Nature's Design's: The Biology of Survival

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Abstract. Life has existed on earth for at least 3.95 billion years. All along, the flame of life has been successfully passed on from generation to generation, and species to species across an immense temporal span. This includes at least five mass-extinction events that wiped out over 70% of all species in each such biotic crisis. Against such immense odds, life has learned to thrive despite repeat assaults. And the ingenuity embedded within natures designs has been an integral part of this inspiring story. For example, the ancient bacterial flagellum is powered by the Mot Complex which is part of a perfectly circular nanoscale rotary engine. It is obvious that nature came upon the wheel much before human arrival (i.e., at least as far back as 2.7 billion years). Many are the design lessons that may be gleaned from studying nature. This paper looks at the immense evolutionary design-laboratory that nature evolves its designs within, and frames it alongside an Axiomatic/Complex-Adaptive/Stigmergic Systems perspective.

Keywords: Axiomatic Design; Biological Systems; Stigmergy; Emergence; Complex Adaptive System; Evolution.

1 Introduction

Form and function are discernable across the biological order; for example, form in anatomy and its corresponding function in physiology. Unfortunately, research in the world of modern biology is currently divorced from that of design-theory. Yet each discipline could benefit from studying the other. From a design perspective (and subject to environment/precedent constraints), form seems to be following function (e.g., the elbow joint of the fore-arm for bringing food to the mouth). The fundamental problem associated with design in biology, is that of agency. Thus, while the act of design implies a purposeful designer, biological "designs" operate bereft of such agency, and therefore explicit intent. If no designer is standing by the biological artifact in question; if there are no design documents in the biological archives, how could the intention of function be properly inferred and ascribed? In this paper, we try to bridge the seemingly insurmountable gap between design-theory and biological "designs," without getting derailed by "intelligent design" polemics.

In Section 2, we establish the stigmergic teleology for biological designs. This helps bring biological designs into the normal design discourse. Section 3 discusses the organic/biological genesis of the design motto "*form follows function,*" and its linkages to the axiomatic framework. In Section 4, the design of the bacterial flagellum which compotes well with the axiomatic framework has been captured. Section 5 discusses the dynamics of evolution from a design matrix perspective.

2 Stigmergic Teleology of Biology

As Prof. Dawkins asserts in [1]:

*The total amount of suffering per year in the natural world is beyond all decent contemplation. During the minute that it takes me to compose this sentence, thousands of animals are being eaten alive, many others are running for their lives, whimpering with fear, others are slowly being devoured from within by rasping parasites, thousands of all kinds are dying of starvation, thirst, and disease....The universe that we observe has precisely the properties we should expect if there is, at bottom, **no design**, no purpose, no evil, no good, nothing but pitiless indifference.* (Emphasis added.)

It was Darwin who first made known the ordering principle of natural selection in biology [2]:

One general law, leading to the advancement of all organic beings, namely, multiply, vary, let the strongest live and the weakest die.

Yet Darwin was acutely aware of the absurdity of the designerly lacuna [2]:

To suppose that the eye with all its inimitable contrivances for adjusting the focus to different distances, for admitting different amounts of light, and for the correction of spherical and chromatic aberration, could have been formed by natural selection, seems, I confess, absurd in the highest degree. When it was first said that the sun stood still and the world turned round, the common sense of mankind declared the doctrine false; but the old saying of Vox populi, vox Dei, as every philosopher knows, cannot be trusted in science....The difficulty of believing that a perfect and complex eye could be formed by natural selection, though insuperable by our imagination, should not be considered subversive of the theory.

It is not that Darwin did not believe his theory; on the contrary, he was quite willing to oppose the common sense (i.e., "Vox populi, vox Dei") of his time. Yet there is something unsatisfactory about how function and form (i.e., design) come together without any role for the designer.

If a top-down role is problematic, is it perhaps possible to establish a bottom-up, boot-strapping role for design? Four supportive concepts [3] (Stigmergy, Complex

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Adaptive Systems, Knowledge Hierarchies & Emergence) need to be briefly reviewed to help shift the problem of biological design into a bottom-up approach.
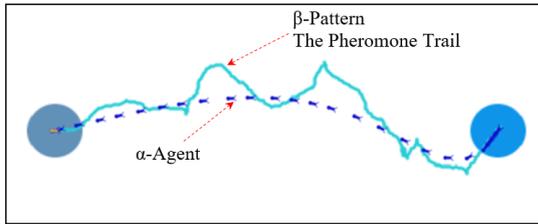
Fig. 1. Stigmergic trails (using NetLogo [4])

