# Concepts of homology and related terms

Objectives

➢ **Homology**

➢ **Types of homology**

➢ **Analogy**

➢ **Homology vs similarity**

Homology

- Richard Owen's original definition of homology (1843): "***the same organ in different animals under every variety of form and function***."

- Homologies are traits present in two or more organisms that were inherited from the common ancestor of those organisms. The human five-fingered hand and the five-toed foot of a lizard, for example, were both inherited from our common ancestor that lived more than 300 Mya.
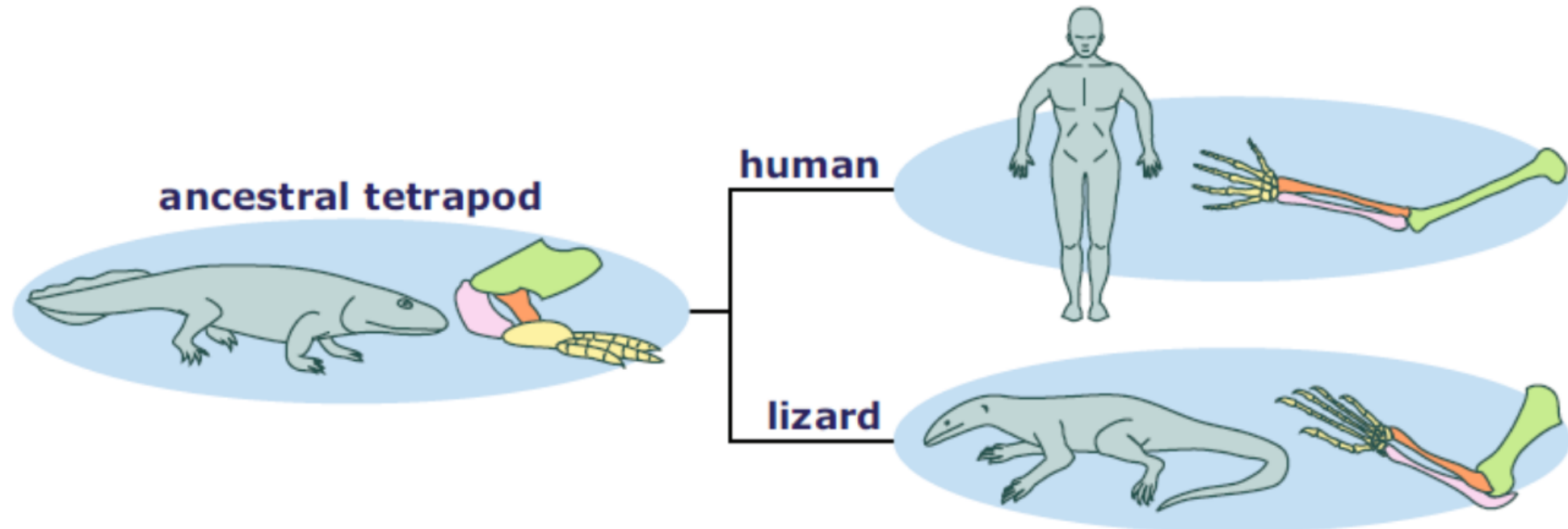
Homology

- Homology is the **study of similarities between organisms to determine common ancestors** based on **genes, physiology or development**. The structures or genes that fall under homology are referred to as being **homologous**.

Bat wing

Bird wing

Bones shown in the same color are homologous.

Human

Bat
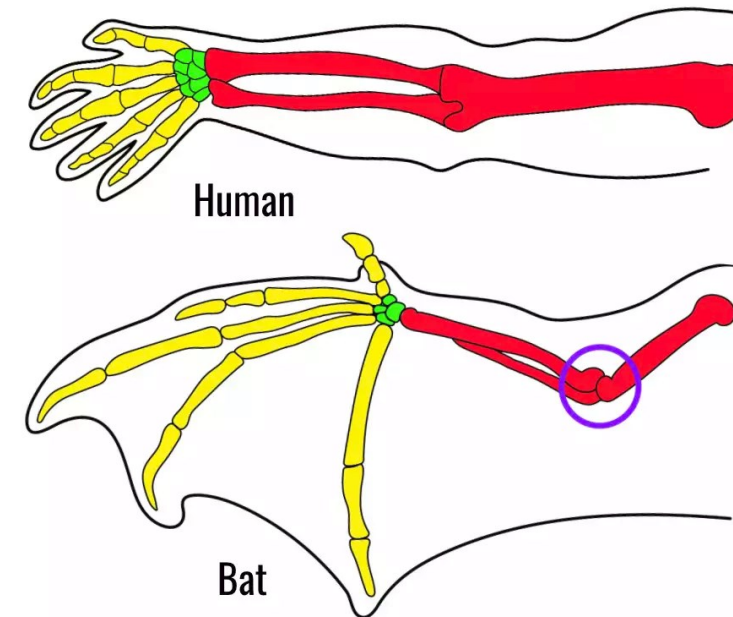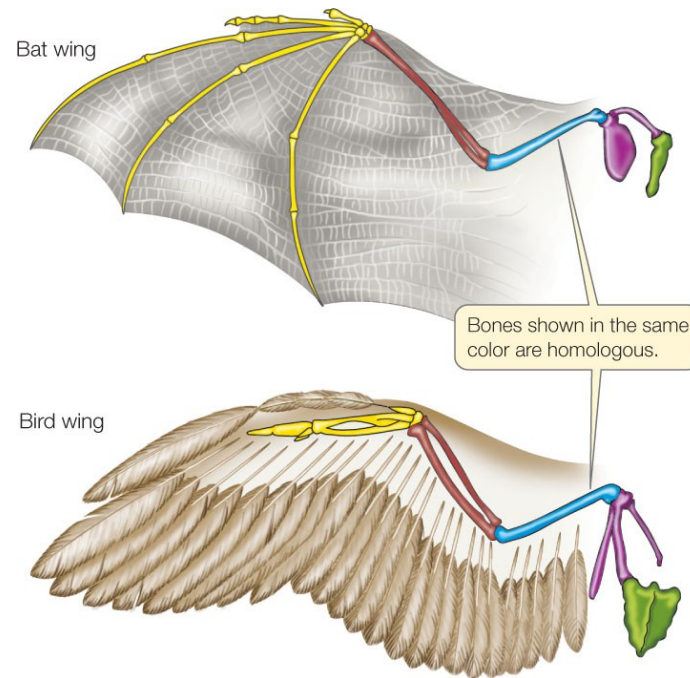
- **The bones are homologous, the wings are not:** These forelimbs originate from a common ancestor and are thus homologous structures. On the functional level, however, birds' and bats' wings are not homologous because both species have independently evolved to fly.

