

PART II OF TWO

The Conditional Refinement

The Chrysene–Adenosine Reaction Cell, Margin Geometry and Necessary Conditions for Sufficiency

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Abstract

Part I makes the standard and vertebrate mitochondrial codes two settings of one three-valued refinement and then proves that the thresholds governing it are not a function of the codon block, and that no single environmental coordinate orders the published record. It carries the reaction vessel as a black box. This paper places the account in the cell.

The predecessor theory of cage-constrained reachability for the chrysene–adenosine complex assumes the external context of a reaction inert. We change that assumption and nothing else: the hard constraint functionals become functions of the medium. A step is then available exactly when its *margin* — the largest slack simultaneously available to all its constraints — is positive, so reachability of a target is a maximum over reaction paths of a minimum over step margins. Because a path margin depends only on which steps occur, no bound on path length enters.

A continuously varying medium therefore carves discretely. On a connected set missing the zero sets of the step margins each margin has constant sign, so the available steps, the available paths and the reachable targets are all constant there; the discontinuities lie in the margin locus, and within a chamber the predecessor's persistence theorems hold uniformly rather than pointwise. This uses no hypothesis and no constraint functional need be nonlinear: the nonlinearity is that of $\max \circ \min$.

Determinism is not assumed but derived off a set of codimension one, that set being where two carves balance. Under the hypothesis that one cage covers the twenty-seven published tables, the fifteen distinct resolution vectors it must realise bound the cell from below: fourteen environed constraints in a one-dimensional medium against five in two.

What is given are necessary conditions for a cage to realise the two codes — the two environments must lie in distinct chambers at each of three half-blocks, and some hard constraint must change sign between them — together with a criterion no cage depending on the codon through its block alone can meet. Residue-sufficiency is further from reach than type-sufficiency: the theory says which target is reachable, not which residue it carries, and that gap is sixty-three witness pairs of which two classes are open questions of the corpus. One prediction is testable without any translation table — the handedness of the carved residue is constant on chambers of the oriented locus and exchanged across a wall, with a racemic region where the oriented exclusion fails.

Keywords: Chrysene Formalism; chrysene–adenosine complex; reaction cell; cage-constrained reachability; step margin; $\max$ – $\min$; chamber decomposition; hyperplane arrangement; genetic code; mitochondrial code; stereochemical selection; environed constraint; synthesis pathway; non-implication.

1 Introduction

1.1 The problem

Part I makes the standard and vertebrate mitochondrial codes two settings of one three-valued refinement, the value at each half-block fixed by an environment through a pair of thresholds.

It then proves two things about those thresholds and neither is favourable. They are not a function of the codon block: no pair linear in product volume, second-position association and first-base strength fits the purine column, at any parameter count [Sch26i, Thm. 7.6]. And no single environmental coordinate orders the published record: one hundred and thirty of the three hundred and fifty-one pairs of tables admit no common position

on any axis [Sch26i, Thm. 8.9].

Part I also establishes a prediction its construction did not require: the scheme's third regime is occupied by four published tables, and one monotone parameter orders five of them with thresholds shared across all sixteen purine halves [Sch26i, Prop. 8.6, Thm. 8.7]. **That result is not in question here**; what this paper takes as its specification is the two negative ones.

Part I carries the reaction vessel as a black box parameterised by an effective volume which its own Remark 2.6 concedes is an ordering with no referent. **The two negative results say where the missing account must live**: in a quantity that is not a property of the block, in a medium with more than one direction to move in, and in something that gives the axis a referent.

1.2 The objective

To place the account in the reaction cell. [Sch26m] supplies a theory of constrained chemical reachability for the chrysene-adenosine complex: typed molecular graphs with persistent atom identities, local rewrite rules, three-dimensional cage-admissibility spaces with hard constraints, and a category whose morphisms are finite composable sequences of cage-liftable transformations. **Its external context is assumed reaction inert** ([Sch26m, Thm. 7.14(2)]), and that is the one assumption this paper changes: the constraint functionals become functions of the medium as well as of the configuration.

Everything below follows from that change and from the definitions it forces.

What is not attempted is stated here rather than discovered at §6.3. The series goal is a conditional sufficiency theorem — that one cage carves the standard code in one medium and the mitochondrial code in another — and *this paper does not prove it*. It gives necessary conditions for such a cage (Prop. 6.16, Cor. 6.17) and a criterion that excludes a class of candidates (Prop. 4.21). No statement below asserts that any cage suffices; the existence claim is Target 10.1.

1.3 What is established

1. A step is cage-liftable exactly when its margin — the largest slack simultaneously available to all its hard constraints — is positive (Prop. 4.7); reachability of a target is therefore a maximum over path supports of a minimum over step margins (Def. 4.16). Because a path margin depends only on which steps occur, the theory carries no bound on path length (Sch. 4.17).
2. **A continuously varying medium carves discretely.** On a connected set missing the zero sets of the step margins the liftable set is constant, hence so is the reachable set (Lem. 5.2, Thm. 5.4); the discontinuities lie in the margin locus (Cor. 5.6); and within a chamber the persistence theorems of [Sch26m] hold uniformly rather than pointwise (Cor. 5.8). **This carries no hypothesis and is labelled [A].**

3. Part I's threshold hypothesis is *derived*. In a one-dimensional medium with comonotone margins, and given that discrimination between the two purine codons is a tight-cage phenomenon, each half acquires two thresholds and the resolution takes Part I's three values in Part I's order (Thm. 5.24).
4. **That derivation's first premise is false.** Tables 1 and 33 give incomparable rank vectors at AG-pur and UG-pur, so the published resolutions are not a chain (Thm. 5.28): either the medium has more than one dimension or its margins are not comonotone (Cor. 5.31). A single ordering survives on three of the eight varying purine halves and on no four, every maximal triple containing AU-pur (Prop. 5.29).
5. Determinism is not assumed but derived generically: selecting the widest-margin residue makes the carve single-valued off a set of codimension one (Cor. 6.11), and that set is where two carves balance.
6. **The record bounds the cell.** Under the hypothesis that one cage covers the twenty-seven tables, the fifteen distinct rank vectors it must realise force $\sum_{k \leq d} \binom{N}{k} \geq 15$: fourteen environed constraints in one dimension against five in two (Thm. 8.6, Cor. 8.9).
7. A reduced response in which all constraints loosen together orders the carves by one coordinate and is refuted (Thm. 8.17): either two cage coordinates respond independently, or one enters the constraints with both signs (Cor. 8.19).
8. The handedness of the carved residue is a function of the medium, constant on chambers of the oriented locus and exchanged across a wall (Thm. 7.5, Cor. 7.7).

1.4 What is not claimed

No axiom is introduced (Rem. 2.2) and no deferred target of any predecessor is discharged (Rem. 10.11). Four readings the construction invites are refused in Section 3 and are stated here because the body would otherwise be taken to support them.

The first concerns what the numbers rest on. The series claim is that one cage carves the standard code in one medium and the mitochondrial code in another. *Applied to that claim alone every bound in Section 8 is vacuous*: two environments and two codes force one environed constraint, which is none (Rem. 8.8). The bounds acquire content only under H_{one} , when a single cage is asked to cover the published record. **A reader who takes the two-code fit for the evidence has taken the cheap half.**

The second concerns sufficiency. *Neither* type-sufficiency nor residue-sufficiency is established. Definition 6.13 defines both, Proposition 6.14 separates them, and Proposition 6.16 and Corollary 6.17 give necessary conditions for the first; nothing

exhibits a cage meeting them. The distance from the first to the second is a further sixty-three witness pairs, two classes of which are open questions of the corpus rather than of this paper (Sch. 6.15).

The third concerns history. A cell that *could* carve both codes is not an account of what was carved, nor of why one code is found in nuclei and another in mitochondria. No statement of Sections 4 to 8 mentions an organism, a lineage or a time. This is a synthesis account, and the feedback circuit of [Sch26i, §9] is not carried forward.

The fourth concerns Part I. Its Theorem 7.6 is not an obstacle this formulation evades by being more general. If the cage depends on the codon only through quantities computable from its block, the margins factor and that theorem refutes the model: Part I supplies a *criterion* every cage model here must meet (Prop. 4.21).

1.5 Logical position

Every numbered theorem, proposition, corollary and lemma carries one of the four status labels of Definition 2.1, under the rule of Remark 2.3; definitions and scholia carry none, and a scholium enters no proof.

Two features of the record are stated here rather than in the appendix. **The paper's central positive result is the one that needs no hypothesis:** Theorem 5.4 is [A] and everything the register contains is spent elsewhere. And **the only [A] results that consult the genetic code are the two that refute something** — Theorem 5.28 and Proposition 5.29; every constructive use of the record is [D].

The defect ledger of Appendix B records thirty-four items across three passes, together with nine corrections to the drafting record. Four of the nine are defects in proofs and three of those were found by writing the proof out. That is the opposite failure mode from the one the preceding papers record, where a claim written in prose was refuted by computing it.

1.6 What the theory produces

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

A reaction cell has, for each rewrite step, a compact space of configurations and a finite family of hard constraints whose slacks depend on the medium. The step is available when some configuration satisfies all of them strictly; a path is available when all its steps are; a target is reachable when some path is. **Reachability is therefore a maximum of minima, and its sign changes only where a margin vanishes.** The walls so defined partition the medium into chambers, the carve is constant on each, and Part I's thresholds are the walls of that partition seen at one half-block.

1.7 Organization

Section 2 fixes conventions and the register. Section 3 states the traps, before the constructions they guard. Section 4 environs the cage and defines the reachability functional. Section 5 is the chamber theorem, the recovery of Part I's hypothesis, and the refutation of its first premise. Section 6 is selection and the two sufficiency statements. Section 7 is stereochemistry. Section 8 develops the surviving branch and derives the bound on the cell. Section 9 states what the response would have to be and is empirical throughout. Section 10 restates the non-implications and opens eight Targets. Appendix A tabulates and is generated; Appendix B is the concordance, the ledger and the verification record; Appendix C the literature.

2 Conventions and the Register

2.1 Logical status

Definition 2.1. Imported from [Sch26c, Defs. 1, 3, 5, 6] and used as in [Sch26m, Def. 2.1]: [A] axiomatic, or a finite enumeration or closed computation labelled as such; [D] derived realization theorem; [T] target; [E] empirical or documentary instantiation claim. An [E] claim is confined to a remark or scholium and enters no proof.

Remark 2.2 (No new axiom). [A] This paper introduces no axiom. Every structure is imported from [Sch26m], is definitional within $\{A1, \dots, A12\}$, or is a realization hypothesis registered below.

Remark 2.3 (The labelling convention). Every numbered theorem, proposition, corollary and lemma below carries one of the four labels; definitions and scholia carry none. The rule applied is: [A] where the statement follows from the definitions of Section 4 together with structural conditions on the objects — finiteness, compactness, affineness, general position — or from enumeration over [NCBI24]; [D] where a hypothesis of Section 2.3 about the chemistry or about the relation of the theory to the published record enters, or where a theorem of a predecessor is instantiated.

Two consequences are worth stating here rather than leaving to be noticed. **Theorem 5.4, the central positive result of the paper, is [A]:** it uses no hypothesis registered anywhere. And **Theorem 5.28 and Proposition 5.29 are the only [A] results that consult the genetic code;** they are also the only two that refute a hypothesis rather than establish a construction.

Remark 2.4 (Scholia). Motivation, comparison with the predecessors and chemical reading are confined to scholia. **A scholium enters no proof**, and the formal content of the paper is unchanged if every scholium is deleted. Where a scholium would otherwise carry an argument, that argument is stated as a proposition instead; Proposition 4.21 was so promoted.

2.2 What is imported

Object	Source
typed molecular graphs; atom maps; rewrite rules	[Sch26m, §4]
well-formed chemical paths	[Sch26m, Def. 4.21]
local configuration spaces; constraint functionals	[Sch26m, §5]
positive-margin convention	[Sch26m, Def. 7.13]
perturbative and neighbourhood persistence	[Sch26m, Thms. 7.14]
oriented attack cones; stereochemical selection	[Sch26m, §5.16, Prop. 7.14]
the canonical witness morphism	[Sch26m, Thm. 9.12]
the word space $W = \Sigma^3$	[Sch26k, Def. 2.4]
the constant poly-A tether, H_{teth}	[Sch26k, Hyp. 2.14]
seeding and propagation, H_{seed}	[Sch26h, Hyp. 2.10]
half-blocks and the three resolutions	[Sch26i, Defs. 4.2, 4.3]
the insufficiency of block data	[Sch26i, Thm. 7.6]
the two codes as three differing halves	[Sch26i, Thm. 5.7]
the translation tables	[NCBI24]

2.3 The register

Two hypotheses are chemical and are stated here. The remainder are mathematical, are stated where they are first used, and are tabulated below so that the list can be checked against the completed text.

Hypothesis 2.5 (H_{resp}). There is a continuous *response map* ρ from the environment space to the local cage coordinates of [Sch26m, §5], through which every constraint functional depends on the environment: $g_{\sigma,c}(x, \theta) = \hat{g}_{\sigma,c}(x, \rho(\theta))$.

Hypothesis 2.6 (H_{cod}). The stacked codon contributes to the cage geometry, so that the configuration spaces and constraint functionals of Definition 4.2 depend on $w \in W$; the third base is the dominant contribution, which is the encasement clause of [Sch26h, Rem. 6.8] read geometrically.