Stigmergy [5] denotes call to work based on local signs or markings (such as the ant trail in the adjacent Fig. 1) left by biological agents (α) at some time in the past and during the course of their work (either as a side-effect of the said work or as something in addition to the work). These markings aggregate to provide organizational directives (β-logic) available at various levels, both within the environment as well as within and between agents. Thus, even though there is no one controlling the set of agents in a top-down sense, there is nevertheless system-wide control being established in a bottom-up sense.
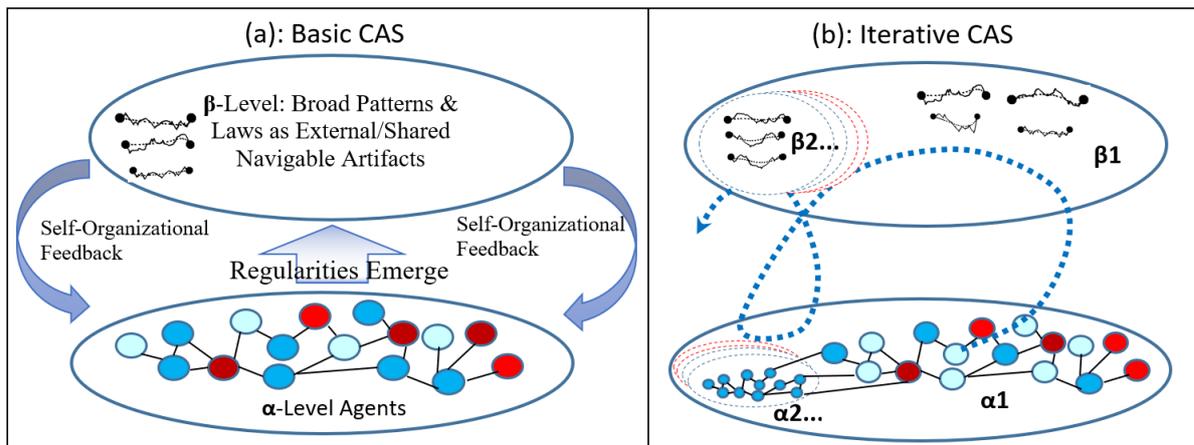

Fig. 2. Complex Adaptive System: Basic vs. Iterative (Reproduced with Permission [3])

Stigmergic ordering is well established across all scales (micro-meso-macro) of biological systems. For example, the pheromone markings that an agent ant (αi) leaves behind as it navigates an unknown terrain helps it to navigate back home instead of being lost (with near-certain death as its fate). And if perchance, it does chance upon a choice food item, these same pheromone patterns (βj) help rally other ant agents to jointly haul the food back to the nest. While biological in origin, the pheromone droppings are not alive. Yet in aggregate, these markings help organize a swarm of ants in a purposeful pursuit. The ants themselves need not be aware of the bigger picture; all that is required is that certain chance mutations have enabled a certain species to be the first in secreting the pheromone droppings. And from then on, the Darwinian survival of the fittest would give it reproductive dominance.

Stigmergic ordering helps biological systems evolve and adapt to form higher levels of complexity under the rubric of Complex Adaptive System's (CAS) and Complex Adaptive System of Systems (CASoS). As Prof. Holland describes it [6], CAS's "*are systems that have a large number of components, often called agents that interact and adapt or learn.*" Holland then proposed a two-tiered system as shown in Fig. 2a above. The lower α-tier follows a fast-dynamic and is engaged in the flow of resources between diverse agents; while the upper β-tier

follows a slow-dynamic that captures stigmergic artifacts and aggregates from these which are then emitted system-wide as stigmergic signals that help the agents organize and scale.
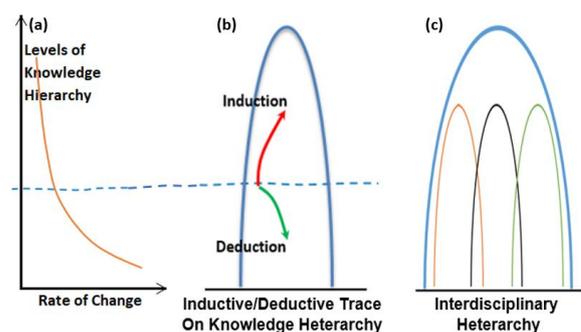
Fig. 3. Knowledge Hierarchy/Interdisciplinary Heterarchy (Reproduced with Permission [3])

When considering the production of knowledge corpus, humans may also be considered as stigmergic agents. The knowledge that we create helps organize human activities in myriad ways beyond the original intent. In other words, the production of human knowledge (as a β-tier aggregate) is itself a CAS process [3]. The form of human knowledge has a conical structure to it; i.e., by the very nature of abstractions, there are many more concretes than

abstractions. Likewise, there are many more abstractions versus abstraction-of-abstractions. Such pyramidic structuring results from our cognitive need to reduce the complexity of whatever we are dealing with into something manageable. For example, Occam's razor (which asserts that one should not make more assumptions than the minimum needed) is an example of such a cognitive need. The end result is that human knowledge has a pyramidic structure as shown in Fig. 3b above. Here, the inductive arch is the upward flowing trace that is involved in creating higher-level generalizations. In contrast, a deduction is the downward flowing trace involved in the application of the induced generalizations. But human knowledge is not the output of any one agent; it instead captures the sum-total of such population-wide outpourings that are painstakingly curated and accumulated across time. And when multiple domains are mapped side-by-side along with their shared conceptual linkages, the various hierarchies map onto a heterarchical span (Fig. 3c) that share and cross-pollinate across the domain barriers. Fig. 3a captures the rate of change across the hierarchy.
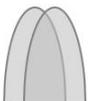
Fig. 4. Ontological vs. Epistemological Emergence (Reproduced with Permission [3])

Now consider the problem of emergence. Reductionism (i.e., whole is the sum of its parts), attempts to reduce all existents to a minimal set. In contrast, emergentism (i.e., the whole is more than the sum of its parts), tracks systemic properties that evaded the reductionist capture. Fundamental existents and concepts in biology (such as life, consciousness, etc.) pertain to emergent properties.