Homoplasy

What is Homoplasy?

The counterpart of homology is usually considered to be homoplasy.

A homoplasious trait is a similarity among organisms that was not inherited from the common ancestor of those organisms.
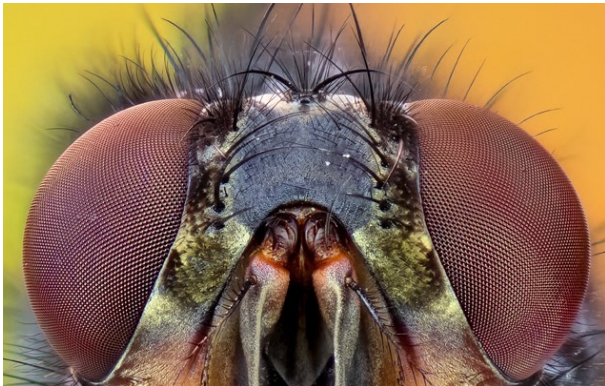
Homology

Homologies at many levels

Though we tend to think of homologies in terms of anatomy (e.g., the tetrapod limb, insect wing, or vertebrate eye), any heritable trait—anything that can be directly or indirectly encoded in DNA—can be a homology.

1. **Which organisms are being compared?** The complex lens eye is homologous among humans, lizards, and fish, but the same trait is homoplasious between humans and squid, having evolved independently in vertebrates and mollusks. Simply identifying a trait as homologous or homoplasious is meaningless unless we know which lineages are being considered.

2. **What specific aspect of the trait is being compared?** Taking another example from eye evolution, we need to know whether we are considering the entirety of a complex structure (e.g., a lens-type eye), the lens itself, the proteins that make up that lens, the genes that encode those proteins, or the genetic triggers that cause those genes to be turned on in developing eyes. Each aspect of this trait may have a slightly different evolutionary story. Vertebrates, for example, have homologous, lens-based eyes, though some of the crystallin proteins that make up those lenses exhibit homoplasy. Different proteins have been recruited at different points in our evolutionary history to build vertebrate lenses.

3. **Does the function of the trait matter?** To make matters even more complex, analyses of homology may also need to consider the function of the trait. Zeta-crystallin provides a striking example. This molecule is present in modern llamas and guinea pigs—and appears to have been inherited from their common ancestor, making the molecule itself homologous in these two groups. However, in that ancient common ancestor, zeta-crystallin likely performed the job of catalyzing chemical reactions and did not form part of the lens, as it now does in llamas and guinea pigs—making zetacrystallin homoplasious as a lens component in these two groups.

Homology

Relation with Gene

Homology

What are the types of homology?

| Type		Description
Orthologs		Genes that diverged by speciation are orthologous. They may or may not have the same function.
Paralogs		Genes that originate from an ancestral duplication and reside within the same species are paralogous.
	In-paralogs (symparalogs)	A subtype of paralogs. Genes that have duplicated **after** the last speciation event are in-paralogs.
	Out-paralogs (alloparalogs)	A subtype of paralogs. These are genes that duplicated **before** the latest speciation event.
	Ohnologs	A subtype of paralogs. A whole-genome duplication results in ohnologous genes. They have a common origin and have diverged an identical length of time.
Xenologs		A transfer of genes, by means other than direct decent from parents to offsprings from one organism to another, results in xenologous genes.
	Homoeologs	A subtype of xenologs. The hybridization of genes from two separate species produces Homoeologous genes.

Homology

1. Orthologs: B_1-B_2, A_1-A_2 and A_{1b}-A_2 are orthologous genes. The genes A_1 and A_{1b} are co-orthologous with A_2.

2. Paralogs: A-B.

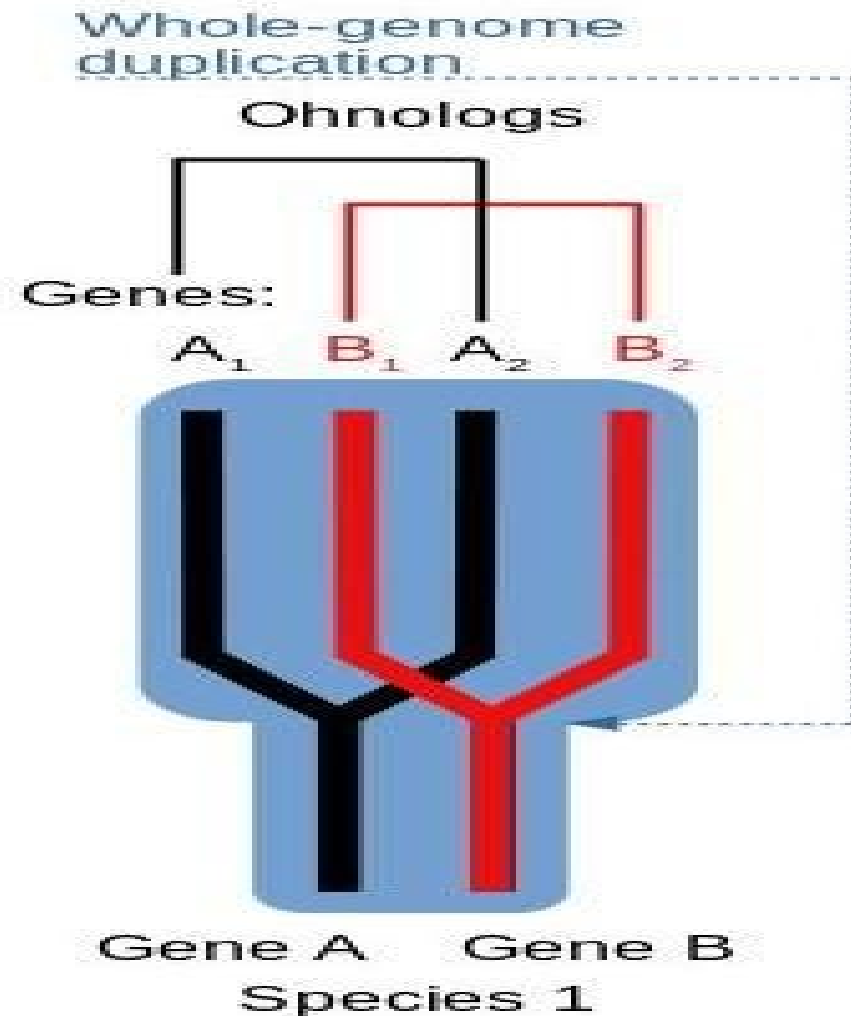   2.1 In-paralogs (symparalogs, duplicated after last speciation): A_1-A_{1b}.

