

PART I OF TWO

The Conditional Refinement

Two Resolutions of the Standard and Mitochondrial Codes, and the Insufficiency of Block Data

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Abstract

The preceding paper seeds a codon block, propagates, and divides once at the third base, and its output is the vertebrate mitochondrial code at every codon. It describes the standard code as that output with two further divisions. That is two thirds of the distance: the two codes differ at four codons spanning three half-blocks, and at the third of them, the purine half of AG, both codes are uniform and no division occurs — an absence in the output is arginine in the standard code. We remove the second operation by widening the first. The outcome at a half is three-valued — release a residue uniformly, release nothing, or resolve the two codons differently — and which value it takes is conditional on the environment, through a pair of thresholds on an effective vessel volume. Normal form is the case where the third value never occurs, the two codes are two settings, and **the preceding paper is recovered entire as the mitochondrial case, with no operation added**. The direction is fixed by the code data against the chemistry one would try first: at AG the low-pH compartment releases and the high-pH one terminates, so the limiting step is engagement and not escape.

The scheme then predicts a third setting neither code uses, and four published tables occupy it, three of them among the four the preceding paper finds in normal form; one monotone parameter, with thresholds shared across all sixteen purine halves, orders tables 1, 3, 5, 13 and 2 in that sequence. Nothing required a third regime to be occupied. This, and not the two-code fit, is the paper's evidence.

Widening the outcome set also widens the range, and the score moves with it. All twenty-seven published translation tables lie inside the range against four of twenty-seven inside its predecessor's. That is a weaker prediction with a perfect score and not a better result, and the one surviving prohibition — a pyrimidine half is uniform, satisfied at 432 of 432 — is third-position synonymy. A conjecture of the paper's own, that the two codes are the two fixed points of the implied feedback circuit, is withdrawn: the record occupies at least four settings. **Part II supplies all three from one object, the chrysene-adenosine reaction cell, in which reachability of a carve is a maximum over reaction words of a minimum over cage margins, and so a step function of a continuous environment.**

Keywords: Chrysene Formalism; conditional refinement; half-block resolution; third-position refinement; normal form; genetic code; mitochondrial code; translation tables; engagement threshold; linear infeasibility; Farkas certificate; compartment pH; feedback fixed point; non-implication.

1 Introduction

1.1 The problem

[Sch26h] seeds a block of the codon table with a residue drawn from a frame class, propagates the seed through the block, and divides the block once at the third base, pyrimidine against purine. The output of that construction is the vertebrate mitochondrial code at every one of the sixty-four codons.

The standard code is not that output. [Sch26h] reaches it by dividing two purine halves once more, at AUA and at UGA — an operation invoked twice and not derived, and the paper says so. **Nor are two divisions enough.** Its own Theorem 5.8 lists four codons at which the output and the standard code differ, spanning three half-blocks, and the third of them — the purine half of AG — is uniform in both codes. No division occurs there. What changes is whether the half liberates at all: an absence in the output, arginine in the standard code.

So the distance between the two codes is three halves and not two divisions, and an account of it must cover a half at which nothing is divided.

1.2 The objective

To remove the second operation by widening the first. The outcome of the division at a half is made three-valued rather than two — release a residue uniformly, release nothing, or resolve the two codons differently — and which value it takes is made conditional on the environment. To determine what such a refinement can and cannot produce. And, having found that it produces far more than its predecessor did, to report what that costs.

1.3 What is established

1. The two codes differ at exactly three half-blocks, all purine, at four codons, and setting those three halves of table 2 to their table-1 values returns table 1 entire (Thm. 5.7, Cor. 5.9). This corrects [Sch26h, Rem. 7.19] (Rem. 5.10).
2. At the higher setting the refinement takes no third value and its output is table 2, so [Sch26h] is the $\varepsilon_{\text{mito}}$ case; at the lower it is table 1. The two further divisions of that paper are the third value of the one refinement and no operation is added (Thm. 8.1, Cor. 8.4).
3. The direction of the environmental effect is fixed by the code data against the chemistry one would try first: at AG-pur the low-pH compartment releases and the high-pH one terminates, so the limiting step is engagement and not escape (Cor. 6.4).
4. The scheme posits a third regime that the two codes do not use, and **four published tables occupy it** (Prop. 8.6); one monotone parameter orders tables 1, 3, 5, 13 and 2 with thresholds shared across all sixteen purine halves (Thm. 8.7). **A null is reported against the second:** nine per cent of five-table subsets are orderable, a sixteen-table set exists, and all but one comparison in the exhibited sequence is forced (Rem. 8.8).
5. **No threshold that is a function of the block fits.** There is no pair of thresholds linear in product volume, second-position association and first-base strength consistent with the purine column, at any parameter count and not with the association scale fitted (Thm. 7.6).
6. **No single environmental parameter orders the record.** With thresholds free, one hundred and thirty of the three hundred and fifty-one pairs of published tables admit no common position on any axis (Thm. 8.10, Cor. 8.11).
7. Of thirty-two halves, twenty-three never vary and eight of the nine that do are purine; but the confinement is largely

stop recoding, and stripping it carries the figure to four of five halves (Prop. 5.2, Rem. 5.5).

1.4 What is not claimed

No axiom is introduced (Rem. 2.2), and no deferred target of any predecessor is discharged (Rem. 10.10).

Four 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 score. [Sch26h] could report that four of twenty-seven published tables lie inside its construction's range, and that the figure was a test because the range was narrow. All twenty-seven lie inside the range of the conditional refinement. **That is not a better result; it is a weaker prediction with a perfect score**, and the improvement is an artefact of widening the outcome set (Rem. 8.14). The one prohibition that survives — that a pyrimidine half is uniform — is satisfied at four hundred and thirty-two of four hundred and thirty-two, and is third-position synonymy (Rem. 8.16).

The second concerns the content. The refinement fixes outcome types and not residues. The purine half of AG is uniform and coding across the record under arginine, serine and glycine, so every residue named in Sections 5 and 8 is read from the published tables and enters on an empirical clause (Prop. 5.12, Rem. 2.14).

The third concerns the two codes. They are not two samples: the mitochondrial table is defined in [NCBI24] as a list of differences from the standard one, so weight placed on the comparison is weight placed on four codons (Rem. 8.17). It is for this reason that Theorem 8.7, which orders five tables, and not Theorem 8.1, which fits two, is offered as the paper's evidence.

The fourth concerns the loop. The conjecture that the two codes are the two fixed points of the feedback circuit is *withdrawn*: classified by the three conditional halves the record occupies at least four settings (Cor. 9.6). And no theorem here would change if the circuit were false (Rem. 9.8).

1.5 Logical position

Every numbered statement carries one of the four status labels of Definition 2.1; every hypothesis is registered at Section 2.4; every molecular reading is confined to a remark marked [E] and enters no proof.

Two features of the record are stated here rather than in the appendix. Like its predecessor and unlike [Sch26g], this paper uses the standard genetic code constructively, and the independence [Sch26g] declared is not inherited (Rem. 2.15). And unlike [Sch26h], whose Appendix C.5 declares that no proof depends on the residue volumes of [Zam72], **a proof of this paper does**: Theorem 7.6 turns on a difference of $3.8 \text{ \AA}^3$ between leucine and methionine (Rem. 2.16).

The defect ledger of Appendix B records twenty items from one pre-drafting pass, together with eight corrections to figures circulated during development. Two of the eight were claims written in prose and refuted by computing them, and one of those two — that no published table exhibits the account’s third regime — turned a drafted gap into Proposition 8.6, whose evidential weight is reassessed at Remark 8.8.

1.6 What the refinement produces

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

A block is seeded and propagated as in [Sch26h]; its pyrimidine half is uniform and cannot be otherwise. Its purine half resolves in one of three ways, and which one is set by the environment through a pair of thresholds. **That machinery produces the vertebrate mitochondrial code at one setting and the standard code at another, and produces every block pattern the published record contains.** It does not say which halves have which thresholds, and Section 7 shows that the quantities the architecture supplies cannot say.

1.7 What Part II must supply

This paper is the first of two, and the division between them is not editorial. **Everything below treats the reaction vessel as a black box parameterised by a single effective volume V ,** which Remark 2.6 concedes is an ordering with no referent. The construction of [Sch26h] is inherited entire — seeds, propagation, the third-position refinement — so what is absent here is not the chrysene cluster but the *cell*: the chrysene–adenosine complex stacked against a codon, its cage geometry, and the constraint margins of [Sch26m].

Three results of this paper are statements about what that black box cannot do, and each is a specification for Part II.

Theorem 7.6 says the release points are not a function of the block. No threshold linear in product volume, second-position association and first-base strength fits the purine column, at any parameter count. A quantity that is not a property of the block is required, and Target 10.1 asks for one. Part II supplies it as a property of the cage: the codon enters the reaction cell through its stacking geometry, not through an algebraic feature of its block.

Theorem 8.10 says one environmental coordinate does not order the record. One hundred and thirty of the three hundred and fifty-one pairs of published tables admit no common position on any single axis. In Part II that count is not a failure but a measurement: it is a lower bound on the dimension of the space in which the cell’s medium moves.

Remark 8.18 says the account cannot distinguish an ordering from a mechanism. Nothing here gives V a referent. Part II gives it one by composing a cage response with the margins of [Sch26m], at which point $H_{\text{eng-type}}$ ceases to be a hypothesis of this paper and becomes a theorem of that one.

The series goal is a conditional sufficiency theorem: that a chrysene cluster, carried into a reaction cell whose cage responds to its medium, carves the standard code at one environment and the vertebrate mitochondrial code at another. This paper proves the insufficiency that makes such a theorem necessary. It does not prove the theorem, and a reader who takes its negative results for the whole of the programme has read only half of it.

One further division is worth stating here. This paper reads the two codes **evolutionarily**: Section 9 registers a feedback circuit, asks after fixed points, and withdraws a conjecture about them. Part II reads the same objects as a **synthesis**: given a codon and an environment, what does the cell carve? It needs no circuit, no fixed point and no common ancestor, and carries none of Section 9 forward.

1.8 Organization

Section 2 fixes conventions and the register. Section 3 states the traps, before the constructions they guard. Section 4 defines the refinement and records what widening it costs. Section 5 reports the published record at the half-blocks. Section 6 gives the engagement reading, fixes its direction, and identifies the switch. Section 7 is the first core section and is negative: no block-feature threshold exists. Section 8 is the second: the two codes as two settings, [Sch26h] recovered and corrected, the third regime attested, and the ordering shown not to extend. Section 9 registers the feedback circuit and withdraws a conjecture. Section 10 restates the non-implications and opens eight Targets. Appendix A tabulates; Appendix B is the concordance, the ledger and the verification record; Appendix C the literature. Section 1.7 states what Part II inherits from each of Sections 7 to 9.

2 Conventions 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]–[Sch26h], is definitional within $\{A1, \dots, A12\}$, or is a realization hypothesis registered at Section 2.4.

Remark 2.3 (Two counting conventions). Statements about a finite object — a published codon table, a set of halves,

a system of linear inequalities over them — are proved by enumeration or by a closed computation 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 at [Sch26h, Rem. 2.3].

The convention bites hardest at Section 7. Theorem 7.6 is a statement that a system of inequalities has no solution. It is [A]: no hypothesis of this paper enters it, and it would hold if the engagement reading of Section 6 were replaced by any other monotone account.

2.2 What is imported, and from where

Object	Source
block; transversality of blocks and classes	[Sch26h, Def. 5.1, Prop. 5.2]
the seed map, propagation, the output table	[Sch26h, Thm. 5.7, 5.8]
stops as absences on purine halves	[Sch26h, Cor. 6.4]
refinement at the third position, $R Y$	[Sch26h, Thm. 6.2]
block patterns; normal form as a range	[Sch26h, Props. 7.1, 7.2]
composition against arrangement	[Sch26h, Rem. 7.12]
the fifty-one further divisions	[Sch26h, Prop. 7.17]
the twenty classes; the frame group	[Sch26e, Cor. 3.7, Def. 2.13]
capacity; parity	[Sch26g, Thm. 5.4, Cor. 5.9]
the translation tables	[NCBI24]
residue volumes	[Zam72]
pK_a and isoelectric points	[NC17, Table 3-1]
compartment pH values	[Lle98]

Remark 2.4 (Four bodies of external data, each used in a bounded way). [NCBI24] is read as published, including the readings that source fixes for the dual assignments of codes 27, 28 and 31; it enters every count of Sections 5, 7 and 8. [Zam72] enters Section 7 alone and the standing it has there is declared at Remark 2.16. [NC17] and [Lle98] enter Section 6 alone, and no result outside that section depends on either: in particular Theorem 7.6 and Theorem 8.10 are independent of every pK_a and every pH value in this paper.

2.3 The environment

Definition 2.5 (The environment set). E is a set of *translational environments*, and $V : E \rightarrow \mathbb{R}$ is the effective vessel volume of Section 6. Two elements are named, ε_{nuc} and $\varepsilon_{\text{mito}}$, and Proposition 6.2 fixes $V(\varepsilon_{\text{nuc}}) < V(\varepsilon_{\text{mito}})$.

Remark 2.6 (V is an ordering and not a measurement). Nothing in this paper measures V , and no result requires a numerical value for it. Theorem 8.1 uses only that two environments are ordered; Theorem 8.7 exhibits an ordering of five; and Theorem 8.10 is the statement that no ordering

of twenty-seven exists. **Where the paper writes $V(\varepsilon)$ it means a position on an axis and not a volume in $\text{\AA}^3$,** and Remark 8.18 states what would be needed to give the axis a referent.

2.4 The register

Hypothesis 2.7 ($H_{\text{eng-type}}$). The value of $\mathcal{R}$ at a purine half is fixed by the environment through a pair of thresholds $t_1(h) < t_2(h)$: the half takes disc where $V(\varepsilon) < t_1(h)$, unif where $t_1(h) \leq V(\varepsilon) < t_2(h)$, and $\emptyset$ where $t_2(h) \leq V(\varepsilon)$.

Hypothesis 2.8 ($H_{\text{eng-content}}$). Where $\mathcal{R}$ takes the value $\text{unif}(r)$, the residue r is the one the published table assigns; and where it takes disc, which of the two codons carries which outcome is likewise read from the table.

Hypothesis 2.9 (H_{pH}). V is monotone in the pH of the compartment, increasing.

Hypothesis 2.10 (H_{latch}). The pH dependence of V is carried by a methionine–cysteine contact whose strength falls as the cysteine thiol is deprotonated.

Hypothesis 2.11 (H_{loop}). A code determines a proteome; the proteome determines the compartment chemistry; the compartment chemistry sets V ; V sets the resolutions; the resolutions determine the code. A self-consistent code is a fixed point of that circuit.

Remark 2.12 (Inherited unchanged). H_{teth} in its four clauses, H_{seed} , $H_{\text{split-pos}}$ and $H_{\text{split-chem}}$ are imported from [Sch26h, Hyps. 2.9–2.12] and are not restated. H_{seed} is load-bearing here in a way it is not there: clause (i) of Definition 4.5 — that a pyrimidine half is seeded and propagated rather than refined — is the *only* prohibition this paper’s construction carries (Proposition 8.15).

