The Role of Evolution in Machine Intelligence

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If the human brain were so simple that we could understand it, we would be so simple that we couldn’t.

Emerson Pugh

1 Introduction

Two categories of development influence the behavior of an intelligent being: (1) lifetime learning or *ontogenesis* and (2) evolution or *phylogenesis*. The ontogenetic development of an organism includes learning from the knowledge and experience accrued over a single lifespan. The phylogenetic development of a species includes the knowledge accrued over the course of evolution, which is passed from generation to generation through the genome.

Research in developing intelligent machines can be categorized as either ontogenetic or phylogenetic, as in table 1. The bulk of current research efforts (2021) in the development of machine intelligence belongs to the ontogenetic category. The primary phylogenetic development is implicit in the lineage of research papers and software. In these artifacts we see certain neural network architectures, optimization procedures, and regularization techniques persist and evolve over time.

Evidence supports the importance of phylogenesis in the development of machine intelligence. This evidence further suggests an underinvestment in research in digital phylogeny. In order to understand our investment options, I describe the “phylogenetic stack”. This stack begins with the near *tabula rasa* environment of emergent evolution and proceeds to more assumption-filled starting points culminating in purely ontogenetic machine learning. I assess these various starting points by their ability to yield intelligent machines. Since nature is the only system that has developed human-like intelligence, I am limited to inductions from a sample size of one. Nevertheless, I rely on natural evolution to guide in my analysis.

Ultimately, I aim to shed light on where in the phylogenetic stack to invest. Given a limited research budget, we want to know which stage would yield the largest return on investment,
Table 1: A broad categorization of current approaches to develop machine intelligence as either ontogenetic or phylogenetic.

| Ontogenetic Development | Phylogenetic Development |
|-------------------------|--------------------------|
| Deep learning           | Architecture research    |
| Supervised learning     | Evolutionary algorithms  |
| Unsupervised learning   | Evolution of evolvability|
| Reinforcement learning  | Emergent evolution       |

where the product is intelligent machines. My first-order suggestion is to diversify our research portfolio. We should invest more broadly across the phylogenetic stack. My second-order hypothesis is that meta-evolutionary algorithms (c.f. section 3.2) may yield an optimal trade-off between the many factors influencing the development of machine intelligence.

2 Investing in Phylogeny

Three motivations, not meant to be comprehensive, for increasing investment in the phylogeny of machine intelligence are:

1. The computation dedicated to natural evolution far exceeds that used in ontogenesis.
2. Automation leads to less biased and more rapid progress.
3. Intelligence is too complex to design by hand.

Computation The bulk of the computation which resulted in the intelligence of humans occurred during evolution. The ontogenesis of an individual leads to remarkable intelligence in only a few years, far surpassing the best machines in generality. However, the genome, which allows for this, is the result of nearly four billion years of evolutionary computation. Of course, the types of computation are quite different. One may argue that the learning during the lifetime of an individual is “smart” whereas the computation occurring in an evolutionary process is “dumb”, and hence the two cannot be compared. However, the difference in time scales is approximately a factor of $10^9$. Even considering the difference in efficiency between the two computational processes, phylogenesis likely merits more computational resources than are currently allocated to it.

Automation Just as deep learning eradicated the need for human-in-the-loop feature engineering, evolutionary algorithms should eradicate the need for neural network architecture engineering. Similarly, traveling further down the stack of computational models of artificial life will reduce the need for hand-engineered evolutionary algorithms. Human-in-the-loop algorithm improvement (i.e. research) can also lead to bias which can yield suboptimal results or hard to overcome local optima. Trend following biases research towards exploitation
of existing models rather than exploration of new models and algorithmic niches. To further the analogy, the implicit fitness function optimized by researchers may be littered with sub-optimal critical points making the higher peaks of intelligence difficult to reach.

Complexity We understand fairly well the low-level mechanisms which participate in intelligent behavior. For example the cell is well understood at the molecular level. We also understand the core units of the brain including neurons, their connections, and how they transmit signals at a granular level. However, we understand less about the decoding of the genome and the complex network of interacting proteins which yield the central nervous system capable of developing intelligence. We also understand little about the high-level neural mechanisms from which intelligent behavior emerges.

We may be more successful developing machine intelligence as an emergent property of a simpler-to-specify system rather than through more direct human-in-the-loop design. In modern deep learning, we have surpassed the threshold of explainable complexity. Researchers typically don’t know why one neural network architecture is more accurate than another. Furthermore, and uncontroversially, the scale and complexity of current learning algorithms will need to grow, possibly multiple orders of magnitude, before they exhibit a more general intelligence.

