Open-Ended Dynamics of Prediction Games

Dissertation Proposal
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Background

A core research concern of the artificial life community is the study of *open-ended evolutionary systems*, which can be broadly defined as evolving systems that never settle into a single stable equilibrium state. The Earth's biosphere provides the most obvious example of an open-ended system, as new and ever more complex forms of life have evolved over time. However, the emergence of new species through *coevolution* provides a challenge for traditional evolutionary models such as the *replicator equation* which requires the set of species and interactions to be fixed and prestated. Rather than model open-ended systems as, for example, a set of diffential equations, the recommended approach is to present "general evolution" as an algorithmic update equation; rather than integrating this equation, we must let it evolve and study the *statistics* of its output (see Chapter 5 in (Thurner et al., 2018)). Open areas of research in the field include the establishment of metrics such as *activity* and *complexity* for quantifying open-ended behavior, the identification of systems believed capable of open-ended growth, and methods for visualizing and interpreting evolutionary dynamics given often massive amounts of data produced in novel contexts (Packard et al., 2019; Stepney, 2021; Dolson et al., 2020).

Pioneering work in the field of open-ended evolution includes the identification of punctuated equilibria within a variation of the iterated prisoner's dilemma in Lindgren and Nordahl (1994), the self-replicating machine code of Tierra and Avida (Ray, 1992; Ofria and Wilke, 2004) and the evolutionary activity statistics of Channon (2001). While more recent work such as the Chromaria environment has produced systems that exhibit features of open-endedness by certain metrics (Adams et al., 2017; Soros and Stanley, 2014), an unambiguously open-ended system has yet to be developed and is considered to be one of the "grand challenges" of artificial life. The dynamics of these systems in general are agreed to be poorly understood, but novel analytical frameworks such as the *Measurements of Open-Ended Dynamics in Evolutionary Systems* (MODES) Toolbox have been proposed to in an effort to better characterize them (Dolson et al., 2019).

The DEMO Lab of Jordan Pollack has produced much work in the related area of *coevolutionary algorithms* (CEAs). CEAs have found practical use on a number of difficult problems, such as the sorting networks of Hillis (1990)

and the game playing strategies of Rosin and Belew (1995). It has been argued in Arulkumaran et al. (2019) that the success of some deep reinforcement learning systems such as AlphaStar can be partly attributed to the use of competitive coevolutionary principles. However, experimental work by the DEMO Lab showed that coevolutionary systems are prone to unique pathologies that may stall adaptive progress in certain domains (Watson and Pollack, 2001). Theoretical work by the lab led to the development of algorithms specifically to address these pathologies (Noble and Watson, 2001; De Jong and Pollack, 2004; De Jong, 2004).

More recently, the lab has begun to explore the potential of coevolutionary dynamics to create systems capable of open-ended complexity growth (Harrington and Pollack, 2019; Moran and Pollack, 2019). This work was cited by Ken Stanley, a leader in the artificial life community, as of special interest in a survey paper of the field (Stanley, 2019). Work by this author (Willkens and Pollack, 2022) proved that previous hypotheses regarding conditions necessary for open-ended growth in these systems, such as the presence of both cooperative and competitive interactions, in fact do not hold in the general case. Moreover, certain systems were found to be sensitive to the selection method employed, with more sophisticated coevolutionary algorithms producing dramatically greater rates of complexity growth. It is difficult to picture the behavior of these systems from static images and plots alone, and so interested readers are encouraged to view the presentation slides for the 2022 ALIFE conference which include a number of dynamic neural network visualizations.

Work accepted for publication in the 2023 Conference on Artificial Life, "MODES Analysis of Prediction Games," showed that the complexity growth observed in the original work by Moran and Pollack (2019) cannot be interpreted on face value, and that it may possible for nonadaptive yet highly complex strutures to emerge through coevolutionary processes. My work has shown that intuitions often fail us when it comes to understanding the dynamics of these systems and reveals the need for a new set of analytical perspectives when approaching them.

Chapter 1: Introduction

The introduction will outline the general aims of the dissertation, summarize the prior literature on the subject, and provide an overview of the necessary terminology.

The intent of this work is to pave the way for the understanding and creation of truly open-ended systems through a careful statistical analysis of a set of novel yet simple systems known to exhibit forms of open-ended genotypic complexity growth. We identify these systems as *coevolutionary prediction games*. They are some of the simplest systems known to produce such behavior and are therefore ideal for simulation and analysis. The goal is to better describe the dynamics of these systems and identify general principles that may apply to more complex applications such as generative modeling and multi-agent reinforcement learning

problems, as well as features of the natural world.

The substantive contributions of this work include the following:

1. The first analytical treatment of prediction games considered as a general class of coevolutionary systems, employing the MODES Toolbox as the primary framework;

2. The introduction of two new prediction game domains, the *Continuous Prediction Game* and the *Harmonic Prediction Game*

3. The introduction of a new artificial organism model based on the *Genetic Program Parse Tree* (GP-Tree) of Koza (1992).

4. The introduction of a novel visulization and analytical technique, *Qualitative Dynamical Evolutionary Stable State Analysis* (Q-DESSA)

In our experiments, we study the coevolutionary dynamics of populations of *artificial organisms* within *coevolutionary ecosystems*. Organism genotypes are represented as *heterogenous graphs* corresponding to phenotypes that take the form of *abstract machines*. A coevolutionary system comprises populations of organisms and interactions that take place between them within a given *interactive domain*. These interactions often have either a "cooperative" or "competitive" nature, in which two organisms will have aligned or opposing interests, respectively.

