Cuvier's objection, morphogenesis and the evolution of evolvability

Abstract
The french biologist Georges Cuvier was a prominent early opponent of evolution. Cuvier claimed that evolution was impossible because any change to existing body plans would be deleterious. Mathematically Cuvier's objection agrees with the formally proven "No free lunch" theorems for search and learning. What is interesting is why Cuvier was wrong in the case of biological evolution. This paper uses the evolution and morphogenetics of metazoan animals as the example for discussion.

It is shown that highly evolvable genoptype→phenotype parameterizations are exceptional, and must capture required mutual information between components of viable phenotypes. Parameterisation through the mechanisms of morphogenesis is essential to the evolvability of animals, especially: cell lines, relative anatomical coordinates, sequential growth, and remodelling on environmental information.

Natural selection can act on gene-specific mutability and gene regulatory networks, leading to evolvable parameterizations. Such evolution of evolvability may be a necessary component of biological evolution.

Keywords: Cuvier's objection, parameterisation, morphogenesis, evolution of evolvability

Introduction

The failure of artificial evolution to reproduce the evolvability and innovation observed in biological evolution, [Packard et al 2019] suggests that some necessary part of the mechanism of biological evolution has not been understood.

The concept of evolvability has been in use since Thomson [1931: pp228, 231],[Crother and Murray, 2019.] and with it the realisation that there is something to be explained. Brown [2014] examined the use of the term in biology, and defined the concept of evolvability as "*an abstract, robust, dispositional property of populations, which captures the joint causal influence of their internal features on the outcomes of evolution*".

Dawkins [1989] recognised the importance of embryological development parameterising the phenotype space in an efficient way, relevant to fitness, and that most parameterisations are highly inefficient. Wagner and Altenberg [1996] reviewing evolution in biology and computer science, found "*mutation, recombination and selection is not universally effective*", and identified the emergence of modularity as an important factor in evolvability.

There is empirical evidence that evolution of evolvability occurs in biology, which raises the question of whether this occurs adaptively. Payne and Wagner [2019] identified three categories of factors of evolvability (i)"*molecular mechanisms that create phenotypic heterogeneity*", (ii) robustness, (iii) "the topographic features of an adaptive landscape".

Izquierdo and Fernando [2008] showed in a simple model of gene networks, "*that transcription factor binding matrices (TFBM) evolve to positively constrain phenotypic variability in response to*

transcription factor binding sequence mutations". Sundaram and Wysocka [2020] identified "*transposable elements as a potent source of diverse cis-regulatory sequences in mammalian genomes*", noting that transposable elements compose more than half the human genome.

This theoretical and empirical background informs the hypothesis tendered in this paper, that certain mechanisms of metazoan morphogenesis and DNA mutation play a critical role in the evident evolvability of biological species.

Cuvier's objection

The supposed '*impossibility*' of evolution of animal bodies was one of the original objections to evolution in biology. In the "*Sacred Ibis debate*" of 1802, and "*The Great Debate*" of 1829 [Curtis et al 2018], Cuvier argued for the fixity of species, asserting "*the varieties keep within certain limits fixed by nature*" [Cuvier 1825], that any deviation from existing morphology would be detrimental due to loss of critical function. In particular Cuvier highlighted the need for body parts to fit and work together.

The "*fixity*" of biological species has been proven wrong by the fossil specimens and discoveries in genetics and morphogenesis that accumulated after Cuvier's lifetime. However the problems predicted by Cuvier appear to match those encountered in artificial evolution - that the shape of non-trivial fitness functions often limits the range of adaptation achievable by evolutionary methods.

Mutual information

Cuvier's objection highlights the mutual information between parts that is required to create a working mechanism. This applies whether the information is matching mechanical components (curvature of opposing joint faces, lengths of bones and tendons, muscle contraction and joint excursion), or biochemical systems (e.g. the induction of enzymes required for a pathway).

Distribution of mutations

In biology genetic mutations having some phenotypic effect are common [Acuna-Hidalgo et al 2016]. While some mutations are eliminated by early death in parental germ-line cells or embryos, this does not explain the constrained phenotypic variation observed. Given the observed degree of phenotypic variation, if variation of parts were approximately uniform and independent, a significant proportion of dysfunctional phenotypes would be expected. However the phenotypic variation observed in biological species arising from genetic mutation, is substantially constrained to a range of viable phenotypes. i.e. offspring with dysfunctional bodies due to mismatched parts are very rare. This implies that mutation is somehow constrained to preserve the required mutual information.