The categories of machine-learning algorithms are sometimes depicted as a layer cake [36]. Figure 1 is one take on this layer cake analogy but with the addition of evolution and the ontogenetic and phylogenetic stages of development demarcated. The size of each layer represents the relative amount of data or computation needed to achieve intelligent behavior. Research and resource allocations can draw inspiration from figure 1. The implication is that we are underinvested in the phylogenetic development of machine intelligence.
Figure 2: Four starting points in the phylogenetic stack are shown horizontally at the top in order of increasing assumptions required. Stacked vertically on the left are many of the core modeling components present (explicitly or implicitly) in every evolutionary process. The colored regions indicate whether the model is emergent, learnable, or fixed. The arrows indicate how a given model changes regions across the phylogenetic stack.

3 The Phylogenetic Stack

We describe four potential starting points from which to develop intelligent machines beginning near the bottom of the phylogenetic stack and culminating with purely ontogenetic development. These starting points are: 1) emergent evolution, 2) meta-evolutionary algorithms, 3) evolutionary algorithms, and 4) machine learning. For each starting point, we discuss common models of computation and some of the key assumptions required for starting at that level. While we have quantized the phylogenetic stack into four starting points, the space between these points is not empty. Other, potentially more optimal starting points may exist between them. Figure 2 shows a summary of the four starting points, and their relationships to the core modeling components explicit or implicit in any evolutionary process.

3.1 Emergent Evolution

In emergent evolution, the goal is to setup a dynamical system in which an evolutionary process emerges. In particular, the designer may not specify the rules of replication or, for example, explicitly seed the environment with self-replicating structures. Instead, the designer specifies a simpler computation model from which an evolutionary process can emerge. Following Dennett [13], we define an evolutionary process as consisting of indi-
viduals or groups of individuals which exhibit self-replication with potential mutations in a competitive environment.

Some example computation models include artificial chemistries [15] and cellular automata (CA) [47]. In both approaches a state space and a transition model must be specified. The state space includes a description of the current set of individuals as well as any additional resources. The transition model specifies the rules which govern the propagation of the state from one time to the next. These two broad components include many important, nearly axiomatic, properties of the system. For example, resource constraints are included in the state space and conservation laws may be implicitly included or explicitly specified in the transition model.

One of the challenges with large-scale assumption-free simulations is simply recognizing the emergence of interesting behavior. The existence of self-replicating individuals and other features of an evolutionary process may not be immediately apparent. In order to recognize interesting behavior in these systems one must define carefully what it means to be “interesting” and create tools capable of measuring this. For example, compression-based [74] and prediction-based metrics [6] can be used to measure the complexity of the states generated by a cellular automata. One challenge is finding measures which capture the zone between the extremes of trivial and purely random behavior, both of which are undesirable.

Emergent evolution obviates the need to specify by hand difficult-to-design processes which are likely to be critical to the development of machine intelligence. For example, the “evolution of evolvability” [11] may naturally emerge from a model which yields an evolutionary process. This improvement in the rate of evolution may be important to the emergence of intelligent behavior. Similarly, while indirect encodings can be used in traditional evolutionary algorithms [5, 60, 62], and genotype-to-phenotype mappings may even be learned [46], the space of such mappings can be explored with less bias by starting further down in the phylogenetic stack.

### 3.2 Meta-Evolutionary Algorithms

We use the term “meta-evolutionary algorithm” (MEA) to refer to an evolutionary algorithm (EA) for which the usually fixed components can themselves be evolved. Any EA must specify at least a genotype-to-phenotype mapping (or use a direct encoding), an evaluation process (typically a hand-designed fitness function), and a reproduction process (typically mutation combined with crossover). Usually these models are fixed and only the genotype is adapted. A partial MEA allows at least one of these components to evolve along with the rest of the algorithm. A complete MEA allows all of them to evolve.

The distinction between MEAs and emergent evolution (c.f. section 3.1) is that an MEA may seed the initial models. The initial population may already possess the ability to self-replicate as well as a preliminary genotype-to-phenotype function. In emergent evolution these abilities must emerge from the simulation.
A benefit of MEAs over emergent evolution is that they retain the ability to modify the key components of phylogenesis (replication, recombination, etc.) without the computational burden required for their discovery. Arguably the emergence of these components is not the critical aspect of the ability of phylogenesis to yield intelligence. Perhaps more important is simply their adaptability.

The umbrella category of MEAs encompasses concepts such as the “evolution of evolvability” (evo-evo) [11], evolutionary development (evo-devo) when applied to learning genotype-to-phenotype mappings, and other intrinsic (as opposed to extrinsic or hard-coded) processes [48, 64]. These have all been active topics in the evolutionary biology literature for decades but are not yet central to the application of EAs in developing machine intelligence.

