23.xi.

1. applications

2. summary

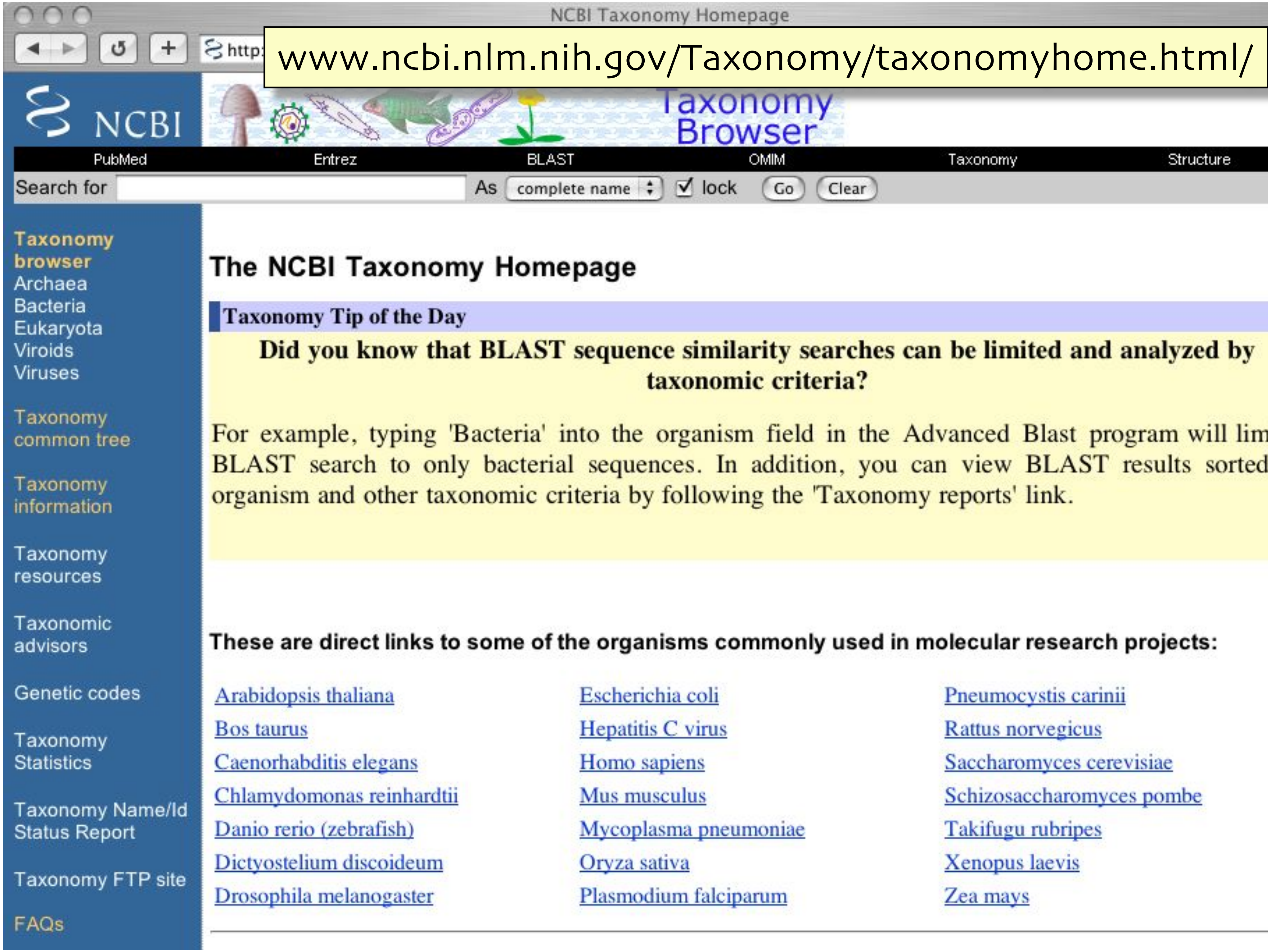
Applications

phylogenetic classification provides best GENERAL REFERENCE system for arranging biological information of numerous taxa

indispensable tool for searching information

unavoidable changes in classification are challenge for database development

structure of databases has to be flexible & their parts have to be small enough to allow easy incorporation of changes www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/



The NCBI Taxonomy Homepage

Taxonomy Tip of the Day

Did you know that BLAST sequence similarity searches can be limited and analyzed by taxonomic criteria?

