

Seeded Assignments on the Chrysene Registry

Transversality, Third-Position Refinement, and the Mitochondrial Code as Normal Form

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Abstract

A frame class is not a codon block: the two partitions of the sixty-four words are transverse, meeting in at most one word, so a residue attached to a class is not thereby attached to a codon. And by the parity obstruction of the preceding paper no map constant on classes can produce the standard genetic code, every class having size two or four while the code assigns methionine and tryptophan to one codon each. We exhibit a construction that crosses the gap: a seed map placing a class's residue at one codon, propagation filling the block, and a refinement dividing a block at the third base into its pyrimidine and purine halves.

Seventeen seeds suffice, with deficiency zero and three classes to spare; exactly eight hundred and forty seed maps achieve it and none is distinguished. The bound of twenty survives the crossing — every residue placed is seeded by a class — while the fibres are freed, so the parity obstruction does not apply. The construction outputs the vertebrate mitochondrial code, at every one of the sixty-four codons; the standard code is that output with two further divisions, at AUA and UGA. Its four stop codons are absences, two purine halves failing to liberate.

The central results concern what such a construction can produce. A block admits normal form — uniform, or two uniform halves — only if its residue pattern is (4) or (2, 2), and the construction produces exactly those; normal form is therefore its range and not a regularity discovered of the genetic code. Of nine candidate refinements, three positions by three partitions, exactly one brings either code near normal form: refinement at the first or second position leaves all sixteen groups outside, under every partition. Holding each block's residues fixed and randomising within it, both codes attain the minimum their composition permits, at probabilities 1.4×10^{-3} and 1.5×10^{-4} ; arrangement is perfect in both and composition is where they differ. A hypothesis of the preceding paper is withdrawn, every stop codon of the output being an absence.

The test is reported at its score. The construction's own output is one of the four of twenty-seven published translation tables that lie inside the range, all four mitochondrial; twenty-three do not, and the further division they would require is needed fifty-one times at eight distinct blocks, of which this paper accounts for two. The parity obstruction is also bounded: it excludes the standard code and does not exclude the mitochondrial one, which has no odd fibre yet splits nineteen of twenty classes. Unlike its predecessor this paper uses the standard genetic code constructively, and says so.

Keywords: Chrysene Formalism; registry classes; frame group; transversality; seed map; system of distinct representatives; third-position refinement; normal form; genetic code; mitochondrial code; parity obstruction; non-implication.

1 Introduction

1.1 The problem

A frame class is not a codon block. The twenty classes of [Sch26e] partition the sixty-four words of a chrysene cluster by

the frame group; the blocks of a codon table partition the same sixty-four words by their first two bases; and the two partitions are transverse, meeting in at most one word (Proposition 5.2). So a residue attached to a class is not thereby attached to a codon, and something must carry it across.

The difficulty is not merely technical. [Sch26g] proves that

no map constant on classes produces the standard genetic code: every class has size two or four, so every fibre of such a map is even, while the standard code assigns methionine to one codon and tryptophan to one. Whatever carries a residue from a class into a codon table must therefore *break* class-constancy, and must do so without losing the bound of twenty that class-constancy supplied.

1.2 The objective

To exhibit a map that does both: a *seed map* placing a class's residue at one codon, *propagation* filling the block, and a *refinement* dividing a block at the third base. To determine what such a construction can and cannot produce. And, having found that it produces codes of one restricted kind, to test whether the published genetic codes are of that kind — and to report the score rather than the successes.

1.3 What is established

- Seventeen seeds suffice: the demands are simultaneously satisfiable with deficiency zero, exactly eight hundred and forty seed maps achieve it, and three classes are left over (Theorem 5.7, Proposition 5.14). No residue is seeded twice, serine being seeded once for both of its blocks (Proposition 5.12).
- The construction outputs **the vertebrate mitochondrial code**, at every one of the sixty-four codons, and the standard code is that output with two further divisions, at AUA and UGA (Theorem 5.8). Its four stop codons are **absences**, the purine halves of UA and AG not liberating (Corollary 5.9).
- The bound of twenty survives. Every residue placed is seeded by a class, so the repertoire is bounded even though the fibres are not class-functional and may be odd (Theorem 5.17, Remark 5.19).
- Fourteen of the sixteen blocks of the standard code are in normal form for the third position under the purine/pyrimidine partition, and two are not (Theorem 6.2). Every stop codon of the output is an **absence** rather than a designation, and H_{stop} of [Sch26f] is withdrawn (Corollary 6.4).
- Of nine candidate refinements — three positions by three partitions — exactly one brings either code near normal form; refinement at the first or second position leaves all sixteen groups outside, under every partition (Theorem 7.5).
- A block admits normal form only if its residue pattern is (4) or (2, 2), and the construction produces exactly those (Propositions 7.1, 7.2). Both codes attain the minimum their composition permits, at probabilities 1.4×10^{-3} and 1.5×10^{-4} under a within-block null (Theorems 7.9, 7.10).
- Four of the twenty-seven published translation tables lie inside the construction's range; twenty-three do not, and the further division they would require is needed fifty-one times at eight distinct blocks (Theorem 7.13, Proposition 7.17).
- Two facts about the partition: base complementation is a frame operation under exactly the eight Watson–Crick assignments, and the biological reverse complement under none (Propositions 4.14, 4.15).

1.4 What is not claimed

No axiom is introduced (Remark 2.2); A3, A4, A5, A7, A9, A10 and A11 are unused; and no deferred target of any predecessor is discharged (Remark 9.11).

Three readings the construction invites are refuted in Section 3 and are stated here because the body would otherwise be taken to support them.

The first concerns the phrase *normal form*. It is the construction's *range*, not a regularity discovered of the genetic code: seeding, propagation and one refinement can produce nothing else. Finding a code inside the range is therefore a test, and its value is the score — four of twenty-seven.

The second concerns the identity at Theorem 5.8. The construction was built against the standard code — its demands, its candidate classes and its seeds all read that table — so agreement with the mitochondrial code is a consequence of the construction and not an independent fit to mitochondrial data. And the two codes are not independent objects: the second is defined in [NCBI24] as four differences from the first, so weight placed on the comparison is weight placed on those four codons.

The third concerns the seed map. There are eight hundred and forty, no criterion selects one, and the witness exhibited is a witness.

1.5 Logical position

Every numbered statement carries one of the four status labels of Definition 2.1; every hypothesis is registered at Section 2.5; every molecular reading is confined to a remark marked [E] and enters no proof.

One feature of the record is stated here rather than in the appendix, because a reader arriving from the preceding paper will otherwise carry a claim forward that does not hold. [Sch26g] declares that the standard genetic code enters no hypothesis and no construction of that paper. **This paper is the opposite case:** the demand graph of Section 5 is built from the standard code, the refinement of Section 6 is verified against it, and Section 7 is a statement about published tables. Sections 5 to 7 depend on that datum entirely and Section 4 not at all (Remark 2.16).

The defect ledger of Appendix B records seventy-six items across five pre-drafting passes, together with four corrections to figures circulated during development — the last of them

found by writing the verification script, which had until then only confirmed drafted sections.

1.6 What the construction produces

Stated once, here, and not left to be assembled from three sections.

Excision assigns a residue to each frame class. A seed map carries it into one codon of a block; propagation fills the block; a refinement at the third position separates the pyrimidine half from the purine half. **That machinery produces a code in normal form and can produce nothing else.** The standard code is such a code together with two further divisions, at UG and AU; the vertebrate mitochondrial code needs none.

1.7 Organization

Section 2 fixes conventions, the assignment and the register. Section 3 states the traps, before the constructions they guard. Section 4 identifies the carrier and what fixes its frame. Section 5 builds the seed map and determines the table it outputs. Section 6 introduces the refinement and separates what is proved of it from what is not. Section 7 is the core: normal form as the construction's range, the nine candidates, the decomposition into composition and arrangement, the audit, and what is left undone. Section 8 bounds the parity argument. Section 9 restates the non-implications and inventories the Targets. Appendix A tabulates; Appendix B is the concordance, the ledger and the verification record; Appendix C the literature.

2 Conventions, the Assignment, and the Register

2.1 Logical status

Definition 2.1 (Status labels). Imported from [Sch26c, Defs. 1, 3, 5, 6] and used as in [Sch26a, Def. 2.7]: **[A]** axiomatic; **[D]** derived realization theorem; **[T]** target; **[E]** empirical instantiation claim. An **[E]** claim is confined to a remark and enters no proof.

Remark 2.2 (No new axiom). **[A]** This paper introduces no axiom. Every structure below is imported from [Sch26d], [Sch26e], [Sch26f] or [Sch26g], is definitional within $\{A1, \dots, A12\}$, or is a realization hypothesis registered at Section 2.5.

Remark 2.3 (Two counting conventions). Statements about a finite object — a set of words, a group acting on it, a published codon table — are proved by enumeration and labelled

[A]. Each is instantiated once, by a corollary labelled **[D]**, as a statement about clusters under the hypotheses named there. The two are kept apart, as in [Sch26d, Rem. 3.9] and [Sch26g, Rem. 2.3].

2.2 Provenance

Proposition 2.4 (Provenance). ***[A]** The site set and the stacking direction are supplied by A6; the two attachment sets, hence the species alternation, by A1; the non-collapse of the marker by A2; the oriented perimeter cycle by A8; and the constraint functionals by A12. No constituent is supplied by A3, A4, A5, A7, A9, A10 or A11.*

Remark 2.5. A7 being unused, nothing here concerns the order dependence of an encoded word and [Sch26d, Thm. 4.17] is not invoked.

2.3 The assignment

Definition 2.6 (Letter assignment). Throughout,

$$FF = A, \quad FB = C, \quad BF = G, \quad BB = U,$$

so that $\text{reg}^{-1}(0) = \{A, U\}$ and $\text{reg}^{-1}(1) = \{C, G\}$: the registry partition is carried to the **Watson–Crick** partition.

Remark 2.7 (This is a re-choice, not a relabelling). [Sch26f, Def. 2.16] adopts an assignment carrying the registry partition to the amino/keto partition; Definition 2.6 does not. The eight assignments compatible with a given partition differ by an element of $\mathcal{N}$ acting on the source, so all counts are unchanged — but the codon carried by each class changes, and the coding table and both block operators of [Sch26f] are rebuilt under the present assignment. This is a re-choice of the datum [Sch26e, Target 7.7] leaves open and is recorded as one, not as a change of notation. Two reasons for the partition are given at Remark 4.16.

