# Summary of Introduction to Evolutionary Biology

v0.3

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## **Preface**

This document aims to summarize the lecture Introduction to Evolutionary Biology as it was taught in the autumn semester of 2017. Unfortunately I can't guarantee that it is complete and free of errors. You can contact me under **glebert@student.ethz.ch** if you have any suggestions for improvement. The newest version of this summary can always be found here: https://n.ethz.ch/~glebert/

#### 1 Introduction

**Definition**: Evolution means biological change over time **Technical basis**: Phenotypes of individuals that are encoded by heritable genotypes vary in a population and their frequencies change

## 1.1 History

**Aristotle**: Ladder of nature / perfection

Carl von Linné: Systematic classification of life

James Hutton & Charles Lyell: Gradual long-term

processes shaped earth (Uniformitarianism)

Jean-Baptiste de Lamarck: Inheritance of acquired

characteristics (Lamarckian evolution)

Charles Darwin: Evolution is descent with modifica-

tion and results in survival of the fittest

#### 1.2 Microevolution

direct observation: small time-scales  $\rightarrow$  short-term changes

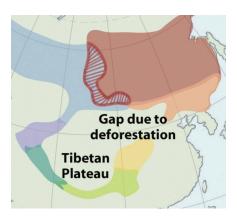
Evidence of Microevolution:

- 1) Observation from natural populations
  - Bacterial adaptation to antibiotic stress
  - Soapherry bug adaptation to fruit
- 2) Observation from living anatomy Vestigal and rudimentary traits
  - Kiwi wings
  - Human coccyx (Steissbein)
  - Human arrector pili muscle (Haaraufrichter-Muskel)
  - (Appendix might be safe house for good gut bacteria)

#### 1.3 Speciation

Speciation is the process that results in one species splitting into two or more. One example for this are ring species. They occur when one species spreads slowly around a geographical area to which they don't spread.

By the time they meet up again the differences between the populations are too big to interbreed. One example for this is the Siberian Greenish Warbler (the hatched area is where no interbreeding occurs with two populations present).



#### 1.4 Macroevolution

indirect observation: long time-scales  $\rightarrow$  long-term changes

Evidence of Macroevolution:

- 1) Successions & Extinctions
  - Law of succession: pattern of correspondence between fossile and recent forms from the same locale Comparative anatomy: Georges Cuvier argued that certain species are extinct. Recent macrofauna is only a fraction of all that ever existed
- 2) Transitional forms
  - Darwinian evolution predicts intermediate forms between a species and its ancestor (e.g. *Microrap*tor gui and *Archaeopteryx* between dinosaurs and modern birds
- 3) Homologies (Owen: "the same organ in different animals under every variety of form and function) can be found through comparative anatomy and comparative embryology. The similarity is due to inheritance from a common ancestor. They are phenotypically and genetically defined and enable the use of model organisms.

Some molecular homologies are

- the universal genetic code: bases and codons
- the small-subunit (SSU) ribisomal RNA genes

## 2 Natural selection

Natural selection is the process underlying adaptive evolution

#### 2.1 Darwins postulates of evolutionary change

Evolutionary change over time is a deductive implication of four postulates.

- 1) All populations contain variable individuals
- 2) Variation among individuals is, at least in part, heritable
- **3**) Some individuals are more successful at surviving and reproducing than others
- 4) Survival and reproduction of individuals are not random; but individuals with the most favorable variation given the environment are those better at surviving.

These postulates can be tested in real world populations (e.g. Darwin's finches from the Galapagos islands). One has to be careful to not misinterpret biasing factors. For example heritability measures can be skewed by misidentified paternity, misidentified maternity, food quality or maternal effects such as egg quality.

## 2.2 Definition

Natural selection acts on individuals (more specifically, phenotypes), its consequences occur in populations as allele frequency changes.

#### 2.3 Darwinian vs. Lamarckian evolution

Different processes proposed for the same pattern.

