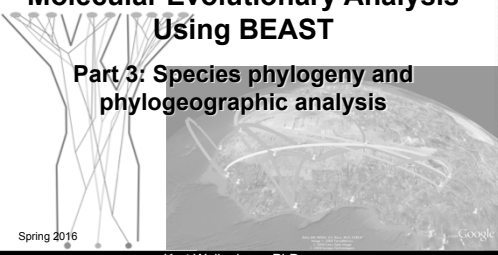


National Institute of Allergy and Infectious Diseases

## Molecular Evolutionary Analysis Using BEAST


### Part 3: Species phylogeny and phylogeographic analysis

Spring 2016



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Bioinformatics and Computational Biosciences Branch  
Office of Cyber Infrastructure and Computational Biology

 National Institute of Allergy and Infectious Diseases

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## 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

The screenshot shows the BEAST software interface. The 'Import Traits' dialog is open, displaying a file explorer window. The file explorer shows a directory structure with folders like 'Desktop', 'Documents', and 'Downloads'. A file named 'continuousTraits' is selected in the 'Downloads' folder. The BEAST interface shows various tabs like 'Partitions', 'Trees', 'States', etc.

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### Phylogeography: Import Locations

The screenshot shows the BEAST software interface. The 'Create partitions from trait...' dialog box is open, showing a list of traits and their corresponding values. The list includes traits like 'hOH10\_97.2', 'hWVa01\_93.2', 'NY01\_03.4', etc., with values ranging from 41.053 to 42.996. The dialog also shows a 'Clock rate' of 1.0 and a 'Nucleotide group' of 'GTR+I+G4'. The BEAST interface shows various tabs like 'Partitions', 'Trees', 'States', etc.

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### Phylogeography: Import Locations

Partition Name	File Name	Type	Sites	Data Type	Site Model	Clock Model	Partition Type
RAxML	RAxMLData_47	47	2811	nucleotide	RAxML	1 RAxML	1 RAxML
Locations	RAxMLLocations_47	47	2	continuous	location	1 RAxML	2 RAxML

Data: 47 taxa, 2 partitions. Fix clock rate to 1.0 in nucleotide\_group. © Copyright BEAST File...

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### Phylogeography

#### SPREAD

Spatial Phylogenetic Reconstruction of Evolutionary Dynamics

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

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### Running BEAST

## DEMO

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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/): <http://collab.niaid.nih.gov/sites/research/SIG/Bioinformatics/>

**1. Select a Subject Matter**

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

**2. Select a Topic**

**View:**

- Seminar Details
- Handout and Reference Docs
- Relevant Links
- Seminar Recording Links

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## Retrieving Slides/Handouts

**This lecture series**

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## Retrieving Slides/Handouts

**Those slides**

**Last lecture**

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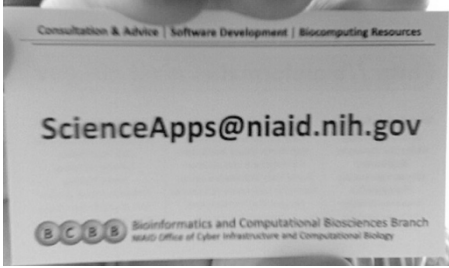
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**Questions?**



Consultation & Advice | Software Development | Biocomputing Resources

**ScienceApps@niaid.nih.gov**

BCBB Bioinformatics and Computational Biosciences Branch  
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**Thank you**



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