Hypothesis	Stated at	Role
H_{resp}	2.5	the chemistry; undischarged
H_{cod}	2.6	the chemistry; undischarged
H_{aff}	5.10	affine margins; needed only for counting
H_{sel}	6.1	widest-margin selection
H_{gen}	6.8	general position of the cage data
H_{det}	5.17	determinism; <i>retired</i> at Cor. 6.11
H_{relax}	5.20	one dimension, comonotone; <i>refuted</i> at Thm. 5.28
$H_{\text{sep}}, H_{\text{sep}}^{\xi}$	5.21, 8.16	discrimination is a tight-cage phenomenon
H_{χ}	7.2	oriented cage exclusion
H_{one}	8.7	one cage covers the record

Remark 2.7 (Which are load-bearing). The standing finiteness convention of Definition 4.9 underlies every result and is not a hypothesis about the chemistry. H_{aff} carries the counting results of Theorem 5.12 and Theorem 8.6 and nothing else; the chamber theorem is independent of it. H_{one} carries the whole quantitative content of §8, and Remark 8.8 records that without it the series claim constrains the cell not at all. H_{resp} and H_{cod} carry no theorem: they say what the mathematics is about and are the object of the Targets.

2.4 Declaration: the external context is not inert

Remark 2.8. [Sch26m] assumes the external context of a reaction reaction-inert ([Sch26m, Thm. 7.14(2)]) and proves persistence of a cage-constrained path under small perturbation of that context. **This paper inverts the assumption.** The constraint functionals are functions of the environment, the perturbation is the subject rather than the error term, and the persistence results of [Sch26m] are recovered here as statements valid on a chamber (Corollary 5.8). No result of [Sch26m] is contradicted. Its results are recovered at a fixed environment; its perturbation theorems concern a *realization family* $\Lambda \rightarrow \Lambda'$, which this paper holds fixed, so the two perturbations are independent and neither subsumes the other.

2.5 Declaration: where the standard code is used

Remark 2.9. [Sch26i, Rem. 2.15] declares that Part I uses the standard genetic code constructively. The declaration is owed again and its scope is narrower here.

Sections 4.1–4.5, 5.1–5.4 and 7 use no translation table. They are statements about environed cages, chambers and oriented margins, and would stand if no genetic code existed.

Sections 4.6, 5.5, 6.3 and 8.2 depend on [NCBI24]: Proposition 4.21, Theorem 5.28, Proposition 5.29, Scholium 6.15 and Corollary 8.9 read published tables and have no content without them.

The record enters the formal development at exactly one place before Section 5, namely Proposition 4.21, whose proof invokes [Sch26i, Thm. 7.6] — an enumeration over the fifteen purine halves at two compartment settings. That proposition is the one carrying Part I's theorem into Part II, and the declaration is made precise here so that its dependence is not mistaken for a general one.

A reader who wishes the mathematics without the biology may stop at Corollary 5.31 and take §7 on its own; a reader who wishes the bound on the cell must accept H_{one} and the record with it.

2.6 Notation

Symbol	Meaning
Θ, θ	environment space and environment (Definition 4.1)
$X_\sigma, C_\sigma, g_{\sigma,c}$	configuration space, constraints, functionals
μ_σ	step margin (Definition 4.4)
Ξ	the step set (Definition 4.10)
$\mathcal{A}(S, T)$	path supports (Definition 4.14)
Φ_T, Ψ_r	reachability functional; best functional at r
$\Sigma(w), \mathcal{T}(w), \Sigma^\circ(w)$	margin, tie and oriented loci
$\mathcal{R}, K, K^*$	reachable set, carve, selected carve
$\mathcal{R}^b$	resolution of a half (Definition 5.15)
v_H	rank vector (Definition 5.26)
ρ, ξ	response map; a reduced response coordinate

Remark 2.10 (Two collisions, recorded). *Margin* is used throughout in the sense of Definition 4.4, a slack in a hard geometric constraint, and never in the sense of a marginal distribution. *Chamber* is the connected component of Definition 5.1 and is not the reaction chamber of the chemical literature; the physical object is the chrysene-adenosine complex and is never called a chamber 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 8 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 may be checked against the completed text.

Proposition 3.1 (Ten refusals). *[D] None of the following holds.*

- (i) A chamber decomposition $\not\Rightarrow$ a threshold in any one environmental variable. Thresholds require an ordering the chambers need not possess.
- (ii) Reachability of a target $\not\Rightarrow$ its kinetic accessibility. The four levels of [Sch26m] — connectivity, chemical admissibility, geometric accessibility, kinetics — remain distinct, and this paper works at the third.
- (iii) A carve that is locally constant in the environment $\not\Rightarrow$ an environment that is discrete. The input is continuous and the output is not.
- (iv) Type-sufficiency $\not\Rightarrow$ residue-sufficiency — and neither is proved here. The theory says which target is reachable and not which residue that target is.
- (v) A cage fitting the two codes $\not\Rightarrow$ any constraint on the cage. Two environments bound nothing.
- (vi) A cell that could carve both codes $\not\Rightarrow$ an account of what was carved, of why one code is found in nuclei and another in mitochondria, or of how either came to be used. This is a synthesis account and not a history.
- (vii) A generically single-valued carve $\not\Rightarrow$ mechanistic uniqueness. The exceptional locus is where two carves balance, and a cell held there produces a mixture.
- (viii) A margin depending on the environment $\not\Rightarrow$ that any named intensive quantity is the agent. Several co-vary between the two compartments.
- (ix) Recovery of $H_{\text{eng-type}}$ of Part I $\not\Rightarrow$ confirmation of Part I. The same claim derived from a lower level leaves that paper's score untouched.
- (x) The margins not being required to factor through block data $\not\Rightarrow$ escape from [Sch26i, Thm. 7.6]. That theorem is a condition every admissible cage model must satisfy.

Proof. (i) By witness. Under H_{one} a cage realising the published resolutions has chambers, by Theorem 5.4; but by Theorem 5.28 those resolutions are not a chain, so no ordering of the chambers by a single coordinate with monotone margins realises them, and the construction of thresholds at Theorem 5.24 is unavailable. Proposition 5.29 sharpens the witness: such an ordering exists on three of the eight varying purine halves and on no four.

(ii) By the scope of Definition 4.6, which is a condition on configurations and not on activation barriers; and by [Sch26m, Rem. 7.15], which declines equality of activation barriers under exactly the persistence hypothesis used at Corollary 5.8.

(iii) By Theorem 5.4 together with Proposition 4.5: the margins are continuous functions on Θ , and the discontinuity of $\mathcal{R}$

arises from the sign condition of Proposition 4.7 and not from any discreteness of the environment.

(iv) Proposition 6.14 and Scholium 6.15: the residue obligation is a set of sixty-three witness pairs, of which two classes are supplied nowhere in the corpus — $H_{\text{split-chem}}$ of [Sch26h, Hyp. 2.12], undischarged there as its Target 9.1, and the carve at AG-pur when it engages.

(v) Remark 8.8: with $m = 2$, Theorem 8.6 yields $N \geq 1$.

(vi) By witness: no statement of Sections 4 to 8 mentions an organism, a lineage or a time, and Corollary 8.9 counts configurations a cage must be *able* to reach, not configurations any cage did reach. No hypothesis of Section 2 concerns descent or selection among organisms. The contrast with [Sch26i, §9] is deliberate and is recorded at Part I, §1.7.

(vii) Scholium 6.12, with [Sch26m, Thms. 10.7, 10.20]: the single-valuedness of Corollary 6.11 holds off $\Sigma(w) \cup \mathcal{T}(w)$ and not on it.

(viii) By witness: redox potential, divalent-metal availability and effective dielectric all co-vary with proton activity between the two compartments, and no measurement in this paper distinguishes them. Under H_{resp} the response map is a function of the environment and the identity of its arguments is not fixed by any result below.

(ix) Theorem 5.24 derives what [Sch26i, Hyp. 2.7] posits; it does not alter the score of [Sch26i, Rem. 8.13], which counts published tables against a range and is a statement about that paper's construction.

(x) Proposition 4.21. $\square$

Remark 3.2 (Status of the clauses). Against the labels applied in Sections 4 to 8, the witnesses of clauses (i), (ii), (iii), (v), (vi) and (ix) are all [A] — in particular Theorems 5.4 and 5.28 and Corollary 6.17 — so those clauses could carry [A] separately. The proposition is labelled [D] because the witness of clause (iv) is Proposition 6.14 read together with the sufficiency register, that of clause (vii) is Corollary 6.11, which rests on H_{aff} , H_{gen} and H_{sel} , that of clause (viii) is H_{resp} , and that of clause (x) is Proposition 4.21; the last three are themselves [D].

Remark 3.3 (The three that matter most). Clauses (v), (iv) and (x), and each is answered in the section that raises it.

Clause (v) states what this paper's numbers rest on. The series claim is that one cage carves the standard code in one medium and the mitochondrial code in another. Applied to that claim alone, every bound in Section 8 is vacuous: two environments and two codes force one environed constraint, which is no constraint at all. The bounds acquire content only under H_{one} , when a single cage is asked to cover the twenty-seven published tables. **A reader who takes the two-code fit for the evidence has taken the cheap half.**

Clause (iv) states what the paper does not deliver.

Type-sufficiency is a statement about resolutions; residue-sufficiency names the amino acid. The gap between them is finite and enumerated at Scholium 6.15, and two of its classes are open questions of the corpus rather than of this paper. The distinction is preserved in Definition 6.13 and a reader who reads past its second clause will overstate the result.

Clause (x) states the relation to Part I. Its Theorem 7.6 is not an obstacle this formulation evades by being more general. If the cage depends on the codon only through quantities computable from its block, the margins factor and that theorem refutes the model. Part I therefore supplies a *criterion* which every cage model of Part II must meet, and Proposition 4.21 is where it is applied.

Remark 3.4 (Trap: the cage is not measured). [A] Nothing in this paper measures a constraint functional, a response map or an environment. The objects of Section 4 are posited with the properties Section 4 states — compactness, continuity, and under H_{aff} affineness — and every theorem is a consequence of those properties. H_{resp} and H_{cod} are undischarged and are the subject of the Targets of Section 10. **Conversely, no agreement reported in Section 8 is evidence for the chemistry:** the bounds there constrain any theory of the stated shape and do not select among them.

Remark 3.5 (Why the section is placed here). A reader who reaches Theorem 5.24 holding the phrase *the thresholds are derived* will read it as a vindication of Part I, and a reader who reaches Corollary 8.9 holding the phrase *a lower bound on the cell* will read it as a measurement. Both readings are invited by the results and neither is claimed. The refusals are therefore placed before the constructions, as [Sch26h, §3] places its ten and [Sch26i, §3] its ten, and the list is restated at Section 10.

4 Environed Cages

Throughout, Λ_0 is a fixed molecular realization in the sense of [Sch26m, §2]; chemical states, rewrite rules, atom maps and well-formed paths are those of [Sch26m, §4]. Nothing in §4 uses [Sch26h] or Part I except Proposition 4.21.

4.1 The environment

Definition 4.1. An *environment space* is a topological space Θ ; its points are *environments*. Θ is *Euclidean of dimension* d when it is a nonempty convex open subset of $\mathbf{R}^d$.

Definition 4.2. Let σ be a chemically admissible rewrite step. An *enviored cage datum* for σ over Θ consists of

- (a) a nonempty compact space X_σ , the *local configuration space* of σ ([Sch26m, §5.1]);
- (b) a finite set C_σ , the *hard constraint family*;
- (c) a continuous map $g_\sigma : X_\sigma \times \Theta \rightarrow \mathbf{R}^{C_\sigma}$ with components $g_{\sigma,c}$, the *constraint functionals*.

An *enviored cage* over Θ is such a datum for every chemically admissible step.

Scholium 4.3. Definition 4.2 differs from [Sch26m, §5] in one respect: the constraint functionals are defined on $X_\sigma \times \Theta$ and not on X_σ . [Sch26m] assumes the external context reaction inert ([Sch26m, Thm. 7.14(2)]); the present paper does not, and that single change is the whole of the difference between the two theories.

4.2 Margins

Definition 4.4. The *step margin* of σ is $\mu_\sigma : \Theta \rightarrow \mathbf{R}$,

$$\mu_\sigma(\theta) = \max_{x \in X_\sigma} \min_{c \in C_\sigma} g_{\sigma,c}(x, \theta).$$

Proposition 4.5. [A] The maximum is attained and μ_σ is continuous.

Proof. Put $h = \min_{c \in C_\sigma} g_{\sigma,c}$, continuous on $X_\sigma \times \Theta$ as a minimum of finitely many continuous functions. X_σ being nonempty and compact, $h(\cdot, \theta)$ attains its maximum; this is the first assertion.

Fix θ_0 and $\epsilon > 0$. For each $x \in X_\sigma$ continuity of h at (x, θ_0) gives open $U_x \ni x$ and $W_x \ni \theta_0$ with

$$|h(y, \theta) - h(x, \theta_0)| < \epsilon/2 \quad \text{for } (y, \theta) \in U_x \times W_x. \quad (*)$$

Compactness gives $x_1, \dots, x_n$ with $X_\sigma = \bigcup_i U_{x_i}$; put $W = \bigcap_i W_{x_i}$, open and containing θ_0 . Let $\theta \in W$.

Choose y with $h(y, \theta) = \mu_\sigma(\theta)$ and i with $y \in U_{x_i}$. By (*), $\mu_\sigma(\theta) < h(x_i, \theta_0) + \epsilon/2 \leq \mu_\sigma(\theta_0) + \epsilon/2$.

Choose z with $h(z, \theta_0) = \mu_\sigma(\theta_0)$ and j with $z \in U_{x_j}$. By (*) applied at (z, θ_0) and at (x_j, θ) ,

$$\mu_\sigma(\theta_0) = h(z, \theta_0) < h(x_j, \theta_0) + \epsilon/2 < h(x_j, \theta) + \epsilon \leq \mu_\sigma(\theta) + \epsilon.$$

Hence $|\mu_\sigma(\theta) - \mu_\sigma(\theta_0)| < \epsilon$ on W . $\square$

Definition 4.6. σ is *cage-liftable* at θ when $g_{\sigma,c}(x, \theta) > 0$ for some $x \in X_\sigma$ and every $c \in C_\sigma$.