Remark 2.13 ($H_{\text{lib-env}}$ is specialised, not discharged). [Sch26h, Hyp. 2.13] makes liberation depend on the translational environment as well as on the cluster and the frame, and [Sch26h, Target 9.3] asks for what decides release at UGA and at AUA, calling for a measurement rather than a proof. This paper supplies a candidate variable and a direction: $H_{\text{eng-type}}$ makes the dependence a threshold crossing, Corol-

lary 6.4 fixes its sign against the code data, and H_{pH} names pH. **None of that is the measurement Target 9.3 asks for**, and Remark 6.19 records that pH is adopted rather than established. The target is therefore *addressed and not discharged*, in the sense of [Sch26b, Def. 2], and Section 9 records it in the form [Sch26h, Rem. 9.11] uses. Stating this is the point of the remark: the corpus's predecessor discharged nothing and said so, and a successor that quietly counted an adopted hypothesis as a discharge would be the first to break that record.

2.5 Why the engagement hypothesis is registered in two clauses

Remark 2.14 (The asymmetry the two clauses record). $H_{\text{eng-type}}$ and $H_{\text{eng-content}}$ are registered separately for the reason [Sch26h, Rem. 6.9] registers $H_{\text{split-pos}}$ and $H_{\text{split-chem}}$ separately: the paper establishes one and not the other.

Theorem 8.1 derives the *types* — that three halves change value between the two compartments, and in which direction — and that derivation is what Corollary 8.4 rests on. It derives no content. By Proposition 5.12 the purine half of AG is uniform and coding under arginine, serine and glycine across the record, so $\text{unif}(r)$ does not determine r ; and by Proposition 5.14 the value disc covers three chemically distinct outcomes. **A single hypothesis covering both would conceal that asymmetry**, and a theorem labelled [D] that silently read its residues off the target table would be the error this corpus has twice been caught in.

$H_{\text{eng-content}}$ accordingly carries [E] and enters no proof. Every occurrence of a named residue in Sections 5 and 8 — the arginine at AGA, the isoleucine at AUA, the absence at UGA — is on its authority and not on the refinement's.

2.6 Declaration: the standard code is used constructively

Remark 2.15 (Inherited from [Sch26h, Rem. 2.16], and owed again). [Sch26g] declares that the standard genetic code enters no hypothesis and no construction of that paper; [Sch26h] declares the opposite of itself, in the same form, because its demand graph is built from that table.

This paper is the second case and the declaration is owed again. Every count of Section 5 is over [NCBI24]; the resolutions of Theorem 8.1 are read from tables 1 and 2; the products of Section 7 are the residues those tables assign; and the orderings of Section 8 are orderings of published tables. Sections 5 to 8 depend on that datum entirely and Sections 3 and 4 depend on it not at all. Nothing here re-establishes the independence [Sch26g] claimed and a reader must not carry it forward.

2.7 Declaration: the residue volumes change standing

Remark 2.16 ([Zam72] is load-bearing here). [Sch26h, §C.5] declares that the residue volumes are used there only to show that two differences have opposite sign, and that no proof of that paper depends on them.

A proof of this paper does. Theorem 7.6 and Corollary 7.7 turn on leucine at 166.7 against methionine at 162.9, a difference of $3.8 \text{ \AA}^3$, and on tryptophan at 227.8 against arginine at 173.4. A transcription error in either of the first two would invalidate the first obstruction, though not the second, which has a margin of $54.4 \text{ \AA}^3$. The change of standing is declared here in the form Remark 2.15 uses, and the values were checked against [Zam72] as published.

2.8 Notation

Symbol	Meaning
$\mathcal{R}$	the conditional refinement, on halves $\times E$
$\text{unif}(r), \emptyset, \text{disc}$	the three resolutions (Definition 4.3)
h	a half-block; there are thirty-two
$t_1(h), t_2(h)$	the two thresholds of $H_{\text{eng-type}}$
E, V	environments and the effective vessel volume
$\varepsilon_{\text{nuc}}, \varepsilon_{\text{mito}}$	nucleoplasm and mitochondrial matrix
$XY\text{-pyr}, XY\text{-pur}$	the two halves of the block XY
pattern (4), (2, 2), ...	as at [Sch26h, Prop. 7.1]

Remark 2.17 (One collision, recorded). $\emptyset$ denotes a half at which liberation does not proceed and is **not** the value $\text{unif}(*)$; Remark 4.4 says why the distinction is load-bearing. $\mathcal{R}$ is free across the corpus. *Resolution* is used throughout in the sense of Definition 4.3 and never in the sense of a resolution of a module or a singularity, neither of which occurs here.

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 9 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 published code lying inside the range of the conditional refinement $\nRightarrow$ the account is confirmed. All twenty-seven lie inside, and they do so because the*

third value widens the range to every block pattern the record contains.

- (ii) *Per-half thresholds existing $\nRightarrow$ the threshold is a function of the block. No function of product volume, second-position association and first-base strength fits the purine column.*
- (iii) *The two codes being ordered by one monotone parameter $\nRightarrow$ the published record is so ordered. It is not, and the failure is not marginal.*
- (iv) *Variation being confined to purine halves $\nRightarrow$ evidence for an engagement account. The confinement is largely stop recoding, and this construction places the stops on purine halves itself.*
- (v) *The latch being built from the code's own products $\nRightarrow$ an account of how V is first set. A product-built latch presupposes the products.*
- (vi) *$\mathcal{R}(h, \varepsilon) = \text{unif}(r) \nRightarrow$ the value of r . The refinement fixes that a residue is released and not which.*
- (vii) *$\mathcal{R}(h, \varepsilon) = \text{disc} \nRightarrow$ one outcome. The published record contains three chemically distinct ones under that value.*
- (viii) *pH correlating with compartment $\nRightarrow$ pH is the switch. Redox potential, viscosity and divalent-metal availability co-vary with it, and nothing here separates them.*
- (ix) *Every pyrimidine half of the record being uniform $\nRightarrow$ a finding of this construction. It is third-position synonymy.*

Sch26h being recovered as a special case $\nRightarrow$ [Sch26h] being superseded. Recovery is the stronger relation, and one claim of that paper is corrected rather than absorbed.

Proof. (i) By Proposition 4.9, which exhibits the four patterns the refinement reaches, with the count at Remark 8.14; check V27.

(ii) By witness: UU-pur against AU-pur requires a negative volume coefficient and UG-pur against AG-pur a positive one, neither pair admitting the other two terms (Corollary 7.7); checks V15, V16.

(iii) By witness: one hundred and thirty of the three hundred and fifty-one pairs of tables admit no common ordering, the smallest being tables 32 and 33 (Corollary 8.11); checks V23–V26.

(iv) By witness: stripping the deviating instances that involve a stop codon in either reading carries the figure from eight of nine halves to four of five, and from forty-eight instances to nineteen (Remark 5.5); check V5. That the standard code's

three stops all have a purine third base, and are absences on purine halves by [Sch26h, Cor. 6.4], is what makes the two predicates near-equivalent.

(v) Corollary 6.17.

(vi) By witness: AG-pur is uniform and coding across the record under arginine, serine and glycine (Proposition 5.12); check V9.

(vii) By witness: of the fifty-one instances of disc, thirty place the A codon on the block's pyrimidine product, twenty leave it with no product at all, and one gives a residue that is neither (Proposition 5.14); check V10.

(viii) By inspection: the two compartments differ in redox potential, viscosity and divalent-metal availability as well as in pH, and no measurement here distinguishes them (Remark 6.19).

(ix) By witness: the regularity holds at four hundred and thirty-two of four hundred and thirty-two pyrimidine halves and is the third-position synonymy of the standard code, which this paper does not establish (Remark 8.16); check V28.

(x) Remarks 5.10 and 8.5: [Sch26h, Thm. 5.8] is preserved and is the $\varepsilon_{\text{mito}}$ case (Corollary 8.3), while [Sch26h, Rem. 7.19] is corrected, the two divisions it names being two thirds of the distance between the codes. $\square$

Remark 3.2 (Status of the clauses). Clauses (iii), (iv), (vi), (vii), (ix) and (x) are refuted by witnesses using no hypothesis of this paper and could carry [A] separately. The proposition is labelled [D] because (i) and (ii) refer to the construction and (v) and (viii) to the register of Section 2.

Remark 3.3 (The three that matter most). Clauses (i), (ii) and (iii), and each is answered in the section that raises it.

Clause (i) states what kind of statement this paper makes. Its predecessor's central result was that its construction could produce nothing but codes in normal form, so that an attested code inside the range was a test, with a score of four of twenty-seven ([Sch26h, Rem. 7.4]). Widening the refinement to three values dissolves that test: the range becomes every pattern in the record and the score becomes twenty-seven of twenty-seven. **The improvement is an artefact and a reader must not take it for a confirmation.** Section 8.5 is written to prevent it, and Remark 4.10 states the cost at the point the third value is introduced rather than after the benefit is collected.

Clause (ii) states what the paper failed to do. Having given each half a pair of thresholds, the natural next step is to say what sets them, and the candidates the architecture supplies are the volume of the product and the association at the second base, with the first-base strength added when those two fail. None of the three combinations works, and Section 7 reports the failure as its principal result rather than fitting a fourth parameter. This corpus has been caught

presenting a forced object as a found one; presenting a saturated fit as a finding would be the same error in a different dress.

Clause (iii) states the limit of what did work. One monotone parameter orders the two codes, and extends to three further tables that nothing required it to reach (Theorem 8.7). It does not order the record. Both belong in the paper and the second is not a footnote to the first: the same table, 21, that exhibits the predicted third regime is also the table that breaks the ordering.

Remark 3.4 (Trap: the two codes are not two samples). [A] Restated from [Sch26h, Rem. 3.4] because this paper's subject is the comparison that remark guards. The vertebrate mitochondrial table is defined in [NCBI24] as a list of differences from table 1, so any statement of the form *the two codes are two resolutions of one refinement* is a statement about four codon reassignments. It is developed at Remark 8.17, and it is why Theorem 8.7 rather than Theorem 8.1 is offered as the evidence of Section 8.

Remark 3.5 (Trap: the chemistry is not tested here). [A] As at [Sch26h, Rem. 3.5]. H_{pH} and H_{latch} are registered and undischarged, and Section 6 is empirical throughout. Nothing in Sections 5, 7 or 8 tests them: those sections are counts over [NCBI24] and feasibility statements about thresholds, and they would stand if the chemical reading were replaced by another monotone account of the same direction. Conversely, no agreement reported there is evidence for the chemistry.

Remark 3.6 (Why the section is placed here). A reader who reaches Section 8 holding the phrase *two resolutions of one refinement* will read the twenty-seven of twenty-seven as a confirmation, and will do so whether or not one is claimed; the reading is invited by the recovery of [Sch26h], by the correction at Remark 8.5, and by the third regime turning out to be occupied. The refutations are therefore placed before the constructions, as [Sch26h, §3] places its ten, and the list is restated at Section 10.

4 The Conditional Refinement

This section states the operation the paper is about. It is short: one definition carries the whole difference from [Sch26h], and the two propositions below record what that difference does and does not buy.

4.1 Blocks and halves

Definition 4.1 (Block). A *block* is a set of four codons agreeing in their first two bases. There are sixteen. This is [Sch26h, Def. 5.1] and is imported unchanged; *block* is never interchanged with *class*, the two partitions being transverse ([Sch26h, Prop. 5.2]).

Definition 4.2 (Half-block). The *pyrimidine half* of a block is its two codons with third base in $\{U, C\}$, and its *purine half* the two with third base in $\{A, G\}$. There are thirty-two halves, sixteen of each kind.

4.2 The resolution of a half

Definition 4.3 (Resolution). The *resolution* of a half is one of three values:

Value	The half	Pattern contributed
$\text{unif}(r)$	releases the residue r at both its codons	uniform
$\emptyset$	releases nothing at either	uniform, non-coding
disc	resolves its two codons differently	non-uniform

Remark 4.4 (Two values and a third). [Sch26h] has the first two and not the third. Its refinement divides a block at the third base and assigns each half a residue or an absence ([Sch26h, Hyp. 2.11], Cor. 6.4), which is exactly $\text{unif}(r)$ and $\emptyset$; the third value is what this paper adds, and Corollary 8.4 is the whole of what adding it buys.

$\emptyset$ is *not* $\text{unif}(\ast)$ and the distinction is load-bearing. A half that liberates a stop designation and a half that liberates nothing are different objects, and [Sch26h, Cor. 6.4] is the argument that the published stops are the second: absences, not designations. The notation is kept separate so that the argument is not quietly undone here.

4.3 The refinement

Definition 4.5 (The conditional refinement). Let E be a set of translational environments. The *conditional refinement* is a map

$$\mathcal{R} : \text{halves} \times E \longrightarrow \{\text{unif}(r), \emptyset, \text{disc}\},$$

subject to two clauses, both inherited:

- (i) on a pyrimidine half $\mathcal{R}$ takes the value $\text{unif}(r)$ of the block's seed, for every environment, the pyrimidine half being seeded and propagated rather than refined ([Sch26h, Hyp. 2.10]);

- (ii) on a purine half $\mathcal{R}$ is free, and which value it takes is fixed by the environment through $H_{\text{eng-type}}$.

Remark 4.6 (Where the conditionality sits). Clause (i) is the only prohibition the refinement carries, and Proposition 8.15 reports that the published record obeys it at all four hundred and thirty-two pyrimidine halves. Clause (ii) is the whole content of the paper, and Sections 6 to 8 are about what fixes it.

Nothing in this definition says which value a purine half takes. That is supplied, for two environments, by Theorem 8.1; it is *not* supplied as a function of the block by Theorem 7.6, which is negative.

4.4 Normal form

Proposition 4.7 (Normal form). *[A] A block is in normal form when each of its halves is uniform, and a code is in normal form when all sixteen of its blocks are. Then a code is in normal form if and only if $\mathcal{R}$ takes no disc value on it, $\emptyset$ counting as uniform.*

Proof. By Definition 4.3, a half is non-uniform exactly when its two codons resolve differently, which is the definition of disc. $\square$

Remark 4.8 (The proposition is an identity of definitions). It carries [A] and is proved in a line, and it is stated because [Sch26h, Def. 6.1] defines normal form on the codon table while Definition 4.5 defines $\mathcal{R}$ on halves, and the two must be shown to agree before [Sch26h, Prop. 7.2] can be recovered at Corollary 8.3. **It is not a verification item:** coding it confirms the transcription and not the claim, and Appendix B records it as carried by argument in the manner of [Sch26h, V7].

The clause about $\emptyset$ is not decorative. Tables 2, 3, 5 and 13 are in normal form and carry empty halves; without the clause the recovery of [Sch26h, Thm. 7.13] would fail at exactly the four tables that paper finds.

4.5 What the third value does to the range

Proposition 4.9 (Patterns). *[A] Write the pattern of a block for the multiset of multiplicities of the residues it carries, as at [Sch26h, Prop. 7.1]. Under Definition 4.5:*

Purine half	Block pattern	Reachable by [S
$\text{unif}(r)$, r the seed	(4)	yes
$\text{unif}(r)$, r not the seed	(2, 2)	yes
$\emptyset$	(2, 2) with a non-coding half	yes
disc, the A codon on the seed	(3, 1)	no
disc, otherwise	(2, 1, 1)	no

So the conditional refinement reaches all four patterns occurring in [NCBI24], where the refinement of [Sch26h] reaches two.

Remark 4.10 (This is a cost before it is a gain). [Sch26h, Prop. 7.2] is the statement that its construction produces codes in normal form *and no others*, and its Remark 7.4 makes the consequence explicit: the range being narrow is what makes an attested code inside it a test. Proposition 4.9 widens the range to every pattern the record contains, and **a construction that forbids nothing predicts nothing**. The accounting is done at Remark 8.14 and should be read with this proposition rather than after it. Clause (i) of Proposition 3.1 states the point before either.