Ontology is the study of entities that exist. Epistemology is the meta-level study of our knowledge of those entities. As shown in [3], emergence may be considered either ontologically or epistemologically (Fig. 4). Ontological emergence is irreducible to its constituent parts; for example, the phenomenon of life is irreducible to its ultimate physical constituents. Ontologically, life is thus a novel property irreducible to its physical constituents regardless of the state of our knowledge about it. In contrast, an epistemologically emergent awareness is a novel concept that is not reducible to our knowledge of the constituent parts; i.e., it needs overarching emergent concepts rendered as white dots in panel-EI/Fig. 4. The panels are marked with the leading letters of the intersecting coordinates; for example, ER denotes epistemologically-reducible. EI may be

associated with OR, for example in making sense of the rainbow in ancient times (e.g., bow for the warrior gods). There can also be erroneous EI without the corresponding OI (for example, the four humors in ancient holistic medicine as well as the error of the afore-mentioned "intelligent design"). Most often, our awareness of OI precedes our theorizing about it and thus formulating a corresponding EI. Many of the emergent properties (such as life and consciousness) are currently in the state of OI without having advanced to the state of EI yet.

Having briefly reviewed the four requisite themes (i.e., Stigmergy, CAS, Knowledge Hierarchies & Emergence), we are now in a position to consider the challenge of bottom-up teleology in biological systems.

Historically, the field of teleology was established by Aristotle for studying "*final-causation*" (which roughly translates to function). Humans are paradigm examples of this view as they are self-conscious and sufficiently self-aware to recognize internal intentions that may be vocalized and probed. This view was then anthropomorphically extended to include the behavior of animals and plants. Each such extension required loosening the anthropomorphic strings to include lower-level conscious, and vegetative actions [7]. But in each of these cases, the teleological intent is invested at the agent level, and not across a collection of agents. We need stigmergic teleology to help us step beyond the agent level.

Consider once again, the ant-trail across a soil track. Soil, stand-alone is not teleological. But when a critical mass of ants (in search of food), embed their pheromone droppings in the soil-bed, it then becomes imbued with teleological directiveness to help the ant-colony successfully scavenge for food. A stand-alone Robinson-Crusoe ant could not have triggered such a collective endeavor; for the pheromone trail would have evaporated and vanished in due course. Also, just a few ants could not have sustained the trail as it would have likewise vanished. Instead, it required a critical mass of ants to constantly replenish the evaporating pheromone scent markings. In other words, the stigmergic goal did not precipitate at the α_i, stand-alone ant level; it instead required a critical mass of ant agents that needed guidance across many α_i-β_j cue-and-response cycles. It is at this critical tipping-point that the ant-trail (along with its marching ants) may be said to be teleologically invested. Thus, given the problem context of the ant-trail (as a means for path-finding for food), it is precisely this critical mass of ants as a unit that is minimally and independently teleologically invested.

Stigmergic teleology works across all scales, including the micro-level. For example, Tabony reports the existence of molecular level stigmergic mechanisms within the cell-biology of the tubulin protein [8]:

...they self-organize and develop other higher-level emergent phenomena by a process where individual micro-tubules are coupled together by the chemical trails they produce by their own reactive growing and shrinking.

β-level stigmergic markings are not restricted to happen in the environment (i.e., pheromone excretions into the soil for the ant-trail); it could also be entrapped within the agent as DNA messaging and shared either vertically (i.e., genetic reproduction to create new agents) or laterally (transformation, transduction, and conjugation) between existing agents.

All design involves searches through massive design spaces. Using lateral gene transfer, bacterial colonies are able to evolve antibiotic resistance at a rapid pace. Even though bottom-up stigmergic design is non-conceptual, it is immensely efficient in scale and scope. Imagine if the underlying stigmergic design patterns & principles were to be rendered conceptually legible?

Stigmergic teleology is a bottom-up emergence of function at the β-level that helps guide and orchestrate the covered agent activities at the α-level. Also, it is bottom-up stigmergic teleology that could have helped Darwin overcome the aforementioned absurdity of the top-down designerly lacuna.

3. Biology of Form Follows Function

It was architect Louis Sullivan (father of the iconic skyscraper design, and mentor to Frank Lloyd Wright) who first coined the phrase "*form follows function*" in [9]:

Whether it be the sweeping eagle in his flight, or the open apple-blossom, the toiling work-horse, the blithe swan, the branching oak, the winding stream at its base, the drifting clouds, over all the coursing sun, form ever follows function, and this is the law. Where function does not change, form does not change...It is the pervading law of all things organic and inorganic, of all things physical and metaphysical, of all things human and all things superhuman, of all true manifestations of the head, of the heart, of the soul, that the life is recognizable in its expression, that form ever follows function. This is the law.

In the above origination of the pithy formulation, Sullivan has an expansive inclusiveness to the concept of form. By form, he doesn't merely mean the shape or configuration of something; instead, it is the existential manifestation of a thing in all its "*physical and metaphysical*" properties. In the world of design, these are the design-parameters (i.e., DP's) that the designer is trying to assemble and configure. In other words, "*form follows function*" is indeed the familiar mapping between Design Parameters (DP's) and Functional Requirements (FR's) in the axiomatic world. Depending on the scale at which the design is operating (micro-meso-macro), biological forms may range from quantum mechanics (that underlies photo-synthesis), molecular biology of the cell (that underlies DNA replication), physics of the cellular transport (such as the Mot Complex), anatomy of the organ and tissue systems (such as respiratory, digestive), etc.

In all of these manifestations, since there are no agent-designers available for interrogation about the governing functions at large, all the hidden FR↔DP mappings need to be induced and reverse-engineered to help understand the operative principles of stigmergic designs that are available in nature.

