THE LIVING ADDRESS

Transcription Termination and RNA Processing

The Clock and the Cut

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In which the reading of the address is found to run at a fixed tempo — a clock set not by need but by the warmth of the field itself — and the raw copy is then edited, cut and capped and spliced, so that the message is separated from the vast address-space around it, the very stretch science calls junk.

Tau (T) is the living fabric of time itself — the sole substance of which all physical reality is composed. Every particle, force, wavelength, and conscious experience is a structured configuration of T-flow. There is no gravity, no electromagnetic force, no strong nuclear force as separate entities: all are registers of the single T-field operating across dimensional levels. The conservation law $d\Sigma T=0$ governs all change: T is never created or destroyed, only redistributed.

Introduction — Through the Force of Time

The chapter that follows is, in the conventional telling, how a transcript is elongated, how transcription ends, and how the raw RNA is processed into its finished form. Read through the Universal Force of Time, it is where the reading is found to run on a clock set by the field itself, and where the raw copy is edited to separate the message from the vast address-space around it.

Chapter Four showed the reading begun. This chapter shows it run and end — and the first thing to notice is that it runs at a fixed tempo. Once a gene is being read, the letters are laid at a steady pace, about sixty a second, and — this is the telling part — the pace is the same whether the cell is racing or resting. It is not set by demand. It is set by temperature, and in the reading of this book heat is nothing but the local density of the time-fabric. The tempo of reading is therefore a clock of the field: a T-metronome, ticking at a rate the register sets, not the cell. As in copying, regulation lives at the beginning; the running itself is clockwork.

Watch, too, how the reading is made to stop. The commonest full stop is a hairpin rich in guanine and cytosine — the three-bond pair — that stalls the machine, followed by a run of uracils whose grip, the weak two-bond kind, lets the machine slip free. The very lattice primes that clamp the base pairs, two and three, now punctuate the reading itself:

the three-bond clamp calls the pause, the two-bond grip calls the release. Start and stop are lattice operations.

The heart of the chapter is the editing. The raw transcript of a gene is not the finished message; it is capped at the front with a backward-set guanine — a protective stamp written, note, on the Venus base — and, above all, it is spliced: long stretches called introns are cut out and discarded, and the remaining pieces, the exons, are joined into the mature message. Mainstream biology has never had a satisfying account of why so much of a gene is thrown away. This book does. If most of the genome is address-space — the coordinate that locates a living thing in the field, the very stretch science dismisses as ‘junk’ — then splicing is exactly the separation of the message from the address, performed in real time: the coordinate cut out of the instruction, the instruction alone sent on to be built.

So the puzzle the biologist notes but cannot explain — why the cell should so carefully remove most of what it just copied — is, in this reading, no puzzle at all. The removed part was never message. It was address, and the cell is separating the two.

Carry this into the chapter: the reading of the address runs on a T-clock set by the warmth of the field, is punctuated by the lattice primes 2 and 3, and is edited — capped, cut, and spliced — to separate the T-message (the exons) from the T-address-space (the introns) that surrounds it.

SECTION 5.1

The Tempo of Reading

In the last chapter we watched the reading-head settle on a promoter and begin. Now we let it run — and the first thing to notice, before any of the machinery, is that it runs at a steady beat. Once transcription is under way, the polymerase does not race or dawdle according to how badly the cell wants the product. It lays down the letters of the RNA copy at a fixed tempo, measured and even, like a metronome. And the tempo is quick: in a bacterium, roughly sixty letters a second. A gene of a thousand letters is read out in under half a minute; a long one in a few minutes; and always at the same unhurried, unhurriable pace.

This steadiness is worth dwelling on, because it is easy to miss how strange it is. You might expect a cell in a great hurry — growing fast, doubling every twenty minutes — to read its genes faster than a cell that is barely ticking over. It does not. Measure the reading rate in a fast-growing culture and in a slow one, at the same temperature, and it comes out the same. The cell does not control the speed of reading at all. It controls, as we saw, only the choice of what to read and when to begin. Once begun, the reading is clockwork. So what, then, sets the beat of the clock?

SECTION 5.2

A Clock Set by Heat

The answer is temperature. Warm the cell and the reading quickens; cool it and the reading slows; and at any fixed temperature the rate is fixed, whatever the cell's haste or leisure. The tempo of reading is a function of heat, and of heat alone. To a conventional biochemist this is unremarkable — all chemical reactions go faster when warmer. But recall what this book holds heat to be. Temperature, in the Force of Time, is not a separate thing that molecules happen to have; it is the local density of the time-fabric itself, the very T of which everything is made, measured as warmth. Heat is T.

