A Natural Definition of Life

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Abstract

Numerous definitions of life have been proposed to date. Nevertheless, a consensus remains elusive, as existing definitions ultimately fail to identify the fundamental elements that distinguish living from inanimate matter. Consequently, robust counterexamples and arbitrary constraints have systematically undermined their significance. Here, we show that all cellular processes can be unified within a single conceptual framework we term *imperiosis*, and identify the universal characteristic of cell death from which the concept of *cell life* is established. By integrating both concepts, we derive a single principle that appears both necessary and sufficient to define life: *Life is Self-compartmentalizing Imperiosis*. From this perspective, our proposed definition naturally captures the foundations of life, offering unique explanatory and predictive power. Notably, it explains and resolves the long-standing ambiguity regarding the status of viruses, predicts a new taxonomy of life forms beyond life as we know it, explicitly defines the minimal life form, and shows that the two leading origin-of-life hypotheses represent two facets of the same phenomenon. Finally, the versatility and scale-free nature of imperiosis provides an unprecedented theoretical basis for understanding biological properties and organization at both intra- and intersystem levels across diverse contexts.

Introduction

It is always fascinating how everyone has a sense of what life is, yet struggles to provide a definition that is recognized or accepted by others. Life is found in nearly every accessible environment on Earth's surface, from the coldest polar regions to the hottest deserts, the highest mountain peaks, and the deepest ocean trenches, as well as far below the surface. Life is so ubiquitous that it appears paradoxical that no consensus has been reached on how to define it.

Hundreds of definitions of life have been proposed to date[1,2,3]. Their diversity reflects the range of biological traits identified through the field-based expertise of the respective authors. Physicists might be more sensitive to thermodynamic principles, biochemists to chemical network properties, computer scientists to information processing mechanisms, biologists to behavioral characteristics, etc. Each view, with some degree of overlap, highlights a different foundational aspect of what constitutes life, without ever capturing its essence. Regardless of their origins, all definitions suffer from the same drawbacks, *i.e.* robust counterexamples and *ad hoc* constraints[4].

In her influential book *The Quest for a Universal Theory of Life*, philosopher of science Carol Cleland identified the root of these drawbacks: trying to define life today is like trying to define

water before the rise of molecular theory. Until the late eighteenth century and the publication of Lavoisier's paper demonstrating that water is not elementary, scientists were limited to defining water based on its observable properties, such as its ability to dissolve substances. This approach led to the misclassification of substances as water (*e.g.* nitric acid) and *ad hoc* explanations shaped more by prevailing philosophical ideologies (*e.g.* phlogiston theory) than by systematic science, mirroring attempts at defining life[5].

Debates about the nature of things are often settled through conceptual breakthroughs: profound shifts in understanding that provide explanatory and predictive power, usually by identifying a universal yet previously hidden characteristic shared by, or distinguishing, objects of debate. For example, water is now known to be composed of *atoms* (H_2O); jade is recognized as consisting of *two minerals* (jadeite and nephrite); space and time are understood to be *intertwined*; the existence of the phylum taxon is justified by *gene expression patterns*[6]; and Archaea is recognized as a *distinct* domain of life.

Simply put, identifying the universal feature that leads to a radical conceptual change in how living organisms are thought of is key to settling the nature of life.

Unifying cellular processes

If there is one concept on which the biology community is fully agreed, it is that the cell is the fundamental unit of life, *i.e.* the smallest common entity, shared by all forms of life, in which the central dogma of molecular biology (CDMB) operates. The CDMB describes the key mechanisms of transcription and translation, which give rise to the cell's functional molecules: RNAs and proteins. Ultimately, all cellular processes emerge from the interplay between these two types of molecules. However, the CDMB does not capture their modes of action, nor is it intended to do so.

RNAs and proteins are fundamentally different in their chemical nature (nucleotide polymer vs. amino acid polymer) and highly diverse in both composition and function, so much so that each has given rise to distinct and productive fields and subfields of research. The broad spectrum of techniques, applications, concepts, and interconnections that has emerged from these research areas is intimately associated with the notion of complexity that pervades the study of biology.

The recognition of this complexity, though necessary for practical discoveries, has obscured the unifying concept underlying the functions of RNAs and proteins. Regardless of whether this function involves catalysis (*e.g.* enzymes, ribozymes), scaffolding (*e.g.* structural proteins, long non-coding RNAs), sensing (*e.g.* receptors, riboswitches), or otherwise, all such processes are ultimately governed, directly or indirectly, by one general principle.