As in emergent evolution, some degree of open-endedness may be important to allow the system to develop sufficiently interesting behavior. Similarly, measuring the complexity of the evolved organisms will likely be necessary to identify non-standard yet intelligent behavior. We elaborate on these common challenges in section 5.

### 3.3 Evolutionary Algorithms

Evolutionary algorithms (EAs) have thus far led to limited improvements in state-of-the-art machine learning. They have been used over the past several decades to tune model architecture and hyper-parameters for a given machine-learning problem [41, 43, 51, 61]. However, these results are mixed, with little adoption in practice. Manual tuning, grid search, random search, and Bayesian optimization make up the bulk of currently used methods [4]. Genetic algorithms, a subset of EAs, are widely used. They are especially useful when solving optimization problems over large discrete spaces, which are not amenable to first and higher-order gradient-based methods [44].

Three key components of an EA are 1) the genotype encoding and corresponding mapping to the phenotype (or lack thereof for direct encodings), 2) the fitness function, and 3) the reproduction process which includes crossover and mutation. Following the discussion in section 3.2, we refer to these as the meta-models of the EA.

The sub-optimality of the meta-models could account for the underutilization of EAs in machine-learning. Human-in-the-loop design usually performs better. Continuing to improve these models directly is one route to enable the development of machine intelligence with EAs. Early research in indirect genotypes for evolving modular neural networks showed promise in learning complex functions [24]. In comparison to a direct encoding, the indirect encoding solved more difficult problems much faster [25]. This and related approaches are worth revisiting at the much larger scale attainable with today’s hardware and data.

Alternatively, taking a step down the phylogenetic stack to MEAs could be more effective. Whether MEAs or human-in-the-loop design is the best path for finding more optimal genotype-to-phenotype mapping, fitness functions, and reproduction models depends on the computational burden of discovery. Hybrid approaches are also possible.
Regardless of the approach, more sophisticated meta-models will likely be critical to the phylogenesis of machine intelligence. For example, a directly encoded genotype will scale poorly to the complexity of the underlying phenotype. All organisms in nature indirectly encode their phenotype in DNA. The mapping from the genotype to the phenotype involves a sophisticated regulatory network dictating gene expression. This process plays a key role in enabling the complex phenotypes of plants and animals, let alone human intelligence.

Another possibility is that EAs are missing one or more key ingredients other than the three described above. These components might be necessary for a continual push towards ever greater complexity or open-endedness. We discuss the challenge of complexity and open-endedness, which is common to most of the phylogenetic stack, in section 5.2.

3.4 Machine Learning

The three pillars of machine learning are supervised learning, unsupervised learning, and reinforcement learning (c.f. figure 1). These three approaches are often used in conjunction with one another; representing a continuous space of techniques rather than three isolated points. For example, semi-supervised learning techniques lies on the line between fully supervised and unsupervised learning. Similarly, reinforcement learning often relies on imitation learning in which a high value action from a given state is provided by an expert [54]. This amounts to learning from labeled data, yielding a hybrid between fully supervised and reinforcement learning.

A natural question to ask is if exploring the simplex spanned by these three techniques is likely to lead to the development of human-like machine intelligence. If not, we should attempt to understand the missing ingredients.

Focusing exclusively on these three pillars of machine learning is too narrow. Machine-learning researchers study a broad array of related problems and approaches. These include many subfields such as life-long (or continual) learning, multi-task learning, active learning, few-shot learning, domain adaptation, transfer learning, and meta-learning. These subfields typically aim to enable an approach based on one of the fundamental learning pillars to generalize to more tasks (life-long or continual learning, and multi-task learning) or to more rapidly generalize to a given task (active learning and k-shot learning), perhaps by taking advantage of previous knowledge (domain adaptation, transfer learning, and meta-learning).

Improving the rate of generalization of machines to a given task and enabling generalization to more tasks are arguably the most important missing criteria for machines to exhibit human-like intelligence. However, Tesler’s theorem [67] and his corresponding dictum “intelligence is whatever machines have not done yet” (often referred to as the AI Effect [27]) hint that developing human-like machine intelligence may be more subtle.

