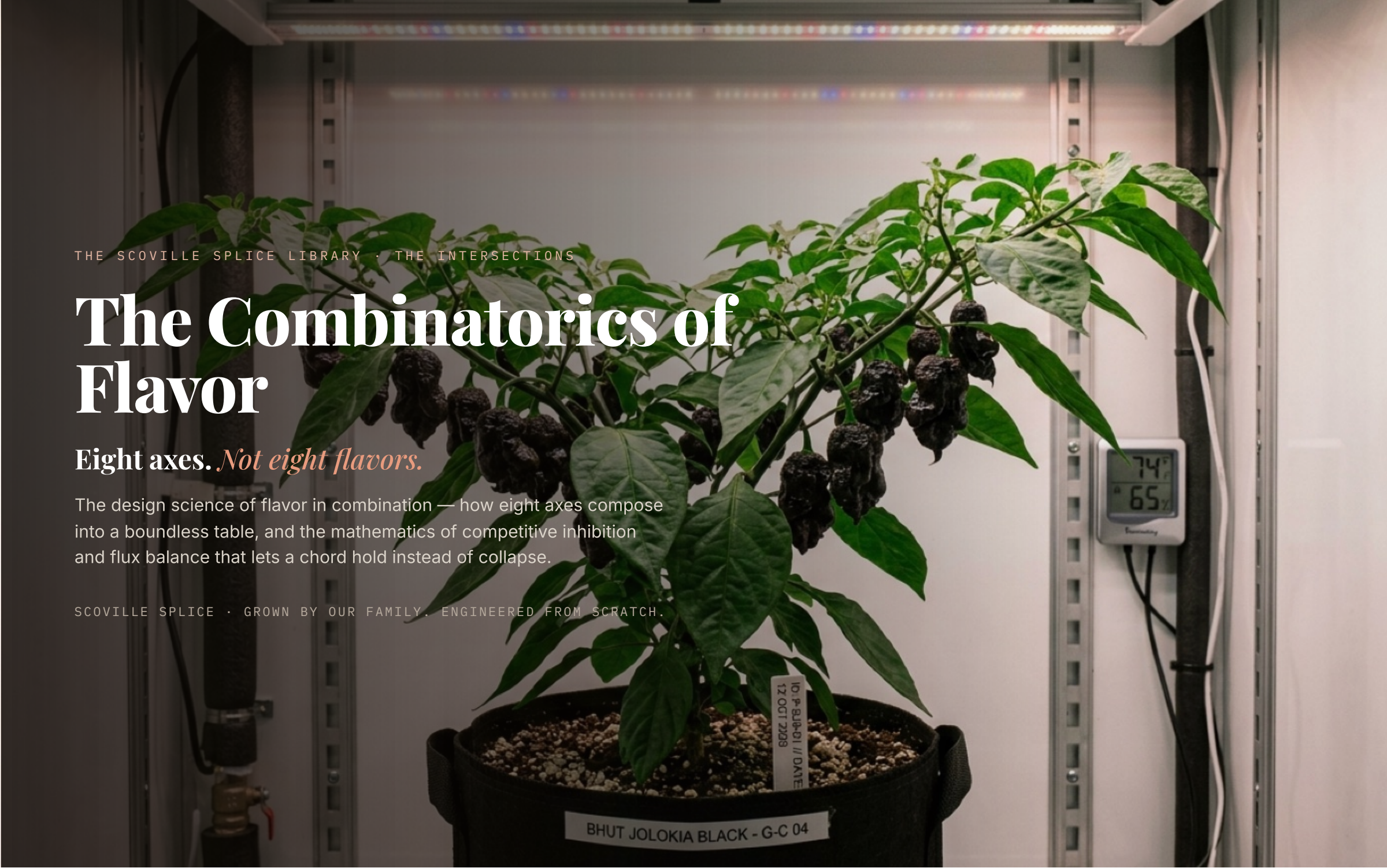


THE SCOVILLE SPLICE LIBRARY · THE INTERSECTIONS

The Combinatorics of Flavor

Eight axes. *Not eight flavors.*

The design science of flavor in combination — how eight axes compose into a boundless table, and the mathematics of competitive inhibition and flux balance that lets a chord hold instead of collapse.

SCOVILLE SPLICE · GROWN BY OUR FAMILY. ENGINEERED FROM SCRATCH.

Contents

01 Opening essay · The space between the axes

02 Chapter 1 · The arithmetic of the table — eight axes, a boundless menu.

03 Chapter 2 · The flavor vector — a taste is a point in eight dimensions.

04 Chapter 3 · Why two tastes are not their sum — composition, not addition.

05 Chapter 4 · Three kinds of competition — name the layer, reach for the tool.

06 Chapter 5 · The receptor can't listen twice — competitive inhibition, exactly.

07 Chapter 6 · The mask — perception, suppression, and the subtraction trick.

08 Chapter 7 · One pathway, many ends — the shared carbon trunk.

09 Chapter 8 · The cofactor bottlenecks — what every branch spends besides carbon.

10 Chapter 9 · Flux balance — the model that holds the ratio.

11 Chapter 10 · The stability–efficacy frontier — ranking what the fold can bear.

12 Chapter 11 · The design loop, composed — propose, build, taste, and the honest CV.

13 Chapter 12 · Two axes at once — the dual-axis library.

14 Chapter 13 · Swicy — heat laddered into sweetness.

15 Chapter 14 · Savory depth — umami, multiplied by kokumi.

16 Chapter 15 · Bitter-sweet — subtraction and lift together.

17 Chapter 16 · Cool-burn — the intersection inside one receptor pair.

18 Chapter 17 · Three axes at once — the triple-axis library.

19 Chapter 18 · The full chord — eight budgets, one fruit.

20 Chapter 19 · Reading a composed scorecard — the shape of a blend.

21 Chapter 20 · The combinatorial frontier — what we have not yet built, and the line we hold.

22 Chapter 21 · A closing note · the composition we don't yet score — flavor, and the body that reads it.

Opening essay · The space between the axes

Eight axes. When the Iyengar Flavor Index was new, that number felt like the whole map. Heat through TRPV1, the trigeminal fire channel. Sweetness through the clasped TAS1R2·TAS1R3 pair. Umami through mGluR1 and the TAS1R1·TAS1R3 clamp. The quiet subtraction of bitterness at TAS2R38. Kokumi at the calcium-sensing receptor, a taste with no taste of its own. Cool-burn at TRPM8, which reads cold and answers to menthol. Pungency through TRPA1, the sharp channel of mustard and wasabi. And the dry grip of astringency, which is not a taste at all but a touch — tannins precipitating the proline-rich proteins that keep saliva slick. Eight pathways through which a plant actually speaks to the body, each reduced to a single honest number by the same plain line:

$$\mathbf{IFI(c) = 1{,}000 \times EC_{50}(reference) \div EC_{50}(candidate)}$$

EC_{50} is the concentration at which a stimulus drives its receptor to half of full response — loudness, not amount. Invert it against a fixed reference, scale by a thousand, and a tomato, a chili, and a cup of tea can be read against one another on one page. We could stand in the greenhouse at dawn and read a plant the way you read coordinates. Each axis carries its own reference constant — a stated convention, the way Scoville's scale is defined by a dilution threshold, not a measured literature value — so IFI scores on different axes are calibrated against different reference points and cannot be directly compared across axes as if they shared one scale.

But no plant our family has ever loved tastes like one axis. A tomato split open at the table is umami and sweetness and a faint astringent bite from the skin — all at once, and in a particular proportion, and it is the proportion, not any single number, that makes you stop and close your eyes. Flavor is a chord, not a note. Eight axes do not give you eight flavors; they give you the enormous space *between* them, and that space is where nearly everything worth eating actually lives.



The founders walking the research greenhouse at dawn — where the question that became this book was first asked: not how loud is one axis, but how do eight of them stand together.

Count that space honestly and its size is the first surprise. Forget magnitude for a moment and ask only which of the eight axes a flavor expresses — is it heat, or heat *and* sweetness, or heat *and* sweetness *and* kokumi? That is a choice of subsets of eight things, and there are $2^8 - 1 =$ **255** of them: 255 distinct axis-signatures before a single score is set. Now let the scores back in. Each axis is not on-or-off but a continuous reading from zero to the Index's per-axis ceiling of 5,000, and the boundless part arrives: a flavor becomes a point in an eight-dimensional space, and between any two points there is always another. Our realized libraries are deliberate samples of that continuum — **8,400** constructs in the dual-axis library alone, **2,800** more in the triple, a chosen set of coordinates drawn from the ~19,000 across the whole platform. The matrix we publish — 42 host organisms down one side, 8 axes across the top, **336** organism-by-axis cells — is only the coarsest grid laid over a continuum that does not end.

You cannot, though, simply add two flavors together, and this is the hard, beautiful fact the rest of the book is about. Receptors compete for the same attention; some of them literally share a protein subunit, so that turning one up turns another down. Metabolic pathways draw on the same shared trunk of carbon, the same pool of the cofactor SAM, the same reducing power, so that asking a plant for more of one axis can quietly leave it less of another. Push heat up and sweetness can collapse. Chase umami and the kokumi you wanted underneath it can go flat. Composition is not addition — it is a system of constraints — and designing in combination means *solving* that system: competitive inhibition, at the receptor and in the plant's own chemistry, and flux balance, the model that finds the proportions that will actually hold in a living fruit.

There is one gift hidden inside all that constraint, and it is worth naming on the first page because the whole book bends toward it. Not every pair fights. A few multiply. Kokumi, working the calcium-sensing receptor, has no flavor to contribute — what it contributes is *gain*, a hand on the volume knob of the tastes around it, so that umami laid under kokumi reads louder than either could alone. The space between the axes is not uniformly hostile. It has valleys where axes suppress one another and ridges where they amplify, and the map of those valleys and ridges — the interaction matrix — is the single most useful object a flavor designer can hold.

This is also why a platform, and not a breeding program, is the right tool. You cannot taste your way across an eight-dimensional space one summer at a time; a breeder who wants a specific chord has to stumble onto it and then hope it is stable. We name a coordinate and go straight to it — compute the allocation, rank the edits for the ones the fold can bear, write them in, and set the result on a table to see whether the model told the truth. The computing was one pair of hands at a keyboard, late, working a single thread until the numbers resolved. The table that judged the result was never one person's.

We did not learn to compose flavor to prove that it could be done. We learned it because the meals we most want to set in front of the people we love are never single notes. They are balanced, whole,

many things at once — the way a plant grown toward its fullest is many things at once, flavor and nourishment in the same ripeness. This book is the arithmetic underneath that table.



PART I OF V

The Count

the size of the space · the flavor vector · why two tastes are not their sum

Chapter 1 · The arithmetic of the table — *eight axes, a boundless menu.*

COMBINATORICS · IFI-M · the size of the design space

Start with the smallest version of the question, and the number is already large. Set magnitude aside and ask only which of the eight axes a flavor lights — not how brightly, only which. That is a choice of a subset from a set of eight, and basic counting gives the total at once: each axis is independently in or out, two possibilities apiece, $2^8 = 256$ subsets, minus the empty one that is no flavor at all. **255 distinct axis-signatures.** Before a single EC_{50} is measured, before any score is chosen, the pure yes-or-no combinatorics of eight channels already names 255 different kinds of thing a plant could be.

They are not evenly distributed, and the distribution is the first thing a designer should internalize, because it tells you where the library's effort has to go. Break the 255 down by how many axes are lit, and the counts are the eighth row of Pascal's triangle:

AXES LIT	NAME	COUNT	FORMULA
1	monad (single note)	8	`C(8,1)`
2	dyad (pair)	28	`C(8,2)`
3	triad (triple)	56	`C(8,3)`
4	tetrad	70	`C(8,4)`
5	pentad	56	`C(8,5)`
6	hexad	28	`C(8,6)`
7	heptad	8	`C(8,7)`
8	the full chord	1	`C(8,8)`

Add the column and it checks: 8 + 28 + 56 + 70 + 56 + 28 + 8 + 1 = 255. The shape is a bell. There are only eight ways to be a single pure note and only one way to be everything at once, but there are seventy ways to light exactly four axes — the fat middle of the distribution, the register where most genuinely complex food actually lives. A great mole, a long-fermented sauce, a fine aged wine: none of them is a single loud axis and none is the full chord. They are tetrads and pentads, four or five things held in proportion, which is precisely the part of the space that is hardest to reach by tasting and easiest to reach by design.



The research plot — every plant in it a coordinate someone chose to actually grow, out of a space with no edge. The library is a deliberate sampling of a continuum.

Now let the scores back in, and the countable becomes continuous. Each of the eight axes is not a switch but a dial, a reading that runs from zero to the Index's per-axis normalization maximum of 5,000. A flavor is therefore not a subset but a *point* — an ordered list of eight numbers, a coordinate in an eight-dimensional cube 5,000 units on a side. Between any two such points there is always a third, and the menu stops being a list and becomes a volume. This is why the library can keep minting forever without ever repeating itself: there is no last flavor, only the next coordinate no one has named yet.

What we actually build is a chosen sampling of that volume, and the counts are deliberate rather than incidental. The **dual-axis library** holds 8,400 constructs spread across the 28 possible pairs. The **triple-axis library** holds 2,800 across the 56 possible triples. Divide and a pattern falls out that the rest of this book will keep returning to:

> Dual: 8,400 constructs ÷ 28 pairs = **300 per pair.** Triple: 2,800 constructs ÷ 56 triples = **50 per triple.**

The sampling density collapses by a factor of six as you add the third axis — not because triples matter less, but because each one is harder to build, harder to keep stable, and harder to hold in proportion, so each realized triple represents far more design effort per construct than a dual does. We have densely furnished the room of pairs and sparsely furnished the room of triples, and at the far corner of the whole space, where all eight axes light at once, we have placed exactly one object: a single cultivar, **Phoenix**, the only eight-dimensional point the platform has ever grown. The combinatorics is not decoration. It is a map of where the work gets expensive.

It is worth being precise about what the 336-cell matrix is and is not, because it is the figure people quote and the easiest to misread. Forty-two host organisms times eight axes is 336 organism-by-axis intersections — a tidy grid, and a real one; every cell is a question we can ask of a plant ("what is this organism's umami ceiling?"). But the grid is not the space. The grid asks only *which organism expresses which single axis.* The space asks *in what proportion all eight stand together in one fruit*, and that question has no finite grid, only the continuum and our sampling of it. The matrix is the index's table of contents. The combinatorics is the book.

Put a number on just how continuous the space is, because "effectively boundless" should not be a hand-wave in a book about counting. Suppose we refuse to split hairs finer than the Index can reliably resolve and quantize each axis into steps of fifty points across its 0-to-5,000 range — a hundred distinguishable levels per axis, which is already coarser than our assays read. Eight axes at a hundred levels each is 100^8 = **10^{16} distinguishable flavor points** — ten quadrillion, from a quantization deliberately made crude. The realized libraries, ~19,000 constructs in all, sample that space at a density of roughly one point in a trillion. We are not running out of flavors. We have barely begun to occupy the space, and every book in this library that "names another cell" is choosing one more of those quadrillion points to actually grow.

The combinatorics is also what lets a single library throw off sixty-four books without repeating itself, and the grammar is worth stating because it is the engine of the whole program. A book can be a **row** of the matrix — one organism across all its axes, the organism monographs. It can be a **column** — one axis across all its organisms, the eight axis volumes. It can be a single **cell** — one organism-axis intersection explored to its floor. Or it can be a **region** — a diet, a cuisine, a tier, a band of the space carved out by something other than the grid lines. This book is a region of a different kind: not a row or a column but the *relationships between* the columns, the off-diagonal structure the grid cannot show. The matrix has 336 cells; the space between them, where composition lives, is the rest of the library's subject and the whole of this volume's.

So the design problem, stated plainly, is a problem of *coordinates and constraints.* A brief is a point you want to reach — four numbers, or eight, a target silhouette on the radar. The constraints are everything that stands between you and that point: receptors that will not report two neighbors independently, a plant that cannot spend the same carbon twice, enzymes that will not fold if you push them too hard. The next two chapters give the coordinate its formal shape and then name the force that bends every straight line between two points: the fact, mechanical and unavoidable, that flavors do not add.

Chapter 2 · The flavor vector — *a taste is a point in eight dimensions.*

MATHEMATICS · $v \in \mathbb{R}^8$ · the geometry of a scorecard

If a flavor is a point, then it has an address, and writing the address down the same way every time is the small formal act that makes everything downstream possible. We write a flavor as a **vector** — an ordered list of its eight axis scores, always in the same order, always on the same 0-to-5,000 scale:

```
v = (H, S, U, B, K, C, P, A)
```

Heat, Sweetness, Umami, Zero-Bitter, Kokumi, Cool-burn, Pungency, Astringency. The order is a convention, nothing more, but conventions are how a library stays legible across sixty-four books: every scorecard in this series is this vector, drawn as a radar instead of printed as a row. The radar's eight spokes are the eight components; the shape you see is the vector made visible. Learning to read combination is, in the most literal sense, learning to read a point in $\mathbb{R}^8$ by its shadow on an octagon.

Take the flagship as the worked example, because we will return to it a dozen times. **Phoenix** — SS-0096 — is the vector

```
v = (4200, 1100, 1800, 2200, 1900, 800, 252, 1400).
```



Phoenix (SS-0096) in cross-section — a single eight-dimensional point made flesh. Every pair and triple in this book is a shadow this fruit casts onto a lower-dimensional plane.

Writing a flavor as a vector buys three things immediately, and each one earns its keep in the design loop.

The first is **magnitude** — how much total flavor a thing carries, independent of its character. The Euclidean norm, the straight-line distance from the origin, is the honest measure: $\|v\| = \sqrt{(H^2 + S^2 + U^2 + \cdots + A^2)}$. For Phoenix, the sum of squares is $4200^2 + 1100^2 + 1800^2 + 2200^2 + 1900^2 + 800^2 + 252^2 + 1400^2 = 17{,}640{,}000 + 1{,}210{,}000 + 3{,}240{,}000 + 4{,}840{,}000 + 3{,}610{,}000 + 640{,}000 + 63{,}504 + 1{,}960{,}000 = 33{,}203{,}504$, so $\|v\| \approx 5{,}762$. A mild culinary pepper with everything but a modest heat near zero might have a norm of 1,500.

The norm is why a superhot and a sauce built from it are different objects even when they share a silhouette: one is the same unit vector scaled up. Magnitude and direction are separable, and separating them is the first thing the vector does for you.

The second is **distance** — how far apart two flavors are, which is exactly the question a formulator asks when matching a target or protecting a house profile batch to batch. The distance between two vectors is the norm of their difference, ‖u − v‖. Set the near-pure early rung of the flagship ladder, Ember, at roughly u = (1570, 150, 200, 150, 150, 0, 150, 150) — two axes meaningfully lit — against Phoenix, and the difference vector is dominated by the seven axes Phoenix grew in that Ember never had. The distance is large not because the heat moved (1,570 to 4,200 is a real climb, but a single axis) but because seven other coordinates went from near-zero to substantial. The ladder from a monad to the full chord is a journey across the space, not up a single line, and the distance metric is what makes "across" quantitative.

Distance and magnitude together answer "how much" and "how far," but there is a third question the vector answers that neither of them touches — *character*, the shape of a flavor independent of its loudness. Two flavors can point the same direction in $\mathbb{R}^8$ at different magnitudes: a concentrated designed cultivar and a dilute sauce built from it are, ideally, the *same flavor at two volumes* — the same proportions, the same silhouette, scaled. The measure that captures sameness-of-character is the **cosine similarity**, the cosine of the angle between two vectors:

$$\cos\theta = (u \cdot v) \div (\|u\| \cdot \|v\|).$$

It runs from 1 (identical direction — same character, any volume) down toward 0 (orthogonal — unrelated flavors). This is the metric a sauce-maker actually wants when scaling a cultivar into a formula: not "is the delivered product as *loud* as the cultivar" (it should not be — it is diluted) but "does it hold the same *proportions*," cos θ near 1 even as the magnitude falls. Distance would flag the dilution as a mismatch; cosine similarity sees through the volume to the shape. A composed flavor has a character you can hold constant while you turn it up or down, and separating character from magnitude — direction from norm — is the geometry that lets a single cultivar seed a whole range of products that all taste *of the same thing* at different strengths.