2.4 Imported objects

Object	Source
marker; non-collapse	[Sch26d, Def. 3.3, Pro
vessel; the binaries $b_1, b_2; \Sigma_0$	[Sch26d, Defs. 3.10, 3
the structural group; ρ, τ and their fixed points	[Sch26d, Props. 4.7, 4.8]
frame; frame-setters; the torsor structure	[Sch26d, Defs. 6.1, 6.2]
decomposition of the frame action	[Sch26d, Prop. 6.7]
initiator	[Sch26d, Def. 9.1]
frame group $\text{Fr} = \langle \text{flip}, \text{rev} \rangle$	[Sch26e, Def. 2.13]
structured alphabet; the count over its word space	[Sch26e, Def. 4.1, Ler
class sizes two and four, profile eight and twelve	[Sch26e, Cor. 3.7]
transversality of blocks and classes	[Sch26f, Rem. 6.3]
capacity; parity; the production clauses	[Sch26g, Thm. 5.4, Cor. 5.9]
residue volumes	[Zam72]
the translation tables	[NCBI24]

steric hindrance and electrostatics together — and not by size alone.

Hypothesis 2.13 ($H_{\text{lib-env}}$). Liberation depends on the translational environment as well as on the cluster and the frame.

Remark 2.14 (Why the split is two hypotheses). $H_{\text{split-pos}}$ is proved at Theorem 6.2; $H_{\text{split-chem}}$ is not proved anywhere, and Corollary 6.7 refutes the first account one would try for it. A single hypothesis covering both would conceal that asymmetry.

Remark 2.15 (Imported hypotheses, and one not carried). $H_{\text{mk}}, H_{\text{stack}}, H_{\text{frm}}$ and H_{ind} are imported unchanged from [Sch26d, Hyps. 2.6–2.11], and $H_{\text{prod}}(0), (0'), (1), (2)$ from [Sch26g, §2.5].

H_{stop} of [Sch26f, Hyp. 2.22] is **not** carried: two of the three designations it makes are consequences of Corollary 6.4, and the third is treated at Remark 7.19. Withdrawing a hypothesis is recorded here because the ledgers of this corpus have more often added them.

2.5 The register

Definition 2.8 (Excision and liberation). Ξ denotes the *excision* map, assigning to each frame class the residue formed at that cluster. ϖ denotes the *liberation* predicate, deciding whether the residue formed is released. The composite is the *production* of the cluster.

Hypothesis 2.9 (H_{teth}). In four clauses, each load-bearing.

- (i) The tether is a constant poly-A strand, one adenine–chrysene unit per coding unit.
- (ii) Its register with the coding strand is non-Watson–Crick, so that the tether is constant irrespective of the codon; and the intervening catalyst of the original cluster is displaced and enters no registry.
- (iii) The tether carries a chemical chain polarity.
- (iv) It is attached at the same ring and in the same orientation at every unit.

Hypothesis 2.10 (H_{seed}). Excision seeds a block at the codon it shares with the seeding class, on the pyrimidine half of a block whose halves carry distinct residues, and the seed propagates within the block.

Hypothesis 2.11 ($H_{\text{split-pos}}$). A block carrying two residues is divided at the third position, pyrimidine against purine.

Hypothesis 2.12 ($H_{\text{split-chem}}$). The residue on the purine half is determined by the reaction vessel — hydrogen bonding,

2.6 Declaration: the standard code is used constructively

Remark 2.16 (The inverse of [Sch26g, Rem. 2.4]). Its predecessor declares that the standard genetic code enters no hypothesis and no construction of that paper, and lists the hypotheses deliberately absent so that the claim can be checked.

This paper is the opposite case and the declaration is owed in the same form. The demand graph of Section 5 is built from the standard code; the refinement of Section 6 is verified against it; and the audit of Section 7 is a statement about published tables. Sections 5 to 7 depend on that datum entirely, and Section 4 depends on it not at all. A reader arriving from [Sch26g] must not carry its independence claim forward: it is not inherited, and nothing in this paper re-establishes it.

2.7 Naming

Remark 2.17 (Three substitutions and two collisions). *Excision* and *liberation* name the two chemical operations. Excision is a term of art in homology theory; neither this paper nor [Sch26c] uses homology, so the collision is nominal and is recorded rather than avoided, as Δ against $\Delta_{\mathbf{k}}$ was recorded at [Sch26g, Rem. 2.23].

ϖ , not ρ , denotes the liberation predicate: ρ is the fixed-

point-free element of the structural group at [Sch26d, Prop. 4.7] and is used in that sense throughout Section 4. Ξ is free across the corpus. *Block* is reserved for the four codons agreeing in their first two bases (Definition 5.1) and *class* for a frame orbit; the two are transverse and are never interchanged.

2.8 Notation

Symbol	Meaning
Ξ	excision; a map on the twenty classes
ϖ	liberation; a predicate on the sixty-four codons
X	the class set; $ X = 20$
Fr	the frame group $\langle \text{flip}, \text{rev} \rangle$
ρ, τ	the structural group elements of [Sch26d, Prop. 4.7]
$R Y, M K, W S$	purine/pyrimidine, amino/keto, Watson–Crick
pattern (4), (2, 2), ...	the multiset of residue multiplicities in a block

3 Traps and Non-Implications

The governing restraint of the formalism is that restoring a foundational object never licenses restoring an unproved implication of it [Sch26b, §3.1]. This section states what Sections 4 to 7 do not establish, and states it first. Each clause is refuted by a witness named in its proof; the section adds no argument and exists so that the list can be checked against the completed text.

Proposition 3.1 (Non-implications). *[D] None of the following holds.*

- (i) *A code lying in normal form $\not\Rightarrow$ normal form is a property discovered of that code. Normal form is the range of the construction of Sections 5 and 6, and finding a code inside it is a test.*
- (ii) *Four tables inside the range $\not\Rightarrow$ the construction is confirmed. Twenty-three of twenty-seven lie outside it.*
- (iii) *The audit of Theorem 7.13 $\not\Rightarrow$ a frequency or a probability. The tables are phylogenetically related and mostly curated as perturbations of one of them.*
- (iv) *The block AU lying outside normal form in twenty-two tables $\not\Rightarrow$ a structural fact about that block. It is the predicate “AUA is read as isoleucine” under another description.*
- (v) *The null of Theorem 7.10 $\not\Rightarrow$ anything about which block patterns occur. It holds composition fixed and speaks only of arrangement.*
- (vi) *Theorem 7.5 $\not\Rightarrow$ that the refinement is distinguished among all groupings of the codon table. Nine candidates were examined.*

- (vii) *Theorem 5.17 $\not\Rightarrow$ a bound independent of [Sch26g, Thm. 5.4]. It is that theorem relayed through the seeds.*
- (viii) *The existence of a seed map $\not\Rightarrow$ a canonical one. There are three hundred and twelve and no criterion is offered.*
- (ix) *Parity $\not\Rightarrow$ that no code is reachable by a class-functional operator. It excludes the standard code and does not exclude the vertebrate mitochondrial code.*
- (x) *Two classes unassigned $\not\Rightarrow$ the Hall deficiency of [Sch26f, §5]. The numbers agree and the quantities do not.*

Proof. (i) and (ii) by Proposition 7.2, which shows the construction produces patterns (4) and (2, 2) and no others, together with Theorem 7.13.

(iii) By inspection of [NCBI24]: tables 4, 6, 10, 11, 12, 15, 16, 25, 26, 29, 30 and 32 each differ from table 1 at one or two codons, so the entries are not independent draws and no sample space is defined.

(iv) By witness: across all twenty-seven tables the two predicates agree, so neither can be evidence for the other; check V13.

(v) By construction of the null at Theorem 7.10, which permutes within blocks and therefore leaves every block pattern unchanged.

(vi) By inspection of Theorem 7.5: three positions and three partitions were examined and no other grouping was.

(vii) Remark 5.18.

(viii) Proposition 5.14.

(ix) By witness: the vertebrate mitochondrial code has fibre sizes twelve of two, seven of four and two of six, hence no odd fibre, and [Sch26g, Cor. 5.9] is silent on it. That it is nonetheless not class-functional is Proposition 8.5, and the obstruction there is not parity.

(x) Remark 5.21, whose witness is that class 11 is matched in every maximum matching of the adjacency while being unassigned here. $\square$

Remark 3.2 (Status of the clauses). Clauses (iii), (iv), (vi), (viii) and (x) are refuted by witnesses using no hypothesis and could carry [A] separately. The proposition is labelled [D] because (i), (ii) and (v) refer to the construction and (ix) to the hypotheses of [Sch26g].

Remark 3.3 (The three that matter most). Clauses (i), (ii) and (viii) are the ones on which a reader is most likely to over-read, and each is answered in the section that raises it. Clause (i) states what kind of statement Section 7 makes. The construction can produce nothing but codes in normal form, so the normal-form result is a prediction and its value

depends entirely on the score. A reader who takes it for an independent regularity of the genetic code has read the section backwards, and Section 7.1 is written to prevent that.

Clause (ii) states the score. Four tables of twenty-seven lie inside the range. That is the number the paper has, it is not presented as a success, and Section 7.5 records the fifty-one further divisions the remaining tables would require.

Clause (viii) states what the construction leaves free. Three hundred and twelve seed maps achieve full coverage; the witness exhibited at Theorem 5.7 is one of them; no principle selects it. This corpus has twice been caught presenting a forced object as a discovered one ([Sch26f, ledger item 20], and the anchors it withdrew); presenting an unforced one as canonical would be the inverse error and is avoided here by stating the count wherever the map is used.

Remark 3.4 (Trap: the two codes are not two samples). [A] Sections 7.3 and 7.4 compare the standard and vertebrate mitochondrial codes, and the comparison is informative because the two differ at four codons. It is not a comparison of two independent objects: the mitochondrial table is defined in [NCBI24] as a list of differences from the standard one. Statements of the form *the mitochondrial code attains normal form and the standard code does not* therefore report a property of four codon reassignments, and any weight placed on them is weight placed on those four.

Remark 3.5 (Trap: the chemistry is not tested here). [A] $H_{\text{split-chem}}$ and $H_{\text{lib-env}}$ are registered and undischarged, and Remarks 6.8 and 7.19 are [E]. Nothing in Sections 5 to 7 tests them: the construction's structural content — transversality, coverage, the range, the refinement position — is independent of what the vessel does chemically, and would stand if the chemical account were replaced. Conversely, no agreement reported here is evidence for the chemical account.

Remark 3.6 (Why the section is placed here). A reader who reaches Section 7 holding the phrase *normal form* will read it as a discovered regularity of the genetic code, and will do so whether or not one is claimed; the reading is invited by the audit, by the smallness of the probabilities at Theorem 7.10, and by the fact that four published tables attain it. The refutations are therefore placed before the constructions, as [Sch26e, Rem. 3.17] places its two and [Sch26g, §3] places its seven, and the list is restated at Section 9.

4 The Carrier

4.1 The composite stack

Definition 4.1 (Composite stack). After the first transformation the coding strand carries three nucleotide–chrysene units and the poly-A strand three adenine–chrysene units. The two are paired in the register of $H_{\text{teth}}(\text{ii})$, and the A-tethered chrysene is interleaved between successive nucleotide pairings. The resulting stack has six units and three vessels, the A-tethered chrysenes serving as the catalyst units and the nucleotide-bearing chrysenes as the substrate units.

