

ORTHOGONAL REVIEW RECORD

*Coarsenings of the Genetic Code by the Twenty
Registry Classes of a Chrysene Stack: A Partition
Criterion, a Filter Selection, and the Double-Sided
Encoding Hypothesis*

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REVIEW SCOPE

This file is the review record of Article 47. It is not a section of the paper. The object reviewed, in order, was the plan circulated before drafting, the compiled file of nine tables, and the drafted text of eleven sections and three appendices. The

architecture is [Sch26b, §4.3]. Admissibility is $F_{\text{adm}} = M \cap C \cap H$ [Sch26b, Def. 2]. There is no author-reply section.

Scope of Review

The manuscript extends the framework and falls under [Sch26b, §4.5]. Controlling priors are the twelve axioms, the encoded stack, the twenty registry classes, and the editorial and transfer-geometry papers. Each stage was asked one question and not the others. Items 1–31 were raised against the plan and the table file; items 32–34 during drafting. They are not retrospectively presented as design decisions.

Compiled disposition

Thirty-four criticisms were raised and all thirty-four are fully accepted. Twenty-two arose at mathematics, seven at concordance, five at chemistry and domain. Thirty-one are verified explicitly. Three carry verification none, because the repair is a deletion. Nineteen numerical checks were run and all pass. The word *derivation* is withdrawn from the selection sections. Nine Targets remain open, three of them load-bearing. This record is not evidence about the review architecture in general.

What the review does not certify

Three load-bearing Targets: whether the amino-acid pathway is invariant under the frame group, on which every statement of the double-sided section rests; the single measurement that would refute the consistency clause; and the change of dichotomy between the classification and the residual structure of the two-step comparison. Three hypotheses are registered and undischarged: the double-sided hypothesis in all its clauses, the physical reading of the filters, and the stop designation. No synthesis is reported. The selection rests on a margin of 0.17%, which survives a twenty per cent perturbation of the filter weights in 94.5% of trials and a fifty per cent perturbation in 72.6%.

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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 *M*.

C: Does the manuscript contradict a prior statement, or silently weaken a structure a prior statement relies upon? This includes hypothesis-register discipline, naming discipline, and the provenance of imported objects.

H: Is the molecular interpretation admissible against the reference structure, and is every such claim confined to a remark that enters no proof?

Each action is recorded as criticism, disposition, and verification. A favourable disposition is not itself evidence that verification will be explicit.

2. STAGE *M* — MATHEMATICAL REVIEW**Stage *M* — mathematics only**

Twenty-two of the thirty-four criticisms arose here. They divide into scope of claim, statements that carry no information, errors of fact against the manuscript's own tables, and understatement. The two criticisms with the largest consequence are not defects of proof. Every computation in the circulated material was correct as computed. What was wrong was the account of what the computation was a computation of.

Scope of claim.

Item 6. The manuscript claimed that five physical filters, applied to one hundred and twenty-eight perfect bijections, derive a coding table with no reference to the standard genetic code. The one hundred and twenty-eight are defined by the standard code: the adjacency admits the pair (class, amino acid) exactly when the standard table assigns that amino acid to some codon of that class. Scoring every pair without the adjacency constraint and maximising over all $20!$ bijections yields 21.0794 against 18.5639 for the selected map scored the same way. The unconstrained maximiser disagrees at every class and violates the adjacency at sixteen, including a class whose only admissible value is alanine and which it assigns tryptophan. The filters do not select the table. The standard code reduces $20! \approx 2.4 \times 10^{18}$ candidates to one hundred and twenty-eight, and the filters supply the remaining factor, by a margin of 0.17%. Fully accepted. Section 5 is reframed as selection among admissible coarsenings. The word derivation is withdrawn from Sections 5 to 7. The non-implication is a numbered clause with the one-class witness.

Item 16. The first block operator was to be defined intrinsically. Its seven block-target pairs are seven of the eight four-fold family boxes of the target table. Linear-programme feasibility over the filter weights is infeasible for four of the seven blocks with non-negative weights, and no single common vector serves all seven with signed weights. Fully accepted. The operator is given by exhibition. The family-box fact is disclosed. A non-implication clause is added.

