

# Tree Editing & Visualization

Lisa Pokorny & Marina  
Marcet-Houben

(with help from Miguel Ángel Naranjo Ortiz)

# Data Visualization

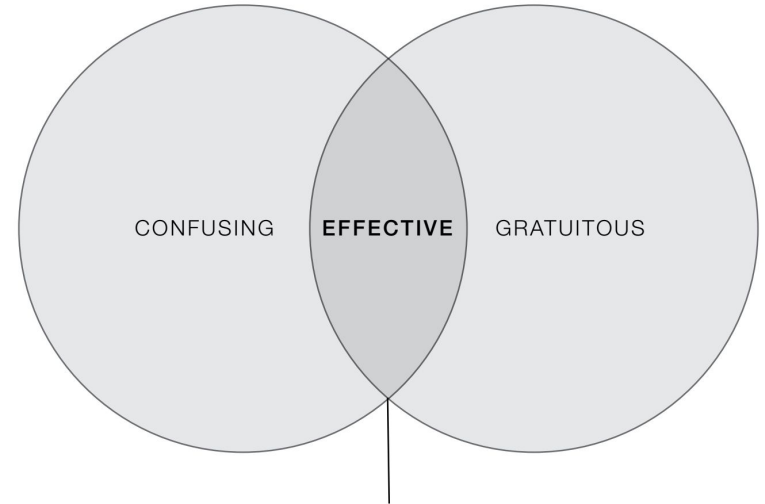
“Strive to give your viewer the greatest number of useful ideas in the shortest time with the least ink in the smallest space”

Tufte, E. The Visual Display of Quantitative Information (Graphic Press, Cheshire, Connecticut, USA, 2007).

## VISUALIZATION SWEET SPOT

INFORMATION-RICH

INFORMATIVE



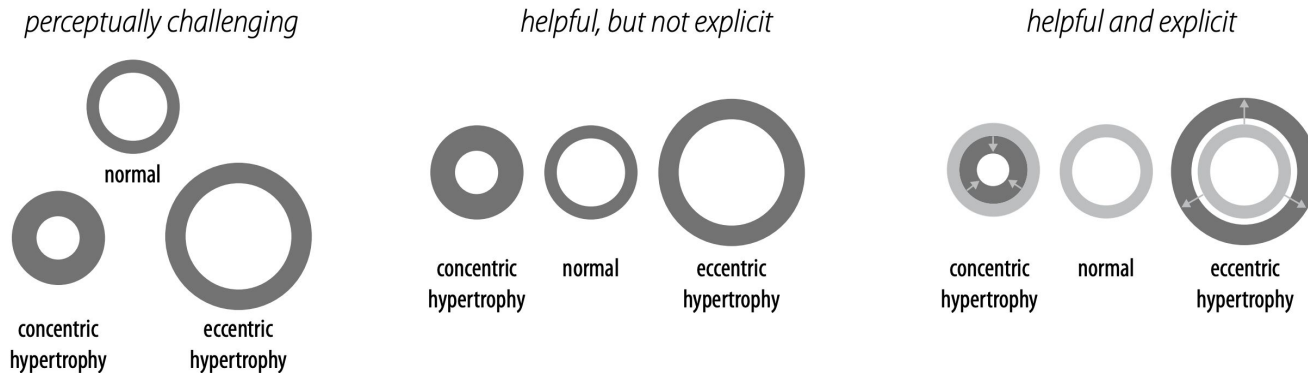
**CLEAR MESSAGE**

**HIGH DATA-TO-INK RATIO**

**ACCESSIBLE COMPLEXITY**

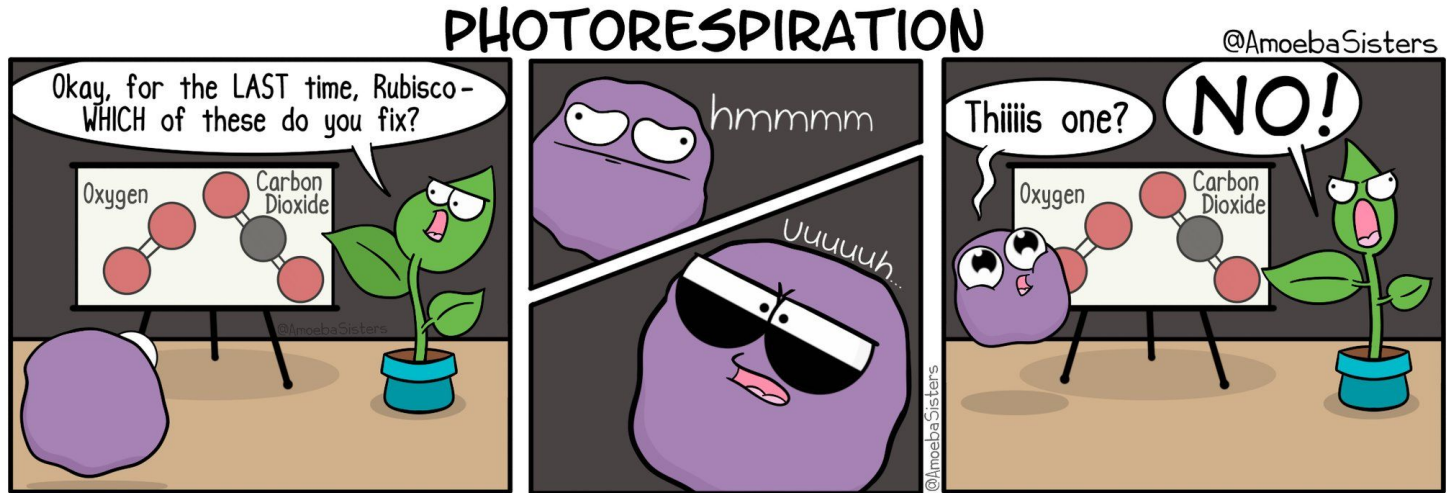
# Data Visualization

- Satisfy your audience, not yourself
- Don't merely display data, explain it
- Be aware of bias in evaluating effectiveness of visual forms
- Patterns are hard to see when variation is due to both data and formatting



# Data Visualization

- Know your message and stick to it (context musn't dilute message).
- Choose effective encoding (to explore your data) and design (to communicate concepts).



# Data Visualization

How do we get from data to visualization?

## TOP-DOWN

redundancy  
consistency  
conciseness  
clarity  
focus & emphasis  
salience & relevance  
truth, accuracy & detail

INFORMS



SATISFIES

## BOTTOM-UP

data encoding  
symbols  
color  
typeface  
arrows  
line weight  
alignment

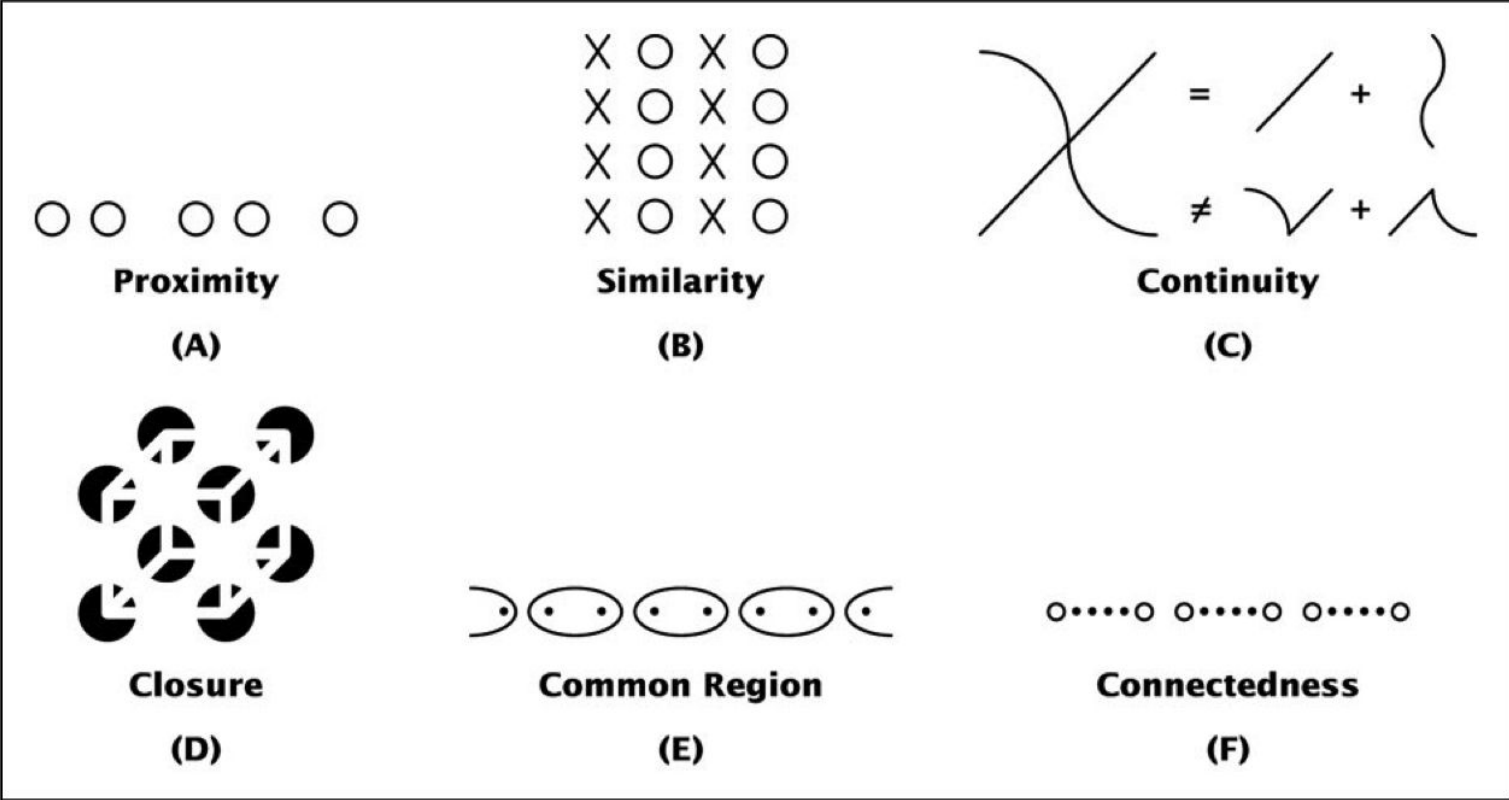
# Data Visualization

How do we get from data to visualization?

- **properties of the data / data type**
  - Phylogenies (cladograms, phylograms, chronograms, cloudograms, etc.)
  - Networks (reticulograms, tanglegrams, etc.)
- **properties of the image / visual encoding**
  - What? Points, lines, labels...
  - Where? 2D, 3D(?)
  - How? Size, shape, texture, color, hue...
- **the rules of mapping data to image**
  - Principles of grouping
  - etc.

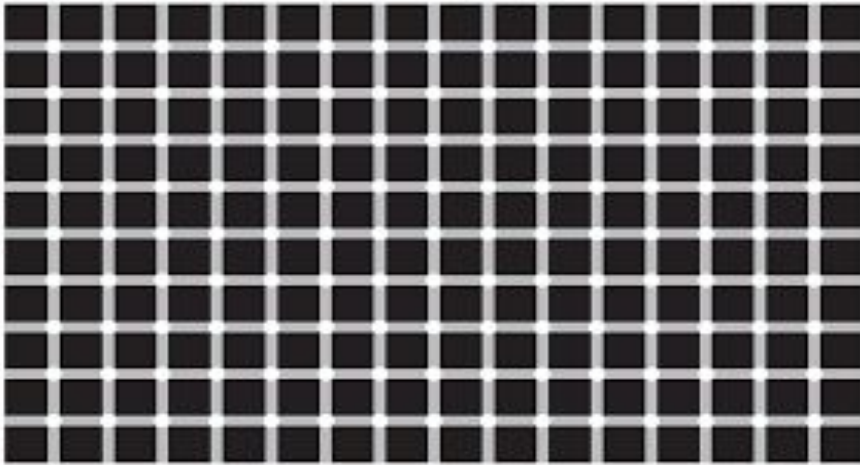
	Points	Lines	Areas	Best to Show
Shape		<i>Possible, but too Weird to Show</i>	<i>Cartogram</i>	<i>Qualitative Differences</i>
Size			<i>Cartogram</i>	<i>Quantitative Differences</i>
Color Hue				<i>Qualitative Differences</i>
Color Value				<i>Quantitative Differences</i>
Color Intensity				<i>Qualitative Differences</i>
Texture				<i>Qualitative &amp; Quantitative Differences</i>

# Principles of Grouping

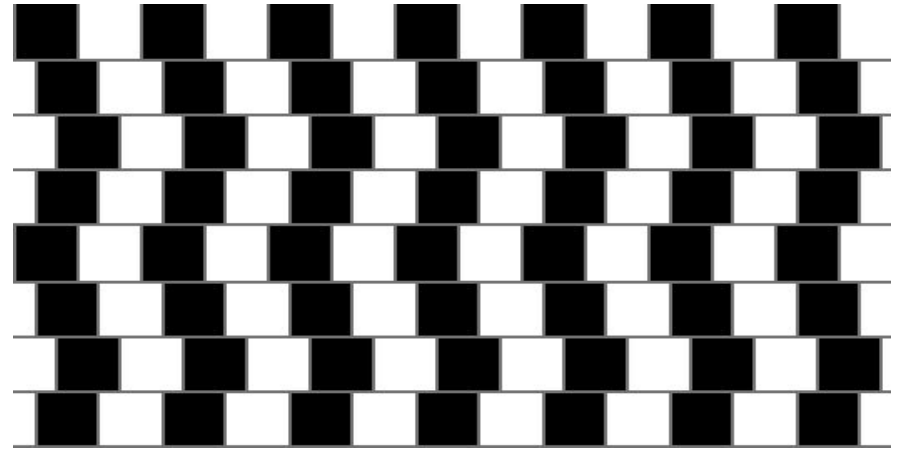


# Optical Illusions

Hermann Grid



Café Wall



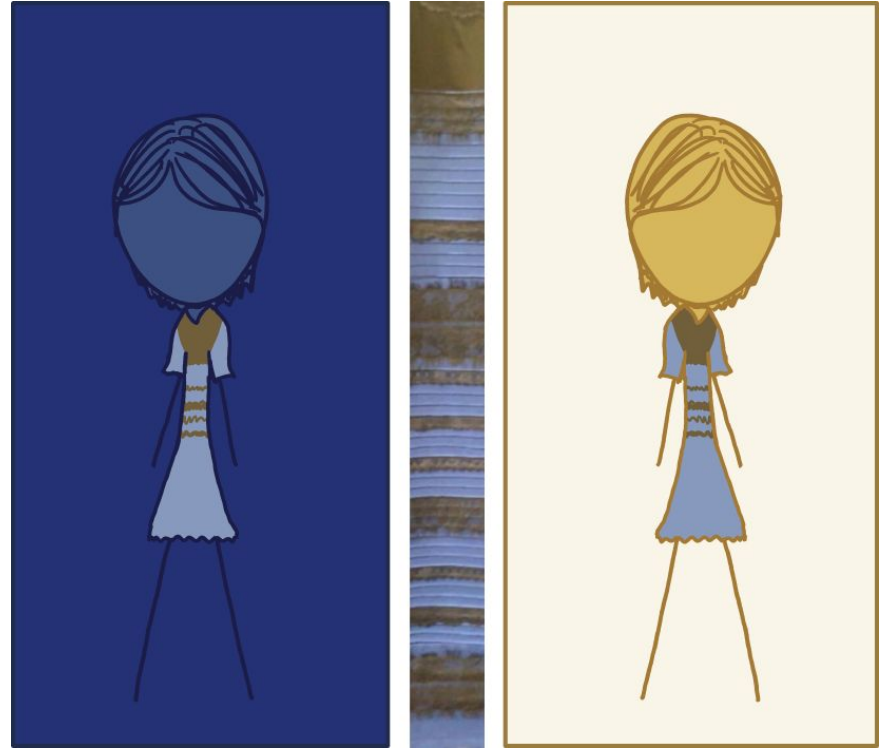


# Color



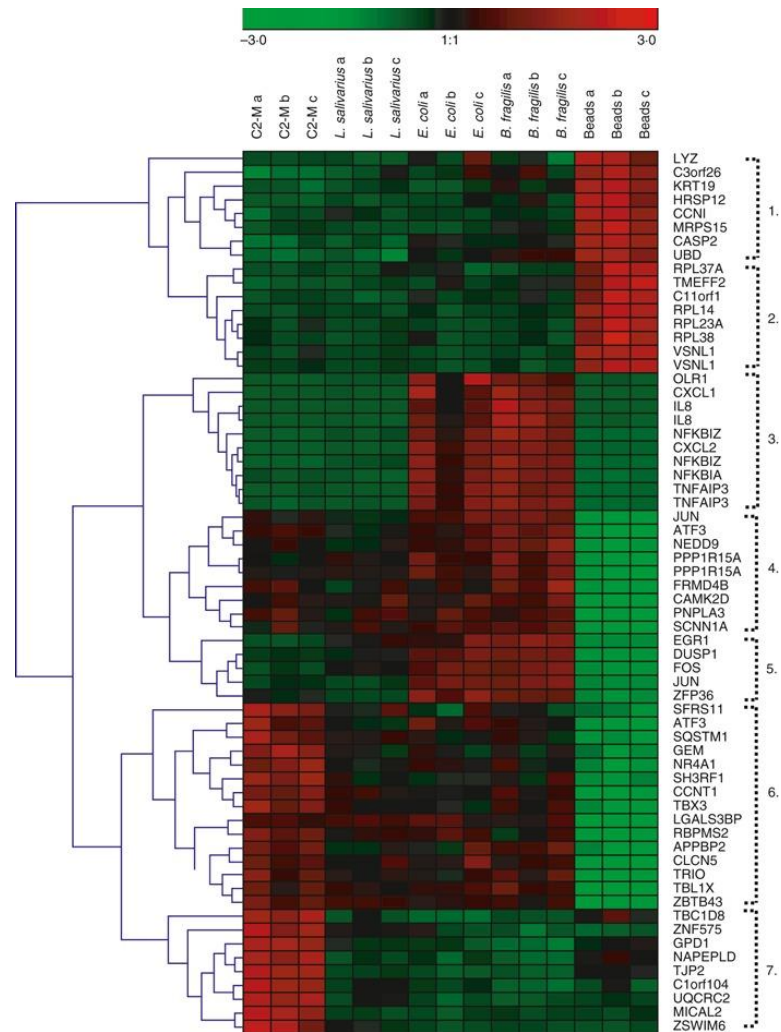
# Color Context

Context affects your color perception



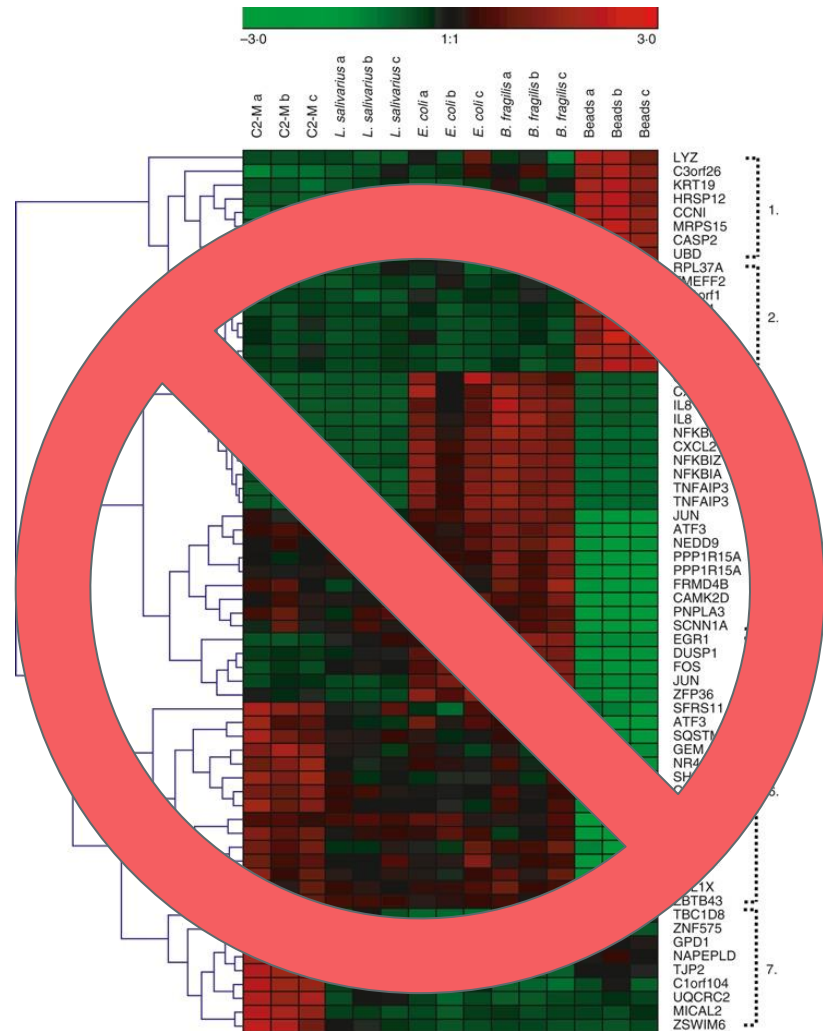
# Color Context

Context affects your color perception



# Color Context

Context affects your color perception



# Color Blindness



# Color Blindness

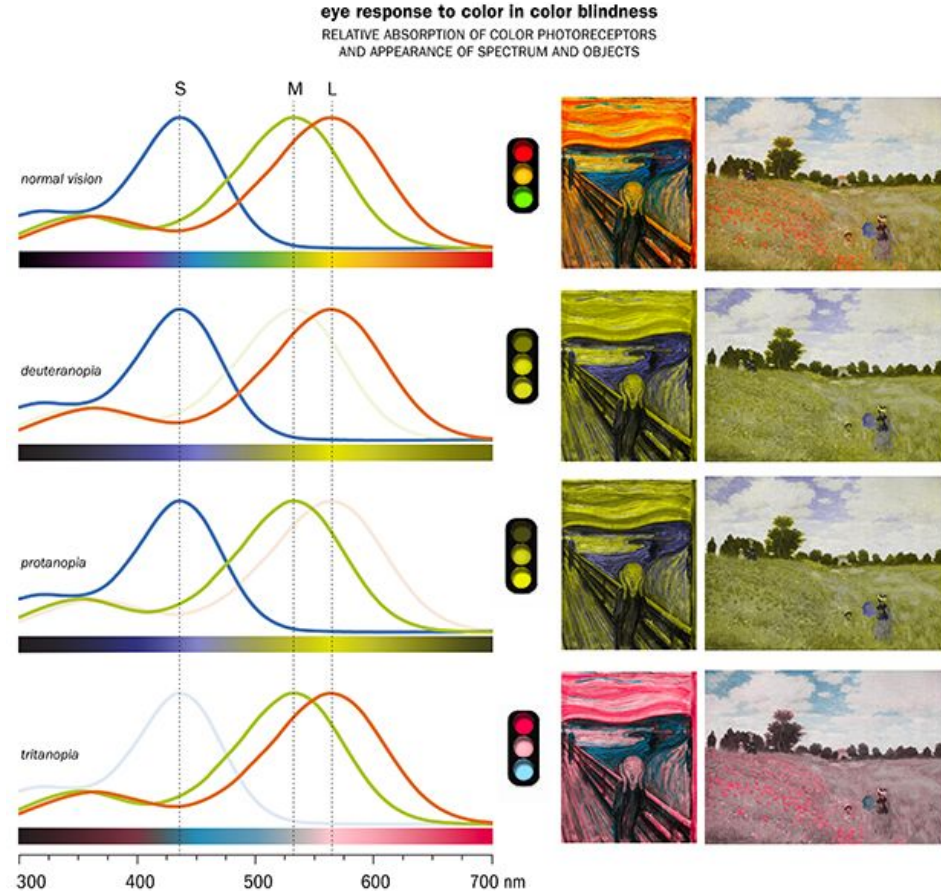
## COLOR PALETTES FOR COLOR BLINDNESS

In an audience of 8 men and 8 women, chances are 50% that at least one has some degree of color blindness. When encoding information or designing content, use colors that is color-blind safe.

[Color Oracle](#) is a good and free color blindness simulator for Windows, Mac and Linux.

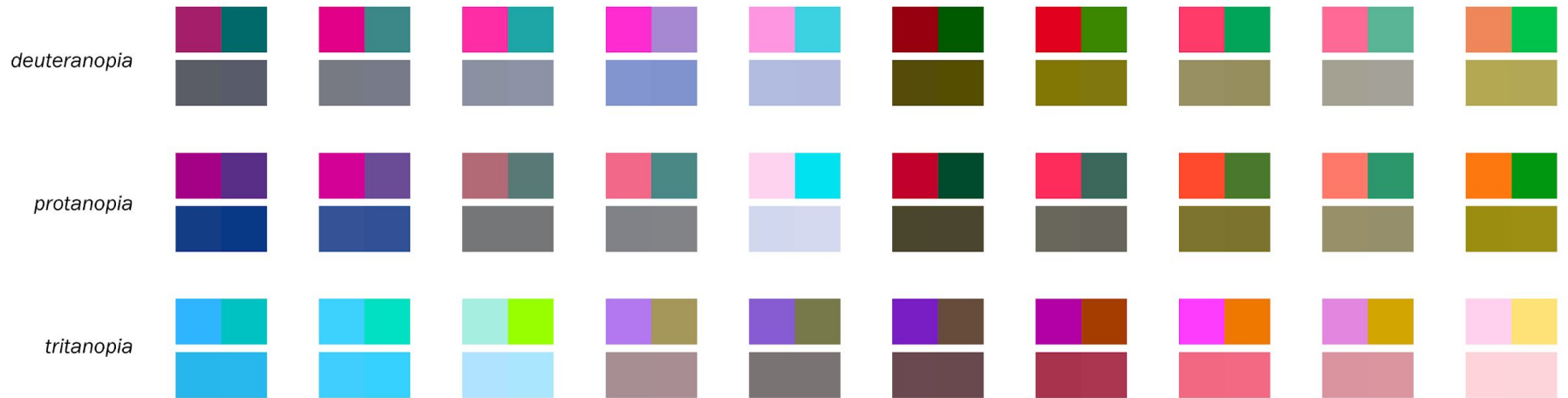
## COLOR RECEPTORS ARE REDUCED OR ABSENT IN COLOR BLINDNESS

The normal human eye is a 3-channel color detector. There are three types of photoreceptors, each sensitive to a different part of the spectrum. Their combined response to a given wavelength produces a unique response that is the basis of the perception of color.



