

Closure, Carry and the Ladder

Bacteria and viruses read through the Vacuum.Net Theory

J. Konstapel, Constable Research, Leiden — 29 October 2026

Read through the Vacuum.Net Theory, bacteria and viruses do not differ in whether they are alive. They differ in what their closure passes on to the next scale: a ring carries, a meeting carries nothing.

The ground

The theory begins with a single act. There is one strand, and a distinction is the strand returning to a place it has been (N1). Nothing is distinguished before that return: no inside, no outside, no object. What we ordinarily call a thing is a loop the strand makes on itself.

Beneath the axioms lies the trinity: the three values -1 , 0 , $+1$, whose sum is zero. Read as the digits of balanced ternary, they add by the digit rule. A sum keeps its residue mod 3 at its own scale and passes the rest on as a carry to the next scale (T1).

A loop persists if and only if it lies in a closed window, and a window is three consecutive trits. It closes when its sum vanishes mod 3. Of the 27 possible windows, exactly 9 close (T2, T3). What does not close passes on as tension. Closure is the selection rule; there is no external selector (N2).

Two further axioms matter here. At every node the passages are ordered: the first passage fixes the direction, and later passages are taken relative to it, so the net carries its history as its shape (N3). And merged into blocks, the coarse strand obeys the same rules again: what does not close at one scale is the material of the next (N5).

That is the whole apparatus used below. No notion of life, organism, function or purpose enters it.

Three closures, and what each carries

Every closed trit word reduces completely, one step at a time, to three elementary closures and nothing else: a standing 0 of length one, a meeting x , $-x$ of length two, and a ring x , x , x of length three. No open word reduces at all (T7).

The difference that matters here is not the length but the carry. A standing and a meeting close with carry 0: nothing passes to the next scale. A ring closes with carry ± 1 , because $1 + 1 + 1 = 10$ and $T + T + T = T0$ in balanced ternary. A ring therefore closes at its own scale and becomes one passage of the next — the rule of N5, stated as arithmetic (T7.1).

That single arithmetic fact carries the whole reading below. Two wholes can both be closed, and be wholly unlike in what they do to the scale above them.

Closure	Length	Carry	Consequence
Standing	1	0	Persists; contributes nothing upward
Meeting	2	0	Persists only as a pair; contributes nothing upward
Ring	3	± 1	Persists and becomes one passage of the next scale

A word that closes in every window is not merely closed somewhere: it repeats one closed window, and there are exactly nine such words for every length (T8). These are the fixed points of the register's rewrite (T10) — the eigenforms of a form that reproduces itself under its own operation.

Bacteria and viruses as kinds of closure

Read this way, a free-living bacterium is a ring. It closes on its own account, repeating its own closed window, and its carry passes upward: it becomes one passage of a colony, a biofilm, a mat, and in the endosymbiotic case a passage of a cell.

A virus is a meeting. It closes only together with the ring of something else. The biological record says the same thing in its own vocabulary: a viral genome carries no information for generating metabolic energy or for protein synthesis, so it depends on the host cell for both ([Ratti et al., via University of Bologna](#); [lecture notes, King Saud University](#)). On its own it contributes nothing to the scale above.

Neither statement says a bacterium is alive and a virus is not. The distinction the theory draws is not about life. It is about carry.

The interesting cases sit between the two. Giant viruses of the family *Mimiviridae* encode parts of the translation apparatus that was long held to divide cells from viruses: tupanviruses carry up to 70 tRNAs, 20 aminoacyl-tRNA synthetases and 11 translation factors, the largest translational apparatus known in the virosphere ([Abrahão et al. 2018](#);

[Silva et al., PLoS Genetics 2017](#)). Part of the ring is carried internally; the rest is still borrowed.

The same ground is approached from the other side. *Candidatus Carsonella ruddii*, the endosymbiont of the psyllid *Pachypsylla venusta*, has a genome of 159,662 base pairs encoding 182 genes, against roughly 4,000 in *Escherichia coli*. Its gene set is not sufficient for DNA replication, transcription and protein synthesis, and the authors conclude it can no longer be considered an independent organism ([Tamames et al., BMC Evol. Biol. 2007](#); [Nakabachi et al., Science 2006, via ScienceDaily](#)). In a related psyllid the symbiont *Psyllophila* completes a tryptophan pathway that *Carsonella* leaves unfinished, so neither closes alone ([mSystems 2023](#)).