Each interaction, which is performed in pairwise fashion between all members of two interacting populations, yields some measure of *fitness* to each individual involved. Using the results of these interactions, a *coevolutionary algorithm* produces members of the next generation. A *selection function* chooses which members have the greatest likelihood to reproduce. For each class of artificial organisms, we define a set of *mutation operators* to be stochastically applied to each parent to produce a child with a modified genotype; in all our experiments reproduction is performed asexually.

We provide here a summary of the artificial organisms under consideration in this dissertation:

1. The *Deterministic Finite State Machine* (DFSM) introduced in Moran and Pollack (2019)

2. The *GNARL Recurrent Neural Network* with operators defined in Willkens and Pollack (2022)

3. The *Genetic Program Parse Tree* (GP-Tree) based on the Artificial Ant of Koza (1992) with modifications novel to this dissertation

We consider four interactive domains:

1. The *Linguistic Prediction Game* (LPG) introduced in Moran and Pollack (2019)

2. The *Collision Game* introduced in Willkens and Pollack (2022)

3. The *Continuous Prediction Game* novel to this dissertation

4. The *Harmonic Prediction Game* also novel to this dissertation

We consider two selection functions:

1. *Fitness Proportionate Selection* (FPS) where the probability of selection is proportional to the fitness of the organism

2. *Discovery of Search Objectives* (DISCO), a new selection function based on work by the DEMO Lab specifically to address coevolutionary pathologies (Liskowski and Krawiec, 2016)

We employ two analytical paradigms:

1. The *Measurements of Open-Ended Dynamics in Evolutionary Systems* (MODES) Toobox introduced by Dolson et al. (2019)

2. The *Q-DESSA* framework novel to this dissertation

CoEvo

It is necessary to perform these experiments under the same conditions and with the same analytical framework. For this purpose, the CoEvo framework has developed. Comprising over 8,000 lines of Julia code, the framework is designed to be modular and extensible and is equipped with an extensive test suite. Genotypes are stored on disk in stable JLD2 dataformat along with random seeds and other metadata. It is possible to "revive" organisms at any point in the evolutionary timeline to evaluate their complexity, study their interactions, and continue their evolutionary progress in a reproducible way.

The framework will be the first of its kind to provide a unified interface for high-performance simulation and analysis of arbitrary coevolutionary systems. A link to the repository can be found at here; it is currently being refactored and prepared for public release.

Open Science

The disseration shall be undertaken in the spirit of open science movement (Vicente-Saez and Martinez-Fuentes, 2018). All code and data will be made public to members of the scientific community as it is produced. Progress will be performed in the open-notebook style, with regular status reports accessible via the Internet.

Chapter 2: Analytical Methods and Complexity Growth

Chapter 2 shall outline the statistical methods and analytical approaches to be applied to the experimental results.

The MODES Toolbox

The *MODES Toolbox* is a set of metrics and analytical techniques introduced in Dolson et al. (2019) to better understand the open-ended potential of evolutionary systems in terms of change, novelty, complexity, and ecology. The toolbox is shown to produce results supporting current intuitions and understanding of systems such as rugged NK landscapes and the Avida digital evolution platform (Lenski et al., 2003; Kauffman and Levin, 1987).

Before applying the metrics to data resulting from an evolutionary system, it is beneficial to first screen out deleterious and neutral genotypes so that the focus is placed on truly adaptive mutations. The primary tool for this is the *persistence filter*, which has its roots in *coalescence theory*, an area of theoretical population genetics (Fu and Li, 1999). This is done by identifying the *persistent lineages* according to a sliding window of length t generations. Coalescence theory predicts that in the absence of selective pressure, a single individual is expected to become the sole common ancestor of the entire population in a median time of $2N$ generations, where N is the population size; this value typically becomes much smaller when selective pressure is present. At each generation $A-t$, each reproductive individual passes on to its offspring a unique identifier, which is passed on their offspring in turn if they are able to reproduce. This continues for t generations until A is reached, whereupon the identifiers are collected from members of the current population such that the persistent individuals from generation $A-t$ can be retrospectively identified.
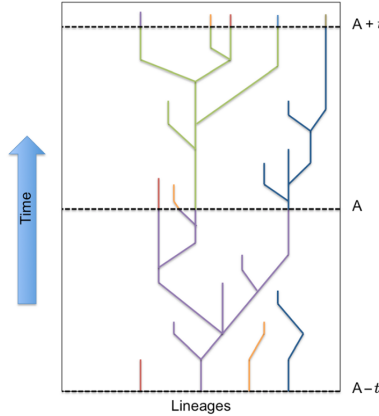

Figure 1: Illustration of persistence filtering taken from Dolson et al. (2019). At timepoint A, the purple lineage has proven to be persistent and therefore the original component from $A-t$ will be considered meaningful. Similarly, the green and blue lineages persist to timepoint $A+t$, and so the original green and blue components will be considered meaningful as they existed at timepoint A.

This step alone dramatically reduce the volume of data for processing, at

least by a factor of N, but there is more that can be done. It is recommended to identify the *informative sites* of these persistent genotypes to prune noncoding genetic material. A simple means of doing so is the *knockout* technique: For each site in the genotype, remove that site and observe the fitness effect for that individual in its original environment. If the fitness either remains the same or increases, this is evidence that the site is nonadaptive or not meaningful and can therefore be pruned. There are downsides to this approach as it fails to capture interactions between sites. This work will explore the possible use of alternative heuristics; preliminary experiments using an incremental fitness-preserving pruning method using information relating to the age of the genes have been promising.