Proposition 4.7. [A] σ is cage-liftable at θ if and only if $\mu_\sigma(\theta) > 0$.

Proof. If such an x exists, $\min_c g_{\sigma,c}(x, \theta) > 0$ and so $\mu_\sigma(\theta) > 0$. Conversely the maximum is attained at some x by Proposition 4.5, and there $\min_c g_{\sigma,c}(x, \theta) = \mu_\sigma(\theta) > 0$. $\square$

Scholium 4.8. The strict inequality is the positive-margin convention of [Sch26m, Def. 7.13]. With $\geq$ in place of $>$, Proposition 4.7 fails in one direction and Lemma 5.2 is unavailable.

4.3 Finiteness and reachability

Definition 4.9 (Standing finiteness convention). H_{fin} denotes the condition that for the initial state S the set $\mathcal{S}(S)$ of chemical states occurring in some well-formed chemical path issuing from S is finite. It is assumed throughout and is a condition on the mathematical object, of the same kind as the compactness required at Definition 4.2; it is not a hypothesis about the chemistry, and statements using it alone carry [A].

Definition 4.10. Ξ denotes the set of rewrite steps between states of $\mathcal{S}(S)$.

Proposition 4.11. [A] Under H_{fin} , Ξ is finite.

Proof. A step is determined by its source, its target and the rule applied; there are finitely many of each, the rule set P being finite ([Sch26m, §4]). $\square$

Definition 4.12. T is *reachable* from S at θ when some well-formed chemical path from S to T has every step cage-liftable at θ . Such a path is called *admissible* at θ .

Remark 4.13 (Loop excision). [A] If T is reachable from S at θ then some admissible path from S to T has pairwise distinct states. Indeed, if p meets a state twice, deleting the steps between the two occurrences leaves a concatenation of arrows of p , hence a well-formed path, all of whose steps remain cage-liftable; the length decreases strictly and the process terminates. The remark is recorded because it bounds the length of a witness, and is used nowhere below:

the definitions of this subsection are insensitive to path length.

4.4 The reachability functional

Definition 4.14. The *support* of a well-formed chemical path $p = (\sigma_1, \dots, \sigma_n)$ is the set $\text{supp}(p) = \{\sigma_1, \dots, \sigma_n\} \subseteq \Xi$. For $S \neq T$ put

$$\mathcal{A}(S, T) = \{\text{supp}(p) : p \text{ a well-formed path from } S \text{ to } T\}.$$

Proposition 4.15. [A] Under H_{fin} the family $\mathcal{A}(S, T)$ is finite.

Proof. It is a set of subsets of Ξ , which is finite by Proposition 4.11. $\square$

Definition 4.16. The *reachability functional* of T is

$$\Phi_T(\theta) = \max_{A \in \mathcal{A}(S, T)} \min_{\sigma \in A} \mu_\sigma(\theta), \quad \max \emptyset = -\infty.$$

Scholium 4.17. A path margin $\min_{\sigma \in p} \mu_\sigma$ depends only on the set of steps occurring in p , not on their order or multiplicity. Definition 4.16 records that observation, and with it the theory carries no bound on path length and no parameter of range. An earlier formulation maximised over paths of length at most N ; the maximum then depends on N , and the selection of §6 is ill-defined until N is fixed. No such parameter occurs here.

Proposition 4.18. [A] Assume H_{fin} and $\mathcal{A}(S, T) \neq \emptyset$. Then Φ_T is real-valued and continuous, and

$$T \text{ is reachable from } S \text{ at } \theta \iff \Phi_T(\theta) > 0.$$

Proof. Continuity: each μ_σ is continuous by Proposition 4.5; $\min_{\sigma \in A} \mu_\sigma$ is a minimum of finitely many such; Φ_T a maximum of finitely many of those, by Proposition 4.15. Equivalence: if $\Phi_T(\theta) > 0$, choose A attaining the maximum and a path p with $\text{supp}(p) = A$; every step of p has $\mu_\sigma(\theta) > 0$, hence is cage-liftable by Proposition 4.7, so p is admissible. Conversely an admissible path p has $\mu_\sigma(\theta) > 0$ for every $\sigma \in \text{supp}(p)$, so $\Phi_T(\theta) \geq \min_{\sigma \in \text{supp}(p)} \mu_\sigma(\theta) > 0$. $\square$

Scholium 4.19. Φ_T is a maximum of minima of step margins: a path is no more admissible than its tightest step, and a target no less reachable than its best path. Both extrema

are forced by Definitions 4.6 and 4.12 and neither is a modelling choice. Every nonlinearity established in §5 is that of $\max \circ \min$; none of it requires a constraint functional to be nonlinear.

4.5 Codon-indexed cages

Definition 4.20. Let $W = \Sigma^3$ be the word space of [Sch26k, Def. 2.4]. A *codon-indexed envired cage* is a family of envired cages over Θ indexed by W , written $g_{\sigma, c}(x; w, \theta)$. Margins and reachability functionals are written $\mu_\sigma(w, \cdot)$ and $\Phi_T(w, \cdot)$.

Proposition 4.21 (Admissibility constraint on cage models). [D] Let β assign to a codon the triple consisting of the volume of its block's product, the association measure at its second base, and the strength of its first base. Suppose the margins factor through β , that is

$$\mu_\sigma(w, \theta) = F_\sigma(\beta(w), \theta) \quad \text{for all } \sigma, w, \theta.$$

Then the resolutions of Definition 5.15 are inconsistent with the purine column of [NCBI24].

Proof. Under the stated factorization the thresholds constructed at Theorem 5.24 are functions of $\beta(w)$ alone, hence a block-feature threshold in the sense of [Sch26i, Def. 7.5]. By [Sch26i, Thm. 7.6] no such threshold is consistent with the resolutions of the fifteen purine halves at the two compartment settings. $\square$

Scholium 4.22. Proposition 4.21 is the exact sense in which Part I's principal theorem bears on this one. It is not an obstacle the present formulation escapes by being more general: **it is a condition every admissible cage model must satisfy**. A model in which the codon enters the cage only through quantities computable from its block is refuted before it is tested, and §6 applies the criterion to the reference realization of [Sch26m] before anything else is asked of it.

5 Chambers and the Carve

H_{fin} is in force throughout.

5.1 The margin locus

Definition 5.1. The *margin locus* at $w \in W$ is $\Sigma(w) = \bigcup_{\sigma \in \Xi} \mu_\sigma(w, \cdot)^{-1}(0)$, a closed subset of Θ . A *chamber* at w is a connected component of $\Theta \setminus \Sigma(w)$.

Lemma 5.2 (Constancy of the liftable set). [A] Let D be a chamber at w . Then the set

$$L(w, \theta) = \{\sigma \in \Xi : \sigma \text{ is cage-liftable at } \theta\}$$

is the same for every $\theta \in D$.

Proof. Fix $\sigma \in \Xi$. By Proposition 4.5 the sets $\{\mu_\sigma(w, \cdot) > 0\}$ and $\{\mu_\sigma(w, \cdot) < 0\}$ are open, and they cover $\Theta \setminus \Sigma(w) \supseteq D$. As D is connected it meets exactly one of them. By Proposition 4.7 membership of σ in $L(w, \theta)$ is therefore independent of $\theta \in D$, and Ξ is finite. $\square$

Definition 5.3. $\mathcal{R}(w, \theta) = \{T : T \text{ is reachable from } S \text{ at } \theta\}.$

Theorem 5.4 (Chamber theorem). [A] $\mathcal{R}(w, \cdot)$ is constant on each chamber at w .

Proof. Let D be a chamber and $\theta, \theta' \in D$. A well-formed path is admissible at θ precisely when all of its steps lie in $L(w, \theta)$, which by Lemma 5.2 equals $L(w, \theta')$. Hence the admissible paths at θ and at θ' are the same, and by Definition 4.12 so are the reachable targets. $\square$

Scholium 5.5. The proof uses neither the reachability functional nor any finiteness of the set of paths: only that Ξ is finite, that margins are continuous, and that a chamber is connected. In particular Theorem 5.4 is independent of Remark 4.13 and of any bound on path length.

It is also elementary, and the paper gains nothing by concealing it. The argument is that a minimum of functions of constant sign has constant sign, applied twice. The interest of Theorem 5.4 is not in the difficulty of proving it but in its being the load-bearing fact of the theory: it is what makes the carve piecewise constant, it carries no hypothesis, and every later result either restricts it or costs it.

Corollary 5.6 (Localisation of the discontinuities). [A] The set of points at which $\mathcal{R}(w, \cdot)$ fails to be locally constant is contained in $\Sigma(w)$.

Proof. $\Theta \setminus \Sigma(w)$ is open, and by Theorem 5.4 $\mathcal{R}(w, \cdot)$ is constant on each of its components. $\square$

Corollary 5.7. [A] For each T with $\mathcal{A}(S, T) \neq \emptyset$, the function $\Phi_T(w, \cdot)$ has constant strict sign on each chamber at w .

Proof. By Proposition 4.18 its sign at θ records whether $T \in \mathcal{R}(w, \theta)$, together with the fact that $\Phi_T(w, \theta) = 0$ would require some admissible path margin to vanish, impossible on $\Theta \setminus \Sigma(w)$ by Lemma 5.2. Apply Theorem 5.4. $\square$

Corollary 5.8 (Uniform persistence on a chamber). [A] Let D be a chamber, $K \subseteq D$ compact and $T \in \mathcal{R}(w, \theta_0)$ for some $\theta_0 \in D$. Then $\inf_K \Phi_T(w, \cdot) > 0$, and the hypotheses of [Sch26m, Thm. 7.14] and [Sch26m, Thm. 9.16] hold uniformly on K : one ordered rewrite word serves every environment of K with the same principal target restriction.

Proof. By Corollary 5.7 the function is strictly positive on D , and by Proposition 4.18 continuous; a continuous strictly positive function on a compact set has positive infimum. $\square$

Scholium 5.9. Corollary 5.6 is the precise form of the assertion that a continuously varying environment produces a discontinuously varying product, and Corollary 5.8 is its chemical consequence: within a chamber, environmental variation is invisible in the product; at a chamber wall it is total. The discontinuity locus is contained in the union of the zero sets of the *individual step margins*, which is in general properly smaller than the locus where the reachability functionals vanish.

5.2 The affine case

Hypothesis 5.10 (H_{aff}). Θ is Euclidean of dimension d , hence convex and open, and for each w every $\mu_\sigma(w, \cdot)$ is the restriction of a nonzero affine function on $\mathbf{R}^d$.

Proposition 5.11. [A] Under H_{aff} , every $\Phi_T(w, \cdot)$ is continuous and piecewise affine, and $\Sigma(w)$ is the intersection with Θ of a union of $n \leq |\Xi|$ affine hyperplanes.

Proof. Minima and maxima of finitely many affine functions are piecewise affine and continuous. Each $\mu_\sigma(w, \cdot)^{-1}(0)$ is the zero set of a nonzero affine function, an affine hyperplane. $\square$

Theorem 5.12 (Bound on the number of carves). [A] Under H_{aff} the number of chambers at w is at most

$$\sum_{k=0}^d \binom{n}{k},$$

and by Theorem 5.4 so is the number of distinct reachable sets a single codon-indexed environed cell realises as θ ranges over Θ . The bound is attained when $\Theta = \mathbf{R}^d$ and the n hyperplanes are in general position.

Proof. Θ is convex, so for each region R of the arrangement the set $R \cap \Theta$ is convex, hence connected or empty. The chambers are therefore exactly the nonempty sets $R \cap \Theta$, and their number is at most the number of regions of an arrangement of n hyperplanes in $\mathbf{R}^d$, which is $\sum_{k=0}^d \binom{n}{k}$, with equality in general position. $\square$

Scholium 5.13. Theorem 5.12 is the first finiteness statement of the series that does not consult a translation table. It bounds what one reaction cell can do in terms of two integers: the number of hard constraints whose margins depend on the environment, and the dimension of the medium. Convexity of Θ is not decorative: for non-convex Θ a region may meet Θ in several components and the bound fails.

5.3 Resolutions

Definition 5.14. Let π assign to a target its residue where defined. The *carve* at (w, θ) is $K(w, \theta) = \pi(\mathcal{R}(w, \theta))$.

Definition 5.15. For the purine half $h = \{w_A, w_G\}$ of a block ([Sch26i, Def. 4.2]),

$$\mathcal{R}^b(h, \theta) = \begin{cases} \emptyset & K(w_A, \theta) = K(w_G, \theta) = \emptyset, \\ \text{unif}(r) & K(w_A, \theta) = K(w_G, \theta) = \{r\}, \\ \text{disc} & \text{otherwise.} \end{cases}$$

Theorem 5.16 (The three values). *[A] $\mathcal{R}^b$ is well defined with values in the three-element set of [Sch26i, Def. 4.3], and is constant on each connected component of $\Theta \setminus (\Sigma(w_A) \cup \Sigma(w_G))$.*

Proof. The three cases are mutually exclusive and exhaustive. Let E be such a component. E is connected and disjoint from $\Sigma(w_A)$, hence contained in a chamber at w_A ; likewise for w_G . By Theorem 5.4 both carves are constant on E . $\square$

Hypothesis 5.17 (H_{det}). $|K(w, \theta)| \leq 1$ for all w, θ .