For example, typing 'Bacteria' into the organism field in the Advanced Blast program will lim BLAST search to only bacterial sequences. In addition, you can view BLAST results sorted organism and other taxonomic criteria by following the 'Taxonomy reports' link.

These are direct links to some of the organisms commonly used in molecular research projects:

Arabidopsis thaliana
Bos taurus
Caenorhabditis elegans
Chlamydomonas reinhardtii
Danio rerio (zebrafish)
Dictyostelium discoideum
Drosophila melanogaster
Escherichia coli
Hepatitis C virus
Homo sapiens
Mus musculus
Mycoplasma pneumoniae
Oryza sativa
Plasmodium falciparum
Pneumocystis carinii
Rattus norvegicus
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Takifugu rubripes
Xenopus laevis
Zea mays

Basic principles of classification

Farris, J.S. 1979. The information content of the phylogenetic system. *Systematic Zoology* 28: 483-519.

Cladistic classification (Farris 1979):

1. enables presentation of information about terminals most economically
2. minimizes exceptions

minimization of homoplasy

3. provides best possible estimate about characters that are still unknown (not yet studied)

classification can be used to plan future studies

objection: classification of several traditional taxa has to be updated

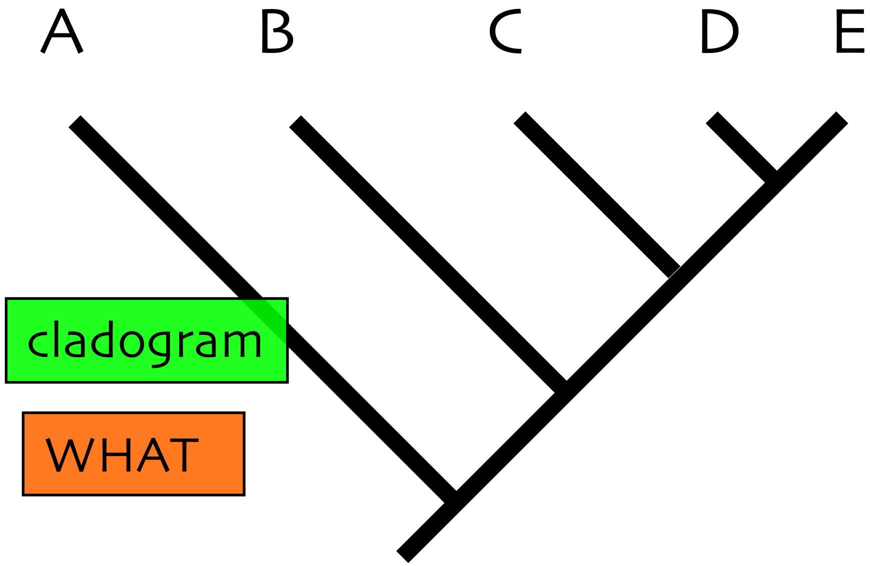
...stable classification.... represents the perpetuation of ignorance (Gaffney 1979)

Application of results

1. biogeography
2. evolutionary biology & ecology
3. applied biology
4. nature conservation