Once the persistent individuals and meaningful genotypic sites have been identified, the core MODES metrics can be applied at each generation interval A given a window size of t:

1. **Change**: A count of the number of unique persistent genotypes at generation A that are different than those at generation $A - t$;

2. **Novelty**: A count of the number of persistent genotypes in generation A that have not been seen at all in the intervals preceding it;

3. **Complexity**: The greatest count of informative sites among all persistent genotypes at generation A;

4. **Ecology**: The Shannon entropy obtained from measuring the proportion of the persistent population occupied by each unique genotype at generation A. This metric provides an intuitive notion of diversity or evenness, as its value grows higher as a greater number of unique genotypes occupy more equal proportions of the population.

Q-DESSA

The MODES toolbox provides an excellent set of analytical tools for explicating core dynamics of evolutionary systems. However, while we get an overall sense of the growth and behavior of the system, we do not gain a sense of how two systems that exhibit similar MODES dynamics might differ. For example, two systems might both exhibit cycling behavior, evidenced by a negative slope of the novelty metric. But we do not get a sense of the frequency of the cycles, the geometry of the genotype space, or the regions in which those cycles occur.

The visualization framework presented in Dolson et al. (2020), in particular the *lineage trajectories* drawn over a fitness landscape, provides inspiration for how to approach this problem. The problem is that in our coevolutionary setting, the fitness function is not fixed and we have multiple populations of interacting individuals.

Q-DESSA (Qualitative Dynamical Evolutionary Stable State Analysis) is a proposed method for analyzing these aspects of potentially open-ended systems. The method employs a graph neural network component trained in an unsupervised fashion over the dataset of persistent organisms filtered using MODES. An

advantage of all the models considered in our prediction game is that they have a natural graph representation, and so this method can be applied in similar fashion to each. We collect together the set of all persistent individuals across all trials of all ecosystems for a given artifical organism type. An approach such as the *UGraphEmb framework* (Ding et al., 2019) may be employed to obtain graph-level embeddings that reflect the *graph edit distance* between the genotypes of the organisms. In such a fashion we can derive a vector space in which the embeddings of the two graphs preserve their graph-graph proximity.

In Ding et al. (2019), the resulting embeddings are reduced in dimensionality using *t-distributed Stochastic Neighbor Embedding* (t-SNE) and visualized in a 2D space (Van der Maaten and Hinton, 2008). However, it is known that t-SNE may prioritize local structure at the expense of global structure, which can introduce significant distortion resulting in misleading interpretations; to mitigate this, we plan to experiment with the recent PaCMAP dimensionality reduction method which is believed to produce a better tradeoff between local and global structure (Wang et al., 2021). The UGraphEmb framework uses the *graph edit distance* as a measure of similarity between graphs, which we plan to implement using the GEDLIB C++ framework (Blumenthal et al., 2019). Experiments are currently being performed using the difference between the Laplacian spectra of the graphs as a measure of similarity as in de Lange et al. (2014), which is fast to compute but provides less precision as edge and node label information is lost.
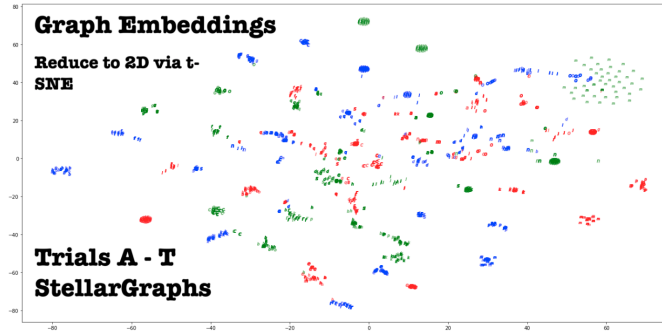

Figure 2: This figure from preliminary experiments represents the reduced embeddings of GNARL neural networks, where the colors denote the species of each organism and the letters A-T represent the trial number 1-20. This was produced using the StellarGraph Python library from experimental data taken from the final generation. Despite some distortion and error, the resulting embeddings capture the intuitive notion that members of one population tend to be clustered together in the embedding space. The full Q-DESSA approach would produce lineage trajectories for organisms that pass the MODES filter.

As an analogy, we may borrow concepts from the dynamical systems theory

of Strogatz (2000), considering each 2D reduced embedding as a *phase point* in a dynamical system. In this sense, each point taken from a lineage at generation A, $A + t \dots$ forms a *trajectory* in the phase space. The path the trajectory takes reflects the evolutionary dynamics of the system, and by considering the trajectories taken by different species within each ecosystem, we can better understand the evolutionary relationship between each population. It may be possible then to qualitatively identify the presence of evolutionary stable states as well as to classify them according to the terminology of Watson and Pollack (2001):

1. *Disengagement*: When the trajectories of two or more population do not leave some *fixed-point region* of the space. As these systems are out of equilibrium, and there always exists the mutational possibility of components being added or removed from the genome and we do not expect a true fixed point to emerge. But orbits constrained within a region reflect that the populations have disengaged evolutionarily and that no more complex adaptations are expected to occur.

2. *Convention chasing*: When the trajectories of two or more populations orbit between two or more *semi-stable regions*. This is a situation where populations cycle through a limited number of adaptive solutions and better solutions either do not exist or are not reachable through mutation.