5 The Empirical Spine

This section reports what the published record does at the thirty-two half-blocks. It is prior to the mechanism of Section 6 and independent of it: every figure below is a count over [NCBI24] and none of them uses $H_{\text{eng-type}}$ or $H_{\text{eng-content}}$. Where a figure is consistent with the mechanism without being evidence for it, Remark 5.5 says so, and it is the most important paragraph in the section.

5.1 A counting convention, stated once

Remark 5.1 (Twenty-seven tables, twenty-five strings). Two conventions govern every count in this paper.

Duplication. The twenty-seven translation tables of [NCBI24] carry only **twenty-five distinct assignment strings**: tables 1 and 11 are identical at all sixty-four codons, and so are tables 27 and 28. Counts below are reported over the twenty-seven *as published*; the duplication is declared and not corrected, in the manner of [Sch26h, Rem. 7.16], because the published record and not a sample space is what is being measured. Check V1.

Baseline. “Varies” without qualification means *takes more than one value across the twenty-seven*. A count of variation at a half is the number of tables whose resolution there differs from **table 1**. The choice of baseline is stated because one figure depends on it entirely (Remark 5.4).

5.2 Where the conditionality lives

Proposition 5.2 (The twenty-three and the nine). *[A] Of the thirty-two half-blocks, **twenty-three take the same resolution in all twenty-seven tables**. Of the nine that vary, **eight are purine halves**; the only pyrimidine half that ever varies is CU-pyr, in table 3 alone, where the whole CU block reads threonine.*

Proof. By enumeration over the thirty-two halves and the twenty-seven tables; check V2. $\square$

Proposition 5.3 (Variation by half). *[A] Counted against table 1 in the sense of Remark 5.1:*

Half	Tables	Half	Tables
UG-pur	15	CU-pur	3
UA-pur	12	AA-pur	3
AG-pur	8	UC-pur	1
AU-pur	5	UU-pur	1
		CU-pyr	1

Eight of the nine are purine halves, as the names record. There are forty-nine deviating table-half instances in all, forty-eight of them on purine halves.

Proof. By enumeration; check V3. $\square$

Remark 5.4 (At UG-pur the standard code is in the minority). The figure 15 at UG-pur is the one that moves with the baseline. Across the twenty-seven, the purine half of UG reads (W, W) in thirteen tables and (*, W) in twelve, with (C, W) and (G, W) once each. **The standard code's reading is the minority reading**, and against the modal value rather than against table 1 the count is 14. The rest of this paper narrates the standard code as the baseline, and this is the one place where that narration is arbitrary. Check V4.

Remark 5.5 (The confinement is consistent with the account and is not evidence for it). Proposition 5.2 invites a reading it does not support, and the reading must be refused here rather than in the conclusion.

First, all three stop codons of the standard code have a purine third base, and [Sch26h, Cor. 6.4] makes them *absences on purine halves by construction*. The predicate “variation sits on a purine half” is therefore substantially entailed by the predicate “variation is stop recoding”, which is a fact about what the curated record contains and not about engagement. **Second**, the margin is carried by those instances. Strip every deviating table-half instance involving a stop codon

in either reading, and the figures fall from **eight of nine halves and forty-eight of forty-nine instances** to **four of five halves and nineteen instances**. Check V5.

The concentration survives the strip; the margin does not. What Proposition 5.2 establishes is that the published record varies on the purine side, which is *consistent with* an engaged-versus-marginal account and with several competitors, and which this construction partly forces. It is clause (iv) of Proposition 3.1 that is at issue, and it is stated there before the constructions it guards.

Remark 5.6 (And no probability is claimed). [Sch26h, Rem. 7.16] declines to read its audit as a frequency because the tables of [NCBI24] are phylogenetically related and most are curated as small perturbations of table 1. The same declinature is owed here and for a sharper reason: **twenty-four of the twenty-seven tables lie within four codons of table 1** and the farthest, table 3, lies at six; check V6. Two nulls were computed and neither licenses a probability.

A null treating the forty-nine deviating instances as independent draws returns 9×10^{-14} . It is worthless: the instances are not independent, and by Remark 5.1 two pairs of tables are byte-identical.

A placement null — the twenty-four distinct non-standard strings, each table's count of deviating halves held fixed and placed uniformly among the thirty-two — puts both the concentration and the purine share outside the sampled range. That null ignores phylogeny entirely, and Remark 5.5 accounts for the same concentration without any appeal to engagement. **The placement figure is reported as a placement statistic and no frequency is claimed.**

5.3 The two codes differ at three halves

Theorem 5.7 (The whole difference). *[A] The standard code and the vertebrate mitochondrial code take different resolutions at **exactly three of the thirty-two half-blocks**, and **all three are purine halves**:*

Half	Table 1	Table 2	Differs
AG-pur	(R, R)	(*, *)	yes
AU-pur	(I, M)	(M, M)	yes
UG-pur	(*, W)	(W, W)	yes
UA-pur	(*, *)	(*, *)	no

The other twenty-nine halves are identical.

Proof. By enumeration; check V7. $\square$

Remark 5.8 (Why UA is in the table). The fourth row is not a fourth difference and is marked so. UA-pur is carried because it is the fourth coupled block and because it constrains the mechanism of Section 6 at both compartment settings: it is the one half required to lie beyond threshold in *both* environments. A reader who counts rows rather than reading the last column will count four differences and there are three.

Corollary 5.9 (The three halves are sufficient). *[A] Setting the three halves of Theorem 5.7 to their table-1 resolutions in table 2 returns table 1 at every one of the sixty-four codons.*

Proof. Immediate from Theorem 5.7, the remaining twenty-nine halves being identical; check V8. The four codons that move are AGA, AGG, AUA and UGA, which are exactly the four at which [Sch26h, Thm. 5.8] records its construction's output as differing from the standard code. $\square$

Remark 5.10 (A correction to [Sch26h]). The corollary is enumeration over a finite object and carries [A] by the convention of [Sch26h, Rem. 2.3]; it is instantiated under $H_{\text{eng-type}}$ at Section 8, where the corresponding statement about resolutions at the two compartment settings carries [D].

It also corrects its predecessor. [Sch26h] describes the standard code in seven places as its construction's output *with two further divisions*, at AUA and UGA, and [Sch26h, Rem. 7.19] states that those two divisions are the whole distance between the two. **They are two thirds of it.** The count of divisions is right and the claim that they exhaust the distance is not: the third differing half is AG-pur, which is *uniform in both codes*, so no division occurs there and none is needed — what changes is the content, an absence in the output against arginine in the standard code. Three halves separate the codes, at four codons; two are divisions and one is a change of liberation status. [Sch26h, Thm. 5.8] lists the four codons correctly and [Sch26h, Rem. 5.10] anticipates the difficulty, cautioning that the mathematics does not distinguish UA from AG and does not predict that they behave alike.

Closing that gap with a single operation is what this paper is for, and the three-valued refinement of Section 4 is the operation.

The correction is asserted against a paper that stands uncorrected as printed. [Sch26h] appears in this volume with Remark 7.19 as quoted, and no erratum has been issued at the time of writing. A reader consulting both will find them in contradiction on this point, and this remark, not that one, is the reading the present author holds.

Remark 5.11 (Two kinds of difference, and why one refinement covers both). At AU and UG the standard code takes the *third* value of Definition 4.3 and the mitochondrial code does not. At AG both codes resolve uniformly and the *content* differs — a residue against an absence. A two-valued refinement together with a further division must treat these as two mechanisms; the three-valued refinement of Definition 4.5 covers both.

It covers both at the level of outcome type and not below it. What the refinement does not supply is treated immediately below and is the reason H_{eng} is registered in two clauses at Section 2.

5.4 What the refinement does not determine

Proposition 5.12 ($\text{unif}(r)$ does not determine r). *[A] Across the twenty-seven tables the purine half of AG takes five distinct resolutions: $\text{unif}(R)$ in nineteen tables, $\text{unif}(S)$ in four, disc as (S, K) in two, $\emptyset$ in one and $\text{unif}(G)$ in one. In particular it is uniform and coding under three different residues.*

Proof. By enumeration; check V9. $\square$

Remark 5.13 (The consequence for Theorem 5.7). Proposition 5.12 is why the register of Section 2 carries $H_{\text{eng-type}}$ and $H_{\text{eng-content}}$ separately, in the form [Sch26h, Rem. 2.14] uses for $H_{\text{split-pos}}$ and $H_{\text{split-chem}}$.

The refinement decides *that* a half releases uniformly. It does not decide *what*. So the entry (R, R) in the first row of Theorem 5.7 is read off table 1 and is not derived here, and the same holds of I at AUA and of the absence at UGA. Stated without this remark, Theorem 5.7 would be a theorem labelled [A] carrying a derivation it does not perform, which is the error [Sch26h, Rem. 9.4] records under a different name.

Proposition 5.14 (The third value is not one outcome). *[A] Summed over the twenty-seven tables there are fifty-one instances of the value disc , and they fall into three chemically distinct outcomes:*

<i>The A-codon of the half</i>	<i>Instances</i>
<i>carries the block's pyrimidine product</i>	30
<i>carries no residue, the G-codon carrying one</i>	20
<i>carries a residue that is neither</i>	1

The standard code carries one instance of each of the first two, at the two halves this paper is about: AU-pur is (I, M) , the A-codon falling back to isoleucine, the product of the pyrimidine half; and UG-pur is $(*, W)$, the A-codon yielding

nothing.

Proof. By enumeration; check V10. $\square$

Remark 5.15 (A discrimination and a failure are not the same event). [E] In the intended reading a carve that stops short of the second transformation and an engagement that fails outright are different events with different causes, and Proposition 5.14 shows the published record contains both under one value of $\mathcal{R}$. Nothing in Definition 4.5, in Section 6 or in Section 7 selects between them. Widening the codomain to four values would remove the difficulty and is not attempted here; Target 10.3 records it. This remark enters no proof.

5.5 One half that never varies

Proposition 5.16 (CG). [A] *The block CG reads R, R, R, R in all twenty-seven tables. Both of its halves are invariant, and the conditionality of arginine in the published record lives entirely at AG-pur.*

Proof. By enumeration; check V11. $\square$

Remark 5.17 (CG is not a curiosity). Proposition 5.16 is placed here rather than among the counts of Section 5.2 because it is load-bearing later. CG-pur and AG-pur carry the same product, arginine, and the same base at the second position. Any threshold that is a function of those two quantities assigns the two halves one value, and by Propositions 5.3 and 5.16 they are the most and the least conditional halves in the record. This is the first of the two obstructions of Theorem 7.6, and it is available already from the counts of this section.

6 The Engagement Threshold

Section 5 reports that the purine halves vary and the pyrimidine halves do not. This section gives the reading under which that happens, fixes its direction against the code data, and identifies the switch. It establishes no threshold function; Section 7 shows that no threshold function of the available block quantities exists.

6.1 The direction, and the account that is rejected

Remark 6.1 (The account first tried). [E] The first chemical account ran as follows. Higher pH deprotonates the cysteine thiol; more thiolate weakens the methionine–cysteine contact; a weakened contact admits a larger effective cage; and a larger cage makes escape of the product easier. Alkaline

conditions would then *ease* release.

Each step is sound and the thiolate arithmetic of Proposition 6.8 is retained from it unchanged. **Its endpoint is inverted for this architecture** and is recorded here so that a reader does not reconstruct it. This remark enters no proof.

Proposition 6.2 (The datum that fixes the direction). [A] *At AG-pur the low-pH compartment releases arginine and the high-pH compartment terminates: table 1 reads (R, R) and table 2 reads (*, *) (Theorem 5.7, first row). By [Lle98] the nucleoplasm, which is continuous with the cytosol through the nuclear pore complexes, sits at pH 7.2–7.4, and the mitochondrial matrix at 7.8–8.0, the difference being maintained by proton pumping across the inner membrane.*

Remark 6.3 (The compartment values are external data). The two ranges are the only quantities in this section not computed from a definition, and the whole direction of the account rests on their order. They are declared here in the manner of the [NCBI24] block: taken from [Lle98] as published, not reconstructed. All arithmetic below is evaluated at the endpoints 7.2 and 8.0.

Corollary 6.4 (The escape account predicts the reverse). [A] *An account in which high pH eases release makes the high-pH compartment the releasing one at AG-pur. Proposition 6.2 is the opposite. No adjustment of the thiolate fraction repairs this, the sign of the prediction being independent of its magnitude.*

6.2 The correction: the limiting step is engagement

Remark 6.5 (Engagement, not escape). [E] Failure at a purine half is failure to *engage, stabilise and carve* — not failure to escape. A larger effective volume does not free the product; it fails to hold the reactants.

This reading is not new here. [Sch26h, Rem. 5.11] gives it already, of the two non-coding halves: 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 does not proceed. What this paper adds is that the same failure is *graded* and that the environment sets where a half falls on it. With that single substitution the same monotone $V(pH)$ reproduces every row of Theorem 5.7:

Effective volume	Outcome at the half
tight (low pH)	engages, carves, discriminates A from G
intermediate	engages, carves, does not discriminate
relaxed (high pH)	fails to engage — no product

The nucleoplasm sits low: AG engages and gives arginine, and AU and UG discriminate, giving the patterns (3, 1) and (2, 1, 1) of [Sch26h, Prop. 7.1]. The matrix sits high: AG fails to engage, and AU and UG resolve coarsely. UA is beyond threshold in both, which is why it carries no difference and yet constrains the account (Remark 5.8). This remark enters no proof; it is the content of $H_{\text{eng-type}}$.

Remark 6.6 (Three outcomes require two thresholds at a half). A monotone $V(pH)$ and one threshold per half generate two outcomes. The scheme of Remark 6.5 requires **two** thresholds at each half, $t_1(h) < t_2(h)$, with $\mathcal{R}(h, \varepsilon) = \text{disc below } t_1(h)$, unif between them and $\emptyset$ above $t_2(h)$. The point is arithmetical and is made because the two numbers are easy to confuse: the *two thresholds* of this remark and the *parameters* a threshold might be a function of are different quantities, and Section 7 is about the second.

Remark 6.7 (What the twenty-three invariant halves contribute). The halves of Proposition 5.2 that never vary are not spectators of this account. A half uniform at both compartment settings requires $t_1(h) \leq V_{\text{nuc}}$ and $t_2(h) > V_{\text{mito}}$, which is a pair of constraints on the same two thresholds. Section 7 takes the whole purine column and not the conditional halves alone, and this is why.

6.3 The pH sensor

Proposition 6.8 (The thiolate fraction). *[A] The cysteine thiol has $pK_R = 8.33$ [NC17, Table 3-1]. With $f_{S^-} = (1 + 10^{pK_R - pH})^{-1}$,*

pH	7.2	7.4	7.8	8.0
f_{S^-}	6.9 %	10.5 %	22.8 %	31.9 %

*a rise of **twenty-five percentage points**, and a 4.62-fold change, across the compartment range of Proposition 6.2.*

Proof. By evaluation; check V12. $\square$

Proposition 6.9 (Which side chain the gradient reaches). *[A] Of the residues the latch and the conditional halves involve, the side-chain ionisation across $7.2 \rightarrow 8.0$ is, from*

[NC17, Table 3-1]:

Group	pK_R	$7.2 \rightarrow 8.0$	Points	Ratio
Cys thiol	8.33	6.90 $\rightarrow$ 31.87 %	24.97	4.62
Tyr phenol	10.07	0.135 $\rightarrow$ 0.844 %	0.71	6.26
Arg guanidinium	12.48	99.999 $\rightarrow$ 99.997 %	0.00	1.00
Met, Trp	—	no ionisable side chain	—	—

Proof. By evaluation; check V13. $\square$

Remark 6.10 (Which measure, and why it matters). The two columns disagree and the disagreement must be stated rather than resolved silently. **On fold change tyrosine moves more than cysteine;** only on absolute population does cysteine lead, and there it leads by a factor of thirty-five. The absolute measure is the right one here, and the reason is structural rather than chemical: a latch is a population of contacts, and what modulates an effective volume is the fraction of them altered, not the multiple by which a negligible fraction grows. A group at $pK_R = 10.07$ delivers seven tenths of one percent across the whole compartment range and cannot latch anything. The claim this paper makes is therefore that the cysteine thiol is **the only ionisable side chain in the relevant set whose pK_R lies near enough to the interval to change a substantial fraction of contacts across it**, and the ratio column is printed so that a reader who computes it is not misled.

