

National Institute of Allergy and Infectious Diseases


**Phylogenetics and Sequence Analysis**

**Lecture 5**

**Making Publication-Quality Tree Figures**

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

Fall 2015



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**Course Organization**

- Building a clean sequence
- Collecting homologs
- Aligning your sequences
- Building trees
- **Further Analysis**



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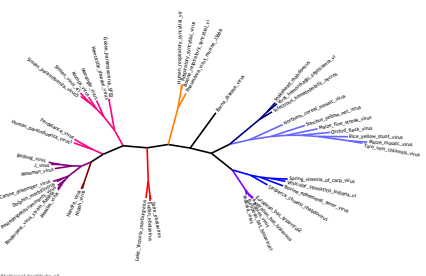
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**Making publication-quality tree figures**



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## Lecture Organization

- Review: what is a tree?
- Tree file formats: Newick and Nexus
- Graphics file formats
- FigTree, Dendroscope
- iTOL
- Inkscape



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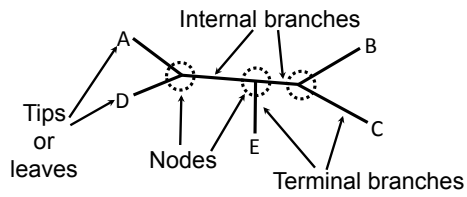
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## What is a phylogenetic tree?



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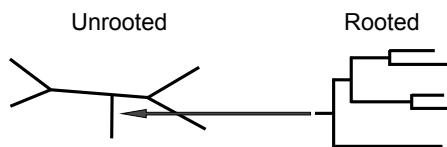
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## What is a phylogenetic tree?



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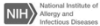

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### Phylogenetic tree file formats

- Newick format - PHYLIP
- Nexus format – PAUP\*, MrBayes, BEAST


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### Phylogenetic tree file: Newick

#### PHYLIP

```

9 1
(((ILlArhesus:0.02931,ILlAhuman:0.02931):0.09645,
(ILlAdog:0.05607,ILlAcat:0.05607):0.04686,(((ILlAsheep:
0.01216,ILlAcow:0.01216):0.06007,ILlApig,0.07223):
0.00147,ILlAhorse:0.07370):0.02282):0.08661,ILlAarat:
0.21237);
    
```


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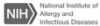

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### Phylogenetic tree file: Nexus (MrBayes)

```

#NEXUS
[ID: 8724605752]
begin trees;
[Note: This tree contains information on the topology, branch lengths
(if present), and the probability of the partition indicated by the
branch.]
tree con_50_majrule = (ILlAhuman:0.022432,(ILlArhesus:0.008931,ILlAmangabey:
0.022870)1.00:0.030817,((((ILlAcow:0.003160,ILlAwaterbuffalo:
0.018619)1.00:0.007481,(ILlAsheep:0.007825,ILlAgoat:
0.007331)1.00:0.011332)1.00:0.046620,ILlAllama:0.041926)1.00:0.014634,(ILlApig:
0.071037,ILlAdolphin:0.098194)0.74:0.006705)1.00:0.022253,ILlAhorse:
0.063677)0.85:0.010744,(ILlAcat:0.055612,ILlAdog:
0.058409)1.00:0.058163)1.00:0.029893,(ILlAarat:0.262258,ILlArabbit:
0.146540)0.97:0.025183)1.00:0.094752);
[Note: This tree contains information only on the topology
and branch lengths (mean of the posterior probability density).]
tree con_50_majrule = (ILlAhuman:0.022432,(ILlArhesus:0.008931,ILlAmangabey:
0.022870):0.030817,((((ILlAcow:0.003160,ILlAwaterbuffalo:0.018619):0.007481,
(ILlAsheep:0.007825,ILlAgoat:0.007331):0.011332):0.046620,ILlAllama:0.041926):
0.014634,(ILlApig:0.071037,ILlAdolphin:0.098194):0.006705):0.022253,ILlAhorse:
0.063677):0.010744,(ILlAcat:0.055612,ILlAdog:0.058409):0.058163):0.029893,(ILlAarat:
0.262258,ILlArabbit:0.146540):0.025183):0.094752);
end;
    
```


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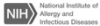