# Color Blindness

## indistinguishable colors in color blindness



































<http://mkweb.bcgsc.ca/colorblind>

<http://mkweb.bcgsc.ca/colorblind/>

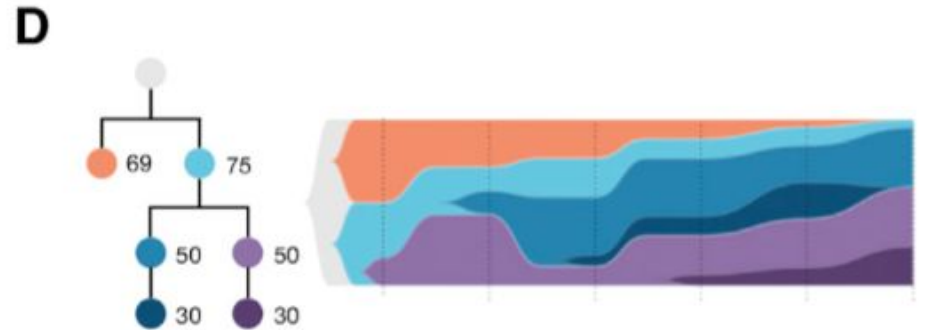
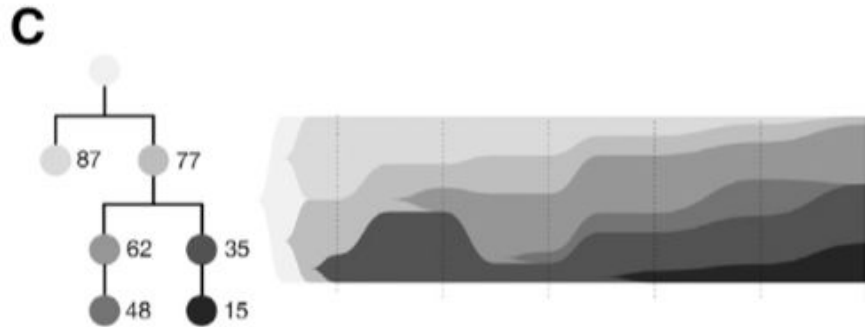
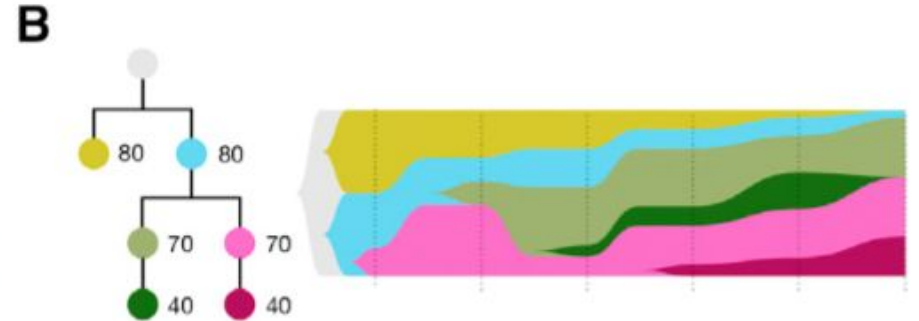
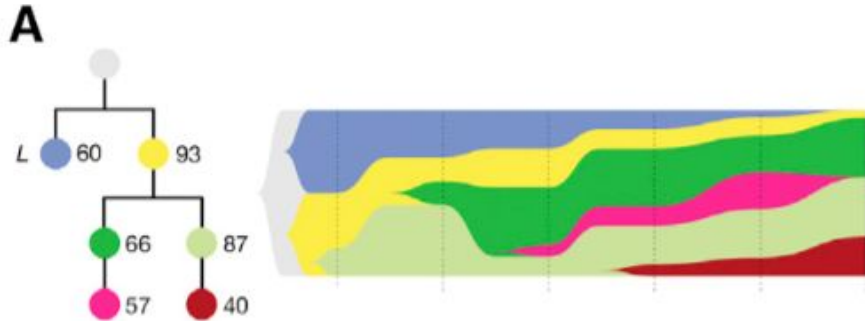
# Color Blindness – Palettes

- General advice: <http://ifly.iam.u-tokyo.ac.jp/color/>
- Cartography: <http://colorbrewer2.org/>
- R plotting system (ggplot2):  
[http://www.cookbook-r.com/Graphs/Colors \(ggplot2\)/#a-colorblind-friendly-palette](http://www.cookbook-r.com/Graphs/Colors (ggplot2)/#a-colorblind-friendly-palette)

	Original	Simulation				Hue	for Photoshop, Illustrator, Freehand, etc.		for Word, Power Point, Canvas, etc.
		Protan	Deutan	Tritan			C,M,Y,K (%)	R,G,B (0-255)	R,G,B (%)
1					Black	- °	(0,0,0,100)	(0,0,0)	(0,0,0)
2					Orange	41°	(0,50,100,0)	(230,159,0)	(90,60,0)
3					Sky Blue	202°	(80,0,0,0)	(86,180,233)	(35,70,90)
4					bluish Green	164°	(97,0,75,0)	(0,158,115)	(0,60,50)
5					Yellow	56°	(10,5,90,0)	(240,228,66)	(95,90,25)
6					Blue	202°	(100,50,0,0)	(0,114,178)	(0,45,70)
7					Vermillion	27°	(0,80,100,0)	(213,94,0)	(80,40,0)
8					reddish Purple	326°	(10,70,0,0)	(204,121,167)	(80,60,70)



# Color Blindness – Luminance



# Font Types

## Arial

Arabic Typesetting  
Aparajita  
AngsanaUPC  
Angsana New  
Andalus  
**ALGERIAN**  
**Aharoni**  
Agency FB  
AGaramondPro-Regular  
*AGaramondPro-Italic*  
**AGaramondPro-BoldItalic**  
AGaramondPro-Bold  
AdobeSongStd-Light  
AdobeMyungjoStd-Medium  
AdobeMingStd-Light  
AdobeKaitiStd-Regular  
**AdobeHeitiStd-Regular**  
AdobeHebrew-Regular  
*AdobeHebrew-Italic*  
*AdobeHebrew-BoldItalic*  
AdobeHebrew-Bold  
**AdobeGothicStd-Bold**  
**AdobeFanHeitiStd-Bold**  
AdobeFangsongStd-Regular  
AdobeArabic-Regular  
*AdobeArabic-Italic*  
*AdobeArabic-BoldItalic*  
AdobeArabic-Bold  
*ACaslonPro-SemiboldItalic*  
ACaslonPro-Semibold  
ACaslonPro-Regular  
*ACaslonPro-Italic*  
*ACaslonPro-BoldItalic*  
ACaslonPro-Bold

## Cambria

Calisto MT  
Californian FB  
Calibri  
*Brush Script Std*  
*Brush Script MT*  
BrowalliaUPC  
Browallia New  
**Broadway**  
**Britannic**  
Bradley Hand ITC  
**Bookshelf Symbol**  
Bookman Old Style  
**Bookman**  
**Book Antiqua**  
Bodoni MT Poster Compressed  
Bodoni MT Condensed  
**Bodoni MT Black**  
Bodoni MT  
**BlackoakStd**  
*Blackletter ITC*  
BirchStd  
**Bernard MT Condensed**  
**Berlin Sans FB Demi**  
Berlin Sans FB  
Bell MT  
**Bauhaus**  
BatangChe  
Batang  
Baskerville Old Face  
AvantGarde  
Arial Unicode MS  
Arial Rounded MT  
Arial Narrow  
**Arial Black**

## DotumChe

Dotum  
DokChampa  
DilemmaUPC  
DFKai-SB  
David  
DaunPenh  
Curlz MT  
Courier New  
Courier  
CordiaUPC  
Cordia New  
Corbel  
COPPERPLATE GOTHIC LIGHT  
Copperplate Gothic  
**CooperBlackStd-Italic**  
**CooperBlackStd**  
**Cooper Black**  
Constantia  
**Comic Sans MS**  
Colonna MT  
Chiller  
CHARLEMAGNESTD-BOLD  
ChaparralPro-Regular  
*ChaparralPro-Italic*  
**ChaparralPro-BoldIt**  
**ChaparralPro-Bold**  
Century Schoolbook  
Century Gothic  
Century  
Centaur  
**CASTELLAR**  
Candara  
Cambria Math

## Gautami

Garamond  
Gabriola  
*French Script ITC*  
*Freestyle Script*  
FreesiaUPC  
FrankRuehl  
**Franklin Gothic Medium Cond**  
**Franklin Gothic Medium**  
**Franklin Gothic Heavy**  
**Franklin Gothic Demi Cond**  
**Franklin Gothic Demi**  
Franklin Gothic Book  
**Forto**  
Footlight MT Light  
GOTHIC  
FELIX TITLING  
FangSong  
Euphemia  
EucrosiaUPC  
Ευχλιδ Στρωβολ  
E M T  
E M  
Euler Fraktur  
Euclid  
Estrangelo Edessa  
Eras Medium ITC  
Eras Light ITC  
**Eras Demi ITC**  
Eras  
**ENGRAVERS MT**  
**Elephant**  
*Edvardian Script ITC*  
Ebrima

## KodchiangUPC

Khmer UI  
**Kartika**  
Kalinga  
Kaiti  
Jutee ITC  
**Jokerman**  
JasmineUPC  
Iskoola Pota  
IrisUPC  
*Interreal Roman*  
Imprint MT Shadow  
**Impact**  
**HoboStd**  
High Tower Text  
Helvetica-Narrow  
Helvetica  
Harrington  
Harlow Solid  
Haettenschweiler  
GungsuChe  
GungsuH  
GulimChe  
Gulim  
**GOUDY STOUT**  
Goudy Old Style  
Gloucester MT Extra Condensed  
Gisha  
Gill Sans Ultra  
Gill Sans MT Ext Condensed  
Gill Sans MT Condensed  
Gill Sans MT  
Gigi  
GothicStd  
Georgia

## Lucida Fax Regular

**Lucida Fax Demibold**  
Lucida Fax  
**Lucida Console**  
*Lucida Calligraphy*  
**Lucida Bright Demibold**  
Lucida Bright  
**LITHOSPRO-REGULAR**  
**LITHOSPRO-BLACK**  
LilyUPC  
Levenim MT  
*LetterGothicStd-Slanted*  
*LetterGothicStd-BoldSlanted*  
**LetterGothicStd-Bold**  
*LetterGothicStd*  
Leelawadee  
Latha  
Lao UI  
*Namoth Script*  
**Kristen ITC**  
KozMinPro-Regular  
KozMinPro-Medium  
KozMinPro-Light  
**KozMinPro-Heavy**  
KozMinPro-ExtraLight  
**KozMinPro-Bold**  
KozMinPr  
KozGoPro-Regular  
KozGoPro-Medium  
KozGoPro-Light  
**KozGoPro-Heavy**  
KozGoPro-ExtraLight  
**KozGoPro-Bold**  
KozGoPr  
Kokila

## IN TYPOGRAPHY

# Font Types However...

Serifs are the small lines tailing from the edges of letters and symbols, separated into distinct units for a typewriter or typesetter

Check out my sweet serifs!



**Serif fonts are easier to read in printed works**

This is because the serif make the individual letters more distinctive and easier for our brains to recognise quickly. Without the serif, the brain has to spend longer identifying the letter because the shape is less distinctive.

Sans-serif is a typeface that does not have the small projecting features called "serifs" at the end of strokes.

Modern, Minimal, Magnificent, I am Sans



**Sans serif fonts are better on the web**

An important exception must be made for the web. Printed works generally have a resolution of at least 1,000 dots per inch; whereas, computer monitors are typically around 100 dots per inch.

# Dyslexia

Dyslexia is the most common learning disability. It is the most recognized of reading disorders, however not all reading disorders are due to dyslexia.

Some see dyslexia as distinct from reading difficulties arising from other causes, such as a neurological condition with vision or hearing, or poor or inadequate reading instruction. There are three subtypes of dyslexia (phonological, surface and orthographic), although individual cases of dyslexia are better explained by specific underlying neurological factors and co-occurring conditions (e.g. attention-deficit/hyperactivity disorder, math disability, etc.). Although it is considered to be a specific language-based learning disability in the research literature, dyslexia also affects one's general academic skills. Researchers at MIT found that people with dyslexia exhibit a wide range of abilities.

# Dyslexia Friendly Text

- Use a plain, evenly spaced sans serif font, e.g., Arial, Verdana, Trebuchet, Calibri, **ComicSans**, Century Gothic...
- Font size should be 12-14 point or larger
- Use dark coloured text on a light (not white) background
- Avoid underlining and *italics*: these tend to make the text appear to run together; use **bold** instead
- AVOID TEXT IN BLOCK CAPITALS!
- Use left-justified with ragged right edge
- Avoid narrow columns
- Line spacing of 1.5 is preferable
- Use bullet points and numbering rather than continuous prose

# Dyslexia Friendly Font Types – OpenDyslexic

## OpenDyslexic

Free, OpenSource Dyslexia Typeface

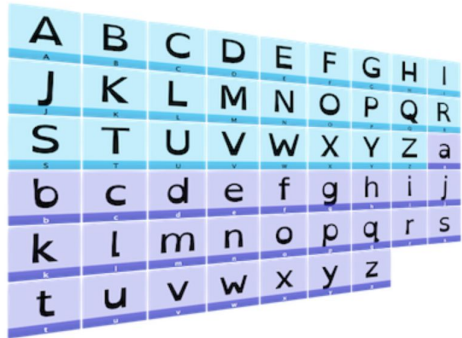
search here ...

[Get it Free](#) [Browse Products](#) [Get it Free](#) [License](#) [News](#) [About](#) [Try it!](#) [FAQ](#)

# OpenDyslexic

OpenDyslexic is a new open source font created to increase readability for readers with dyslexia. The typeface includes regular, bold, italic, and bold-italic styles. It is being updated continually and improved based on input from dyslexic users. OpenDyslexic is free for Commercial and Personal use.

[Download Now!](#)



# Dyslexia Friendly Font Types – Lexie Readable

 K-TYPE

[Home](#) [Fonts](#) [Free Fonts](#) [Kernel](#) [My Account](#)



## Lexie Readable

Lexie Readable (formerly Lexia Readable) was designed with accessibility and legibility in mind, an attempt to capture the strength and clarity of Comic Sans without the comic book associations. Features like the non-symmetrical b and d, and the handwritten forms of a and g may help dyslexic readers. You can read more about the story behind Lexie Readable in the [Kernel](#).

Lexie Readable now includes a full complement of Latin Extended-A characters and numerous subtle outline improvements.

The Regular and Bold weights can be downloaded and used freely without a licence by educational and charitable institutions as well as by individuals.

The **Basic Family** includes Regular, Italic, Bold and Bold Italic. The **Heavy** package includes a Heavy Outline version.

Download the Regular & Bold Free for Personal, Educational or Charity Use: [Download](#)

# Dyslexia Friendly Font Types – Dyslexie



Dyslexie font is patented



Size  
A A

Background

Language  
🇳🇱 🇬🇧



d  
Dyslexie font



Books/Apps

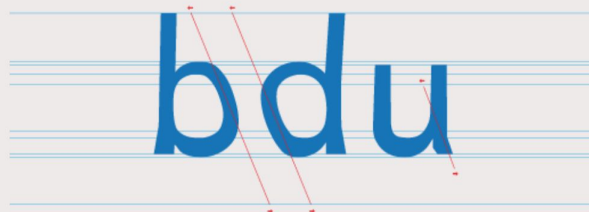


## How the Dyslexie font works

To show you what makes the Dyslexie font different from other fonts, we will show you the 9 main features below.

### 02 Slanted parts

Characters which look quite similar have been adapted by changing the tails, to reduce the similarity and avoid the problem of mirror letters.



1 2 3 4 5 6 7 8 9

see all slides



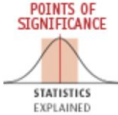




# **ESSENTIALS OF DATA VISUALIZATION**

THINKING ABOUT DRAWING DATA + COMMUNICATING SCIENCE

## RESOURCES



# Insights into Data Visualization: 8-part mini-series

This video series focuses on relevant and practical concepts in scientific data visualization. Our aim is to make you think more clearly about visual presentation and to make you a better communicator.

Each video in the series presents fundamental ideas and is designed to provide constraints and guidance to your thoughts about communicating your data. The purpose of scientific data visualization is not merely to inform but also to answer and generate hypotheses.

Though few firm rules exist when it comes to how to achieve clarity—whatever the communication medium—we must meet core requirements such as consistency, redundancy and appropriate mapping between relevant and salience. We present these essential topics using biological data as examples. But if you're not a biologist, don't worry. Instead, think about the data structure rather than meaning and you'll be fine.

## Resources

Each video is about 15 minutes long and comes with a slide deck of the images used in the video, exercise and suggested solutions.

[Download all course materials.](#)

## Episodes

### 1 DATA ENCODING

MAKE IT EASY TO ANSWER RELEVANT QUESTIONS.

[watch](#) | [PDF](#) | When you think of data visualization, the first ideas that come to mind are a scatter plot, or a bar chart, a box plot or a network diagram. These are all data encodings—methods that relate data values to the positions, sizes and shapes of the lines or symbols that appear on the screen or in a figure. There are many data encodings—which do you choose?

### 2 SHAPES AND SYMBOLS

INTUITIVELY ENCODE ROLE AND RELEVANCE.

[watch](#) | [PDF](#) | Shapes and glyphs are really important. They make up the heart of a lot of data plots. Your default should be the circle. If you need different shapes, try to map the classes as intuitively as possible onto the shapes. Use less prominent symbols for data that are less relevant (such as reference data included for context).

### 3 COLOR

USE IT FOR EMPHASIS AND VISUAL SEPARATION.

[watch](#) | [PDF](#) | Color is one of the most exciting ways in which you can completely screw over your visualization. What can start off as a great diagram can be absolutely ruined by a lack of color judgment. When using color, ask yourself—do I need it? Try to work around it using grey tones from Brewer palettes. If you succeed, you're in a perfect place to use spot color, sparingly, for emphasis.



#### 4 UNCERTAINTY

DON'T MAKE ERRORS IN ERROR BARS.

[watch](#) | [PDF](#) | Knowing the limits of your knowledge is very important. In biology, it's important to be able to sample the extent of biological variation. And so being able to show this and other forms of variation in measurements or any computed values in visualizations is very important—it addresses reproducibility and your capacity to make statistical inference. Often this is done with error bars. Ironically, there's a lot of error associated with the use of and interpretation of error bars.



#### 5 DESIGN

ORGANIZE AND CLARIFY.

[watch](#) | [PDF](#) | Design plays a large role in data visualization. Think of design as choreography for the page. In our context it's not merely driven by aesthetic, but function. Although there's always room for aesthetic—gently applied—and I really encourage you to find your own and continue to refine it. But always remember, be understood before being articulate. Be legible before being attractive! Your goal here isn't to make inroads on the global stage of aesthetic studies. Become a good visual explainer. It's harder ... and more worth doing.

2017  $\pi$  DAY



#### 6 NOTHING

NO DATA, NO INK.

[watch](#) | [PDF](#) | Data-to-ink ratio, taken to the extreme: if there is no data to show, no ink should be used. The idea of “no data to show” may correspond to a variety of scenarios. There may be sincerely no data to show—no values were collected. Or, there are no significant changes to see. Where possible, you should use empty space to indicate lack of data or lack of change in data. You should never be distracted by something that isn't relevant and empty space is not distracting—it really just provides contrast to adjacent elements, which presumably correspond to actual data or actionable data.



#### 7 LABELS

RESPECT TYPE AND USE IT TO ESTABLISH HIERARCHY.

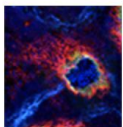
[watch](#) | [PDF](#) | Open up a journal or your favourite text book. Find a figure. There's probably some labels in there. Maybe it's a multi-panel figure and the labels are the titles. Maybe there are some callouts that tell you what the parts are. If it's a plot there are probably axis labels and tick labels and maybe a legend with some labels. There's usually several informational layers in the image, each with their own labels. These labels should reflect that these layers are different. They should also reflect the relative importance of these layers.



#### 8 PROCESS

CREATING A VISUALIZATION FOR SCIENTIFIC AMERICAN GRAPHIC SCIENCE: FROM START TO FINISH.

[watch](#) | [PDF](#) | Let's now look at the process of designing a visualization from scratch—from the encoding all the way to design. This was a graphic I did for the [June 2015 issue of Scientific American](#). It appeared on the Graphic Science page.



© 1999–2019 [Martin Krzywinski](#) | [contact](#) | [Genome Sciences Centre](#)  $\subset$  [BC Cancer Research Center](#)  $\subset$  [BC Cancer](#)

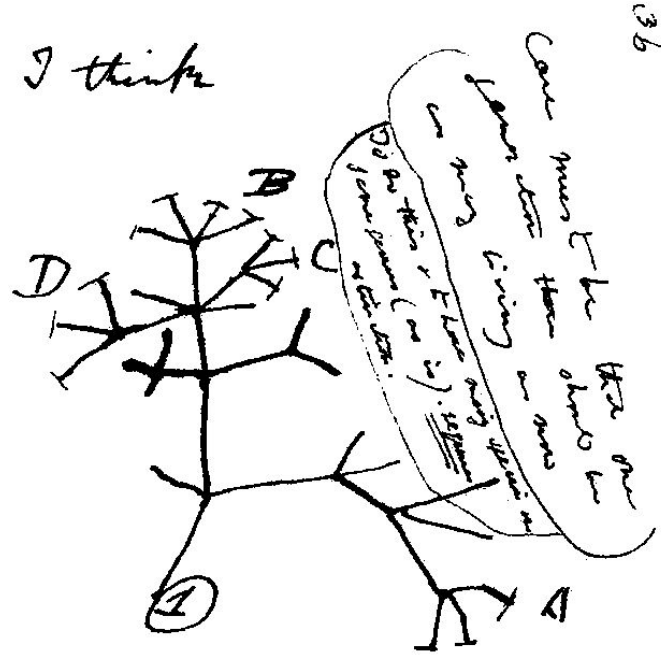
# Phylogenetic Tree Visualization

- Web Portals

- Software

- Toolkits

- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)



# Phylogenetic Tree Visualization

- **Web Portals:**

- Phylo.IO @ <http://phylo.io>
- Interactive Tree of Life viewer (iTOL) @ <http://itol.embl.de>
- EVOLVIEW @ <http://www.evolgenius.info/evolview>

- **Software:**

- FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
- DensiTree @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
- TreeGraph2 @ <http://treegraph.bioinfweb.info>

- **Toolkits:**

- PYTHON library: ETE toolkit @ <http://etetoolkit.org>
- R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
- JavaScript library: jsPhyloSVG @ <http://www.isphylosvg.com>

- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)

# Phylogenetic Tree Visualization

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- EVOLVIEW @ <http://www.evolgenius.info/evolview>

- **Software:**

- FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
- DensiTree @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
- TreeGraph2 @ <http://treegraph.bioinfweb.info>

- **Toolkits:**

- PYTHON library: ETE toolkit @ <http://etetoolkit.org>
- R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
- JavaScript library: jsPhyloSVG @ <http://www.isphylosvg.com>

- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)

# Web Portals

- **Phylo.IO** @ <http://phylo.io>
- **Interactive Tree of Life viewer (iTOL)** @ <http://itol.embl.de>
- **EVOLVIEW** @ <http://www.evolgenius.info/evolview>
- **Others:**
  - **PHYLOViZ Online** @ <https://online.phyloviz.net/index>, (10-min YouTube tutorial: <https://www.youtube.com/watch?v=hmbmurFV6ik>)
  - **Archaeopteryx-js** @ [http://www.phyloxml.org/archaeopteryx-js/bcl2\\_js.html](http://www.phyloxml.org/archaeopteryx-js/bcl2_js.html)
  - **TreeLink** @ <http://www.treelinkapp.com>
  - **T-REX** @ <http://www.trex.uqam.ca>
  - **AQUAPONY** @ <http://www.lirmm.fr/~cazaux/AQUAPONY/>
  - etc.

# Phylo.IO

Very simple and intuitive, fast

Allow to export tree figures as images (.svg)

Quite limited

1' demo @ <https://www.youtube.com/watch?v=IOQK3CP8GIA>



# Phylo.IO demo

Phylo.io

Version: 1.0.0 (04/28/2016 15:06:36)

View Compare

Tree: *Untitled*

Paste your tree or drag and drop your tree file here

Small Example Tree  
Large Example Tree

Render ▶ Clear

Settings  
Share  
Help

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1. Choose view for a single tree, Compare for two trees
2. Add your trees into the text boxes in newick format
3. Click "Render"

# Phylo.IO demo



**Phylo.io**  
Version: 1.0.0 (04/28/2016 15:06:36)

View Compare

Tree: *Untitled*

```
((sba:0.0398495207632660886
1,
(sca:0.2421230719967884248
4,
(cgl:0.29957965624763355228
,
(((kla:0.3282900962783522613
7,ago:0.352170853400062044
97):0.05741546733669361524
,
sba
sca
cgl
kla
ago
skl
kwa
yii
lel
cal
ctr
pst
pgu
dha
sce
spa
smi
sku
```

Small Example Tree 1

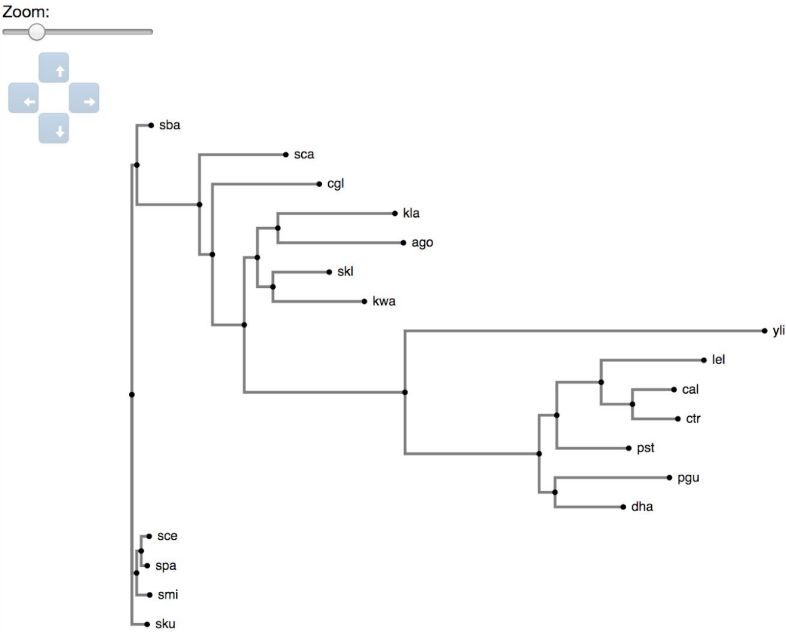
Large Example Tree

2 **Render** **Clear**

Settings

Share

Help



SVG

# Phylo.IO demo

**Phylo.io**  
Version: 1.0.0 (04/28/2016 15:06:36)

View Compare

Tree: *Untitled*

```
((sba:0.0398495207632660886
1,
(sca:0.2421230719967884248
4,
(cgl:0.2995796562476335228
,
(((kla:0.3282900962783522613
7,ago:0.352170853400062044
97):0.05741546733669361524
```

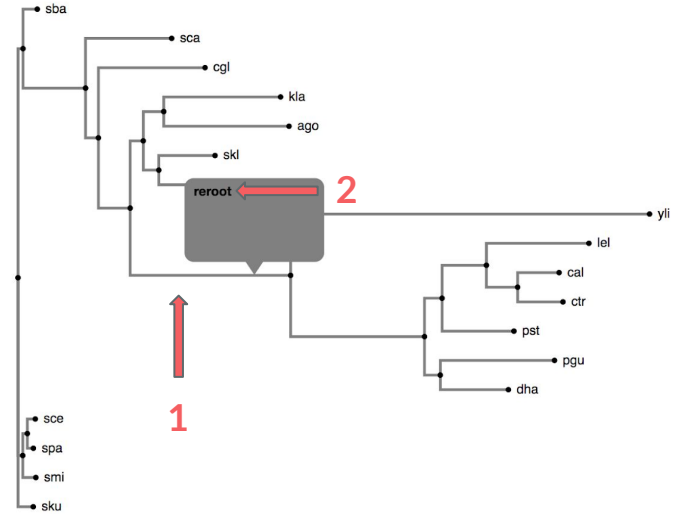
Small Example Tree  
Large Example Tree

Render Clear

Settings  
Share  
Help

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Zoom:



SVG

# Phylo.IO demo

**Phylo.io**  
Version: 1.0.0 (04/28/2016 15:06:36)

View Compare

Tree: *Untitled*

```
((sba:0.0398495207632660886  
1,  
(sca:0.2421230719967884248  
4,  
(cgl:0.29957965624763355228  
,  
(((kla:0.3282900962783522613  
7,ago:0.352170853400062044  
97):0.05741546733669361524
```

