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*Seeded Assignments on the Chrysene Registry: Transversality, Third-Position Refinement,
and the Mitochondrial Code as Normal Form*

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Review scope

This file is the review record of Article 50. It is not a section of the paper. The object reviewed, in sequence, was fifteen concept outlines, of which five received a full pass (versions 3, 5, 7, 11 and 14); the drafted text of ten sections and three appendices; and the supplementary verification script. The architecture is [Sch26b, §4.3]. There is no author-reply section.

Scope of Review

The manuscript extends the framework and falls under [Sch26b, §4.5]. Its mathematics is light and its inheritance heavy. It imports a classification, a capacity bound and a parity obstruction,

and adds a matching argument, an enumeration and an audit. It uses the standard genetic code constructively, which neither predecessor did. Concordance was therefore expected to be active, and it was.

Compiled disposition

Seventy-six criticisms were raised across five pre-drafting passes, and all seventy-six are fully accepted. Forty-eight confirmed a caution the outline had itself anticipated. Twenty-eight were new: fifteen mathematical, twelve concordance, one chemistry. Eighteen numerical checks pass. The manuscript withdrew more than it added. One hypothesis of a predecessor is withdrawn, one prior corollary is bounded, two carriers are superseded rather than repaired, and a deferred pair is abandoned. Five corrections to figures circulated during development are recorded separately. Nine Targets remain open, three of them load-bearing.

Before the domain pass, not disposed

Three chemical claims a proof uses are referred. Clause (iii) of H_{teth} , the chain polarity, decides between sixty-four states and thirty-six; below sixty-four, Sections 5 to 7 have no object. $H_{\text{split-chem}}$ must account for two families of opposite sign; a size rule has been refuted. $H_{\text{lib-env}}$ must identify what decides release at UGA and AUA.

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1 The three questions

M: is each numbered statement valid at the strength claimed? A correct computation offered as establishing more than it establishes fails the test. *C*: does the manuscript contradict a prior statement, or silently weaken a structure a prior statement relies on, including register, naming and provenance? *H*: is the molecular interpretation admissible, and is every such claim confined to a remark entering no proof?

2 Stage *M* — mathematical review

Stage *M* — fifteen new items

Scope of claim, arithmetic, and one class of error the corpus has not previously recorded. The two items that changed the manuscript more than any others are not defects of proof. One defect was found by writing the verification script, after five review passes had confirmed the section.

Scope of claim. Against outline 5: excision applied to classes deleted codons, so every fibre of the composite was a subset of one class. In the standard code only methionine and tryptophan have all their codons within one class, and those are precisely the two the parity obstruction of [Sch26g] forbids a class-functional operator to assign. The construction could form fibres of the right shape only where it was forbidden to act. The assignment is separated from the repertoire, the fibres are freed, and the bound of twenty is relayed through the seeds. Against outline 14: normal form was presented as a property the genetic codes were found to have. It is the construction's range. Seeding, propagation and one refinement produce patterns (4) and (2,2) and nothing else. Section 7.1 now opens by saying so, and the section reports a test with a score rather than a discovery.

Arithmetic and calibration. A count of $16 + 4 = 20$ was offered as structure. It is arithmetic, the code having twenty residues, and was removed. A deferred pair was presented as chemically motivated and proved to be one of forty-three admissible pairs. A seed-map count of 3,326,976 was cited for a superseded construction. A figure of twenty-three tables was miscounted for twenty-two, and is not independent of the assignment it counts. A null giving a mean of 15.97 violations destroyed the structure it was meant to test and was replaced by a within-block null.

Found by coding. The demand construction was drafted informally and, when coded, proved inconsistent: two blocks in the same structural position were handled differently. Correcting it changed the seed count from eighteen to seventeen, the map count from 312 to 840, the spares from two to three, and removed a claim that arginine uniquely required two seeds. This is the first item in the corpus found by writing a verification script rather than by reading the text.

