Chipmunks plan!

Two part question:

1. Are there demographic explanations for the introgression/direction of introgression at the sub-species boundaries?

Methods:

Splatche vs continuous?

Is there time scale information on movement in the introgressive boundary?

How old does it seem to be?

What are the historic movement patterns?I am going

2. What are the genomic expectations for patterns of introgression between hybridizing lineages?

- How does linkage lead to the buildup of neutral genetic variation around differentially selected sites?

- How does linkage between selected sites lead to co-adapted gene complexes

Methods:

CoalSim?

Parameters: r, s, m ??? – anything else?

treat linkage groups as linear…

Questions:

What does the transcriptome data look like? 1000 bp?

200-400 bp

How well understood are rec rates in chipmunks.

Advantages of analytic vs. simulation based methods…

How to model recombination…

What if I treat it as blocks, with a certain rec. rate between each…

What are expectations

NOT PURSUING.

3. What about cytonuclear incompatibilies? What if there is recombination in the organellar genomes?

BCA

cecile lenet - gene tree species tree estimation in sysbio online….

Deepest introgression-

Tamias

aminius ruficaudaus

Thinking about differences in patterns of inheritance between different chunks-

I think I should focus on demographic models of mtDNA introgression-

+ maybe cyto nuclear incomp?