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### Phylogenetic tree file: Nexus (BEAST)

```

#NEXUS
Begin taxa;
  Dimensions ntax=50;
  Taxlabels
  SWIP      'A/Beijing/01/2009_135_2009_37'
           'A/Zhejiang/1/2009_143_2009_392'
  ;
End;
Begin trees;
  Translate
  SWIP      1 'A/Beijing/01/2009_135_2009_37',
           50 'A/Zhejiang/1/2009_143_2009_392'
  ;
tree TREE1 = [&#x27;&#x27;(((49[rate_range=(3.65693396208952E-10,2.5712819974047436E-5),
height_951_HPD=(0.1149999999999999,0.1150000000000000), SWIP ],
18[rate_range=(9.44777643108012E-11,1.8901175119338495E-5), SWIP ]);
353.789381869338997,
SWIP
height_range=(40.25394728353271,2270915.338655316),length=0.0);
End;

```


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### Graphics File Formats

pdf: Portable Document Format

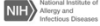

- Very portable and editable

png: Portable Network Graphics

- Portable and editable
- Format of Macintosh screen shots

svg: Scalable Vector Graphics

- Easily editable
- Can't be imported into PowerPoint


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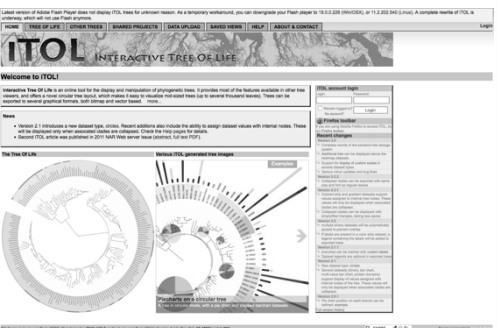


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### Making a Tree Figure: iTOL


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### Making a Tree Figure: FigTree



Latest Version - v1.4

<http://tree.bio.ed.ac.uk/software/figtree/>

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### Making a Tree Figure: Dendroscope

Dendroscope  
Software for visualizing phylogenetic trees and rooted networks.

- Download Dendroscope 3 [here](#).
- See our [book on phylogenetic trees and networks...](#)




### Dendroscope 3

by Daniel H. Huson  
with contributions from Benjamin Albrecht, Philippe Gambette, Leo van Iersel, Celine Scornavacca and others.

[www.ab.informatik.uni-tuebingen.de/software/dendroscope](http://www.ab.informatik.uni-tuebingen.de/software/dendroscope)

Dendroscope 3 - An interactive viewer for rooted phylogenetic trees and networks

<http://ab.inf.uni-tuebingen.de/software/dendroscope/welcome.html>

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### Editing a Tree Figure: Inkscape



<http://inkscape.org>

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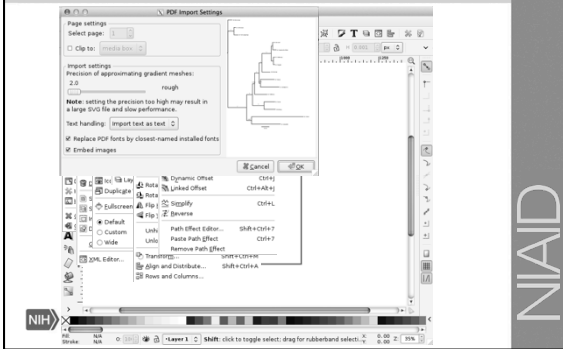
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### Editing a Tree Figure: Inkscape



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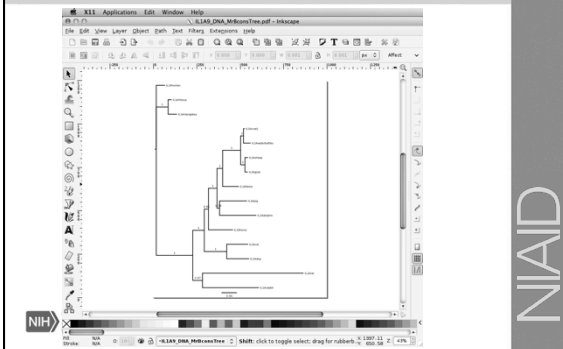
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### Editing a Tree Figure: Inkscape