The third is **projection** — the move that lets us teach composition two axes at a time. To read a dual-axis slice of a full vector, you simply ignore the other six components and keep the two you care about; geometrically, you are casting the eight-dimensional point onto a two-dimensional plane and reading its shadow. This is why we can read a real dual-axis example off Phoenix without building a separate cultivar for every pair: project the full vector onto the heat-sweet plane and you have a genuine swicy coordinate, (H, S) = (4200, 1100); project it onto the umami-kokumi plane and you have a genuine savory-depth coordinate, (U, K) = (1800, 1900). The flagship contains all 28 of its pairwise projections at once. Much of Part IV is nothing but this projection, done deliberately, one plane at a time.

A caution lives inside the geometry, and it is the whole reason the book is not finished at this chapter. The vector tells you where a flavor *sits* on the Index — the measured loudness of each axis, read against its own receptor. It does not tell you how those eight loudnesses will *interact* when they arrive on a tongue together. Two vectors with identical coordinates could, in principle, taste different if the physical mix that produces them loaded one axis in a way that masks another; conversely, the perceived result of a vector is not the plain sum of its components, because the components interfere. The vector is the specification. The interaction is the physics. A designer who confuses the map for the territory — who believes that because he has specified eight numbers he has specified a taste — will build a scorecard that reads beautifully and a fruit that eats like mud. The next chapter is that warning, made exact.

But do not lose the gift under the caution. The reason to insist on the vector, on the fixed order and the shared ceiling and the honest norm, is that it turns an art into a geometry you can compute in. A breeder's "a little hotter, a touch sweeter, more backbone" becomes a displacement, a direction and a distance in $\mathbb{R}^8$, and a direction and a distance are things a flux model can be asked to travel. The poetry of the table does not survive the translation into coordinates — nothing does — but the *reachability* of the table does. You cannot compute your way to why a meal moved someone. You can compute your way to the point on the Index where that meal lives, and grow it.

Chapter 3 · Why two tastes are not their sum — *composition, not addition.*

MODEL · the interaction matrix · linear hope, quadratic reality

The intuition that fails first is the kitchen intuition: that to build a hot-sweet pepper you take a hot one and a sweet one and meet in the middle. It is a reasonable belief and it is wrong, and watching exactly *how* it is wrong is the beginning of real composition. Stack a high IFI-H against a high IFI-S naïvely — two loud axes, specified side by side — and the two do not average into a balanced middle. They interfere. The heat reads first and loudest, the brain spends its attention there, and the sweetness arrives muffled, present on the scorecard and absent on the tongue. The sum of two intended flavors is very often a third, unintended one, and the third one is usually a muddle.



Research trays of a candidate line — where a composition that looks balanced on paper is set on the tongue to find out whether the axes interfere. The page is a hypothesis; the mouth is the experiment.

Here is the failure stated as arithmetic, because stating it as arithmetic is what lets us fix it. The *linear hope* is that the perceived vector equals the specified vector — that perception **p** is just **v**, each axis reporting its own loudness and minding its own business:

> linear hope: $\mathbf{p}_i = \mathbf{v}_i$

The *quadratic reality* is that each perceived axis is its own loudness plus a sum of interaction terms, one for every other axis it shares a mouth with:

```
reality: pᵢ = vᵢ + Σⱼ Wᵢⱼ · g(vᵢ, vⱼ)
```

Read it slowly, because this one line is the thesis of the book. **p** is what you perceive; **v** is what you specified and the Index measured. **W** is an eight-by-eight **interaction matrix** — a table with a number for every ordered pair of axes, the coefficient that says how much axis *j* bends axis *i*. And $g(v_i, v_j)$ is the shape of the bending, some function that is small when either axis is quiet and grows when both are loud — which is why the trouble is always worst exactly where you most wanted both axes present. The interaction term is a *product*; products are zero when either factor is zero and large when both are large. Interference is not a flaw in strong flavors. It is a property of strong flavors standing together.

Everything turns on the signs in **W**. A negative W_{ij} is **suppression** — axis *j* quiets axis *i*, the way a loud bitter buries a sweet, the way heat pulls focus from a sugar. A positive W_{ij} is **synergy** — axis *j* amplifies axis *i*, the way kokumi lengthens umami, the way removing bitterness uncovers the sweetness that was always there. A near-zero W_{ij} is **orthogonality** — two axes that genuinely mind their own business, rare but real, and a gift when you find one because it means you can set both without either paying for the other. The matrix is not symmetric in general: heat suppresses the *perception* of sweetness more than sweetness suppresses the perception of heat, so W(S←H) and W(H←S) differ, and the order you notice things in is written into that asymmetry.

We can sketch the matrix's character — not every coefficient, which fills a later chapter, but the neighborhoods, so the shape is in hand before the mechanism is:

PAIR	SIGN	WHAT HAPPENS	WHERE IT HAPPENS
Umami × Kokumi	+ +	kokumi multiplies savory body	receptor (CaSR gain)
Zero-Bitter × Sweet	+	removing bitter uncovers sweet	perception (unmasking)
Heat × Umami	+	savor makes heat read as *food*	perception (cross-modal)
Heat × Pungency	+	two sharp channels summate	receptor (co-localized)
Sweet × Umami	−	shared receptor subunit competes	receptor (shared TAS1R3)
Bitter × Sweet (raw)	−	each masks the other	perception (mixture suppression)
Heat × Cool	∓	fire and ice, held in contradiction	receptor (TRPV1 ⇄ TRPM8)
Heat × Astringency	0	near-independent	different modalities

The presence of both signs in that table is the entire reason composition is a craft and not a formula. If every interaction were suppression, design would be a grim exercise in damage control — pick your one axis, accept that everything else you add subtracts

from it. If every interaction were synergy, design would be trivial — pile it all on, watch it all grow. Reality is mixed, and mixed is interesting: some pairs you *fight* (push against the suppression with ratio and sequencing and subtraction), and some pairs you *ride* (let the synergy do your work, spend less to get more). The skill is knowing which is which before you build, and the interaction matrix is how we write that knowledge down so it does not have to be rediscovered by every tasting.

There is a deeper structure under **W**, and it is the structure that organizes Parts II and III. The interactions do not all live in the same place. Some are set at the **receptor** — two molecules at one site, or two channels on one nerve, or two dimers competing for one shared protein — and those you solve with receptor pharmacology, with which agonist at what EC_{50} arriving in what order. Some are set in the **metabolism**, upstream of taste entirely, where two axes are built from the same carbon and the same cofactors and cannot both be maximized from a fixed supply — and those you solve with flux balance, with a budget allocated on purpose. And some are set in **perception**, in the brain that integrates eight channels into one experience and lets them mask and color one another — and those you solve partly by subtraction, turning a masking signal down so the masked one surfaces with nothing added. Three layers, three toolkits. Naming the layer an interaction lives in is the first move of every hard composition, and it is where Part II begins.

Composition, then, is the discipline of designing *with* the matrix instead of against it. It means specifying not two scores but a relationship — a ratio, a sequence, a figure-ground of which axis sits under which — and then solving for the construct that holds the relationship once the receptors and the chemistry and the brain have all had their say. A dual-axis cultivar that lands tastes deliberate rather than murky for exactly this reason: it was never a stack of two loud things hoping to coexist. It was a solution to $\mathbf{p = v + WG(v)}$, run backward — a **v** chosen so that the **p** it produces is the one we meant.



PART II OF V

The Collisions

three layers · the shared receptor · the mask · the shared trunk · the shared cofactor

Chapter 4 · Three kinds of competition — *name the layer, reach for the tool.*

MECHANISM · receptor · metabolism · perception

When two axes fight, they fight in one of three places, and naming the place is the first diagnostic move of every composition, because the place decides the tool. Build long enough and you learn to hear which layer a collision lives in the way a mechanic hears which bearing is failing — and the whole of Part II is teaching that ear.

The first place is the **receptor** itself, the molecular front door where a flavor molecule meets the protein that will report it. Competition here is physical and immediate: two molecules reaching for one binding site and each slowing the other's access; two channels wired to the same nerve so that a strong signal on one raises the threshold of its neighbor; or — the sharpest case we know — two different taste receptors built from one *shared* protein subunit, so that assembling more of one receptor leaves literally fewer parts to assemble the other. Receptor competition you resolve with pharmacology: which agonist, at what EC_{50}, how much of it, arriving in what order. It is the layer where the Index's own currency, the EC_{50}, does the work, because the whole fight is about EC_{50}s shifting in each other's company.

The second place is the **metabolism**, upstream of taste entirely, inside the plant, before a single molecule has reached a tongue. Flavor molecules are not free; they are built, enzyme by enzyme, from a shared pool of carbon and a shared set of cofactors that every branch of the pathway draws on at once. Push flux toward capsaicin and that carbon is no longer available to the branch that was building a sweetening glycoside; spend the cell's SAM on one methylation and another methylation goes hungry. Metabolic competition you resolve not with pharmacology but with *accounting* — flux-balance analysis, a budget written as a linear program and allocated on purpose. This is the layer a breeder cannot see and cannot reach, because it is not about the fruit's flavor at all; it is about the plant's chemistry, two steps before the flavor exists.

The third place is **perception**, downstream of both, in the brain that takes eight separate channels and integrates them into the single unified experience we call *taste.* The channels are not summed cleanly; they mask and color one another. Bitterness suppresses the sweetness sitting right beside it. A loud trigeminal burn pulls attention off a quiet savory floor. Cooling re-colors the *meaning* of a sweetness without changing its receptor at all. Perceptual competition is the subtlest because it lives in no molecule and no gene — it is a property of the integrator, not the ingredients — and

you resolve it partly by subtraction (turn the masking signal down and the masked one surfaces on its own, with nothing added) and partly by *sequencing* (arrange which axis arrives first and which lingers, since the brain weighs onset and finish differently).

Nearly every real composition is some mixture of the three, and the mixtures are where the craft lives. Swicy — heat against sweetness — is mostly a perceptual collision (the burn stealing the sugar's attention) laid over a mild metabolic one (both drawing, distantly, on the same carbon). Savory depth — umami under kokumi — is a receptor collaboration (CaSR potentiating the umami receptor) with a metabolic cost (both the glutamate and the γ-glutamyl peptides have to be grown). Bitter-sweet balance is a perceptual gift (unmasking) reached through a metabolic edit (attenuating the bitter compound at its source). The three-layer model is not a taxonomy for its own sake. It is a troubleshooting tree: when a composition reads wrong on the tongue, you ask *which layer*, and the answer tells you whether to reach for the receptor assay, the flux model, or the subtraction.

The diagnostic works because the three layers leave *different fingerprints*, and the two instruments we read a candidate with — the cell-based assay that returns the measured vector, and the trained human panel that returns the perceived one — disagree in layer-specific ways. When the assay and the panel *agree* that an axis is low, the fault is upstream: either the receptor competed the molecule away (and the assay will show its EC_{50} shifted in company) or the plant never built it (and the flux model will show a branch pinned at a constraint). When the assay reads an axis correctly but the panel does *not* perceive it, the fault is in the integrator — a masking or a sequencing, the perceptual layer — because the molecules are present and the receptor reports them and only the brain is discounting them. The gap between the two instruments is the diagnostic; the layer is read off the gap.

Work the tree as a table, because this is the page a designer actually keeps at the bench:

SYMPTOM AT THE TABLE	LIKELY LAYER	HOW WE CONFIRM IT	THE TOOL TO REACH FOR
An axis you specified is simply missing	receptor competition	assay shows its EC_{50} shifted upward in company	re-ratio; change agonist or order of arrival
Two axes present, but the dish reads *muddy*, neither clean	perception (masking)	panel splits from assay; the assay vector is correct	subtract the mask; stage the release
An axis caps below what its single-axis line promised	metabolism (shared carbon)	flux model shows a binding precursor constraint	widen the supply; reallocate the branch
The whole fruit is weak, and varies batch to batch	metabolism (cofactor / fold)	flux-variability wide; ΔΔG margin thin	re-select edits on the stability frontier

Run that table on a failing swicy — heat loud, sweetness specified but absent, the dish reading hot-and-thin. The assay returns the sweetness at its specified value; the panel does not perceive it. Assay-correct, panel-blind: the fingerprint of the perceptual layer, a masking, the burn stealing the sugar's attention. So you do not reach for the flux model and you do not raise the sweetener — both would

be the wrong tool for the wrong layer. You stage the release so the sweetness arrives a beat before the heat, and the axis that was always present surfaces. Name the layer, reach for the tool: the three chapters that follow take the layers one at a time, in the order a diagnosis most often runs them — the receptor, then the mask, then the budget beneath both.

Chapter 5 · The receptor can't listen twice — *competitive inhibition, exactly.*

MECHANISM · the receptor layer · the shared TAS1R3 subunit

A receptor is a lock, and a flavor molecule is a key, and the honest measure of a key is its EC_{50} — the concentration at which it drives the lock to half of full response. The whole Index rests on it: a low EC_{50} is a loud molecule, and inverted against a reference it becomes a high IFI. In isolation this is clean. In a real mouth, keys arrive together, and the arithmetic of the lock changes in a way that has a textbook name.

Competitive inhibition is the first and cleanest case. Two molecules fit the same site; while one is bound, the other cannot be; each therefore slows the other's access, and the effective EC_{50} of each shifts *upward* — you need more of it to reach half-response — in exact proportion to how much competitor is present. The pharmacology is a century old and admits a single clean equation. If a competitor sits at concentration [I] and binds its site with dissociation constant K_i, the agonist's effective half-activation becomes

$$EC_{50}' = EC_{50} \times (1 + [I] \div K_i).$$

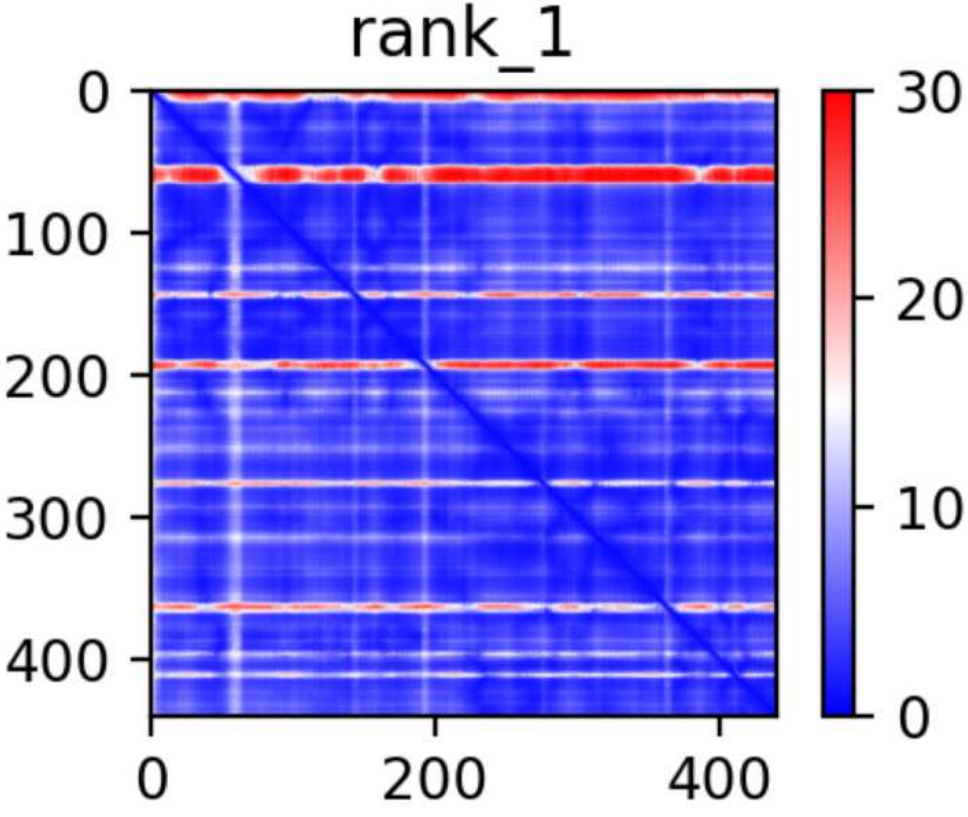
Push that through the Index and the consequence for composition is immediate and a little humbling. Because IFI is 1,000 × EC_{50}(ref) ÷ EC_{50}, and the competitor has multiplied the denominator by (1 + [I]/K_i), the perceived IFI in company is the isolated IFI divided by the same factor:

$$IFI' = IFI \div (1 + [I] \div K_i).$$

Now the numbers bite. Set a competitor at its own K_i, so [I]/K_i = 1: the factor is 2, and the axis you measured at IFI 2,000 alone delivers **1,000** in company — half, gone, not because the molecule changed but because it is no longer listening to that molecule alone. Raise the competitor to three times its K_i and the factor is 4; your 2,000 becomes **500.** This is why the platform scores composites *as composites*, measured in combination against the receptor, and never trusts that two axes verified alone will add. The isolated IFI is true. The context moves it, and competitive inhibition says exactly how far.

The most beautiful instance of receptor competition in all of taste is not two molecules at one site but two *receptors* built from one shared part, and it sits right in the middle of the eight axes. Sweetness is read by a receptor assembled from two subunits,

TAS1R2 and TAS1R3. Umami, in its taste-bud form, is read by a receptor assembled from **TAS1R1 and TAS1R3.** Look at what they share: **TAS1R3 is a subunit of both.** The sweet receptor and the umami receptor are not independent locks — they are two locks that must be built from a common pile of the same hinge, and the pile is finite.



The AlphaFold predicted-aligned-error map for one of our modeled acyltransferases — the kind of structural confidence read we use to understand where a protein's domains move independently and where they are coupled. Shared-subunit receptors pose the same coupling question at the level of taste itself.

Write the sharing as a conservation law, because that is what it is and the law is the design constraint. Let the total TAS1R3 available on a taste cell be a fixed pool, T. It is partitioned three ways — into sweet dimers, into umami dimers, and into unpaired monomer:

> **T = [TAS1R2·TAS1R3] + [TAS1R1·TAS1R3] + [TAS1R3]_free.**

A fixed total, split among competing demands, held in balance — the reader who has met the next part of the book will recognize the shape before its name, because it is the receptor-level twin of the mass-balance law that governs metabolism. Now the composition problem on the sweet-umami plane becomes visible as more than central masking. When a strong umami ligand stabilizes the TAS1R1·TAS1R3 dimer, it pulls TAS1R3 out of the shared pool, leaving fewer hinges to build sweet dimers from; the sweet receptor's *available* population falls, and a fixed dose of sweetener reads quieter. Sweet and umami compete not only in the brain but in the sheer inventory of the protein that reads them both — which is the mechanistic reason S×U is one of the genuinely sub-additive pairs, and why a tomato's sweetness and its savor have to be *co-designed*, grown in a deliberate ratio, rather than each maximized and hoped to coexist.

The thermal axes give the other great receptor collision, and it is a collision of *channels wired to one nerve* rather than dimers sharing a part. **TRPV1** reads heat and answers to capsaicin; **TRPM8** reads cold and answers to menthol; they are the two ends of a single thermal story, often co-expressed on the same trigeminal endings. A plant

carrying both is not blending two flavors — it is holding a controlled contradiction, a fruit that tells the nerve *hot* and *cold* at once. The percept does not cancel to nothing; it resolves into the strange, legible doubleness the tongue calls fire-and-ice, and we will build it on purpose in the cool-burn chapter. The lesson here is only that the collision is physical and local: two channels, one nerve, and a brain receiving a signal it has no single word for.

And the pungency channel, **TRPA1**, closes the receptor layer with a case of near-*collaboration.* TRPA1 answers to the sharp electrophiles — allyl isothiocyanate from mustard and wasabi, cinnamaldehyde from cinnamon, allicin from garlic — and it is frequently co-expressed with TRPV1 on the very same peptidergic neurons. Activate both and the signals summate and cross-sensitize rather than compete: heat and pungency *reinforce*, which is why a mustard-sharp heat feels larger than the sum of a plain heat and a plain sharpness. Co-localization can cut either way — toward contradiction, as with TRPV1 and TRPM8, or toward amplification, as with TRPV1 and TRPA1 — and which way it cuts is written in the wiring, not the wish. Composition begins the moment you admit the receptor can't listen twice at once, and then learn, pair by pair, whether its single ear favors one axis, splits between them, or hears them louder together.

Chapter 6 · The mask — *perception, suppression, and the subtraction trick.*

MECHANISM · the perceptual layer · mixture suppression · Zero-Bitter as a lever

Past the receptors, the eight channels converge on one integrator, and the integrator does not add. This is the perceptual layer, the one with no gene and no molecule of its own, and its governing fact is a century of psychophysics distilled to a sentence: **the perceived intensity of a taste in a mixture is almost always less than its intensity alone.** Mix two tastes and each is quieter than it was by itself. The phenomenon is called *mixture suppression*, and it is the reason a flavor is not the stack of its parts even after every receptor has reported honestly.