What do the AMPA receptor, RNA-polymerase, ribosome, and glycogen phosphorylase have in common? Despite being fundamentally different in structure and function, they all operate according to the same core mechanistic logic: input $\rightarrow$ gate $\mapsto$ output. In each case, an external input, *i.e.* glutamate, dNMP, codon, or phosphoryl group, triggers a conformational response

within the functional molecule, resulting in a specific output, *i.e.* influx of sodium (Na^+), ribonucleotide addition, amino acid addition, or glycogen breakdown into glucose subunits, respectively[7,8,9,10]. Any functional RNA or protein that is controlled by an external input can be described by the input → gate ↦ output (IGO) logic. This includes molecules responsive to physical stimuli, such as the G-protein-coupled receptor rhodopsin[11] (light → rhodopsin ↦ GTP-bound Gα release) or the RNA thermometer FourU[12] (high temperature → FourU ↦ opening of AgsA mRNA). Even molecular functions that do not necessarily generate an "active" biochemical product, such as sequestration or scaffolding, still conform to a degenerated form of the same logic: input → gate ↦ [input-gate], where [input-gate] becomes itself an input or a gate for downstream IGO-based processes. This is evident in regulatory elements like micro-RNAs, long non-coding RNAs, or decoy receptors, where input-induced gating controls downstream availability or inhibition without producing a conventional output, but participates in downstream controlled reactions[13,14,15].

The IGO logic naturally captures fundamental molecular properties that are universal in living systems but often lack a coherent unifying framework. The core principle can be formalized as follows:

Let $I = \{i_1, i_2, ..., i_n\}$ with $n \in \mathbb{N}$ be any set of input(s), $G = \{g_1, g_2, ..., g_m\}$ with $m \in \mathbb{N}$ be any set of gate(s), and $O = \{o_1, o_2, ..., o_p\}$ with $p \in \mathbb{N}$ any set of output(s). If g accepts multiple inputs or produces multiple outputs simultaneously (*i.e.*, requires all to be present at once), the corresponding sets will be indicated with brackets []. If g can accept different inputs independently or consecutively, or produce any single output, parentheses () will be used. "∨" denotes the logical OR, "→" denotes any types of interaction, and "↦" denotes any processes (*e.g.* chemical reaction) induced by the interaction of I with G. The precursors required for the process, if any, are not represented (*e.g.* for a chemical reaction, only the product(s) are represented, not the substrates).

The most general form of the IGO logic can then be written:

$$\mathbf{[I] \vee (I) \rightarrow G \mapsto [O] \vee (O)}$$

From the general form, any control-based biological molecular functions or properties can be derived, including plasticity, redundancy, promiscuity, tight regulatory control, signal transduction, sensing, feedback loop, transport, scaffolding, inhibition, sequestration/decoy, anabolism and catabolism (table 1).

Table 1: Systematic Derivation of Biological Functionality from IGO (Input-Gate-Output) Framework.

Biological function/property	**IGO logic**	**Definition**	**Examples***	**References**
Plasticity	(I) → g ↦ (O)	A gate responds to diverse inputs with diverse outputs	Ribosomes, polymerases, pleiotropic g protein coupled receptors	8,9,16
Redundancy	(I) → g ↦ o (I) → G ↦ o	A gate produces same output from diverse inputs – Diverse gates produce same output.	Genetic code degeneracy Analogous enzymes	17,18
Promiscuity	i → g ↦ (O)	A gate responds to one input with diverse outputs	Promiscuous enzymes	19
Tight Regulatory Control	[I] → g ↦ [O] ∨ (O)	A gate responds to diverse inputs simultaneously	Multi-factor dependent transcription initiation/elongation	20
Signal Transduction Sensing	i → g ↦ o	One-to-one correspondence between input and output mediated by a gate	Kinase cascade, hormone receptors, riboswitches	21,22,23
Feedback Loop	i → g ↦ i	A gate responds to its own output	Metabolic enzymes such as hexokinase (negative feedback loop), RelA (positive feedback loop).	24,25
Transport	i → g ↦ F	A gate generates a mechanical force.	Motor proteins *e.g.* myosin motor: actin (input) and myosin head (gate) bind which release ADP + Pi and produce F (outputs).**	26
Scaffolding Inhibition/Sequestration/Decoy	i → g ↦ [i-g]	Gate/input pairs form new functional gates or input themselves	LnRNA and/or protein mediated catalytic complex formation; miRNA-mRNA complex, reversible inhibitor protein	13,14,15

Anabolism	i → g ↦ o	Controlled synthesis of one molecule "o" from precursors (not shown)	Biosynthesis enzymes (amino acids, glucose, etc.) *e.g.* pyruvate carboxylase activated by acetyl-CoA	27
Catabolism	i → g ↦ [O]	Controlled breakdown of one molecule into many	Digestive enzymes (amylase, lipase, protease, etc.) *e.g.* Amylase activated by chloride ions	28

*Non-exhaustive. In addition, numerous meta-examples can be found for each category when interconnected IGO logic is considered (as in complex metabolic pathways or regulatory networks).

