Tree Editing & Visualization

Lisa Pokorny & Marina Marcet-Houben

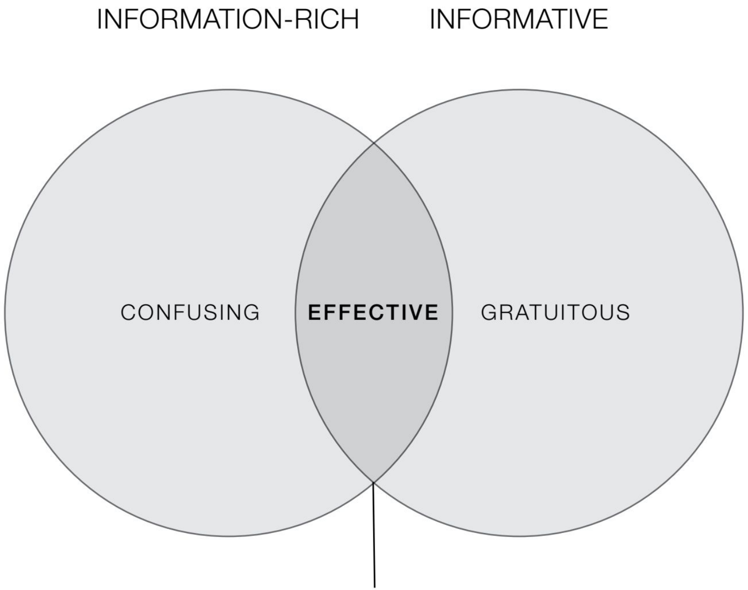
(with help from Miguel Ángel Naranjo Ortiz)

Data Visualization

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

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

VISUALIZATION SWEET SPOT



CLEAR MESSAGE

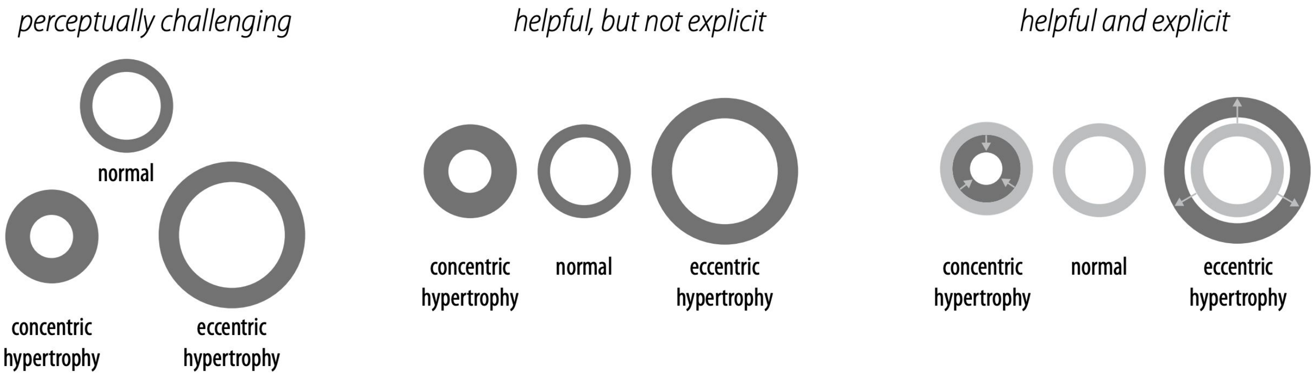
HIGH DATA-TO-INK RATIO

ACCESSIBLE COMPLEXITY

http://mkweb.bcgsc.ca/vizbi/2013/krzywinski-visual-design-principles-vizbi2013.pdf

Data Visualization

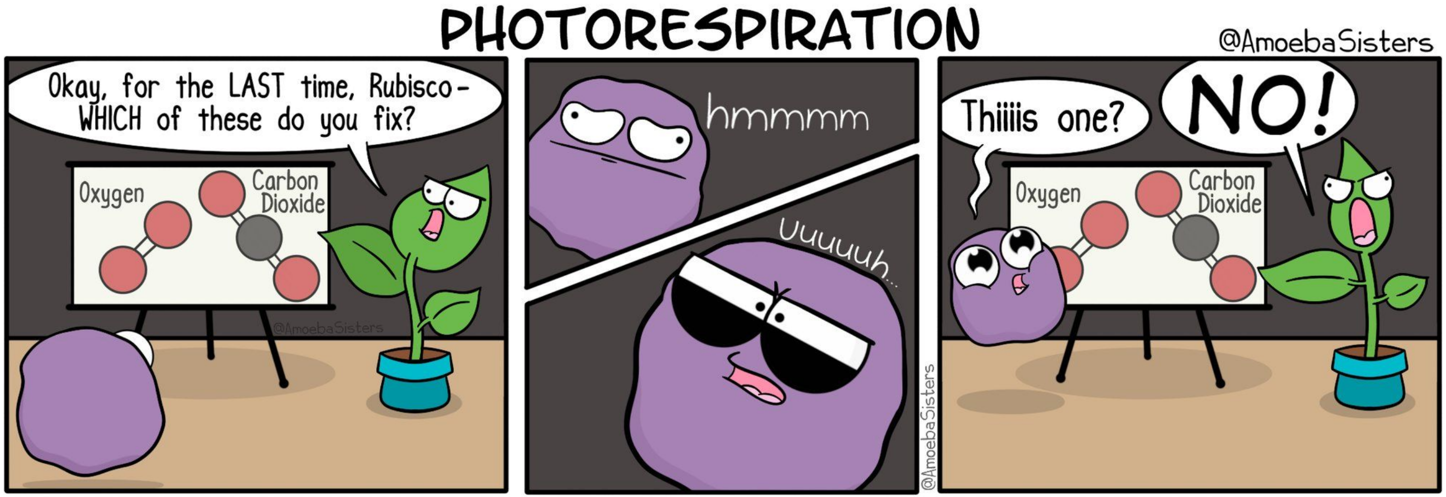
- Satisfy your audience, not yourself
- Don’t merely display data, explain it
- Be aware of bias in evaluating effectiveness of visual forms
- Patterns are hard to see when variation is due to both data and formatting



http://mkweb.bcgsc.ca/vizbi/2013/krzywinski-visual-design-principles-vizbi2013.pdf

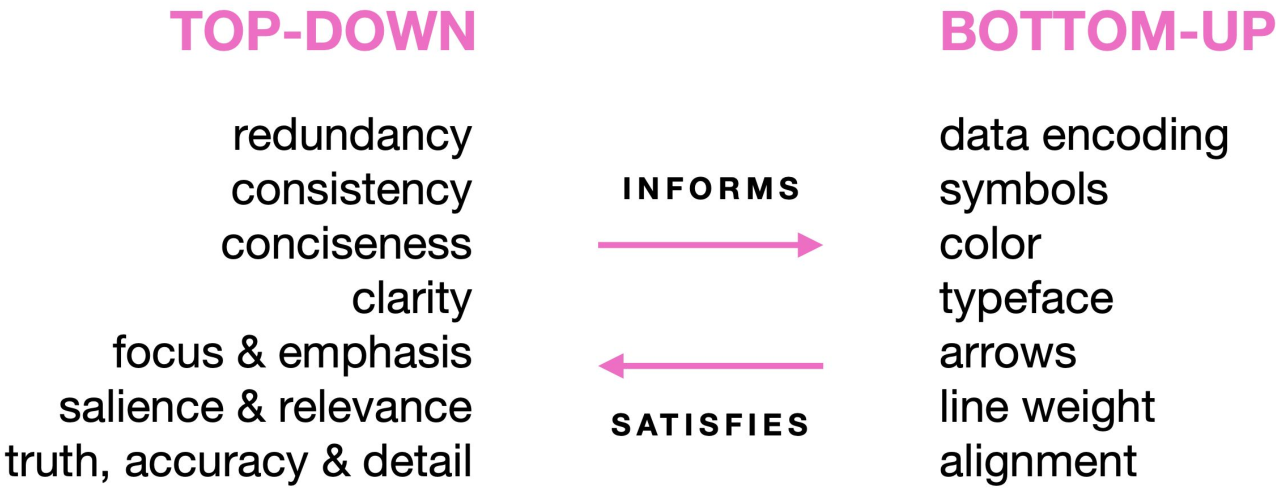
Data Visualization

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



Data Visualization

How do we get from data to visualization?



TOP-DOWN

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

INFORMS →

← **SATISFIES**

BOTTOM-UP

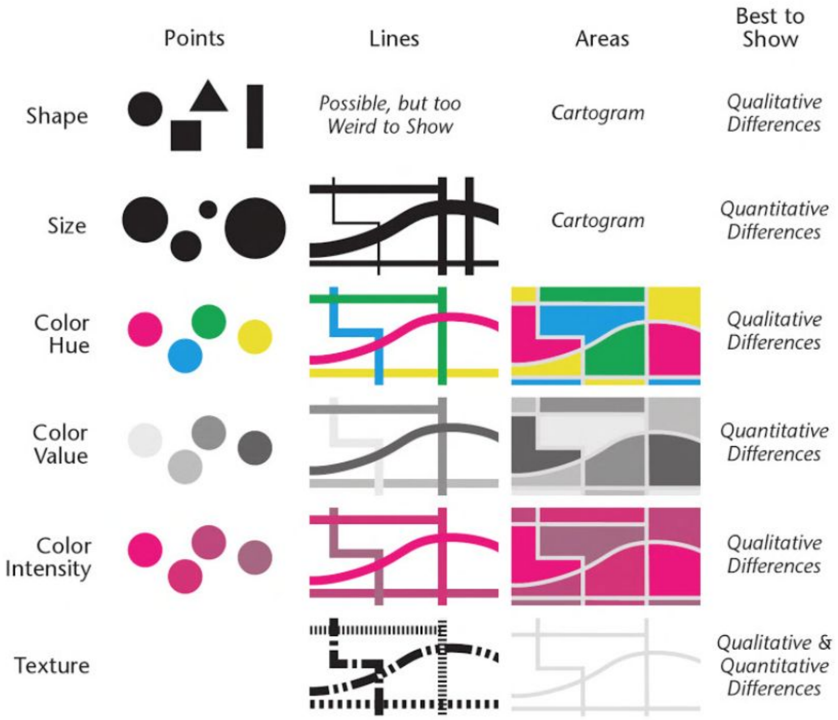
data encoding
symbols
color
typeface
arrows
line weight
alignment

http://mkweb.bcgsc.ca/vizbi/2013/krzywinski-visual-design-principles-vizbi2013.pdf

Data Visualization

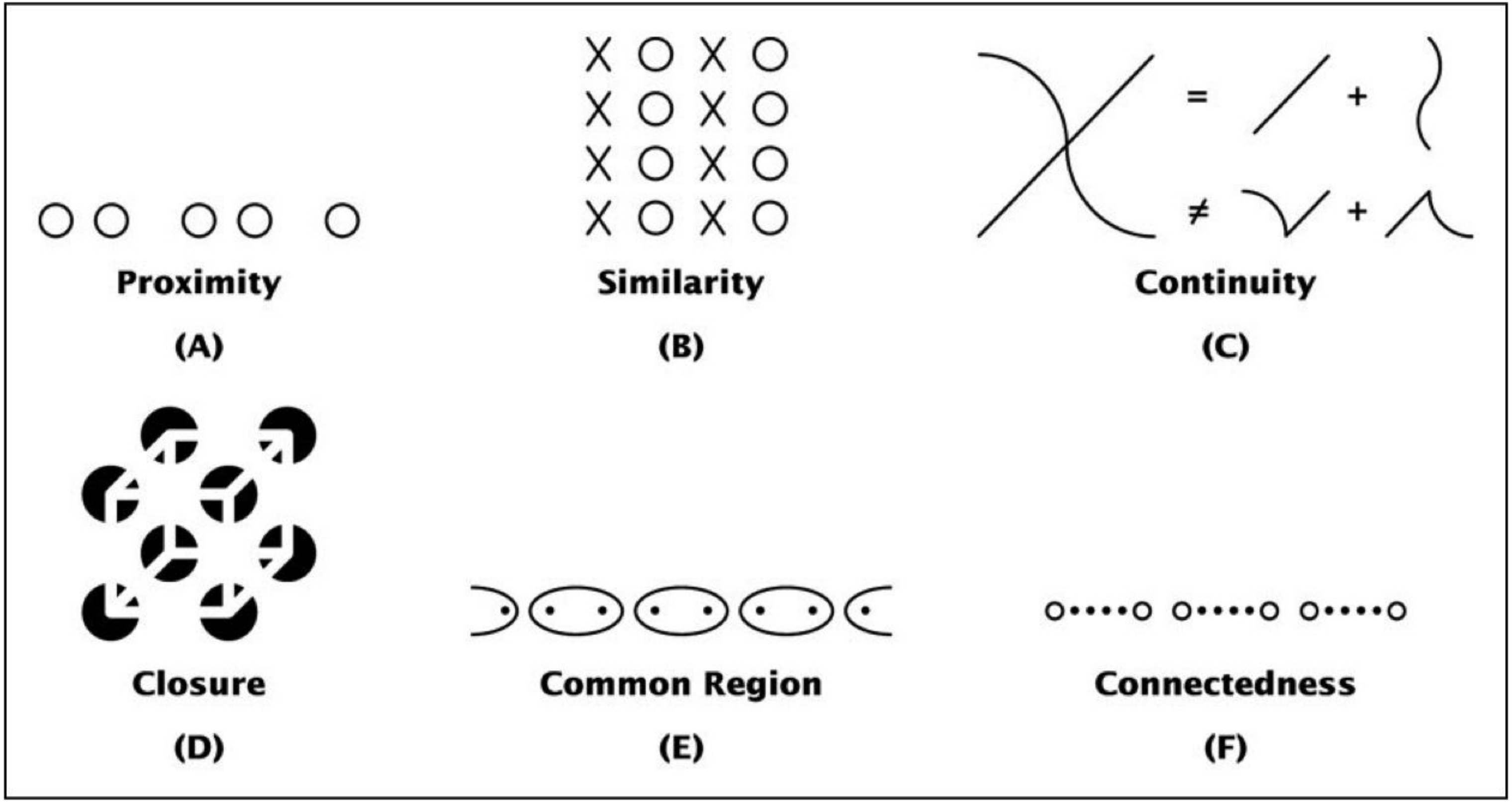
How do we get from data to visualization?

- **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.



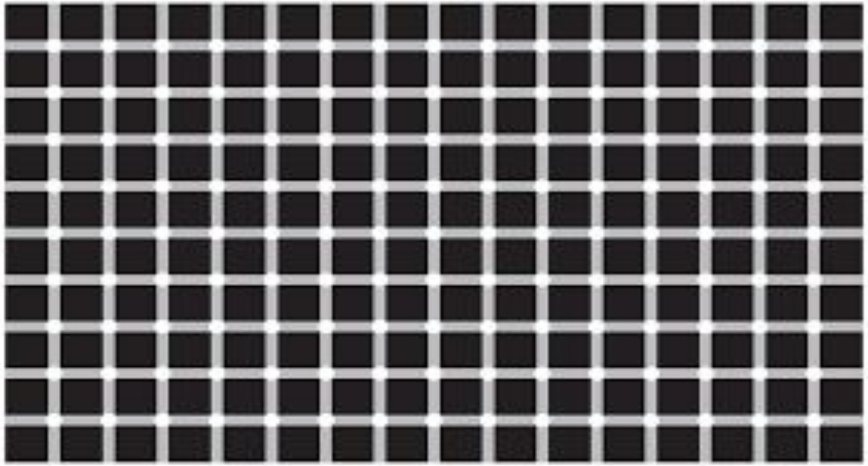
Krygier & Wood. 2011. *Making Maps: A Visual Guide to Map Design for GIS*. Guilford Press

Principles of Grouping

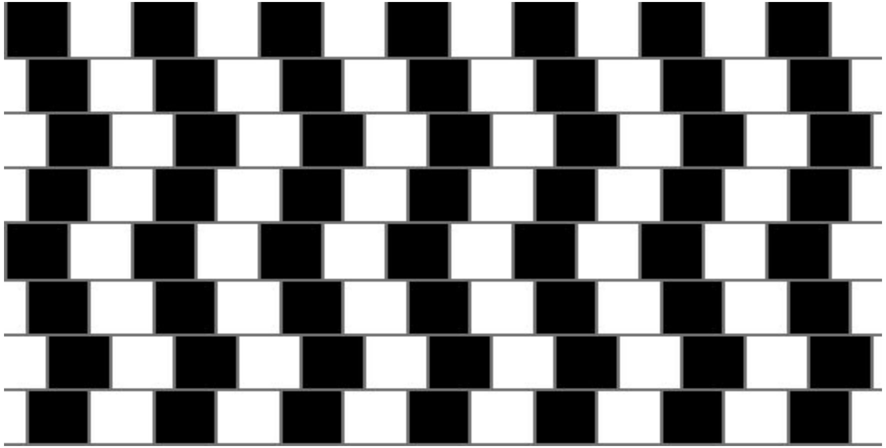


Optical Illusions

Hermann Grid



Café Wall

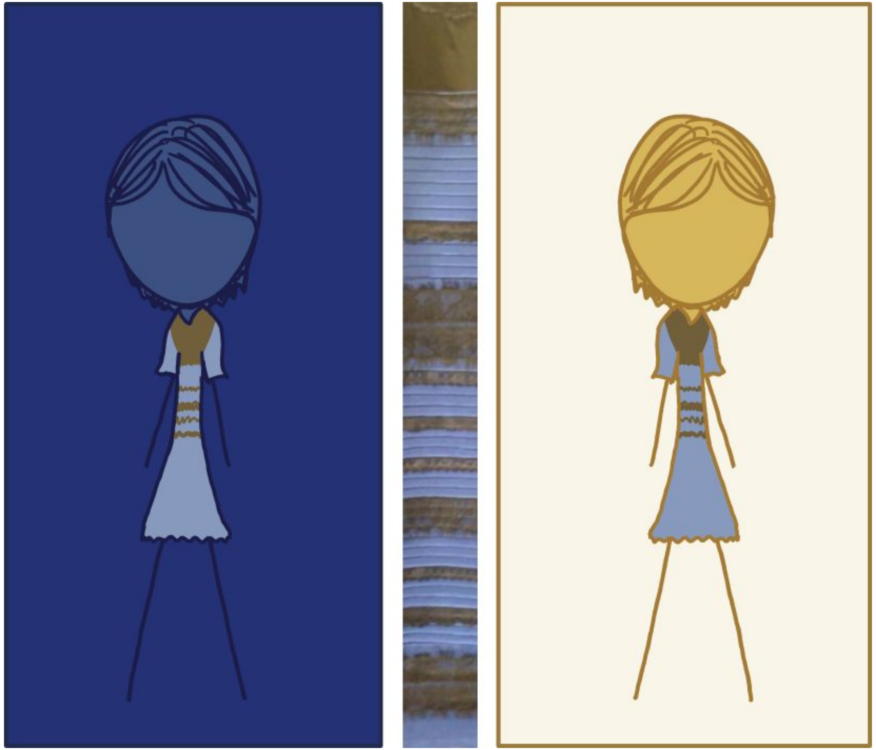


https://en.wikipedia.org/wiki/List_of_optical_illusions

Color

Color Context

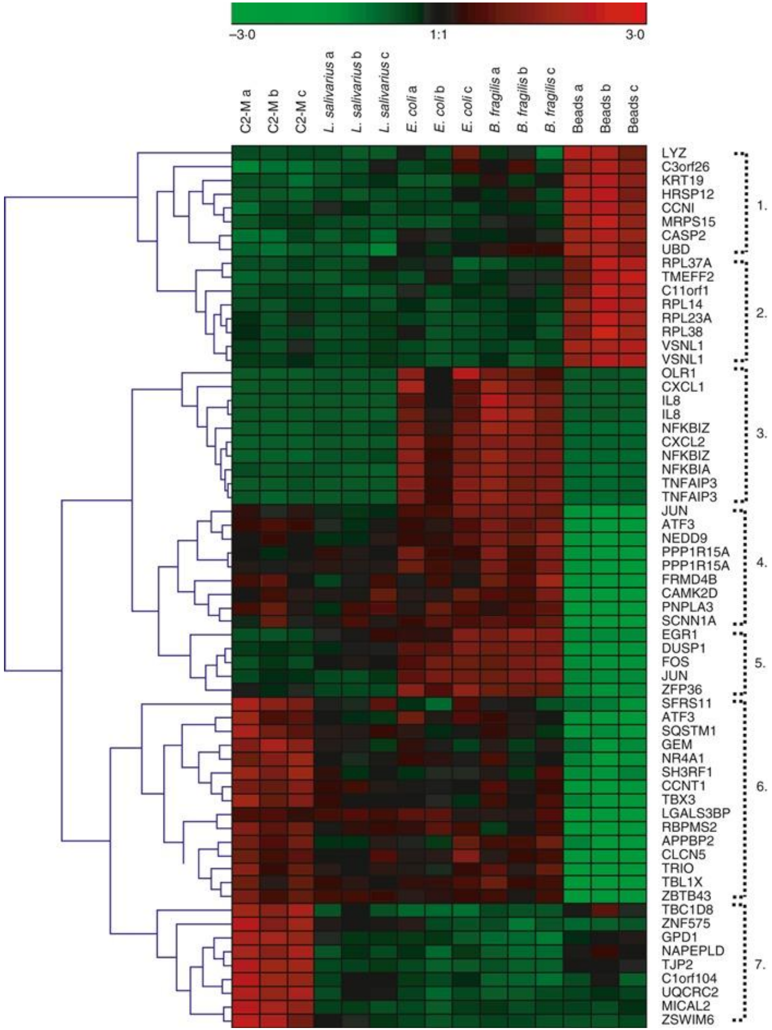
Context affects your color perception



https://xkcd.com/1492/

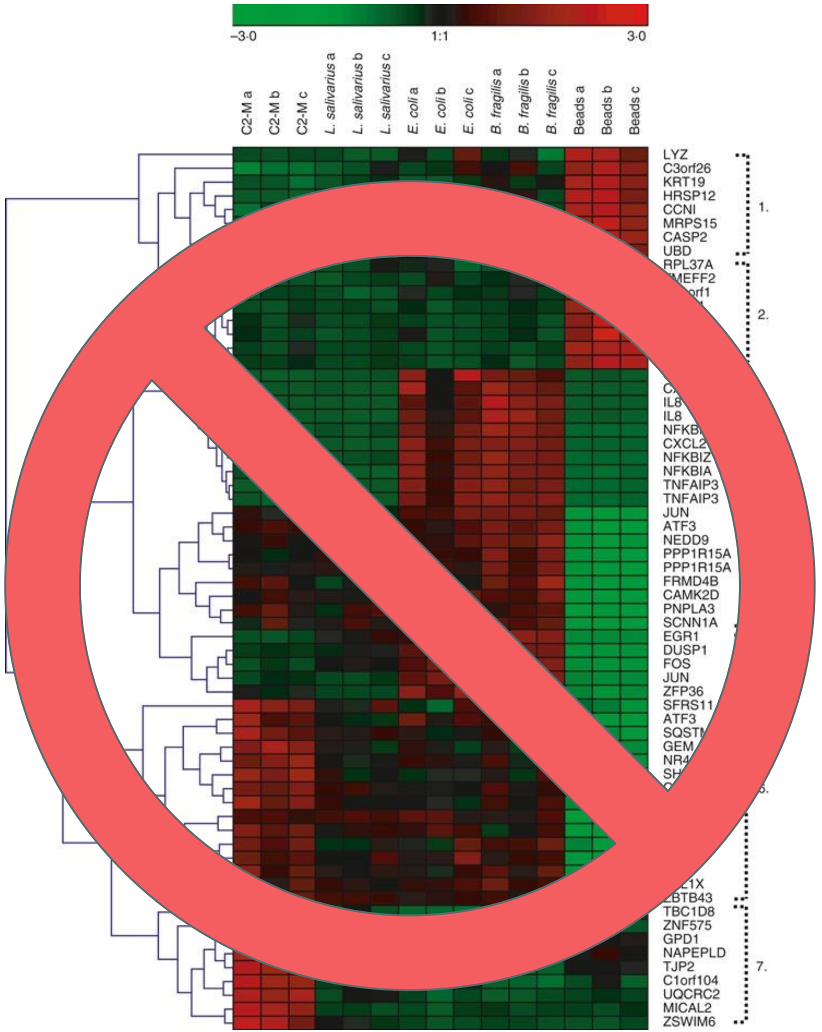
Color Context

Context affects your color perception



Color Context

Context affects your color perception



Color Blindness

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

Color Blindness

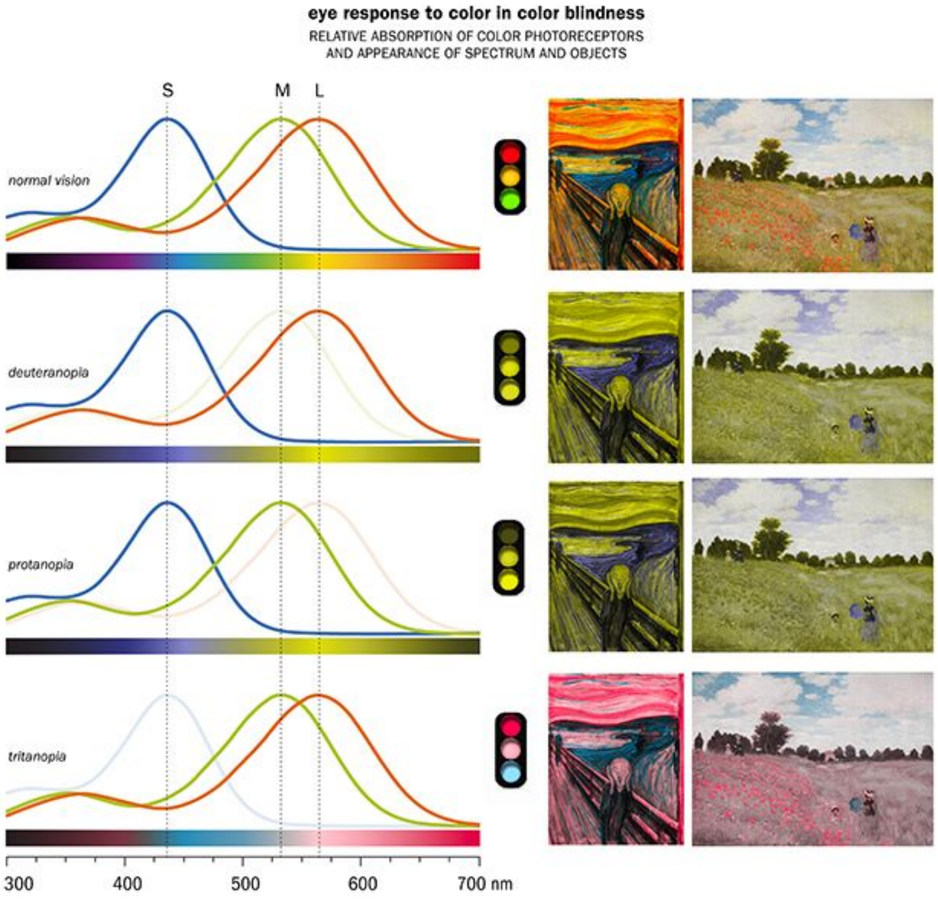
COLOR PALETTES FOR COLOR BLINDNESS

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.

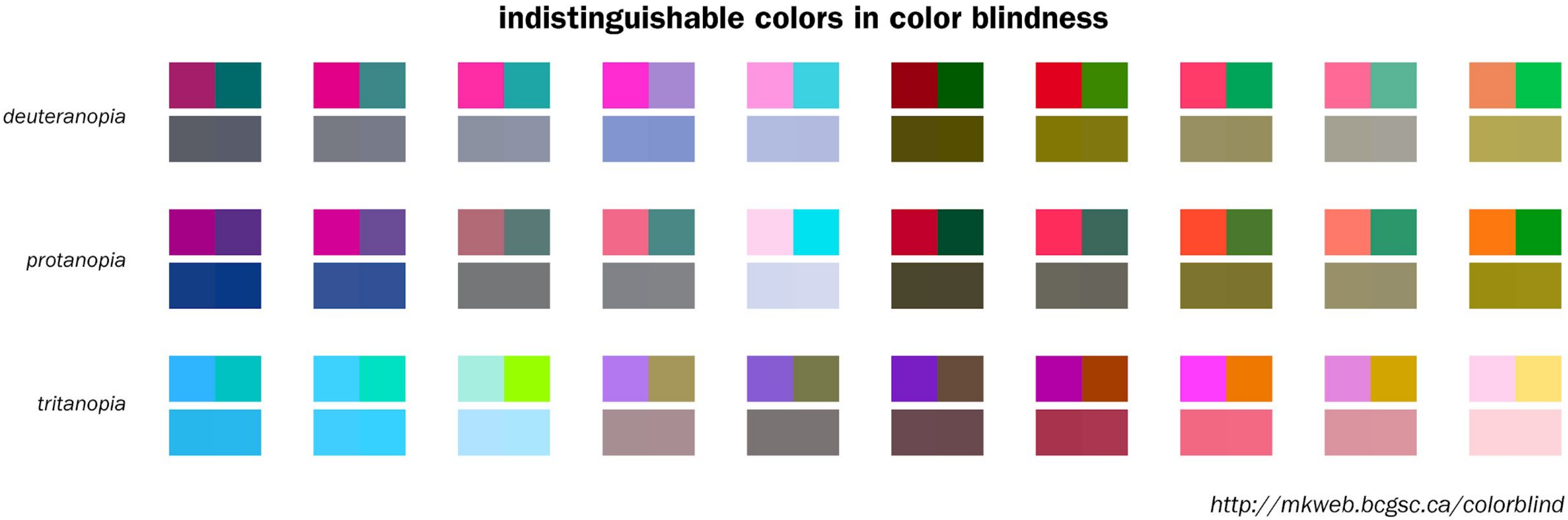
COLOR RECEPTORS ARE REDUCED OR ABSENT IN COLOR BLINDNESS

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.



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

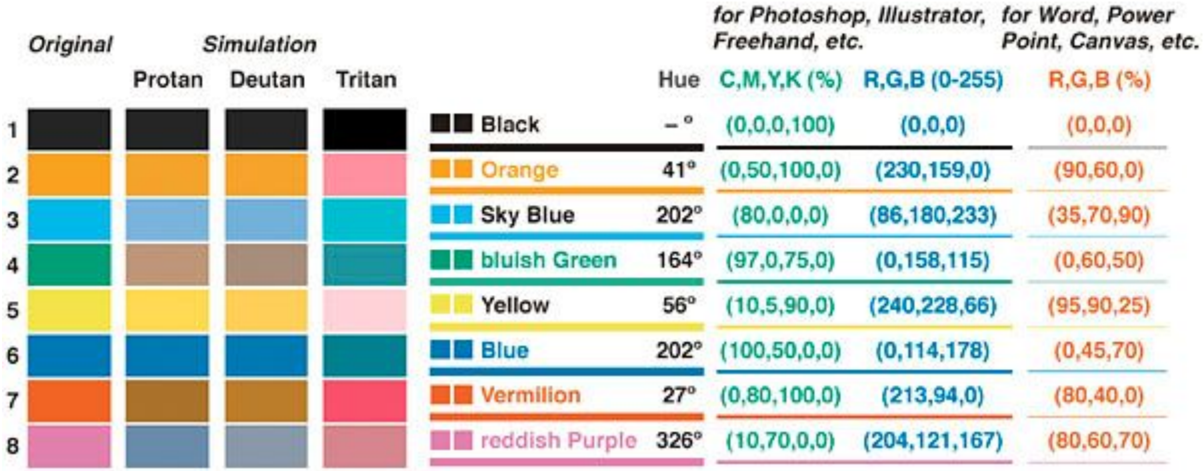
Color Blindness



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

Color Blindness – Palettes

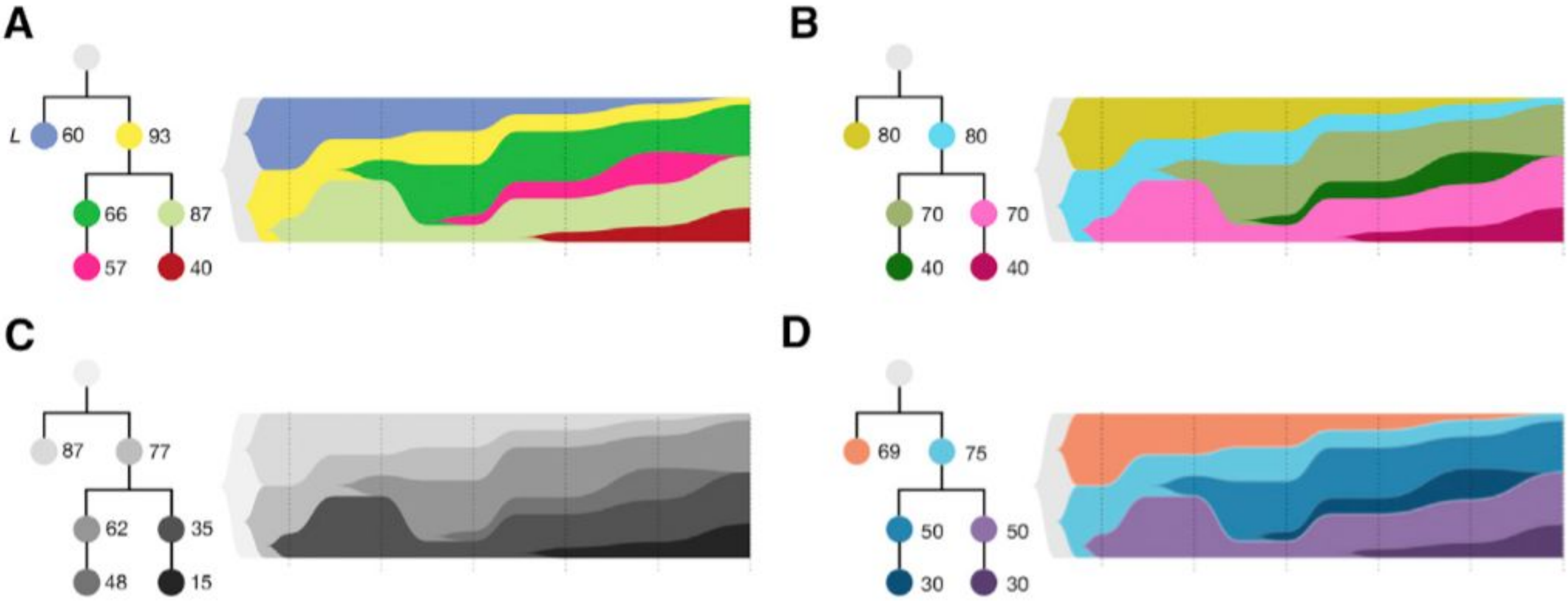
- General advice: http://jfly.iam.u-tokyo.ac.jp/color/
- Cartography: http://colorbrewer2.org/
- R plotting system (ggplot2): http://www.cookbook-r.com/Graphs/Colors_(ggplot2)/#a-colorblind-friendly-palette



	Original	Simulation Protan	Simulation Deutan	Simulation Tritan		Hue	for Photoshop, Illustrator, Freehand, etc. C,M,Y,K (%)	for Photoshop, Illustrator, Freehand, etc. R,G,B (0-255)	for Word, Power Point, Canvas, etc. 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	■	■	■	■	Vermilion	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://jfly.iam.u-tokyo.ac.jp/color/

Color Blindness – Luminance



Krzywinski. 2016. *Mol. Cell* 62:652–656.

