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The Chrysene Formalism as Candidate Mathematics and Candidate Biogenesis: A Quantitative and Categorical Survey of Volume 1, Number 2

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Abstract

This paper is the editorial introduction to Volume 1, Number 3 of the *Annals of the Chrysene Formalism* and a retrospective, categorical, and quantitative survey of the twenty-one papers of Volume 1, Number 2. Number 2 differs from Number 1 in three measurable respects: its subject matter concentrates on the combinatorial origin of the genetic code; its mean paper length is 32.7 pages against 12.5; and every paper was reviewed under the orthogonal criteria of mathematical validity, framework concordance, and chemical admissibility, with no paper under the undifferentiated Level 1 protocol. Six papers — those carrying the critical formalism and the critical genetic-code results — received multi-pass review; fifteen received a single orthogonal round of editor review and revision. We formalize both tiers, state precisely what each certifies, and record the consequence-weighted rule by which papers were allocated between them. The corpus is classified by the categories, basis of argument, and formal techniques of the predecessor survey, extended conservatively where Number 2 required it. The genetic-code results are stratified into combinatorial theorems that use no code table, constructions that take a published table as input, and chemical mechanisms stated under named premises; for the first stratum we give complete proofs of the registry-class count and of the even-fibre parity obstruction. We argue that Number 2 advances the pure-mathematics thesis through new proved results and printed self-corrections, and sharpens the biogenesis thesis by replacing the Identification Hypothesis, within the code sub-series, by narrower premises that terminate in specific measurements. Neither thesis is established. We close by setting the program of Number 3: the protocell, its upstream material sources, and the representation of the formalism's mathematics in protocell components, each such representation stated as a realization hypothesis rather than as an identity.

Keywords: Chrysene Formalism; genetic code; registry classes; frame group; parity obstruction; protocell; orthogonal review; AI-augmented peer review; biogenesis; bibliometric survey.

1 Introduction: The Editorial Mandate after Number 2

The predecessor survey [Sch26l] stated two theses against the twelve-axiom core of [Sch26m]: that the axiomatic system constitutes a candidate field of pure mathematics (Thesis A), and that its reference molecule is worth pursuing as a candidate mechanism of biogenesis (Thesis B). It stated both with their unproved premises attached, and it identified the Identification Hypothesis Φ and the absence of experimental synthesis as the largest gap beneath Thesis B.

Volume 1, Number 2 comprises the twenty-one papers indexed 39–59, spanning pages 476–1162. Relative to Number 1 it changed three things at once: what was studied, at what length, and under what review. This paper records those changes as a checkable classification and states what each change does and does not establish. Its objectives are:

1. to record the provenance role of the patent filings in Number 2, and to correct the predecessor survey (Section 2);
2. to recall, with proofs where they are short, the results by which Number 2 extended the formal core (Section 3);
3. to define the two orthogonal review tiers of Number 2, state what each certifies, and record the rule by which papers were allocated between them (Section 4);

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4. to report the corpus's quantitative and categorical structure (Sections 5–6);
5. to restate Theses A and B against the Number 2 evidence, with the genetic-code results stratified by logical dependence (Section 7);
6. to report the evidence Number 2 adds to the constrained-collaborator argument (Section 8);
7. to state the corpus's limitations without euphemism (Section 9); and
8. to set the program of Number 3 (Section 10).

2 Provenance and Corrections

In Number 1 the patent record [Sch25a, Sch25b] fixed the reference structure against which chemical admissibility H is evaluated. In Number 2 it also supplies specific structural data used inside proofs. Two instances are load-bearing.

1. The chain-polarity arrow of [Sch26e]: US 12,473,247 B2 exhibits a $(6, 12)$-disubstituted chrysene remnant on adenine that anchors a phospholipid bilayer and from whose poly-A tail a coding strand departs. Under the identification of that arrow with reversal, the residual frame group is trivial and the pairs (class, relative frame) number 64.
2. The base assignment of [Sch26q], under which the orientation pattern of a chrysene stack is named by nucleobases, is the assignment specified in the filing.

Both uses are *documentary*: they import a structure from an external record that the review process did not generate. Neither is experimental evidence that the structure forms. We retain the qualification of [Sch26e] without change: if the identification of the arrow is refused, two lemmas stand and the corresponding target remains open.

Remark 1 (Corrections to the predecessor survey)**.** *Following the precedent of [Sch26l], which recorded a citation inconsistency in [Sch26m], we record the following corrections to [Sch26l]. None affects a result.*

1. *The final paragraph of its Section "Looking Ahead" terminates mid-sentence. The completion, supplied here by the editor, is that the Identification Hypothesis and the absence of experimental synthesis are not addressed by either opening paper of Number 2, and are not, at the time of that writing, addressed by any paper scheduled for Number 2.*
2. *The paragraph introducing its pipeline figure is printed twice in succession.*
3. *Its first-page footer reads "First published . . . Vol. 1, No. 1"; it should read No. 2.*
4. *Its PDF metadata title is that of [Sch26t].*
5. *Its appendix on operator algebras refers the sequence algebra to the section on the review pipeline; the intended reference is the section on mathematical preliminaries.*

3 The Formal Core as Extended by Number 2

We recall the results of Number 2 on which later sections depend. Results whose proofs are short are proved here; the others are stated in the notation of their source and cited.

3.1 The encoded stack and the frame group

Definition 1 (Marker assignments and frame group)**.** *Let $N \geq 1$. A* stack *of $2N$ sites carries a binary marker at each site; its* marker assignments *form the set $\Omega_N := \{0,1\}^{2N}$. Define involutions of Ω_N by*

$$\varphi(x)_i := 1 - x_i, \qquad \rho(x)_i := x_{2N+1-i} \qquad (1 \leq i \leq 2N). \tag{1}$$

The frame group *is $\mathrm{Fr} := \langle \varphi, \rho \rangle$. The maps φ and ρ are involutions, and they commute, since $\varphi\rho(x)$ and $\rho\varphi(x)$ both have i-th coordinate $1 - x_{2N+1-i}$. As $\varphi \neq \rho$, $\mathrm{Fr} = \{1, \varphi, \rho, \varphi\rho\} \cong (\mathbb{Z}/2)^2$. The orbits of Fr on Ω_N are the* registry classes.

Definition 1 is the presentation of [Sch26s], with φ acting as complementation, consistent with its use in [Sch26e]. By the maximal-frame-invariant theorem of [Sch26p], every quantity attributable to the assembly rather than to its reading factors through the quotient Ω_N/Fr.

Theorem 1 (Registry-class count [Sch26s])**.** *For every $N \geq 1$:*

1. *$|\Omega_N/\mathrm{Fr}| = 2^{2N-2} + 2^{N-1}$;*
2. *every orbit has cardinality 2 or 4, and none has cardinality 1;*
3. *exactly 2^N orbits have cardinality 2, and $2^{2N-2} - 2^{N-1}$ have cardinality 4.*

In particular, for $N = 3$ there are 20 registry classes, 8 of cardinality 2 and 12 of cardinality 4; for $N = 4$ there are 72.