The "No free lunch" theorems

Evolutionary algorithms operate within the constraints defined by the "No Free Lunch" theorems for search and learning, [Wolpert and Macready 1995, 1997, 2005], [English 1996], [Wolpert 2012]. These impose an absolute mathematical constraint, that the better-than-random-search performance of an evolutionary algorithm is specific to a particular problem domain and parameterisation of the domain. This is because

1. any evolutionary algorithm contains implied prior information about the distribution of desirable solutions as a function of the genotype and the distribution of mutations,

2. for every possible correlation between a given evolutionary algorithm and fitness function, it is mathematically possible to write another fitness function with the opposite correlation, giving correspondingly worse than random search performance.

The “prior” of evolution

The fundamental prior expectation of evolutionary algorithms, is that phenotype fitness correlates with genotype, at least for local subspaces of the genotype. This is required for there to exist gradients in fitness as function of genotype, which cause an evolutionary algorithm to progressively discover genotypes of higher fitness.

For most biological genomes the metaphorical picture is modified by the possibility of neutral mutations that do not by themselves alter phenotype fitness. Consequently evolution may resemble percolation through a network of genotypes, producing intermittent step changes in fitness [Harvey and Thompson 1996]. This does not alter the requirement for correlation between phenotype fitness and genotype.

Effects of parameterisation

Consider Cuvier’s objection in the context of a naive artificial genome parameterisation for components of a phenotype that must co-vary in order to produce a viable phenotype - for example the curvature of joint faces, parameterised by voxelisation in 3D space. All the viable phenotypes can easily be expressed by this genome, but they are separated from each other in genotype space by many individual voxel changes that are extremely damaging to the function of the phenotype. Such parameterisations have limited evolvability.

Only those genome parameterisations which contain the required information about the dependencies within the set of viable phenotypes, will produce the correlation of genotype with phenotype fitness. Fully evolvable parameterisations (with no local optima) for a given problem, form a very small subset of the mathematically possible parameterisations. Proportionally, this subset is equal to the reciprocal of the Kolmogorov algorithmic complexity of the required mutual information between parts for viable phenotypes of the species. Larger sets of parameterisations may exist containing partial information about the constraints. These result in breaking the fitness function into multiple local optima in genotype space.

The most compact subset of highly evolvable parameterisatons describe only viable variations. These present a genotype space orders of magnitude smaller than less evolvable parameterisations. This difference can change evolutionary improvement of fitness from intractable to highly tractable.

Mechanisms underlying evolution in metazoan animals

This section lays out a high level view of morphogenetics and genetic mutation, covering only those details required in order to explain (1) the ‘problem’ being solved by biological evolution, (2) how the parameterisation of phenotypes by biological genomes encodes the required prior information about the problem, (3) how this information can be acquired through natural selection.

Search domain of phenotypes

The bodies of animals are diverse in appearance and abilities, but very similar in composition and construction. Large highly mobile animals are all metazoan bilateria, dominated by a few highly adaptable phyla. These phyla define base materials, tissues, and basic body plans that conserve topology and morphogenesis.

Two types of information about phenotype fitness are required,

1. co-dependence internal to anatomy and physiology,
2. dependence on the external environment – requirements of the niche.

Morphogenesis

Morphogenesis is the interaction of many cells descended from a single zygote, to construct a multicellular organism. Key features of how morphogenesis generates phenotype are

1. Branching tree of epigenetic cell lines encoding body part identities,
2. Convergence of epigenetic cell lines to a smaller number of tissue generating cell types,
3. Parameterization of anatomical topology on local anatomical coordinates produced by morphogen diffusion gradients,
4. Sequential growth and refinement, patterning finer details with respect to structures generated in preceding stages,
5. Remodelling of tissues on cell environmental information, especially mechanical forces.

The mechanisms underlying these are (in)activation of transcription factor genes, inheritance of epigenetic state by daughter cells, and inter-cellular communication by chemical diffusion of morphogens. These enable the direction of cell behaviours used to define body structures, including clock-and-wavefront, gap-and-pair, cell taxis, adhesion and sorting.