In the quest for survival against immense odds, biological agents have been instruments of stigmergic design across vast temporal expanses. Or as recounted in [10]:

Trapped within the sparse coils of the DNA (which consists of about 1.5 GB of DVD-sized data), one may witness the essence of the Information Axiom operating in a self-organizing context. Herein, the genetic code orchestrates the embryonic self-articulation and development of a complex living entity (consisting of about 150 zettabytes of data and requiring about 30 Manhattan-size datacenters to merely store) that can struggle, adapt and thrive in heretofore novel and unknown environments with ever changing risks and opportunities.

4. Bacterial Flagellum Design

The flagellum is for sensing, orienting, and locomotion of cells of organisms in low Reynolds number (high viscosity relative to mass) media. Flagellum is Latin for a whip. Flagella are found on all three main branches of the evolutionary tree: prokaryotes (e.g., E. coli), archae (e.g., Methanococcus voltae) and eukaryotes (e.g., sperm). Prokaryotes use rotary movement at the flagellar base for propulsion. In other words, the wheel that is embedded in the motor was invented by nature much before human arrival–and at least as far back as 2.7 billion years.

For a bacterium that is around 2-3 microns in length, its flagella are about 10–30 nm in diameter and 5–20 μm in length (Fig. 5a). The basic function of the flagellum is for locomotion. The sensory organelle for a bacterium is the array of methyl-accepting chemotaxis proteins (MCP's) embedded in the inner membrane. MCP's are sensitive to changes in the environment such as chemicals (attractants/repellents), temperature, pH, etc. The protein wheel structure of the nanoscale molecular rotary engine has its (cell-membrane embedded) stator composed of the Mot Complex (MotA/MotB). The rotor consists of 4 protein complexes (FliF, FliG, FliM, and FliN). The last three of these also act as a molecular switch that enables clockwise (CW) and counterclockwise (CCW) switching based upon messaging signals from MCP. The stator-rotor engine is powered by the Proton Motive Force (PMF) pump that uses electrochemical potential difference to build up a proton gradient across the inner cytoplasmic membrane [11]. Stand-alone (i.e., without the attached flagellum), the rotor can operate in the 20,000-100,000-rpm range; with the attached flagellum, it reaches 200-1000 rpm. As there is no ignition key for the flagellar motor, it keeps rotating. Rotation is stopped using the EpsE protein that attaches to the FliF-complex of the rotor and acts as a clutch to stop the flagellum, resulting in a stationary bacterium [12]. With femtoampere currents being generated, the energy consumption is minuscule
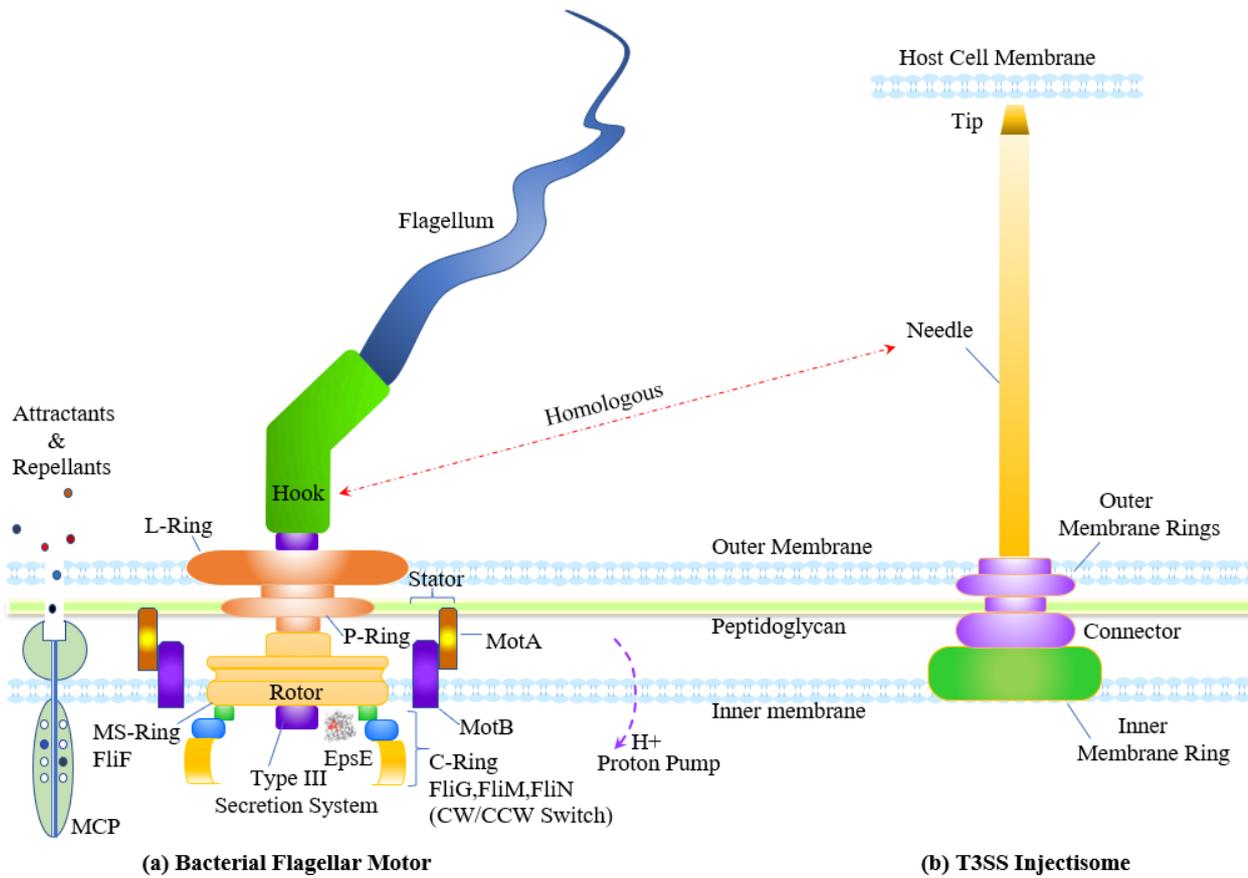
Fig. 5. The Flagellar Mot Complex vs. T3SS Injectisome (Adapted from Wikipedia [14,15])