This is a reason to prefer the thiol, not an argument excluding other agents entirely; Remark 6.19 records what it does not exclude.

Proposition 6.11 (Arginine is not the sensor). *[A] Arginine has been proposed as the sensor on the ground that it is the residue whose assignment changes at AG-pur. Three evaluations from [NC17, Table 3-1] refuse it:*

- (i) *The guanidinium group, $pK_R = 12.48$, is protonated to 99.999 % at 7.2 and 99.997 % at 8.0. It does not titrate across the interval, and by Proposition 6.9 it is the least responsive group in the set.*
- (ii) *The α -amino group, $pK_2 = 9.04$, moves only from 98.6 % to 91.6 % — seven percentage points against the thiol's twenty-five, and on the backbone rather than the side chain.*
- (iii) *$pI(\text{Arg}) = 10.76$ lies well above both compartment values. **Moving from 7.2 to 8.0 therefore moves arginine toward its isoelectric point, not away from it.***

Proof. By evaluation; check V13. $\square$

Corollary 6.12 (The solubility argument reads backwards). *[A] An account in which alkalisation releases arginine by raising its solubility is refuted by clause (iii): the change is toward the isoelectric point, at which solubility is least. The argument is recorded because it is the one a reader constructs on being told that the conditional residue at AG-pur is arginine, and because its failure is not obvious from the direction of the pH change alone.*

Remark 6.13 (One pK_a set, named). Every dissociation constant and isoelectric point in this section is [NC17, Table 3-1], declared as external data in the manner of the [NCBI24] block. The set is used entire and is not mixed with another: its isoelectric points are the means the same table's pK_a values give, at Cys 5.02, Tyr 5.66, Arg 10.76, Trp 5.89 and Met 5.74, and all five reproduce. The declaration is made because an earlier draft of this paper did mix two compilations, printing a guanidinium protonation of 100.000 % — which requires $pK_R \approx 13.8$ — beside $pI = 10.76$, which requires 12.48. Neither figure was wrong of its own set and the pair was impossible. The defect is recorded at Appendix B.6 and is the reason this remark exists.

Remark 6.14 (A closed form for the latch). *[E] If a functional form is wanted, the two protonation states of the thiol give*

$$K_{MC}^{\text{eff}}(pH) = f_{SH} K_{MC}^{SH} + f_{S^-} K_{MC}^{S^-},$$

and $K_{MC}^{SH} > K_{MC}^{S^-}$ gives $dK_{MC}^{\text{eff}}/d pH < 0$, with

$$V(pH) = V_0 + \Delta V f_{S^-}(pH), \quad \Delta V > 0.$$

The monotonicity is all that Remark 6.5 uses, and by Proposition 6.9 the thiol is the only side chain in the set that supplies it. Neither V_0 nor ΔV is determined here, and Section 7 shows that determining them would not suffice. This remark enters no proof.

6.4 The latch is feedback and not structure

Proposition 6.15 (The latch is built from products). *[A] The chrysene complex contains neither cysteine nor methionine. Both are products of the code the complex produces.*

Corollary 6.16 (An instantiation of H_{loop}). *[D] A methionine–cysteine latch therefore cannot be an intrinsic part of the vessel. If it exists it is the code's own products modulating the vessel that makes them, which is a concrete instance of H_{loop} and not a further hypothesis. It is also a*

chemical instance of [Sch26h, Target 9.8], which proposes cysteine with methionine, and tyrosine with tryptophan, as pairs produced by coordinated vessels; that target is not discharged here, and the latch is one candidate mechanism for the first pair and says nothing of the second. This is the strongest reason this paper has for preferring the latch to a generic pH sensor, and it is a structural reason rather than a chemical one.

Corollary 6.17 (Maintenance, not initiation). *[D] A latch built from products cannot set the initial value of V , nothing having yet been made. Whatever the latch does, it does after the code is running. The initial setting requires a separate account, which this paper does not give; Target 10.4.*

Remark 6.18 (The corollary is stated in the same paragraph). Corollaries 6.16 and 6.17 are kept adjacent deliberately. The first is the argument for the latch and the second is its cost, and a presentation that separated them would let a reader take the feedback reading as an origin account. It is not one.

6.5 What is adopted, and what is not excluded

Remark 6.19 (pH is adopted, not established). Redox potential, viscosity and divalent-metal availability all covary with pH between nucleoplasm and matrix, and nothing in this paper separates them. pH is *adopted* as the switch, on the strength of Proposition 6.8 and Remark 6.10, and H_{pH} is registered at Section 2 accordingly.

That pH correlates with compartment does not make pH the switch, and clause (viii) of Proposition 3.1 states this before the construction that uses it. Any of the covarying quantities would drive Remark 6.5 equally well; what the section establishes is the *direction* of the effect (Corollary 6.4), which is common to all of them, and not the identity of the agent.

Remark 6.20 (What this section does not do). Nothing above assigns a threshold to a half. Remark 6.5 says that each half has a pair of thresholds and that V crosses them in a fixed order; it does not say which halves have which, and Remark 6.7 records that the invariant halves constrain the answer as much as the conditional ones do.

Section 7 asks whether the thresholds are a function of the quantities the architecture supplies — product volume, association at the second position, and strength at the first — and answers that they are not (Theorem 7.6). Remark 5.17 has already given the first half of that answer from the counts of Section 5.

7 Thresholds: A Negative Result

Section 6 gives each half a pair of thresholds and says that $V(pH)$ crosses them in a fixed order. It does not say which half has which. This section asks whether the thresholds are a function of the quantities the architecture supplies, and answers that they are not.

The result is negative and is the paper's principal one. It is stated in the form [Sch26h, Cor. 6.7] uses at the level below, where the first account of the pyrimidine–purine transformation is refuted by its own numbers: an account that cannot be made to fit is worth more to the reader than a fit with enough free parameters to be guaranteed.

7.1 Scope

Remark 7.1 (Purine halves only). Both candidate quantities — the volume of the product and the association of the second base with the tether — are properties of a *block*, so neither can separate a block's two halves. The point is not abstract: UA-pur codes in all twenty-seven tables and UA-pur terminates in fifteen, and under any block-level assignment the two carry identical coordinates.

This section is therefore about purine halves, and the pyrimidine halves are handled where [Sch26h] handles them, by the encasement clause of [Sch26h, Rem. 6.8]: a complex fully encased at a pyrimidine third base is stable. **The invariance of the pyrimidine halves reported at Proposition 5.2 is accordingly an assumption of this section and not something it explains.**

Definition 7.2 (The product of a half). The *product* of a purine half is the residue its G codon carries, that residue being the one released wherever the half engages at all. Fifteen of the sixteen purine halves have one.

Remark 7.3 (UA-pur is excluded, and why that is not a convenience). UA-pur is the sixteenth and has no product: it does not code in table 1, so Definition 7.2 assigns it nothing. It is tempting to supply one by block analogy — tyrosine, at 193.6 Å³ — and an earlier draft of this paper did, resting an argument on it. Two things refuse the choice. Across the twenty-seven tables UA-pur codes in twelve and for five different residues — Gln 143.8, Glu 138.4, Leu 166.7, Tyr 193.6, Trp 227.8 — with glutamine modal and *smaller* than isoleucine, so the analogy picks one value out of a range that spans 89 Å³. And the analogy is against the general pattern: in seven of the eight blocks whose halves differ, the purine half's residue is not the pyrimidine half's. The product at UA-pur is Target 10.2 and is not assumed here. Check V14.

Remark 7.4 (The standing of [Zam72]). [Sch26h, §C.5] declares that the residue volumes are used there only to show that two differences have opposite sign, and that no proof depends on them. **In this section a proof does.** Theorem 7.6 turns on Leu 166.7 against Met 162.9, a difference of 3.8 Å³, and on Trp 227.8 against Arg 173.4. The change of standing is declared here in the form [Sch26h, Rem. 2.16] uses for the standard code, and the four values were checked against [Zam72] as published.

7.2 The refutation

Definition 7.5 (A block-feature threshold). A *block-feature threshold* assigns to each purine half h the pair

$$t_i(h) = a_i \text{vol}(h) + b_i \alpha(h) + c_i w(h) + d_i, \quad i = 1, 2,$$

where $\text{vol}(h)$ is the volume of the product of h , $\alpha(h)$ is any real-valued measure of association at the second base, $w(h)$ is 1 when the first base is weak and 0 when it is strong, and $\mathcal{R}(h, \varepsilon)$ is disc below $t_1(h)$, unif between $t_1(h)$ and $t_2(h)$, and $\emptyset$ above $t_2(h)$, per Remark 6.6.

Theorem 7.6 (No block-feature threshold fits). [A] *There is no block-feature threshold consistent with the resolutions of the fifteen purine halves of Definition 7.2 at ε_{nuc} and $\varepsilon_{\text{mito}}$. The system is infeasible at one, two and three parameters, and remains infeasible when the association measure α is fitted rather than fixed in advance.*

Proof. By linear programming over the thirty regime constraints and the fifteen orderings $t_1(h) < t_2(h)$; check V15. The obstruction is exhibited directly at Corollary 7.7, which uses no linear algebra. $\square$

Corollary 7.7 (The obstruction, without reference to any scale). [A] *Two pairs of halves, each sharing a second base and a weak first base, so that within each pair only the volume term can distinguish them:*

Pair	Shared	Volumes	The larger	Its r
UU-pur, AU-pur	U at 2, weak at 1	Leu 166.7, Met 162.9	UU	unif
UG-pur, AG-pur	G at 2, weak at 1	Trp 227.8, Arg 173.4	UG	disc

*The first pair requires $t_1(\text{UU}) \leq V_{\text{nuc}} < t_1(\text{AU})$ with a volume difference of +3.8 Å³, hence $a_1 < 0$. The second requires $t_1(\text{AG}) \leq V_{\text{nuc}} < t_1(\text{UG})$ with a volume difference of +54.4 Å³, hence $a_1 > 0$. **The volume coefficient is required to take both signs.** Neither α nor w enters either pair.*

Proof. By evaluation of Definition 7.5 at the four halves; check V16. $\square$

Remark 7.8 (The convention does not rescue it). Definition 7.2 takes a disc half's product to be its G-codon residue. Under the other convention — the A-codon residue — AU-pur carries isoleucine, and by [Zam72] isoleucine and leucine are *equal* at $166.7 \text{ \AA}^3$. UU-pur and AU-pur then have identical coordinates (166.7, U, weak) and different resolutions, which is an outright collision rather than a sign contradiction. The refutation holds under either convention and by a different argument in each. Check V16.

Proposition 7.9 (A second obstruction, geometric). *[A] Take α on the unit-spaced Watson–Crick rank $U > G > A > C$. In the plane of (volume, association), AG-pur lies strictly inside the triangle spanned by AA-pur, AU-pur and UG-pur, at barycentric weights (0.438, 0.438, 0.123). AG-pur is the only one of the four that fails to engage at $\varepsilon_{\text{mito}}$, so t_2 must separate it from the other three; a point interior to a hull is separated from its vertices by no linear functional. Check V17.*

Remark 7.10 (Which obstruction to rely on). The two are not of equal strength and the difference should be stated. Corollary 7.7 holds for *every* association measure and every first-base term, because neither appears in either pair; it is the one Theorem 7.6 rests on. Proposition 7.9 is stated for one choice of α and would move under another. It is given because it is visible on a plot and because it locates the difficulty at AG-pur, which is where Section 5 already put it.

Remark 7.11 (The first-base term rescues CG and orders nothing). Remark 5.17 gives the shortest form of the difficulty: CG-pur and AG-pur carry the same product and the same second base, and are the least and the most conditional halves in the record. A first-base term separates them, C being strong and A weak, and that is why w appears in Definition 7.5 at all.

It does nothing inside the conditional set. All four of UA, AG, AU and UG have weak first bases, so w is constant across them and orders none of them. The model is three-parameter and two of the three are active where the section's question is asked. That is worth saying plainly, because a reader who sees a parameter added in response to Proposition 5.16 will expect it to have bought something here, and it has not.

7.3 What is refuted, and what is not

Remark 7.12 (Sections 4 to 6 are untouched). Theorem 7.6 refutes no part of the account that precedes it. The three-valued refinement, the direction of the engagement effect, the pH sensor and the latch all require only that per-half thresholds *exist*, which they trivially do: sixteen halves may be given thirty-two numbers. What is refuted is that those numbers are a function of the block quantities the architecture supplies.

This is clause (ii) of Proposition 3.1, and Corollary 7.7 is the witness its proof names.

Remark 7.13 (Composition and arrangement, one level down). [Sch26h, Rem. 7.12] separates two things the phrase *normal form* runs together: arrangement, which its construction accounts for, and composition, which it does not. The same separation recurs here and at the level of the conditionality rather than of the code. **This paper accounts for the arrangement of the conditionality — that it falls on purine halves, that it takes three values, that the two codes are two settings of one refinement — and not for its composition, which is the question of which halves are conditional.** Theorem 7.6 is the statement that composition is not reachable from the block features, and Target 10.1 is what remains.

It also bears on [Sch26h, Target 9.9], which asks whether one mechanism is available at eight blocks and why the standard code's exceptions are UG and AU rather than another pair. This paper answers the second question negatively and does not answer the first: no function of product volume, second-position association and first-base strength picks out that pair, and the target survives in the sharper form Target 10.1 gives it.

Remark 7.14 (Two accounts recorded as refuted, so that they are not reintroduced). **One parameter on first-two-base strength.** Refuted by UA-pur against AU-pur: both blocks carry two weak bases, and the first terminates at both compartment settings while the second engages at both.

One parameter on product volume. Refuted at AG-pur against AU-pur — 173.4 against 162.9, with AG required to be the *less* tolerant — and this holds whichever residue is supplied at UA-pur. The refutation is stated there and not at UA deliberately: the UA version turns on the counterfactual of Remark 7.3 and this one does not. Check V15.

7.4 Where the further divisions fall

Remark 7.15 (Strong and weak first bases). A count worth recording, and worth discounting in the same breath. Over the twenty-seven tables, of the fifty-one blocks requiring a further division ([Sch26h, Prop. 7.17]), **forty-nine sit on blocks whose first base is weak**; no block with two strong bases in its first two positions ever requires one, and every block with two weak bases does. Check V19.

Three qualifications, and together they are why this is a remark and not a subsection.

It is a *first-base* statement and not a two-base one. The two exceptions are CU, whose first base is strong and whose second is weak; and of the eight mixed blocks, four ever require a division and four never do, so the strong/weak pair has no purchase that the first base alone does not have.

The strong-strong half of it is close to forced. All four strong-strong blocks are already fourfold degenerate in table 1, and twenty-four of the twenty-seven tables lie within four codons of table 1, the farthest at six; check V6. A block that is fourfold degenerate in table 1 and perturbed at four codons across the whole record is unlikely to acquire a (3, 1) pattern, whatever the mechanism.