Proposition 4.2 (It is a stack). [D] Under H_{teth} the composite of Definition 4.1 alternates in species in the sense of [Sch26d, Def. 3.1], the interleaved A-tethered chrysenes supplying the catalyst sites.

Remark 4.3 (The displaced catalyst). Clause (ii) of H_{teth} states that the intervening catalyst of the original cluster is displaced and enters no registry. The clause is doing work and is not an aside: it is why the composite has six units rather than more, and why no registry entry arises between a tether unit and a coding unit. An architecture placing the tether at additional *sites* rather than complexing it within one refines the twenty classes into thirty-six; see Remark 4.17.

4.2 The carrier is a word space

Proposition 4.4 (The alphabet is structured). [D] Under the assignment of Section 2.3 the nucleobase alphabet $\{A, C, G, U\}$ with the partition $\{A, U\} \mid \{C, G\}$ is a structured alphabet in the sense of [Sch26e, Def. 4.1].

Theorem 4.5 (Twenty classes). [A] The word space of a structured alphabet at length N carries $2^{2N-2} + 2^{N-1}$ frame classes. At $N = 3$ there are **twenty**, of sizes two and four in the profile eight and twelve.

Sch26e, Lem. 4.5. with [Sch26e, Cor. 3.7]. The statement is imported and not reproved; it was verified directly under the present assignment at check V1 of Appendix B. $\square$

Remark 4.6 (No transport argument is needed). The carrier is a word space over a structured alphabet, which is the object [Sch26e, Lem. 4.5] is about. Theorem 4.5 is therefore that lemma applied, not a result transported from the marker presentation to a new one. Earlier plans for this paper did

require such a transport and are recorded at Remark 4.17.

Remark 4.7 (U and T). Relabelling U as T carries the partition $\{A, U\} \mid \{C, G\}$ to $\{A, T\} \mid \{C, G\}$, the same partition of the same four-element set, and by [Sch26g, Prop. 4.11] the classification is independent of the labelling. The codon tables of [NCBI24] are published with T ; U is used here and the two are interchangeable throughout. The formalism is indifferent to the substitution; the chemistry is not, thymine being 5-methyluracil, and no claim is made either way.

4.3 The tether and the frame

Proposition 4.8 (Why the tether can be constant). *[D] Under the non-Watson–Crick register of $H_{\text{teth}}(\text{ii})$ the tether strand is independent of the codon. Under a Watson–Crick register it would be determined by the codon and would distinguish no frame.*

Proposition 4.9 (The tether is palindromic). *[A] As a word the tether is AAA. Since τ fixes the aligned letters and A is aligned under the assignment of Section 2.3, $\text{rev}(AAA) = AAA$: the tether is fixed by reversal.*

Corollary 4.10 (What each datum fixes). *[A] The states remaining when the tether fixes:*

<i>Tether fixes</i>	<i>Residual group</i>	<i>States</i>
<i>nothing</i>	Fr	20
<i>the projection reference only</i>	$\langle \text{rev} \rangle$	36
<i>the reading direction only</i>	$\langle \text{flip} \rangle$	32
<i>both</i>	trivial	64

By Proposition 4.9 the tether’s pattern fixes the projection reference and **cannot** fix the reading direction, so its pattern alone leaves thirty-six.

Remark 4.11 (Chain polarity is load-bearing). Clause (iii) of H_{teth} supplies what the pattern cannot: a poly-A chain carries a chemical polarity the formalism does not represent, and the reading direction is fixed by the chain. With (i), (ii) and (iii) together the frame is determined. **Without (iii) the state count is thirty-six and no map onto a sixty-four-codon table exists**, so the clause is as load-bearing as the constancy and is registered as such. It is Target 9.7.

Corollary 4.12 (Sixty-four). *[D] With the frame fixed, the pairs (class, relative frame) number $8 \times 2 + 12 \times 4 = 64$, which is the domain of a codon table.*

Remark 4.13 (One tether, one frame, one code). A single poly-A strand serves every cluster along it, so the section it supplies is *global*: one frame for all clusters, hence one codon table and one handedness across all codons. A per-cluster reference would give per-cluster frames and nothing would require the resulting tables to agree.

4.4 Why Watson–Crick

Proposition 4.14 (Complementation is a frame operation only under Watson–Crick). *[A] Base complementation is fixed-point-free, and ρ is the unique fixed-point-free element of the structural group of [Sch26d, Prop. 4.7]. Hence complementation coincides with flip under exactly the eight assignments carrying the registry partition to $\{A, U\} \mid \{C, G\}$, and under none of the other sixteen.*

Proposition 4.15 (Reverse complementation never is). *[A] The reversing elements of the frame group are rev and fliprev , acting letterwise as τ and $\tau\rho$, each of which fixes exactly two letters by [Sch26d, Prop. 4.8]. A fixed-point-free map equals neither. Hence the biological reverse complement is a frame operation under no assignment.*

Remark 4.16 (Two reasons, and one consequence). The Watson–Crick partition is adopted for stability, which is empirical, and because it is the unique partition under which complementation is a symmetry of the classification at all, which is Proposition 4.14 and is not. The corpus has no other argument for a partition on symmetry grounds. Proposition 4.15 has a consequence worth stating. Strand complementarity is available to the formalism and strand reading direction is not, so a DNA:RNA duplex is an *external datum* — like the initiator and like the tether — and not a symmetry. It can break the frame; it cannot halve the registry.

4.5 Superseded architectures

Remark 4.17 (Two models raised and abandoned). Two earlier carriers were considered and are recorded because each was abandoned for a reason that constrains the chemistry. An architecture placing the tether at its own *sites* in the stack creates registry entries between tether and coding unit

of the form $m_j + c$. These are invariant under flip and are genuinely new information, and the count refines from twenty to **thirty-six**. Complexing the tether *within* a site creates no such entry. A constant is not informationless when the thing beside it varies; it is informationless when it is complexed into the same site.

An architecture treating the composite as a binary marker alphabet raised three further questions — whether the composite alternates in species, whether a composite site carries a marker at all, and how many tether units pair with how many coding units — all of which dissolve once the carrier is recognised as a word space over the nucleobase alphabet, which is what the chemistry supplies. These are recorded as *superseded* rather than repaired: they were consequences of a model the chemistry does not use, and the distinction is one the ledgers of this corpus have not previously had occasion to draw.

5 The Seed Map

Excision gives a residue to each of the twenty frame classes. It does not give a codon table: a class is not a block, and the two partitions of the sixty-four codons are transverse. This section supplies the map that carries a residue from a class into the codon table, and establishes what it can and cannot reach.

5.1 Blocks, and their relation to the classes

Definition 5.1 (Block). A *block* is a set of four codons agreeing in their first two bases. There are $4^{N-1} = 16$ of them at $N = 3$.

Proposition 5.2 (Transversality). [A] A block and a frame class meet in at most one codon.

Proof. By enumeration; check V2 of Appendix B. The statement is [Sch26f, Rem. 6.3] and is imported. $\square$

Remark 5.3 (What transversality buys). It is what makes the construction below well defined. A class assigned a residue can seed at most one codon of any block, so no block receives two seeds from one class and the propagation of Definition 5.6 is unambiguous. It is also what makes the construction necessary: because the two partitions are transverse, a residue attached to a class is not thereby attached to a block, and something must carry it across.

5.2 Seeds, demands and propagation

Definition 5.4 (Seed map). Let Ξ be the excision map of Section 2. A *seed map* assigns to each frame class at most one residue, subject to: a class may be assigned the residue r only if the class contains a codon that the standard code assigns r . A class so assigned *seeds* r at each block in which it holds such a codon; by Proposition 5.2 that is at most one codon per block.

Definition 5.5 (Demand). A *demand* is a residue together with the set of blocks in which it must be seeded. Where a single class holds a codon for that residue in every such block, the demand is one; where no class does, the demand is split into one demand per block. Seeds sit on the pyrimidine half of a block whose halves carry distinct residues, per H_{seed} .

Definition 5.6 (Propagation). *Propagation* assigns the seed's residue to every codon of its block; where the block is refined in the sense of Definition 6.1, to every codon of the seeded half.

5.3 Coverage

Theorem 5.7 (Full coverage). [A] The demands of Definition 5.5 number seventeen and are simultaneously satisfiable by seventeen distinct classes. The deficiency is zero, and three classes are left unassigned. One witness:

Residue	Seeded at	Class	Residue	Seeded at	Class
Phe	UU pyr	1	Met	AU pur	15
Ser	UC + AG pyr	4	Thr	AC	2
Tyr	UA pyr	3	Asn	AA pyr	10
Cys	UG pyr	13	Val	GU	7
Trp	UG pur	14	Ala	GC	6
Leu	CU	9	Asp	GA pyr	5
Pro	CC	18	Gly	GG	8
His	CA pyr	19	spare: 11, 17, 20		
Arg	CG	12			

The five residues not listed — leucine at UU, glutamine, lysine, glutamate and arginine at AG — are supplied by the refinement of Section 6 and require no seed.

Proof. By bipartite matching on the demand graph; check V4 of Appendix B. The witness is one solution of many and is exhibited for concreteness; see Proposition 5.14. $\square$

Theorem 5.8 (The construction outputs the vertebrate mitochondrial code). *[D] Seeding as above, propagating, and refining as in Section 6 assigns every one of the sixty-four codons, and the resulting table is the vertebrate mitochondrial code, [NCBI24, table 2], at every codon.*

It differs from the standard genetic code at exactly four codons:

Block	construction	standard	mitochondrial
AU	I, I, M , M	I, I, I, M	I, I, M, M
UG	C, C, W , W	C, C, *, W	C, C, W, W
AG	S, S, *, *	S, S, R , R	S, S, *, *

All other blocks agree with both codes. All twenty residues are placed.

Proof. By construction; check V4b of Appendix B, which builds the table from the seeding rule and compares it codon by codon with [NCBI24]. $\square$

Corollary 5.9 (The four stops are absences). *[D] The purine halves of UA and AG are non-coding, liberation not proceeding there, so the output assigns no residue to UAA, UAG, AGA or AGG. These are precisely the four stop codons of the vertebrate mitochondrial code, and each is an **absence** rather than a designation.*

Remark 5.10 (What the identity means, and what it does not). Theorem 5.8 is the paper's most concrete claim and should be read before Section 7. The construction does not merely produce *some* code in normal form; it produces a code that is *attested*, and the standard code is that output with two further divisions, at AUA and UGA — exactly the pair Remark 7.19 treats.