Proof. For $g \in \mathrm{Fr}$ let $\mathrm{Fix}(g) := \{x \in \Omega_N : gx = x\}$. We have $|\mathrm{Fix}(1)| = 2^{2N}$. Since $\varphi(x)_1 \neq x_1$ for every x, $\mathrm{Fix}(\varphi) = \varnothing$. A point of $\mathrm{Fix}(\rho)$ is a palindrome and is determined by $(x_1, \dots, x_N)$, so $|\mathrm{Fix}(\rho)| = 2^N$. A point of $\mathrm{Fix}(\varphi\rho)$ satisfies $x_i = 1 - x_{2N+1-i}$ for all i; because $2N$ is even no coordinate is paired with itself, so such a point is determined by $(x_1, \dots, x_N)$ and $|\mathrm{Fix}(\varphi\rho)| = 2^N$. Burnside's lemma [Rot95] gives

$$|\Omega_N/\mathrm{Fr}| = \tfrac{1}{4}\big(2^{2N} + 0 + 2^N + 2^N\big) = 2^{2N-2} + 2^{N-1},$$

which is (1). For (2), the stabilizer Fr_x of any x excludes φ. It cannot contain both ρ and $\varphi\rho$, since it would then contain their product φ. Hence $|\mathrm{Fr}_x| \in \{1, 2\}$ and the orbit of x has cardinality 4 or 2. For (3), $\mathrm{Fix}(\rho) \cap \mathrm{Fix}(\varphi\rho) \subseteq \mathrm{Fix}(\varphi) = \varnothing$, so exactly $2^N + 2^N = 2^{N+1}$ points have stabilizer of order 2; they fill $2^{N+1}/2 = 2^N$ orbits of cardinality 2. The remaining $2^{2N} - 2^{N+1}$ points fill $(2^{2N} - 2^{N+1})/4 = 2^{2N-2} - 2^{N-1}$ orbits of cardinality 4. □

Corollary 1 (Capacity ratio [Sch26v])**.** *For every $N \geq 1$,*

$$\frac{|\Omega_N/\mathrm{Fr}|}{4^N} = \frac{1}{4} + 2^{-(N+1)} < 1. \tag{2}$$

Consequently the classical sufficiency argument, that 4^N words must at least cover the products, distinguishes no value of N. The reading length three is not derived from it.

Proof. Divide Theorem 1(1) by 2^{2N}; the right side is at most $\frac{1}{4} + \frac{1}{4} < 1$. □

In [Sch26v] the stack length is fixed at six units ($N = 3$) on chemical grounds, independently of codons and of the alphabet size. The count 20 and the reading length 3 are then two consequences of one input; neither is used to justify the other. The same paper proves that the map from clusters to classes is a bijection, so a class is a physical cluster and not an equivalence class of descriptions. Two premises carry the product ceiling: that a product depends on the marker assignment alone, and that the pathway does not involve the initiator. If the frame data are data of the cluster rather than re-descriptions of it, the count is 32 rather than 20 [Sch26v].

3.2 The parity obstruction

Definition 2 (Class-functional assignment)**.** *Let W be a set of* 64 *words and $\beta : W \to \Omega_3$ a bijection. A map $c : W \to Y$ into any set Y is* class-functional with respect to β *if $c \circ \beta^{-1}$ is constant on every* Fr*-orbit of Ω_3.*

Proposition 2 (Even fibres [Sch26v, Sch26i])**.** *If c is class-functional with respect to some β, then $|c^{-1}(y)|$ is even for every $y \in Y$.*

Proof. $\beta(c^{-1}(y))$ is a union of Fr-orbits, each of cardinality 2 or 4 (Theorem 1(2)), and β preserves cardinality. □

Corollary 2. *Let c_{std} and c_{mt} be the standard and vertebrate mitochondrial genetic codes, regarded as maps from the* 64 *codons to the amino acids together with a stop symbol.*

1. *c_{std} is class-functional with respect to* no *bijection β, since $c_{\mathrm{std}}^{-1}(\mathrm{Met}) = \{\mathrm{AUG}\}$ and $c_{\mathrm{std}}^{-1}(\mathrm{Trp}) = \{\mathrm{UGG}\}$.*
2. *Every fibre of c_{mt} has even cardinality. Proposition 2 therefore does not exclude it.*

Even fibres are necessary, not sufficient, for class-functionality. Under the identification of [Sch26i], c_{mt} splits nineteen of the twenty registry classes, and so is not class-functional with respect to that β. Corollary 2(2) asserts only that parity is not the obstruction.

Proof. (1) is immediate from Proposition 2; note that the conclusion holds for every β, because fibre cardinalities do not depend on β. For (2), the vertebrate mitochondrial table [EO] assigns AUA to Met and UGA to Trp, so both fibres have cardinality 2. Leu, Ser, Ala, Gly, Pro, Thr, Val, Arg and the stop symbol (UAA, UAG, AGA, AGG) have fibres of cardinality 6 (Leu, Ser) or 4 (the others). The remaining ten amino acids — Phe, Tyr, His, Gln, Asn, Lys, Asp, Glu, Cys and Ile — have fibres of cardinality 2. □

Corollary 2 is the exact content of the statement, repeated across [Sch26v, Sch26i, Sch26f, Sch26q], that parity excludes the standard code and is silent on the mitochondrial one. A finer obstruction, one that sees multi-valued classes by a clause other than fibre parity, was sought in [Sch26f] and remains open.

3.3 Transversality

Proposition 3 (Transversality [Sch26i, Sch26k])**.** *Under the identification of [Sch26i], the partition of the* 64 *words into the* 20 *registry classes and their partition into the* 16 *codon blocks (words sharing their first two letters) are transverse: a class and a block meet in at most one word.*

By Proposition 3, a residue attached to a class is not thereby attached to a codon. The seed–propagate–refine construction of [Sch26i] crosses this gap, and in [Sch26k] the pair (word, residue) is shown to be minimal Neyman-sufficient for the excision map [LS50, Bas55].

3.4 Certified extension and transfer geometry

Definition 3 (Certification frontier [Sch26d])**.** *For a theorem θ with recorded proof routes, the* certification frontier $\mathrm{Front}_n(\theta)$ *is the family of inclusion-minimal sets of uncertified, admission-requiring premises over those routes.*

If $\varnothing \notin \mathrm{Front}_n(\theta)$, no recorded route supports assertoric certification of θ, and each frontier element yields a conditional theorem. In [Sch26d], theoretical scission is the least fixed point of a support operator on a directed proof-support hypergraph. It removes exactly the unsupported region when certified support is withdrawn, and it retains every theorem with a surviving grounded proof. This is the formal counterpart of the deferred-theorem convention of [Sch26l].