Small Example Tree  
Large Example Tree

Render Clear

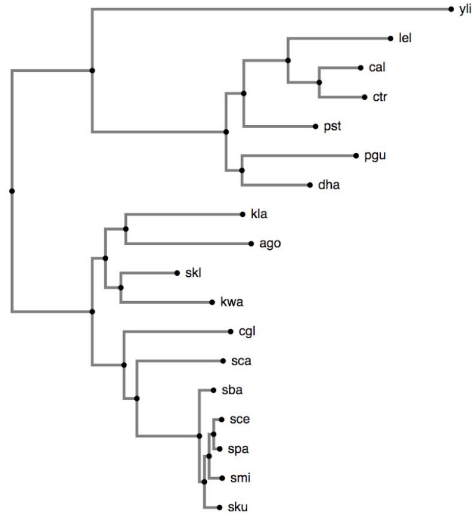
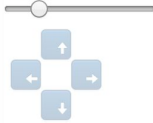
Settings **1**

Share

Help

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Zoom:



# Phylo.IO demo



1 → **Auto-Collapse Depth:** - 2 +

**Internal Labels:**

- None
- Branch Labels/Support
- Length
- Similarity

**Adjust Tree Style:**

Line Thickness

2 → [Slider]

Node Size

3 → [Slider]

Font Size

[Slider]

Use Lengths

Move To Best Corresponding Node on Highlight Click

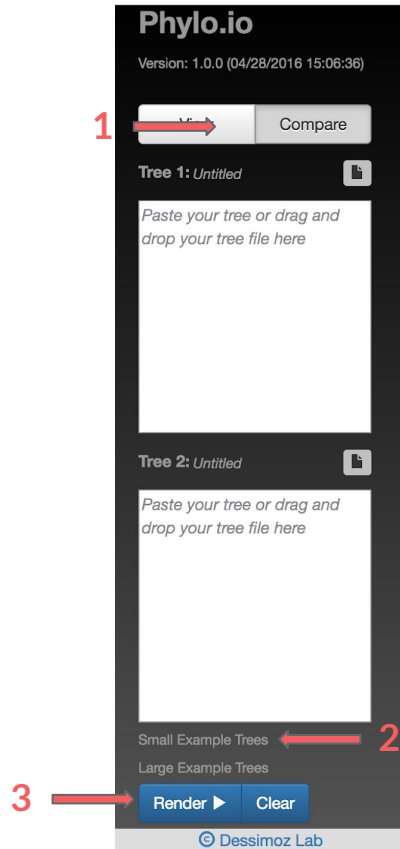
Zoom: [Slider]

Navigation: [Up, Down, Left, Right]

↓ SVG

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# Phylo.IO demo



1. Choose view for a single tree, Compare for two trees
2. Add your trees into the text boxes in newick format
3. Click "Render"

# Phylo.IO demo

**Phylo.io**  
Version: 1.0.0 (04/28/2016 15:06:36)

View Compare

Tree 1: *Untitled*

```
((yli:1.0085614391793067,(((lel:0.2880678599618948,(cal:0.11643570498932501,ctr:0.12746420698315983):0.0877413194006926):0.12449843844102518,pst:0.20187483296288805):0.04951181210826987,(pgu:0.3208350693977453,dha:0.19121342958249643):0.047,skl:kwa),sca:cgl),sba:0.04645932805874481569,(smi:0.03315550229946162553,(spa:0.01466907419174275952,sce:0.02383733069302066895):0.01620853054082276729):0.01834962617511207497):0.06496501071301066799,(sca:0.2192849714635205504
```

Small Example Trees  
Large Example Trees

Render Clear

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Zoom:

2.22

Zoom:

4.03

reroot reorder

1 2

SVG SVG

# Phylo.IO demo

Tree 1: Untitled

```
((yli:1.0085614391793067,
(((lel:0.2880678599618948,
(cal:0.11643570498932501,ctr
:0.12746420698315983):0.087
7413194006926):0.124498438
44102518,pst:0.20187483296
288805):0.0495118121082698
7,
(pgu:0.3208350693977453,dh
a:0.19121342958249643):0.04
```

Tree 2: Untitled

```
5,dha:0.177977065464032413
46):0.04249479494672471491
):0.29326816910580705278,yli
:0.72911704942210797675):0.
31199925135971823265):0.06
946141605430436461,cgl:0.27
125751484306920291):0.0367
8319509837457008):0.090113
50505801994648,sku:3.28511
106679567399524):0.0;
```

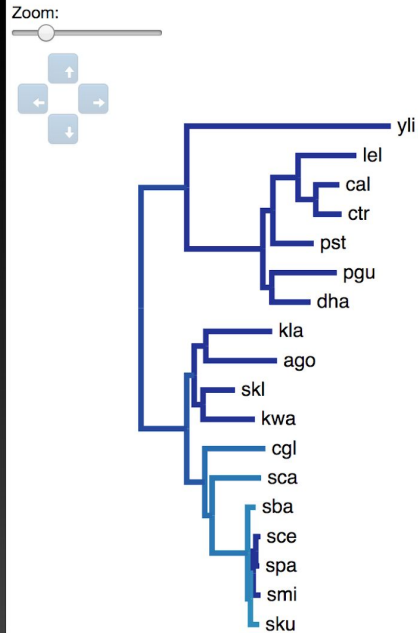
Small Example Trees  
Large Example Trees

Render Clear

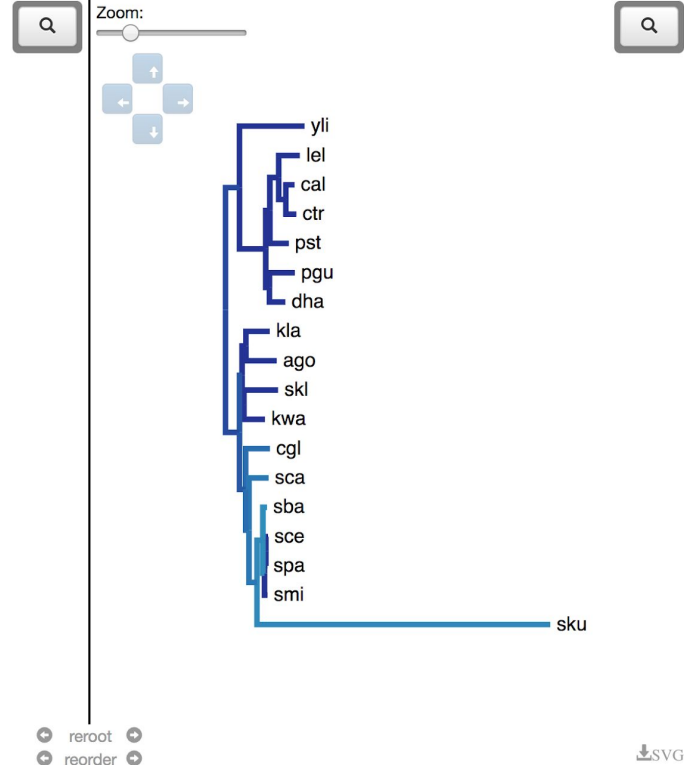
Similarity to most common node:

0 1

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2.22



5.04



# Phylo.IO demo

The image displays two side-by-side screenshots of the Phylo.IO web application interface, demonstrating tree manipulation features.

**Left Screenshot (Version 2.22):**

- Panel 1 (Left):** Shows a list of taxon identifiers and their associated values, such as `:0.12746420698315983):0.087`.
- Panel 2 (Middle):** Displays a phylogenetic tree with blue branches and labels for taxa: `yli`, `lel`, `cal`, `ctr`, `pst`, `pgu`, `dha`, `kla`, `ago`, `skl`, `kwa`, `cgl`, `sca`, `sba`, `sce`, `spa`, `smi`, and `sku`.
- Panel 3 (Right):** Contains a settings sidebar with options for "Small Example Trees", "Large Example Trees", "Render", "Clear", and a "Similarity to most common node" color scale from 0 to 1.

**Right Screenshot (Version 5.04):**

- Panel 1 (Left):** Shows the same phylogenetic tree as the left screenshot.
- Panel 2 (Middle):** The tree is zoomed in, and a context menu is open over the `lel` node. The menu options are: `collapse >`, `collapse all >`, `swap subtrees >`, and `highlight >`. A red arrow labeled "1" points to the `collapse all >` option, and another red arrow labeled "2" points to the `lel` node.
- Panel 3 (Right):** The tree is zoomed out, showing the `sku` taxon at the bottom.

**Bottom Panel:**

- On the far left, a red arrow labeled "3" points to the "Share" button in the settings sidebar.
- At the bottom center, the version number `2.22` is displayed.
- At the bottom right, the version number `5.04` is displayed.

# Phylo.IO demo

:0.12746420698315983):0.087  
7413194006926):0.124498438  
44102518,pst:0.20187483296  
288805):0.0495118121082698  
7,  
(pgu:0.3208350693977453,dh  
a:0.19121342958249643):0.04

Tree 2: Untitled

```
((sba:0.0464593280587448156  
9,  
(smi:0.0331555022994616255  
3,  
(spa:0.0146690741917427595  
2,sce:0.023837330693020668  
95):0.01620853054082276729  
):0.01834962617511207497):0  
.06496501071301066799,  
(sca:0.2192849714635205504
```

Small Example Trees  
Large Example Trees

Render Clear

Similarity to most common node:  
0 1

Settings  
Share

© Dessimoz Lab

Zoom: [input] [input] Zoom: [input] [input]

Link to share tree visualisation ← **6-month lasting link**

<http://phylo.io/#a99d9e055e852c5eda49eba43097ef72#d73a7bda61923e42bacaf89979306d>

SVG reoot reorder SVG

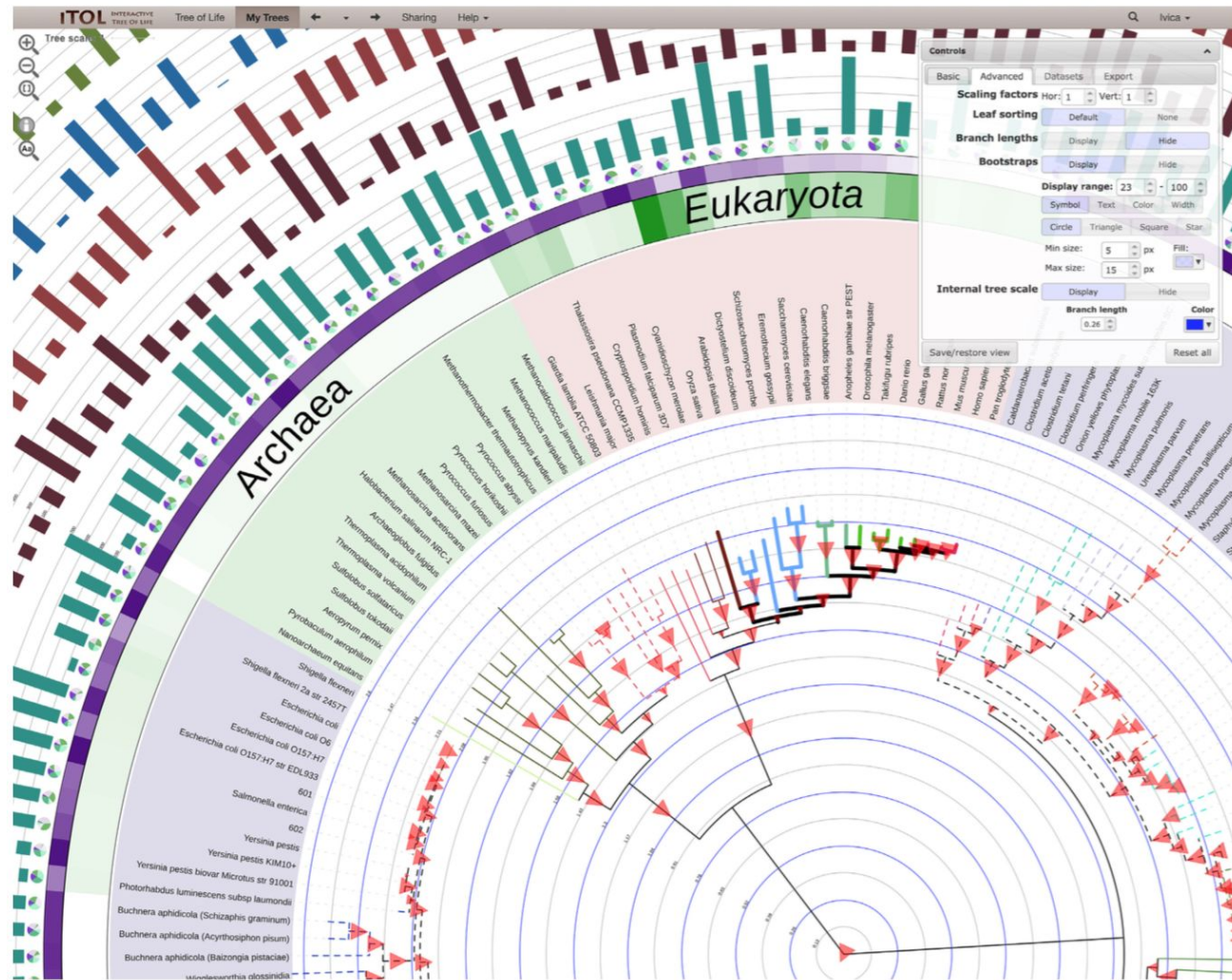
2.22 5.04

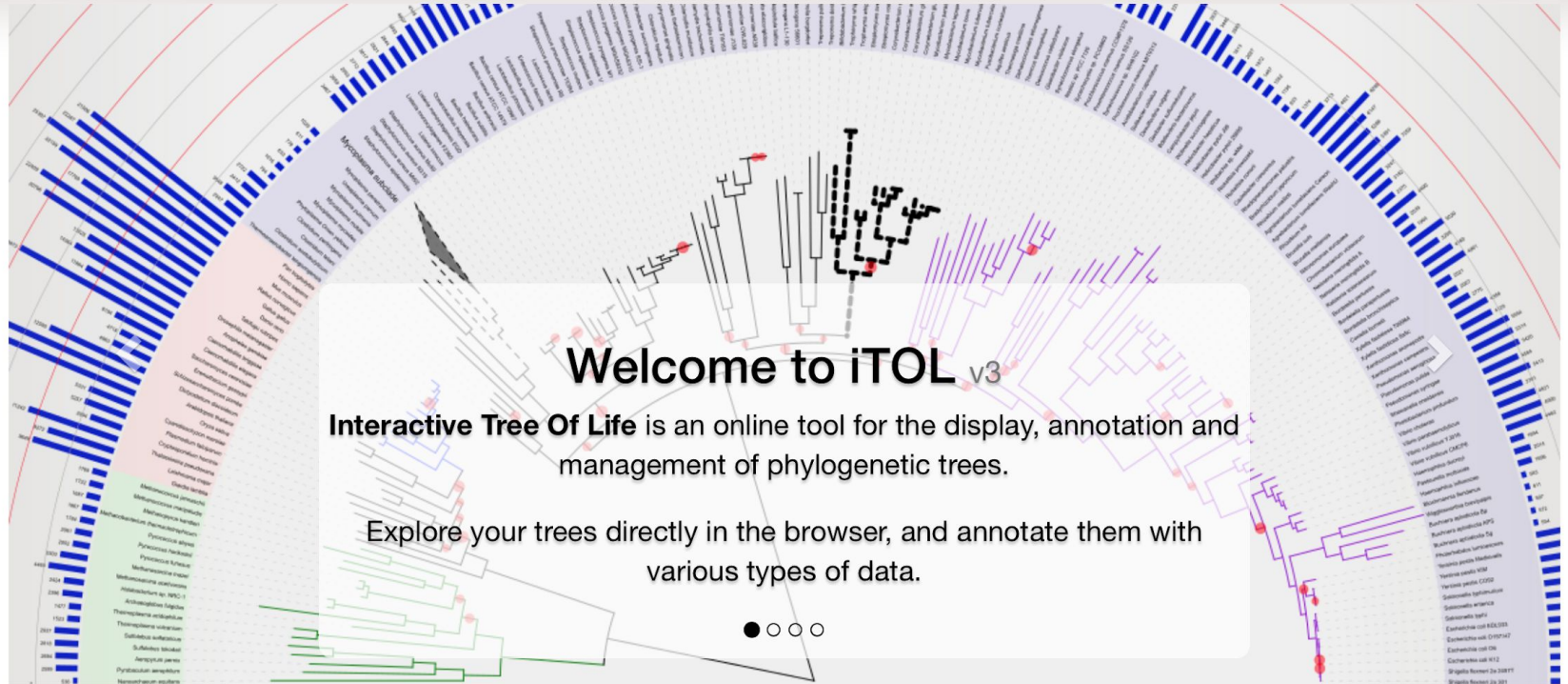
# Web Portals

- Phylo.IO @ <http://phylo.io>
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- EVOLVIEW @ <http://www.evolgenius.info/evolview>
- Others:
  - PHYLOViZ Online @ <https://online.phyloviz.net/index>, (10-min YouTube tutorial: <https://www.youtube.com/watch?v=hmbmurFV6ik>)
  - Archaeopteryx-js @ [http://www.phyloxml.org/archaeopteryx-js/bcl2\\_js.html](http://www.phyloxml.org/archaeopteryx-js/bcl2_js.html)
  - TreeLink @ <http://www.treelinkapp.com>
  - T-REX @ <http://www.trex.uqam.ca>
  - AQUAPONY @ <http://www.lirmm.fr/~cazaux/AQUAPONY/>
  - etc.

# iTOL

- Web based
- Highly customizable/programmable
- Interactive interface
- Able to export trees in several formats
- Tree storing allowed
- Able to load really large trees





# iTOL demo – Uploading Data

1. Go to <http://itol.embl.de/>
2. If you wish to save your trees from session to session you may register
3. Go to Upload. There, you can copy our\_tree.nw or save it locally and upload it as Newick, Nexus or PhyloXML format. Then click upload!

# our\_tree.nw

```
(Centruroides:1.866817169516780e-01,Synsphyronus:3.982413562183681e-01,((Lip  
histius:1.586096567169307e-01,(Mastigoproctus:1.453966099439421e-01,Damon:1.  
332103864420345e-01)1.00:1.959232427470038e-02)1.00:2.980038140121848e-02,((  
Limulus:1.976959421750321e-01,(Peripatopsis_long_iso:3.261872681877993e-01,S  
cutigera:2.212767162268583e-01)1.00:1.057606285127356e-01)1.00:1.75486204668  
1610e-02,((Eremobates:1.924502405585649e-01,(Ixodes:3.038900301437783e-01,Te  
tranychus:7.026474543095570e-01)0.93:3.270977853676584e-02)0.93:2.1597666642  
09322e-02,(Metasiro:2.402845336869420e-01,((Ricinoides:1.810767667451328e-02  
,R_karschii:1.949305408859397e-02)1.00:2.919091302746515e-02,(Pseudocellus:4  
.098385269473430e-02,(Cryptocellus_Bocas:2.548915750691317e-02,Cryptocellus_  
becki:2.383929304335081e-02)1.00:2.194619857092223e-02)1.00:1.13747331795313  
1e-02)1.00:1.342660962530040e-01)1.00:1.510542954930570e-02)0.93:1.019147450  
482914e-02)0.93:1.829267541645866e-02)0.93:2.236446951190263e-02);
```

# iTOL demo – Uploading Data

Use this page to upload and visualize a new phylogenetic tree. It should be in a plain text file and in a supported format (Newick, Nexus or PhyloXML). You can also use *.jplace* files generated by RaxML or pplacer. Please check the [help pages](#) for detailed instructions.

Trees uploaded anonymously will be stored for 30 days, and are not protected from modifications by other users. If you want to keep them private and protected, or have multiple trees to visualize, we recommend creating [an iTOL personal account](#). If you already have an account, please [login first](#).

Datasets and other annotation should be dragged and dropped directly onto the interactive tree. Please check the [help pages](#) for detailed instructions and dataset template files.

Upload  
your tree  
here

Upload a new tree

Tree name:  optional

Paste your tree into the box below, or select a file using the Tree file selector. You can also simply drag and drop the tree file onto the page.

Tree text:

Tree file:  Ningún archivo seleccionado

If you have trouble uploading your tree or datasets, please [contact us](#).

Paste your  
tree here

Tree text:

Tree file:

 Ningún archivo seleccionado

If you have trouble uploading your tree or datasets, please [contact us](#).



# iTOL demo – Control Panel

Once in the graphical interface we can go to control panel where we can change different representation values:

- Normal, circular or unrooted trees
- Branch length
- Support
- Tree scale
- Export image
- Datasets (More about this later)
- Others (Try toying around!)

# iTOL demo – Control Panel

ITOL INTERACTIVE TREE OF LIFE

Tree of Life Upload Sharing Help Login

Tree scale: 0.1

Centruroides  
Synsphyronus  
Liphistius  
Mastigoproctus  
Damon  
Limulus  
Peripatopsis long iso  
Scutigera  
Eremobates  
Ixodes  
Tetranychus  
Metasiro  
Ricinoides  
R karschii  
Pseudocellus  
Cryptocellus Bocas  
Cryptocellus becki

Controls

Basic Advanced Datasets Export

Display mode Circular Normal Unrooted

Parameters 0 rotation

Invert Yes No

Branch lengths Use Ignore

Labels Aligned At tips Off

Label shift 0 Dashes On Off

Label font Arial

Font style 20 px B I

Branch lines 1 px

Save/restore view Reset all

Look how many options!

# iTOL demo – Poking the Branches (& Nodes)

We can select any node or leaf by clicking on it. A new menu pops up that allows several functions. The menu is slightly different if the node is internal:

- Reroot the tree in that node
- Collapse or prune (remove) the node (only internal)
- Rotate node (only internal)
- Style:
  - Labels
  - Branch color, thickness, style...
  - Color ranges

# iTOL demo – Poking the Branches (& Nodes)

Tree scale: 0.1

After clicking in this node we get this menu

- Centruroides
- Synsphyronus
- Liphistius
- Mastigoproctus
- Damon
- Limulus
- Peripatopsis long iso
- Scutigera
- Eremobates
- Ixodes
- Tetranychus
- Metasiro
- Ricinoides
- R karschii
- Pseudocellus
- Cryptocellus Bocas
- Cryptocellus becki

Node functions

- Collapse node
- Rotate node
- Add node to pruned tree
- Copy leaf labels to clipboard
- Editing**
- Color >
- Style >
- Leaf labels >
- Tree structure >

# iTOL demo – Datasets

iTOL allows a huge range of plots to compliment a tree:

<http://itol.embl.de/help.cgi#annot>

You can attach many types of data to your phylogenetic tree.

Examples:

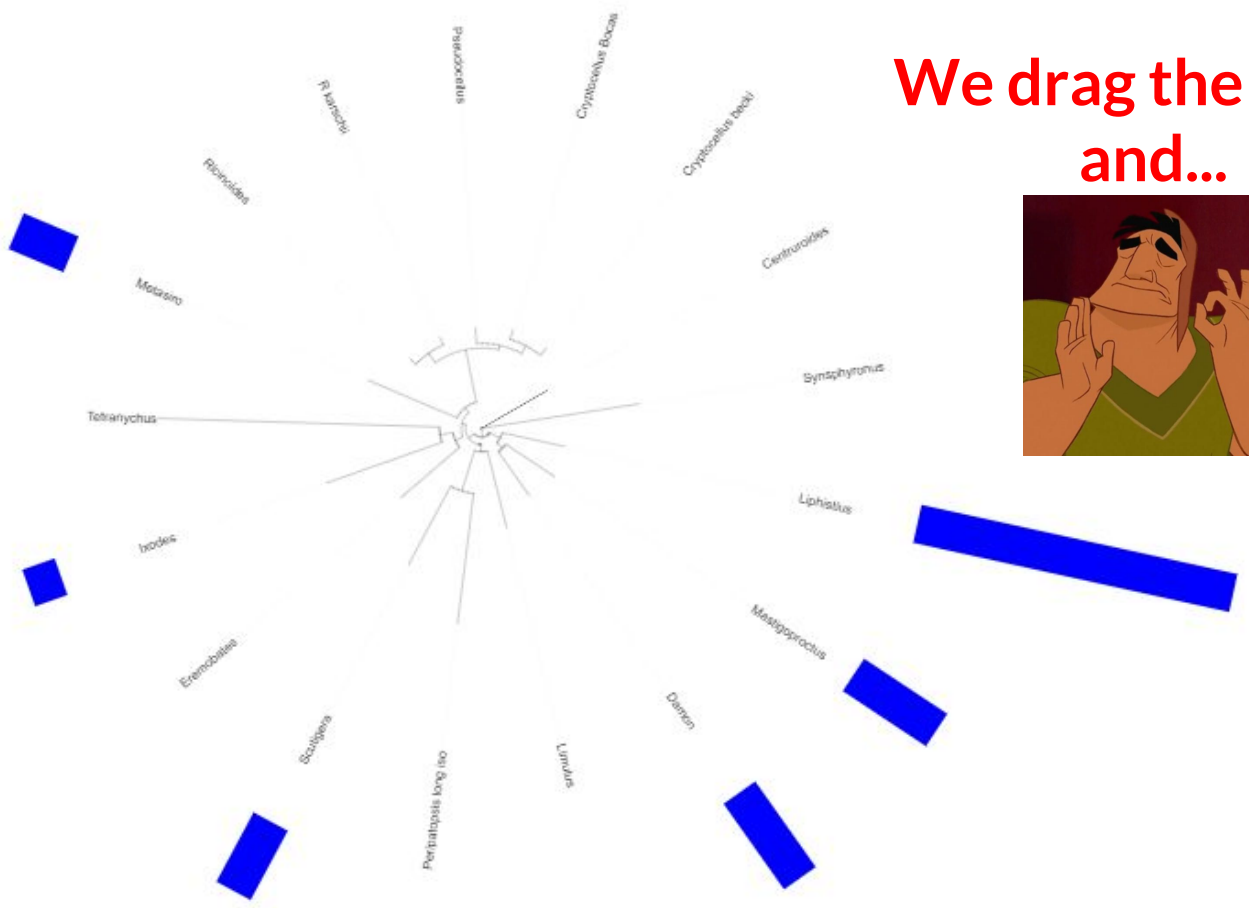
1. Histogram with the number of genes in a given family for each organism
2. Pie chart representing relative frequencies of transposon families
3. Horizontal connections between nodes to represent HGT
4. Phenotypic characters for each branch
5. Protein architecture for each branch

# iTOL demo – Datasets

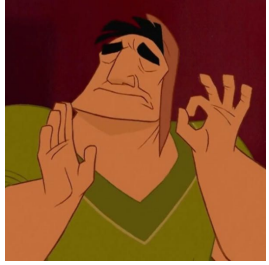
1. Dataset type
  2. Separator (Space, TAB or comma)
  3. Name of the dataset
  4. Other characteristics
  5. Data (from now on we will indicate the node ID and plot values)
- ```
DATASET_SIMPLEBAR
SEPARATOR TAB
DATASET_LABEL simple_bar_testing
COLOR #0000ff
WIDTH 1000
DATA
Ixodes 34
Scutigera 78
Metasiro 59
Liphistius 321
Damon 104
Eremobates 12
Mastigoproctus 99
```



Tree scale: 0.1



We drag the file in  
and...