Begin with the single-taste law, because the mixture law is built on it. A receptor's response to a stimulus of concentration C follows a saturating curve — the Beidler form, a Langmuir isotherm wearing a taste-science name:

```
R ÷ R_max = C ÷ (C + K).
```

Response rises steeply from zero, then bends over and flattens as the sites fill; K is the concentration at half-maximum, which is EC_{50} by another name. Perceived *intensity* then scales as a power of the stimulus — Stevens' law, $\psi = k \cdot C^n$ — with an exponent n that differs by taste. The two laws together already tell you that doubling a concentration never doubles a sensation; the curves are bent, and bent curves do not add like straight lines.

Mixture suppression bends them further. When two tastes occupy the mouth together, central processing — lateral inhibition among taste channels, attention finite and drawn to the loudest — discounts each. The classic measurements are unambiguous: a sweetness and a bitterness presented together are *each* perceived as weaker than when presented alone, and the stronger the partner, the deeper the discount. Sugar hides quinine; quinine hides sugar. This is not receptor competition — sweet and bitter share no subunit — it is the integrator refusing to pass both signals at full volume.



A tea leaf in cross-section — the plant that carries bitterness and astringency and a brothy savor in one leaf, every cup of it an exercise in which signal the brain lets through and which it masks.

Here is where the masking law stops being an obstacle and becomes a *tool*, and it is one of the most elegant moves in the whole library. If bitterness suppresses sweetness, then *removing* bitterness must **release** sweetness — uncover a sweetness that was already present in the food, already on the tongue, merely held down by the bitter signal lying across it. And removing bitterness is precisely what one of our eight axes does. **IFI-B, Zero-Bitter**, is the axis of attenuation: it turns down the report of the bitter receptor TAS2R38 by twenty to sixty-five percent, not by adding anything but by quieting the warning. So Zero-Bitter is a sweetness lever that adds no sugar. Lift it and the sweetness already in a dark chocolate, a coffee, a brassica, a grape rises on its own, unmasked, because the hand that was holding it down has been lifted.

Put rough numbers on the gift, because the gift is quantitative. Suppose a food's intrinsic sweetness would read 1,400 on the Index in a clean mouth, but a co-present bitterness suppresses it by forty percent, so the eater perceives only about 840. Attenuate the bitter axis enough to cut that suppression in half — from forty percent down to twenty — and the perceived sweetness climbs toward 1,120 with *not one additional unit of sweetener added.* You have raised a flavor by subtracting its mask. This is the arithmetic under the bitter-sweet books — under reduced-bitterness coffee that tastes sweeter black, under a dark chocolate that keeps its structure and sheds its harshness — and it is the clearest proof that the perceptual layer, read correctly, gives back as much as it takes.

The phenomenon has a name in the psychophysics — **release from mixture suppression** — and sweetness is not the only axis it gives back. Bitterness masks *umami* as surely as it masks sweet, so a debittered savory reads deeper for the same reason a debittered sweet reads louder: the mask lifted, the floor surfaces. A brassica tuned down on its bitter warning tastes not only less harsh but more savory, the glutamate it always held suddenly audible. One subtraction, two axes released — which is why the Zero-Bitter lever is worth so much more than its single column suggests, and why the interaction matrix shows it running synergy with sweet *and* umami at once. There is an asymmetry worth marking, too, because it governs which direction the subtraction is worth running: the suppression is not symmetric in strength. A strong bitter buries a modest sweet far more than a modest sweet buries a strong bitter, because the louder,

more alarming signal commands more of the integrator's limited attention. Bitterness is an evolutionary alarm — the taste of the alkaloid, the warning the body keeps loud on purpose — so it masks more than it is masked, and that asymmetry is exactly why *attenuating the bitter* buys more perceived flavor than adding the sweet ever could. You turn down the loud alarm, and everything quieter in the room becomes audible at once.

Sequencing is the perceptual layer's second lever, quieter than subtraction but real. The brain weighs a taste's *onset* and its *finish* differently; an axis that arrives first stamps the experience, and an axis that lingers defines the memory of it. Capsaicin's burn builds slowly and stays; sweetness is quick and fades. So the same two scores, H and S, can be composed to read heat-forward or sweet-forward depending on which the physical matrix releases first and which it holds — a fast-dissolving sugar on the surface with the capsaicin bound in the flesh reads as sweet-then-hot; the reverse reads as hot-then-sweet. We cannot always control release in a living fruit as finely as a confectioner controls it in a panned sweet, but the principle governs how a composed cultivar is *used*, and the cookbooks downstream of this shelf lean on it constantly: the order of arrival is part of the composition, even when the vector is fixed.

The perceptual layer is the hardest of the three to measure, because it lives in a person and not in an assay, which is why every composite score in this library is finally checked against a trained human panel and not left to the cell-based reading alone. When the panel and the assay disagree, it is almost always the perceptual layer speaking — a masking or a sequencing the molecules alone did not predict — and the rule we hold is the one the whole company is built on: when the model and the tongue disagree, it is the model we correct. The mask is real. You design around it, you exploit it where it gives, and you never pretend the receptor reading was the whole truth of what a person will taste.

Chapter 7 · One pathway, many ends — *the shared carbon trunk.*

MECHANISM · the metabolic layer · PAL → C4H → 4CL → HCT → COMT

Walk upstream from the flavor to the chemistry and the third kind of competition is waiting, and it is the one no tongue ever feels directly and no receptor assay ever sees. It is set inside the plant, in the branching of a single metabolic trunk, days before the fruit is picked. Most of what we tune does not come from eight separate factories. It comes from one trunk line that runs through every vascular plant on Earth — the **phenylpropanoid pathway** — branching again and again into the molecules that become color, defense, structure, and taste.

The trunk begins where primary metabolism hands off to secondary: with the amino acid **phenylalanine**, itself the end of the shikimate pathway, the plant's great converter of photosynthetic carbon into aromatic rings. From phenylalanine the committed sequence runs:

> **PAL → C4H → 4CL → HCT → COMT**

Phenylalanine ammonia-lyase (**PAL**) strips the amino group to make cinnamic acid — the committed, rate-setting first step, the valve on the whole trunk. Cinnamate-4-hydroxylase (**C4H**) hydroxylates it to *p*-coumaric acid. 4-coumarate-CoA ligase (**4CL**) activates it as a CoA thioester, the currency the downstream branches spend. Hydroxycinnamoyl transferase (**HCT**) and caffeoyl-CoA *O*-methyltransferase and its relatives (**COMT**) carry the carbon toward the ferulate and caffeate pool. And from that pool the branches leave:

BRANCH OFF THE TRUNK	TERMINAL CHEMISTRY	AXIS IT FEEDS
Vanillylamine → capsaicinoids (pAMT, Pun1/CS)	heat molecules	**H** · Heat
Monolignols → lignin	structure (not flavor)	—
Chalcone synthase → flavonoids → proanthocyanidins	tannins	**A** · Astringency
Flavan-3-ols, procyanidins	bitter polyphenols	**B** · Zero-Bitter (what we attenuate)
Ferulate → vanillin → vanillin derivatives	vanilla, kokumi-adjacent	**K** · Kokumi
Phenylpropenes (eugenol, methyl ethers)	clove/cinnamon sharpness	**P** · Pungency

In the pepper, four terminal enzymes finish the heat specifically — **pAMT** (the aminotransferase that makes vanillylamine), **Pun1/CS** (the capsaicin synthase / acyltransferase that condenses it with the fatty-acyl chain), and the fatty-acid-side enzymes **KAS** and **BCAT** that build and brand that branched chain. But every one of those terminal steps begins by drawing on the same ferulate-and-phenylalanine pool that the tannin branch, the vanillin branch, and the phenylpropene branch draw on too.



A research tray of a developing line — where the question stops being "which flavor" and becomes "which branch gets the carbon." A shared trunk is a shared budget, and the budget is fixed before the fruit is ripe.

A shared trunk is a shared budget, and this is the metabolic echo of competitive inhibition. Direct more flux down the capsaicin branch and that carbon is no longer available to the branch that was building a tannin or a vanillin; the plant does not make more total aromatic carbon on command, it makes *different proportions* of a supply that photosynthesis and the shikimate pathway set upstream. "Just add more astringency" to a hot pepper is, at the metabolic level, a request to split a fixed pool more ways — and if the pool does not grow, the heat you already built has to shrink to pay for it. This is why a naïve stack fails in the plant as surely as it fails on the tongue: the fruit cannot spend the same carbon twice, and the branches that make two different axes are often two taps on one line.

Follow the trunk one step further upstream and the size of the budget comes into view, because the phenylalanine that starts the sequence is itself the product of a longer road — the **shikimate pathway**, the plant's great converter of primary carbon into aromatic rings. Shikimate begins with two molecules the cell draws straight from central metabolism: phosphoenolpyruvate (PEP) from glycolysis and erythrose-4-phosphate (E4P) from the pentose-phosphate pathway. Seven enzymatic steps condense them through shikimate itself to chorismate, the branch point from which phenylalanine, tyrosine, and tryptophan all leave. So the whole eight-axis flavor budget traces back, in the end, to how much PEP and E4P the plant can spare from running itself — which is to say to light, to leaf area, to the vigor of the grown plant. When the flux model says a composition needs a *wider trunk*, this is the valve it means: not the phenylpropanoid steps themselves, but the shikimate supply feeding them, and widening it is why a composed cultivar is also, quietly, a cultivar grown with its vigor protected. A starved plant has a narrow trunk and cannot afford a loud chord.

The trunk also feeds things that are not flavor at all, and this is the competition a designer forgets at their peril. The largest single draw on the phenylpropanoid pathway in most plants is **lignin** — the structural polymer that stiffens stems and vessels, built from the same monolignols that branch off the ferulate pool — and after lignin come the defense compounds the plant makes when stressed, flavonoids and phenolics marshaled against pests and ultraviolet light. These are not axes we score, but they spend from the same

account the axes draw on, and they do not politely wait their turn: a plant under stress will pour phenylpropanoid flux into defense and leave the flavor branches starved, which is one reason a composed cultivar's silhouette can drift if it is grown hard. Part of designing a stable composition is therefore agronomic as much as genetic — growing the plant unstressed enough that the trunk's output goes where the model allocated it, rather than being commandeered by a frightened plant building walls. The budget is shared not only among the flavors but between the flavors and the plant's own body, and the model that allocates it has to respect both.

The constraint has a gift folded inside it, and the gift is the entire reason the company exists. Because PAL through COMT runs in *every* vascular plant, a method proven in Capsicum is a method that transfers. The same branch-point logic that laddered heat in a pepper — identify the valve, rank the edits, reallocate the flux — can modulate a proanthocyanidin in a grape, a glucosinolate-adjacent sharpness in a brassica, a catechin in a tea. Five of the platform's seven engineering modules transfer unchanged to any organism with a sequenced genome, precisely because the trunk they act on is universal. The budget is shared across axes *within* a plant; the *grammar* for spending it is shared across all plants. What remains, in every organism and every composition, is to allocate the trunk on purpose rather than by accident — and allocation on purpose is a mathematical problem with a name, which is the subject of the chapter after next.

But first the trunk has a second scarcity under it, subtler than carbon and just as binding, because the branches do not only spend carbon. They spend *cofactors* — the small shared currencies that activate and decorate every intermediate — and the cofactors are competed for across pathways that share no carbon at all. That is the deepest layer of the metabolic collision, and it is where two axes on opposite sides of the plant can still fight over a molecule neither of them is made of.

Chapter 8 · The cofactor bottlenecks — *what every branch spends besides carbon.*

MECHANISM · the metabolic layer · SAM · NADPH · malonyl-CoA · BCAA

Carbon is the obvious budget, the one you can draw as a branching tree. Under it run four others — the activated cofactors — and they are the reason axes that share no pathway can still starve one another. A cofactor is a small molecule the cell makes at a finite rate and hands to enzymes across the whole metabolism; when two distant branches both demand it, they compete for a pool neither of them appears, on a pathway map, to touch. These are the hidden couplings in the interaction matrix, the ones that surprise a designer who was watching only the carbon.

The first and most binding is **SAM** — *S*-adenosylmethionine, the cell's universal methyl donor. Every time a pathway attaches a methyl group, it spends one SAM and leaves behind *S*-adenosylhomocysteine, which must be recycled before the methyl pool refills. Methylations are everywhere in flavor: **COMT** on the phenylpropanoid trunk methylates caffeate toward ferulate on the road to both capsaicin and vanillin; the **N-methyltransferases** that build caffeine (a bitter molecule) spend three SAM per caffeine; the *O*-methyltransferases that finish many phenylpropenes and the vanillin derivatives spend their own. So **heat, zero-bitter, kokumi, and parts of pungency all draw on one SAM pool** — four axes, chemically unrelated at the branch tips, coupled at the methyl donor. Compose a cultivar that wants loud heat *and* a vanillin-rich kokumi *and* a modulated bitter chemistry, and the three can collide not over carbon but over SAM, each methylation waiting in line for a cofactor the cell regenerates only so fast.

The second is **NADPH**, the reducing currency — the electrons that run every reductive step. The phenylpropanoid branches reduce and hydroxylate at many points; the fatty-acid branch that builds capsaicin's acyl chain reduces at every elongation; the terpenoid routes that make the cooling monoterpenes reduce heavily. Heat, astringency, and cool-burn therefore share a draw on NADPH, which the plastid must supply from photosynthesis and the pentose-phosphate pathway. Reducing power is rarely the single hardest bound, but it is the one that couples a composition to the *light* the plant received — a reminder that a flavor budget is, at bottom, a solar budget, and that a cultivar grown dim is a cultivar given less to spend.



A candidate on the microscope stage — the point in the loop where a composition's feasibility stops being a question of taste and becomes a question of whether the cell could afford to build it at all.

The third is the **acetyl-CoA / malonyl-CoA** pool, the two-carbon currency of everything built by chain extension. Malonyl-CoA feeds the fatty-acid synthase that builds capsaicin's branched 8-methyl-nonanoyl chain, and it feeds **chalcone synthase**, the first committed enzyme of the flavonoid-and-tannin branch — so **heat and astringency compete for malonyl-CoA directly**, a second coupling between the same two axes that already share the phenylpropanoid trunk's carbon. When two axes are coupled in two places at once — carbon *and* a cofactor — their interaction coefficient in the matrix is large and stubborn, and no amount of perceptual cleverness will fix in the mouth what the plant could not afford to build in the first place.

The fourth is the branched-chain amino acid pool, routed through **BCAT**, the branched-chain aminotransferase. Capsaicin's defining feature — the branched methyl near the end of its acyl tail, the thing that makes capsaicin *capsaicin* and not a generic fatty amide — comes from valine and leucine metabolism by way of BCAT. This one is mostly heat's private draw, but it is worth naming because it shows that even a single axis can be bottlenecked at a cofactor-like branch point, and that laddering heat to its ceiling means feeding a pathway most of the cell's machinery was built for other purposes entirely.

Gather the four into one table, because the table *is* the hidden half of the interaction matrix — the couplings you would never find by tasting, only by accounting:

SHARED CURRENCY	BRANCHES THAT SPEND IT	AXES COUPLED
SAM (methyl donor)	COMT; caffeine N-MTs; vanillin & phenylpropene O-MTs	H · B · K · P
NADPH (reducing power)	phenylpropanoid reductions; fatty-acid elongation; monoterpene synthesis	H · A · C
Malonyl-CoA (C_2 extension)	capsaicin acyl chain (KAS); chalcone synthase → flavonoids	H · A
2-oxoglutarate / Glu (amino pool)	GS/GOGAT, GDH1 → free glutamate; γ-glutamyl peptides	U · K
BCAA (via BCAT)	capsaicin's branched acyl chain	H
IPP / DMAPP (isoprenoid)	menthol and the cooling monoterpenes	C · P

Read the right-hand column as a second, invisible interaction matrix, and two lessons fall out that govern all of Part III. The first: **the couplings are not only antagonistic.** The 2-oxoglutarate / glutamate row couples umami and kokumi *constructively* — the same amino pool that fills free glutamate for umami also supplies the γ-glutamyl peptides that drive kokumi, so growing one makes the other cheaper, which is part of why savory depth is the friendliest composition we build. The second: **a composition's hardest constraint is often a cofactor, not a flavor.** When the flux model tells us a triple is infeasible, the binding constraint is frequently SAM or malonyl-CoA, not carbon — a bottleneck you relieve by engineering *supply* (upregulating the regeneration of the cofactor) rather than by trading one axis against another. You cannot see these walls from the tongue, and you cannot see them from the scorecard. You can only see them from the budget — which is why the next chapter stops describing the collisions and starts solving them, by writing the whole plant's chemistry as a system of balances and asking a model to find the allocation that holds.



PART III OF V

The Solution

flux balance · the stability frontier · the loop that composes

Chapter 9 · Flux balance — *the model that holds the ratio.*

METHOD · flux-balance analysis · S·v = 0 · the price of an axis

Flux-balance analysis is how you turn a shared budget into a specification, and it is the mathematical heart of designing in combination. You write the plant's metabolism as a **stoichiometric network** — every reaction a column, every metabolite a row, every entry how many molecules go in or out — and then you impose the one law a steady-state living system cannot break: what flows into each internal pool must flow back out. Nothing accumulates without bound; nothing is created from nothing. In the compact notation that has organized metabolic engineering for thirty years,

$$S \cdot v = 0,$$

where S is the stoichiometric matrix and v is the vector of all the reaction fluxes you are solving for. That single matrix equation, written across hundreds or thousands of reactions at once, is just mass conservation applied everywhere simultaneously — and it carves the space of all *conceivable* flux distributions down to the far smaller space of the ones a real cell could actually sustain. The reader who met the shared-TAS1R3 conservation law in Chapter 5 is meeting its metabolic twin here: a fixed total, partitioned among competing demands, balanced at every node.

Conservation alone does not pick an answer; it only rules out the impossible ones. To choose among the feasible, you add two more ingredients. First, **bounds** — every reaction has a capacity, $lb_i \le v_i \le ub_i$, set by how much enzyme the plant can make, by thermodynamic direction, by what the promoters we install will allow. Second, an **objective** — a direction in flux space you want to push as far as the conservation and the bounds permit. For a microbe the textbook objective is growth; for us it is a target flavor, a weighted combination of the branch outputs that corresponds to the vector we are trying to reach. Put the three together and the problem has a familiar name to anyone who has ever allocated a scarce resource:

$$\text{maximize } c^{\top}v \text{ subject to } S\cdot v = 0,\ lb \le v \le ub.$$

A linear program. Its answer is not a flavor but an *instruction* — a complete flux distribution, a number for every reaction, that says push here, hold there, and this is the proportion your carbon and cofactor budgets will actually bear.

Work it small, because the small version makes the whole thing concrete. Take the ferulate pool from the phenylpropanoid trunk and call its supply φ. Three flavor branches draw on it — the capsaicin branch (heat), the tannin branch (astringency), the vanillin branch (kokumi) — plus a maintenance draw the plant cannot skip. Conservation at the pool is a single balance:

```
φ = v_H + v_A + v_K + v_maintenance.
```

Suppose, in round units, that reaching IFI-H 4,200 costs v_H = 70, reaching IFI-A 1,400 costs v_A = 25, reaching IFI-K 1,900 costs v_K = 30, and maintenance takes 10. The total demand is 135. If the plant's supply is φ = 120, the balance cannot close — **135 of demand against 120 of supply, infeasible** — and the model does not shrug; it tells you precisely which way out exists. Either you raise φ (upregulate PAL and the shikimate pathway that feeds it, widening the trunk) until supply meets demand, or you trade an axis down until demand meets supply. There is no third option where all three axes stay loud on a trunk too narrow to carry them, and the honesty of that "no" is exactly what a breeder working by taste never gets told until a season is lost.



The sequencer bench — where a flux solution stops being a diagram and becomes a sequence to write. The computing proposes the allocation; the edit commits it; the table decides whether the model told the truth.

The most useful thing the linear program gives back is not the optimum itself but the **shadow price** — the dual variable attached to each binding constraint, which says how much the objective would improve if that constraint were relaxed by one unit. At the binding ferulate balance, the shadow price of φ is *the marginal flavor per unit of precursor* — literally the price of an axis, quoted in carbon. If widening the trunk by one unit buys sixty more points of IFI-H, then heat costs about 1/60 of a precursor-unit per Index point at that margin, and you can compare it directly against what an extra unit would buy on the astringency branch or the kokumi branch. Composition becomes an *economic* decision with real prices: when two axes compete for the same precursor, the shadow prices tell you which one to spend the next scarce unit on, and when to stop

spending and widen the supply instead. This is the quantitative form of the sentence we keep repeating — a flavor has to be paid for, in carbon, from the same account another flavor is spending.