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
BrushScriptStd
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
Blackadder ITC
BirchStd
Bernard MT Condensed
Berlin Sans FB Demi
Berlin Sans FB
Bell MT
Bauhaus
BatangChe
Batang
Baskerville Old Face
AvantGarde
Arial Unicode MS
Arial Rounded MT
Arial Narrow
Arial Black

DotumChe
Dotum
DokChampa
DilleniaUPC
DFKai-SB
David
DaunPenh
Curlz MT
Courier New
Courier
CordiaUPC
Cordia New
Corbel
COPPERPLATE GOTHIC LIGHT
Copperplate Gothic
CooperBlackStd-Italic
CooperBlackStd
Cooper Black
Constantia
Consolas
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 MT
Freestyle Script
FreesiaUPC
FrankRuehl
Franklin Gothic Medium Cond
Franklin Gothic Medium
Franklin Gothic Heavy
Franklin Gothic Demi Cond
Franklin Gothic Demi
Franklin Gothic Book
Forte
Footlight MT Light
[illegible]
FELIX TITLING
FangSong
Euphemia
EucrosiaUPC
Euχλιδ Σψμβολ
𝔼 𝕄 𝕋
ℰ ℳ 𝒪
Euclid Fraktur
⟶⇕ℓ○○ ⟶⟶↦
Euclid
Estrangelo Edessa
Eras Medium ITC
Eras Light ITC
Eras Demi ITC
Eras
ENGRAVERS MT
Elephant
Edwardian Script ITC
Ebrima

KodchiangUPC
Khmer UI
Kartika
Kalinga
KaiTi
Juice ITC
Jokerman
JasmineUPC
Iskoola Pota
IrisUPC
Informal Roman
Imprint MT Shadow
Impact
HoboStd
High Tower Text
Helvetica-Narrow
Helvetica
Harrington
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
Gigi
GiddyupStd
Georgia

Lucida Fax Regular
Lucida Fax Demibold
Lucida Fax
Lucida Console
Lucida Calligraphy
Lucida Bright Demibold
Lucida Bright
LITHOSPRO-REGULAR
LITHOSPRO-BLACK
LilyUPC
Levenim MT
LetterGothicStd-Slanted
LetterGothicStd-BoldSlantec
LetterGothicStd-Bold
LetterGothicStd
Leelawadee
Latha
Lao UI
Kunstler 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

IN TYPOGRAPHY

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

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.

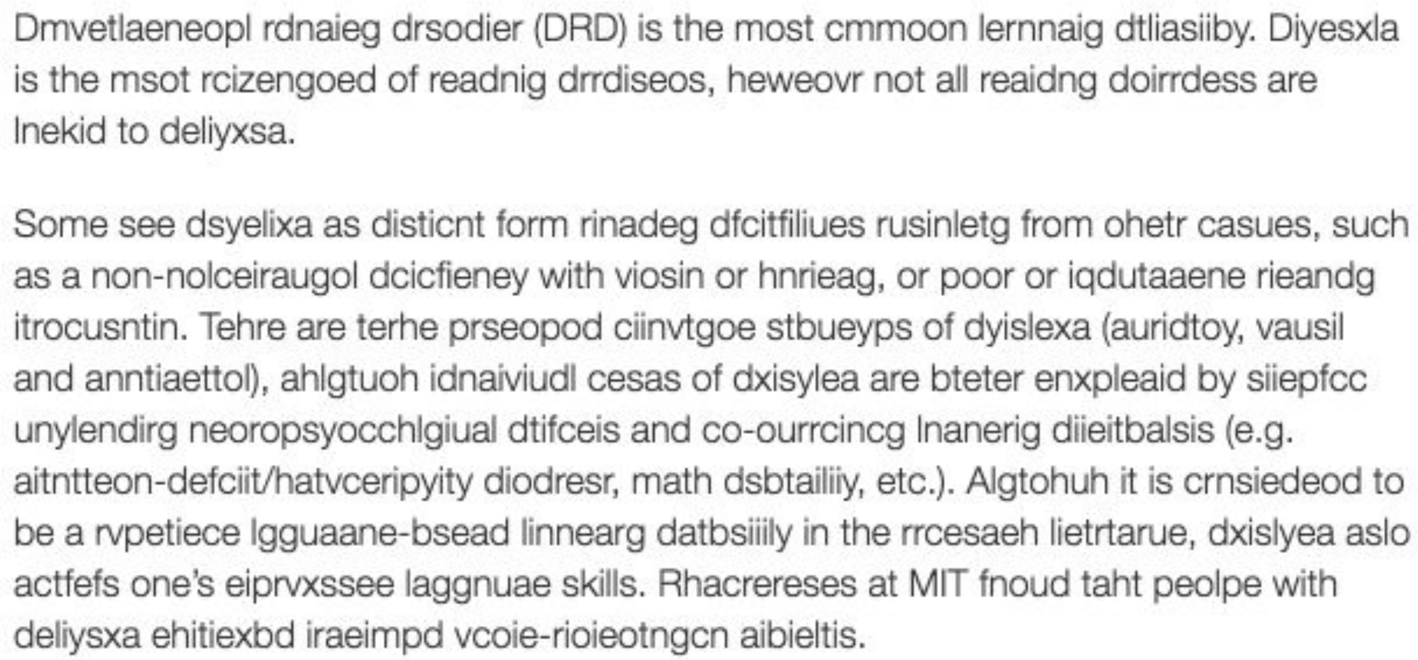
Modern, Minimal, Magnificent, I am Sans

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.

However...

Dyslexia



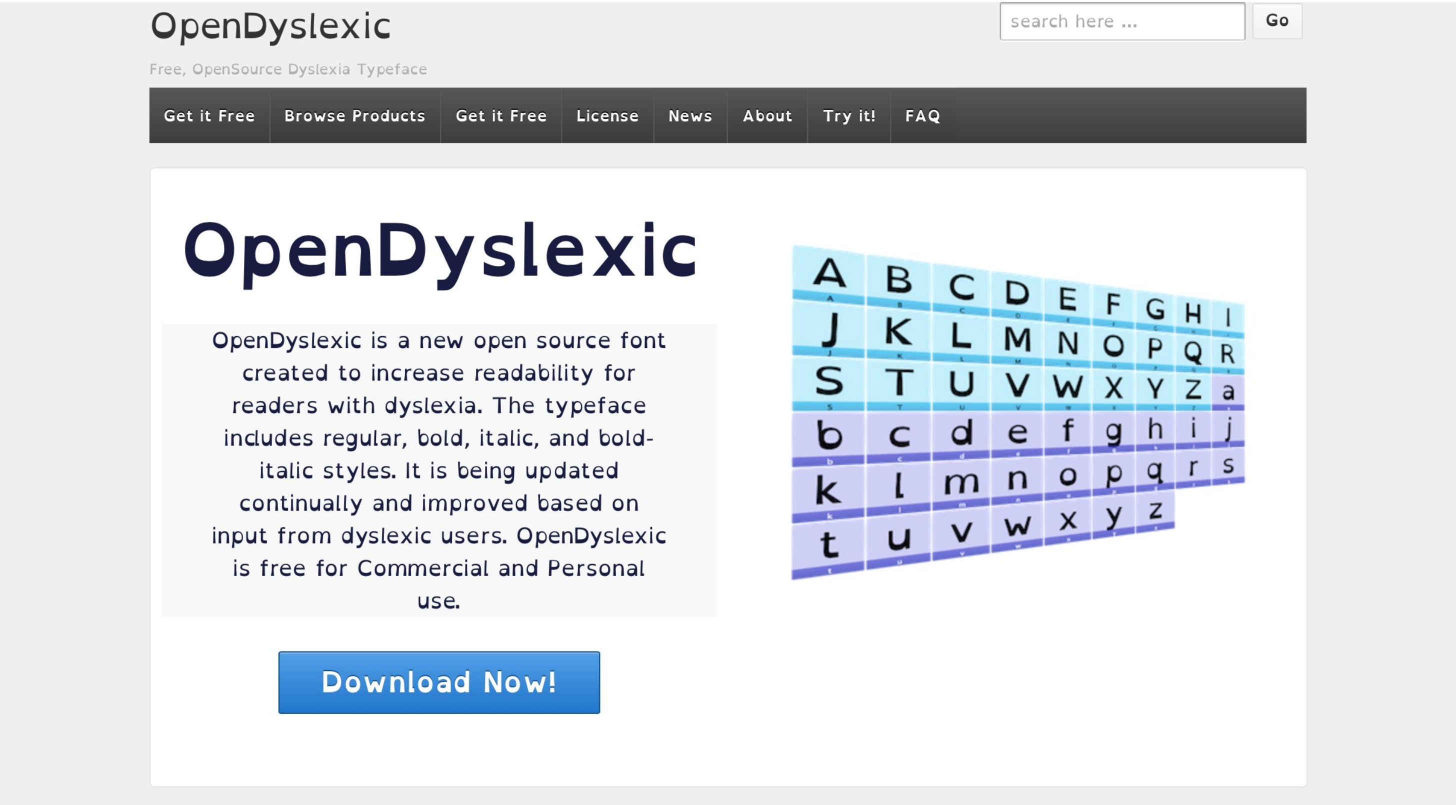
Dmvetlaeneopl rdnaieg drsodier (DRD) is the most cmmoon lernnaig dtliasiiby. Diyesxla is the msot rcizengoed of readnig drrdiseos, heweovr not all reaidng doirrdess are lnekid to deliyxsa.

Some see dsyelixa as disticnt form rinadeg dfcitfiliues rusinletg from ohetr casues, such as a non-nolceiraugol dcicfieney with viosin or hnrieag, or poor or iqdutaaene rieandg itrocusntin. Tehre are terhe prseopod ciinvtgoe stbueyps of dyislexa (auridtoy, vausil and anntiaettol), ahlgtuoh idnaiviudl cesas of dxisylea are bteter enxpleaid by siiepfcc unylendirg neoropsyocchlgiual dtifceis and co-ourrcincg lnanerig diieitbalsis (e.g. aitntteon-defciit/hatvceripyity diodresr, math dsbtailiiy, etc.). Algtohuh it is crnsiedeod to be a rvpetiece lgguaane-bsead linnearg datbsiiily in the rrcesaeh lietrtarue, dxislyea aslo actfefs one’s eiprvxssee laggnuae skills. Rhacrereses at MIT fnoud taht peolpe with deliysxa ehitiexbd iraeimpd vcoie-rioieotngcn aibieltis.

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



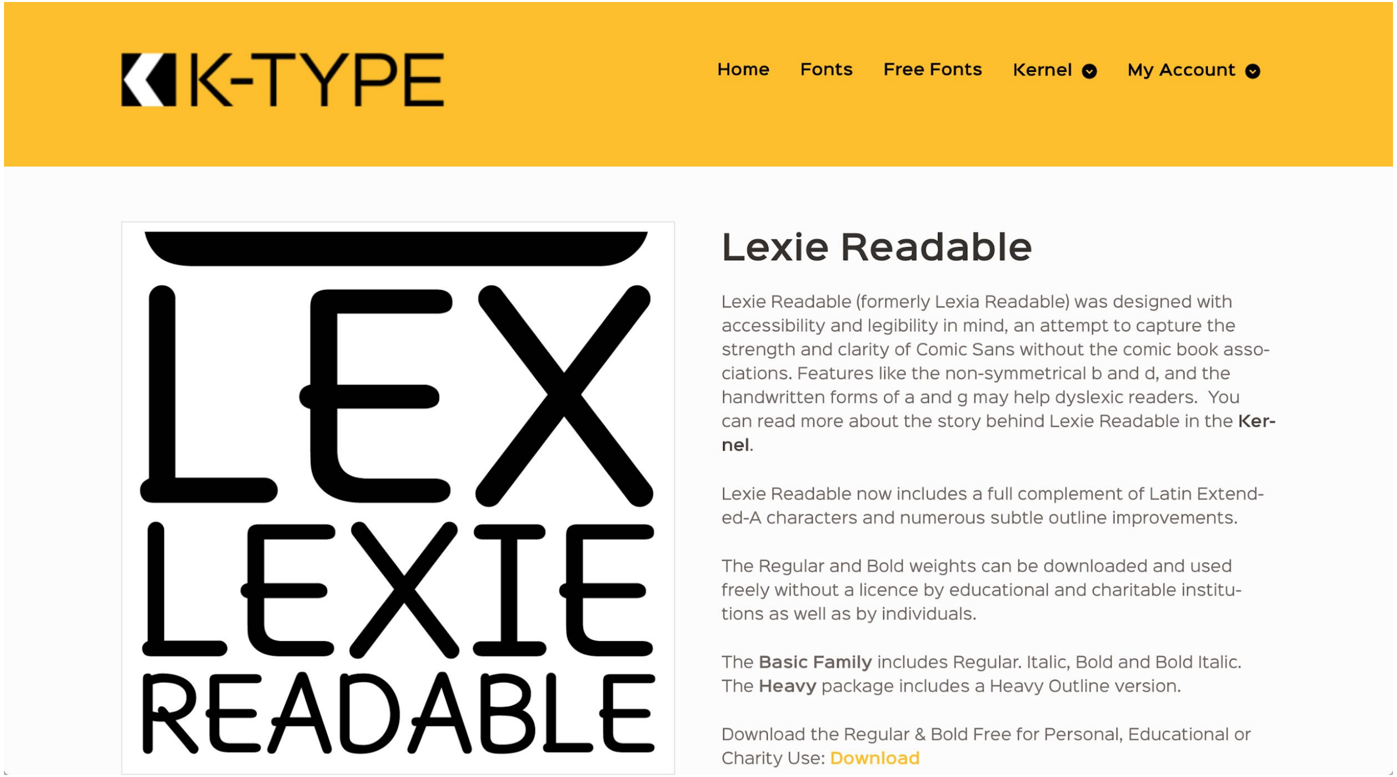
OpenDyslexic

Free, OpenSource Dyslexia Typeface

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.

Dyslexia Friendly Font Types – 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**.

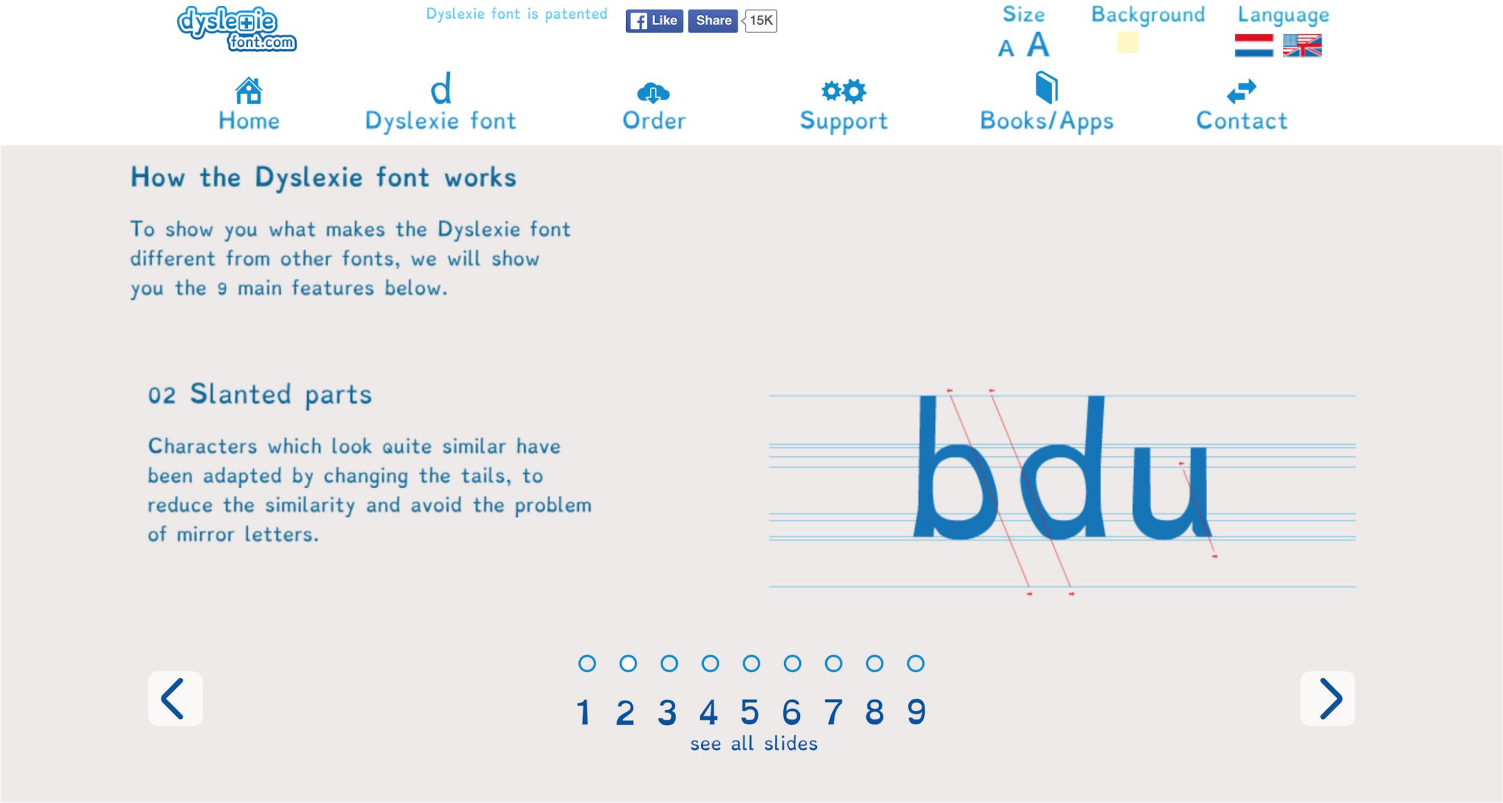
Lexie Readable now includes a full complement of Latin Extended-A characters and numerous subtle outline improvements.

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



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.

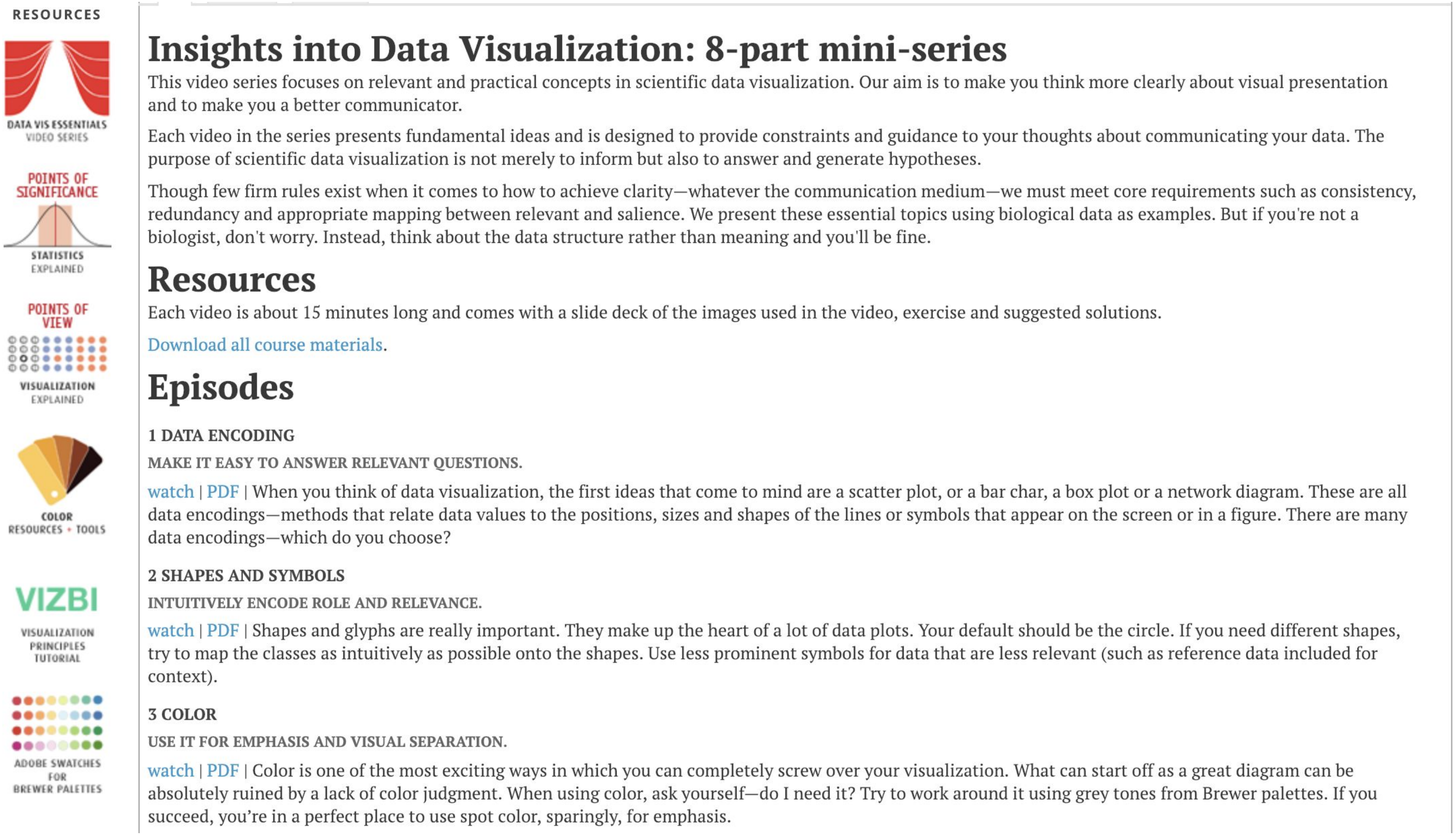
02 Slanted parts

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

ESSENTIALS OF DATA VISUALIZATION

THINKING ABOUT DRAWING DATA + COMMUNICATING SCIENCE

http://mkweb.bcgsc.ca/essentials.of.data.visualization/



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 char, 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.

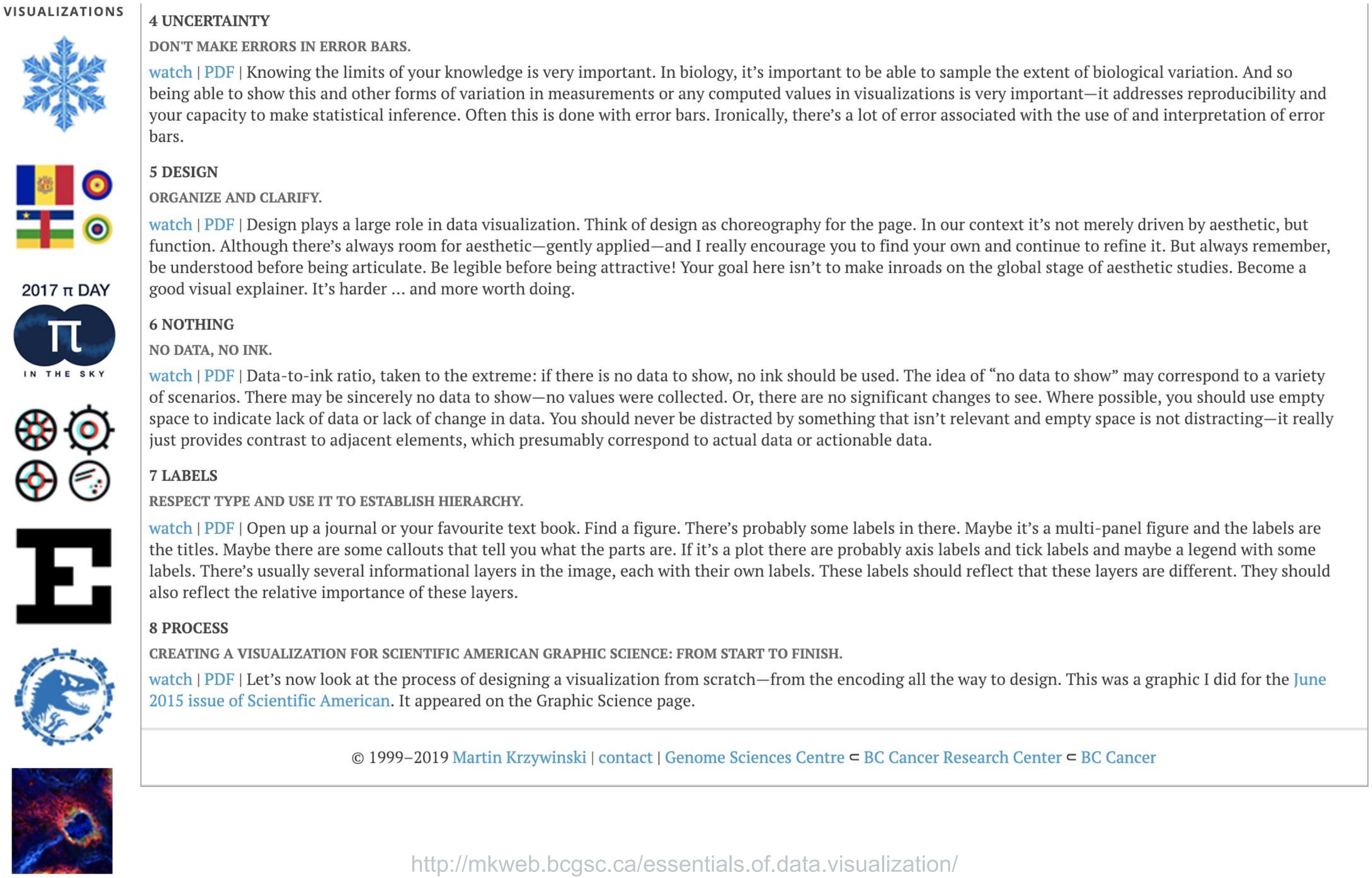
watch | PDF | Shapes and glyphs are really important. They make up the heart of a lot of data plots. Your default should be the circle. If you need different shapes, try to map the classes as intuitively as possible onto the shapes. Use less prominent symbols for data that are less relevant (such as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

http://mkweb.bcgsc.ca/essentials.of.data.visualization/



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.

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.

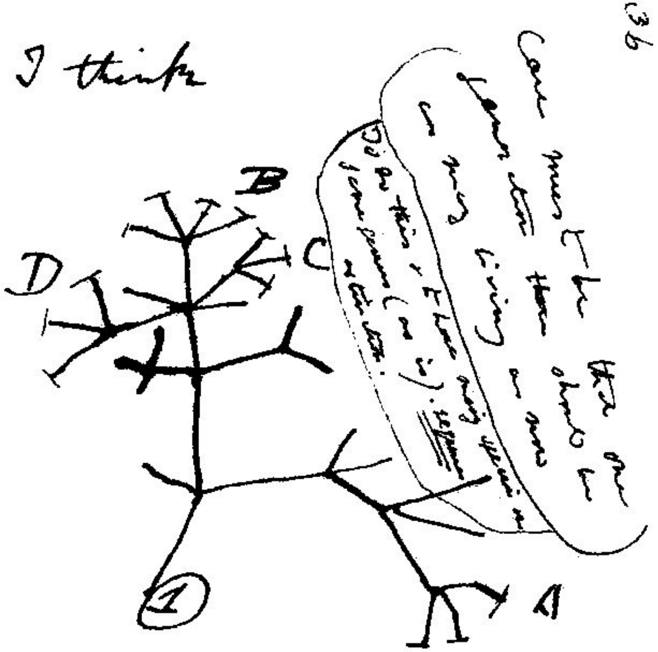
http://mkweb.bcgsc.ca/essentials.of.data.visualization/

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**

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**

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.

Phylo.IO

Very simple and intuitive, fast

Allow to export tree figures as images (.svg)

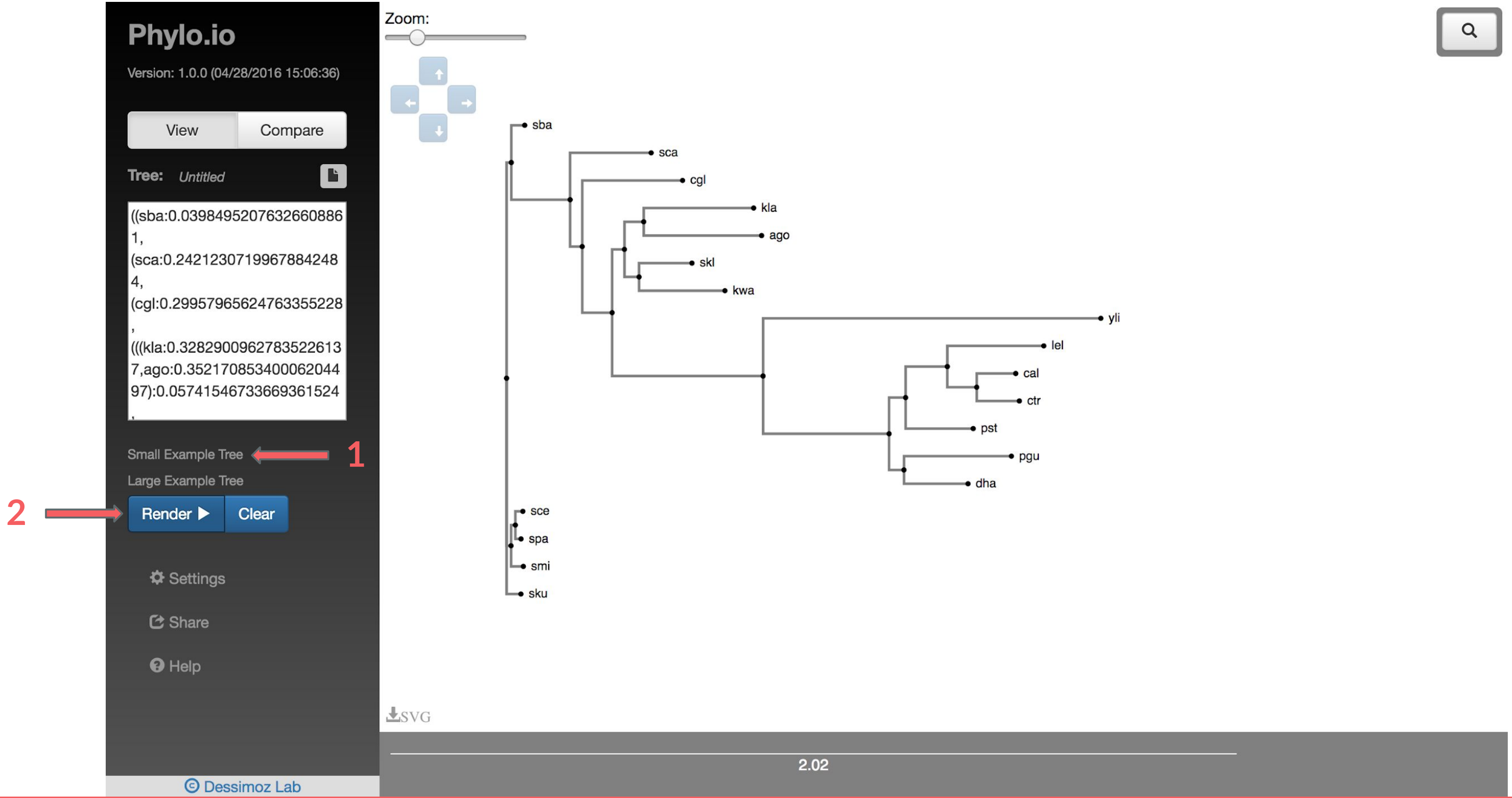
Quite limited

1’ demo @ https://www.youtube.com/watch?v=IOQK3CP8GlA

Phylo.IO demo

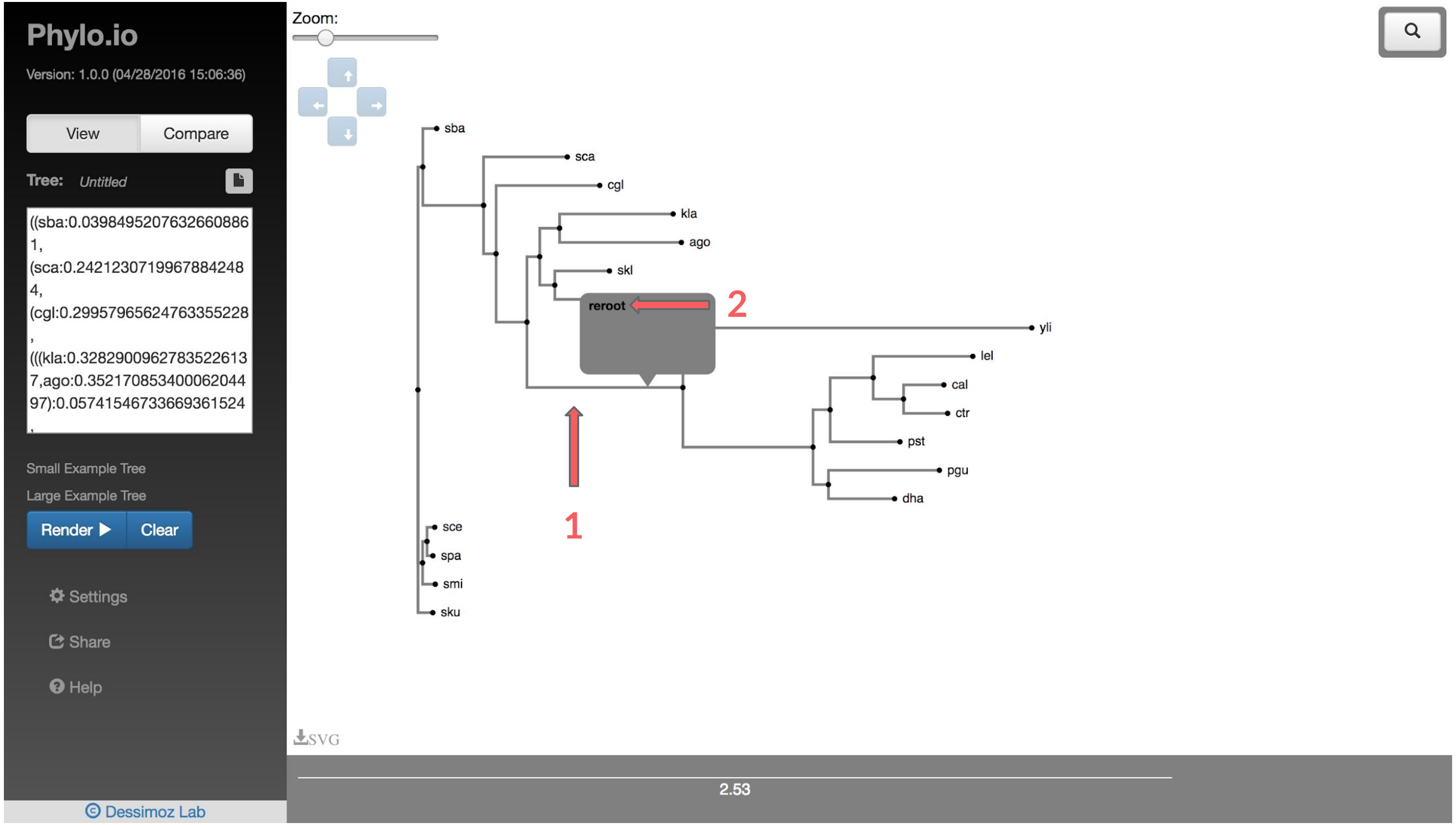
1. Choose view for a single tree, Compare for two trees
2. Add your trees into the text boxes in newick format
3. Click "Render"

