

Tree Editing & Visualization

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Marcet-Houben

(with help from Miguel Ángel Naranjo Ortiz)

Data Visualization

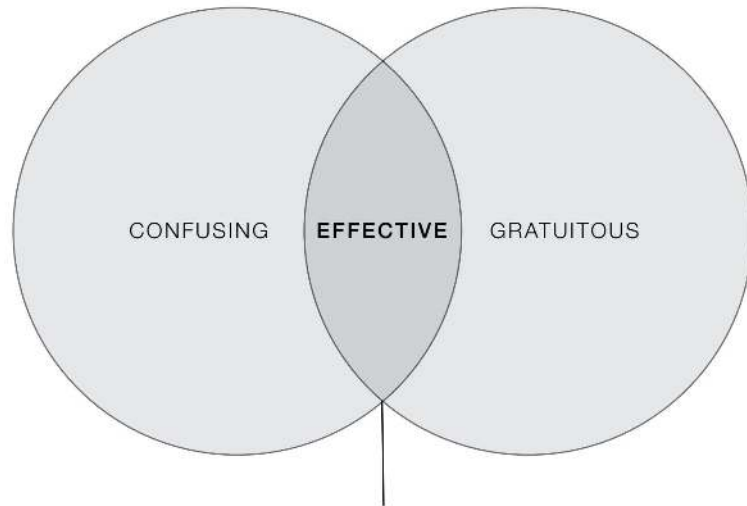
“Strive to give your viewer the greatest number of useful ideas in the shortest time with the least ink in the smallest space”

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

VISUALIZATION SWEET SPOT

INFORMATION-RICH

INFORMATIVE



CLEAR MESSAGE

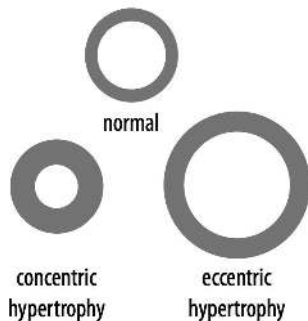
HIGH DATA-TO-INK RATIO

ACCESSIBLE COMPLEXITY

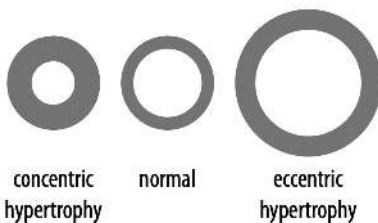
Data Visualization

- 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

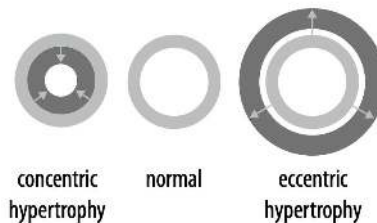
perceptually challenging



helpful, but not explicit

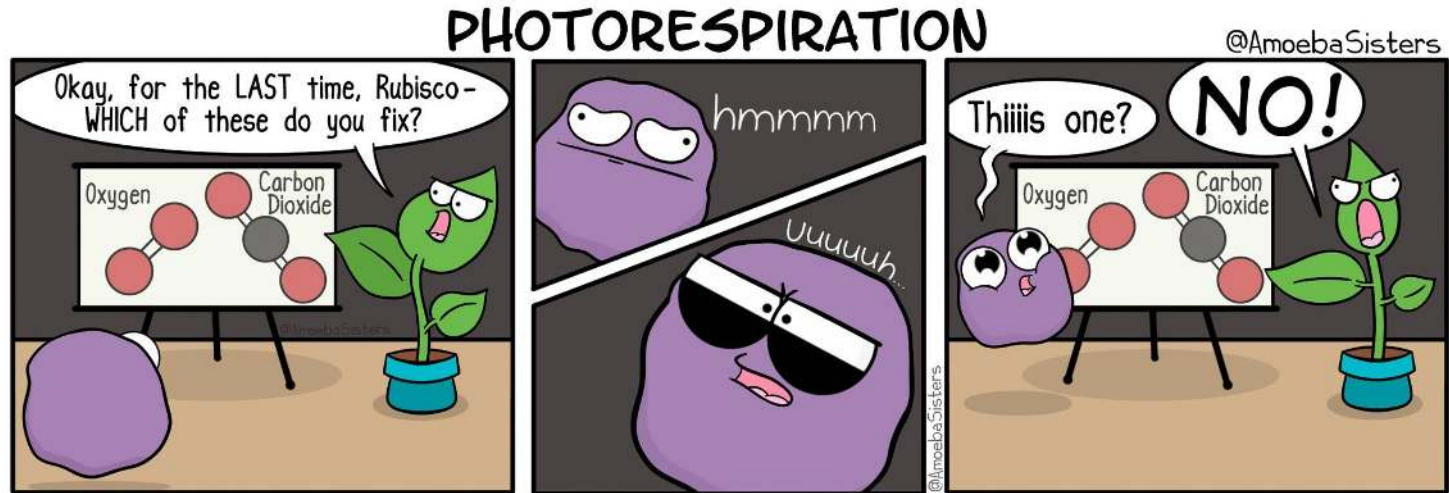


helpful and explicit



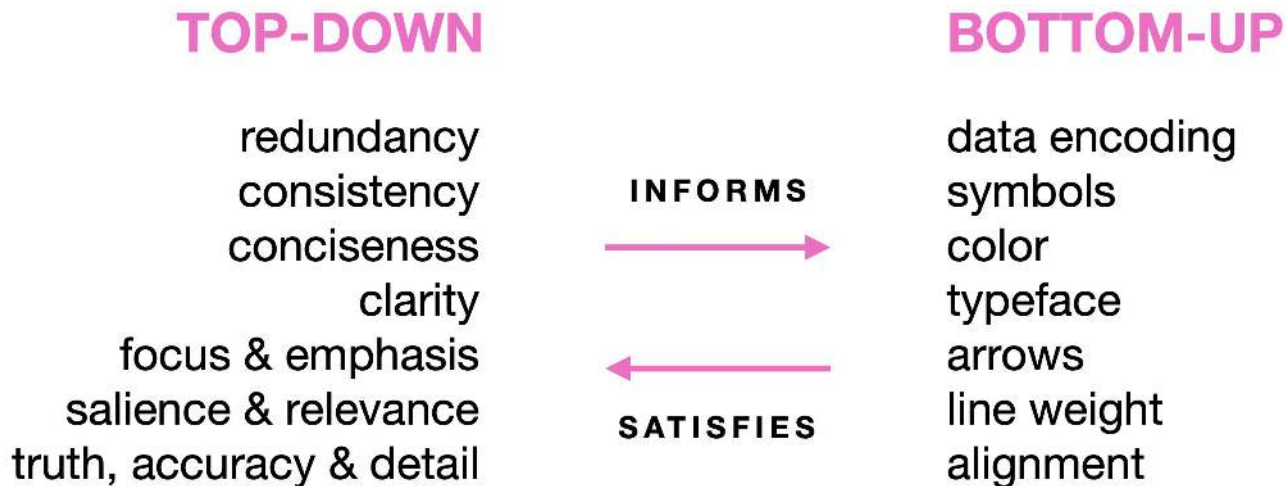
Data Visualization

- 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?



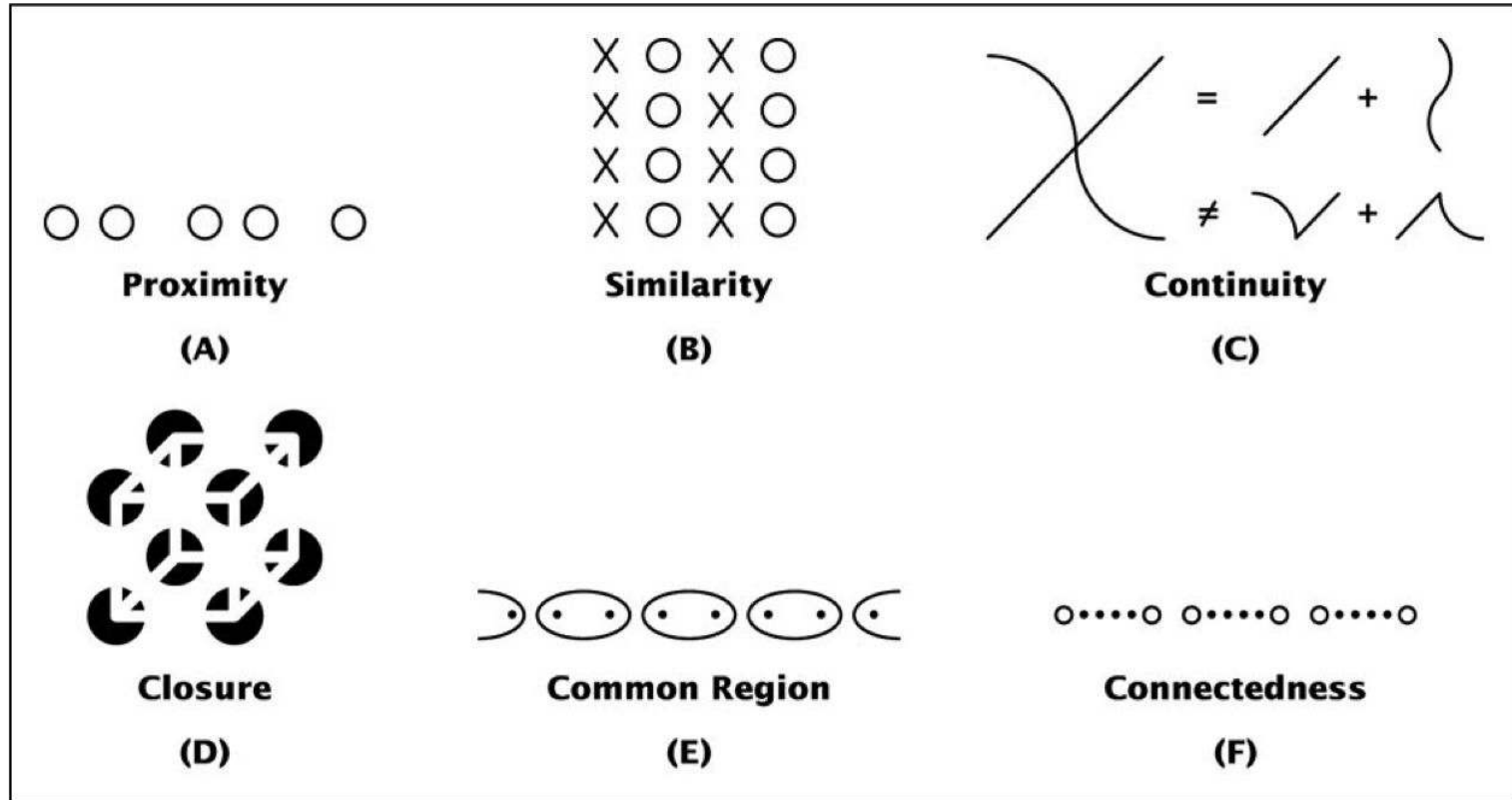
Data Visualization

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.

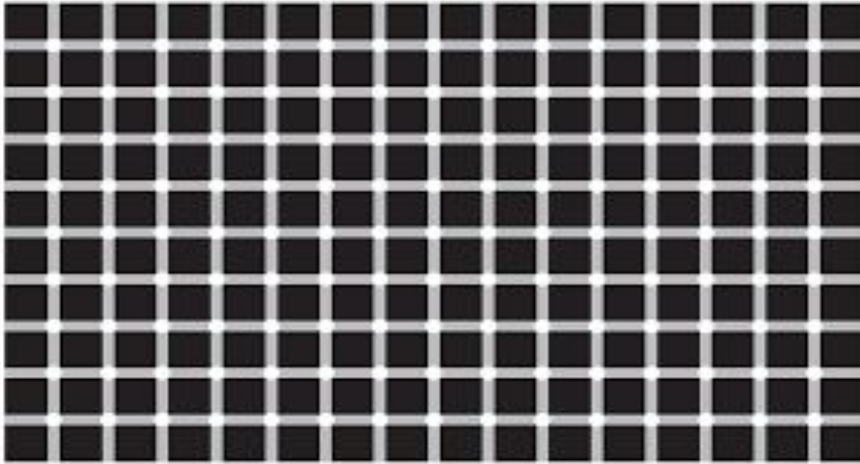
	Points	Lines	Areas	Best to Show
Shape		<i>Possible, but too Weird to Show</i>	<i>Cartogram</i>	<i>Qualitative Differences</i>
Size			<i>Cartogram</i>	<i>Quantitative Differences</i>
Color Hue				<i>Qualitative Differences</i>
Color Value				<i>Quantitative Differences</i>
Color Intensity				<i>Qualitative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

Principles of Grouping

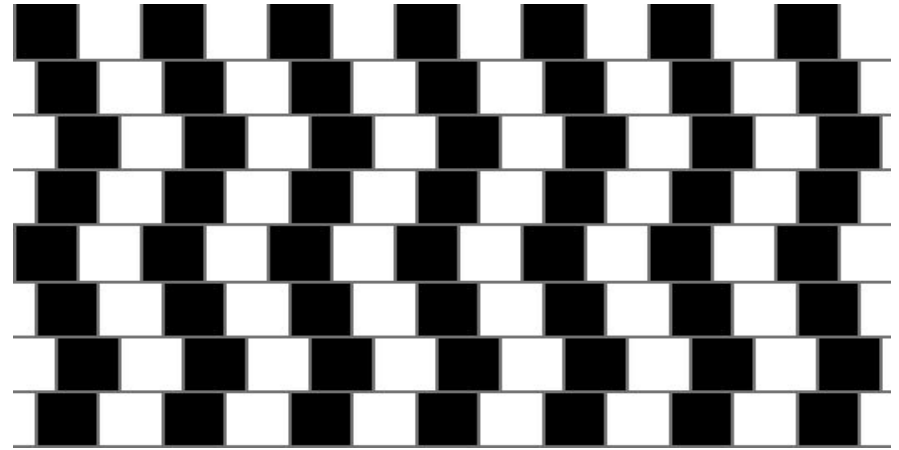


Optical Illusions

Hermann Grid



Café Wall

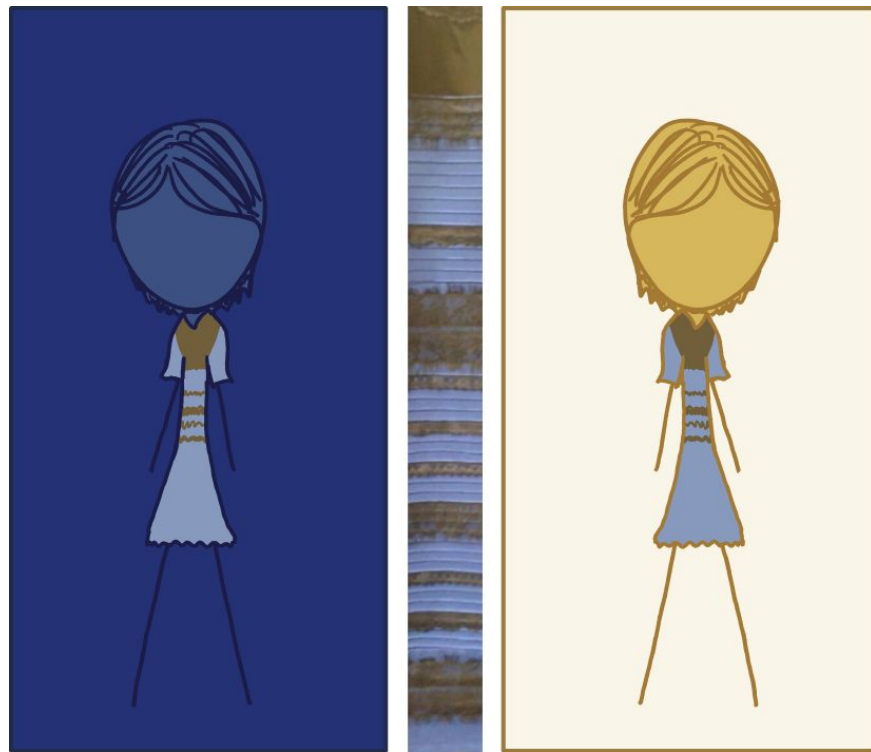


Color



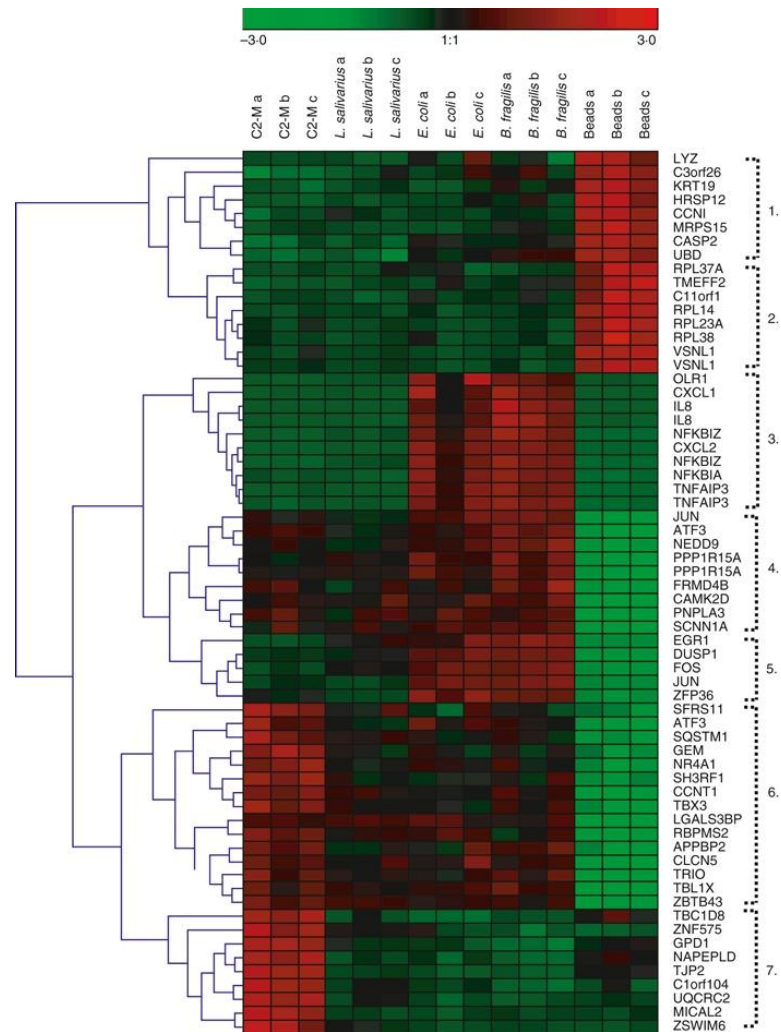
Color Context

Context affects your color perception



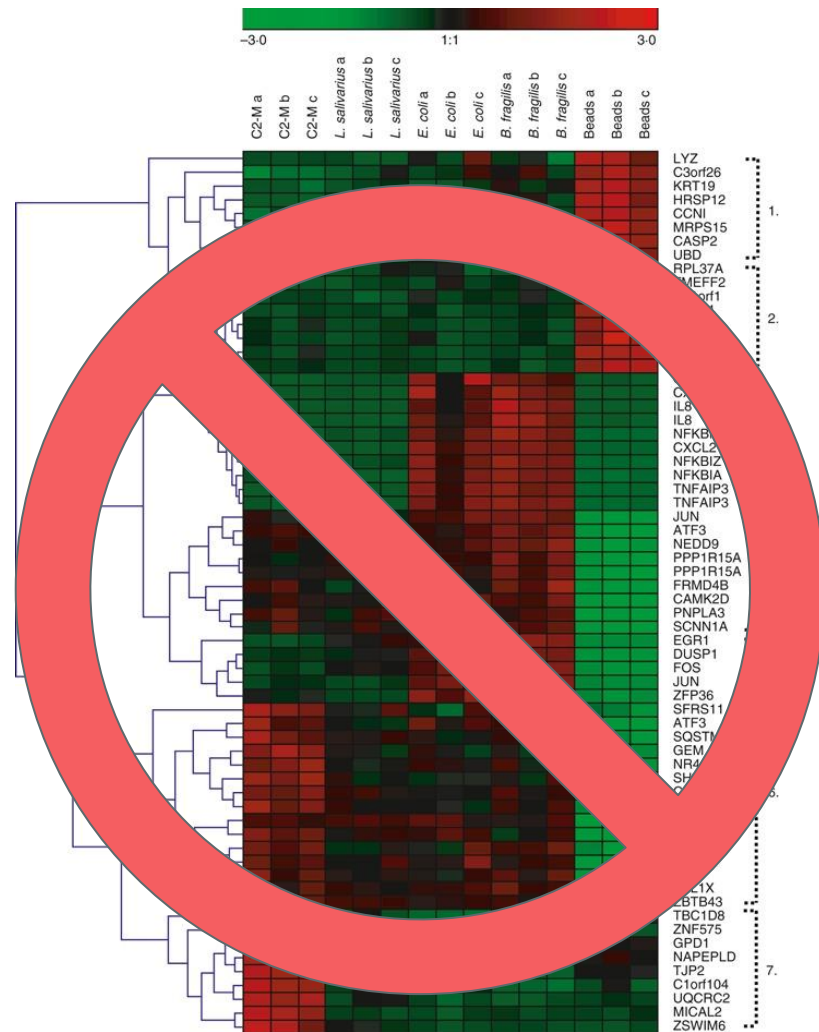
Color Context

Context affects your color perception



Color Context

Context affects your color perception



Color Blindness



Color Blindness

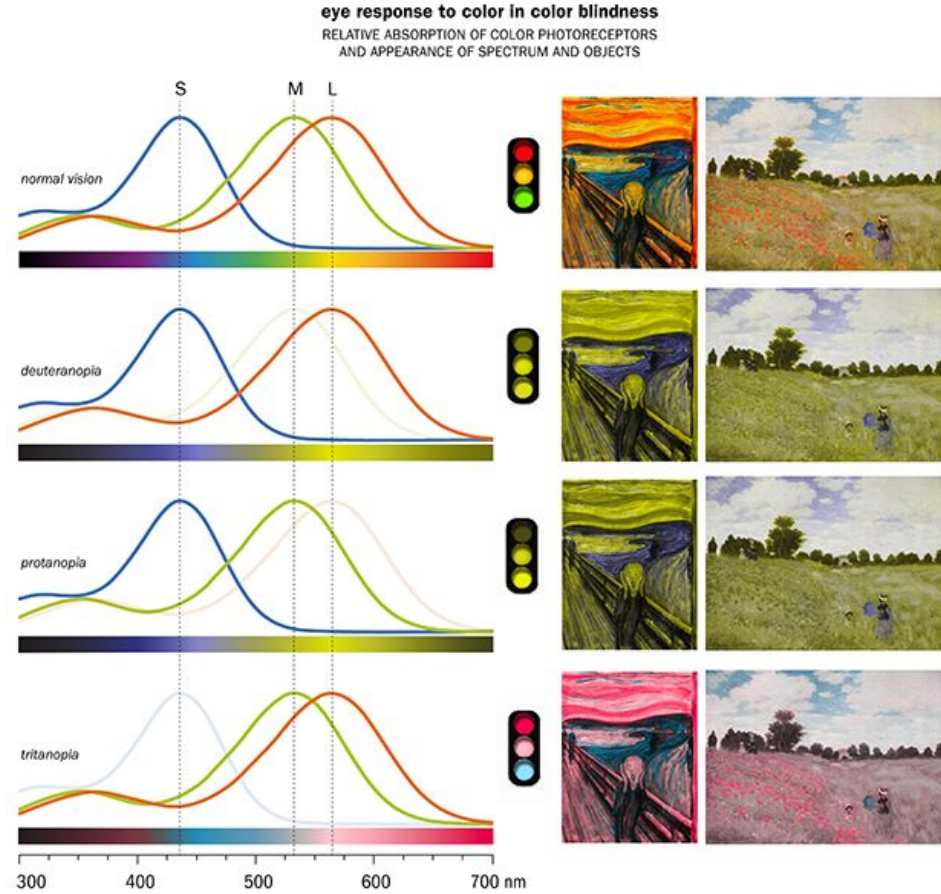
COLOR PALETTES FOR COLOR BLINDNESS

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.