3. *Open-ended behavior*: When the transient phase of the trajectory continues indefinitely, and there are no fixed points or semi-stable regions. Open-ended growth necessarily implies open-ended behavior, as a lineage with genotypes that tend to grow over time without bound will not remain within any region.

Fig. 1: Definition of the random variable τ_n.

From: Universal exploration dynamics of random walks

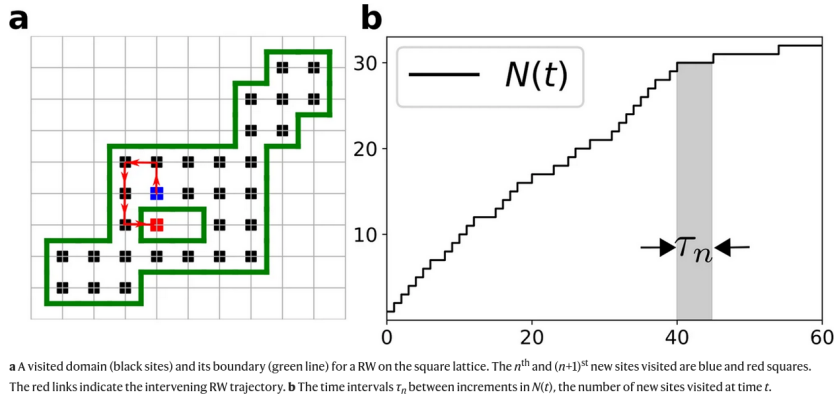**a** A visited domain (black sites) and its boundary (green line) for a RW on the square lattice. The nth and $(n+1)$st new sites visited are blue and red squares. The red links indicate the intervening RW trajectory. **b** The time intervals τ_n between increments in $N(t)$, the number of new sites visited at time t.

Figure 3: Site visitations and waiting time plot, taken from Regnier et al. (2023)

To quantify these notions in a stastical fashion, we propose that the theory of random walks could be applied as in Regnier et al. (2023). By dividing the embedding space into a lattice, we can examine metrics such as the number of distinct sites visited by a lineage, as well as the waiting time τ_n, which is the time taken to reach a new, distinct site. This will only approximate the true dynamics of the underlying system given the inevitable distortion of dimensionality reduction and training error, but it could provide more insight than the MODES metrics in isolation.

Chapter 3: The Linguistic Prediction Game and the Complexity of DFSMs

This chapter will finish work begun in Moran and Pollack (2019) and continued in a paper accepted for publication in the 2023 Conference on Artificial Life titled "MODES Analysis of Prediction Games."

The *linguistic prediction game* is a simple two-player coevolutionary domain. For an infinite sequence of timesteps, each player simultaneously emits a bit. If the game is *cooperative*, then players share the same goal: either to match (or mismatch) the bit provided by the other. In a *competitive* interaction, however, only one player is rewarded for matching (or mismatching) bits. Neither player is aware of the nature of their relationship upon starting the game, and their decisions must be made based solely on the patterns of bits produced.

Organisms in the game take the form of *deterministic finite state machines* (DFSMs). Each state has either a 0 or 1 label, corresponding to the bit emitted at that state, and two transition links. The bit emitted by the other player determines which of the links to choose to transition to the next state. Due to the discrete nature of the machines, a loop eventually must occur. The simulation ends once such a loop is detected, and the score for each player is determined by taking the average of all their scores in the loop.
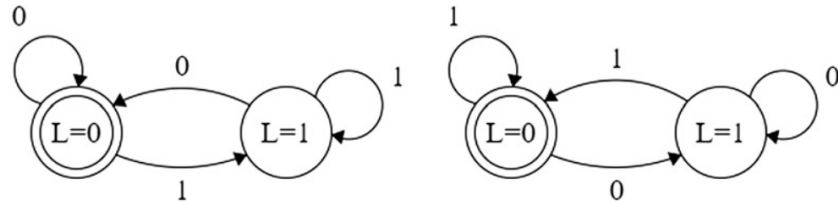

Figure 4: Two examples of DFSM organisms. Node labels indicate the symbol to be emitted at that state, while transition labels indicate the symbol emitted by the other that causes the transition to occur.

Evolution begins with identical populations consisting of a single *start state* with two links to itself. There is an equal probability that one of four mutations

will occur: (1) Add state, (2) remove state, (3) flip state label, (4) reassign link.
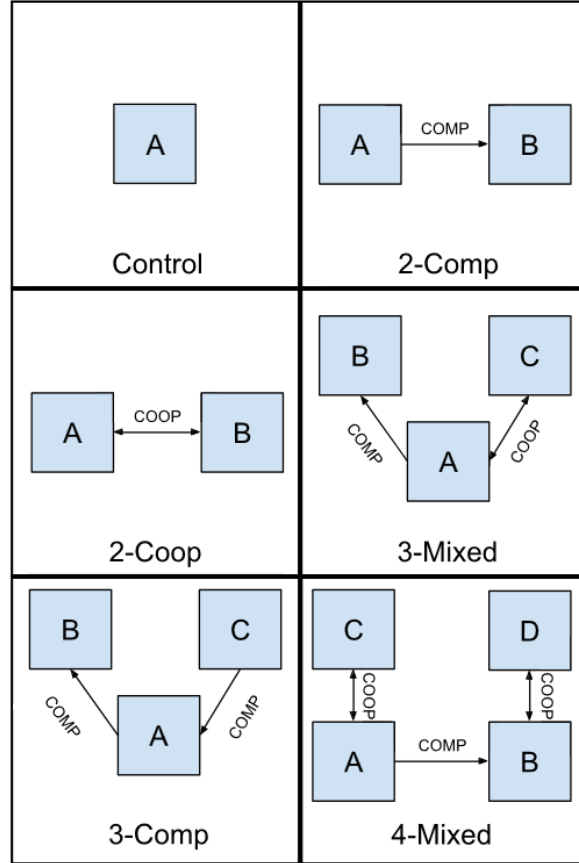