Two refinements matter enough to name, because they are how FBA earns its place in a *combinatorics* book specifically. The first is that real compositions bind on **more than one constraint at once** — the ferulate balance *and* the SAM balance *and* the malonyl-CoA balance, three inequalities whose feasible region is a polytope in flux space, with the optimum sitting at a vertex where several constraints meet. A triple-axis design is hard precisely because it tends to pin against several walls simultaneously, leaving the vertex with no slack, which is the formal reason the triple library is sampled six times more sparsely than the dual. The second is **flux variability analysis** — asking, once the objective is fixed, how much each individual flux could still move without changing the result. A branch with wide variability is a robust axis, forgiving of the plant's day-to-day noise; a branch pinned to a single value is a fragile one, and fragility in a flux is fragility in a flavor. Flux variability is where the model first predicts a cultivar's reproducibility — the coefficient of variation we will have to defend in the field — long before a single seed is sown.

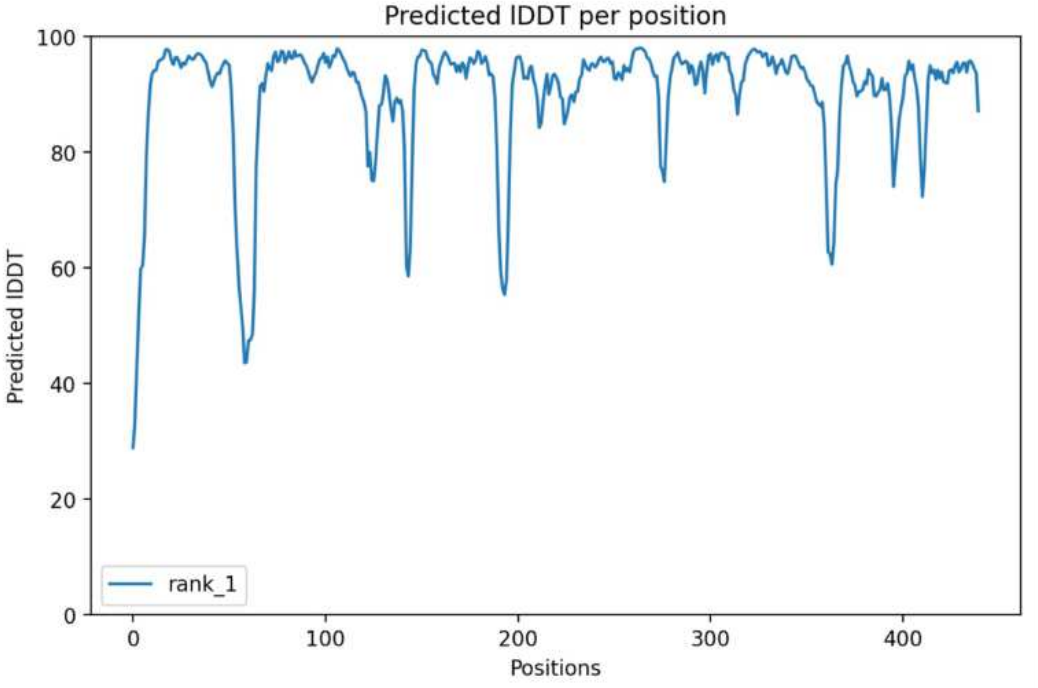
The model is also where the honest shape of this company lives. The computing — the network, the objective, the search for the vertex — was one pair of hands at a keyboard, late, working a single thread until the numbers resolved. But a flux solution is only a hypothesis until something grown from it is set on a table and tasted, and that part was never one person's. The family ate the candidates. The model proposed the allocation; the table decided whether it was *food*; and a ratio was not "right" until both agreed. The linear program finds what the plant *can* bear. It cannot find what a person at a table will *love*, and we have never pretended the two are the same optimization.

Chapter 10 · The stability–efficacy frontier — *ranking what the fold can bear.*

METHOD · ESM2 · efficacy × stability · ΔΔG · CRISPR

Every axis you add to a composition is another enzyme you have to perturb, and every perturbation is a small bet against the fold. A mutation that pushes a branch harder is worthless if it leaves the enzyme too unstable for the plant to carry — efficacy without stability is a protein that never folds, a flavor that never grows. And composition *multiplies* that risk in a way single-axis design never has to face: eight axes means eight budgets, which means eight enzymes perturbed, which means eight places the protein machinery can quietly fail. The full chord is not eight times as hard to build as one note. It is harder than that, because the failures compound.

So before a single edit is written, candidate mutations are ranked on a frontier with two axes of its own — the same kind of two-dimensional trade-off we have been drawing for flavors, now drawn for proteins. A protein language model, **ESM2**, reads a proposed enzyme variant and predicts both halves at once: how much the change should shift the branch's catalytic output (**efficacy**), and how well the fold will survive it (**stability**, read as ΔΔG, the change in folding free energy, where a negative number means the variant is *more* stable than the wild type). Plot every candidate substitution as a point in that plane and the useful ones separate from the merely dramatic. A mutation that raises activity but costs four kilocalories of stability is a cliff you do not step off; a mutation that raises activity *and* stabilizes the fold is free money, and there are more of those than intuition expects.



The Pun1 / AT3 acyltransferase model, coloured by pLDDT confidence — the binding domain and active-site cleft resolved sharply enough to reason about which residues set catalysis and which hold the fold. The two design edits (double variant S39L+L345G) that made Phoenix's heat reachable were chosen on a plot like this.

The discipline is to keep only the **Pareto-optimal** candidates — the ones that are not beaten on *both* axes by some other candidate. A mutation dominated on both efficacy and stability is discarded no matter how exciting one of its numbers looks; the frontier is the set of edits where you cannot gain activity without surrendering stability or vice versa, and the final choice is a point *on* that frontier, chosen for how much fold margin the whole composition can still spare once every other axis has taken its bite. In a single-axis cultivar, the budget for destabilization is generous — one enzyme, one bet, plenty of margin. In a full-spectrum cultivar, the margin is shared across every perturbed enzyme, and the frontier is where you decide how to ration it.

You can read the whole method in one construct. **Phoenix**'s heat was made reachable by two substitutions — the double variant **S39L+L345G** in the Pun1 acyltransferase — surfaced by the model, scored on the efficacy–stability frontier, and written in with CRISPR. (C175S, a structural annotation that our modelling identified as preventing a disulfide misfold, ΔΔG −0.9, was not included in the shipped construct.)

EDIT	EFFECT	ΔΔG (KCAL/MOL)
S39L	binding affinity ↑ at the N-terminal lip	−2.1
L345G	steric relief in the active-site cleft	−1.8
C175S (structural annotation — not in shipped construct)	removes a mis-pairing cysteine, prevents misfold	−0.9

Read the ΔΔG column and the quiet brilliance of the selection shows itself: **every one of the design edits is negative.** The two shipped edits that raised catalytic throughput also *stabilized* the fold — combined ΔΔG for the design edits is about −3.9 kcal/mol, a protein left meaningfully sturdier than the wild type even as its output climbed. This is not luck. It is what the frontier is *for*: among all the ways to push the capsaicin branch, the model found the two design edits that pushed it while strengthening the very enzyme that had to carry seven other axes' worth of perturbation alongside it. A less careful program would have chased the single most activating mutation, paid for it in stability, and discovered the cost only when the plant failed to thrive.

A word on why the ΔΔGs can be treated additively, because the additivity is what makes the combinatorics tractable. For substitutions that sit far apart on the fold — different domains, non-interacting side chains — the change in folding free energy is, to a good first approximation, the *sum* of the individual changes. That additivity is a gift: it means the fold budget behaves like the carbon budget, a quantity you can allocate linearly, spending so much destabilization here and so much there and checking the total against the protein's melting margin. It is also a warning, because additivity can fail — two mutations whose side chains touch can destabilize far more together than apart, an epistatic cliff the sum does not see — which is exactly why the model scores

combinations, not just singles, and why a candidate triple is re-evaluated as a triple before it is ever cut. The frontier is drawn for the composition, not for the mutation.

The frontier is what keeps an ambitious composition *buildable* instead of merely imaginable. Anyone can write a vector with all eight axes loud; the question is whether the enzymes that would produce it can all fold in one cell at one time, and that question is answered not at the table and not in the flux model but here, in the plane of efficacy against stability, one perturbed protein at a time, their destabilizations summed against a shared margin. The flux model says the plant can *afford* the flavor. The frontier says the plant can *fold* the machinery that makes it. Only when both say yes does an edit get written — and even then, the writing is just a better hypothesis, which the next chapter sets on a table.

Chapter 11 · The design loop, composed — *propose, build, taste, and the honest CV.*

METHOD · the loop · ≤7% coefficient of variation · model and tongue

Put the three methods end to end and they close into a loop — the same loop that laddered a single pepper's heat, now run with eight numbers in the brief instead of one. It has four stations, and a composed cultivar goes around it as many times as it takes for the model's proposal and the table's verdict to finally agree.

Propose. The brief is a vector — a target silhouette on the radar, two or three or eight coordinates we mean to reach. The flux model takes it and returns an allocation: which branches to push, which to hold, and whether the budget can bear the whole brief or whether some axis must yield. Where the allocation calls for an enzyme to work harder, the stability–efficacy frontier returns the specific edits that will push it without breaking the fold. The output of this station is not a plant; it is a *design* — a flux distribution and a list of ranked substitutions, a complete hypothesis about how to stand at a named point in eight-dimensional space.

Build. CRISPR writes the chosen edits into the host genome, under the fruit-and-stage-specific promoters that keep the changes where they belong — in the ripe fruit, late, and not in the leaf or the root that have their own metabolism to run. For a composed cultivar this is several edits at once, sometimes across several enzymes, and the construct library records every one: the 8,400 dual-axis constructs and the 2,800 triples are not 11,200 attempts at a handful of flavors but a *library* spanning pathways, promoters, and genetic backgrounds, each a documented point in the space with its edits and its measured result.

Grow and score. The plant is grown out, and its fruit is measured twice — once by the cell-based assay that reads each axis's EC_{50} against its own receptor and returns the vector, and once by a trained human panel that reads the *perceived* result, the integrated experience the assay cannot see. Scoring a composite is where the three-layer model earns its keep: when the assay vector and the panel disagree, the gap is almost always the perceptual layer — a masking or a sequencing the molecules alone did not predict — and the gap tells us whether to adjust the ratio, the release, or the model.

Taste. And then the fruit is set on a table, among people who did not design it, and eaten as food. This is the station no assay replaces and the one the whole company is built around. The model proposed; the panel measured; the table decides whether the thing is *good* — whether the composition that reads balanced on a radar

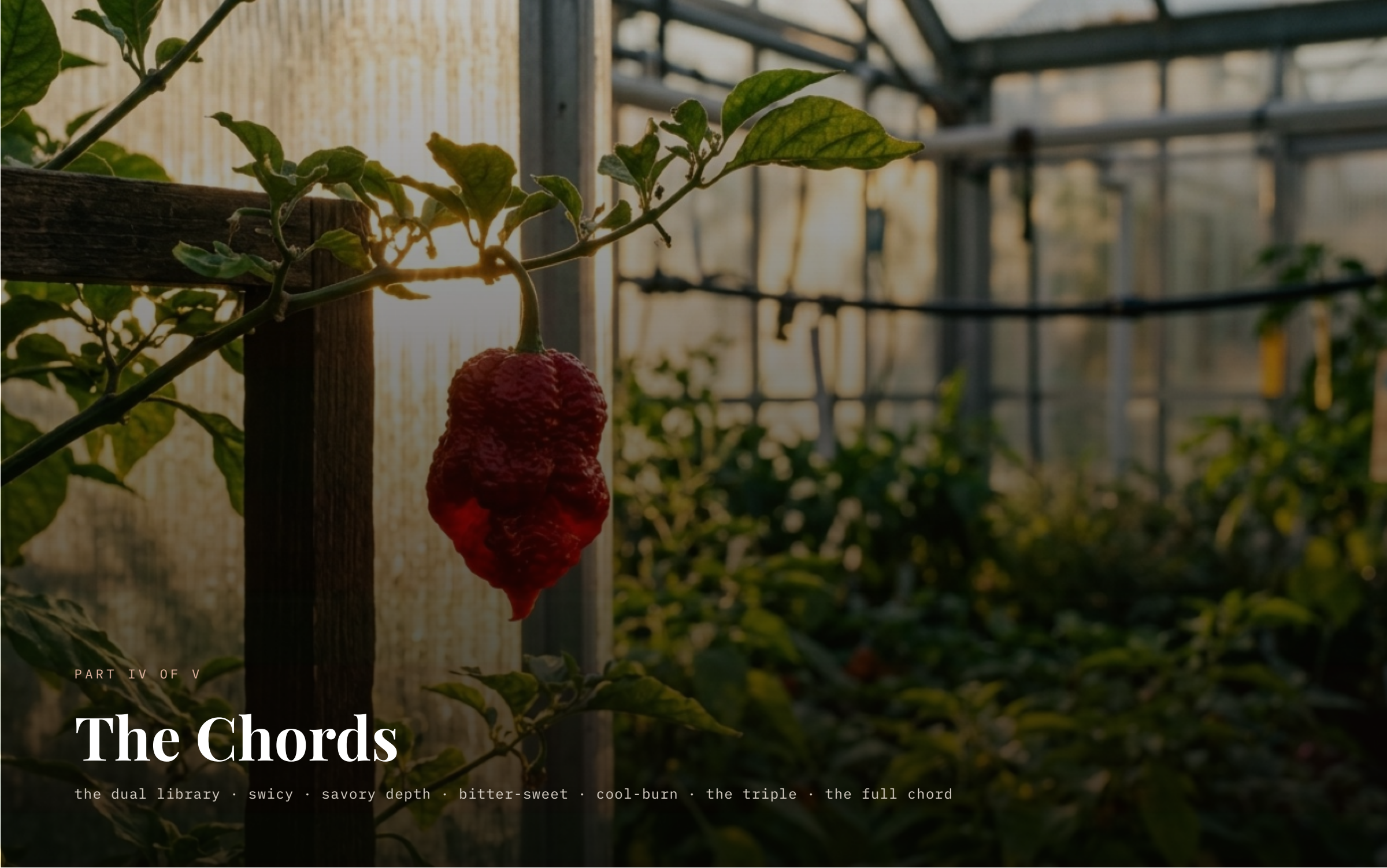
actually eats like something you would want to feed the people you love. A vector can be correct and a fruit can still be wrong, and only the table knows the difference.



A composed candidate in the controlled chamber — grown, measured, and waiting for the only test the model cannot run: whether it is food someone would choose.

The loop's hardest promise is reproducibility, and composition makes the promise harder to keep in a way worth stating plainly. A single-axis cultivar has to hit one number batch after batch; we hold every axis to a **coefficient of variation of seven percent or better** — the standard deviation no more than seven percent of the mean, a tight band for a living thing. A composed cultivar has to hit *all* its numbers at once, and the naïve fear is that the variation compounds — that eight axes each wobbling by seven percent produce a silhouette that wobbles far more. It does not, and the reason is the whole argument for designing at the source rather than blending at the plant. The axes of a composed cultivar are not eight independent ingredients dosed together, each with its own error; they are the outputs of *one* flux solution in *one* fruit, co-regulated by the same promoters responding to the same ripening, so their variations are correlated rather than independent. Flux variability analysis — the wiggle-room calculation from the flux chapter — is run *as part of the design*, and a solution that sits on a sharp, high-variability vertex is rejected in favor of one that sits in a robust, low-variability basin, even at some cost in peak score. We do not only design the flavor. We design the *stability* of the flavor, and we pay for it where it is cheap — in the model — rather than discovering its absence where it is ruinous, in a shipped batch.

There is a temptation, running this loop, to let the model have the last word — to trust the vector because the vector is precise, and precision feels like truth. We hold the opposite rule, and it is the rule that keeps the lushness of this whole library honest: **when the model and the tongue disagree, it is the model we correct.** The flux solution, the ESM2 frontier, the assay vector — all of them are instruments for reaching a place the tongue has already judged worth reaching, and none of them overrules the judgment. The computing was one pair of hands, and those hands were serving a table they did not outrank. That is the shape of the company, and it is the shape of the loop: a machine for proposing flavors, pointed at a question only people eating together can answer.



PART IV OF V

The Chords

the dual library · swicy · savory depth · bitter-sweet · cool-burn · the triple · the full chord

Chapter 12 · Two axes at once — *the dual-axis library.*

COMPOSITION · IFI-M · the M2 library · 8,400 constructs · 28 pairs

With the mechanism in hand and the methods closed into a loop, the design space opens one dimension at a time, and the first room is the largest we have furnished: the **dual-axis library**, 8,400 constructs spread across the 28 possible pairs — the 300-per-pair sampling density from the opening arithmetic. A dual-axis design is specified the way you would name a point on a map, two coordinates in a two-dimensional slice of the full eight, and then solved for with the flux model so the pair holds rather than fights. Every pair in this room sits somewhere on the interaction matrix, and before furnishing it chord by chord it is worth laying the whole matrix out, because the table *is* the atlas of this room — the 28 doors, each labeled with the layer it collides in, the sign of its interaction, and where in the living world it is already native:

PAIR	LAYER	SIGN	SIGNATURE / NATIVE ORGANISM
H × S	perception	−	*swicy* — burn steals the sugar's attention; strawberry sweet-heat
H × U	perception	+	savor makes heat read as *food* — Phoenix
H × B	perception	+	debittering cleans the line of a heat
H × K	metabolic	+	kokumi gives a burn a body to sit in
H × C	receptor	∓	*cool-burn* — TRPV1 ⇄ TRPM8, fire and ice
H × P	receptor	+	co-localized TRPV1/TRPA1 — a sharp, mustard-edged heat
H × A	orthogonal	0	a heat with a dry, tannic finish
S × U	receptor	−	shared TAS1R3 subunit — tomato
S × B	perception	+	unmasking — sweeter black coffee, darker chocolate
S × K	receptor	+	CaSR gain lengthens a sweetness
S × C	perception	+	cooling freshens and brightens sweet
S × P	perception	0/−	a sweet cut by a sharp top-note
S × A	perception	∓	sweetness tempers astringency — grape / wine
U × B	perception	+	savor cleaned of a bitter overlay
U × K	receptor	++	*savory depth* — CaSR multiplies umami; soybean, yeast
U × C	orthogonal	0	rare; a cool savory, lightly explored
U × P	metabolic	+	a savory sharpness — garlic
U × A	perception	0/−	brothy savor against tannin — tea
B × K	perception	+	body plus the lifted bitter guard — cacao
B × C	metabolic	+	debittered and cooling — orange
B × P	orthogonal	0	lightly coupled
B × A	metabolic	−	shared polyphenol chemistry — grape, tea, cacao
K × C	orthogonal	0	a cool with a body
K × P	metabolic	+	kokumi and sharpness together — garlic (K/P)
K × A	mouthfeel	∓	body against grip, a textural balance
C × P	receptor	+	sharp-cool — menthol and mustard, the Sichuan tingle
C × A	orthogonal	0	cooling with a dry edge
P × A	orthogonal	0/−	a sharp top against a dry base

Read the sign column down and the shape of the whole room appears: a handful of outright synergies to *ride* (U×K most of all, then the unmaskings S×B and U×B, then the CaSR-sweet gain), a handful of genuine fights to *solve* (S×U at the shared receptor, H×S in perception, B×A in the metabolism), one controlled contradiction to *hold* (H×C), and a broad plain of near-orthogonal pairs where both axes can be set with little tax. A designer entering this room does not treat all 28 doors alike. The synergies are cheap and the fights are dear, and the matrix is how you know which is which before you spend a season finding out.

Different organisms are native to different doors, and the index records where each already lives — which intersections a plant will take to most easily, and where our construct counts have therefore gone deepest:

ORGANISM	NATIVE INTERSECTION	CONSTRUCTS
Habanero	Full / multi (F/M)	3,190
Tomato	Sweetness × Umami (S/U)	2,040
Black Mustard	Pungency × multi (P/M)	2,790
Peppermint	Cool × multi (C/M)	2,360
Grape	Bitter × Astringency (B/A)	1,610
Stevia	Sweet × full/multi (S/F/M)	910
Garlic	Kokumi × Pungency (K/P)	560
Soybean	Umami × Kokumi (U/K)	360
Tea	Umami × Bitter × Astringency (U/B/A)	280
Yeast	Umami × Kokumi (U/K)	240

There is one specimen, though, that occupies every door at once, and it becomes our teacher for the rest of this part. Because **Phoenix** (SS-0096) registers on all eight axes, its single eight-dimensional coordinate *contains* all 28 pairs as projections — read any two components and you have a real, grown, designed dual-axis example without building a separate cultivar for it. We do not have to invent the swicy point or the savory-depth point or the cool-burn point. We can read each one off the flagship, two numbers at a time, and spend the next five chapters doing exactly that: the same fruit, cast onto five different planes, each plane a lesson in a different corner of the interaction matrix.