# iTOL demo – Datasets

You can add as many datasets as you want and visualize them

Once added, you can modify the global parameters through the interactive interface

A number of templates and examples are provided



Tree scale: 1



We can change color, width, etc. Now is thinner and red

**Controls**

Basic | **Advanced** | Datasets | Export

Dataset simple\_bar\_testing

Legend color

Type Simple bar chart

Left margin 150 px

Maximum width 1400 px

Show internal values Yes No

Border style 3 px

Display value Yes No

Bar shift 0

Bar height factor 0.5 x

Bar zero at 0 dataset value

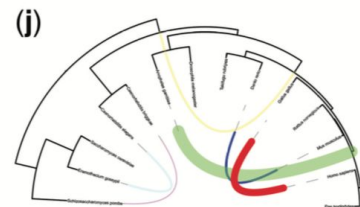
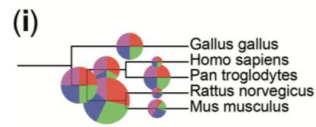
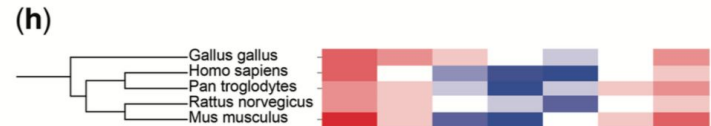
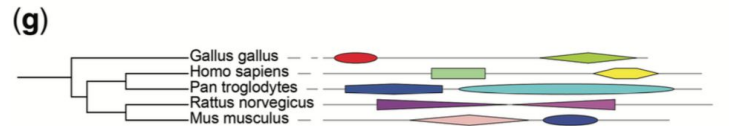
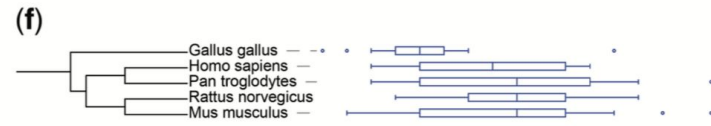
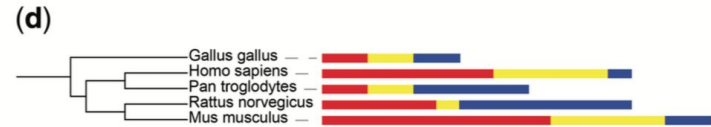
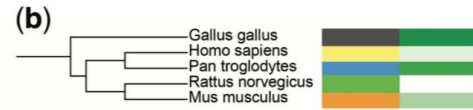
**Datasets**

simple\_bar\_testing

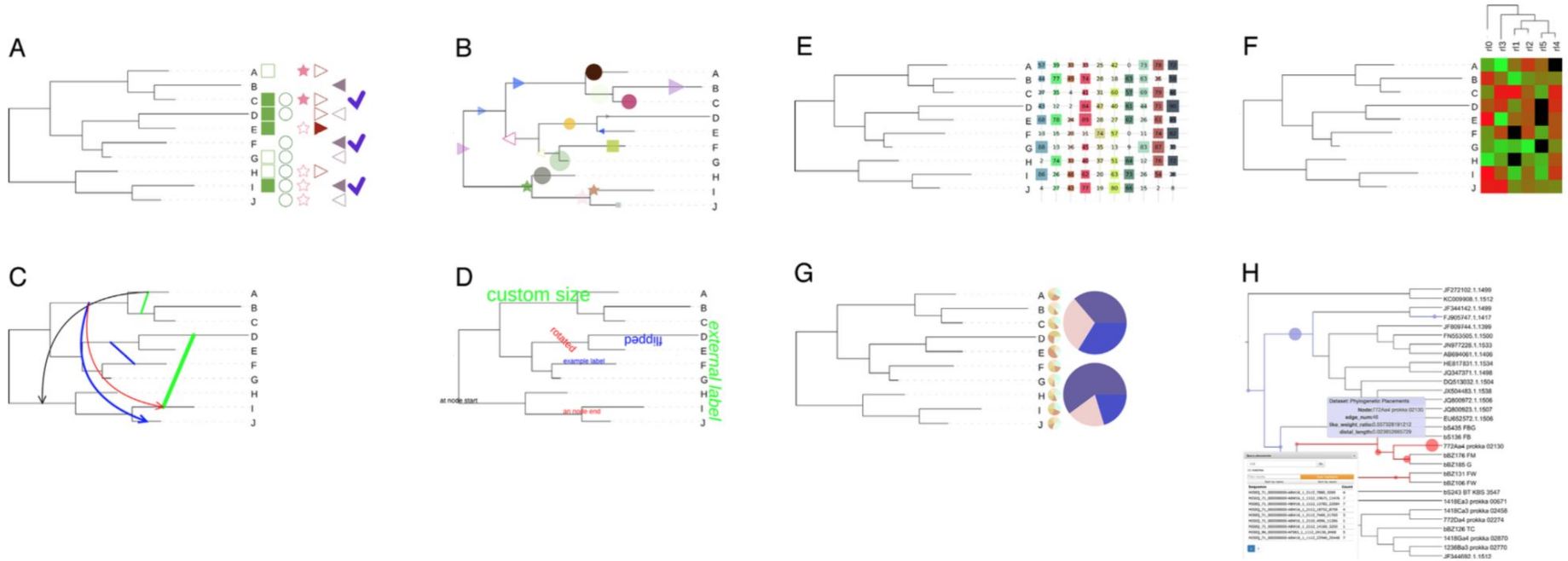
simple\_piechart\_testing

Switch on-off datasets

# iTOL - Dataset Templates



# iTOL - Even More Templates



# Web Portals

- Phylo.IO @ <http://phylo.io>
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- Others:
  - PHYLOViZ Online @ <https://online.phyloviz.net/index>, (10-min YouTube tutorial: <https://www.youtube.com/watch?v=hmbmurFV6ik>)
  - Archaeopteryx-js @ [http://www.phyloxml.org/archaeopteryx-js/bcl2\\_js.html](http://www.phyloxml.org/archaeopteryx-js/bcl2_js.html)
  - TreeLink @ <http://www.treelinkapp.com>
  - T-REX @ <http://www.trex.uqam.ca>
  - AQUAPONY @ <http://www.lirmm.fr/~cazaux/AQUAPONY/>
  - etc.

# EVOLVIEW

Web based

Interactive interface

Exporting tree images in several formats allowed

Highly customizable, programmable

Trees can be stored

Claims to be able to operate with thousands of leaves/tips

# EVOLVIEW



- DEMONS (16 trees)
- SHOWCASES (7 trees)
- showcase 01
- showcase 02
- showcase 03
- showcase 04
- showcase 05
- ss
- shmbian

Basic Advanced Annotation upload Export

«

The main interface area is currently empty, showing a large white space. A vertical scrollbar is visible on the left side of this area.

# EVOLVIEW



## DEMOS (16 trees)

yeast duplications

ensembl compara 2011

a demo of datasets

bars

leaf decoration and stroke

protein domains

group label

group label style 3

group label style 4

dotplots

Charts

with strokes

rect without strokes

heatmaps

column plots

bootstrap value styles

parentheses in leaf names

multiple bootstrap values

TimeLine

## SHOWCASES (7 trees)

Basic Advanced Annotation upload Export

pdf png jpeg tiff nwk nxs nhx xml

### Example of dot plot

● dot 1

● dot 2

● dot 3

● 4

● 8

● 12

● 16

### rect dotplots without strokes

■ dataset 1

■ dataset 2

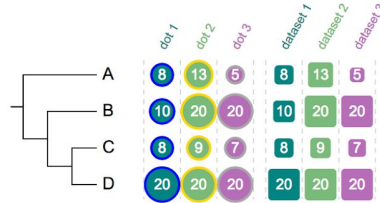
■ dataset 3

■ 4

■ 8

■ 12

■ 16



# EVOLVIEW demo

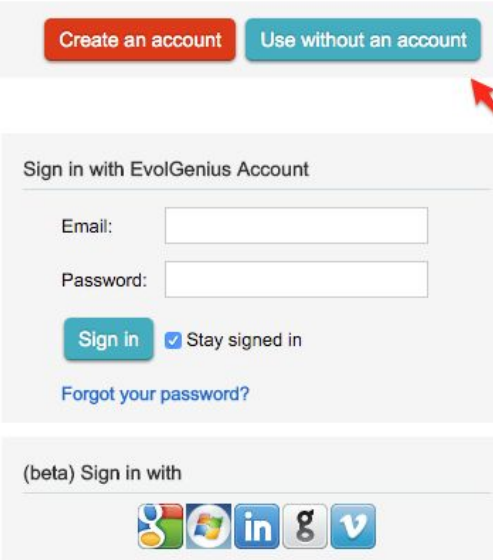
## A quick start

In this "quick start", we'll show you step-by-step how to use this tool to display and customise a tree:

- add a new tree (and a new project),
- change the branch and leaf colors of the tree by uploading some datasets,
- add two extra datasets to the tree,
- play around with the tree and its uploaded datasets, and
- export the customized tree as a pdf file as well as other formats

## Add a new tree to a new project

- at the "login" page, click "Use without an account" 



Create an account Use without an account

Sign in with EvolGenius Account






Email:

Password:

Sign in  Stay signed in

[Forgot your password?](#)

(beta) Sign in with



# EVOLVIEW demo

- at the "mytrees" page, click the folder icon on the "Basic" tab (the only icon that's clickable if no tree is active). in the popup window, enter the following contents and click the button "Submit" at the bottom:

Project: new project

Name: test tree

Data: (chicken, ((mouse, rat), (chimp, human)));



Basic Advanced Annotation upload Export

Upload a new tree

Project: new project ← 2

Name: test tree ← 3

Format: newick (also phyip)

Data: 1 (chicken, ((mouse, rat), (chimp, human))); ← 4

Or upload: Seleccionar archivos ningún archivo seleccionado

Cancel Submit

# EVOLVIEW demo

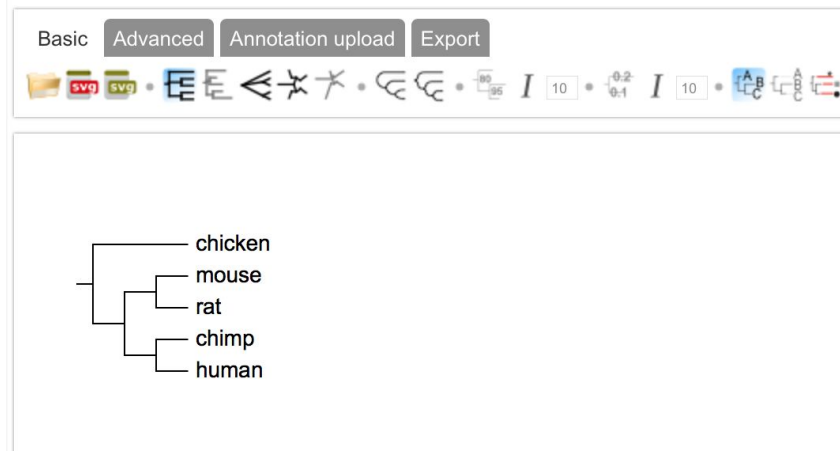
- at the "mytrees" page, click the folder icon on the "Basic" tab (the only icon that's clickable if no tree is active). in the popup window, enter the following contents and click the button "Submit" at the bottom:

Project: new project

Name: test tree

Data: (chicken, ((mouse, rat), (chimp, human)));

- the tree will be shown as the following if there is no error in your input:



# EVOLVIEW demo

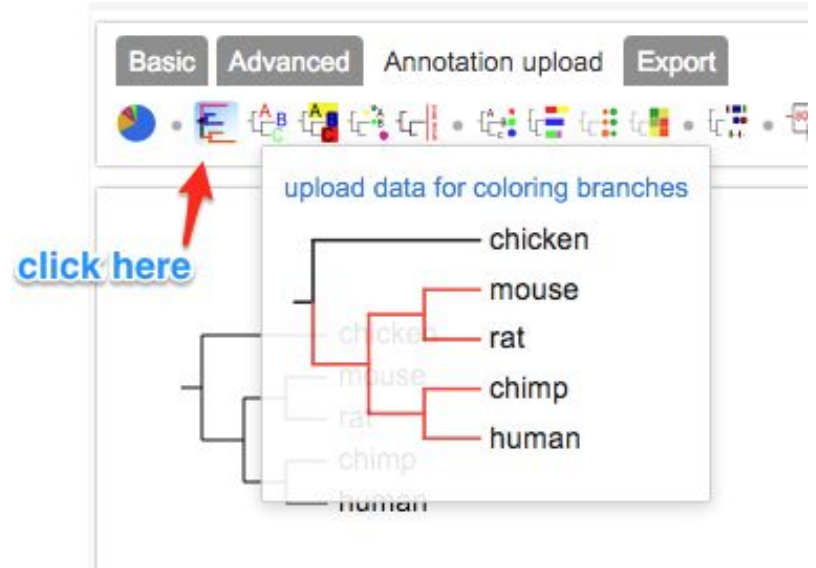
## Change the branch and leaf colors of the tree

in the following we'll add several datasets to change the appearances of the tree.

Let's use the same tree again:

```
(chicken, ((mouse, rat), (chimp, human)));
```

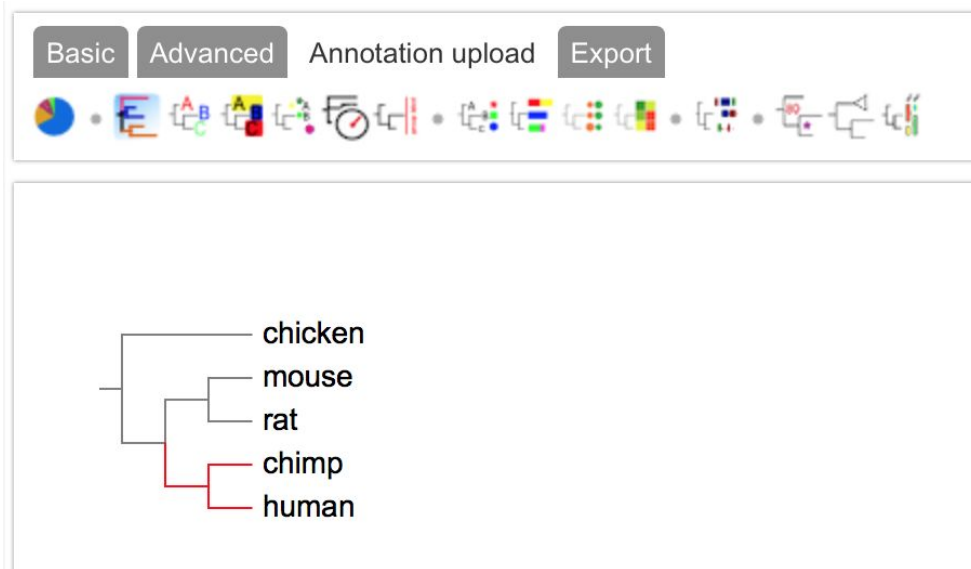
- First of all add a dataset named "branch colors" to change the colors of the branches by clicking the "branch colors" icon on the "Annotation upload" tab:



# EVOLVIEW demo

```
## lines start with # are annotations; you can put an annotation line anywhere in this dataset, provided that
## the # is the first character of the line let the dataset begin: all fields of a line are separated by 'tab'
## first all, color all branches with 'grey'
human,chicken    grey  ad
## and then highlight the branches connecting human and chimp
human,chimp red    ad
```

- After applying the dataset:



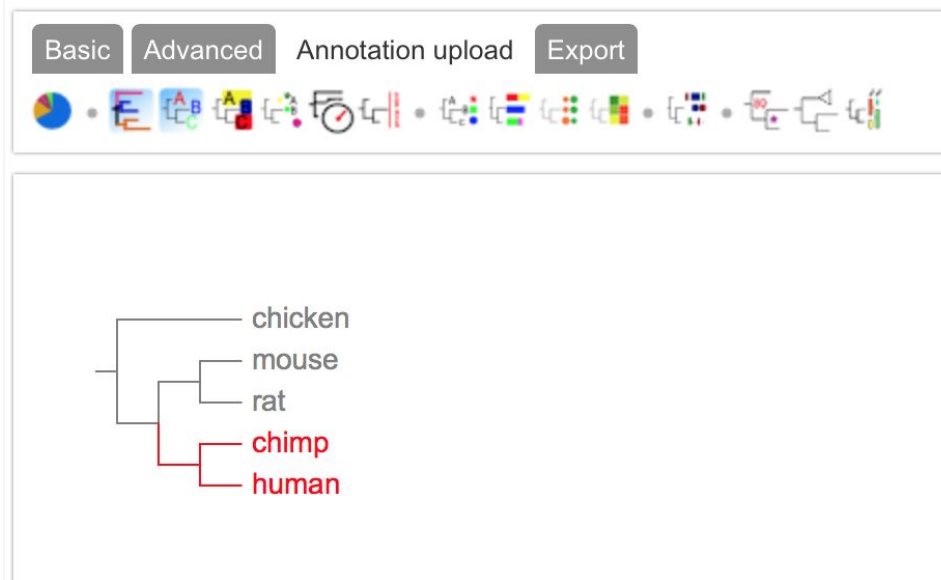
# EVOLVIEW demo

- then add another dataset to change colors of the tree leaves to match the colors of their corresponding branches by clicking the "tree leaf colors" icon on the "Annotation upload" tab:

```
## Let the dataset begin
## Each line of the 'data part' consists three fields sparated by a 'tab' character:
## - The first field specifies the location on the tree; for example 'human' indicates the leaf node
##   representing 'human' or the branch connecting to this leaf node, while 'human,mouse' indicates
##   the internal node representing the last common ancestor (LCA) of human and mouse
## - The second field specifies the color to be applied to the corresponding nodes / branches
## - The third field is optional; it can be one the following 'key-words':
##     ad: the color will be applied to all decendents of the node specified by the first field
##     prefix: the color will be applied to all leaf nodes (or connecting branches) whose names
##     start with the string in the first field
##     suffix: the color will be applied to all leaf nodes (or connecting branches) whose names
##     end with the string in the first field
##     anywhere: the color will be applied to all leaf nodes (or connecting branches) whose names
##     contain the string in the first field
## first all, color all leaves to 'grey'
human,chicken      grey  ad
## then, highlight human and chimp with 'red'
human,chimp red    ad
```

# EVOLVIEW demo

- then add another dataset to change colors of the tree leaves to match the colors of their corresponding branches by clicking the "tree leaf colors" icon on the "Annotation upload" tab:



The screenshot displays the EVOLVIEW software interface. At the top, there are four tabs: "Basic", "Advanced", "Annotation upload", and "Export". The "Annotation upload" tab is currently selected. Below the tabs is a toolbar containing various icons for file operations, tree manipulation, and visualization. The main area of the interface shows a phylogenetic tree with five tips: "chicken", "mouse", "rat", "chimp", and "human". The branches leading to "chimp" and "human" are highlighted in red, indicating that the tree leaf colors have been updated to match the colors of their corresponding branches.

# EVOLVIEW demo

## Add pie charts to the tree

From this section we'll add some more complicated datasets to the tree.

First of all, some pie charts; the pies will be displayed on the tree branches.

- click the "piechart" icon on the "Annotation upload" tab:
- copy and paste the following to the text box of the popup dialog box:

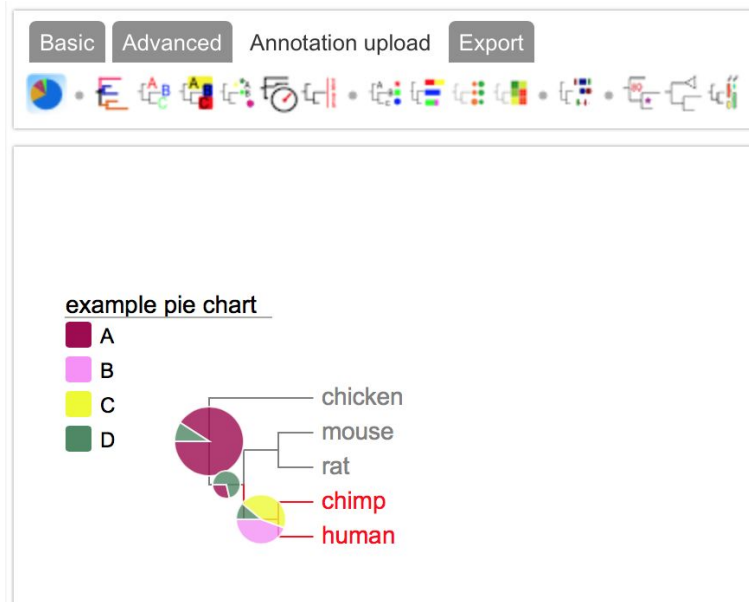
```
## Created on May 25, 2011
## Before the 'data section', now we have a new section that contains lines starting with '!'; this section
## is called the 'modifier section' because it's used to change / modify the default behaviors of the dataset
!Groups           A,B,C,D
!colors           #9F0251,#f88ef9,#effc00,#4D8963
!legendstyle      rect
!title            example pie chart
!maxradius        20
!minradius        8
!opacity          0.8
chicken,human    50,0,0,5
mouse,human      10,0,0,25
chimp,human      0,20,20,5
```

# EVOLVIEW demo

## Add pie charts to the tree

From this section we'll add some more complicated datasets to the tree.  
First of all, some pie charts; the pies will be displayed on the tree branches.

- click the "piechart" icon on the "Annotation upload" tab:
- copy and paste the following to the text box of the popup dialog box:



The screenshot shows the EVOLVIEW software interface. At the top, there are four tabs: "Basic", "Advanced", "Annotation upload", and "Export". Below the tabs is a toolbar with various icons, including a pie chart icon. The main area displays a phylogenetic tree with pie charts on the branches. A legend titled "example pie chart" is shown on the left, with four categories: A (dark red), B (pink), C (yellow), and D (green). The tree shows a large pie chart on the branch leading to "chicken", and smaller pie charts on the branches leading to "mouse", "rat", "chimp", and "human".

example pie chart

- A
- B
- C
- D

chicken  
mouse  
rat  
chimp  
human



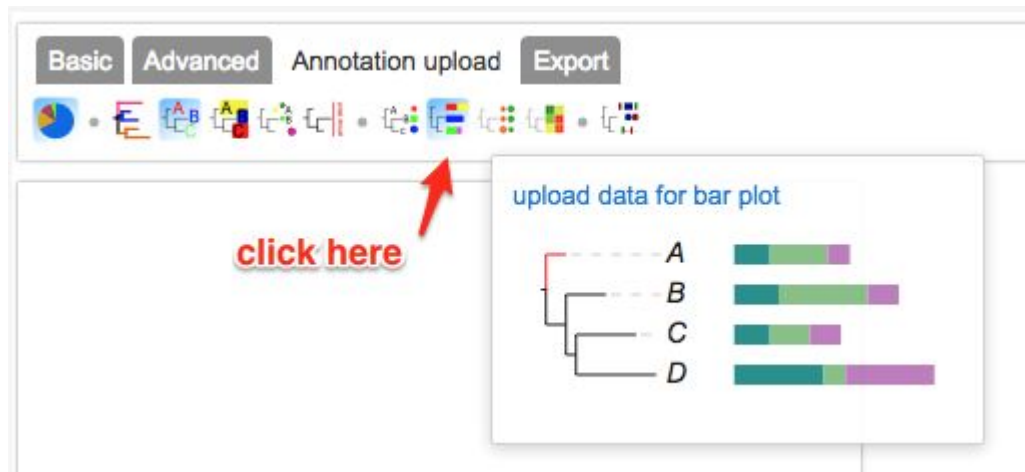
# EVOLVIEW demo

## Add bar plots to the tree (next to the leaf labels)

Here we'll add some bar plots to the tree; the bars will be plotted next to the leaf labels.

- first of all, click the "bar plots" icon on the "Annotation upload" tab:
- choose a name for the dataset and copy and paste the following to the text area in the popup dialog box:

```
##barplots
!groups          a,b,c
!colors          darkblue,darkgreen,darkred
!showLegends     0
!plotwidth       100
!align
!grid
chicken          2,3,1
mouse            8,9,2
human            20,3,4
chimp           10,20,1
rat              4,6,5
```



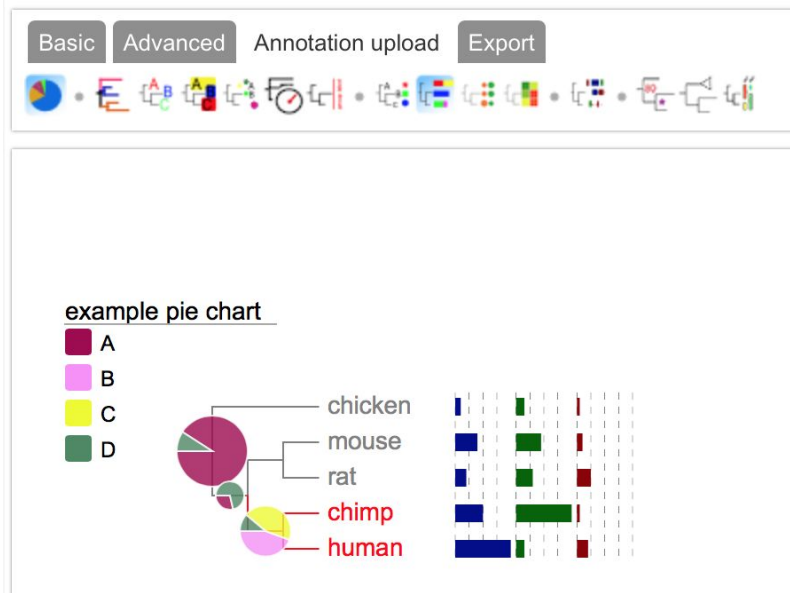
The screenshot shows the EVOLVIEW software interface. At the top, there are four tabs: "Basic", "Advanced", "Annotation upload", and "Export". The "Annotation upload" tab is selected. Below the tabs is a toolbar with various icons, including a bar plot icon. A red arrow points to this icon with the text "click here". Below the toolbar is a large text area. A popup dialog box is open, titled "upload data for bar plot". The dialog shows a tree diagram with four leaf nodes labeled A, B, C, and D. Next to each node is a horizontal bar plot with three segments: dark blue, dark green, and dark red. The segments are colored according to the legend in the dialog.

# EVOLVIEW demo

## Add bar plots to the tree (next to the leaf labels)

Here we'll add some bar plots to the tree; the bars will be plotted next to the leaf labels.

- first of all, click the "bar plots" icon on the "Annotation upload" tab:
- choose a name for the dataset and copy and paste the following to the text area in the popup dialog box:



The screenshot shows the EVOLVIEW software interface. At the top, there are four tabs: "Basic", "Advanced", "Annotation upload", and "Export". The "Annotation upload" tab is selected. Below the tabs is a toolbar with various icons, including a pie chart icon. The main area displays a tree visualization with pie charts at the leaf nodes. The pie charts are labeled with "chicken", "mouse", "rat", "chimp", and "human". To the right of the tree is a bar plot with vertical bars of different colors (blue, green, red) corresponding to the categories A, B, C, and D. A legend on the left identifies the categories: A (dark red), B (pink), C (yellow), and D (green).

example pie chart

- A
- B
- C
- D

chicken  
mouse  
rat  
chimp  
human

# EVOLVIEW demo

## Add colored objects/ shapes to the tree (next to the leaf labels)

Here we'll add a dataset called "color strips / colored shapes".

