

# BIS101 F2013 Lecture 7:

## Macroevolution and Phylogenetics

### Notes

TEST!!

Halloween!

### Reading

All of Ch. 17. Check syllabus for updates. HW and reading updates as we go along

### Phylogenetics

Study of relationships among genes and species. Important for understanding not just how things are related, but using that information to learn about function, mechanistic basis of function, both of genes and phenotypes.

Go through C4 tree.

Then bat/dolphin. Draw out inference if dolphin/bat closest. One or multiple ?

Then add cow and ask gain vs. loss ?

Then look at real phylogeny. Gain multiple times. So similar or different genetic basis ?

Predict different, but in this case similar. What does that tell you? Limited number of genes that can be changed to gain echolocation. Actually same parts of some of these genes changed in same way!

### Inferring function:

How do we know how much of the genome is functional?

Well, let's look at a gene, makes a transcript, and a protein. Functional ?

Human exome (?) is 100Mb (how much ?). But human genome is ? (3Gb)

What about the rest?

Draw human, chimp, orangutan, cow. Draw a sequence present in only human and one present in all of them. Which more likely to be functional ?

# How to build?

Usually use gene sequences to determine relatedness. For example:

Raccoon

ATGGGA

Bear

ATGGGA

Cat

AACGGT

Mongoose

AACGGA

Platypus

GTCTTA

**Parsimony** (?) method. Method that requires the fewest changes -- the simplest.

Draw one wrong tree. Redraw better tree.

Really people use whole genomes and very complex statistical methods. We will not go into these details.

Draw tree, label nodes. Define **outgroup** allowing you to put an ancestral root on the tree.

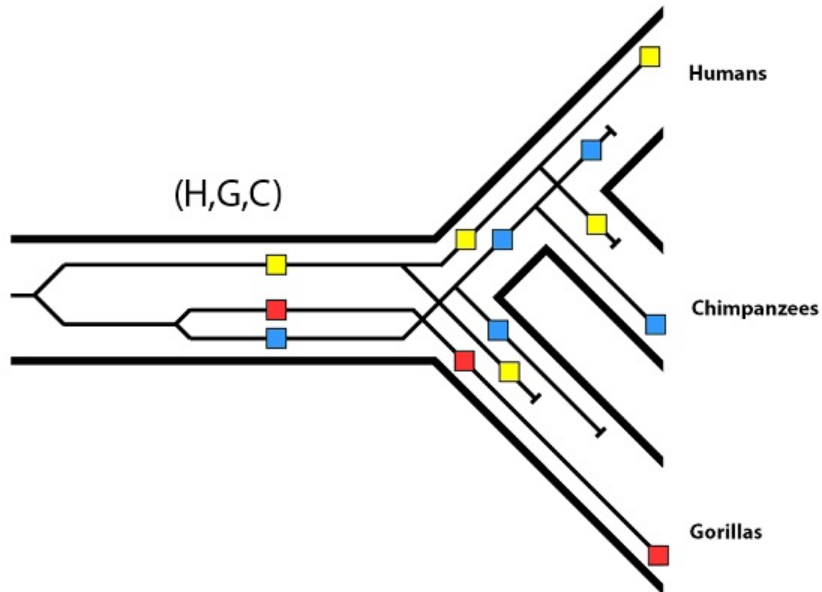
Does this mean platypus is "basal" or "ancestral" to all mammals? No. Explain same distance

## Gene tree vs. species tree

This has assumed all Cats have one sequence. This works for distantly related lineages where all differences are fixed.

But populations are polymorphic for different gene sequences. And multiple alleles segregating.

Draw species tree of humans, chimps, gorillas.



We actually predict this to be common. In fact 25% genes are more related to gorilla than chimp. And 1% closer to orangutan than chimp!

## Gene duplication

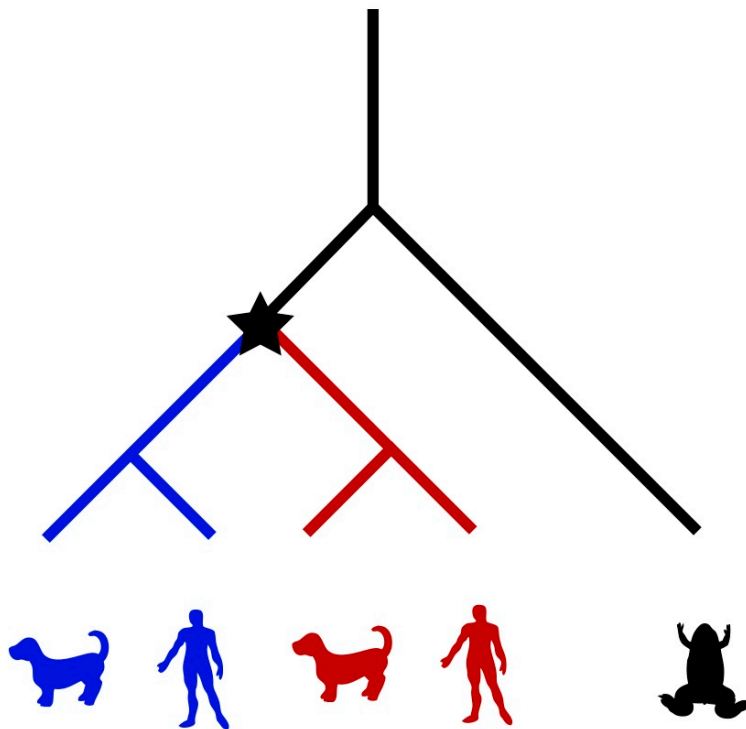
**Homolog** closely related gene.

Genes can be copied and duplicated over time, and gene families can grow and shrink.

This leads to two kinds of homologs.

**ortholog** vs **paralog**

separated by speciation vs. separated by duplication



But draw star earlier. Key to difference is identifying where on tree duplications have occurred. Then just ask how genes are separated by tracing back.

Remove human and ask ortholog/paralog.

Draw genes at tips and at duplication event

define **synteny**

draw how synteny can inform which gene is ortholog.

fates of a new gene duplicate: Subfunctionalization vs. neofunctionalization vs. pseudofunctionalization

what would happen to a pseudogene over time?

## Gene evolution

What will happen to new deleterious mutations ?

**Purifying selection** removes new deleterious mutations. Important genes with functions will be under stronger ? or weaker purifying selection?

How to identify.

Define **nonsynonymous** and **synonymous** changes?

Which is more likely to be functional ?

Which is more likely to be deleterious ?

If both have no effect on function, expect equal proportions of such changes.

Can compare gene sequences along a phylogeny and count nonsyn and syn changes per bp. if  $dN/dS \ll 1$ , constraint! if  $dN/dS \gg 1$ , rapid adaptation!