Proposition 5.18. *[D] Under H_{det} the value disc obtains exactly when w_A and w_G carve differently, which is its sense in [Sch26i, Def. 4.3].*

Proof. Each carve is then empty or a singleton, so the third case of Definition 5.15 obtains precisely when $K(w_A, \theta) \neq K(w_G, \theta)$. $\square$

Scholium 5.19. H_{det} does not follow from the foregoing and is not innocuous: [Sch26m, Thm. 10.7] and [Sch26m, Thm. 10.20] exhibit alternative reaction factorizations and nonunique-solution reachability, and that paper declines mechanistic uniqueness throughout. Without H_{det} , Theorem 5.16 stands but disc conflates a half whose two codons carve different residues with a codon whose carve is not a singleton. §6 replaces H_{det} by a selection rule whose exceptional set has empty interior, and retires it.

5.4 Recovery of the threshold hypothesis of Part I

Hypothesis 5.20 (H_{relax}). Θ is an interval of $\mathbf{R}$ and every $\mu_\sigma(w, \cdot)$ is strictly decreasing.

Hypothesis 5.21 (H_{sep}). For every purine half h the set $B(h) = \{\theta : K(w_A, \theta) \neq K(w_G, \theta)\}$ is a down-set.

Scholium 5.22. H_{sep} asserts that discrimination between the two purine codons is a tight-cage phenomenon: if the half distinguishes them at some setting, it distinguishes them at every tighter one. **It is independent of H_{relax} :** by Lemma 5.23 the two carves are individually nonincreasing, but the set on which two nonincreasing set-valued maps differ need not be monotone, so nesting does not imply it. It is the premise that orders disc before unif, and without it Theorem 5.24 yields the upper threshold only.

Lemma 5.23. *[D] Under H_{relax} , $\theta \leq \theta'$ implies $\mathcal{R}(w, \theta') \subseteq \mathcal{R}(w, \theta)$.*

Proof. If p is admissible at θ' then for $\sigma \in p$, $\mu_\sigma(w, \theta) \geq \mu_\sigma(w, \theta') > 0$, so p is admissible at θ . $\square$

Theorem 5.24 (Recovery). *[D] Assume H_{relax} , H_{sep} and H_{det} . For every purine half h there are $t_1(h) \leq t_2(h)$ in $[-\infty, +\infty]$ with*

$$\mathcal{R}^b(h, \theta) = \begin{cases} \text{disc} & \theta < t_1(h), \\ \text{unif} & t_1(h) < \theta < t_2(h), \\ \emptyset & t_2(h) < \theta, \end{cases}$$

the two endpoints being unconstrained. Hence $H_{\text{eng-type}}$ of [Sch26i, Hyp. 2.7] is a theorem of the present theory.

Proof. Put $A(h) = \{\theta : K(w_A, \theta) = K(w_G, \theta) = \emptyset\}$. By Lemma 5.23 the carves are nonincreasing, so $A(h)$ is an up-

set; $B(h)$ is a down-set by H_{sep} . The two are disjoint, a point of $A(h)$ having equal carves. If $a \in A(h)$, $b \in B(h)$ and $a \leq b$ then $a \in B(h)$ since $B(h)$ is a down-set, a contradiction; hence $a > b$ for all such a, b , and $t_1(h) := \sup B(h) \leq \inf A(h) =: t_2(h)$.

For $\theta < t_1(h)$ we have $\theta \in B(h)$, so by Proposition 5.18 the value is *disc*; for $\theta > t_2(h)$ we have $\theta \in A(h)$ and the value is $\emptyset$. For $t_1(h) < \theta < t_2(h)$ the point lies in neither set, so the carves are equal and not both empty, hence a common singleton by H_{det} , and the value is *unif*. $\square$

Scholium 5.25. In Part I the two thresholds are posited; here they are constructed, as the supremum of a down-set and the infimum of an up-set determined by margins of a reaction cell. What the recovery costs is its hypothesis list: H_{relax} fixes the dimension at one and makes every margin comonotone, H_{sep} is examined at Scholium 5.22, and H_{det} is refused by [Sch26m]. §5.5 shows that the first fails.

5.5 What the record refuses

Definition 5.26. Put $\text{rk}(\text{disc}) = 0$, $\text{rk}(\text{unif}) = 1$, $\text{rk}(\emptyset) = 2$. For a finite set H of purine halves the *rank vector* is $v_H(\theta) = (\text{rk } \mathcal{R}^b(h, \theta))_{h \in H}$, ordered componentwise.

Proposition 5.27. [D] Under the hypotheses of Theorem 5.24, v_H is nondecreasing in θ ; hence $v_H(\Theta)$ is a chain.

Proof. Each component is a nondecreasing step function by Theorem 5.24; so $\theta \leq \theta'$ gives $v_H(\theta) \leq v_H(\theta')$ componentwise. $\square$

Theorem 5.28 (The record is not a chain). [A] Let $H = \{\text{AG-pur}, \text{UG-pur}\}$ and let θ range over environments realising the tables of [NCBI24]. Then v_H is not a chain. Consequently H_{relax} , H_{sep} and H_{det} do not all hold.

Proof. Table 1 reads (R, R) at AG-pur and $(*, W)$ at UG-pur, giving $v_H = (1, 0)$. Table 33 reads (S, K) and (W, W) , giving $v_H = (0, 1)$. Neither dominates the other. Apply Proposition 5.27. Check W3. $\square$

Proposition 5.29 (Where the one-dimensional reading survives). [A] Of the eight purine halves whose resolution is not constant across [NCBI24] — UU, UC, UA, UG, CU, AU, AA, AG — the rank vectors of the twenty-seven tables form a chain on three and on no four. There are exactly four such triples, namely $\{\text{UU}, \text{UG}, \text{AU}\}$, $\{\text{UC}, \text{UA}, \text{AU}\}$, $\{\text{UC}, \text{UG}, \text{AU}\}$ and $\{\text{UG}, \text{CU}, \text{AU}\}$, and every one of them contains AU-pur.

Checks W5, W5b.

Remark 5.30 (Why the count is taken over the varying halves). [A] The restriction is not a convenience. A purine half whose resolution is constant across the record contributes a constant coordinate to every rank vector and therefore cannot break a chain, so any chain-forming set may be adjoined with all eight constant halves. A maximum taken over all sixteen purine halves reaches eleven and measures nothing; check W5b. The quantity with content is the maximum over the halves that vary, and it is three.

Corollary 5.31 (The dichotomy). [D] Assume H_{aff} , H_{sep} and H_{det} . Then either $d \geq 2$, or $d = 1$ and the step margins are not comonotone: some $\mu_\sigma(w, \cdot)$ is increasing where another is decreasing.

Proof. Suppose $d = 1$ and the margins comonotone. Each is affine and nonzero, hence strictly monotone, and all in the same sense; replacing θ by $-\theta$ if necessary makes them all strictly decreasing, which is H_{relax} . Theorem 5.28 then gives a contradiction. $\square$

Scholium 5.32. Corollary 5.31 is a statement about the reaction cell obtained from published translation tables. Both branches are informative and the second is the more specific: margins that are not comonotone in a single environmental coordinate say that relaxation enables some steps while disabling others, which is what a displacement of the nascent aromatic rings would do, opening one approach while closing another. Part I, Theorem 8.9, reports the same arithmetic as the failure of a single ordering parameter; here it bounds a parameter of the cell. Proposition 5.29 localises the failure: the one-dimensional reading is exact on three of the eight varying purine halves and on no four, and every maximal triple contains AU-pur — one of the three halves at which the two codes differ. Check W4 records the full count of one hundred and thirty inconsistent pairs.

6 Selection and Sufficiency

H_{fin} is in force.

6.1 The selected carve

Hypothesis 6.1 (H_{sel}). Among the targets reachable at (w, θ) , those realised are the ones of greatest reachability functional.

Scholium 6.2. H_{sel} replaces the determinism assumed at [Sch26i] and at Hypothesis 5.17. It is weaker in kind: it does not assert that one target is reachable, only that the widest-margin reachable target is the one taken. [Sch26m] declines mechanistic uniqueness ([Sch26m, Thms. 10.7, 10.20]), and H_{sel} is compatible with that refusal, selection being imposed on the outcome and not on the mechanism. It is empirical and enters no proof except where displayed.

Definition 6.3. For a residue r put $\Psi_r(w, \theta) = \max\{\Phi_T(w, \theta) : \pi(T) = r\}$, the maximum over the finitely many targets carrying r , and $-\infty$ if there are none.

Definition 6.4. The *selected carve* at (w, θ) is

$$K^*(w, \theta) = \arg \max \{\Psi_r(w, \theta) : \Psi_r(w, \theta) > 0\},$$

a set of residues, empty when $\mathcal{R}(w, \theta) = \emptyset$.

Definition 6.5. The *tie locus* at w is

$$\mathcal{T}(w) = \bigcup_{r \neq r'} \{\theta \in \Theta \setminus \Sigma(w) : \Psi_r(w, \theta) = \Psi_{r'}(w, \theta) > 0\},$$

the union over unordered pairs of distinct residues.

Proposition 6.6. [A] For $\theta \in \Theta \setminus (\Sigma(w) \cup \mathcal{T}(w))$ with $\mathcal{R}(w, \theta) \neq \emptyset$, the set $K^*(w, \theta)$ is a singleton.

Proof. Finitely many residues occur, and at least one has $\Psi_r > 0$ by Proposition 4.18; the maximum is attained. Two distinct residues attaining it would place θ in $\mathcal{T}(w)$. $\square$

Theorem 6.7 (Selection chamber theorem). [A] $K^*(w, \cdot)$ is constant on each connected component of $\Theta \setminus (\Sigma(w) \cup \mathcal{T}(w))$.

Proof. Let E be such a component. E is connected and misses $\Sigma(w)$, so lies in a chamber; by Theorem 5.4 the set $\mathcal{R}(w, \cdot)$, and hence the set of residues r with $\Psi_r > 0$, is constant on E , by Corollary 5.7. For two such residues $r \neq r'$ the function $\Psi_r(w, \cdot) - \Psi_{r'}(w, \cdot)$ is continuous, being a difference of maxima of finitely many continuous functions, and vanishes nowhere on E , which misses $\mathcal{T}(w)$. Being continuous on a connected set it has constant sign, so the order of the Ψ -values is constant on E and so is the maximiser. $\square$

6.2 Genericity, and the retirement of H_{det}

Hypothesis 6.8 (H_{gen}). For all distinct residues r, r' , the functions $\Psi_r(w, \cdot)$ and $\Psi_{r'}(w, \cdot)$ agree on no nonempty open subset of Θ .

Definition 6.9. A property of θ holds *generically at w* when it holds off a closed subset of Θ with empty interior.

Proposition 6.10. [A] Assume H_{aff} and H_{gen} . Then $\Sigma(w) \cup \mathcal{T}(w)$ is closed with empty interior and Lebesgue measure zero in Θ .

Proof. $\Sigma(w)$ is a union of at most $|\Xi|$ affine hyperplanes by Proposition 5.11. Fix $r \neq r'$. By Proposition 5.11 the functions $\Psi_r(w, \cdot)$ and $\Psi_{r'}(w, \cdot)$ are piecewise affine; take a finite polyhedral subdivision of Θ on which both are affine. On a cell P their difference is affine, so its zero set is P or a polyhedron of dimension at most $d - 1$. The first case is excluded by H_{gen} when P has nonempty interior, and cells without interior already have dimension at most $d - 1$. Finitely many pairs and cells give a finite union of closed sets of dimension at most $d - 1$, which is closed with empty interior and of measure zero; the closure of $\mathcal{T}(w)$ adds nothing of interior. $\square$

Corollary 6.11 (H_{det} is retired). [D] Assume H_{aff} , H_{gen} and H_{sel} . Then the *selected carve* is single-valued generically at every w , and generically the resolution computed from K^* takes the value `disc` exactly when w_A and w_G carve different residues.

Proof. Propositions 6.6 and 6.10; the second assertion is Proposition 5.18 with H_{det} replaced by that single-valuedness, which is all its proof uses. $\square$

Scholium 6.12. H_{det} asserted determinism at every environment and was refused by [Sch26m, Thms. 10.7, 10.20]. Corollary 6.11 delivers it off a set of measure zero, from H_{sel} together with a general-position proviso. **The trade is a chemical hypothesis for a genericity one**, and it should be recorded as a trade and not as a removal: H_{gen} excludes a set of cage data of measure zero, but it excludes it by fiat, and a cage whose two carves coincide identically on an open region is not absurd.

The exceptional set is not an inconvenience to be hidden. It is the locus at which two carves are exactly balanced, a cell held there produces a mixture, and that is the formal counterpart of [Sch26m]’s nonuniqueness theorems. Under H_{aff} and H_{gen} it has codimension one.

6.3 The two sufficiency statements

Definition 6.13. Let t_1, t_2 denote the assignments of [NCBI24, tables 1 and 2]. A codon-indexed environed cage *type-suffices* when there are $\theta_{\text{nuc}}, \theta_{\text{mito}} \in \Theta$ such that for every purine half h ,

$$\mathcal{R}^b(h, \theta_{\text{nuc}}) = \text{res}_{t_1}(h), \quad \mathcal{R}^b(h, \theta_{\text{mito}}) = \text{res}_{t_2}(h),$$

where res takes the resolution type only; and *residue-suffices* when in addition the residues agree, at all sixty-four codons.

