$M^{u,v} = \text{diag}(u) M \text{diag}(v) = \begin{pmatrix} 0.98 & 0.04 & 0 \\ 0.0025 & 0.485 & 0.02 \\ 0 & 0 & 0.25 \end{pmatrix},$$

and this is exactly the structure matrix of $\mathcal{A}$ in the rescaled natural basis $f_i = v_i^{-1} e_i$. The population is subject to strong, genotype-dependent selection, yet its inheritance algebra is unchanged up to isomorphism, and no algebraic invariant of the mechanism reveals that selection is acting.

Invisible in the algebra, visible in the dynamics. Invisibility does not mean the regime has no consequences. In the frequency dynamics of Section 4, a composition $p(t)$ is updated by $p(t+1) \propto p(t) \text{diag}(u) M \text{diag}(v)$, normalized to total frequency one. For the unselected mechanism M , whose rows are stochastic, genotype 3 is absorbing and reachable, so every initial composition with $p_2 > 0$ converges to $(0, 0, 1)$: the resistant type fixes. Under the invisible regime above, the $\{1, 2\}$ block of $\text{diag}(u) M \text{diag}(v)$ has trace 1.465 and determinant 0.4752, hence Perron root 0.9802, which exceeds the remaining diagonal entry 0.25; the long-run composition is the dominant left eigenvector, normalized to total frequency one,

$$(0.9234, 0.0746, 0.0020),$$

independently of the (interior) initial condition: the wild type dominates and the resistant type is held at a mutation–selection remnant. Figure 2 displays the divergence of the two trajectories from a common initial composition. This is the behaviour predicted by Proposition 4.7: the regime satisfies $u_i v_i^2 \equiv 1$ but $u_i v_i = (1, \frac{1}{2}, \frac{1}{4})$, so it is invisible without being dynamically equivalent to neutrality.

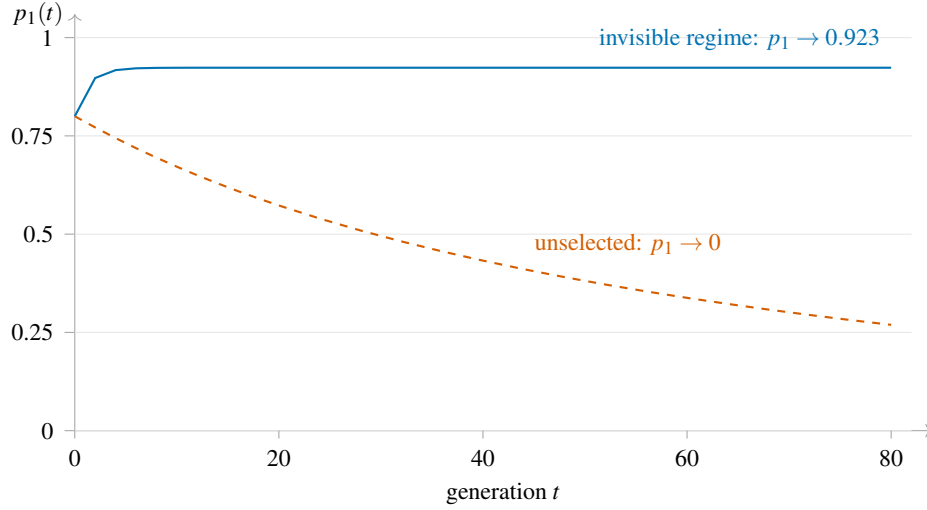


FIGURE 2. Wild-type frequency $p_1(t)$ from the initial composition $p(0) = (0.8, 0.15, 0.05)$. Under the unselected mechanism (dashed) the resistant type fixes and $p_1 \rightarrow 0$; under the algebraically invisible regime $u = (1, \frac{1}{4}, \frac{1}{16})$, $v = (1, 2, 4)$ (solid) the composition converges to $(0.9234, 0.0746, 0.0020)$. The two populations carry isomorphic inheritance algebras throughout.

The same regime that is undetectable in the inheritance algebra reverses the long-run outcome for the population. The example thus separates the two levels of description precisely: the algebra carries the structure of the inheritance mechanism, the frequency dynamics carry the composition of the population, and the invisibility theorem asserts that selection along the trade-off curve moves the second without moving the first.

Visible selection. By contrast, pure viability selection favouring only the resistant type, $u = (1, 1, 1)$ and $v = (1, 1, 2)$, is visible: the logarithmic displacement of the structure constants is not in $\text{Im } B_\Gamma$, the least-squares residual to that subspace being 0.775 rather than 0. Corollary 4.6 expresses this in general: uncompensated selection changes the isomorphism type.