Chapter 13 · Swicy — *heat laddered into sweetness.*

COMPOSITION · IFI-H × IFI-S · TRPV1 × TAS1R2·R3 · the perceptual fight

Begin with the pair the whole market is asking for, because it is also the cleanest example of a *perceptual* collision solved by ratio. Heat against sweetness — the composition the trade has started calling *swicy* — looks on paper like it should never fight at all. Capsaicin works TRPV1, a trigeminal channel; sweetness clasps the TAS1R2·TAS1R3 pair, a gustatory receptor; different locks, different nerves, no shared subunit, no shared precursor to speak of. By the orthogonality of their receptors the two should simply coexist. And yet in the mouth they collide, because the collision is not at the receptor — it is in the integrator, where a loud TRPV1 signal pulls focus and the brain reads the sweetness arriving behind it as thinner than its score. Swicy is a mask (Chapter 6) wearing the disguise of an addition.



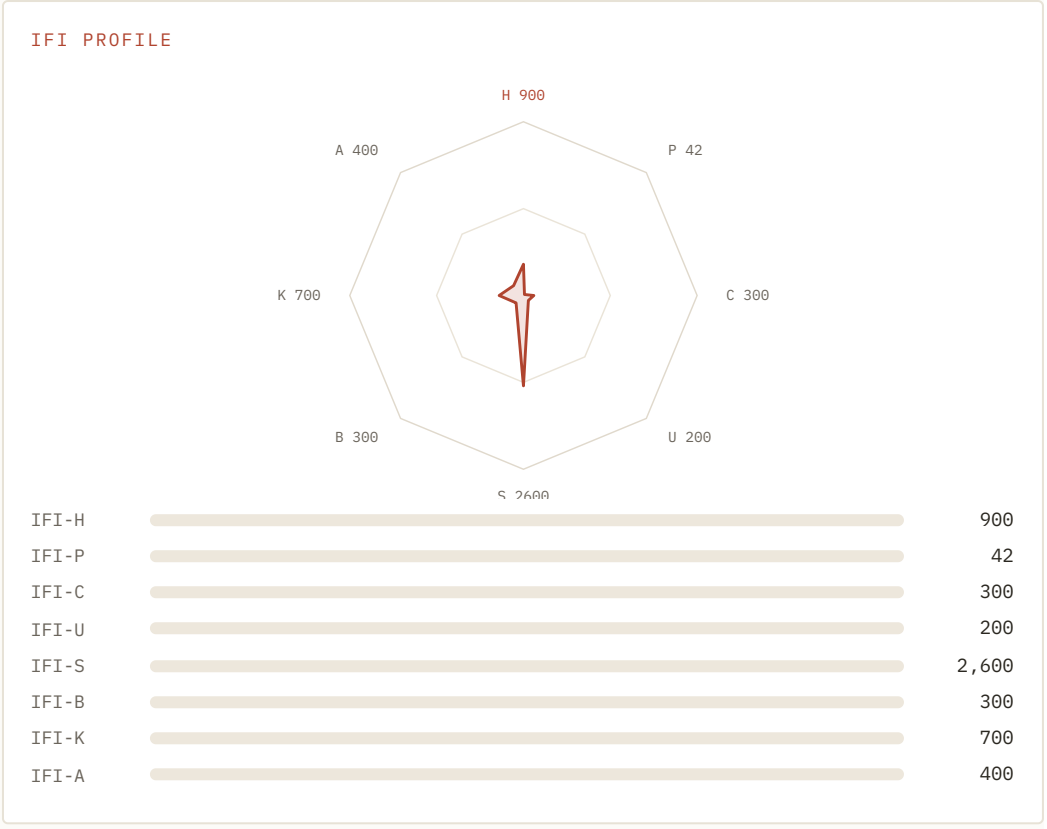
A sweet-heat strawberry — the dessert frontier's emblem, sweetness as the headline and heat as the lift that makes it read louder. The same two axes as a hot-sweet pepper, composed the other way up.

Because the fight is perceptual, the fix is perceptual: you do not try to make the two axes equal — equal, they muddle — you decide which is figure and which is ground, and you compose the ratio and the release so the ground survives under the figure. Read Phoenix projected onto the heat-sweet plane and you see a point chosen, not stumbled into:

AXIS	SCORE	ROLE
IFI-H · Heat	4,200	the headline, at the top of the ladder
IFI-S · Sweetness	1,100	grown in *underneath*, not added on top

A heat of 4,200 would erase most sweetness presented beside it; a sweetness of 1,100, composed to sit *under* the burn and release a half-beat before it, survives — because the flux model paid for both from the same budget and the perceptual tuning placed the sugar where the heat would not step on it. The number 1,100 is not large, but it is not meant to be large; it is meant to be *present*, a floor of sweetness the eater registers as the burn arrives and remembers as the burn fades.

The dessert frontier is this exact move composed upside down, and it is where swicy becomes joyful rather than merely clever. Our roadmap's **Strawberry *Sweet Heat*** line — Warm Kiss, Sugar Burn, Candied Fang, Devil's Dessert — makes sweetness the headline and heat the lift, a trace of capsaicin grown into a berry so that the sweetness reads *louder* for the warmth standing behind it. Same plane, opposite corner, one grammar. Here is a swicy preparation scored as a dish — a sweet-heat strawberry, barely warmed, spooned over a cold thick yogurt with a crack of flaky salt:



Read the silhouette and the composition is legible at a glance: sweetness forward at 2,600, a real but subordinate heat at 900 arriving late, a lift of cool at 300 and a kokumi body at 700 from the yogurt that keeps the sweetness from reading flat. This is swicy as the body actually wants it — the warmth making the sweet feel like more than sugar, the whole thing balanced rather than loud. The strawberry carries its own gentle nourishment, and we grew the heat

into the fruit rather than dosing it on, so what reaches the table is one plant doing two things at once, the way a plant grown toward its fullest always does.

Swicy is, underneath, a *sequencing* problem as much as a ratio problem, and this is the lever that separates a muddle from a delight. The two axes do not share a timescale. Sweetness is fast — the TAS1R2·TAS1R3 receptor reports almost the instant sugar reaches it, and the signal fades as the sugar clears. Capsaicin is slow and stubborn — it binds TRPV1 lipophilically, builds over seconds, and lingers for minutes because it does not rinse away. Set the two side by side at equal volume and the fast one is gone before the slow one arrives, leaving a sweetness you barely registered and a heat with nothing to balance it. The fix is to compose the *onset*: a sweetness released at the surface, quick and bright, handing off to a heat grown into the flesh that arrives a beat behind and carries the finish. The best swicy is never heard as a chord struck at once; it is heard as a phrase — sweet, then warm — and the phrasing is designed, not left to chance.

The dessert frontier reads the same two axes as a ladder, tilting the figure-ground from sweet-led to heat-led one cultivar at a time. Our roadmap's Strawberry *Sweet Heat* line is that ladder made into fruit:

CULTIVAR	IFI-S	IFI-H	WHAT IT TASTES LIKE
Warm Kiss	2,800	300	a ripe berry with a blush of warmth on the finish
Sugar Burn	2,600	700	sweetness first, heat arriving as it fades
Candied Fang	2,300	1,300	a real bite living inside the candy
Devil's Dessert	1,900	2,200	sweet and hot at a dead level, neither yielding

Climb the two middle columns and you are watching the figure-ground invert: at Warm Kiss the heat is a rumor under a loud sweetness; by Devil's Dessert the two stand level and the eater's attention is pulled back and forth between them, which is its own kind of pleasure. Every rung is the same pair of axes — the same plane of the interaction matrix — sampled at a different ratio, and the ladder is how a line is built: not one flavor, but a parametrized family across a two-dimensional slice.

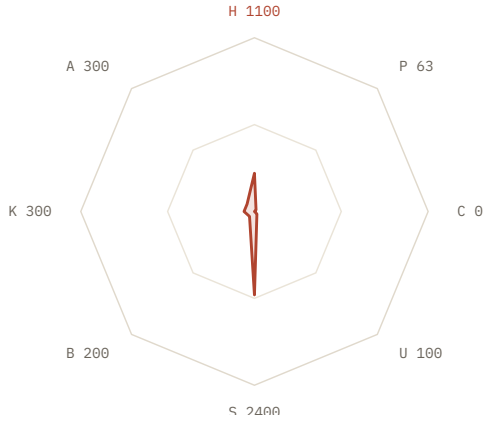
Sweet-heat strawberry hot honey · a swicy you can pour

Built on Candied Fang, or the ripest berries and a whisper of a mild designed chili. This is a condiment that keeps the phrasing — sweetness leading, heat landing late — so it can carry the composition onto anything you pour it over. *A note from our kitchen: this is the first thing we hand a skeptic, over a soft cheese; the argument usually ends on the second cracker.*

Honey (or warmed agave, to keep it vegan)	240 g
Sweet-heat strawberries (Candied Fang target), hulled and quartered	150 g
A mild designed chili (microdose), thinly sliced	1 small
Lemon zest	1 strip
Flaky salt	1 pinch
Cider vinegar	1 tsp

1. Warm the honey gently with the sliced chili and the lemon zest to just under a simmer — never a boil, which flattens the berry's top notes. Hold at a bare steam for ten minutes; capsaicin is oil-soluble and patient, and a low, slow infusion places the heat on the *finish* where swicy wants it.
2. Add the strawberries and the salt, then pull the pan from the heat. Let the berries slump in the residual warmth for fifteen minutes — softened, not dissolved.
3. Stir in the vinegar. The bright acid keeps the sweetness from cloying and sharpens the hinge where the heat takes over from the sugar.
4. Strain for a clear pour, or leave the fruit in for a spoonable version. Taste the phrasing: the heat should land a full beat behind the sweetness. If it arrives too soon, the chili cooked too hard — next time infuse cooler and longer.

IFI PROFILE



IFI-H	1,100
IFI-P	63
IFI-C	0
IFI-U	100
IFI-S	2,400
IFI-B	200
IFI-K	300
IFI-A	300

Over a roast squash, a seared halloumi, a plain thick yogurt, or warm cornbread, this is the swicy phrase made portable — and the proof that a composition, once solved in the plant, can be carried to a hundred tables without being re-solved at each one.

Chapter 14 · Savory depth — *umami, multiplied by kokumi.*

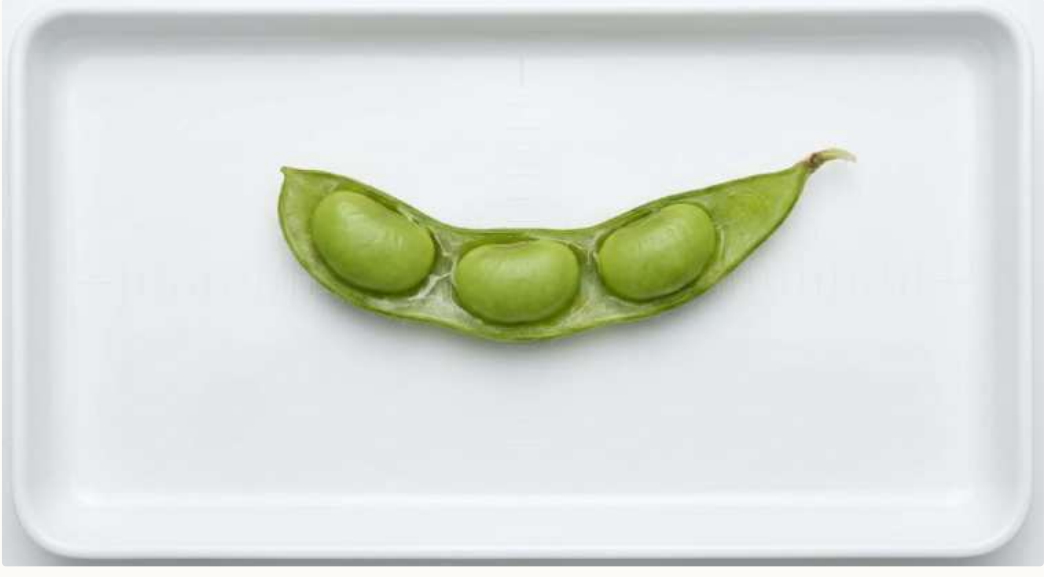
COMPOSITION · IFI-U × IFI-K · mGluR1 × CaSR · the receptor synergy

Not every pair fights, and the most-requested combination we build is also the friendliest — umami and kokumi, the savory round and the thing that gives it a body. Here composition is genuinely more than the sum, because the collision is at the receptor and the receptor *collaborates.* Umami is free glutamate finding mGluR1 and the TAS1R1·TAS1R3 clamp, the receptors that report *here is nourishment.* Kokumi has no taste of its own; it is **γ-glutamyl peptides** — glutathione, γ-Glu-Val-Gly and their kin — working the **calcium-sensing receptor, CaSR**, and what they modulate is not a flavor but a *gain.* Lay kokumi under umami and the CaSR signal multiplies the umami response: the savory does not add to the body, the body amplifies the savory.

Write the synergy as the gain it is, because the functional form is the whole point. Where a competitive inhibitor divided the IFI (Chapter 5), a kokumi potentiator *multiplies* it:

> **IFI-U′ = g(K) × IFI-U, with g(K) > 1 and rising with kokumi occupancy.**

That single sign flip — multiply instead of divide, a factor greater than one instead of less — is the difference between the two hardest-working pairs in the library. S×U divides, because sweet and umami compete for one shared subunit. U×K multiplies, because kokumi is a gain on a receptor it does not itself occupy for taste. The same umami glutamate, under a loud enough kokumi, reads a third again as savory as it would alone, and the eater perceives not two tastes but one deeper one.

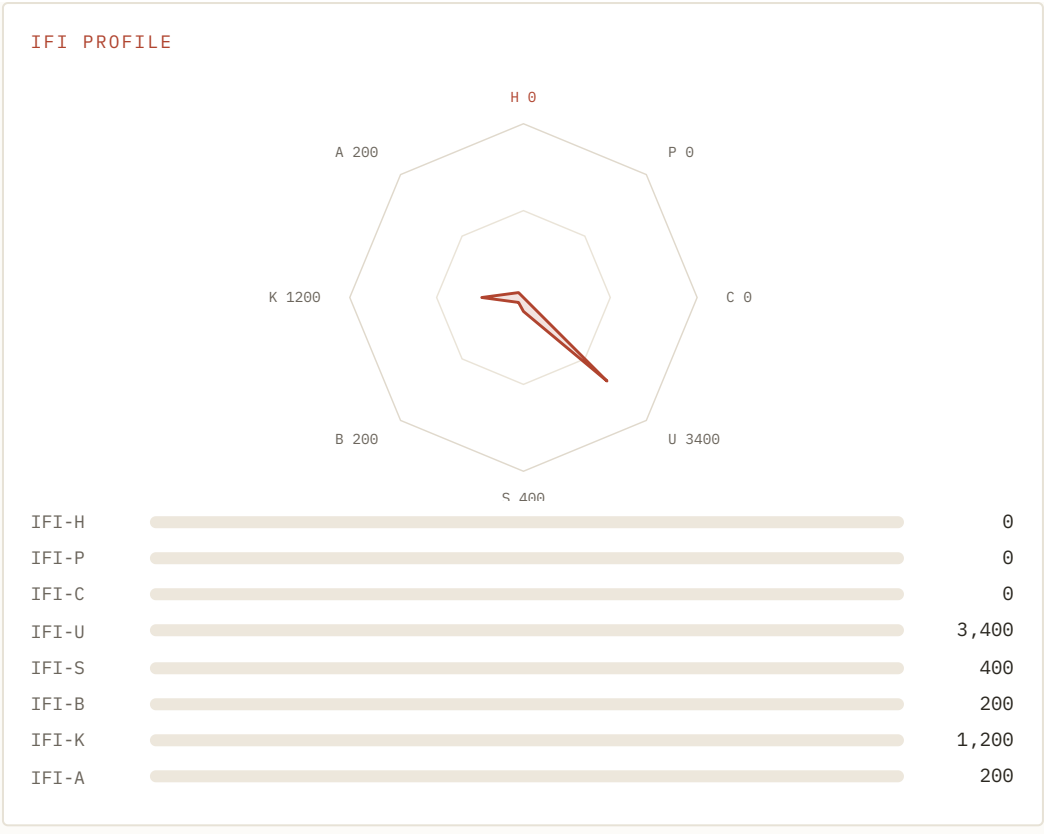


Soybean in cross-section — native to the umami-kokumi door (U/K, 360 constructs), a single legume carrying both the glutamate and the peptides that multiply it. Much of our savory work is the attempt to grow the multiplier and the multiplicand into one plant.

Read Phoenix on the savory plane and the design intent is visible in the near-balance:

AXIS	SCORE	ROLE
IFI-U · Umami	1,800	the savory pull of mGluR1
IFI-K · Kokumi	1,900	the gain that makes it last

The two land almost level, 1,800 against 1,900, and the near-balance is deliberate: enough glutamate to be clearly savory, enough kokumi gain to multiply rather than merely accompany it. The organisms born to this door are tuned the same way — **Soybean** (360 constructs, U/K) and **Yeast** (240, U/K), each grown to carry both halves, and the restored tomato given its free glutamate back to an IFI-U of 2,600, three times the glutamate the shipping fruit was bred down to and nearly ten times as loud on the receptor because savor does not track concentration in a straight line. The composition is what turns that glutamate into *depth*: a savory floor with a body under it, grown rather than boiled, so a vegetarian pot reaches the roundness a long stock gives without the stock. Here is that floor scored as a preparation — a clear broth of restored tomato and engineered shiitake, nothing else:



Umami clears 3,400 — higher than either ingredient reaches alone, because the glutamate of the tomato and the guanylate of the mushroom press on the same receptor and the kokumi body at 1,200 multiplies the whole — and the bowl reads deep and quenching and complete, a savor that fills the mouth and stays. Depth without a stockpot, richness without a long day of fat: the savory floor a plant-first kitchen stands on, grown in rather than cooked down.

There are, in fact, *two* multiplications stacked in that bowl, and it is worth separating them because together they are the most efficient flavor arithmetic we know. The first is the umami axis's own internal synergy — the one between free glutamate and the 5′-ribonucleotides, IMP and GMP, that dock beside it and hold the receptor's trap shut. That synergy was quantified decades ago in the equivalent-umami-concentration equation, $EUC = \Sigma(a_i \cdot b_i) + 1218 \cdot (\Sigma\, a_i \cdot b_i)(\Sigma\, a_j \cdot b_j)$, where the second term — a *product* of the amino-acid sum and the nucleotide sum, scaled by a large constant — is the synergy. Run a modest kombu-and-shiitake extract through it (glutamate 0.10, aspartate 0.02 g/100 g; guanylate 0.015, inosinate 0.005) and the product term alone contributes $1218 \times (0.1015 \times 0.0395) \approx 4.8$, so the mix tastes as savory as nearly *five grams* of straight glutamate — a roughly fiftyfold amplification from quiet ingredients placed so the receptor multiplies them. The second multiplication is the kokumi gain layered *on top* of that: the γ-glutamyl peptides — glutathione, and the potent γ-Glu-Val-Gly — working the calcium-sensing receptor to apply a further factor $g > 1$ to the whole savory reading. Nucleotide synergy within the umami, kokumi gain over the umami: two products stacked, which is why savory depth built from the right pairing reads so much louder than the sum of its grams.

The calcium-sensing receptor earns one more line, because it is the quiet mechanism under the whole friendly pair. CaSR is a class-C G-protein-coupled receptor — the same structural family as the umami receptor mGluR1 and the sweet-and-umami T1R clamp, a family built around a large hinged extracellular domain — but on the taste cell it reports no flavor of its own. What it does is modulate: occupied by a γ-glutamyl peptide, it potentiates the cell's response to sweet, umami, and salty and lends the sensation its *continuity*, the thickness and mouth-filling persistence that cooks call body. This is why kokumi is the axis you feel but cannot name, and why it is the designer's favorite collaborator: it adds no taste to argue with the others, only a hand on their collective volume. Soybean and yeast are native to this door (U/K, 360 and 240 constructs) precisely because each already carries both halves — the glutamate and the peptides — in one organism, and much of our savory work is the attempt to grow the multiplier and the multiplicand into a single host a cook can reach for whole.