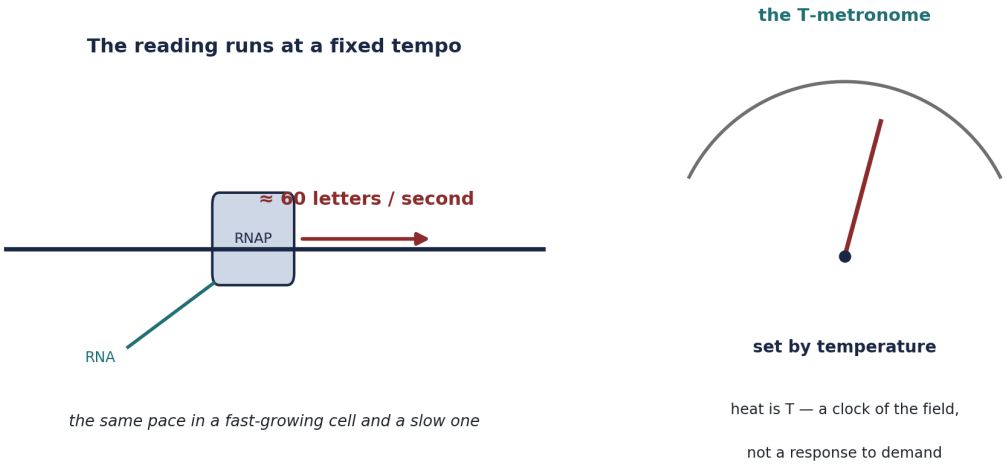

Figure 5.1. The tempo of reading. Once a gene is being transcribed, the polymerase lays down letters at a fixed rate — about sixty a second in a bacterium — the same whether the cell is growing fast or slow. The pace is set by temperature, and temperature is the local density of the time-fabric: the reading runs on a clock of the field, a T-metronome, not a response to demand.

So when we say the reading runs at a rate set by temperature, we are saying something the theory takes quite literally: the reading runs at a rate set by the local density of T. The tempo of transcription is a clock of the field — a T-metronome, ticking at whatever rate the local register of the time-fabric dictates. The cell does not wind this clock; it inherits it, from the warmth it sits in, which is to say from the flow of the one substance through it. And this is not the only clock of its kind we shall meet. In the very next chapter we will find protein-building keeping step with this same beat — the two great reading processes of the cell locked to one tempo — and later still we shall find the same principle at the scale of the planet, where the turning of the Earth is another clock the field keeps. The steady sixty-a-second of transcription is the first of these clocks to be measured, and the plainest: the field, keeping time.

KEY IDEA

Once begun, transcription runs at a fixed tempo — about sixty letters a second in a bacterium — set by temperature, the same fast or slow. Since heat, in this book, is the local density of T, the tempo of reading is a clock of the field: a T-metronome the cell inherits from the warmth it sits in, not a rate it sets by demand.

SECTION 5.3

Where the Reading Stops

A reading must end as well as begin, and the way it ends is a small marvel of the lattice. The commonest full stop written into a bacterial gene is a two-part signal, and each part is built from one of the two smallest primes we have met so clamping the base pairs of Chapter Two. First comes a stretch rich in guanine and cytosine — the three-bond pair, the strong one — arranged so that the RNA, as it emerges, folds back and pairs with itself into a tight little hairpin. That hairpin, gripping itself with its strong three-bond clasps, jams awkwardly in the machine and brings the polymerase to a halt. Then, immediately after, comes a run of the letter uracil, whose pairing with the DNA template is the weakest bond in all of nucleic acid chemistry — a feeble two-bond grip. With the machine stalled by the hairpin and the strand held only by that weakest of grips, the whole thing lets go, and the RNA is released.