Phylo.IO demo



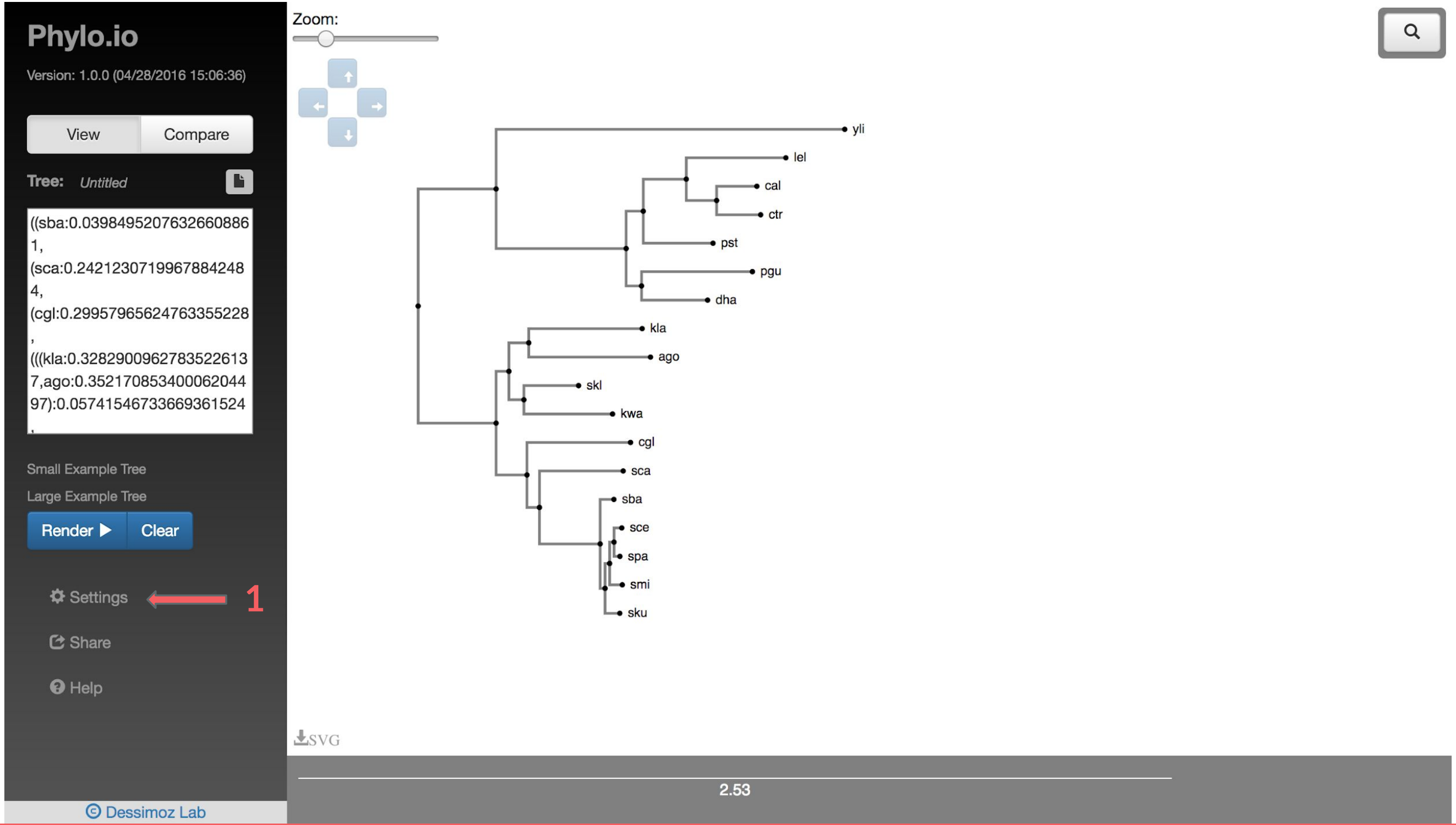
```
((sba:0.03984952076326608861,
(sca:0.24212307199678842484,
(cgl:0.29957965624763355228
,
(((kla:0.32829009627835226137,ago:0.35217085340006204497):0.05741546733669361524
```

Phylo.IO demo



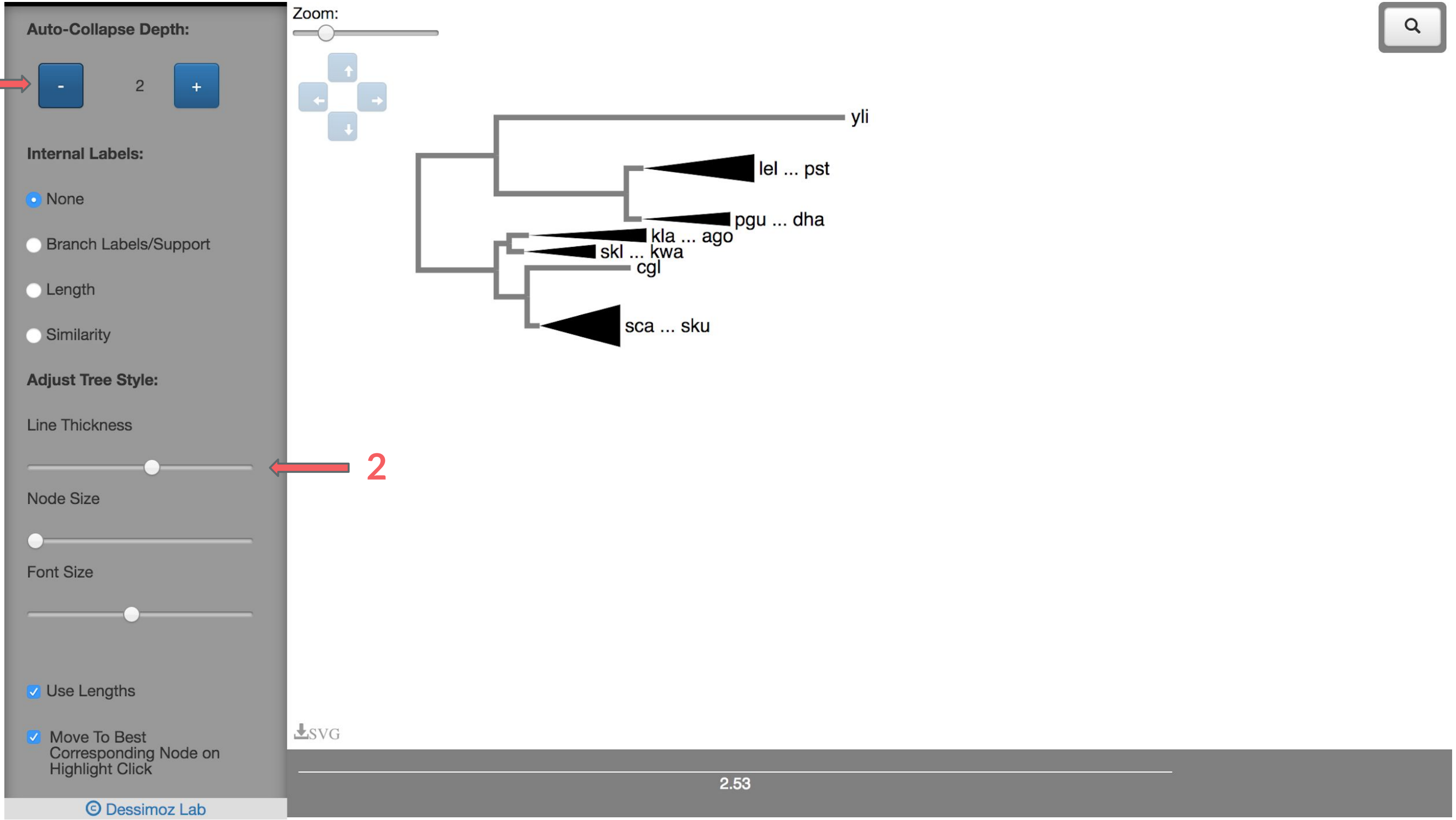
```
((sba:0.03984952076326608861,
(sca:0.24212307199678842484,
(cgl:0.29957965624763355228
,
(((kla:0.32829009627835226137,ago:0.35217085340006204497):0.05741546733669361524
,
```

Phylo.IO demo



((sba:0.03984952076326608861,
(sca:0.24212307199678842484,
(cgl:0.29957965624763355228
,
(((kla:0.32829009627835226137,ago:0.35217085340006204497):0.05741546733669361524
,

Phylo.IO demo



Auto-Collapse Depth:

- 2 +

Internal Labels:

● None

○ Branch Labels/Support

○ Length

○ Similarity

Adjust Tree Style:

Line Thickness

Node Size

Font Size

☑ Use Lengths

☑ Move To Best Corresponding Node on Highlight Click

Ⓒ Dessimoz Lab

1

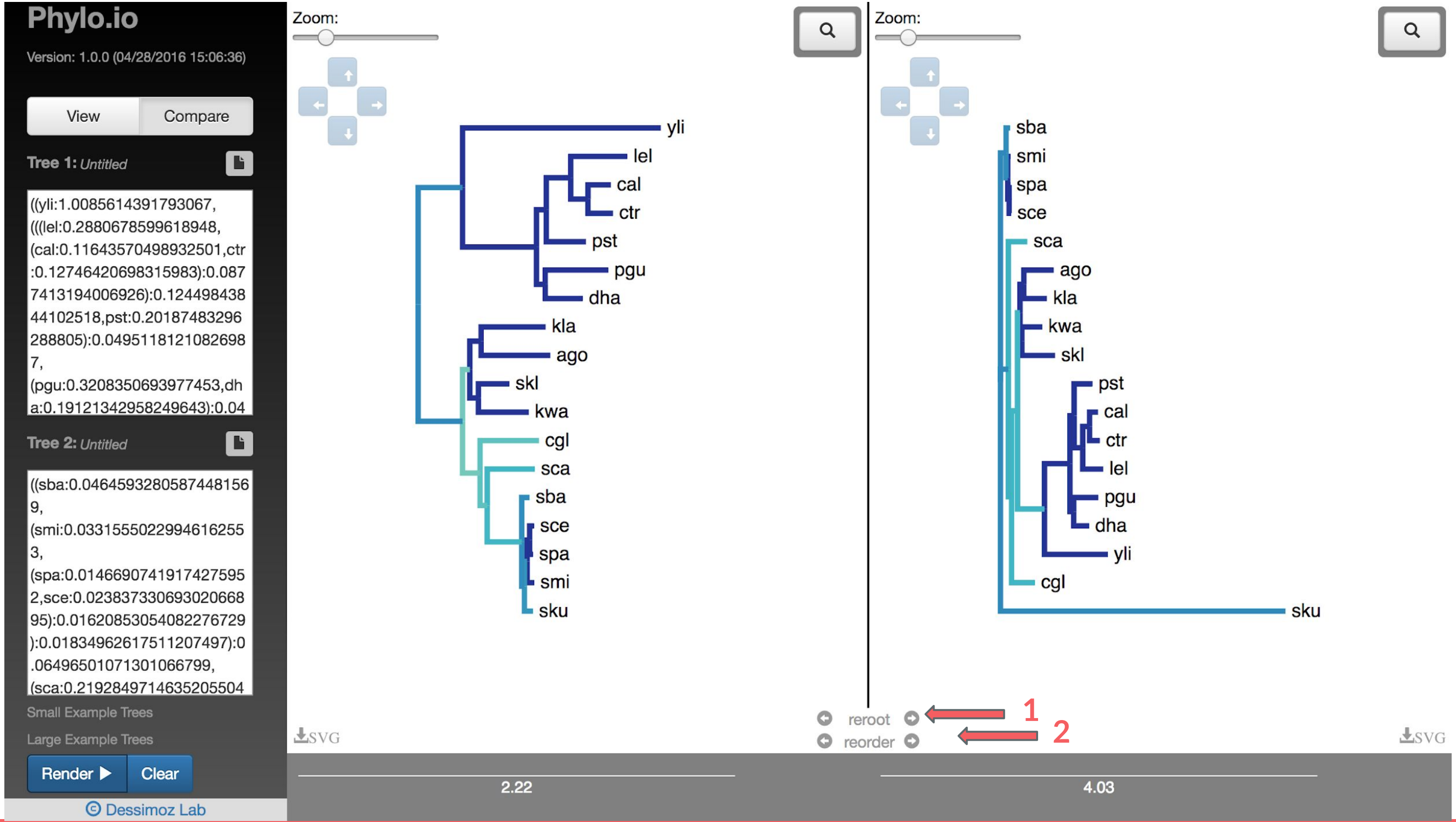
2

3

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



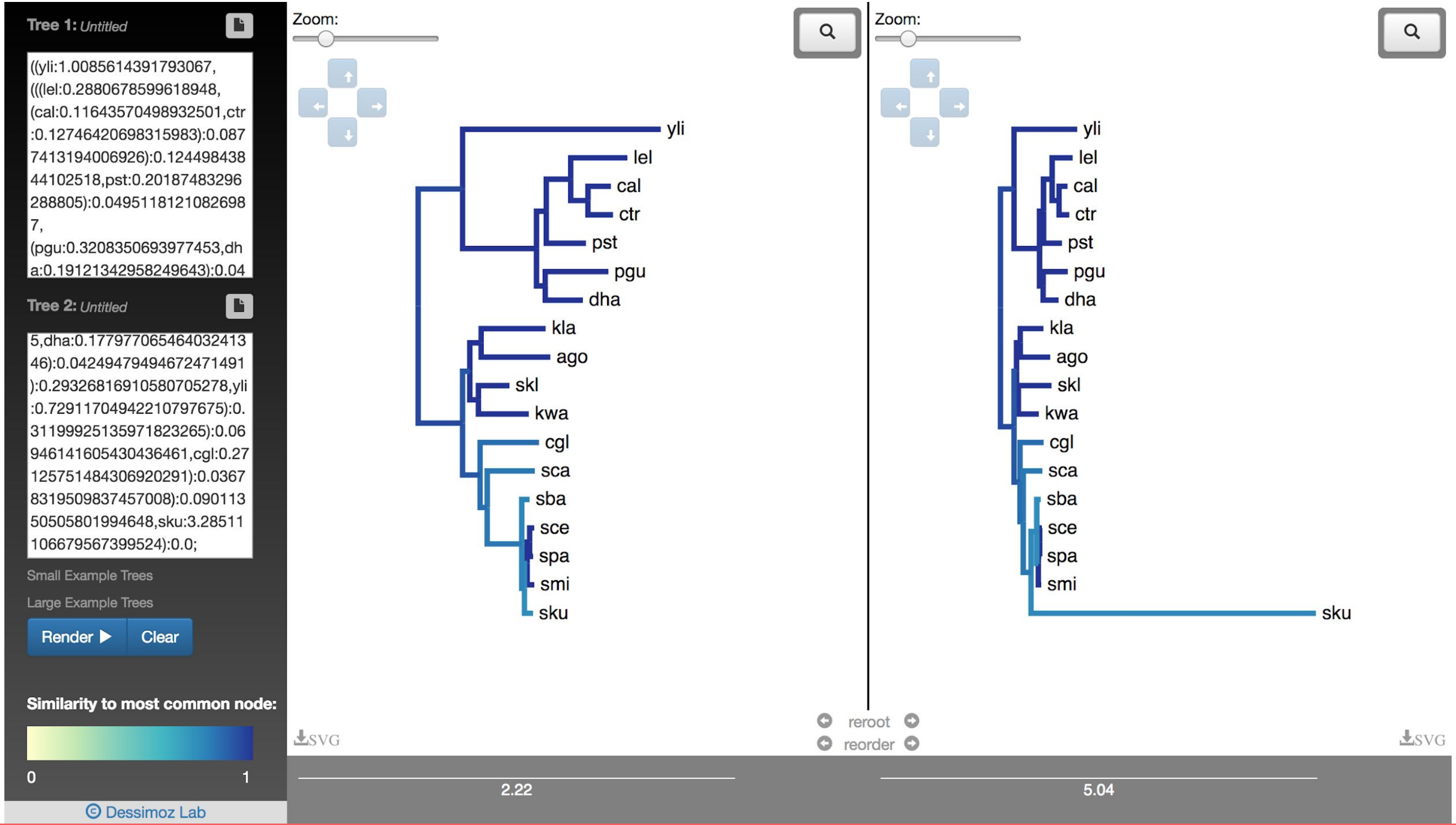
Tree 1: *Untitled*

```
((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:0.0238373306930206668
95):0.0162085305408227672 9
):0.0183496261751120749 7):0
.0649650107130106679 9,
(sca:0.2192849714635205504
```

Phylo.IO demo



Tree 1: *Untitled*

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

Tree 2: *Untitled*

```
5,dha:0.17797706546403241З
46):0.04249479494672471491
):0.29326816910580705278,yli
:0.72911704942210797675):0.
3119992513597182З265):0.06
94614160543043646l,cgl:0.27
125751484306920291):0.0367
8319509837457008):0.090113
50505801994648,sku:3.28511
106679567399524):0.0;
```

Small Example Trees

Large Example Trees

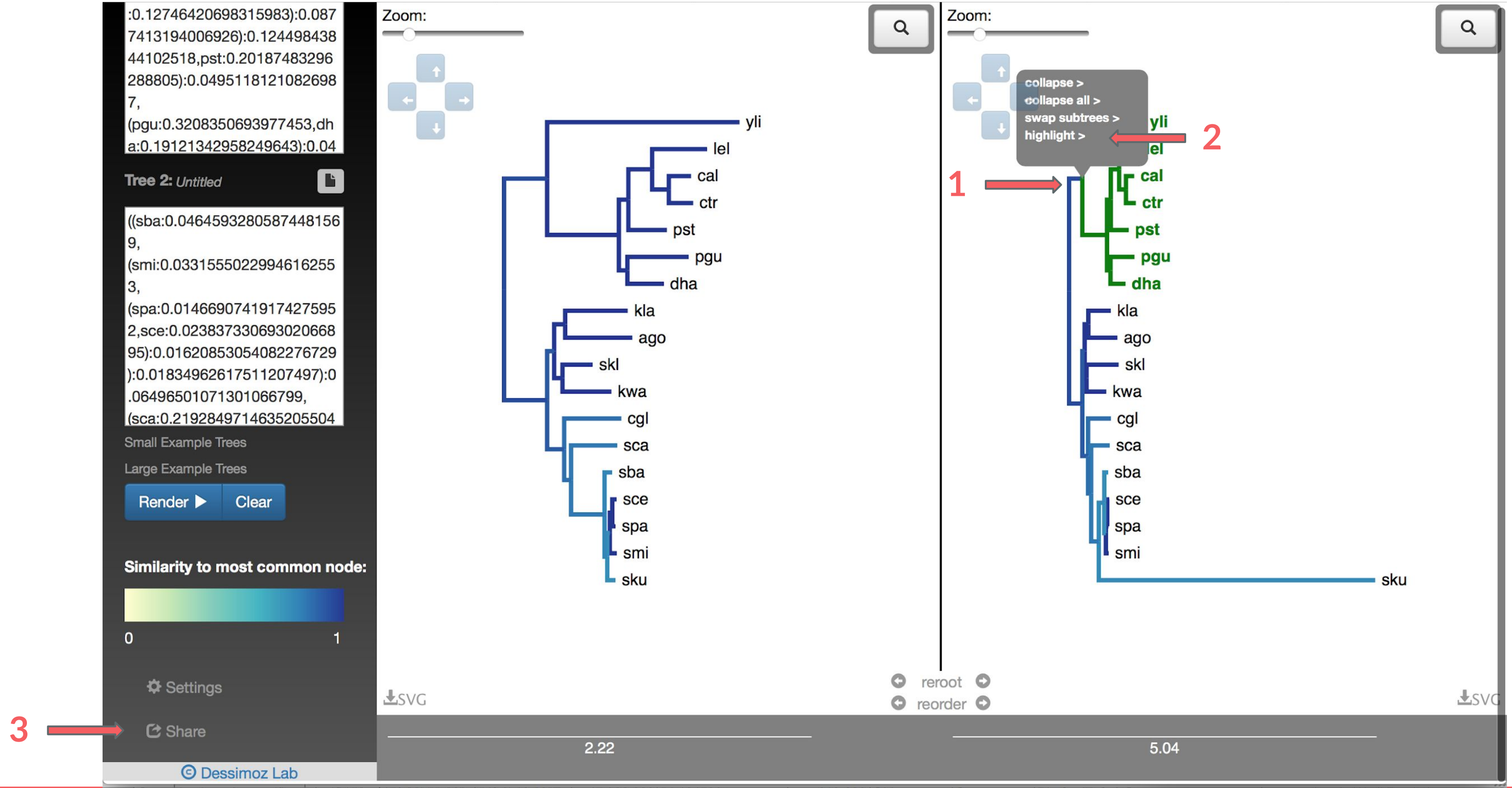
Render ▶ Clear

Similarity to most common node:

0 1

Dessimoz Lab

Phylo.IO demo

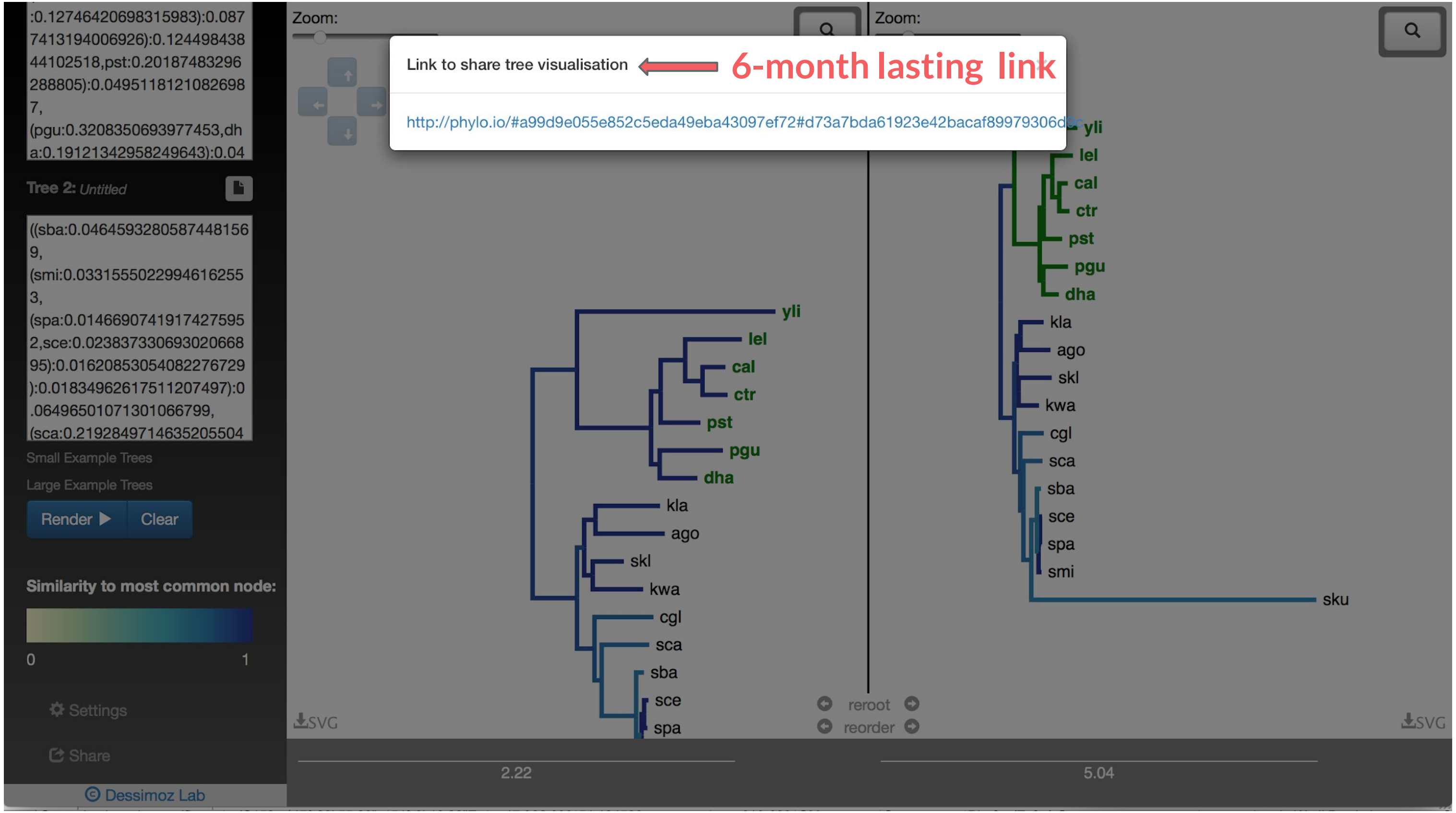


```
:0.12746420698315983):0.087
7413194006926):0.124498438
44102518,pst:0.20187483296
288805):0.0495118121082698
7,
(pgu:0.3208350693977453,dh
a:0.19121342958249643):0.04
```

Tree 2: *Untitled*

```
((sba:0.0464593280587448156
9,
(smi:0.0331555022994616255
3,
(spa:0.0146690741917427595
2,sce:0.0238373306930206668
95):0.0162085305408227672 9
):0.0183496261751120749 7):0
.064965010713010667 99,
(sca:0.2192849714635205504
```

Phylo.IO demo



Link to share tree visualisation

6-month lasting link

http://phylo.io/#a99d9e055e852c5eda49eba43097ef72#d73a7bda61923e42bacaf89979306d9c

```
:0.12746420698315983):0.087
7413194006926):0.124498438
44102518,pst:0.20187483296
288805):0.0495118121082698
7,
(pgu:0.3208350693977453,dh
a:0.1912134295824964З):0.04
```

Tree 2: *Untitled*

```
((sba:0.04645932805874481560
9,
(smi:0.0331555022994616255
3,
(spa:0.0146690741917427595
2,sce:0.0238373306930206668
95):0.01620853054082276729
):0.01834962617511207497):0
.06496501071301066799,
(sca:0.2192849714635205504
```

Web Portals

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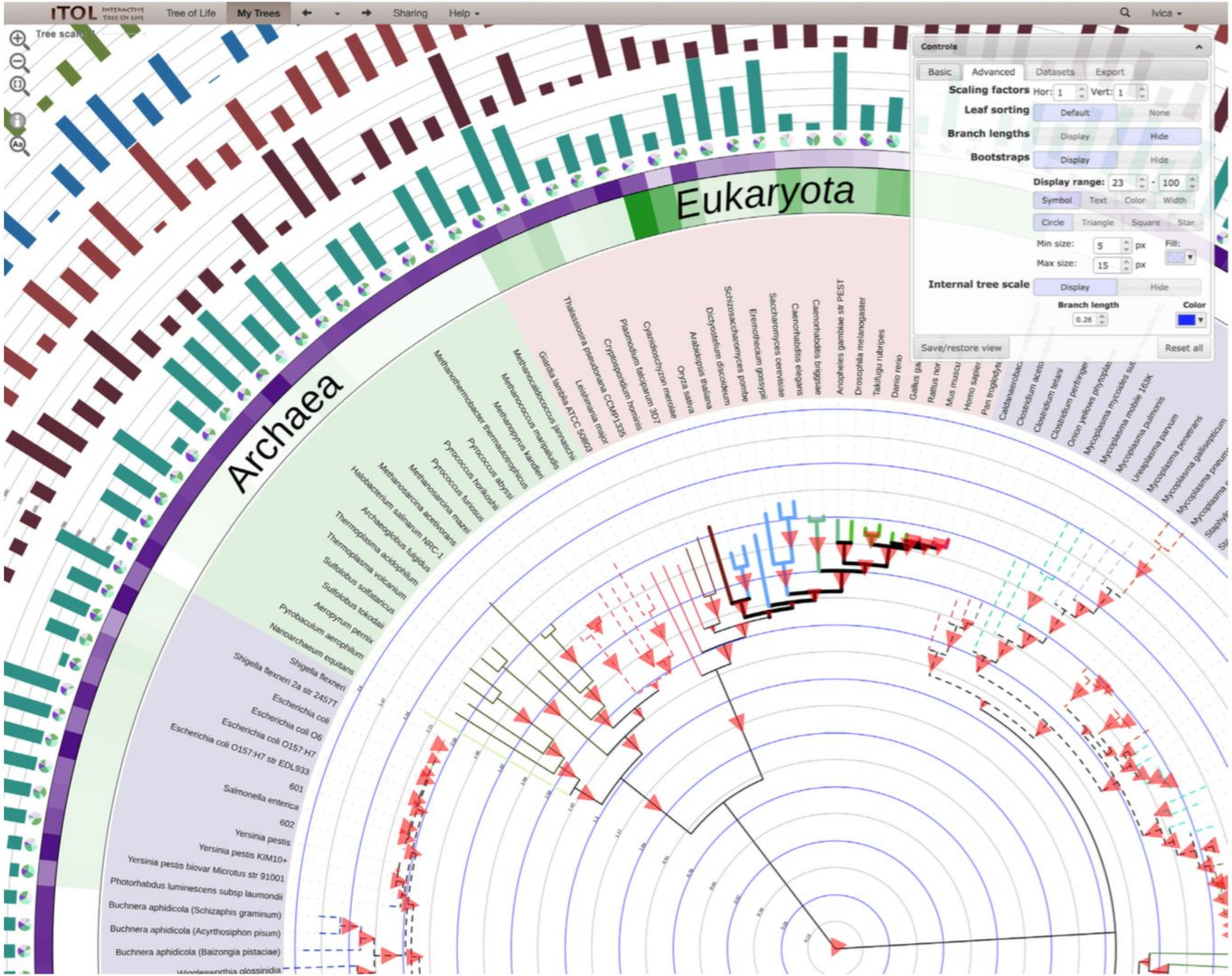
- Others:
    - **PHYLOViZ Online** @ https://online.phyloviz.net/index, (10-min YouTube tutorial: https://www.youtube.com/watch?v=hmbmurFV6ik)
    - **Archaeopteryx-js** @ http://www.phyloxml.org/archaeopteryx-js/bcl2_js.html
    - **TreeLink** @ http://www.treelinkapp.com
    - **T-REX** @ http://www.trex.uqam.ca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

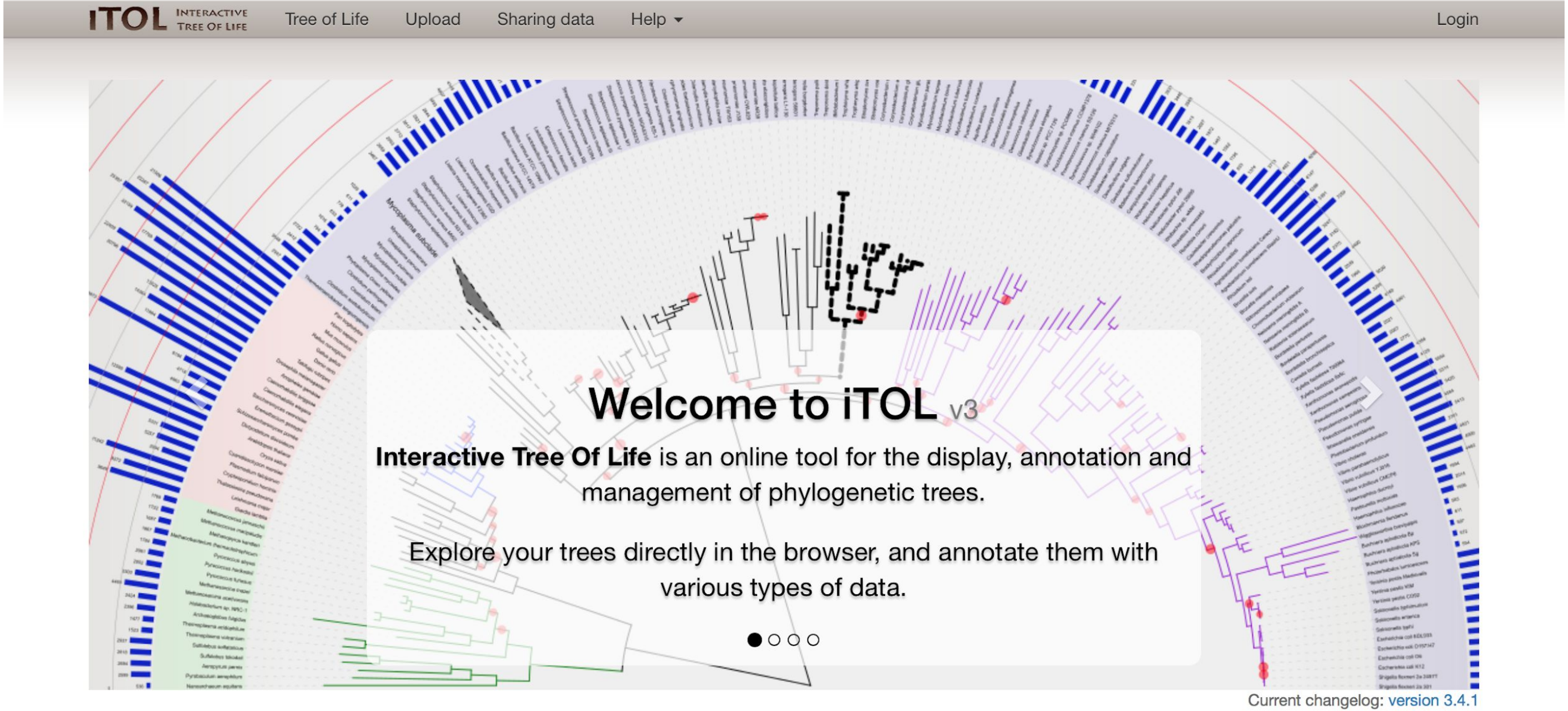
iTOL

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



Scaling factors Hor: 1 Vert: 1
Leaf sorting: Default | None
Branch lengths: Display | Hide
Bootstraps: Display | Hide
Display range: 23 - 100
Symbol | Text | Color | Width
Circle | Triangle | Square | Star
Min size: 5 px
Max size: 15 px
Fill:
Internal tree scale: Display | Hide
Branch length: 0.26
Color

iTOL



Welcome to iTOL v3

Interactive Tree Of Life is an online tool for the display, annotation and management of phylogenetic trees.