In [Sch26j], the unitary-orbit H_∞ distance between transfer realizations is an extended pseudometric whose zero set is transfer isomorphism, which is logically independent of molecular-graph isomorphism. Its well-posedness requires that the active region carry no mode embedded in the continuum of a second fibration yet orthogonal to every channel into it. The paper shows the formalism's own explicit model to have infinite gain. In [Sch26a], survival — robust stability together with invariance of the admissible domain — is certified by a single L^1 peak-gain ball under a uniform constraint-margin hypothesis [DDB95]. The integrated return amplitude is bounded below by π divided by the width of the composite spectrum, so the certifiable disturbance amplitude is bounded above by the fibration, not by the design.

Remark 2 (Growth of the deferred program)**.** *Number 2 adds twelve deferred targets in [Sch26j] and four in [Sch26a], two of them load-bearing. It records fourteen and twelve non-implications respectively. Targets 9.4 and 9.7 of the code sub-series remain open [Sch26f, Sch26e]. The infinite gain of the explicit model is the obstacle most directly relevant to Section 10: any physical realization claimed to survive persistent disturbance must first be shown to be well posed.*

4 Editorial Methodology: Two Orthogonal Tiers

4.1 Definitions

We retain the admissible foundational region $F_{\mathrm{adm}} = M \cap C \cap H$ and the criticism–revision–verification decomposition $(\mathrm{crit}(R), \mathrm{rev}(R), \mathrm{ver}(R))$ of [Sch26l].

Definition 4 (Review protocol)**.** *A* review protocol *is a finite sequence $(E_1, \ldots, E_k)$ of* review events*, each consisting of a review stage $s(E_\ell) \in \{M, C, H, E, \mathrm{Meta}\}$ applied to a manuscript state, followed by a revision of that state. Here M, C, H are the mathematical, concordance, and chemistry/domain stages, E is an editor stage assessing all three criteria, and* Meta *is the meta-review classifying each prior criticism as resolved, partially resolved, unresolved, or no longer applicable.*

Definition 5 (The two tiers of Number 2)**.**

1. *A paper is reviewed in tier* O_{m} *(*orthogonal, multi-pass*) if its protocol contains events with stages M, C, H, in that order, followed by an event with stage* Meta*. The stages may be run jointly or one at a time, and a revision that alters mathematical content returns the manuscript to M.*
2. *A paper is reviewed in tier* O_{s} *(*orthogonal, single-round*) if its protocol is a single event of stage E, assessing the manuscript against M, C and H, followed by one revision based on the referee comments.*

Proposition 4 (What each tier records)**.**

1. *In tier* O_{m}*, every criticism raised at M, C or H is examined by a later event, namely the meta-review.*
2. *In tier* O_{s}*, no criticism is examined by a review event other than the one that raised it.*

Proof. (1) The meta-review follows the M, C and H events and, by Definition 4, classifies each prior criticism. (2) The protocol has exactly one review event. □

Proposition 4 holds by construction of Definition 4. It states what the protocols are, not what any particular review did. Its empirical counterpart is the claim that every criticism raised in each of the six O_{m} reviews was in fact classified at meta-review, and that claim can be checked only where review-provenance records exist. With that distinction, the proposition states precisely the difference between the tiers. Both apply the orthogonal criteria; both record criticism and revision. Only O_{m} supplies an independent record that each repair was examined. Accordingly, membership in F_{adm} is *assessed* for every paper of Number 2 and *verified* for the six papers of tier O_{m}. Review-provenance records in the sense of [Sch26b] were kept where available.

4.2 The allocation rule

The following rule is a reconstruction, stated after the review of Number 2, of the judgments by which that review was allocated. Its test is its prospective application to Number 3 (Section 10).

Definition 6 (Consequence-weighted allocation)**.** *A paper j is assigned to O_{m} if at least one of the following holds:*

(a) Foundational: *j revises the axiomatic core, or constructs the object on which a subsequent sub-series rests.*

(b) Evidential: *j's principal result would, if correct, bear on matters outside the corpus. This covers agreement with a premise fixed before the result was obtained, and resolution of a defect identified by a predecessor.*

(c) Apparently natural: *j's principal result reproduces a pattern expected on independent grounds, and that pattern is not an input to j.*

Otherwise j is assigned to O_{s}.

Clause (c) rests on the observation that a result which looks natural is the result a reviewer is least inclined to contest; it is where confirmation is most costly. Clause (c) excludes results whose agreement with an observed pattern is explained by that pattern being an input. Such results declare their dependence themselves (Section 7.2). In particular, clause (c) does not select [Sch26i] or [Sch26n]. The agreement of their outputs with the vertebrate mitochondrial and standard tables is explained by demand read from, and settings fitted against, those tables, as both papers state.

Remark 3 (Application to Number 2)**.** *Clause (a) selects [Sch26m, Sch26p, Sch26s]. Clause (b) selects [Sch26s, Sch26v] and [Sch26u]; clause (c) selects [Sch26q]. The union is* $\{40, 44, 45, 48, 57, 59\}$*, which is the set of papers reviewed in O_{m}. Three applications illustrate the clauses.*

1. The sulfur pair. *[Sch26r] co-synthesizes the two sulfur-requiring structures on a single chrysene unit. In doing so it shows that homochirality is lost: the initiation point of the amino acid differs for one of the two sulfurs. [Sch26u] resolves this defect at a co-facial chrysene–chrysene junction, at which the internal sulfur's sense is forced and homochirality is retained. A paper that repairs a defect found by its predecessor carries the weight of both, and it was reviewed accordingly (clause (b)).*
2. Structural consistency. *[Sch26q] supplies the formation pathways of the twenty structures and returns results that appear natural: block degeneracy follows a rule at sixteen of sixteen blocks. It also recovers, from block structure alone, the base partition specified in the filing (clause (c)).*
3. The count twenty. *The filings associate chrysene clusters with coding before the count of Theorem 1 was available, and [Sch26v] fixes the carrier length on chemical grounds (clause (b)). The evidential weight of this agreement is assessed in Remark 7.*

Remark 4 (Relation to the stated scope)**.** *[Sch26l] designated full orthogonal review for three classes — framework revisions, computational or hardware assemblies, and healthcare claims — and Level 1 for all others. Number 2 departed from that designation in two respects. First, Level 1 was retired: every paper received orthogonal review, which narrows the admissibility gap further than was promised. Second, multi-pass review was allocated by Definition 6 rather than by subject class; in particular [Sch26h], a molecular crossbar proposal within the computational-assembly class, received O_{s}. Definition 6 supersedes the scope of [Sch26l]. Like that scope, it is an editorial risk judgment and not a theorem. It was recorded after the issue was reviewed, and it is stated here so that Number 3 can be allocated by it in advance.*

