

Phylogenomics Introduction

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1 Introduction

Looking at relationships between more distance taxa, when they last shared common ancestry and time when they last shared common ancestry. Interested in understanding these things to gain understanding of how traits evolve.

Pseudoreplication sampling many points which aren't independent of each other but treating them as if they were.

Phylogenies work by taking DNA sequences then aligning, look for the shared patterns of base states. Once have branches should be able to add time on branches as can assume that mutations happen at a constant rate. Looking at genes which go to fixation, very few between populations that are different.

2 What we can measure

Most recent common ancestor, time to most recent common ancestor, generate a gene tree from the data, infer degree of evolution by looking at the lengths of the branches. All branches on tree aren't equal length which shows that evolution doesn't always happen at the same rate. 2 things affect rate of evolution: mutation rate and generation time.

Incomplete lineage sorting helps us determine phylogenies. Can get disagreement between lineage of a gene and that of the population.

3 Gene tree vs species tree

Can only measure gene trees and from them want to infer the species trees. Gene trees don't always show the same branching pattern as their species tree which contains them. Short branches are more difficult to resolve,

effective...

Any one gene you look at may be a bad representation of the species tree as a whole, The more independent loci sampled the more the gene tree will approximate the species tree.

4 Divergence times

Need an absolute time to hang on the tree to get an idea of how fast things are happening on the tree. Need some independent bit of information e.g fossil. Also need to know how it links to the tree.

What makes a good fossil calibrator?

Fossils only give some information, only gives a minimum time when divergence could have occurred.