Proposition 6.14. [A] *Type-sufficiency is a condition on $\mathcal{R}^b$ alone and hence, by Theorem 5.16, on the chamber structure. Residue-sufficiency is equivalent to the existence, for each codon w and each of the two settings, of an admissible path at that setting whose selected target satisfies $\pi(T) = t(w)$.*

Proof. The first assertion is immediate from Definitions 5.15 and 6.13. For the second, by Definitions 4.12 and 6.4 the selected residue at (w, θ) is π of a maximiser over reachable targets, and a target is reachable exactly when an admissible path reaches it. $\square$

Scholium 6.15 (The residue obligation is finite and enumerable). Proposition 6.14 makes the difference between the two statements explicit and, more usefully, *finite*. Residue-sufficiency requires a witness path for each distinct pair (w, r) with $r = t_1(w)$ or $r = t_2(w)$ and r a residue; check W6 records that there are sixty-three such pairs: the two tables agree at sixty codons, fifty-eight of them coding and two carrying a stop in both, and differ at four codons — AGA, AGG, AUA, UGA — spanning the three halves of [Sch26i, Thm. 5.7]. Only AUA contributes two obligations, being coding in both tables and differently.

Two of the obligations are not supplied anywhere in the corpus and should be named. **The first is $H_{\text{split-chem}}$ of [Sch26h, Hyp. 2.12]**, which fixes the residue on a divided purine half and is that paper's Target 9.1, undischarged. **The second is the carve at AG-pur when it engages:** [Sch26h] makes that half an absence, [Sch26i, Prop. 5.12] records it uniform-and-coding across the published record under arginine, serine and glycine, and no paper of the corpus says which. Both are questions of the same kind — exhibit a rewrite word — and both are chemistry rather than mathematics.

The present paper proves neither. It gives necessary conditions for type-sufficiency at Proposition 6.16 and Corollary 6.17, and a criterion excluding a class of cages at Proposition 4.21; *no statement of this paper asserts that a cage type-suffices*, and the existence claim is Target 10.1.

Residue-sufficiency lies a further sixty-three obligations off. A reader who takes a necessary condition for the theorem it is necessary for has read Definition 6.13 past its second clause and Proposition 6.16 past its antecedent.

Proposition 6.16 (What type-sufficiency requires of the chamber structure). [A] *If a codon-indexed environed cage type-suffices, then for each of the three halves at which t_1 and t_2 differ ([Sch26i, Thm. 5.7]) the environments θ_{nuc} and θ_{mito} lie in distinct chambers, and for each of the remaining twenty-nine halves they may lie in the same one.*

Proof. If the two environments lay in one chamber at both codons of a half, then by Theorem 5.16 the resolution there would agree, contradicting the assumed disagreement at the three halves. The second clause is vacuous, no constraint being imposed. $\square$

Corollary 6.17. [A] *Under H_{aff} , a type-sufficing cage has at least one environed constraint, and the segment from θ_{nuc} to θ_{mito} meets $\Sigma(w)$ for at least one codon w of each of the three differing halves.*

Proof. By Proposition 6.16 the two environments lie in distinct chambers at such a codon. Θ is convex, so the segment joining them lies in Θ ; being connected and meeting two distinct components of $\Theta \setminus \Sigma(w)$, it meets $\Sigma(w)$. Were no constraint environed, every $\Sigma(w)$ would be empty and Θ a single chamber, contradicting Proposition 6.16. $\square$

Scholium 6.18. Corollary 6.17 is the minimal quantitative content of the series claim: *some* hard constraint of the reaction cell must change sign between the two compartments, at a codon of AG, AU or UG. It is a necessary condition and not the sufficiency statement of Definition 6.13, which this paper does not prove; and it is not conditional on H_{sel} , on H_{sep} or on H_{det} ; it follows from convexity and Theorem 5.4 alone. It is also, by Proposition 4.21, a constraint that no cage depending on the codon only through its block can satisfy.

7 Stereochemical Selection

[Sch26m] fixes the stereochemistry of the carved residue by an *oriented* cage condition: the desired and opposite attack cones A_{χ^*} and $A_{\chi^{\text{opp}}}$ at c_α are separated by the local oriented plane, and a strictly positive oriented margin places every admissible desired trajectory at nonzero distance from that boundary ([Sch26m, §7.19]). This section environs that condition. Nothing here uses [Sch26h] or Part I.

7.1 The oriented margin

Definition 7.1. Let σ be an amino-installation step at c_α . An *oriented constraint family* for σ is a pair of hard constraint families C_σ^* , C_σ^{opp} , whose configuration spaces are the restrictions of X_σ to A_{χ^*} and $A_{\chi^{\text{opp}}}$ respectively. The associated margins, formed as in Definition 4.4, are written μ_σ^* and μ_σ^{opp} .

Hypothesis 7.2 (H_χ). For every w and every θ outside $\mu_\sigma^*(w, \cdot)^{-1}(0) \cup \mu_\sigma^{\text{opp}}(w, \cdot)^{-1}(0)$, exactly one of $\mu_\sigma^*(w, \theta)$, $\mu_\sigma^{\text{opp}}(w, \theta)$ is positive.

Definition 7.3. Under H_χ the *chirality selector* is the function $\chi(w, \theta) \in \{\chi^*, \chi^{\text{opp}}\}$ naming the cone whose margin is positive.

Definition 7.4. The *oriented locus* is $\Sigma^\circ(w) = \Sigma(w) \cup \mu_\sigma^*(w, \cdot)^{-1}(0) \cup \mu_\sigma^{\text{opp}}(w, \cdot)^{-1}(0)$.

7.2 Chambers of the oriented locus

Theorem 7.5. [D] Assume H_χ . Then $\chi(w, \cdot)$ is constant on each connected component of $\Theta \setminus \Sigma^\circ(w)$.

Proof. Let E be such a component. By Proposition 4.5 the functions $\mu_\sigma^*(w, \cdot)$ and $\mu_\sigma^{\text{opp}}(w, \cdot)$ are continuous and vanish nowhere on E ; E being connected, each has constant sign there, so by H_χ the selector is constant. $\square$

Corollary 7.6. [D] Assume H_χ and H_{sel} . The selected carve together with its stereochemical assignment is constant on each connected component of $\Theta \setminus (\Sigma^\circ(w) \cup \mathcal{T}(w))$.

Proof. Such a component misses $\Sigma^\circ(w) \supseteq \Sigma(w)$ and $\mathcal{T}(w)$, so Theorem 6.7 gives constancy of the carve and Theorem 7.5 constancy of χ . $\square$

Corollary 7.7 (The switch). [D] Let E, E' be components of $\Theta \setminus \Sigma^\circ(w)$ adjacent across a point of $\mu_\sigma^*(w, \cdot)^{-1}(0)$ at which $\mu_\sigma^{\text{opp}}(w, \cdot)$ does not vanish. Then χ takes the value χ^* on one of E, E' and χ^{opp} on the other.

Proof. $\mu_\sigma^*(w, \cdot)$ changes sign across the point, being continuous and vanishing there while not vanishing identically on either side; by H_χ , $\mu_\sigma^{\text{opp}}(w, \cdot)$ has the opposite sign on each side. Apply Definition 7.3. $\square$

Proposition 7.8 (At most one switch in one dimension). [D] Assume H_χ , $d = 1$, and that $\mu_\sigma^*(w, \cdot)$ is affine and nonzero. Then $\chi(w, \cdot)$ changes value at most once on Θ .

Proof. A nonzero affine function on an interval vanishes at most once, so $\mu_\sigma^*(w, \cdot)$ has at most one sign change; by H_χ the selector is determined by that sign. $\square$

Scholium 7.9 (What H_χ excludes). H_χ is the strong oriented cage exclusion of [Sch26m, §7.19], environed. It requires exactly one cone to carry a positive margin, and so excludes the case in which both do. That case is not pathological: both attack trajectories are then cage-admissible and the cell carves without stereochemical selection, which is to say racemically. The locus on which H_χ fails is a further wall of the same kind as those of Definition 7.4, and the prediction of Corollary 7.7 is accompanied by a second: between a region of one handedness and a region of the other there may lie a region of neither.

Scholium 7.10. Theorem 7.5 and Corollary 7.7 assert that the handedness of the carved residue is a function of the medium: one reaction cell, one codon, one ordered rewrite word, and a change of chirality on crossing a wall of the oriented locus. **This is the one prediction of the series that can be tested without reference to any translation table.** It uses neither [Sch26h] nor Part I, and it does not depend on H_{sel} , H_{sep} or H_{aff} ; it requires only H_χ and the continuity of Proposition 4.5. Proposition 7.8 says further that in a one-dimensional medium with an affine oriented margin the switch occurs once, so the prediction is not merely of variability but of a single crossing.

8 The Response, and What the Record Bounds

Corollary 5.31 leaves two branches: the medium has dimension at least two, or it has dimension one and the step margins are not comonotone. This section develops the second, and then derives from the published record a bound that holds on both.

8.1 One dimension without comonotonicity

Definition 8.1. A family of real functions on an interval is *comonotone* when all its members are nondecreasing or all are nonincreasing.

Proposition 8.2 (Chambers are intervals). [A] Assume H_{aff} with $d = 1$, comonotonicity not assumed, and let n be the number of distinct nonconstant margin functions $\mu_{\sigma}(w, \cdot)$. Then $\Sigma(w)$ is a set of at most n points and there are at most $n + 1$ chambers at w , each an open interval.

Proof. Each nonconstant affine function on an interval vanishes at most once, its zero possibly lying outside Θ , so $\Sigma(w)$ has at most n points; the complement of $k \leq n$ points in an interval has $k + 1$ components, each an interval. $\square$

Proposition 8.3 (Nesting fails). [A] Assume H_{aff} with $d = 1$ and suppose some $\mu_{\sigma_+}(w, \cdot)$ is increasing while some $\mu_{\sigma_-}(w, \cdot)$ is decreasing, each vanishing in the interior of Θ . Then the conclusion of Lemma 5.23 fails: the reachable set is not nonincreasing in θ .

Proof. Let θ_+ be the zero of $\mu_{\sigma_+}(w, \cdot)$. For $\theta < \theta_+ < \theta'$ the step σ_+ is not cage-liftable at θ and is cage-liftable at θ' by Proposition 4.7. Any target reachable only by paths through σ_+ therefore lies in $\mathcal{R}(w, \theta') \setminus \mathcal{R}(w, \theta)$. $\square$

Scholium 8.4. Proposition 8.3 identifies the exact point at which the recovery of Part I's threshold hypothesis breaks down in the second branch. Theorem 5.24 rests on Lemma 5.23, and Lemma 5.23 rests on comonotonicity. Without it, relaxation is not loss: a wider cage disables the steps that need a tight one and enables those that need room, and the reachable set moves rather than shrinks.

8.2 A lower bound on the cell, from the record

Definition 8.5. Let H be a finite set of purine halves and W_H the set of codons of its members. The *enviored count* $N(H)$ is the number of distinct nonconstant functions among the $\mu_{\sigma}(w, \cdot)$ for $\sigma \in \Xi$ and $w \in W_H$.

Theorem 8.6 (Complexity bound). [A] Assume H_{aff} with Θ Euclidean of dimension d . If the codon-indexed enviored cage realises m distinct rank vectors $v_H(\theta)$ as θ ranges over Θ , then

$$\sum_{k=0}^d \binom{N(H)}{k} \geq m.$$

Proof. Put $\Sigma_H = \bigcup_{w \in W_H} \Sigma(w)$, a union of at most $N(H)$ affine hyperplanes by Proposition 5.11 and Definition 8.5. Let E be a connected component of $\Theta \setminus \Sigma_H$. For each $w \in W_H$, E is connected and misses $\Sigma(w)$, so lies in a chamber at w ; by Theorem 5.16 the resolution of every $h \in H$

is constant on E , hence so is v_H . Therefore m is at most the number of components of $\Theta \setminus \Sigma_H$, which by the argument of Theorem 5.12 — Θ being convex — is at most the number of regions of an arrangement of $N(H)$ hyperplanes in $\mathbf{R}^d$, namely $\sum_{k \leq d} \binom{N(H)}{k}$. $\square$

Hypothesis 8.7 (H_{one}). One codon-indexed enviored cage, with one constraint family, realises the resolutions of every published table of [NCBI24] at suitable environments.

Remark 8.8 (The two-code claim bounds nothing). Applied to the series claim alone — two environments and the two codes of [Sch26i, Thm. 5.7] — Theorem 8.6 has $m = 2$ and yields $N \geq 1$: a single enviored constraint suffices. **Every quantitative statement below rests on H_{one} and not on the series claim.** The vacuity is recorded rather than passed over, being the honest measure of how little a fit to two objects constrains the cell.

Corollary 8.9 (What the published record forces). [D] Assume H_{one} . Taking H to be the sixteen purine halves, the record exhibits $m = 15$ distinct rank vectors, whence

$$d = 1 \Rightarrow N \geq 14, \quad d = 2 \Rightarrow N \geq 5, \quad d = 3 \Rightarrow N \geq 4.$$

Taking H to be the three conditional halves, $m = 5$ and $d = 1 \Rightarrow N \geq 4$. Check W7, W8.

Proof. Theorem 8.6 with the stated m , solving $\sum_{k \leq d} \binom{N}{k} \geq m$ for the least admissible N . $\square$

Remark 8.10 (Is the bound binding?). [A] $N(H)$ counts distinct nonconstant margin functions over the codons of H — thirty-two codons when H is the sixteen purine halves — and **nothing in this paper bounds Ξ** . A reaction cell of the kind [Sch26m] describes has many steps, so N may run to hundreds, and a lower bound of fourteen is then no constraint at all.

The bound is therefore not known to be binding, and the paper does not claim that it is. What Corollary 8.9 establishes is the form of the constraint and the comparison between its branches, not that either branch is tight. Estimating N for the reference realization of [Sch26m, Thm. 9.12] is Target 10.9, and until it is done the corollary should be read as saying what a bound on the cell would look like rather than as supplying one.

Remark 8.11 (H_{one} is a strong hypothesis). [E] Hypothesis 8.7 asks one cage, with one constraint family, to realise

the resolutions of every published table. **This is not a mild idealisation.** The twenty-seven tables come from organisms separated by the whole of eukaryotic and bacterial divergence, and their translational machinery differs in more than the medium. A reader who grants H_{one} grants that the differences among those organisms which bear on the curve are differences of environment and not of cage.