        2.2 Out-paralogs (alloparalogs, duplicated before last speciation): A_1-B_1, A_{1b}-B_1 and A_2-B_2.
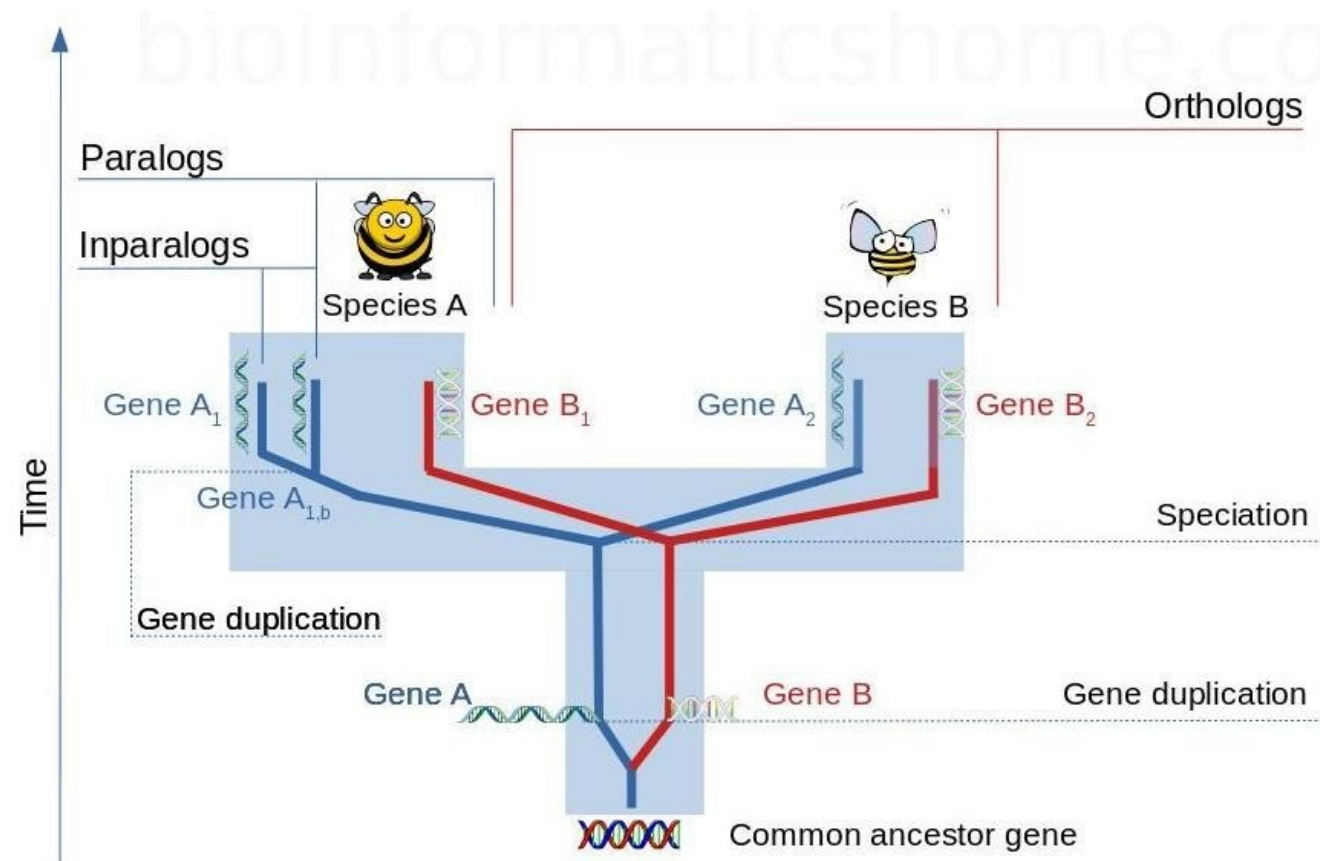
Homology

2.3 Ohnologs (duplication of whole genome): The third subtype of paralogs. These are genes that are a result of a duplication of a whole genome.

Homology

3. Xenologs (Lateral or horizontal gene transfer):

- A transfer of genes from one organism to another, unrelated, organism results in xenologous genes. This process is known as lateral (horizontal) gene transfer. Lateral gene transfer can occur among unrelated organisms, differing from the vertical gene transfer in which gene transfer is from parents to offsprings.