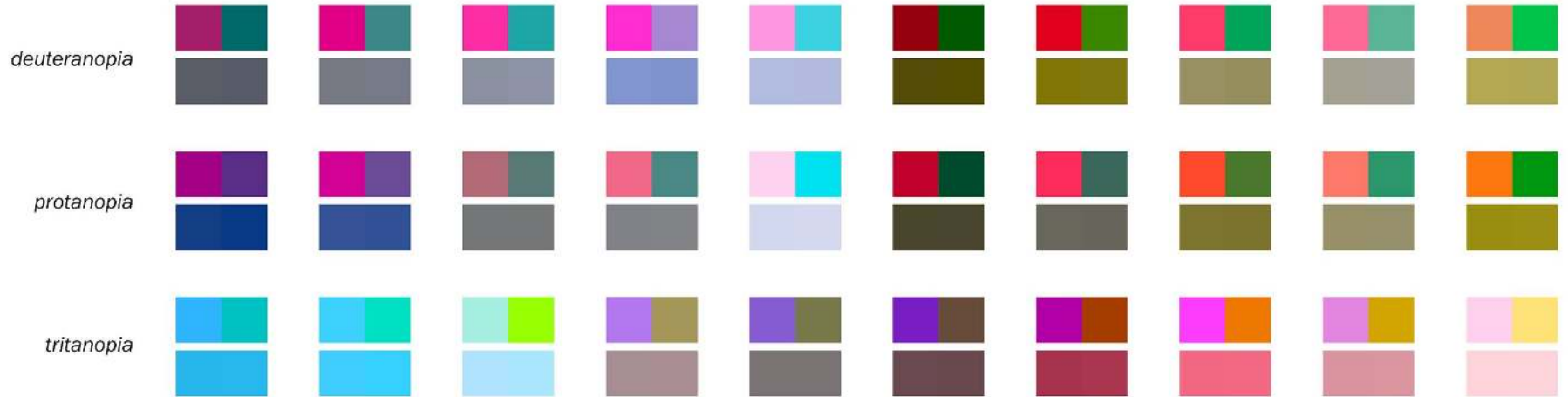
COLOR RECEPTORS ARE REDUCED OR ABSENT IN COLOR BLINDNESS

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>

Color Blindness – Palettes

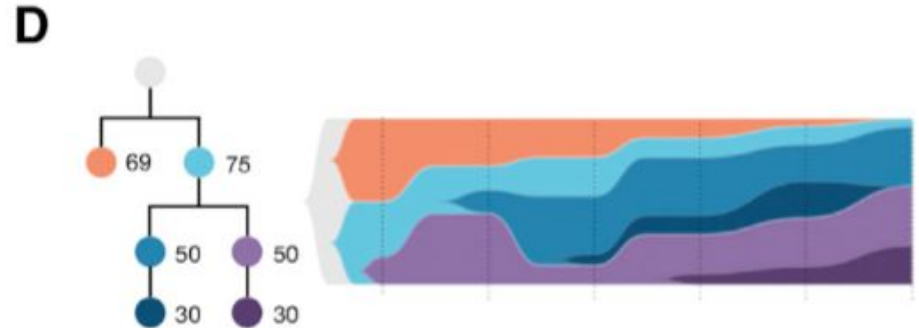
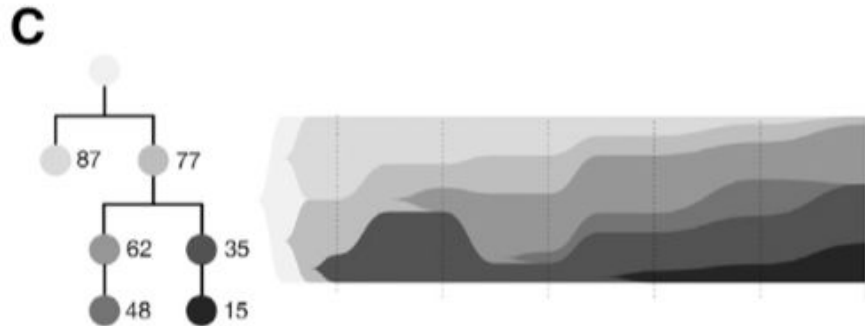
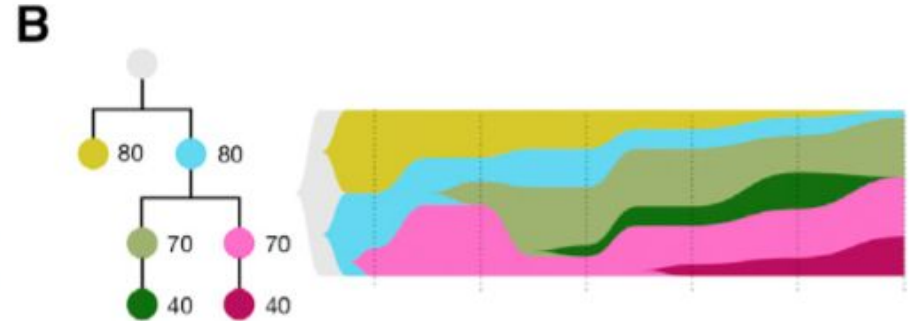
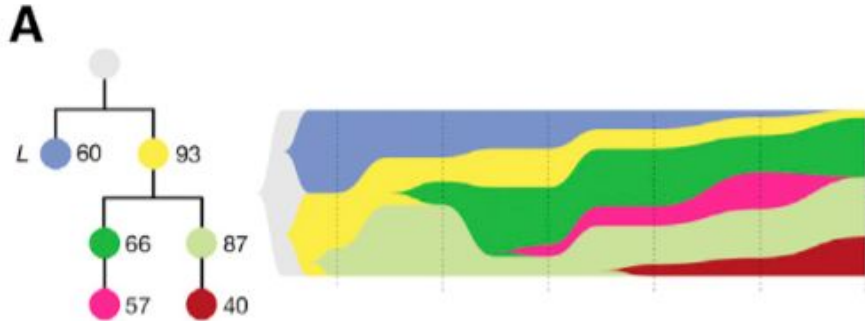
- General advice: <http://ifly.iam.u-tokyo.ac.jp/color/>
- Cartography: <http://colorbrewer2.org/>
- R plotting system (ggplot2):

[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)

<http://ifly.iam.u-tokyo.ac.jp/color/>

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

BirthStd

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

DilleniaUPC

DFKai-SB

David

DaunPenh

Curly MT

Courier New

Courier

CordiaUPC

Cordia New

Corbel

COPPERPLATE GOTHIC LIGHT

Copperplate Gothic

CooperBlackStd-Italic

CooperBlackStd

Cooper Black

Constantia

Cosolas

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

Forté

Footlight MT Light

FLUX

FELIX TITLING

FangSong

Euphemia

EucrosiaUPC

Ευχλιδ Σημβολ

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KodchiangUPC

Khmer UI

Kartika

Kalinga

Kaiti

Julius ITC

Jokerman

JasmineUPC

Iskoola Pota

IrisUPC

Informal Roman

Imprint MT Shadow

Impact

HoboStd

High Tower Text

Helvetica-Narrow

Helvetica

flarrington

Harlow Solid

Haettenschweiler

GungsuhChe

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

Gill Sans

Gill Sans

Gill Sans

Lucida Fax Regular

Lucida Fax Demibold

Lucida Fax

Lucida Console

Lucida Calligraphy

Lucida Bright Demibold

Lucida Bright

LITHOSPRO-REGULAR

LITHOSPRO-BLACK

UlyUPC

Levenim MT

LetterGothicStd-Slanted

LetterGothicStd-BoldSlanted

LetterGothicStd-Bold

LetterGothicStd

Leelawadee

Latha

Lao UI

Navarrothe 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

Font Types However...

IN TYPOGRAPHY

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 a neurodevelopmental disorder (DRD) is the most common learning disability. Dyslexia 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 non-verbal cognitive deficit with vision or hearing, or poor or inadequate reading instruction. There are three subtypes of dyslexia (phonological, surface and mixed), although individual cases of dyslexia are better explained by multiple underlying neurological factors and co-occurring learning disabilities (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 learning skills. Researchers at MIT found that people with dyslexia exhibit impaired voice-recognition 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

[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!

A	B	C	D	E	F	G	H	I
J	K	L	M	N	O	P	Q	R
S	T	U	V	W	X	Y	Z	a
b	c	d	e	f	g	h	i	j
k	l	m	n	o	p	q	r	s
t	u	v	w	x	y	z		

Dyslexia Friendly Font Types – Lexie Readable

 K-TYPE

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



LEX
LEXIE
READABLE

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

 Like  Share 15K

Size  Background  Language  

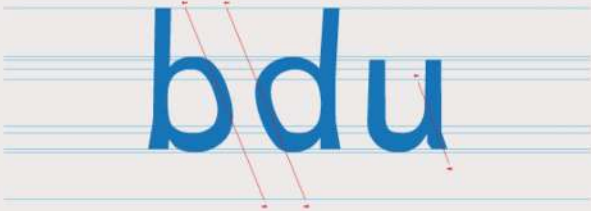
 Home  Dyslexie font  Order  Support  Books/Apps  Contact

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

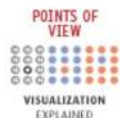
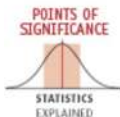




ESSENTIALS OF DATA VISUALIZATION

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.

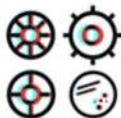
2017 π DAY



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.

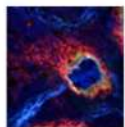
[watch](#) | [PDF](#) | Open up a journal or your favourite text book. Find a figure. There's probably some labels in there. Maybe it's a multi-panel figure and the labels are the titles. Maybe there are some callouts that tell you what the parts are. If it's a plot there are probably axis labels and 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.



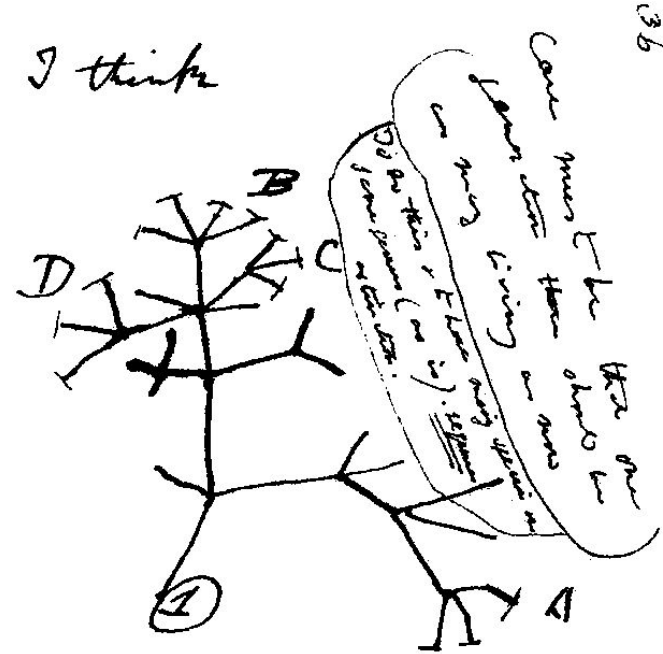
Phylogenetic Tree Visualization

- Web Portals

- Software

- Toolkits

- 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.jsphylosvg.com>

- https://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software

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- 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

Web Portals

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- **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
 - **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

 Dessimoz Lab



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

The image shows the Phylo.io web application interface. On the left is a dark sidebar with the following elements:

- Phylo.io** logo and version information: Version: 1.0.0 (04/28/2016 15:06:36)
- Buttons: **View** and **Compare**
- Tree name: **Tree: Untitled**
- A text box containing a Newick tree format string:

```
((sba:0.03984952076326608861,(sca:0.24212307199678842484,(cgl:0.29957965624763355228,(((kla:0.32629009627835226137,ago:0.35217085340006204497):0.05741546733669361524
```
- Links: **Small Example Tree** (with a red arrow labeled '1' pointing to it) and **Large Example Tree**
- Buttons: **Render** (with a red arrow labeled '2' pointing to it) and **Clear**
- Settings: **Settings**, **Share**, and **Help**
- Footer: **© Dessimoz Lab**

On the right is the main area displaying a phylogenetic tree. Above the tree is a **Zoom:** slider and a set of four directional arrows (up, down, left, right). The tree has two main clades. The top clade includes taxa: sba, sca, cgl, kla, ago, skl, kwa, yli, lol, cal, ctr, pst, pgu, and dha. The bottom clade includes taxa: sce, spa, smi, and sku. A search icon is located in the top right corner. At the bottom of the interface, there is a status bar with a download icon and the text **SVG**, and a version number **2.02**.

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
🔗 Share
📖 Help

© Dessimoz Lab

Zoom:

1 2

reroot

SVG

2.53

Phylo.IO demo

Phylo.io
Version: 1.0.0 (04/28/2016 15:08:36)

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

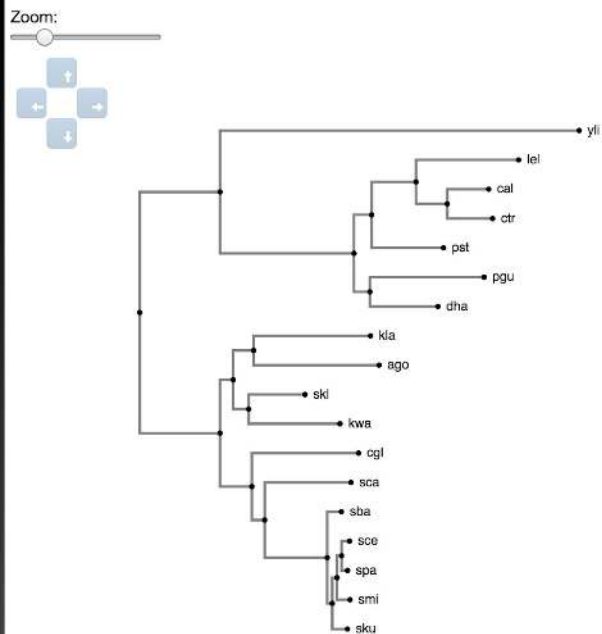
Render Clear

⚙ Settings ← 1

🔗 Share

📖 Help

© Dessimoz Lab



Phylo.IO demo

1 →

Auto-Collapse Depth: - 2 +

Internal Labels:

- ☒ None
- ☐ Branch Labels/Support
- ☐ Length
- ☐ Similarity

Adjust Tree Style:

Line Thickness

2 →

Node Size

3 →

Font Size

☒ Use Lengths

☒ Move To Best Corresponding Node on Highlight Click

Zoom: [Slider]

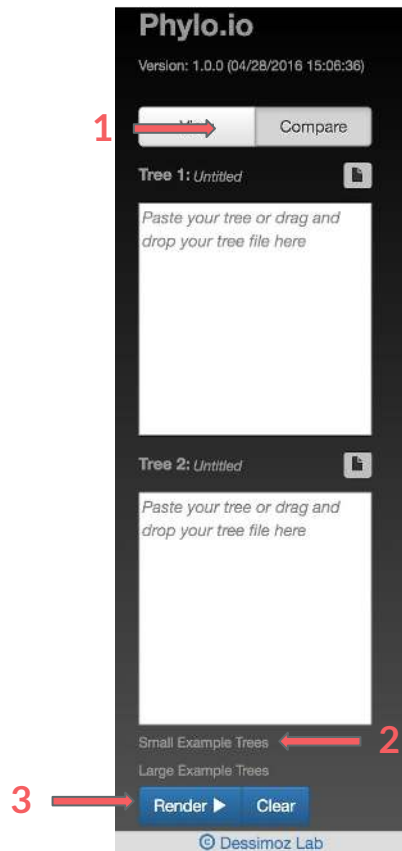
↓ SVG

2.53

© Dessimoz Lab

Search [Q]

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

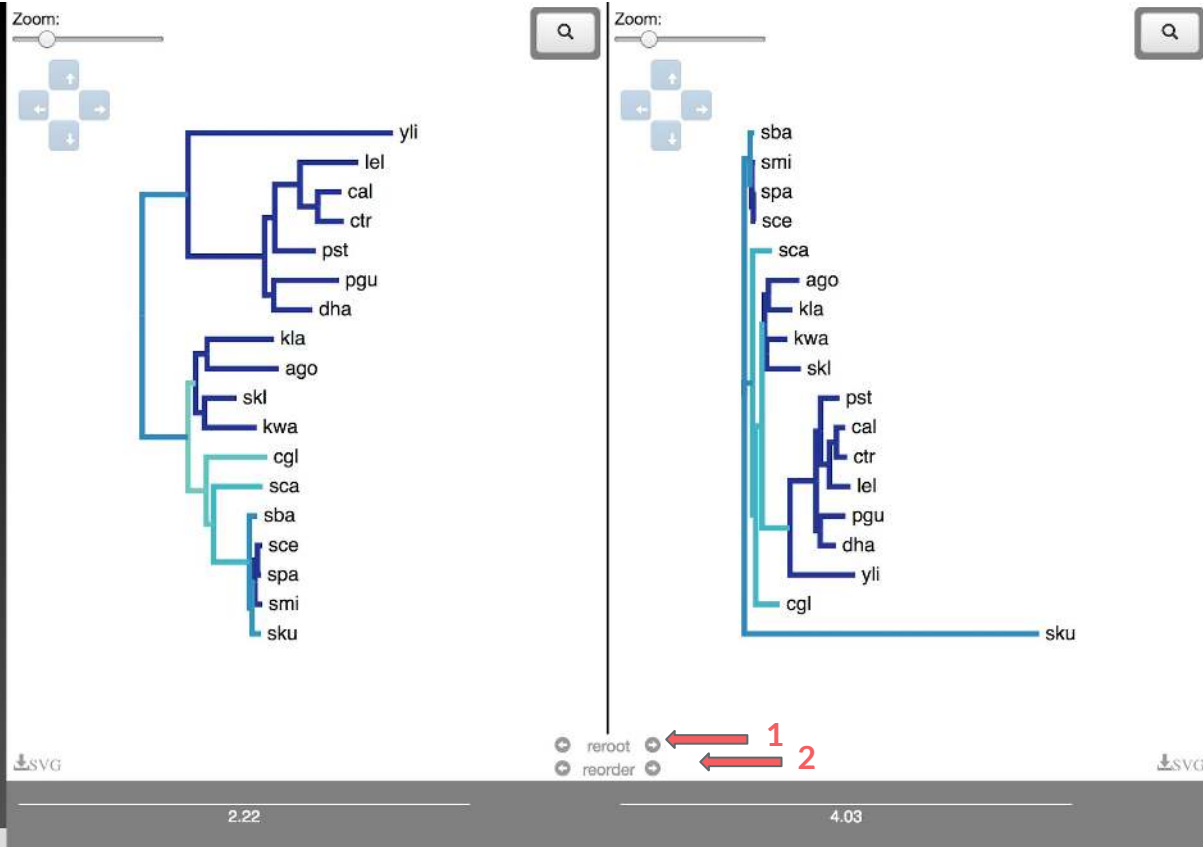
Tree 2: *Untitled*

```
((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
```