And it is not this corpus's to discover: it is the family-box regularity, and it should be attributed rather than presented as new.

What it does not do is support Theorem 7.6's replacement. An earlier plan for this paper kept the count because a first-base term was independently wanted by a threshold model. Remark 7.11 removes that reason: the term is inert among the conditional halves. The count stands as a description of where the further divisions fall and as nothing more.

Proposition 7.16 (First-base strength against the varying halves). *[A] Of the nine halves that vary across the twenty-seven tables (Proposition 5.2), seven sit on blocks with a weak first base and two on blocks with a strong one, against nine and fourteen among the twenty-three invariant halves. By instance, forty-five of the forty-nine deviations sit on weak first bases. Fisher's exact test, one-sided, gives $p = 0.057$.*

Proof. By enumeration; check V18. $\square$

Remark 7.17 (The figure is not significant and is not used as if it were). $p = 0.057$ does not reach the conventional threshold, the halves are not independent for the reasons of Remark 5.6, and no hypothesis of this paper depends on the proposition. It is reported because the question was asked and the answer is weakly affirmative, and because a reader who computes it and finds 0.057 should find it here rather

than conclude it was suppressed.

8 The Two Codes as Two Resolutions

Everything before this section is either a count over the published record or a reading of the vessel. This section puts them together.

One caution governs the whole of it and is stated here rather than at its end. The vertebrate mitochondrial table is defined in [NCBI24] as a list of differences from table 1, so the two codes are not two independent objects, and weight placed on any comparison of them is weight placed on four codons (Remark 8.17). It is worth saying what survives if table 2 is set aside entirely: Proposition 5.2, Remark 5.5 and Proposition 5.12 are counts over the record and stand; **Theorem 8.1 does not, having nothing to compare.** It recovers [Sch26h] as a special case, corrects one claim of that paper, finds the account's third setting attested where nothing required it to be, and then reports the two prices: the range grows, and the ordering does not extend to the record.

8.1 The two settings

Theorem 8.1 (The two resolutions). *[D] Under $H_{\text{eng-type}}$ and the scheme of Remark 6.5, with $V(\varepsilon_{\text{nuc}}) < V(\varepsilon_{\text{mito}})$ by Proposition 6.2:*

Half	$\mathcal{R}$ at ε_{nuc}	$\mathcal{R}$ at $\varepsilon_{\text{mito}}$
AG- <i>pur</i>	unif	$\emptyset$
AU- <i>pur</i>	disc	unif
UG- <i>pur</i>	disc	unif
UA- <i>pur</i>	$\emptyset$	$\emptyset$
the remaining twenty-eight	unchanged	unchanged

The derived content of the theorem is the table above: three half-blocks change resolution between the two settings, and in which direction. With the residues supplied by $H_{\text{eng-content}}$, which is [E], and the remaining codons by the seed map of [Sch26h, Thm. 5.7], the output is [NCBI24, table 2] at $\varepsilon_{\text{mito}}$ and table 1 at ε_{nuc} at every one of the sixty-four codons — that extension being carried by the empirical clause and the predecessor, not by the refinement (Remark 8.2).

Proof. The resolutions are Theorem 5.7; that the three halves determine the rest is Corollary 5.9; the ordering of regimes is Remark 6.5. Check V20. $\square$

Remark 8.2 (What is derived and what is imported). The theorem is [D] for outcome *types* and for nothing else. By Proposition 5.12 the value $\text{unif}(r)$ does not determine r , so the arginine at AGA, the isoleucine at AUA and the absence at UGA enter through $H_{\text{eng-content}}$, which is [E]; and

by Remark 5.15 the value *disc* does not say whether the A codon falls back to the pyrimidine product or yields nothing (Target 10.3). **The theorem says that three halves change and in which direction; it does not say into what.**

8.2 [Sch26h] is the mitochondrial case

Corollary 8.3 (Recovery). *[D] At $\varepsilon_{\text{mito}}$ the refinement takes no *disc* value, so by Proposition 4.7 its output is in normal form, and by Theorem 8.1 that output is table 2. This is [Sch26h, Thm. 5.8] with [Sch26h, Prop. 7.2], and that construction is the $\varepsilon_{\text{mito}}$ case of this one.*

Corollary 8.4 (The second operation is not a second mechanism). *[D] [Sch26h] reaches the standard code by a further division, invoked at UG and at AU and not derived. Under Theorem 8.1 those two divisions are the value *disc* of the one refinement at a lower setting of V . No operation is added; the outcome set is widened.*

Remark 8.5 (And the recovery is a correction). Corollary 8.4 accounts for two of the three halves at which the codes differ. The third is AG-pur, where no division occurs in either code — the half is uniform in both — and what changes is whether it liberates at all. **That is the half [Sch26h] does not count**, and its Remark 7.19 states that the two divisions are the whole distance between the codes; they are two thirds of it. Remark 5.10 records the correction and this is where it is repaired, the three-valued refinement covering the third half by the same mechanism as the other two.

8.3 The third setting is attested

Proposition 8.6 (The intermediate regime). *[A] Remark 6.5 posits three regimes, of which Theorem 8.1 uses two. At an intermediate V the scheme requires AG-pur to engage uniformly while AU-pur and UG-pur have ceased to discriminate — all three uniform at once.*

Four published tables are in that state: 3 yeast mitochondrial, 5 invertebrate mitochondrial, 13 ascidian mitochondrial and 21 trematode mitochondrial. All four are mitochondrial, and three of them are three of the four [Sch26h, Thm. 7.13] finds in normal form. Check V21.

Theorem 8.7 (A five-table ordering). *[A] There exist a value V_t for each of the tables 1, 2, 3, 5, 13 and thresholds $t_1(h) < t_2(h)$ for each of the sixteen purine halves such that*

every resolution in all five tables is the one the scheme of Remark 6.5 assigns. The ordering is $V_1 < V_3 = V_5 = V_{13} < V_2$. Check V22.

Remark 8.8 (A null for the ordering, and what survives it). *[A] An earlier version of this section offered Theorem 8.7 as the paper's evidence, on the ground that nothing selected which tables should occupy the regime. That claim does not survive its own null and is withdrawn.*

Two tables are orderable by a single monotone parameter with free per-half thresholds exactly when their rank vectors are comparable componentwise, so an orderable set is a clique in the comparability graph on the twenty-seven tables. Computing it: **seven thousand two hundred and twenty-six of the eighty thousand seven hundred and thirty five-table subsets are orderable, nine per cent**, and a simultaneously orderable set of *sixteen* tables exists — for instance $\{1, 2, 3, 4, 5, 6, 10, 11, 13, 15, 16, 22, 25, 29, 30, 32\}$. The paper exhibits five where sixteen are available. Check V31. Most of the exhibited ordering is moreover forced. **Table 2 dominates all twenty-six other tables**, being the only one with an empty half at AG-pur, so its position at the top follows from the rank convention and is not a finding; and **tables 3, 5 and 13 have identical rank vectors**, so the tie $V_3 = V_5 = V_{13}$ is forced. Check V32. **One comparison of Theorem 8.7 is not forced: that table 1 lies strictly below tables 3, 5 and 13.** Check V33.

What survives is a consistency statement and not a statistical feat: the standard code sits on the tight side of the intermediate mitochondrial tables, and one threshold assignment accommodates all five at all sixteen purine halves.

The paper's positive content lies elsewhere and is structural. It is Corollary 8.4, that the two further divisions of [Sch26h] are the third value of one refinement and no operation is added; and Remark 5.10, that the distance between the codes is three halves and not two divisions. Neither is a count over tables and neither has a null to fail. Proposition 8.6 — that a regime the two codes do not use is occupied at all — is a genuine if weak confirmation, and it is the most the record supports.

Two cautions of the earlier version are retained and still apply: the four tables are mitochondrial and phylogenetically related, so this is not four independent confirmations (Remark 5.6); and the fitted V is an ordering and not a measurement.

Scholium 8.9. *The section that reports the placement null at Remark 5.6 and the range cost at Remark 8.14 could not consistently omit this one. The omission in the earlier version was an inconsistency in practice rather than in standard, and it is recorded at Appendix B.6.*

8.4 The ordering does not extend to the record

Theorem 8.10 (No single monotone parameter orders the published codes). *[A] There is no assignment of a value V_i to each of the twenty-seven tables, together with thresholds $t_1(h) < t_2(h)$ at the sixteen purine halves, realising every resolution in the record. This holds with the thresholds free — no functional form assumed, and in particular independently of Theorem 7.6. Check V23.*

Corollary 8.11 (The obstruction is a pair). *[A] One hundred and thirty of the three hundred and fifty-one pairs of tables cannot be ordered at all: each such pair has one half at which the first table is the tighter and another at which the second is. The smallest witness needs one half each way — tables 32 and 33, where UG-pur discriminates in 32 and is uniform in 33 while AG-pur does the reverse. Checks V24, V25.*

Remark 8.12 (The failure reaches the series the paper is about). It would be convenient if the unorderable pairs were confined to the exotic tables, and they are not. Adding table 21 to the five of Theorem 8.7 already breaks the ordering, and tables 4 and 21 are unorderable by themselves: at AU-pur table 4 discriminates where 21 is uniform, and at AA-pur table 21 discriminates where 4 is uniform. Check V26. Both are mitochondrial, and table 21 is one of the four exhibiting the intermediate regime.

So Proposition 8.6 and Theorem 8.10 bear on the same tables and pull in opposite directions, and the paper must state both. Three of the four intermediate tables extend the ordering; the fourth breaks it.

Remark 8.13 (What the two theorems together say). **A single environmental parameter accounts for the two codes, extends to three more, and fails on the record.** That is the whole of the positive claim and the whole of its limit.

The failure is not of the chemistry and not of the three-valued refinement. It is of the assumption that one scalar orders every translational environment: two compartments differing in several respects at once (Remark 6.19) will not in general place their halves on one axis, and Corollary 8.11 is the record saying so. A second axis is Target 10.5, and AA-pur and CU-pur are where to look: they are implicated in fifty-five and thirty-two of the unorderable pairs while carrying no part of the two-code account.

8.5 What the widening costs

Remark 8.14 (The price of the recovery). [Sch26h, Prop. 7.2] establishes that its construction produces codes in normal form and no others, and [Sch26h, Rem. 7.4] draws the consequence: normal form being the range, finding a code inside it is a test, reported at its score of four of twenty-seven.

Widening the outcome set to three values widens the range, and the score moves with it. A purine half taking disc gives its block pattern (3, 1) or (2, 1, 1), so the three-valued refinement reaches all four block patterns where the two-valued one reached two, and **twenty-seven of twenty-seven** published tables lie inside the widened range against four of twenty-seven inside the narrow one. Check V27.

Twenty-seven of twenty-seven is *not* a better result than four of twenty-seven. **It is a weaker prediction with a perfect score**, and the improvement is an artefact of the widening. Clause (i) of Proposition 3.1 states this before the section is reached.

What is bought for the loss is Corollary 8.4, the two codes ceasing to need two mechanisms, and Theorem 8.7, which is a prediction the narrow construction could not have made. What is not bought is any account of which halves take which value: that is Theorem 7.6 and it is negative.

Proposition 8.15 (The one surviving prohibition). *[A] The widened construction forbids exactly one thing: that a pyrimidine half take the value disc, that half being seeded and propagated rather than refined ([Sch26h, Hyp. 2.10]). Of the four hundred and thirty-two pyrimidine halves in the published record — sixteen blocks in each of twenty-seven tables — none does. Check V28.*

Remark 8.16 (And the prohibition is not this corpus's to discover). The figure is the whole of what the construction still forbids and it is satisfied, and it must be discounted in the same breath, on the discipline of Remark 7.15: that a third base may be read U or C without changing the residue is third-position synonymy, among the oldest regularities recorded of the genetic code, and predicting it is predicting something already known.

The discriminating content of this paper has therefore moved out of the range and into the environment — from *is this code in the range*, which Section 8.5 shows is now nearly vacuous, to *does a setting of V say which halves take which value*. Theorem 8.7 answers yes for five tables and Theorem 8.10 answers no for twenty-seven.

8.6 Two cautions carried forward

Remark 8.17 (The two codes are not two samples). [Sch26h, Rem. 3.4] states the caution and it applies with more force here, the comparison being this paper's subject. The vertebrate mitochondrial table is defined in [NCBI24] as a list of differences from table 1, so *the two codes are two resolutions of one refinement* reports a property of four codon reassignments, and weight placed on Theorem 8.1 is weight placed on those four. Nor are the three halves four independent observations: AG-pur supplies two of the four codons and the others one each.

Theorem 8.7 is less exposed to this objection, resting on five tables rather than two; but by Remark 8.8 it is not the evidence the earlier version took it for, and the section's positive content is the structural results named there.

Remark 8.18 (What would discriminate). Two things, neither performed here. An intervention of the kind [Sch26h, Target 9.3] asks for: move V — through pH or through whichever co-varying quantity of Remark 6.19 is the agent — and read whether a half's resolution moves with it in the predicted direction. That is a measurement and not a proof. Or a compartment pH for the four tables of Proposition 8.6. The account places them between nucleoplasm and matrix on a monotone axis; if that axis is pH, their matrix pH should lie between 7.4 and 7.8, and if it does not, either the axis is one of the co-varying quantities or Theorem 8.7 is an ordering without a referent. **This is the sharpest test the paper admits and it is not performed.**

9 The Feedback Loop as a Registered Conjecture

H_{loop} is the least supported object in this paper and the section is written accordingly: it states the circuit, reports the one concrete element the paper supplies, records what the record says about it — which is not what the conjecture said — and opens three Targets. **Nothing in Sections 5 to 8 is evidence for it**, and Section 9.4 says so at the point the conjecture is put.

9.1 The circuit

Remark 9.1 (What H_{loop} asserts). A code determines a proteome; the proteome determines the compartment's redox handling, metal chemistry and pH; those set V ; V sets the resolutions at the purine halves; and the resolutions are the code. The circuit closes, and a code that reproduces itself around it is a fixed point.

The hypothesis is registered at H_{loop} and is used nowhere.

It is stated because the alternative — leaving the circularity implicit in an account whose switch is built from the code's own products — would be worse.

9.2 The one concrete element

Remark 9.2 (The latch is inside the loop, not outside it). By Proposition 6.15 the chrysene complex contains neither cysteine nor methionine; both are products of the code the complex makes. A methionine–cysteine latch is therefore not a part of the vessel but the code's own output modulating the vessel, which is Corollary 6.16.

This is the paper's only concrete instance of the circuit, and it is worth stating what makes it more than a restatement of H_{loop} : the latch was not chosen to instantiate the loop. It was arrived at in Section 6 as the only ionisable side chain in the relevant set whose pK_R lies near the compartment interval, and the fact that it is built from products is a consequence discovered afterwards. A generic pH sensor would have served Section 6 equally well and would have sat outside the circuit entirely.

Remark 9.3 (And it cannot start the circuit). Corollary 6.17 is the cost and is restated here because this is the section where a reader will try to read the loop as an origin account. A latch built from products presupposes the products. **The loop as this paper has it is a maintenance mechanism and not an initiation one**, the initial setting of V is not accounted for, and that is Target 10.4.

9.3 The conjecture, and what the record does to it

Remark 9.4 (The conjecture as it stood). The natural conjecture, and the one this paper set out with, is that the standard and the vertebrate mitochondrial codes are **two** fixed points of the circuit, reached by two convergence paths from a common ancestor. It has the shape the account invites: two compartments, two settings of V , two codes.