5 Quantitative Portrait of Volume 1, Number 2

Definition 7 (Corpus)**.** *Let $J := \{39, 40, \dots, 59\}$ index the papers of Volume 1, Number 2, and let $I := \{1, \dots, 38\}$ index those of Number 1. The Number 2* corpus *is the indexed family*

$$\mathcal{K}_2 := \big(\pi_j, \mathrm{pp}_j, \Gamma(j), \mathrm{Cat}(j), \mathrm{Basis}(j), T(j), \mathrm{Tier}(j), \mathrm{Mod}(j)\big)_{j \in J}, \tag{3}$$

where π_j, pp_j, $\mathrm{Cat}(j)$, $\mathrm{Basis}(j)$ and $T(j)$ are as in [Sch26l], over the vocabularies extended in Definition 8. $\Gamma(j)$ is the cluster of Section 6, $\mathrm{Tier}(j) \in \{\mathsf{O}_{\mathrm{m}}, \mathsf{O}_{\mathrm{s}}\}$ *(Definition 5), and* $\mathrm{Mod}(j)$ *is the reviewing model family. Table 1 lists $\mathcal{K}_2$.*

The corpus spans 687 pages, against 475 for the thirty-eight papers of Number 1. The mean paper length is therefore $687/21 \approx 32.7$ pages against $475/38 = 12.5$, a ratio of about 2.6. Because the Number 2 distribution is skewed by [Sch26c] (80 pp.), [Sch26m] (72 pp.) and [Sch26h] (64 pp.), we also report medians: 29 pages (range 9–80) against 11 (range 5–23). The six papers of tier O_{m} occupy 214 pages and the fifteen of tier O_{s} occupy 473. Papers appeared between 30 September and 11 October 2026.

5.1 Extension of the classification

Number 2 could not be classified within the vocabularies of [Sch26l]. Two papers, a survey and a review-methodology

Table 1: The Number 2 corpus $\mathcal{K}_2$. Cat: PM Pure Mathematics & Algebraic Foundations; CB Cosmological & Biological Emergence; QA Quantum Architectures & Computing; ED Editorial & Review Methodology. Basis: Mol molecular; Math mathematical; Meth methodological. Model family: Cl Claude (Opus 5.5, Opus 5.0, Sonnet 3.7); GPT ChatGPT 4.6; Gk Grok 4.6; Mix ChatGPT 4.6 (author side) with ChatGPT 4.6, Gemini 3.1 Pro (Extended) and Grok 4.6 (editor side). Model families are the same on both sides except for Art. 40.

Art.	Ref.	pp.	Cluster	Cat	Basis	Tier	Model
39	[Sch26l]	476–488	Γ_7	ED	Meth	O_s	Cl
40	[Sch26m]	489–560	Γ_1	PM	Math	O_m	Mix
41	[Sch26b]	561–581	Γ_7	ED	Meth	O_s	Cl
42	[Sch26d]	582–602	Γ_1	PM	Math	O_s	Cl
43	[Sch26j]	603–645	Γ_2	PM	Math	O_s	GPT
44	[Sch26p]	646–675	Γ_3	PM	Math	O_m	Cl
45	[Sch26s]	676–704	Γ_3	PM	Math	O_m	Cl
46	[Sch26a]	705–729	Γ_2	PM	Math	O_s	GPT
47	[Sch26g]	730–767	Γ_4	CB	Math	O_s	Cl
48	[Sch26v]	768–793	Γ_4	CB	Mol	O_m	Cl
49	[Sch26h]	794–857	Γ_6	QA	Mol	O_s	Cl
50	[Sch26i]	858–882	Γ_4	CB	Math	O_s	Cl
51	[Sch26k]	883–913	Γ_4	CB	Math	O_s	Gk
52	[Sch26e]	914–925	Γ_4	CB	Mol	O_s	Gk
53	[Sch26f]	926–934	Γ_4	CB	Math	O_s	Gk
54	[Sch26c]	935–1014	Γ_5	CB	Mol	O_s	Cl
55	[Sch26n]	1015–1047	Γ_4	CB	Math	O_s	Cl
56	[Sch26o]	1048–1075	Γ_5	CB	Mol	O_s	Cl
57	[Sch26q]	1076–1106	Γ_4	CB	Mol	O_m	Cl
58	[Sch26r]	1107–1136	Γ_5	CB	Mol	O_s	Cl
59	[Sch26u]	1137–1162	Γ_5	CB	Mol	O_m	Cl

case study, argue from neither chemistry nor a new formal result, and several techniques of Number 2 are absent from the twenty-element vocabulary $\mathcal{T}$. We therefore extend the classification, and we state the extension as a definition so that its effect on Number 1 is explicit.

Definition 8 (Extended classification)**.** *Let* $C' := C \sqcup \{\kappa_8\}$*, with* κ_8 *= Editorial & Review Methodology. Let* $\mathcal{B}' := \{\mathsf{Mol}, \mathsf{Math}\} \sqcup \{\mathsf{Meth}\}$*, and* $\mathcal{T}' := \mathcal{T} \sqcup \mathcal{T}_{\text{new}}$*, where* $\mathcal{T}_{\text{new}}$ *comprises eight techniques:*

- *combinatorics/matching theory;*
- *chemical graph rewriting/reaction theory;*
- *mathematical logic/model theory;*
- *linear systems/state-space theory;*
- *variational/max–min optimization;*
- *spectral/scattering theory;*
- *statistical inference;*
- *corpus and case-study coding.*

The extended maps $\mathrm{Cat}', \mathrm{Basis}', T'$ *on* $I \sqcup J$ *satisfy* $\mathrm{Cat}'|_I = \mathrm{Cat}$*,* $\mathrm{Basis}'|_I = \mathrm{Basis}$ *and* $T'|_I = T$*.*

Proposition 5 (Conservativity on Number 1)**.** *Every count, share, and cross-tabulation reported in [Sch26l] for* I *is unchanged under Definition 8.*

Proof. Each reported quantity is a function of $(\mathrm{Cat}, \mathrm{Basis}, T)$ restricted to I, which the extension leaves fixed. □

The cost of conservativity must be stated with it. For $\tau \in \mathcal{T}_{\text{new}}$ the count $|T'^{-1}(\tau) \cap I| = 0$ records that τ was not assessed on I, not that it is absent from I. Comparisons across issues for techniques in $\mathcal{T}_{\text{new}}$ are therefore lower bounds on the Number 1 side.

5.2 Distributions

Remark 5 (Empirical finding: concentration)**.** *By direct tabulation (Table 2),* $|\mathrm{Cat}'^{-1}(\kappa_{\cos}) \cap J| = 12 > |J|/2$*. The Cosmological & Biological Emergence share rises from* 34.2% *in Number 1 to* 57.1% *in Number 2, and the Pure Mathematics share from* 15.8% *to* 28.6%*. Four of the seven Number 1 categories have no Number 2 paper.*

Sixteen of the twenty-eight techniques of $\mathcal{T}'$ occur in Number 2. Thermodynamics and statistical mechanics, the most frequent technique of Number 1 (11 papers), and algebraic topol-

Table 2: Category distribution in Numbers 1 and 2, $|\mathrm{Cat}'^{-1}(\kappa)|$.