Figure 5: Figure taken from Moran and Pollack (2019)

The primary ecosystems to be studied include the following:

1. In the *Control* ecosystem, populations evolve without the presence of selective pressure. The results are used to interpret the open-ended behavior of the other ecosystems. In general, genetic drift will lead the size of the organisms will increase gradually over time due to the fact that the number of states is bounded at one.

2. The *Two-Species Competitive* (Comp) ecosystem involves two populations: one whose members seek to match bits, and another whose members seek to mismatch.

3. In the *Two-Species Cooperative* (Coop) variety, both seek either to match or to mismatch.

4. In the *Three-Species Mixed* (3-Mixed) variety, one "host" species is in a cooperative relationship with one population and a competitive relationship with a "parasitic" other.

5. In the *Three-Species Competitive* (3-Comp) variety, all three species are in competition.

6. In the *Four-Species Mixed* (4-Mixed) two cooperating pairs of species are linked by a single competitive relationship.

It was argued that ecosystems possessing only cooperative or competitive interactions tend to plateau in terms of complexity, there defined as the count of the number of states once a DFSM is pruned using *Hopcroft's algorithm* (Hopcroft, 1971). Meanwhile, *mixed* ecosystems were believed to hold the potential for *unbounded growth*, there determined as when the slope of the line of best fit to the mean complexity growth of a population exceeds that of a control or "shadow" ecosystem that lacks selection pressure.

A number of hypotheses were proposed to explain the behavior of the systems. These include that primarily cooperative species are more likely to exhibit growth; that *convention chasing* may be responsible for cycles between competitive species, leading to *evolutionary stable states*; and that clusters of competitive interactions appear to choke growth in larger configurations, leading to *degenerate ecosystems* (Ficici and Pollack, 1998; Watson and Pollack, 2001). However, more comprehensive theoretical and statistical justification was left for future work, as the volume and apparent intricacy of the machines and their interactions made manual inspection and analysis intractable over evolutionary timescales.
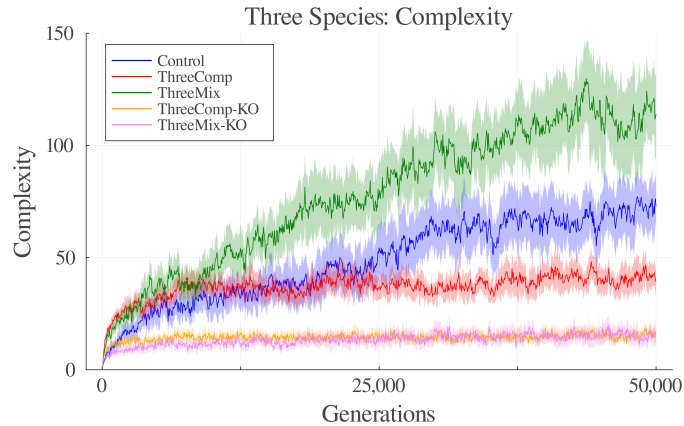
Figure 6: Figure taken from the upcoming publication "MODES Analysis of Prediction Games" The complexity growth of the *adaptive knockout* group (3-Mixed-KO, pink line), is well below that of the Hopcroft group (3-Mixed, green line). This suggests that the observed growth is largely nonadaptive, but the mechanisms behind this behavior are not yet understood and will be a subject of investigation.

Goals

This chapter will employ MODES Toolbox, the Q-DESSA method, and the DISCO selection method to answer the following open scientific questions:

1. Is the complexity growth observed in mixed ecosystems adaptive or nonadaptive upon application of the MODES metrics? Preliminary evidence suggests that a large portion of the growth is nonadaptive.

2. Can competitive ecosytems be statistically shown to demonstrate convention-chasing or cycling behavior?

3. Preliminary experiments suggest that the original work by Moran and Pollack (2019) failed to adequately characterize the behavior of various ecosystems given different "competitive" and "cooperative" configurations. Can the underlying dynamics be better characterized and understood?

Chapter 4: The Collision Game and the Growth of GNARL Networks

The Collision Game

See the presentation slides for the 2022 ALIFE conference which include a number of dynamic visualizations.

The *collision game* is a parameterized finite-horizon two-player game introduced in Willkens and Pollack (2022) that takes place on a real-valued one-dimensional number line. On timestep zero, each agent is assigned a position on the line such that they are some distance apart. At every timestep, each agent emits two real-valued outputs between -1.0 and 1.0. The first is a *movement* value, which is summed with the agent's current position value to determine its position at the next timestep, while the second is a *communication* value.

At the start of the next timestep, each player is provided with the distance between their two respective positions along with the communication value of the other agent. Each then determines new action and communication values, and so on. The episode ends upon one of two conditions: If the position of the agent that began with the lesser value becomes greater than or equal to the position of the other, the game is over and the interaction is classified as a *collision*; however, if the agents fail to collide by some specified timestep, it is an *evasion*.