Three cautions. The construction was built against the standard code: its demands, its candidate classes and its seeds all read that table (Definition 5.4), so the identity with table 2 is a *consequence* of the construction and not an independent fit to mitochondrial data. The mitochondrial table is itself defined in [NCBI24] as four differences from table 1, so the identity is a statement about those four codons (Remark 3.4). And that the purine halves of UA and AG both fail to liberate is a chemical claim, registered at $H_{\text{lib-env}}$ and carried by Remark 5.11; the mathematics does not distinguish the two blocks and does not predict that they behave alike.

Remark 5.11 (The two non-coding halves). *[E] In the intended reading UA and AG behave alike for the same reason: a purine at the third position within the poly-A-*

tethered enclosure does not engage, does not stabilise, and does not carve out a product, so liberation simply does not proceed. The mechanism is that of Remark 6.8 with the outcome absent rather than altered. This remark enters no proof.

Proposition 5.12 (The serine overlap). *[A] Serine occupies UC and the pyrimidine half of AG, and classes 4 and 17 each hold a serine codon in both. One seed therefore serves both blocks.*

*Consequently AG requires no second seed: its pyrimidine half is already seeded, and its purine half is left to the refinement. **No residue requires more than one seed.***

Proof. By enumeration; check V6 of Appendix B. $\square$

Remark 5.13 (What the overlap buys). The seed released at AG is not merely saved; it is spent elsewhere. Without the overlap the demands number eighteen against twenty classes, and it is the overlap that leaves three spare rather than two. It is also what makes Corollary 5.9 available: a second seed at AG would have placed a residue on its purine half, and the block could not then have been one of the two that terminate.

5.4 How many seed maps

Proposition 5.14 (The count). *[A] Exactly 840 seed maps achieve full coverage, leaving eighty-seven distinct triples of unassigned classes. Eight classes — 3, 5, 9, 10, 14, 15, 16, 19 — are assigned in all 840.*

Proof. By exhaustive enumeration of the demand graph's perfect matchings; check V5. $\square$

Remark 5.15 (The eight are an invariant of the formulation, not of the classification). Proposition 5.14 is a statement about the demand graph of Definition 5.5, and that graph encodes three choices: that seeds sit on the pyrimidine half, that serine is served by one class spanning two blocks, and that AG is refined rather than seeded twice. Change any of them and the eight move. They are therefore an invariant of the stated formulation and are not offered as a property of the twenty classes.

Remark 5.16 (The seed map is a free parameter). Eight hundred and forty is small enough to state and too large to ignore. No criterion selecting one is offered here, and Target 9.5 proposes testing the 840 against a numerical

model of the tether–chrysene complex to determine whether the intersection is a single map. Until that is done the seed map is a choice, and the witness of Theorem 5.7 is a witness.

5.5 The bound on the repertoire

Theorem 5.17 (Repertoire bound). *[D] Every residue the construction places is seeded by a class, and distinct residues require distinct seeds. Hence the image of the assignment has at most $|X| = 20$ elements.*

Proof. Immediate from Definition 5.4: a residue appears in the table only where propagated from a seed, a seed is a class assigned that residue, and a class is assigned at most one residue. $\square$

Remark 5.18 (This is the capacity theorem relayed, not a new bound). Theorem 5.17 gives the same number as [Sch26g, Thm. 5.4] and gives it for the same reason: the seeds are classes and the classes number twenty. It is the capacity theorem transported through the seed map and is not independent of it. What it adds is only that the transport survives a construction whose *fibres* are not class-functional — which is the point of Remark 5.19 — and it should not be presented as a second bound on the same quantity.

Remark 5.19 (Why the fibres are free). [Sch26g, Cor. 5.9] excludes any class-functional operator from producing the standard code, every fibre of such an operator being even while the standard code has two singleton fibres. The assignment built here is not class-functional: propagation carries a residue to codons of a block, and the block is transverse to the class. Its fibres may therefore span classes and may be odd, and the corollary does not apply to it. Nothing in [Sch26g] is contradicted; that result governs functions on X , and this is not one.

5.6 The unassigned classes

Proposition 5.20 (Spares). *[A] Seventeen classes are assigned and three are not. In the witness of Theorem 5.7 these are classes 11, 17 and 20, and every residue their codons carry is already reached, so each can only be redundant.*

Remark 5.21 (The spares are not the Hall deficiency). The adjacency of [Sch26f, §5] has Hall deficiency two under the Watson–Crick partition, and two classes are unassigned here. The numbers agree and the quantities do not. Nine classes can be left unmatched in some maximum matching

of that adjacency, and class 11 can be left unmatched in none of them; the two unassigned here are determined by the demand graph and not by the adjacency. The agreement is arithmetic and is recorded so that it is not read as structure.

Remark 5.22 (What the spares produce). Under $H_{\text{prod}}(1)$ of [Sch26g] every class produces a residue, so three residues are produced and placed nowhere. The paper does not say what becomes of them. That is Target 9.2, and it is the first thing a reader should ask of Theorem 5.7.

6 The Third-Position Refinement

Propagation fills a block with its seed. This section introduces the second operation, which divides a block in two, and separates what the paper proves about it from what it does not.

6.1 Position

Definition 6.1 (Refinement). A *refinement* of the codon table is a pair: a position $p \in \{1, 2, 3\}$ and a partition of the four bases into two classes of two. A block — the four codons agreeing outside p — is *in normal form* for that refinement when it is uniform, or when each of its two halves is uniform. A code is in normal form when all sixteen of its blocks are.

Theorem 6.2 (Where the standard code is in normal form). *[A] Of the sixteen blocks of the standard genetic code, fourteen are in normal form for the third position under the purine/pyrimidine partition, and two are not: UG, whose purine half carries a stop and tryptophan, and AU, whose purine half carries isoleucine and methionine. In particular every block whose two halves each carry one residue is in normal form, without exception.*

Proof. By enumeration of the sixteen blocks; check V3 of Appendix B. $\square$

Remark 6.3 (The statement has to be made this way). It is tempting to write that every block carrying two residues is in normal form. That is false: AU carries isoleucine and methionine, two residues, and is not in normal form, its isoleucine occupying three codons and its methionine one. The correct division is by the *pattern* of a block and not by the number of residues it carries, and it is made at Proposition 7.1.

Corollary 6.4 (Stop codons are absences). *[D] The blocks UA and AG are in normal form with non-coding purine halves. Under H_{seed} a codon carries a residue only where one is seeded or propagated, so UAA, UAG, AGA and AGG carry none: they are **absences and not designations**. These are the four stop codons of the code the construction outputs (Corollary 5.9).*

Remark 6.5 (H_{stop} is removed from the register). [Sch26f, Hyp. 2.22] registers the designation of three codons as non-coding, because no axiom supplies it and the class surjection of [Sch26e, Prop. 3.15(ii)] has no element outside a fibre. **Every stop codon of the code this construction outputs is a consequence of Corollary 6.4**, and the hypothesis is not carried here. The standard code's third stop, UGA, is not a stop in that output at all: it is treated at Section 7.5 as one of the two further divisions by which the standard code is reached.

6.2 Transformation

The position is uniform. What happens across the division is not, and the simplest account of it is refuted by its own numbers.

Proposition 6.6 (The two families). *[A] For the four blocks whose halves carry distinct residues and which are not treated at Section 7.5, the residue volumes of [Zam72] are*

Block	pyrimidine	Vol.	purine	Vol.	Δ
AA	Asn	114.1	Lys	168.6	+54.5
GA	Asp	111.1	Glu	138.4	+27.3
CA	His	153.2	Gln	143.8	−9.4
UU	Phe	189.9	Leu	166.7	−23.2

The differences are of both signs.

Corollary 6.7 (Size is not the discriminant). *[A] No rule of the form the purine half carries the larger residue, or its converse, holds across the four. The first would fail at CA and UU, the second at AA and GA, and the widest failure is UU, where the rule would make leucine larger than phenylalanine, false by $23.2 \text{ \AA}^3$.*

Remark 6.8 (The reaction vessel). *[E] In the intended reading the division is a matter of stability and not of size. The cluster is a reaction vessel, and hydrogen bonding between tether and codon, steric hindrance and electrostatics all enter. A complex fully encased at a pyrimidine third base is stable; a purine there destabilises it and a further loss*

of CO_2 follows, at each arm of the upper ring. Loss of CO_2 makes the product smaller, which is the sign observed at UU and CA and the opposite of that observed at AA and GA; so the two families of Proposition 6.6 are not one transformation. This remark enters no proof.

Remark 6.9 (Why the hypothesis is registered in two clauses). $H_{\text{split-pos}}$ and $H_{\text{split-chem}}$ of Section 2.5 are registered separately because the paper establishes one and not the other. Theorem 6.2 proves the position; the transformation is Remark 6.8, is empirical, and is not derived — and Corollary 6.7 shows that the first account one would try is wrong. A single hypothesis covering both would conceal that asymmetry, which is the error [Sch26g, Rem. 4.6] records under a different name.

7 Normal Form

7.1 Normal form is the range of the construction

The order of this section matters and is stated at its head. Normal form is not a property the genetic codes were found to have. It is what the construction of Sections 5 and 6 can produce, and what follows is a *test* of whether natural codes fall inside it.

Proposition 7.1 (Which patterns admit normal form). *[A] Write the pattern of a block for the multiset of multiplicities of the residues it carries. A block is in normal form for some arrangement of its residues if and only if its pattern is (4) or (2, 2). The patterns (3, 1) and (2, 1, 1) are in normal form under no arrangement. A (2, 2) block is in normal form for exactly one of the three ways of pairing its four codons.*

Proof. Each half of a block has two codons, so a half is uniform only if its two codons carry one residue. A pattern with a residue of odd multiplicity places that residue in a half with a second residue, and that half is not uniform; (3, 1) and (2, 1, 1) each have such a residue. For (2, 2) the two halves must be the two residue classes, which is one of the $\binom{4}{2}/1 = 3$ pairings. $\square$

Proposition 7.2 (The range of the construction). *[D] Under H_{seed} and $H_{\text{split-pos}}$, a block receiving one seed and no refinement has pattern (4); a block receiving one seed and a refinement, or two seeds one in each half, has pattern (2, 2). No other pattern arises. Consequently **the construction produces codes in normal form, and produces no others**.*

Proof. Propagation assigns the seed's residue to every codon of the block, giving (4). A refinement divides the block into its pyrimidine and purine halves and assigns one residue to each,

giving (2, 2); two seeds, one per half, give the same. A pattern (3, 1) or (2, 1, 1) requires a division of four codons into parts of sizes 3 and 1, or 2, 1 and 1, and the pyrimidine/purine cut divides them 2 and 2. $\square$

Remark 7.3 (The construction outputs one table). Proposition 7.2 says the construction produces codes in normal form. Theorem 5.8 says which one: **the vertebrate mitochondrial code**, at every codon. So the audit below is not a search for a member of the range that happens to be attested — the construction names one, and the question is what the rest of the published record does. The standard code is that output with two further divisions, at AUA and UGA.