- click the "color strips" icon on the "Annotation upload" tab:
- copy and paste the following to the text area in the popup dialog box:

```
##color strips
!groups      a,b,c,d
!colors      blue,green,gray,red
!type        rect,circle,star,strip
!showlegends 1
human        red,green,blue,purple
chimp        purple,darkred,lightgreen,lightblue
mouse        lightblue,yellow
chicken      darkgreen,gray,pink,gray
rat          gray,orange,pink,orange
```

The screenshot shows the EVOLVIEW software interface. The 'Annotation upload' tab is selected, and a popup dialog titled 'upload data for color shapes and strips' is open. A red arrow points to the 'color strips' icon in the toolbar, with the text 'click here' below it. The popup dialog displays a tree structure with four groups (A, B, C, D) and five columns of colored shapes and symbols. The columns are labeled 'strip', 'check', 'rect', 'star', and 'circle'. The shapes are colored according to the legend in the text above.

|   | strip     | check      | rect       | star | circle    |
|---|-----------|------------|------------|------|-----------|
| A | red       | green      | blue       | star | green     |
| B | purple    | darkred    | lightgreen | star | darkred   |
| C | lightblue | lightgreen | lightblue  | star | lightblue |
| D | darkgreen | green      | pink       | star | gray      |

# EVOLVIEW demo

Add colored objects/ shapes to the tree (next to the leaf labels)

Here we'll add a dataset called "color strips / colored shapes".

- click the "color strips" icon on the "Annotation upload" tab:
- copy and paste the following to the text area in the popup dialog box:

The screenshot shows the EVOLVIEW interface with the 'Annotation upload' tab selected. Below the toolbar, there is a preview area containing:

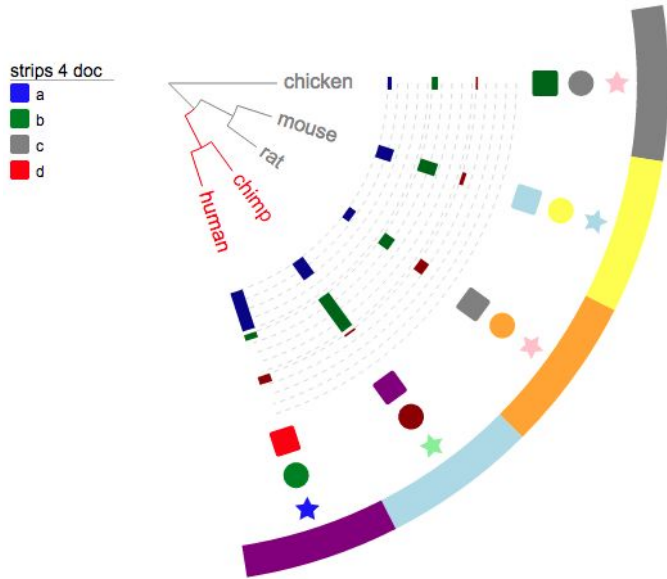
- example pie chart**: A legend with four categories: A (purple), B (pink), C (yellow), and D (green). To the right is a pie chart with four segments corresponding to these colors, connected by lines to a phylogenetic tree.
- color strips**: A legend with four categories: a (blue), b (green), c (grey), and d (red). To the right is a phylogenetic tree with colored bars (strips) next to the leaf labels, corresponding to these categories.

The phylogenetic tree in the preview shows a root branching into 'chicken' and 'mouse', which then branches into 'rat', 'chimp', and 'human'.

# EVOLVIEW demo

Play around and then export the tree to pdf file

- Try different display mode:



- Then download the plot as a PDF file:



[click here](#)

# Phylogenetic Tree Visualization

- **Web Portals:**
  - Phylo.IO @ <http://phylo.io>
  - Interactive Tree of Life viewer (iTOL) @ <http://itol.embl.de>
  - EVOLVIEW @ <http://www.evolgenius.info/evolview>
- **Software:**
  - FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
  - DensiTree @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
  - TreeGraph2 @ <http://treegraph.bioinfweb.info>
- **Toolkits:**
  - PYTHON library: ETE toolkit @ <http://etetoolkit.org>
  - R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
  - JavaScript library: jsPhyloSVG @ <http://www.isphylosvg.com>
- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)

# Software

- **FigTree** @ <http://tree.bio.ed.ac.uk/software/figtree/>
- **DensiTree** @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
- **TreeGraph2** @ <http://treegraph.bioinfweb.info>
- **Others:**
  - **TreeView** @ <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>
  - **NJplot** @ <http://doua.prabi.fr/software/njplot>
  - **Dendroscope** @ <http://ab.inf.uni-tuebingen.de/software/dendroscope/>
  - **Spread3** @ <https://github.com/phylogeography/Spread3>
  - **SeaView** @ <http://doua.prabi.fr/software/seaview>
  - etc.

# FigTree



## FigTree

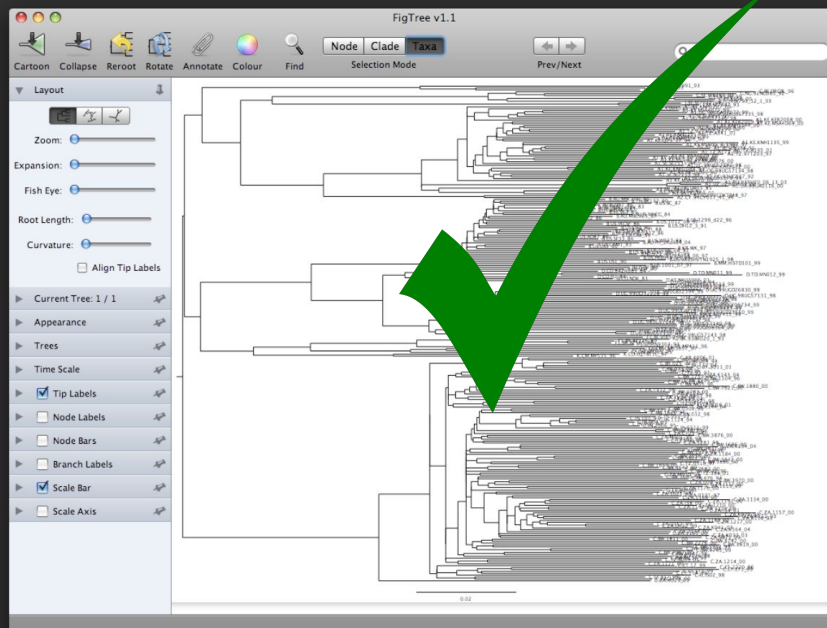
FigTree is designed as a graphical viewer of phylogenetic trees and as a program for producing publication-ready figures. As with most of my programs, it was written for my own needs so may not be as polished and feature-complete as a commercial program. In particular it is designed to display summarized and annotated trees produced by BEAST.

Subscribe to the Figtree Announcement mailing list:

Email:

[Visit this group](#)

This mailing list is for announcements of new versions of FigTree only.






## FigTree



Latest Version - v1.4.3

Bug fixes

Downloads

-  **FigTree v1.4.3.dmg**  
Macintosh OS X executable version. This requires Java 1.6 or better which is installed by Mac OS X Snow Leopard (10.6).  
Downloads: 1
-  **FigTree v1.4.3.zip**  
Windows executable version. This is a ZIP archive.  
Downloads: 1
-  **FigTree\_v1.4.3.tgz**  
Java executable version. Will run on any system with Java 1.5 or better installed, including Linux and Mac OS X. This archive is tarred and gzipped.  
Downloads: 1

New features:



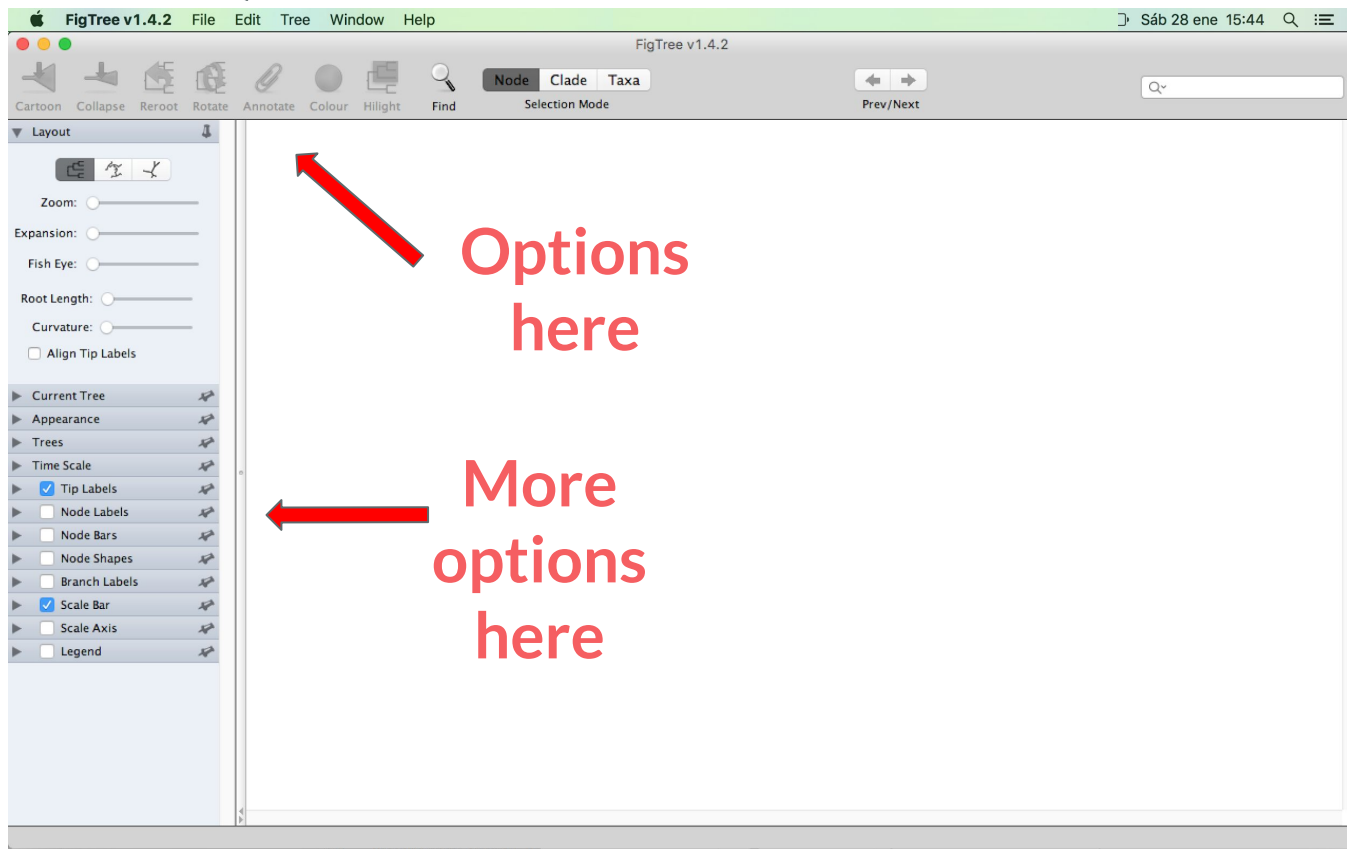
# FigTree

## Features:

- Cross-platform graphical tree display
- Three different tree styles: rectangular, polar and radial
- Display of node heights, branch lengths, support values and other annotations
- Node height range bars if available
- Collapse of clades into triangles
- Colouring of branches and tip labels
- Colouring by annotation (for example, support values)
- Quick search for tip labels or partial tip labels
- Printing and export as PDF graphics

# FigTree

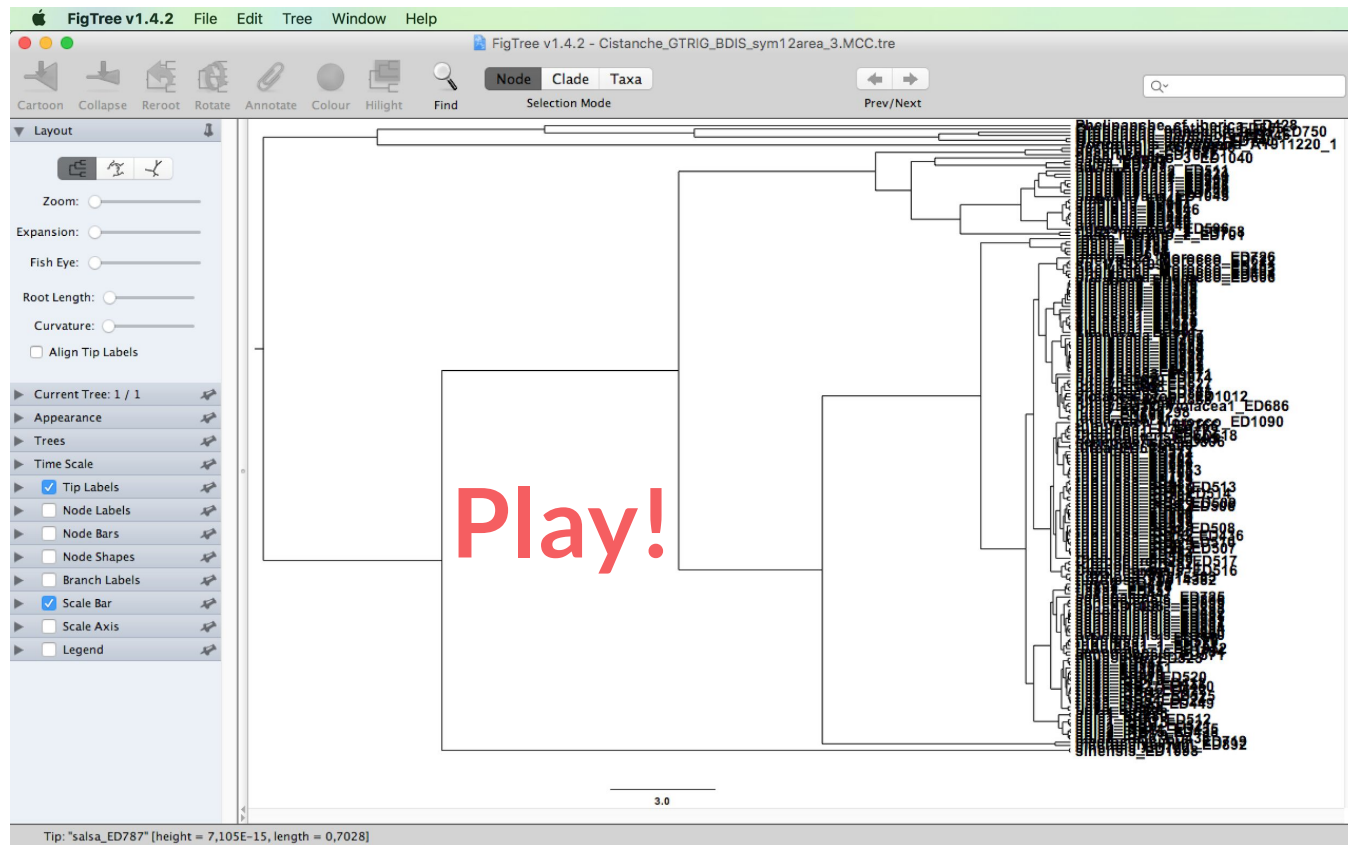
Open files  
here



Options  
here

More  
options  
here

# FigTree



# Software

- **FigTree** @ <http://tree.bio.ed.ac.uk/software/figtree/>
- **DensiTree** @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
- **TreeGraph2** @ <http://treegraph.bioinfweb.info>
- Others:
  - **TreeView** @ <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>
  - **NJplot** @ <http://doua.prabi.fr/software/njplot>
  - **Dendroscope** @ <http://ab.inf.uni-tuebingen.de/software/dendroscope/>
  - **Spread3** @ <https://github.com/phylogeography/Spread3>
  - **SeaView** @ <http://doua.prabi.fr/software/seaview>
  - etc.

# DensiTree

## Contents:

[INTRODUCTION](#)

[DOWNLOAD/INSTALLATION](#)

[META DATA](#)

[GEOGRAPHY](#)

[FAQ/How to's](#)

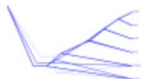
[SUPPORT & LINKS](#)

[WHAT IS NEW](#)

[ACKNOWLEDGMENTS](#)

## Introduction

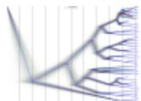
Bayesian hierarchical clustering methods provide a powerful tool for phylogenetic analysis, linguistic research and hierarchical clustering in general such as applied in marketing, political science, customer preference grouping etc. Bayesian methods use MCMC sampling which results in a large number of trees representing the distribution over all possible hierarchies. DensiTree is a program for qualitative analysis of sets of trees. To get an impression of the capabilities of DensiTree, have a look at the gallery below (click thumb nails to get larger image).



Show only consensus trees. This set shows that there is very little uncertainty in the topology of most of the tree, except for the few splits near the root.



Show only consensus trees. This highlights the uncertainty inside the clades, but shows that the split at the root into two groups is very certain (split into progressive and conservative politicians).



Show tree height by height grid and height bar. This tree set nicely demonstrates the increase in uncertainty of the node heights going from the leaves to the root.



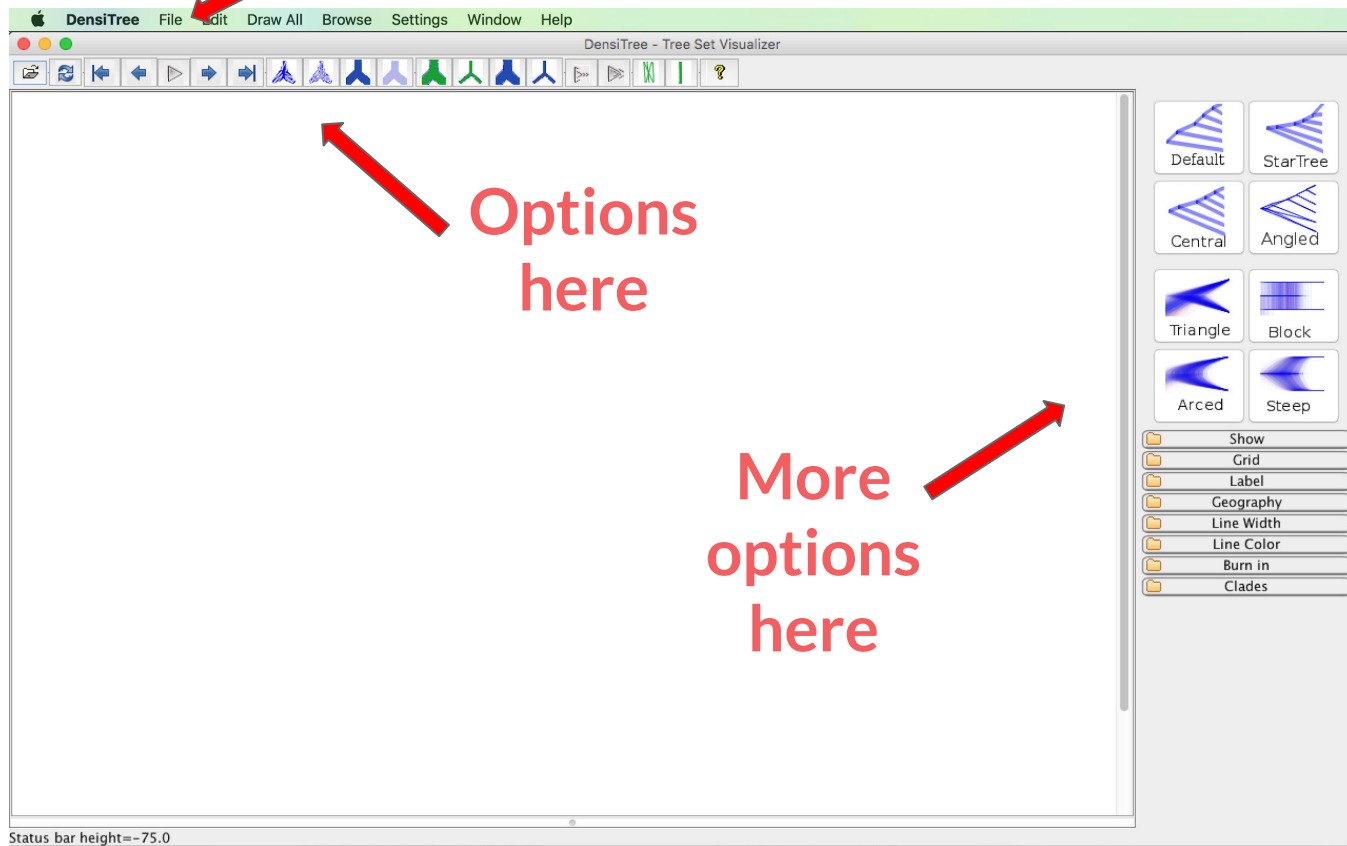
As Figure preceding but in block trees. This tree set was generated with calibration points, which show up as dense node heights, for example, the parent of Rrr and Bbb.



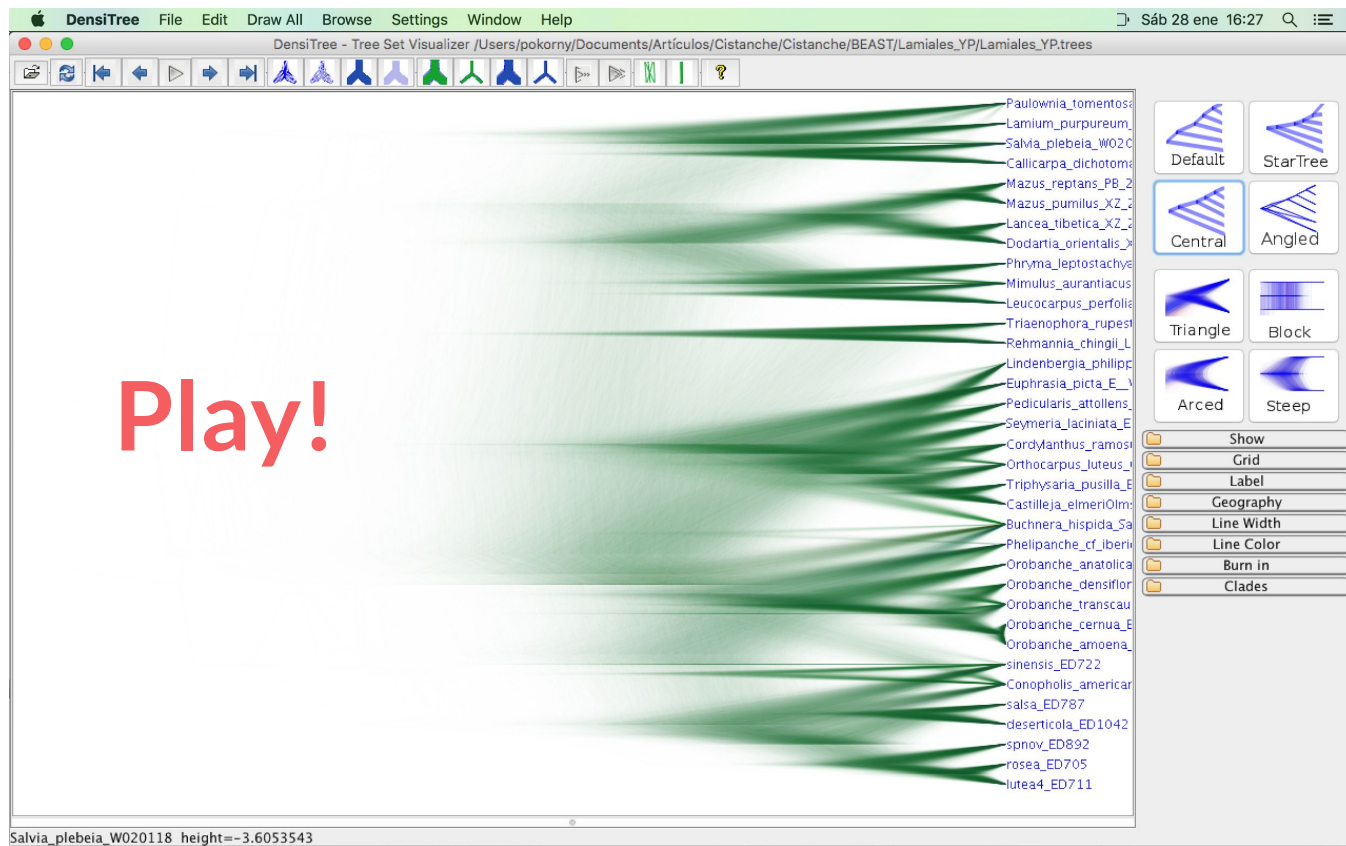
Decreased width of consensus trees, only consensus trees drawn. Intensity of consensus trees needed to be increased considerably. This is useful when there is large uncertainty in the topology and hence many consensus trees (over 900 in this example) with little overlap. Without intensity increase they would not show up and only a white image would be shown.