One possibility for the missing link is enabling some degree of open-ended behavior by the machine [42]. Generative adversarial models [19] and reinforcement learning models which engage in self-play [57, 66] are a step towards open-endedness [26]. Assuming fixed data
Figure 3: On the horizontal axis is a timeline of the evolution of intelligent life in billions of years since the formation of Earth. Certain landmarks are indicated, such as the emergence of multicellularity or the Cambrian explosion. For each point on the timeline, we provide an estimate of the complexity of the most advanced organisms.

distributions and model hypothesis spaces, these models usually reach a fixed point. Drift in the complexity of the data distribution and hypothesis space may enable a larger degree of open-endedness.

4 Assessing Starting Points

Research in the phylogenetic stage of development can be thought of as moving further down the stack in the computational infrastructure giving rise to intelligence. The further down the stack we go, the fewer assumptions we need to make. This is beneficial. The more assumptions about the underlying computational model and algorithms we make, the more likely they are to be incorrect and hence limiting to the emergence of intelligence. However, the further down the stack we go, the more we rely on undirected but interesting behavior to emerge. This likely requires substantially more computation since much of the computation will be wasted on uninteresting behavior. In this case, we also require some notion of “interesting” and an ability to identify behavior as such. In a massive simulation, merely determining if an evolutionary process has emerged can be difficult. Furthermore, identifying the intelligent behavior itself can also be problematic. In an undirected assumption-free simulation, emergent intelligence may be incomparable to that which we are used to observing in animals and humans. I describe in more detail the challenges and paths forward for identifying and measuring intelligence and the more nebulous “complexity” in section 5.3.

Deciding where in the phylogenetic stack to invest in research requires navigating complex trade-offs. I explore these trade-offs from a few angles.
4.1 Evolutionary Time and Complexity

The complexity of the organisms present at a given stage of evolution can help determine where to start in a digital simulation. As the complexity of the organism grows, determining which properties are important to encode in silico and how to encode them becomes more challenging. This suggests starting with as simple a system as possible. However, the simpler the starting point, the greater the computational time required to yield human-like intelligence.

We observe the relationship between complexity of various organisms and the time required to evolve human intelligence from the first appearance of that organism. This can guide our choice of where to start in the phylogenetic stack. Assume the quality of a starting point $S$ is proportional to the sum of the complexity of the most advanced organism at that point $C(S)$ and the time-to-intelligence $T(S)$ (where both $C(S)$ and $T(S)$ are appropriately scaled). We look for the starting point by finding the minimizer:

$$S^* = \arg \min_S C(S) + T(S). \quad (1)$$

Upon finding $S^*$, we can evaluate the evolutionary models present at that point. This evaluation can inspire where in the digital phylogenetic stack (c.f. figure 3) to begin based on which models are emergent, learned, or fixed.

Figure 3 shows a timeline of the evolution of intelligence since the formation of Earth. At each point we estimate the complexity of the most advanced organism present at that time. The complexity in figure 3 is based on the judgement of the author and is not intended to be definitive. A more quantitative approach could use for example the size of the genome. However, this suffers from the well-known C-value paradox [68]. Another approach could be to estimate the information carrying capacity in bits of the central nervous system of the most advanced organism. Sagan [52, p. 26] gives an example of both approaches, yielding curves with a similar shape as that of figure 3.

Interestingly, figure 3 has a knee shape with a bend roughly around 3.5 billion years at the development of macroscopic multicellular organisms. The development of macroscopic multicellular organisms was soon followed by the Cambrian explosion and the genus Homo. However, while unicellular organisms developed soon after the cooling of the Earth, multicellular organisms are believed to have taken much longer. This point in evolutionary history may be difficult to discover by a more assumption-free evolutionary process. On the other hand, we understand a large portion of the processes which govern simple multicellular organisms. They are considerably less complex than the many larger organisms that evolved during and after the Cambrian explosion. Because of this, simulation of an evolutionary

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1 A similar problem arises, aptly dubbed the G-value paradox, when using the number of genes instead of the C-value (mass of DNA) [28].

2 This is an estimate for the emergence of macroscopic multicellular organisms, however; evidence exists that smaller and simpler multicellular organisms emerged for the first time more than 2 billion years ago [29].
process starting at a digital analog of multicellularity may yield an optimal trade-off in the amount of direct design required and computation needed to observe emergent intelligence.

The next step is to determine the digital analog of evolution at the time of the initial macroscopic multicellular organisms. When multicellular organisms emerged, nature was already equipped with several key components of an evolutionary process. The environment itself consisted of finite resources engendering competition and natural selection under complex fitness landscapes. Also present was a large diversity of self-replicating organisms such as the eubacteria, archaea, and both of the unicellular eukaryotes (protozoans) and multicellular eukaryotes (metazoans). All of these organisms had (and have) a common method to store information (DNA), and a related genotype-to-phenotype decoder (RNA, ribosomes, proteins, etc.). Mutation and recombination existed at the very least via random errors produced during DNA cloning and through exchanging DNA in plasmids. However, many of these core components continued to develop including crossover and sexual reproduction, more sophisticated machinery for decoding genes, and more complex fitness landscapes due in part to feedback from the growth of biotic life in the environment.