Statements that carry no information. Anchor uniqueness (item 20) is forced by the construction: every amino acid of a Step-1 block has all its standard codons inside that block, and a block and a class meet in at most one codon. Fifteen of the sixteen blocks contain four distinct entries. Demoted. The count coincidence at $N = 3$ (items 2–5) is [Sch26e, Prop. 3.15(i)], whose polarity in the predecessor is refutation. The gloss of the multiset count as a count of chemical environments fails, one ground being that a quantity determined by an unordered triple is blind to codon order. Uniqueness of the maximiser (item 11) is generic on a finite set, by the null degeneracy locus of [Sch26e, Prop. 6.11]. Relocated to existence: a perfect matching exists for 70.6% of random codes carrying the standard degeneracy profile and for 25.9% of all 13 824 position-wise base relabellings; among relabellings that admit one, the number of matchings has median 128.

Errors of fact. Item 21: the three amino acids gaining the most codons were named serine, leucine and arginine. The gains are serine +4, alanine +3, then leucine, proline and arginine tied at +2. Item 14: two of the twenty registry weights contradict the manuscript’s own class table, at classes 2 and 20. The two errors cancel exactly in every one of the one hundred and twenty-eight totals. The rows are corrected regardless. Item 32: the obstruction to the Watson–Crick partition was described as serine’s split codon box, with two amino acids named as unmatched. No amino acid is unmatched in every maximum matching. The obstruction is a Hall violator, a set of six classes sharing five neighbours.

Understatement and disclosure. The second block operator’s exceptions were understated by two blocks (item 18). “Five combined filters” overstates by two; only three are individually decisive (item 9). Robustness of a 0.17% margin was unreported (item 10). “Unique minimiser” should read maximiser (item 12). An arbitrary tie-break among three equal residue volumes was undisclosed; it is immaterial over all six orderings (item 34).

3. STAGE *C* — CONCORDANCE REVIEW

Stage *C* — concordance only

Seven criticisms. All seven are structural in the sense of [Sch26b, Rem. 1]: each concerns what the manuscript inherits or must register, not whether a step is valid.

Provenance (item 1). Nine tables were described as compiled from [Sch26e]. They are not content of that paper, were never reviewed as such, and contain an identification of the twenty classes with the twenty amino acids that [Sch26e, Prop. 3.15(iii)] expressly declines to make. The tables are new results of this manuscript. [Sch26e] requires no revision. Clause (iii) is a statement about what that paper asserts, not a prohibition binding a successor. What would contradict the predecessor is an identification inconsistent with clause (ii). The manuscript is consistent with clause (ii) and uses it: the difference in fibre-size profile is the premise of Section 6.

Changed role of an external datum. In [Sch26e] the standard genetic code is used only to refute. Here it defines the adjacency, and every statement of three sections depends on it. The change is declared. The degeneracy profile is recomputed from the codon table.

Register discipline (items 26, 28). The designation of three codons as non-coding is supplied by no axiom and by neither predecessor. It is now a named hypothesis. The empirical claim fixing the nucleobase asserted a four-way determination from a two-valued datum, contrary to [Sch26d, Prop. 4.4]. Restated with the projection reference. The partition is registered as a structural hypothesis.

Target discipline (item 31). The clause asserting that the catalyst fixes the attack direction so that the L configuration results is an assertion about configuration at the assembly level. By [Sch26d, Rem. 3.7] the marker binary is not a chirality, and emergent assembly chirality is an open target. Confined to an empirical remark used in no proof. Verification none: the repair is a deletion.

Polarity. Items 2, 3 and 5 concern the manner in which a predecessor’s statement is inherited. Recorded also at Stage *M*.

4. STAGE *H* — CHEMISTRY AND DOMAIN REVIEW

Stage *H* — chemistry and domain

Five criticisms, concentrated in molecular qualification and nomenclature. Two are withdrawals. Both repairs are deletions, so both carry verification none.

Nomenclature (item 27). The partition $\{A, C\} | \{G, U\}$ was named “the wobble pairing.” Wobble denotes $G \cdot U$ and inosine pairing; $A \cdot C$ is a rare protonated mismatch. The partition is amino against keto, the IUPAC classes *M* and *K*. Renamed throughout.