** Activation steps are conceptually similar to signal transduction.

The IGO architecture reflects a universal design principle underlying both the activity and synthesis of functional RNAs and proteins, and, by extension, the operation of all cellular processes. Even functional molecules with uncontrolled activity, if any, still fall under the framework of IGO-based logic, at least with respect to their synthesis.

We propose that this logic constitutes the fundamental unit from which life is built. To capture this concept, we introduce the term *imperiosis*, derived from the Latin *imperiosus*, meaning "commanding", combined with the Greek suffix *-osis*, denoting a process. Imperiosis thus refers to a "controlled process", and serves as a conceptual foundation for understanding molecular function across all domains of life.

Where the central dogma describes the flow of genetic information, and homeostasis ensures system stability, imperiosis offers a framework for understanding how molecular units conditionally operate, *i.e.* receiving signals, integrating them through structural gates, and generating adaptive outcomes. It is not a molecule, nor a reaction, but a logic, a pattern that recurs across all levels of molecular life. However, imperiosis on its own does not constitute life, just as hydrogen and oxygen alone are not water, but merely its constituents. For example, a PCR machine executes imperiosis (cycles of molecular recognition, gating, and output generation) but remains non-living.

Since imperiosis is fundamentally a process, this leads us to the critical question: "What type of imperiosis gives rise to life itself?"

The universal characteristic of cell death

If there is one phenomenon that can naturally shed light on the essence of life, it is death. Death is intrinsically linked to life, as it marks its conclusion. Since the cell is the fundamental unit of life, understanding cell death across all domains of life is of primary importance for defining life.

Cell death can be classified into two categories: programmed cell death (PCD) and accidental cell death (ACD)[29]. PCD is a tightly regulated process involving numerous distinct mechanisms such as apoptosis, autophagy, necroptosis, pyroptosis, and ferroptosis, each characterized by specific molecular pathways and progressive morphological changes (Table 2). The morphological changes associated with PCD depend on the organelles involved, yet all reflect impairment of cellular compartmentalization (*i.e.* organelle and/or biomolecular condensate decay), inevitably converging toward a common endpoint: cell lysis (global loss of compartmentalization via disruption of the plasma membrane and release of cellular contents, either into the extracellular environment or within a phagolysosome). ACD, by contrast, is an uncontrolled process, typically involving direct plasma membrane rupture or necrosis, which can be triggered by factors such as physical or chemical injury, or infection. Necrosis is characterized by a series of morphological changes, including organelle loss and cell swelling that ultimately lead to rupture of the plasma membrane and the release of cellular contents into the extracellular environment. Thus, despite being functionally distinct, PCD and ACD mechanisms ultimately obey one unifying principle: the loss of compartmentalization.

Table 2: A comparative overview of cell death mechanisms.

Type of cell death	**Key pathways involved**	**Key morphological changes**	**References**
Necrosis	Uncontrolled External injuries	Organelle disruption, Cell Swelling, Plasma Membrane Breakdown, Cell Lysis	30
Apoptosis	Several pathways exists that require specific triggering signals to begin an energy-dependent cascade of molecular events (*e.g.* extrinsic, intrinsic, and perforin/granzyme)	Cell Shrinkage, Chromatin Condensation, Membrane Blebbing, Apoptotic Body (AB) Formation, Phagocytosis, AB Membrane Breakdown, AB lysis	31
Oncosis	Four distinct pathways: loss of cell membrane integrity, inhibition of ATP synthesis, opening of MPTP, or ion balance disorder	Organelle and Cell Swelling, chromatin aggregation, Membrane Blebbing, Nuclear disruption, Plasma Membrane Breakdown, Cell Lysis	32
Necroptosis	RIPK1 and RIPK3 form a heterodimer complex promoting oligomerization of MLKL,which translocates towards the plasma membrane	Membrane Permeabilization, Cell Swelling, Plasma Membrane Breakdown, Cell Lysis	33
Eryptosis	Numerous pathways are associated with eryptosis, including Ca2+ signaling, ROS signaling, Ceramide signaling, etc.	Cell Shrinkage, Membrane Blebbing, Increased Granularity, Phagocytosis (macrophage), Plasma Membrane Breakdown, Cell lysis	34
Ferroptosis	Erastin inhibits the import of cystine, leading to glutathione depletion and inactivation of the phospholipid peroxidase glutathione peroxidase 4 (GPX4)	Reduced Mitochondrial Volume, Loss of Mitochondiral cristae, Outer Mitochondrial Membrane Rupture, Late Plasma Membrane Breakdown, Cell Lysis	30,35