Overall, these observations point to a meta-evolutionary algorithm as a good starting point. An MEA can yield an optimal trade-off between wasted computation spent on the emergence of evolutionary behavior and artificial barriers to machine intelligence from poorly specified models.

### 4.2 Computation and Assumptions

The number of assumptions required at each starting point can serve to guide the decision of where to begin the development of a computational model leading to intelligence. Fewer assumptions imply a larger state space of results achievable by the simulation. This decreases the chance that the designer inadvertently removes areas in the state space where intelligent behavior is likely to develop. The trade-off is that exploring the larger space requires more computation.

We define an assumption as any modeling choice which narrows the state space that the simulation would have had access to without the assumption. From this definition we can also assign a magnitude to each assumption based on the amount that it shrinks the search space of the simulation compared to that of the assumption-free version. Let $A(S)$ be the cumulative magnitude of the assumptions for a given starting point, $S$, and $T(S)$ be the computation time required to develop machine intelligence. A good starting point is one which minimizes the sum of the properly scaled assumptions and computation time:

$$S^* = \arg \min_S A(S) + T(S). \quad (2)$$

Figure 4 depicts four of the possible starting points in the phylogenetic stack ordered by increasing magnitude of assumptions required. The bottom arrow indicates that the computation time, $T(S)$, increases in the opposite direction.
Emergent evolution requires the fewest assumptions. Possibly any model computationally equivalent to a universal Turing machine is sufficient for intelligent behavior to eventually emerge. Wolfram’s “Principle of Computational Equivalence” \cite{73} suggests that such Turing complete models are abundant in nature. Even the simplest digital systems such as elementary cellular automata can be computationally universal \cite{9}. While these universal systems are all equivalent in what they can simulate, they may not be equal in the likelihood and amount of computation required to evolve intelligent behavior. Hence, the assumption of which class of models to use and selection of the specific model within that class may be critical.

Meta-evolutionary algorithms and evolutionary algorithms require strictly more assumptions than a model of emergent evolution. In MEAs, the self-replicating individuals and a core set of meta-models (a genotype-to-phenotype map, a reproductive model, and a fitness landscape) are pre-specified but adaptable. The assumptions implicit in EAs are greater in magnitude than MEAs as the meta-models themselves do not adapt – only the genotype is evolved.

Machine learning requires a greater cumulative magnitude of assumptions than an evolutionary algorithm. As an example, in a typical use of deep neural networks, the designer specifies the model architecture, learning criterion, optimization algorithm, and regularization. An EA operates on a family of model architectures, whereas a machine-learning algorithm operates on a single, typically hand-designed architecture. If the EA uses an expressive indirect encoding of the phenotype (architecture) then the relative magnitude in assuming a single architecture is even greater.

Identifying interesting behavior becomes more difficult with fewer assumptions. In a simulation of artificial life the goal may be to observe emergent evolution and intelligent behavior. Identifying self-replicating individuals undergoing mutation and selection may be difficult in a massive simulation. Intelligent behavior may take an unfamiliar form and can be even more difficult to identify. This requires care in specifying and measuring intelligence and any other types of complex behaviors we intend to observe.
4.3 Contingency and Convergence

The prior sections assess starting points based on the initial complexity and magnitude of the assumptions required. Optimal starting points are those which minimize the trade-off between these and the computation time required to evolve intelligence. We used natural evolution as a guide for the computation time in section 4.1 and left computation time mostly unspecified in section 4.2. This estimate of computation time does not address the potential contingency of human-like intelligence in natural evolution. Perhaps nature was simply lucky and evolved intelligence much more quickly than expected. Or perhaps nature was unlucky and intelligence could have evolved much more quickly. We attempt to understand on average how much time would be required to evolve human-like intelligence. This can then guide where in the phylogenetic stack to initiate a digital evolutionary system.

Throughout this section we rely on nature to support our arguments. An important consideration is which of the processes found in nature are necessary to translate into a digital simulation and which parts are artefacts of the natural world and irrelevant to the digital analog. We discuss this consideration in more detail in section 5.1.