Remark 7.4 (This is a prediction, not a discovery). Proposition 7.2 is what licenses the rest of the section and it is also what limits it. Because normal form is the construction's image, finding a code in normal form is evidence for the construction and finding one outside it is evidence against; but neither is a property discovered independently of the construction. Sections 7.4 and 7.5 report the test and the score, and the score is not favourable at the level of all published codes.

7.2 The refinement is distinguished, not stipulated

An objection arises immediately. The construction groups codons by their first two bases and divides at the third, so a code built that way will look regular at the third position, and Theorem 6.2 may record nothing but the grouping. It does not, and the following settles it.

Theorem 7.5 (Nine candidates, one fit). *[A] The number of blocks not in normal form, over the three refining positions and the three partitions of the base alphabet into two classes of two:*

Code	Partition	Position 1	Position 2	Position 3
standard	R Y	16	16	2
standard	M K	16	16	8
standard	W S	16	16	8
mitochondrial	R Y	16	16	0
mitochondrial	M K	16	16	8
mitochondrial	W S	16	16	8

Proof. By enumeration; check V8 of Appendix B. $\square$

Corollary 7.6. *[A] Refinement at the first or second position leaves every one of the sixteen groups outside normal form, for both codes and under every partition. At the third position the other two partitions leave eight. One combination of nine brings either code near normal form.*

Remark 7.7 (The objection is answered). Had third-position regularity been an artefact of grouping by the first two bases, it would hold under $M|K$ and $W|S$ as well, the grouping being the same. It gives eight violations there. The position and the partition are therefore both findings.

7.3 Composition and arrangement

Proposition 7.8 (Block patterns). *[A] The standard code has eight blocks of pattern (4), six of (2, 2), one of (2, 1, 1) at UG and one of (3, 1) at AU. The vertebrate mitochondrial code has eight of (4) and eight of (2, 2).*

Theorem 7.9 (Both codes attain their minimum). *[D] By Proposition 7.1 the standard code has two blocks that cannot be in normal form under any arrangement, and the mitochondrial code has none. Each attains that bound: every block that can be in normal form is, fourteen of fourteen for the standard code and sixteen of sixteen for the mitochondrial.*

Theorem 7.10 (The arrangement null). *[A] Hold each block's multiset of residues fixed and randomise which of its four codons carries which. The probability that every eligible block falls in normal form is $(1/3)^6 \approx 1.4 \times 10^{-3}$ for the standard code, which has six (2, 2) blocks, and $(1/3)^8 \approx 1.5 \times 10^{-4}$ for the mitochondrial, which has eight.*

Proof. The (4) blocks are in normal form under every arrangement and the ineligible blocks under none, so only the (2, 2) blocks contribute, independently, each with probability $1/3$ by Proposition 7.1. Simulation over 200,000 samples gives 0.00149 and 0.00015; check V11. $\square$

Remark 7.11 (The null, and why this one). The null holds composition fixed and asks about arrangement alone, which is the question a refinement is about. A weaker null — permuting residues across all sixty-four codons, preserving only the profile of fibre sizes — destroys the block structure entirely and puts the mean at 15.97 violations against a maximum of sixteen; it establishes only that the code is not a random permutation of its own profile, and is not used

here. The choice of null is stated because the figure depends on it entirely.

Remark 7.12 (The decomposition is the result). Theorem 7.9 separates two things that the phrase *normal form* runs together. *Arrangement* is perfect in both codes. *Composition* is where they differ: the standard code has two blocks whose residue patterns make normal form unattainable however their codons are arranged, and the mitochondrial code has none. Nothing in Sections 5 and 6 bears on composition, and Target 9.9 records that as the paper’s central omission.

7.4 The test, and the score

Theorem 7.13 (The audit). [A] *Over the twenty-seven translation tables of [NCBI24], the number outside normal form for the third position under purine/pyrimidine is*

Blocks outside	Tables
0	2 vertebrate mit., 3 yeast mit., 5 invertebrate mit., 13 a
1	4, 21, 27, 28, 31
2	1 standard, 6, 9, 10, 11, 24, 25, 29, 30
3	12, 14, 15, 16, 23, 26, 32, 33
4	22

Four of twenty-seven lie inside the range of the construction; twenty-three do not. All four are mitochondrial; no nuclear, bacterial or plastid code attains it.

Proof. The tables were taken from [NCBI24] as published, not reconstructed, and the audit is check V12. □

Proposition 7.14 (What reassigning AUA does). [A] *Reading AUA as methionine carries AU from pattern (3, 1) to (2, 2). Five tables do so, and four of them are in normal form; the exception, table 21, lies outside at AA for an unrelated reason.*

Remark 7.15 (A figure that is not what it appears). The block AU lies outside normal form in twenty-two of the twenty-seven tables, which invites a structural reading. It does not carry one: across all twenty-seven, “AU is outside normal form” and “AUA is read as isoleucine” are the *same predicate*, agreeing on every table. The figure counts how many tables leave AUA unchanged. It is reported here so that a reader who computes it is not misled by it.

Remark 7.16 (The audit is not a probability). The tables of [NCBI24] are phylogenetically related and most are curated as small perturbations of table 1. A count over them measures the published record, not a sample space, and no frequency is claimed. Three further cautions. Tables 27, 28 and 31 carry dual assignments — UGA as stop or tryptophan in 27, all three stops dual in 28, UAG and UAA as glutamate or stop in 31 — and the published string fixes one reading; all three lie at one block outside, so the ambiguity bears on their placement, and the reading used is the published one. Whether AGA and AGG are mitochondrial stops is disputed [Tem10]; the audit was run both ways and the AG block is in normal form under either. And UGA is read as tryptophan in all animal mitochondria while AUA is read as methionine in most metazoan mitochondria, so the two are not one fact.

7.5 What is left undone

Proposition 7.17 (The fifty-one). [A] *A block outside patterns (4) and (2, 2) requires a further division inside one half. Summed over the twenty-seven tables there are **fifty-one** such blocks, thirty-three of pattern (3, 1) and eighteen of (2, 1, 1), at eight distinct blocks: AU twenty-two times, UG fourteen, UA six, AA three, CU and AG twice each, UC and UU once each.*

Remark 7.18 (The claim of this paper is restricted accordingly). This paper treats the further division at two blocks only, UG and AU in the standard code, where it accounts for UGA against UGG and for AUA against AUG. **It does not account for the other forty-nine.** The number is stated because it is the honest measure of the remainder, and because a mechanism available at eight different blocks is a stronger claim than this paper makes. Whether one such mechanism exists is Target 9.9.

Remark 7.19 (UGA and AUA). [E] In the intended reading the purine half of UG yields tryptophan, the largest residue of the set, whose release is sterically marginal; where the translational environment permits release the site codes, and where it does not the site terminates. The same at AU for methionine. That is the content of $H_{\text{lib-env}}$, which makes liberation depend on the environment as well as on the cluster and the frame, and it is why the same codon is read differently in the two codes. This remark enters no proof. These two divisions are the *whole* distance from the construction’s output to the standard code. By Theorem 5.8 the output is the vertebrate mitochondrial code exactly, and the standard code is reached from it by dividing the purine halves of UG and AU once more — at UGA, where tryptophan

is not released and the site terminates, and at AUA, where methionine is not released and isoleucine is read instead.

8 Parity, and the Limit of Its Reach

Section 5 observes that the assignment built here is not class-functional and that the parity obstruction of [Sch26g] therefore does not apply to it. This section states what that obstruction does reach, and — more usefully — what it does not.

Proposition 8.1 (Parity). *[A] Every frame class has size two or four. Hence every fibre of a map that is constant on classes has even cardinality.*

Sch26e, Cor. 3.7. for the sizes; a fibre of a class function is a union of classes. $\square$

Corollary 8.2 (The standard code is not class-functional). *[A] The standard code assigns methionine to AUG alone and tryptophan to UGG alone. Two fibres of odd cardinality, so by Proposition 8.1 no map constant on classes produces it. This is [Sch26g, Cor. 5.9] and is imported.*

Corollary 8.3 (A start codon is not class-functional). *[A] A start codon is uniquely specified, hence is the codon of a singleton fibre. By Proposition 8.1 no singleton fibre arises from a class function. Therefore the start codon of the standard code cannot arise in a class-functional phase.*

Remark 8.4 (What the corollary costs and what it buys). Corollary 8.3 uses parity and nothing else: no chemistry, no seed map, no refinement. It is the cheapest statement in the paper and, within the standard code, the strongest. What it does not do is generalise, which is the content of the next proposition.

Proposition 8.5 (Parity is silent on the mitochondrial code). *[A] The vertebrate mitochondrial code has fibre sizes twelve of two, seven of four and two of six, and therefore no singleton fibre and no odd fibre at all. Proposition 8.1 does not exclude it. It is nonetheless not class-functional: nineteen of the twenty classes carry more than one residue under it, exactly as under the standard code.*

Proof. By enumeration; checks V16 and V17 of Appendix B. $\square$

Remark 8.6 (The second obstruction is not identified). Proposition 8.5 is a limitation and is stated as one. The parity argument is often read as showing that no genetic code can be class-functional; it shows that of the standard code, and the vertebrate mitochondrial code is a counterexample to the general reading. Both codes fail to be class-functional and they fail for different reasons, only one of which this paper can name.

The unnamed one may be the more interesting. Parity is a coarse invariant — it sees only the parity of fibre sizes — and the mitochondrial code evades it while still splitting nineteen of twenty classes. What separates a code that is class-functional from one that merely has even fibres is Target 9.4, and it is the question this section leaves open.

Remark 8.7 (A convergence, recorded and not used). *[A]* The mitochondrial code is the code the construction of Sections 5 and 6 produces, by Theorem 7.13; it is also the code parity fails to exclude, by Proposition 8.5. The two facts point the same way and are established by unrelated arguments — the first by the range of the construction, the second by fibre parity. The convergence is recorded. It is not used, and no claim is made from it: a code with no odd fibre and a code in normal form are different conditions, and the paper has not shown that either implies the other.

9 Non-Implications Restated, and Targets

9.1 The non-implications in one line each

- (i) Normal form is the construction's range, so a code lying in it is a test and not a discovery (Prop. 3.1(i), 7.2).
- (ii) Four tables of twenty-seven lie inside; twenty-three do not (3.1(ii), Thm. 7.13).
- (iii) The audit is not a frequency; the tables are not independent (3.1(iii), Rem. 7.16).
- (iv) The AU figure is the AUA predicate (3.1(iv), Rem. 7.15).
- (v) The null speaks of arrangement and not of composition (3.1(v), Rem. 7.11).
- (vi) Nine candidate refinements were examined, not all groupings (3.1(vi), Thm. 7.5).
- (vii) The repertoire bound is the capacity theorem relayed (3.1(vii), Rem. 5.18).
- (viii) Three hundred and twelve seed maps; none is canonical (3.1(viii), Prop. 5.14).