- Notably, bacteria transfer genetic material among themselves to gain antibiotic resistance or virulence. Lateral gene transfer is the major contributor to disease outbreaks and the rise of hyper-virulent human pathogens.
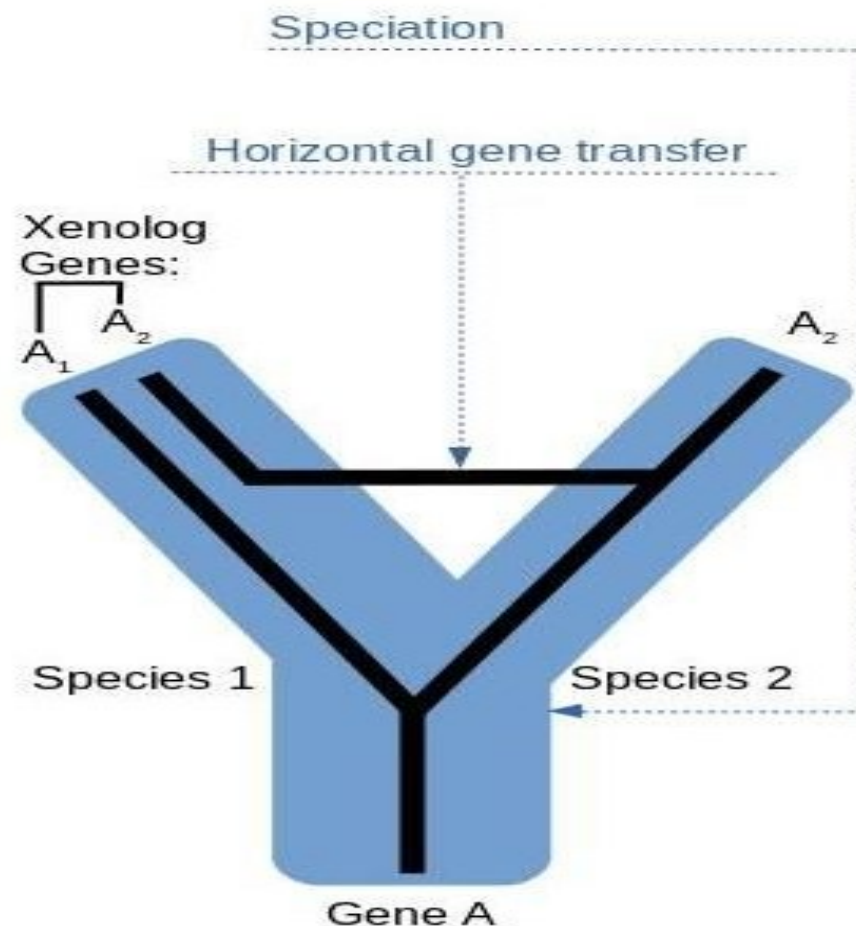
- However, lateral gene transfer is not limited to bacteria. It can occur between, and among, various organisms. For example, bacteria to fungi, plants, insects, and animals, plant to plant, plants to animals, fungi to insects, are a few known cases, but there are many other.

Homology

3.1 Homoeologs: The hybridization of genes from two separate species produces Homoeologous genes. These are genes that a speciation event has separated. When hybridized together, they are homoeologs.
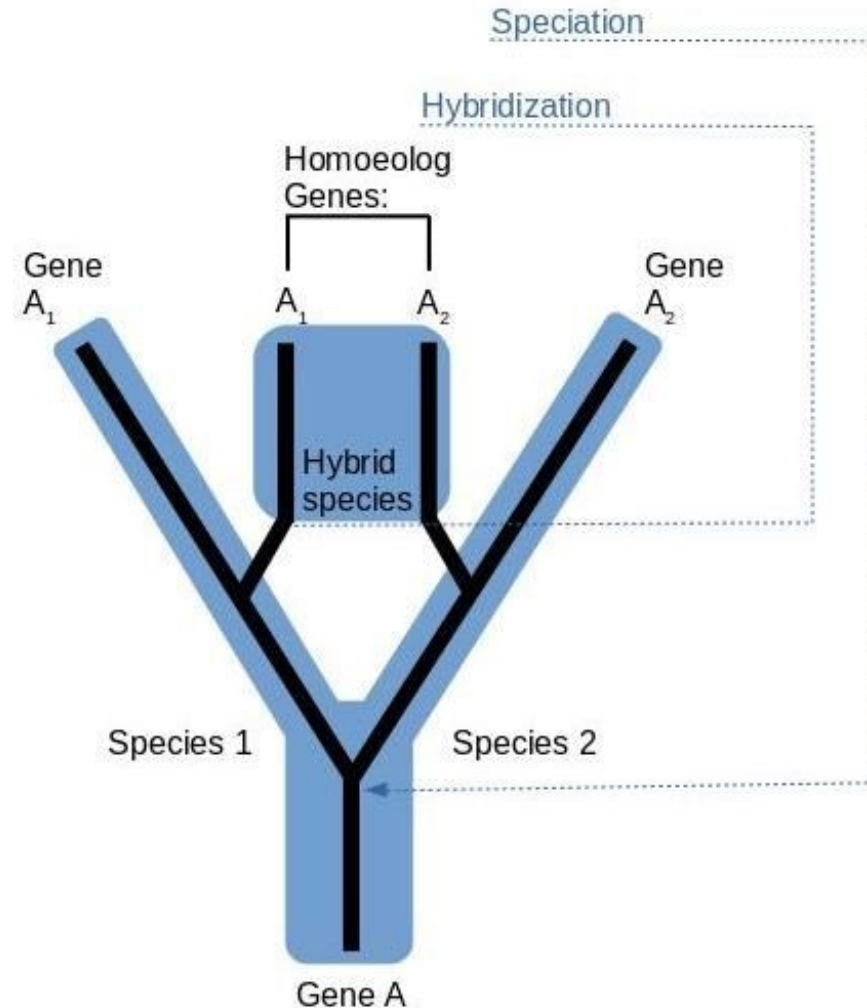
Homology vs Homoplasy

The similarity among structures may be due to
(1) common ancestry (which is homology)
(2) convergent evolution,
(3) parallel evolution,
(4) reversals or unknown random events.