The linguistic prediction game and the collision game differ in various ways: The former is infinite-horizon, with discrete actions and a one-dimensional action space; meanwhile, the latter has finite-horizon episodes, real-valued actions, and a two-dimensional action space. Moreover, the collision game features three classes of interaction:

- *Affinitive*: If the episode terminates with a collision, both agents are rewarded with a single point; otherwise neither agent is rewarded. We classify this as a *cooperative* relationship as both interests are aligned.

- *Avoidant*: Both agents are rewarded if no collision occurs and are given nothing otherwise. This also is a *cooperative* relationship, but one incentivizing a different pattern of behavior.

- *Adversarial*: One species is assigned the role of predator, the other the prey. If the episode ends with a collision, the predator is awarded a point while the prey receives nothing, and vice-versa. This is a *competitive* relationship due to the misalignment of their goals.

We note that the reward in the linguistic prediction game is real-valued, while in the collision game it is discrete. But there are strong similarities between the two games: They can be easily mapped to various ecosystem topologies, agents begin with ignorance of their partner's identity, different flavors of competitive and cooperative interactions are involved, and there is room for diverse strategies to emerge.

GNARL Networks

The abstact machine chosen to represent the organism model in this experiment is the recurrent GNARL network as described in Angeline et al. (1994). GNARL networks evolve both their weights and topologies starting from a minimal state.

	Collision	Evasion
Affinitive	(1, 1)	(0, 0)
Avoidant	(0, 0)	(1, 1)
Adversarial	(1, 0)	(0, 1)

Table 1: Payoffs for the collision game

Our networks here have two input nodes corresponding to the distance and communication value of the other agent, one bias node, and two output nodes corresponding to the movement and communication actions. The first generation has zero hidden nodes and zero connections.

Each node output is the weighted sum of all incoming connections passed through a nonlinear function. We use the *tanh* activation function for all connections so that output is bound in the range $[-1.0, 1.0]$. Each node retains this output value as a hidden state; in the case of a self-loop, the state value from the prior activation is weighted and likewise included in the sum. The movement action of the *greater* (or rightmost) agent is negated in simulation, so that an output of 1.0 always corresponds with moving towards the other agent and -1.0 with retreat.
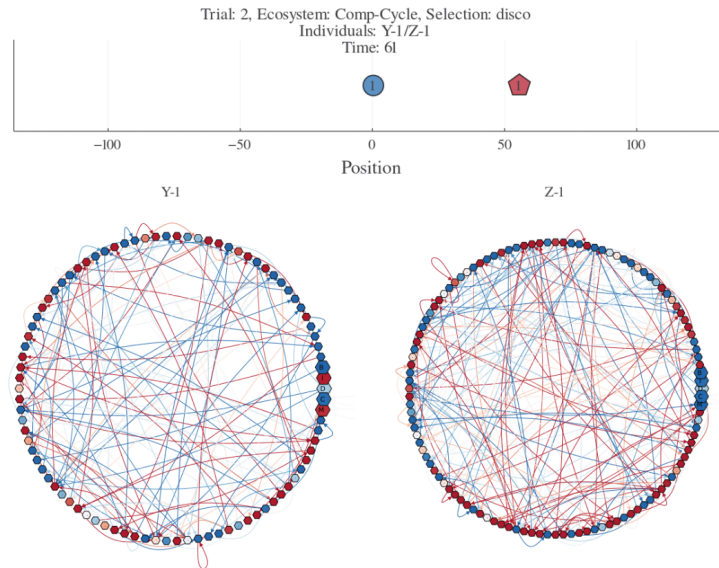

Figure 7: Complex GNARL Networks at one timestep of an interaction in the collision game (Willkens and Pollack, 2022). The state of each node and its weighted outputs is represented by color, with red being values close to -1.0 and blue being values close to 1.0.

Goals

In Willkens and Pollack (2022), it was found that rates of complexity growth followed different patterns than those predicted by Moran and Pollack (2019). Moreover, for all the ecosystem configurations considered, fitness-proportionate selection failed to produced unbounded complexity growth, while the DISCO selection method succeded in some. This chapter will investigate the following questions using the MODES Toolbox and the Q-DESSA method:

1. How does the DISCO selection method affect evolutionary dynamics such that unbounded complexity growth is produced in the collision game?

2. Is the complexity growth adaptive or nonadaptive by the standards of the MODES Toolbox?

3. Will open-ended transients be observed upon application of the Q-DESSA method?

Chapter 5: The Continuous and Harmonic Prediction Games with Genetic Programming

Here we introduce two new domains predicted to exhibit open-ended characteristics.

The first, the *continuous prediction game*, may be considered a variant of the linguistic prediction game. The game can be envisioned as a pursuit about the unit circle. Each agent has a position corresponding to a point on the unit circle, beginning at the same point. At each timestep, each agent is given a scalar observation corresponding to the arclength distance between the two agents Each agent then produces a scalar action value, which is applied to produce a rotation of that point on the unit circle. The distance between the two points is measured and subjected to a scoring function and the process repeats for a given number of timesteps. The overall score is the average over all timestep scores in the episode and is illustrated in Figure 8.

In this game, a "cooperative" interaction is defined as one in which each agent is rewarded for minimizing the distance between the two points on each timestep, while in a "competitive" interaction, one will seek to minimize the distance while the other is rewarded for maximizing it.