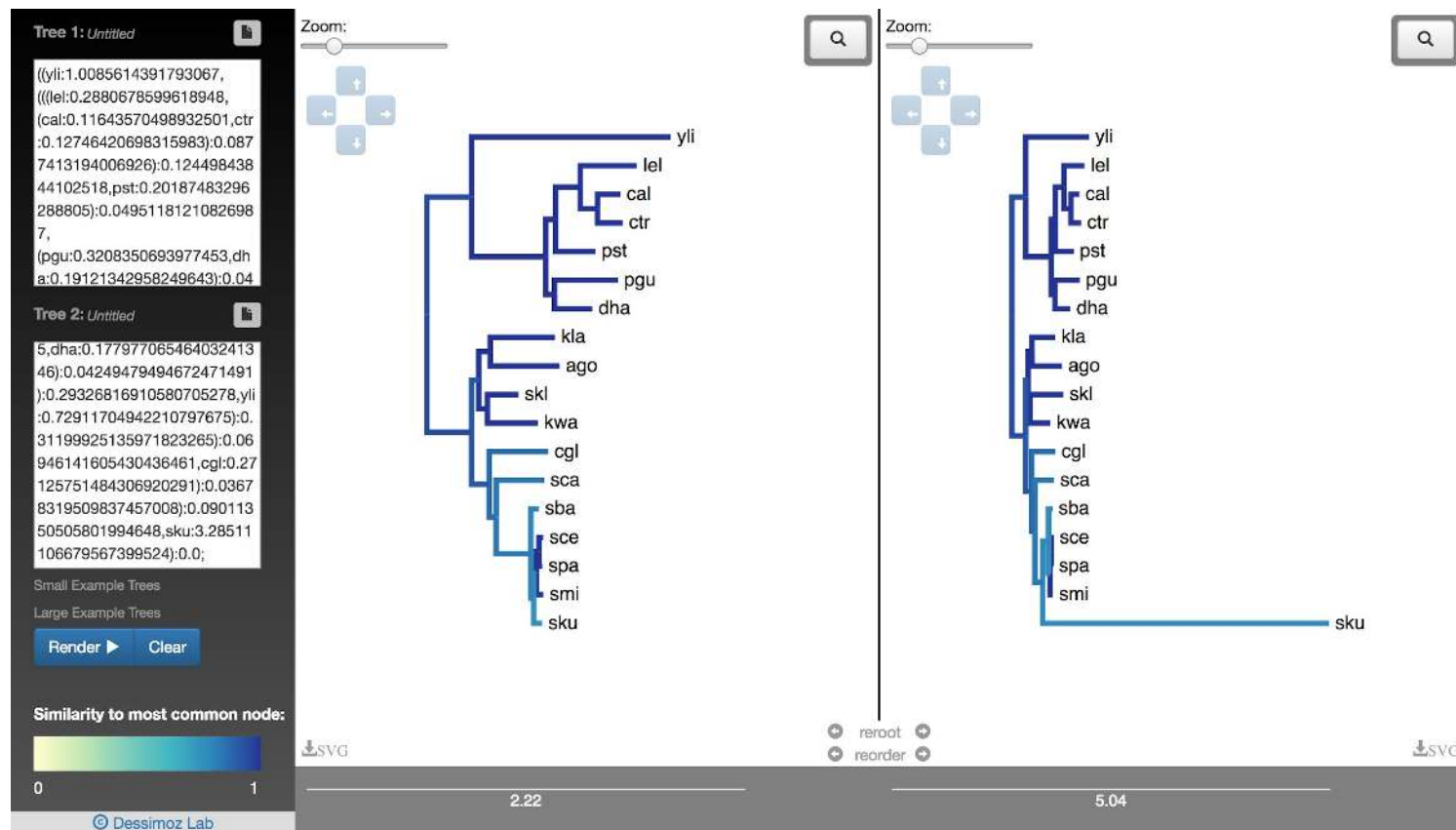
Small Example Trees
Large Example Trees

Render Clear

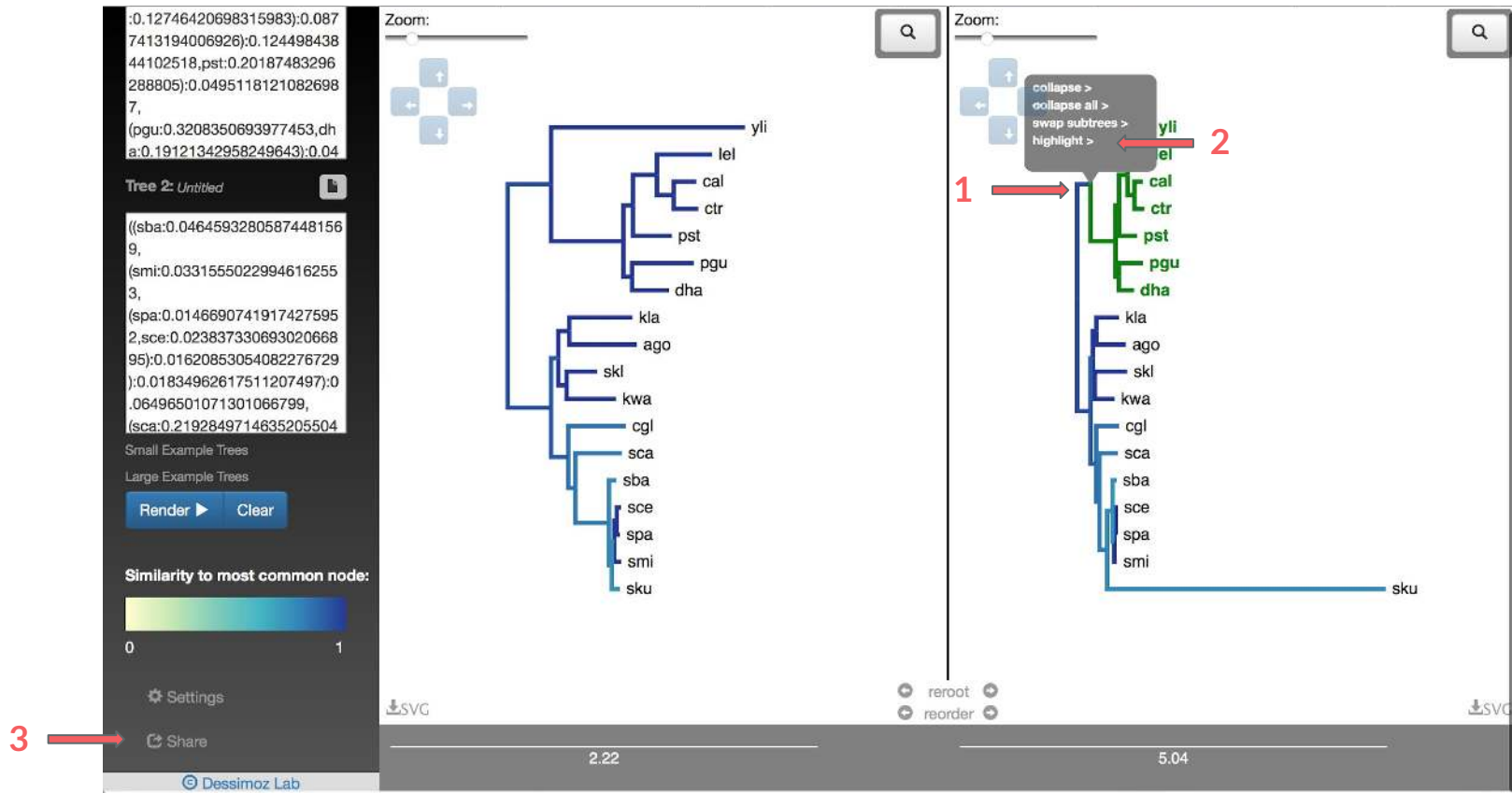
© Dessimoz Lab



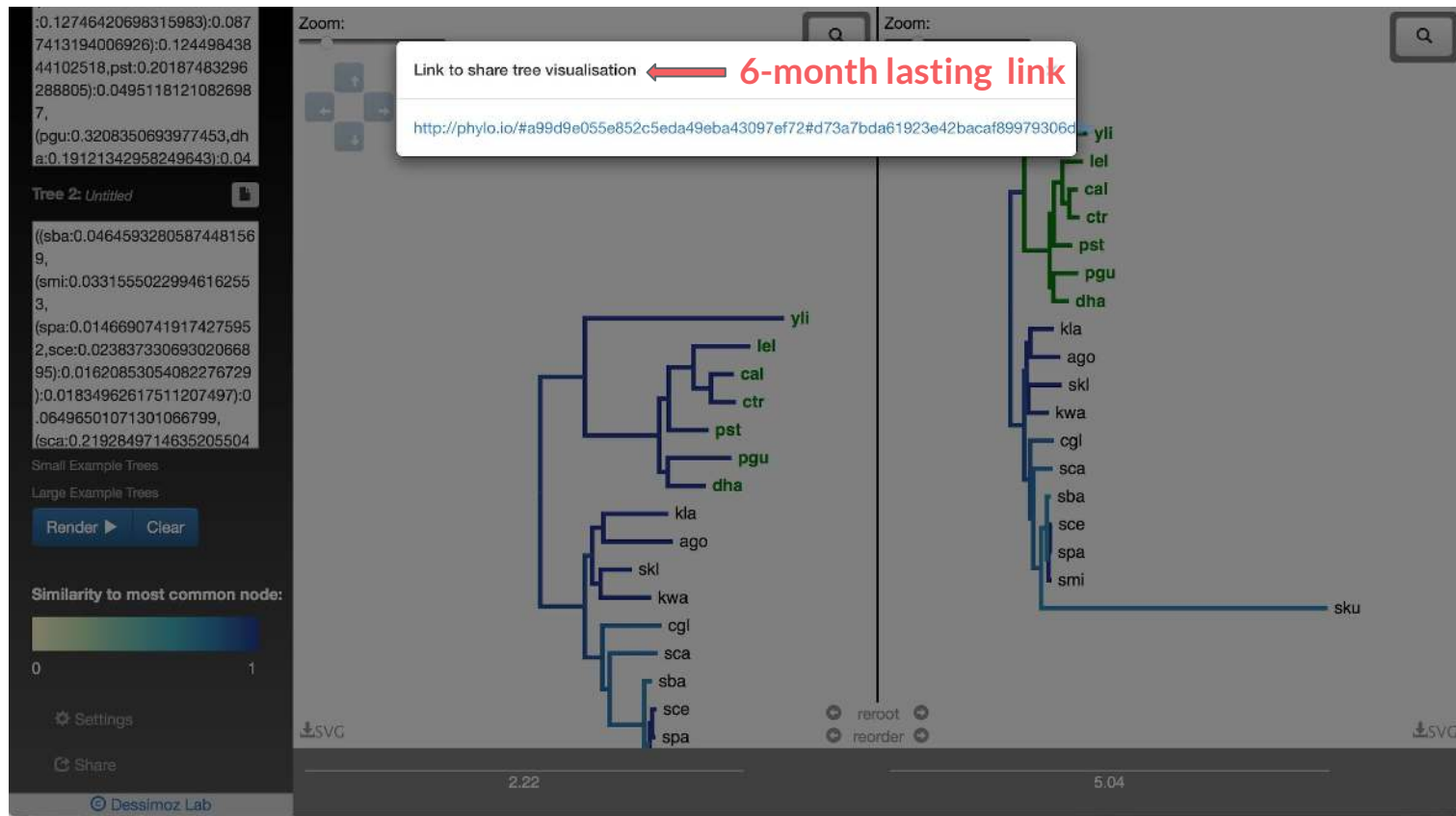
Phylo.IO demo



Phylo.IO demo



Phylo.IO demo

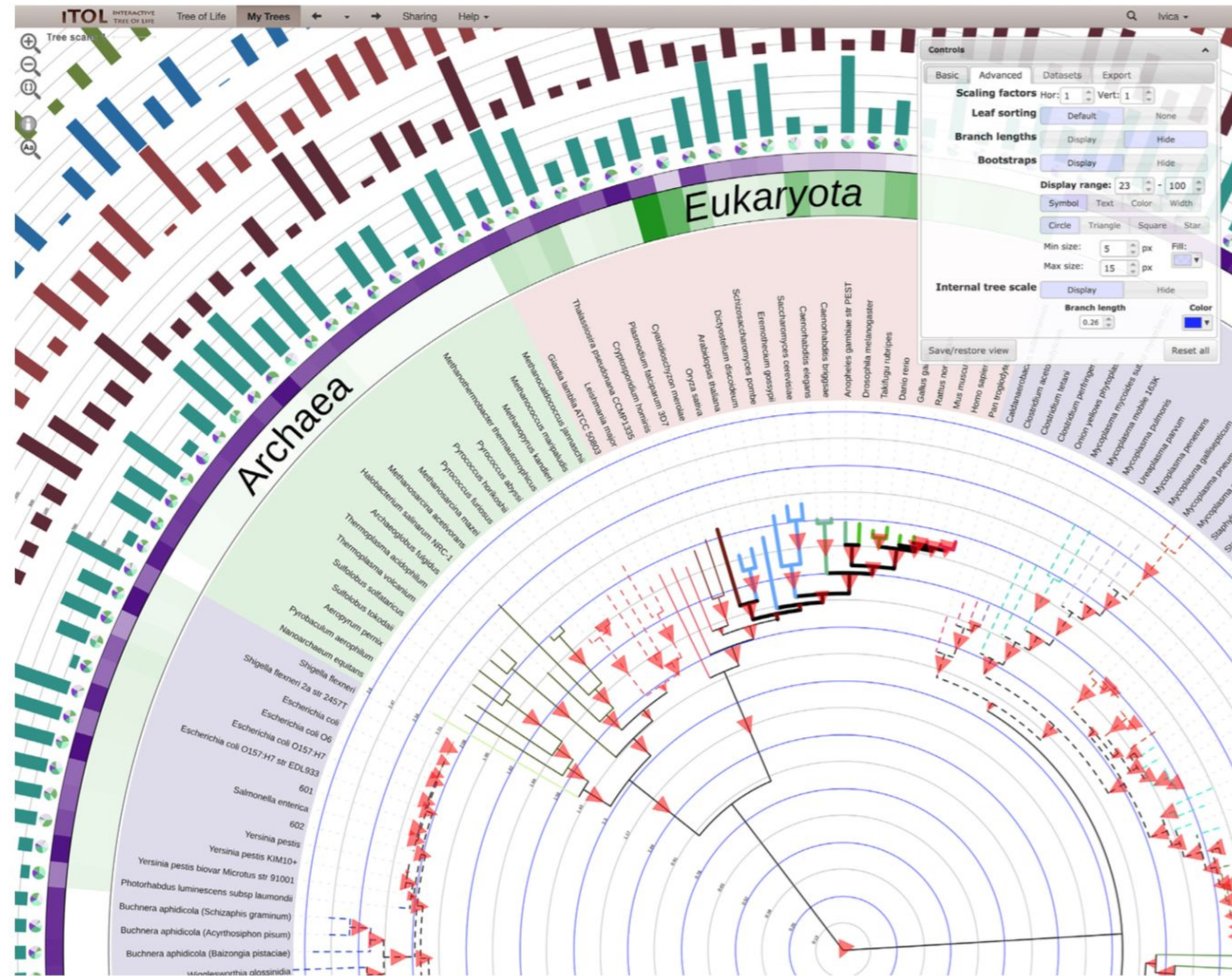


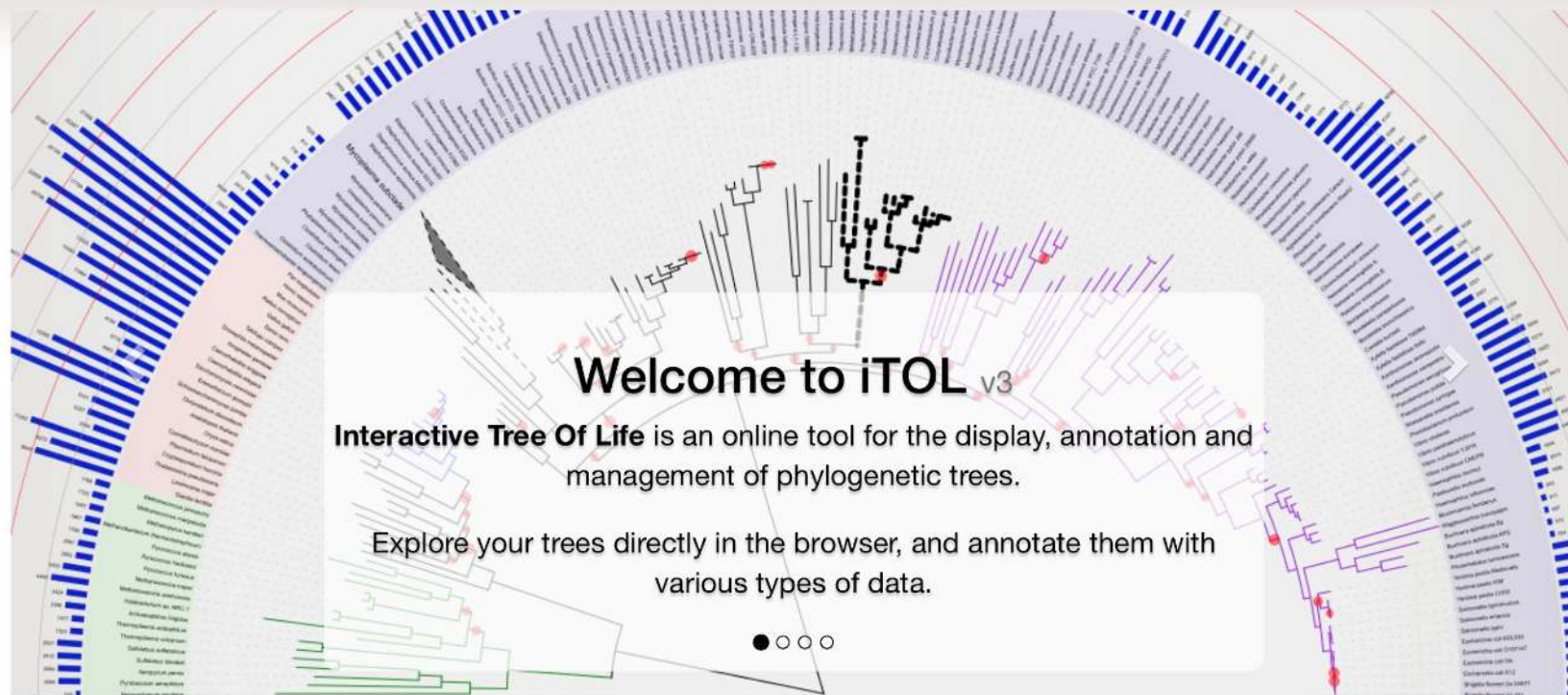
Web Portals

- **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
 - **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 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:

Seleccionar archivo

Ningún archivo seleccionado

Upload

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

Upload
your tree
here

Paste your
tree here

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

The image displays the iTOL (Interactive Tree Of Life) web interface. The top navigation bar includes the iTOL logo, "Tree of Life", "Upload", "Sharing", "Help", and a "Login" link. On the left, a vertical toolbar contains icons for zooming in (+), zooming out (-), information (?), and text formatting (Aa). The main area shows a phylogenetic tree with a "Tree scale: 0.1" slider at the top left. The tree is rooted and has a scale bar. To the right of the tree, a list of taxa is displayed, including: Centruroides, Synsphyronus, Liphistius, Mastigoproctus, Damon, Limulus, Peripatopsis long iso, Scutigera, Eremobates, Ixodes, Tetranychus, Metasiro, Ricinoides, R karschii, Pseudocellus, Cryptocellus Bocas, and Cryptocellus becki. On the right side, a "Controls" panel is open, showing various settings for the tree display. The "Basic" tab is selected, and the "Display mode" is set to "Normal". Other settings include "Parameters" (0° rotation), "Invert" (No), "Branch lengths" (Use), "Labels" (Aligned), "Label shift" (0), "Dashes" (On), "Label font" (Arial), "Font style" (20 px), "Branch lines" (1 px), and "Reset all" button.

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

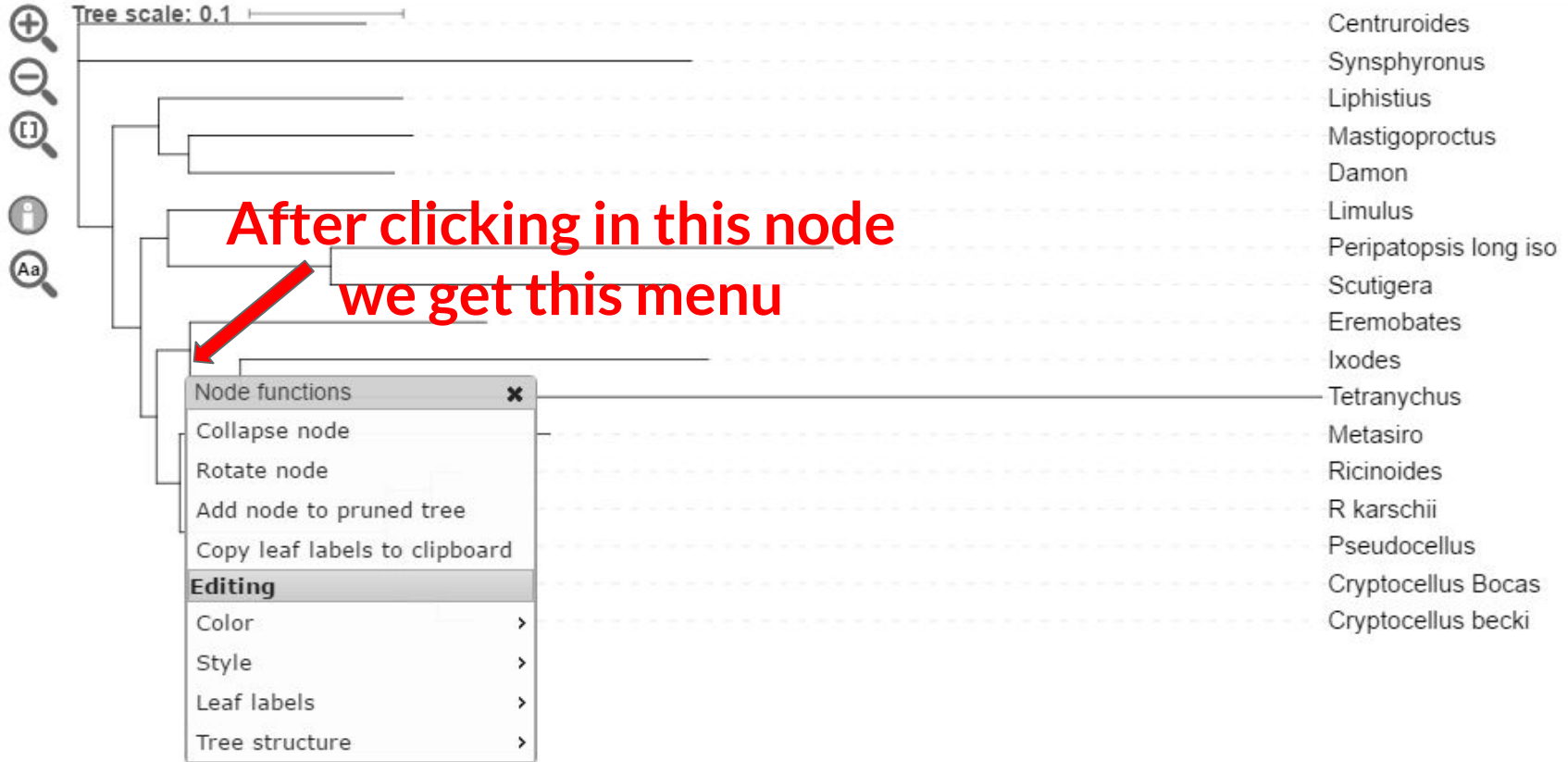
Look how many options!