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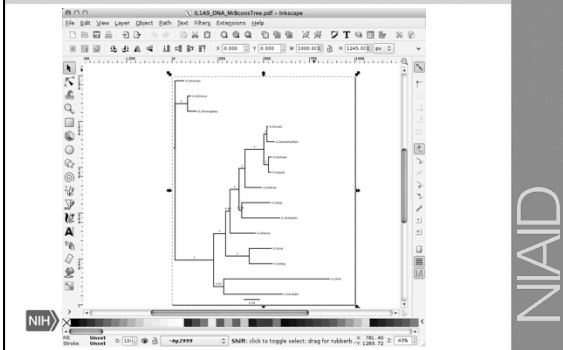
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### Editing a Tree Figure: Inkscape



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### Editing a Tree Figure: Inkscape

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### Editing a Tree Figure: Inkscape

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### Editing a Tree Figure: Inkscape

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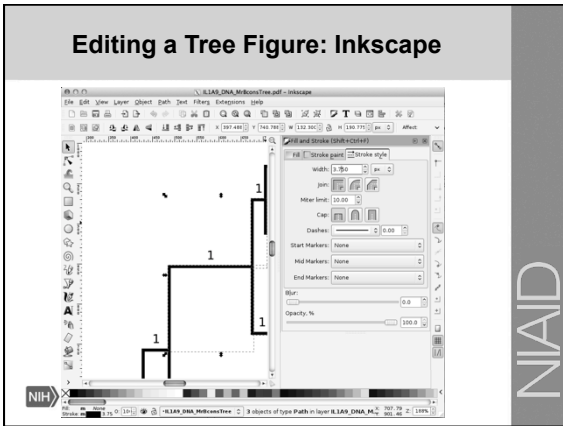
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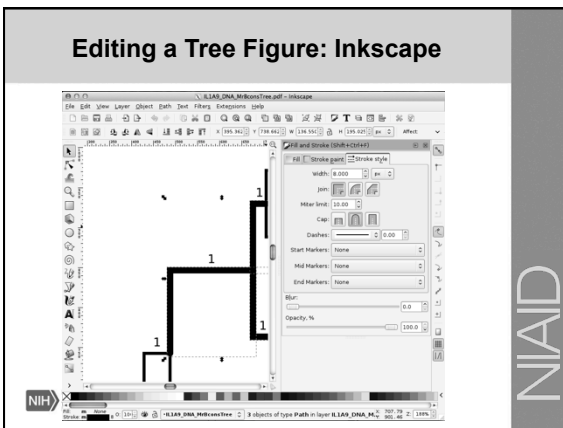
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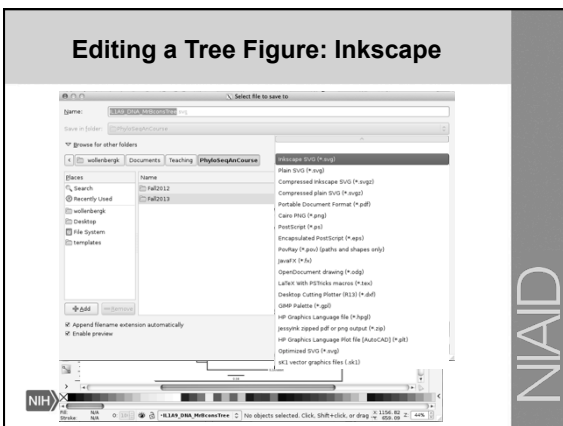
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## Seminar Follow-Up Site

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

**This file**

**This lecture**

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## Questions?

Consultation & Advice | Software Development | Bioinformatics Resources

**ScienceApps@niaid.nih.gov**

**BCCBB** Bioinformatics and Computational Biosciences Branch  
NIH/OD Office of Cyber Infrastructure and Computational Biology

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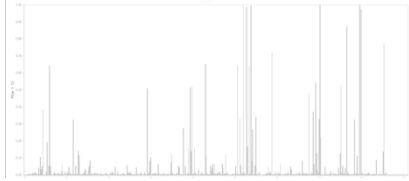
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## Next

Tuesday, 1 December at 0930

### Selection Analysis Using HyPhy

$0 \leftarrow \omega \rightarrow \infty$



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