Explore your trees directly in the browser, and annotate them with various types of data.

Current changelog: version 3.4.1

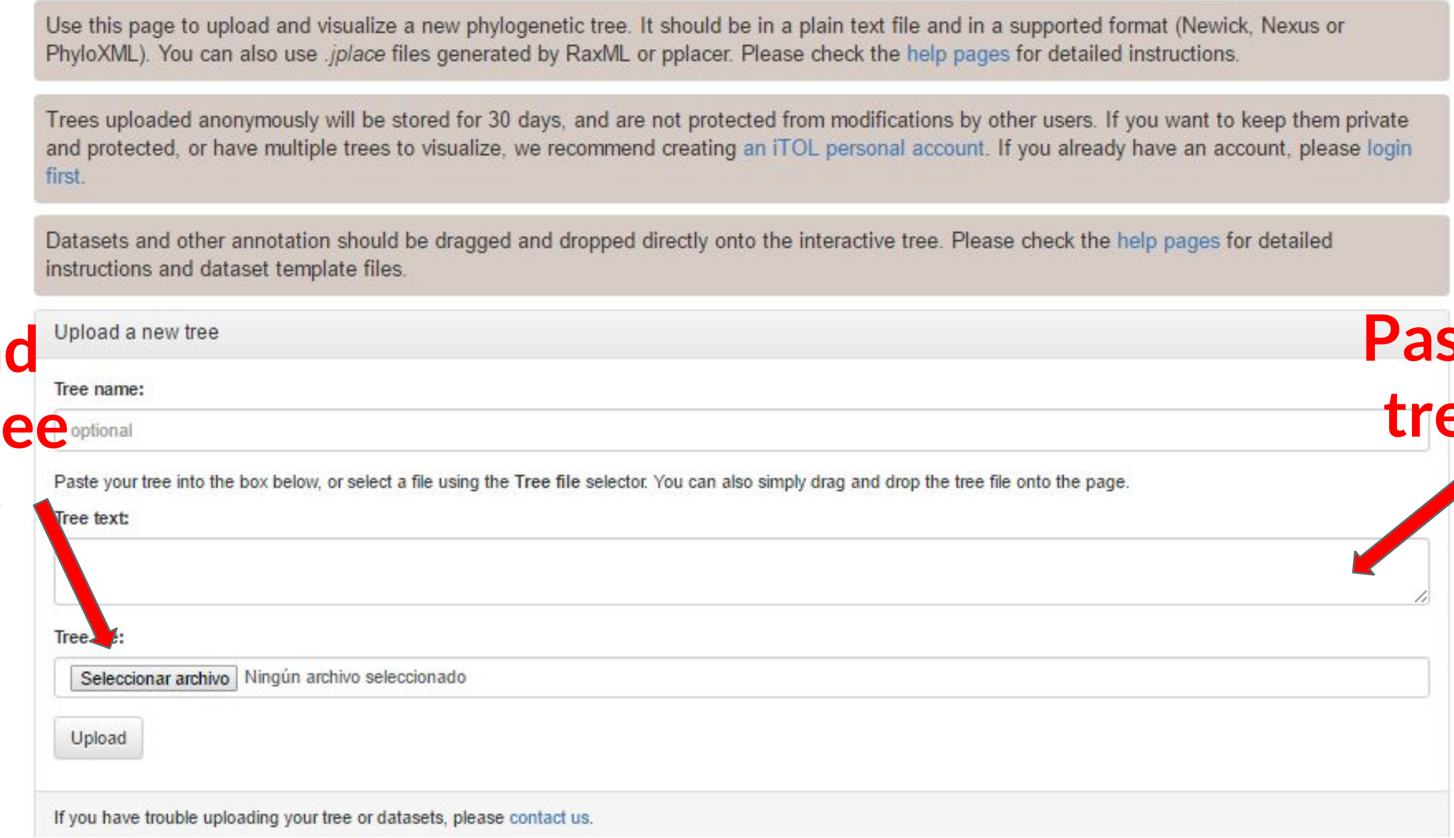
iTOL demo – Uploading Data

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,((Liphistius: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,Scutigera:2.212767162268583e-01)1.00:1.057606285127356e-01)1.00:1.754862046681610e-02,((Eremobates:1.924502405585649e-01,(Ixodes:3.038900301437783e-01,Tetranychus:7.026474543095570e-01)0.93:3.270977853676584e-02)0.93:2.159766664209322e-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)1.00:1.137473317953131e-02)1.00:1.342660962530040e-01)1.00:1.510542954930570e-02)0.93:1.019147450482914e-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:

Ningún archivo seleccionado

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 were 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

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

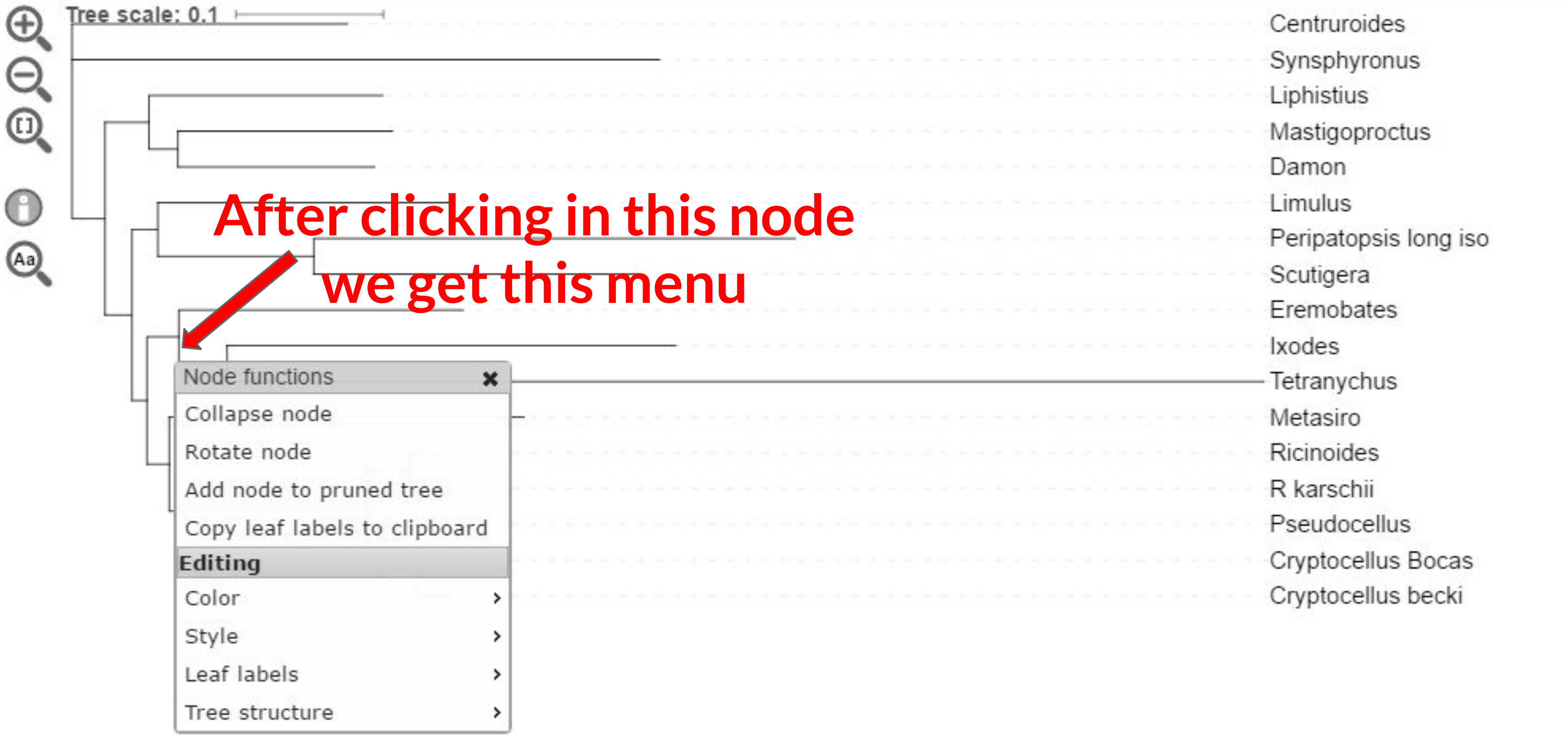
Look how many options!

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)



After clicking in this node we get this menu

iTOL demo – Datasets

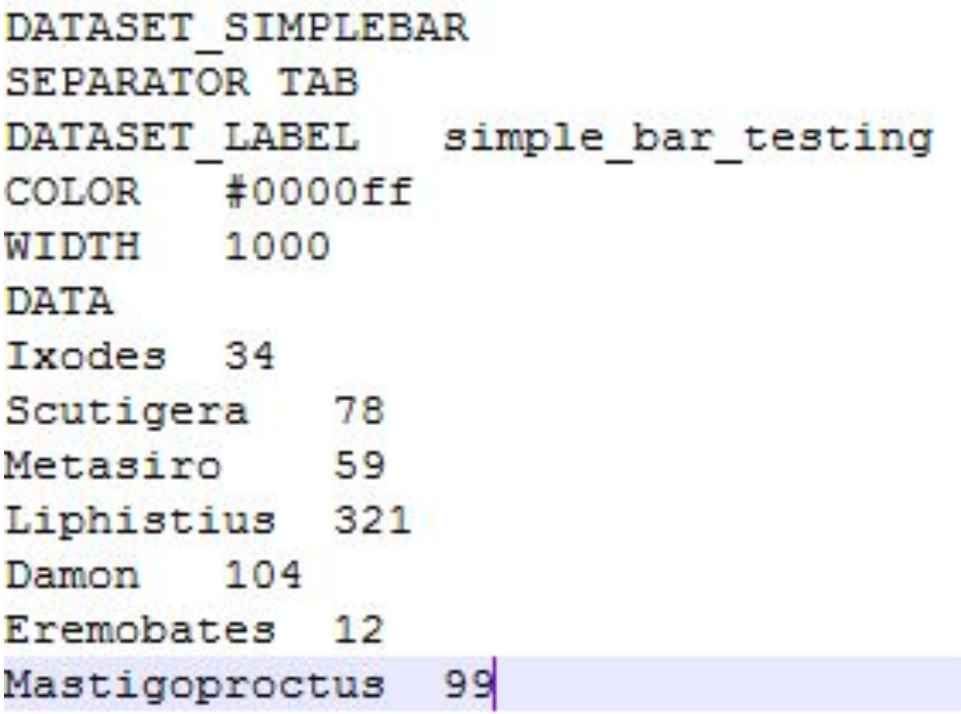
iTOL allows a huge range of plots to compliment a tree:
http://itol.embl.de/help.cgi#annot

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
```

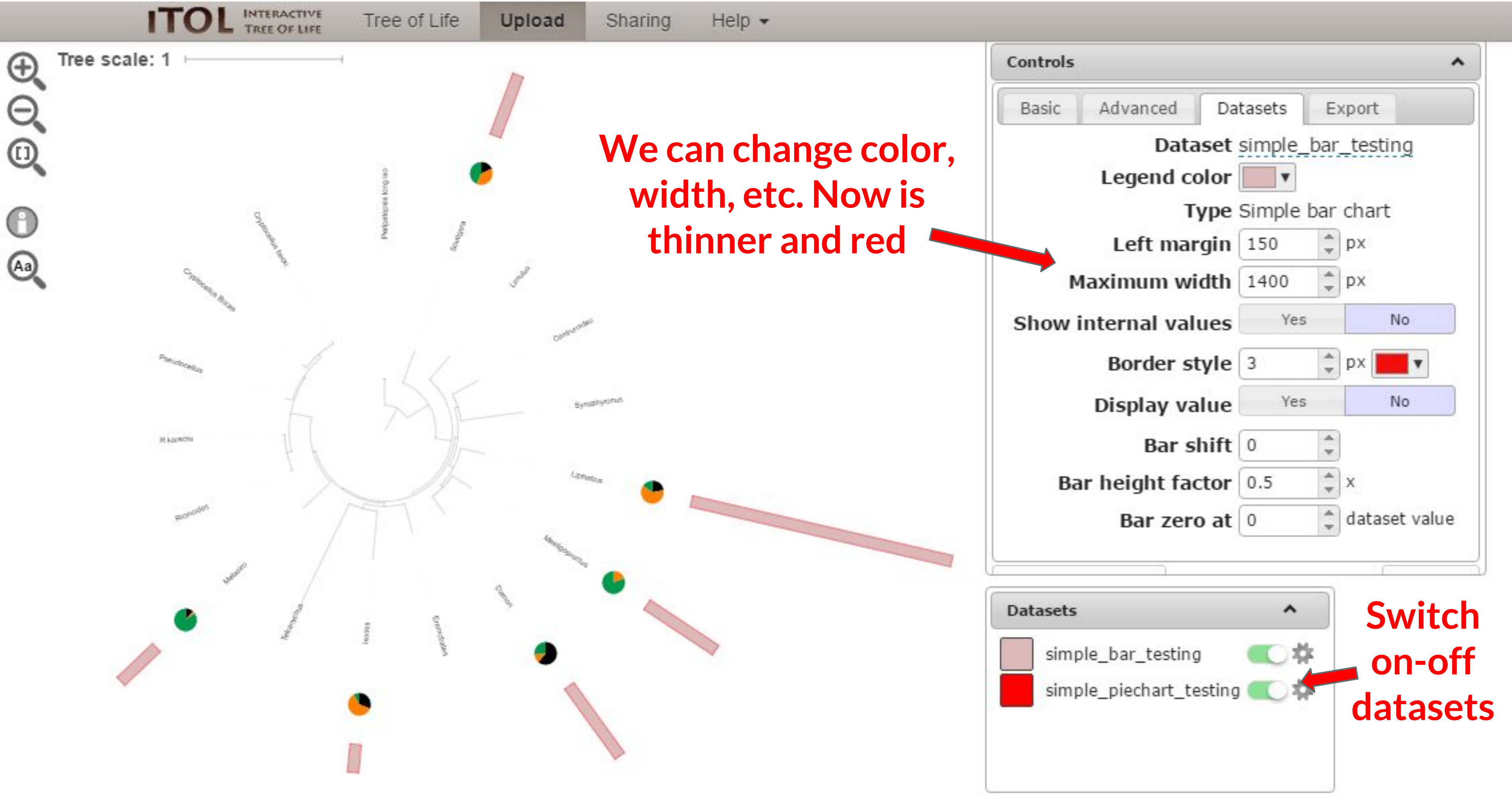
We drag the file in and...

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



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

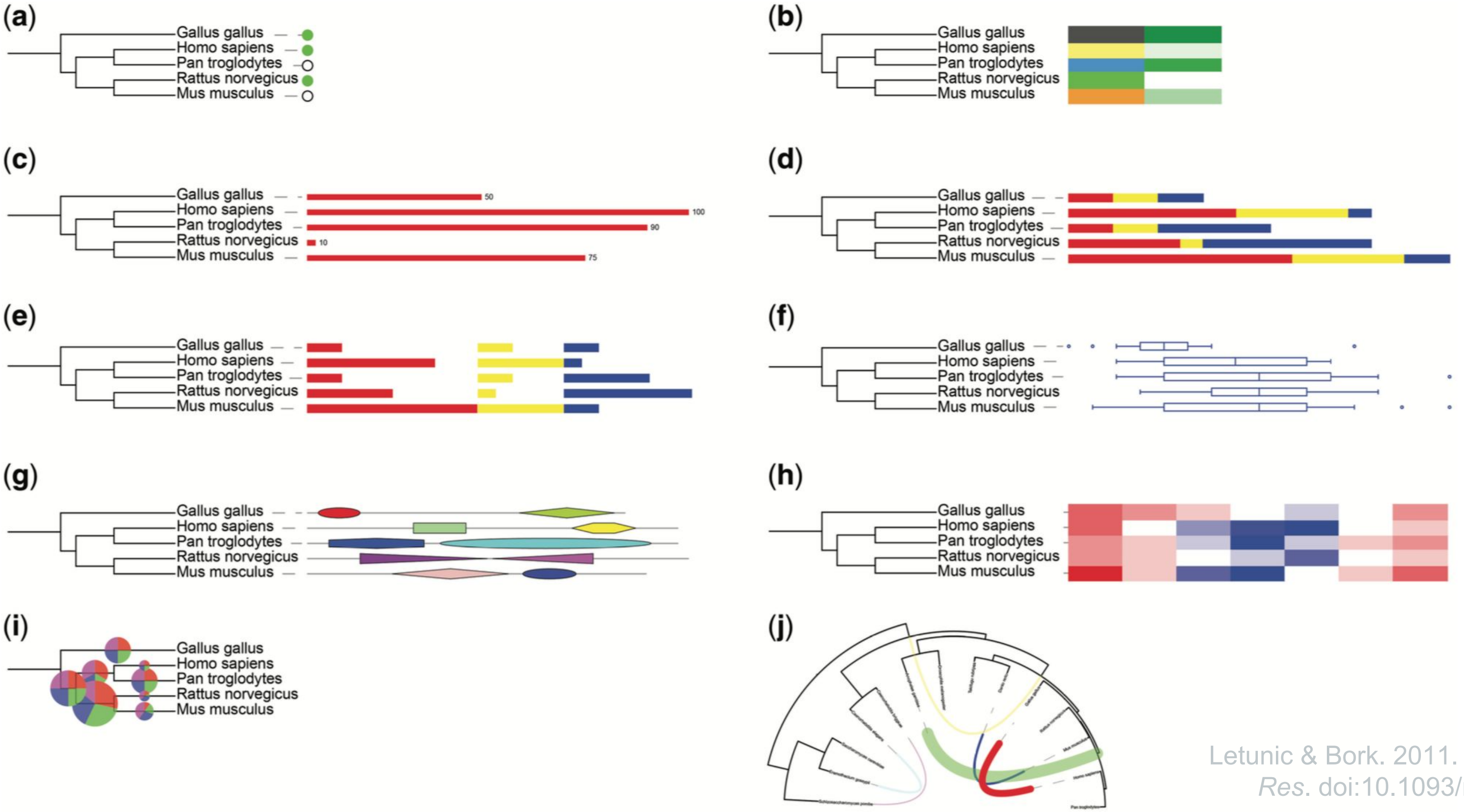
Datasets

- 🟥 simple_bar_testing
- 🟥 simple_piechart_testing

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

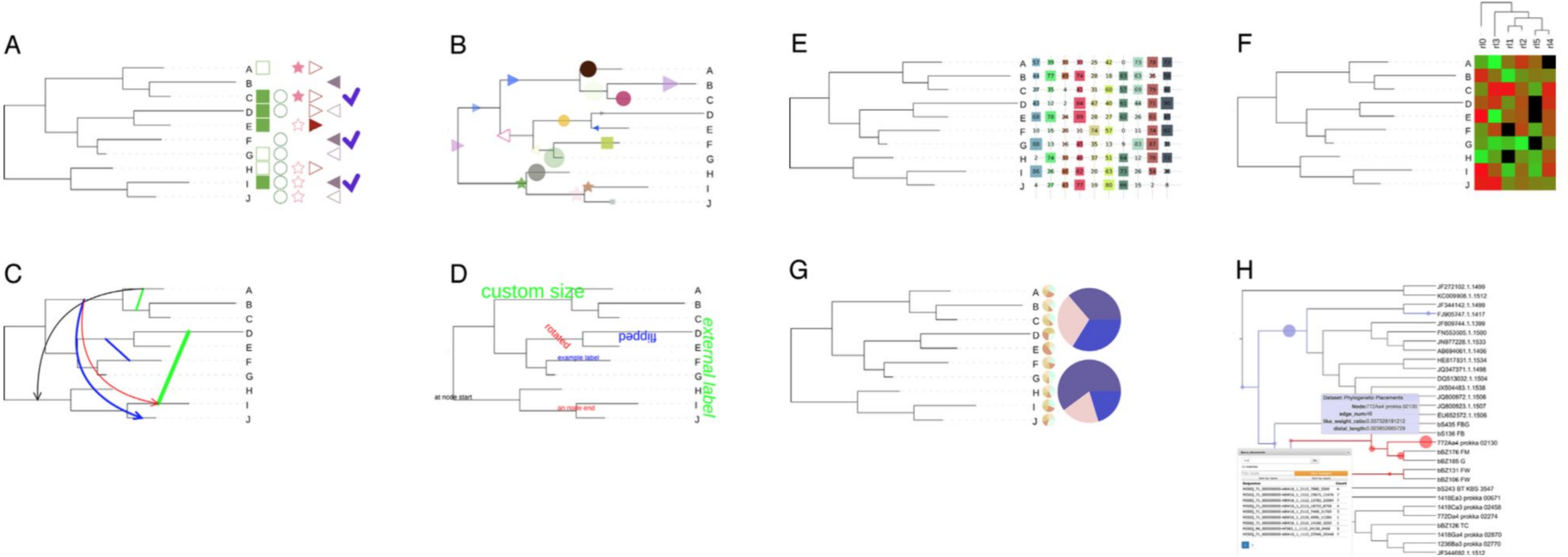
Switch on-off datasets

iTOL – Dataset Templates



Letunic & Bork. 2011. *Nucleics Acids Res*. doi:10.1093/nar/gkr201

iTOL – Even More Templates



Letunic & Bork. 2016. *Nucleics Acids Res.* 44. doi:10.1093/nar/gkw290

Web Portals

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- Others:
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    - **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.

EVOLVIEW

Web based

Interactive interface

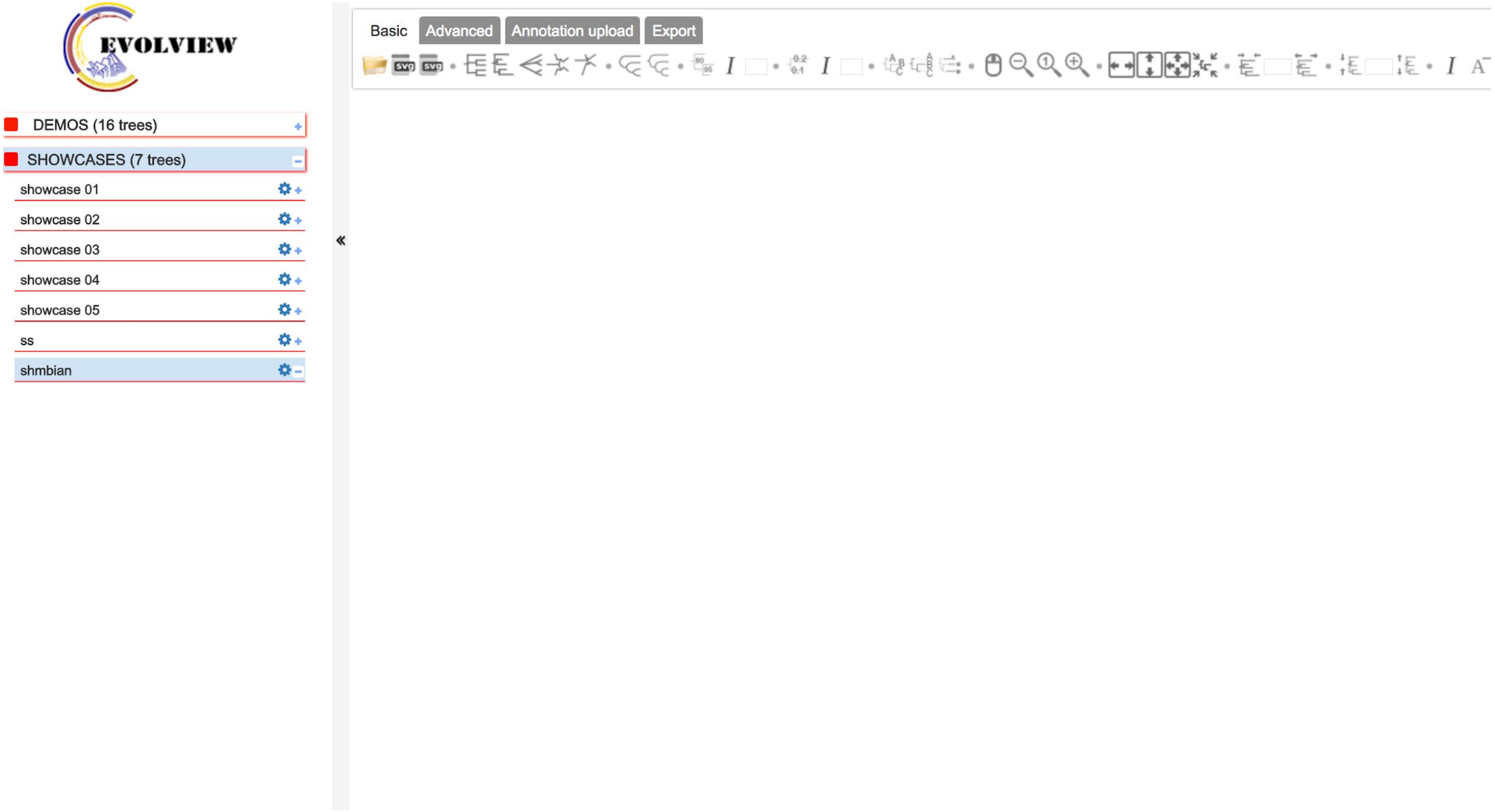
Exporting tree images in several formats allowed

Highly customizable, programmable

Trees can be stored

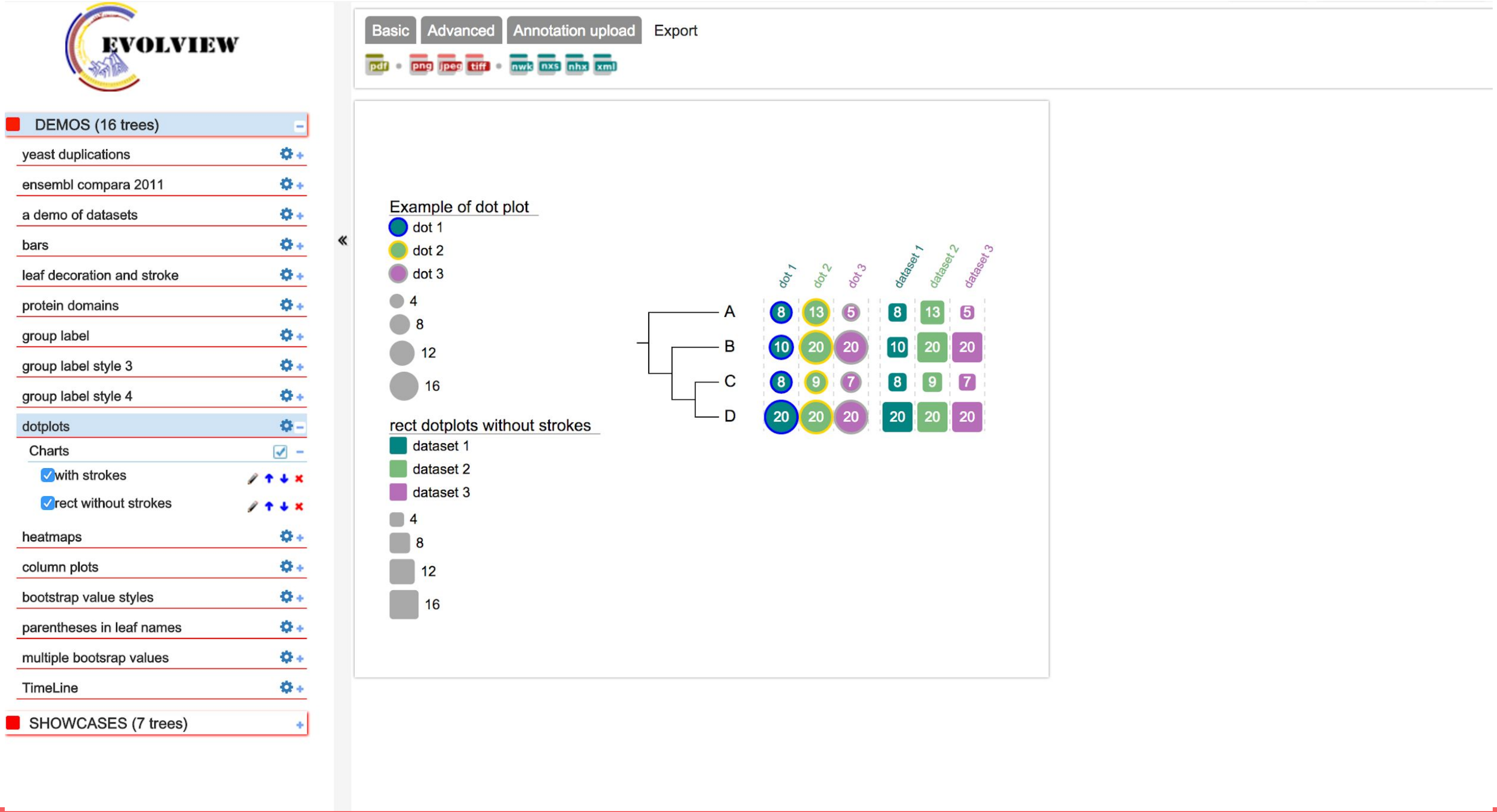
Claims to be able to operate with thousands of leaves/tips

EVOLVIEW



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 bootsrap values
TimeLine
SHOWCASES (7 trees)
Basic
Advanced
Annotation upload
Export
pdf
png
jpeg
tiff
nwk
nxs
nhx
xml
Example of dot plot
dot 1
dot 2
dot 3
4
8
12
16
rect dotplots without strokes
dataset 1
dataset 2
dataset 3
4
8
12
16
dot 1
dot 2
dot 3
dataset 1
dataset 2
dataset 3
A
B
C
D
8
13
5
8
13
5
10
20
20
10
20
20
8
9
7
8
9
7
20
20
20
20
20
20

EVOLVIEW demo

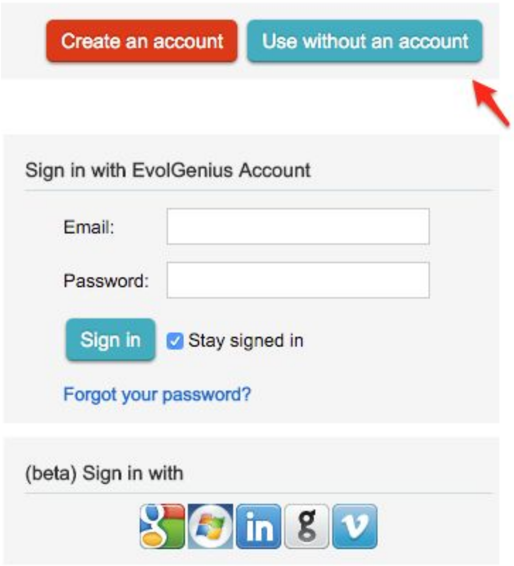
A quick start

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

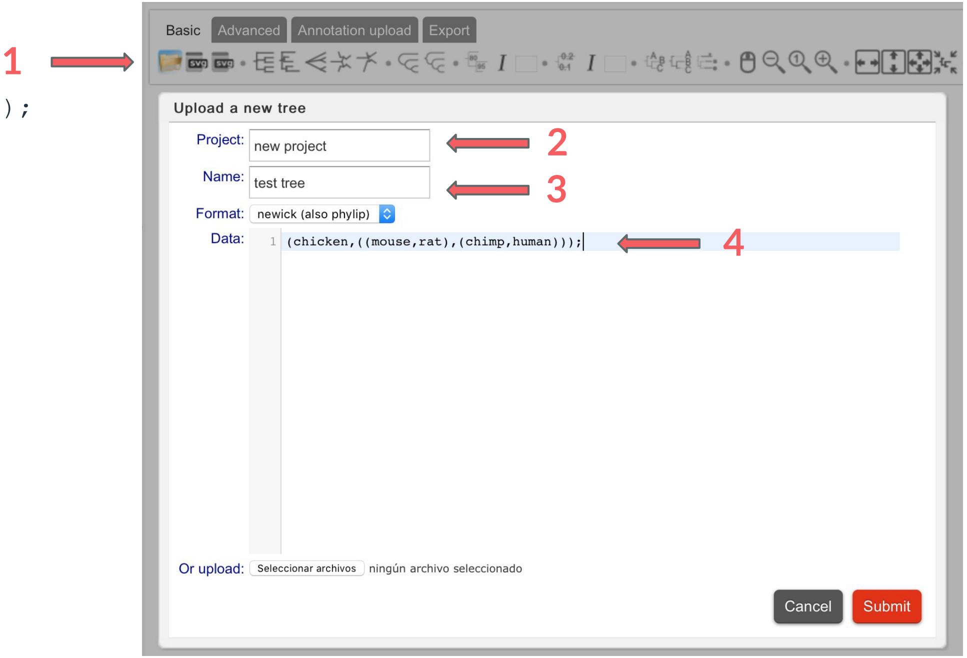
- at the "login" page, click "Use without an account"



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)));
```