Pyroptosis	Inflammasome activates caspase-1, which cleaves gasdermin D, leading to oligomerization and the formation of pores in the plasma membrane.	Cell Swelling, Membrane Blebbing, Nuclear Condensation, Membrane Pore Formation, Plasma Membrane Breakdown, Cell Lysis	29,30
Paraptosis	IGF-IR-dependent signaling in its downstream signaling pathways, including MAPKs and JNK, ROS-mediated cellular damage or the accumulation of misfolded proteins.	Cytoplasmic vacuolization, Mitochondria and ER swelling, Progressive vacuole enlargement, Plasma Membrane breakdown, Cell Lysis	36
Parthanatosis	DNA damage leads to PARP1 hyper-activation, PAR accumulation, and AIF nucleus translocation from mitochondria.	Mitochondrial & Nuclear Integrity Loss, DNA fragmentation, Plasma Membrane Breakdown, Cell Lysis	37
Alkaliptosis	pH-induced alkalization, mainly through the activation of JTC801, which promotes the transcriptional repression of CA9 by NF-κB.	Similar to Necroptosis	30,38
Methuosis	Macropinocytosis and defective macropinosome recycling induced by unrestricted activation of Rac1 by Ras(G12V).	Cytoplasmic Vacuolization, Vacuole Expansion, Cell Swelling, Plasma Membrane Breakdown, Cell Lysis	39
Oxeiptosis	ROS-induced KEAP1/PGAM5/AIFM1 pathway.	Similar to Apoptosis	40
Sarmoptosis	Mitochondrial dysfunction stimulates a Sarm1-dependent cell destruction pathway in sensory neurons.	Mitochondrial swelling, Axonal Fragmentation, Membrane swelling, Plasma Membrane breakdown, Cell Lysis	41
NETosis	Various stimuli such as bacteria, fungi, viruses, LPS, CaI, or PMA induce NETosis via diverse pathways.	Cell Rounding, Chromatin Swelling, Nuclear Envelope and Plasma Membrane Breakdown, Cell Lysis	42
Entosis	Various triggers induce cytoskeletal changes via Rho/ROCK signaling and myosin II activation.	Engulfment of a live cell by another, Inner Cell Lysis	43
Anoikis	Lack of ECM contact or the engagement with inappropriate ECM fails to activate pro-survival signals leading to intrinsic or extrinsic apoptosis.	Similar to Apoptosis	44
Cornification	Active caspase-14 contributes to filaggrin degradation, and keratins and other proteins are cross-linked by transglutaminases.	Plasma membrane replaced by cross-linked proteins/lipids, Organelle Disintegration, Flattening/Dehydration, Desquamation	45
Immunological Cell Death (ICD)	DAMPs released during ICD bind to PRRs on the surface of dendritic cells (DCs) that ultimately activate innate and adaptive immune responses	Similar to Apoptosis	46

Mitotic Cell Death (MCD)	Various endogenous and exogenous factors induce MCD by affecting DNA replication via cell cycle checkpoints, chromosome segregation, or microtubule function.	Nuclear Disruption, Chromosome Abnormalities, Mitochondria permeabilization, Progression to apoptosis, necrosis, or autophagy	47
Autophagic Dependent Cell Death (ADCD)	Regulated by the PI3K-mTOR signal transduction pathway upstream of autophagy-associated genes (ATG) and the Beclin1 Complex.	Autophagosome formation, Organelle Swelling and Fragmentation, Autolysosome formation, Cell structure clearance.	46
Autosis (subtype of ADCD)	Class III PI3K complexes and Na+/K+-ATPase are two major mediators of autosis, which interact through Beclin 1 and alpha subunits.	Swelling and Fragmentation of ER, Autophasome, Autolysosome and empty vacuole formation, Mitochondria disruption, Nuclear swelling, Organelle clearance, Plasma membrane rupture, Cell lysis	48,49
Lysosome Dependent Cell Death (LDCD)	Numerous agents and molecules can induce LDCD, including ROS, Bcl-2 family proteins, Caspases, etc.	Lysosomal membrane permeabilization leading to necrosis or apoptosis.	50
Cuproptosis	Accumulation of Cu that drives ROS production causing mitochondrial and DNA damage, and inhibition of the ubiquitin-proteasome system.	Mitochondrial Shrinkage, ER damage, Chromatin rupture, Plasma Membrane Breakdown, Cell lysis	51

The mechanisms described above have been extensively established in mammalian model organisms. However, similar processes have also been identified in the other three eukaryotic kingdoms, *i.e.* plants[52], fungi[53], and protists[54]. Although PCD was long thought to be unique to eukaryotic cells, studies over the past two decades have established the existence of programmed cell death in bacteria as well. Numerous forms of bacterial PCD have now been identified, rivaling those of eukaryotes in diversity[55,56]. Once again, despite this mechanistic diversity, these processes are characterized by an ordered cellular disassembly that ultimately leads to cell lysis, *i.e.* loss of compartmentalization. Finally, direct, unequivocal evidence of programmed cell death in archaea is still lacking. However, indirect evidence does exist from genomic analyses showing the presence of caspase homologs[57], such as metacaspases and orthocaspases (enzymes related to those involved in bacterial and eukaryotic cell death), as well as toxin–antitoxin (TA) systems[58] (well known to induce apoptosis-like cell death in bacteria). Moreover, infection of the archaeon Sulfolobus solfataricus with the SIRV2 virus can trigger the expression of a CRISPR-associated toxin that causes cell death (chromosome degradation and morphological changes followed by cell lysis), suggesting an inducible programmed cell death pathway[59,60].

