Natural Computation and Self Organization in Monkey Behavior

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Abstract: The temporal structure of animal behavior may be an untapped yet fundamental source of information about an animal's behavioral ecology and health. However, little is known about which pattern properties might be relevant or might reveal differences in behavior patterns of individuals. We investigated the activity patterns of 14 adult female macaques on Koshima Island, Japan. Focal sampling was used to record 56 activity sequences (4/individual, ranging from 17-68 minutes) of discretely categorized locomotion. From these time series we calculated entropy rates (Hmu) and excess entropy (E). Preliminary analysis reveal that there is more structure in monkey locomotion time series than a biased coin! However, the strongest correlation of Hmu and E were still with the percent of the observation the monkey was active, and no clear trends were found with individual monkey characteristics such as age or rank. Further analysis will include construction of epsilon machines from the sequences to calculate additional metrics including statistical complexity. Future studies will utilize biotracking technology to collect longer sequences with greater precision and finer time scale.

Introduction

Complex patterns in nature were once considered to be indescribable by mathematics unstructured, unpredictable, and random. Yet, with access to new technology and increased computing power, the emerging field of complexity science is providing tools to quantify this 'roughness' in nature. Complexity science explores the organization, structure and behavior of all types of systems, and though an official definition of 'complexity' is still debated, it is generally agreed that complex systems share common qualitative properties such as emergent collective behavior, information production and processing, and adaptation over time (Mitchell, 2009). The notion of 'biological computation' has become increasingly popular, proposing that living systems function as natural information processes (Flack, 2014; Mitchell, 2011; Denning, 2007). Viewing an animal with its diverse behavioral outputs as a complex system offers a holistic approach to understanding behavioral processes, instead of maintaining a reductionist view which describes several driving components of behavior separately. An animal's behavior is a product of many different things on many different time scales: evolutionary history of the species, genetic composition, rearing influences, interactions with other animals, current environment, past environment, hormones, health state, physiology, etc. (and all of these things also interact with each other). Hence, an animal is basically a black box, with measurable behavioral outputs.

Multiple features of an animal's behavior can be measured; for instance, we often see summary statistics such as frequency, count, speed, or duration. However, beyond such summary statistics, pattern qualities can also be measured as sequences can have very different structure even with the same overall amount of behavior. This structure may hold important differences between the behavior patterns of individuals; for example, animals living in the same group might move on average about the same amount every day if the group travels together, but some may take more breaks, or move in longer bouts depending on their health or social interactions. Another instance, an organism may need to eat some amount of food each day to survive, but may forage in different number of times of different durations, and we know that the patterns and quantities of meals influence our metabolism and health. Indeed, emergent spatiotemporal patterns may offer important information about the underlying state of an animal system. Natural systems tend to balance order and disorder resulting in structural complexity, and a certain level of behavioral diversity (on a gradient between invariably deterministic and random) is fundamental to survival (Crutchfield, 2012). Complex structure is thought to give a system efficiency, stability, and resilience (West, 1990). There has even been a proposed 'theory of complexity loss in aging and disease', which postulates that healthy systems output complex multi-scaled variability that allows for adaptive capabilities and breaks down with age or illness (Goldberger et al, 2002). For example, the long-range scaling patterns of human heartbeat and gait dynamics have been shown to deteriorate in markedly pathological conditions (Goldberger et al, 2002b). Measurements of behavioral pattern complexity offers an intriguing avenue to explore many concepts in animal behavior such as optimal animal-environment interaction for resource acquisition, an animal's ability to self-regulate its behavior in response to a changing environment, and pathological behavioral stereotypy. The measurement of behavioral complexity in this regard may be an untapped yet fundamental source of information about an animal's behavioral ecology and health

Background

A small body of work has investigated the pattern structure of animal behavior over time using fractal analyses, a class of complexity measures that estimate fractal dimension which represents the degree of scaling in the distribution of step-lengths or correlation structure of sequences, and the degree of self-similarity and long range correlation in patterns (Peng et al, 1992; Peng et al, 1994). From the branching growth of plants (Escós et al., 1995) to fluctuations in heart beat variability (West, 1990), fractal analyses have been used to characterize organizational complexity over space or time in a diverse array of systems. Previous studies have reported that fractal analysis can detect subtle changes in 'hidden' animal behavioral structure that are missed when using traditional measures such as average durations (Escós et al., 1995; Asher et al., 2009; Seuront & Cribb, 2011). Variability in behavioral sequence complexity detected by such analyses has been linked to many characteristics: differences by sex (social behavior of chimpanzees: Alados & Huffman, 2000; foraging and locomotion behavior in Japanese macaques: MacIntosh et al., 2011), stress level (boat traffic disturbance in dolphin surface behavior: Seuront & Cribb, 2011; resource deprivation in chickens: María et al., 2009), and age (young chickens: María et al., 2009; adult macaques: MacIntosh et al., 2011). In addition, states known to be energetically taxing such as reproduction, clinically impaired health, and parasite infection have been associated with differences in complexity (Japanese macaques: MacIntosh et al., 2011; Spanish Ibex: Alados et al., 1996; chimpanzees: Alados & Huffman, 2000). However, interpretations of the direction in which changes occurred may be flawed due to methodological differences (Eke et al, 2002, Delignieres et al, 2005), and most studies used observational periods that did not exceed 30-60 continuous minutes, which don't allow investigation of correlations at larger time scales that may be necessary for accurate estimations of fractal dimension. Thus, while findings from these studies suggest a promising way to detect changes or differences in behavior pattern and link them to important perturbations, the results are difficult to interpret and thorough investigation of behavior pattern structure is still lacking.

