

## Contents

<b>1</b>	<b>Evolutionary Thinking</b>	<b>3</b>
	Introduction (Lecture) . . . . .	3
<b>10</b>	<b>Studying Adaptation</b>	<b>4</b>
	Hypothesis Testing: Oxpeckers Reconsidered . . . . .	4
	Experimental Design . . . . .	4
<b>4</b>	<b>Evolutionary Trees</b>	<b>5</b>
	How to Read an Evolutionary Tree . . . . .	5
	Inferring Phylogenetic Trees . . . . .	6
<b>3</b>	<b>Natural Selection</b>	<b>7</b>
	Lecture Notes . . . . .	7
	Discussion Questions: Dog Domestication . . . . .	7
<b>6</b>	<b>Mendelian Genetics</b>	<b>9</b>
	. . . . .	9
<b>7</b>		<b>10</b>
	. . . . .	10
<b>8</b>		<b>11</b>
	. . . . .	11
<b>9</b>		<b>12</b>
	. . . . .	12
<b>11</b>		<b>13</b>
	. . . . .	13
<b>12</b>		<b>14</b>
	. . . . .	14
<b>13</b>		<b>15</b>
	. . . . .	15
<b>14</b>		<b>16</b>
	. . . . .	16
<b>16</b>		<b>17</b>
	. . . . .	17
<b>17</b>		<b>18</b>
	. . . . .	18



# 1 Evolutionary Thinking

## Introduction (Lecture)

- ▷ Essential questions of evolutionary biology:
  - Why do organisms look so different?
  - Why develop elaborate sexual traits?
  - Why do organisms senesce?
- ▷ Evolution is mainly an historical science and thus must rely on other methods of reconstructing the past or making inferences about evolutionary forces.
- ▷ **Proximate**: a question about a mechanistic cause; provides an immediate explanation about **how** a mechanistic cause functions.
- ▷ **Ultimate**: **why**, or the reason, a trait or organism is the way it is; an evolutionary explanation.
- ▷ Example of proximate vs ultimate in Galapagos finches:
  - Proximate: developmental growth factor is increased/decreased in some birds.
  - Ultimate: different habits are selected on breaks that maximize food gathering ability.
- ▷ Evolutionary biology's approach to answering questions:
  - **Empirical data**: **observation** studies, experiments; the *comparative method*.
  - **Theory**: **predictions** that use models and mathematical reasoning which can be **tested** with empirical data.
- ▷ Overview of the components of evolution by natural selection:
  - Genetic variation exists, via mutations.
  - Mutations are heritable.
  - There is an advantage to survival and/or reproduction from the mutation.
  - Individuals with the advantage in survival/reproduction are selected for.

## 10 Studying Adaptation

### Hypothesis Testing: Oxpeckers Reconsidered

- ▷ **Adaption:** a trait, or a suite of traits, that increases the fitness of its possessor.
- ▷ No hypothesis for the adaptive value of a trait should be accepted simply because of its plausibility.
- ▷ Oxpeckers and impalas traditionally were thought to have a mutually beneficial existence; oxpeckers ate ticks and impalas provided a safe environment.
- ▷ Experiments on cattle were done to test whether this observation was true:
  - Results show red-billed oxpeckers have no effect tick loads of cattle.
  - Red-billed oxpeckers maintained open wounds, even enlarging existing wounds to feed on the cattle's blood.
  - Red-billed oxpeckers removed hosts' earwax; whether this is good or bad is unclear.
  - Even these results must remain in question, as cattle are not the native host for the birds.
- ▷ Other important points to remember:
  - Differences among populations or species are not always adaptive.
  - Not every trait is adaptive.
  - Not every adaptation is perfect, often the adaptation just happened to work well enough or by chance better than other adaptations.

### Experimental Design

- ▷ Defining and testing effective control groups is critical.
- ▷ Treatments of controls and experimental measures must be handled as close to exactly alike as possible.
- ▷ Randomization is a key technique for equalizing miscellaneous effects and a tool to avoid bias.
- ▷ Reproduction is essential in order to help remove potential outlier effects.
  - Allows for greater understanding of precision, accuracy, and variation by providing more data for statistical tests.