# DensiTree

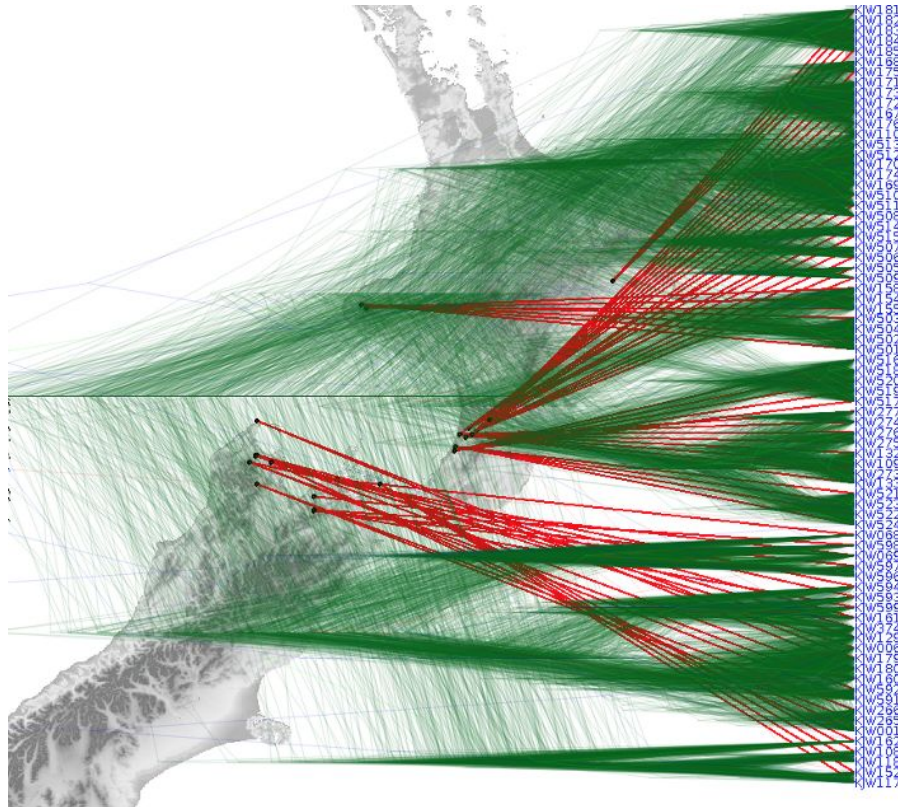
Open files  
here



# DensiTree



# Clouddogram...



<https://www.cs.auckland.ac.nz/~remco/DensiTree/geography.html>



# Cloudogram Fail



<https://www.cs.auckland.ac.nz/~remco/DensiTree/geography.html>

# Cloudogram...

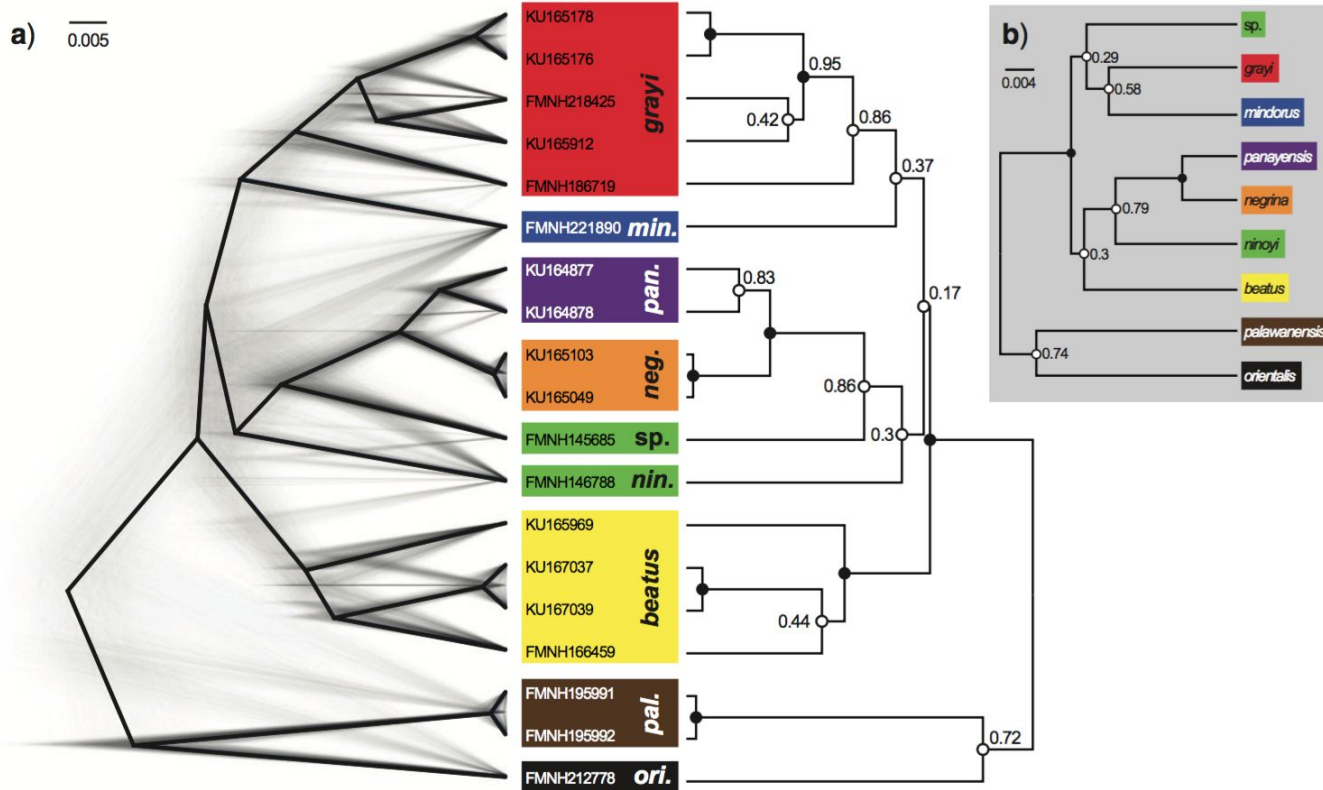


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

# Cloudogram Success

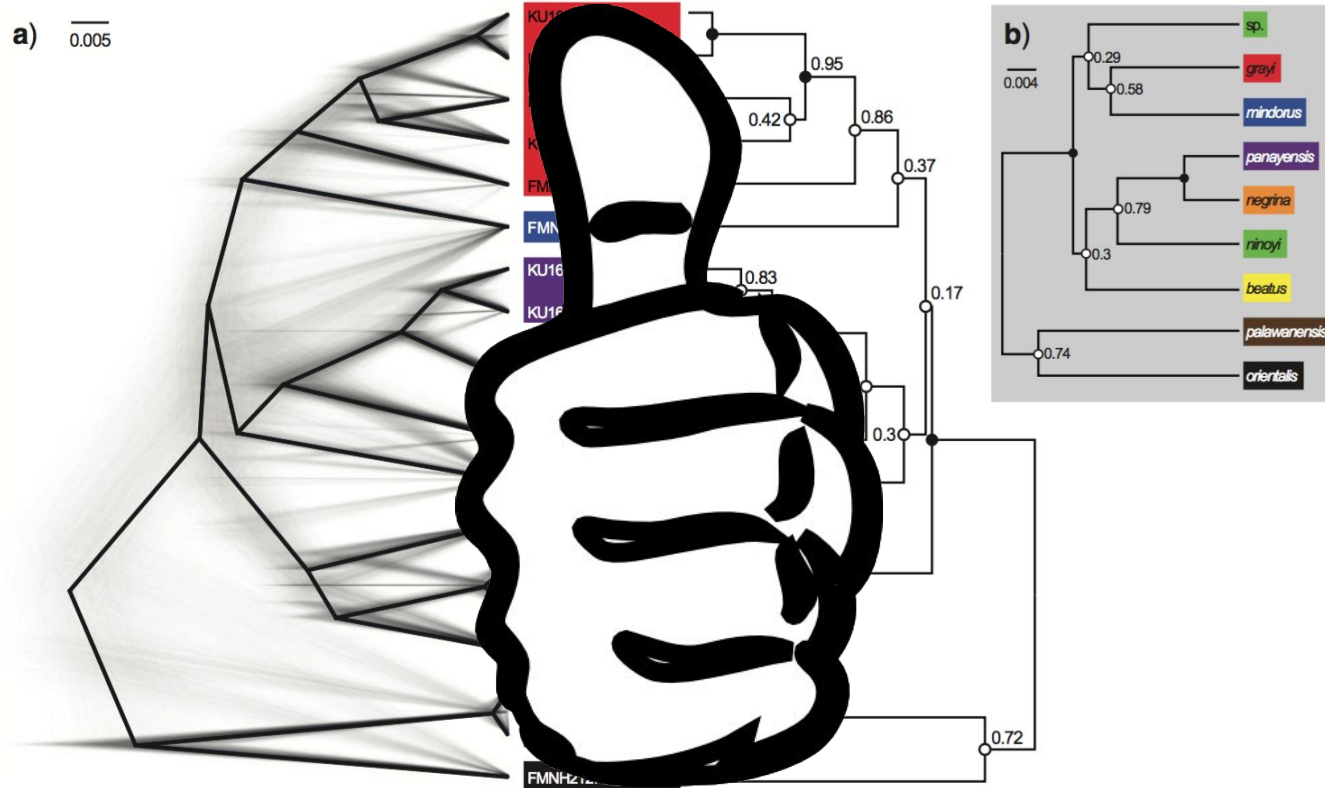


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

# Software

- **FigTree** @ <http://tree.bio.ed.ac.uk/software/figtree/>
- **DensiTree** @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
- **TreeGraph2** @ <http://treegraph.bioinfweb.info>
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  - **Dendroscope** @ <http://ab.inf.uni-tuebingen.de/software/dendroscope/>
  - **Spread3** @ <https://github.com/phylogeography/Spread3>
  - **SeaView** @ <http://doua.prabi.fr/software/seaview>
  - etc.

## TreeGraph 2 - A feature rich and easy to use phylogenetic tree editor

### Download

System requirements  
How to install

### License Help

Alphabetical index  
Video tutorials  
Categories  
Random page

### Development

Subversion repository  
Recent changes  
Documentation

Latest Javadoc  
XTG format

Libraries and tools

### Publications

### Version 1

Subversion repository

### About



### Publication:

Stöver BC, Müller KF:  
TreeGraph 2: Combining  
and visualizing evidence  
from different  
phylogenetic analyses.  
*BMC Bioinformatics* 2010,  
11:7 [Open Access](#)

Highly accessed

TreeGraph  
2.13.0-748 beta

Download

*TreeGraph 2* is a **graphical editor for phylogenetic trees** which allows you to apply lots of graphical formats to the elements of your tree. Moreover, it supports several (visible or invisible) **annotations** (e.g. support values) for every branch or node. These annotations can be imported from *Nexus* tree files or text files containing data in a table (e.g. exported from a spreadsheet program). *TreeGraph 2* is **licensed under GNU General Public License**.

*TreeGraph 2* is developed by **Ben Stöver, Sarah Wiechers, and Kai Müller**.

If you have any questions about *TreeGraph 2* feel free to contact [stoever@bioinfweb.info](mailto:stoever@bioinfweb.info). You can find more software that has been developed by the authors on <http://bioinfweb.info/Software>.

### Citation

*TreeGraph 2* has been published in BMC Bioinformatics:

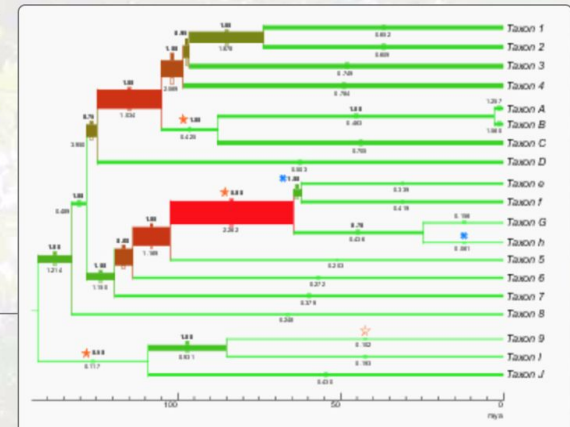
- Stöver B C, Müller K F: *TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses*. *BMC Bioinformatics* 2010, **11**:7
- DOI: 10.1186/1471-2105-11-7 [What is this?]

### Key features

- Read trees in *Newick*, *Nexus* format (including annotations in hot comments), *NeXML* or *PhyloXML*
- Import annotations from text files or combine information from different phylogenetic analyses
- An unlimited number of numerical or textual annotations on every branch
- Export trees to various vector and (anti-aliased) pixel graphic formats (e.g. *PDF*, *SVG*, *EMF* or *PNG*)
- Many global and element specific formats like line width or color and text formats
- Versatile editing and formatting options, such as automatically setting branch widths or colors according to the value of any attached data
- Editing operations like *rerooting*, *ladderizing* or *moving* and *collapsing* nodes or *copying* or *manually creating* whole clades

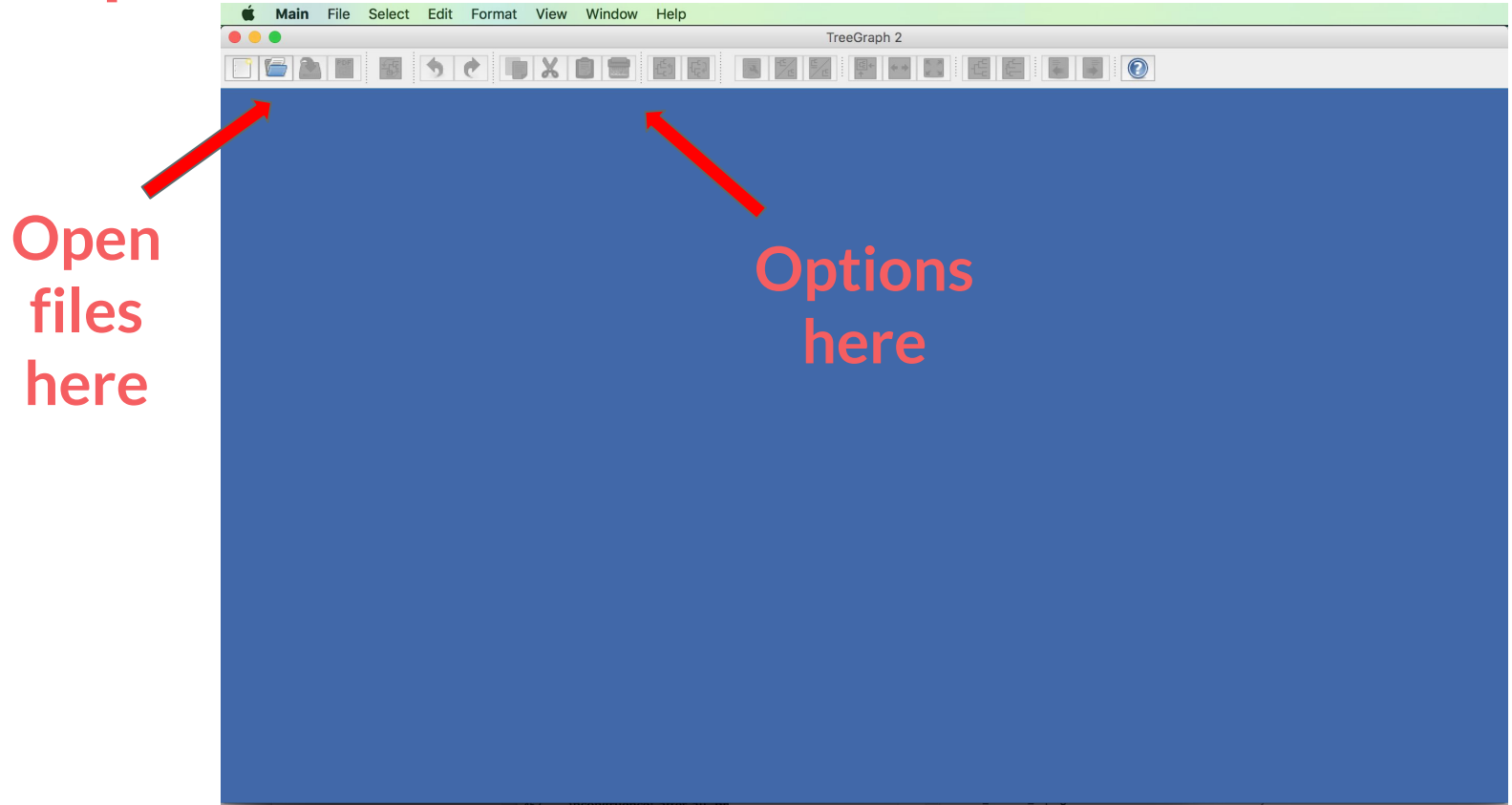
### Getting started

- Download *TreeGraph 2*
- Documentation (help system)
- Tutorials

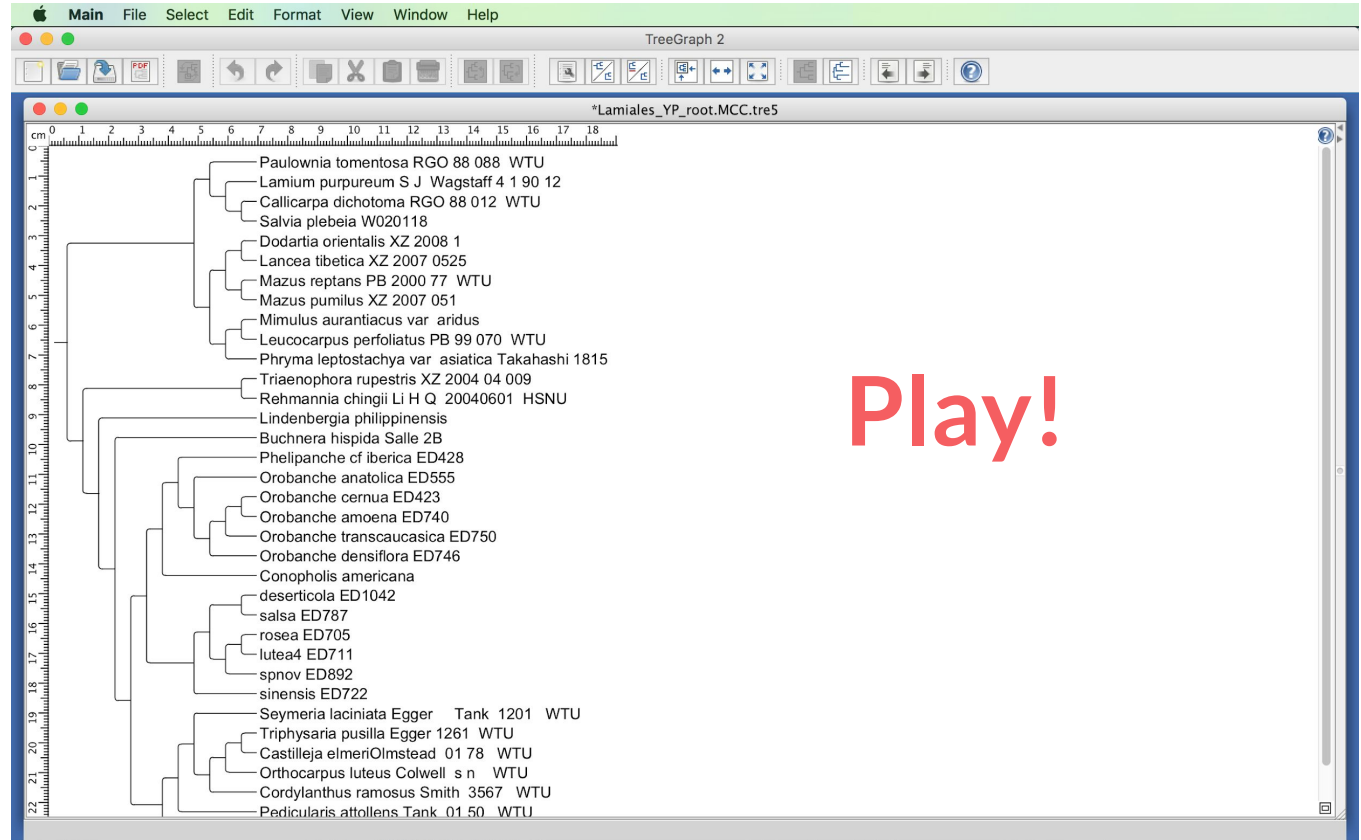


Example of some possible formats in *TreeGraph 2* [Enlarge]  
[Download]

# TreeGraph 2



# TreeGraph 2



# TreeGraph 2 – Documentation

## Feature overview

### The application

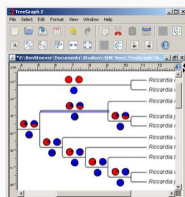
- Main menu
- Tool bar
- Document window
- Synchronizing tree selections

### Import/export

- Open files (Newick, Nexus (including hot comment annotations), NeXML, PhyloXML)
- Adding support values (Merging support values from different analyses)
- Importing node/branch data (Importing annotations from tables)
- Importing ancestral state probabilities
- Exporting commands for ancestral state analyses
- Exporting trees as graphics
- Exporting trees as Newick/Nexus files
- Exporting node/branch data (Exporting annotations to tables)
- Exporting pie chart label colors

### Parts of a TreeGraph 2 document

- Document element
- Node
- Branch
- Label
- Text label
- Icon label
- Pie chart label
- Legend
- Scale bar



### Formatting

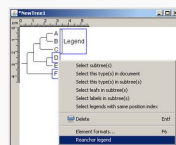
- Element formats
- Document formats
- Set colors by node/branch data (Allows you to display annotations as colors.)
- Set distance values by node/branch data (Allows you to display annotations e.g. as branch widths or text heights.)
- Scaling distance values
- Automatically position labels

### Annotations

- Node/branch data
- Text label
- Hidden node/branch data
- Adding support values
- Copying node/branch data
- Calculating node/branch data (Allows you to calculate annotations by mathematical expressions from other annotations.)
- Deleting node/branch data outside interval
- Data table of the document window

### Tree editing

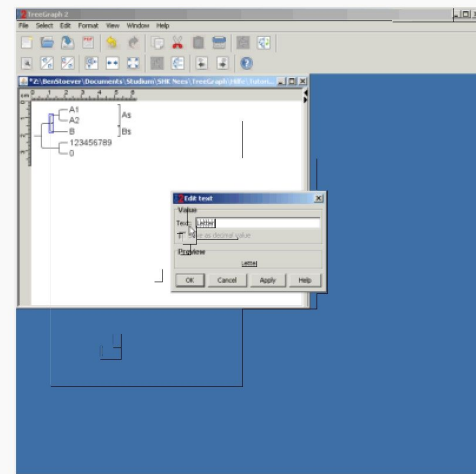
- Inserting nodes
- Collapsing nodes
- Collapsing nodes by support
- Anchoring legends
- Copying/cutting document elements
- Laddering
- Sorting terminal nodes
- Moving nodes
- Rerooting
- Editing text element values
- Changing branch lengths
- Replace text in node/branch data



## Video tutorials

In addition to the articles on single features a set of [screencasts](#) is provided that allow you to learn how to use TreeGraph 2 step by step. Currently the following screencasts are available:

- Combining support values from different analyses in one tree
- Creating trees by hand (e.g. helpful in teaching)
- Displaying taxon counts of the angiosperm orders as branch widths



Additional tutorials can be found at the [tutorial main page](#).



# TreeGraph 2 – Video Tutorials

## Video tutorials

---

### Adding support values

This tutorial shows how to merge support values from different analyses in one tree, which is one of the most important features of TreeGraph 2.

[\[Tutorial overview\]](#) [\[First step\]](#) [\[Download files\]](#)

### Creating trees

TreeGraph 2 is one of very few tree editors that allows creating whole new trees without importing any e.g. Nexus file as well as adding new **document elements** (e.g. **nodes**) to existing trees. This can be very helpful e.g. to rapidly generate a tree for a lecture.

[\[Tutorial overview\]](#) [\[First step\]](#) [\[Download files\]](#)

### Display taxon counts as branch widths

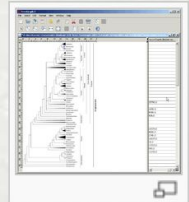
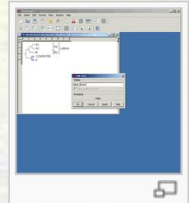
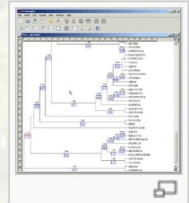
This tutorial demonstrates the ability of TreeGraph 2 to import **node/branch data** from tables and to display numeric values as formats (branch widths in this case). Precisely that means that we will import a text file which contains taxon counts of different angiosperm orders into an angiosperm tree and visualize the data as **branch widths**.

[\[Tutorial overview\]](#) [\[First step\]](#) [\[Download files\]](#)

## Other tutorials

---

- Calculating node/branch data: [Calculating node ages](#)
- Calculating node/branch data: [Converting ancestral character states into probability columns](#)



# Phylogenetic Tree Visualization

- **Web Portals:**
  - Phylo.IO @ <http://phylo.io>
  - Interactive Tree of Life viewer (iTOL) @ <http://itol.embl.de>
  - EVOLVIEW @ <http://www.evolgenius.info/evolview>
- **Software:**
  - FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
  - DensiTree @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
  - TreeGraph2 @ <http://treegraph.bioinfweb.info>
- **Toolkits:**
  - PYTHON library: ETE toolkit @ <http://etetoolkit.org>
  - R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
  - JavaScript library: jsPhyloSVG @ <http://www.jsphylosvg.com>
- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)

# Toolkits

- PYTHON library: ETE3 toolkit @ <http://etetoolkit.org>
- R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
- JavaScript library: jsPhyloSVG @ <http://www.jsphylosvg.com>
- Others:
  - Archaeopteryx @ <https://sites.google.com/site/cmzmasek/home/software/archaeopteryx>
  - PhyD3 @ <https://phyd3.bits.vib.be/index.html>
  - ggtree @ <https://guangchuangyu.github.io/ggtree/>
  - (More on phylogenetics in R here: <https://cran.r-project.org/web/views/Phylogenetics.html>)
  - etc.

# ETE3

- ETE is a python library to manipulate trees. It is used often with large sets of trees because of its ability to perform analyses on many trees automatically.
  - Things within the scope of ETE:
    - Search for orthology / paralogy relationships
    - Search for a given tree topology
    - Identify whether a set of sequences is monophyletic
    - Compare trees
    - Visualize trees
  - Newick tree example:

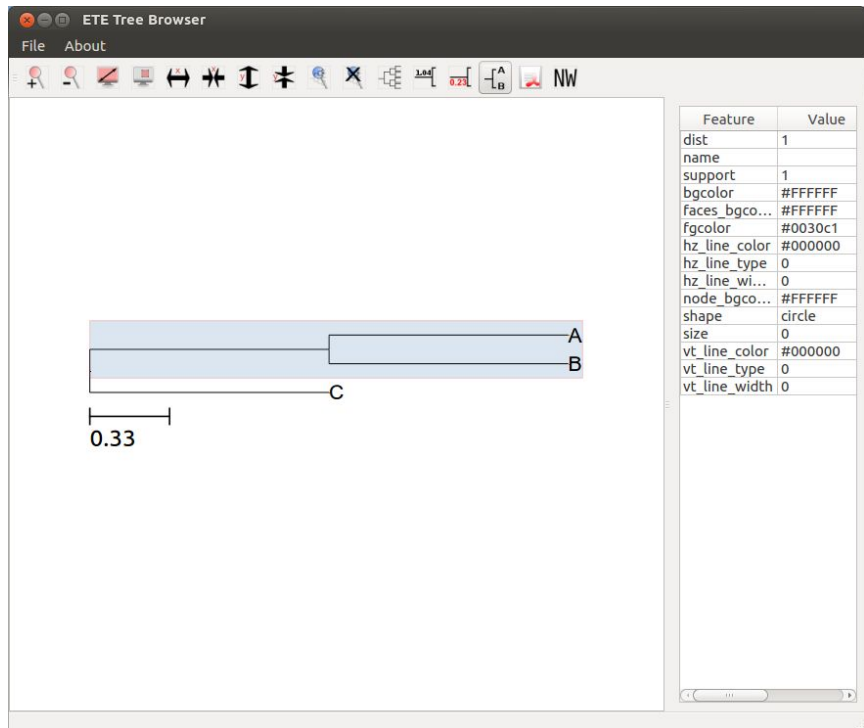
```
(((A:0.1,B:0.2)90:0.2,(C:0.1,D:0.2)80:0.15)70:0.1,E:0.2);
```

# ETE3

Default visualization tool:

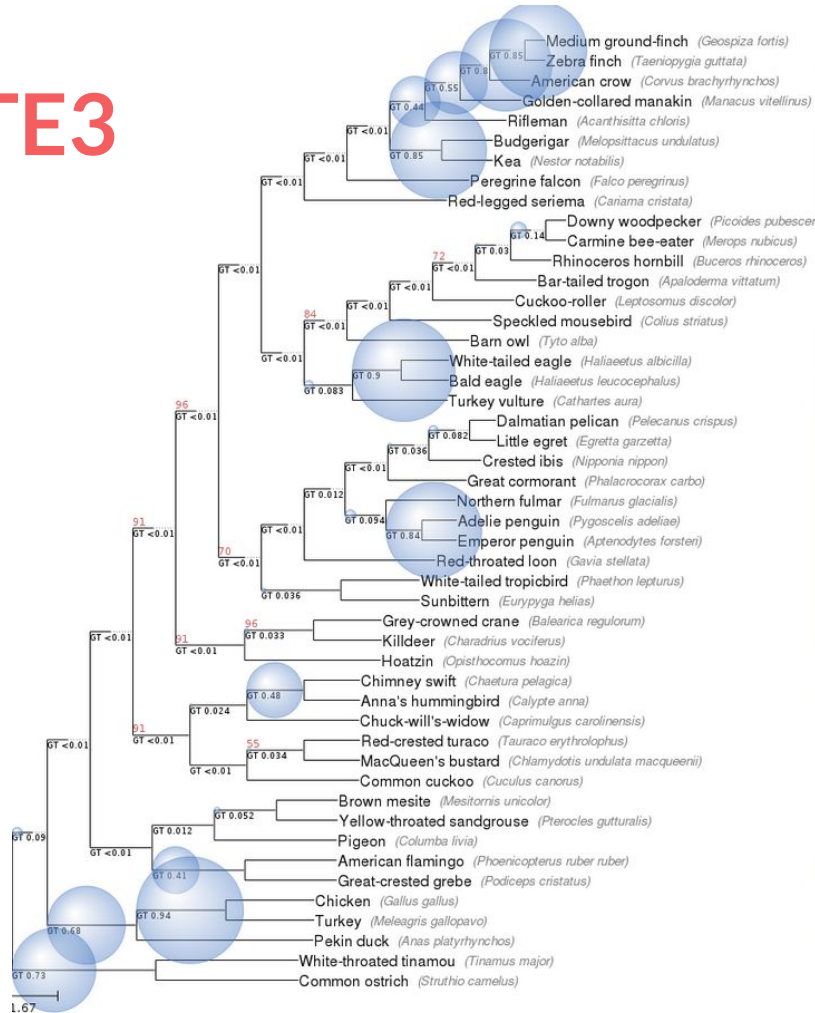
`ete3 view -t INPUT`

Where the INPUT can be a text string of a newick or a file containing a newick



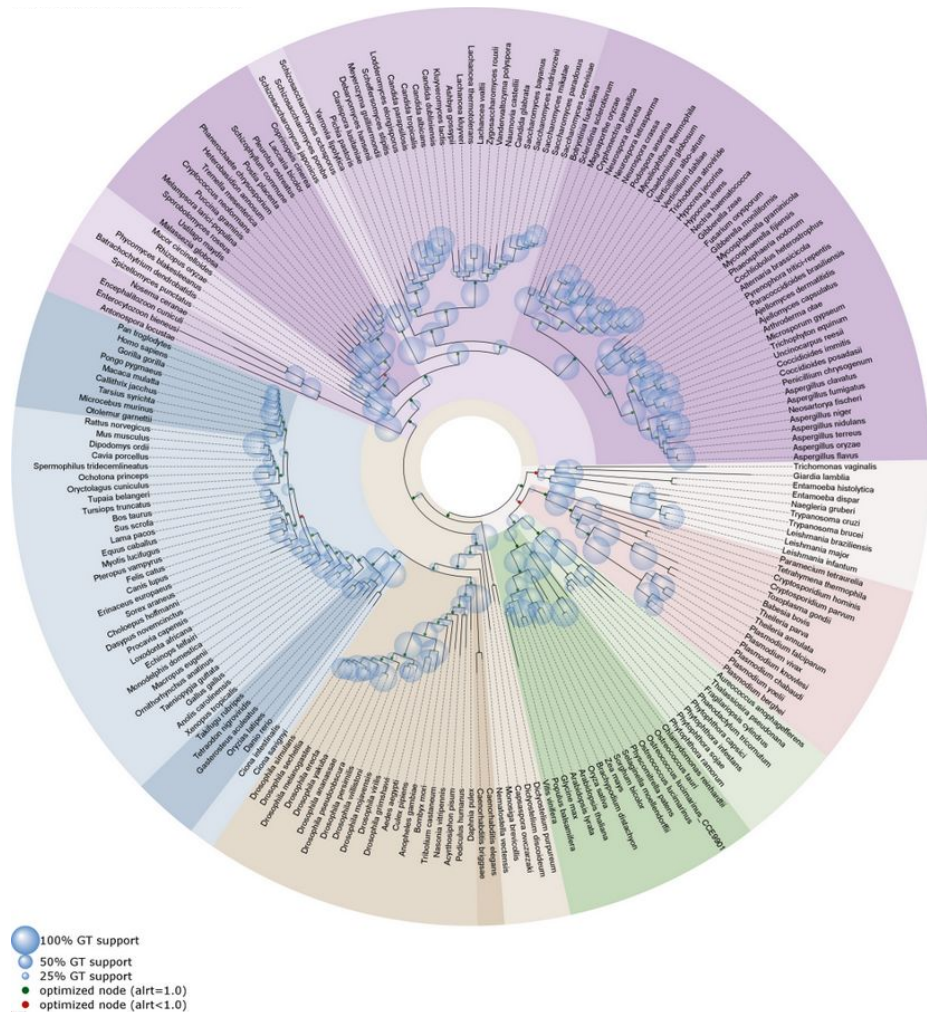
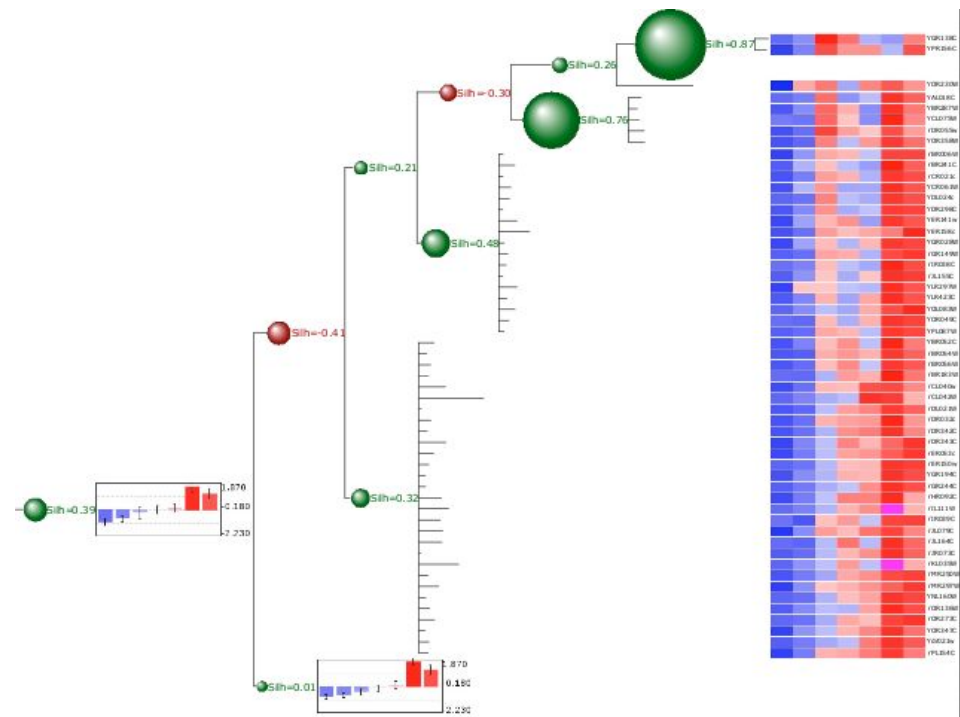
While nice, the default visualization tool is limited

# ETE3



|                          |               |                     |             |                   |                |             |
|--------------------------|---------------|---------------------|-------------|-------------------|----------------|-------------|
| vocal learning           | Neognathae    | Passeriformes       | Passeroidea | Fringillidae      | Emberizinae    | Thraupini   |
| vocal learning           | Neognathae    | Passeriformes       | Passeroidea | Passeroidea       | Estrildidae    | Estrildinae |
| vocal learning           | Neognathae    | Passeriformes       | Corvoidea   | Corvidae          |                |             |
|                          | Neognathae    | Passeriformes       |             | Pipridae          |                |             |
|                          | Neognathae    | Passeriformes       |             | Acanthisittidae   |                |             |
| vocal learning           | Neognathae    | Psittaciformes      |             | Psittacidae       |                |             |
| vocal learning           | Neognathae    | Psittaciformes      |             | Psittacidae       |                |             |
| apex birds-of-prey       | Neognathae    | Falconiformes       |             | Falconidae        |                |             |
| apex birds-of-prey       | Neognathae    | Gruiformes          |             | Cariamiidae       |                |             |
|                          | Neognathae    | Piciformes          |             | Picidae           |                |             |
|                          | Neognathae    | Coraciiformes       |             | Meropidae         |                |             |
|                          | Neognathae    | Bucerotiformes      |             | Bucerotidae       |                |             |
|                          | Neognathae    | Trogoniformes       |             | Trogonidae        |                |             |
|                          | Neognathae    | Coraciiformes       |             | Leptosomidae      |                |             |
|                          | Neognathae    | Coliiformes         |             | Coliidae          |                |             |
| apex birds-of-prey       | Neognathae    | Strigiformes        |             | Tytonidae         |                |             |
| apex birds-of-prey       | Neognathae    | Falconiformes       |             | Accipitridae      | Accipitrinae   |             |
| apex birds-of-prey       | Neognathae    | Falconiformes       |             | Accipitridae      | Accipitrinae   |             |
| apex birds-of-prey       | Neognathae    | Ciconiiformes       |             | Cathartidae       |                |             |
| aquatic and semi-aquatic | Neognathae    | Pelecaniformes      |             | Pelecanidae       |                |             |
| aquatic and semi-aquatic | Neognathae    | Ciconiiformes       |             | Ardeidae          |                |             |
| aquatic and semi-aquatic | Neognathae    | Ciconiiformes       |             | Threskiornithidae |                |             |
| aquatic and semi-aquatic | Neognathae    | Pelecaniformes      |             | Phalacrocoracidae |                |             |
| aquatic and semi-aquatic | Neognathae    | Procellariiformes   |             | Procellariidae    | Procellariinae |             |
| aquatic and semi-aquatic | Neognathae    | Sphenisciformes     |             | Spheniscidae      |                |             |
| aquatic and semi-aquatic | Neognathae    | Sphenisciformes     |             | Spheniscidae      |                |             |
| aquatic and semi-aquatic | Neognathae    | Gaviiformes         |             | Gaviidae          |                |             |
| aquatic and semi-aquatic | Neognathae    | Pelecaniformes      |             | Phaethontidae     |                |             |
| aquatic and semi-aquatic | Neognathae    | Gruiformes          |             | Eurypygidae       |                |             |
| aquatic and semi-aquatic | Neognathae    | Gruiformes          |             | Gruidae           |                |             |
| aquatic and semi-aquatic | Neognathae    | Charadriiformes     |             | Charadriidae      |                |             |
|                          | Neognathae    | Opisthocomiformes   |             | Opisthocomidae    |                |             |
|                          | Neognathae    | Apodiformes         |             | Apodidae          |                |             |
|                          | Neognathae    | Trochiliformes      |             | Trochilidae       |                |             |
|                          | Neognathae    | Caprimulgiformes    |             | Caprimulgidae     | Caprimulginae  |             |
|                          | Neognathae    | Musophagiformes     |             | Musophagidae      |                |             |
|                          | Neognathae    | Gruiformes          |             | Otididae          | Chlamydotis    |             |
|                          | Neognathae    | Cuculiformes        |             | Cuculidae         |                |             |
|                          | Neognathae    | Gruiformes          |             | Mesitornithidae   |                |             |
|                          | Neognathae    | Ciconiiformes       |             | Pteroclididae     |                |             |
|                          | Neognathae    | Columbiformes       |             | Columbidae        |                |             |
| aquatic and semi-aquatic | Neognathae    | Phoenicopteriformes |             | Phoenicopteridae  | Phoenicopterus |             |
| aquatic and semi-aquatic | Neognathae    | Podicipediformes    |             | Podicipedidae     |                |             |
|                          | Neognathae    | Galliformes         |             | Phasianidae       | Phasianinae    |             |
|                          | Neognathae    | Galliformes         |             | Phasianidae       | Meleagridinae  |             |
| aquatic and semi-aquatic | Neognathae    | Anseriformes        |             | Anatidae          |                |             |
|                          | Palaeognathae | Tinamiformes        |             | Tinamidae         |                |             |
|                          | Palaeognathae | Struthioniformes    |             | Struthionidae     |                |             |

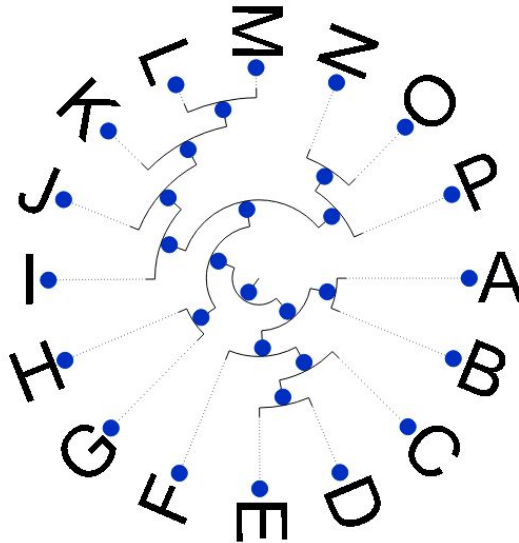
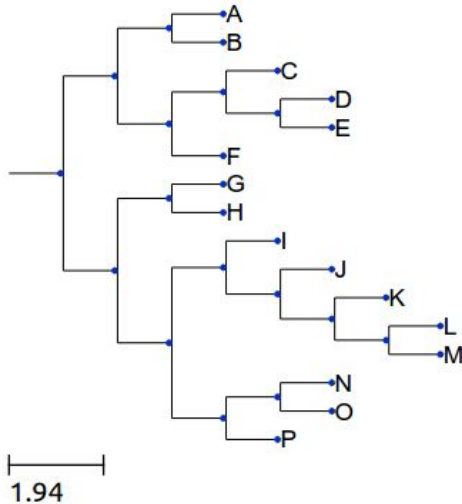
# ETE3



# ETE3

## TreeStyle

- ETE3 can change the visualization of the trees through four parameters: TreeStyle, nodeStyle, faces and layouts.
  - The tree style affects general tree parameters, for instance whether the tree is shown as circular or not:



It can also change whether it shows things such as branch lengths, support, leaf names.

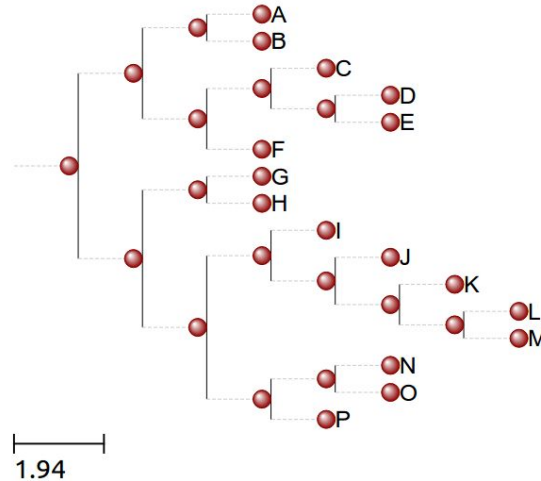
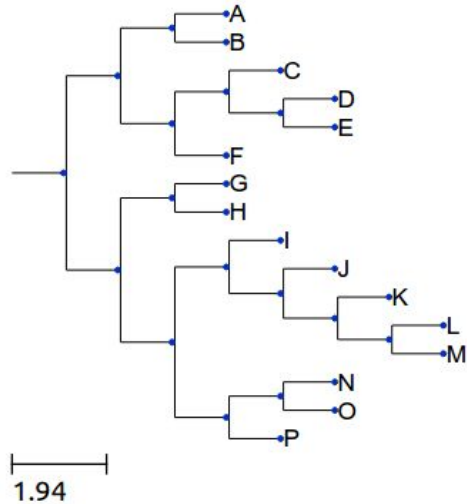
Most importantly it can assign a given layout to a tree (see later).



# ETE3

## NodeStyles

- NodeStyle like treeStyle affects the visualization of individual nodes:

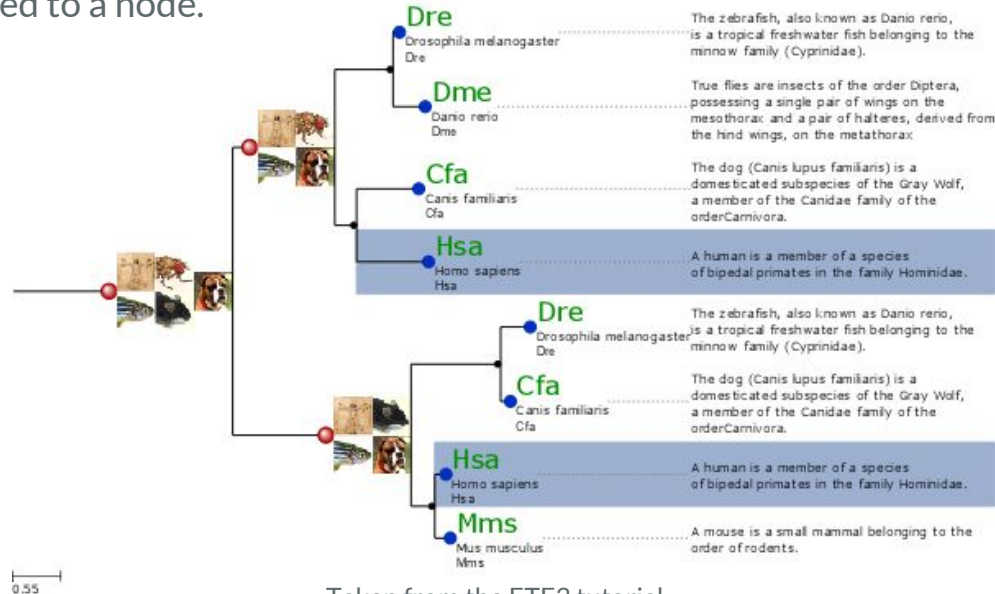


- For instance, the default style for nodes in ETE3 is that they are represented with a blue dot
- This can be modified by calling the node instance and changing some of the characteristics in the node style such as colour or size
- Useful tip: if you don't want them, change the size to 0

# ETE3

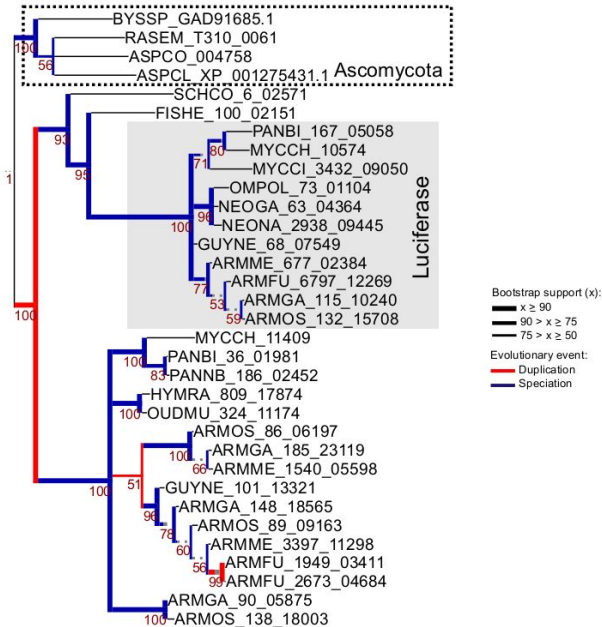
## Faces

- Faces are responsible for adding new elements to the tree. A face can be something as simple as the leaf name, which you can assign a different colour, font or size, or something more complicated as images, plots or geometric elements. Once they have been defined, they need to be associated to a node.



Taken from the ETE3 tutorial

- Layouts are what puts everything together. It's a python function that receives a tree node and receives instructions on how to modify it.



This layout detected the support of each node. If it was below 50 it deleted the node, then it assigned different branch thickness depending on the support. It also coloured the branches according to evolutionary relationships. It deleted the internal node figure and added node support to the image.

Once a tree has been drawn to what you want it, you can render it in pdf or svg format.



# Toolkits

- PYTHON library: ETE3 toolkit @ <http://etetoolkit.org>
- R repository: **PhyTools** @ <https://cran.r-project.org/web/packages/phytools/index.html>
- JavaScript library: jsPhyloSVG @ <http://www.jsphylosvg.com>
- Others:
  - Archaeopteryx @ <https://sites.google.com/site/cmzmasek/home/software/archaeopteryx>
  - PhyD3 @ <https://phyd3.bits.vib.be/index.html>
  - ggtree @ <https://guangchuangyu.github.io/ggtree/>
  - (More on phylogenetics in R here: <https://cran.r-project.org/web/views/Phylogenetics.html>)
  - etc.

# Phytools

R based

This gives you nearly infinite “mathemagical” power, use it wisely

Absurdly powerful drawing tools

Just like ETE, it has many functions beyond tree representation

R is much more specialized than Python



# Phytools demo

First we have to download Phytools. For this, go to R. You can do this by typing 'R' on the terminal or through any R graphic user interface (RStudio, R GUI, QuickR...).

Then we install the package. For this, type:

```
install.packages("phytools", repos="https://cloud.r-project.org")
```

Once finished, check the installation with:

```
packageVersion("phytools")
```

# Phytools demo

Now we load the package with:

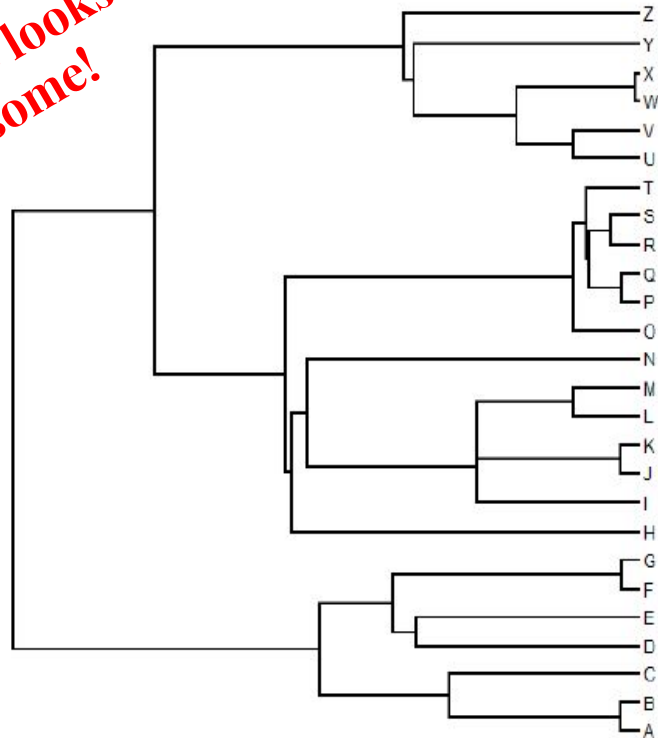
```
require(phytools)
```

Don't you feel all this power already? Let's start simulating a tree and plotting it:

```
tree<-pbtree(n=26,tip.label=LETTERS)
```

```
plotTree(tree)
```

*Our tree looks awesome!*





# Phytools demo

Now we simulate some random data for our amazing tree. We use a Brownian motion function:

```
x<-fastBM(tree)
```

*Remember: You can look at the content of a variable just by typing its name*

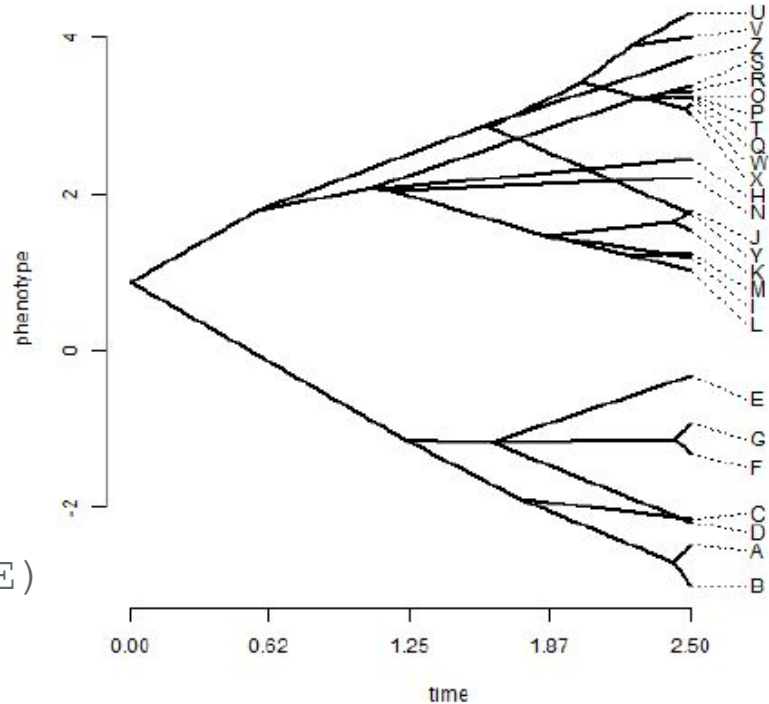
Now we plot a simple traitgram:

```
phenogram(tree,x,spread.labels=TRUE)
```

**This variable stores our tree**

**This one, our data**

**Spread visualization style, show leaf names**



# Phytools demo

Let's try now to represent the values in `x` as dots in the tree. The size indicates the value:

```
dotTree(tree, x, standardize=TRUE)
```

We are going to repeat it now with more data. First we create the data:

```
X<-fastBM(tree, nsim=10)
```

And now we plot again

```
dotTree(tree, X, standardize=TRUE)
```

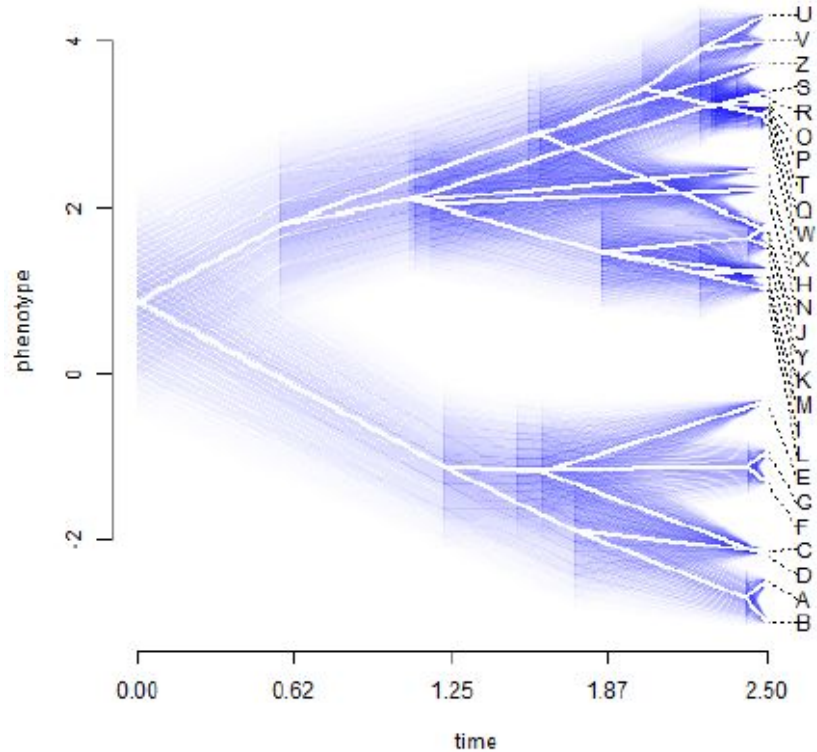
# Phytools demo

Let's try a heat map with our data:

```
phylo.heatmap(tree,X,standardize=TRUE)
```

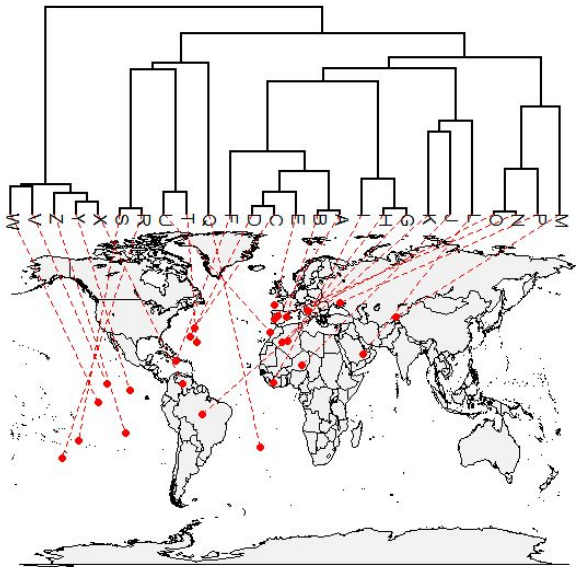
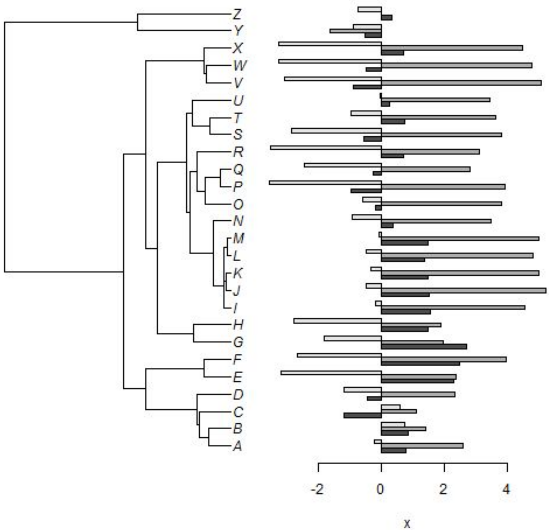
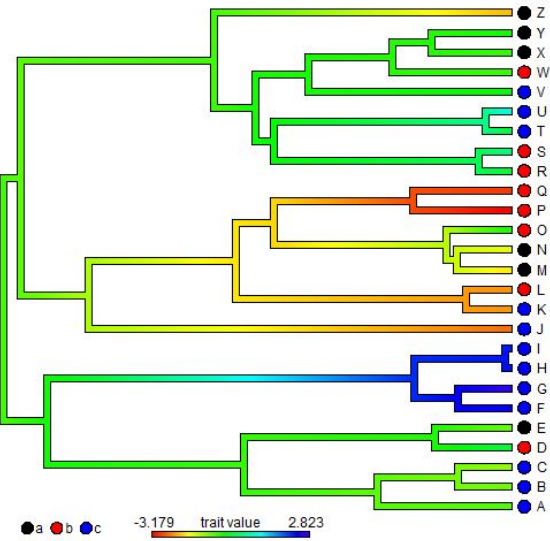
Now some hardcore stuff: Traitgram with the uncertainty of ancestral traits visualized using transparent probability density:

```
fancyTree(tree,type="phenogram95",x=x,s  
pread.cost=c(1,0))
```