Bio-logging and Movement Ecology

MacIntosh et al. (2013) carried out the most comprehensive investigation of scaling properties in a non-human species, and was able to demonstrate that diving sequences of penguins display long-range dependence across at least 2 orders of magnitude by collecting activity data with biologgers across complete foraging trips. While movement data reduce behavior and context to sequences of activity and inactivity, they have long been used as indicators of health and wellbeing, as seen with the recent explosion of self-tracking devices (step counters, fitbit, etc.), and similar technologies have become increasingly more popular for long-term data collection of animal movement. While organization of movement is driven by many internal factors (i.e. metabolism) and external constraints (i.e. terrain) (Macintosh et al, 2011; Paraschiv-ionescu et al, 2008), these patterns are often our only window into the numerous underlying processes of an animal's behavioral ecology (Gurarie et al, 2016). It is the hope of many researchers to be able to detect remotely what specific behavior an animal is doing from movement data. While some progress has been made using methods from machine learning to identity points of change in behavioral states, we ultimately need to understand the deeper structure of movement to successfully implement and interpret these analyses (Guarie et al, 2016). Bio-loggers allow for the finer time units and long continuous sequences necessary for robust complexity analyses to answer basic

questions about behavioral organization - What benefits do certain behavior patterns offer an individual, and what can we learn about the state of an individual from these emergent patterns? At the same time, complexity analyses will allow us to asses precisely what information we are actually acquiring about the movement of animals through bio-logging technology.

To date, no species of animal has been investigated thoroughly enough to understand how much variability exists between individuals in the temporal structure of their activity, and how much this varies within an individual by behavioral state, landscape, and social environment. This knowledge is necessary to create a basic framework to understand and interpret behavioral complexity of animals. This project begins exploring the question: what spatial and temporal patterns are observable in the structure of animal movement?

Dynamical system: Wild Japanese macaques

Japanese macaques (*Macaca fuscata*) were studied on Koshima Island, the birthplace of Japanese Primatology, considered to be one of the most influential research sites in the history of animal behavior. About 95 macaques live on Koshima. This population has been studied since 1948 and all individuals have been identified and marked. Data on general health (e.g. weight), pedigrees and the matrilineal hierarchy (dominance rank and lineage) are available, offering previous knowledge and easy identification of subjects despite living in a free-ranging, naturalistic setting. These macaques have diverse daily routines, spending time grooming on a flat beach, foraging for shellfish on rocky shorelines, traveling across the island over steep forest terrain, and also spending time in tree canopies. Additionally, the population is regularly provisioned with 3kg of wheat 2-3 times per week, creating different social and foraging contexts such that sometimes animals are feeding in close proximity on a finite resource, and other times the group is spread over wide ranges with little feeding competition. Due to the age, personality, and rank diversity of the population, along with the diverse landscape and the multi-faceted nature of macaque societies, this study system is ideal by both species and location to investigate between and within individual differences in behavioral structure.

This study was originally designed to complement an ongoing parasite and reproduction project where a subset of a Japanese macaque population was treated with anthelmintics to clear them of gastrointestinal parasites. Data was collected from 7 treated and 7 control individuals to test the hypothesis that the energetic strain of parasites constrains the organizational complexity of behavior in Japanese macaques. Unfortunately, this fieldwork coincided with Japan's typhoon season, and access to the island was more limited than we had hoped, yielding a smaller data set than planned. More tragically, we speculate the study was compromised due to weather delays in data collection following treatment, such that reinfection was likely to have occurred before the onset of behavioral data collection. However, this dataset now serves as pilot data for investigating differences of behavior pattern based on individual attributes, island location, and behavioral state. A follow-up study will be conducted using bio-logging collars in the Winter of 2017.

Methods: Data Collection and Time Series Analysis

Current data: Observational focal sampling was used to record 56 activity sequences (4/individual for 14 focal animals, ranging from 17-68 minutes) of discretely categorized locomotion. Individual monkeys were followed until they were lost, or up to 68 minutes. Their behavioral states lasting >3 seconds were recorded as time-stamped records 3 seconds after the point of change, and these were then coded as binary sequences of active

or inactive states, one character for each second. The location and terrain of each observation were also recorded.

Future data: I will record sequences of activity and location using a combination of GPS and accelerometry bio-loggers, which will be attached on collars to a subset of animals to continuously record their activity patterns. These data will be coded into multiple fundamental time series, including the overall dynamic body acceleration (ODBA) and binary sequences of activity and inactivity. I will conduct observations alongside bio-logging to validate their measures of activity, and record the behavioral states of the macaques (feeding on provisions, foraging, travel). In addition, I will record data on social interactions of affiliative (grooming, social contact, proximity) and agonistic (aggression and status signaling) behavior.