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)



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:

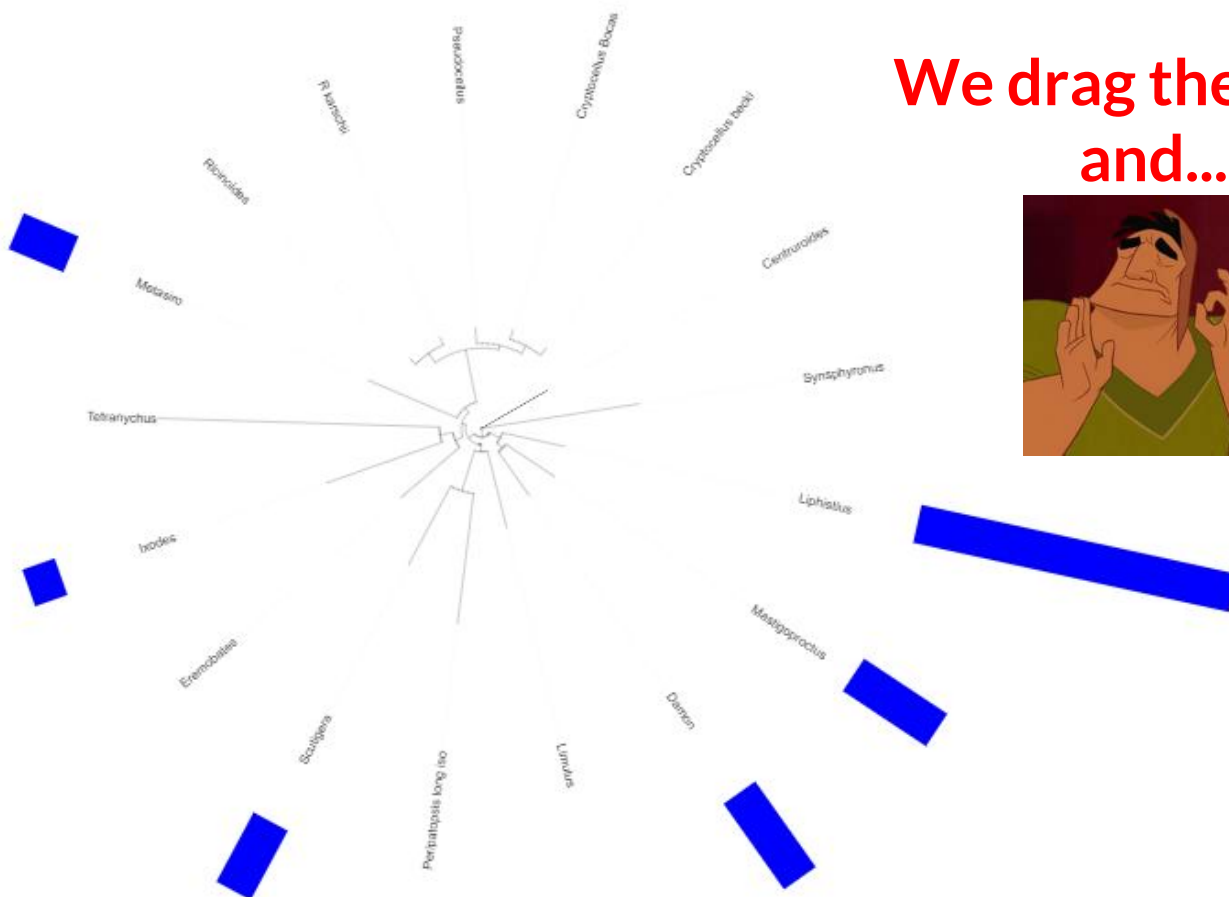
1. Histogram with the number of genes in a given family for each organism
2. Pie chart representing relative frequencies of transposon families
3. Horizontal connections between nodes to represent HGT
4. Phenotypic characters for each branch
5. Protein architecture for each branch

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

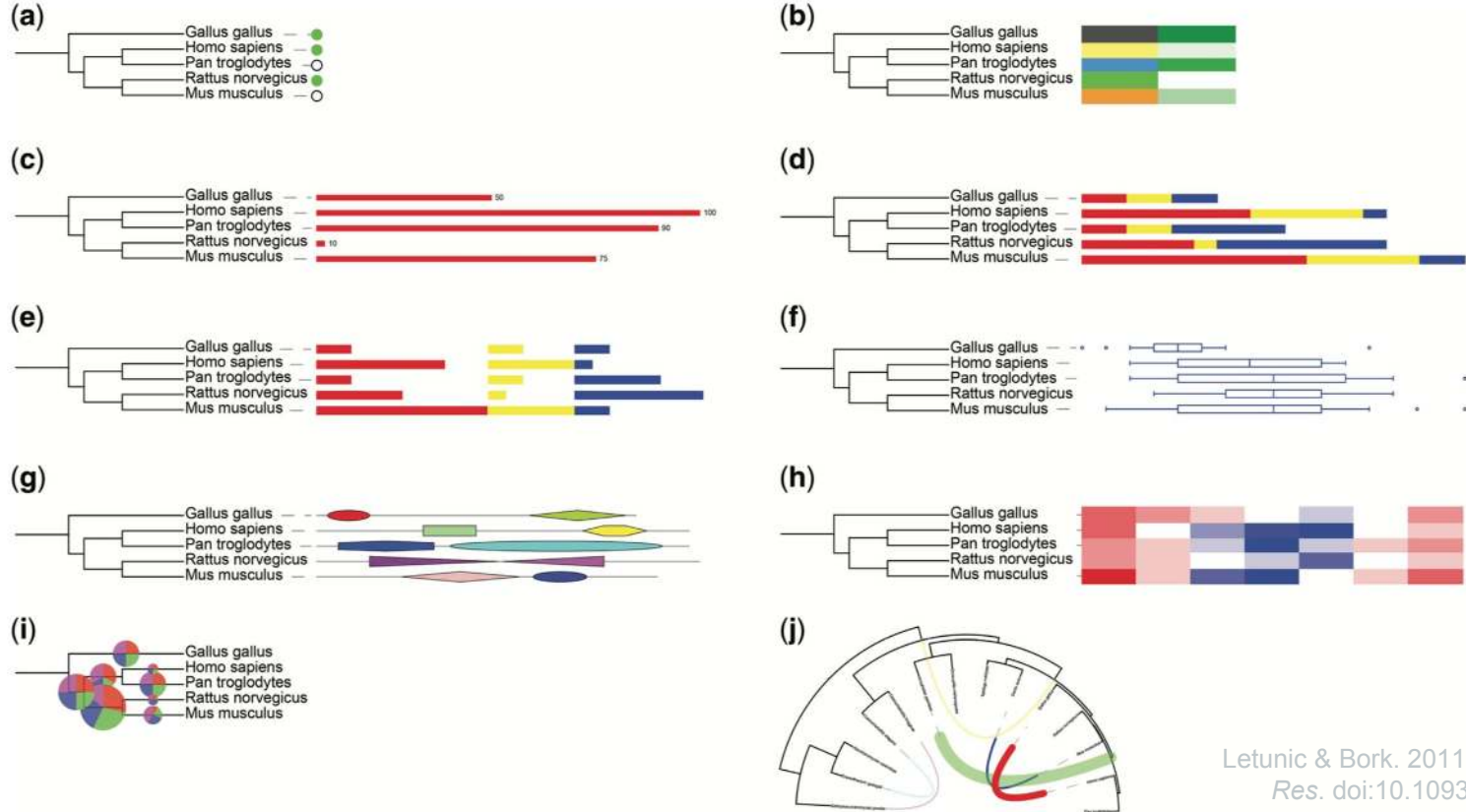
Bar zero at 0 dataset value

### Datasets

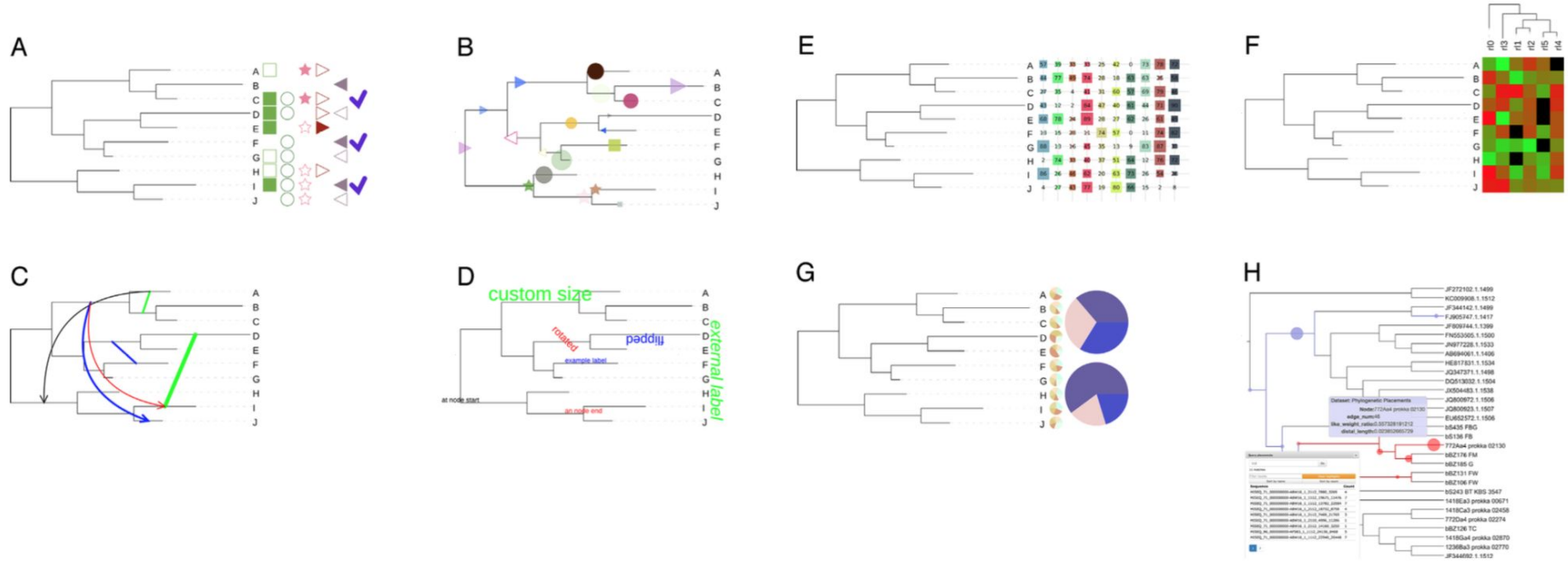
- simple\_bar\_testing ☒
- simple\_piechart\_testing ☒

Switch on-off datasets

# iTOL – Dataset Templates



# iTOL – Even More Templates



# Web Portals

- Phylo.IO @ <http://phylo.io>
- 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.

# 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



|                       |      |
|-----------------------|------|
| ■ DEMOS (16 trees)    | +    |
| ■ SHOWCASES (7 trees) | -    |
| showcase 01           | ⚙️ + |
| showcase 02           | ⚙️ + |
| showcase 03           | ⚙️ + |
| showcase 04           | ⚙️ + |
| showcase 05           | ⚙️ + |
| ss                    | ⚙️ + |
| shmbian               | ⚙️ - |

Basic Advanced Annotation upload Export

# EVOLVIEW

**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 webp eps svg 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

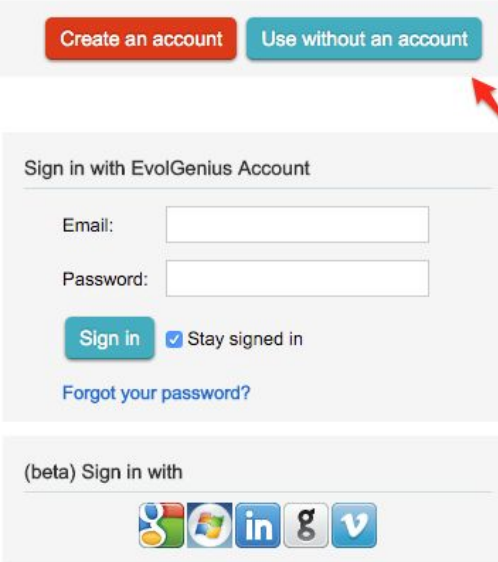
## A quick start

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)));



The screenshot shows the 'Upload a new tree' dialog box in the EVOLVIEW application. The dialog has four tabs: 'Basic', 'Advanced', 'Annotation upload', and 'Export'. The 'Basic' tab is selected. Below the tabs is a toolbar with various icons. The main area of the dialog contains the following fields:

- Project:** A text input field containing 'new project'. A red arrow labeled '2' points to this field.
- Name:** A text input field containing 'test tree'. A red arrow labeled '3' points to this field.
- Format:** A dropdown menu showing 'newick (also phylip)'.
- Data:** A text area containing the Newick tree string: '(chicken, ((mouse, rat), (chimp, human)));'. A red arrow labeled '4' points to this text area.

At the bottom of the dialog, there is a section labeled 'Or upload:' with a button 'Seleccionar archivos' and the text 'ningún archivo seleccionado'. At the bottom right, there are two buttons: 'Cancel' and 'Submit'.

# EVOLVIEW demo

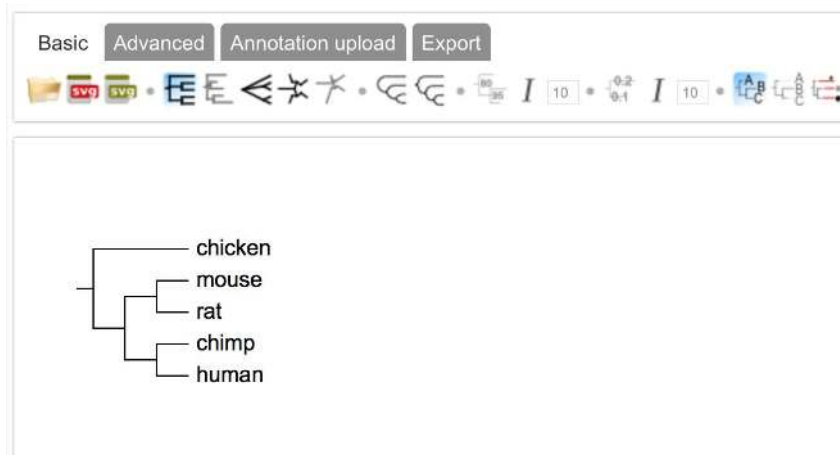
- at the "mytrees" page, click the folder icon on the "Basic" tab (the only icon that's clickable if no tree is active). in the popup window, enter the following contents and click the button "Submit" at the bottom:

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

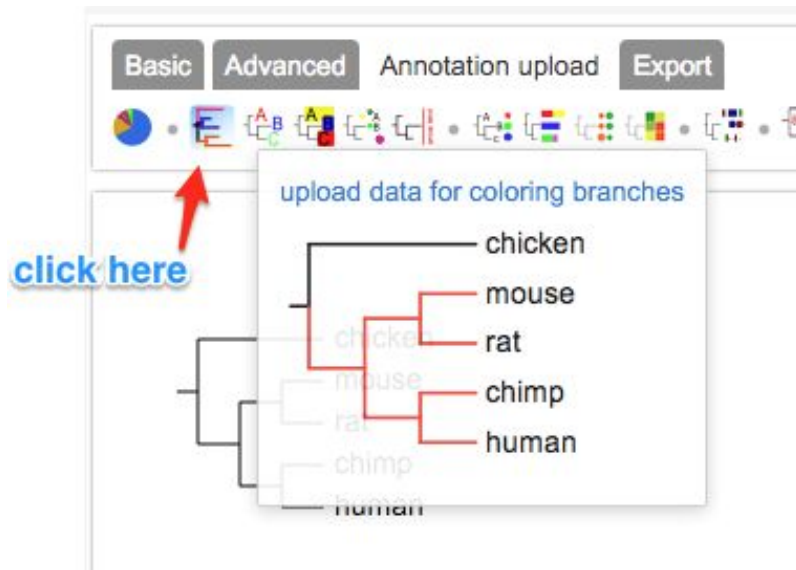
## Change the branch and leaf colors of the tree

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

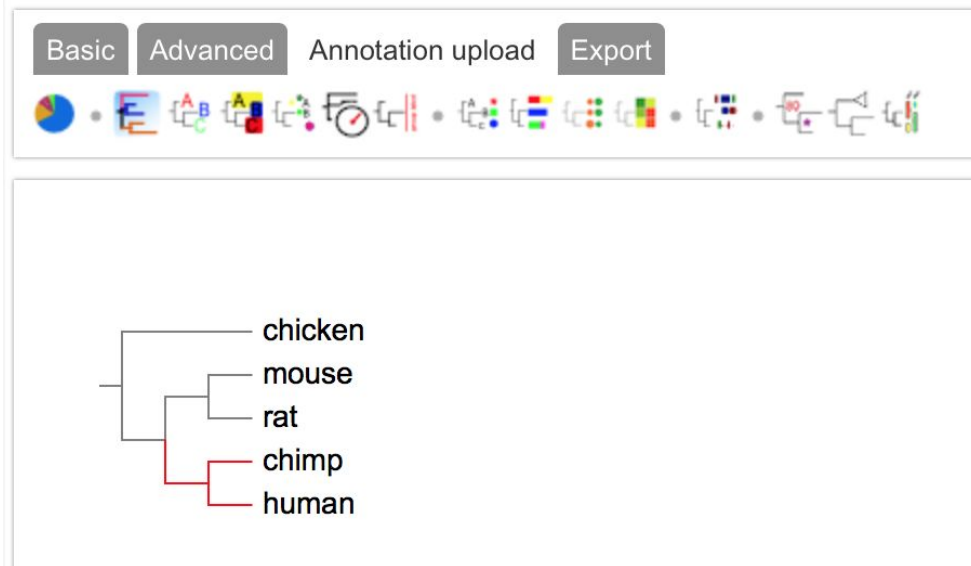
## lines start with # are annotations; you can put an annotation line anywhere in this dataset, provided that  
## the # is the first character of the line let the dataset begin: all fields of a line are separated by 'tab'  
## first all, color all branches with 'grey'

```
human,chicken grey ad
```

## and then highlight the branches connecting human and chimp

```
human,chimp red ad
```

- After applying the dataset:



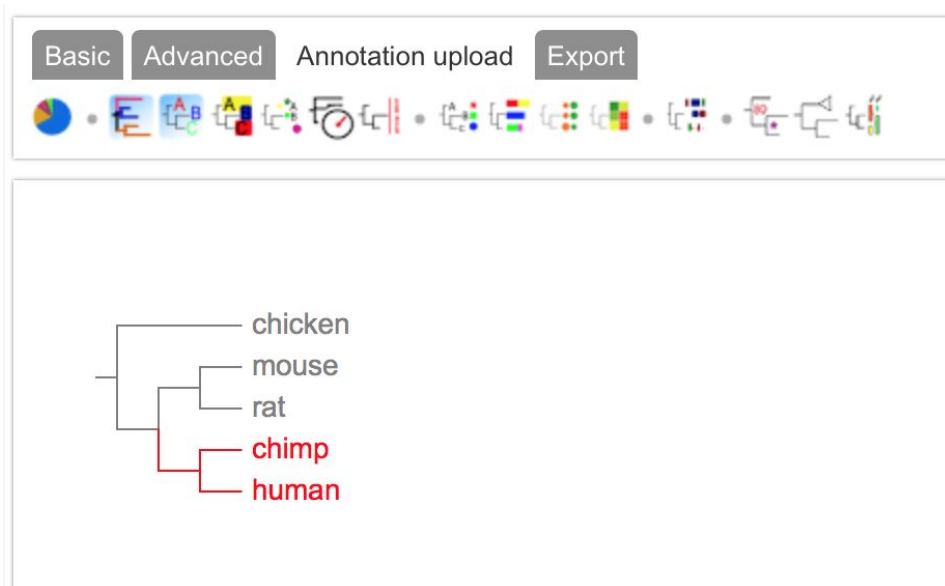
# EVOLVIEW demo

- 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:



# 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
```

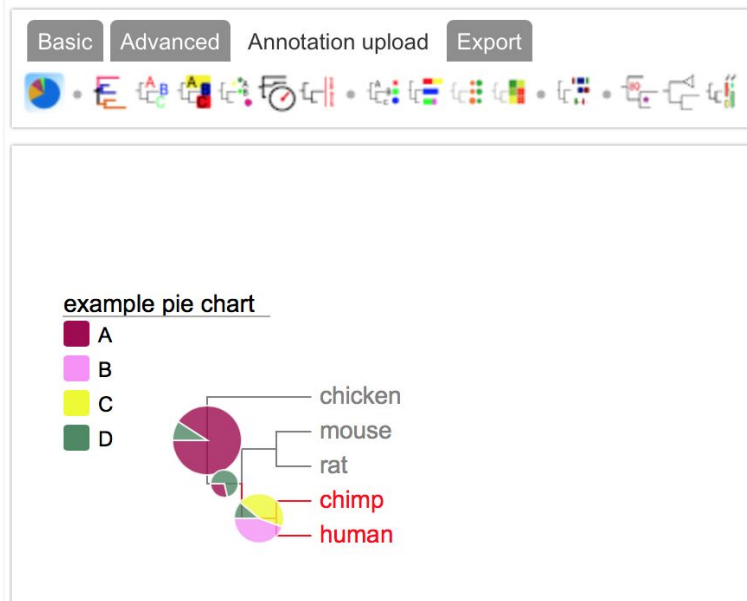
# EVOLVIEW demo

## 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:



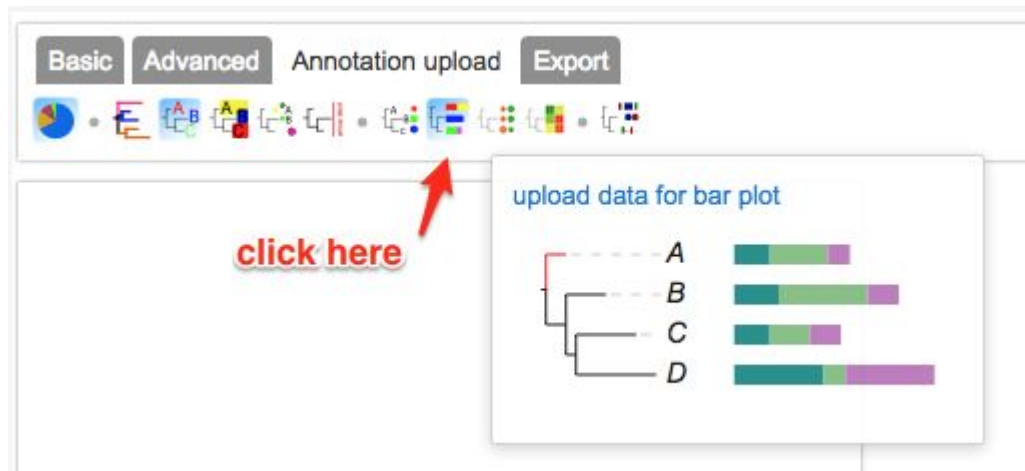
# EVOLVIEW demo

## 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
```