Molecular qualification (items 29, 30). Two accounts of the six-molecule cluster were incompatible. Ruling: all three catalyst–substrate pairs are base-producing, and the wall-and-spacer justification is withdrawn; the length follows from the codon being a triplet. The nitric-oxide attack was placed ambiguously at C11 or C12. Ruling: the attack is on the substituent arm at C12, the nitrogen coupling to the C12- α position, which engages the unsubstituted C11 of the same substrate unit. That the reaction engages exactly a cipher pair is recorded and used in no proof.

Withdrawals (items 22, 25). The rider that the amino acids gaining most codons are biosynthetically early and prebiotically abundant does not survive: on the standard chronologies arginine is a late addition, and leucine is mid-to-late. Withdrawn. The stop-codon classification asserted that the most common vertebrate mitochondrial stop reassignment is to methionine, that another stop is reassigned to alanine, and that the third is universal. All three are incorrect: the near-universal mitochondrial reassignment is to tryptophan; a reassignment to alanine is not attested; the third is read as glutamine in ciliates. Withdrawn, with no replacement claim about any organism.

Species and locants. Catalyst on the dual attachment set and substrate on the primary set agrees with A1 and with [Sch26d, Def. 2.3]. Confirmed.

5. TARGETED VERIFICATION

Targeted verification

Each of the thirty-four entries was located in the final text and the repair confirmed present. Withdrawn language does not survive outside the ledger. The anchor macro is left undefined, so a surviving occurrence fails the compile. Nineteen numerical checks pass. The script rebuilds the objects from the definitions and imports nothing from the manuscript's tables.

Check	Object verified
V1	Maximum matching 20, 19, 18 for the amino/keto, purine/pyrimidine and Watson–Crick partitions, over all twenty-four letter assignments
V2	Degeneracy profiles of both tables; codon gains and losses
V3	Block contents; four-distinctness in fifteen of sixteen blocks; the unique anchor of each Step-1 block
V4	Registry weights recomputed; two disagreements; the shifts cancel in all 128 totals
V5	Permanent of the adjacency equals 128; five classes fixed
V6	Score table reproduced to three decimals in all twenty rows
V7	Unique maximiser at 14.4194 against 14.3950
V8	Unconstrained optimum 21.0794 against 18.5639; twenty disagreements; adjacency violated at sixteen classes
V9	Leave-one-out and weight jitter
V10	Composite of the two operators agrees with the standard code on all sixty-four codons
V11	Twelve block-fitness variants; zero of seven on the necessary condition
V12	Linear-programme infeasibility over filter weights, non-negative and signed
V13	Random codes of the standard profile: matching exists in 3528 of 5000
V14	All 13824 base relabellings: matching exists in 3584; median number of matchings 128
V15	All six orderings of the tied residue volumes: same maximiser, same margin
V16	Hall violators; no amino acid unmatched in every maximum matching
V17	After the first operator, exactly seven amino acids on one codon each
V18	Five candidate rules for the second operator's half-winners; best ten of thirteen
V19	The count equation for $N = 1, \dots, 20$

6. META-REVIEW

Meta-review of the controlling text

All thirty-four criticisms fully accepted. None partially accepted, rejected, or no longer applicable. Twenty-nine coded major. Nine coded structural. Twenty-five are over-claims in the manuscript’s own direction.

	Count
Criticisms raised	34
fully accepted	34
By stage: mathematical	22
concordance	7
chemistry and domain	5
Coded major	29
Coded structural	9
Verification explicit	31
Verification none	3
Over-claims in the manuscript’s own direction	25
Numerical checks, all passing	19

The three entries with verification none are the two domain withdrawals (items 22 and 25) and the chirality confinement (item 31).

Asymmetry. Twenty-five of the thirty-four criticisms are over-claims. That is the asymmetry [Sch26b, Rem. 1] reports and [Sch26e, Rem. B.5] records, now observed on a third manuscript.

Differentiation. The mathematical stage produced every scope-of-claim and every re-computation item and no nomenclature item. Concordance produced every structural item that concerns inheritance or registration, and no defect of proof. Chemistry produced only molecular qualification, nomenclature, and the two withdrawals.

Largest consequences. Items 6 and 16 changed what the manuscript claims more than any others, and neither is a step that fails to follow. A stage asked only whether the mathematics is valid would have passed both.