Category κ	No. 1	No. 2	Vol. 1
Cosmological & Biological Emergence	13	12	25
Pure Mathematics & Algebraic Foundations	6	6	12
Medical & Pharmacological Networks	6	0	6
Applied Topological Engineering	5	0	5
Cryptography & AGI Containment	3	0	3
Financial Networks & Systemic Liquidity	3	0	3
Quantum Architectures & Computing	2	1	3
Editorial & Review Methodology	0	2	2
Total	38	21	59

Table 3: The most frequent techniques in Number 2, $|T'^{-1}(\tau) \cap J|$, with Number 1 counts. A dagger marks $\tau \in \mathcal{T}_{\mathrm{new}}$, which was not assessed on Number 1 (Proposition 5); daggered rows support no comparison between issues.

Technique τ	No. 2	No. 1
Group theory / symmetry	11	8
Combinatorics / matching theory†	10	–
Non-commutative geometry	5	7
Chemical graph rewriting†	5	–
Graph theory / spectral graph theory	4	6
Mathematical logic / model theory†	3	–
Linear systems / state-space theory†	3	–
Variational / max–min optimization†	3	–

ogy (8 papers) do not occur. Further techniques with fewer occurrences: H_∞ robust control, operator algebras, spectral and scattering theory, statistical inference, and corpus coding (2 each); finite fields, category theory, and quantum chemistry (1 each).

On basis, $|\mathrm{Basis}'^{-1}(\mathsf{Math}) \cap J| = 11$ (52.4%), $|\mathrm{Basis}'^{-1}(\mathsf{Mol}) \cap J| = 8$ (38.1%), and $|\mathrm{Basis}'^{-1}(\mathsf{Meth}) \cap J| = 2$ (9.5%); Number 1 had 18, 20 and 0. Of the twenty-one papers, 6 (28.6%) were reviewed in O_m and 15 (71.4%) in O_s. Fifteen (71.4%) used the Claude family on both sides, three used Grok 4.6 on both sides, two used ChatGPT 4.6 on both sides, and one used several models.

6 Categorical Survey of Number 2

Because one category contains twelve of the twenty-one papers, the survey is organized by *cluster*, a partition of J finer than Cat' that follows the predecessor relations stated in the papers themselves (Figure 1).

Definition 9 (Clusters)**.** $\Gamma : J \to \{\Gamma_1, \dots, \Gamma_7\}$ *is the map with fibres*

$\Gamma_1 = \{40, 42\}$, $\Gamma_2 = \{43, 46\}$,
$\Gamma_3 = \{44, 45\}$, $\Gamma_5 = \{54, 56, 58, 59\}$,
$\Gamma_6 = \{49\}$, $\Gamma_7 = \{39, 41\}$,
$\Gamma_4 = \{47, 48, 50, 51, 52, 53, 55, 57\}$.

Proposition 6 (Non-collapse of basis in Number 2)**.** Basis' *is not constant on the fibre* $\mathrm{Cat}'^{-1}(\kappa_{\cos}) \cap J$*, nor on the cluster* Γ_4*.*

Proof. $47, 57 \in \Gamma_4 \subseteq \mathrm{Cat}'^{-1}(\kappa_{\cos})$, with $\mathrm{Basis}'(47) = \mathsf{Math}$ and $\mathrm{Basis}'(57) = \mathsf{Mol}$ (Table 1). □

The witnesses are chosen to avoid the one borderline classification of the issue. The proposition does not depend on the basis of [Sch26v]: within Γ_4, Art. 52 and 57 are Mol and Art. 47, 50, 51, 53 and 55 are Math.

The split in Number 2 is 7 molecular to 5 mathematical within Cosmological & Biological Emergence, against 12 to 1 in Number 1. Category and basis are therefore further from collapse in Number 2 than in Number 1. The basis of [Sch26v] is recorded as Mol because its thesis concerns the products of a physical cluster whose length is fixed on chemical grounds; its method is group-theoretic, and the classification is borderline. No result of this survey depends on it.

Γ_1**, foundations and certification.** [Sch26m] restates the formalism in twelve axioms and proves non-vacuity by an explicit chrysene model. [Sch26d] supplies the theory by which the formalism may grow strictly while its molecular anchor is held fixed.

Γ_2**, transfer geometry and survival.** [Sch26j, Sch26a] construct the transfer metrics of Section 3. Their survival certificate is the formal object that Section 10 proposes to realize as protocell homeostasis.

Γ_3**, the encoded stack and registry classes.** [Sch26p, Sch26s] construct the stack and prove Theorem 1. [Sch26s] explicitly declines any identification with the genetic code. It also refutes two coincidences of counting rather than using them: agreement of class counts between source and target is uninformative, and twenty classes agree with the twenty three-letter multisets only at $N = 3$.

Γ_4**, genetic-code combinatorics.** The largest cluster takes up the question Γ_3 declined. It treats the coarsening criterion [Sch26g], the capacity theorem [Sch26v], the seed construction and its statistical form [Sch26i, Sch26k], chain polarity [Sch26e], finer obstructions [Sch26f], conditional refinement [Sch26n], and codon placement [Sch26q]. Its results are stratified in Section 7.2.

Γ_5**, reaction-cell chemistry.** [Sch26c] gives an existence theory for cage-constrained transformation of

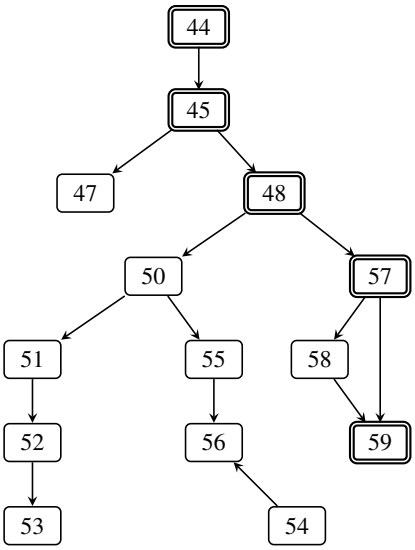


Figure 1: Principal predecessor relations among clusters Γ_3–Γ_5, as stated in the papers. An arrow $j \to k$ means that k takes a result of j as its point of departure. Double-bordered nodes were reviewed in tier O_{m}. The edge 58 → 59 is the homochirality repair of Remark 3(1).

the chrysene–adenosine complex by typed graph rewriting [EEPT06]. Its conditional witness reaches the connectivity C5–C_α(H)(NH_2)–C_β(= O)–O2′Ado with the chrysene C5–C6 bond retained; Table 4 describes this target, interpretively, as an amino-acyl–adenosine linkage. [Sch26o] makes its constraints medium-dependent. [Sch26r, Sch26u] treat the two sulfur-requiring structures. No paper in Γ_5 computes an energy or a barrier.