Proposition 9.5 (Occupancy). [A] *Classify each of the twenty-seven tables by the triple of resolutions at the three conditional halves AG-pur, AU-pur and UG-pur. Of the twenty-seven conceivable triples, five are occupied:*

AG	AU, UG	Tables	Which
disc	disc, unif	2	24, 33
unif	disc, disc	14	1 standard, 6, 10, 11, ...
unif	disc, unif	6	4, 9, 14, 27, 28, 31
unif	unif, unif	4	3, 5, 13, 21
∅	unif, unif	1	2 vertebrate mit.

Four of the five lie on a single chain, which **twenty-five of the twenty-seven tables occupy**; the exceptions are tables 24 and 33, both carrying AG-pur as disc. Check V29.

Corollary 9.6 (The conjecture of two fixed points does not cover the record). [A] *The chain of Proposition 9.5 passes through four distinct settings and the standard and mitochondrial codes occupy two of them. The other two are occupied by ten tables — 4, 9, 14, 27, 28 and 31 at one setting, and 3, 5, 13 and 21 at another — and those are codes of living organisms, presumably as self-consistent as the two this paper began with. A fixed-point account must therefore admit at least four, and with tables 24 and 33 at least five. Check V30.*

Remark 9.7 (The conjecture is revised, not rescued). Remark 9.4 is withdrawn in its stated form. What survives is weaker and is stated as a Target rather than a conjecture: the circuit, if it has fixed points at all, has at least four, and the ordering of Theorem 8.7 suggests they are not scattered but strung along an axis.

Two observations keep even that in proportion. **Five of twenty-seven conceivable configurations is a concentration**, and a concentration is what a discrete-attractor account predicts — but the tables are phylogenetically related and mostly curated as perturbations of table 1 (Remark 5.6), so the concentration is what relatedness predicts too, and nothing here separates the two explanations. And the four settings are ordered by the same axis that Theorem 8.10 shows cannot be extended to the full purine column, so the tidiness is a feature of the three halves this paper selected and not of the record.

9.4 What the spine does not support

Remark 9.8 (Stated where the conjecture is put). The findings of Section 5 — that twenty-three of thirty-two halves never vary, that eight of the nine that do are purine, that the two codes differ at exactly three halves — are *consistent with H_{loop}* and with several accounts that have no loop in them at all. They are not evidence for it, and Remark 5.5 shows that the purine confinement is in substantial part entailed by the construction inherited from [Sch26h] rather

than discovered.

No result of this paper would change if H_{loop} were false. Theorem 8.1, Theorem 8.7, Theorem 7.6 and Theorem 8.10 are statements about published tables and about systems of inequalities over them; each would stand under any account that makes a half's resolution depend monotonically on one environmental quantity, loop or no loop. The loop earns its place in the register by Corollary 6.16 alone.

9.5 The state space is not one-dimensional

Remark 9.9 (What Theorem 8.10 costs the loop). H_{loop} as stated routes the whole circuit through a single scalar: the proteome sets the compartment chemistry, which sets V , which sets the resolutions. If that were right the published record would be ordered by V , and Theorem 8.10 is the statement that it is not — **one hundred and thirty of the three hundred and fifty-one pairs of tables admit no common position on any single axis**, with the thresholds free.

So the circuit's state is at least two-dimensional, and Corollary 8.11 says where the second dimension shows itself: AA-pur and CU-pur are implicated in fifty-five and thirty-two of the unorderable pairs while carrying no part of the two-code account. Whether the second quantity is one of the co-varying candidates of Remark 6.19 — redox potential, viscosity, divalent metals — or something the formalism does not represent is Target 10.5.

This is the most useful thing the negative results of Sections 7 and 8 do for the loop: they do not refute it, and they tell it how many parameters it needs.

9.6 What a test would require

Remark 9.10 (The loop has no state space yet). H_{loop} names five quantities and an arrow between each consecutive pair. It has no state space, no map, and therefore no fixed points in any sense that could be checked — Corollary 9.6 counts occupied settings and not fixed points, and the two are different things until the map is written down. Giving the circuit a state space and a map, and asking how many fixed points it has, is Target 10.8. Until that is done, **the conjecture is a picture and the paper does not claim otherwise**; clause (v) of Proposition 3.1 guards the one inference a reader is most likely to draw from the picture, that a product-built latch explains how the code began.

10 Non-Implications Restated, and Targets

10.1 The non-implications in one line each

- (i) All twenty-seven tables lie inside the range, because the third value widened it; that is a weaker prediction and not a better score (Prop. 3.1(i), Rem. 8.14).
- (ii) Per-half thresholds exist and are not a function of the block (Prop. 3.1(ii), Thm. 7.6).
- (iii) One monotone parameter orders the two codes and does not order the record (Prop. 3.1(iii), Thm. 8.10).
- (iv) The purine confinement is largely stop recoding, and this construction places the stops there itself (Prop. 3.1(iv), Rem. 5.5).
- (v) A product-built latch presupposes the products and cannot start the circuit (Prop. 3.1(v), Cor. 6.17).
- (vi) $\text{unif}(r)$ does not determine r (Prop. 3.1(vi), Prop. 5.12).
- (vii) disc covers three distinct outcomes (Prop. 3.1(vii), Prop. 5.14).
- (viii) pH is adopted as the switch and is not established (Prop. 3.1(viii), Rem. 6.19).
- (ix) The uniformity of the pyrimidine halves is third-position synonymy (Prop. 3.1(ix), Rem. 8.16).

Sch26h is recovered and not superseded, and one of its claims is corrected (Prop. 3.1(x), Rem. 8.5).

Three further traps are stated at the point of use and not repeated as clauses: that the two codes are not two samples (Rem. 8.17); that no result here tests the chemical hypotheses, nor they it (Rem. 3.5); and that V is an ordering and not a measurement (Rem. 2.6).

10.2 Targets

Target 10.1 (What sets the threshold). [T] Determine what fixes $t_1(h)$ and $t_2(h)$, given that no function of product volume, second-position association and first-base strength does (Thm. 7.6). The minimum a candidate must do is separate UU-pur from AU-pur and AG-pur from UG-pur *with the same sign*, which is what Corollary 7.7 shows no block-level quantity can. A quantity that is not a property of the block — a property of the tether register, or of the cluster's neighbours along the strand — is where to look, and the formalism does not currently supply one.

Target 10.2 (The product at UA-pur). [T] Determine what the purine half of UA would release if it engaged. It does not code in table 1, so the formalism assigns it nothing, and across the record it codes in twelve tables for five different residues spanning eighty-nine cubic ångströms (Rem. 7.3). Section 7 excludes the half rather than choose, and the exclusion costs one inequality.

Target 10.3 (Which discrimination). [T] Determine what selects between the outcomes the value disc covers: the A codon falling back to the block's pyrimidine product, thirty instances; yielding nothing, twenty; or a residue that is neither, one (Prop. 5.14). Either a fourth value is added to Definition 4.3 or a rule is given. The first is the stronger paper and is not attempted here.

Target 10.4 (The initial setting). [T] Account for the value of V before any product exists. The latch of H_{latch} is built from cysteine and methionine, which the code makes, so it is maintenance and not initiation (Cor. 6.17). Whatever sets V initially is outside the circuit of H_{loop} and outside this paper.

Target 10.5 (A second axis). [T] Identify the second environmental quantity. One is not enough: one hundred and thirty of the three hundred and fifty-one pairs of published tables admit no common position on any single axis, with the thresholds free (Cor. 8.11). AA-pur and CU-pur are where to look, being implicated in fifty-five and thirty-two of those pairs while carrying no part of the two-code account. Whether the second quantity is one of the co-varying candidates of Remark 6.19 or something the formalism does not represent is open.

Target 10.6 (Which agent). [T] Separate pH from redox potential, viscosity and divalent-metal availability, which co-vary with it between the two compartments. This paper adopts pH on the strength of Proposition 6.9 — the cysteine thiol being the only side chain in the relevant set whose pK_R lies near enough to the interval to move a substantial fraction of contacts across it — and that is a reason to prefer it, not a measurement. An intervention moving one quantity while holding the others is what would settle it. **This is [Sch26h, Target 9.3] and it is not discharged here.** That target asks what decides release at UGA and at AUA and calls for a measurement; this paper supplies a candidate and a direction (Rem. 2.13).

Target 10.7 (The intermediate compartments). [T] Measure the matrix pH of the organisms using tables 3, 5, 13 and 21. Theorem 8.7 places three of them between nucleoplasm and vertebrate matrix on a monotone axis; if that axis is pH, their matrix pH should lie between the 7.4 and 7.8 of [Lle98]. **This is the sharpest test the paper admits**, it requires no new formalism, and a negative result would show either that the agent is one of the co-varying quantities of Target 10.6 or that Theorem 8.7 is an ordering without a referent.

Target 10.8 (A map for the loop). [T] Give H_{loop} a state space and a map, and ask how many fixed points it has. At present the circuit names five quantities and an arrow between each consecutive pair, and has no fixed points in any checkable sense: Corollary 9.6 counts occupied settings, of which there are at least four, and occupied settings are not fixed points until the map is written (Rem. 9.10). By Remark 9.9 the state is at least two-dimensional.

10.3 Which are load-bearing

Remark 10.9 (Three of the eight). Their number is not offered as evidence of anything.

Target 10.1 decides whether the account reaches composition at all. At present it reaches the arrangement of the conditionality and not its composition (Rem. 7.13), which is [Sch26h, Rem. 7.12]’s division recurring one level down, and the paper’s central omission is on the same side of it as its predecessor’s.

Target 10.5 decides how much of the record the account can reach. One parameter reaches five tables and fails on twenty-seven. Until a second is named, Theorem 8.7 is the largest set the account orders and there is no principle saying why it stops there.

Target 10.7 decides whether the axis has a referent. Everything in Sections 6 and 8 is consistent with V being a bookkeeping device that orders tables and corresponds to nothing; the measurement would settle that and nothing else in the paper can.

The remaining five are not load-bearing in the same sense. Targets 10.2 and 10.3 sharpen results already stated; Target 10.4 concerns a phase the paper does not model; Target 10.6 would strengthen an adopted hypothesis without changing any theorem; and Target 10.8 asks for a result stronger than any claimed here.

10.4 Status of the predecessors’ programme

Remark 10.10 (One target addressed, one answered in part, none discharged). No deferred target of [Sch26c]–[Sch26g] is discharged here. Three statements of [Sch26h] change standing and the manner is recorded so that none is mistaken for a discharge.

[Sch26h, Target 9.3], discharging $H_{\text{lib-env}}$, is *addressed and not discharged*: a candidate variable and a direction are supplied and the measurement it asks for is not performed (Rem. 2.13, Target 10.6).

[Sch26h, Target 9.9], which asks whether one mechanism is available at eight blocks and why the standard code’s exceptions are UG and AU rather than another pair, is *answered in part, negatively*: no function of the block quantities the architecture supplies picks out that pair (Thm. 7.6). The first half of the target is untouched and the target survives in the sharper form of Target 10.1.

[Sch26h, Target 9.8], on coordinated vessels, is *touched*: the methionine–cysteine latch is a candidate mechanism for the first of the two pairs that target proposes and says nothing of the second (Cor. 6.16).

Two further dispositions are not targets and are recorded with them. [Sch26h, Rem. 7.19] is **corrected**: the two divisions it names are two thirds of the distance between the codes (Rem. 5.10, Rem. 8.5). And [Sch26h, §C.5] is **inverted**: the residue volumes it declares decorative are load-bearing here (Rem. 2.16).

Finally, one conjecture of this paper’s own development is withdrawn rather than deferred: that the standard and mitochondrial codes are the two fixed points of H_{loop} . The record occupies at least four settings (Cor. 9.6), and a withdrawal is not a proof.

11 Conclusion

The question was what carries the construction of [Sch26h] from the vertebrate mitochondrial code to the standard one. That paper reaches its output by seeding a block, propagating, and dividing once at the third base, and then reaches the standard code by a further division which it invokes twice and does not derive. The answer offered here is that no further operation is required: the one division has a third outcome, and which outcome it takes is set by the environment.

The distinguishing feature is stated first because it governs everything after. Widening the refinement to three values widens its range to every block pattern the published record contains, so the narrow prediction that made [Sch26h, Prop. 7.2] a test is lost, and the score that rises from four of twenty-seven to twenty-seven of twenty-seven rises for that reason and not because anything was confirmed (Rem. 8.14). What is bought for the loss is the removal of a second mechanism, an attested

third setting, and a correction; what is not bought is any account of which halves take which value.

The refinement. A half resolves in one of three ways: it releases a residue at both codons, releases nothing at either, or resolves its two codons differently (Def. 4.3). The pyrimidine half is seeded and propagated and cannot take the third value, which is the construction's only prohibition; the purine half is free, and the environment fixes it (Def. 4.5). Normal form is the case where the third value never occurs, with a non-coding half counting as uniform — a clause that is not decorative, since without it the recovery of [Sch26h, Thm. 7.13] fails at exactly the four tables that paper finds (Rem. 4.8).

The spine. Of the thirty-two halves, twenty-three take the same resolution in all twenty-seven published tables, and eight of the nine that vary are purine halves (Prop. 5.2). The figure invites a structural reading and does not carry one: all three stop codons of the standard code have a purine third base and are absences on purine halves by [Sch26h, Cor. 6.4], so the confinement is in substantial part entailed by the inherited construction, and stripping the deviations that involve a stop carries it from eight of nine halves to four of five (Rem. 5.5). The two codes differ at exactly three halves, all purine, at four codons, and setting those three halves of table 2 to their table-1 values returns table 1 entire (Thm. 5.7).

The engagement reading. The direction is fixed by the code data and not by the chemistry: at AG-pur the low-pH compartment releases arginine and the high-pH one terminates, so an account in which alkalinity eases release predicts the reverse (Cor. 6.4). The limiting step is engagement and not escape — a larger effective volume does not free the product, it fails to hold the reactants — and the reading is [Sch26h, Rem. 5.11]'s, made conditional. The cysteine thiol at pK_R 8.33 moves from 6.9 to 31.9 per cent across the compartment range, twenty-five points, and is the only ionisable side chain in the relevant set that moves a substantial fraction of contacts there; arginine, whose assignment is the one that changes, is refused on three grounds, of which the sharpest is that $7.2 \rightarrow 8.0$ carries it *toward* its isoelectric point (Prop. 6.11). The latch cannot be part of the vessel, cysteine and methionine being products of the code the vessel makes, so it is feedback; and being built from products it cannot set the initial volume (Cor. 6.17).

The recovery, and the correction. At the higher setting the refinement takes no third value and its output is table 2, which is [Sch26h] entire; the two further divisions of that paper are the third value at the lower setting, and no operation is added (Cor. 8.4). The recovery also corrects. [Sch26h] describes the standard code in seven places as its output with two further divisions and states at its Remark 7.19 that those two are the whole distance between the codes. **They are two thirds of it.** The third differing half is AG-pur, which is uniform in both codes, so no division occurs there and none is needed; what changes is whether the half liberates at all (Rem. 8.5). Its own Theorem 5.8 lists the four codons correctly.

What extends. The scheme posits three regimes and the two codes use two. At an intermediate volume AG-pur should engage uniformly while AU-pur and UG-pur have ceased to discriminate, and **four published tables are in that state** — yeast, invertebrate, ascidian and trematode mitochondrial — three of them being three of the four [Sch26h] finds in normal form (Prop. 8.6). One monotone parameter, with thresholds shared across all sixteen purine halves, orders tables 1, 3, 5, 13 and 2 in that sequence (Thm. 8.7). Nothing required a third regime to be occupied and nothing selected which tables should occupy it. Theorem 8.7 rests on five tables where Theorem 8.1 fits two environments to three halves; but by Remark 8.8 neither is the paper's evidence, which is structural.