Thus, cell death, whether regulated or accidental, ultimately results from and is defined by the loss of compartmentalization. Reverse the dynamics, and the concept of "cell life" emerges as the gain and continual maintenance of compartmentalization. Having established imperiosis as the universal molecular process underlying all cellular activities, we are now equipped to propose a natural definition of life.

Definition of Life

Life is *Self-compartmentalizing Imperiosis*.

In other words, life is the physical result of a system of imperiosis coordinating to achieve and maintain compartmentalization from the inside out.

This definition provides the first natural, operational boundary for the living state, free from philosophical or ideological biases (such as teleology). It is logically grounded in a single, universal organizing principle derived from the identification and integration of two unifying concepts: (i) *Cell life*, as opposed to cell death, which captures the ongoing process of being alive; and (ii) *Imperiosis*, which captures the mechanism by which this process is achieved. In this light, the proposed principle appears both necessary and sufficient to define life, offering explanatory and predictive power, as discussed below.

Discussion

Classification of Historically Challenging Cases

Virus:

The proposed definition offers a natural explanation for the long-standing ambiguity regarding the status of viruses as living or non-living entities. Viruses exist in distinct physical and functional states: (i) as dormant particles outside a host cell, and (ii) as genetic material within a host cell, existing in either an active or a dormant form.

In the extracellular state, viral particles are fully compartmentalized (encapsidated), yet lack the capacity to execute imperiosis, that is, they perform no regulated processes to maintain or adapt their compartmentalization. Conversely, once inside a host cell, viral genomes engage in intricate imperiosis (hijacking the host's molecular machinery for expression and replication), but do so without compartmentalizing themselves; indeed, only the newly produced viral copies become compartmentalized before exiting the host[61].

Thus, while viruses do exhibit both fundamental hallmarks of life, *i.e.* compartmentalization and imperiosis, they never manifest them simultaneously or in a self-coordinated fashion. As particles, they are static compartments without imperiosis; as genetic material, they are imperiosis without intrinsic compartmentalization.

Consequently, viruses are non-living entities that are constructed from, and perpetuate through, the very principles underlying life, hence the ambiguity surrounding their status.

Prion:

Similar to viruses, the nature of prions has long been debated in scientific literature. Prions are abnormally folded proteins that can induce normally folded counterparts to adopt the same misfolded conformation through direct protein-to-protein contact. Unlike viruses or bacteria, prions contain no DNA or RNA; their infectivity resides entirely in their aberrant protein

structure[62]. This unique mechanism has blurred the boundary between infectious agents and pure protein biochemistry, challenging traditional definitions of life.

From the perspective of the proposed definition, prions exemplify an imperiosis-only-driven system: the misfolded prion protein (input, i) interacts with the normal protein (gate, g) to produce a misfolded output (o), following the IGO logic ($i \rightarrow g \mapsto g^*$). Prions, therefore, are analogous to PCR reactions, *i.e.* implementing imperiosis (a controlled, propagating process), but not achieving self-compartmentalization. Consequently, prions do not meet the criteria of life, they are self-propagating molecular phenomena constructed from, but not embodying, the fundamental principles of living systems.

Synthetic and artificial life:

The proposed definition of life explicitly demonstrates that life is not inherently rooted in biochemistry; rather, biochemical molecules represent just one possible substrate, not a fundamental prerequisite for life. In this framework, imperiosis is understood as a controlled process whereby any type of input regulates a gate to produce an output, without direct physical interaction between the input and the resulting output. Consequently, any chemical or physical system that implements imperiosis to create or maintain its own compartmentalization qualifies as living under this definition. This principle opens the door to the recognition of non-biochemical and artificial implementations of life where exotic molecular, electronic, or mechanical systems could theoretically achieve living status.

In electronics, logic gates allow or block the flow of electric current; there is no generation of an output that is physically independent of the input signal. Moreover, an electronic circuit cannot construct itself purely through the process it performs, *i.e.* controlling electrical flow. However, when considering larger-scale electronic systems, imperiosis becomes possible: for example, a sensor that performs a mechanical task upon activation embodies input–gate–output logic. Here, the directed electric current acts as the functional equivalent of a conformational change within a protein in biological systems. Thus, in theory, it is conceivable to design an autonomous, imperiosis-driven electronic system capable of building or maintaining itself, provided that we re-conceptualize what constitutes the "building blocks". If the architectural components are engineered properly, such systems could, in principle, meet the criteria of self-compartmentalizing imperiosis.