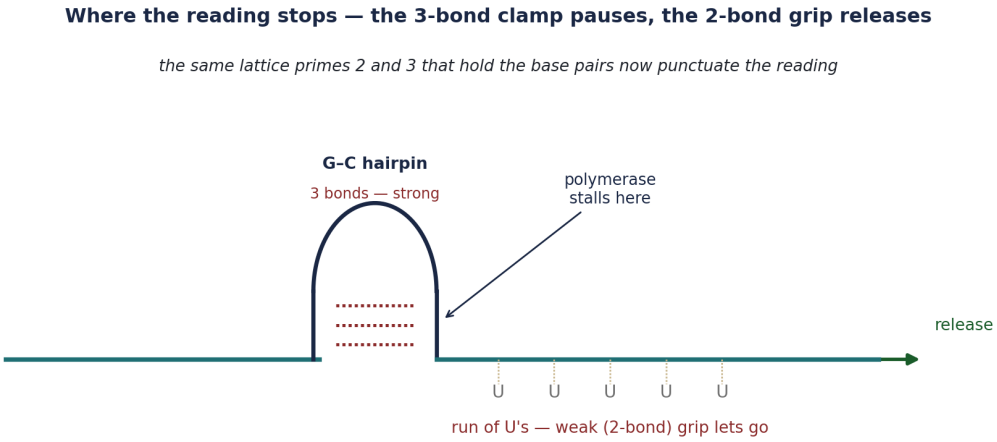

Figure 5.2. Where the reading stops. A guanine–cytosine hairpin — held by the strong, three-bond pairing — stalls the polymerase; a following run of uracils, whose grip is the weak, two-bond kind, then lets the machine slip free. The same lattice primes 2 and 3 that clamp the base pairs now punctuate the reading: the three-bond clamp calls the pause, the two-bond grip calls the release.

Read that mechanism through the lens of the lattice and it is beautifully clean. The reading is paused by the three — the strong, three-bond guanine–cytosine clasp — and

released by the two — the weak, two-bond grip of the uracil run. The very primes that hold the rungs of the ladder together in Chapter Two, and that clamped the pump's ratio in Chapter One, now serve as the punctuation of reading: the three calls the full stop, the two turns the page. Start and stop, in the cell's reading of its address, are lattice operations — the melting-order of the bonds, which the lattice itself ranks, deciding where the machine pauses and where it lets go.

KEY IDEA

The commonest stop signal is a G–C hairpin (the strong three-bond pair) that stalls the polymerase, followed by a run of uracils (the weak two-bond grip) that releases it. The lattice primes 2 and 3 that clamp the base pairs now punctuate the reading — the 3-clamp pauses, the 2-grip releases.

SECTION 5.4

One Reading, Many Pieces

The RNA that comes off the machine is not always ready to use. Often it is a long raw transcript that must be cut into its finished pieces — and the tidiest example is the reading of the genes for the ribosome, the protein-building machine itself. In the bacterium these are gathered into a handful of nearly identical stretches, read as single long transcripts, each of which is then cut by molecular scissors into several distinct finished RNAs: a large one, a small one, a middling one, and a little transfer RNA besides, all snipped from the one growing chain.

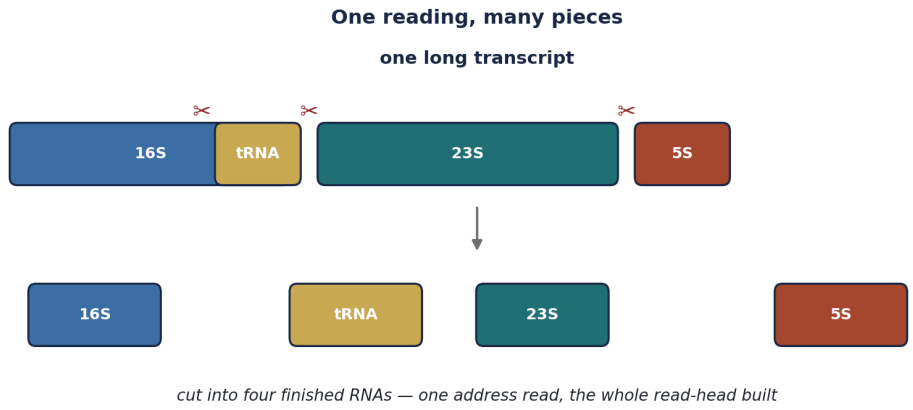

Figure 5.3. One reading, many pieces. The genes for the ribosome are read as a single long transcript, then cut by nuclease enzymes into several finished RNAs — a large, a small, and a middle ribosomal RNA, and a transfer RNA. One passage of the address, read once, yields the whole substance of the read-head.

There is a quiet elegance in this worth naming. One reading of one stretch of the address yields, after cutting, the whole set of parts for a ribosome — the very machine that will go on to read all the other addresses. The node reads a single coordinate and,

from that one reading, assembles the reader that serves the rest. (A small honesty, in passing: the bacterium keeps about seven of these nearly identical gene-clusters, and seven, as we noted for the polymerase's tail in the last chapter, is not a number of the lattice — a drift, not a node, and the book does not pretend otherwise.) The point that matters here is the shape of the thing: the raw transcript is not the product. It is stock, to be cut. And cutting, it turns out, is only the gentlest of the editing the cell performs on what it reads.