Γ_6**, dual-channel information topology.** [Sch26h] is the single Number 2 continuation of Number 1's computing cluster. It proves a finite neuromorphic consistency result on a corrected Hückel model of the chrysene π substrate, without attributing cognition to a molecular channel.

Γ_7**, methodology.** [Sch26l, Sch26b] are the predecessor survey and the review case study.

7 Two Foundational Theses Revisited

7.1 Thesis A

The three conditions of [Sch26l] for a candidate mathematical discipline were a non-vacuous foundation, an established core of proved results, and an actively pursued frontier. Number 2 strengthens the second and third.

1. *Proved results.* Theorem 1, Proposition 2 and its corollary, Proposition 3, the certification-frontier and scission theory of [Sch26d], and the transfer metrics and joint certificate of [Sch26j, Sch26a]. All are proved from the axioms together with explicitly stated hypotheses, and none uses the Identification Hypothesis.
2. *Frontier.* The deferred program grew (Remark 2), and the papers record their own defect ledgers and non-implications.

The disciplinary judgment by which a candidate field becomes an established one remains external to the journal, as [Sch26l] stated.

7.2 Thesis B: the genetic-code results by stratum

Definition 10 (Stratification)**.** *Let $\mathfrak{T}$ denote the set of published translation tables [EO] used in Number 2, and let $\mathcal{R}$ denote the principal genetic-code results of $\Gamma_4 \cup \Gamma_5$. For $r \in \mathcal{R}$ define $\sigma(r) \in \{1, 2, 3\}$ by the following clauses, applied in order:*

(3) $\sigma(r) = 3$ if r asserts chemical existence, selection, or asymmetry under named chemical premises;

(2) otherwise, $\sigma(r) = 2$ if an element of $\mathfrak{T}$ is a hypothesis of r or an input to a construction in r;

(1) otherwise, $\sigma(r) = 1$.

A table to which r is applied only as the object tested — as c_{std} is tested against Proposition 2 in Corollary 2 — is neither a hypothesis of r nor an input to it.

Because the clauses are applied in order, σ is a function on $\mathcal{R}$. A result that both asserts a chemical selection and is compared with observed tables, such as the forced placement of [Sch26q], lies in stratum 3.

Proposition 7 (Independence of stratum 1 from the code)**.** *Every result of stratum 1 holds for every assignment of residues to registry classes. In particular, Proposition 2 constrains every candidate code, observed or not.*

Proof. By Definition 10, no element of $\mathfrak{T}$ is a hypothesis of a stratum-1 result or an input to a construction in it, so its proof uses no property of any code. A table to which the result is applied enters only as the object of the conclusion. □

For stratum 2 the corresponding statement fails by definition, and the editorial position is the one the papers take themselves. Agreement of a construction's output with a table that is among its inputs is evidence of *consistency*, not of *derivation*.

- [Sch26g] states before its construction that its adjacency is built from the standard code, and that coarsenings exist for about seventy per cent of codes with the standard degeneracy profile.
- [Sch26i] states that, unlike its predecessor, it uses the standard code constructively.

Table 4: Principal genetic-code results of Number 2 by stratum (Definition 10) and review tier.

σ	Result	Ref.	Tier	Status
1	Twenty registry classes; orbits of size 2 or 4	[Sch26s]	O_m	Proved (Thm. 1)
1	Cluster–class bijection; product ceiling 20; reading length 3	[Sch26v]	O_m	Proved under two named premises; 32 if frames are data
1	Even fibres; the standard code is not class-functional	[Sch26v]	O_m	Proved (Prop. 2, Cor. 2)
1	Parity bounded: silent on the mitochondrial code, which splits 19 of 20 classes	[Sch26i]	O_s	Proved
1	Class and block partitions transverse	[Sch26i, Sch26k]	O_s	Proved
2	Amino/keto partition admits a coarsening; one of 128 bijections selected	[Sch26g]	O_s	Coarsening, not derivation
2	Seed–propagate–refine yields the vertebrate mitochondrial table	[Sch26i, Sch26k]	O_s	Demand read from the standard table
2	Three-valued conditional refinement; both codes as settings	[Sch26n]	O_s	All 27 tables in range; third setting occupied
3	Conditional reachability of an amino-acyl–adenosine linkage	[Sch26c]	O_s	Existence under hypotheses
3	Chamber decomposition; handedness constant on chambers	[Sch26o]	O_s	Necessary conditions; one table-free prediction
3	Structure space; forced placement of the sulfur pair	[Sch26q]	O_m	Placement unique, matches neither code
3	Sulfur pair on one unit; disulfide exclusion at 1.02 Å	[Sch26r]	O_s	Homochirality lost; aldehyde/alcohol asymmetry
3	Co-facial junction; frame, start, and homochirality	[Sch26u]	O_m	Five named premises; no energies

- [Sch26n] states that widening the outcome set brings all twenty-seven tables into range, which is a weaker prediction with a perfect score and not a better result. It locates its evidence instead in the occupation, by four published tables, of a third setting that nothing required to be occupied.

Remark 6 (Structural, not chronological, ordering)**.** *In [Sch26i, Sch26n] the vertebrate mitochondrial table is the output of the simpler construction, and the standard table is reached by further divisions or as a second setting of the same refinement. This ordering is* structural*. The mitochondrial case was treated first because it poses fewer questions, the standard case then being resolved as a setting of the three-valued refinement. It is not a claim about evolutionary priority, and it does not contest the phylogenetic account in which vertebrate mitochondrial reassignments are derived from the standard code [OJWM92, KFL01].*

Remark 7 (On the status of the count twenty)**.** *Theorem 1 yields twenty classes for the six-unit cluster. The filings [Sch25a, Sch25b], published in 2025, associate chrysene clusters with coding. The count was first published in [Sch26s] in October 2026. Four qualifications determine what this agreement is evidence of.*

1. *The carrier was fixed independently of the count: by the filings, and in [Sch26v] on chemical grounds. The integer* 20 *is therefore not a fitted parameter.*
2. *The number of proteinogenic amino acids was known before the count. The agreement is a retrodiction, not the prediction of an unknown quantity.*
3. *Twenty is a ceiling. Equality requires in addition that every class produce an amino acid and that distinct classes produce distinct ones [Sch26v].*
4. *The count is* 32*, not* 20*, if the frame data are data of the cluster rather than re-descriptions of it.*

The agreement is therefore consistency with a premise fixed in advance*. That is stronger than a post-hoc fit and weaker than a prediction. We record it in that category and in no stronger one.*

What Number 2 changes for Thesis B is the form of its premises, not their discharge. The Number 1 cluster was conditional throughout on Φ. Within Γ_4 and Γ_5, Φ is replaced by premises named paper by paper, and [Sch26k, Sch26e] state that they do not use Φ. The sub-series ends in an undecided alternative [Sch26q]: either the consistency relation is wrong at two exchanges, or the observed codes stand two exchanges

from an assignment that structural consistency selects and that is neither of them. [Sch26u] inherits this alternative whole. It also ends in a short list of measurements:

- the remnant oxidation-level asymmetry of [Sch26r], decidable by a single product analysis;
- the chamber-wise handedness of [Sch26o];
- the filter-independent assignments of [Sch26g], one decidable by a single measurement.