("*just one ten-quadrillionth of a watt*" [13]). As Prof. Namba recounts in [13]: "*This structure is basically 100% energy efficient. It is an extremely exquisite nanomachine.*"

Decoupled, Lower-Diagonal Propulsion Design

Fig. 6. The Flagellar Mot Complex Design

The flagellar hook is a molecular universal joint. Traditional universal joints have a center block that helps transmit the rotary motion across axes that are inclined with each other. The molecular flagellar hook is able to do the same in far more degrees of axis inclination and with

no center block transfer mechanism. Instead, the molecular sleeve of the hook reshapes and reorients itself in a flexible manner.

The bacterial locomotion is a biased random walk. Unlike a pure random walk that has uniform probabilities in all possible degrees of freedom, a biased random walk has non-uniform probabilities (i.e., biases) in certain preferred directions. Thus, when the MCP on the flagellum senses favorable environments in the direction that it was moving in, it signals the CW/CCW switch in the rotor to continue along CCW. However, when MCP senses unfavorable environments in the direction that it was moving in, it initiates the CW/CCW switch to reverse into CW mode. This switch initiates the bacterial tumble that results in a random change in the direction of locomotion, but away from the non-favorable environment.

With the above review of the main elements of the flagellar system, the overall design can now be traced [16] as shown in Fig. 6. The locomotion of the flagellated bacterium may be observed in three distinct cases:

- **M: Motion** towards attractants or away from repellants
- **ML: Motionless** state (such as when in a biofilm)
- **CD: Change-of-direction** via tumbling

The design leads with the sensory organelle MCP that provides the discriminatory signal to the flagellar engine to move towards an attractant, to move away from a repellant, or to stay stationary in a satisfactory environment. The PMF pump provides the motive energy for the rotating elements. With the EpsE protein detached from FliF, the rotating elements are engaged in the normal CCW direction (Case M). In contrast, when EpsE is attached to FliF, the rotating elements are disengaged resulting in a stationary organism (Case ML). Whenever the MCP proteins detect unfavorable conditions in the direction of motion, it signals the basal elements of the rotating flagellum (i.e., FliG, FliM, and FliN) to switch the rotating direction from the default CCW to CW. This triggers the random tumbling of the bacterium (Case CD). During the process of tumbling, when the sensory elements detect itself oriented in a favorable position, the signal to switch to the default forward-propelling CCW is sent. The hook (at the protruding base of the flagellum) serves as a universal-joint for transmitting the torque. And finally, the flagellum provides the propulsive thrust against the low Reynolds medium.

Many of the functions and structures (and the underlying proteins) observed in the bacterial flagellum have also been found in the non-rotating Injectisome-T3SS (Type Three Secretion System) used by bacteria in injecting poisons such as the bubonic plague (bacterium Yersinia Pestis) into a eukaryotic target (Fig. 5b). For example, the hook is homologous between the flagellum and the T3SS needle.

Three possibilities exist regarding the order of evolution between Injectisome-T3SS and the flagellar complex:

- Bacterial flagellum preceded Injectisome-T3SS
- Injectisome-T3SS preceded bacterial flagellum
- Co-evolution of bacterial flagellum and Injectisome-T3SS from a common ancestor

Current research has yet to conclude on the proper evolutionary lineage. Nevertheless, it is important to understand the evolutionary dynamic pressures on the underlying design matrix. In the following section, we look at the evolutionary dynamic of the FR↔DP Design Matrix.

5. Design Matrix Dynamics & Evolution

From recent evidence of microbial by-products found in rocks from north-eastern Canada, it is now clear that life has existed for at least 3.95 billion years [17]. The last 500 million years have witnessed five major mass extinction events that wiped out over 70% of all species in each such biotic crisis (Fig. 7).

The causes for the mass extinctions are varied and include massive volcanic basalt-flood events, asteroid strikes, sea-level changes, changes in the atmospheric gas concentrations, etc. While 70% of life may have gone extinct, the remaining 30% has learned to thrive despite repeat assaults. And the ingenuity of the design potential embedded within natures evolutionary mechanism has been an integral part of this inspiring story.