ALL organisms have HISTORY, as well as their CHARACTERS

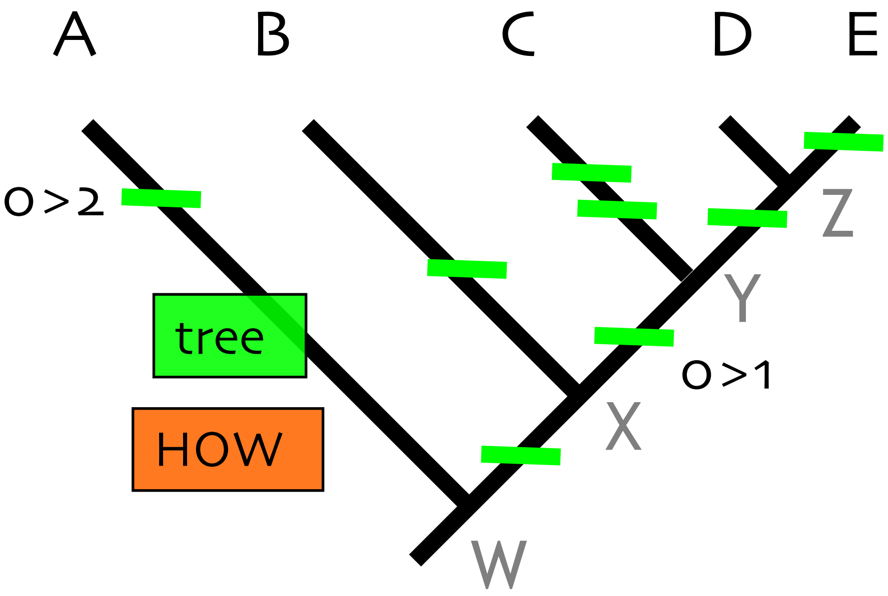
reliable hypotheses about phylogeny are important for ALL fields of biology



sister-group relationships between terminals

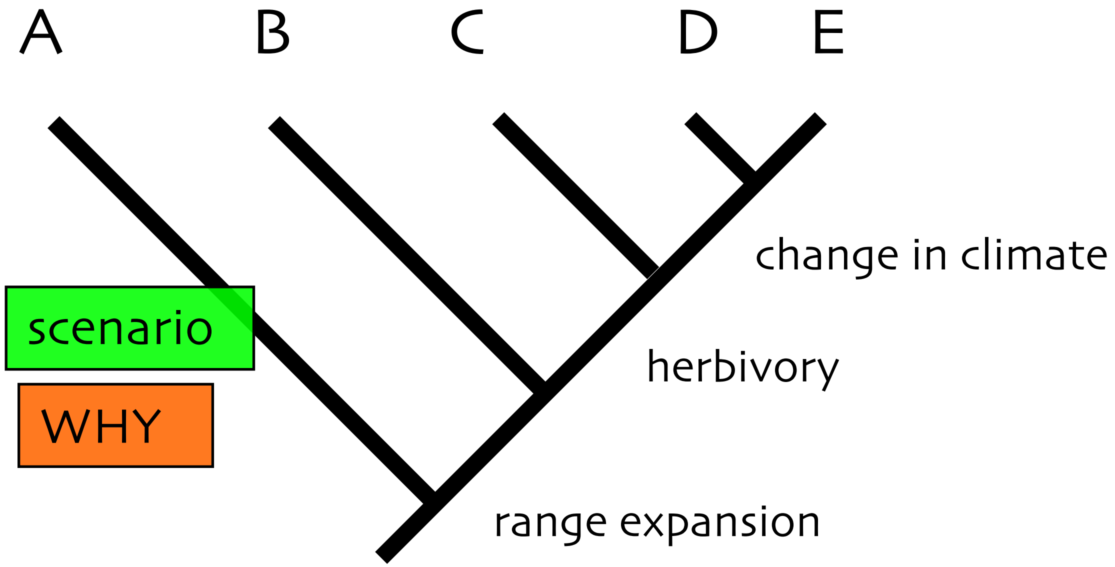
nested set of monophyletic gorups (clades)

(A (B (C (D (E)))))



terminals & their ancestors

<u>CHANGES from ch. state to another</u>



Nelson 1980

Biogeography

organismal ranges dynamic > shrink & enlarge

changes include e.g.:

1) dispersal to new areas

2) fragmentation of former continuous range

speciation **MIGHT** be informative about history of the areas occupied by organisms

reliable hypotheses about phylogeny are needed for these kind of studies of HISTORICAL biogeography

Biogeography

study of distributional areas group by group

parsimony

origins of similar ranges independently unlikely

more parsimonious to try to find explanation from shared HISTORY

null hypothesis: speciations DO tell something about history of the areas

basic question: do phylogenetic hypotheses of different groups of taxa give same hypothesis about areas?