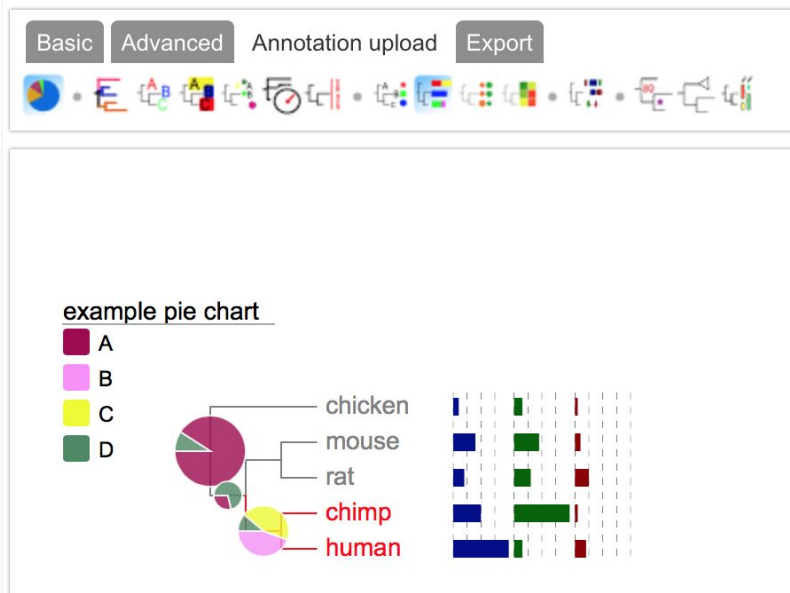


# EVOLVIEW demo

## 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:



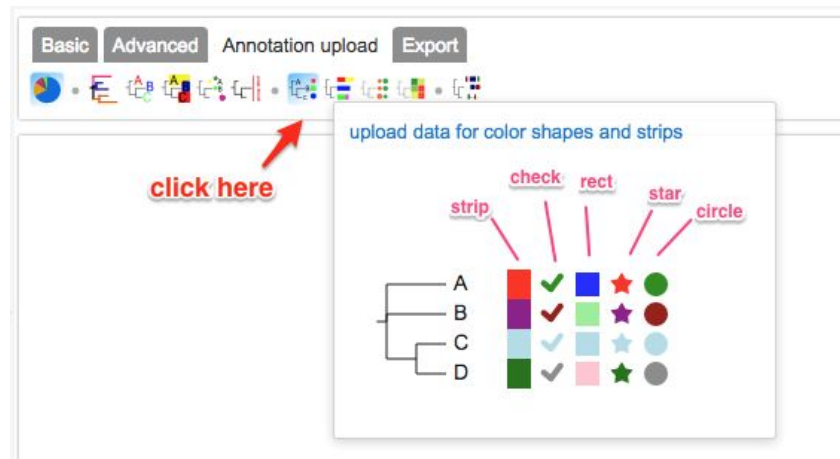
# EVOLVIEW demo

## 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,grey,red
!type rect,circle,star,strip
!showlegends 1
human red,green,blue,purple
chimp purple,darkred,lightgreen,lightblue
mouse lightblue,yellow
chicken darkgreen,grey,pink,grey
rat grey,orange,pink,orange
```



# 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 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. The main area displays a preview of the data being added, which includes a pie chart and a set of color strips.

**example pie chart**

- A
- B
- C
- D

**color strips**

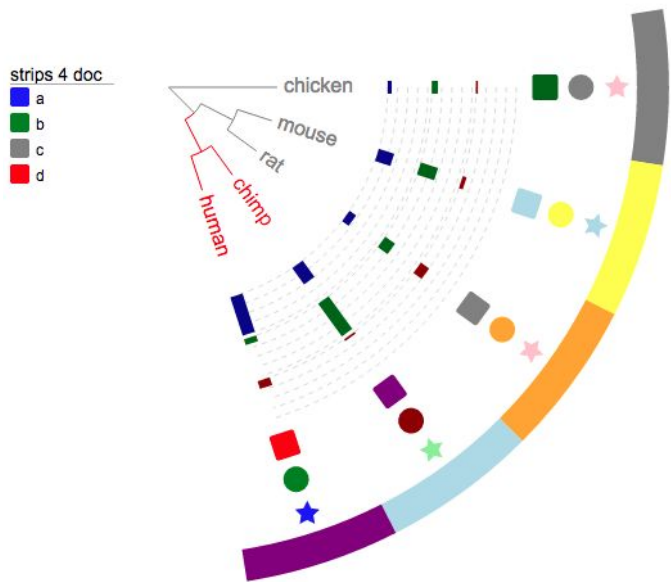
- a
- b
- c
- d

The pie chart shows a tree structure with leaf labels: chicken, mouse, rat, chimp, and human. The color strips are arranged in a grid, with each strip corresponding to a specific color and shape (e.g., blue square, green circle, grey star, yellow triangle).

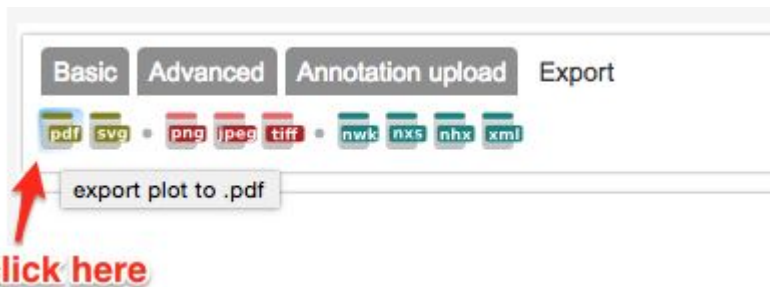
# EVOLVIEW demo

Play around and then export the tree to pdf file

- Try different display mode:



- Then download the plot as a PDF file:



# 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

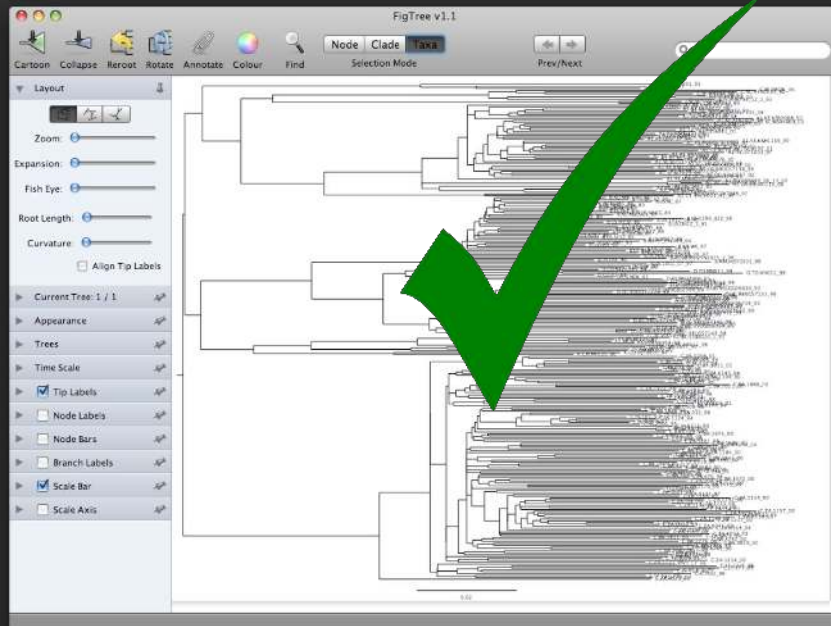
FigTree is designed as a graphical viewer of phylogenetic trees and as a program for producing publication-ready figures. As with most of my programs, it was written for my own needs so may not be as polished and feature-complete as a commercial program. In particular it is designed to display summarized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

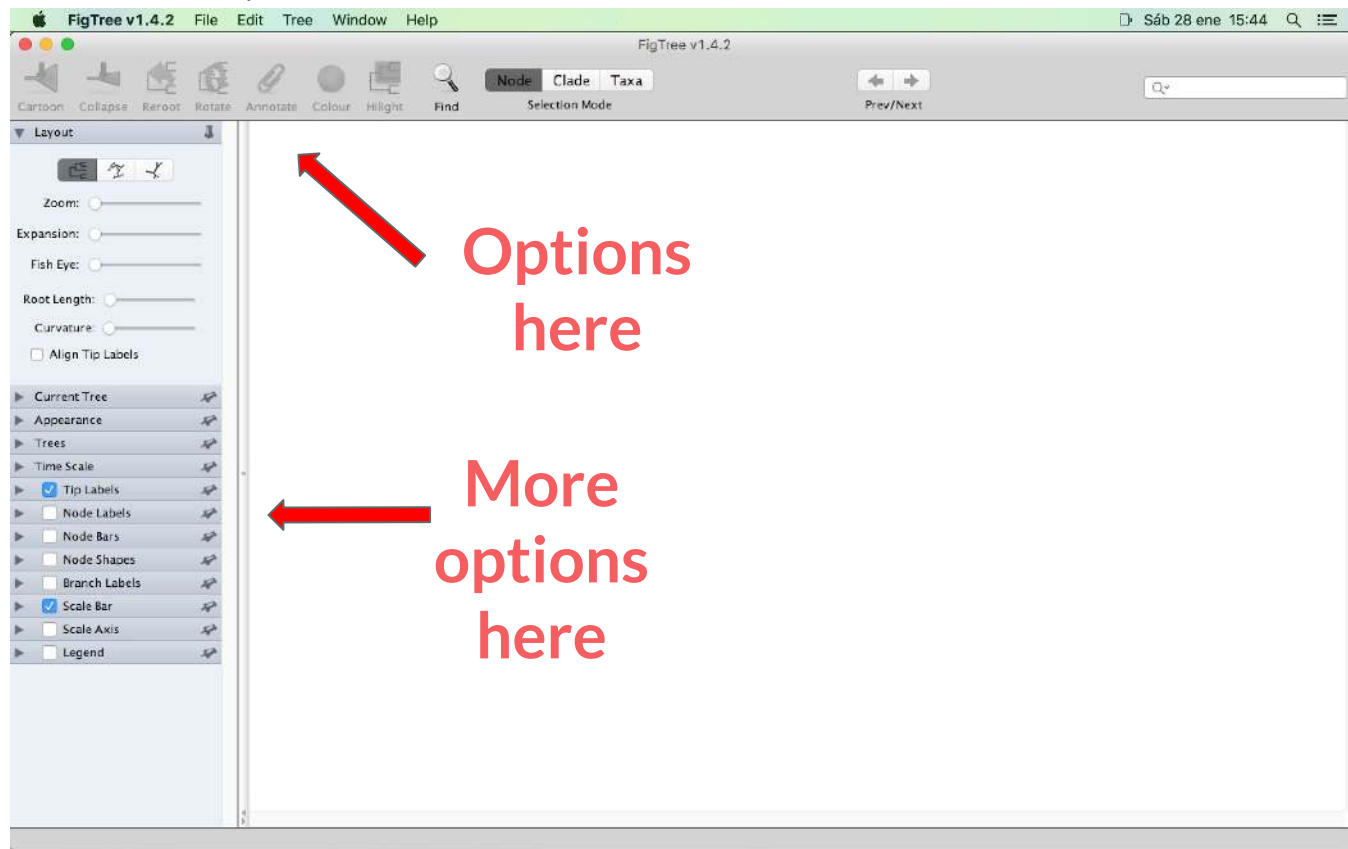
# FigTree

## 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

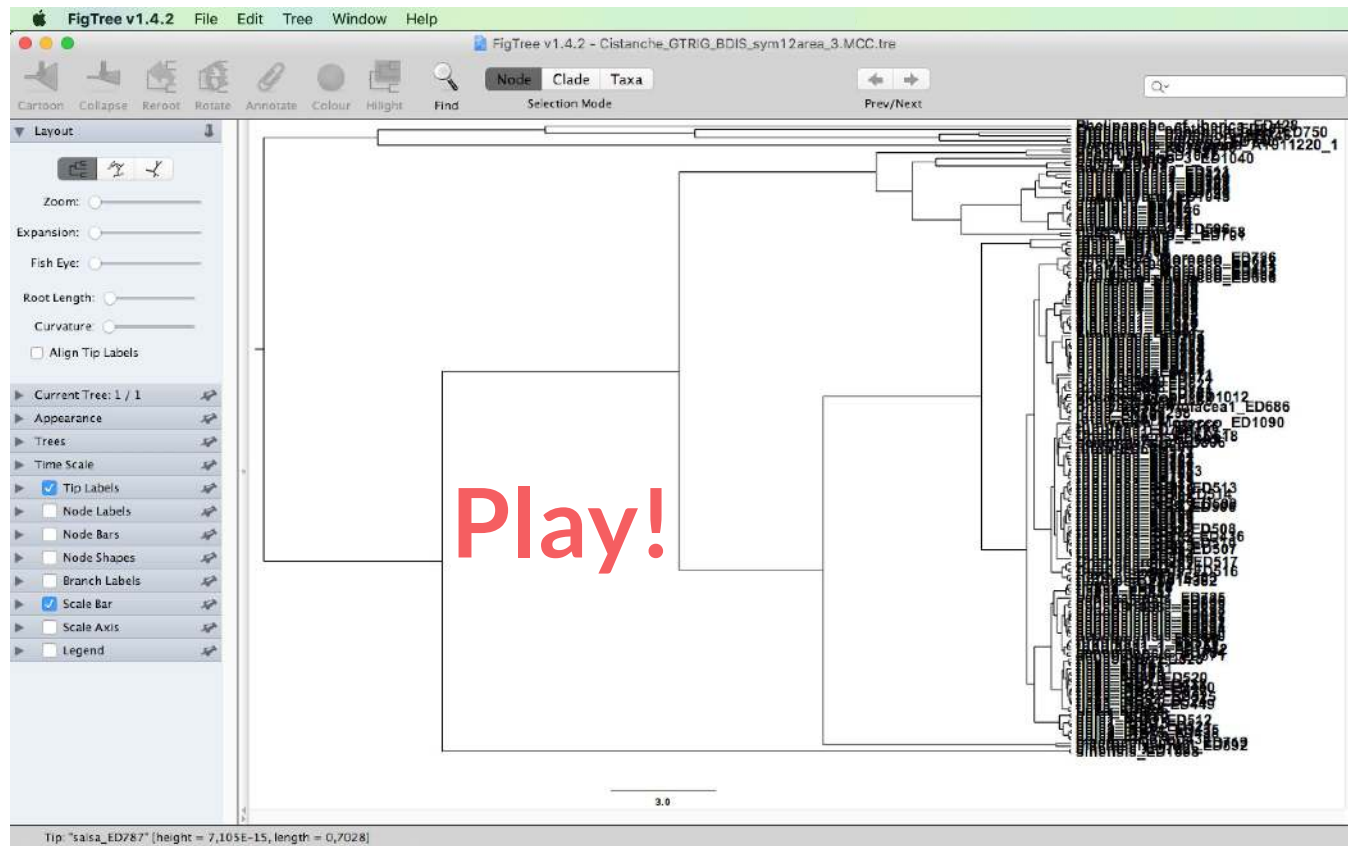
Open files  
here



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](#)

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[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).



root.

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 leafs to the



Rrr and Bbb.

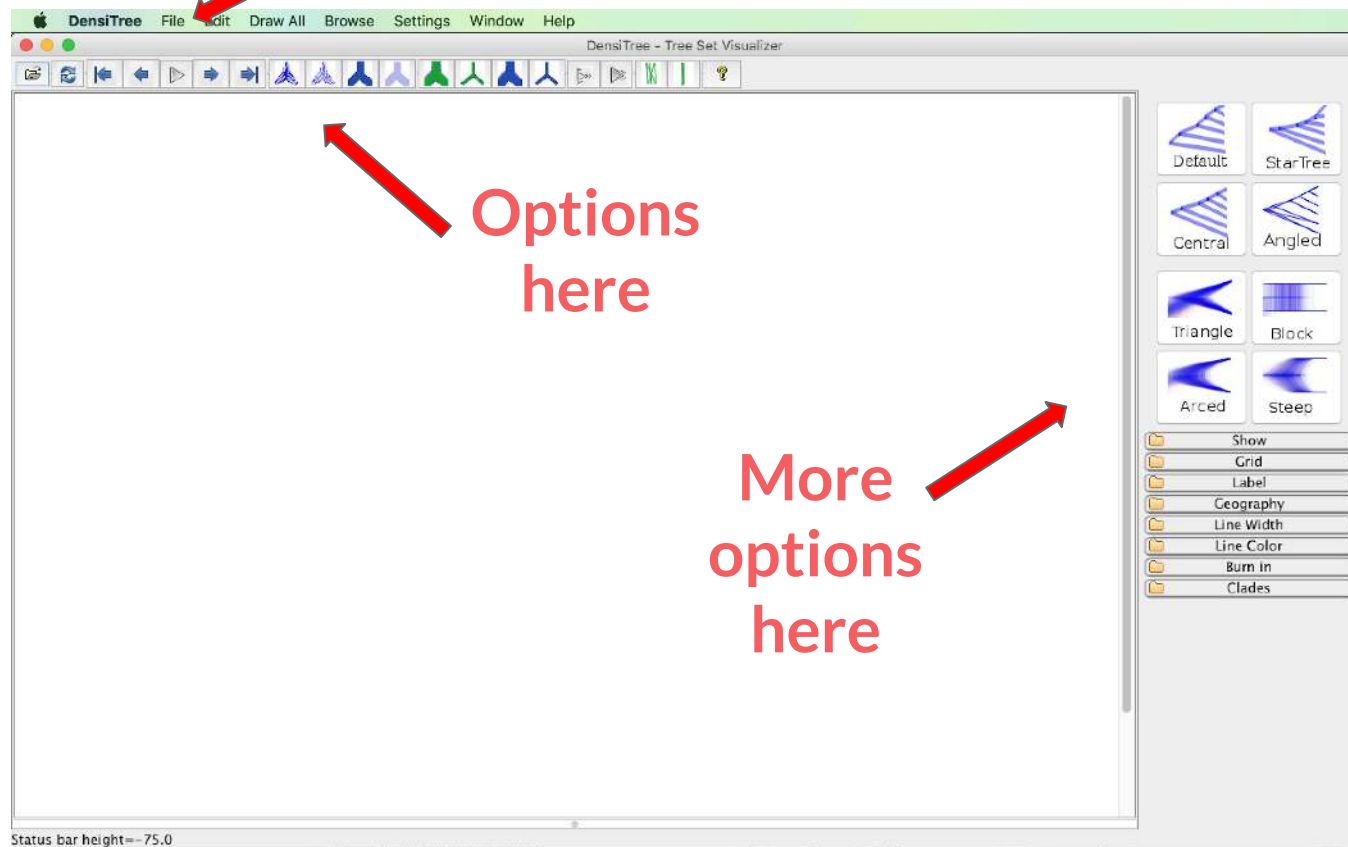
As Figure preceding but in block trees. This tree set was generated with calibration points, which show up as dense node heights, for example, the parent of



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.

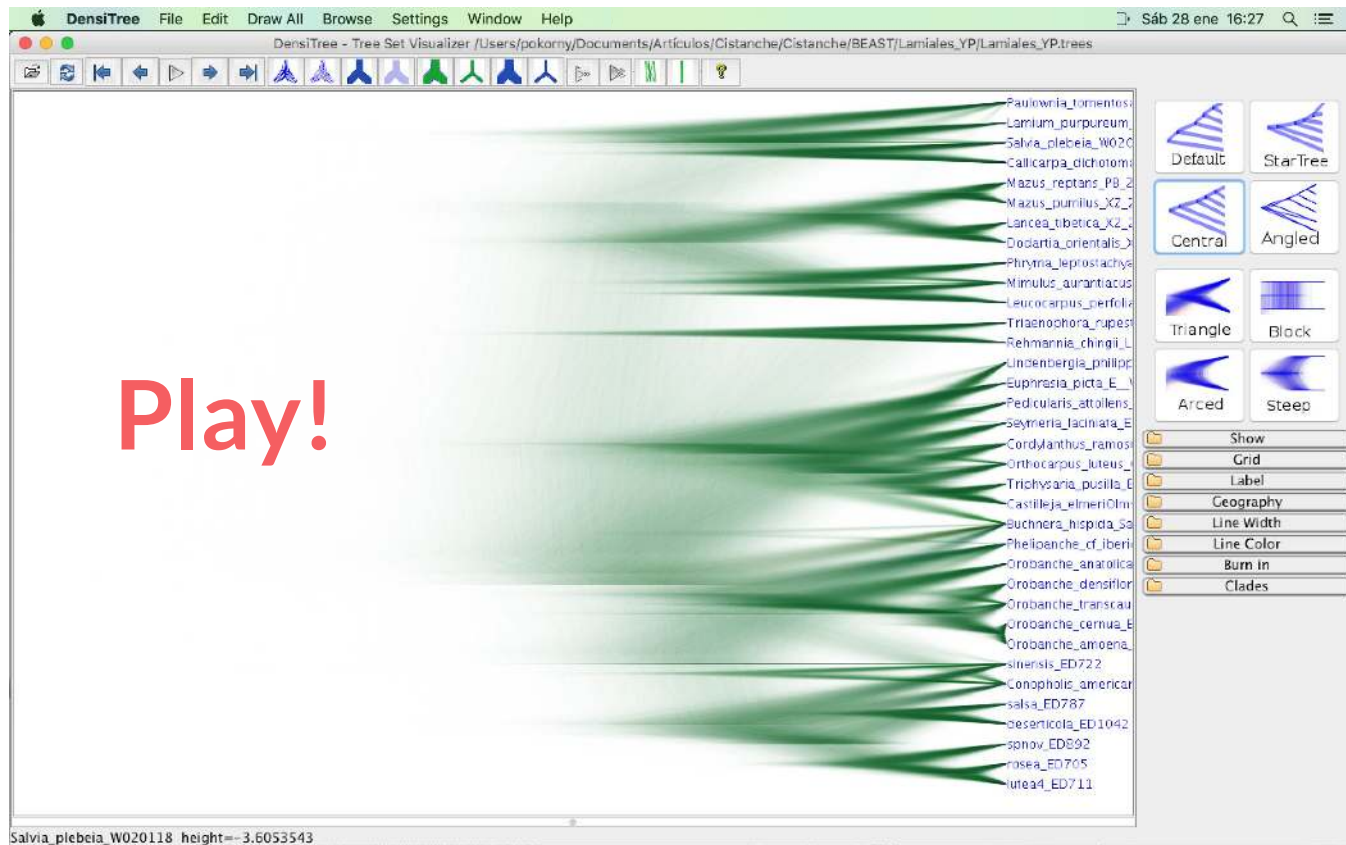
# DensiTree

Open files  
here

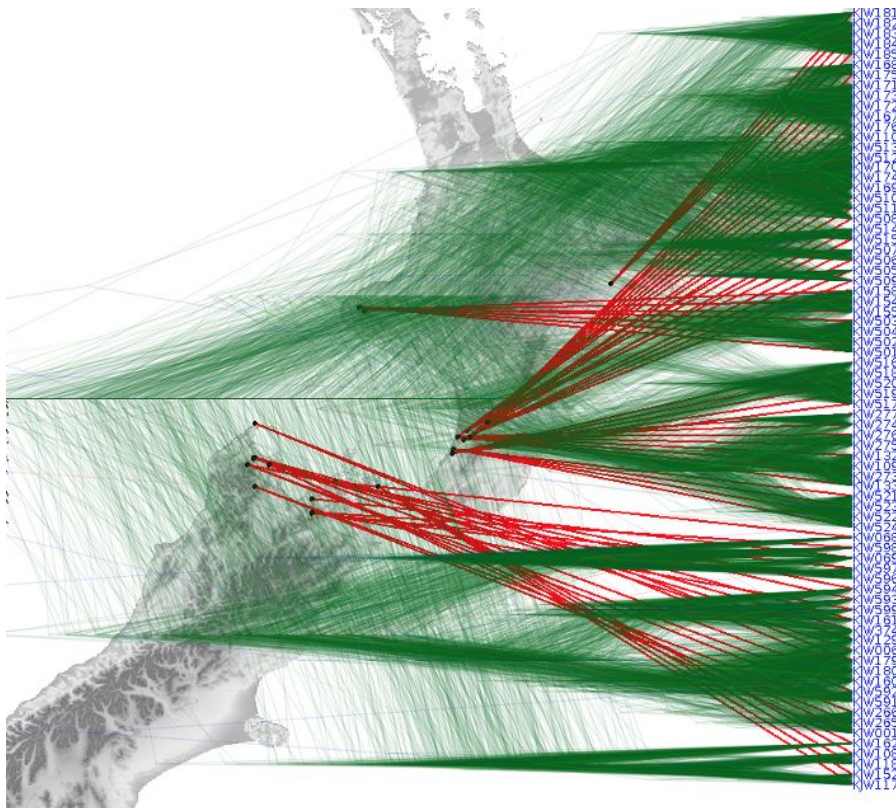


# DensiTree

Play!



# Cloudogram...



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

# Cloulogram Fail



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

# Cloudogram...

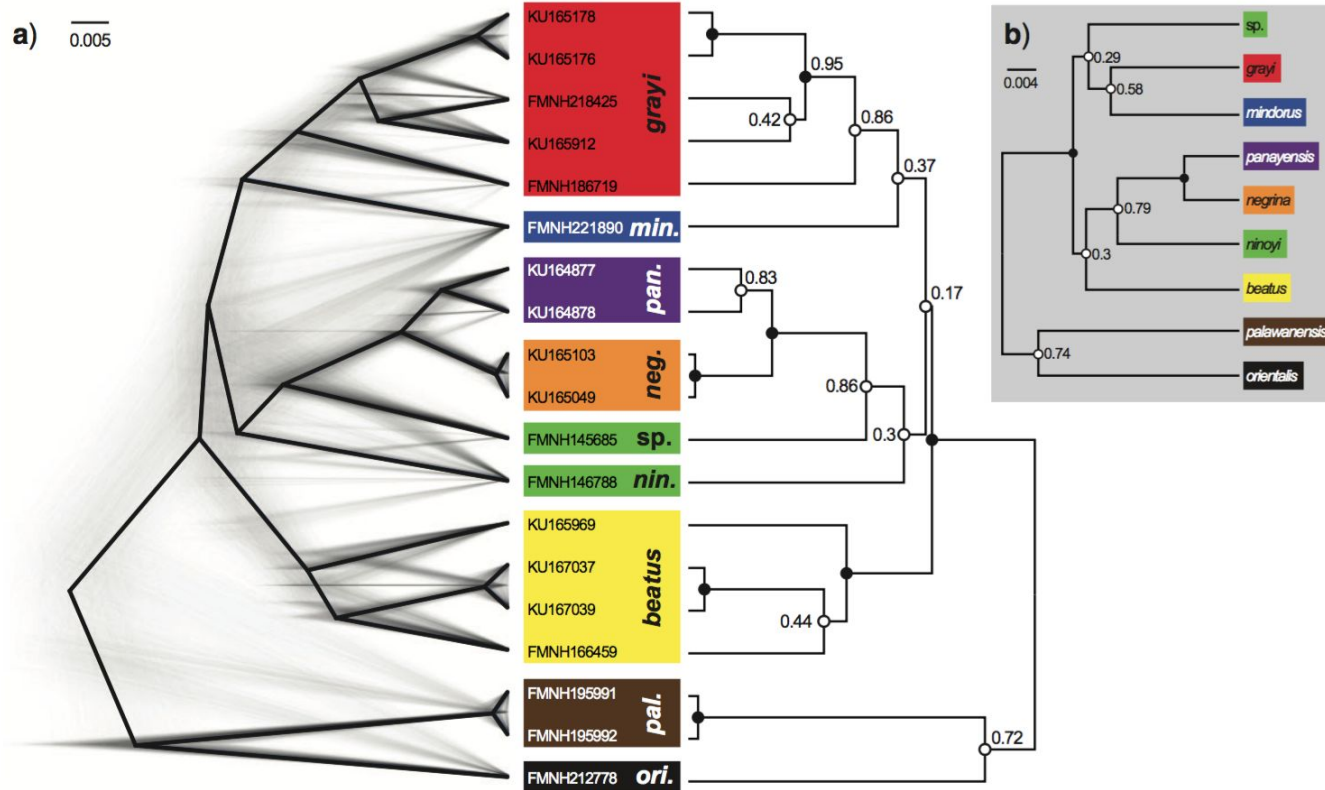


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

# Cloudogram Success

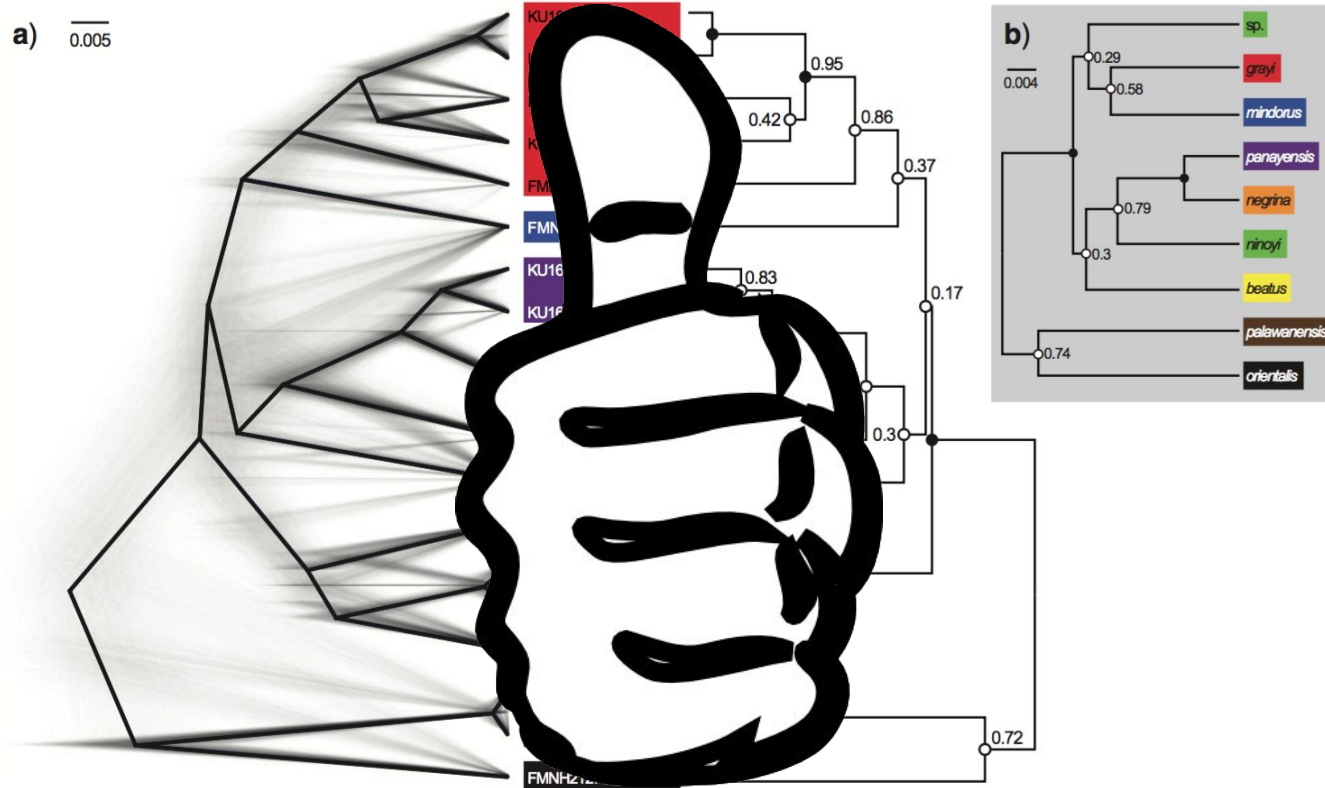


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

# Software

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

## 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:

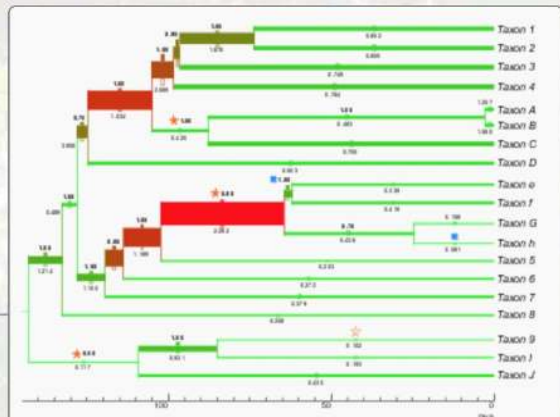
- Stöver B C, Müller K F: *TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses*. *BMC Bioinformatics* 2010, **11**:7
- DOI: [10.1186/1471-2105-11-7](https://doi.org/10.1186/1471-2105-11-7) [What is this?]

### 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

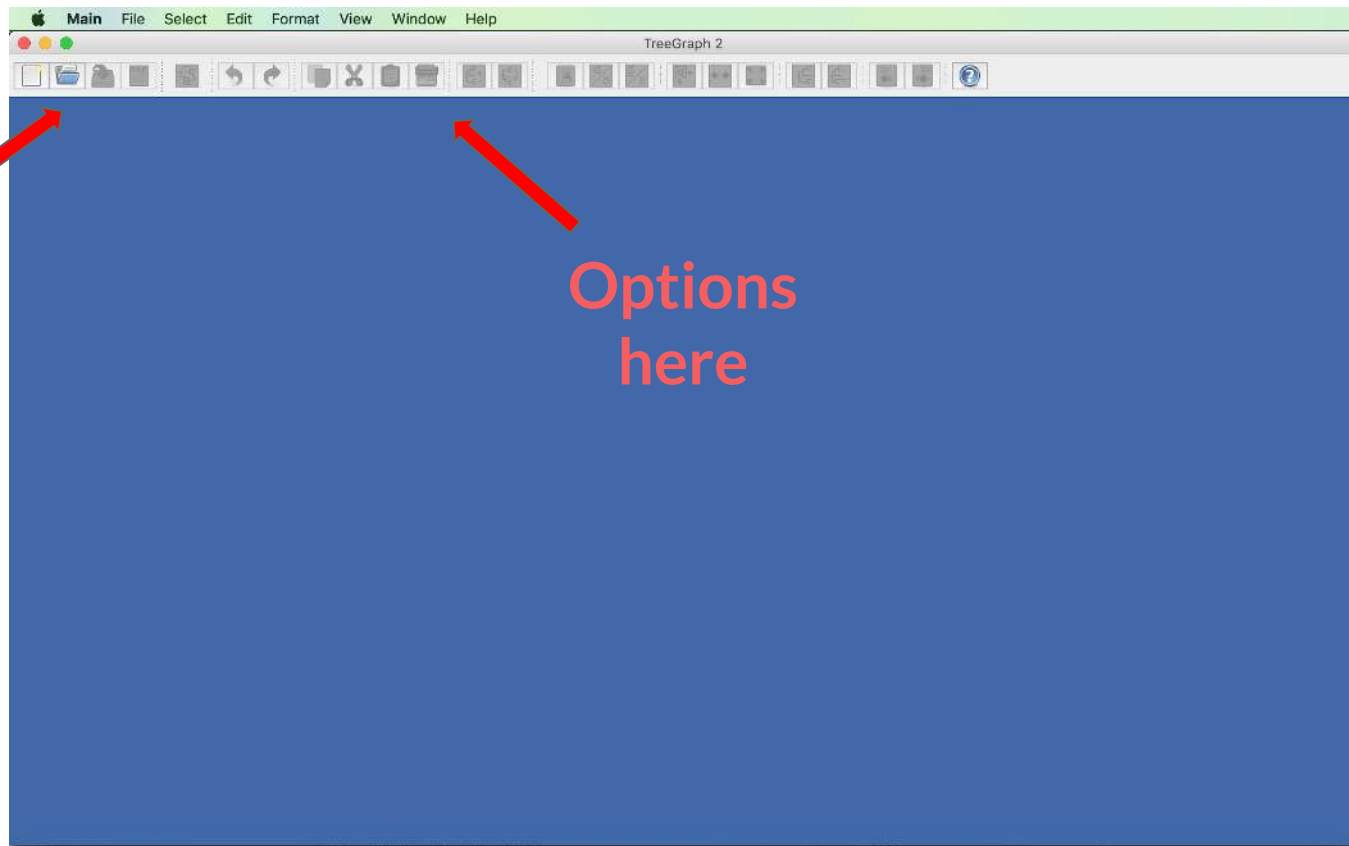


Example of some possible formats in TreeGraph 2 [Enlarge]  
[Download]

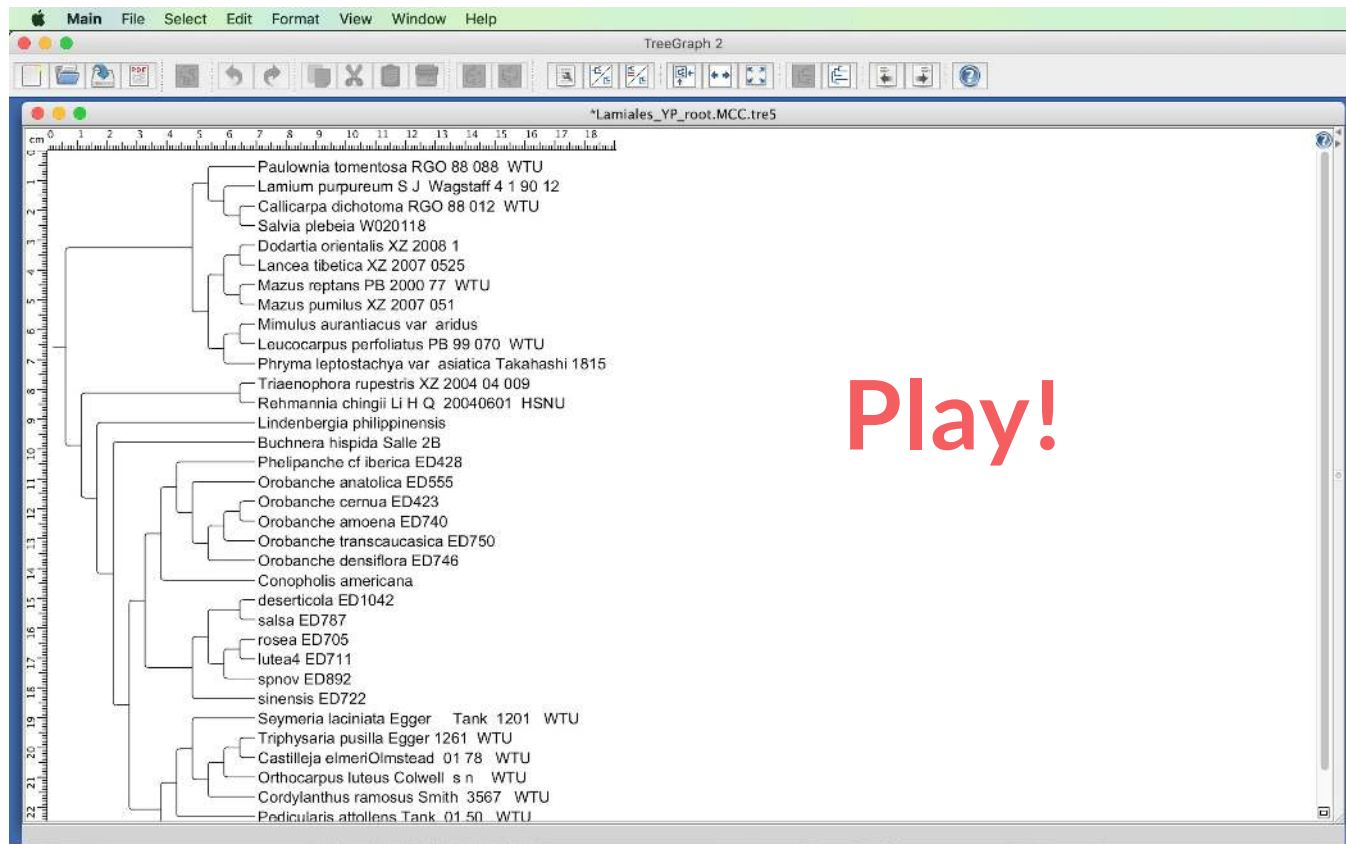
# TreeGraph 2

Open  
files  
here

Options  
here



# TreeGraph 2



Play!

# TreeGraph 2 – Documentation

## Feature overview

### The application

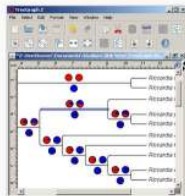
- Main menu
- Tool bar
- Document window
- Synchronizing tree selections

### 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

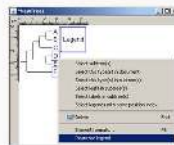
- Element formats
- Document formats
- Set colors by node/branch data (Allows you to display annotations as colors.)
- Set distance values by node/branch data (Allows you to display annotations e.g. as branch widths or text heights.)
- Scaling distance values
- Automatically position labels

## 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

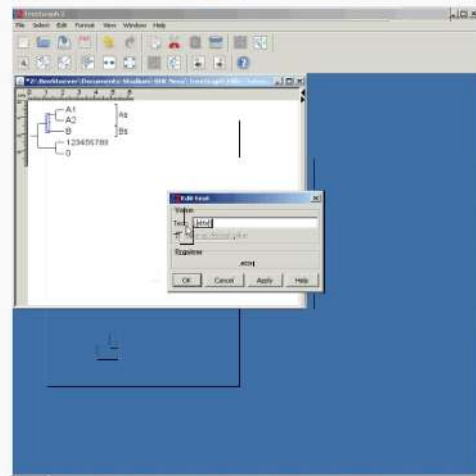
- Inserting nodes
- Collapsing nodes
- Collapsing nodes by support
- Anchoring legends
- Copying/cutting document elements
- Ladderizing
- Sorting terminal nodes
- Moving nodes
- Rerooting
- Editing text element values
- Changing branch lengths
- Replace text in node/branch data



## 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.

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

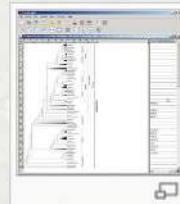
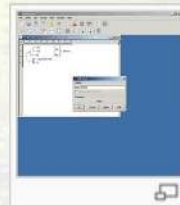
### Display taxon counts as branch widths

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:

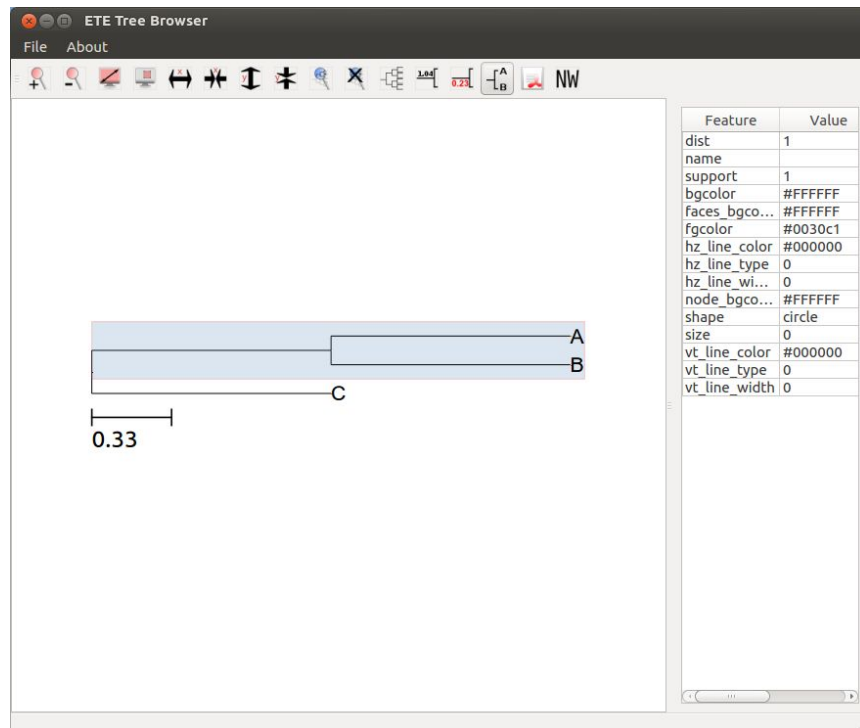
```