The hypothesis is retained because the alternative is to have no quantitative statement at all (Remark 8.8), and it is named, costed and placed at the head of the load-bearing list for that reason. It is not argued for anywhere, and Target 10.8 is where it would be.

Scholium 8.12. Corollary 8.9 is a lower bound on the complexity of the reaction cell, obtained from published translation tables and the convexity of the medium. It is the converse in kind of Theorem 5.12, which bounds from above what a cell of given complexity can do; here the variety of the record bounds from below what the cell must have. The two branches of Corollary 5.31 are costed by it: a one-dimensional medium is admissible but expensive, requiring fourteen environed constraints where two dimensions require five.

8.3 The response is not reduced and coherent

Definition 8.13. The response is *reduced* when there is a continuous $\xi : \Theta \rightarrow \mathbf{R}$ and functions $m_{\sigma,w}$ with $\mu_{\sigma}(w, \cdot) = m_{\sigma,w} \circ \xi$ for all σ, w ; it is *coherently oriented* when in addition every $m_{\sigma,w}$ is nonincreasing.

Lemma 8.14 (Nesting by ξ). *[A] Suppose the response is reduced and coherently oriented. If $\xi(\theta) \leq \xi(\theta')$ then $\mathcal{R}(w, \theta') \subseteq \mathcal{R}(w, \theta)$ for every w .*

Proof. For every σ and w , $\mu_{\sigma}(w, \theta) = m_{\sigma,w}(\xi(\theta)) \geq m_{\sigma,w}(\xi(\theta')) = \mu_{\sigma}(w, \theta')$, the function $m_{\sigma,w}$ being non-increasing. Hence every step cage-liftable at θ' is cage-liftable at θ by Proposition 4.7, so every path admissible at θ' is admissible at θ . $\square$

Remark 8.15 (Nesting alone does not order the resolutions). *[A]* Lemma 8.14 does not by itself make the rank vector monotone, and the point is easy to miss. Let $\xi(\theta) \leq \xi(\theta')$ and let a half have $K(w_A) = K(w_G) = \{r\}$ at θ , so $\mathcal{R}^b = \text{unif}$ of rank 1. Shrinking the carves may empty one of them and leave the other, giving $\mathcal{R}^b = \text{disc}$ of rank 0 at θ' : the rank has *decreased*. Exactly this is why Theorem 5.24 carries H_{sep} , and the same premise is required here.

Hypothesis 8.16 (H_{sep}^{ξ}). For every purine half h the set $B(h) = \{\theta : K(w_A, \theta) \neq K(w_G, \theta)\}$ is a down-set for the preorder $\theta \preceq \theta' \iff \xi(\theta) \leq \xi(\theta')$.

Theorem 8.17 (The response is not reduced and coherent). *[D] Assume the selected curve is single-valued and H_{sep}^{ξ} . If the response is reduced and coherently oriented, then for every finite set H of purine halves the rank vectors $v_H(\Theta)$ form a chain. Consequently, by Theorem 5.28, the response of a cage realising the resolutions of [NCBI24, tables 1 and 33] is not both reduced and coherently oriented.*

Proof. Fix a half h and let $\xi(\theta) \leq \xi(\theta')$. If $\theta' \in B(h)$ then $\theta \in B(h)$ by H_{sep}^{ξ} , so $\text{rk}(\theta) = \text{rk}(\theta') = 0$. If $\theta' \notin B(h)$ and $\theta \in B(h)$ then $\text{rk}(\theta) = 0 \leq \text{rk}(\theta')$. If neither lies in $B(h)$, both carves agree at each of the two environments, and by Lemma 8.14 the common carve at θ' is contained in that at θ ; a singleton contains a singleton or the empty set, so $\text{rk}(\theta) \leq \text{rk}(\theta')$. Hence $v_H(\theta) \leq v_H(\theta')$ componentwise, and any two rank vectors are comparable, $\mathbf{R}$ being totally ordered. Theorem 5.28 exhibits two that are not. $\square$

Scholium 8.18. Theorem 8.17 uses neither H_{aff} nor any hypothesis on the dimension of Θ , and does not require ξ to be monotone or even to be a coordinate: a reduced and coherently oriented response orders the carves by the value of ξ alone, and that order is total because $\mathbf{R}$ is. It does require H_{sep}^{ξ} , by Remark 8.15, and that premise is the same one Theorem 5.24 carries. What has been removed relative to the recovery theorem is the restriction to dimension one and the assumption that the margins are affine.

Corollary 8.19. *[D] Either at least two cage coordinates respond independently to the medium, or a single cage coordinate enters the constraint functionals with both signs.*

Proof. The negation of *reduced* is the first alternative; the negation of *coherently oriented*, given reducedness, is the second. Apply Theorem 8.17. $\square$

Scholium 8.20 (The nascent rings). *[E]* Corollary 8.19 is a statement about the chrysene–adenosine complex derived from codon tables, and its second alternative is the one the architecture makes natural. A displacement of the nascent aromatic rings of the tethered chrysene is a single cage coordinate which does not act on all constraints with one sign: rotating or puckering the ring system opens the approach at one face of c_{α} while closing it at another, so that a motion which relaxes one hard constraint tightens a

second. Under Definition 8.13 such a response is reduced and *not* coherently oriented, and is therefore admitted by Theorem 8.17 where a uniform loosening of the cage is not. This is a reading and enters no proof. What the mathematics supplies is the disjunction of Corollary 8.19 and the cost of each branch at Corollary 8.9; which branch holds is Target 10.2, and it is decided by the sign of $\partial\mu_\sigma/\partial\xi$ for two steps of opposed approach geometry.

9 The Response

This section is empirical in its entirety. It states what H_{resp} would have to mean for the chrysene–adenosine complex, and which branch of Corollary 8.19 each candidate supplies. **Nothing below enters a proof**, and every theorem of Sections 4 to 8 stands if the whole section is deleted.

9.1 What the response map is, and what it is not

Remark 9.1. [E] H_{resp} asserts that the environment acts on the constraint functionals only through the local cage coordinates: a change of medium moves the geometry, and the geometry decides admissibility. It does not assert which intensive quantities the medium is described by, how many there are, or that the map ρ is known. Clause (viii) of Proposition 3.1 refuses the inference from a margin's dependence on θ to the identity of the agent.

Remark 9.2 (Two things the section does not attempt). [E] It does not compute a constraint functional. [Sch26m] gives the functionals as data of a realization and a computation of them is the certification programme of that paper, not of this one. And it does not choose among the candidates below: the choice is Target 10.5 and would be made by an intervention, not by an argument.

9.2 Candidate arguments of the response map

Remark 9.3 (The table). [E] For each candidate intensive quantity, the cage coordinate it is expected to move and the constraint whose margin then varies:

Quantity	Cage coordinate moved	Margin affected
proton activity	charge on the tether phosphate; protonation of adenine N1 and of ring substituents	electrostatic approach margin at c_α
divalent-metal activity	phosphate clamp; torsions along C6–O–C $_\alpha$ –C $_\beta$	the reach margin for C5–C $_\alpha$ capture
redox potential	oxidation state and planarity of the chrysene ring system; displacement of the nascent aromatic rings	inter-plane separation of the π -stack; the oriented margin of Definition 7.1
effective dielectric	screening of the preceding	all electrostatic margins, weakly

Each row is a reading of [Sch26m, §5] and of the architecture of [Sch26k], and each is separately falsifiable. **The redox row is the only one entered twice:** it bears on the inter-plane separation and on the oriented margin of Section 7, so it alone touches Target 10.6 as well as Target 10.2, and it is the row on which the second branch of Corollary 8.19 rests.

9.3 Which branch each candidate supplies

Remark 9.4. [E] Corollary 8.19 leaves two alternatives: at least two cage coordinates respond independently, or a single coordinate enters the constraint functionals with both signs. The candidates divide between them.

First branch. Proton activity and divalent-metal activity move different coordinates — a charge and a torsion — and there is no reason for their effects to be proportional. Two quantities varying independently between nucleoplasm and matrix supply two coordinates directly.

Second branch. A displacement of the nascent aromatic rings is one coordinate, and it is the candidate that acts with both signs. Scholium 8.20 states the reason: rotating or puckering the ring system opens the approach at one face of c_α while closing it at another, so a motion relaxing one hard constraint tightens a second. Such a response is reduced in the sense of Definition 8.13 and is not coherently oriented, and Theorem 8.17 admits it where a uniform loosening of the cage is refused.

The two are not exclusive and the record does not separate them. What Corollary 8.9 adds is a cost: under H_{one} a one-dimensional medium requires fourteen environed constraints where two dimensions require five, so the second branch is admissible but expensive unless the single coordinate carries many constraints at once — which is precisely what

a ring displacement does.

9.4 What would have to be measured

Remark 9.5. [E] Three measurements would decide the section, and none is performed here.

The sign of $\partial\mu_\sigma/\partial\xi$ for two steps of opposed approach geometry decides the branch (Target 10.2). A computation of one constraint functional over a range of cage coordinates, in the manner of [Sch26m]’s certification programme, supplies ρ for that coordinate (Target 10.4). And an intervention moving one intensive quantity while holding the others decides the agent (Target 10.5).

The first is the cheapest and the most informative, requiring no absolute values: only that two constraints be compared as one coordinate moves.

10 Non-Implications Restated, and Targets

10.1 The non-implications in one line each

- (i) Chambers are not thresholds; an ordering is required and is refuted (Prop. 3.1(i), Cor. 5.31).
- (ii) Reachability is not kinetics (Prop. 3.1(ii), [Sch26m, Rem. 7.15]).
- (iii) A discontinuous output does not require a discontinuous input (Prop. 3.1(iii), Thm. 5.4).
- (iv) Type-sufficiency is not residue-sufficiency (Prop. 3.1(iv), Sch. 6.15).
- (v) Fitting two codes bounds nothing (Prop. 3.1(v), Rem. 8.8).
- (vi) A cell that could carve both codes is not an account of what was carved (Prop. 3.1(vi)).
- (vii) Generic single-valuedness is not mechanistic uniqueness (Prop. 3.1(vii), Sch. 6.12).
- (viii) A margin varying with the medium does not name the agent (Prop. 3.1(viii), Rem. 9.1).
- (ix) Recovering Part I’s hypothesis does not confirm Part I (Prop. 3.1(ix), Thm. 5.24).
- (x) Part I’s Theorem 7.6 is a criterion and not an obstacle escaped (Prop. 3.1(x), Prop. 4.21).

A further refusal is not a clause of Proposition 3.1 because no reader is likely to infer it from a result, but it governs the paper and is stated here: **a necessary condition for sufficiency** $\nRightarrow$

sufficiency. Definition 6.13 is met by no cage exhibited here (Target 10.1).

One further trap is stated at the point of use and not repeated: nothing here is measured (Rem. 3.4).

10.2 Targets

Target 10.1 (Exhibit a sufficing cage). [T] Exhibit a codon-indexed envired cage and two environments $\theta_{\text{nuc}}, \theta_{\text{mito}} \in \Theta$ at which it type-suffices in the sense of Definition 6.13. **This is the series goal and neither part proves it.** Part I derives the resolutions of the two codes from a posited threshold structure; this paper derives that structure from margins and gives necessary conditions on any cage meeting it (Prop. 6.16, Cor. 6.17), together with a criterion excluding those whose margins factor through block data (Prop. 4.21). *No cage is exhibited.*

Under H_{aff} a schematic witness — affine margins stipulated rather than computed — should be constructible, and would settle whether the necessary conditions are jointly satisfiable at all. Such a witness would not discharge Target 10.3, the margins being stipulated, but it would separate *no cage suffices* from *no cage has been produced*, which the paper as it stands does not.

Target 10.2 (Which branch). [T] Decide the alternative of Corollary 8.19: do at least two cage coordinates respond independently to the medium, or does a single coordinate enter the constraint functionals with both signs? It suffices to determine the sign of $\partial\mu_\sigma/\partial\xi$ for two steps of opposed approach geometry at c_α as one cage coordinate is varied. No absolute values are needed, only a comparison of two signs, and by Remark 9.5 this is the cheapest of the three measurements the paper invites.

Target 10.3 (Fix the margins from the geometry). [T] Compute the step margins of Definition 4.4 from the configuration spaces and constraint functionals of [Sch26m, §5], rather than positing them. **This is what separates a theory from a fit.** With the margins free, the chamber structure can be made to realise any finite family of carves and Section 8 has no content; with them fixed, Theorem 5.12 bounds what the cell can do and Corollary 8.9 what it must have, and the two may be compared.

Target 10.4 (The response map). [T] Determine ρ of H_{resp} for at least one cage coordinate: compute one constraint functional over a range of that coordinate, in the manner of the certification programme of [Sch26m], and exhibit the dependence on an intensive quantity of the medium.

Target 10.5 (Which agent). [T] Separate the candidates of Remark 9.3. Proton activity, divalent-metal availability, redox potential and effective dielectric all differ between nucleoplasm and mitochondrial matrix, and no result of this paper distinguishes them. An intervention moving one while holding the others is what would settle it; this is [Sch26h, Target 9.3] in the vocabulary of the present theory and it is not discharged here.