MYA	Era	Period	5 Extinction Events & its respective % Size	Life Forms that went Extinct	Life that Flourished	Likely Causes
	Cenozoic	Quaternary		Non-Avian Dinosaurs (e.g., *T-Rex*)	Mammals	Astroid strike in Chicxulub; Lava Flow in the Deccan Traps
100		Tertiary	~65 MYA (75%)			
	Mesozoic	Cretaceous		Non-Dinosaur Archasaurs, many terrestial reptiles & ambibians	Dinosaurs	Volcanic activity
200		Jurassic	~200-210 (75%)			
		Triassic	~250 (96%)	Largest Extinction; many vertebrates	Dinosaurs	Astroid Strike, Volcanic Activity (Emeishan), Microbes
		Permian		Tropical marine species: corals, sponges, placoderms		Volcanic eruptions (Viluy Traps), meteor strike, anoxic oceans
300	Paleozoic		~360-370 (80%)			
400		Devonian		Small Marine life: Shelled brachiopods, conodonts, trilobites		Massive Glaciation in southern hemisphere triggered by loss of sunlight due to dust from astroid collision in outer space.
			~440 (85%)			
500		Silurian				
		Ordovician				
		Cambrian				
600						
↓			Precambrian			
4,600						

Fig. 7. Big 5 Mass-Extinction Events (Adapted from [18, 19])

In any given ecosystem, there could be environmental (**e**) changes in the habitat as well as evolutionary changes within competing/collaborative (**c**) agents. In general, there could be nine change categories between these two factors (see Fig. 8 below with attached explanatory legends).

	e-	e0	e+
c-	c-e-	c-e0	c-e+
c0	c0e-	c0e0	c0e+
c+	c+e-	c+e0	c+e+

e- : Adverse Environment
eo: Neutral Environment
e+: Favorable Environment
c- : Competitive Agents
c0: Neutral Agents
c+: Coexisting Agents

Fig. 8. Nine Types of Selection Pressures

A few select examples to illustrate the above include:

- **c0e+/c0e-:** An example of the environmental selection pressure could be an ice-age type of climate change into snowy, white-out conditions. In this case, c0e+ selection pressure would favor animals of a lighter colored coat to camouflage itself and survive in the white-out climate better. Likewise, c0e- would put selection pressure on animals with a darker coat to evolve into a lighter shade.
- **c-e0/c+e0:** The ongoing predator/prey arms-race between the rough-skinned Newt (Taricha Granulosa) and the Garter snake (Thamnophis Sirtalis Parietalis) would illustrate the c-e0/c+e0 selection-pressure dynamic. The Newt produces enough tetrodotoxin to kill several adult humans. But

it is safe to handle the Newt as the toxin is safely stored underneath the skin. The Garter snake preys on the poisonous Newt and has to successfully digest the toxic load. In evolutionary time-scales, the competitive advantage has shifted back and forth between these two antagonists. Currently, the competitive advantage resides with the Garter snake (i.e., it is, therefore, c+e0) while the Newt (c-e0) has to evolve and store an even more potent tetrodotoxin load beneath its skin [20].

- **c-e-/c+e+:** About 200 of the 12,000 ant species that exist today are of the invasive kind. By hitch-hiking alongside human global travel patterns, these invasive ant species have triggered dramatic bio-diversity losses with concomitant economic damage. Invasive species in the US alone cost an estimated $138 billion/year [21]. An example of the non-invasive species is L. Paralienus that is local to Central Europe (including Austria, Bosnia, France, Germany, Italy, Spain, Sweden, Switzerland, Turkey, etc.). In contrast the invasive species, L. Neglectus was initially local in its native range near the Black Sea; it is now found all across Europe. Being more adaptable to the human built-environment, it is successfully displacing the local species such as the L. Paralienus. In this example, the L. Paralienus species is facing c-e- selection pressures (both from the urban/built environment as well as the highly adaptable/aggressive invasive species such as L.

Neglectus). In contrast, the invasive L. Neglectus species is facing c+e+ selection pressures (given its higher urban adaptability, its inherent aggressiveness as well as favorable migratory pathways).

- **c0e0:** In 1968, Biologist Motoo Kimura proposed the neutral theory of molecular evolution [22]. It holds that most changes at the molecular level occur from the random genetic drift that does not compromise existing functions and are therefore neutral with respect to natural selection. c0e0 pertains to this possibility. It is, however, possible that such a neutral drift is not neutral (and therefore subject to Darwinian selection) at a later stage when circumstances have changed.

A fundamental question worth considering is to look at how these evolutionary selection pressures impact the design-matrix? In other words, what are the patterns of design-matrix dynamics one should expect to see? For example, where should one expect to see the primitive & conserved genes, proteins, and functions to be more favorably located on the design matrix? Likewise, where should one expect the recent additions and deletions to be located? Also, which areas of the design-matrix are more vulnerable for a knockout. The following discussion uses the design-matrix (Fig. 9) as a theoretical framework to explore the evolutionary dynamics.
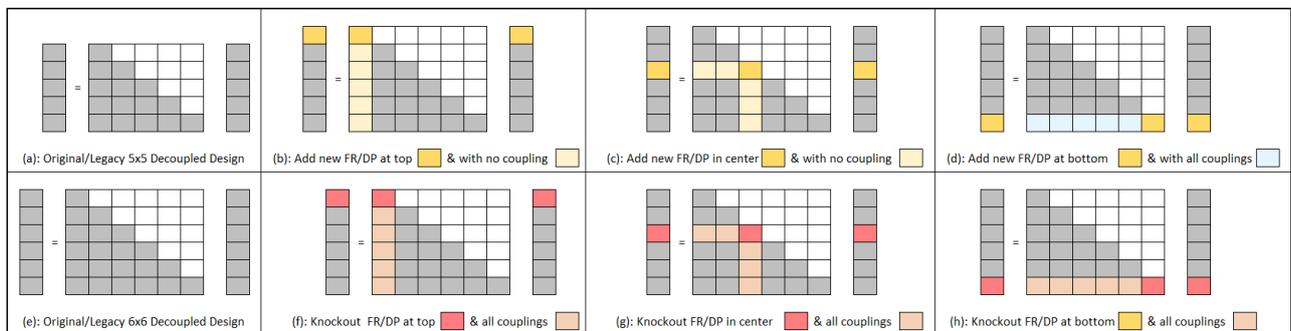
Fig. 9. Design Matrix & Evolutionary Dynamics