SECTION 5.5

The Cap on the Front

In the larger, compartmented cells — the eukaryotes — the editing goes much further, and it begins the moment the reading does. Almost as soon as the front end of a messenger RNA emerges from the polymerase, the cell fits it with a cap: a single guanine, chemically modified and, curiously, set on backward, joined to the front of the message by a reversed linkage found nowhere else in the molecule. The cap protects the message from being chewed up from the front, helps carry it out to the workshops, and helps the protein-builders recognise it as a message worth reading.

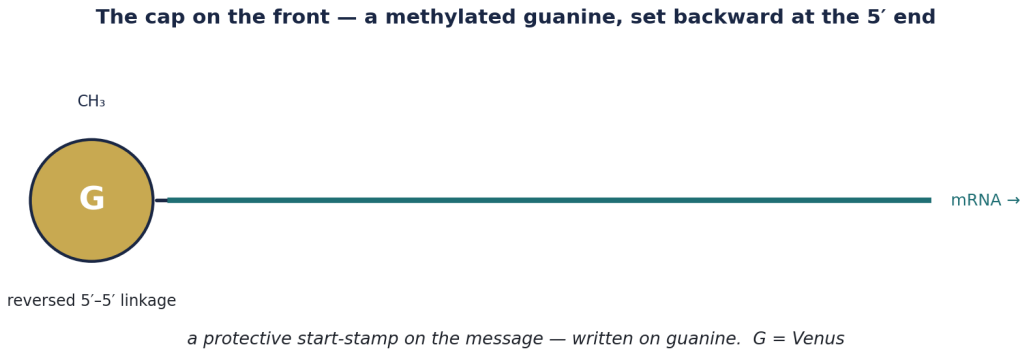

Figure 5.4. The cap on the front. The front end of a eukaryotic messenger RNA is fitted with a modified guanine, set backward in a reversed linkage — a protective start-stamp that marks the message and speeds its reading. The cap is written on guanine: G = Venus.

Notice the base the cap is written on: guanine. In the map of Chapter Two, guanine is the base of Venus. It is a small thing, and the book does not lean its whole weight upon it — but set it beside the findings of Chapter Three, where the cell's clock was kept on adenine, the Earth, and its sun-damage taken on thymine, Mercury, and a pattern continues to fill in. The protective start-stamp on the message is written on the Venus base. Each of the four letters, as the chapters accumulate, keeps turning up in the role its planet would suggest; and the cap is one more entry in that quietly lengthening ledger.

SECTION 5.6

The Great Editing

Now the deepest cut of all, and the strangest fact in this whole chapter. When a eukaryotic gene is read, the raw transcript that comes off the machine is far longer than the message it contains — because the message is interrupted. Scattered along the gene, between the stretches that actually code for the protein, lie long tracts that do not; and the raw transcript faithfully copies all of it, coding and non-coding alike. The cell then performs an astonishing act of editing: it cuts out every one of the non-coding tracts — the introns — and splices the remaining coding pieces — the exons — end to end into the finished message. Whole stretches of what was just laboriously copied are excised and thrown away, and only the joined remainder is sent on to be built.