A program that ends in a list of measurements that could fail is the honest form of progress toward Thesis B.

8 AI as a Constrained Collaborator: Number 2 Evidence

[Sch26l] argued that binding generation to an external reference changes what review detects, on the evidence of one retrospective case study [Sch26b]. Number 2 adds evidence of a different kind: papers that correct their predecessors in print.

Remark 8 (Empirical finding: printed self-correction)**.** *By inspection of the Number 2 papers:*

- *[Sch26j] records five corrections to the prior corpus in a concordance table, together with a self-identified defect ledger.*
- *[Sch26a] records three corrections to [Sch26j], one of them to a hypothesis on which that paper's invariance theorem rests.*
- *[Sch26i] withdraws a stop-codon hypothesis of [Sch26v], and [Sch26n] withdraws a conjecture of its own.*
- *[Sch26r] identifies the loss of homochirality that [Sch26u] repairs.*
- *[Sch26s, Sch26g] refute coincidences of counting that would have favored their conclusions.*

A process evaluated only on internal coherence has no reason to produce such records; a process held to an external reference and to orthogonal criteria does. The records are therefore consistent with the constrained-collaborator thesis. They do not demonstrate its mechanism: no unconstrained arm exists against which the frequency of self-correction could be compared. The evidence is limited in the same ways as before. It comes from one coder and, for twenty of twenty-one papers, one model family per paper on both sides of review (Section 9.5).

9 Limitations and Open Problems

9.1 The admissibility gap, narrowed

Level 1 was retired in Number 2, so the gap of [Sch26l] no longer arises from an undifferentiated coherence judgment. By Proposition 4, membership in F_{adm} is verified by an independent review event for six papers and assessed in a single event for fifteen. Several stratum-2 and stratum-3 results on which Number 3 builds lie in the second group (Table 4). Each was assessed against all three criteria and revised on the referee's comments, and that is what this survey asserts of them.

9.2 The Identification Hypothesis and experimental confirmation

No paper of Number 2 proves Φ or reports synthesis, and no paper of Γ_5 computes an energy or a barrier. Experimental protocols have been developed for Number 3; experimental work is scheduled for Numbers 4 and 5. The editorial design is that the mathematics be completed first, so that experiment confirms rather than explores. That design carries one obligation, which we adopt: each prediction must be recorded, with its decision criterion, before the corresponding experiment is performed (Section 10).

9.3 Dependence of stratum 2 on published tables

Agreement of stratum-2 constructions with the published tables is evidence of consistency, not of derivation (Section 7.2). The undecided alternative of [Sch26q] is the sub-series's principal open problem.

9.4 The deferred program

The deferred program is larger after Number 2 than before (Remark 2). Its growth is evidence for Thesis A and a measure of what is not yet established. The infinite gain of the explicit model is an obstacle to every survival claim made of a physical realization.

9.5 Independence and reproducibility

Twenty of twenty-one papers used one model family on both sides of review, so the independence of author-side and editor-side review is, as in Number 1, independence of pass and not of system. The Claude entries span three model versions because model availability changed during use; this is a disclosure, not a source of independence. Review-provenance records were kept where available, not uniformly. The classifications of Sections 5–6 are the work of a single coder, and their vocabularies were extended during the survey (Definition 8).

9.6 Copying of the carrier

Number 2 treats the reading of the carrier and the production of residues from it. No paper treats the copying of the poly-A–chrysene carrier. A protocell account requires it.

10 Looking Ahead: Volume 1, Number 3

Number 3 turns to the protocell. It evaluates the upstream sources of the materials that Number 2 presupposes; it represents the formalism's mathematics in protocell components; and it positions the genetic-code results of Number 2 within that representation.

10.1 Upstream sources

Several Number 2 results are conditional on premises about inputs. In [Sch26r, Sch26u], sulfur arrives as a disulfide and does not afterwards migrate; in [Sch26o], the medium supplies constraint margins; throughout Γ_5, chrysene, adenosine, and phospholipid are assumed available in the stated configurations. These premises are where the account meets the world before any reaction occurs. Evaluating their upstream source converts premises about the medium into claims about supply, which can be checked.

10.2 Representation as hypothesis

Proposition 8 (Protocell statements are not consequences of the axioms)**.** *Let L be the signature of Axioms A_1–A_{12}, $L' \supsetneq L$ a signature containing a symbol for a protocell component, $\mathcal{A}$ the twelve axioms, and P an L'-sentence. Then $\mathcal{A} \models P$ if and only if every L'-expansion of every model of $\mathcal{A}$ satisfies P. In particular, if some expansion of some model of $\mathcal{A}$ falsifies P, then $\mathcal{A} \not\models P$.*

Proof. The models of $\mathcal{A}$ as an L'-theory are exactly the L'-expansions of its L-models, since $\mathcal{A}$ places no condition on the symbols of $L' \setminus L$. □

Remark 9 (An instance)**.** *Let $\mathfrak{R}^{\mathrm{ex}}$ be the explicit model of $\mathcal{A}$ that witnesses non-vacuity in [Sch26m], with structural state set X. Let $L' := L \cup \{\mathrm{Mem}\}$, with* Mem *a unary predicate on X read as "is a membrane state". Let P_{mem} be the sentence $\exists x \in X\, \mathrm{Mem}(x)$, the weakest claim any membrane representation requires. The expansion of $\mathfrak{R}^{\mathrm{ex}}$ interpreting* Mem *as $\varnothing$ falsifies P_{mem}. Hence $\mathcal{A} \not\models P_{\mathrm{mem}}$: even the existence of a membrane component must be supplied by a realization hypothesis. The same holds for every L'-sentence that implies P_{mem}. In particular it holds for any identification of the membrane states with a nonempty part of the boundary of Ω_{adm}.*

Proposition 8 fixes the form that every Number 3 statement linking the formalism to the protocell must take. Such a statement must be a deferred theorem in the sense of [Sch26l]: $\mathcal{A} \cup H_\rho \models P_\rho$ with $\mathcal{A} \not\models P_\rho$, where H_ρ is a named *realization hypothesis* for a representation ρ. Stating such a representation as an identity would reintroduce Φ under another name. The non-implication $d_C^*(x, y) = +\infty \not\Rightarrow$ autonomous physical scission of [Sch26l] is a specific instance: the boundary of the admissible domain is not, by itself, a membrane.