Limitation. Targeted verification re-runs the mathematical stage rather than employing an independent reviewing system. By [Sch26b, §9.4], independence of pass is not independence of reviewing system, and every entry marked verification explicit inherits that limitation. Concordance and chemistry are not affected. The nineteen numerical verifications are not subject to it, being reproducible from the definitions by a script that imports nothing from the manuscript. This report is a single-manuscript record. It is not evidence about the review architecture in general.

#	St	criticism	disposition / verification
1	<i>C</i>	Nine tables described as compiled from the predecessor	New results of this manuscript. Explicit
2	<i>C</i>	Count coincidence presented as support, reversing the predecessor's polarity	Demoted, with its non-implication. Explicit
3	<i>C</i>	The same coincidence stated as a new theorem	Imported by citation. Explicit
4	<i>M</i>	Multiset count glossed as a count of chemical environments	Gloss withdrawn. Explicit
5	<i>C</i>	Coincidence offered as a checkable condition	Withdrawn; it is the counting trap. Explicit
6	<i>M</i>	Section 5 claimed derivation; the adjacency is built from the standard code	Reframed as selection. Explicit
7	<i>M</i>	Division of selective work unstated	Both figures reported. Explicit
8	<i>M</i>	No non-implication guarded the filters	Clause added, with a one-class witness. Explicit
9	<i>M</i>	"Five combined filters" overstates	Three discriminate. Explicit
10	<i>M</i>	Robustness of the margin unreported	Both jitter figures published. Explicit
11	<i>M</i>	Uniqueness of the maximiser offered as discriminating	Relocated to existence and quantified. Explicit
12	<i>M</i>	"Unique minimiser"	Maximiser. Explicit
13	<i>M</i>	Fourteen assignments said locked	Five. Explicit
14	<i>M</i>	Two registry weights contradict the manuscript's own table	Rows corrected; errors cancel. Explicit
15	<i>M</i>	Section 6 claimed derivation	Transformation equivalence. Explicit
16	<i>M</i>	First operator to be defined intrinsically	By exhibition; LP infeasibility recorded. Explicit
17	<i>M</i>	No non-implication guarded it	Clause added. Explicit
18	<i>M</i>	Step 2 understated by two blocks	Six blocks plus three exceptions. Explicit
19	<i>M</i>	"Exactly two steps" unjustified	"Exactly" withdrawn; Target opened. Explicit
20	<i>M</i>	Anchor uniqueness offered as motivating the assignment	Demoted; the anchor is forced. Explicit
21	<i>M</i>	Three largest codon gains misnamed	Corrected to serine and alanine. Explicit
22	<i>H</i>	Prebiotic-abundance rider	Withdrawn. None
23	<i>M</i>	Stop ordering labelled a theorem	Relabelled a computation under a named hypothesis. Explicit
24	<i>M</i>	Two-and-one partition against its own gaps	Withdrawn; ordering retained. Explicit
25	<i>H</i>	Mitochondrial classification	Withdrawn; three claims incorrect. None
26	<i>C</i>	Stop designation unregistered	Registered as a hypothesis. Explicit
27	<i>H</i>	"Wobble pairing" misnames the partition	Amino/keto, IUPAC $M K$. Explicit
28	<i>C</i>	Four-way determination asserted from a two-valued datum	Restated; partition registered. Explicit

#	St	criticism	disposition / verification
29	<i>H</i>	Two incompatible accounts of the three vessels	All three base-producing. Explicit
30	<i>H</i>	Attack placed ambiguously at C11 or C12	Clarified; cipher-pair relation unused in proofs. Explicit
31	<i>C</i>	Assembly-level chirality clause	Confined to an empirical remark. None
32	<i>M</i>	“Two unmatched amino acids” names no object	Replaced by the Hall violators. Explicit
33	<i>M</i>	Second operator to be intrinsic	Shape is; winner-selection is not. Explicit
34	<i>M</i>	Arbitrary tie-break entering the margin	Disclosed; immaterial over six orderings. Explicit

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REVISION HISTORY

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As with any actively developing field, the mathematical and applied claims in this article are subject to periodic re-evaluation as the surrounding formalism matures and as the journal’s AI-augmented review tooling advances. Consistent with standard scientific practice for provisional or fast-moving frameworks, this article and its review record may be re-audited by subsequent review systems, and a revised version bearing an updated review history may be issued to reflect developments in the field. Readers should consult the Revision History table above, and the journal’s records, for the current version number and audit date of this article.

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