A contingent phenotype (or species, phylum, etc.) in evolution is one which, while possibly predictable or explainable in hindsight, is not probable. The contingent phenotype is one of many likely alternatives that could have occurred subject to very slight deviations in initial conditions or external influences. Gould [20] suggests that contingency plays a large role in evolution, citing as evidence the Cambrian radiation of diverse phyla followed by a seemingly arbitrary culling. By this logic the development of humans may be highly unlikely to occur again if we were to replay the course of evolution. However, this does not imply that intelligence itself is unlikely.

An evolutionary niche dictates the likelihood of a phenotype emerging based on two factors: 1) the strength of selection for the given phenotype in the niche and 2) the capacity of the niche. The strength of selection for a phenotype is dictated by how much it benefits an organism’s ability to reproduce. A higher strength of selection within a niche leads to convergent evolution. The evolution of a highly convergent phenotype in a given niche will be robust to initial conditions and external perturbations. The capacity of the niche dictates the degree of parallel evolution. The same phenotype can evolve in different organisms if the niche has a high capacity for it. Together these characteristics of an evolutionary niche dictate the level of contingency or likelihood of observing a given phenotype.

We observe with some confidence that nature does not have a high capacity for human-like intelligence. It has evolved only once in history and does not appear to be evolving in parallel in any contemporary species. Estimating the degree of convergence of intelligence is more difficult. Conway Morris [8] argues that evolution is highly convergent and human-like intelligence is not only predictable but probable.3

3Somewhat ironically, Conway Morris is one of the three primary re-discoverers of the Burgess shale which is the pillar that Gould [20] builds his case of contingency around.
As examples, we consider the contingency of two possible “major transitions” in natural evolution [58]. First consider the hypothesized endosymbiotic merger of the archaea and eubacteria which resulted in the modern eukaryote with its energy generating mitochondria [39]. Lane [35] argues that this merger is extremely contingent and unlikely to be a convergent result in evolution (and therefore also unlikely to evolve in parallel). Lane [35] also argues that the merger of the two prokaryotes was a necessary condition for the growth of the genome\(^4\) and hence the development of more complex multicellular organisms and ultimately human-like intelligence.

Another major transition is the evolution of multicellular organisms from unicellular organisms. Multicellularity has evolved independently at least 25 times [23]. The spontaneous self-organization of cells into larger groups appears to be highly convergent in natural evolution. This suggests that multicellularity has a strong reproductive benefit and that discovering it in an evolutionary process is not so difficult. As far as digital evolutionary systems go, encoding modularity as an analog to multicellular organisms may benefit evolvability. However, even if one does not directly encode such a phenotype, the convergence in natural evolution suggests that this may also emerge naturally in a sophisticated simulation.

\section{Challenges in Evolving Intelligence}

\subsection{Biological Relevance}

Thus far we have somewhat egregiously conflated natural evolution with digital evolution. Nature has certainly inspired the design of digital algorithms, a few of which include genetic algorithms, neural networks, and swarm intelligence [17]. However, carelessly following nature’s path may be suboptimal or even misleading.

Consider flight which has evolved independently four times across four major animal classes.\(^5\) Flying in nature is thus relatively convergent. Despite the propensity for evolution to discover flight, directly designing airplanes using the principles of aeronautics is a better approach. Alternatively, consider the wheel. The wheel is simple to design but is thought to have evolved in nature only once, namely in the flagellum used for forward locomotion by prokaryotes [34].

Human-like intelligence falls in a different regime than either of the above examples. It is neither simple to design directly nor is it highly convergent in evolution. Which route is

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\(^4\)The argument goes roughly as follows. In order to grow beyond a certain limit, cellular energy production must scale linearly with cell volume. Bacterial energy production uses the cell membrane to create the proton gradient required for respiration. This scales with surface area and not volume, and hence puts a limit on cell size. Local organelles which produce energy throughout the volume of the cell enable linear scaling of energy production with the volume of the cell. However, in order to regulate energy production at a granular level, the mitochondria need local genetic information (the co-location for redox regulation hypothesis [1]). The simplest (and perhaps only plausible) way for this to evolve is if one cell engulfs another.

\(^5\)Flight evolved independently in mammals (bats), birds, insects and reptiles (pterosaurs).
easier, or even feasible, is yet to be determined. Even if human-like intelligence is easier to discover with evolution, a direct approach may yield a more efficient and usable design.

Many processes or phenotypes in natural evolution may be important to drive the complexity and diversity needed to ultimately yield intelligent behavior. Consider a few examples:

- Non-coding DNA may serve as a substrate for mutation which is more likely to yield non-deleterious mutations. We may need analogous scratch space in the digital genotype.

- Multicellularity and other kinds of modularity could be important for the “evolution of evolvability” [11]. Incorporating this in any direct encoding of an evolutionary algorithm may yield more rapid and responsive evolution.