What does not extend. Two negative results, and they are the paper's principal content.

The thresholds are not a function of the block. No pair of thresholds linear in product volume, second-position association and first-base strength fits the purine column, at any parameter count, and not with the association scale fitted either (Thm. 7.6). The obstruction needs no linear algebra: UU-pur and AU-pur share a second base and a weak first base and differ by $3.8 \text{ \AA}^3$, with the larger the one that does *not* discriminate; UG-pur and AG-pur share a second base and a weak first base and differ by $54.4 \text{ \AA}^3$, with the larger the one that *does*. The volume coefficient is required to take both signs, and neither of the other two terms enters either pair (Cor. 7.7).

And one environmental parameter does not order the record. With the thresholds free and no functional form assumed, no assignment of a value to each of the twenty-seven tables realises every resolution: **one hundred and thirty of the three hundred and fifty-one pairs admit no common position on any single axis**, the smallest witness being tables 32 and 33, where UG-pur discriminates in one and AG-pur in the other (Cor. 8.11). The failure is not confined to the exotic tables: adding table 21 to the five already breaks the ordering, and table 21 is one of the four exhibiting the predicted third regime (Rem. 8.12).

The loop. The latch being built from products is the paper's one concrete instance of H_{loop} , and it was not chosen to be one: it was arrived at on pK_a grounds and turned out afterwards to sit inside the circuit (Rem. 9.2). The conjecture the account invites — that the two codes are the two fixed points — does not survive the record. Classified by the three conditional halves, the twenty-seven tables occupy five of twenty-seven conceivable configurations, four of them on a single chain that twenty-five tables lie on, and the standard and mitochondrial codes occupy two of the four (Prop. 9.5). A fixed-point account must admit at least four, and the conjecture is withdrawn rather than deferred (Cor. 9.6). What the negative results give the loop in return is a count: its state is at least two-dimensional (Rem. 9.9).

What is not done. No axiom is introduced (Rem. 2.2). No deferred target of any predecessor is discharged; [Sch26h, Target 9.3] is addressed, its Target 9.9 answered in part and negatively, its Target 9.8 touched, its Remark 7.19 corrected,

and its Appendix C.5 inverted, the residue volumes it declares decorative being load-bearing here (Rem. 10.10, Rem. 2.16). Ten non-implications are recorded and eight Targets opened, of which three are load-bearing.

Three limits deserve restating rather than leaving to the list. The refinement fixes outcome *types* and not content: AG-pur is uniform and coding across the record under arginine, serine and glycine, so the residues named in Sections 5 and 8 are read from the published tables and enter on $H_{\text{eng-content}}$, which is empirical (Rem. 2.14). The two codes are not two samples, the mitochondrial table being defined as a list of differences from the standard one, so weight placed on the comparison is weight placed on four codons (Rem. 8.17). And V is an ordering and not a measurement: everything in Sections 6 and 8 is consistent with its being a bookkeeping device that ranks tables and corresponds to nothing (Rem. 2.6).

What remains. A single refinement with a third outcome removes the second operation, recovers its predecessor as one case, corrects that predecessor's account of the distance to the standard code, and predicts a third setting which four published tables occupy. It does not say which halves are conditional, and Section 7 shows that the quantities the architecture supplies cannot say. It orders five tables and not twenty-seven, and Section 8 shows that one parameter cannot. **The paper accounts for the arrangement of the conditionality and not for its composition**, which is [Sch26h, Rem. 7.12]'s division recurring one level down and on the same side of it.

And this is where Part II begins. The three results just restated are the specification it works to: a quantity that is not a property of the block (Thm. 7.6), a medium with more than one direction to move in (Thm. 8.10), and a referent for the axis (Rem. 8.18). Part II supplies all three from one object, the chrysene–adenosine reaction cell of [Sch26k] carrying the cage margins of [Sch26m]: the codon enters through stacking geometry rather than block algebra, the medium moves the cage through several coordinates at once, and reachability of a carve is a maximum over reaction words of a minimum over margins — a quantity that is a step function of a continuous environment. The series goal is the conditional sufficiency theorem that one cluster, in two media, carves the two codes. **What this paper establishes is that no account which leaves the cell out can reach it.**

The sharpest question is Target 10.1 and the sharpest test is Target 10.7. The second requires no new formalism: if the axis of Theorem 8.7 is pH, the matrix pH of the organisms using tables 3, 5, 13 and 21 lies between the 7.4 and 7.8 of [Lle98]. Nothing else in this paper could distinguish an ordering from a mechanism, and the measurement has not been made.

A Tables

Every table in this appendix is a computation, regenerated by the supplementary script from the definitions of Section 4 and, where a codon table is read, from [NCBI24] as published. Nothing here is transcribed by hand. Throughout, $u(r)$ abbreviates $\text{unif}(r)$ and $d(x, y)$ abbreviates disc with x at the A codon and y at the G codon.

A.1 The conditional halves across the published record

id	Code	AG-pur	AU-pur	UG-pur	Setting
24	Rhabdopleuridae mitochondrial	$d(S, K)$	$d(I, M)$	$u(W)$	<i>off chain</i>
33	Cephalodiscidae mitochondrial	$d(S, K)$	$d(I, M)$	$u(W)$	<i>off chain</i>
1	Standard	$u(R)$	$d(I, M)$	$d(*, W)$	low
6	Ciliate, dasycladacean, hexa..	$u(R)$	$d(I, M)$	$d(*, W)$	low
10	Euplotid nuclear	$u(R)$	$d(I, M)$	$d(C, W)$	low
11	Bacterial, archaeal, plant p..	$u(R)$	$d(I, M)$	$d(*, W)$	low
12	Alternative yeast nuclear	$u(R)$	$d(I, M)$	$d(*, W)$	low
15	Blepharisma nuclear	$u(R)$	$d(I, M)$	$d(*, W)$	low
16	Chlorophycean mitochondrial	$u(R)$	$d(I, M)$	$d(*, W)$	low
22	Scenedesmus obliquus mit.	$u(R)$	$d(I, M)$	$d(*, W)$	low
23	Thraustochytrium mitochondrial	$u(R)$	$d(I, M)$	$d(*, W)$	low
25	Candidate division SR1	$u(R)$	$d(I, M)$	$d(G, W)$	low
26	Pachysolen tannophilus nuclear	$u(R)$	$d(I, M)$	$d(*, W)$	low
29	Mesodinium nuclear	$u(R)$	$d(I, M)$	$d(*, W)$	low
30	Peritrich nuclear	$u(R)$	$d(I, M)$	$d(*, W)$	low
32	Balanophoraceae plastid	$u(R)$	$d(I, M)$	$d(*, W)$	low
4	Mold, protozoan, coelenterat..	$u(R)$	$d(I, M)$	$u(W)$	low
9	Echinoderm and flatworm mit.	$u(S)$	$d(I, M)$	$u(W)$	low
14	Alternative flatworm mit.	$u(S)$	$d(I, M)$	$u(W)$	low
27	Karyorelict nuclear	$u(R)$	$d(I, M)$	$u(W)$	low
28	Condylostoma nuclear	$u(R)$	$d(I, M)$	$u(W)$	low
31	Blastocrithidia nuclear	$u(R)$	$d(I, M)$	$u(W)$	low
3	Yeast mitochondrial	$u(R)$	$u(M)$	$u(W)$	intermediate
5	Invertebrate mitochondrial	$u(S)$	$u(M)$	$u(W)$	intermediate
13	Ascidian mitochondrial	$u(G)$	$u(M)$	$u(W)$	intermediate
21	Trematode mitochondrial	$u(S)$	$u(M)$	$u(W)$	intermediate
2	Vertebrate mitochondrial	$\emptyset$	$u(M)$	$u(W)$	high

Five of the twenty-seven conceivable configurations are occupied (Proposition 9.5); four lie on one chain, which 25 of the twenty-seven tables occupy, and tables 24 and 33 lie off it. The UA-pur column is omitted: it is $\emptyset$ in 15 of the twenty-seven and is excluded from Section 7 by Remark 7.3.

A.2 The nine halves that vary

Half	Table 1	Deviating	Distinct	Values taken
UG-pur	$d(*, W)$	15	4	$u(W) \times 13, d(*, W) \times 12, d(C, W) \times 1, d(G, W) \times 1$
UA-pur	$\emptyset$	12	8	$\emptyset \times 15, u(Q) \times 3, d(Y, *) \times 2, d(*, L) \times 2, u(E) \times 2, d(*, Q) \times 1, u(Y) \times 1, d(*, W) \times 1$
AG-pur	$u(R)$	8	5	$u(R) \times 19, u(S) \times 4, d(S, K) \times 2, \emptyset \times 1, u(G) \times 1$
AU-pur	$d(I, M)$	5	2	$d(I, M) \times 22, u(M) \times 5$
CU-pur	$u(L)$	3	4	$u(L) \times 24, u(T) \times 1, d(L, S) \times 1, d(L, A) \times 1$
AA-pur	$u(K)$	3	2	$u(K) \times 24, d(N, K) \times 3$
UU-pur	$u(L)$	1	2	$u(L) \times 26, d(*, L) \times 1$
UC-pur	$u(S)$	1	2	$u(S) \times 26, d(*, S) \times 1$
CU-pyr	$u(L)$	1	2	$u(L) \times 26, u(T) \times 1$

Twenty-three of the thirty-two halves take one value throughout. Eight of the nine above are purine halves; CU-pyr is the exception and varies in table 3 alone. Counts are deviations from table 1 (Remark 5.1).

A.3 The fifty-one instances of the third value

Outcome at the A codon	Instances	By half
A carries the block's pyrimidine product	30	AU-pur 22, AA-pur 3, CU-pur 2, AG-pur 2, UG-pur 1
A carries no residue	20	UG-pur 12, UA-pur 6, UU-pur 1, UC-pur 1
A carries a residue that is neither	1	UG-pur 1
total	51	at 8 halves

The count of fifty-one agrees with [Sch26h, Prop. 7.17], which reaches it by block pattern rather than by resolution. The division into three outcomes is Proposition 5.14 and is the content of Target 10.3.

A.4 The purine column, and why no block-feature threshold fits

Half	Product	Vol.	Pos. 2	Pos. 1	$\varepsilon_{\text{nuc}} \rightarrow \varepsilon_{\text{mito}}$
UU-pur	L	166.7	U	weak	unif $\rightarrow$ unif
UC-pur	S	89.0	C	weak	unif $\rightarrow$ unif
UA-pur	—	—	A	weak	empty $\rightarrow$ empty
UG-pur	W	227.8	G	weak	disc $\rightarrow$ unif
CU-pur	L	166.7	U	strong	unif $\rightarrow$ unif
CC-pur	P	112.7	C	strong	unif $\rightarrow$ unif
CA-pur	Q	143.8	A	strong	unif $\rightarrow$ unif
CG-pur	R	173.4	G	strong	unif $\rightarrow$ unif
AU-pur	M	162.9	U	weak	disc $\rightarrow$ unif
AC-pur	T	116.1	C	weak	unif $\rightarrow$ unif
AA-pur	K	168.6	A	weak	unif $\rightarrow$ unif
AG-pur	R	173.4	G	weak	unif $\rightarrow$ empty
GU-pur	V	140.0	U	strong	unif $\rightarrow$ unif
GC-pur	A	88.6	C	strong	unif $\rightarrow$ unif
GA-pur	E	138.4	A	strong	unif $\rightarrow$ unif
GG-pur	G	60.1	G	strong	unif $\rightarrow$ unif

The product of a half is its G-codon residue (Definition 7.2); UA-pur has none. **The obstruction of Corollary 7.7 can be read off this table.** UU-pur and AU-pur agree in both remaining columns and differ by $3.8 \text{ \AA}^3$, the larger being the one that does not discriminate; UG-pur and AG-pur likewise agree and differ by $54.4 \text{ \AA}^3$, the larger being the one that does.

A.5 Ionisation across the compartment range

Group	pK	7.2	7.4	7.8	8.0
Cys thiol, deprotonated	8.33	6.9	10.5	22.8	31.9
Tyr phenol, deprotonated	10.07	0.135	0.213	0.534	0.844
Arg guanidinium, protonated	12.48	99.999	99.999	99.998	99.997
Arg α -amino, protonated	9.04	98.6	97.8	94.6	91.6

Percentages. pK values are [NC17, Table 3-1]; the compartment range is [Lle98]. Methionine and tryptophan have no ionisable side chain. The cysteine thiol moves 25.0 percentage points across the range and the tyrosine phenol 0.71; on fold change the order reverses, which is Remark 6.10.

B Concordance, Ledger, and Verification

B.1 Scope

This appendix records, for every prior statement the paper touches, whether it is preserved, extended, restated, specialised, corrected, inverted, bounded, not applicable or noted, against the criterion C of [Sch26b, Def. 2]. Four entries require comment before the tables, because each changes the standing of a prior result rather than citing it: [Sch26h, Rem. 7.19] is *corrected* (Rem. 8.5); [Sch26h,

Hyp. 2.13] is *specialised* (Rem. 2.13); [Sch26h, Rem. 5.11] is *extended* (Rem. 6.5); and the declaration of [Sch26h, §C.5] about the residue volumes is *inverted* (Rem. 2.16).

B.2 Concordance with [Sch26h]

Prior statement	Disposition
Thm. 5.8, the output is table 2	Preserved, and is the $\varepsilon_{\text{mito}}$ case of Thm. 8.1 (Cor. 8.3)
Rem. 7.19, two divisions are the whole distance	Corrected. Three halves separate the codes; two are divisions and the third, AG-pur, is uniform in both codes and changes only whether it liberates (Rem. 5.10, Rem. 8.5)
Cor. 6.4, stops are absences on purine halves	Preserved and made load-bearing: it is why the purine confinement of Prop. 5.2 is partly entailed rather than found (Rem. 5.5)
Hyp. 2.10, H_{seed}	Preserved and made load-bearing: clause (i) of Def. 4.5 is the construction's only prohibition (Prop. 8.15)
Hyp. 2.13, $H_{\text{lib-env}}$	Specialised , not discharged: a threshold form, a direction and a candidate variable are supplied (Rem. 2.13)
Rem. 5.11, the two non-coding halves	Extended. Its reading — a purine third base does not engage, stabilise or carve — is made graded and conditional (Rem. 6.5)
Props. 7.1, 7.2, patterns and the range	Preserved, and the range is <i>widened</i> : the third value reaches all four patterns where two were reached (Prop. 4.9, Rem. 8.14)
Thm. 7.13, the audit	Preserved; its four tables are recovered as the $\emptyset$ and intermediate settings (Cor. 8.3, Prop. 8.6)
Rem. 7.12, composition against arrangement	Preserved and extended one level down: this paper accounts for the arrangement of the conditionality and not its composition (Rem. 7.13)
Prop. 7.17, the fifty-one	Preserved; recovered by resolution rather than by pattern (Prop. 5.14)
Cor. 6.7, size is not the discriminant	Preserved, and its pattern reused one level up: Thm. 7.6 refutes the threshold account as Cor. 6.7 refutes the size account
Rem. 6.9, the two-clause registration	Preserved; the same form is used for $H_{\text{eng-type}}$ against $H_{\text{eng-content}}$ (Rem. 2.14)
Rem. 2.3, two counting conventions	Preserved (Rem. 2.3)
Rem. 2.16, the constructive declaration	Preserved and owed again in the same form (Rem. 2.15)
Rem. 3.4, the two codes are not two samples	Preserved and made sharper, the comparison being this paper's subject (Rem. 8.17)
§C.5, the residue volumes are decorative	Inverted. A proof of this paper depends on them (Rem. 2.16)
Target 9.3, discharge $H_{\text{lib-env}}$	Addressed, not discharged (Target 10.6)
Target 9.8, coordinated vessels	Touched: the latch is a candidate for the Cys–Met pair and says nothing of Tyr–Trp (Cor. 6.16)
Target 9.9, which blocks are further divided	Answered in part, negatively: no function of the block quantities picks out the pair (Thm. 7.6); survives as Target 10.1

B.3 Concordance with the earlier corpus

Prior statement	Disposition
[Sch26e, Cor. 3.7], the class profile	Preserved; not used directly, this paper working at the level of blocks
[Sch26g, Thm. 5.4], the capacity bound	Preserved; untouched, no residue being placed here that [Sch26h] did not place
[Sch26g, Cor. 5.9], parity	Not applicable. The conditional refinement changes no fibre of either code; the codes compared are those [Sch26h] compares
[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
A1–A12	Preserved; no axiom added (Rem. 2.2)

B.4 Chemical scope

Remark B.1 (What is before the domain pass). [E] H_{pH} and H_{latch} are chemical and undischarged, and H_{loop} is a conjecture with no state space (Rem. 9.10). Of these, H_{pH} is the one a reading depends on: by Rem. 6.19 redox potential, viscosity and divalent-metal availability co-vary with pH between the compartments and nothing here separates them, so every occurrence of pH in Section 6 may be read as *the quantity that co-varies* without altering a single theorem.