Imagine a decoupled legacy design with a 5x5 or a 6x6 design matrix as shown in Figs. 9a & 9e. The following are some of the interesting design-matrix dynamics from an evolutionary perspective:

- Figs. 9a→9b: The new system attempts to add a fresh new FR and its corresponding DP at the very top row of the design matrix. Care is taken to make sure there are no other spurious coupling terms associated with this DP that compromise any other FR in the system. With no coupling terms to compromise the existing system, it is more than likely that such an addition wouldn't be expensive to meet.
- Figs. 9a→9c: A singleton FR/DP addition could also be made as any of the new rows without much expense; it is effectively orthogonal to the existing system. Likewise, if such a singleton FR/DP pair

currently exists in the legacy system, it would not wreak havoc if it had to be knocked-out.
- Figs. 9a→9d: This case adds an FR/DP row at the very bottom along with full coupling with every other DP that preceded and located above the new addition. Such an addition would be minimally disruptive as it can keep the legacy functions intact.
- Figs. 9e→9h: This is the knockout case which is the reverse of the above case of Figs. 9a→9d. And similar to the above case, such a knockout would be minimally disruptive as it can keep the remaining functions intact.
- Figs. 9e→9f & 9g: These are knockout cases (with significant couplings) from the top & middle-zone areas. Given that the couplings also need to be knocked out, such deletions can be expensive.

There are many more similar transitions that the system could be subjected to. But in broad terms, here are some general patterns one could expect:

- FR/DP pairs at the top of the design-matrix with appropriate couplings (Fig. 9f) are likely to be more primitive, not easily knocked-out and therefore, highly conserved.
- Singleton FR/DP additions (Fig. 9b, 9c) could, in time, come to serve as the origination point for new sub-systems.
- FR/DP pairs at the bottom of the design-matrix (even with appropriate couplings) could be easily knocked-out as well as added into the system without wrecking system-wide havoc (Fig. 9d, 9h).

To illustrate the above dynamic, consider the central dogma of molecular biology which highlights the directionality of genetic information flow along the following schema: DNA ↔ RNA→Protein. The DNA is first transcribed into various RNA components (i.e., mRNA, tRNA & rRNA). Once transcribed, the genetic information is then translated into the requisite polypeptides the cell needs. Located in the cytoplasm of the cell, ribosomes are protein factories that help translate the information contained within the mRNA into the actual protein that the cell requires. Proteins are constituted from a palette of 20 amino-acids. Casting the above self-organization occurring within the cell in an iterative-CAS framework (see section 2), if the amino-acids are α_1-level entities, information captured in the RNA/DNA are β_1/β_2 patterns; and ribosomes are higher-level α_{2+} entities. Higher the entity in the CAS heterarchic-hierarchy, lower is the rate of change (similar to Fig. 3.a). It is this differential rate of change that is likely operative in the differential rates of genetic conservation across evolutionary time-scales. For example, consider the manufacture of the ribosome that also needs to be periodically manufactured/replenished. The requisite information for the manufacture of these protein-factory ribosomes is transcribed into the rRNA fragment (as mentioned above). The ribosome contains a small subunit (SSU) as well as a large subunit (LSU). Bacterial, archaeal as well as plastid SSU's are denoted 16S in reference to the centrifugal sedimentation rate (Svedberg unit) they occupy. In contrast, eukaryotes such as humans have their respective SSU in the 18S sedimentation level. With this terminology in place, one may recognize the significance of the highly-conserved SSU component of the rRNA. Its conservation derives from the ubiquitous role it plays in all protein synthesis processes. Random mutations that compromise its foundational protein-making function faces strong selection pressures against it becoming prevalent. Even so, SSU rRNA does suffer change. But that change is occurring at such an infinitesimal pace that it helps trace the very tree of life across evolutionary time-scales. Or as Prof. Rogers indicates in [23]:

The SSU rRNA molecules are highly conserved, such that bacterial ribosomal rRNA can be compared with archaeal SSU rRNA and eukaryotic SSU rRNA. This characteristic led Carl Woese and George Fox to characterize the rRNA from a broad range of organisms to form the first phylogenetic tree based on molecular characters and led to finding an entirely new taxon of life, the Archaea.

The SSU rRNA is an example of the FR/DP pairing that is primitive, highly conserved and not easily knocked-out:

- FR: Create gene-specific protein-making machinery
- DP: Ribosome as the custom, gene-specific, protein-making factory.

Without the machinery for making proteins, the cell is effectively dysfunctional. The SSU sRNA, therefore, occupies the very top rungs of the design-matrix equation (as shown in Fig. 9f). The SSU sRNA is one example of the design-matrix based dynamic patterns that agree with current research. But if this could be verified across an ensemble of similar cases, such an approach could help provide valuable guidance in allied domains such as healthcare, animal care, farming, drug discovery, etc.