- (ix) Parity excludes the standard code and not the mitochondrial one (3.1(ix), Prop. 8.5).
- (x) The two unassigned classes are not the Hall deficiency (3.1(x), Rem. 5.21).

Three further traps are stated at the point of use and not repeated as clauses: that the two codes compared in Section 7 are not two samples (Rem. 3.4); that no result here tests the chemical hypotheses, nor they it (Rem. 3.5); and that the eight classes used in every seed map are an invariant of the formulation and not of the classification (Rem. 5.15).

9.2 Targets

Target 9.1 (The split transformation). [T] Derive $H_{\text{split-chem}}$. Proposition 6.6 exhibits two families of opposite sign and Corollary 6.7 refutes a size rule, so a single transformation must account for both signs. The UU case is the widest failure of the size rule and is where an account should be tested first.

Target 9.2 (The spare classes). [T] Determine what the two unassigned classes produce. Under $H_{\text{prod}}(1)$ of [Sch26g] every class produces a residue, so two are produced and placed nowhere. Whether they are discarded, duplicate a seeded residue, or are the source of a datum this paper does not model is open, and by Remark 5.22 it is the first question Theorem 5.7 invites.

Target 9.3 (The environmental variable). [T] Discharge $H_{\text{lib-env}}$: identify what decides release at UGA and at AUA, given that the same codon releases in one translational setting and not in another. A measurement, not a proof.

Target 9.4 (The second obstruction). [T] Characterise what prevents the vertebrate mitochondrial code from being class-functional. Parity is silent on it by Proposition 8.5, yet nineteen of its twenty classes carry more than one residue. A sufficient condition finer than fibre parity would apply to both codes and would subsume Corollary 8.2.

Target 9.5 (Collapsing the seed maps). [T] Test the three hundred and twelve seed maps of Proposition 5.14 against a numerical model of the tether–chrysene complex and determine whether the admissible ones intersect in a single map. If they do not, the seed map remains a free parameter and the paper’s constructions are correspondingly weaker; that outcome should be reported as readily as the other.

Target 9.6 (Agreement with the block operators). [T] Determine whether seeding with propagation and one refinement agrees with the two block operators exhibited at [Sch26f, §6]. **The scopes differ** — that paper’s first operator fills seven blocks and its second acts on six of nine remaining, against sixteen blocks here — so the two constructions are not the same object and the comparison is not of like with like.

Target 9.7 (Chain polarity). [T] Discharge clause (iii) of H_{teth} : establish that the poly-A chain’s polarity fixes the reading direction. By Corollary 4.10 this decides between sixty-four states and thirty-six, and without it no map onto a sixty-four-codon table exists.

Target 9.8 (Coordinated vessels). [T] Test whether cysteine with methionine, and tyrosine with tryptophan, are produced by coordinated reaction vessels rather than independently. The vertebrate mitochondrial code is where to test it: there UG, AU and UA are all two-and-two, and each proposed pair draws one residue from a pyrimidine half and one from a purine half of different blocks. **That cross-block symmetry is an observation and is not evidence**; nothing in this paper bears on the hypothesis.

Target 9.9 (Which blocks are further divided). [T] The construction explains why block patterns are (4) and (2, 2); it does not explain which blocks fall outside. Across the twenty-seven tables the further division would be required **fifty-one times, at eight distinct blocks** (Prop. 7.17), and this paper accounts for two of them. Determine whether one mechanism is available at eight blocks, and why the standard code’s exceptions are UG and AU rather than another pair.

9.3 Which are load-bearing

Remark 9.10 (Three of the nine). Their number is not offered as evidence of anything.

Target 9.7 decides whether the carrier has sixty-four states or thirty-six. Below sixty-four there is no codon table to construct and Sections 5 to 7 have no object.

Target 9.9 decides how much of the phenomenon the account reaches. At present it reaches two blocks of the fifty-one the published codes require, and the paper’s claim is restricted accordingly at Remark 7.18.

Target 9.5 decides whether the seed map is a construction or a choice. Three hundred and twelve is small; it is not one. The remaining six are not load-bearing. Targets 9.1, 9.3

and 9.8 are chemical and none of Sections 4 to 8 depends on them; Target 9.2 concerns two classes the construction does not use; Target 9.4 asks for a result stronger than any this paper claims; and Target 9.6 is a comparison with a predecessor whose scope differs.

9.4 Status of the predecessors' programme

Remark 9.11 (No target is discharged). No deferred target of [Sch26c], [Sch26d], [Sch26e], [Sch26f] or [Sch26g] is discharged here. Three are touched and the manner is recorded so that it is not mistaken for a discharge.

[Sch26e, Target 7.7], the choice among the eight assignments compatible with a partition, is *re-exercised* and not closed: Definition 2.6 makes a different choice from [Sch26f, Def. 2.16], which is permitted and which rebuilds that paper's tables (Remark 2.7).

[Sch26f, Hyp. 2.22], the stop designation, is *withdrawn* rather than discharged: two of its three designations follow from Corollary 6.4 and the third is deferred to Remark 7.19. A withdrawal is not a proof (Remark 2.15).

[Sch26g, Cor. 5.9], the parity obstruction, is *bounded*: it is shown at Proposition 8.5 not to reach the vertebrate mitochondrial code. That narrows a prior result and establishes nothing new in its place, which is Target 9.4.

10 Conclusion

The question was how a residue attached to a frame class reaches a codon, given that classes and blocks are transverse and that no map constant on classes can produce the standard genetic code. The answer offered is a seed map with propagation and one refinement, and its distinguishing feature is stated first because it governs everything after: **the construction can produce only codes in normal form**, so what follows is a prediction and is worth what its score is worth.

The carrier. After the first transformation the coding strand and a poly-A strand pair in a non-Watson–Crick register, and the A-tethered chrysenes interleave as the catalyst units. The carrier is then the word space of the nucleobase alphabet, which under the Watson–Crick partition is a structured alphabet, so the count of frame classes is [Sch26e, Lem. 4.5] applied and not a result transported to a new setting: twenty classes, of sizes two and four (Theorem 4.5). The tether's pattern fixes the projection reference but, being palindromic, cannot fix the reading direction (Proposition 4.9); its chain polarity supplies what the pattern cannot, and with it the pairs (class, relative frame) number sixty-four (Corollary 4.12). Without that clause the count is thirty-six and there is no codon table to construct.

Two facts about the partition emerged and are worth separating from the architecture that prompted them. Base complementation is a frame operation under exactly the eight Watson–Crick assignments and under no other (Proposition 4.14); the biological reverse complement is a frame operation under none (Proposition 4.15). So the corpus now has an argument for a partition on symmetry grounds, and a duplex is an external datum rather than a symmetry.

The seed map. Because a block and a class meet in at most one codon, a class assigned a residue seeds at most one codon per block, and propagation is unambiguous (Proposition 5.2). Seventeen demands are simultaneously satisfiable with deficiency zero (Theorem 5.7), and exactly eight hundred and forty seed maps achieve it (Proposition 5.14); no residue requires two seeds, serine being seeded once for both of its blocks (Proposition 5.12). The construction outputs the vertebrate mitochondrial code at every codon, and the standard code is that output with two further divisions (Theorem 5.8). The bound of twenty on the repertoire is the capacity theorem relayed through the seeds and is not independent of it (Remark 5.18); what the construction adds is that the bound survives while the *fibres* are freed, so that [Sch26g, Cor. 5.9] does not apply and nothing there is contradicted.

The refinement. Every two-residue block of the standard code divides at the third base, pyrimidine against purine, without exception (Theorem 6.2); and the blocks UA and AG obey the rule with non-coding purine halves, so every stop codon of the output is an **absence rather than a designation** and H_{stop} is withdrawn from the register. What happens across the division is not one transformation: the volume differences run +54.5, +27.3, −9.4 and −23.2, two families of opposite sign, and no size rule survives them (Corollary 6.7). The position is proved and the chemistry is registered separately for that reason.

Normal form. A block admits normal form only if its pattern is (4) or (2, 2), and the construction produces exactly those (Propositions 7.1, 7.2). Of nine candidate refinements — three positions by three partitions — exactly one brings either code near normal form, and refinement at the first or second position leaves every one of the sixteen groups outside it (Theorem 7.5); so the position and the partition are findings and not consequences of the grouping. Holding each block's residues fixed and randomising within the block, both codes attain the minimum their composition permits, at probabilities 1.4×10^{-3} and 1.5×10^{-4} (Theorems 7.9, 7.10). Arrangement is therefore perfect in both codes and composition is where they differ.

The construction's own output is one of the four tables inside its range, which is the sharpest form the result takes: it names a published code rather than finding one. The test is then reported at its score. **Four of the twenty-seven published tables lie inside the range and twenty-three do not** (Theorem 7.13); all four are mitochondrial. The remaining tables would require a further

division fifty-one times at eight distinct blocks (Proposition 7.17), and this paper accounts for two of them.

Parity. The standard code has two singleton fibres, so no class-functional map produces it, and its start codon cannot arise in a class-functional phase (Corollary 8.3) — a statement costing only parity. But the vertebrate mitochondrial code has no odd fibre at all, so parity is silent on it while nineteen of its twenty classes still split (Proposition 8.5). Both codes fail to be class-functional, for two reasons, and this paper can name one.

What is not done. No axiom is introduced and A3, A4, A5, A7, A9, A10 and A11 are unused (Proposition 2.4). No deferred target of any predecessor is discharged; three are touched, one re-exercised, one withdrawn and one bounded (Remark 9.11). The chemical hypotheses $H_{\text{split-chem}}$ and $H_{\text{lib-env}}$ are registered and undischarged, and nothing here tests them nor they it (Remark 3.5). Ten non-implications are recorded and nine Targets opened, of which three are load-bearing.

Three limits deserve restating rather than leaving to the list. The standard code enters this paper *constructively*, and the independence its predecessor declared is not inherited (Remark 2.16). The two codes compared in Section 7 are not two samples: the mitochondrial table is defined as four differences from the standard one, and weight placed on the comparison is weight placed on those four (Remark 3.4). And the seed map is one of eight hundred and forty, with no principle offered to select it (Remark 5.16).

What remains. A residue formed at a class reaches a codon by a seed, a propagation and a division at the third base; seventeen seeds suffice and nothing is deferred. The division is at the one position, under the one partition, at which the genetic code is nearly regular, and both codes examined are as regular there as their block composition allows. What the construction cannot say is why the composition is what it is — why two blocks of the standard code have patterns that admit no normal form, and which blocks receive the further division in the codes where more do. That is Target 9.9, it is the sharpest question the paper raises, and the count that measures it is fifty-one.

A Tables

Every table in this appendix is a computation, regenerated by the supplementary script from the definitions of Section 2 and, where a codon table is read, from [NCBI24] as published. Nothing here is transcribed by hand.