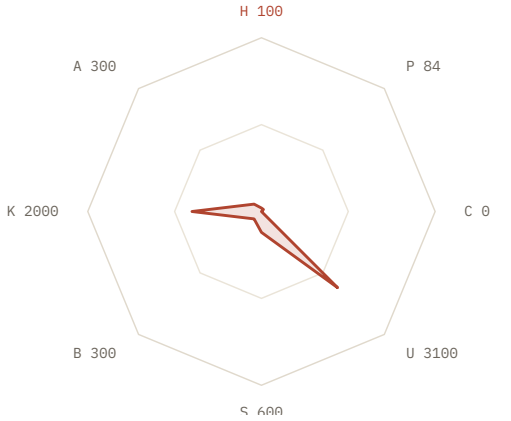
Restored-tomato and shiitake braise · savory depth, no stock

A braise that reaches the roundness of a long bone stock from plants alone, because the depth is grown into the ingredients rather than extracted over hours. Built on the restored tomato (U 2,600), engineered shiitake for the guanylate, and a kokumi lift from soy and yeast. *We make this on the first cold night of the year; no one ever asks where the meat is.*

Restored tomatoes (umami-tuned), halved	600 g
Dried engineered shiitake	25 g
Kombu	1 piece (10 cm)
Water	800 ml
Tamari or soy sauce	2 tbsp
Engineered nutritional yeast (U/K)	1 tbsp
Firm tofu or cooked white beans	350 g
Garlic (K/P), sliced	3 cloves
Olive oil, spring onion, toasted sesame	to finish

1. Cold-steep the kombu and dried shiitake in the water for thirty minutes, then warm slowly to just below a simmer and hold ten minutes. Lift the kombu before it turns slick; leave the shiitake to keep giving up its guanylate.
2. Meanwhile, roast the halved tomatoes cut-side up with the garlic and a little oil at 200 °C for twenty-five minutes, until they collapse and caramelize at the edges — concentration without losing the free glutamate to a hard boil.
3. Slide the roasted tomatoes and garlic into the mushroom broth, add the tamari and the yeast, and simmer gently fifteen minutes. Fold in the tofu or beans to warm through.
4. Taste for the *floor*: it should read deep and complete before any salt, the glutamate and guanylate and the kokumi peptides all pressing the same receptors at once. Finish with spring onion and sesame. Serve over rice or good bread.

IFI PROFILE



IFI-H	100
IFI-P	84
IFI-C	0
IFI-U	3,100
IFI-S	600
IFI-B	300
IFI-K	2,000
IFI-A	300

Umami at 3,100 and kokumi at 2,000 standing together is savory depth as a dish rather than a diagram — the two tall spokes of the U×K door, grown into a pot that asks for no stock and no apology. It is the plainest demonstration we own that the friendliest corner of the interaction matrix is also the most nourishing one, since the late ripeness that filled the tomato's glutamate filled its lycopene in the same motion.

Chapter 15 · Bitter-sweet — *subtraction and lift together.*

COMPOSITION · IFI-B × IFI-S · TAS2R38 × TAS1R2·R3 · the unmasking

This pair is unlike the others, because one of its axes is a *subtraction.* Every other axis adds a signal; IFI-B *removes* one, attenuating the bitter report of TAS2R38 by twenty to sixty-five percent. Composing it with sweetness means running two levers in the same direction — down on the bitter, up on the sweet — toward a single lift. And there is a gift folded into the ordering, the unmasking from Chapter 6 made into a design principle: because bitterness centrally *masks* sweetness, turning the bitter signal down **uncovers** sweetness that was already in the food, before you have added a grain of anything.



Grape in cross-section — native to the bitter-astringent door (B/A, 1,610 constructs), where softening the bitter guard without stripping the structure is the whole art. The same unmasking lifts a dark chocolate and a black coffee.

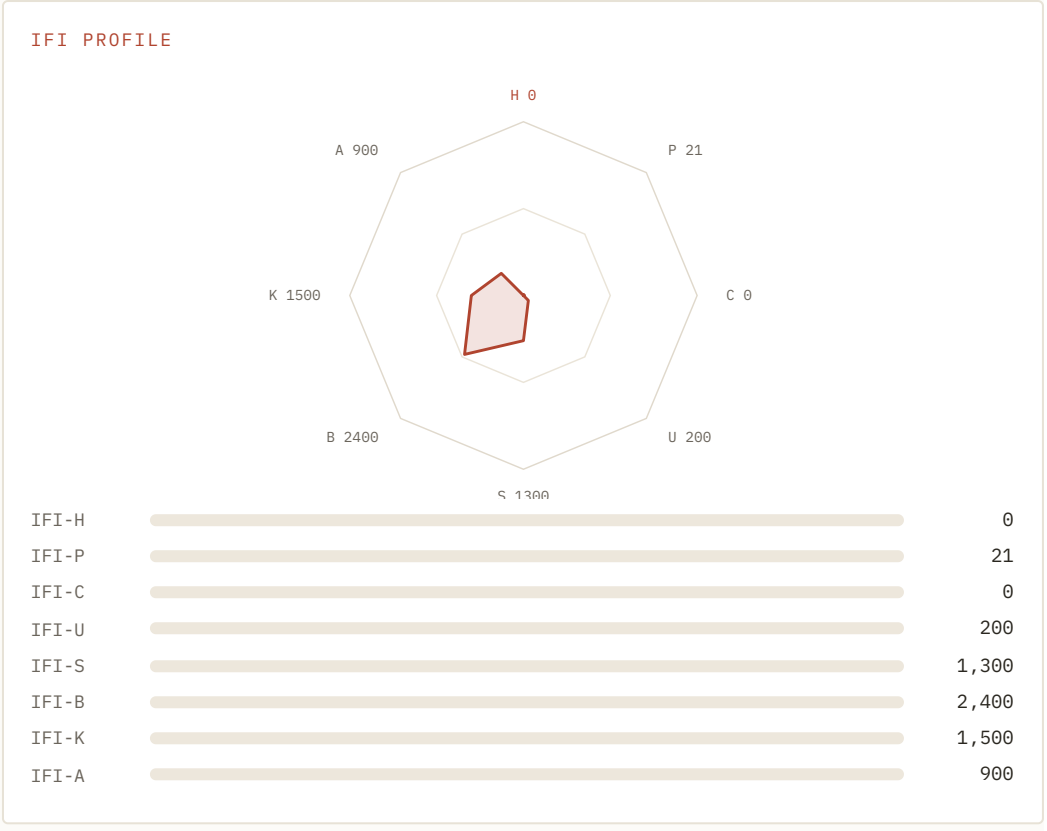
Read Phoenix on the bitter-sweet plane and the subtraction and the addition are held together:

AXIS	SCORE	ROLE
IFI-B · Zero-Bitter	2,200	the bitter guard, turned down
IFI-S · Sweetness	1,100	the sweetness it uncovers and lifts

An IFI-B of 2,200 is a substantial easing of the TAS2R38 warning, and against it a composed sweetness of 1,100 reads far louder than the number alone would promise — because, as the unmasking arithmetic showed, part of the sweetness is not added but *released*,

a signal that was always present and merely held down. Recall the rough figures: a sweetness that would read 1,400 in a clean mouth but was suppressed to 840 by a co-present bitter climbs back toward 1,120 when you halve the suppression, with no sweetener added at all. Two levers, one lift, and half the lift paid for by subtraction.

This is the lever under coffee, under cacao, under the dark and tannic pleasures that people love *against* their bitterness rather than for it. It is also where the metabolic coupling we flagged in the matrix — B×A, bitter and astringency drawing on shared polyphenol chemistry — has to be respected: in a grape, a tea, a cocoa bean, the bitter compounds and the astringent tannins come off the same branch, so attenuating the bitter without stripping the structure is a flux problem, not a blunt deletion. The grape, native to this door at 1,610 constructs (B/A/M), is where we have learned it best: soften the guard, keep the backbone. Here is a bitter-sweet preparation scored — a dark drinking chocolate from debittered cacao, unsweetened but for what the subtraction uncovers:



The zero-bitter axis does the heaviest work at 2,400, and watch what rises in its shadow: a sweetness of 1,300 in a cup with very little added sugar, a kokumi body at 1,500 that the bitterness had been hiding, an astringency pulled back to a soft 900 so the structure reads as grip rather than scrape. The chocolate tastes sweeter and rounder and kinder than its sugar content can explain, because most of what you taste was released, not added. It is the gentlest arithmetic in the book — a flavor lifted by taking something

away — and it is the one that most quietly serves the body, since the sweetness you did not have to add is sugar the eater did not have to be given.

The metabolic coupling named in the matrix — B×A, bitter and astringency drawing on the same polyphenol branch — is the reason this composition is a flux problem and not a deletion. In a coffee, a cacao, a grape, the bitter compounds and the astringent tannins are cousins off one line: the flavan-3-ols and their condensed polymers, the proanthocyanidins, built through the branch that runs flavan-3-ol synthesis by way of the reductases **ANR** and **LAR**. Delete the branch and you lose the structure with the bitterness; what you want instead is to *retune* it — shift the degree of polymerization and the proportion of the harshest small polyphenols while keeping the longer tannins that give a dark chocolate its spine and a wine its grip. This is why Zero-Bitter is an *attenuation*, 20 to 65 percent and no more, rather than a switch: the flux model finds the allocation that quiets the warning without hollowing the body, holding the B axis down and the A axis at a deliberate, structured level. Coffee (40 constructs, B) and cacao live or die on exactly this restraint — a debittering that leaves the dark intact.

Work the unmasking once more with numbers, because the gift is worth proving twice. Take a black coffee whose intrinsic sweetness — the caramelized sugars of the roast — would read about 900 on the Index in a clean mouth, but which a co-present bitterness suppresses by half, so the drinker perceives only ~450 and reaches for sugar to compensate. Attenuate the bitter axis to cut that suppression from 50 percent to 20, and the perceived sweetness climbs toward 720 with nothing added to the cup. The drinker who would have stirred in two spoons now needs none, not because the coffee was sweetened but because its own sweetness was *uncovered*. Multiply that across a day's cups and a year's drinkers and the subtraction is not only a flavor move; it is sugar that never had to be poured.

Black coffee, uncovered · the sweetness you did not add

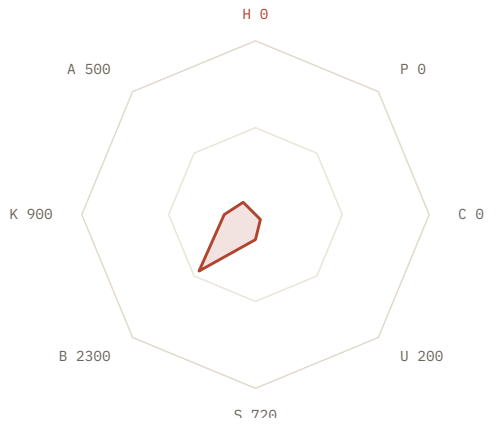
Built on Coffee-B, the bitter-attenuated bean, brewed clean so the unmasking does the sweetening. No sugar — the point is to taste what the subtraction releases. *Brew it once beside an ordinary dark roast, side by side, and the difference is not subtle.*

Debittered coffee (Coffee-B target), medium-coarse grind	32 g
Water, 94 °C	520 g

1. Rinse the filter and warm the vessel; discard the rinse water so no papery note rides along to be mistaken for bitterness.
2. Add the grounds, start a timer, and pour just enough water to saturate — about 70 g — for the bloom. Wait forty-five seconds; a debittered bean still degasses, and the bloom still matters.
3. Pour in slow concentric stages to 520 g over the next two and a half minutes, keeping the bed level. A debittered coffee forgives a slightly longer contact time because the compounds that would turn harsh have been turned down — so you can pull more body without pulling more bite.

4. Taste black, before any instinct to sweeten. The cup should read round and faintly sweet on its own, the roast sugars standing where the bitterness used to lie across them. If you still reach for sugar, the bean was under-attenuated, not under-sweetened.

IFI PROFILE



IFI-H	0
IFI-P	0
IFI-C	0
IFI-U	200
IFI-S	720
IFI-B	2,300
IFI-K	900
IFI-A	500

A sweetness of 720 in a cup with no sugar in it is the whole bitter-sweet thesis in one reading: the Zero-Bitter axis at 2,300 lifting a sweetness that was always present and merely masked. It is the kindest arithmetic in the library, and the one most quietly in the body's service — a flavor raised by subtraction, and a sweetness the drinker was spared from having to add.

Chapter 16 · Cool-burn — *the intersection inside one receptor pair.*

COMPOSITION · IFI-H × IFI-C · TRPV1 ⇄ TRPM8 · the held contradiction

Cool-burn is the pair that proves the thesis bare, because its two axes are already an intersection before you compose anything. **TRPM8** reads cold and answers to menthol; **TRPV1** reads heat and answers to capsaicin; they are the two ends of one thermal story, often wired to the same trigeminal endings. A plant carrying both is not blending two flavors — it is holding a single sensation in contradiction with itself, telling one nerve *hot* and *cold* at once. Fire and ice are not far apart on the Index. They are the same ruler, read from opposite ends, and the composition is the controlled collision of Chapter 5 made into a flavor on purpose.



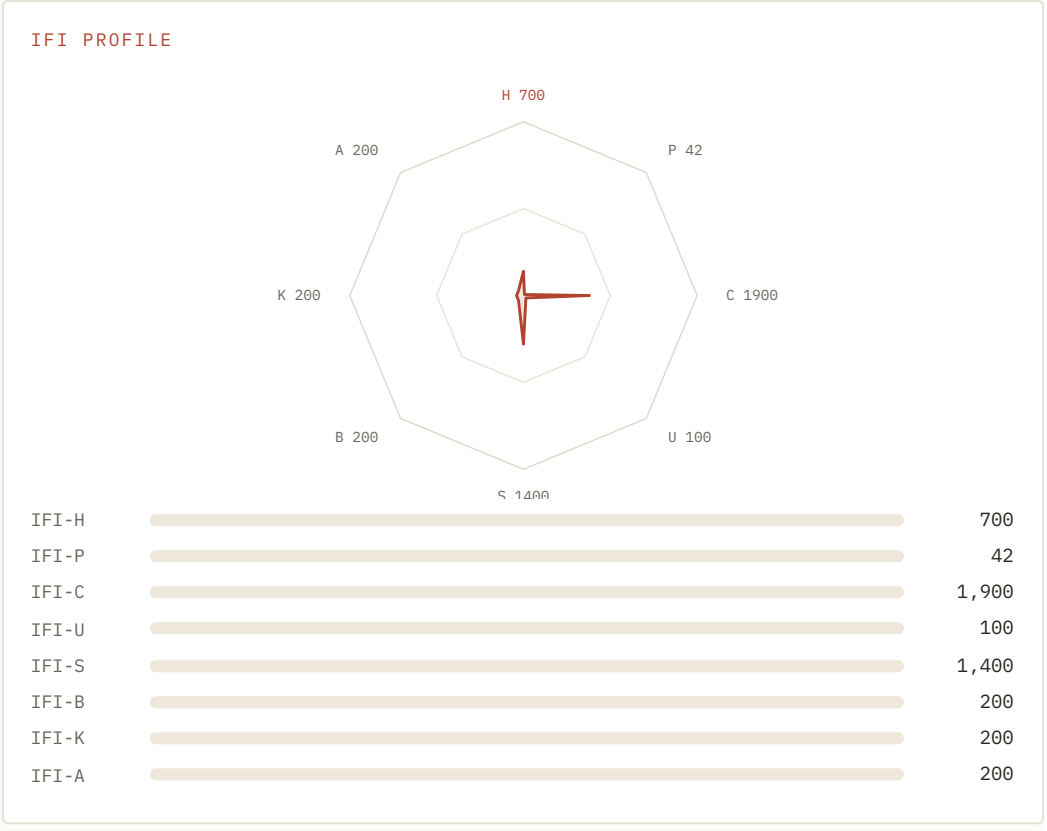
Peppermint — native to the cool door (C/M, 2,360 constructs), carrying the five-gene menthol pathway that builds cooling where the Index reads none. Set against heat, cool becomes the rarest trick we own.

Read Phoenix carrying a thread of cool against its wall of heat:

AXIS	SCORE	ROLE
IFI-H · Heat	4,200	capsaicin at TRPV1, the full burn
IFI-C · Cool-Burn	800	menthol-side cooling at TRPM8, set against it

Eight hundred of cool beneath 4,200 of heat is not a cancellation — it is a *shape.* The cool does not lower the temperature of the burn; the two channels are distinct proteins and the capsaicin does not stop firing TRPV1 because menthol is firing TRPM8. What the cool does is draw a cold line through the middle of the heat, a doubled

reading the tongue cannot quite resolve and cannot stop chasing — the reason a mentholated heat feels like it moves, arriving hot and finishing cold or the reverse, where a plain heat only sits. Built to stand alone, cool-burn is the clean rush of engineered **Peppermint** (2,360 constructs, C/M) and its five-gene menthol pathway, cooling grown where none grew. Built against heat, it is the single clearest demonstration in the library that a sensation is only a receptor, and a receptor can be set against its opposite by design. Here is a cool-burn preparation scored — a chilled cucumber and mint agua fresca with a thread of grown-in chili warmth:



Cool forward at 1,900, a sweetness of 1,400 to carry it, and a heat of 700 arriving underneath as a slow warmth the cold keeps circling — the drink reads as *motion*, a temperature that will not hold still. This is the composition at its most refreshing and its most instructive: nothing here cancels, everything coexists, and the pleasure is in the contradiction the two thermal channels report to one nerve that has no single word for it.

It is worth naming the cool side's chemistry, because the cooling that fights the heat is built, not borrowed, and its pathway is one of the most elegant in the plant world. Menthol is a monoterpene, and peppermint assembles it down a short committed route from geranyl diphosphate — the five-to-seven-step pathway the index calls, in shorthand, the five-gene menthol pathway. Limonene synthase (**LS**) cyclizes the GPP to (−)-limonene; a cytochrome-P450 limonene-3-hydroxylase (**L3H**) oxidizes it; then a cascade of a dehydrogenase and a run of reductases — isopiperitenol dehydrogenase (**IPD**), isopiperitenone reductase (**IPR**), the isomerase and pulegone reductase (**PR**), and menthone reductase (**MMR**) — walks the carbon through isopiperitenone and pulegone and menthone to (−)-menthol. Engineered Peppermint carries 2,360 constructs tuning exactly that cascade, which is why the cool side of a cool-burn is a *designed* loudness and not a flavoring dropped in: the menthol is grown, and the TRPM8 it speaks to is a real channel with a real EC_{50}, scored on the Index like any other axis.

Keep one distinction clear, because the two great "cool" sensations are not the same receptor and the book maps them with care. Menthol's cool is a *steady* cooling — TRPM8 opened and held, a clean cold that sits. The tingling buzz of Sichuan pepper is something else: hydroxy-α-sanshool works largely by *blocking* the two-pore background potassium channels (the KCNK family) and nudging TRPA1, which leaves the touch neurons firing in a rhythmic, roughly fifty-hertz flutter the mouth reads as vibration rather than temperature. Both land on the IFI-C axis in our bookkeeping because both are thermomodulatory cousins the eater files under "cool," but the mechanisms are distinct — a held cold versus a buzzing tingle — and a designer composing a cool-burn chooses which cold they mean. Here, against heat, we mean menthol's steady kind.