Upload a new tree

Project: new project

Name: test tree

Format: newick (also phylip)

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

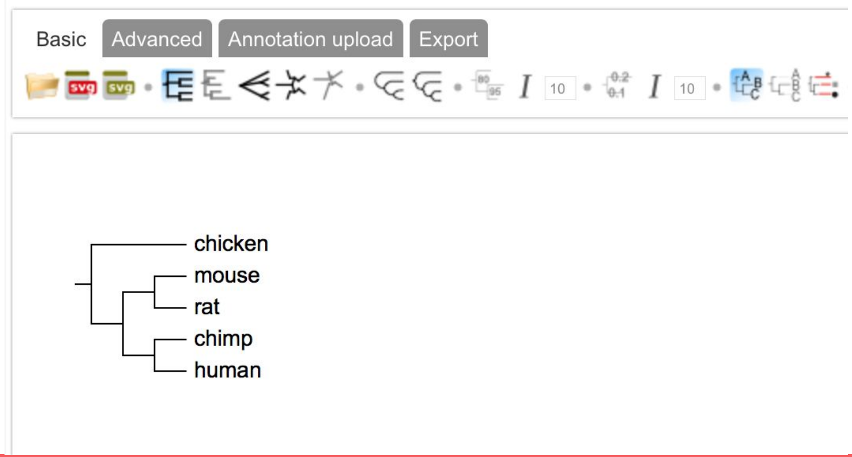
Or upload: Seleccionar archivos ningún archivo seleccionado

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:

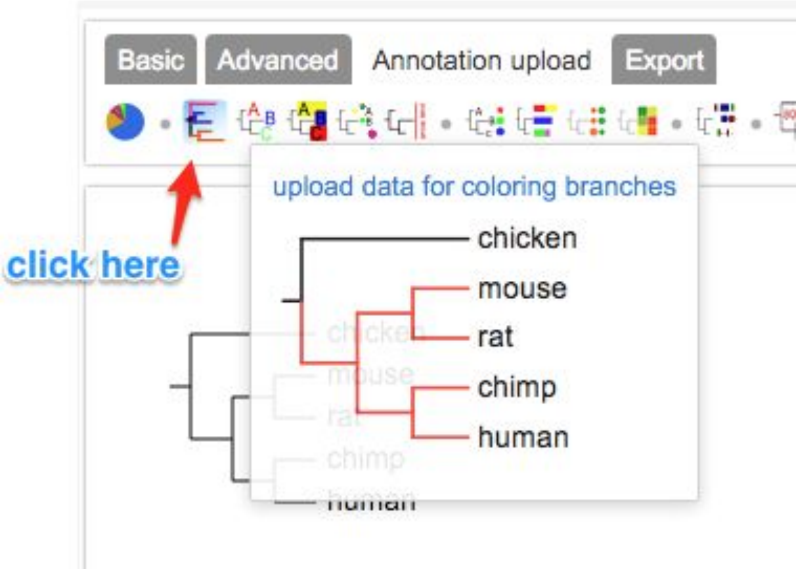


EVOLVIEW demo

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)));`

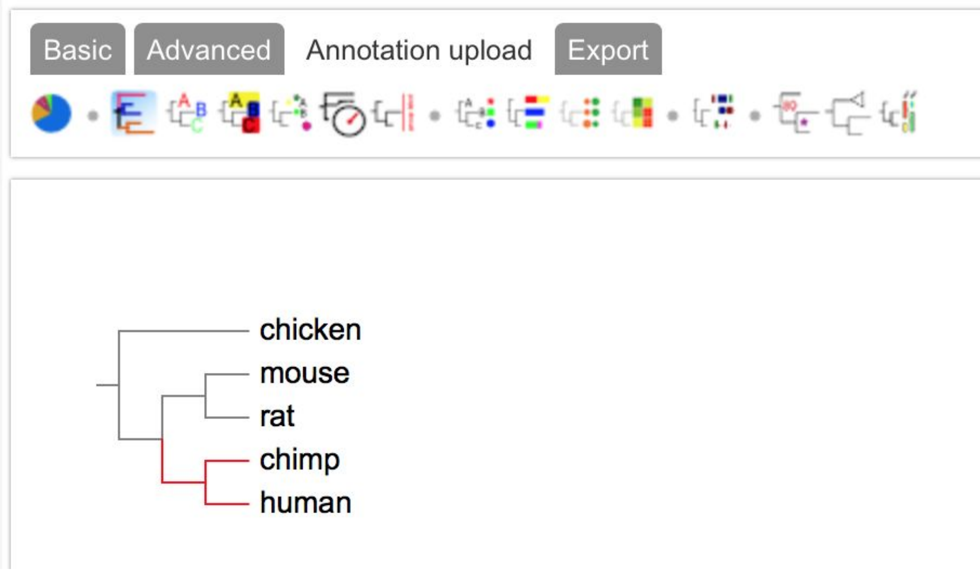
- First of all add a dataset named "branch colors" to change the colors of the branches by clicking the "branch colors" icon on the "Annotation upload" tab:



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:



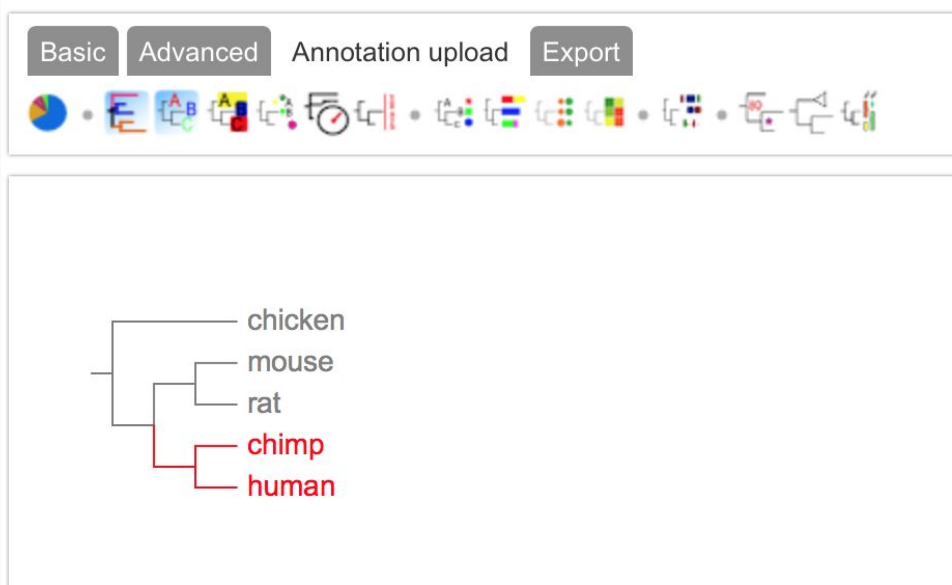
EVOLVIEW demo

- 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 ancester (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:

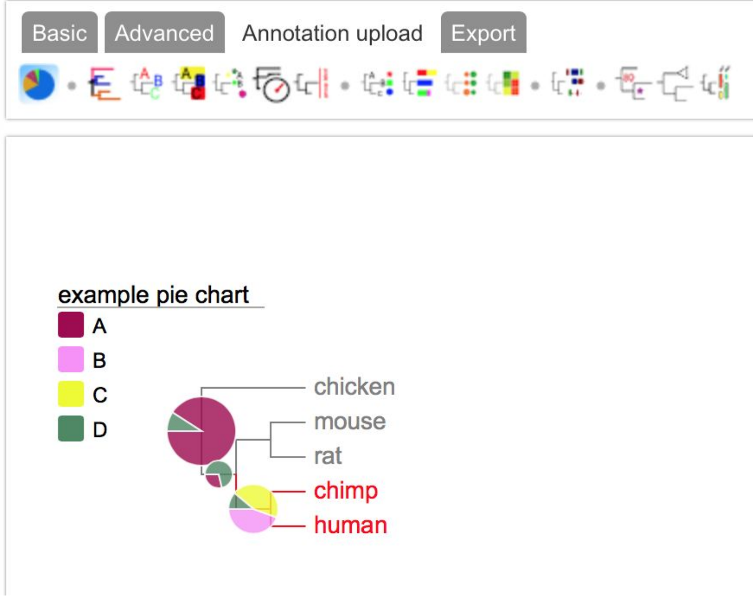
```
## Created on May 25, 2011
## Before the 'data section', now we have a new section that contains lines starting with '!'; this section
## is called the 'modifier section' because it's used to change / modify the default behaviors of the dataset
!Groups           A,B,C,D
!colors           #9F0251,#f88ef9,#effc00,#4D8963
!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:



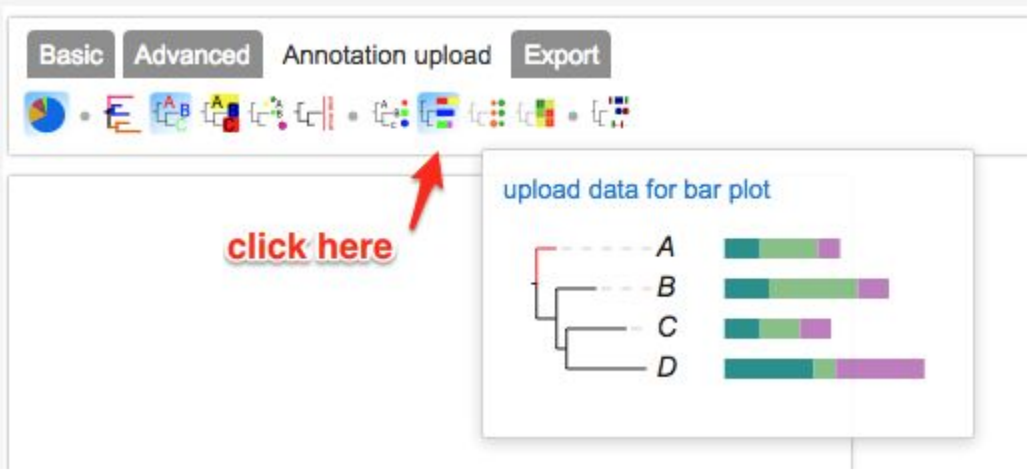
EVOLVIEW demo

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
```

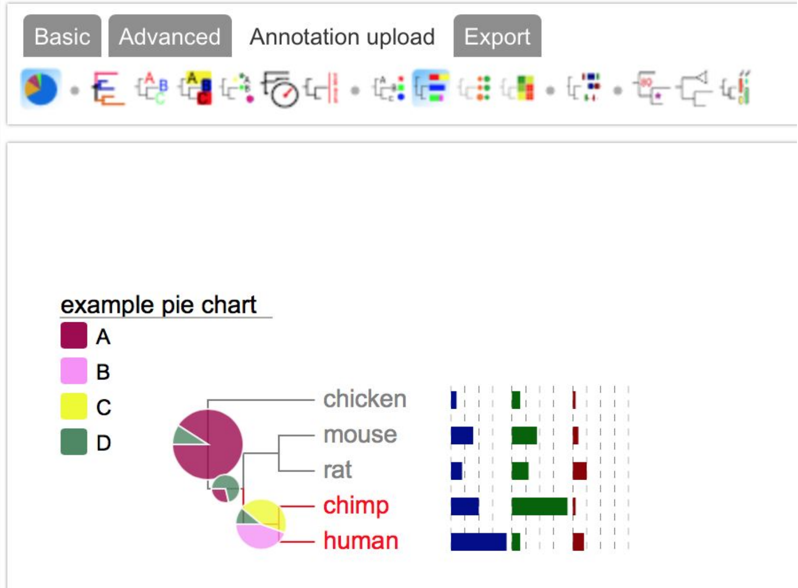


EVOLVIEW demo

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:



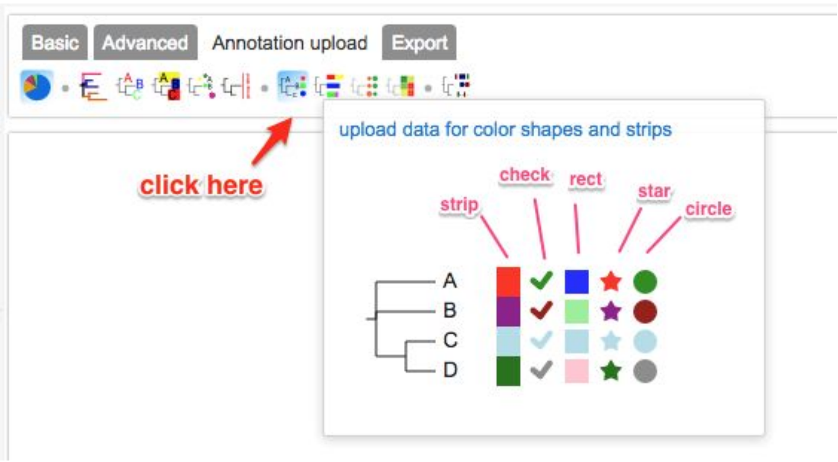
EVOLVIEW demo

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
```

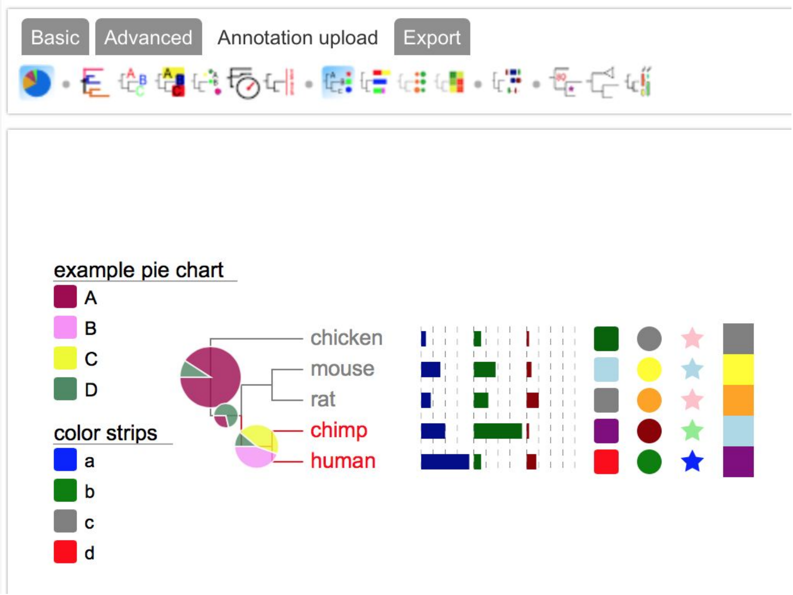


EVOLVIEW demo

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

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

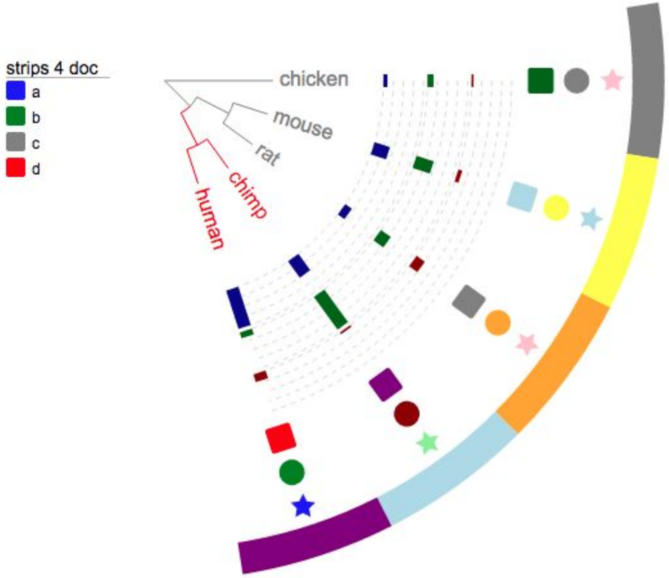
- click the "color strips" icon on the "Annotation upload" tab:
- copy and paste the following to the text area in the popup dialog box:



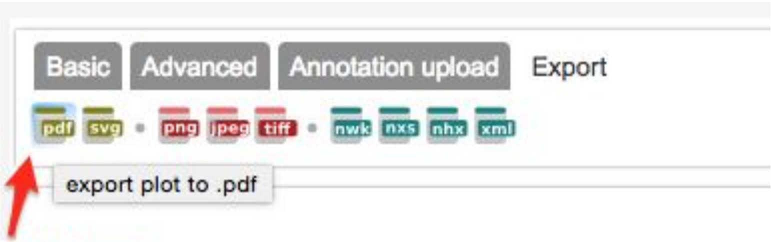
EVOLVIEW demo

Play around and then export the tree to pdf file

- Try different display mode:



- Then download the plot as a PDF file:



click here

Phylogenetic Tree Visualization

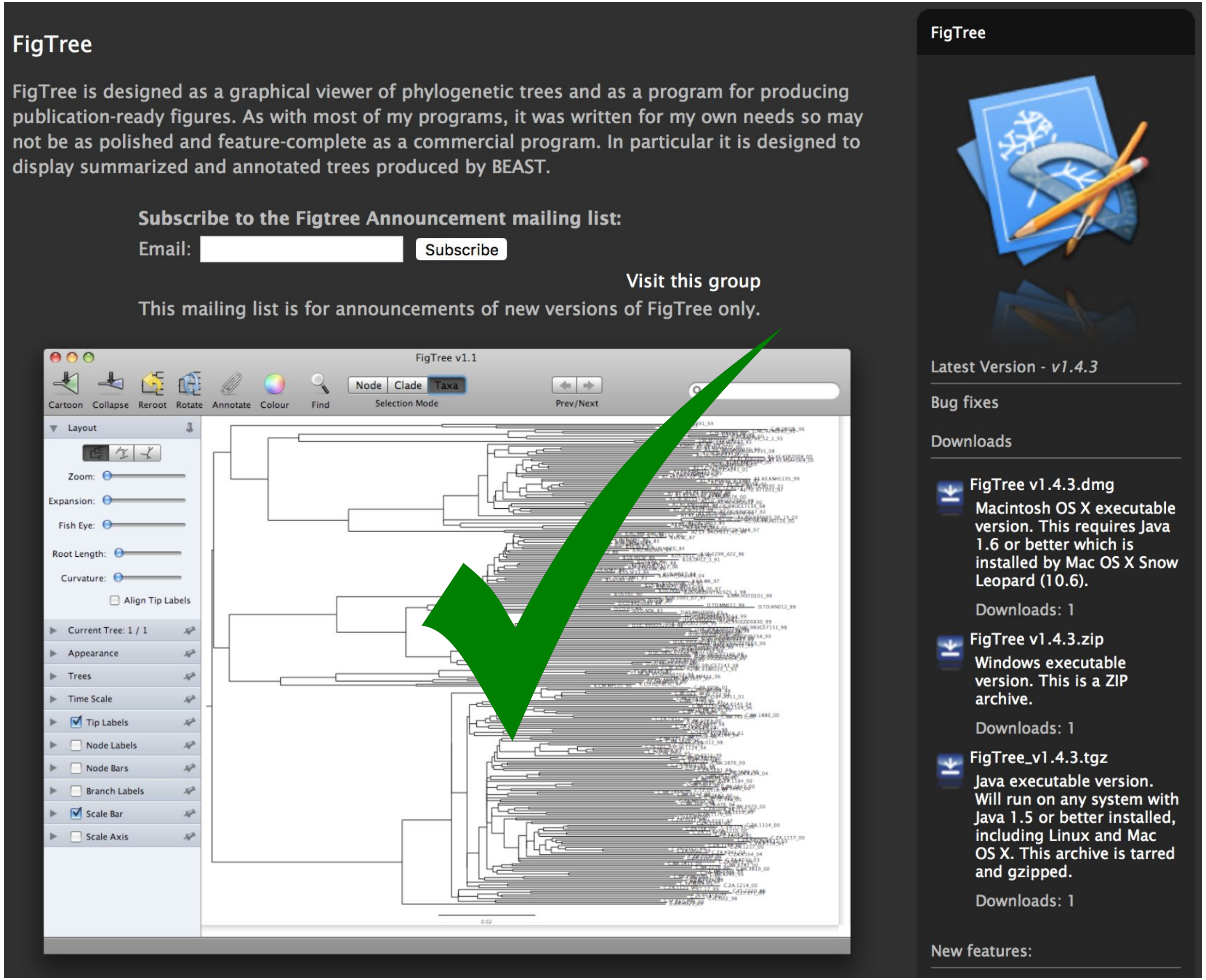
- Web Portals:
    - Phylo.IO @ http://phylo.io
    - Interactive Tree of Life viewer (iTOL) @ http://itol.embl.de
    - EVOLVIEW @ http://www.evolgenius.info/evolview
- **Software:**
    - FigTree @ http://tree.bio.ed.ac.uk/software/figtree/
    - DensiTree @ https://www.cs.auckland.ac.nz/~remco/DensiTree/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

- 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: ☐ Subscribe

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:

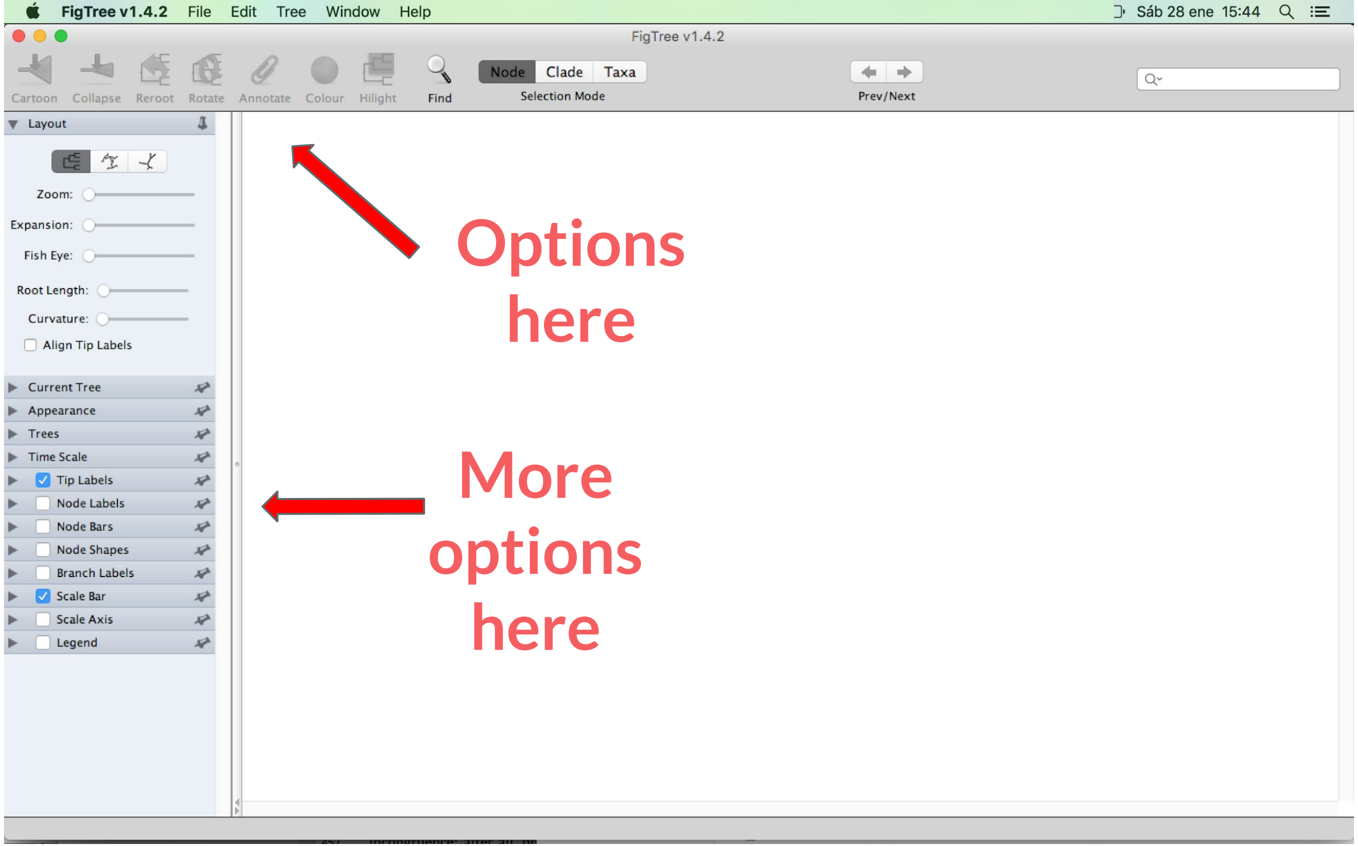
FigTree

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



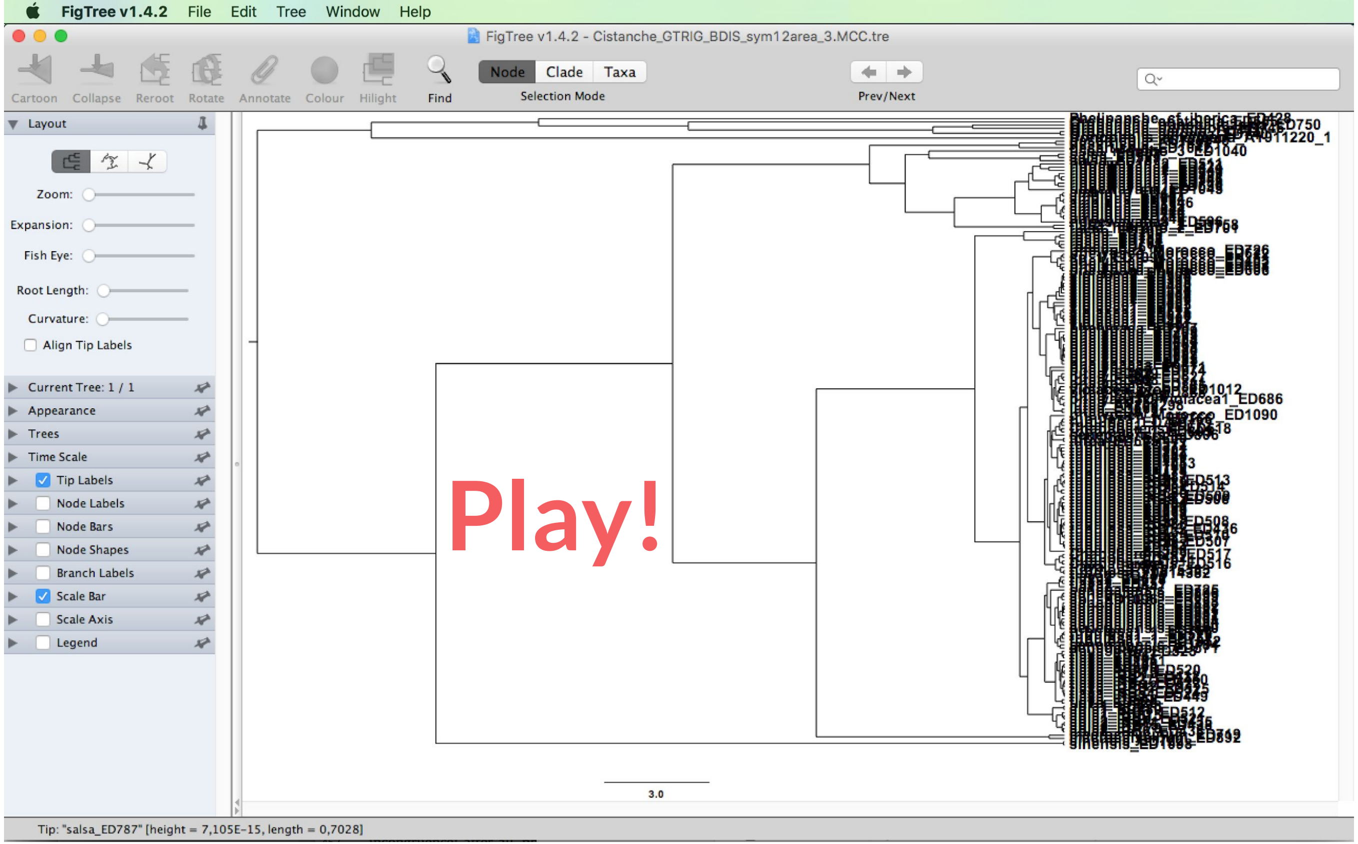
☐ Align Tip Labels

- Current Tree
- Appearance
- Trees
- Time Scale
- ☑ Tip Labels
- ☐ Node Labels
- ☐ Node Bars
- ☐ Node Shapes
- ☐ Branch Labels
- ☑ Scale Bar
- ☐ Scale Axis
- ☐ Legend

Options here

More options here

FigTree



☐ Align Tip Labels

☑ Tip Labels

☐ Node Labels

☐ Node Bars

☐ Node Shapes

☐ Branch Labels

☑ Scale Bar

☐ Scale Axis

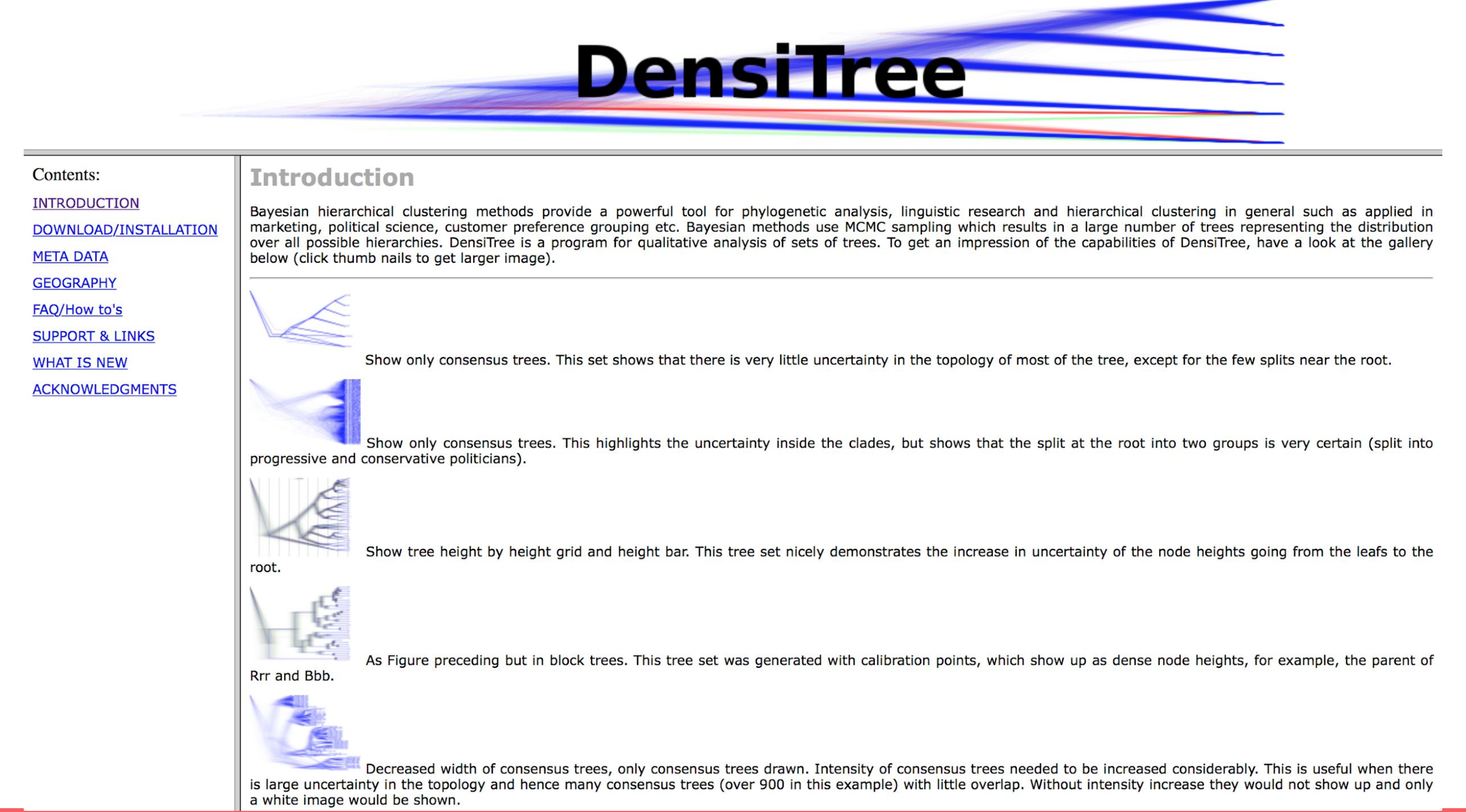
☐ Legend

Tip: "salsa_ED787" [height = 7,105E-15, length = 0,7028]

Play!

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.



Introduction

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

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

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

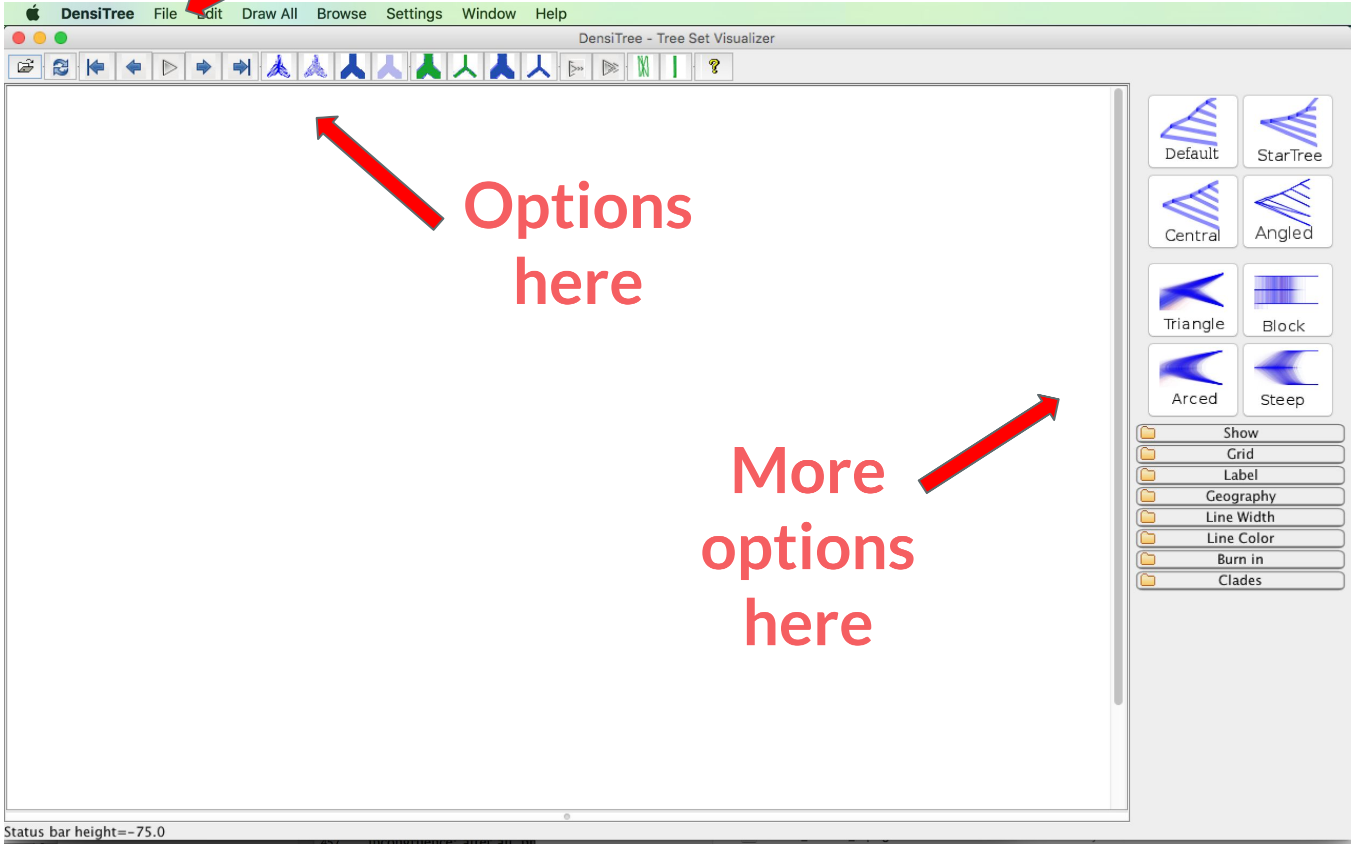
Show tree height by height grid and height bar. This tree set nicely demonstrates the increase in uncertainty of the node heights going from the leafs to the root.

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

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

DensiTree

Open files here

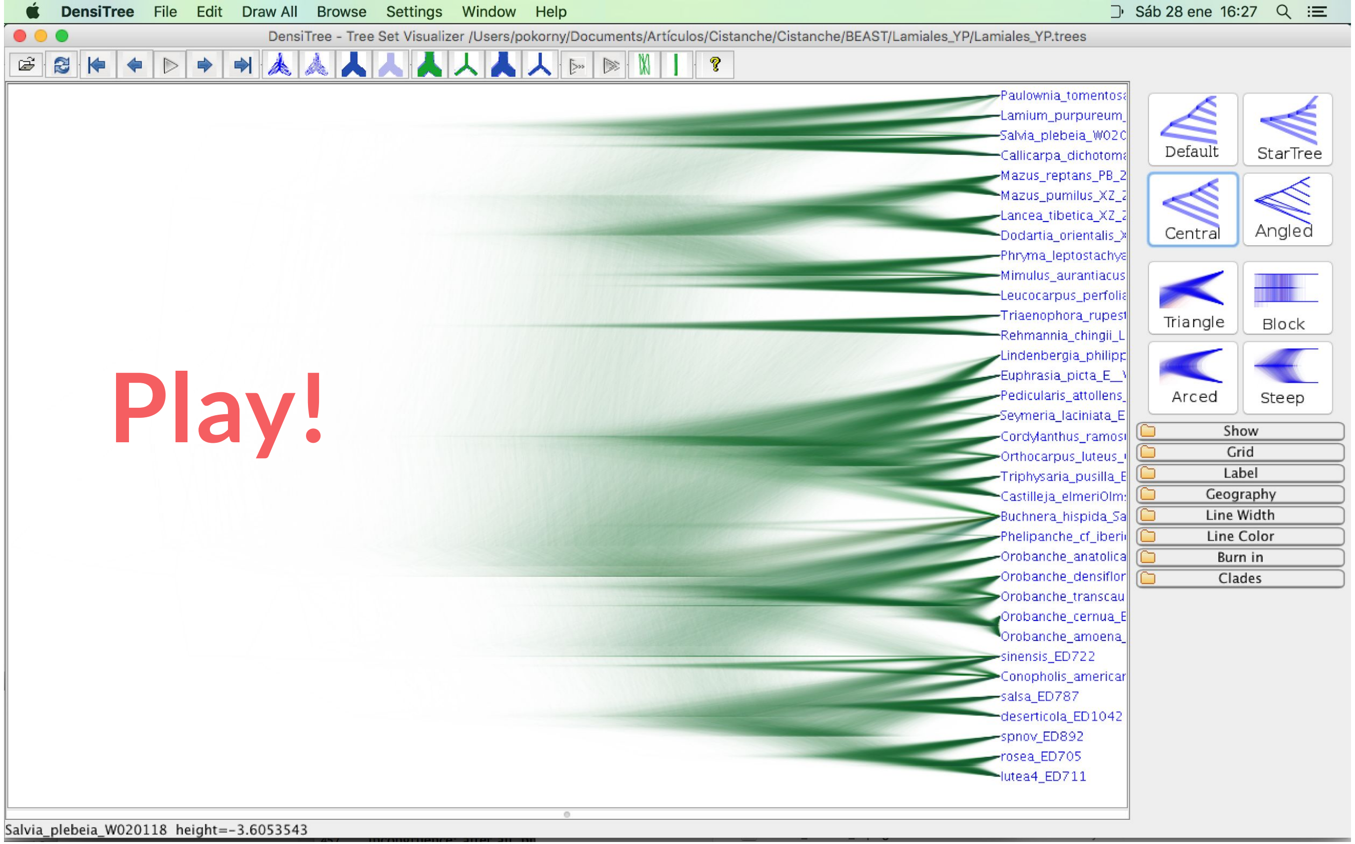


Status bar height=-75.0

Options here

More options here

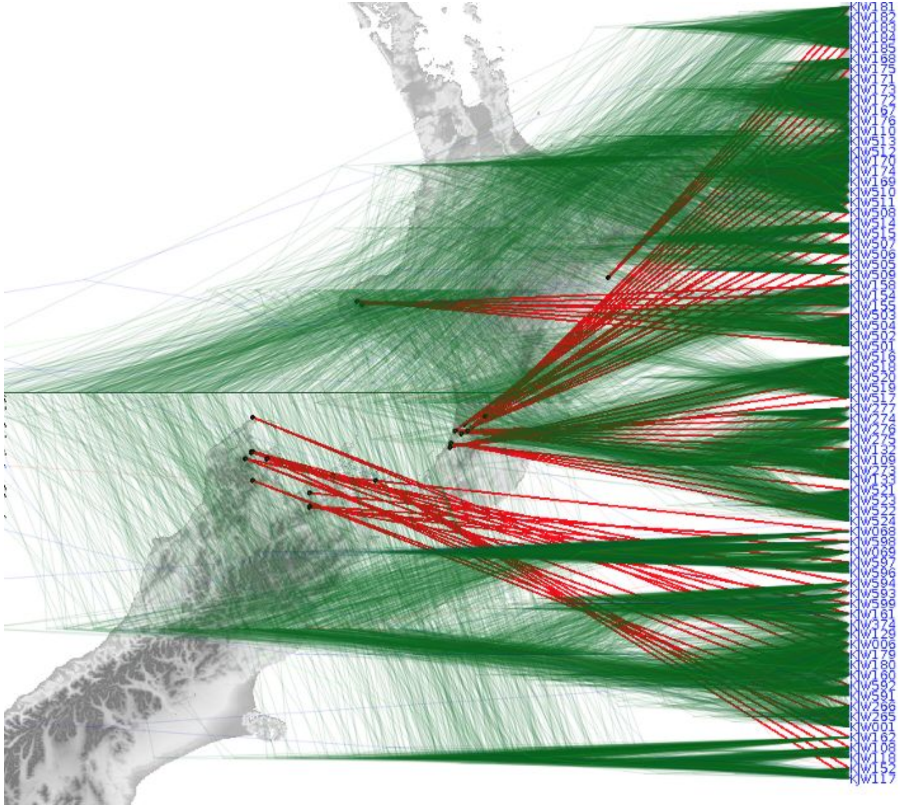
DensiTree



Salvia_plebeia_W020118 height=-3.6053543

Play!

Cloudogram...



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

Cloudogram Fail

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

Cloudogram...

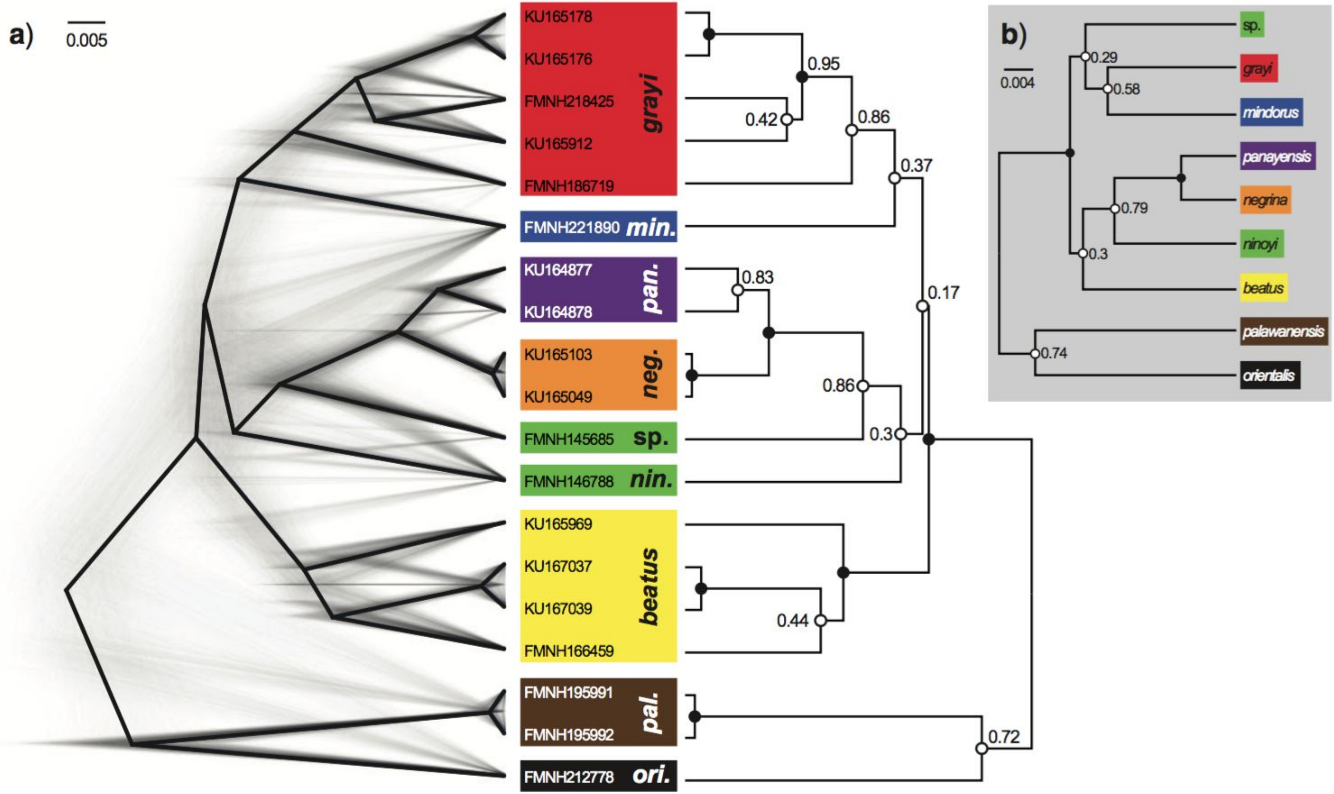


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

Cloudogram Success

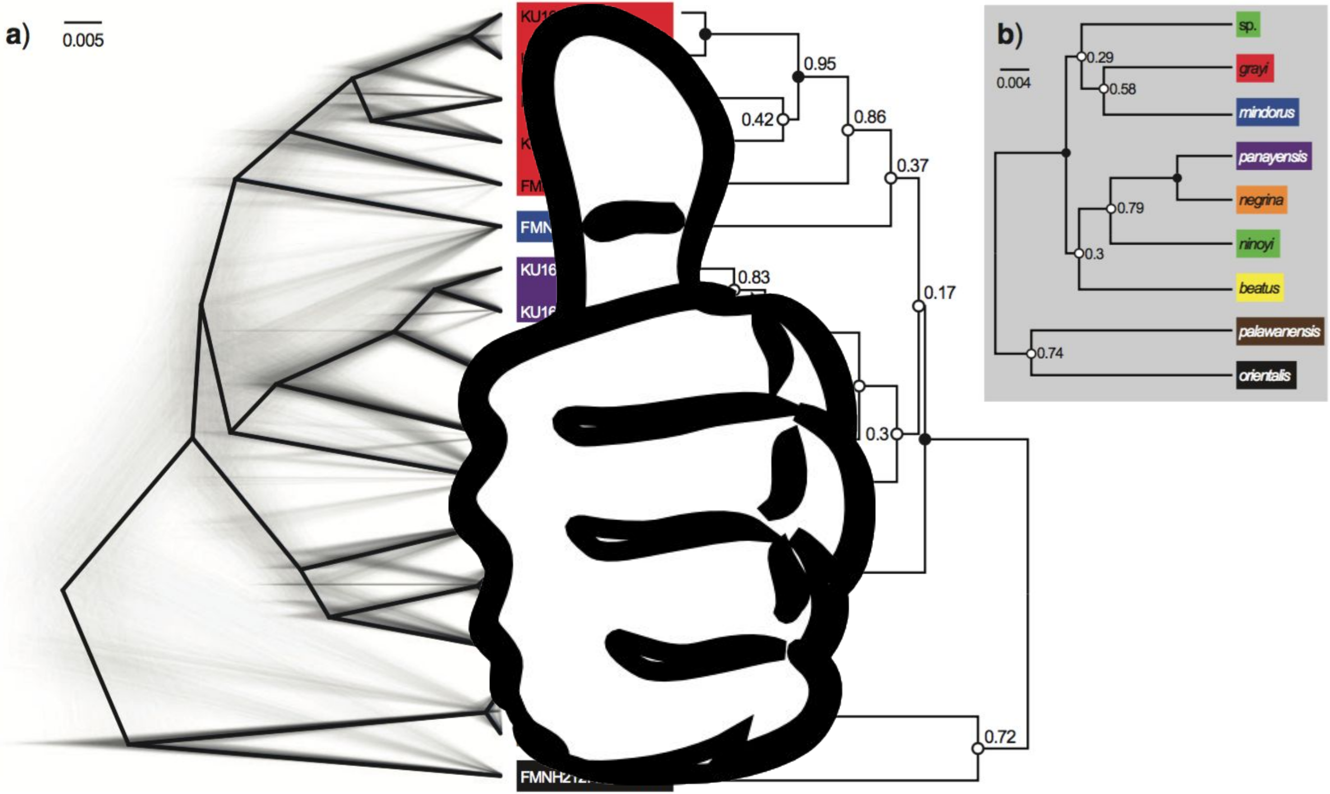


Fig. 3. Giarla & Esselstyn. 2015. *Syst. Biol.* 64(5):727–740.

Software

- **FigTree** @ http://tree.bio.ed.ac.uk/software/figtree/
- **DensiTree** @ https://www.cs.auckland.ac.nz/~remco/DensiTree/
- **TreeGraph2** @ http://treegraph.bioinfweb.info
- Others:
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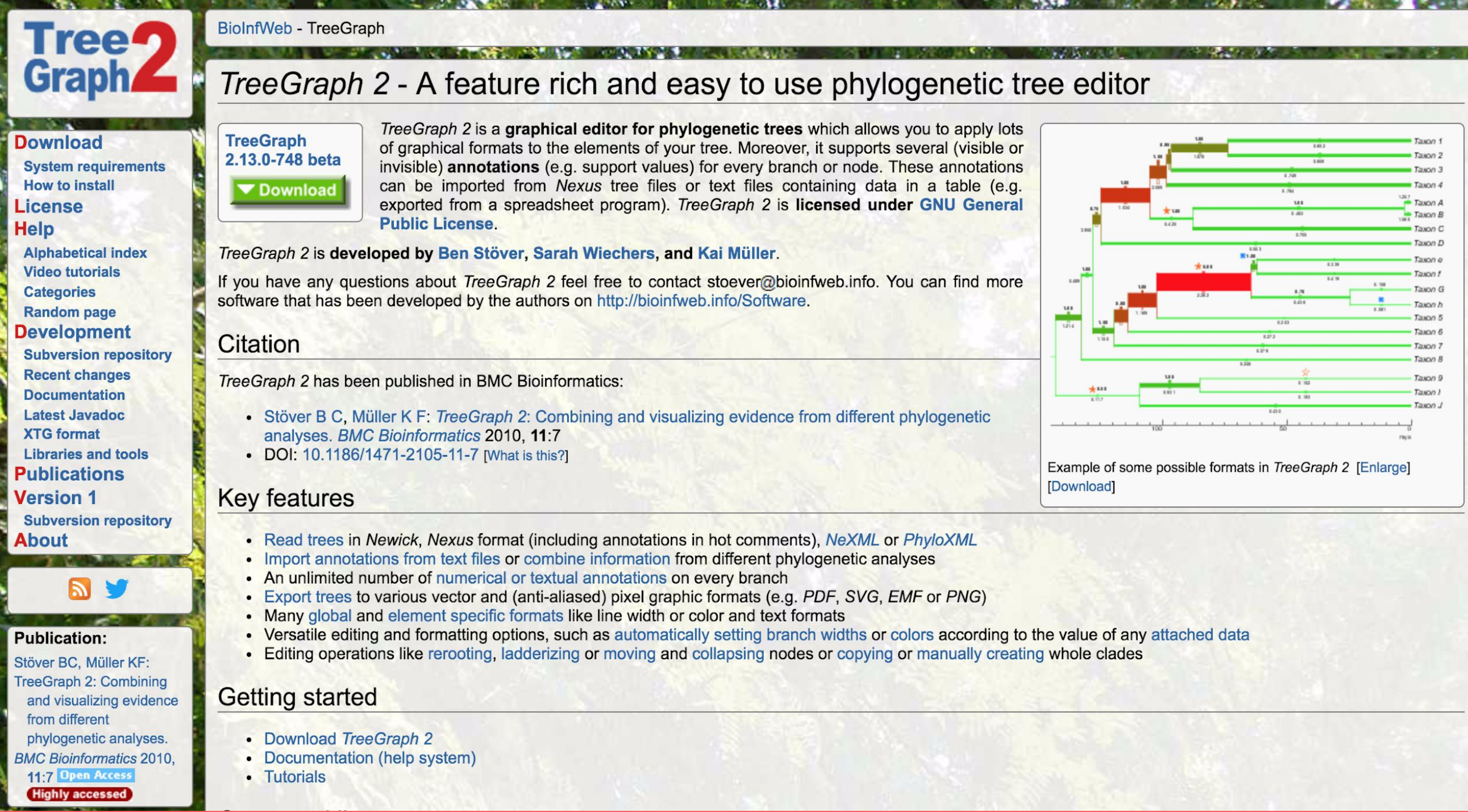
    - **NJplot** @ http://doua.prabi.fr/software/njplot
    - **Dendroscope** @ http://ab.inf.uni-tuebingen.de/software/dendroscope/
    - **SpreaD3** @ https://github.com/phylogeography/SpreaD3
    - **SeaView** @ http://doua.prabi.fr/software/seaview
    - etc.



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

BioInfWeb - TreeGraph

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

TreeGraph 2.13.0-748 beta

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. You can find more software that has been developed by the authors on http://bioinfweb.info/Software.

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

Citation

TreeGraph 2 has been published in BMC Bioinformatics:

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

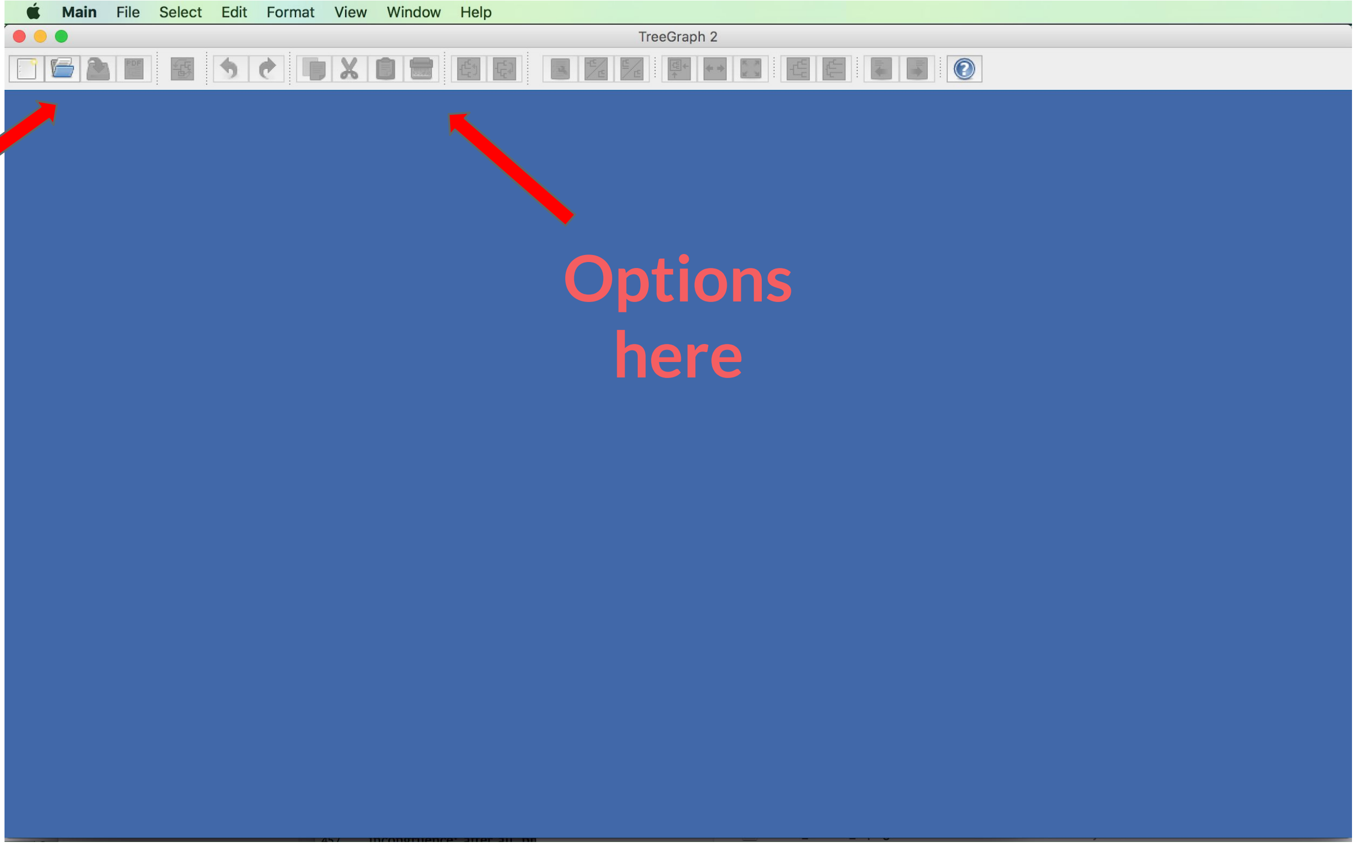
Key features

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

Getting started

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

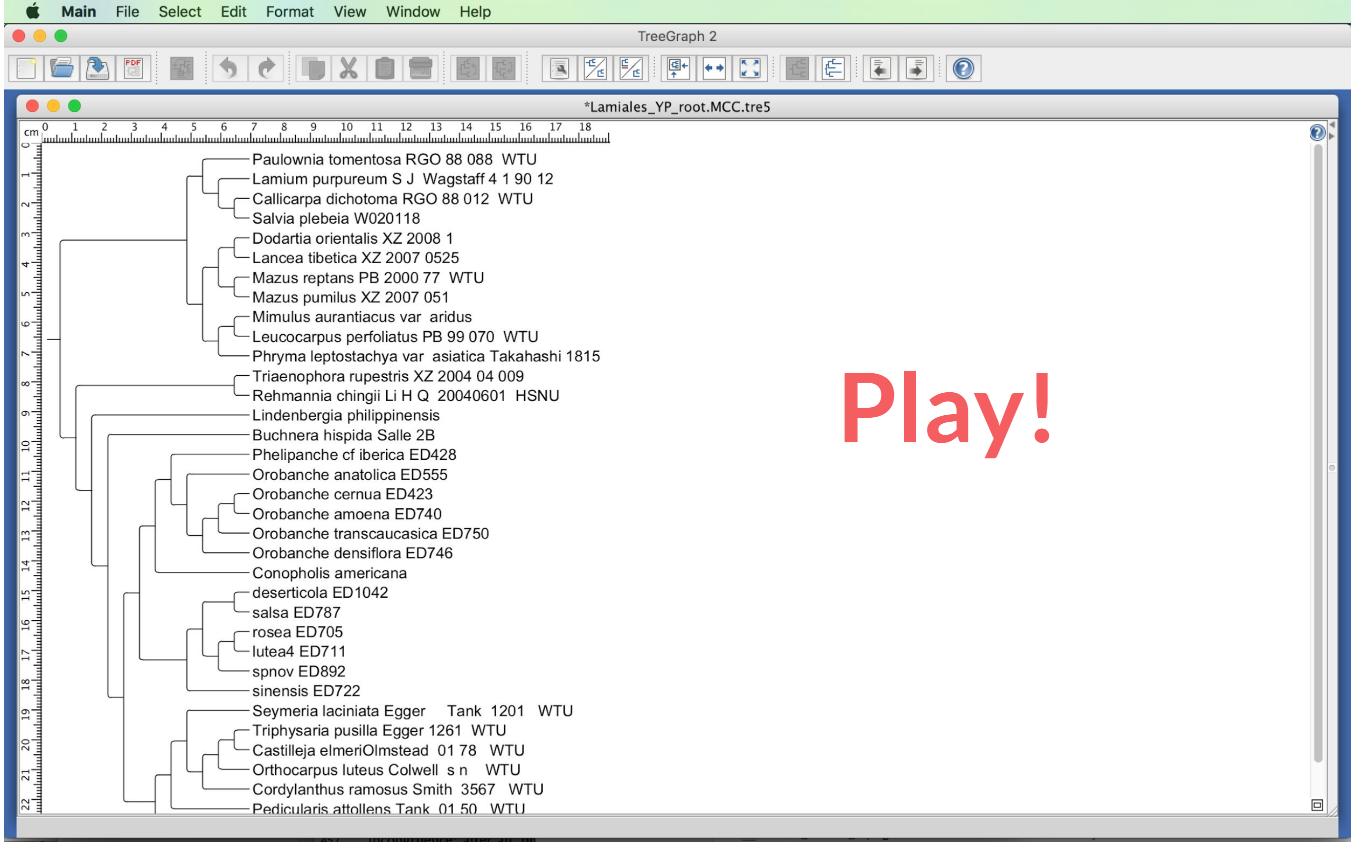
TreeGraph 2



Open files here

Options here

TreeGraph 2



Play!

TreeGraph 2 – Documentation

Feature overview

The application

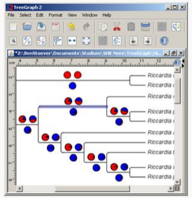
- Main menu
- Tool bar
- Document window
- Synchronizing tree selections

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

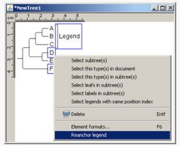
- Element formats
- Document formats
- Set colors by node/branch data (Allows you to display annotations as colors.)
- Set distance values by node/branch data (Allows you to display annotations e.g. as branch widths or text heights.)
- Scaling distance values
- Automatically position labels

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

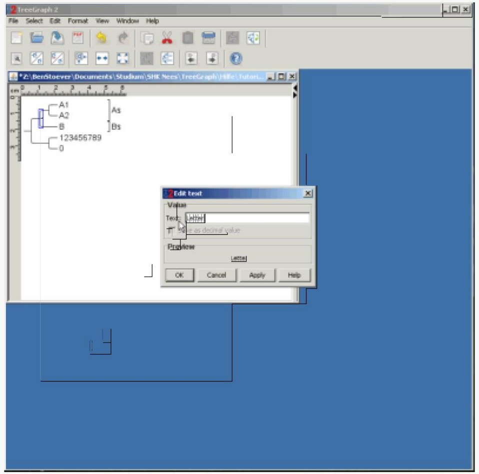
- Inserting nodes
- Collapsing nodes
- Collapsing nodes by support
- Anchoring legends
- Copying/cutting document elements
- Laddering
- Sorting terminal nodes
- Moving nodes
- Rerooting
- Editing text element values
- Changing branch lengths
- Replace text in node/branch data



Video tutorials

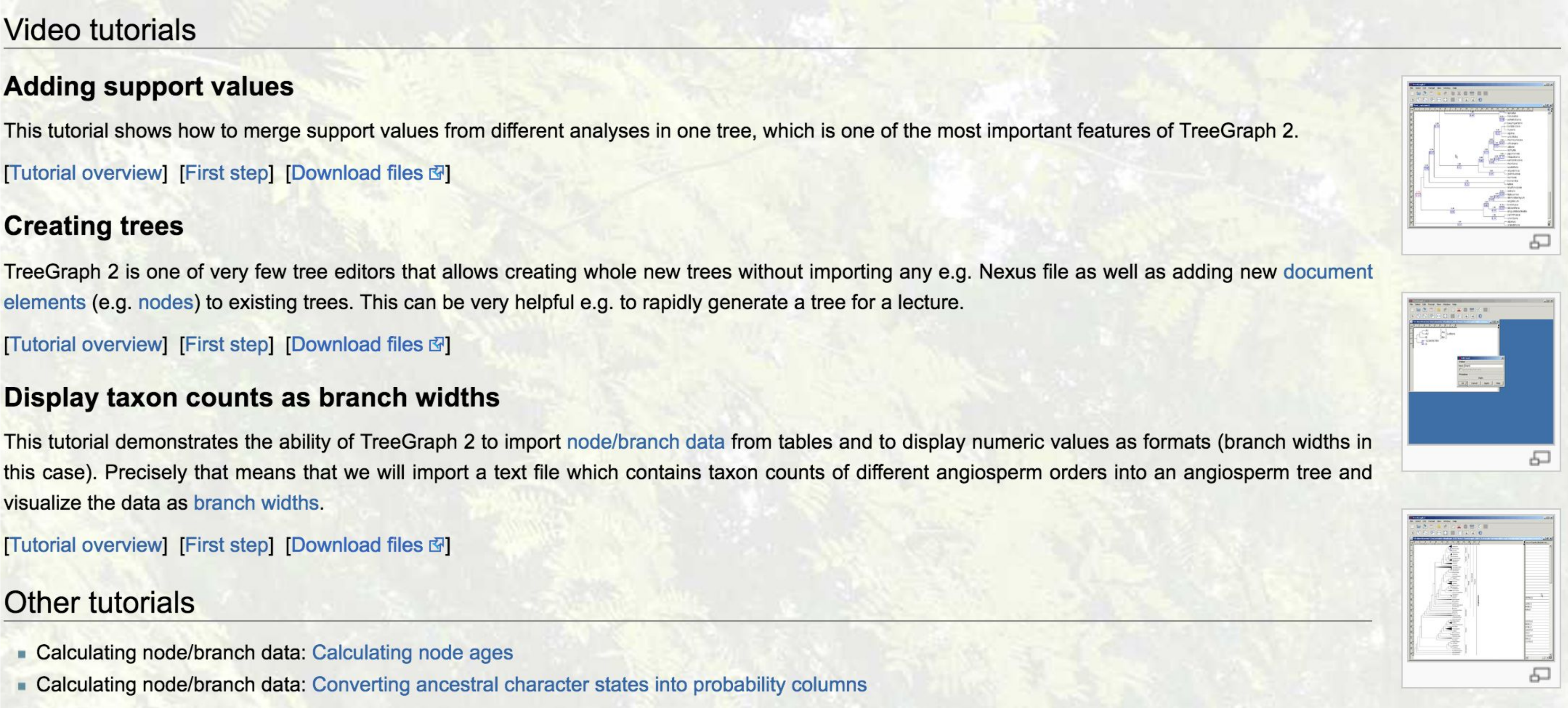
In addition to the articles on single features a set of screencasts is provided that allow you to learn how to use TreeGraph 2 step by step. Currently the following screencasts are available:

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



Additional tutorials can be found at the tutorial main page.

TreeGraph 2 – Video Tutorials



Video tutorials

Adding support values

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

[Tutorial overview] [First step] [Download files]

Creating trees

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

[Tutorial overview] [First step] [Download files]

Display taxon counts as branch widths

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

[Tutorial overview] [First step] [Download files]

Other tutorials

- Calculating node/branch data: Calculating node ages
- Calculating node/branch data: Converting ancestral character states into probability columns

Phylogenetic Tree Visualization

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

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

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:

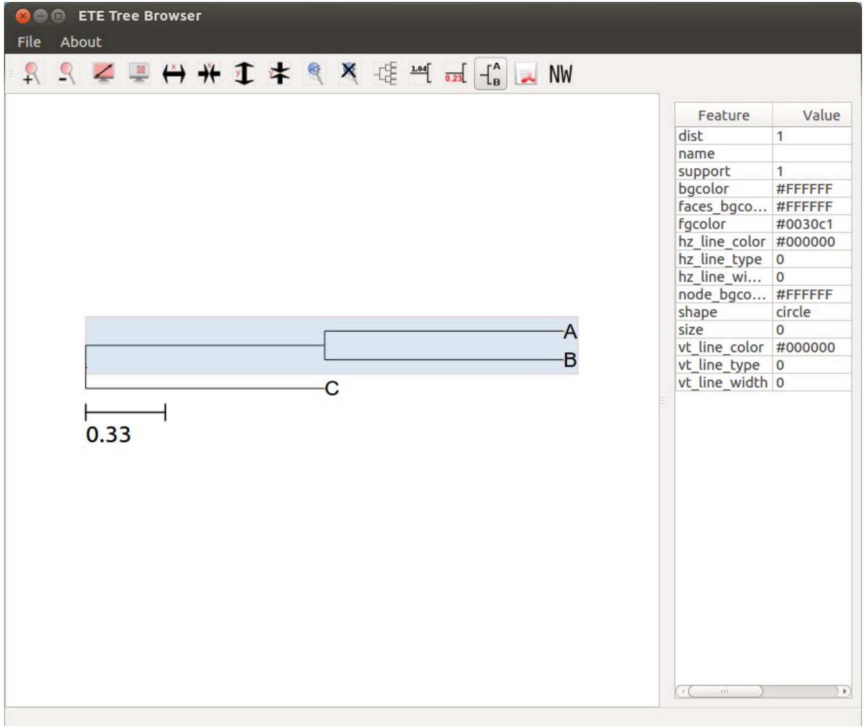
(((**A**:0.1,**B**:0.2)90:0.2,(**C**:0.1,**D**:0.2)80:0.15)70:0.1,**E**:0.2);

ETE3

Default visualization tool:

ete3 view -t INPUT

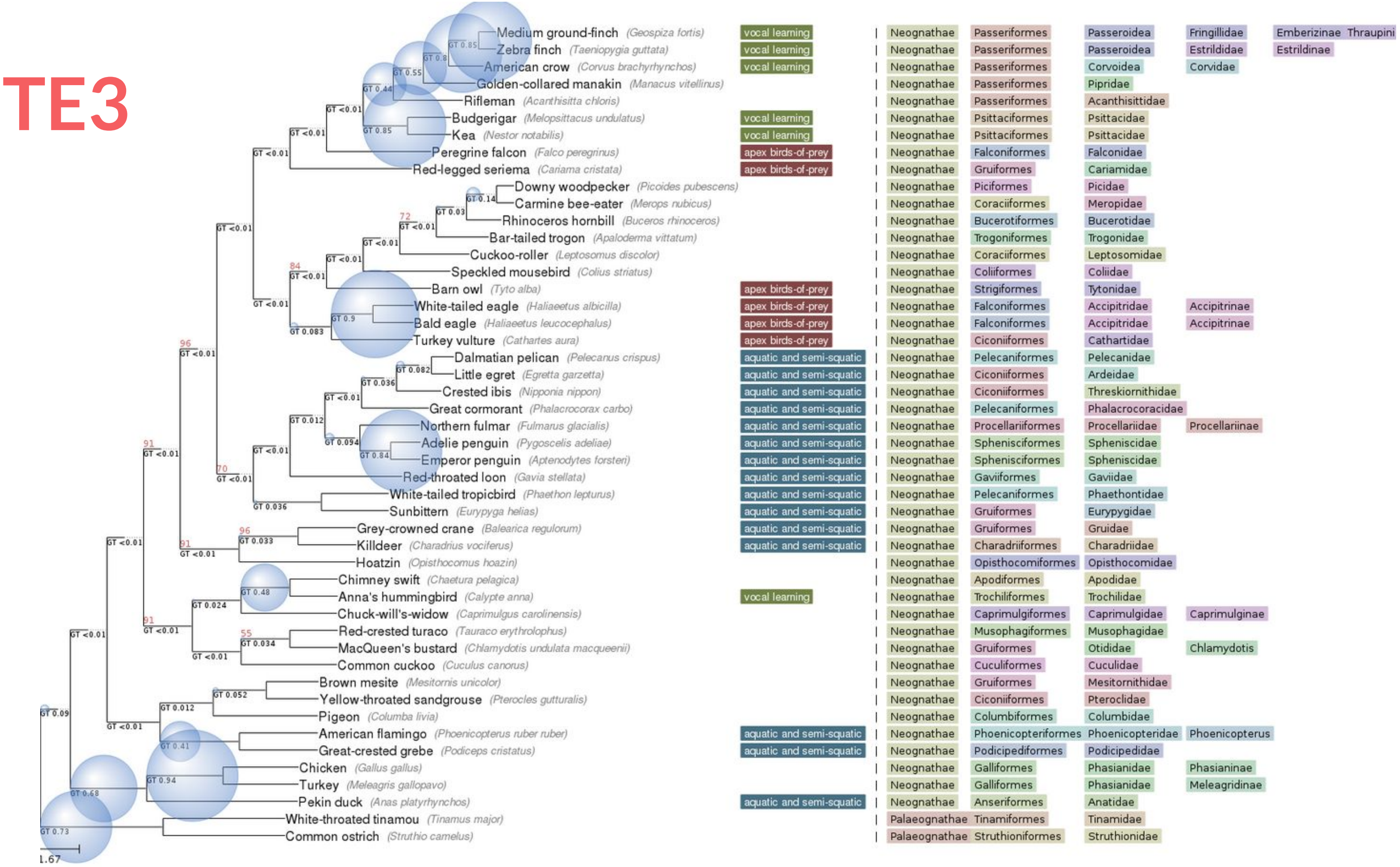
Where the INPUT can be a text string of a newick or a file containing a newick



Feature	Value
dist	1
name	
support	1
bgcolor	#FFFFFF
faces_bgco...	#FFFFFF
fgcolor	#0030c1
hz_line_color	#000000
hz_line_type	0
hz_line_wi...	0
node_bgco...	#FFFFFF
shape	circle
size	0
vt_line_color	#000000
vt_line_type	0
vt_line_width	0

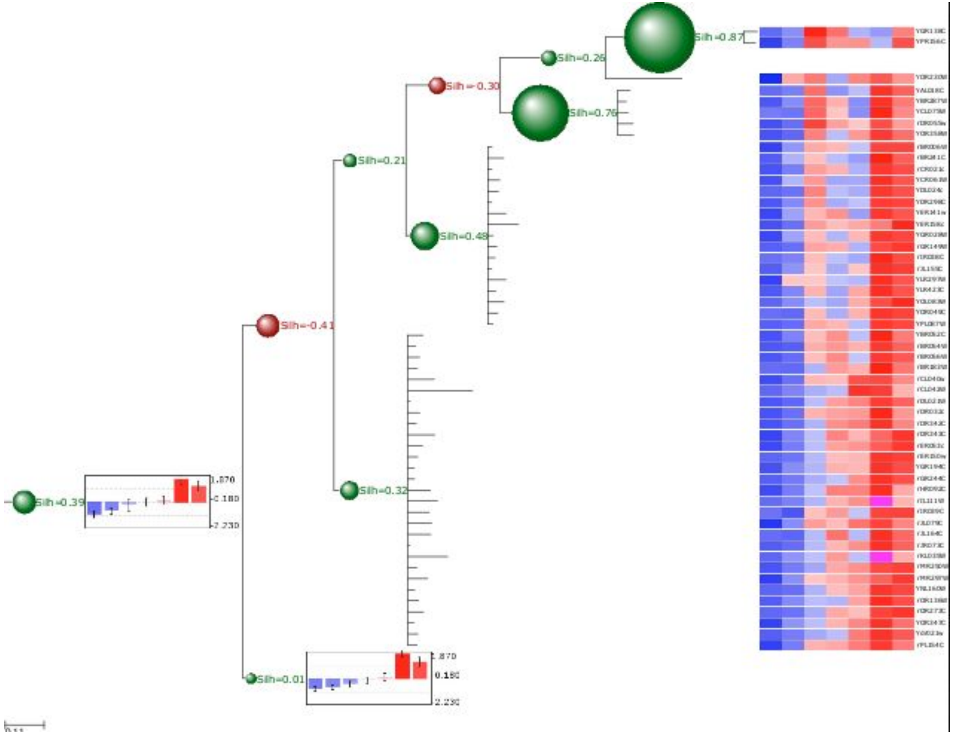
While nice, the default visualization tool is limited

ETE3

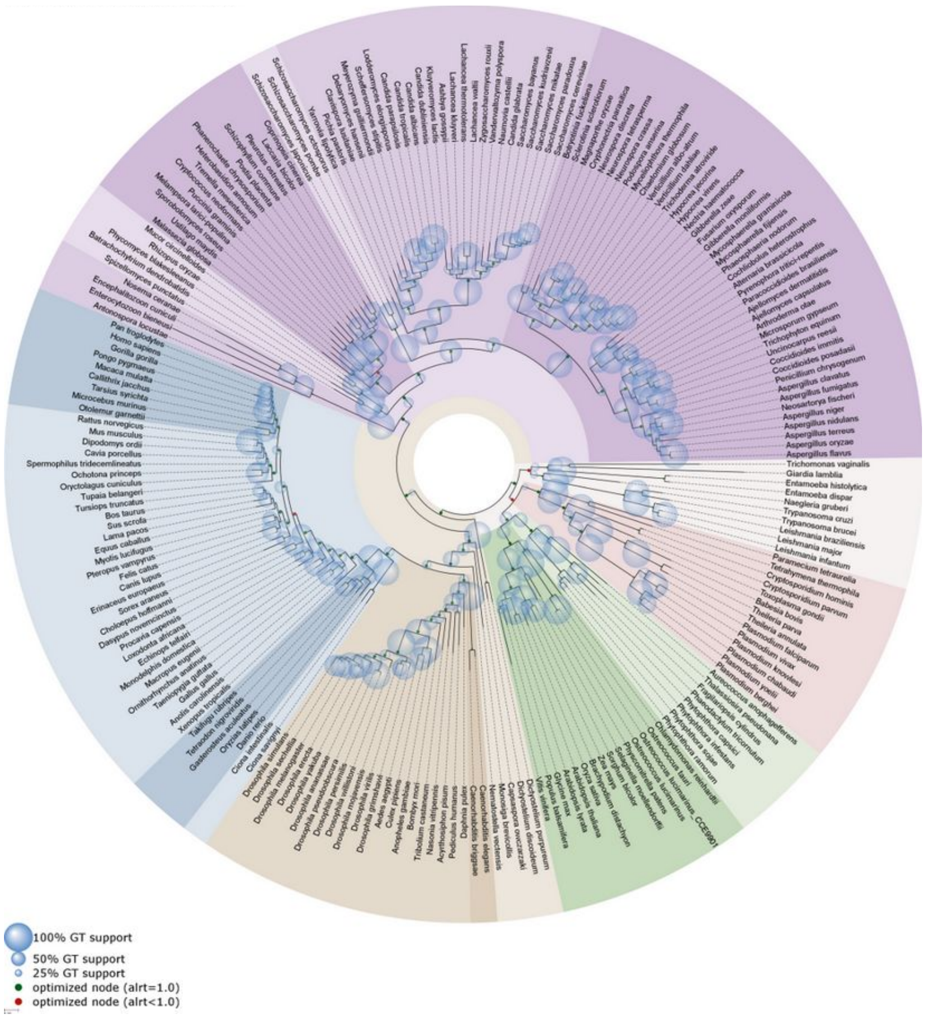


Medium ground-finch (Geospiza fortis) | vocal learning | Neognathae | Passeriformes | Passeroidea | Fringillidae | Emberizinae Thraupini
Zebra finch (Taeniopygia guttata) | vocal learning | Neognathae | Passeriformes | Passeroidea | Estrildidae | Estrildinae
American crow (Corvus brachyrhynchos) | vocal learning | Neognathae | Passeriformes | Corvoidea | Corvidae
Golden-collared manakin (Manacus vitellinus) | Neognathae | Passeriformes | Pipridae
Rifleman (Acanthisitta chloris) | Neognathae | Passeriformes | Acanthisittidae
Budgerigar (Melopsittacus undulatus) | vocal learning | Neognathae | Psittaciformes | Psittacidae
Kea (Nestor notabilis) | vocal learning | Neognathae | Psittaciformes | Psittacidae
Peregrine falcon (Falco peregrinus) | apex birds-of-prey | Neognathae | Falconiformes | Falconidae
Red-legged seriema (Cariama cristata) | apex birds-of-prey | Neognathae | Gruiformes | Cariamidae
Downy woodpecker (Picoides pubescens) | Neognathae | Piciformes | Picidae
Carmine bee-eater (Merops nubicus) | Neognathae | Coraciiformes | Meropidae
Rhinoceros hornbill (Buceros rhinoceros) | Neognathae | Bucerotiformes | Bucerotidae
Bar-tailed trogon (Apaloderma vittatum) | Neognathae | Trogoniformes | Trogonidae
Cuckoo-roller (Leptosomus discolor) | Neognathae | Coraciiformes | Leptosomidae
Speckled mousebird (Colius striatus) | Neognathae | Coliiformes | Coliidae
Barn owl (Tyto alba) | apex birds-of-prey | Neognathae | Strigiformes | Tytonidae
White-tailed eagle (Haliaeetus albicilla) | apex birds-of-prey | Neognathae | Falconiformes | Accipitridae | Accipitrinae
Bald eagle (Haliaeetus leucocephalus) | apex birds-of-prey | Neognathae | Falconiformes | Accipitridae | Accipitrinae
Turkey vulture (Cathartes aura) | apex birds-of-prey | Neognathae | Ciconiiformes | Cathartidae
Dalmatian pelican (Pelecanus crispus) | aquatic and semi-squatic | Neognathae | Pelecaniformes | Pelecanidae
Little egret (Egretta garzetta) | aquatic and semi-squatic | Neognathae | Ciconiiformes | Ardeidae
Crested ibis (Nipponia nippon) | aquatic and semi-squatic | Neognathae | Ciconiiformes | Threskiornithidae
Great cormorant (Phalacrocorax carbo) | aquatic and semi-squatic | Neognathae | Pelecaniformes | Phalacrocoracidae
Northern fulmar (Fulmarus glacialis) | aquatic and semi-squatic | Neognathae | Procellariiformes | Procellariidae | Procellariinae
Adelie penguin (Pygoscelis adeliae) | aquatic and semi-squatic | Neognathae | Sphenisciformes | Spheniscidae
Emperor penguin (Aptenodytes forsteri) | aquatic and semi-squatic | Neognathae | Sphenisciformes | Spheniscidae
Red-throated loon (Gavia stellata) | aquatic and semi-squatic | Neognathae | Gaviiformes | Gaviidae
White-tailed tropicbird (Phaethon lepturus) | aquatic and semi-squatic | Neognathae | Pelecaniformes | Phaethontidae
Sunbittern (Eurypyga helias) | aquatic and semi-squatic | Neognathae | Gruiformes | Eurypygidae
Grey-crowned crane (Balearica regulorum) | aquatic and semi-squatic | Neognathae | Gruiformes | Gruidae
Killdeer (Charadrius vociferus) | aquatic and semi-squatic | Neognathae | Charadriiformes | Charadriidae
Hoatzin (Opisthocomus hoazin) | Neognathae | Opisthocomiformes | Opisthocomidae
Chimney swift (Chaetura pelagica) | Neognathae | Apodiformes | Apodidae
Anna's hummingbird (Calypte anna) | vocal learning | Neognathae | Trochiliformes | Trochilidae
Chuck-will's-widow (Caprimulgus carolinensis) | Neognathae | Caprimulgiformes | Caprimulgidae | Caprimulginae
Red-crested turaco (Tauraco erythrolophus) | Neognathae | Musophagiformes | Musophagidae
MacQueen's bustard (Chlamydotis undulata macqueenii) | Neognathae | Gruiformes | Otididae | Chlamydotis
Common cuckoo (Cuculus canorus) | Neognathae | Cuculiformes | Cuculidae
Brown mesite (Mesitornis unicolor) | Neognathae | Gruiformes | Mesitornithidae
Yellow-throated sandgrouse (Pterocles gutturalis) | Neognathae | Ciconiiformes | Pteroclidae
Pigeon (Columba livia) | Neognathae | Columbiformes | Columbidae
American flamingo (Phoenicopterus ruber ruber) | aquatic and semi-squatic | Neognathae | Phoenicopteriformes | Phoenicopteridae | Phoenicopterus
Great-crested grebe (Podiceps cristatus) | aquatic and semi-squatic | Neognathae | Podicipediformes | Podicipedidae
Chicken (Gallus gallus) | Neognathae | Galliformes | Phasianidae | Phasianinae
Turkey (Meleagris gallopavo) | Neognathae | Galliformes | Phasianidae | Meleagridinae
Pekin duck (Anas platyrhynchos) | aquatic and semi-squatic | Neognathae | Anseriformes | Anatidae
White-throated tinamou (Tinamus major) | Palaeognathae | Tinamiformes | Tinamidae
Common ostrich (Struthio camelus) | Palaeognathae | Struthioniformes | Struthionidae
GT 0.85
GT 0.8
GT 0.55
GT 0.44
GT <0.01
GT 0.85
GT 0.14
GT 0.03
72
GT 0.9
GT 0.083
84
96
GT 0.082
GT 0.036
GT 0.012
GT 0.094
GT 0.84
91
70
GT 0.036
96
GT 0.033
GT 0.48
GT 0.024
55
GT 0.034
GT 0.052
GT 0.012
GT 0.41
GT 0.94
GT 0.68
GT 0.09
GT 0.73
1.67

ETE3



Silh=0.87
Silh=0.26
Silh=-0.30
Silh=0.76
Silh=0.21
Silh=0.48
Silh=-0.41
Silh=0.32
Silh=0.39
1.870
0.180
-2.230
Silh=0.01
1.870
0.180
-2.230

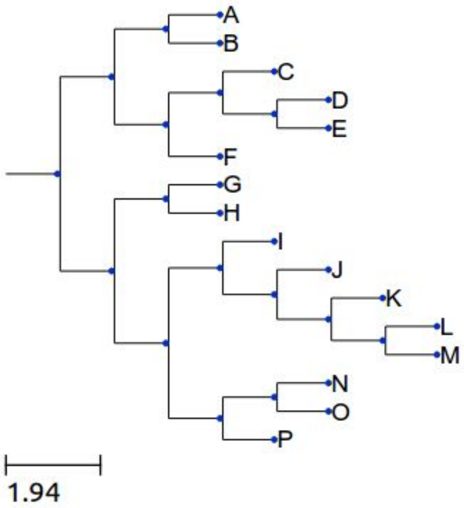


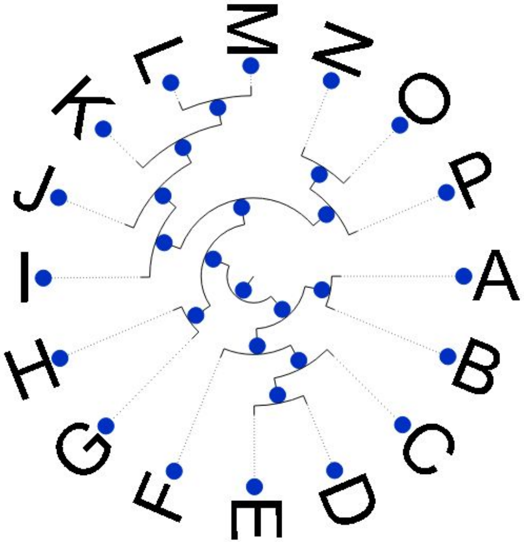
100% GT support
50% GT support
25% GT support
optimized node (alrt=1.0)
optimized node (alrt<1.0)

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:



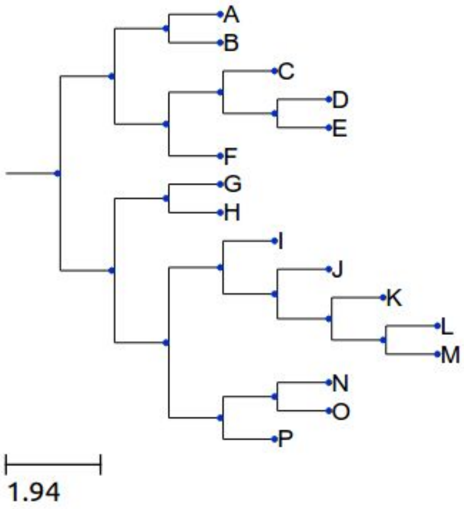


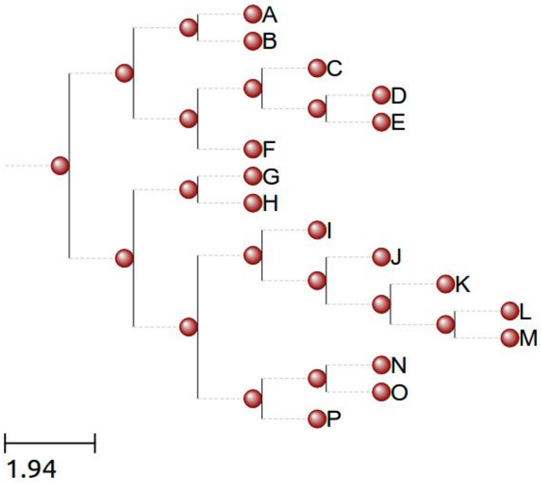
It can also change whether it shows things such as branch lengths, support, leaf names.

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

NodeStyles

- NodeStyle like treeStyle affects the visualization of individual nodes:

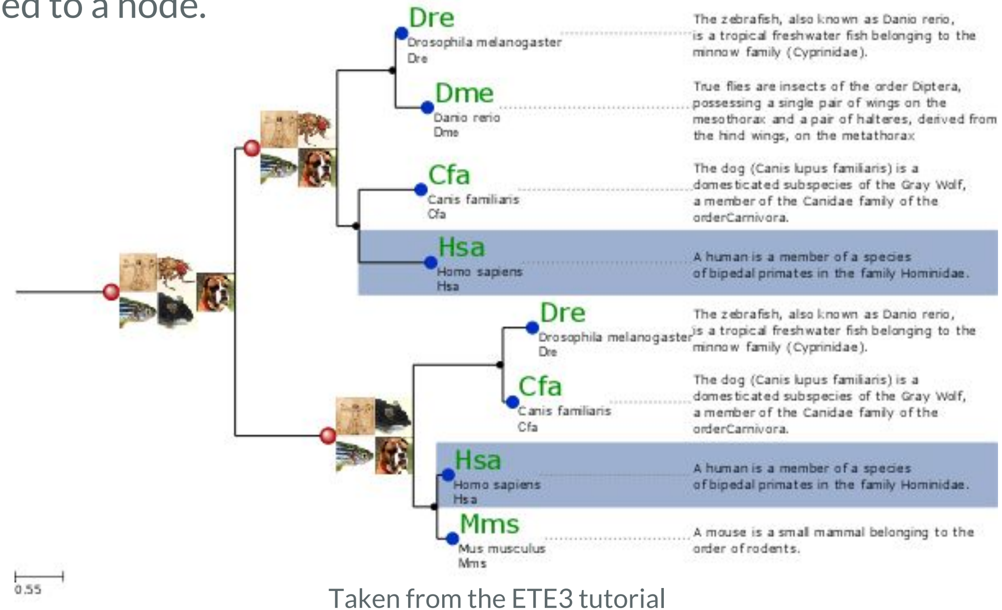




- For instance, the default style for nodes in ETE3 is that they are represented with a blue dot
- This can be modified by calling the node instance and changing some of the characteristics in the node style such as colour or size
- Useful tip: if you don’t want them, change the size ot 0

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.



The zebrafish, also known as Danio rerio, is a tropical freshwater fish belonging to the minnow family (Cyprinidae).

True flies are insects of the order Diptera, possessing a single pair of wings on the mesothorax and a pair of halteres, derived from the hind wings, on the metathorax

The dog (Canis lupus familiaris) is a domesticated subspecies of the Gray Wolf, a member of the Canidae family of the orderCarnivora.

A human is a member of a species of bipedal primates in the family Hominidae.

The zebrafish, also known as Danio rerio, is a tropical freshwater fish belonging to the minnow family (Cyprinidae).

The dog (Canis lupus familiaris) is a domesticated subspecies of the Gray Wolf, a member of the Canidae family of the orderCarnivora.

A human is a member of a species of bipedal primates in the family Hominidae.

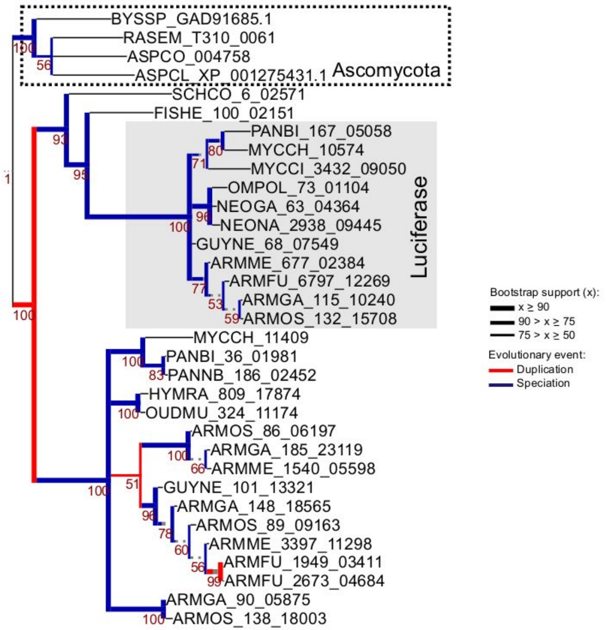
A mouse is a small mammal belonging to the order of rodents.

Taken from the ETE3 tutorial

ETE3

Layouts

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

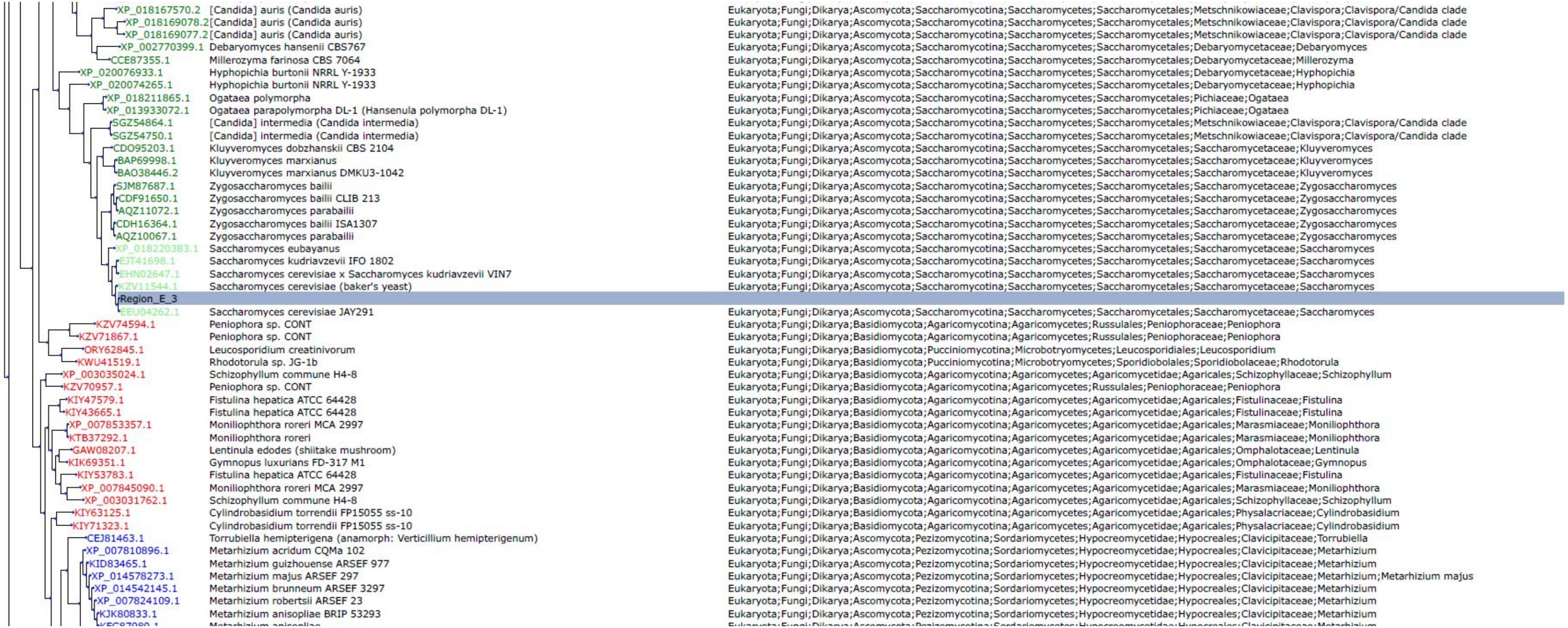


This layout detected the support of each node. If it was below 50 it deleted the node, then it assigned different branch thickness depending on the support. It also coloured the branches according to evolutionary relationships.
It deleted the internal node figure and added node support to the image.

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

ETE3

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



XP_018167570.2	[Candida] auris (Candida auris)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Metschnikowiaceae;Clavispora;Clavispora/Candida clade
XP_018169078.2	[Candida] auris (Candida auris)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Metschnikowiaceae;Clavispora;Clavispora/Candida clade
XP_018169077.2	[Candida] auris (Candida auris)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Metschnikowiaceae;Clavispora;Clavispora/Candida clade
XP_002770399.1	Debaryomyces hansenii CBS767	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Debaryomycetaceae;Debaryomyces
CCE87355.1	Millerozyma farinosa CBS 7064	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Debaryomycetaceae;Millerozyma
XP_020076933.1	Hyphopichia burtonii NRRL Y-1933	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Debaryomycetaceae;Hyphopichia
XP_020074265.1	Hyphopichia burtonii NRRL Y-1933	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Debaryomycetaceae;Hyphopichia
XP_018211865.1	Ogataea polymorpha	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Pichiaceae;Ogataea
XP_013933072.1	Ogataea parapolymorpha DL-1 (Hansenula polymorpha DL-1)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Pichiaceae;Ogataea
SGZ54864.1	[Candida] intermedia (Candida intermedia)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Metschnikowiaceae;Clavispora;Clavispora/Candida clade
SGZ54750.1	[Candida] intermedia (Candida intermedia)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Metschnikowiaceae;Clavispora;Clavispora/Candida clade
CDO95203.1	Kluyveromyces dobzhanskii CBS 2104	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Kluyveromyces
BAP69998.1	Kluyveromyces marxianus	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Kluyveromyces
BAO38446.2	Kluyveromyces marxianus DMKU3-1042	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Kluyveromyces
SJM87687.1	Zygosaccharomyces bailii	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Zygosaccharomyces
CDF91650.1	Zygosaccharomyces bailii CLIB 213	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Zygosaccharomyces
AQZ11072.1	Zygosaccharomyces parabailii	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Zygosaccharomyces
CDH16364.1	Zygosaccharomyces bailii ISA1307	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Zygosaccharomyces
AQZ10067.1	Zygosaccharomyces parabailii	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Zygosaccharomyces
XP_018220383.1	Saccharomyces eubayanus	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces
EJT41698.1	Saccharomyces kudriavzevii IFO 1802	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces
EHN02647.1	Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces
KZV11544.1	Saccharomyces cerevisiae (baker's yeast)	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces
Region_E_3		
EEU04262.1	Saccharomyces cerevisiae JAY291	Eukaryota;Fungi;Dikarya;Ascomycota;Saccharomycotina;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces
KZV74594.1	Peniophora sp. CONT	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Russulales;Peniophoraceae;Peniophora
KZV71867.1	Peniophora sp. CONT	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Russulales;Peniophoraceae;Peniophora
ORY62845.1	Leucosporidium creatinivorum	Eukaryota;Fungi;Dikarya;Basidiomycota;Pucciniomycotina;Microbotryomycetes;Leucosporidiales;Leucosporidium
KWU41519.1	Rhodotorula sp. JG-1b	Eukaryota;Fungi;Dikarya;Basidiomycota;Pucciniomycotina;Microbotryomycetes;Sporidiobolales;Sporidiobolaceae;Rhodotorula
XP_003035024.1	Schizophyllum commune H4-8	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Schizophyllaceae;Schizophyllum
KZV70957.1	Peniophora sp. CONT	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Russulales;Peniophoraceae;Peniophora
KIY47579.1	Fistulina hepatica ATCC 64428	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Fistulinaceae;Fistulina
KIY43665.1	Fistulina hepatica ATCC 64428	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Fistulinaceae;Fistulina
XP_007853357.1	Moniliophthora roreri MCA 2997	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Marasmiaceae;Moniliophthora
KTB37292.1	Moniliophthora roreri	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Marasmiaceae;Moniliophthora
GAW08207.1	Lentinula edodes (shiitake mushroom)	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Omphalotaceae;Lentinula
KIK69351.1	Gymnopus luxurians FD-317 M1	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Omphalotaceae;Gymnopus
KIY53783.1	Fistulina hepatica ATCC 64428	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Fistulinaceae;Fistulina
XP_007845090.1	Moniliophthora roreri MCA 2997	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Marasmiaceae;Moniliophthora
XP_003031762.1	Schizophyllum commune H4-8	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Schizophyllaceae;Schizophyllum
KIY63125.1	Cylindrobasidium torrendii FP15055 ss-10	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Physalacriaceae;Cylindrobasidium
KIY71323.1	Cylindrobasidium torrendii FP15055 ss-10	Eukaryota;Fungi;Dikarya;Basidiomycota;Agaricomycotina;Agaricomycetes;Agaricomycetidae;Agaricales;Physalacriaceae;Cylindrobasidium
CEJ81463.1	Torrubiella hemipterigena (anamorph: Verticillium hemipterigenum)	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Torrubiella
XP_007810896.1	Metarhizium acridum CQMa 102	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium
KID83465.1	Metarhizium guizhouense ARSEF 977	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium
XP_014578273.1	Metarhizium majus ARSEF 297	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium;Metarhizium majus
XP_014542145.1	Metarhizium brunneum ARSEF 3297	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium
XP_007824109.1	Metarhizium robertsii ARSEF 23	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium
KJK80833.1	Metarhizium anisopliae BRIP 53293	Eukaryota;Fungi;Dikarya;Ascomycota;Pezizomycotina;Sordariomycetes;Hypocreomycetidae;Hypocreales;Clavicipitaceae;Metarhizium

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

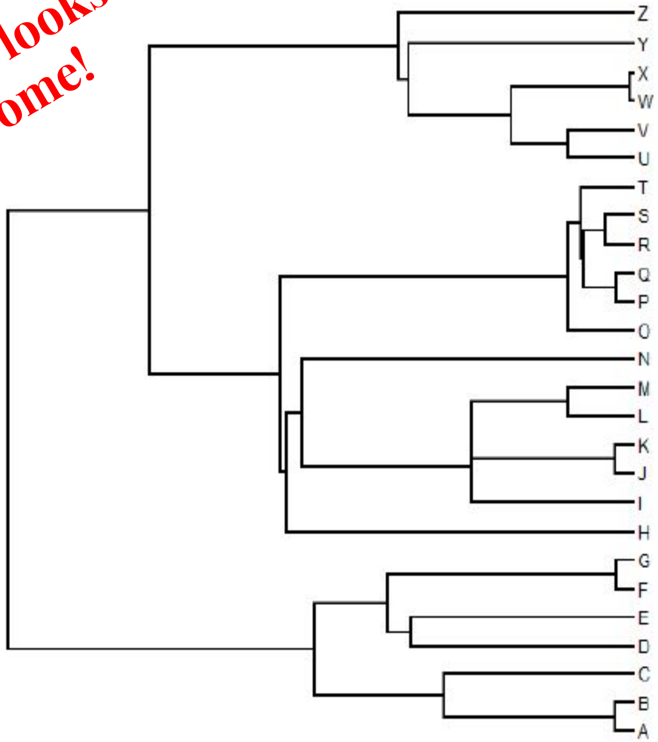
Now we load the package with:

```
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

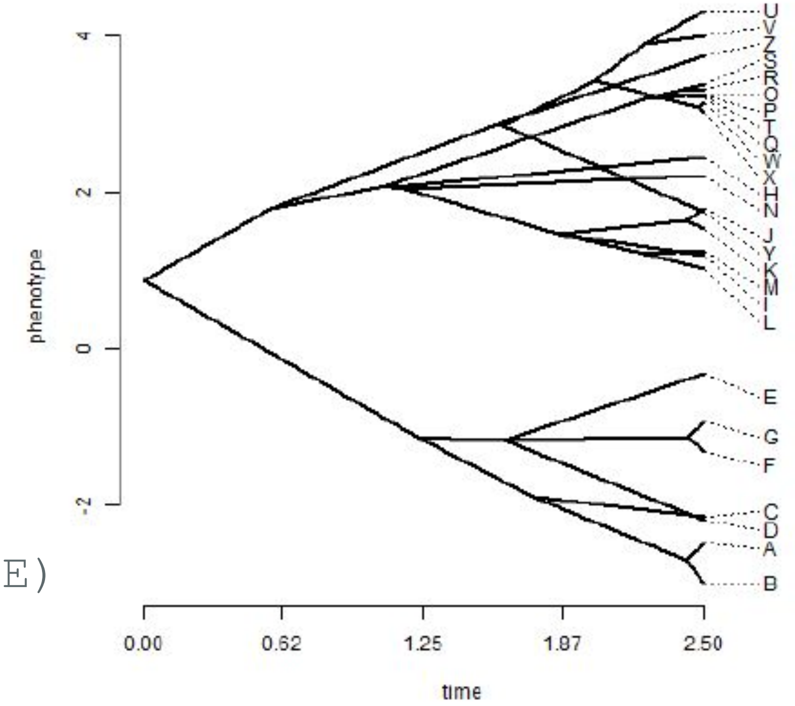
Now we plot a simple traitgram:

```
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)
```