Selection-invariants. With $m = 6$, $n = 3$ and $c(\Gamma) = 1$, Theorem 5.4 gives $6 - 6 + 1 = 1$ selection-invariant: the bipartite support graph has exactly one cycle, the 4-cycle on rows 1, 2 and columns 1, 2. Its monomial is the cross ratio $\rho_{12,21}$ (the quadruple $i = 1, j = 2, k = 2, l = 1$) on the wild-type/single-mutant block,

$$\rho = \frac{a_{12}a_{21}}{a_{11}a_{22}} = \frac{\mu\nu}{(1-\mu)(1-\mu-\nu)} = 2.10 \times 10^{-4},$$

the interaction between the two directions of mutation, normalized by the two fidelities. Its value is unchanged by the visible regime above, as it must be, and it is the one number an observer can extract from the mechanism knowing nothing about the selective environment. Everything else about the six rates can be produced by a suitable regime.

Balanced form. The full structure matrix lacks total support: the entry a_{23} lies on no positive diagonal of M , reflecting the irreversibility of the second mutation, so Theorem 6.1 does not apply to M as a whole. The reversible block on genotypes 1, 2 is fully indecomposable, and its balancing regime, normalized by $u_1 = 1$, is

$$u = (1, 1.42149), \quad v = (1.00582, 0.71488),$$

unique up to the reciprocal-scalar substitution, carrying the block to the doubly stochastic matrix

$$\begin{pmatrix} 0.985702 & 0.014298 \\ 0.014298 & 0.985702 \end{pmatrix},$$

symmetric because the block has a single cross ratio and balancing removes all main effects. The off-diagonal entry 0.014298 is the canonical mutation rate of the mechanism, the value the two asymmetric rates $\mu = 0.02$ and $\nu = 0.01$ share once the selective advantage distinguishing wild type from mutant has been normalized away; it is ρ in disguise, since for a symmetric doubly stochastic 2×2 matrix with off-diagonal ε one has $\rho = \varepsilon^2 / (1 - \varepsilon)^2$.

Ideals. The hereditary subsets of Γ are $\{3\}$ and $\{1, 2, 3\}$, so $\mathcal{A}$ has exactly one proper nonzero basic ideal, $\mathbb{K}e_3$: the resistant type, having lost reversion, is the only evolutionarily closed proper class. By Proposition 7.1 this is true in every selected algebra $\mathcal{A}^{u,v}$ with u, v positive, however extreme. Imposing lethality on the resistant type — biologically, a second intervention exploiting a collateral sensitivity of the resistant genotype — deletes the edges $2 \rightarrow 3$ and $3 \rightarrow 3$ (Figure 1, right); the susceptible pair $\{1, 2\}$ becomes hereditary and the selected algebra is degenerate, since the resistant row's entire support was lethal (Proposition 7.3(ii)). The mechanism closes over the susceptible types, which is the algebraic form of the treatment goal. Table 1 collects the numerical invariants of the mechanism.

TABLE 1. Invariants of the three-genotype resistance pathway. Dimensions are of real vector spaces, or of groups of regimes, as appropriate.

Quantity	Value
genotypes n , rates $m = \mathcal{E} $	3, 6
$\text{rank } B_\Gamma$, structural degrees of freedom $m - \text{rank } B_\Gamma$	3, 3
$\text{rank } C_\Gamma$, $\dim \ker C_\Gamma$	5, 1
dimension of all selection regimes	6
dimension of invisible regimes $\dim \ker C_\Gamma + \text{rank } B_\Gamma$	4
selection-invariants $m - \text{rank } C_\Gamma$	1
proper nonzero basic ideals	1

9. DISCUSSION

The formalism developed here inserts selection into the algebra of inheritance, not into the dynamical system the algebra generates. The central outcome is a rigidity theorem: the algebra sees a selection regime only through the combination $u_i v_i^2$, so an entire multi-parameter family of strong selective pressures leaves no algebraic trace. The prediction has an unambiguous form. If fecundity and viability advantages are measured for each genotype of a uniparental population and the products $u_i v_i^2$ are found to be equal across genotypes, then no property of the inheritance algebra distinguishes the selected population from the unselected one, notwithstanding that all genotype frequencies differ. Within the formalism the exponent is a structural consequence, not a fitted parameter (Remark 4.5), so what an experiment would be testing is the adequacy of the evolution algebra as a model of the inheritance process. The test itself requires genotype-resolved measurements of both fitness components in a uniparental system — brood or division counts for the fecundities u_i and survival-to-reproduction assays for the viabilities v_j — of the kind produced by microbial experimental evolution and by mitochondrial heteroplasmy lines; the quantity to examine is the constancy of $u_i v_i^2$ across genotypes. The experimental difficulty should not be understated: standard competition assays estimate only the composite fitness $u_i v_i$, which by Proposition 4.7 is the dynamically relevant combination but not the algebraically relevant one, so the test requires life-stage-resolved data separating the

two channels. A failure of constancy admits two readings — selection is acting visibly, or the evolution-algebra model is inadequate for the system — and discriminating between them requires the independent fit of the inheritance model itself. Because departures from constancy act linearly on the moduli coordinates of Section 5, near-trade-off regimes are near-invisible, and the detectability of selection from structural data degrades continuously rather than abruptly.

Table 2 collects the dictionary between the biological and the algebraic sides of the paper.

TABLE 2. The correspondence established in this paper.