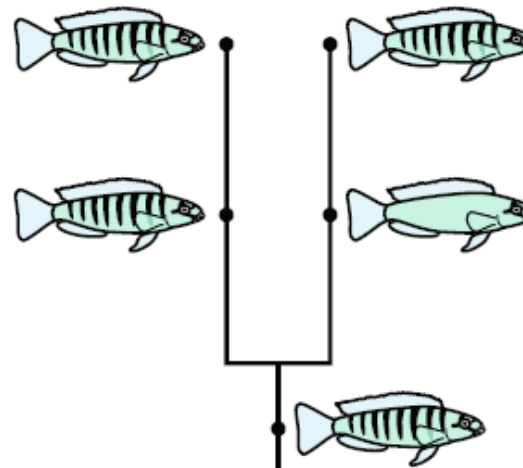The similarity of structures or functions caused by other reasons than common lineage is homoplasmious.

Consequently, the degree of similarity is useful for hypothesis generation but not alone enough to define a homology.
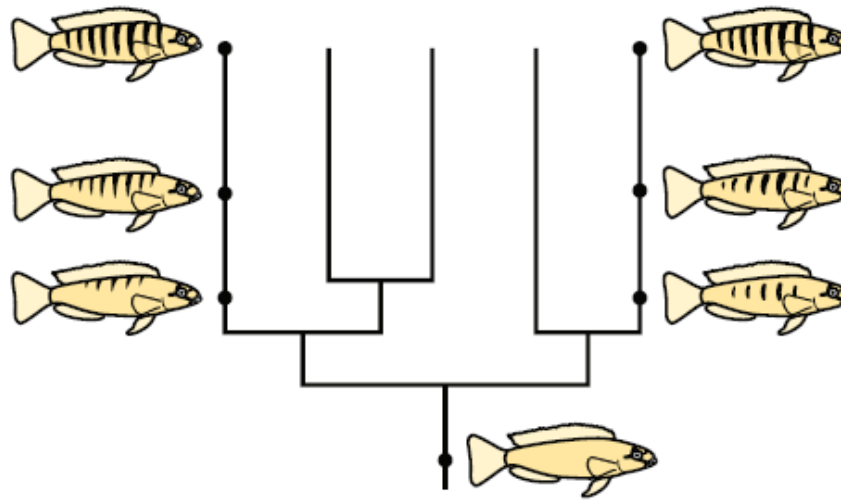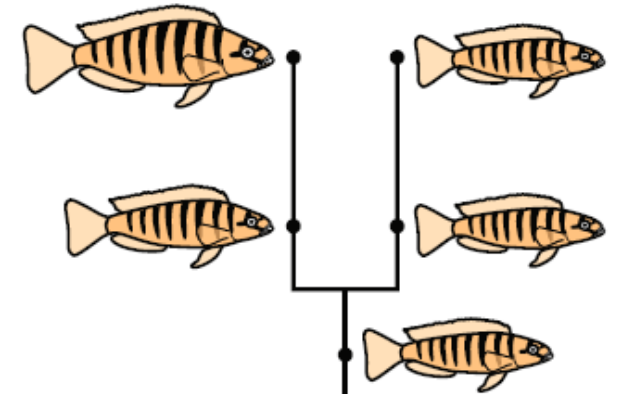

a convergent evolution
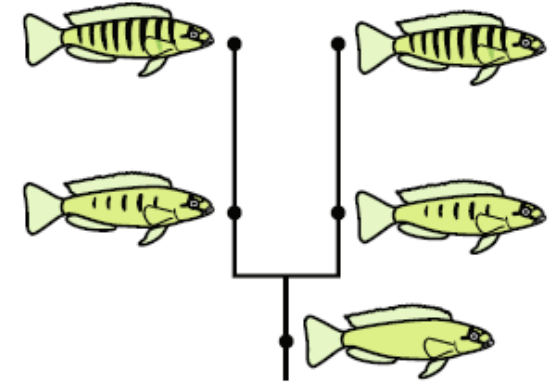
b parallel evolution

**c** evolutionary reversal

d homology

Homology vs Analogy

What is Analogy?

- Analogies, on the other hand, are similar traits that evolved through convergent evolution.

- Analogous genes are genes that have identical or similar function but don't share a common ancestor and are therefore unrelated as opposed to homologous genes. The main processes that result in analogous genes or structures are **convergent evolution**, **parallel evolution** and reversals.