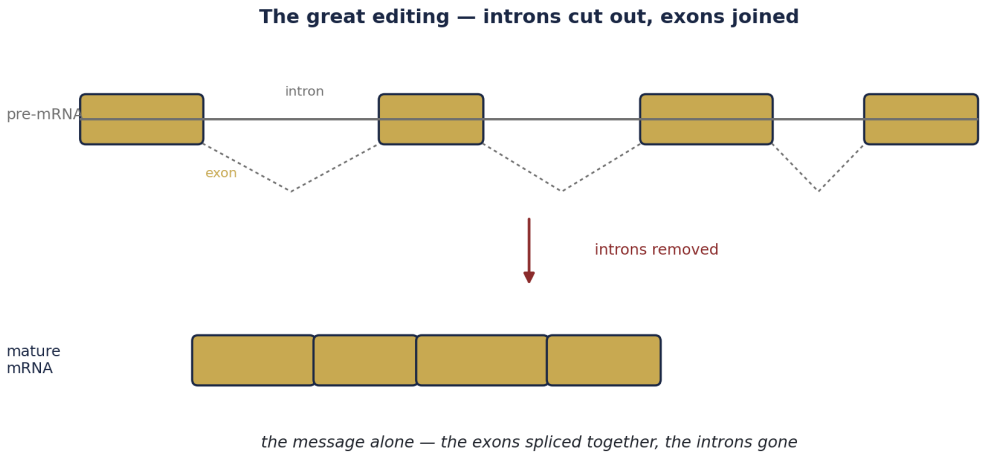

Figure 5.5. The great editing. A eukaryotic gene is read as a long raw transcript containing both coding stretches (exons) and non-coding stretches (introns). The cell then splices out every intron and joins the exons end to end, sending on only the finished message. Most of what was copied is cut out and discarded.

The standard textbook is admirably honest about how puzzling this is. It describes the splicing in exact detail — and then admits, of the whole business of cutting genes apart and stitching them back together, that “why the modifications occur is not clear.” It is a genuine mystery of mainstream biology: why should a cell copy out a great deal of sequence only to cut most of it away? Why carry the introns at all, if they are only to be removed? The recipe view of the genome has no good answer. But the address view, this book will argue, has a very good one indeed.

SECTION 5.7

Message and Address

Here is the answer. If the genome is not merely a recipe but an address — a coordinate that locates the living thing in the field — then it must carry two quite different kinds of thing along its length: the message, the instructions for what to build, and the address itself, the coordinate that says which node this is and where. In Chapter One we met the claim that the roughly ninety-eight parts in a hundred of the human genome that code for no protein — the stretch science dismisses as junk — are not junk at all but the address-space, the coordinate system of the living thing. The introns are that address-space, threaded in among the coding exons. And splicing is nothing other than the separation of the two: the cutting of the coordinate out of the instruction, so that the instruction alone goes forward to be built.

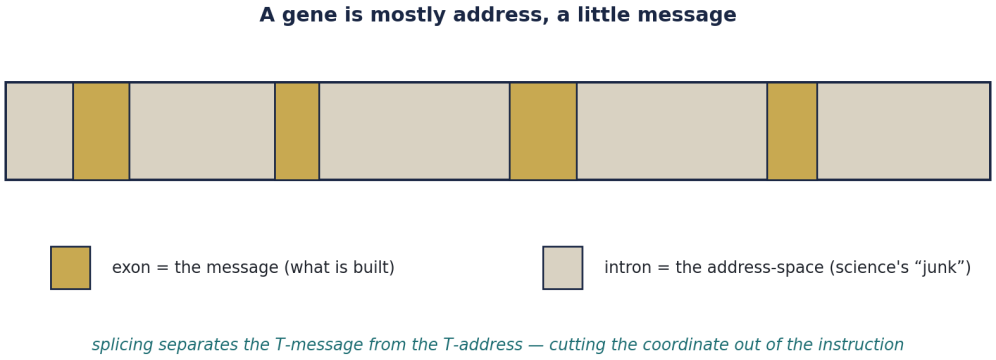

Figure 5.6. Message and address. A gene is mostly non-coding (the introns, in this reading the address-space — science's 'junk') with a little coding sequence (the exons, the message) scattered through it. Splicing separates the two: the T-message is joined and sent on, the T-address is cut away.

Seen so, the mystery dissolves. Of course the cell copies the whole gene, introns and all: the raw transcript is a copy of a stretch of the address, and an address is address and message intermixed. And of course the cell then cuts the introns out before building: you do not feed the coordinate to the factory, only the instruction. The splicing that baffles the recipe view is exactly what the address view predicts — a living thing separating, in real time, the part of its coordinate that says what to build from the part that says who and where it is. The removed part was never message, and never meant to be built. It was address, and the cell knows the difference, and acts on it, every time it reads a gene.

KEY IDEA

The introns cut out in splicing are, in this reading, the T-address-space — the coordinate stretches science dismisses as 'junk' — threaded among the coding exons, the message. Splicing separates the two: the coordinate cut out of the instruction. The biologist's open puzzle — why copy so much only to discard it — is the address view's plainest prediction.

SECTION 5.8

The Tail and the Nucleus

Two smaller finishing touches complete the picture, and both fit the theme. First, the far end of a eukaryotic message is fitted with a long tail of a single repeated letter — a run of adenines, the poly-A tail — that stabilises the message and times its eventual destruction, a clock of a different kind counting down the message's working life. And note, once more, the letter: the tail that governs the message's lifespan is written on adenine, the Earth base, the same base on which Chapter Three found the cell keeping time. Time, again, on the Earth.