10.3 Position of the genetic-code results

Within the representation of Table 5, the Number 2 results take four positions.

1. *Carrier and reading.* Chain polarity orients the strand [Sch26e]; the co-facial junction sets the frame and the start, and retains homochirality [Sch26u].
2. *Capacity.* Theorem 1 and Proposition 2 are properties of the carrier. By Proposition 7, they hold in every protocell realization that contains it.
3. *Setting.* The settings of the conditional refinement [Sch26n] become compartment variables. Stratum 2 results become predictions exactly when a protocell model fixes those variables independently of the tables and then yields the setting.
4. *Placement.* The undecided alternative of [Sch26q] becomes a question the protocell can pose: whether constraints of supply or delivery at the boundary or at the junction select the observed placement over the structurally selected one.

10.4 Review and confirmation

Number 3 will be allocated between O_{m} and O_{s} by Definition 6, stated in advance. Every paper asserting a protocell representation satisfies clause (a). Its experimental protocols will be accompanied by a register of predictions, each with a decision criterion fixed before the experiments of Numbers 4 and 5. The register begins with the three measurements of Section 7.2.

11 Conclusion

Number 2 narrowed the journal's subject from biogenesis in general to the combinatorial origin of the genetic code. It reviewed every paper under orthogonal criteria, and it lengthened the papers roughly two-and-a-half-fold. Its strongest results are combinatorial theorems about the chrysene cluster: twenty registry classes of sizes two and four, and an even-fibre obstruction excluding the standard code from any class-functional

Table 5: Representations proposed for Number 3. Each row is a realization hypothesis H_ρ in the sense of Proposition 8, not an identity.

Protocell component	Corpus anchor	Formal object	What the hypothesis must supply
Boundary	Chrysene remnant anchoring a phospholipid bilayer [Sch25b, Sch26e]	Admissible domain Ω_{adm} and d_C^* (A_{12})	A physical mechanism for the boundary that $d_C^* = +\infty$ alone does not supply
Information carrier	Poly-A–chrysene complex; RNA with tethered chrysene [Sch26e, Sch26q, Sch26u]	Sequence algebra; encoded stack; registry classes [Sch26p, Sch26s]	Copying of the carrier (Section 9)
Production	Reaction cell [Sch26c, Sch26o, Sch26r, Sch26u]	Max–min margin reachability; chambers	The internal variables that fix the constraint margins
Compartment	Effective vessel volume; pH regimes [Sch26n]	Medium-dependent margins [Sch26o]	Whether interior and exterior realize the code settings in distinct chambers
Homeostasis	—	Survival certificate [Sch26j, Sch26a]	A realization of finite gain
Homochirality	Lattice step-defect; chamber handedness; co-facial junction	Oriented-locus chambers	Reconciliation of the mechanisms of Number 1 and Number 2
Division	—	Dynamical scission (deferred)	Not available until the deferred target is discharged

assignment. Both hold independently of any code table, and both were proved here in full. Its constructions recover the published tables they take as input. Its chemistry is stated under named premises, with no energy computed and no synthesis performed, and its central placement question is undecided.

Against Thesis A, Number 2 adds proved results, a larger frontier, and printed self-correction. Against Thesis B, it replaces an unproved global identification by local premises that end in measurements. Neither thesis is established. Number 3 places these results inside a protocell representation whose every link to the formalism is a stated hypothesis, and it evaluates the upstream sources of the materials on which the representation depends. The editorial mandate is unchanged: to supply the formal apparatus and the review architecture by which results that are true can be distinguished from results that only appear to be.

A Mathematical Literature Relevant to Number 2

As in [Sch26l], none of the subjects below is claimed to be novel in isolation. The purpose is to identify the established machinery each cluster of Number 2 draws upon.

A.1 Finite group actions and matchings

Theorem 1 is an application of Burnside's lemma to a Klein four-group acting on binary words [Rot95]. The coarsening criterion of [Sch26g] and the seed bound of [Sch26i] are statements about matchings in bipartite incidence structures, for which Hall's theorem [Hal35] supplies the deficiency formula used.

A.2 Statistical sufficiency

The minimal-sufficiency and ancillarity results of [Sch26k] use the Lehmann–Scheffé theory of sufficiency and completeness [LS50]. The non-applicability of Basu's theorem [Bas55] recorded there turns on the dependence of the frame coordinate on the class.

A.3 Spectral and scattering theory; robust control

The well-posedness criterion of [Sch26j] concerns modes embedded in a continuum; the standard framework is the limiting absorption principle [Agm75]. The H_∞ and peak-to-peak (L^1) gains of [Sch26j, Sch26a] are treated in [ZDG96] and [DDB95], respectively.

A.4 Graph rewriting

The reaction category of [Sch26c] is generated by typed graph-rewrite rules. The algebraic theory of such rules, including the double-pushout construction, is developed in [EEPT06].

A.5 The genetic code and its variants

The published translation tables are those maintained by NCBI [EO]. The frozen-accident account [Cri68], the evidence for code variation and its mechanisms [OJWM92], and the evolvability of the code [KFL01] supply the background against which Remark 6 is stated. The statistical optimality of the standard code [FH98] is relevant to any future claim that a construction selects it.

A.6 Protocells

The decomposition of Table 5 into container, carrier and metabolism follows the chemoton [Gán03] and its modern statements [SBL01, RCD+04].

B Verification and Formal Proof

Two artifacts accompany this article, each published with its own dossier.

1. The harness `verify_A89.py` executes 137 checks in sixteen blocks, in exact integer and rational arithmetic only; all pass. It recomputes Theorem 1 for $N = 1, \ldots, 8$, Proposition 2 over all 2^{20} unions of registry classes, Corollary 2 against NCBI tables 1 and 2, and every count, share, median and page figure of Section 5 from the Volume 1 ledger. Each printed decimal is certified by the bound $2|ns - rd| < d$, and each certificate fails when its figure is moved by one unit in the last place.

2. The Lean 4 file `acf-89-proof.lean` (Lean 4.12.0, core only) proves 85 statements by `decide`; `#print axioms` reports no axiom for any of them.

Both certify the formal content of this article and the arithmetic performed on its classifications. Neither certifies the classifications, which are editorial judgments (Section 9.5).

> **Remark 10** (The identification behind Proposition 3)**.** *Let the three letters of a codon occupy consecutive pairs of sites, and let each letter carry a marker pair. Over all* 24 *assignments of letters to marker pairs, the harness finds that Proposition 3 holds for every assignment. Both tables split exactly nineteen of the twenty classes, leaving* {AGU, UCA} *unsplit, for exactly the eight assignments under which complementation of markers is Watson–Crick complementation; under the other sixteen, both split all twenty. The statement following Corollary 2 is to be read under an identification of the first kind, as the use of complementation in [Sch26e] indicates.*

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