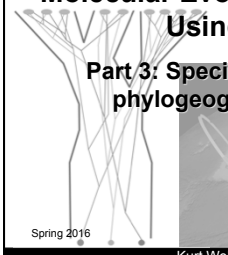
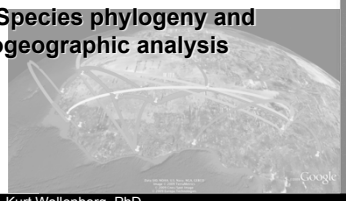
National Institute of Allergy and Infectious Diseases

Molecular Evolutionary Analysis Using BEAST

Part 3: Species phylogeny and phylogeographic analysis





Spring 2016

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Kurt Wollenberg, PhD
Phylogenetics Specialist
Bioinformatics and Computational Biosciences Branch
Office of Cyber Infrastructure and Computational Biology

Course Organization

- Introduction to Bayesian phylogenetics
- Introduction to BEAST
- Building a Bayesian phylogeny
- Incorporating sample time in the phylogeny
- Estimating demographic parameters
- Estimating species trees from gene trees
- Estimating ancestral trait states (esp. geography)

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Lecture Organization

- Gene trees vs. species trees.
- Estimating parameter values at ancestral nodes.
- Incorporating time and location information - Phylogeography
- BEAST Analysis Demo

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Gene trees vs Species trees

- Demographic effects
- Incomplete lineage sorting

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Gene trees vs Species trees

Demographic effects

- Population bottlenecks reduce coalescent intervals.
- Migration of lineages among populations.

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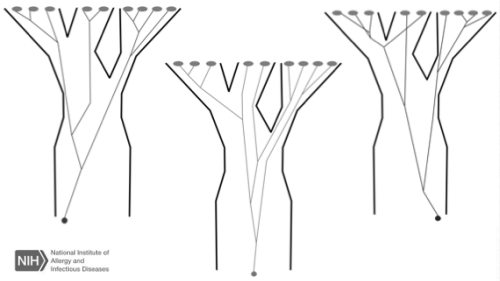
Gene trees vs Species trees

Incomplete lineage sorting



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Running BEAST

DEMO

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Phylogeography

- Bayesian estimation of ancestral states
- Adding location data to the analysis
- Mapping the coalescent phylogeny onto a map.

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Phylogeography

- Discrete diffusion model
  - Location names
- Continuous location estimation
  - Latitude/longitude

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Phylogeography: Import Locations

The Traits File

Traits	Lat	Long
hOH10_97.2	41.053	-80.706
hWVa01_93.2	40.505	-80.575
NY01_03.4	41.057	-73.794
NY03_03.4	42.934	-76.565
NY04_03.4	42.617	-75.037
NY12_03.4	42.996	-78.170
NY516_92.5	42.137	-75.888
NY771_92.5	41.125	-74.015
PA.R89_89.6	40.803	-75.031
PA11_04.7	40.033	-78.480
PA13_04.7	40.871	-79.930

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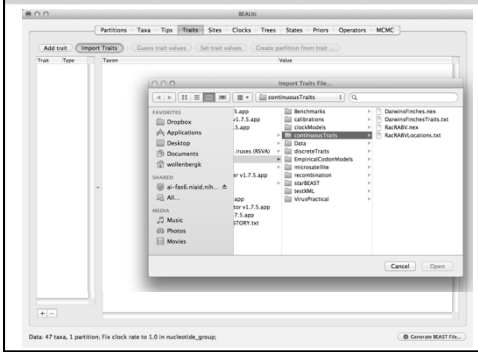
Phylogeography: Import Locations



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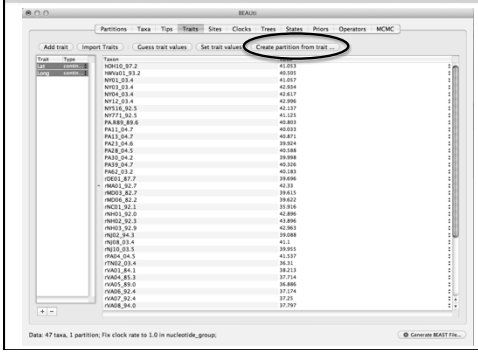
Phylogeography: Import Locations



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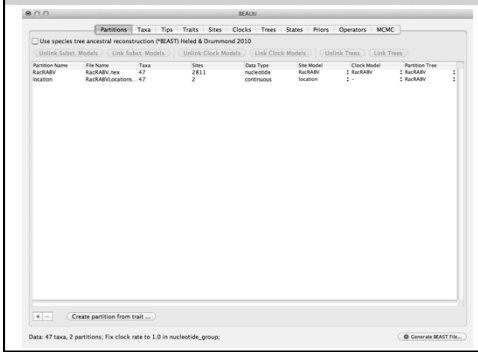
Phylogeography: Import Locations



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Phylogeography

SPREAD

Spatial **P**hylogenetic **R**econstruction of **E**volution**A**ry **D**ynamics

- Separate, stand-alone software
- Permits visualization of Bayesian phylogeographic analysis results
  - Can output KML files for use in Google Earth.

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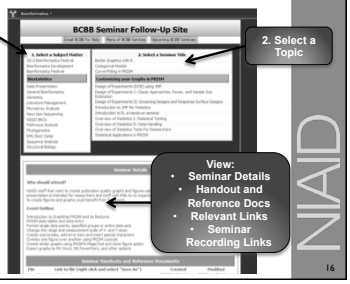
Seminar Follow-Up Site

- For access to past recordings, handouts, slides visit this site from the NIH network: http://collab.niaid.nih.gov/sites/research/SIG/Bioinformatics/



Recommended Browsers:
- IE for Windows,
- Safari for Mac (Firefox on a Mac is incompatible with NIH Authentication technology)

Login
- If prompted to log in use "NIH\" in front of your username

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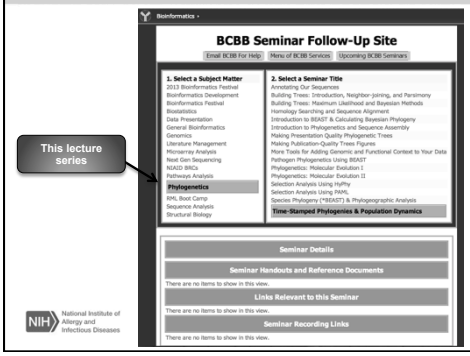
Retrieving Slides/Handouts



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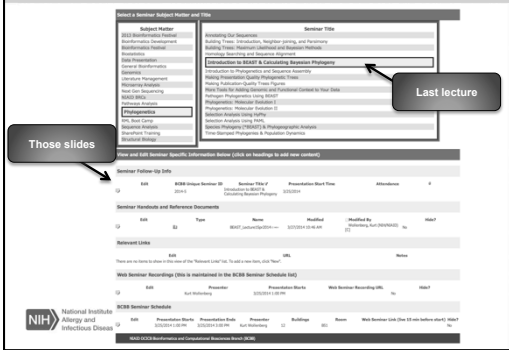
Retrieving Slides/Handouts



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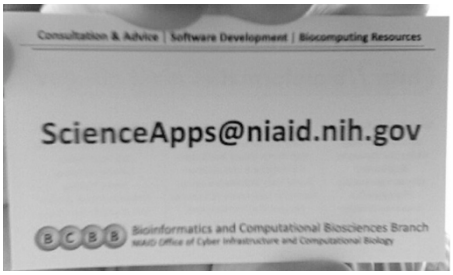
Questions?



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Thank you

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