Second, and tellingly, a great deal of the RNA a eukaryotic cell reads never leaves the nucleus at all. Much of what is transcribed is edited, and then simply kept — retained in the nuclear compartment, never exported to be built into protein. To the recipe view this looks wasteful: why read so much that is never used? To the address view it is natural: much of what the cell reads is not a message to be built but a coordinate to be consulted, and a coordinate need never leave home. The reading of the address is not always a prelude to construction. Often it is the field simply keeping its own registry in order, within the walls of the node, with nothing sent out at all.

SECTION 5.9

What the Editing Is Keeping

Gather the chapter. We found that the reading of the address, once begun, runs at a fixed tempo — about sixty letters a second — set by temperature and so, in this book, by the local density of T: a clock of the field, a T-metronome the cell inherits rather than sets. We found the reading stopped by a signal built from the lattice primes, the three-bond hairpin calling the pause and the two-bond uracil grip calling the release. We found one reading of one stretch yielding, after cutting, the whole substance of the reader itself. We found the message capped at the front with a modified guanine — the Venus base — and tailed at the back with adenines, the Earth base that keeps time. And we found, at the heart of it, the great editing: the cell cutting the introns — the address-space, science's junk — out of the raw transcript and splicing the exons, the message, together, separating in real time the part of the coordinate that says what to build from the part that says who and where.

Not one measurement has been altered. The rate is still sixty a second; the hairpin still stalls the machine; the introns are still spliced out. What has changed is that the chapter's central puzzle — the one the textbook itself confesses it cannot explain, why the cell should copy so much only to cut most away — stops being a puzzle. In the address view it is the plainest thing in the world: the cell is separating message from address, because its genome is both. The tempo is a clock of the field; the punctuation is the lattice; and the editing is the parting of the coordinate from the instruction. Reading,

in a cell, is not a simple photocopy. It is the field consulting its registry, on its own clock, and sorting message from address as it goes.

KEY IDEA

The thesis of the chapter: the reading of the address runs on a T-clock and is edited to separate message from address. The tempo is set by heat (= T); the stops by the lattice primes 2 and 3; and splicing cuts the intron address-space out of the exon message — answering, in the address view, the very puzzle mainstream biology leaves open.

SECTION 5.10

Why This Should Matter to You

There is a consequence of the great editing that touches your own body directly, and it turns the splicing from a curiosity into one of the deepest sources of your complexity. Because a gene is read as separable pieces, the cell can join those pieces in more than one way — keeping this exon, dropping that one — and so build several different proteins from a single gene, according to which cell is reading and under what conditions. The same coordinate, spliced differently, yields different messages. This is much of the reason you are as intricate as you are with so few genes: the human coordinate is read and re-edited into a far larger number of messages than there are genes to begin with. Your richness lies not only in what your address says, but in the many ways the cell chooses to cut and join it.

And where the cutting goes wrong, so does the body. A great many inherited diseases turn out to be failures of splicing — an intron mistakenly kept, an exon wrongly dropped, the message garbled not because the coordinate was mistyped but because it was mis-edited. In this book's terms, the address was sound but the parting of message from address failed, and the wrong instruction went forward. Understanding the editing is therefore not an academic nicety; it is, increasingly, the ground of real medicine, where correcting a splice can correct a disease. We have watched the address written, copied, and now read and edited. In the next chapter we turn to what the message finally builds — the proteins — and find the machines of the cell folded, like everything else, to the numbers of the lattice.

The Numbers at a Glance

The tempo, the punctuation, and the editing of the reading — and the reading the Force of Time gives each. Every biological fact is left exactly as measured.

Feature	What the cell does	The Force of Time reading
Elongation tempo	~60 letters/second, temperature-set	a T-metronome — heat is T, a clock of the field
Same in fast & slow cells	rate independent of growth	the running is clockwork; only the start is gated
Termination	G–C hairpin, then a run of U's	3-bond clamp pauses, 2-bond grip releases — lattice primes
5′ cap	modified guanine, reversed linkage	start-stamp on the Venus base (G)
3′ poly-A tail	a run of adenines, times decay	lifespan clock on the Earth base (A)
Splicing	introns cut out, exons joined	message parted from address — the coordinate cut from the instruction
Non-coding introns	copied, then discarded	the T-address-space (science's 'junk'), separated from the message

References

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