Axiomatic Design highlights the hierarchical structure of design. As Prof. Suh highlights in two separate instances in [16]:

- *Everything we do in design has a hierarchical nature to it. That is, decisions must be made in order of importance by decomposing the problem into a hierarchy.... When such a hierarchical nature of decision making is not utilized, the process of decision making becomes very complex.*
- *The designer must recognize and take advantage of the existence of the functional and physical hierarchies. A good designer can identify the most important FRs at each level of the functional tree by eliminating secondary factors from consideration. Less-able designers often try to consider all the FRs of every level simultaneously, rather than making use of the hierarchical nature of FRs and DP's.*

Hierarchies also show up in nature's designs. Capturing these hierarchies may have significant value. But this involves meticulous reverse engineering of nature's FR-DP design complex. However, this needs to be accomplished without the benefit of any closely aligned prior art and its documentation. In reverse-engineering any given product, the iterative, top-down, forward flow between FR→DP is reversed into an iterative, bottom-up, FR←DP reverse flow [24-26]. In the case of nature's designs, the fundamental problem that exists in regard to the above reverse engineering exercise is that of hydrating natures FR←DP hierarchies in a bottom-up sense. This is because there is no explicit prior art that lends a helping hand in the bottom-up structuring of the FR←DP hierarchies. In this context, the suggestion in [25] to consider the system evolution is of considerable significance:

The first step is to study the previous systems in order to identify system evolution.... The resources needed to investigate system evolution are: standards, patents, instruction for use, safety data sheets, accident reports and other applicable resources related to the system.

Using phylogenetic trees (for example, as created using the highly conserved SSU rRNA, and discussed above),

one may be able to trace the subtle additions and subtractions between functioning organisms and their respective genomes. The requisite bottom-up, hierarchical mapping may be obtained by casting the overall phylogenetic tree of life into a total FR←DP mapping. Current genomic research is unaware of the axiomatic design [27]. This is to be expected as the very concept of design is looked down upon when considering nature's designs. Nevertheless, hydrating the genomic FR←DP mapping in a bottom-up sense has significant and strategic value.

Consider, for example, the human genome project that concluded in 2003:

- The human genome has approximately 3.42 billion nucleotides spread across 23 linear chromosomal pairs in the nucleus.
- Only 2% of the human genome codes for genes (that number approximately 35,000) with instructions for making proteins.
- Rest 98% of the human genome (i.e., the non-protein coding region) was considered as "junk DNA", a term coined in 1972 by geneticist Susumu Ohno [28].
- The idea that there is "junk DNA" runs counter to the Information Axiom [16] which seeks to minimize the information content in a design.
- Firstly, the non-coding genome may be performing the role of a ready-made inventory of body part templates kept in reserve for a rainy day. These may have been functional in the past, but are silenced and non-functional in the current environment [29].
- Now consider the problem of regulating and orchestrating the immense complexity of the highly adaptable and dynamic genomic system. Transposons or jumping genes were discovered in the 1940s by the Nobel laureate and Maize geneticist, Prof. Barbara McClintock. Transposons were considered as part of junk DNA until 1965 when it was shown by Prof. McClintock that these "junk DNA" elements had a regulatory role in turning genes on and off. Transposons make up more than 40% of the human genome [30]. And like the SSU sRNA, transposons are highly conserved.
- Regulatory structures create hierarchies as well as heterarchic hierarchies. Transcription Factors (TF's) are proteins that attach to the DNA to control the rate of DNA→RNA transcription. There are close to 2600 TFs that regulate the human genome. As Yu and Gerstein assert in [31]:

  The relationships between TFs and their target genes can be modeled in terms of directed regulatory networks. These relationships, in turn, can be readily compared with commonplace ''chain-of-command'' structures in social networks, which have characteristic hierarchical layouts.

Reversing-Engineering the FR←DP mapping in the genomic context involves reverse-engineering the design trace that is embedded in the central dogma of molecular biology, i.e., DNA ↔ RNA→Protein. This exercise needs to be done with meticulous care using tools from disciplines such as complex adaptive systems, data-sciences, bio-informatics, and phylogenetics. In all this, the neglected Functional Domain needs to be kept center-stage.

6. Conclusions

This is the very first foray into looking at naturally occurring biological designs in the wild as an immense creative laboratory that spans across geologically vast temporal expanses. Conclusions, contributions as well as shortcomings include:

i. Bottom-up stigmergic teleology is an original proposition in this paper. It could help understand designs in the biological realm without the need for an agent-designer. Given the variety and the immense quantity of biological artifacts available for study, such designs could dramatically enrich the theory of design.

ii. Despite the lack of an agent-designer, biological designs do comport well with the axiomatic design framework.

iii. A design-based approach to biology could aid as a didactic tool in helping organize the vast complexity of biological sciences.

iv. Bringing insights from axiomatic design-matrix dynamics into the realm of biology, genomics, and evolution could help articulate and capture the hidden functions that are operative across various biological scales (micro/meso/macro), including that of the "junk DNA."

v. The design principles of self-organization and self-assembly that underlie biological morphogenesis [32] have yet to be fully understood. The above discussion fails to consider the "manufacturing process" design of the biological artifact. Thus, while the primary design map (FR↔DP) of the flagellum complex has been considered, the equally deserving, self-assembling DP↔PV mapping (DNA↔RNA→Protein→Morphogenesis) needs further research.

vi. It is impossible to capture the richness of the scale and scope of biological designs in such a short report.

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