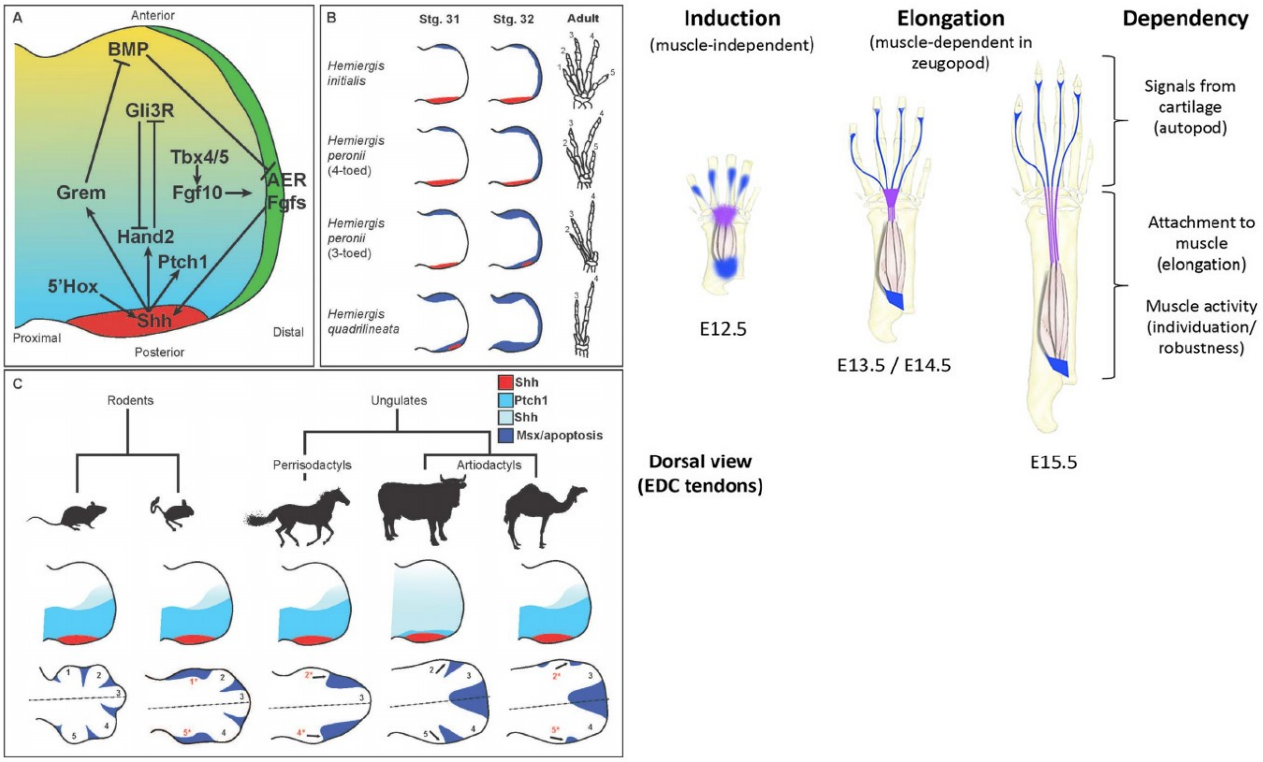

Fig 1 Patterning of topology in morphogenesis.
Left: Morphogen gradients in the mammalian limb bud establish local anatomical coordinates that control morphogenesis. From fig1 of [Young and Tabin, 2017].
Right: Musculoskeletal integration at the mammalian wrist, initial topology formed on morphogen gradients with respect to bone primordia, followed by bone growth, muscle and tendon remodelling. From fig 8 of [Huang et al 2015]

Patterning of topology

The body symmetry of bilateria is formed by breaking the omni-directional symmetry of the blastocoel to establish dorso-ventral and cranio-caudal body axes, by competitive inhibition of morphogen secretion. In chordates the somites and axial body regions are established by the clock-and-wavefront mechanism and Hox gene activation. The limb buds are located with respect to the Hox cell-type, embryonic tissue layers and morphogen gradients. The limb buds in turn generate new internal morphogen gradients which control the definition of the limb segments, and subsequent division into bone primordia, joints, muscles, tendons, and associated nerves and vessels. Epigenetic cell types allow recognition and adhesion to connect required topology, including myotendon junctions, and tendon insertions on bones. Equivalent mechanisms exist in other phyla [Sadler 2018], [McGeady et al 2017].