3 Stage *C* — concordance review

Stage *C* — twelve new items

Four changed the manuscript’s structure. Two carriers are superseded, not repaired. Three prior results are touched in three distinct ways: re-exercised, withdrawn, and bounded.

An undeclared change of role. [Sch26g] declares that the standard genetic code enters no hypothesis and no construction of that paper. This manuscript uses the code constructively: the demand graph is built from it, the refinement verified against it, the audit a statement about published tables. A reader arriving from the predecessor would have carried its independence claim forward. A remark in the inverse form names the sections that depend on the datum and the one that does not.

Two carriers superseded. An architecture placing the poly-A tether at its own sites creates registry entries between tether and coding unit and refines the twenty classes into thirty-six. An architecture treating the composite as a binary marker alphabet raised questions of species alternation, of whether a composite site carries a marker, and of tether cardinality. Both were abandoned once the carrier was recognised as a word space over the nucleobase alphabet. Each abandonment constrains the chemistry. The corpus’s ledgers had not previously drawn the disposition *superseded*.

Three prior results. [Sch26e, Target 7.7] is re-exercised: the manuscript chooses Watson–Crick where [Sch26f] chose amino/keto, which leaves all counts unchanged and rebuilds that paper’s tables. [Sch26f, Hyp. 2.22], the stop designation, is withdrawn: every stop codon of the code the construction outputs is a consequence of a corollary, and a withdrawal is not a proof. [Sch26g, Cor. 5.9], the parity obstruction, is bounded: it excludes the standard code and does not exclude the vertebrate mitochondrial code, which has no odd fibre yet splits nineteen of twenty classes.

Naming. ρ was reused for the liberation predicate and is reserved by [Sch26d, Prop. 4.7]; renamed ϖ . Excision collides nominally with its homological sense and is recorded rather than avoided.

4 Stage *H* — chemistry and domain review

Stage *H* — one new item

The mathematical content uses no molecular datum. The chemical content is six registered hypotheses and two [E] remarks. One locant ambiguity was disposed. Three statements are before the domain pass and are not disposed here.

The specification places the adenine linkage at “its C2 position” beside the chrysene’s C12. In the formalism v_2 belongs to the dual attachment set of $A1$, and a reader meeting the two in one sentence will take both for chrysene locants. The text states on first use that C2 is adenine’s own ring position.

5 Targeted verification

Targeted verification

Each ledger entry was located and the repair confirmed present. Withdrawn language does not survive outside the ledger. The predecessor’s marker-string macro is left undefined, so a stray marker string fails the compile. Eighteen numerical checks pass. The script rebuilds the objects from the definitions and imports nothing from the manuscript’s tables. The twenty-seven translation tables are reproduced from [NCBI24] and are the only external data.

Check	Object verified
V1	Word space: 64 states, 20 classes, profile eight and twelve
V2	A block and a class meet in at most one codon
V3	Fourteen of sixteen blocks of the standard code in normal form; the two outside are AU and UG
V4	Seventeen demands, maximum matching seventeen, deficiency zero
V4b	The table the construction outputs is the vertebrate mitochondrial code at all sixty-four codons, and differs from the standard code at four
V5	Exactly 840 seed maps; 87 spare triples; eight classes used in all
V6	Serine seeded once for two blocks; no residue seeded twice
V7	The construction yields patterns (4) and (2, 2) only
V8	The nine-combination table: 16/16/2 and 16/16/0; other partitions eight
V9	Block patterns of both codes
V10	Both codes attain the minimum their composition permits
V11	Within-block null: 0.00149 and 0.00015 over 200,000 samples
V12	The full audit of all twenty-seven tables; distribution 4/5/9/8/1
V13	“AU outside” and “AUA is Ile” agree on all twenty-seven
V14	Fifty-one blocks outside (4) and (2, 2), at eight distinct blocks
V15	The AGA/AGG dispute does not affect the audit
V16	Fibre sizes: the standard code has two singletons, the mitochondrial none
V17	Neither code is constant on the classes; nineteen of twenty split in each

6 Meta-review

Meta-review of the controlling text

All seventy-six criticisms fully accepted. None partially resolved, unresolved, or no longer applicable. The manuscript withdrew more than it added. This is the first of the three recent records to reduce the standing commitments of the corpus.