Outside of electronics, analogous possibilities for imperiosis-driven systems can be envisioned, for example, within solid-phase chemistry by exploiting solid–solid phase transitions[63] or dynamically disordered solids as platforms for imperiosis logic[64]. Additionally, it is important to emphasize that compartmentalization is not limited to membrane-bound environments. In fact, compartmentalization may also be achieved through energy gradients. For instance, Floroni et al. (2025) demonstrated the feasibility of both transcription and translation within a thermally induced confinement[65]. Naturally, for such a system to qualify as an "exotic" life form under our proposed definition, its compartmentalization must emerge as a result of imperiosis rather than from externally imposed physicochemical conditions. Lastly, one could even envision life forms based

purely on physical reactions involving nuclear processes, rather than chemical, provided that imperiosis can exist in such systems.

Regarding the creation of synthetic cells that closely mimic biological systems, the field is approaching the realization of our proposed definition of life. Notably, the two essential aspects of this definition have each been demonstrated separately in recent years. Blanken et al. (2020) provided compelling experimental evidence of imperiosis-driven phospholipid biosynthesis: cell-free expressed enzymes, encoded in a synthetic minigenome, catalyzed the formation of phospholipids within liposome-based artificial cells[66]. However, the yield of synthesized phospholipids in this system was too low to enable de novo membrane formation or sustained maintenance of the compartment. In parallel, Fracassi et al. (2025) demonstrated, for the first time, the generation and maintenance of dynamic artificial cell membranes from a synthetic phospholipid metabolic pathway[67]. Yet, this pathway was not imperiosis-driven as it relied on non-controlled, non-catalyzed chemical reactions. Therefore, if such a metabolic pathway could be catalyzed in a controlled, imperiosis-guided manner such as by synthetic enzymes encoded in a synthetic minigenome or by molecular components responsive to external inputs, a genuine synthetic biological life form, as defined by self-compartmentalizing imperiosis, could be claimed.

A New Taxonomy of Life Forms – Life Beyond Life As We Know It

As outlined in the previous section, our proposed definition of life explicitly demonstrates that replication is not a fundamental aspect of life; rather, replication emerges as a potential outcome of self-compartmentalizing imperiosis, in direct contrast to prevailing views.

This potential paradigm shift is supported by common biological observations. For instance, soil microbiomes exhibit a wide range of replication rates and biomass distributions. However, the largest proportion of standing microbial biomass consists of oligotrophic or dormant (non-dividing) taxa[68]. In other words, the vast majority of microorganisms in natural environments are not best defined by their ability to replicate, but by their persistent biological activity, *i.e.* by their engagement in imperiosis. Another example is provided by considering cell turnover in higher organisms, such as humans[69]. Not all tissues undergo continuous renewal: most brain neurons and the cells of the eye lens persist for the organism's lifetime without replicating. Adipocytes and muscle cells, which together comprise approximately 75% of total cellular mass, account for only about 5% of total cellular turnover due to their exceptionally long lifespans, implying that, in these tissues, little to no cellular replication occurs during adulthood. Furthermore, it is well established that under stress, both prokaryotic and eukaryotic organisms can suspend or drastically reduce reproductive activity. Taken together, these observations underscore that replication is, in many instances, a minority process within living systems and not a defining feature. Rather, it is the ongoing, regulated activity that is central in those instances.

Evolution, defined as the change in heritable characteristics of populations over successive generations, depends intrinsically on replication. More specifically, for evolution through replication to occur, an organism's functional components must be encoded on a substrate capable of variation (SCV). However, within the framework of our proposed definition, SCV arises only

as a particular, non-essential type of input. This insight broadens the potential paradigm shift introduced earlier: evolution, though central to the history and diversity of life on Earth, is no longer a defining, universal feature of life as such. Rather, it is a property that can emerge only in self-compartmentalizing imperiosis systems with both replication capacities and encoded elements on variable substrate.

From these considerations emerges a natural taxonomy of life forms, derived from their self-compartmentalizing imperiosis properties (SCIP). For clarity, we define as:

- Non-replicative: a life form possessing a compartment without division ability;
- Replicative: a life form possessing a compartment with division ability;
- Non-encoded: a life form lacking inputs or gates that are themselves products of imperiosis;
- Encoded: a life form with at least one input or gate that is itself a product of imperiosis.
- Spontaneous: imperiosis-independent (*e.g.* triggered by environmental pH variation or osmotic pressure, etc.)