In the language used here: *Carsonella* has outsourced most of its ring and now closes only as a meeting.

Not a boundary but a mixture

Biology keeps asking where chemistry ends and life begins, and keeps finding a grey zone instead of an answer. In this reading the question is malformed. There is no property of being alive that a thing either has or lacks. There is only closure, and what that closure passes on.

Nothing in the theory is itself vague. A window closes or it does not (T2). A closure is a standing, a meeting or a ring, and nothing else (T7). What varies continuously is something different: the proportion in which a given whole is built from meetings and from rings, and therefore how much carry it sends upward.

The second source of apparent vagueness is scale. What fails to close at one scale may close at the next (N5). *Carsonella* does not close alone; *Carsonella* together with its insect does. Whether something qualifies depends on the scale at which the question is asked, and the theory makes that dependence explicit instead of leaving it as an embarrassment.

The biological record is consistent with a gradient rather than a line. *Carsonella* is described as standing at the frontier between cell and organelle, and the giant viruses are said to have blurred the roots of the tree of life ([Tamames et al. 2007](#); [Silva et al. 2017](#)). Those are two independent groups describing, in the vocabulary of components, what the carry rule describes as a proportion.

Seams: closure is not enough

When two closed windows meet in one word, the joint between them is a seam. The seam is closed if and only if the second window is the same as the first. Over all 81 ordered pairs there are 9 closed seams, 36 with one open window and 36 with two (T11).

This is a sharper condition than it first appears. Both parties being closed in themselves does nothing for the joint. Of the nine closed windows available to the second party, exactly one leaves no tension. Order must be shared, not merely possessed.

That reframes symbiosis and infection without appealing to aggression or defence. Gut flora and mitochondria are not harmless; after a long common history they run in the same order. A novel pathogen is not malicious; it brings a different order. The difference lies in the seam, not in a property of either party.

The record offers a case in which the tension is absorbed in a third way: not by matching order, but by adding a loop. The virophage mavirus integrates into the genome of the flagellate *Cafeteria*. When the giant virus CroV infects that host, mavirus is reactivated and suppresses CroV production. The infected cell still dies, but the surrounding population survives ([Fischer & Hackl, Max Planck Institute](#); [Racaniello, Virology Blog](#)). Closure is not restored at the scale of the cell. It is restored one scale up.

The ladder is a count, not a size

Merged into blocks, a coarse passage contains exactly $2^a \cdot 3^b$ passages of the finest scale, after a merges of meetings and b merges of rings. On the ring ladder each step multiplies by three (T15). The ladder therefore counts passages. It does not measure length, and reading it as a length is the first mistake to avoid.

Taking the atom as the finest passage and average atomic mass as 2×10^{-26} kg, the depths come out as follows. Masses are order-of-magnitude figures, so each depth carries roughly half a step of uncertainty.

	Mass (kg)	Atoms	Ring steps ($\log_3$)
Protein	1×10^{-22}	5×10^3	7.8
Ribosome	4×10^{-21}	2×10^5	11.1
Ebola virion	1×10^{-19}	5×10^6	14.0
Mimivirus	1×10^{-17}	5×10^8	18.2
<i>E. coli</i>	1×10^{-15}	5×10^{10}	22.4
Human cell	1×10^{-12}	5×10^{13}	28.7
Human body	7×10^1	3.5×10^{27}	57.7

The choice of the atom as the finest passage is a choice, not a result. It shifts every depth by the same constant, so the absolute numbers say little. The differences do not depend on it:

- virion to bacterium: 8.4 steps
- bacterium to human cell: 6.3 steps
- human cell to human body: 29 steps

The last figure is the one worth sitting with. The distance from a single cell to a whole body is larger than the entire distance from an atom to a cell. On this ladder, most of the work is not in building a cell. It is in stacking them.

Two ladders that never meet

Meetings merge by two, rings by three, and the two ladders never coincide: $2^n \neq 3^k$ for all integers other than $n = k = 0$ (T16, proved). A whole built from both kinds of closure therefore closes exactly at no depth whatever. Something is always left over.