Homology vs Analogy
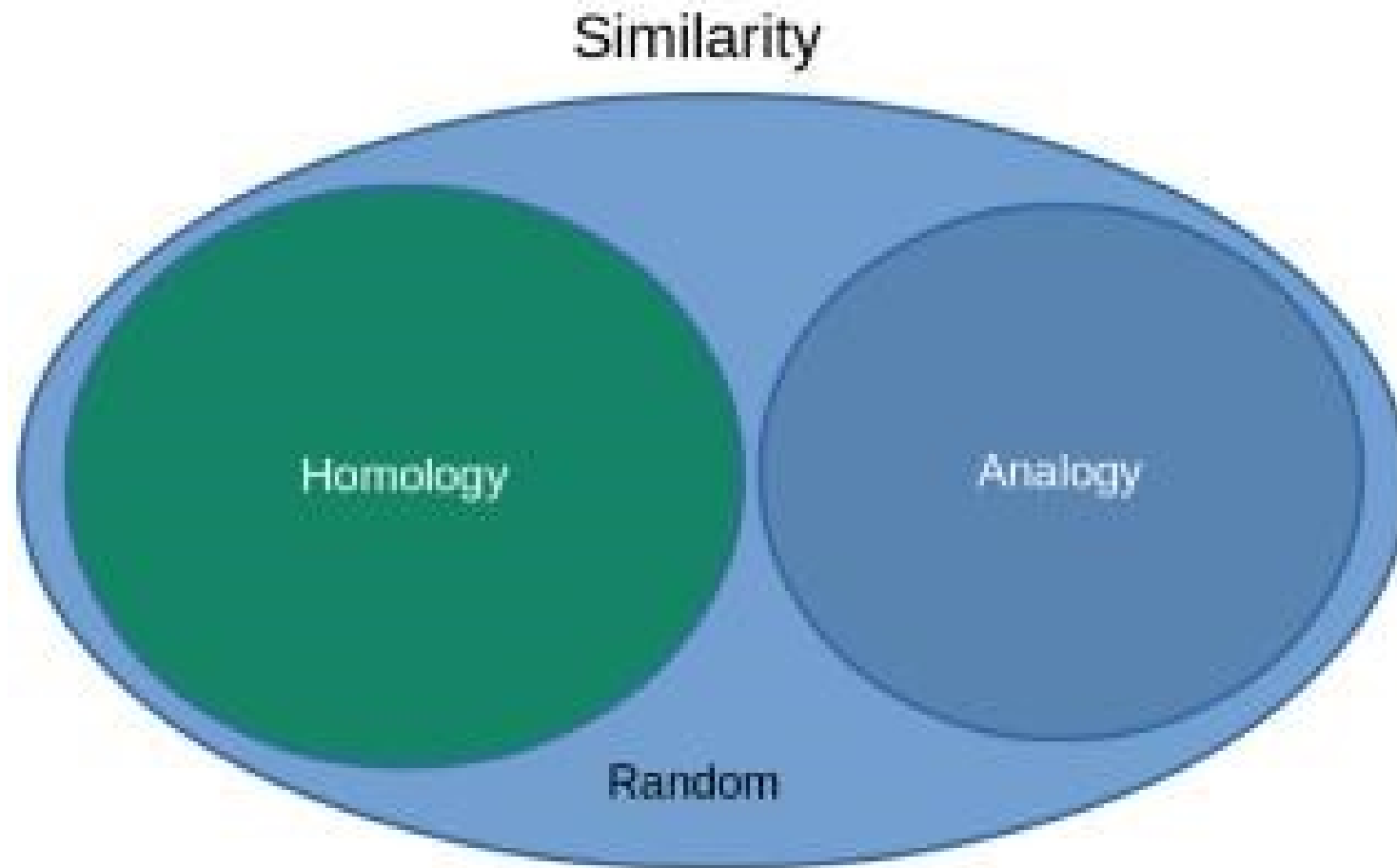
Processes resulting in homoplasious genes

1. Convergent evolution
- When two unrelated species over time develop similar structures or genes, we collectively name the processes as convergent evolution. At the genetic level of the hierarchy, we can classify the convergent evolution into *independent* and *collateral genetic evolution*.

1.1 Independent evolution: When unrelated mutations occur in separate populations or species, we name the processes as *independent evolution.*

Bat wing

Bones shown in the same color are homologous.

Bird wing
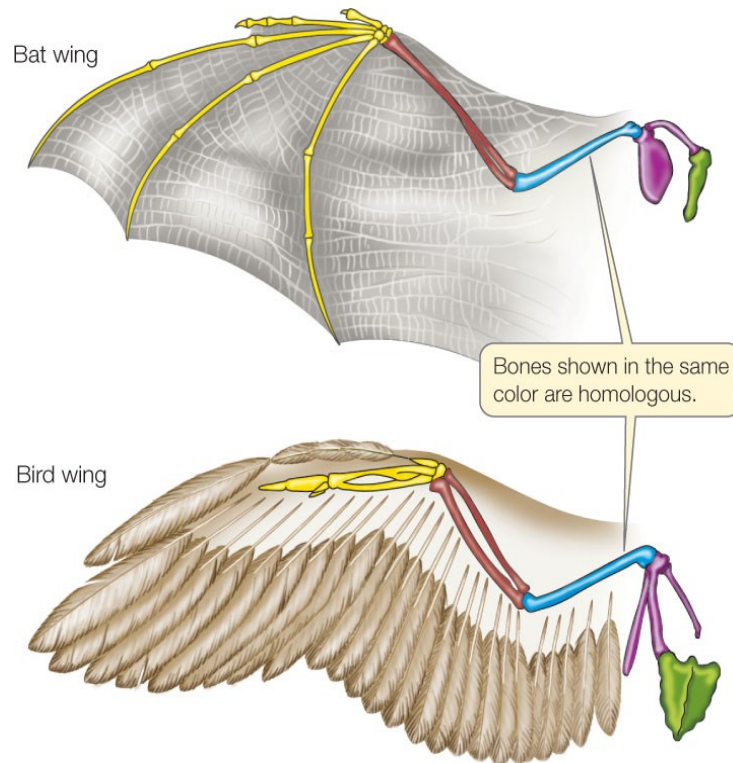
Processes resulting in homoplasious genes

1.2 Collateral evolution*: Collateral evolution* can occur by (1) a selection of polymorphic alleles that exist in an ancestral population, or by (2) hybridization of genetic material between two divergent populations or species.