From these definitions, basic SCIP categories are as follows:

SCIP categories:

1. **SCIP-0:** Non-replicative, non-encoded
2. **SCIP-1A:** Spontaneously replicative, non-encoded
3. **SCIP-1B:** Replicative, non-encoded
4. **SCIP-2:** Non-replicative, encoded
5. **SCIP-3A:** Spontaneously replicative, encoded
6. **SCIP-3B:** Replicative, encoded

This taxonomy is a direct consequence of our proposed definition of life and offers a new paradigm in which life is no longer confined by its chemistry or cherry-picked characteristics. Instead, it delineates natural categories of life that extend well beyond canonical life forms. As such, this framework directly addresses the long-standing "N=1 problem" in biology and offers conceptual guidelines for the search and systematic evaluation of alternative forms of life, including those predicted by the shadow biosphere hypothesis[70].

Lastly, it is important to emphasize that the simplest case of encoded imperiosis, as presented above, does not involve inputs capable of variations. The potential for variation constitutes an additional property, from which new classes of imperiosis can be defined, *i.e.* (i) imperiosis with inputs capable of variation (ICV) that do not alter output properties, and (ii) ICV imperiosis that alter the output properties (structure, function, etc.). Furthermore, life forms can be differentiated by the degree of dependency among their imperiosis reactions, *i.e.* by the number of inputs or gates that are themselves products of imperiosis, and the resulting network-level parameters (*e.g.* connection density, degree distribution, diameter, clustering coefficient). Consequently,

imperiosis meta- and sub-properties provide a basis for defining additional categories or subcategories of life.

Overall, the SCIP framework both unifies the known diversity of terrestrial life and opens a path for predicting, creating, discovering, and categorizing life as it might exist elsewhere on Earth or across the cosmos.

Theoretical Minimal Life Forms

The SCIP framework provides a rational basis for defining minimal life forms (MLFs). Based on our definition of life, any life form can be described as an n-imperiosis system, *i.e.* a system composed of *n* imperiosis reactions.

Key annotations:

|: such as

⇒: If … Then

*: self-assembling ability

≈: dynamic variation around an equilibrium point

$\lesssim^{0/1}$: division ability (0 = conditions for division not met; 1 = conditions met)

"**:**": denotes a state change

~**:** time course

i → g ↦ o reads "input i interacts with gate g, which catalyzes the formation of output o"

$\approx[*o]^{I,G,O,C}$: a self-assembled, dynamically maintained compartment from o_1* encapsulating the sets of imperiosis elements I, G, O and C. For example, I = {i}, G = {g}, O = {*o}, and C is the set of *p* chemical precursors used by the gates in G to produce outputs in O, such as C = {c_1… c_p}.

$\approx[*o_1\lesssim^{0}]^{I,G,O,C}$: same as above, but with latent division ability

$[*o_1\lesssim^{0}]^{I,G,O,C}$: same as above, but outside equilibrium

$[*o_1\lesssim^{1}]^{I,G,O,C}$: ready to divide

Using these annotations, we present below imperiosis systems for the MLF in the SCIP-0 category, which represents the simplest possible life form, and in the SCIP-3B category, which represents the simplest canonical life form.

- **MLF SCIP-0: 1-imperiosis system**

$$\left\{ i_1 \rightarrow g_1 \mapsto {*o_1} \mid \approx [{*o_1}]^{I,G,O,C} \right.$$

- **MLF SCIP-3B: 3-imperiosis system**

$$\left\{ \begin{array}{l} i_1 \rightarrow g_1 \mapsto {*o_1} \mid \approx [{*o_1}\zeta^0]^{I,G,O,C} \\ i_2 \rightarrow g_2 \mapsto g_1 \\ i_3 \rightarrow g_3 \mapsto o_2 \mid o_2 \rightarrow \approx [{*o_1}]^{I,G,O,C} : [{*o_1}\zeta^0]^{I,G,O,C} \sim [{*o_1}\zeta^1]^{I,G,O,C} \\ [{*o_1}\zeta^1]^{I,G,O,C} \Rightarrow 2 \cdot \{ \approx [{*o_1}\zeta^0]^{I,G,O,C} \} \end{array} \right.$$

In the SCIP-3B example above, the output o_2 could act as a regulatory factor controlling compartment curvature, ultimately enabling division[71]. The input i_2 may represent the concentration of o_1 precursors. Imperiosis elements need not be entirely distinct, enabling the exploration of more complex imperiosis dependencies.

These minimal life form representations demonstrate how our proposed definition of life can be concretely applied to define the simplest systems meeting the criteria for life. By formalizing MLFs across the SCIP taxonomy, we establish a clear set of reference models that can guide both theoretical exploration and experimental construction of living systems.

