

## Lecture 16: 1 Nov 2018

**Andrew**

1. (Halfway through lecture) Thylacine vs Wolf skulls
  - (a) How do we deal with convergence?
  - (b) Thylacine have pouches and raise offspring in pouches - conflict in phylogenetic dataset.
  - (c) Thylacine: face says put me near dogs, but pouches say with kangaroos
2. Phylogenetic Reconstruction: metric of distance in two things you're interested in. Distance based approach = phenetics.
  - (a) Phenetics: based on overall similarity (i.e. distance) start with the two most similar taxa and work outwards. Distance between too, or branch length. Can lead to discordance (e.g. stingray). Is dependent on rate constancy (or rate heterogeneity) in evolution. Rate of substitution among sites
  - (b) Overtime, genetic divergence is a function of time since isolation. Mutations accumulate separately in each population.
  - (c) The Molecular Clock: time vs number of amino acid changes per site
  - (d) Different genes tick at different rates. Histones are very slow. Depends on intensity of negative selection acting against mutations in the gene.
  - (e) Can use molecular data - because in a more rate constant way. Morphological information can be misleading.
3. How do we do phylogenetic reconstruction without molecular data?
4. Cladistics:
  - (a) Homology: present from a common ancestor, derived from same source. Forelimb example.
    - i. Derived: changes from common ancestor
    - ii. Ancestral: preserved ancestral state
  - (b) Ancestral character states can be misleading. Can be used on basis of derived character states.
5. Understanding the importance of microbes at a molecular level: history of life is about microbes. We are a tiny twig on enormously complicated tree of life