Analysis: It has been suggested that no single statistical measure can quantify the complexity of a system and instead a 'toolkit' of metrics should be utilized to explore different qualities of complicated processes (Goldberger et al, 2002). Therefore, it is my eventual goal to calculate a series of measures that describe different pattern attributes in order to investigate specifically how behavior patterns vary, and which variations relate to variables of interest. Currently, I have calculated *entropy rates (Hmu)* of sequences, which represents the amount of randomness or surprise in a pattern (such that it is maximized in a fair coin process). I have also estimated *excess entropy (E)*, a measure of memory or predictable information in a sequence. These values were estimated by calculating the slope (Hmu) and intercept (E) of the block entropy curve created by plotting word length by Shannon entropy (- \sum p log p) of the distribution of binary words of a given word length in the sequences.

Results

Section 1 - Exploration of a sequence

I began by investigating the properties of one sequences from the monkey Omoto during a foraging bout on the rocky shore of the island that lasted 4104 seconds. Below is the temporal structure of active (blue) and inactive (white) bouts over this observation.





To the left is a plot of the distribution of bout lengths of activity and inactivity. Most bouts were short, with a few very

Below are return maps of the sequence which show the lengths of (1) active bouts followed by inactive bouts, (2) active bouts followed by the previous active bout, and (3) inactive bouts followed by the previous inactive bout.



Again, we see that the majority of active and inactive bouts are very short. Long bouts of activity or inactivity are usually followed by short bouts of activity or

Section 2 - Randomization of sequences

In order to see if the block entropy of word frequency distribution method would actually detect any structure in the sequences, I randomized a subset of sequences by shuffling the characters, and by shuffling the bouts of activity and inactivity. Below we see entropy by word length plots of these sequences. The fully randomized sequences look like biased coins, with intercepts likely at 0, and straight block entropy curves that relate to the % of activity in the observation (i.e. the bias of the coin). The actual data look quite different – they would have non-zero intercepts (excess entropy), and entropy rates that aren't predicted merely by their % activity. The data with shuffled bouts looks the same as the real data, and most block entropies were the same with the exception of the larger word lengths, which varied from actual data by only thousandths of points. This is not entirely surprising - since most bouts are small and of similar length, the word frequencies likely didn't vary much from the real data, especially with short word lengths.



Section 3 – Hmu and E of all sequences

I plotted block entropy curves for 54 of the sequences to see how much variability existed in Hmu and E estimates. The colors represent which of the 14 focal individuals the sequences came from. I fit these points to lines to get the slope and intercept.



I made several plots with these measures to begin exploring what is driving the variability we see. Below are plots of Hmu and E for each focal individual. There exists a fair amount of variability within most individuals.



To check these metric's dependence on the length of the sequences, I plotted by sequence duration (seconds). There did not seem to be any relationship here, which is good and expected.





Forest Location

Mix

Mix

Rocks

Beach

Hmu by % Active

However, both Hmu and E were correlated with the % activity in the sequence.



The % activity is also related to the terrain/location in which the observation occurred. In fact, in previous analysis of these data, the only significant finding was that % activity was predicted by location, such that they are least active on the beach. In other words, we have shown with science, that monkeys like to relax on the beach.

Given the relationship between Hmu and E with % active, it is not surprising we see a very similar relationship between Hmu and E with location (plots below).





Finally, I plotted Hmu against E. While these values are not mathematically required to be correlated, in these data they appear to be loosly related. It seems like a lot of the variability may likely be driven by different amounts of activity in the sequences. Looking at the primary behavioral state of the sequence (what behavioral context was occurring during the majority of the sequence: travel, forage, social interaction, rest) might be valuable.

There appeared to be no relationship between Hmu and E with age, rank, or whether or not the monkey had an infant.

Conclusion

While there is nothing striking sticking out from these measures with regards to specific attributes of the monkeys, it seems as though the structure of monkey activity has less randomness and more memory than a biased coin, which is at least encouraging.

Future Directions

The next step is to model epsilon machine representations of these sequences. To start, I will try to model them as an alternating renewal process between active and inactive states

(Marzen et al, 2015). An epsilon machine is a unique, predictive, and minimal representation of a process, and models a generative scheme of a pattern (Crutchfield, 2012). Using Baysian inference, I will determine which epsilon machine models could have produced the sequences, and estimate an array of complexity measures from the weighted averages of a posterior distribution of possible generative machines. Beyond Hmu and E, several complexity measures can be calculated from epsilon machines, all of which represent several independent properties of sequence structure (Crutchfield & Feldman, 2003). For instance, *statistical complexity* represents the amount of 'hidden' information required to make an accurate prediction. *Transient information* represents the amount of information that needs to be extracted before an observer can 'synchronize' with a process. All of these metrics represent different properties of a sequence, and could relate to different attributes of individual monkeys, or functions of behavioral states. These methods provide a framework to make precise interpretations about differences in movement patterns.



Example of an alternating renewal process machine from Marzen et al, 2015.

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