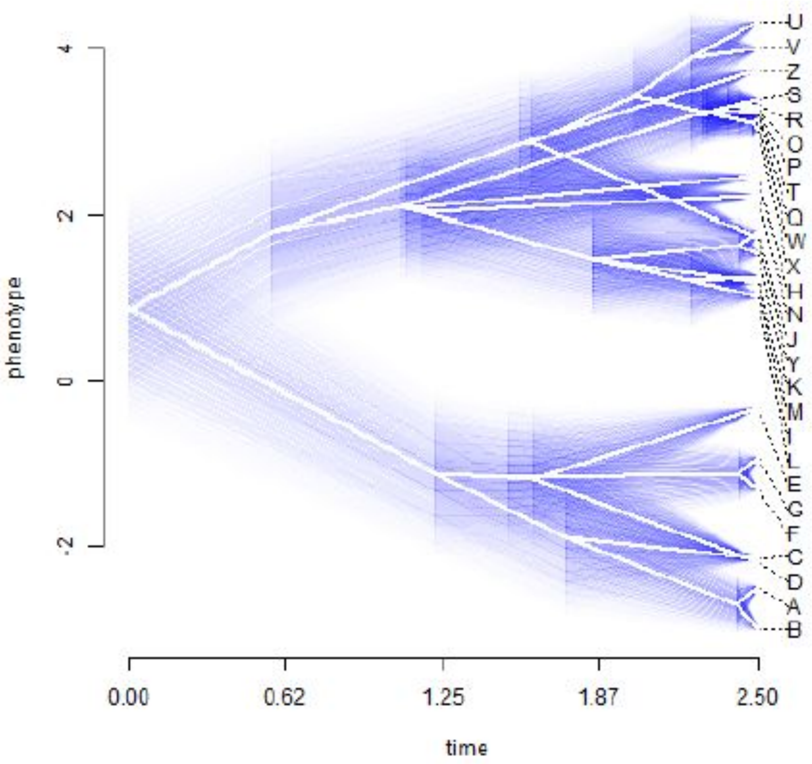
Phytools demo

Let’s try a heat map with our data:

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

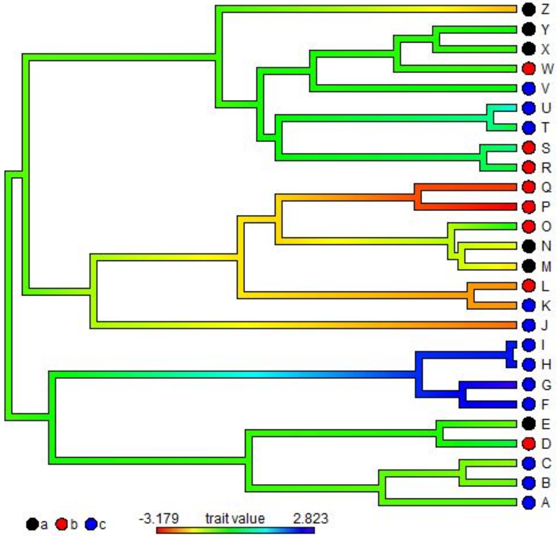
Now some hardcore stuff: Traitgram with the uncertainty of ancestral traits visualized using transparent probability density:

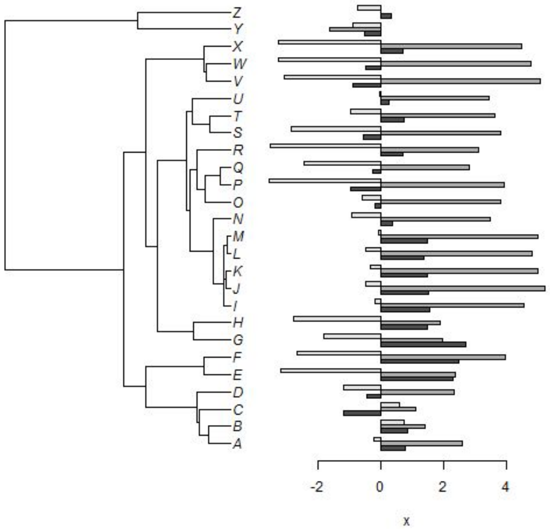
```
fancyTree(tree,type="phenogram95",x=x,spread.cost=c(1,0))
```

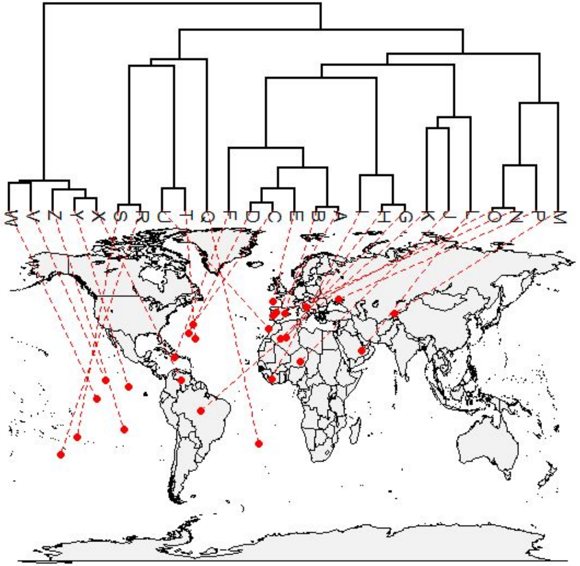


Much more here → http://www.phytools.org/Cordoba2017/ex/15/Plotting-methods.html

Phytools Examples

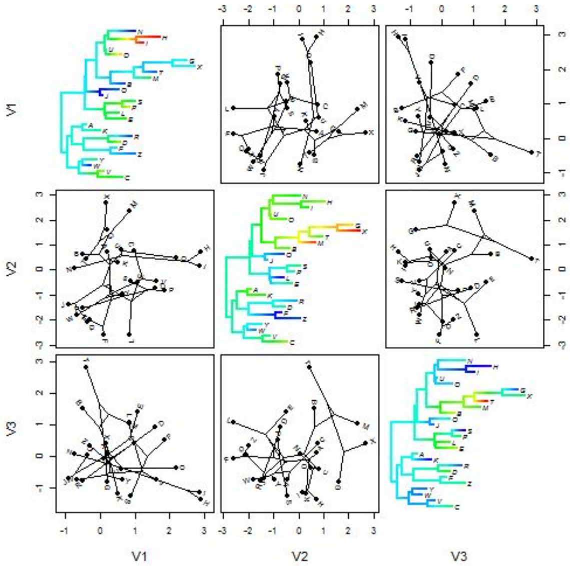


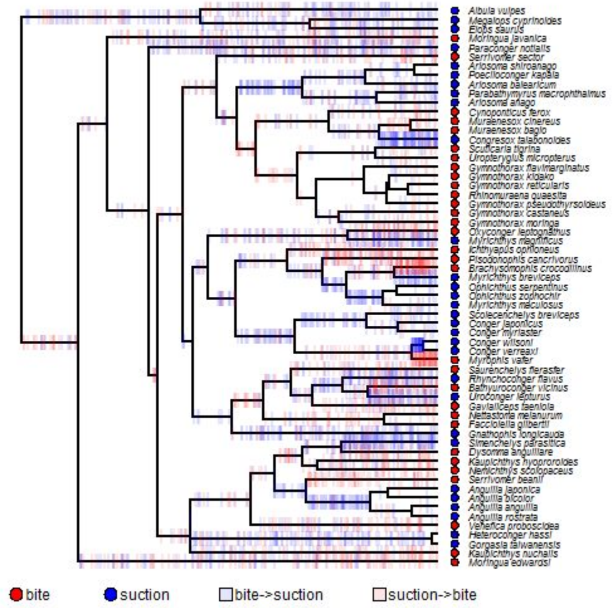




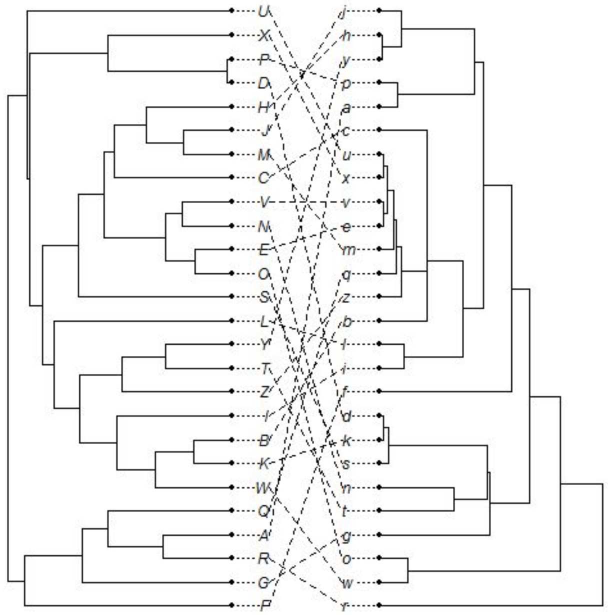
http://blog.phytools.org/

Phytools Examples





● bite ● suction ☐ bite->suction ☐ suction->bite



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.

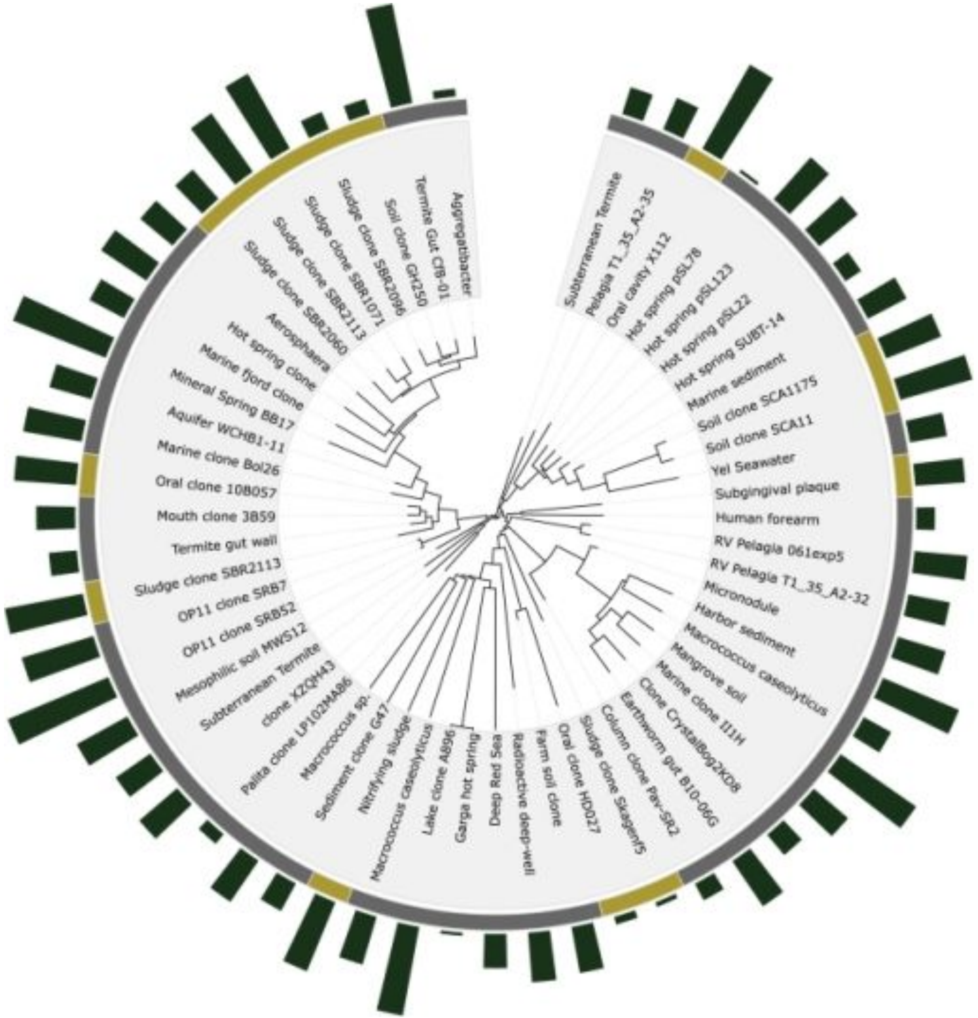
jsPhyloSVG

JavaScript based

Much more focused on user side web visualization

Very simple syntax

A bit limited compared to other options

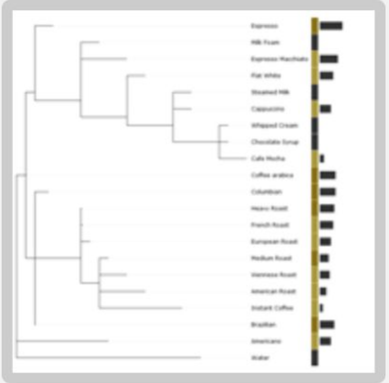


How can jsPhyloSVG help me?

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

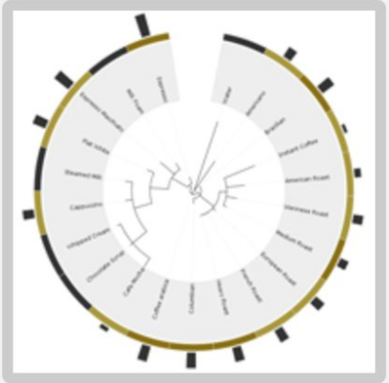
Here is a quick example of how to render a **rectangular** phylogenetic tree:

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



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

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

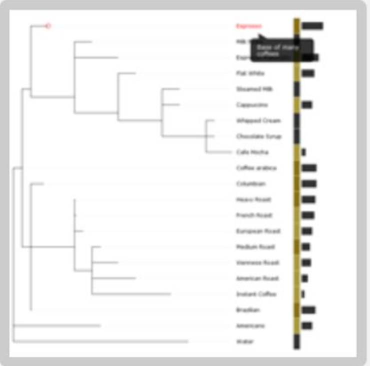


What about interactive features?

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:

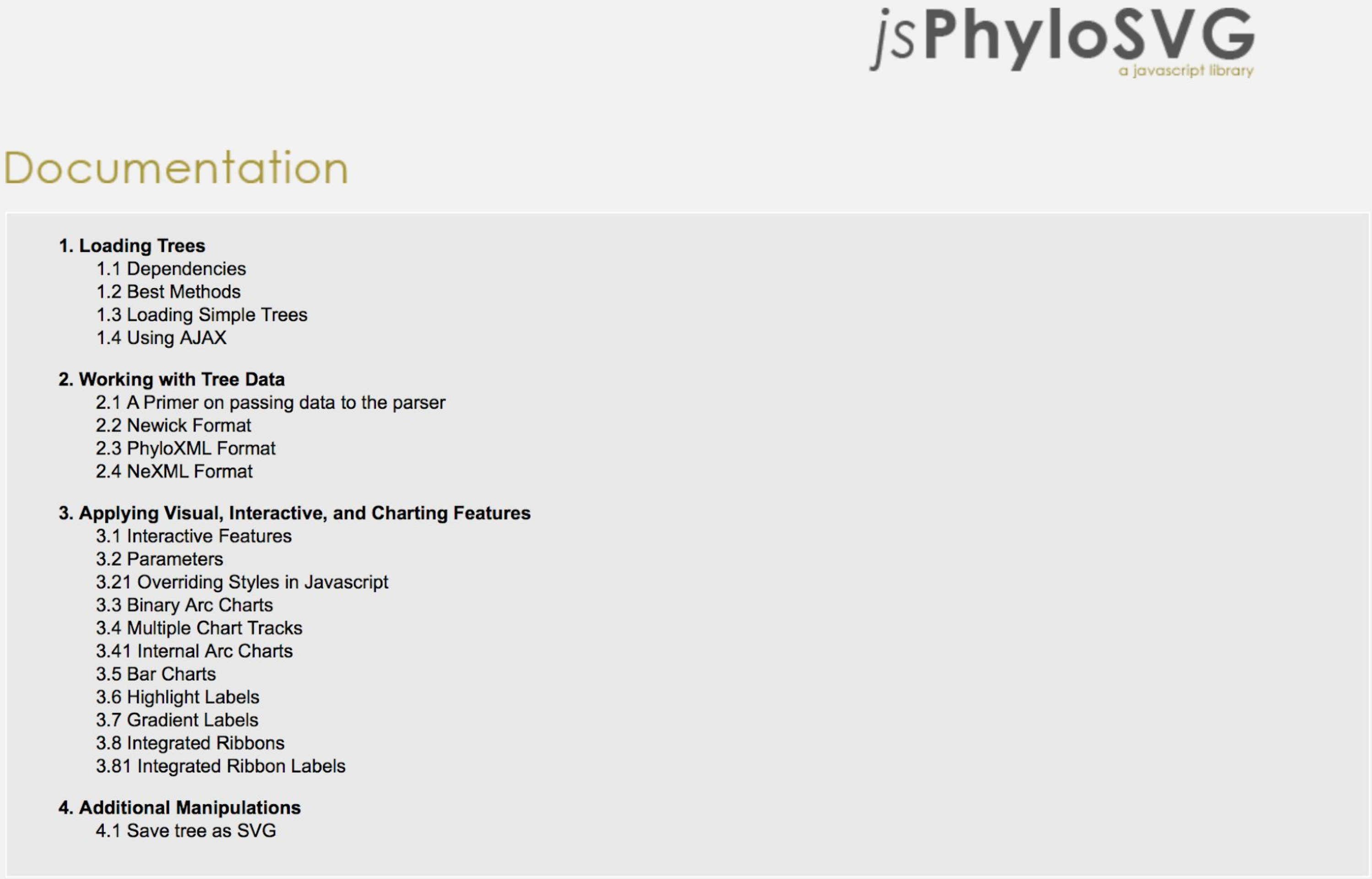
```xml
<clade>
<name>Subterranean Termite</name>
<branch_length>0.17793</branch_length>
<annotation>
    <desc>GQ502663.1 Gut clone Cf8-01 </desc>
    <uri>http://www.jsphylosvg.com/GQ502663 </uri>
</annotation>
</clade>
```



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.



jsPhyloSVG
a javascript library

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

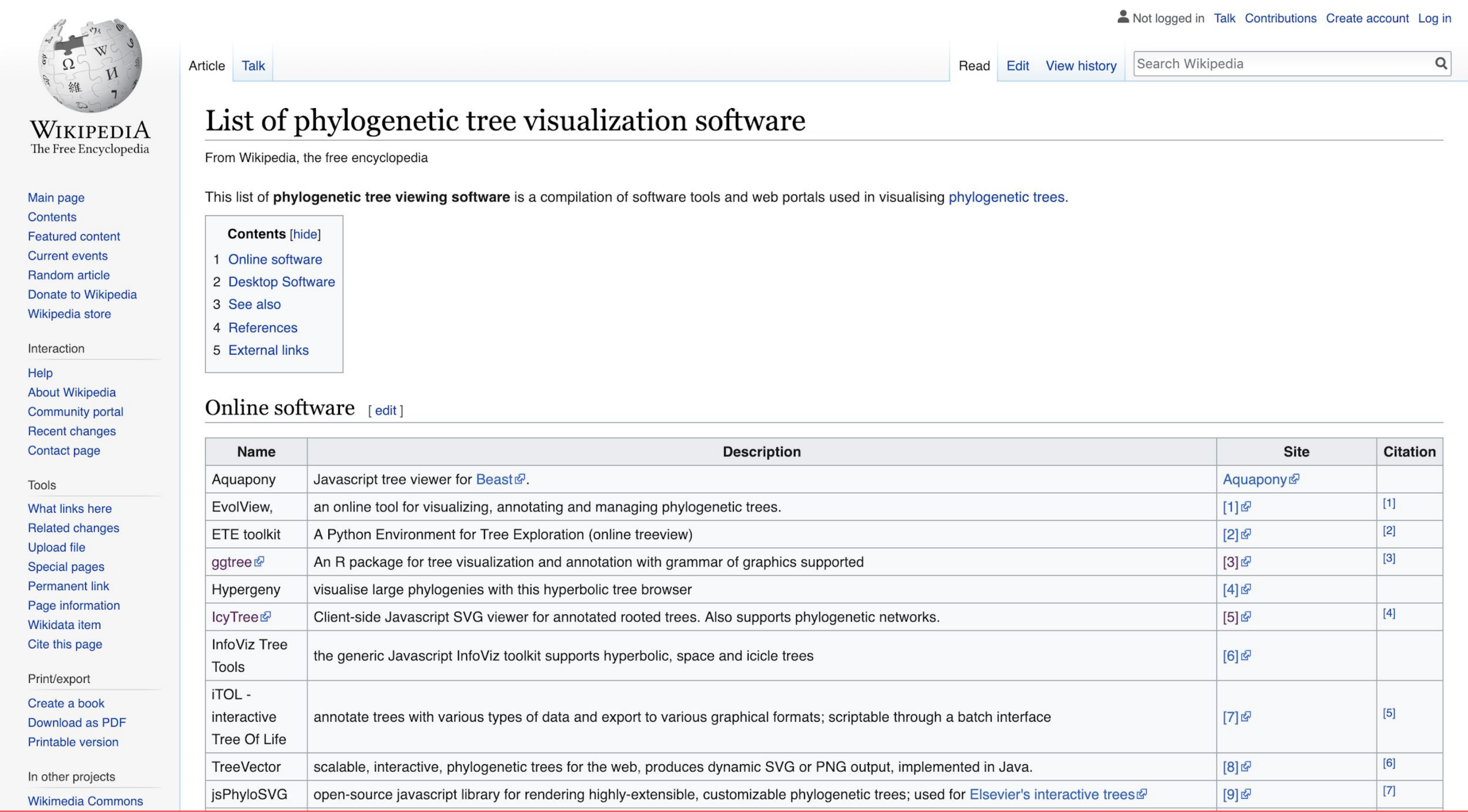
4. Additional Manipulations
    4.1 Save tree as SVG

http://www.jsphylosvg.com/documentation.php

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.jsphylosvg.com

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



List of phylogenetic tree visualization software

From Wikipedia, the free encyclopedia

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

Contents [hide]
1 Online software
2 Desktop Software
3 See also
4 References
5 External links

Online software [edit]

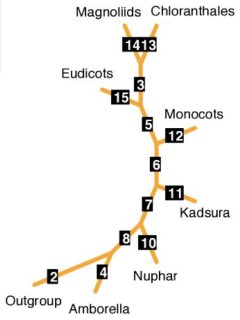
Name	Description	Site	Citation
Aquapony	Javascript tree viewer for Beast.	Aquapony	
EvolView,	an online tool for visualizing, annotating and managing phylogenetic trees.	[1]	[1]
ETE toolkit	A Python Environment for Tree Exploration (online treeview)	[2]	[2]
ggtree	An R package for tree visualization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

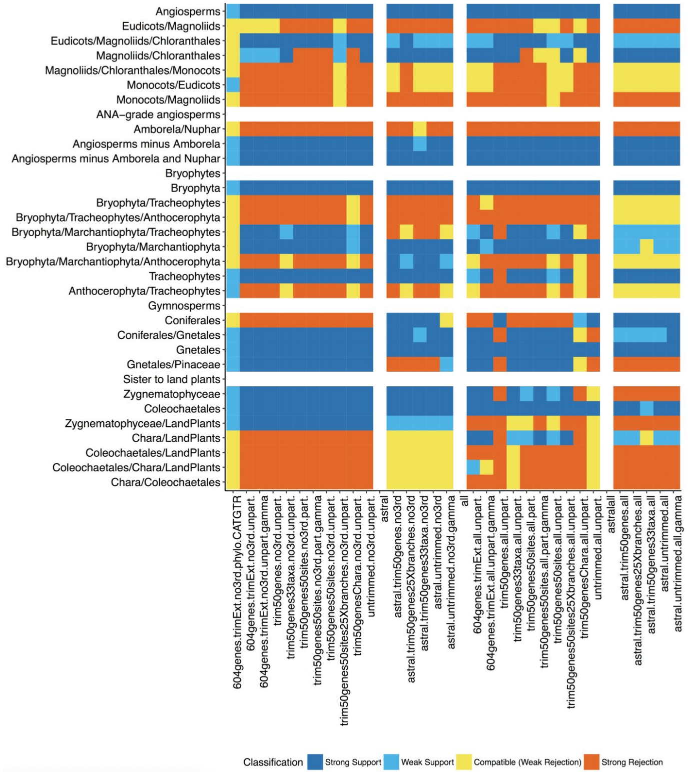
Phylogenetic Tree Visualization

- **Web Portals:**
  - Phylo.IO @ http://phylo.io
  - Interactive Tree of Life viewer (iT ol.embl.de
  - EVOLVIEW @ http://www.evolge view
- **Software:**
  - FigTree @ http://tree.bio.ed.a
  - DensiTree @ https://www ree/
  - TreeGraph2 @ http://t
- **Toolkits:**
  - PYTHON library: ETE
  - R repository: PhyTools @ ackages/phytools/index.html
  - JavaScript library: jsPhy losvg.com
- **https://en.wikipedia.o iki/List_of_phylogenetic_tree_visualization_software**

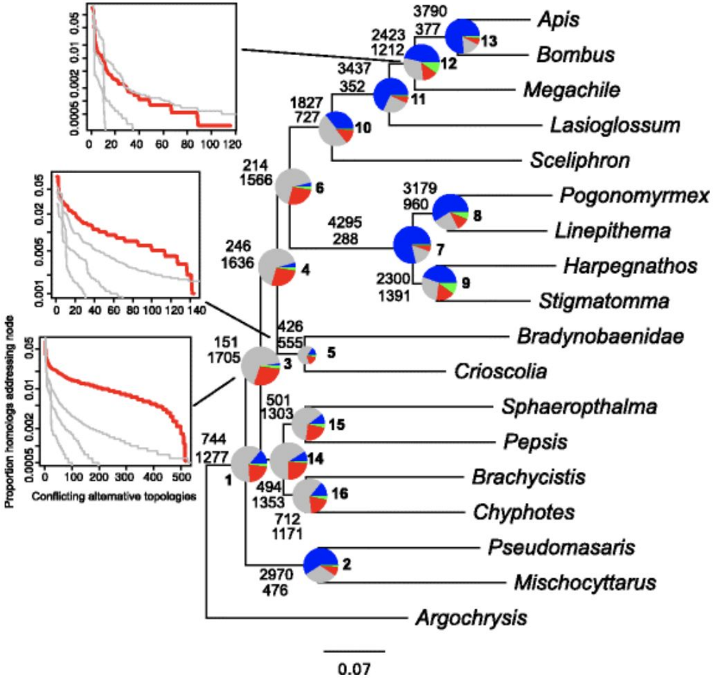
Phylogenetic Conflict Visualization

- **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

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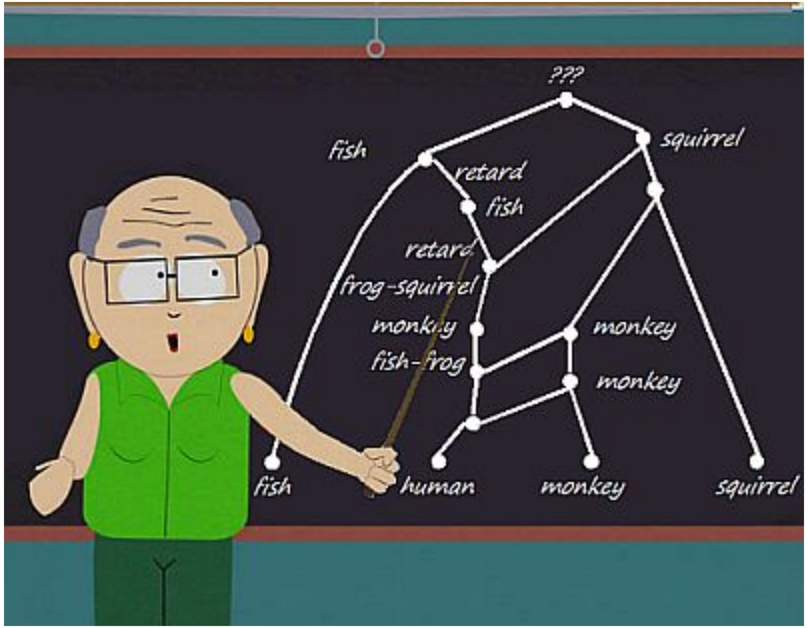
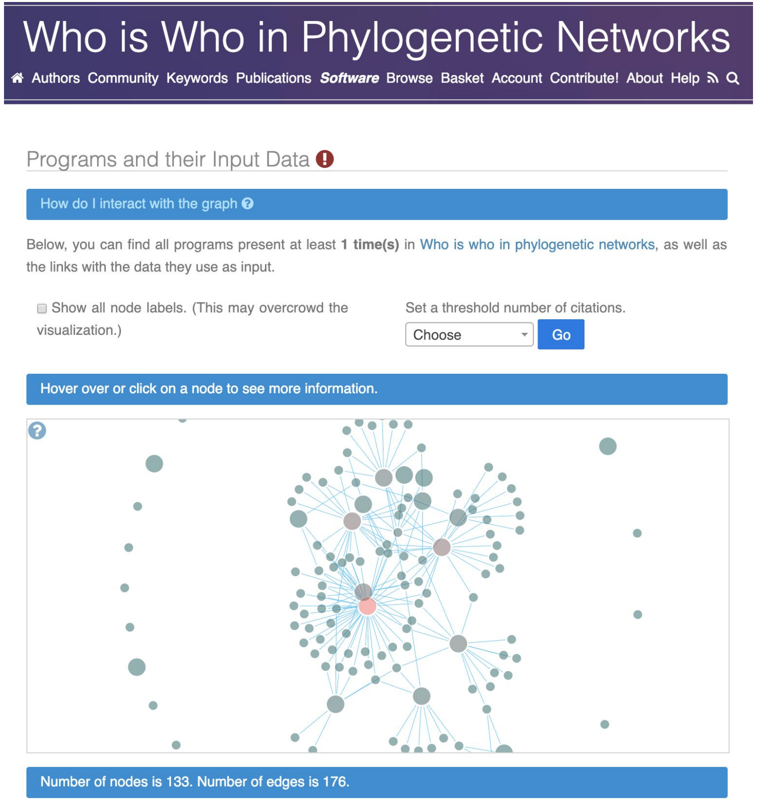
Phylogenetic Network Visualization





Programs and their Input Data

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.

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

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.

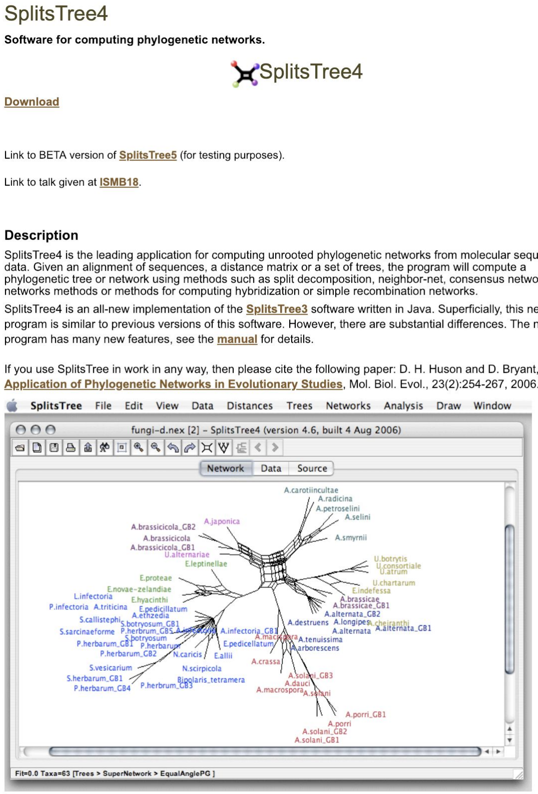
Feature List:

- 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.

SplitsTree4

Download

Link to BETA version of SplitsTree5 (for testing purposes).

Link to talk given at ISMB18.

Description

SplitsTree4 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.

Fit=0.0 Taxa=63 [Trees > SuperNetwork > EqualAnglePG]

Visualization Challenge

ポケモン Phylogeny