## 4 Evolutionary Trees

### How to Read an Evolutionary Tree

- ▷ **Phylogeny:** aka evolutionary tree or phylogenetic tree, is a diagram showing the history of divergence and evolutionary change. Essentially, it's the **genealogical relationships** of organisms based on descent with modification.
  - **Taxa:** the units you are analyzing, e.g. certain species or DNA sequences.
    - **Character:** a feature or trait present among the taxa of interest, e.g. teeth of mammals or nucleotides of DNA sequences.
      - *Character state(s):* an **alternative condition** of a character, which are able to evolve one to another, e.g. pointed/flat teeth of mammals.
    - **Ancestral character:** a trait that was **possessed by the common ancestor**.
    - **Derived character:** a trait the was **not possessed by the common ancestor** and instead **evolved** in at least one of the descendants.
      - **Synapomorphy:** derived character state shared by **two or more** taxa and used to define a clade of taxa.
      - **Autapomorphy:** derived character state in only **one** taxon.
    - **Outgroup:** a taxon or taxa that are used to root the phylogeny or determine ancestral character states.
    - **Ingroup:** the set of taxa that are the focus of the phylogeny.
  - **Nodes:** points at which the tree splits; represents mutations, speciation events, or **character changes**.
  - **Anagenesis:** descent with modification, but **no speciation**.
  - **Cladogenesis:** **speciation**, origin of clades.
    - **Clade:** also known as a **monophyletic group**, an ancestor and **all** of its descendants.
    - **Paraphyletic group:** a group of organisms consisting of an ancestor and **some** of its descendants.
  - **Sister:** a taxa or clade that are most closely related to each other; they **share the most recent** common ancestor.
- ▷ **Homology:** similarity due to common descent; **continuity** of a trait, character, or character state through time.

- *Homologous trait*: found in a taxa that inherited the trait from a common ancestor.
- ▷ **Homoplasy**: or analogous, similarity in the characters or traits in different taxa due to convergent evolution, parallelism, or reversal, but **not due to common descent**.
  - **Convergent evolution**: similar traits due to selective forces and **not shared ancestry**.
  - **Parallelism**: convergent evolution in **recently diverged** taxa.
  - **Reversal**: derived traits or character states that revert to the ancestral form.

### Inferring Phylogenetic Trees

- ▷ **Parsimony**: the hypothesis of relationshipsthat requires the **smallest number of character changes** is most likely to be correct.
  - Based on **derived** traits(synapomorphies).
  - Reconstruction using parsimony:
    1. Code characters.
    2. Make up a taxon x character matrix.
    3. Search for synapomorphies, and theshortest tree.
      - Outgroups can help polarize the characters.
  - **Treelength**: a measure of evolutionary change using parsimony.
    - Shortest tree length produces most parsimonious tree.
    - Length determined by number of synapomorphies.
    - Homoplasious characters increase tree length.
- ▷ **Distance Methods**: converts a sequence alignment to genetic distances between pairs of sequences.
  - Branch length is proportional to genetic differences.
- ▷ **Baysian**
- ▷ **Bootstraping**

### 3 Natural Selection

#### Lecture Notes

▷

#### Discussion Questions: Dog Domestication

##### ▷ Background and Goals

- What hypotheses about dog domestication are examined in this paper?
  - The origin of domestic dogs was the main focus; genetic data suggested East Asia, but fossil data suggested Europe and Siberia.
- What predictions do these hypotheses make? What would the expected phylogenetic trees look like under each of these hypotheses (i.e. what are the expected topologies)?
  - Dogs and wolves would fall under a monophyletic group from a particular area indication origin.

##### ▷ Methods

- What taxa were sampled for this study?
  - Hypothesis was tested using DNA extracted to trace mitochondrial genomes from 18 prehistoric canids and 20 modern wolves from Eurasian and American origin.
- What gene sequences were used for this study?
  - Wolves, dogs, including divergent breeds, recently published chinese indigenous dogs, and coyotes. (148 mitochondrial genomes)
- What phylogenetic methods were used to reconstruct the phylogenetic tree in Figure 1?
  - Maximum likelihood, coalescence, and bayesian.

##### ▷ Results and Discussion

- In Figure 1, which wolf sequence is most closely related to the extant dog clade A, and what geographic region is it from?
  - Argentina (pre-Columbian within clade A)
- In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?
  - Dog clade C, Germany, 14,700 years ago.

- Based upon Figure 1, how many times does it appear that modern extant dogs could possibly have been domesticated?
  - Figure 1 suggests 4, but the the authors state, "the inferred recent divergence of clade B from wolves now found in Sweden and Ukraine implies that is might represent a mitochondrial genome introgressed from wolves rather than one established by domestication."
- What was the topology of the phylogenetic tree that was recovered, and therefore, which hypothesis was supported?
  - The findings support the conclusion that legacy of dogs derives from wolves of European origin.
  - Analysis of coalescence times support divergence time of >15,000 years ago.
  - Past mitochondrial and Y chromosome analysis suggested non-European, but had less supported data than these findings.

▷ Conclusions

- What are the major conclusions of the paper?
  - Three of four modern dog clades are more closely related to sequences from ancient European rather than extant wolves with divergence times >15,000 years ago.
- Was the taxonomic sampling sufficient to rule out alternative hypotheses?
  - Ancient panel did not contain specimens from Middle East or China. No, no ancient dog remains older than 13,000 years are known from those regions.
  - The mtDNA sequence tree is well supported, but represents a single genetic locus. Independent loci could offer more power to resolve phylogenetic relations.



## 6 Mendelian Genetics























**18**



**20**