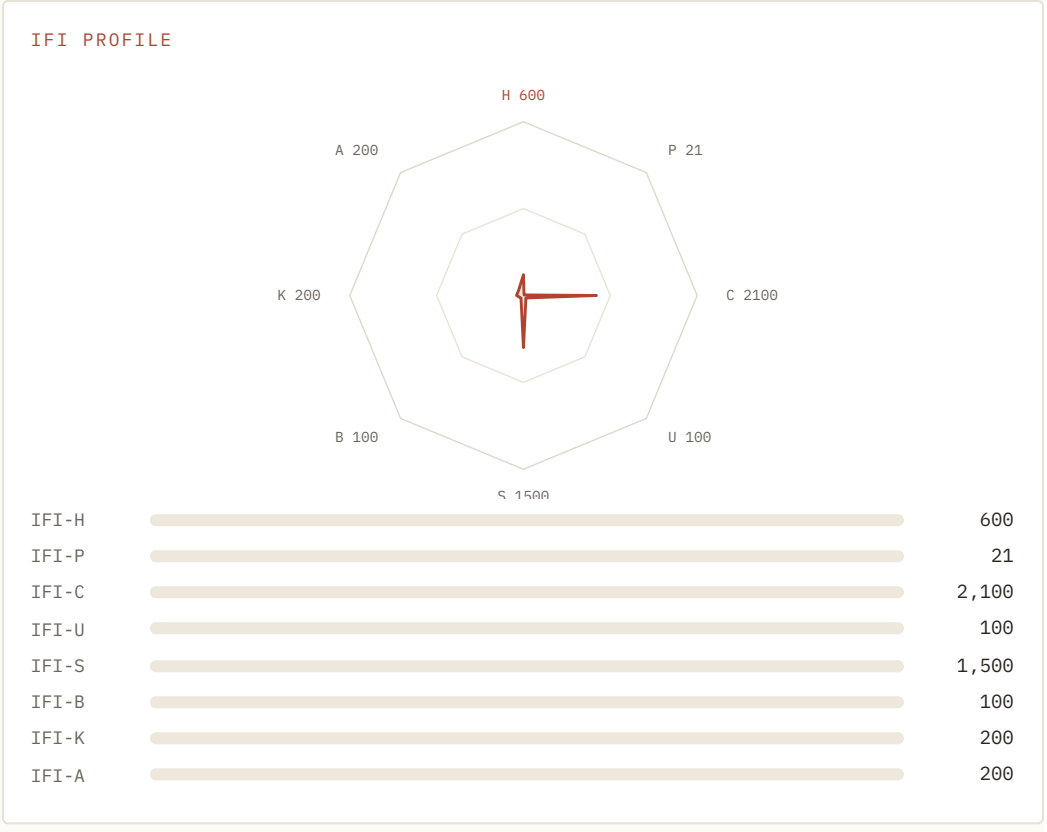
Cucumber-mint cooling granita · a thread of warmth beneath the cold

Built on engineered Peppermint (C 2,360) and a microdose of grown-in heat, frozen so the cold is literal and the menthol-cool rides on top of it while the warmth rises from underneath. *The children ask for this one; the adults are quietly astonished that something so cold can also be, faintly, hot.*

Cucumber, peeled and seeded	500 g
Engineered peppermint leaves (C/M)	20 g
Lime juice	60 ml
Cane sugar or agave	70 g
Water	150 ml
A mild designed chili (microdose), seeded	1/2 small
Flaky salt	1 pinch

1. Warm the water and sugar to a bare syrup, drop in half the mint off the heat, and steep ten minutes; the menthol is freely extracted and needs no boiling. Strain.
2. Blend the cucumber, lime, salt, the remaining fresh mint, and the chili with the cooled syrup until smooth. Taste: the heat should sit at the very bottom, a rumor.

3. Pour into a shallow tray and freeze, dragging a fork through the crystals every thirty minutes for about three hours, until it is loose, glittering shards.
4. Serve immediately in chilled glasses. The sequence is the point — the ice gives literal cold, the menthol gives a second cold that *moves*, and the chili rises last as a warmth the cold keeps circling back over. Three temperatures, one spoon.



Cool at 2,100 over a heat of 600 is fire and ice composed to refresh rather than to astonish — the TRPM8 and TRPV1 channels both firing, the brain handed a contradiction it cannot resolve and does not want to. It is the clearest proof in the kitchen that a sensation is only a receptor, and a receptor can be set against its opposite and served cold.

Chapter 17 · Three axes at once — *the triple-axis library.*

COMPOSITION · IFI-M · the M3 library · 2,800 constructs · 56 triples

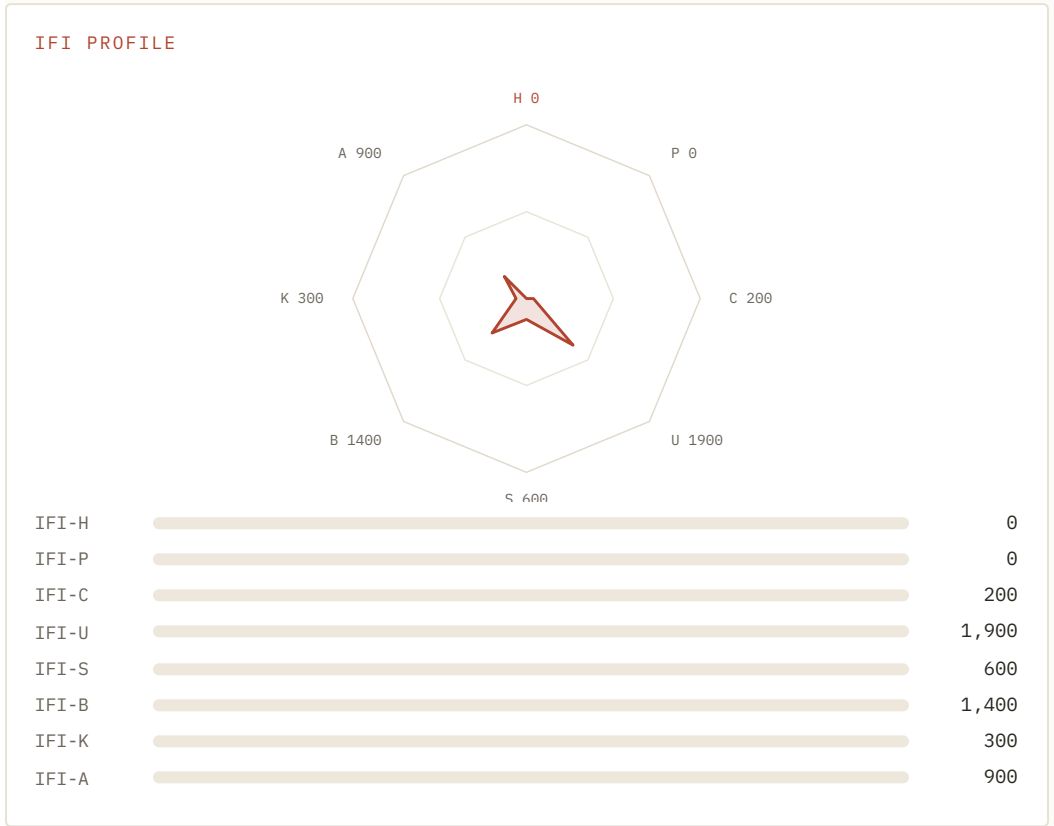
Add a third axis and the arithmetic turns strict. There are 56 possible triples, C(8,3), and the realized triple-axis library holds 2,800 constructs across them — **fifty per triple**, a sixth of the dual library's density, and the thinness is not neglect but difficulty. Three branches to balance means three draws on the same carbon and cofactor budgets and three folds to keep stable; the flux model is now solving against several binding constraints at once, pinned to a vertex of the feasible polytope with no slack left (Chapter 9). This is the altitude where composition stops forgiving mistakes, and where a platform earns its keep most plainly — you cannot find a stable triple by tasting, because the space of three-axis points is too large to wander and the stable region within it too narrow to stumble on. You compute the allocation, rank the edits against a shared fold margin, and trust the loop.



Tea — a natural triple, umami and bitterness and astringency held in one leaf (U/B/A, 280 constructs). The cup that most people drink is already a three-axis composition, written by the plant before anyone could score it.

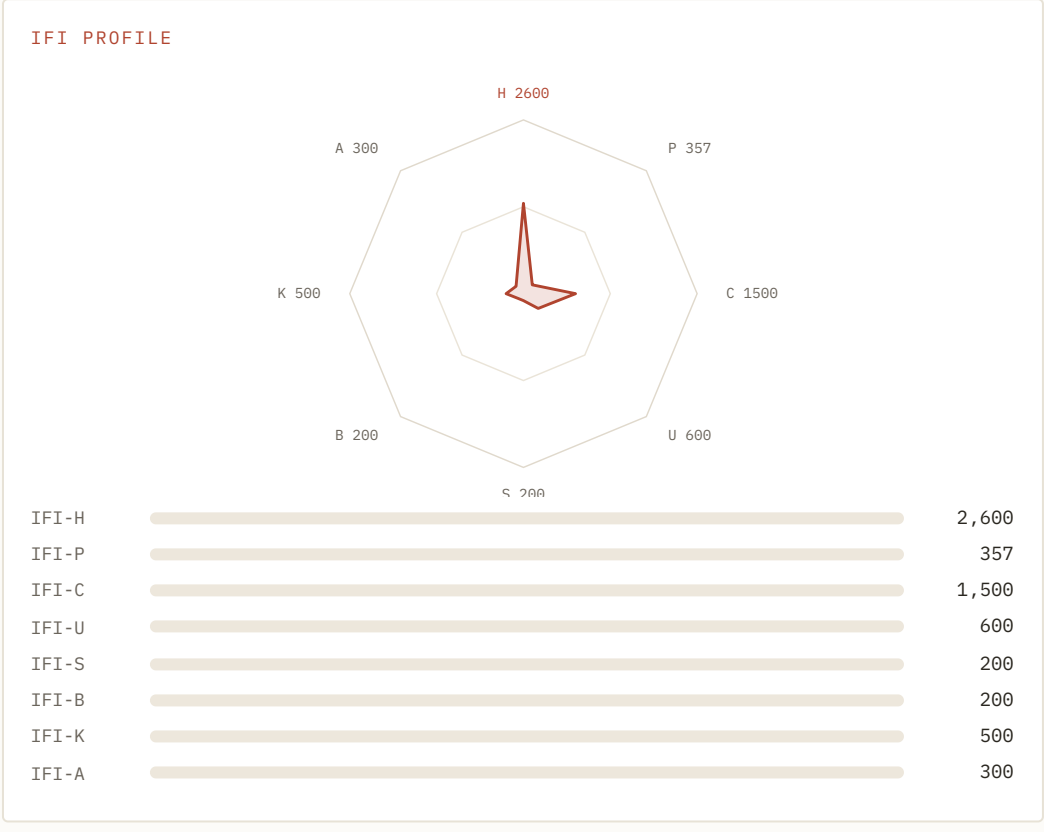
Nature furnishes two triples worth studying before we build our own, because each teaches a different face of three-axis design. The first is **tea** — *Camellia sinensis*, native to the U/B/A door at 280 constructs — where umami (the theanine savor), bitterness (the catechins and caffeine), and astringency (the tannins) all arise from one leaf and all trade against one another through the plant's nitrogen metabolism and the grower's shade. A cup of fine green tea is a three-axis composition the plant wrote and the brewer tunes,

and it is the clearest proof that triples are not exotic: the most-drunk beverage on earth after water is a triad. Scored as the leaf delivers it:



Umami forward at 1,900, the zero-bitter axis doing real work at 1,400 to keep the catechins in their place, astringency pulled back to a soft grip at 900 — a triad held in balance, cool and green and quenching.

The second natural triple is older than the Index and written in a wok: **mála**, the numbing-heat of Sichuan, a three-axis composition centuries before anyone could score it. Heat from the chili, IFI-H at TRPV1. The cool, tingling buzz of the Sichuan pepper — hydroxy-α-sanshool working the thermal and sharp channels — read on the Index as IFI-C, the cool-burn axis. And the bright, lifting pungency that carries the whole thing, IFI-P at TRPA1, the channel of the fermented bean paste and the aromatics, native to **Black Mustard** at 2,790 constructs (P/M). Three receptors, three budgets, one sensation the mouth integrates as a single astonishing event — heat and tingle and sharpness that the brain cannot quite separate. Scored as a mála chili oil, the triad composed on purpose:



Read the two dominant spokes — H 2,600, C 1,500 — plus the pungency channel at P 357 (by the revised AITC convention constant) standing together without any one swallowing the others, and you are reading the triple-axis problem solved: a flux allocation that funded all three branches against a shared budget, and a fold margin rationed across the enzymes each branch required. To design mála is to hand the model a three-coordinate target and ask for the proportion that holds, which is the composition problem at the altitude where it stops forgiving — and the altitude where, with only fifty constructs per triple to show for it, every realized point is dear.

The reason a triple is so much dearer than a pair repays one more look, because it is the quantitative spine of this whole part. A dual-axis design pins against one or two binding constraints and leaves the flux solution some slack — the flux-variability range stays wide, the axis is robust, the coefficient of variation stays easily inside seven percent. A triple tends to pin against three or four constraints at once — carbon *and* SAM *and* malonyl-CoA, say — which drives the optimum to a tight vertex of the feasible polytope where the variability range collapses and the plant has almost no room to wobble before an axis slips. That tightness is why the realized triples number only fifty per combination against the pairs' three hundred: not because triples are less wanted, but because each one demands a flux solution robust enough to survive a living plant's daily noise, and robust solutions in a pinned-down polytope are rare and hard-won. The combinatorial bell says there are 56 triples to build; the flux geometry says each will cost roughly six times the effort per construct — and the library's shape, dense in pairs and sparse in triples, is that cost made visible.

Mála chili crisp · the numbing-heat triad in a jar

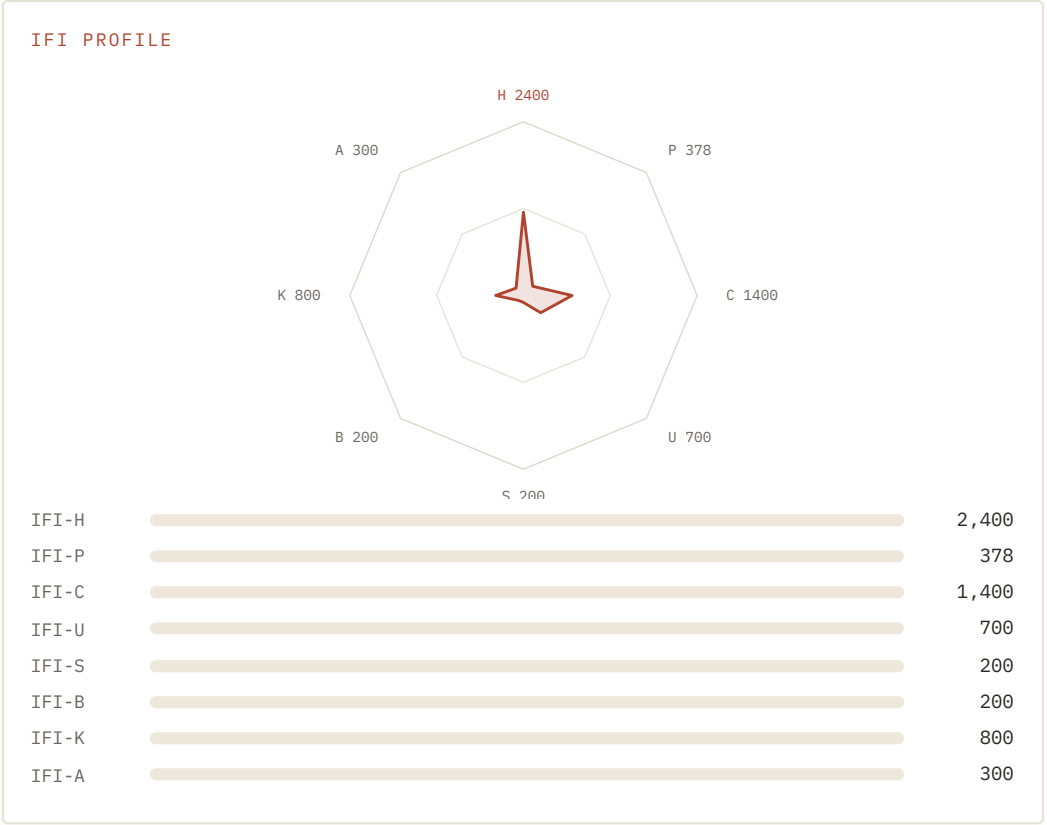
The three-axis composition that a Sichuan kitchen has made for centuries, built here on a designed heat cultivar, real Sichuan peppercorn for the tingle, and a pungent aromatic base. Vegetarian, and all the better for it — the depth comes from the alliums and the ferment, not from meat. *This jar lives in our refrigerator door; it goes on everything, which is the whole argument for learning to compose a triple.*

Neutral oil (grapeseed or peanut)	300 ml
Designed chili flakes (heat cultivar)	40 g
Sichuan peppercorns, lightly toasted	15 g
Garlic (K/P), thinly sliced	6 cloves
Ginger (P), julienned	30 g
Star anise	2
Fermented black beans or bean paste	2 tbsp
Toasted sesame seeds	2 tbsp
Soy sauce and a pinch of sugar	to season

1. Put the chili flakes and half the toasted, coarsely cracked Sichuan peppercorns in a heatproof bowl with the sesame — this is the bed the hot oil will bloom.
2. Warm the oil gently with the garlic, ginger, star anise, and the remaining peppercorns over low heat, letting the aromatics fry slow and pale-gold, fifteen minutes; low and slow keeps the garlic

sweet and draws the tingling amides out of the husks without scorching them.

3. When the garlic is crisp and the oil is fragrant, stir in the fermented beans for a last minute, then pour the whole hot mixture — oil and solids — over the chili-and-peppercorn bed. It will roar and bloom; stand back.
4. Season with soy and a pinch of sugar, cool, and jar. Rest a day before using: the three axes marry as it sits, the heat settling under the tingle, the pungency lifting both. Taste for the triad — heat you feel, a buzz that vibrates, a sharpness that carries.



Heat, pungency, and cool-tingle standing at H 2,400, P 378, C 1,400 with a savory floor beneath them is mála as the mouth actually receives it: three channels firing at once — TRPV1, TRPA1, and the KCNK-flutter of the sanshool — that the brain refuses to separate into parts. It is the oldest triple-axis composition on earth, and the proof that long before anyone could score a chord, a kitchen could compose one by hand and hold it for a thousand years.

Chapter 18 · The full chord — *eight budgets, one fruit.*

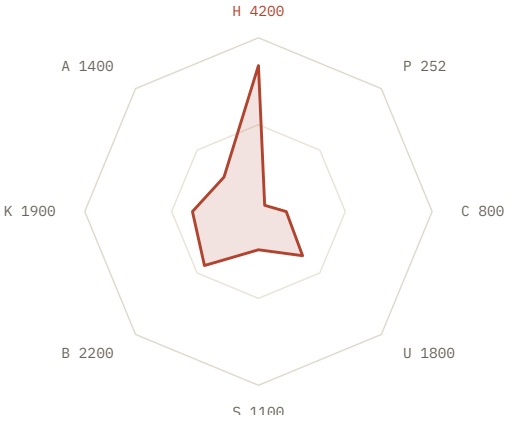
COMPOSITION · IFI-F · all 8 axes · Phoenix · SS-0096

At the far corner of the space, where all 255 axis-signatures resolve to their single maximal one and the only subset left to choose is the whole set, sits the only cultivar we have ever designed to register on every axis at once. **Phoenix** — SS-0096 — is the eight-dimensional point itself, not a projection of it, and every pair and triple in this book has been a shadow it cast onto a lower plane. Here, at last, is the whole fruit, un-projected:



Phoenix under specimen isolation — the single eight-axis point the platform has ever grown, and the proof that the entire space is addressable rather than merely mappable.

IFI PROFILE





AXIS	SCORE	AXIS	SCORE
IFI-H · Heat	4,200	IFI-S · Sweetness	1,100
IFI-P · Pungency	252	IFI-B · Zero-Bitter	2,200
IFI-C · Cool-Burn	800	IFI-K · Kokumi	1,900
IFI-U · Umami	1,800	IFI-A · Astringency	1,400

Its heat is the headline — IFI-H 4,200, corresponding to **our model's prediction of approximately 2.95 million Scoville heat units**, the highest design target yet specified in a commercial construct — but read the whole radar and the point of the thing is the company that heat keeps. Eight budgets, allocated at once from one shared trunk, held in proportion by the flux model: bitterness attenuated to 2,200, kokumi and umami grown in near 1,900 and 1,800, a designed astringent finish at 1,400, a sweetness of 1,100 beneath the burn, a pungent sharpness at 252 (by the revised AITC convention constant), a thread of cool at 800. The double variant — **S39L+L345G** — the two design edits from the frontier, their stabilities combining to roughly −3.9 kcal/mol — made the heat reachable; the flux model made the other seven *coherent* instead of chaotic, and the fold margin held because the edits that raised the heat also strengthened the enzyme that had to carry everything else.

Hold the full vector against the ladder it sits atop, because the ladder is the clearest picture of composition happening — the octagon filling in rung by rung as the flagships climb from a near-pure note toward the whole chord:

CULTIVAR	SKU	PREDICTED SHU	IFI-H	AXES LIT
Ember	SS-0087	~866K	1,570	2/8
Cinder	SS-0088	~1.05M	2,290	3/8
Blaze	SS-0091	~1.72M	2,630	4/8
Wildfire	SS-0092	~1.96M	2,930	5/8
Firestorm	SS-0094	~2.47M	3,490	6/8
Solara	SS-0095	~2.72M	3,980	6/8
Phoenix	**SS-0096**	**~2.95M**	**4,200**	**8/8**

SHU values are computational predictions from our flux model, not certified measurements.