Target 10.6 (The stereochemical switch). [T] Test Corollary 7.7 at the bench: one cell, one codon, one ordered rewrite word, and a change of handedness in the carved residue on crossing a wall of the oriented locus. Under H_{aff} with $d = 1$, Proposition 7.8 predicts a single crossing; Scholium 7.9 predicts that where H_χ fails the carve is racemic. **This is the only prediction of the series testable without reference to a translation table.**

Target 10.7 (The carve at AG-pur). [T] Exhibit a rewrite word whose selected target at θ_{nuc} carries arginine at the purine half of AG. [Sch26h] makes that half an absence and [Sch26i, Prop. 5.12] records it uniform-and-coding across the published record under arginine, serine and glycine; no paper of the corpus says which. With $H_{\text{split-chem}}$ of [Sch26h, Hyp. 2.12] — that paper's Target 9.1, undischarged — this is the whole of the distance from type-sufficiency to residue-sufficiency (Sch. 6.15).

Target 10.8 (Is one cage enough). [T] Decide H_{one} . The hypothesis that a single codon-indexed environed cage covers the twenty-seven published tables is assumed in Section 8 and tested nowhere. It could fail in two ways: no single constraint family suffices, or the environments required are not realised in any cell. **Every quantitative statement of this paper depends on it** (Rem. 8.8).

Target 10.9 (The chamber count). [T] Compute the number of chambers of the reference realization of [Sch26m, Thm. 9.12] under a stated response, and compare it with the bound of Theorem 5.12 and with the fifteen configurations the record exhibits (Cor. 8.9). A count materially above fifteen would say the cell is more versatile than the record requires; materially below, that one cage cannot cover it.

10.3 Which are load-bearing

Remark 10.10 (Four of the nine). Their number is not offered as evidence of anything.

Target 10.1 decides whether the series has a theorem. The goal of both parts is a conditional sufficiency statement, and neither part proves one; until a cage is exhibited, the necessary conditions of §6.3 are conditions on an object not shown to exist.

Target 10.3 decides whether the paper has content. Section 8 bounds the cell from below and Section 5 from above, and both bounds are statements about margins; if the margins are fitted rather than computed, the bounds describe the fit. **Target 10.8** decides whether the bounds apply to anything. The series claim alone forces nothing (Rem. 8.8), so the whole quantitative content of Section 8 rests on a hypothesis stated there and tested nowhere.

Target 10.2 decides the architecture. Corollary 8.19 offers two readings of the chrysene–adenosine complex and the record does not choose between them; the measurement is cheap and the answer changes what Section 9 may assert. The remaining five are not load-bearing in the same sense. Targets 10.4 and 10.5 would strengthen hypotheses that carry no theorem; Target 10.6 tests a prediction whose failure would not disturb Sections 4 to 6; Target 10.7 concerns a statement the paper declines to make; and Target 10.9 compares two bounds neither of which is asserted to be tight.

10.4 Status of the predecessors' programme

Remark 10.11. No deferred target of [Sch26c]–[Sch26m] is discharged here.

[Sch26i, Target 10.1], what sets the threshold, is *answered in form and not in content*: Theorem 5.24 constructs the thresholds from margins of a reaction cell, and Target 10.3 records that the margins themselves are not computed.

[Sch26i, Target 10.5], a second environmental axis, is *sharpened*: Corollary 5.31 replaces the request for a second axis by a dichotomy, and Corollary 8.9 costs each branch.

[Sch26h, Target 9.1] and [Sch26h, Target 9.3] are *restated in the present vocabulary* at Target 10.7 and Target 10.5, and neither is advanced.

[Sch26m]'s reaction-inert declaration is *inverted* (Rem. 2.8), and its persistence theorems are recovered as statements valid on a chamber (Cor. 5.8). Nothing of that paper is contradicted.

Finally, one hypothesis of this paper's own development is *retired* rather than discharged: H_{det} , replaced at Corollary 6.11 by a selection rule and a general-position proviso. A retirement is not a proof.

11 Conclusion

Part I asks what separates the standard genetic code from the vertebrate mitochondrial one and answers that the two are two settings of a single three-valued refinement, with the value at each half-block fixed by the environment through a pair of thresholds. It then proves that those thresholds are not a function of the codon block, and that no single environmental coordinate orders the published record. Those are the two results this paper takes as its specification.

The reply is that the thresholds are margins of a reaction cell. The chrysene–adenosine complex of [Sch26k], carrying the cage-admissibility structure of [Sch26m], has for each rewrite step a configuration space and a finite family of hard constraints; the step margin is the largest slack simultaneously available to all of them, and the step is cage-liftable exactly when that margin is positive (Prop. 4.7). Making the constraint functionals depend on the medium is the single change this paper makes to [Sch26m], whose external context is assumed inert (Rem. 2.8).

The mathematics is then $\max \circ \min$ and nothing more. A path is no more admissible than its tightest step and a target no less reachable than its best path, so reachability is a maximum over path supports of a minimum over step margins (Def. 4.16); and because a path margin depends only on which steps occur, the theory carries no bound on path length and no parameter of range (Sch. 4.17).

The nonlinearity follows from the sign structure alone. On a connected set missing the zero sets of the step margins, each margin has constant sign, so the set of liftable steps is constant, so the admissible paths are constant, so the reachable set is constant (Lem. 5.2, Thm. 5.4). **A continuously varying medium therefore produces a discontinuously varying product**, the discontinuities confined to the margin locus (Cor. 5.6), and within a chamber the persistence theorems of [Sch26m] hold uniformly rather than pointwise (Cor. 5.8). None of this requires a constraint functional to be nonlinear, and none of it requires the environment to be discrete (Prop. 3.1(iii)).

Part I's hypothesis is recovered as a theorem, at a stated price. Under a one-dimensional medium with comonotone margins, and the premise that discrimination between the two purine codons is a tight-cage phenomenon, each half acquires two thresholds and the resolution takes Part I's three values in Part I's order (Thm. 5.24). The thresholds are constructed, as the supremum of a down-set and the infimum of an up-set. The price is the hypothesis list, and the first of its entries fails: tables 1 and 33 give rank vectors (1, 0) and (0, 1) at the halves AG-pur and UG-pur, which are incomparable, so the published resolutions are not a chain (Thm. 5.28). Either the medium has more than one dimension, or its margins are not comonotone (Cor. 5.31); and the one-dimensional reading is exact on three of the eight varying purine halves and on no four (Prop. 5.29).

Determinism is not assumed but derived, generically. Selecting the widest-margin residue makes the carve single-valued

off the margin and tie loci, which under affineness and a general-position proviso have codimension one (Prop. 6.10, Cor. 6.11). The exceptional locus is not concealed: it is where two carves balance, a cell held there produces a mixture, and that is the formal counterpart of [Sch26m]'s refusal of mechanistic uniqueness. What has been traded is a chemical hypothesis for a genericity one, and Scholium 6.12 records the trade as a trade.

The record bounds the cell. If one cage is asked to cover the twenty-seven published tables, the fifteen distinct rank vectors it must realise force $\sum_{k \leq d} \binom{N}{k} \geq 15$, whence fourteen environed constraints in a one-dimensional medium against five in two dimensions (Thm. 8.6, Cor. 8.9). This is the converse in kind of Theorem 5.12, which bounds from above what a cell of given complexity can produce. **It also costs the two branches of the dichotomy against each other:** a one-dimensional medium is admissible but expensive unless its single coordinate carries many constraints at once, which is what a displacement of the nascent aromatic rings would do.

That displacement is the second branch, and the mathematics states it without the chemistry. A response factoring through one cage coordinate with all constraints loosening together orders the carves by that coordinate alone, and the order of **R** is total, so the rank vectors would form a chain (Lem. 8.14, Thm. 8.17). They do not. Hence either two cage coordinates respond independently, or one enters the constraints with both signs (Cor. 8.19) — a motion opening the approach at one face of c_α while closing it at another.

One prediction is testable without any translation table. The oriented cage exclusion of [Sch26m, §7.19], environed, makes the handedness of the carved residue a function of the medium: constant on chambers of the oriented locus and exchanged across a wall (Thm. 7.5, Cor. 7.7), with a single crossing in a one-dimensional medium (Prop. 7.8) and a racemic region where the exclusion fails (Sch. 7.9).

What is not done. No axiom is introduced (Rem. 2.2). No deferred target of any predecessor is discharged (Rem. 10.11). No constraint functional, response map or environment is measured (Rem. 3.4). And **the paper proves neither sufficiency statement:** it gives necessary conditions for a cage to realise the two codes (Prop. 6.16, Cor. 6.17) and a criterion excluding a class of candidates (Prop. 4.21), and exhibits no cage (Target 10.1). Residue-sufficiency lies further off again: the theory says which target is reachable, not which residue that target is, and the gap is sixty-three witness pairs of which two classes are open questions of the corpus (Sch. 6.15).

Three limits deserve restating rather than leaving to the list. **The series claim bounds nothing:** two environments and two codes force a single environed constraint, and every number in Section 8 rests on the separate hypothesis that one cage covers the record (Rem. 8.8, Target 10.8). **The margins are posited and not computed**, so the bounds of Sections 5 and 8 describe the posited family until Target 10.3 is discharged. And **Part I's negative theorem is not escaped:** a cage depending on the

codon only through quantities computable from its block is refuted before it is tested (Prop. 4.21).

What remains. A reaction cell whose cage responds to its medium carves discretely; the walls at which the carve changes are the zero sets of its margins; Part I's thresholds are constructed from those zero sets, as the supremum of a down-set and the infimum of an up-set (Thm. 5.24); and the variety of the published record is a lower bound on how many such walls the cell must have. What the series has not shown is that any particular cell has them. The sharpest question is Target 10.3 and the sharpest test is Target 10.2, which asks only for the comparison of two signs as one cage coordinate moves, and which decides between the two readings of the complex that the genetic code leaves open.

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 d, u and $\emptyset$ abbreviate the three resolutions of Definition 5.15, of ranks 0, 1 and 2 in the sense of Definition 5.26.

A.1 The purine halves at which the record varies

Tables	UU	UC	UA	UG	CU	AU	AA	AG
22	u	d	d	d	u	d	u	u
15, 16, 32	u	u	d	d	u	d	u	u
14	u	u	d	u	u	d	d	u
33	u	u	d	u	u	d	u	d
23	d	u	$\emptyset$	d	u	d	u	u
6, 29, 30	u	u	u	d	u	d	u	u
12, 26	u	u	$\emptyset$	d	d	d	u	u
27, 28, 31	u	u	u	u	u	d	u	u
1, 10, 11, 25	u	u	$\emptyset$	d	u	d	u	u
9	u	u	$\emptyset$	u	u	d	d	u
24	u	u	$\emptyset$	u	u	d	u	d
4	u	u	$\emptyset$	u	u	d	u	u
21	u	u	$\emptyset$	u	u	u	d	u
3, 5, 13	u	u	$\emptyset$	u	u	u	u	u
2	u	u	$\emptyset$	u	u	u	u	$\emptyset$

The eight columns are the purine halves whose resolution is not constant across the record; the remaining eight are u throughout and are omitted, so the rank vector over all sixteen purine halves is determined by this table. There are 15 distinct rows, which is the m of Corollary 8.9.

A.2 The three conditional halves

Tables	AG	AU	UG	rank	Setting
24, 33	d	d	u	(0, 0, 1)	<i>off chain</i>
1, 6, 10, 11, 12, 15, ... (14 in all)	u	d	d	(1, 0, 0)	low
4, 9, 14, 27, 28, 31	u	d	u	(1, 0, 1)	low
3, 5, 13, 21	u	u	u	(1, 1, 1)	intermediate
2	$\emptyset$	u	u	(2, 1, 1)	high

5 of the twenty-seven conceivable triples are occupied. Exactly 1 pair of them is incomparable in the componentwise order, namely (1, 0, 0) and (0, 0, 1); that pair is the witness of Theorem 5.28, realised by tables 1 and 33.

A.3 Where a single ordering survives

Of the 8 purine halves whose resolution is not constant across the record, the rank vectors of the twenty-seven tables form a chain on **3** and on no 4. There are 4 such sets:

UU, UG, AU
UC, UA, AU
UC, UG, AU
UG, CU, AU

Every one of them contains AU-pur. The count is taken over the varying halves because a constant half contributes a constant coordinate and cannot break a chain: adjoining all 8 constant halves to any of the sets above leaves a chain of 11, which measures nothing. This is Proposition 5.29 and Remark 5.30.

A.4 The two bounds

n	$d = 1$	$d = 2$	$d = 3$	$d = 4$
2	3	4	4	4
4	5	11	15	16
6	7	22	42	57
8	9	37	93	163
12	13	79	299	794
16	17	137	697	2517

Above: $\sum_{k \leq d} \binom{n}{k}$, the bound of Theorem 5.12 on the number of chambers, hence on the number of distinct curves one cell can realise.
 Below: its converse at Corollary 8.9, the least envired count N compatible with the m distinct rank vectors the record exhibits.

Halves taken as H	m	$d = 1$	$d = 2$	$d = 3$
the three conditional halves	5	≥ 4	≥ 3	≥ 3
the four coupled halves	10	≥ 9	≥ 4	≥ 4
all sixteen purine halves	15	≥ 14	≥ 5	≥ 4

Both tables are vacuous without H_{one} : applied to the two codes alone, $m = 2$ and every entry reads ≥ 1 (Remark 8.8).

A.5 The residue obligation

Distinct (codon, residue) witness pairs	63
codons at which tables 1 and 2 agree	60
of which coding	58
of which stop in both	2
codons at which they differ	4

The differing codons and their obligations:

Codon	table 1	table 2	obligations
AGA	R	$\emptyset$	1
AGG	R	$\emptyset$	1
AUA	I	M	2
UGA	$\emptyset$	W	1

Only AUA contributes two, being coding in both tables and differently. This is the obligation of Scholium 6.15; two of its classes are supplied nowhere in the corpus.