A. jamaicensis

A. planirostris

Unknown

Artibeus schwartzi

Processes resulting in homoplasious genes

2. Parallel evolution

- In theory, parallel evolution is the **development of identical or similar traits in separate species**; Thus, the resulting characteristics are **analogous**.
- In practice, *parallel evolution* is difficult to distinguish from *collateral evolution by shared ancestry*. One way is to examine the ancestors of each species and see if they share a similar trait. If ancestors lack the feature, we hypothesize that evolution is *parallel*, otherwise *collateral evolution by shared ancestry.*
- Only in the *parallel evolution* process, the result is *analogous* genes, structures, and traits, and *collateral evolution by shared ancestry* produces homologs.
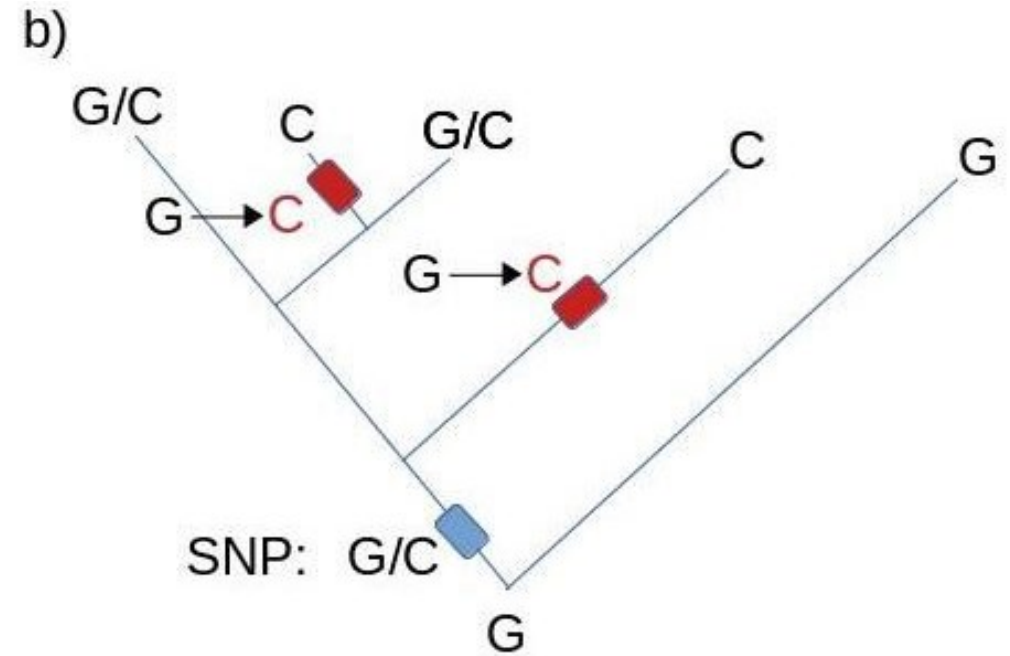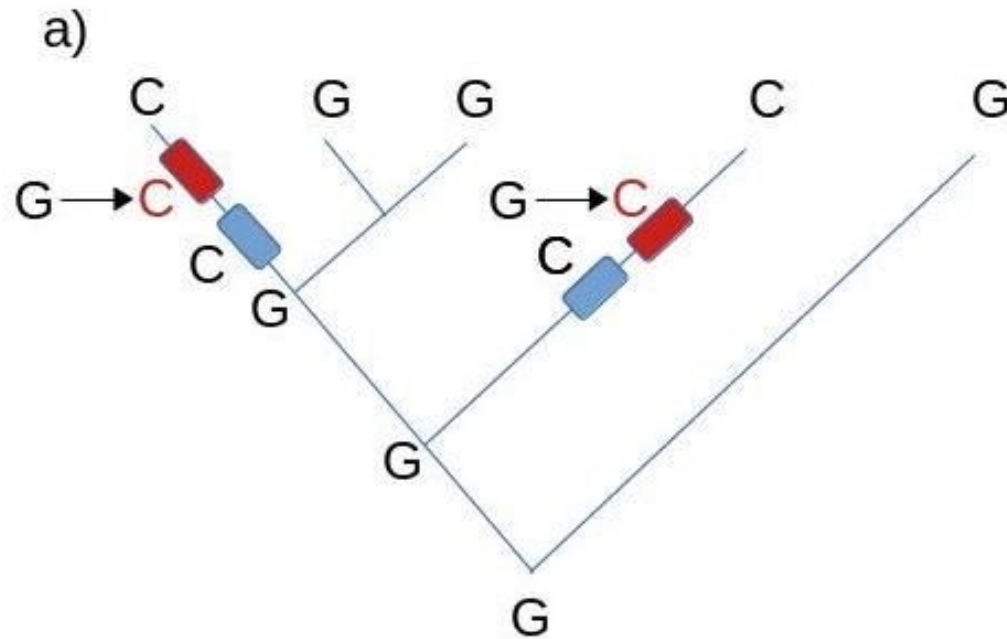
a) The ancestral state G evolved into two separate progenitors, G. The blue rectangles represent the original G alleles, and the red boxes illustrate substitutions of G into C alleles. b) In collateral evolution by shared ancestry, a mutation has occurred (blue box). This mutation is later taken up by several descendants (red boxes).

Processes resulting in homoplasious genes

2. Parallel evolution

Monarch butterfly caterpillar
(***Danaus plexippus***)

Red milkweed beetle
(***Tetraopes tetrophthalmus***)

**Oleander aphids**
(***Aphis nerii***)

Large milkweed bug
(***Oncopeltus fasciatus***)

Homology and Similarity

MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAIPDIARHTLHINLSAGLEPVAAECLAKMSRLFDLQCN
PQIVNGALGRLGAARPGLRLPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQRLAAADPQALKALGM
PLKRAEALIHLANAALEGTLPMTIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQAKDVFLPDDYLIKQRFPGMTPAQIRRYAERWK
PWRSYALLHIWYTEGWQPDEA