SHARED, common explanation for geographical information conveyed by separate, independent lineages

comparison of hypotheses of phylogeny with geological information

Biogeography

1. monophyletic groups chosen with members present in numerous areas
2. cladistic analysis of all groups
3. names of terminals replaced with areas where they occur

many S Hemisphere groups ideal for this kind of study

formerly continuous areas fragmented

now separated by vast spaces of oceans

N Hemisphere?

Biogeography

organismal ranges dynamic > shrink & enlarge

changes induced e.g. by:

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speciation MIGHT be informative about history of the
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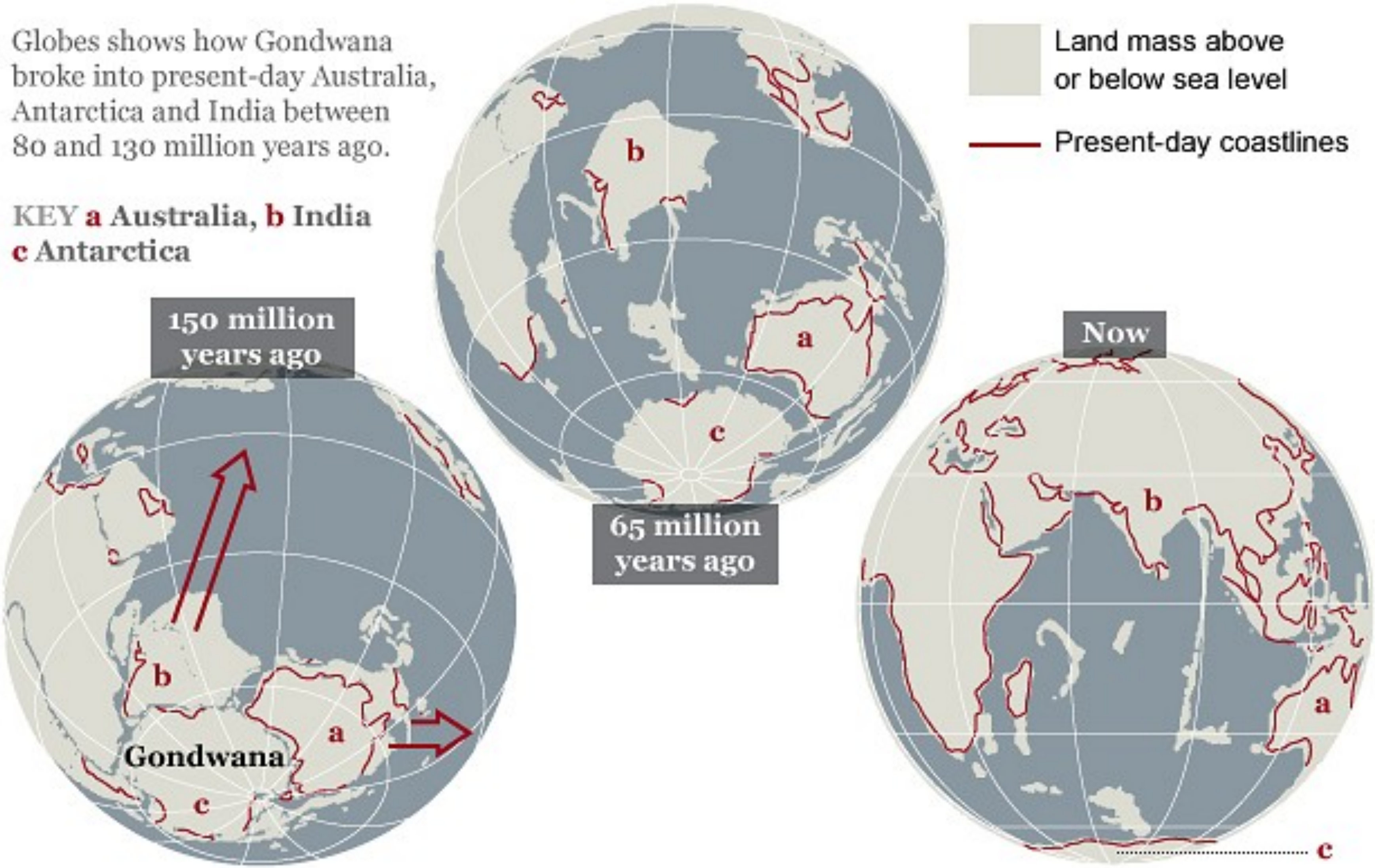