Remodelling

The initial geometry formed on morphogen gradients is far simpler than that of the mature foetus. Overall size, proportion and shape are extensively remodelled, while maintaining the original topology. This requires that all body parts grow in coordination with each other, in both size and composition, to arrive at a well integrated body with all parts matching size, shape and material properties. The mechanism is remodelling of tissues both passive and active, on environmental signals including mechanical forces, whole body physiology, and local morphogens. The rules of remodelling are defined by the behaviour of tissue cell types.

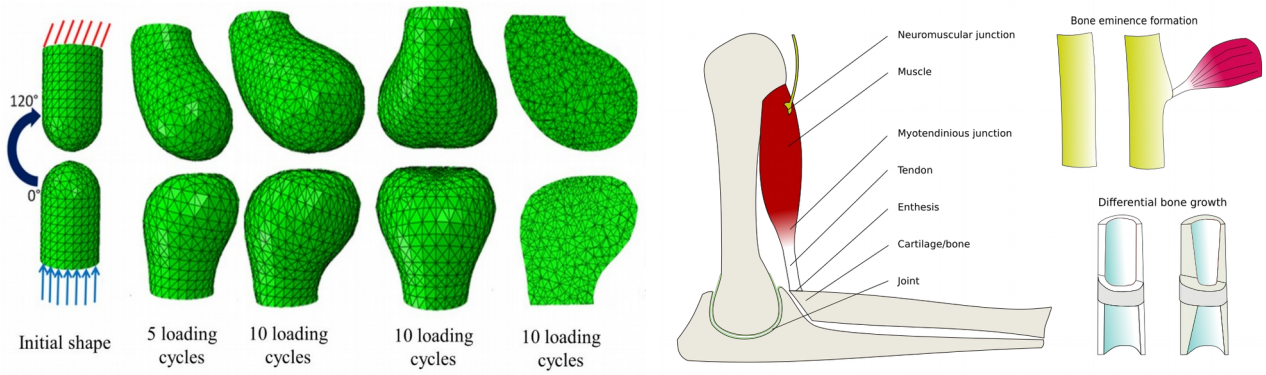

Fig 2. Left: Passive mechanical remodelling of opposing joint faces of bone primordia, joint capsule and menisci not shown. Reproduced with permission from [Giorgi 2015]
Right: Active remodelling of musculoskeletal tissues produces well matched components. From [Hockings and Howard 2020], drawn from data in [Felsenthal and Zelzer, 2017]

Summary of morphogenesis

• Body structure is formed through the process of morphogenesis as a function of cell behaviour.
• Cell behaviour depends on cell line, diffusion of morphogens, and mechanical forces.
• **These allow the co-dependencies of viable phenotypes to be expressed as cell behaviour.**

Genotypes and epigenetic regulation

The cell behaviours of morphogenesis are determined by epigenetic regulation, of a single genome common to all the cells of the organism. However cell lines have different regions of the genome permanently silenced, by epigenetic modifications that are inherited by descendant cells.

Protein coding DNA makes only 1-2% of most metazoan genomes. Cis-regulatory DNA elements are sparsely distributed in the non-protein coding DNA associated with each gene cluster.

Key points of genotype and epigenetic regulation

1. The genes encode the proteins that form the structure, enzymes, morphogens, and receptors used in the process of morphogenesis.
2. Epi-genetic regulation controls which genes are active.
3. Gene regulatory networks produce stable cell types.
4. Trans-regulatory factors epigenetically encode the current state of a cell.
5. Cis-regulatory elements encode the behavioural repertoire of all cell types.

The information that describes a species, and the co-dependencies of viable phenotypes of its niche, is encoded in the cis-regulatory elements of the genome. The set of genes defines the morphogenetic toolkit from which diverse species can evolve. Together these provide a compact encoding of required information of viable phenotypes. This encoded genetic information is much less than the sequence of base pairs.

Mutation of DNA

The ways in which the DNA mutates, and the distribution of those mutations determine the steps which evolution can take in generating new phenotypes from the existing population. It is essential therefore to consider:

1. what is present in the DNA sequence
2. how it affects mutation of the genome
3. the effects of that mutation on phenotype.