The second, the *harmonic prediction game*, springs from the observation that the "distance" function in such prediction games is ultimately arbitrary, and that multidimensional outputs and inputs may be interpereted in creative ways. If a domain provides sufficient adaptive pressure and coevolutionary tension, we could expect to observe various forms of open-ended complexity across a wider range of representations.
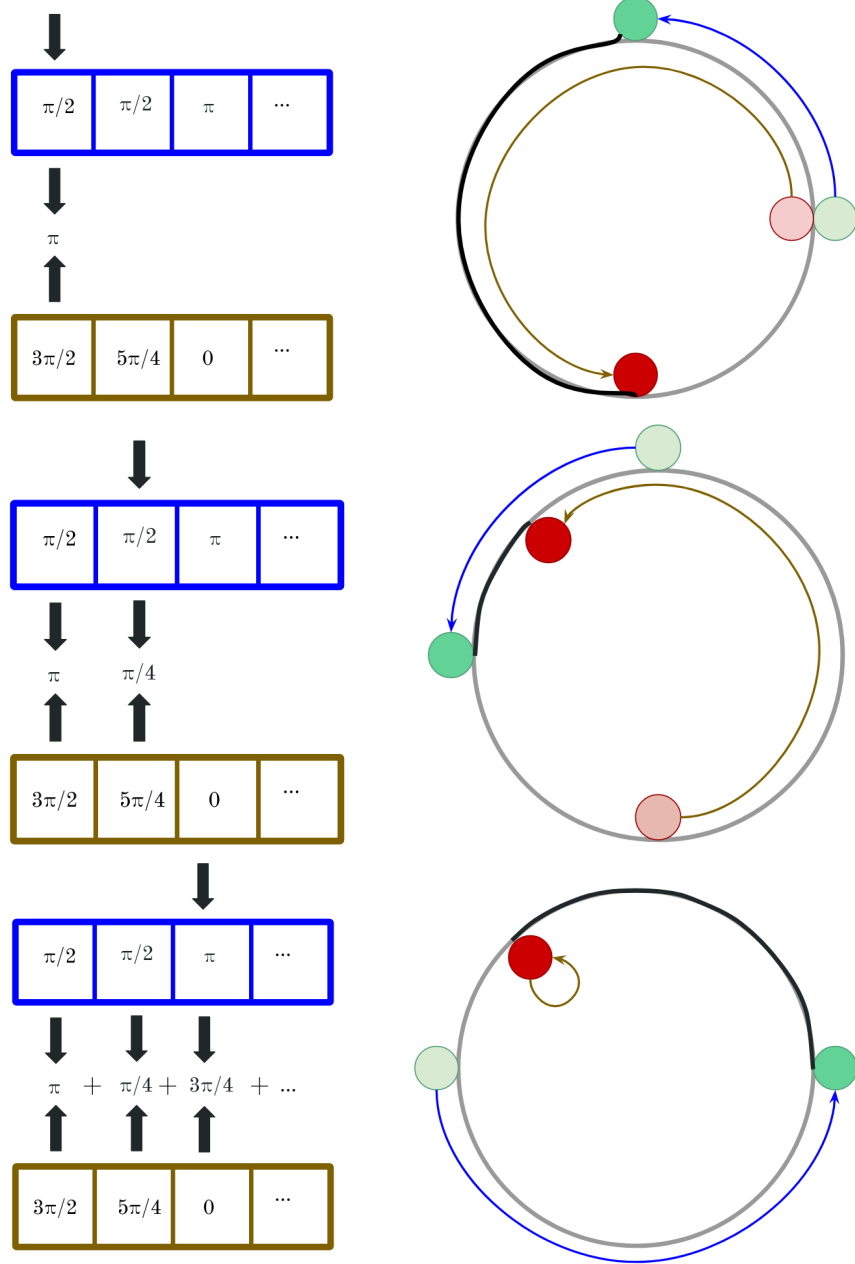
Figure 8: Example of scoring in the continuous prediction game.

The harmonic prediction game interprets each scalar observation as the frequency of a synthesized tone. As an alternative "distance" metric, we may use

a *dissonance model* such as that of Sethares (2005) as presented in Cook (2017) and shown in Figure 9. The interval created by the harmony of the two tones may be then measured using the dissonance model; a "cooperative" interaction is one in which both are rewarded for producing harmony, while a "competitive" interaction corresponds to when one agent is rewarded for producing harmony, while the other is rewarded for producing dissonance. The resulting score is not expected to reflect human aesthetic prefences, but we predict the emergence of patterns that are neither trivial nor random.
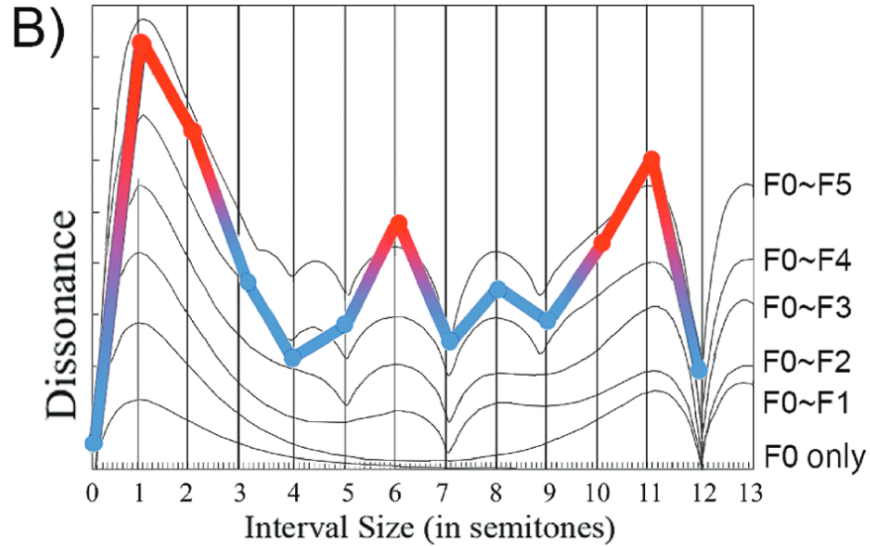

Figure 9: Dissonance model shown in Cook (2017). The colored line represents the empirical curve of perceived dissonance reported by human subjects, while the black lines represents the addition of overtones to the theoretical model of Sethares (2005).