	Count
Criticisms raised across five passes	76
fully accepted	76
Confirming a caution the outline anticipated	48
New items	28
mathematical	15
concordance	12
chemistry and domain	1
Corrections to circulated figures	5
Numerical checks, all passing	18

Found by coding, not by reading. Five review passes confirmed the seed construction. Writing the verification script required stating the demand rule precisely enough to execute, and the statement proved inconsistent between two blocks in the same structural position. The checks should be coded before the section they verify is drafted.

Largest items were not defects of proof. Both concern what a correct computation was a computation of: the shape of the fibres, and the range of the construction. That is the fourth and fifth instance of the pattern in this corpus.

Length. Fifteen outline versions. Most of the length was spent on three architectures that were tried and abandoned. A tether placed between sites refines the classes to thirty-six. A composite marker alphabet raises questions the word space does not. A deferral scheme cannot select its own deferred pair. A shorter development would have reached a working construction sooner and would not have established that the alternatives fail.

What the review does not certify

Nine Targets are open, three load-bearing: the chain polarity, which decides sixty-four states against thirty-six; which blocks receive the further division, where the manuscript accounts for two of the fifty-one the published codes require; and the collapse of the 840 seed maps, which decides whether the seed map is a construction or a choice. Six hypotheses are registered and undischarged, of which one a proof depends on. Four of twenty-seven published tables lie inside the construction's range. The identity between the construction's output and [NCBI24, table 2] is a consequence of a construction built against table 1, and the two tables differ by four codons. It is not an independent fit to mitochondrial data, and the manuscript says so.

Limitation

Targeted verification re-runs the mathematical stage. By [Sch26b, §9.4], every explicit verification inherits that limitation. Concordance and chemistry are not affected. The eighteen numerical checks are not subject to it, with the new qualification that the script itself found a defect, so its correctness is load-bearing in a way it has not previously been. This report is a single-manuscript record.

7 Corrections to figures circulated during development

These are not criticisms of the manuscript. The criticism/revision/verification convention of [Sch26b, Def. 3] does not cover them.

1. A duplex analysis was run with the biological reverse complement in place of the formalism’s flip-reversal. The two differ. The corrected analysis is the proposition that the reverse complement is a frame operation under no assignment.
2. The deficiency of the seeding construction was reported as one and attributed entirely to arginine. It is two: arginine accounts for one and a seven-demand Hall violator for the other.
3. The count of tables whose AU block lies outside normal form was reported as twenty-three. It is twenty-two, and is not independent of the AUA assignment.
4. The seed construction was drafted with two blocks in the same structural position handled differently. Corrected: seventeen demands, 840 seed maps, three spares, no residue seeded twice. Found by writing the verification script.
5. The refinement at AG was first drafted as supplying arginine on the purine half, which left the output differing from both published codes. On the ruling that AG behaves as UA does, the purine half is non-coding and the output is the vertebrate mitochondrial code exactly. No demand, map or spare count changes.

References

- [NCBI24] A. Elzanowski and J. Ostell. The Genetic Codes. National Center for Biotechnology Information. Last update 23 September 2024.
- [Sch26b] C. D. Schaper. The chrysene formalism as candidate mathematics and candidate biogenesis. *Annals of the Chrysene Formalism* 1(2):476–488, 2026.
- [Sch26d] C. D. Schaper. The encoded stack. *Annals of the Chrysene Formalism* 1(2):646–675, 2026.
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- [Sch26f] C. D. Schaper. Coarsenings of the genetic code by the twenty registry classes. *Annals of the Chrysene Formalism* 1(2):730–767, 2026.
- [Sch26g] C. D. Schaper. Why three and why twenty. *Annals of the Chrysene Formalism* 1(2):768–793, 2026.

Revision history

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