Effect of DNA patterns on mutability

Apart from cis-regulatory elements, non-protein coding DNA contains many repeating patterns of various classes [Trent 2012]. Insertion or removal of segments of DNA may shuffle, duplicate or insert cis-regulatory or protein coding DNA [Sundaram and Wysocka 2020],[Shendure and Akey 2015],[Chuong et al 2017].

DNA patterns that may affect mutability include:

short tandem repeats

1. increase variability by insertion/deletion errors,
2. replication slippage and slipped strand mis-pairing, and
3. increase chance of crossing over [Gemayel et al 2010], [Gymrek et al 2016] .

cross over hot spots

Meiotic crossing over with homologous chromosomes occurs predominantly at PRDM9 binding sites [Paigen and Petkov 2018]. Paralogous DNA segments may carry matching PRDM9 binding

sites, leading to unequal crossovers that may insert or remove DNA sequences. The existence of crossover hot spots in proximity to a gene therefore affects its probability of mutating.

transposable elements (T.E.s)

T.E. insertion does not occur randomly. T.E. insertion sites are not ‘typical’ DNA, and have specific characteristics [Liao et al 2000]. Both potential insertion sites associated with host genes and the site tropism of T.E.s are mutable. T.E.s are dependent on the success of the host genome, and evolve to avoid causing deleterious mutations. [Sultana et al 2017].

3D Genome

For a mutation to affect the cis-regulation or protein coding of a gene, it must occur within the topologically associated domain (TAD) to which a gene belongs. Any change that moves a segment of the genome to or from the TAD, will alter the effective mutability of he associated genes e.g binding to the lamina associated domain (LAD), or transfer to a different TAD.

Gene length

Highly conserved genes are shorter and less likely to be a site of mutation. For example ‘housekeeping’ genes believed to be responsible for essential cell functions, have shorter introns indicating selection for compactness [Eisenberg and Levanon 2003].

Karyotypic mutation

Chromosomes are defined by their telomeres and centromeres, which can be added or removed by crossing over. Karyoyptic change is very common between closely related species [Scherthan 2001], and between populations of the same species [Arslan and Zima 2014]. There are documented species with variable chromosome numbers within breeding populations, e.g. the ’common house mouse’ [Nachman and Searle 1995].

The division of the genome into chromosomes affects (i) the possible and probable changes of gene regulation and gene duplication that crossing over can cause in a species, (ii) which genes may assort independently, and (iii) whether two populations can interbreed to produce fertile offspring, or are genetically isolated.

Phenotypic effects

The distribution and effect of mutations determines the distribution of sampling of new phenotypes. Mutations, in rough order of frequency, may have the following effects on morphogenesis:

1. **Tuning regulation of existing gene networks** - may incrementally affect the position, thickness or composition of a tissue layer.
2. **Creating new links in gene networks** - by insertion of cis-regulatory elements receptive to trans-regulatory factors from different regulatory genes - may change where a tissue type is produced, or what stimuli remodelling is sensitive to.
3. **Changing the architecture of the genome** - alters the probabilities of future mutations and therefore the subspace of the genome accessible to evolution.
4. **Changing the number of repeated parts in the body** - e.g. number of ripples in a morphogenetic field.
5. **Creating new structure in the body** - a new cluster of genes providing distinct regulation of morphogenesis of tissue layers and topology.

Summary of mutation of DNA

- The genome does not mutate uniformly with respect to genes.
- DNA patterns influence where mutations occur.
- Most mutation occurs in the regulation of genes, not the protein-coding exons.
- Chromosome architecture affects the probability and possibility of crossing over and gene assortment, and therefore which subspace of the genome is accessible to evolution.
- In this way evolvability is implicitly encoded in the genome, and therefore itself accessible to evolution.

This completes the chain of problem domain, parameterisation, and sampling distribution required to define an evolutionary algorithm. In the multicellular biological version we have an additional intermediate link in the form of morphogenesis by cell behaviour. This facilitates access to the additional environmental information needed to correctly describe the co-dependencies in the phenotype. **The final encoding in the DNA provides a doubly abstracted domain specific language for the efficient expression of the required information of viable phenotypes in evolvable form.**

Expected evolutionary effects

This section discusses the theoretically expected evolutionary effects of the features highlighted in the previous sections.