Genetic Programming

As a third substrate, we will use constructs from the *genetic programming* paradigm to represent our artificial organisms. We use the Artificial Ant automata along with the Symbolic Regression framework as presented in Koza and Poli (2005) as a basis. The difference is that in addition to protected arithmetic operations, we also include operations for writing values to an output tape and reading values produced by the other agent from its own respective output tape. These tapes will begin with a single entry of real value and grow in length over the course of the episode.

Different representations are currently under investigation. The tapes may be read in a circular fashion, where each read operation moves the read head

forward one position, and reaching the end returns the tape to the beginning; see Figure 10 for one simple example. Alternatively, we could employ a non-circular tape with terminals for moving the read head backwards and forwards. Additional computational power could be provided by equipping each organism with a stack, along with operations for pushing and popping values resulting from intermediate calculations.

The tradition depth-based GP mutation operator can be highly destructive and is stochastic in the number of functions added to the tree. Special mutation operations have been defined for our case that are more similar to those employed in the previous two works, only changing the number of functions by at most one while preserving as much of the tree structure as possible.
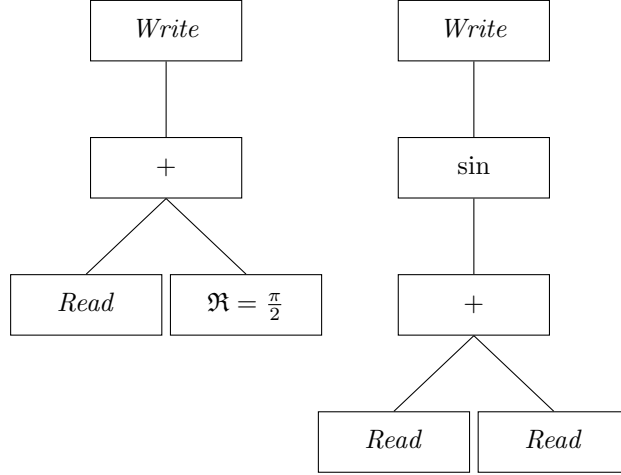

Figure 10: Two simple GP organisms. In this example, the set of functions is $\{Write, +, \sin\}$, while the set of terminals is $\{Read, \mathfrak{R}\}$, where $\mathfrak{R}$ denotes the generation of a random constant. An organism must have a minumum of two nodes: a *Write* node and a *Read* node. In an interaction, each organism begins with an output tape of [0] and operations are performed simultaneously starting with the leftmost terminal and then looping once the root is reached. So the operations peformed by the first organism would be $[Read, \frac{\pi}{2}, +, Write, Read\ldots]$. In the event that *Write* and *Read* operations are performed simultaneously, the *Write* operation is performed first. Sixteen timesteps of interaction between the two results in an output tape for the left organism of $[0, \frac{\pi}{2}, \frac{\pi}{2}, \frac{\pi}{2}, 1 + \frac{\pi}{2}]$ and an output tape for the right of $[0, 0, 1, 0]$.

Goals

The goals of this chapter are to answer the following questions:

1. Is the GP representation capable of producing open-ended complexity growth?

2. How do the continuous and harmonic prediction games compare to other games in terms of complexity when perfomed using analogous ecosystems?

3. How will the resulting interactions be interpreted in terms of human aesthetics and statistical complexity?

4. Can we develop a more unified theoretical framework for interpreting the behavior of these systems given variations in domain and representation?

Chapter 6: Conclusion and Future Work

This section will summarize the results of the previous analysis and discuss various avenues for future work. Depending on the pace of progress, some of this may be included in the final dissertation as experiments are easy to perform using the CoEvo framework. Future work may include:

1. Testing the effects of different organism representations across different interactive domains. For example, we may test the effects of using the GNARL representation in the continuous prediction game, or the effects of using the GP representation in the collision game. It may be that a more powerful computation model is required to produce open-ended complexity in certain ecosystems of the linguistic prediction game.

2. Testing the effects of different selection methods across different interactive domains. It is possible that the DISCO method could unlock complexity growth in the linguistic or continuous prediction games.

3. Testing the effects of varying other hyperparameters, such as the population size. Larger populations may be required to produce open-ended complexity in certain ecosystems.

4. Analyzing the complexity of the interaction timeseries using a technique such as *epsilon machine reconstruction* to observe whether there is a correlation between genotypic complexity and the statistical complexity of phenotypic interaction (Crutchfield, 2012; Bartlett et al., 2022).

A better understanding of the impact of variables such as domain or selection method on complexity growth, as well as the adaptive nature of such growth, would allow a more principled approach to the design of more powerful coevolutionary systems. It is the hope of the author that this dissertation will grant a better understanding of the phenomena of evolutionary complexity growth on a more fundamental level and contribute to the ultimate effort of developing truly open-ended artificial systems.

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