On the origin of life

Origin-of-life research is a highly dynamic and multidisciplinary field, spanning all major scientific disciplines. This intellectual intermingling produced numerous innovative works, which is reflected by the diversity of hypotheses regarding the origin of life. The leading hypotheses are the RNA world hypothesis (genetic information arose first), and the metabolism-first hypothesis (metabolic networks preceded genetics) from which emerged many prebiotic "worlds" favoring different biomolecules for their order and/or relevance of appearance on Earth, including protein (or peptide), lipid, and coenzyme worlds[72]. A virus world has even been proposed in 2006 by Koonin et al.[73]. However, while producing significant scientific advances, this multifaceted approach also highlights the lack of consensus on what "object" should be produced in the first place.

An operational definition of life is not intended to answer the question of the origin of life; rather, such a definition is essential to provide first principles from which (i) theorists can derive pathways potentially leading to the generation of a living entity in a particular environment, and (ii) experimentalists can test those pathways. In other words, a definition of life must provide logical guidance for what pathways should be considered under prebiotic conditions.

The principle of self-compartmentalizing imperiosis dissolves the longstanding dichotomy between "genetic-first" and "metabolism-first" models: at their core, these are both expressions of imperiosis logic. The essential criterion is whether gates or inputs (the elements of imperiosis) are products of imperiosis themselves (encoded origin) or products of standard chemistry (non-encoded origin). From this perspective, the origin of life becomes inherently SCIP-focused. Crucially, the identification of minimal life forms within each SCIP category provides a powerful framework to elucidate the essential properties of imperiosis and compartmentalization required for abiogenesis to occur.

Key questions regarding those properties include:

- What constitutes a plausible prebiotic gate?
- How flexible are prebiotic gates in accepting different inputs?
- To what extent can prebiotic gates be modular, integrating multiple simultaneous inputs?
- Does imperiosis require spatial confinement for its emergence?
- Do gates performing polymerization require specific conditions to emerge, as opposed to gates performing other types of chemical reactions?
- Are polymerized inputs necessary for polymerizing gates?
- Are SCIP categories permeable? Can a life form of one category give rise to another?
- How imperiosis interdependencies emerge?
- Are prebiotic compartments necessarily membrane-delimited?

The simplicity of the founding principle, and the level of abstraction it provides, makes it a powerful tool; not only for framing hypotheses about life's origins but also for guiding experimental and theoretical exploration across chemistry, biology, and synthetic systems.

Concluding remarks

Life is fundamentally dynamic, so it is no coincidence that its core principle is itself a process. The very nature of imperiosis is that it is an encoding process: it establishes a correspondence between two or more entities without requiring direct physical interaction between them. This abstraction not only frees imperiosis from dependence on any specific substrate and captures fundamental biological properties, but also provides remarkable explanatory power across the scales.

Elements of an interconnected imperiosis network can be abstracted as a single "virtual gate" capable of accepting and producing many inputs and outputs simultaneously. By this logic, an entire cell can be regarded as a single gate, just as groups of interconnected cells forming tissues, organs, or entire organisms, can be represented as higher-order gates. Across these scales, the

encoding principle of imperiosis recurs. Above the cellular scale, life becomes an expression of its core principle through a more diverse set of imperiosis elements. This means that, in theory, every aspect of an organism can be explained in terms of imperiosis, from its individuality to its capacities.

What distinguishes a population from its entities is the presence of a unifying upper-level compartment (*e.g.* skin, shell). When that compartment is lost, as in a dead animal decomposing, the larger-scale living entity ceases to exist, even though some of its constituent cells may remain alive. The principle of self-compartmentalizing imperiosis applies directly at multiple levels of organization, from single cells to integrated multicellular individuals, and provides a natural basis for distinguishing between living individualities.

The versatility of imperiosis enables remarkable properties to emerge at the molecular level, which in turn support higher-order phenomena such as resource management and spatiotemporal organization. Its scale-free nature is evident in the capacity of living entities to organize themselves functionally into higher-order organizations that both depend on and extend these properties (*e.g.* colonies, troops, pods, societies, ecosystems), and, more generally, in their capacity to embody the principle of imperiosis. A simple but striking example is the act of reading aloud: electromagnetic waves are converted into acoustic waves through imperiosis, with the human serving as the gate.

Life is self-compartmentalizing imperiosis: a universal process logic that builds, maintains, and coordinates compartments across the scales. From molecular gates to cells, from organisms to ecosystems, imperiosis repeats and reconfigures itself, generating the structures and dynamics associated with living systems. It is a principle abstract enough to transcend chemistry, yet precise enough to guide experiments, classify life forms, and explore life's properties and origins. At every level, from the simplest life form to the most complex biosphere, the process persists, recursively sustaining and reproducing the conditions for its own existence. In this most fundamental sense, life calls life.

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