Biology	Algebra
selective environment (fecundity, viability)	regime $M \mapsto \text{diag}(u)M \text{diag}(v)$, a principal isotope
selection undetectable in the mechanism	$u_i v_i^2$ constant (Theorem 4.4)
selection without long-run consequence	$u_i v_i$ constant (Proposition 4.7)
features no environment can alter	cycle monomials, e.g. cross ratios (Theorem 5.4)
mechanism normalized across environments	doubly stochastic balanced form (Theorem 6.1)
genotype classes closed under inheritance	basic ideals, hereditary subsets (Proposition 7.1)
lethal intervention closing a class	edge deletion creating hereditary sets (Proposition 7.3)
guaranteed extinction	nilpotency of the selected algebra (Proposition 7.3)

Three limitations bound the results. First, the theory is one of regimes, not of trajectories: it classifies deformations of the algebra, and an invisible regime is in general not dynamically neutral, as the example of Section 8 shows by reversing the long-run composition of a population under an algebraically undetectable regime. Proposition 4.7 gives this separation a structural form — dynamical neutrality is cut out by $u_i v_i$ and algebraic invisibility by $u_i v_i^2$, and the two loci meet only in uniform regimes — but a full account of the dynamics of invisible regimes, in particular of the spectra realizable within one isomorphism class, remains open. Second, the invariant theory of Section 5 is developed over $\mathbb{R}_{>0}$. Over a general field the passage from λ_i^2 to λ_i requires square roots, and the relation $x_j = 2x_i$ along edges acquires torsion phenomena governed by the numbers $2^r - 1$ attached to cycles of length r , which is precisely the arithmetic appearing in the diagonal group scheme of Elduque and Labra [11]. A characteristic-sensitive

version of Theorem 5.1 would be a natural continuation, and over $\mathbb{F}_q$ the invariant lattice becomes a genuinely arithmetic object. Third, the model inherits the restriction of evolution algebras themselves to uniparental reproduction; Remark 4.5 indicates that the corresponding trade-off exponent changes for gametic algebras, and the classification of invisible regimes in the Mendelian and gonosomal settings is open — note that the two classes of algebras are genuinely distinct, classical Mendelian algebras not being evolution algebras although arbitrarily small perturbations of them are [36].

Several directions remain open. The interaction of selection with mutation admits the same treatment: mutation in the sense of Gonshor [20] and of Falcón, Falcón and Núñez [22] is an isotopy that adds edges to the digraph, whereas selection by Proposition 7.1 preserves it and by Proposition 7.3 can only delete edges through lethality; the composite operation on the lattice of hereditary subsets is monotone, and identifying its fixed points explicitly would give an algebraic counterpart of mutation–selection balance. The quasispecies reading of Remark 3.3 also admits development: since the cycle monomials are invariant under every change of fitness landscape, they are properties of the mutation scheme Q alone, and the balanced form of Theorem 6.1 furnishes a fitness-independent canonical representative of Q recoverable from data gathered under unknown selection. Whether the balanced normal form of Theorem 6.1 has a variational characterization, as the doubly stochastic scaling does through relative entropy, is a further question with a possible biological reading as a principle of minimal selective distortion. Three biological extensions fall outside the present family of regimes and mark its boundary: selection on parental survival between broods, which acts on the lineage rather than on a single reproduction event and does not factor as $u_i v_j$; interactions in which fecundity depends on the offspring genotype, which break the separability of the two channels; and frequency-dependent selection, in which u and v are functions of the composition p , so that the deformation leaves the category of fixed isotopies altogether. Finally, the results transfer verbatim to any setting in which a finite-state reproduction or transition mechanism is deformed by row and column weights; discrete models of neural population turnover, or of clonal dynamics in tissue, carry the same structure, and the separation between the graph-determined structure and the cycle-monomial invariants, neither of which any weighting can move, carries over without change.

10. CONCLUSIONS

This paper has introduced natural selection into the algebraic theory of uniparental inheritance and determined exactly what the inheritance algebra can and cannot record of it. A selection regime — fecundity weights on parents, viability weights on offspring — deforms an evolution algebra within the class supported on its digraph, and the deformation is undetectable in the isomorphism type precisely along the trade-off $u_i v_i^2 = \text{const}$, the exponent being forced by the quadratic encoding of uniparental reproduction. The quantities that no selective environment can alter are the cycle monomials of the bipartite support graph, cross ratios in the generic case; every positive mechanism possesses an essentially unique selectively balanced normal form; and the genotype classes closed under inheritance are immune to every invertible regime, while lethal regimes create new closed classes and can force extinction, algebraically as nilpotency and dynamically within n generations. Because algebraic invisibility and dynamical neutrality are governed by different exponents and are transversal, structurally cryptic selection is generically consequential for the fate of the population, as the resistance-pathway example shows by reversing fixation. For mathematical biology the framework supplies a computable dictionary (Table 2) translating questions about selective environments — detectability, robustness, normalization, containment, eradication — into invariants of a single algebraic object, and it poses the corresponding questions for sexual inheritance, frequency-dependent selection and finite base fields.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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