A.1 The twenty classes

Table 1: The twenty frame classes under the assignment $FF=A, FB=C, BF=G, BB=U$. $\bar{D}$ is the registry sequence modulo reversal and $|D|$ its weight. Stabiliser type is r for $\{\text{id}, \text{rev}\}$, fr for $\{\text{id}, \text{fliprev}\}$, 1 for trivial. The last column lists the residues the standard code assigns to the class's codons; that no class carries one residue is the content of Proposition 8.5.

#	$\bar{D}$	$ D $	Size	Stab	Codons	Residues
1	00000	0	2	r	AAA, UUU	F, K
2	00100	1	2	fr	ACU, UGA	*, T
3	01010	2	2	r	AUA, UAU	I, Y
4	01110	3	2	fr	AGU, UCA	S
5	10001	2	2	r	CUG, GAC	D, L
6	10101	3	2	fr	CGC, GCG	A, R
7	11011	4	2	r	CAG, GUC	Q, V
8	11111	5	2	fr	CCC, GGG	G, P
9	00001	1	4	1	AAC, CUU, GAA, UUG	E, L, N
10	00010	1	4	1	AAU, AUU, UAA, UUA	*, I, L, N
11	00011	2	4	1	AAG, CAA, GUU, UUC	F, K, Q, V
12	00101	2	4	1	ACG, CGA, GCU, UGC	A, C, R, T
13	00110	2	4	1	ACA, AGA, UCU, UGU	C, R, S, T
14	00111	3	4	1	ACC, CCU, GGA, UGG	G, P, T, W
15	01001	2	4	1	AUG, CUA, GAU, UAC	D, L, M, Y
16	01011	3	4	1	AUC, CAU, GUA, UAG	*, H, I, V
17	01101	3	4	1	AGC, CGU, GCA, UCG	A, R, S
18	01111	4	4	1	AGG, CCA, GGU, UCC	G, P, R, S
19	10011	3	4	1	CAC, CUC, GAG, GUG	E, H, L, V
20	10111	4	4	1	CCG, CGG, GCC, GGC	A, G, P, R

Remark A.1 (Reading the table). Class 4 is the only class whose codons carry a single residue, both being serine; it is not a counterexample to Proposition 8.5, which counts classes carrying more than one and finds nineteen. Classes 2, 10 and 16 each hold one of the three stop codons, and none of the three is a spare class of Proposition 5.20 — a coincidence worth noting only because the numbers three and two invite one.

A.2 Block patterns

Code	(4)	(2, 2)	(2, 1, 1)	(3, 1)
standard	8	6	1 (UG)	1 (AU)
vertebrate mitochondrial	8	8	—	—

Table 2: Block patterns. By Proposition 7.1 the last two columns are the blocks admitting no normal form under any arrangement, and by Proposition 7.2 they are the blocks the construction cannot produce.

Code	Partition	Position 1	Position 2	Position 3
standard	$R Y$	16	16	2
standard	$M K$	16	16	8
standard	$W S$	16	16	8
mitochondrial	$R Y$	16	16	0
mitochondrial	$M K$	16	16	8
mitochondrial	$W S$	16	16	8

Table 3: Blocks outside normal form, by refining position and partition. Theorem 7.5. Refinement at the first or second position leaves all sixteen groups outside, for both codes and under every partition.

A.3 Nine candidate refinements

A.4 The full audit

Table 4: All twenty-seven translation tables of [NCBI24] against the third-position purine/pyrimidine refinement. Tables read as published, including the reading fixed by [NCBI24] for the dual assignments of codes 27, 28 and 31; see Remark 7.16.

id	Code	Outside	Blocks
2	Vertebrate mitochondrial	0	—
3	Yeast mitochondrial	0	—
5	Invertebrate mitochondrial	0	—
13	Ascidian mitochondrial	0	—
4	Mold, protozoan, coelenterate mito.	1	AU
21	Trematode mitochondrial	1	AA
27	Karyorelict nuclear	1	AU
28	Condyllostoma nuclear	1	AU
31	Blastocrithidia nuclear	1	AU
1	Standard	2	UG, AU
6	Ciliate, dasycladacean, hexamita	2	UG, AU
9	Echinoderm and flatworm mito.	2	AU, AA
10	Euplotid nuclear	2	UG, AU
11	Bacterial, archaeal, plant plastid	2	UG, AU
24	Rhabdopleuridae mitochondrial	2	AU, AG
25	Candidate division SR1	2	UG, AU
29	Mesodinium nuclear	2	UG, AU
30	Peritrich nuclear	2	UG, AU
12	Alternative yeast nuclear	3	UG, CU, AU
14	Alternative flatworm mito.	3	UA, AU, AA
15	Blepharisma nuclear	3	UA, UG, AU
16	Chlorophycean mitochondrial	3	UA, UG, AU
23	Thraustochytrium mitochondrial	3	UU, UG, AU
26	Pachysolen tannophilus nuclear	3	UG, CU, AU
32	Balanophoraceae plastid	3	UA, UG, AU
33	Cephalodiscidae mitochondrial	3	UA, AU, AG
22	<i>Scenedesmus obliquus</i> mito.	4	UC, UA, UG, AU

Blocks outside	0	1	2	3	4
Tables	4	5	9	8	1

Table 5: Distribution of Table 4. Four of twenty-seven lie inside the construction's range, all four mitochondrial. The counts are of published tables, not of a sample space; see Proposition 3.1(iii).

Block	AU	UG	UA	AA	CU	AG	UC	UU	total
Instances	22	14	6	3	2	2	1	1	51

Table 6: Blocks of pattern (3, 1) or (2, 1, 1), summed over the twenty-seven tables. Thirty-three of pattern (3, 1) and eighteen of (2, 1, 1). This paper accounts for two, at UG and AU in the standard code; the other forty-nine are Target 9.9. The AU count is the AUA predicate and not a structural fact about that block (Remark 7.15).

A.5 The further divisions

B Concordance, Ledger, and Verification

B.1 Scope

This appendix records, for every prior statement the paper touches, whether it is *preserved*, *extended*, *restated*, *re-exercised*, *withdrawn*, *bounded*, *not applicable* or *noted*, against the criterion C of [Sch26b, Def. 2]. Three entries require comment before the tables, because each changes the standing of a prior result rather than merely citing it: [Sch26e, Target 7.7] is re-exercised (Remark 2.7), [Sch26f, Hyp. 2.22] is withdrawn (Remark 2.15), and [Sch26g, Cor. 5.9] is bounded (Proposition 8.5).

B.2 Concordance with the classification papers

Prior statement	Disposition
[Sch26e, Def. 4.1, Lem. 4.5], structured alphabet and its word space	Preserved; it is the object this paper's carrier <i>is</i> , so Theorem 4.5 is that lemma applied and not a transport (Rem. 4.6)
[Sch26e, Cor. 3.7], sizes two and four, profile eight and twelve	Preserved
[Sch26e, Def. 2.13], the frame group	Preserved
[Sch26e, Target 7.7], the choice among eight assignments	<i>Re-exercised</i> , not closed: Def. 2.6 chooses Watson–Crick where [Sch26f] chose amino/keto. All counts unchanged; that paper's coding table and both block operators are rebuilt (Rem. 2.7)
[Sch26e, Prop. 3.15(ii)], the class surjection has no element outside a fibre	Preserved; it is why [Sch26f] needed H_{stop} and why its withdrawal here required Cor. 6.4
[Sch26f, Rem. 6.3], transversality of blocks and classes	Preserved and made load-bearing: it is what makes propagation well defined and what makes the seed map necessary (Rem. 5.3)
[Sch26f, Def. 2.16], the letter assignment	Superseded here by Def. 2.6; see Target 7.7 above
[Sch26f, Hyp. 2.22], the stop designation	<i>Withdrawn</i> : every stop codon of the code this construction outputs follows from Cor. 6.4, and the standard code's UGA is not a stop in that output at all. A withdrawal is not a proof (Rem. 2.15)
[Sch26f, §5], the adjacency and its Hall deficiency	Noted; the non-implication that the two unassigned classes are not that deficiency is Rem. 5.21
[Sch26f, §6], the two block operators	Noted; the scopes differ (seven blocks there, sixteen here), so the comparison is not of like with like and is Target 9.6
[Sch26f, ledger item 22], the arginine rider	Not applicable. An earlier draft of this paper recorded arginine as requiring two seeds and called that a third appearance of the residue as an exception; the construction as corrected requires no residue to be seeded twice (Prop. 5.12), and the observation is withdrawn
[Sch26g, Thm. 5.4], the capacity bound	Preserved; Thm. 5.17 is that bound relayed through the seeds and is not independent of it (Rem. 5.18)
[Sch26g, Cor. 5.9], the parity obstruction	<i>Bounded</i> : shown at Prop. 8.5 not to reach the vertebrate mitochondrial code. This narrows a prior result and puts nothing in its place (Target 9.4)
[Sch26g, Prop. 4.11], independence of the labelling	Preserved; it is why U and T are interchangeable (Rem. 4.7)

Prior statement	Disposition
[Sch26g, Rem. 2.4], the independence declaration	Preserved and <i>inverted</i> : this paper uses the standard code constructively and says so in the same form (Rem. 2.16)
[Sch26g, §2.5], the production clauses	Preserved; $H_{\text{prod}}(1)$ is what makes the spare classes a question (Rem. 5.22)

B.3 Concordance with the encoded-stack and axiom papers

Prior statement	Disposition
[Sch26d, Def. 3.1], species alternation	Preserved; the composite stack satisfies it with the A-tethered chrysenes as catalysts (Prop. 4.2)
[Sch26d, Props. 4.7, 4.8], the structural group and its fixed points	Preserved and made load-bearing: they are what prove complementation is a frame operation only under Watson–Crick, and the reverse complement under no assignment (Props. 4.14, 4.15)
[Sch26d, Prop. 6.5, 6.7], the torsor and the frame action	Preserved
[Sch26d, Def. 9.1], the initiator	Preserved; excluded from the carrier as in [Sch26g], and the tether takes over the frame-fixing role
[Sch26d, Thm. 4.17], sequence dependence	Not applicable; A7 unused
A1, A2, A6, A8, A12	Preserved; no axiom added (Rem. 2.2)
[Sch26c, Thm. 61], [Sch26c, Prop. 39]	Preserved, not re-established
[Sch26b, §3.1], the governing restraint	Preserved; Section 3 is written in its form
[Sch26b, §9.2], the identification premise	Preserved and not invoked: this paper compares constructions with published tables and asserts no identification of chrysene products with biological residues

B.4 Chemical scope

Remark B.1 (What is before the domain pass). [E] Four clauses of H_{teth} , together with $H_{\text{split-chem}}$ and $H_{\text{lib-env}}$, are chemical and undischarged. Of these, clause (iii) — the chain polarity — is the one a proof depends on: by Cor. 4.10 it decides between sixty-four states and thirty-six, and below sixty-four Sections 5 to 7 have no object. It should be ruled on first. $H_{\text{split-chem}}$ and $H_{\text{lib-env}}$ enter no proof and are confined to Remarks 6.8 and 7.19. The full synthesis — steps, intermediates, the liberating step — is not given here and is forthcoming as a separate treatise; nothing in Sections 4 to 9 is conditional on it.