Body plan

Much of the domain knowledge of how to build bodies lies in the regulatory architecture of the basic body plan. Given the body plan, the diverse adaptations of animals are produced primarily by adjusting geometric and compositional proportions. From the No Free Lunch algorithms [Wolpert 2012] these body plans can only be adapted to particular niches, about which they contain implied information. Little overlap is seen in the niches of animals of fundamentally different body plans. Due to the intractable size of the search space, it is also impossible to prove the non-existence of other undiscovered highly adaptable body plans of potential phyla.

Selection for an axis of evolvability, low mutability

Most possible (not probable) mutations of the genome that have genetic effect, produce malformation, loss of multicellular organisation, or cell death. This is because they lose necessary mutual information for the maintenance of viable anatomy, physiology, identity of a multicellular organism, or even of a living cell. This may include, mutual information between cell homeostatic processes, cell types, tissues, organs and the body as a whole. Such mutations are seen under the influence of external mutagens such as ionising radiation, but much more rarely in normal environmental conditions.

Evolution tends to minimise the likelihood of such dysfunctional mutations arising. Such mutability is a deleterious trait that is heavily selected against by differential survival of offspring over successive generations. Alleles that increase such risks are minimised in the gene pool. This particularly affects DNA encoded gene-specific mutability, such as DNA patterns.

This continuous selection for mutationally-safe genotypes restricts evolution to an evolvable subspace of the set of expressible genomes, in which only certain genes are likely to mutate.

Evolvability of the genome as a whole does not necessitate the evolvability of each gene. There are three alternate outcomes of selection on mutations that alter the evolvability of a gene:

1. Alleles that provide a high rate of safe mutation and some improvement on fitness, are selected for. Such genes must encode any required mutual information between the phenotypic traits they influence. This promotes the accumulation of such information in the genotype.

2. If the new allele of the gene has a high probability of mutation producing non-viable offspring, then the allele is likely to be eliminated from the population.

3. If the new allele has low mutability, such that further mutations leading to non-viable offspring are as rare, then if the new allele at least preserves existing fitness it may increase in frequency in the population.

Note that this process is distinct from the concept of 'purifying selection', in that it minimises mutation of critical genes so preventing the emergence of new alleles, rather than exercising selection on them. This reduction in mutational diversity closes off some potential avenues of evolution, but increases the potential rate of evolution, by concentrating mutations within a subspace where nearly all offspring have viable phenotypes.

An apparent example

An apparent example of these alternate routes of evolution is the notochord of chordates.

(a) In the urochordate sub-phylum the notochord is primarily a mechanical structure, and the body pattern is relatively simple. Within the urochordates, class thaliacea have lost their notochord [Holland 2016]. Here the low mutual information associated with the notochord allowed mutation, (1) above.

(b) In contrast in the vertebrate sub-phylum, signals from the notochord are used in many body patterning processes, critical to the fitnesss of the phenotype. The number of dependent processes mean that mutations which conserve the mutual information, necessary for viable body patterns, are a small subset of possible mutations. In vertebrates not only the phenotypic form of the notochord but also the sequence of the genes regulating it, are highly conserved, [Muller and Wagner 1991], [Maguire et al 2018]. Mutation under purifying selection would be expected to accumulate phenotypically neutral mutations. The rarity of exon shuffling in highly conserved genes indicates low mutability, rather than mutability under purifying selection, [Conant and Wagner 2005].

Here first mutual information about viable vertebrate bodies was accumulated in genes dependent on the notochord, (1) above. This lead to a high probability that mutations to the genes specifying notochord itself would be non-viable, (2) above. Therefore mutations that reduced mutability of the notochord were favoured, (3) above.

Evidence for gene specific evolution of evolvability

There is (i) an observed 100 fold variation in conservation of vertebrate genes, [Lupski 2007], [Michaelson et al 2012], (ii) the presence of molecular mechanisms and DNA patterns controlling mutability, [Shendure and Akey 2015] and (iii) reason to expect strong selective pressure.

Together these indicate an important role for gene specific genetic control of mutability in the evolution of evolvability.