GSEGHRTLASTPALWASIPCPRSELRLDLVLPSGQSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCTVYRGDKSQASRPTPDELE
AVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLLRQDPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFP
SLQALAGPEVEAHLRKLGLGYRARYVSASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTQVADCICLMALDKPQAVPVDV
HMWHIAQRDYSWHPTTSQAKGPSPQTNKELGNFFRSLWGPYAGWAQAVLFSADLRQ
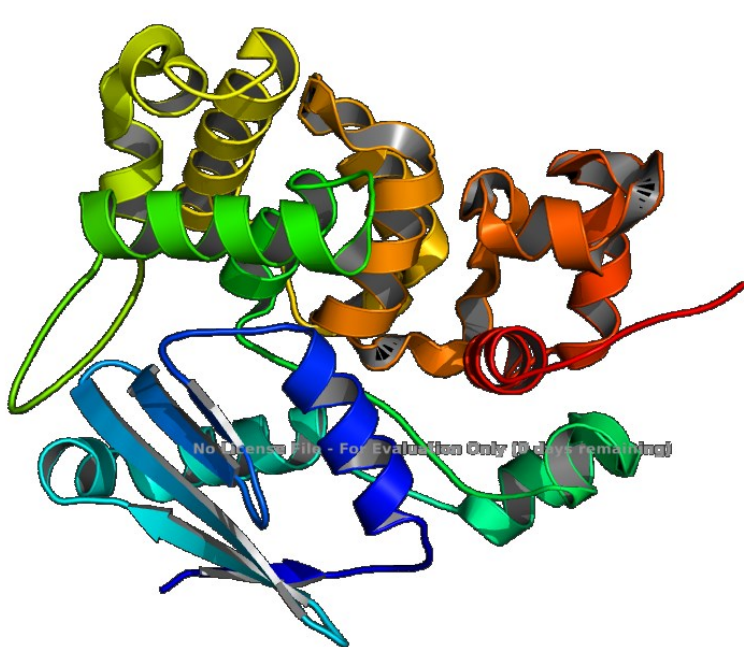
Homology and Similarity

Score	Expect	Method	Identities	Positives	Gaps
32.3 bits(72)	7e-06	Compositional matrix adjust.	34/108(31%)	48/108(44%)	11/108(10%)

```
Query  127  SVAMAAKLTARVAQLYGERL---DDFPEYICFPTPQRLAAADPQA-LKALGMPLKRAEAL  182
            ++A    +  R+ Q +G RL   DD   Y  FP+ Q LA  + +A L+ LG+   RA  +
Sbjct  143  NIARITGMVERLCQAFGPRLIQLDDV-TYHGFPSLQALAGPEVEAHLRKLGLGY-RARYV  200

Query  183  IHLANAALEGT-----LPMTIPGDVEQAMKTLQTFPGIGRWTANYFAL  225
             A A LE          L        E+A K L   PG+G   A+   L
Sbjct  201  SASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTQVADCICL  248
```


E. coli 3-Methyladenine DNA Glycosylase (ALKA)
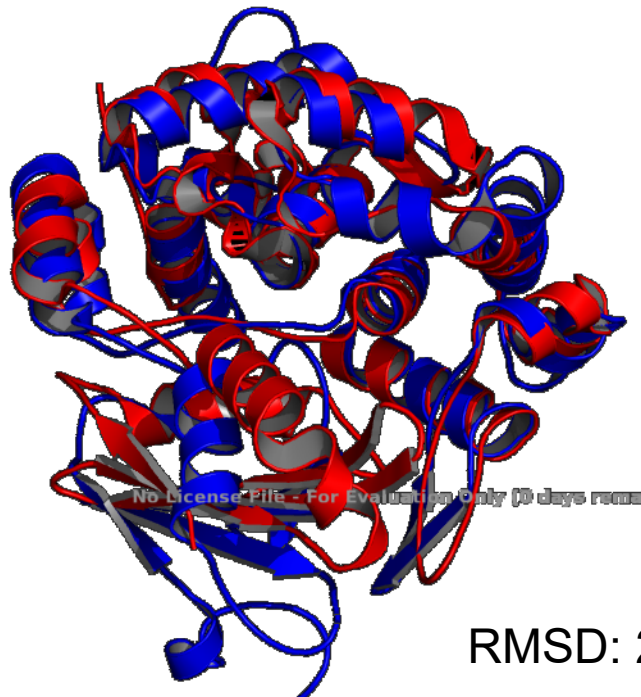
Human 8-Oxoguanine Glycosylase (HOGG1)

RMSD: 2.089 Å

Significance of alignments

GTCC**T**CATAAC**T**CTCTCTAG
||| | ||||| || | || || |||
GTC**G**TCATAAC-CTCTCTAG

- How can we know that sequences are homologous? Homology means that a common ancestor is assumed.

- Even random sequences may reach a high score when aligned optimally, so when is a sequence alignment significant? [This will be discussed later].
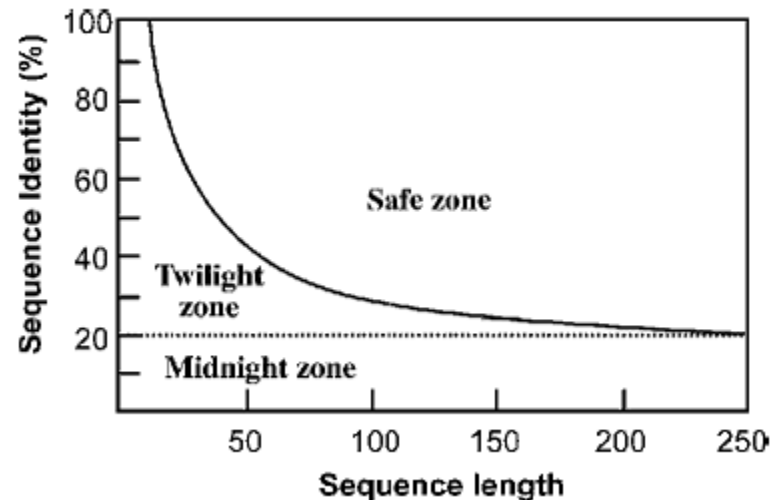
Homology and Similarity

Homology: Statement about common evolutionary ancestry of two sequences. ***Can only be true or false***. We can rarely be certain about this, it is therefore usually a hypothesis that may be more or less probable.

Similarity: Degree of likeness between two sequences, usually expressed as a percentage of similar (or identical) residues over a given length of the alignment. Can usually be easily calculated.

A high degree of similarity implies a high probability of homology
- If two sequences are very similar, the sequences are usually homologous.
- If two sequence are not similar, we don't know if they are homologous.
- If two sequences are not homologous, their sequences are usually not similar (but may be by chance).
- If two sequences are homologous, their sequences may or may not be similar; we don't know.

Thank You