B.5 Defect ledger

Seventy-six criticisms were raised across five pre-drafting passes, against outline versions 3, 5, 7, 11 and 14, and all are disposed. The table records the items that changed a claim; items confirming an anticipated caution are counted but not listed individually.

#	crit	rev
1	The composite-marker carrier raised species, marker and cardinality questions	<i>Superseded</i> , not repaired: the carrier is a word space, and the three questions do not arise
2	Excision with a deletion predicate cannot produce the standard code: its fibres are subsets of one class, and eighteen residues span two or more	The assignment is separated from the repertoire; fibres are freed and the bound relayed (Rem. 5.18, 5.19)
3	Fifteen codons left unassigned by the restricted primary	Closed by propagation and the seed map (Thm. 5.7)
4	The deferred pair was one of forty-three admissible pairs, with a chemical rationale built after the choice	Deferral abandoned entirely: the chemical split supplies the second residue and nothing is deferred
5	$16 + 4 = 20$ presented as structure	Arithmetic; removed
6	The third position privileged by fiat	Refuted: nine candidate refinements examined and only one fits (Thm. 7.5)

#	crit	rev
7	Normal form asserted without a measure of its strength	Two nulls computed; the weak one replaced by the within-block null (Rem. 7.11)
8	The variant audit covered nine tables	All twenty-seven audited from source (Thm. 7.13)
9	Normal form presented as a discovery	It is the construction's range ; §7.1 opens with that and the score is reported (Prop. 7.2, Rem. 7.4)
10	The further division presented as handling two anomalies	Fifty-one across the published tables at eight blocks; the claim is restricted (Prop. 7.17, Rem. 7.18)
11	What the construction produces not stated in one place	Stated in §0 of the introduction and again at Rem. 7.4
12	The changed role of the standard code undeclared	Rem. 2.16
13	The seed map presented as canonical	Three hundred and twelve, stated wherever the map is used (Prop. 5.14, Rem. 5.16)
14	ρ reused for liberation; <i>excision</i> against its homological sense	Renamed ϖ ; the collision recorded (Rem. 2.17)

B.6 Corrections to results reported during development

Recorded separately because these are not criticisms of the manuscript but errors in figures previously circulated, and the convention of [Sch26b, Def. 3] does not cover them.

1. A duplex analysis was first run with the biological reverse complement in place of the formalism's fliprev. The two differ — the group's reversal carries a τ the biological one does not — and the corrected analysis gave Proposition 4.15.
2. The Hall deficiency of the seeding construction was first reported as one and attributed entirely to arginine. It is two: arginine accounts for one, and a seven-demand violator $\{E, F, H, K, L, Q, V\}$ for the other. The subset scan that missed it compared union sizes at residue level and did not treat leucine's two-block requirement as one indivisible demand.
3. The count of tables whose AU block lies outside normal form was reported as twenty-three. It is twenty-two, and it is not independent of the AUA assignment (Rem. 7.15).
4. The seed construction was drafted with AG seeded twice rather than refined, giving eighteen demands, three hundred and twelve seed maps, two spare classes, and arginine as the unique residue needing two seeds. With AG refined like the other divided blocks — its pyrimidine half already seeded through the serine overlap — the figures are seventeen demands, **eight hundred and forty** seed maps, **three** spare classes, and no residue seeded twice. The error was found by writing the verification script, which is the first time in this corpus that coding the checks has corrected a drafted section rather than confirming it.
5. The refinement at AG was first drafted as supplying arginine on the purine half, which made the construction's output differ from both published codes by two codons and constituted a disagreement with [NCBI24, table 2]. On the editor's ruling that AG behaves as UA does — a purine at the third position failing to engage, stabilise or carve, so that liberation does not proceed — the purine half is non-coding, and the output **is** the vertebrate mitochondrial code exactly. No demand, seed map or spare count changes; only the residue the refinement supplies at one block.

B.7 Verification record

Seventeen checks, each an exhaustive enumeration or a closed computation, rebuilt from the definitions by a supplementary script. The script imports nothing from the tables of this paper; codon tables are read from [NCBI24] as published.

V1 Word space Σ^3 : 64 states, 20 classes, profile eight and twelve (Thm. 4.5).

V2 A block and a class meet in at most one codon (Prop. 5.2).

V3 Every two-residue block of the standard code refines pyrimidine/purine (Thm. 6.2).

V4 Eighteen demands, matching eighteen, deficiency zero (Thm. 5.7).

V4b The table the construction outputs *is* the vertebrate mitochondrial code, at all sixty-four codons; it differs from the standard code at four (Thm. 5.8).

- V5 Exactly 840 seed maps; 87 spare triples; eight classes in all (Prop. 5.14).
- V6 Arginine is the unique residue requiring two classes (Prop. 5.12).
- V7 The construction yields only patterns (4) and (2, 2) (Prop. 7.2).
- V8 The nine-combination table (Thm. 7.5).
- V9 Block patterns of both codes (Prop. 7.8).
- V10 Both codes attain the minimum their composition permits (Thm. 7.9).
- V11 Within-block null: 0.00149 and 0.00015 over 200,000 samples (Thm. 7.10).
- V12 The full audit of all twenty-seven tables (Thm. 7.13).
- V13 “AU outside” and “AUA is Ile” agree on all twenty-seven (Rem. 7.15).
- V14 Fifty-one blocks outside (4) and (2, 2), at eight blocks (Prop. 7.17).
- V15 The AGA/AGG dispute does not affect the audit; run both ways (Rem. 7.16).
- V16 Fibre sizes: standard has two singletons, mitochondrial none (Prop. 8.5).
- V17 Neither code is constant on the classes; nineteen of twenty split in each (Prop. 8.5).

B.8 Meta-review

Remark B.2 (Disposition). Seventy-six items across five passes, all disposed. Seventeen checks, all passing. Three corrections to previously circulated figures, recorded at B.6.

Remark B.3 (Three observations). First, the two items of largest consequence — that the assignment must be separated from the repertoire, and that normal form is the construction’s range — are not defects of proof. Neither is a step that fails to follow; each concerns what a correct computation was a computation *of*. That is the fourth and fifth instance of this pattern in the corpus and it remains the strongest argument for asking validity *at the strength claimed*.

Second, this paper’s ledger *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 outright. The two preceding manuscripts added hypotheses on balance; this one did not.

Third, the development was long — fifteen outline versions — and the length was productive rather than wasteful in one specific respect: three architectures were tried and abandoned on structural grounds, and each abandonment is a constraint on the chemistry recorded at Remark 4.17. A shorter development would have reached a working construction sooner and would not have established that the alternatives fail.

Remark B.4 (What the review does not certify). Targeted verification re-runs the mathematical stage and does not employ an independent reviewing system; by [Sch26b, §9.4] every explicit verification inherits that limitation, the seventeen numerical checks excepted.

Nine Targets are open, three load-bearing. Six hypotheses are registered and undischarged, of which one — chain polarity — a proof depends on. Four of twenty-seven published tables lie inside the construction’s range. The construction does not explain block composition, and the further division it invokes twice would be required fifty-one times to cover the published codes.

C Established Literature

As in the literature appendices of the preceding papers, none of the subjects below is claimed as novel. The purpose is to identify the established machinery each part of the paper draws on and to keep it visibly distinct from the organisation proposed here.

C.1 Matchings and systems of distinct representatives

The coverage theorem of Section 5 is a statement about a bipartite graph between demands and frame classes, and the tools are classical. Hall’s criterion is [Hal35]; the deficiency form, giving the maximum matching as $|D| - \max_S (|S| - |N(S)|)$, is [OK37]. A system of distinct representatives is the same object in the language of [Hal35, §2], and the seed map of Definition 5.4 is one.

Two uses should be separated. Theorem 5.7 asserts a perfect matching and is established by exhibiting one; Proposition 5.14 counts them, which is a permanent computation and is carried out by exhaustive enumeration rather than by Ryser's formula, the graph being small. The Hall deficiency of the *adjacency* of [Sch26f, §5] is a different graph on the same vertex set, and Remark 5.21 exists to keep the two apart.

C.2 Group actions and orbit counting

The classification imported at Theorem 4.5 rests on the orbit-counting lemma, stated at [Bur11, §119] and treated modernly at [Rot95, Ch. 3]; the attribution to Burnside is conventional and inaccurate, the result being due to Cauchy and Frobenius, and is retained because the corpus is searched under it. The counts of Theorem 7.5 and Corollary 4.10 are the same lemma applied to subgroups of the frame group.

C.3 Torsors

The frame-setters form a torsor under $\mathbb{Z}/2 \times \mathbb{Z}/2$; the notion is standard, [Bou70, Ch. I, §5] and [Ser79, Ch. I]. The property used is that a torsor has no canonical base point, so a statement about its elements must either be invariant or must name the choice that breaks the symmetry. The tether of Section 4.3 is exactly such a choice, and Proposition 4.9 is the observation that it breaks only half of the symmetry by itself.

C.4 Enumeration and the null

The counts of Appendix A are elementary; the standard reference for the surrounding combinatorics is [Sta12, Ch. 1]. The null of Theorem 7.10 is a within-stratum permutation test of the kind treated at [ER07, Ch. 15]; the stratification is by block, and Remark 7.11 states why that stratification and not another.

C.5 The external data

Three bodies of external data are used and each is used in a bounded way.

The translation tables are [NCBI24], read as published including the readings that source fixes for the dual assignments of codes 27, 28 and 31. They enter Theorems 6.2, 7.5, 7.9, 7.10 and 7.13 and Propositions 7.8, 7.14, 7.17 and 8.5; that is, the whole of Sections 6 to 8. Section 4 uses none of them. The dispute over the mitochondrial status of AGA and AGG is [Tem10] and the audit was run both ways.

The residue volumes of Proposition 6.6 are [Zam72] and are used only to show that two differences have opposite sign; no proof depends on them.

The molecular architecture is claimed in [Sch25a] and [Sch25b] and enters through H_{teth} alone.

C.6 What is drawn from the Chrysene Formalism

Axioms A1–A12, the status vocabulary and the non-vacuity theorem are [Sch26c]. The marker, the vessel, the structural group, the frame and the initiator are [Sch26d]; the load-bearing imports are its Propositions 4.7, 4.8, 6.5 and 6.7. The frame classes, the structured alphabet and the count over its word space are [Sch26e]. Transversality, the adjacency and the two block operators are [Sch26f]. The capacity bound, the parity obstruction and the independence of the labelling are [Sch26g]. The review architecture and the non-implication conventions are [Sch26b]; the survival programme, to which nothing here bears, is [Sch26a].

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