How eight budgets were made to fit in one fruit is worth a paragraph, because it is the flux chapter's logic run at the hardest setting. The binding constraint on the full chord was not carbon — the shikimate trunk can be widened — but the shared methyl donor, **SAM**: four of the eight axes (heat, zero-bitter, kokumi, and part of the pungency) draw on it at once, and the full chord asks for all four, so the SAM-regeneration flux, not the ferulate supply, set the ceiling. The allocation that worked did not trade the axes against one another; it engineered the *supply*, lifting the methionine-cycle regeneration so the methyl pool refilled fast enough to feed four methylating branches in parallel. This is the deepest lesson of the full chord, and it is counter-intuitive: the way you build eight loud axes at once is rarely by sharing a fixed budget more cleverly: it is by finding the

single cofactor that binds and widening *it*, so the competition dissolves rather than being refereed. The model found that SAM was the wall. The edit widened the wall.

There is a delivery side to the full spectrum worth naming, because eight axes arriving on a tongue at the same instant can read as noise rather than a chord — the perceptual layer's revenge on an over-full vector. The full-spectrum composite products (the IFC line, built on this flagship's profile) use **nanoparticle encapsulation** to stage the arrival: axes released on slightly different timescales so the mouth hears them as a sequence — a phrase — rather than a simultaneous blare. Encapsulated delivery is, in the language of Chapter 6, a perceptual-layer tool: it does not change the vector, it changes the *order of arrival*, which is the one variable a living fruit cannot fully set on its own. Composition does not end at the plant wall. It extends into how the composed flavor is carried to the tongue.

A plain word on using it, since the number invites misreading: Phoenix, with our model predicting approximately **2.95 million Scoville heat units**, is not an eating pepper in the ordinary sense, any more than a pure extract is a drink. It is a design instrument and a source — a thing you dilute by orders of magnitude into a sauce, a crisp, a single drop in a pot — and the eight-axis profile is what makes a microdose of it taste like *food* rather than like an assault, because the heat never arrives alone. The umami and kokumi and the eased bitterness ride in with it even at a thousandth of the dose, which is the quiet practical gift of designing the full chord: the company heat keeps scales down with the heat.

Read the last column as the real story. Ember is two axes lit — a shape with two points. By Phoenix the octagon is whole. The heat climbing from 1,570 to 4,200 is the headline anyone notices; the axes count climbing 2 → 8 is the *composition*, the quiet proof that the platform was never only laddering a single number. What Phoenix proves is not that extreme heat is possible — that was settled rungs earlier. It is that **the entire space is addressable** — that you can name all eight coordinates at once and grow the point, hold eight budgets against one trunk, ration one fold margin across eight perturbations, and have the result eat as *one fruit* rather than eight flavors arguing. Everything smaller than this — every dual, every triple, every mild culinary cultivar on the far gentle side of the space — is now a matter of choosing where to stand. The full chord was the hard proof. The rest is the music.



PART V OF V

The Reading

the silhouette · the frontier · the ninth axis

Chapter 19 · Reading a composed scorecard — *the shape of a blend.*

PRACTICE · the silhouette · the brief · the ≤7% band

A multi-axis scorecard is not a list of peaks; it is a *silhouette*, and learning to read combination means learning to read the shape rather than the tallest bar. Because every axis is normalized to the same 0-to-5,000 ceiling, the radar of a tomato and the radar of a superhot are drawn on the same octagon, and you can compare their *forms* — where they bulge, where they go quiet, how balanced or spiky the whole outline is. A composed flavor has a shape you can recognize across the room, the way you know a face before you can name a feature.



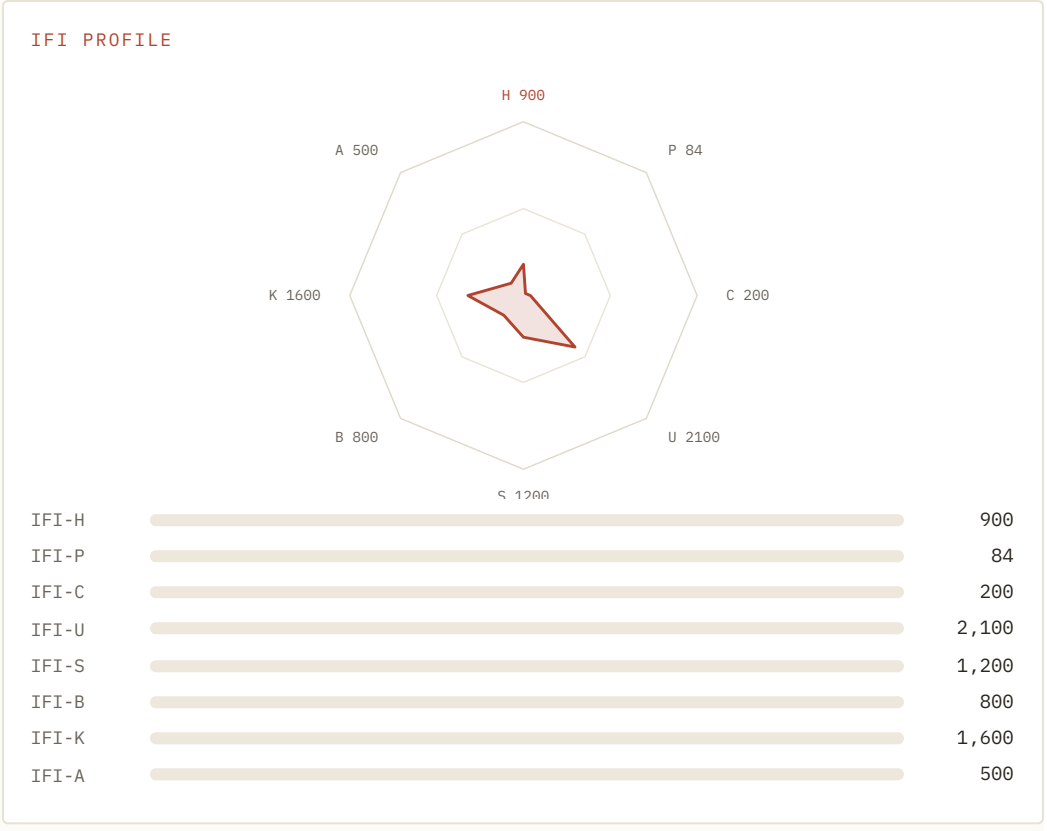
A finished flagship, isolated for the record — the point of reading a scorecard is to hold this fruit's whole silhouette in one glance, not to chase its tallest spoke.

There is a grammar to the shapes, and four forms cover most of what a reader will meet. A **monad** is a star with one long ray — a single-axis cultivar, a pure note, legible and loud and simple. A **dyad** is a shape with two poles, and its character is in the *ratio* of the two: a swicy with heat long and sweet short reads utterly unlike one with the poles reversed, though both light the same two spokes. A **triad** is a triangle, and the eye should check whether it is roughly equilateral — three axes genuinely balanced, the hard-won mála — or a thin sliver where one axis dominates and the other two are alibis. And the **full chord** is the filled octagon, which the eye reads not as eight separate lengths but as an overall *area and roundness* — how much total flavor, how evenly distributed. The experienced reader stops summing spokes and starts seeing gestalts, and the gestalt is usually the brief.

For a formulator, the silhouette *is* the specification, and this is the practical heart of the chapter. You do not order "hot." You order a shape — a target vector, a silhouette you need matched — and the scorecard is both how you write the order and how you check that the order came back right. The check has a number attached, and it is the number the whole platform defends: every axis holds to a **coefficient of variation of seven percent or better**, batch after batch, which means the silhouette you specified is the silhouette you receive, within a tight and stated band, in February as in August. For a composed cultivar this is a stronger promise than for a single-axis

one — every spoke in the band at once, not just the tall one — and it holds for the reason the design loop built in: the axes are co-regulated outputs of one flux solution in one fruit, their variations correlated rather than independent, the robust low-variability vertex chosen over the fragile high-scoring one. A formulator buying a composite is buying a *shape with a tolerance*, and the tolerance is what lets them build a product around it without re-testing every lot.

Read a composite the way the panel does, and a discipline falls out that is worth stating as a rule: **check the quiet spokes first.** The tall axis is self-advertising; it will announce itself on the first taste and it rarely surprises. The composition lives in the short spokes — the kokumi at 700 that keeps a sweetness from reading flat, the astringency at 400 that gives a heat a clean finish, the cool at 300 that makes a drink seem to move. Those are the axes a naïve stack loses first and a real composition protects most carefully, and they are the ones a careful reader audits, because a scorecard that nails its headline and loses its floor has lost the very thing composition was for. Here is a composed culinary cultivar — not a superhot, but a balanced everyday fruit meant for a weeknight pan — scored so the short spokes carry the meaning:



The headline is a gentle heat at 900, reachable by anyone; but run the quiet spokes and the composition appears — umami at 2,100 and kokumi at 1,600 giving the fruit a savory depth that makes a quick dish taste slow-cooked, a sweetness of 1,200 to round it, a debittering touch at 800 so nothing reads harsh. This is the register most of the kitchen actually wants — not the far corner of the space but a well-chosen point near its gentle middle, every axis present

and none of them shouting. A reader who can hold that whole silhouette in one glance can order it, match it, and defend it, which is the entire practical purpose of drawing flavor as a shape.

Make the match quantitative, because a formulator does not trade in impressions but in acceptance windows, and the vector makes both the order and the check into arithmetic. A specification is a *target vector* with a tolerance on each axis — for the cultivar above, the brief is **t** = (900, 1200, 2100, 800, 1600, 200, 400, 500) with each spoke held to the platform's ±7% coefficient of variation. The umami axis, specified at 2,100, therefore carries an acceptance window of 2,100 ± 147, or [1,953, 2,247]; any lot measuring inside it is in spec, any lot outside it is flagged. When a delivered lot is assayed, it returns its own vector **d**, and the single-number match score is the distance between order and delivery, $\|\mathbf{t} - \mathbf{d}\|$ — the same Euclidean norm from Chapter 2, now doing quality control.

Watch it localize a drift. Suppose a lot comes back with every axis on target but umami at 1,950. The match distance is $\|\mathbf{t} - \mathbf{d}\| = \sqrt{(150^2)} = 150$ — small, because only one axis moved — and the per-axis check does the rest of the work: $|2{,}100 - 1{,}950| \div 2{,}100 = 7.1$ percent, a hair outside the ±7 band, so the lot is flagged and the *reason* is already named. The formulator does not reformulate the product or re-test the other seven axes; the distance vector points straight at the umami branch, and the correction is to the glutamate pathway alone. This is the deepest practical gift of composing with vectors: drift is not a vague "the batch tastes off" but a displacement with a direction, and a displacement with a direction is a repair with an address. A house profile — a sauce, a bar, a blend built around a composed cultivar — stays itself across years and lots because the thing being held constant is a point in eight-dimensional space, and any wander from it is measured, localized, and corrected before it ever reaches a tongue.

Why the composite coefficient of variation does not blow up under all this is worth restating in the formulator's terms, because it is the promise they are buying. Eight axes each held to ±7 percent could, if they varied *independently*, produce a silhouette whose overall shape wandered far more than any single spoke. They do not vary independently: they are co-regulated outputs of one flux solution in one fruit, their fluctuations correlated by the shared ripening that drives them all, and the design loop rejected any solution that sat on a high-variability vertex in favor of one in a robust basin. So the silhouette holds as a *shape*, not just as eight separate numbers — which is exactly what a formulator needs, since they are building a product around the gestalt, not around any one axis. The scorecard is the order, the specification, the incoming-QC check, and the drift diagnosis, all in one octagon, and that is why we teach everyone downstream of the platform to read it.

Chapter 20 · The combinatorial frontier — *what we have not yet built, and the line we hold.*

FRONTIER · the sampling map · attributes, never claims

Return, at the end, to the arithmetic that opened the book, because it has one more thing to show — not the size of the space now, but the shape of our *progress across it*, which is the most honest map of where the work stands. Lay the bell of possibility (how many chords exist at each order) beside the reality of what we have built, and the frontier draws itself:

ORDER	CHORDS POSSIBLE	REALIZED SAMPLING	PER CHORD	STATUS
monad (1 axis)	8	the single-axis libraries, thousands of constructs	—	**saturated**
dyad (2 axes)	28	8,400 constructs	~300	**dense**
triad (3 axes)	56	2,800 constructs	~50	**sparse**
tetrad (4 axes)	70	a handful, via full-spectrum-capable lines	few	**frontier**
pentad (5 axes)	56	—	—	essentially unsampled
hexad (6 axes)	28	—	—	unsampled
heptad (7 axes)	8	—	—	unsampled
octad (8 axes)	1	Phoenix · SS-0096	1	the single proof-point

Read it honestly and the frontier is not where a newcomer would guess. We have *saturated* the single axes and *densely sampled* the pairs; we have *sparsely sampled* the triples; and at the extreme far corner we have planted exactly one flag, the octad, as proof that the corner is reachable at all. But look at the fat middle of the bell — the tetrads and pentads, 70 and 56 chords, **126 four-and-five-axis**

combinations, almost none of them built. That is the true frontier of this library: not the full chord, which we reached as a demonstration, but the *balanced middle* — the four- and five-axis flavors where most of the world's genuinely complex food actually lives, and where the combinatorial explosion has so far outrun our sampling. A great mole is a tetrad we have not grown. A fine aged wine is a pentad. The eight-axis fruit was the hard proof of reach; the four-axis fruit, grown cheaply and reliably and at the gentle end of every spoke, is the hard work of coverage, and it is mostly ahead of us.



The research line stretching back toward the frontier — a platform's progress across an eight-dimensional space is measured not in its farthest point but in how much of the balanced middle it has learned to grow reliably.

Set the frontier against the ledger, because the canonical numbers are the frame around all of it. The platform holds on the order of **~19,000 engineered construct designs** in our research library, of which **~225 distinct construct designs** back the **19,500 purchasable product SKUs** (product names are catalogue labels, not each representing a unique sequence) — a reminder that the built library is itself a small, deliberate sampling of a far larger named space, which is a larger sampling of a continuum with no edge. **Forty-two host organisms**, **eight axes**, the **≤7% coefficient of variation** that makes a composite specifiable, **three patents filed**, and **twenty-one peer-reviewed papers** posted open-access under CC BY 4.0 so the method can be checked rather than merely claimed. The combinatorics says the menu is boundless; the ledger says what portion of it is actually on the shelf; and the honesty of the company is in never letting the first number be mistaken for the second.

A word, then, on the line we hold at the frontier, because a combinatorics this powerful invites two kinds of overreach and we decline both. The first is the overreach of the *label.* Because our axes are grown into the plant at the source — the glutamate in the fruit, the debittering in the bean, the kokumi peptides in the legume — a composed flavor arrives *inside* an organism and labels as food, not as a stack of additives dosed into a formula. That is a genuine advantage, and precisely because it is genuine we state it plainly and do not dress it up: the savor was restored, not added; the sweetness was uncovered, not synthesized; the construct is documented, patented where novel, and published where checkable. Source-side engineering earns a clean label by being clean, not by being quiet about what was done.

These are computational designs; Scoville Splice's cultivars and constructs have not been experimentally validated in a laboratory. The designs are built on computational predictions from our flux model, ESM2 stability analysis, and receptor pharmacology — a rigorous basis, and an honest one, and a different thing from a lab-validated result.

The second overreach is the one this whole library refuses hardest: the overreach of the *claim.* Everything in this book is a flavor — a receptor driven, an EC_{50} measured, a silhouette specified — and a flavor is an *attribute*, not a benefit promised to a body. We have said, more than once, that a plant grown toward its fullest flavor is often grown toward its fullest nourishment, because the same late ripeness that pools the glutamate pools the vitamins, the same metabolic maturity carries both. We say it because it is true of the plant's chemistry, and we stop exactly there. No cure, no detox, no health halo, no promise that a composed fruit will do anything for anyone beyond taste the way we designed it to taste. The nourishment is an *intention* in how we grow and a *fact* about ripeness; it is never a claim on a package, and the discipline of holding that line is what lets the quiet through-line of this library stay honest across sixty-four books. Combinatorics gives us enormous reach. The line we hold is that reach is not permission — that the power to compose any flavor is not the power to promise any benefit, and that the difference between an attribute and a claim is a difference we keep on purpose, for the body's sake and the reader's trust.

Chapter 21 · A closing note · the composition we don't yet score — *flavor, and the body that reads it.*

NOURISHMENT · the ninth axis · the arithmetic of a table

There is a composition this book has not drawn, and it is the one our family thinks about most. Every page here has been about allocating a shared budget of carbon and cofactor across the branches that become taste — but the same trunk, the same flux, the same late ripeness that carries umami or sweetness also carries the vitamins, the minerals, the carotenoids and the compounds the body actually draws nourishment from. We proved it on the tomato without meaning to: the late-ripening window that pools the free glutamate is the same window that builds the lycopene and the vitamin C, so the fruit we tuned toward its fullest savor came back richer in the things a body is fed by, in the same motion, from the same metabolic maturity. A plant composed toward its fullest flavor is, almost always, a plant composed toward its fullest nourishment. They were never two problems. They are two readings of one allocation.

So the honest end of a combinatorics of flavor is the admission that there is a ninth axis we do not yet score, and that we are building the column for it with the same rigor and the same restraint the other eight taught us. Imagine the flux model with one more objective in its brief — not only the vector on the tongue but the vector in the body, the vitamins and minerals and bioavailable compounds the same ripeness could carry — and the same linear program asked to find the allocation that holds *both*. Much of the machinery is already in hand: the shared trunk is the same trunk, the shared cofactors the same cofactors, the loop the same loop. What is not yet in hand is the measurement — the receptor-honest, assay-anchored number that would let nourishment sit on the radar beside heat and be *composed* against it rather than hoped for alongside it. That number is the subject of the books further along this shelf, and it is, in truth, the reason we learned combinatorics at all.

The measurement is hard in a way the eight axes were not, and the difficulty is instructive about why we have not simply declared it solved. Every one of the eight has a *receptor* — a single protein whose half-activation gives EC_{50} a clean meaning, so that loudness can be measured against one honest anchor. Nourishment has no such receptor. It is not a taste; it is an outcome, and the outcome depends not only on what the food contains but on what a particular body, with a particular meal around it, can actually *absorb*. Iron in a leaf is not iron in the blood; a carotenoid locked in a raw cell wall is not the same as one freed by gentle cooking and carried on a little fat. The honest analog of EC_{50} here is not how much of a nutrient the food holds but how much the body can *draw* from it — bioavailability, which is a joint property of the food, the matrix it arrives in, and the eater — and measuring that with the rigor we hold

the flavor axes to is genuinely unfinished science, not a number we are coyly withholding. We would rather say *we are still building the ruler* than print a figure the body cannot cash. The restraint is the same one that governs the whole library: an attribute is measured before it is scored, and a benefit is never claimed at all. The ninth axis will go on the radar when we can measure it as honestly as the heat — and not one book sooner.



The founders at dusk, the greenhouse behind them — the table that started the whole question, and the one the arithmetic was always serving.

Because in the end the combinatorics is domestic, and it is worth saying so plainly after twenty chapters of linear programs and interaction matrices. A table set for the people you love is a composition — this much heat so the children can still reach for it, this much savory depth so no one asks where the meat is, this much sweetness to make the whole thing feel like care, this much bitterness eased so the greens get eaten, this much coolness so the summer meal lands light. Every cook who has ever balanced a dish for a particular table, for the people who would actually sit down to it, has solved a constrained optimization in eight dimensions by hand and by heart, without a model, without a number, and gotten it right by the only measure that finally counts, which is whether the people they fed were glad.

We spent years learning to solve that system in a plant — to name a coordinate in the space between the axes and grow the point, to pay for each flavor in carbon from the account another was spending, to ration a fold margin across eight perturbations and have the result eat as one fruit. The mathematics is real and we have shown it in full, because numbers are a form of respect for the reader and because you cannot design what you cannot measure. But the mathematics was never the point. We already knew how to solve this system at the table; the platform only let us solve it in the seed, so that the balance a good cook reaches for would already be grown into the thing they reach for. This book was only ever the arithmetic underneath something we were always going to do anyway: feed the people we love, on purpose, with the fullest flavor and the fullest nourishment we could compose into one living fruit — eight axes, held in proportion, grown toward a table.