No theorem of this paper is conditional on any of the three. Theorems 7.6, 8.7 and 8.10 are statements about [NCBI24] and about systems of inequalities over it, and Theorem 8.1 requires only that two environments are ordered. The full synthesis is not given here and is forthcoming separately.

B.5 Defect ledger

Twenty criticisms were raised in the pre-drafting pass against outline v2, and all are disposed. The table records the items that changed a claim; items confirming an anticipated caution are counted and not listed individually. Ten were anticipated by the outline's own list and confirmed, three of those with their statement adjusted.

#	crit	rev
11	The two-parameter threshold model is refuted by CG-pur against AG-pur, which carry the same product and the same second base, and which the outline itself reported as the least and most conditional halves	Accepted. A first-base term was admitted and then refuted with the rest; Section 7 is a negative result (Thm. 7.6)
12	The refutation of a one-parameter model rested on assigning tyrosine to UA-pur, a half that does not code in table 1	Accepted. The binding failure is at AG against AU and is robust to the assignment; UA-pur is excluded and becomes Target 10.2 (Rem. 7.14)
13	The third value covers three chemically distinct outcomes and nothing selects between them	Accepted; recorded as Prop. 5.14 and Target 10.3, the codomain staying three-valued
14	$\text{unif}(r)$ does not determine r , so a theorem labelled [D] would read its residues off the target table	Accepted; the hypothesis is registered in two clauses (Rem. 2.14)
15	The purine confinement was presented as predicted rather than partly entailed by [Sch26h, Cor. 6.4]	Accepted; both figures are reported, before and after the stop-strip (Rem. 5.5)
16	A three-valued outcome needs two thresholds per half, and the outline had one	Accepted (Rem. 6.6)
17	Counting conventions: twenty-seven tables carry twenty-five distinct strings; the per-half counts are against table 1 and not the mode	Accepted (Rem. 5.1, Rem. 5.4)
18	Normal form iff no third value is definitional and cannot be a verification item	Accepted; carried by argument, and $\emptyset$ declared admissible (Rem. 4.8)
19	The strong/weak count is a first-base statement and is largely forced by the standard code's own degeneracy	Accepted; reduced to a remark with the forcing declared (Rem. 7.15)
20	Two pK_a compilations were mixed, printing a guanidinium protonation requiring one beside an isoelectric point requiring the other	Accepted; [NC17] is used entire and the mixture is recorded at B.6 (Rem. 6.13)

B.6 Referee revisions

One required and three recommended changes were made after review.

#	crit	rev
R1	Theorem 8.7 was offered as the paper's evidence and no null was reported; nine per cent of five-table subsets admit the ordering and a sixteen-table set exists	Accepted. The null is reported at Remark 8.8, the claim withdrawn, and the positive content relocated to Cor. 8.4 and Rem. 5.10; checks V31–V33
R2	Theorem 8.1 claims sixty-four codons where the refinement derives a resolution type at three halves	Accepted; the statement now names what is derived and what is carried by $H_{\text{eng-content}}$ and the seed map

#	crit	rev
R3	The four-codon caveat was conceded once and left to be carried for twenty pages	Accepted; restated at the head of §8, with what survives if table 2 is set aside
R4	The correction to the predecessor is asserted against a paper that stands uncorrected	Accepted; Rem. 5.10 now says so

B.7 Corrections to results reported during development

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

1. The pH effect was first given the opposite direction: higher pH easing release through a larger cage. The chemistry is retained and the endpoint inverted, the code data requiring that the low-pH compartment be the releasing one at AG-pur (Rem. 6.1, Cor. 6.4).
2. A threshold in product volume and second-position association was carried through two outline versions before being refuted. **The refuting datum was printed in the same outline four paragraphs earlier**, at the invariance of CG-pur.
3. UA-pur was assigned the volume of tyrosine by analogy with its block. Across the record that half codes in twelve tables for five residues, the modal one smaller than isoleucine, and the assignment is withdrawn.
4. The arginine figures were drawn from two pK_a compilations at once: a guanidinium protonation of 100.000 per cent, which requires $pK_R \approx 13.8$, beside $pI = 10.76$, which requires 12.48. Neither figure was wrong of its own set and the pair was impossible. [NC17] is now used entire.
5. The cysteine thiol was taken at $pK_R = 8.30$ where [NC17] gives 8.33. All four thiolate fractions and the fold change are restated (Prop. 6.8).
6. The thiol was claimed as the sharpest available switch on a *fold-change* measure, on which tyrosine leads it. The claim is restated on absolute population, where the thiol leads by a factor of thirty-five (Prop. 6.9, Rem. 6.10).
7. Section 8 was first drafted asserting that no published table exhibits the account's intermediate regime. **Four do**, and three of them are three of the four [Sch26h, Thm. 7.13] finds in normal form. The assertion was made in prose and refuted by computing it; what had been drafted as a gap is Prop. 8.6 and Thm. 8.7, the paper's best positive result.
8. The conjecture that the standard and mitochondrial codes are the two fixed points of H_{loop} was carried until the occupancy was counted. At least four settings are occupied and the conjecture is withdrawn (Cor. 9.6).

B.8 Verification record

Thirty-three checks, each an exhaustive enumeration or a closed computation, rebuilt from the definitions by the supplementary script. The script imports nothing from the tables of this paper; codon tables are read from [NCBI24] as published, residue volumes from [Zam72], dissociation constants from [NC17] and compartment pH values from [Lle98].

- V1 27 tables carry 25 distinct strings; 1=11 and 27=28 (§5.1)
- V2 32 halves: 23 invariant, 9 vary, 8 of them purine (§5.2)
- V3 per-half counts vs table 1; 49 instances, 48 purine (§5.2)
- V4 UG-pur: the standard reading is the minority one (§5.2)
- V5 stop-strip: 8/9 halves and 48/49 → 4/5 and 19 (§5.2, 3(iv))
- V6 24 of 27 tables within 4 codons of table 1 (§5.2, 7.4)
- V7 the two codes differ at exactly 3 halves, all purine (§5.3)

V8	setting those 3 halves of table 2 returns table 1	(§5.3)
V9	AG-pur takes 5 resolutions; uniform under R, S, G	(§5.4, 3(vi))
V10	the 51 disc instances split 30 / 20 / 1 by kind	(§5.4, 3(vii))
V11	CG reads R,R,R,R in all 27	(§5.5)
V12	cysteine thiolate at pKR 8.33 [NC17]	(§6.3)
V13	which side chain the gradient reaches; arginine refused	(§6.3)
V14	UA-pur codes in 12 tables for 5 residues	(§7.1)
V15	no block-feature threshold fits the purine column	(§7.2, 3(ii))
V16	the sign obstruction; robust to the product convention	(§7.2, 3(ii))
V17	AG-pur interior to the hull of AA, AU, UG	(§7.2)
V18	varying halves vs first-base strength, Fisher $p=0.057$	(§7.4)
V19	49 of 51 on weak first bases; strong-strong forced	(§7.4)
V20	the two settings output tables 1 and 2	(§8.1)
V21	the intermediate regime is attested: tables 3, 5, 13, 21	(§8.3)
V22	one monotone V orders 1,3,5,13,2	(§8.3)
V23	no monotone V orders all 27, thresholds free	(§8.4, 3(iii))
V24	130 of 351 table pairs are mutually unorderable	(§8.4)
V25	smallest witness: tables 32 and 33 at UG-pur / AG-pur	(§8.4)
V26	the failure reaches the series: tables 4 and 21	(§8.4, 3(iii))
V27	range: 27 of 27 inside, against [Sch26h]’s 4 of 27	(§8.5, 4.5, 3(i))
V28	all 432 pyrimidine halves of the record are uniform	(§8.5, 4.3, 3(ix))
V29	5 of 27 configurations occupied; 25 tables on one chain	(§9.3)
V30	the chain passes through at least four distinct settings	(§9.3)
V31	9 % of five-table subsets are orderable; a 16-table set exists	(§8.3)
V32	table 2 is the global maximum; the tie among 3, 5 and 13 is forced	(§8.3)
V33	one comparison of Thm. 8.7 is not forced	(§8.3)

Normal form iff the refinement takes no third value (Prop. 4.7) is an identity of definitions, is carried by argument, and is **not** a verification item, as [Sch26h] carries its own V7.

B.9 Meta-review

Remark B.2 (Disposition). Twenty items in one pre-drafting pass, all disposed. Thirty checks, all passing. Eight corrections to previously circulated figures, recorded at B.6.

Remark B.3 (Three observations). First, the two items of largest consequence — that the threshold model was refuted by a datum the outline already printed, and that the intermediate regime the draft denied is occupied — are not defects of proof. Neither is a step that fails to follow; each concerns what a correct computation was a computation of, and in both cases the

correction was found by computing a claim that had been written in prose. That is the sixth and seventh instance of this pattern in the corpus.

Second, this paper's ledger corrects a predecessor rather than itself withdrawing a hypothesis. [Sch26h] withdrew one hypothesis of *its* predecessor and bounded one corollary; this paper specialises one hypothesis, corrects one remark, inverts one declaration about external data, and withdraws a conjecture of its own.

Third, the paper's principal results are negative and its range is wider than its predecessor's, which is an unusual combination and is worth naming. A wider range with a perfect score is a weaker claim than a narrow range with a poor one (Rem. 8.14), and what keeps the paper from being weaker overall is Thm. 8.7, which the narrow construction could not have stated at all.

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 thirty numerical checks excepted.

Eight Targets are open, three load-bearing. Five hypotheses are registered and undischarged, of which none is required by a theorem (Rem. B.1). All twenty-seven published tables lie inside the construction's range, and that is a consequence of widening it. One monotone parameter orders five of the twenty-seven and no assignment orders all of them. The paper does not say which halves are conditional, and Section 7 shows the quantities the architecture supplies cannot say.

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 Linear feasibility

Sections 7 and 8 both turn on the *infeasibility* of a system of linear inequalities, which is the only technique the paper uses that its predecessors do not. That a system is infeasible exactly when a non-negative combination of its inequalities yields a contradiction is Farkas's lemma [Far02]; the modern treatment, together with the simplex and interior-point methods by which the systems here were decided, is [Schr86].

Two uses should be separated. Theorem 7.6 and Theorem 8.10 assert infeasibility and are established by the solver; Corollary 7.7 and Corollary 8.11 exhibit the Farkas certificate by hand, in each case a pair of inequalities whose sum is a contradiction. **The hand certificates are what the paper relies on** — a solver's infeasibility report is a computation and the certificate is an argument — and the solver is used to establish that no further certificate was missed.

Proposition 7.9 is the dual observation that a point interior to a convex hull is separated from its vertices by no linear functional, which is the separating-hyperplane theorem [Roc70, §11]; it is stated for one choice of association scale and Remark 7.10 records that it is therefore the weaker of the two obstructions.

C.2 Chains in a partial order

Proposition 9.5 classifies the published tables by a triple of resolutions ordered componentwise, and reports the longest chain. The vocabulary is that of partially ordered sets; the relevant classical result is Dilworth's [Dil50], though the posets here are small enough that the chains and the single incomparable pair are found by enumeration and no theorem is invoked.

C.3 Exact tests

Proposition 7.16 reports Fisher's exact test [Fis35, §21], the hypergeometric tail for a 2×2 table. It is used once, it returns $p = 0.057$, and Remark 7.17 records that the figure is not significant at the conventional threshold and that the halves are not independent, so that the test is reported rather than relied on.

C.4 Acid–base equilibria

The fractions of Proposition 6.8 and Proposition 6.9 are the Henderson–Hasselbalch relation applied to a single group at a stated pK , with the dissociation constants and isoelectric points of [NC17, Table 3-1]. No buffering, no ionic-strength correction and no

local-environment shift is modelled, and none is needed for the comparisons made: every statement in Section 6.3 is an ordering of fractions at two pH values and not a prediction of either.

C.5 Regularities of the genetic code that this paper does not claim

Two regularities appear in this paper as figures and belong to the prior literature. Both are attributed here because each could otherwise be read as a finding of the construction.

That a codon's third base may be read U or C without changing the residue — the uniformity of all four hundred and thirty-two pyrimidine halves of the published record, Proposition 8.15 — is third-position synonymy, and the mechanism proposed for it is the wobble hypothesis [Cri66]. Remark 8.16 states that the construction's one surviving prohibition is satisfied by a regularity that was not in doubt.

That blocks with strong first two bases are fourfold degenerate, so that no such block ever requires the further division — Remark 7.15 — is the family-box pattern, treated as a reading rule at [Lag78]. The count reported there, forty-nine of fifty-one on blocks with a weak first base, is a description of where the further divisions fall and is not offered as an explanation of why.

C.6 The external data

Five 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 every count of Sections 5, 7, 8 and 9 and the whole of Appendix A. Sections 3 and 4 use none of them. The dispute over the mitochondrial status of AGA and AGG is [Tem10]; it bears on AG-pur, which is the half at which the two codes differ most consequentially here, and Proposition 5.12 reports that the half takes five distinct resolutions across the record under either reading.

The residue volumes are [Zam72]. **Unlike in [Sch26h] a proof depends on them**, and Remark 2.16 declares the change of standing and names the margin: $3.8 \text{ \AA}^3$ for the first obstruction and $54.4 \text{ \AA}^3$ for the second.

The dissociation constants and isoelectric points are [NC17, Table 3-1], used entire; B.6 records that an earlier draft mixed two compilations. The compartment pH values are [Lle98], which established by targeted pH-sensitive fluorescent proteins that the resting matrix sits near 8.0 while cytosol and nucleus remain near 7.2. They enter Section 6 alone.

The molecular architecture is claimed in [Sch25a] and [Sch25b] and enters through H_{teth} , inherited unchanged from [Sch26h].

C.7 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 frame classes and the structured alphabet are [Sch26e]. Transversality and the block operators are [Sch26f]. The capacity bound and the parity obstruction are [Sch26g]. **The seed map, propagation, the third-position refinement, normal form as a range, and the output table are [Sch26h]**, and this paper's whole subject is one operation of that construction. The review architecture and the non-implication conventions are [Sch26b]; the survival programme, to which nothing here bears, is [Sch26a].

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