- Genetic crossover and sexual reproduction may be essential to enable exploration in evolution while avoiding error thresholds [3]. Similarly, in emergent evolution we may need to enable approaches which can avoid cascading errors and overcome Eigen’s paradox\(^6\) while maintaining a healthy mutation rate [16].

The features of natural evolution that can improve digital evolution must ultimately be determined empirically. However, qualitatively assessing the important features of natural evolution and their ability to translate to useful digital analogs can help to prioritize research in digital evolution. After all, nature is the only system we know of that has created human-like intelligence.

### 5.2 Complexity and Open-endedness

A drive towards ever greater complexity is arguably one of the key missing criteria from digital evolutionary and learning systems. In natural evolution, the increase in peak complexity is hard to refute despite the term being poorly defined and difficult to measure. A key challenge is understanding what drives evolution’s “arrow of complexity” and how to achieve a similar effect in artificial systems [2].

A related notion is that of open-endedness, of which unbounded complexity growth is a defining characteristic. Recently, open-endedness in artificial systems has become a research goal in and of itself [63]. This has not been without controversy, as coming up with definitions of open-endedness which do not admit trivial solutions has been a challenge [31, 65].

Both open-endedness and complexity are not well-defined terms with disagreement as to their importance and how to measure them. Regardless, some degree of an open-ended drive toward complexity is likely to be important to the emergence of machine intelligence from any of the starting points discussed in section 4. We discuss some possible enablers and drivers of complexity and open-endedness in the context of these starting points.

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\(^6\)Eigen’s paradox argues that given the mutation rates found in nature, without error correction during DNA self-replication the largest possible genome sizes are quite limited. This size limitation is much smaller than the size of a genome which can encode an error correction mechanism.
**Emergent evolution**  One driver of complexity in emergent evolution is the hierarchical construction of higher-level components from lower-level building blocks. For example, in computational chemistries, monomers are constructed from atoms, polymers from monomers, and more complex and even self-replicating molecules from groups of polymers. Rasmussen et al. [50] propose that increasing the complexity of the primitives of such a system is a necessary and sufficient condition for the emergence of higher-order structure. This is related to the generation of open-ended evolution through “cardinality leaps” [53]. A cardinality leap can be achieved through hierarchical construction. For example, a finite set of primitive building blocks can be used to construct a countably infinite number of higher-level structures.

The emergence of higher-level structure from lower-level primitives seems likely to be a key driver of complexity growth in a simulation of emergent evolution. However, complexity on its own is not a sufficient condition for the emergence of self-reproducing organisms. Other properties are likely to be important, including a tendency towards entropy, resource constraints, and possibly other conservation laws.

**EAs and MEAs**  Many theories have been proposed to explain the natural tendency of evolution to grow the complexity of organisms. Some of these include:

- The theory of “passive diffusion” posits that organisms in evolutionary systems grow in complexity purely due to randomness. In a random walk, the probability of arriving at a larger distance from the origin increases with the number of steps. In same way, the probability of developing more complex organisms increases over time [40, 21].

- Red queen effects [69] due to predator-prey arms races and other inter-species coevolutionary dynamics are hypothesized to be drivers of complexity [12].

- Korb and Dorin [33] state that complexity of an evolutionary system (as opposed to organisms) can grow through niche construction. They argue that a given niche creates multiple byproducts which in turn support the development of more than one new niches resulting in exponential growth. We hypothesize in turn that an increase in evolutionary niches can yield more complex coevolutionary dynamics which could in turn yield a growth in organism complexity.

These are but a few plausible explanations for complexity growth in evolutionary systems. Furthermore, these explanations do not preclude one another. Incorporating one or more of these drivers of complexity growth in an EA or MEA will likely aid in the emergence of intelligence.

Evolutionary systems also have features which suppress complexity. Thus avoiding complexity suppressors in a system is also important. For example, natural selection requires mutation, but if the rate of mutation is too high it may induce an error threshold on the length of the genome [3]. Diversity while avoiding error thresholds can be achieved through other mechanisms such as crossover or gene duplication. However, point-wise mutations may
be important to explore the evolutionary landscape at a finer grain.

**Machine learning** The complexity of a machine-learning model is dictated by the hypothesis space and the objective function. Following Occam’s razor, most learning algorithms prefer simpler over more complex models. Regularization allows practitioners to trade-off fitness to the learning objective for simplicity with the intention that this yields models which generalize better to the true data distribution. The reasonable desire to have models which generalize acts a suppressor of complexity.