The miss is small at particular depths. The closure depths are the denominators of the convergents of $\log_2 3$: 1, 2, 5, 12, 41, 53, 306, 665, 15601 (T17). At depth 12 the residue is 1.35 %, the Pythagorean comma; at 53 it is 0.21 %, at 306 it is 0.10 % (T18). It never reaches zero.

The consequence for a living whole is direct. Any such whole mixes closures that carry with closures that do not, so there is a permanent residue. It is not produced by a pathogen, a mutation or a failure. It follows from arithmetic. And by N5 that residue is exactly what constitutes the next scale: without a residue there is no scale above.

One observation, offered as nothing more: of the depths in the table above, only the ribosome at 11.1 falls near a closure depth (12). The rest do not. That may be coincidence, and the order-of-magnitude masses are too coarse to decide it.

Where the residue discharges

A carry moves one scale up, never sideways (T7.1). What does not close in a cell appears at the level of the tissue; what does not close there appears at the level of the body. The residue can only rise until it finds a scale at which it closes.

That changes the central question. Medicine asks what disturbs the equilibrium. On this reading there is no equilibrium to disturb: the residue is permanent, and the question is at what depth it discharges. Locally, within the tissue, across the whole organism, or — as in the virophage case — only at the level of the population, with the individual lost.

The question also stops being about the identity of an invader. Two seams with the same participants can differ entirely, because the seam depends on shared order rather than on what the parties are. A reservoir host and a spillover host meet the same virus and do not meet the same seam.

What the reading does not yield should be said plainly. It gives no case fatality rate, no prediction of who recovers, and no therapy. It is a different bookkeeping of the same facts, and its value is in which questions it makes askable.

What stands where

The Foundations document assigns every statement one of five statuses, and that discipline is kept here.

Element	Standing
The trinity, N1–N5	Assumed
T1, T2, T7.1, T12, T16, T17, T18	Proved — arithmetic
T7, T8, T10, T11, T15	Conditionally proved, under their stated hypotheses
Ring = free-living organism; meeting = virus	Read into the theory here; it carries no status in the document
What the places and passages of a living body are	Open (IX.5)

The third row is the load-bearing one. Foundations makes no physical claim, and the physical reading of the trit rule is listed as an open question. The identification of biological kinds with kinds of closure is therefore a reading, offered because it is coherent and because it reorganises the facts, not because the theory entails it.

Two numerical checks were run for this article rather than taken from the document: in a word that closes everywhere, altering a single trit opens exactly three windows, for all nine such words and every position; and with trits drawn uniformly and independently, a window closes with probability 1/3 (0.3341 over 300,000 draws), while trits derived from a sequence are correlated and close more often. Both agree with T2 and T6.

Sources

The theory. J. Konstapel, *The Vacuum.Net Theory*, Ninth Edition, Constable Research, Leiden, 27 October 2026 — *Foundations* 9.2 and *Physics* 9.0. Theorem numbers above refer to Foundations.

Viruses and the host cell

- [Ratti et al., *Viruses*, via University of Bologna](#) — viral genomes lack the information for ATP generation and protein synthesis.
- [General properties of viruses, King Saud University](#) — obligate intracellular parasitism; absence of ribosomes.

Giant viruses

- [Abrahão et al. 2018, *Nature Communications*](#) — tupanviruses: up to 70 tRNAs, 20 aaRS, 11 translation factors.
- [Silva et al. 2017, *PLoS Genetics*](#) — translation-related genes in mimiviruses.

Reduced endosymbionts

- [Tamames et al. 2007, *BMC Evolutionary Biology*](#) — Carsonella: 159,662 bp, 182 ORFs; the frontier between cell and organelle.
- [Nakabachi et al. 2006, *Science*, via ScienceDaily](#) — the smallest cellular gene set then known.
- [mSystems 2023](#) — *Psyllophila* completes the tryptophan pathway Carsonella leaves incomplete.

Virophages

- [Fischer & Hackl, Max Planck Institute for Medical Research](#) — mavirus integrates into the host genome and protects the population.
- [Racaniello, Virology Blog](#) — independent account of the same work.

Closure to efficient causation

- [Siekmann 2017, *Ecological Complexity*](#) — Rosen's (M,R) systems; organisms as closed to efficient causation, and the argument that this is a postulate to be tested.