((A:0.1,B:0.2)90:0.2,(C:0.1,D:0.2)80:0.15)70:0.1,E:0.2);
```

# ETE3

Default visualization tool:

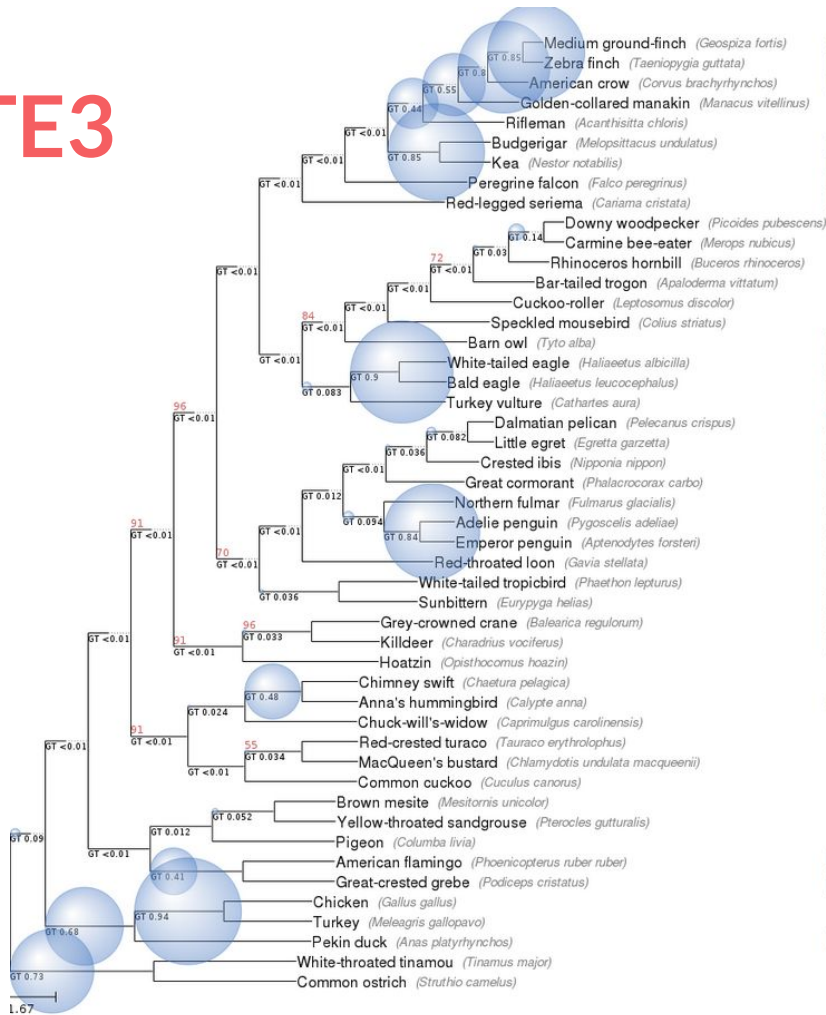
`ete3 view -t INPUT`

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



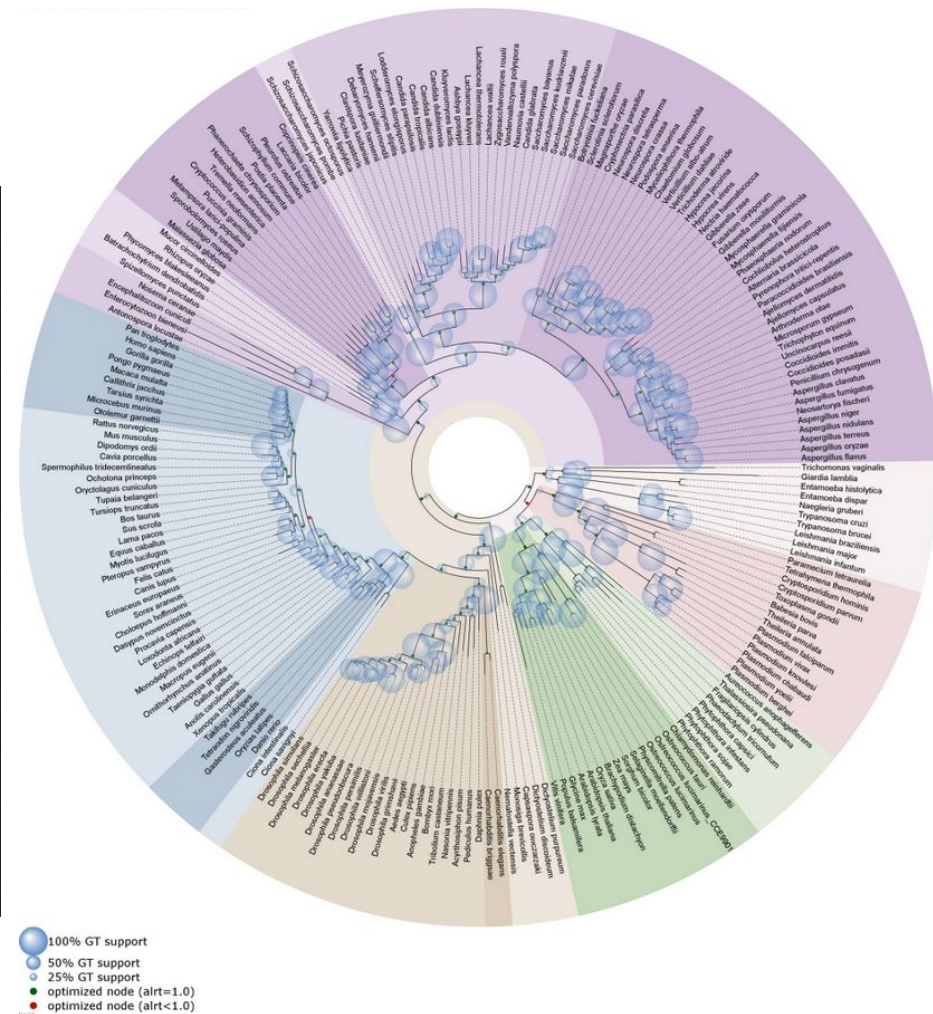
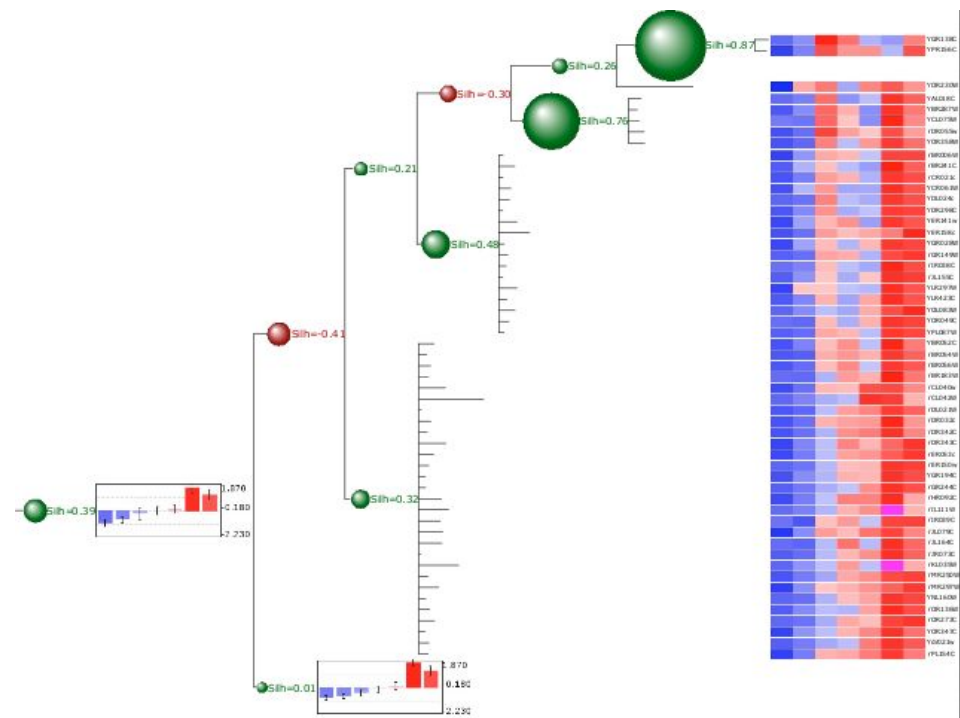
While nice, the default visualization tool is limited

# ETE3



|                          |               |                     |                   |                |             |           |
|--------------------------|---------------|---------------------|-------------------|----------------|-------------|-----------|
| vocal learning           | Neognathae    | Passeriformes       | Passeroidea       | Fringillidae   | Emberizinae | Thraupini |
| vocal learning           | Neognathae    | Passeriformes       | Passeroidea       | Estrildidae    | Estrildinae |           |
| vocal learning           | Neognathae    | Passeriformes       | Corvoidea         | Corvidae       |             |           |
|                          | Neognathae    | Passeriformes       | Pipridae          |                |             |           |
|                          | Neognathae    | Passeriformes       | Acanthistidae     |                |             |           |
| vocal learning           | Neognathae    | Psittaciformes      | Psittacidae       |                |             |           |
| vocal learning           | Neognathae    | Psittaciformes      | Psittacidae       |                |             |           |
| apex birds-of-prey       | Neognathae    | Falconiformes       | Falconidae        |                |             |           |
| apex birds-of-prey       | Neognathae    | Gruiformes          | Carriamidae       |                |             |           |
|                          | Neognathae    | Piciformes          | Picidae           |                |             |           |
|                          | Neognathae    | Coraciiformes       | Meropidae         |                |             |           |
|                          | Neognathae    | Bucerotiformes      | Bucerotidae       |                |             |           |
|                          | Neognathae    | Trogoniformes       | Trogonidae        |                |             |           |
|                          | Neognathae    | Coraciiformes       | Leptosomidae      |                |             |           |
|                          | Neognathae    | Coliiformes         | Colidae           |                |             |           |
| 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    | Ciconiiformes       | 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          |                |             |           |
| vocal learning           | Neognathae    | Trochiliformes      | Trochilidae       |                |             |           |
|                          | Neognathae    | Caprimulgiformes    | Caprimulgidae     | Caprimulginae  |             |           |
|                          | Neognathae    | Musophagiformes     | Musophagidae      |                |             |           |
|                          | Neognathae    | Gruiformes          | Otididae          | Chlamydotes    |             |           |
|                          | 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     |                |             |           |

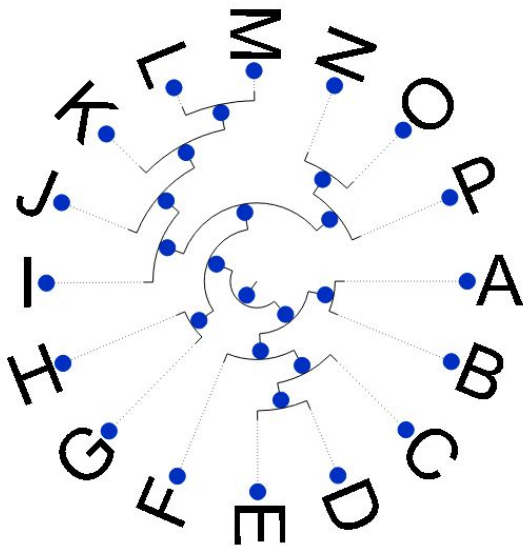
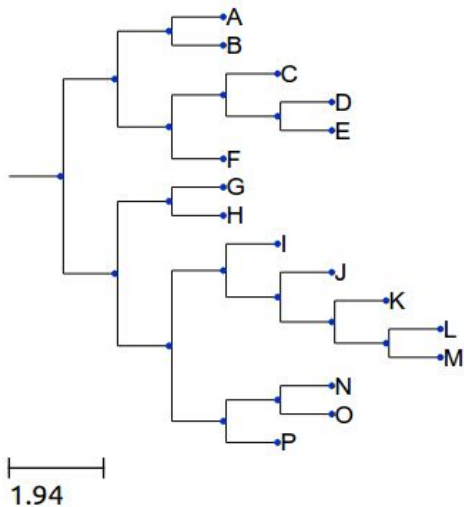
# ETE3



# 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:



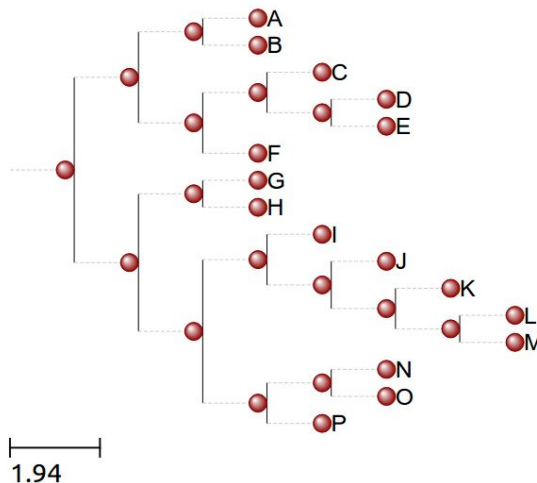
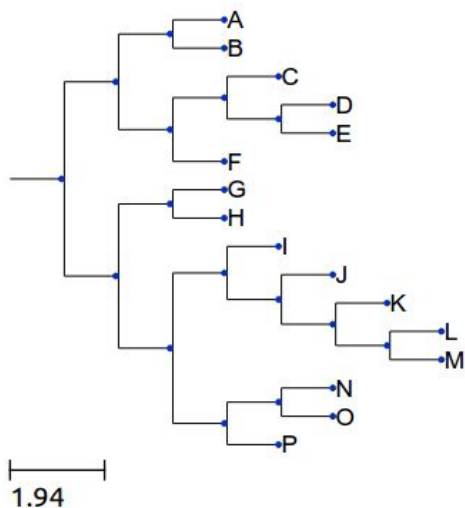
It can also change whether it shows things such as branch lengths, support, leaf names.

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

# ETE3

## NodeStyles

- NodeStyle like treeStyle affects the visualization of individual nodes:

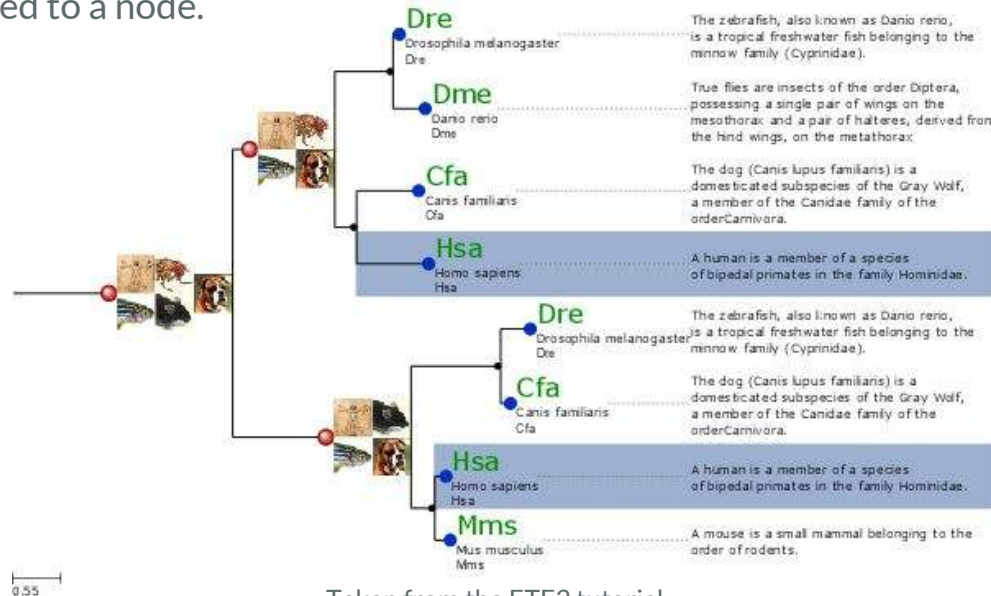


- For instance, the default style for nodes in ETE3 is that they are represented with a blue dot
- This can be modified by calling the node instance and changing some of the characteristics in the node style such as colour or size
- Useful tip: if you don't want them, change the size to 0

# ETE3

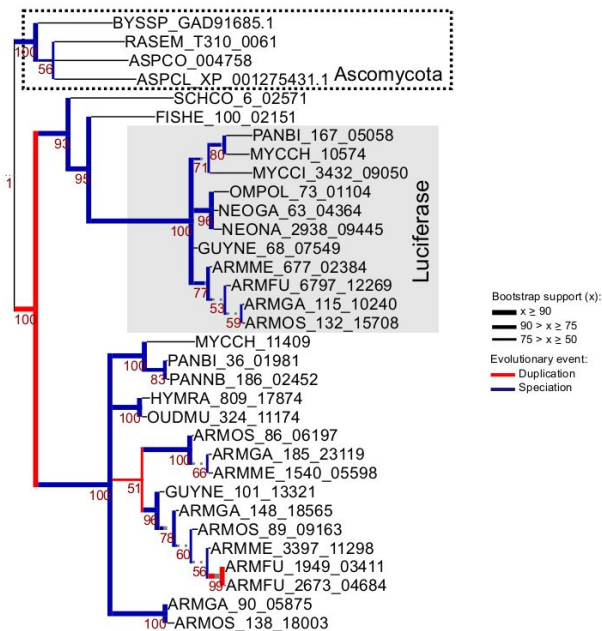
## Faces

- 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

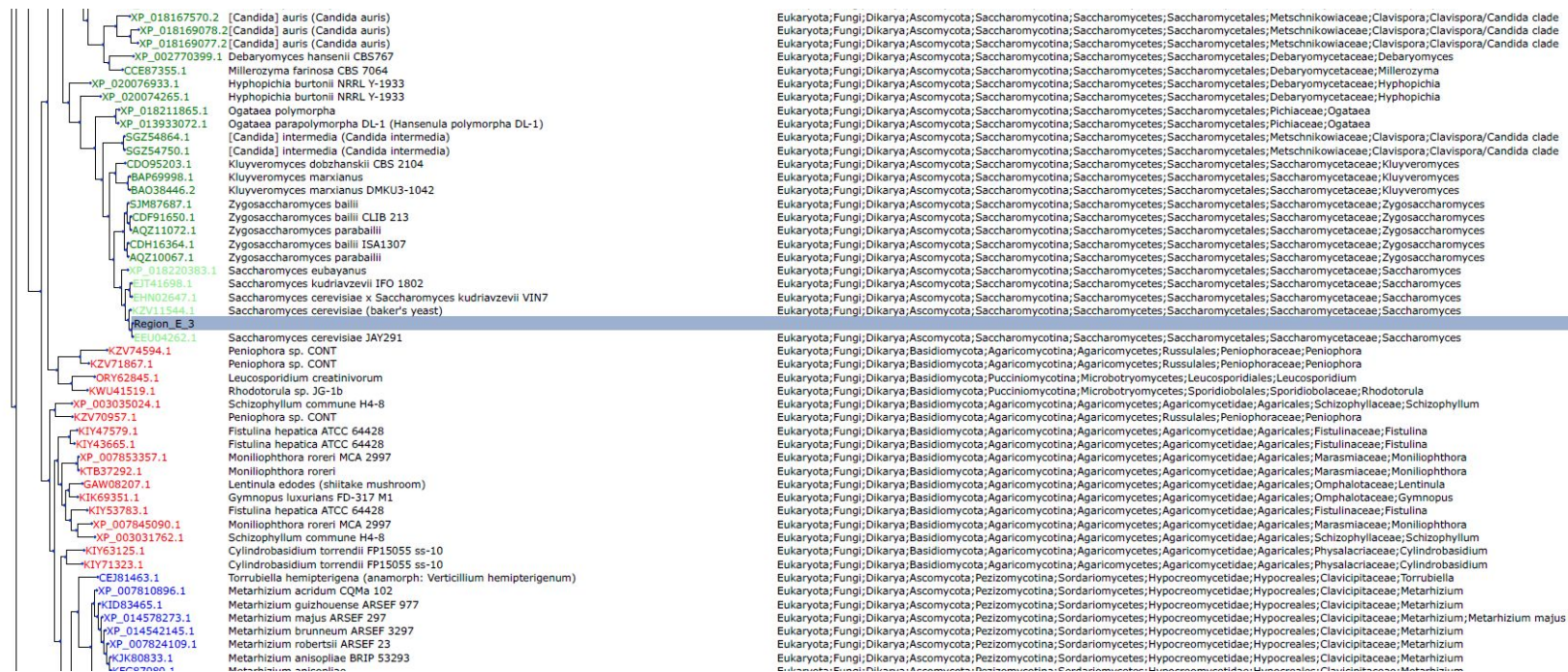
- Layouts are what puts everything together. It's a python function that receives a tree node and receives instructions on how to modify it.



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.

- Why should I bother with ETE visualization when there are so many other tools?



# 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:

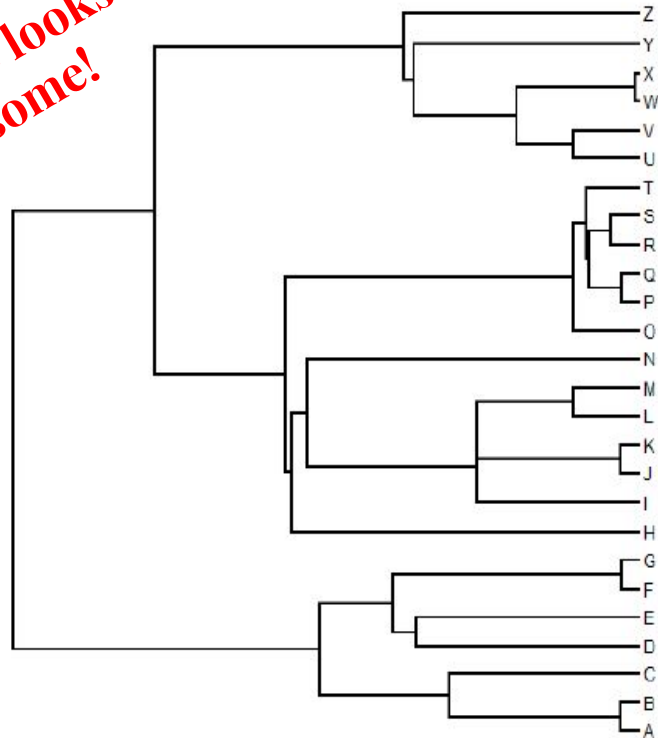
```
require(phytools)
```

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*

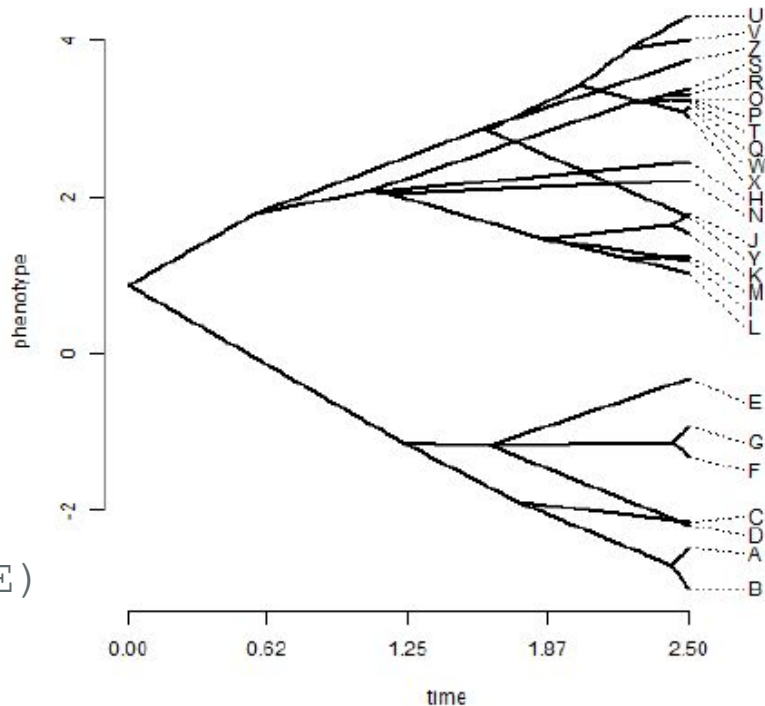
Now we plot a simple traitgram:

```
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)
```

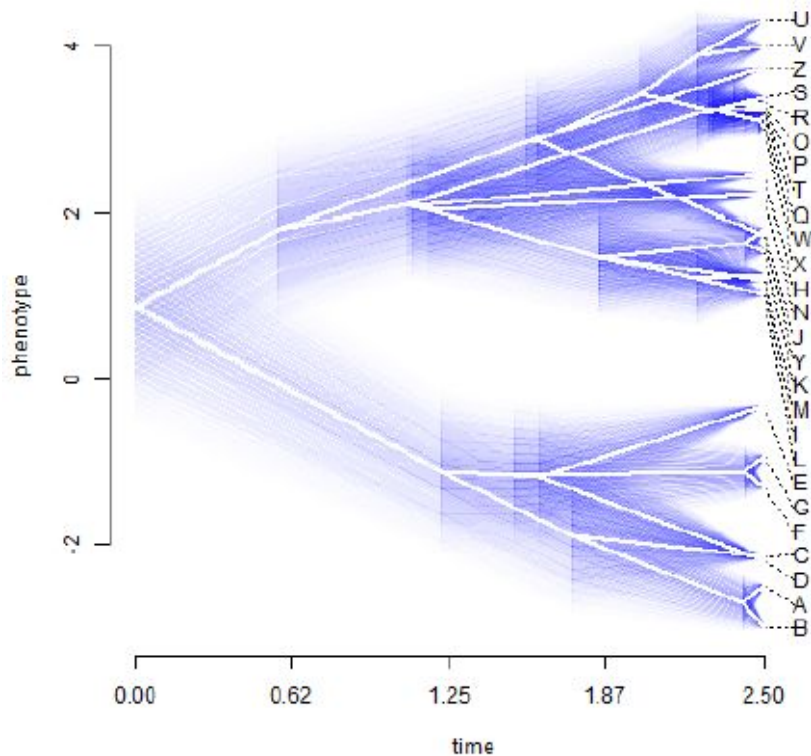
# Phytools demo

Let's try a heat map with our data:

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

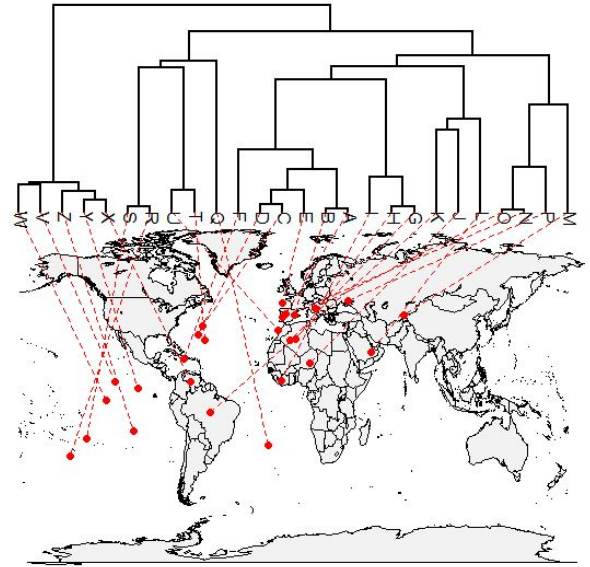
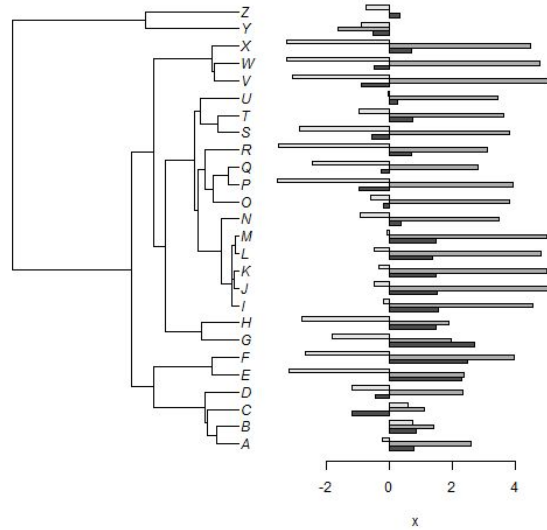
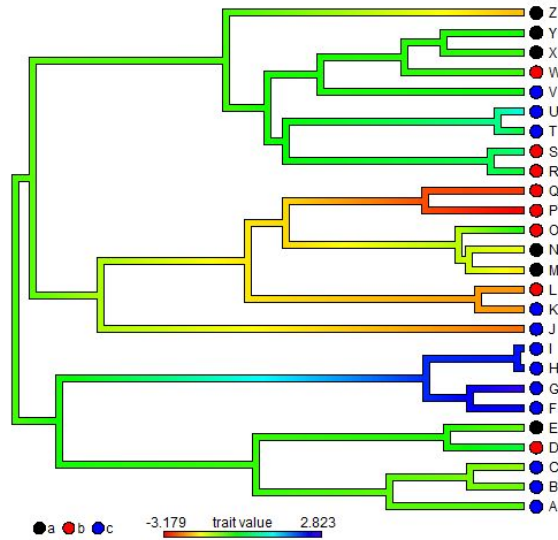
Now some hardcore stuff: Traitgram with the uncertainty of ancestral traits visualized using transparent probability density:

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



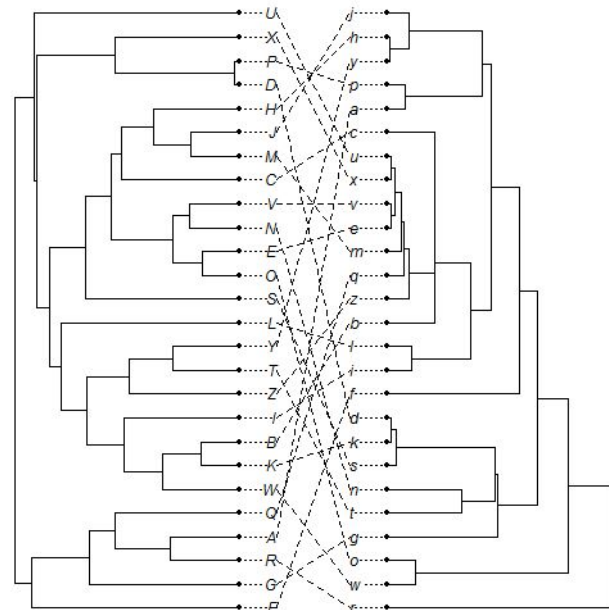
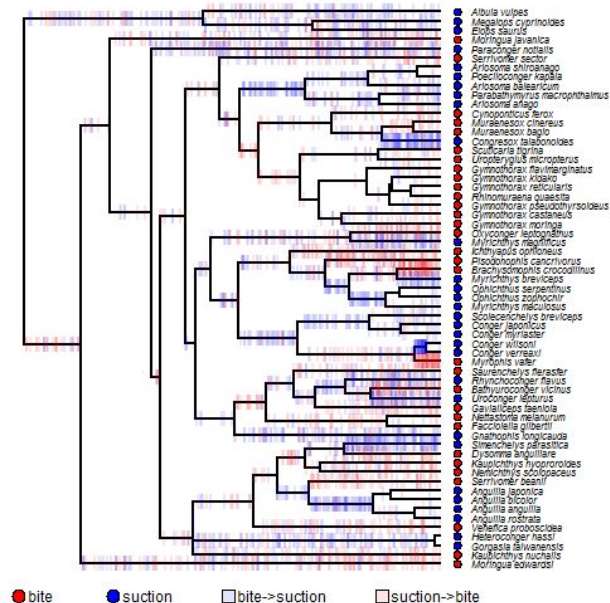
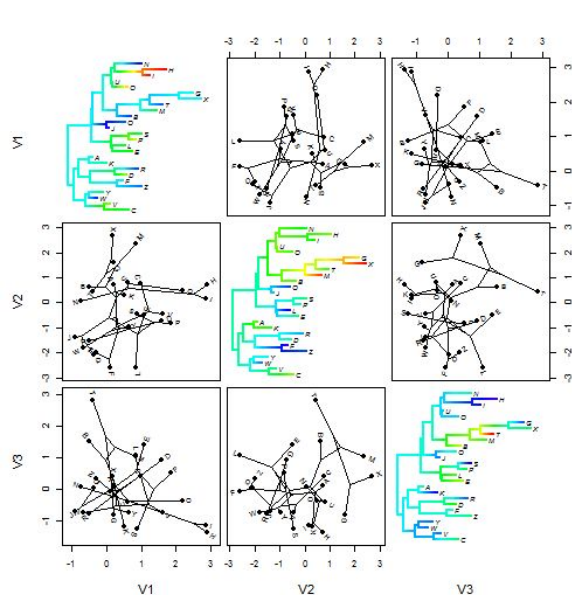
Much more here → <http://www.phytools.org/Cordoba2017/ex/15/Plotting-methods.html>

# Phytools Examples



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

# Phytools Examples



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

# Toolkits

- **PYTHON** library: **ETE3 toolkit** @ <http://etetoolkit.org>
- **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.

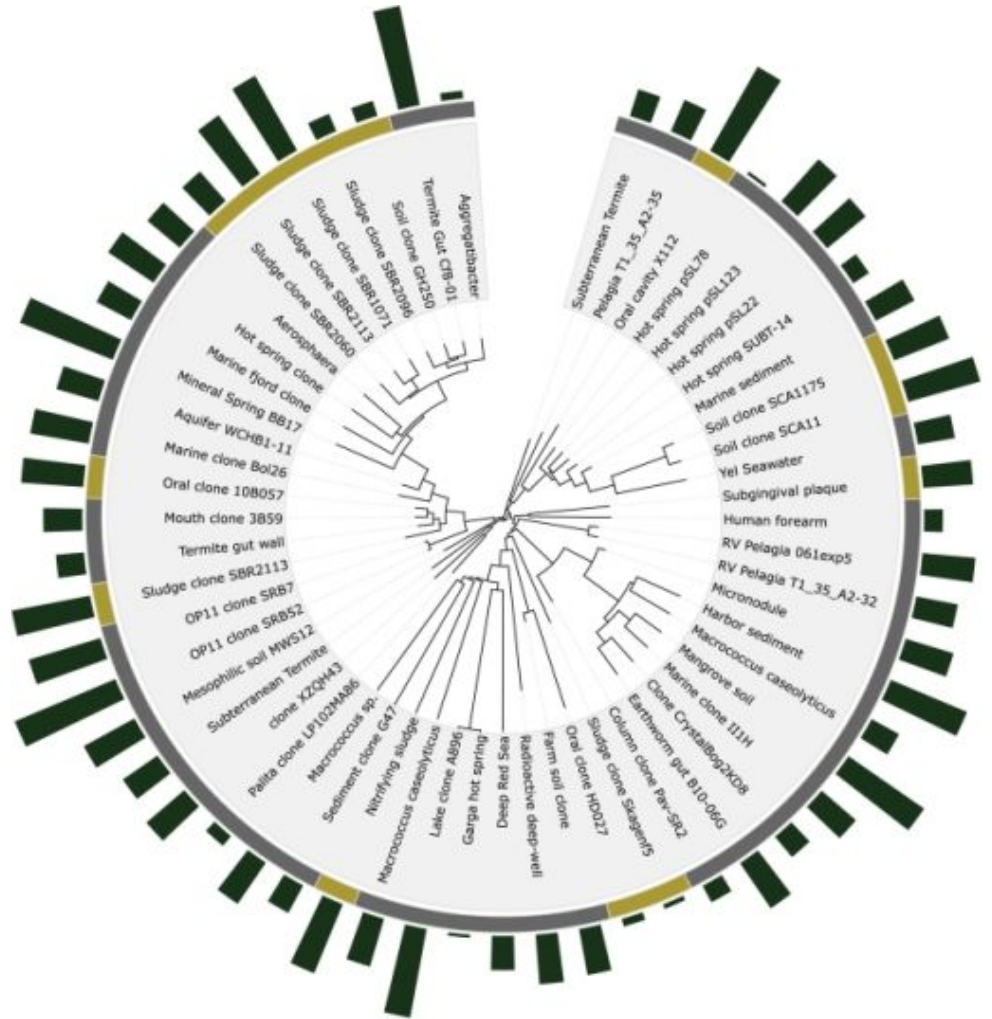
# jsPhyloSVG

JavaScript based

Much more focused on user  
side web visualization

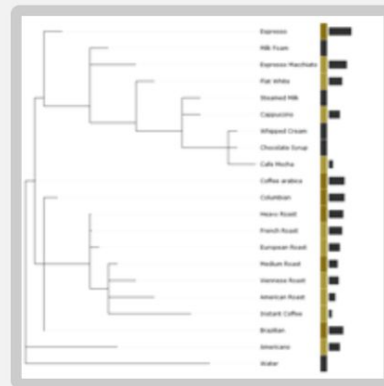
Very simple syntax

A bit limited compared to other  
options

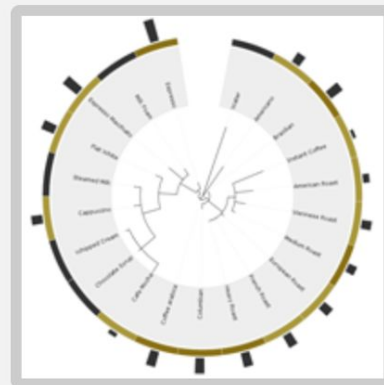


jsPhyloSVG is an open-source javascript library specifically built for rendering highly-extensible, customizable phylogenetic trees. jsPhyloSVG can render complex trees, yet offers a simple method to do so. It leverages the recent XML schema definition specified for phylogenetic trees, [phyloXML](#).