Billerent processes proposed for the same partern.	
No initial variation	Initial variation
Individuals adapt	Selection acts on
during their lifetime	individuals
Inheritance of aquired	Inheritance of
changes/characters	surviving alleles if
(IAC)	environment leads to
	adaptation
$\Rightarrow$ individuals and	$\Rightarrow$ populations evolve
populations evolve	
	No initial variation Individuals adapt during their lifetime Inheritance of aquired changes/characters (IAC)  ⇒ individuals and

Epigenetic modifications are attached to the genetic code and can be passed on to the offspring (up to two generations). Thus their evolutionary relevance is short-term.

#### 2.4 Limits

- Natural selection acts on existing traits
- Natural adaptation does not lead to perfection
- Natural selection is non-random, but it is not progressive
- Natural selection is blind to the future, but tells us tales from the past

#### 2.5 "Perfection" in nature

William Paley argued, that the vertebrate eye is too perfect and complicated to have resulted from natural processes. Thus it must be a creation of a conscious designer. By looking closely at eyes from various chordates one can see that there is a lot of variation in the complexity of the eye. Thus Paleys argument is wrong.

## 3 Phylogenetics

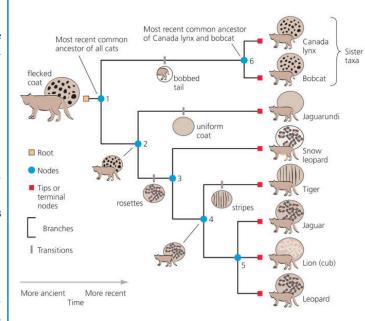
#### 3.1 Evolutionary trees

Evolutionary trees aim to display the course of speciation over time and the relation between species. They start with one common ancestor (the root) and end with multiple species (tips or terminal nodes). Dichotomies (splits of branches into two) in between are called nodes. If phylogeny can't be resolved to dichotomies branches

split into three or more subbranches. This phenomenon is called polytomy. Branches can have transitions where a specific characteristic evolved. The first group or species to split of is called basal.

Trees come in many forms depending on the author and on the kind of data they aim to display. They can be left-right, top-down or even circular.

One should not forget that evolutionary trees are merely hypotheses.



## 3.2 Phylogenetic inference

- Plesiomorphy: A characteristic that is shared between a species and its ancestor
- Apomorphy: A characteristic that is different from an ancestor
- Synapomorphy: Apomorphic and shared between multiple sister taxa. Also called homology
- Autapomorphy: Apomorphic and different from sister taxa
- Monophyletic group: All descendants of one ancestor (at least two taxa). Also called clade.
- Paraphyletic group: A subset of descendants of one ancestor

Classical taxonomic groups are not necessarily monophyletic (e.g. prokaryotes, dicots and fish).

#### 3.3 Tree reconstruction

Pitfalls of trees inferred form phenotypes alone:

- Phenotypes are influenced by genotypes and environment
- Only genotypes are heritable
- Phenotypic similarity due to convergence (analogy / homoplasy; e.g. camera eye in mollusks and teleosts)

Combination of phenotypic and genotypic data (molecular markers) leads to better results. When using molecular markers each nucleotide is seen as an independent character.

If multiple possible trees exist, one can assume that the most parsimonious (least evolutionary steps) is the correct one. If multiple equally parsimonious trees turn up one estimates uncertainty. This is done by bootstrapping which is the generation of data sets made up from the original data set. Data points can be repeated multiple times or be absent altogether. When analyzing these data sets one gets a phylogenetic tree for each. The most likely tree will be the one that comes out the most after the analysis. The certainty of a certain clade is placed at its node and given in percent. This number is the percentage of the replicates in which that particular clade appeared and is also called the bootstrap support of the clade. High bootstrap support means that the clade is a winner across our artificial data set.

Reversals or "back-mutations" can remove synapomorphies.

## 3.4 Answering questions with phylogeny

The following examples illustrate some of the problems that phylogeny can help to solve.

• By looking at when body lice evolved from hair

lice one can estimate when humans started wearing clothes (around 107,000 years ago).

- Forensic scientists were able to conclude which patients got HIV from their dentist and which got it else where.
- In his E. coli long-term experimental evolution project (LTEE) Richard Lenski was able to show that the mutation rate in his bacteria evolved.