Types of innovation and information

Micro-evolution

The establishment of a genome with the distribution of mutations skewed to safe variations that produce viable phenotypes allows rapid micro-evolution within established body plans. This is seen in selective breeding of domestic species, and the rapid evolution of isolated populations of wild species. This may include speciation and radiation into available niches, [de Amorim,et al 2017], [Hendry et al 2007].

While good morphogenetic parameterization can encode established information about mutual dependencies of viable phenotypes, and so facilitate micro-evolution, it cannot encode what has not yet been discovered. This fundamentally separates micro-evolution from true innovation and macro-evolution.

Macro-evolution

Fundamental innovation involves capturing information about new body plans, as opposed to adjusting the parameters of an existing model. By this proposed definition, macro-evolution would be evident in retrospect, as the acquisition of information about viable phenotypes that enables a new radiation of species. This may involve:

1. **New body morphogenetic mechanisms**, including new connections in gene regulatory networks and new body-part genetic identities,
2. **New phenotypic structures** – e.g. feathers from scales, limbs from fins.
3. **New relations of existing structures to the niche** – e.g. tetrapod fish hands for terrestrial locomotion, feathered therapod forelimbs as wings, canine teeth as tusks.

Corollary to Cuvier's objection, there needs to be selective pressure for each step on the way to discovering information about new phenotype-environment relationships. The intermediate species leading to major innovations may be highly specialized, gaining partial access to the potential benefits of the innovation. The need for changing selection pressures suggests environmental evolution of niches as an important driver of innovation.

Why morphogenetic innovation is rare

Many low probability steps are required to 'discover' a new highly evolvable body plan.
Consider the prior probabilities of the following subsets of mutations.

1. Mutationally accessible morphogenetic changes capable of expressing a particular co-dependence in morphology.
2. Changes of morphogenetic co-dependence capable of improving fitness.
3. The subset of (2) that may be useful steps towards a set of innovations sufficient to make a large group of related niches accessible.
4. The subset of (2) that reduce the likelihood of (3), i.e. dead end specialisations.

Increased fitness alone is not sufficient for a mutation to survive and increase within a gene pool.

1. If further mutations have a distribution that produces heightened mortality, then the new morphology is not evolvable,
2. If recombination of the new allele with the existing gene pool tends to produce non-viable or unfit offspring, then the new allele is deleterious, and will be selected against.

Morphogenetic location of major innovations

Innovation is most likely to occur in parts of the phenotype and the gene regulatory network of the body plan, where natural selection does not drive reduction of mutability. This does not preclude

innovation occurring in critical parts of the anatomy – e.g the emergence of the hearing apparatus of terrestrial vertebrates from the jaw mechanism of Devonian tetrapods [Clack et al 2016]. Rather the mutability and structure of the gene network [Izquierdo and Fernando 2008] controlling morphogenesis restricts the distribution of mutations to those with a low probability of producing dysfunctional phenotypes. If the niche provides a gradient of fitness with respect to the range of accessible mutations, then even critical parts of the phenotype can evolve.

Conclusions

It has not previously been appreciated how critical the particular genotype→phenotype parameterization of morphogenesis is to the evolvability of biological species and clades.

Cuvier's objection is a fundamental problem in evolution, closely related to the No Free Lunch theorems. Naive or arbitrary parameterizations are likely to have low evolvability, no better than random search, potentially much worse. Evolvability at the level of micro-evolution requires a genotype parameterization, which contains the required mutual information between the components of viable phenotypes. Such parameterizations are intrinsically domain specific.

Key components of morphogenesis which enable evolvable parameterizations of metazoan animal bodies include:

- The tree of epigenetic cell lines converging to a smaller number of tissue types, through epigenetic silencing of genes, inherited by daughter cells
- Patterning on local anatomical coordinates and relative timing, through inter cellular signalling
- Sequential patterning, growth and refinement
- Remodelling tissues on environmental information

The information about evolvable body plans is captured by the genome though natural selection on gene-specific mutability, and the structure of genetic regulatory networks. This has the effect of constraining the distribution of mutations to a viable subset of phenotypes. This constraint facilitates both rapid micro-evolution, and given the right right accessible niches, innovation leading macro-evolution.

It is anticipated that selection on gene-specific mutability and regulatory network structure, leading to evolution of evolvable genotype→phenotype parameterizations is a widespread component of biological evolution. Given that most possible parameterisations are minimally evolvable, such evolution of evolvability may be a necessary component of biological evolution.

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