```
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);
```



```
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);
```

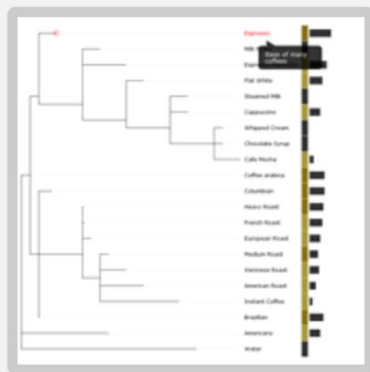


## What about interactive features?

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)



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# 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]

- Online software
- Desktop Software
- See also
- References
- External links

## Online software [\[ edit \]](#)

| Name                            | Description                                                                                                                                            | Site                     | Citation            |
|---------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------|
| Aquapony                        | Javascript tree viewer for <a href="#">Beast</a> .                                                                                                     | <a href="#">Aquapony</a> |                     |
| EvolView,                       | 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.nihs.gov/research/programs-services/clinical-translational-research/branches/phylogenetics/densitree/>
- TreeGraph2 @ <http://treegraph2.bioinformatics.net/>

- **Toolkits:**

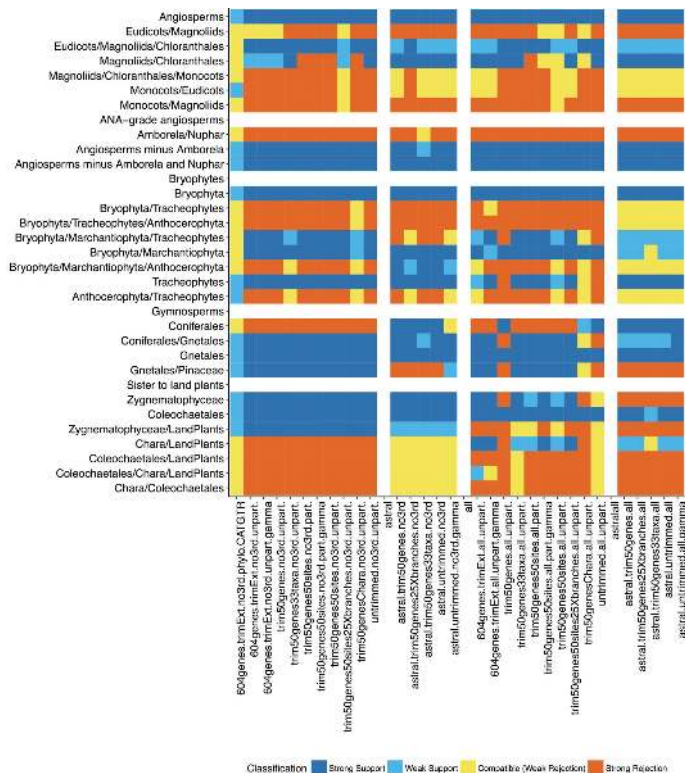
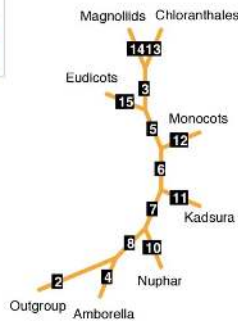
- PYTHON library: ETE3 @ <http://etetoolkit.org/>
- R repository: PhyTools @ <http://phylotools.org/packages/phytools/index.html>
- JavaScript library: jsPhylo @ <http://d3js.org/jsPhylo/>

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

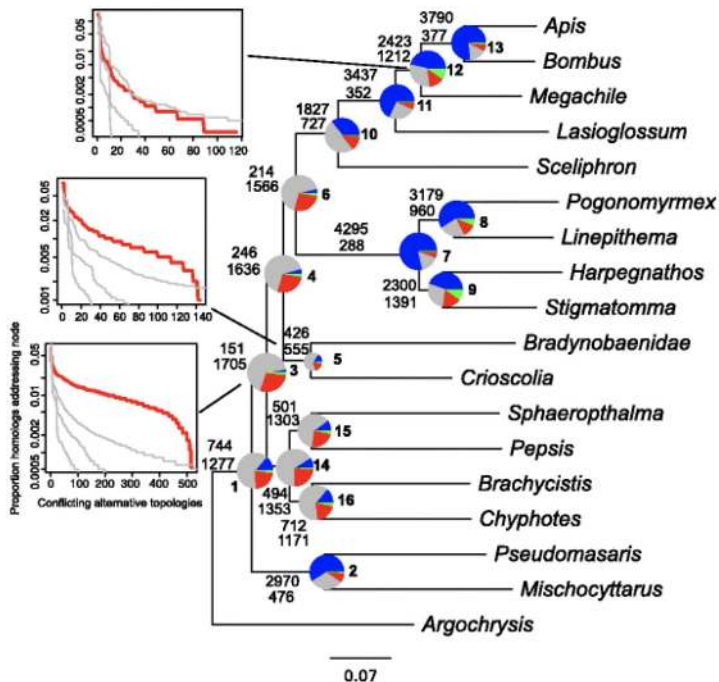


# Phylogenetic Conflict Visualization

- 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.schmiedeknecht.ch/Software/DensiTree/>
- TreeGraph2 @ <http://www.treegraph2.net/>

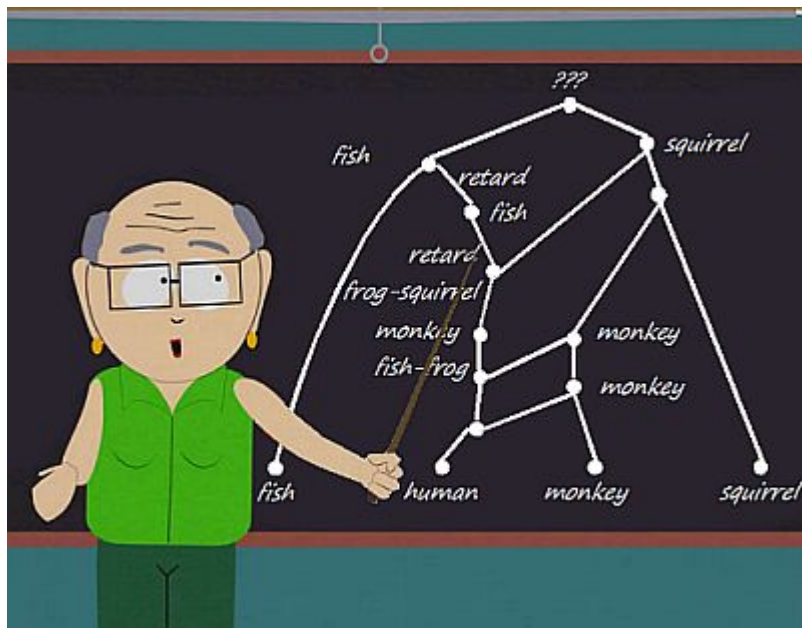
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- PYTHON library: ETE toolkit @ <http://etetoolkit.org/>
- R repository: PhyTools @ <https://cran.r-project.org/web/packages/phytools/index.html>
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- [https://en.wikipedia.org/wiki/List\\_of\\_phylogenetic\\_tree\\_visualization\\_software](https://en.wikipedia.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.

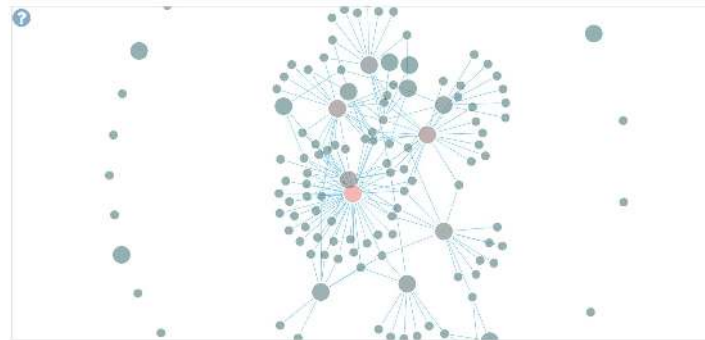
☐ Show all node labels. (This may overcrowd the visualization.)

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



<http://dendroscope.org/>

# Phylogenetic Network Visualization



<http://www.splitstree.org/>

## SplitsTree4

### Software for computing phylogenetic networks



## Download

Link to BETA version of SplitsTree5 (for testing purposes)

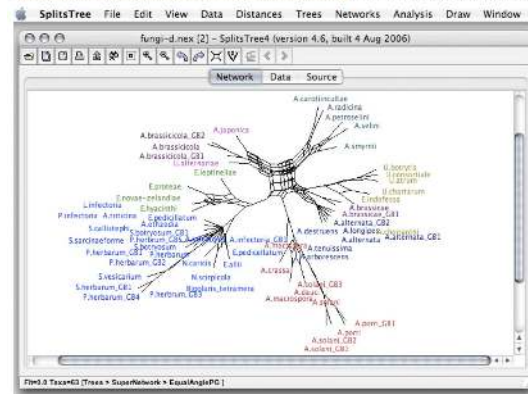
Link to talk given at [ISMB18](#)

### Description

SplitTree4 is the leading application for computing unrooted phylogenetic networks from molecular sequence data. Given an alignment of sequences, a distance matrix or a set of trees, the program will compute a phylogenetic tree or network using methods such as split decomposition, neighbor-net, consensus network, super networks methods or methods for computing hybridization or simple recombination networks.

SplitsTree4 is an all-new implementation of the [SplitsTree3](#) software written in Java. Superficially, this new program is similar to previous versions of this software. However, there are substantial differences. The new program has many new features, see the [manual](#) for details.

If you use SplitsTree in work in any way, then please cite the following paper: D. H. Huson and D. Bryant, **Application of Phylogenetic Networks in Evolutionary Studies**, *Mol. Biol. Evol.*, 23(2):254-267, 2006.



# Visualization Challenge

ポケモン Phylogeny