B Concordance, Ledger, and Verification

B.1 Scope

This appendix records, for every prior statement the paper touches, whether it is preserved, extended, inverted, recovered, specialised or not applicable, against the criterion C of [Sch26b, Def. 2]. Two entries require comment before the tables. [Sch26m]’s **declaration that the external context is reaction inert is inverted** (Rem. 2.8), and that single inversion is the whole of the difference between the two theories. [Sch26i, Thm. 7.6] is **not evaded but applied**, as a criterion every cage model must meet (Prop. 4.21).

B.2 Concordance with [Sch26m]

Prior statement	Disposition
§4, typed graphs and rewrite rules	Preserved and imported entire
Def. 4.21, well-formed paths	Preserved; the support of a path (Def. 4.14) is new and is the only structure added
§5, configuration spaces and constraint functionals	Extended: the functionals acquire a second argument, the environment (Def. 4.2)
Def. 7.13, uniform positive margin	Preserved; the step margin of Def. 4.4 is its pointwise form
Thm. 7.14(2), reaction-inert context	Inverted (Rem. 2.8)
Thms. 7.14, 9.16, persistence	Recovered on a chamber: what those theorems give at a point, Cor. 5.8 gives uniformly on a compact subset of a chamber
Rem. 7.15, no equality of activation barriers	Preserved and made a non-implication, Prop. 3.1(ii)
§5.16, Prop. 5.15, §7.19, oriented exclusion	Environed: the oriented margins of Def. 7.1 are functions of θ , and Cor. 7.7 is the consequence
Thms. 10.7, 10.20, nonuniqueness	Preserved and made load-bearing: they are why H_{det} could not stand and why the tie locus is given a meaning (Sch. 6.12)
Thm. 9.12, the canonical witness	Preserved; not used, and named at Target 10.9 as the realization whose chambers should be counted

B.3 Concordance with Part I and the earlier corpus

Prior statement	Disposition
[Sch26i, Defs. 4.2, 4.3]	Preserved; recovered as Def. 5.15 from reachable sets
[Sch26i, Hyp. 2.7], $H_{\text{eng-type}}$	Derived: posited there, constructed at Thm. 5.24
[Sch26i, Thm. 7.6]	Preserved and applied as a criterion (Prop. 4.21)
[Sch26i, Thm. 8.9, Cor. 8.10]	Preserved; restated as a bound on the cell (Cor. 8.9) rather than the failure of an account
[Sch26i, Thm. 5.7]	Preserved; the three halves are what Prop. 6.16 requires distinct chambers for
[Sch26i, Targets 10.1, 10.5]	Answered in form and sharpened respectively (Rem. 10.11)
[Sch26i, §9], the feedback circuit	Not carried. This is a synthesis account; Prop. 3.1(vi)
[Sch26h, Hyp. 2.10], H_{seed}	Preserved; inherited through Part I
[Sch26h, Hyp. 2.12], $H_{\text{split-chem}}$	Noted and not advanced; one of the two classes of Target 10.7
[Sch26h, Rem. 6.8], encasement	Preserved and read geometrically at H_{cod}
[Sch26k, Def. 2.4], the word space	Preserved; the index set of Def. 4.20
[Sch26k, Hyp. 2.14], H_{teth}	Preserved; inherited unchanged
[Sch26g, Thm. 5.4], capacity	Not applicable; no residue is placed here
[Zam72], residue volumes	Not used. Part I's proof depends on them; no proof of this paper does

B.4 Chemical scope

Remark B.1 (What is before the domain pass). [E] H_{resp} and H_{cod} are chemical and undischarged, and H_{sel} , H_{sep} , H_{sep}^{ξ} and H_{χ} are claims about the behaviour of a cell. **No theorem labelled [A] uses any of them.** In particular Theorem 5.4, Theorem 5.12, Theorem 8.6, Theorem 5.28 and Proposition 5.29 are independent of every chemical hypothesis in the register, and would stand under any account assigning continuous margins to the steps of a rewrite system. The full synthesis is not given here. Section 9 is a reading of what H_{resp} would have to mean and enters no proof.

B.5 Defect ledger

Thirty-four items were raised in three pre-drafting and drafting passes against Sections 4–5, 6–8 and 2–3 with 9–11 respectively, and all are disposed. The table records the items that changed a claim.

#	crit	rev
I.3	The chamber theorem was proved through the reachability functional and so inherited a finiteness hypothesis it does not need	Accepted; reproof from the constancy of the liftable set (Lem. 5.2), and the theorem is [A]
I.7	The dimension corollary was false: a sign change of the parameter cannot make a mixed family comonotone	Accepted; replaced by the dichotomy of Cor. 5.31, whose second branch is developed at §8
I.11	A scholium claimed exemption from [Sch26i, Thm. 7.6]	Accepted; promoted to Prop. 4.21, which states the theorem as a criterion the cage must meet
II.1	The range N made the selected curve ill defined, the functional growing with N	Accepted; Φ_T is a maximum over path <i>supports</i> (Def. 4.16) and no length bound occurs in the paper
II.3	The proposition retiring $H_{\det}$ was false: two functionals may agree on a full-dimensional cell	Accepted; H_{gen} registered, and the trade recorded at Sch. 6.12
II.8	The $d > 1$ case of the reduced-response theorem argued along a monotone path with no reason to exist	Accepted; replaced by nesting under the order of ξ (Lem. 8.14), which needs no dimension hypothesis
II.10	The complexity bound assumed one cage covers the record, which the series claim does not require	Accepted; H_{one} registered and the vacuity of the two-code case printed (Rem. 8.8)
III.1	Sixty-four numbered statements carried no status label	Accepted; forty labels applied under the rule of Rem. 2.3, and the two consequences stated there
III.2	The constructive declaration claimed Section 4 uses no translation table	Accepted; Prop. 4.21 is where the record enters, and the declaration now says so (Rem. 2.9)
III.5	A non-implication refuted a trap no reader would fall into	Accepted; restated as the converse of the paper's own claim, Prop. 3.1(vi)

B.6 Corrections made during drafting

Recorded separately because these are errors in the drafting record rather than criticisms of the manuscript.

1. A finiteness hypothesis was asserted for the set of paths between two states. It is false: nothing forbids a path from revisiting a state, and [Sch26m] carries a length function for that reason.
2. The chamber theorem was proved under that hypothesis. It needs none.
3. The dimension corollary of §5.5 was false as proved, and its repair produced the dichotomy which §8 develops and which Corollary 8.9 costs.
4. A review pass asserted that the reduced-response theorem needs no separation hypothesis. **It does.** Nesting shrinks the curves, and shrinking can empty one curve of a half while leaving the other, carrying *unif* to *disc* and *lowering* the rank; Rem. 8.15 displays the counterexample.
5. The proposition retiring $H_{\det}$ omitted the general-position case in which two functionals coincide on an open set.
6. Sixty-four numbered statements were drafted without status labels, in a paper whose subject is which results survive which hypotheses.
7. The constructive declaration was drafted false.
8. The complexity bound was drafted without naming the hypothesis that carries it.
9. One citation of forty-four into the predecessors was wrong. The other forty-three resolve as printed.

B.7 Verification record

Ten checks, each an enumeration over [NCBI24] as published or a closed computation, rebuilt by the supplementary script. The script imports nothing from the tables of this paper.

W1 the three values of Definition 5.15 all occur in the record (§5.3)

W2 the chamber bound $\sum_{k \leq d} \binom{n}{k}$, as arithmetic (§5.2)

W3	tables 1 and 33 give rank vectors (1, 0) and (0, 1) at AG-pur and UG-pur	(§5.5)
W3b	28 of 351 table pairs are incomparable on those two halves alone	(§5.5)
W4	130 of 351 pairs are incomparable over all sixteen purine halves	(§5.5, §8.2)
W5	the record is a chain on three of the eight VARYING purine halves and on no four; every maximal triple contains AU-pur	(§5.5)
W5b	the eight constant halves may be adjoined freely, so a count over all sixteen is uninformative	(§5.5)
W6	63 distinct residue obligations; 60 agreeing codons, 58 coding; 4 differing	(§6.3)
W7	15 distinct rank vectors over the sixteen purine halves, 5 over the three conditional	(§8.2)
W8	the least environed count: $d = 1 \Rightarrow N \geq 14$, $d = 2 \Rightarrow N \geq 5$, $d = 3 \Rightarrow N \geq 4$	(§8.2)

Appendix A is emitted by a second script from the same objects and is not transcribed by hand.

B.8 Meta-review

Remark B.2 (Disposition). Thirty-four items in three passes, all disposed. Nine checks, all passing. Nine corrections to the drafting record, at B.6.

Remark B.3 (Three observations). First, **four of the nine corrections at B.6 are defects in proofs**, and three of those were found by writing the proof out rather than by computing anything. That is a different failure mode from the one the preceding papers record, where a claim written in prose was refuted by computing it. A Bourbaki-style presentation moves the errors from the figures into the arguments, and it appears to find them at about the same rate.

Second, item 4 of B.6 is a correction of a correction: a review pass claimed a hypothesis could be dropped, and applying the claim showed it could not. The ledger records the sequence rather than the endpoint.

Third, **the paper's central positive result is the one that needs no hypothesis**. Theorem 5.4 carries [A], and everything the register contains is spent on the recovery of Part I's threshold hypothesis, on selection, and on the bounds — none of which is the statement that a continuously varying medium carves discretely.

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 nine numerical checks excepted.

Eight Targets are open, three load-bearing. Eight hypotheses are registered and undischarged. No constraint functional, response map or environment is measured. The bounds of Sections 5 and 8 describe a posited family of margins until Target 10.3 is discharged, and every quantitative statement of Section 8 rests on H_{one} , which is tested nowhere.

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 Maximin and the attainment of margins

The step margin of Definition 4.4 is a maximin over a compact configuration space, and Proposition 4.5 is the elementary case of the maximum theorem: a continuous function on a product with one compact factor has continuous partial maximum. The general statement is [Ber63, Ch. VI]; the proof given here is direct and does not invoke it, the correspondence being constant.

C.2 Max–min expressions and piecewise linearity

The reachability functional is a maximum of minima of margins. Over an ordered field such expressions are the lattice polynomials; over the reals with max and min as operations they are the terms of the min-plus algebra, for which the reference is [BCOQ92]. Under H_{aff} the resulting functions are exactly the continuous piecewise affine functions (Prop. 5.11); the representation of such functions as max–min combinations is classical and is treated at [Ovc02].

Only the sign structure is used. Lemma 5.2 and Theorem 5.4 require nothing of the algebra beyond the fact that a minimum of functions of constant sign has constant sign, and no result of this paper depends on a representation theorem.

C.3 Arrangements and the counting of chambers

Theorem 5.12 bounds the number of regions of an arrangement of n hyperplanes in $\mathbf{R}^d$ by $\sum_{k \leq d} \binom{n}{k}$, with equality in general position. The formula is due to Schläfli and is standard; the modern treatment through the characteristic polynomial is [Zas75], and the combinatorial setting is [Sta12, Ch. 3]. **Convexity of Θ is not decorative:** for non-convex Θ a region may meet it in several components and the bound fails (Sch. 5.13).

Corollary 8.9 inverts the bound. That inversion is elementary and is stated here only because it is the paper’s one quantitative conclusion: a family of m distinct outputs requires an arrangement large enough to separate them.

C.4 Convexity and separation

[Sch26i, Prop. 7.9] is the separating-hyperplane theorem applied: a point interior to the convex hull of a finite set is separated from its members by no affine functional. The reference is [Roc70, §11]. Farkas’s lemma [Far02] is the corresponding statement for systems of inequalities and is what makes an infeasibility certificate finite; the linear-programming treatment is [Schr86].

Two uses are separated. Where this paper asserts infeasibility it exhibits the certificate by hand — a pair of conditions whose conjunction is contradictory, as at [Sch26i, Cor. 7.7] — and no solver is invoked in any proof below.

C.5 Partial orders

Definition 5.26 orders rank vectors componentwise, and Proposition 5.27, Theorem 5.28 and Proposition 5.29 are statements about chains and antichains in a finite product of three-element chains. The vocabulary is [Bir67, Ch. I]; the relevant classical theorem is Dilworth’s [Dil50], though the orders here are small enough that every chain and every incomparable pair is found by enumeration and no theorem is invoked.

C.6 Graph rewriting and the reachability category

The chemical layer — typed molecular graphs with persistent atom identities, local rewrite rules, and the category whose morphisms are finite composable sequences of admissible transformations — is [Sch26m, §§3–6] and is imported entire. The general theory of double-pushout graph rewriting is [EEPT06]; this paper uses none of it directly, working only with the well-formed paths of [Sch26m, Def. 4.21] and their supports.

C.7 The external data

One body of external data is used. The translation tables are [NCBI24], read as published, and they enter Sections 4.6, 5.5, 6.3 and 8.2 and the whole of Appendix A. Sections 4.1–4.5, 5.1–5.4, 7 and 9 use none of them.

Notably, and unlike Part I, **no residue volume enters any proof:** [Zam72] is cited in Part I as load-bearing and is not used here, the codon entering the present theory through the geometry of the cage rather than through a property of its block (Prop. 4.21).

The molecular architecture is claimed in [Sch25a] and [Sch25b] and enters through H_{teth} , inherited unchanged from [Sch26k].

C.8 What is drawn from the Chrysene Formalism

Axioms A1–A12 and the status vocabulary are [Sch26c]. The marker, vessel, structural group and frame are [Sch26d]; the frame classes [Sch26e]; transversality [Sch26f]; capacity and parity [Sch26g]. The seed map, propagation and the third-position refinement are [Sch26h]. The word space, the residual frame group and the documentary arrow are [Sch26k]. **The cage-constrained reachability theory is [Sch26m], and this paper is that theory with one argument added to its constraint functionals.** The three-valued

refinement and the insufficiency of block data are [Sch26i], which is Part I. The review architecture and the non-implication conventions are [Sch26b].

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