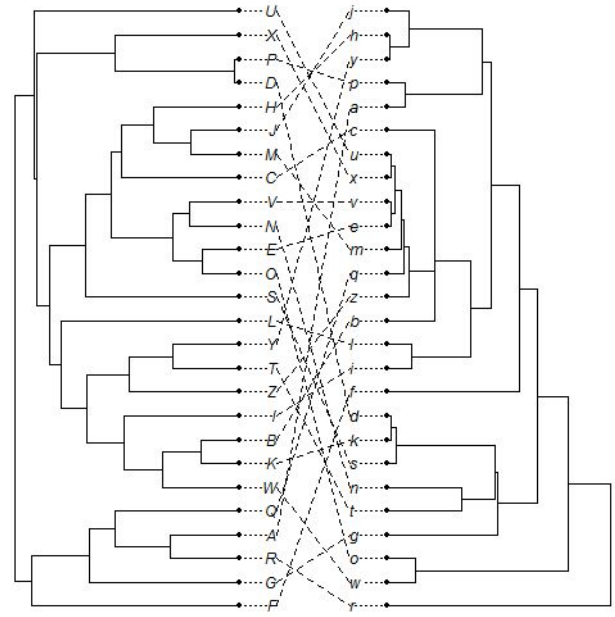
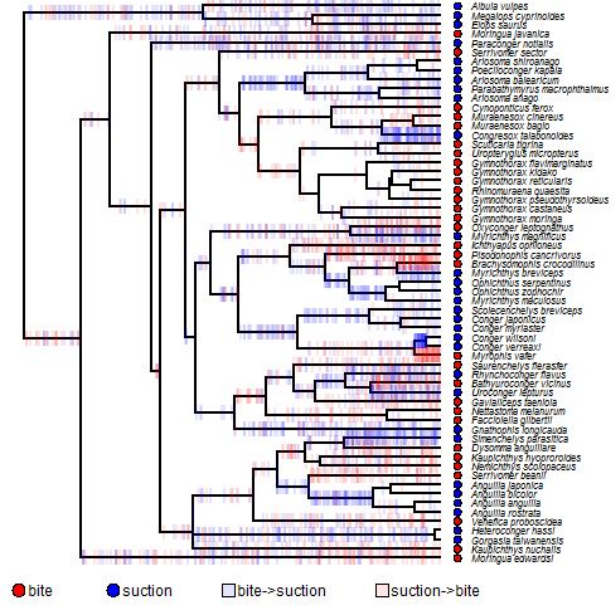
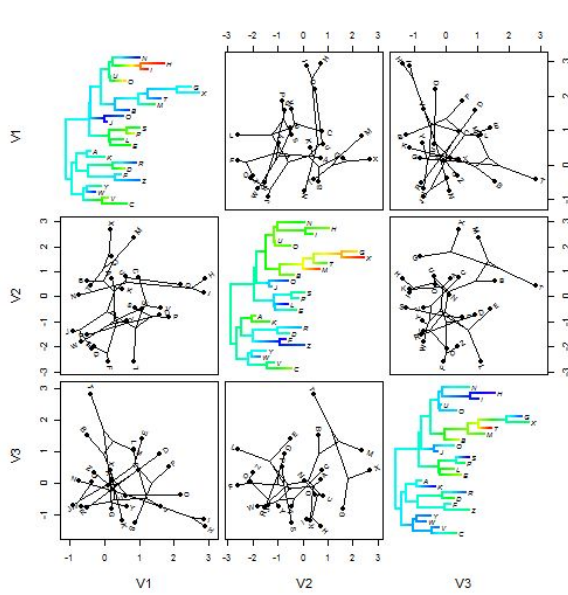
Much more here → <http://www.phytools.org/Cordoba2017/ex/15/Plotting-methods.html>

# Phytools Examples



<http://blog.phytools.org/>

# Phytools Examples



<http://blog.phytools.org/>

# Toolkits

- PYTHON library: ETE3 toolkit @ <http://etetoolkit.org>
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- Others:
  - Archaeopteryx @ <https://sites.google.com/site/cmzmasek/home/software/archaeopteryx>
  - PhyD3 @ <https://phyd3.bits.vib.be/index.html>
  - ggtree @ <https://guangchuangyu.github.io/ggtree/>
  - (More on phylogenetics in R here: <https://cran.r-project.org/web/views/Phylogenetics.html>)
  - etc.

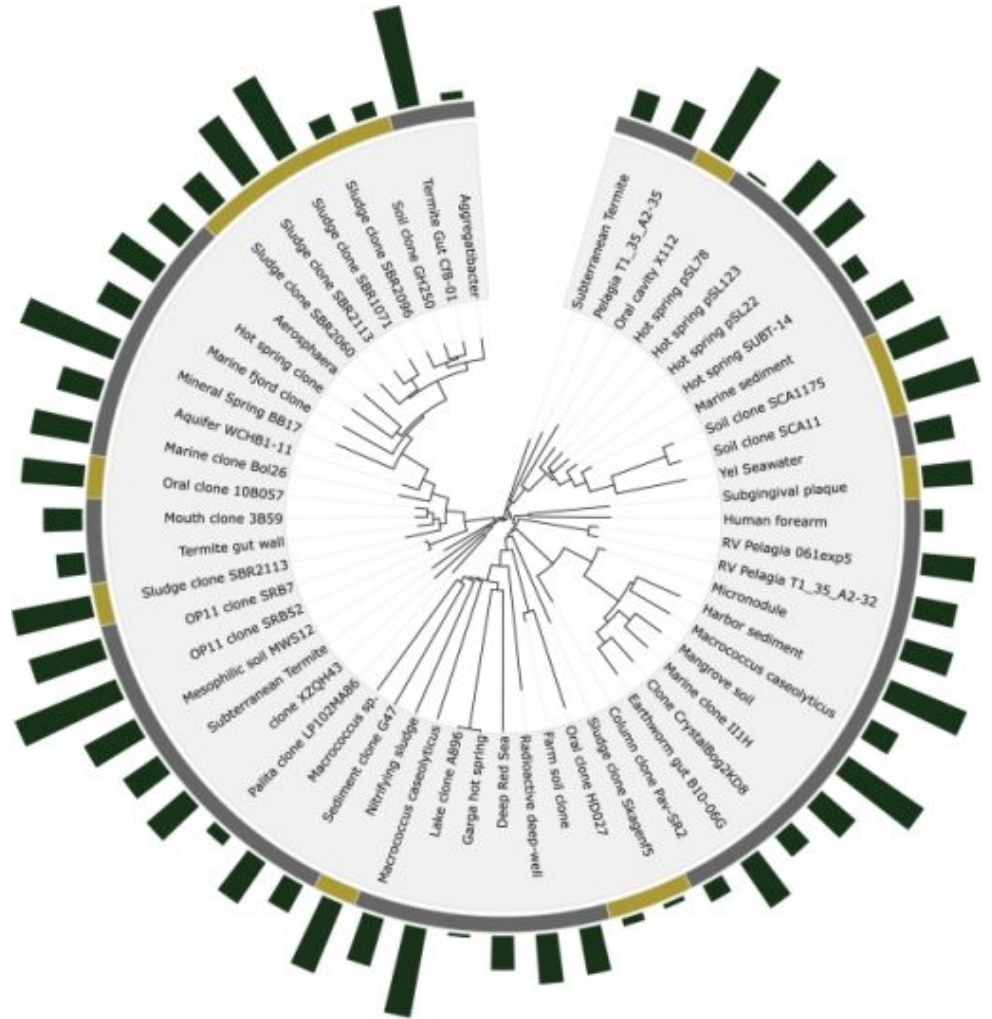
# jsPhyloSVG

JavaScript based

Much more focused on user  
side web visualization

Very simple syntax

A bit limited compared to other  
options

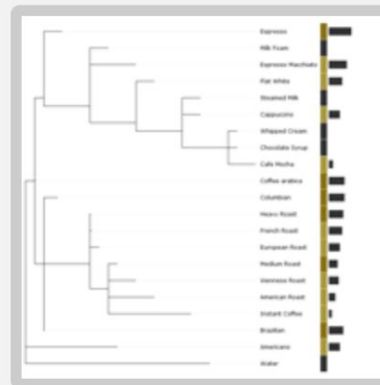


## How can jsPhyloSVG help me?

jsPhyloSVG is an open-source javascript library specifically built for rendering highly-extensible, customizable phylogenetic trees. jsPhyloSVG can render complex trees, yet offers a simple method to do so. It leverages the recent XML schema definition specified for phylogenetic trees, [phyloXML](#).

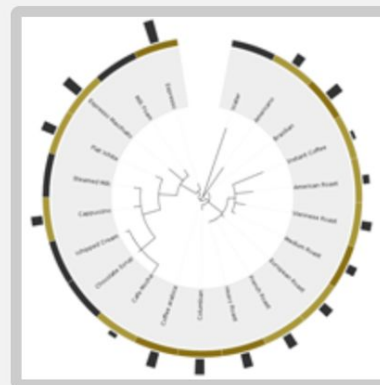
Here is a quick example of how to render a **rectangular** phylogenetic tree:

```
1 phylocanvas = new Smits.PhyloCanvas(  
2   dataObject,    // Newick or XML string  
3   'svgCanvas',  // Div Id where to render  
4   1000, 1000    // Height, Width in pixels  
5 );
```



The same tree, except this time a **circular** tree:

```
1 phylocanvas = new Smits.PhyloCanvas(  
2   dataObject,    // Newick or XML string  
3   'svgCanvas',  // Div Id where to render  
4   1000, 1000,   // Height, Width in pixels  
5   'circular',   // Type of tree  
6 );
```



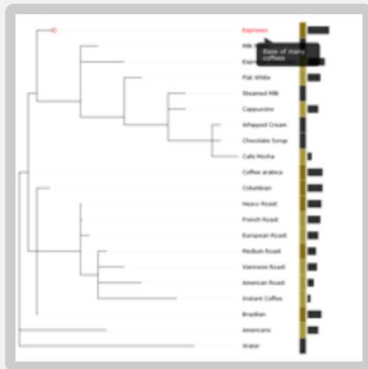


## What about interactive features?

The XML definition already includes the option of adding a hyperlink reference and description. jsPhyloSVG taps into this, and formats the text nodes with this information.

Here's an example of what the XML format looks like:

```
1 <clade>
2 <name>Subterranean Termite</name>
3 <branch_length>0.17793</branch_length>
4 <annotation>
5   <desc>GQ502663.1 Gut clone Cf8-01 </desc>
6   <uri>http://www.jsphylosvg.com/GQ502663 </uri>
7 </annotation>
8 </clade>
```



## Cool. Tell me more!

To get started, take a look at our [documentation](#). You will find plenty of code and examples.

We are always looking for ways to make our library better. So please, [let us know](#) what you like, and how we can make this better for you! If you create extensions, let us know so that the rest of the community can benefit.

## Documentation

### **1. Loading Trees**

- 1.1 Dependencies
- 1.2 Best Methods
- 1.3 Loading Simple Trees
- 1.4 Using AJAX

### **2. Working with Tree Data**

- 2.1 A Primer on passing data to the parser
- 2.2 Newick Format
- 2.3 PhyloXML Format
- 2.4 NeXML Format

### **3. Applying Visual, Interactive, and Charting Features**

- 3.1 Interactive Features
- 3.2 Parameters
  - 3.21 Overriding Styles in Javascript
- 3.3 Binary Arc Charts
- 3.4 Multiple Chart Tracks
  - 3.41 Internal Arc Charts
- 3.5 Bar Charts
- 3.6 Highlight Labels
- 3.7 Gradient Labels
- 3.8 Integrated Ribbons
  - 3.81 Integrated Ribbon Labels

### **4. Additional Manipulations**

- 4.1 Save tree as SVG

# Phylogenetic Tree Visualization Software

- **Web Portals:**
  - Phylo.IO @ <http://phylo.io>
  - Interactive Tree of Life viewer (iTOL) @ <http://itol.embl.de>
  - EVOLVIEW @ <http://www.evolgenius.info/evolview>
- **Software:**
  - FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
  - DensiTree @ <https://www.cs.auckland.ac.nz/~remco/DensiTree/>
  - TreeGraph2 @ <http://treegraph.bioinfweb.info>
- **Toolkits:**
  - PYTHON library: ETE toolkit @ <http://etetoolkit.org>
  - R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
  - JavaScript library: jsPhyloSVG @ <http://www.isphylosvg.com>
- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)



# List of phylogenetic tree visualization software

From Wikipedia, the free encyclopedia

This list of **phylogenetic tree viewing software** is a compilation of software tools and web portals used in visualising *phylogenetic trees*.

## Contents [hide]

- 1 Online software
- 2 Desktop Software
- 3 See also
- 4 References
- 5 External links

## Online software [ edit ]

| Name                            | Description                                                                                                                                            | Site                     | Citation            |
|---------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------|
| Aquapony                        | Javascript tree viewer for <a href="#">Beast</a> .                                                                                                     | <a href="#">Aquapony</a> |                     |
| EvoView,                        | an online tool for visualizing, annotating and managing phylogenetic trees.                                                                            | <a href="#">[1]</a>      | <a href="#">[1]</a> |
| ETE toolkit                     | A Python Environment for Tree Exploration (online treeview)                                                                                            | <a href="#">[2]</a>      | <a href="#">[2]</a> |
| <a href="#">ggtree</a>          | An R package for tree visualization and annotation with grammar of graphics supported                                                                  | <a href="#">[3]</a>      | <a href="#">[3]</a> |
| Hypergeny                       | visualise large phylogenies with this hyperbolic tree browser                                                                                          | <a href="#">[4]</a>      |                     |
| <a href="#">IcyTree</a>         | Client-side Javascript SVG viewer for annotated rooted trees. Also supports phylogenetic networks.                                                     | <a href="#">[5]</a>      | <a href="#">[4]</a> |
| InfoViz Tree Tools              | the generic Javascript InfoViz toolkit supports hyperbolic, space and icicle trees                                                                     | <a href="#">[6]</a>      |                     |
| iTOL - interactive Tree Of Life | annotate trees with various types of data and export to various graphical formats; scriptable through a batch interface                                | <a href="#">[7]</a>      | <a href="#">[5]</a> |
| TreeVector                      | scalable, interactive, phylogenetic trees for the web, produces dynamic SVG or PNG output, implemented in Java.                                        | <a href="#">[8]</a>      | <a href="#">[6]</a> |
| jsPhyloSVG                      | open-source javascript library for rendering highly-extensible, customizable phylogenetic trees; used for <a href="#">Elsevier's interactive trees</a> | <a href="#">[9]</a>      | <a href="#">[7]</a> |

# Phylogenetic Tree Visualization

- **Web Portals:**

- Phylo.IO @ <http://phylo.io>
- Interactive Tree of Life viewer (itol) @ [itol.embl.de](http://itol.embl.de)
- EVOLVIEW @ <http://www.evolgenet.net/evolview/>

- **Software:**

- FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
- DensiTree @ <https://www.nuim.ie/~nuim/~dmi02/densitree/>
- TreeGraph2 @ <http://tree.bio.ed.ac.uk/software/treegraph2/>

- **Toolkits:**

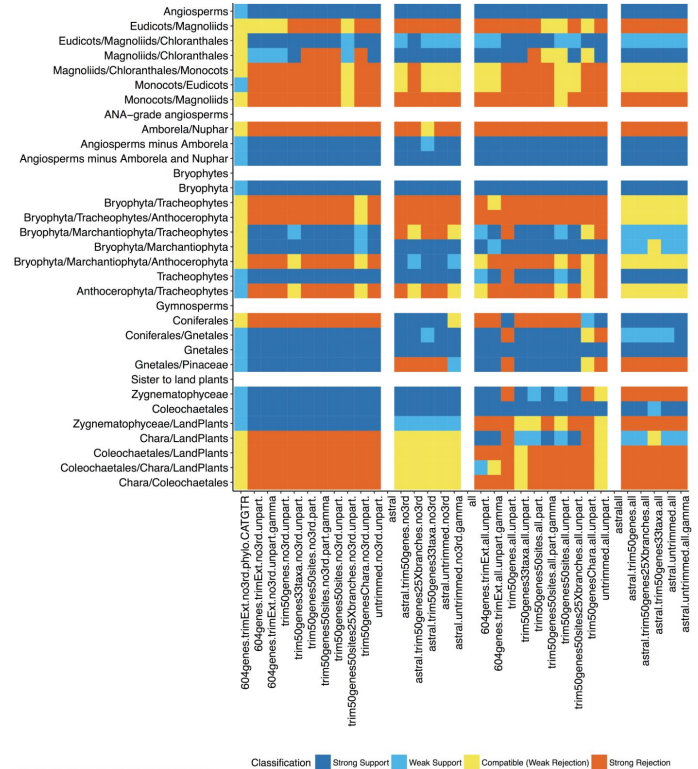
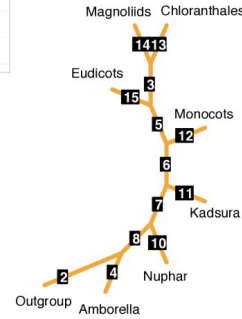
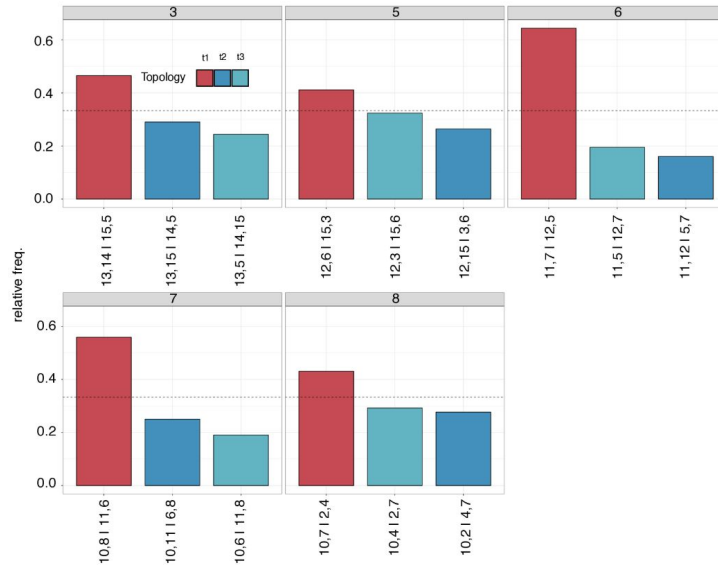
- PYTHON library: ETE @ <http://etetoolkit.org/>
- R repository: PhyTools @ <https://github.com/PhyloToys/PhyTools>
- JavaScript library: jsPhy @ <http://www.jsphy.com/>

- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)

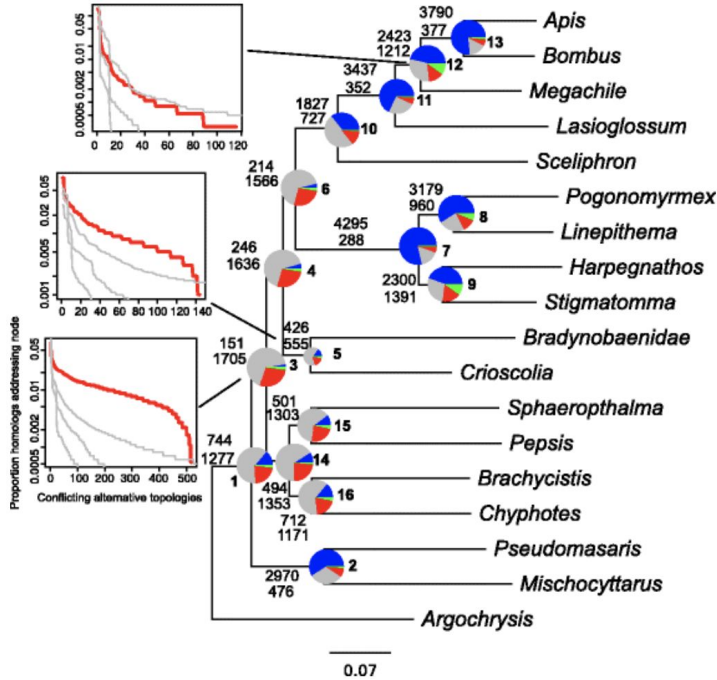


# Phylogenetic Conflict Visualization

- DiscoVista: <https://github.com/esayyari/DiscoVista>



# Phylogenetic Conflict Visualization



Each pie chart has four colors:

- Blue: Concordant gene trees
- Green: Most common conflicting bipartition
- Red: Other conflicting bipartitions
- Gray: Gene trees with no information (missing or unresolved)

- **PhyParts + PieCharts:** <https://bitbucket.org/blackrim/phyparts> & <https://github.com/mossmatters/phyloscripts/tree/master/phypartspiecharts>

# Phylogenetic Tree Visualization

- **Web Portals:**

- Phylo.IO @ <http://phylo.io>
- Interactive Tree of Life viewer @ <http://itol.phylo.io>
- EVOLVIEW @ <http://www.evolview.info>

- **Software:**

- FigTree @ <http://tree.bio.ed.ac.uk/software/figtree/>
- DensiTree @ <http://people.sabanci.ac.tr/~erdinc/densitree/>
- TreeGraph2 @ <http://www.phylo.org/treegraph2/>

- **Toolkits:**

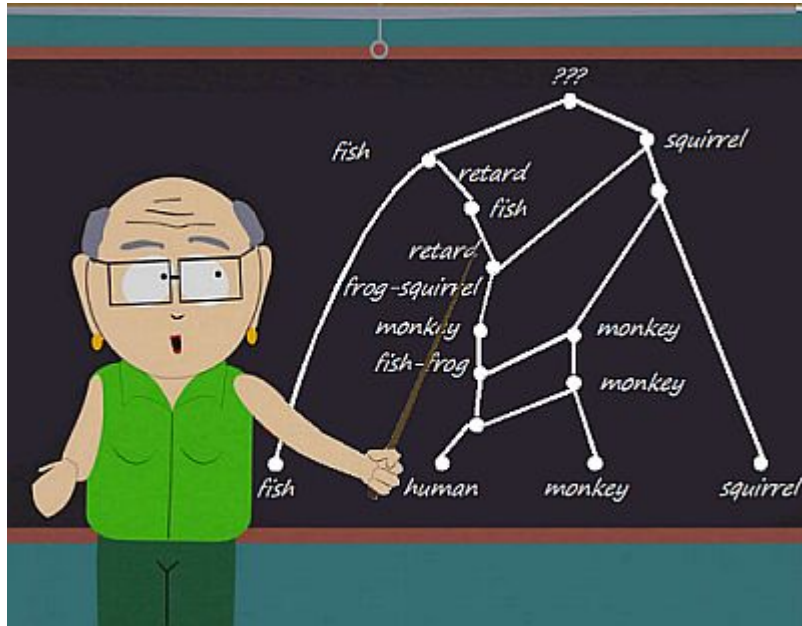
- PYTHON library: ETE toolkit @ <http://etetoolkit.org/>
- R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
- JavaScript library: jsPhyloSVG @ <http://www.isphylosvg.com>

- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software)





# Phylogenetic Network Visualization



## Who is Who in Phylogenetic Networks

🏠 Authors Community Keywords Publications **Software** Browse Basket Account Contribute! About Help 🔍

### Programs and their Input Data !

How do I interact with the graph ?

Below, you can find all programs present at least **1 time(s)** in Who is who in phylogenetic networks, as well as the links with the data they use as input.

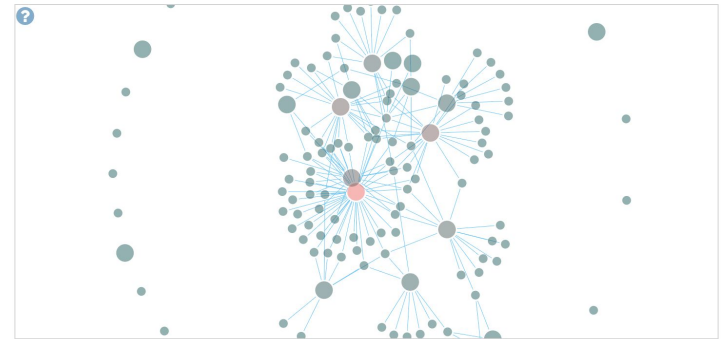
Show all node labels. (This may overcrowd the visualization.)

Set a threshold number of citations.

Choose

Go

Hover over or click on a node to see more information.



Number of nodes is 133. Number of edges is 176.

<http://phylnet.univ-mlv.fr/show.php?keyword=programs#programlist>

# Phylogenetic Network Visualization

## Dendroscope

Software for visualizing phylogenetic trees and rooted networks.

- Download Dendroscope 3 [here](#).
- See our [book on phylogenetic trees and networks...](#)
- Over 20,000 registered users...
- This program is open source, the source is available [here](#).



## 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

Researchers studying phylogenetic relationships need software that is able to visualize rooted phylogenetic trees and networks efficiently, increasingly of large datasets involving hundreds of thousands of taxa. The program should be user friendly (easy to run on all popular operating systems), facilitate interactive browsing and editing the trees and allow one to export the result in multiple file formats in publication quality. In addition, there is a need for a program that allows one to compute rooted phylogenetic networks from trees.

We have developed the platform independent tree and rooted network viewer *Dendroscope* that addresses these issues.

#### Feature List:

- Large trees with hundreds of thousands of taxa can be easily displayed, browsed and edited
- Multiple trees and networks from a single file can be displayed together in an m by n grid
- Novel magnifying features for zooming detailed views (see [screenshots](#));
- Find and replace tool bar that uses regular expressions;
- Subtrees can be collapsed and colored;
- All labels (leaves/inner nodes and edges) can be edited;
- Trees can be rerooted;
- Seven different views are available, including a rectangular, slanted, circular and radial view;
- Input formats: Newick and Nexus, extended-Newick (for rooted phylogenetic networks) and Dendroscope;
- Multiple graphic export formats: .eps, .svg, .png, .jpg, .gif, .bmp, .pdf;
- Trees and networks can be copied and pasted between different windows
- Platform independent (Java, installers for common operating systems available)
- Consensus trees and rooted phylogenetic networks can be computed from a set of trees
- Hybridization networks and tanglegrams for multifurcating trees on unequal taxon sets
- Commandline mode





# Visualization Challenge

ポケモン Phylogeny