Growing complexity in machine learning simply for sake of complexity does not make sense. The driver of complexity must come from more diverse, difficult to achieve, and possibly open-ended learning objectives.

Recently a trend has emerged in machine learning research to construct benchmarks with multiple tasks [71]. Models have been developed which perform well on these benchmarks with minimal task-specific training [14]. This includes models which are able to perform tasks across differing modalities, such as vision and text [38]. As the size, number, difficulty, and diversity of the tasks in these benchmarks grow, so too will the required complexity of a model which can generalize across the full suite.

While encouraging complexity, the trend towards multi-task generalization does not require open-ended learning. As mentioned in section 3.4, open-ended machine learning systems may be important to developing more human-like intelligence [42]. Steps towards achieving this type of open-ended behavior include for example generative adversarial models and self-play in reinforcement learning [26].

### 5.3 Identifying Intelligence

The further down the phylogenetic stack we begin an evolutionary simulation the fewer assumptions we need. These assumptions will have a tendency to lead to more familiar types of intelligent behavior. Conversely, fewer assumptions will make identifying emergent intelligence (or the emergent ability to rapidly evolve intelligence) difficult.

Assuming a close correspondence of intelligence and complexity, one way to identify a system capable of emergent intelligence is to measure complexity. Researchers have attempted to qualitatively assess the features of systems which exhibit complexity [72] However, as simulations grow in size and number, qualitative examination is not scalable.

An alternative approach is to use a single quantitative measure of complexity, of which many have been proposed [37, 45]. Figure 5 demonstrates the typical challenge of measuring complexity. In figure 5a, we see that the most complex systems lie between order and disorder. Common measures of information content such as Shannon entropy [56] or algorithmic information content (AIC; also known as Kolmogorov complexity) [32, 59] grow monotonically with the disorder of the system (fig. 5b).
Several complexity measures have been proposed which in theory peak in the zone of complexity between order and disorder. These include measures such as effective complexity [18], minimum message length [70], statistical complexity [10] and the closely related effective measure complexity [22]. One problem with these measures is that they are not easy to compute. They typically require computing the AIC or the entropy (or related information-theoretic measures) over a large state space. Also, they often require assumptions on the part of the modeler, which degrades their objectivity. Few, if any, practical examples exist which use these measures to compute the complexity of a dynamical system.

Statistical complexity is perhaps the most objective as it does not require any data-specific assumptions to put in practice. Shalizi et al. [55] used statistical complexity to separate circular cellular automata exhibiting sophisticated structure from those which are more ordered and more disordered.

Alternatively, compression-based or prediction-based heuristics can be used to measure complexity [6, 74]. These heuristics were able to correctly order by complexity Wolfram’s four classes of elementary cellular automata [73].

Completely reducing the identification of intelligent behavior or even complexity to a single measure is impractical. Other tools to assist in the scalable identification of these sorts of behaviors will be useful. These include producing summary visualizations [7], and filtering large state spaces for interesting structures [30].

6 A Redistribution

I began by making the case that researchers should investigate more resources in the phylogeny of machine intelligence. Human-like intelligence is hard to design. Automating the process through phylogenesis may be both faster and more objective. Observing nature, I noted that the bulk of the computation which went into producing humans is found in phy-
logenesis over ontogenesis. While the type of computation may differ in value-per-operation, the orders of magnitude more invested in phylogenesis is suggestive.

To investigate more resources in phylogenesis, we must first consider the options. These make up the phylogenetic stack (which is really a spectrum) beginning with emergent evolution and culminating with machine learning.

I assessed each possible starting point from several perspectives. These included the trade-offs between complexity and computation, the trade-offs of assumptions and computation, and the likelihood of intelligent behavior emerging from a given starting point. Throughout, I used nature as a crutch in my analysis. This may be a major flaw, but is unavoidable if we care to make any inductions versus purely deductive speculation. After all, nature is the only system that we know of which has evolved human-like intelligence.

Given the above analysis, determining a starting point in the phylogenetic stack for evolving intelligence in silico remains non-trivial. However, we need not determine precisely where to start since we need not limit ourselves to a single choice. Rather, a more interesting question is how to distribute the resources for research across the phylogenetic stack. My primary conclusion is that we should devote more resources to earlier in the stack.

Within phylogenesis, meta-evolutionary algorithms are well supported as a starting point. They do not suffer the limitations of EAs which have been observed in practice. They also retain many of the benefits of purely emergent evolution while avoiding many of the contingencies. Regardless, by studying simulations of evolution, we will undoubtedly learn more about how to develop machine intelligence – and maybe even a clue or two about the nature of ourselves.

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