Globes shows how Gondwana broke into present-day Australia, Antarctica and India between 80 and 130 million years ago.

telegraph.co.uk

Nothofagus

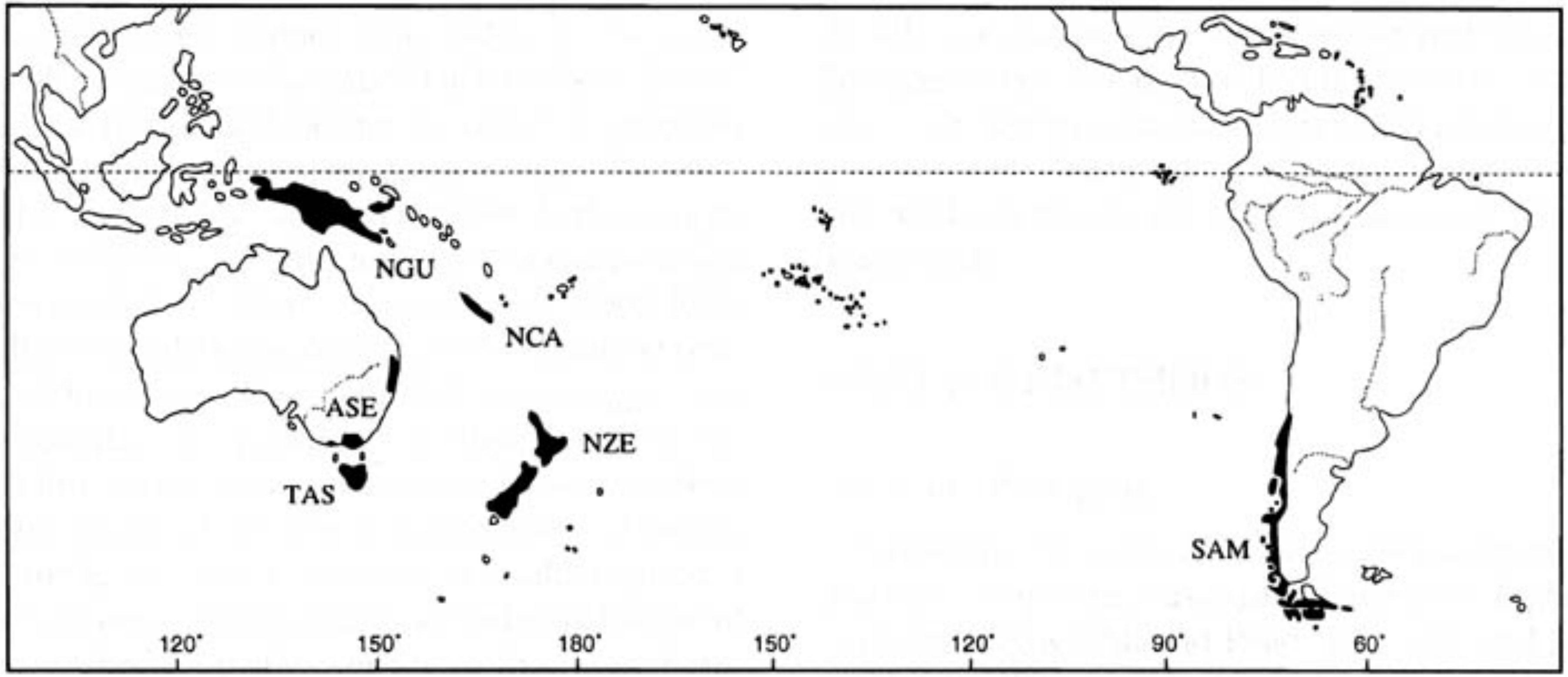
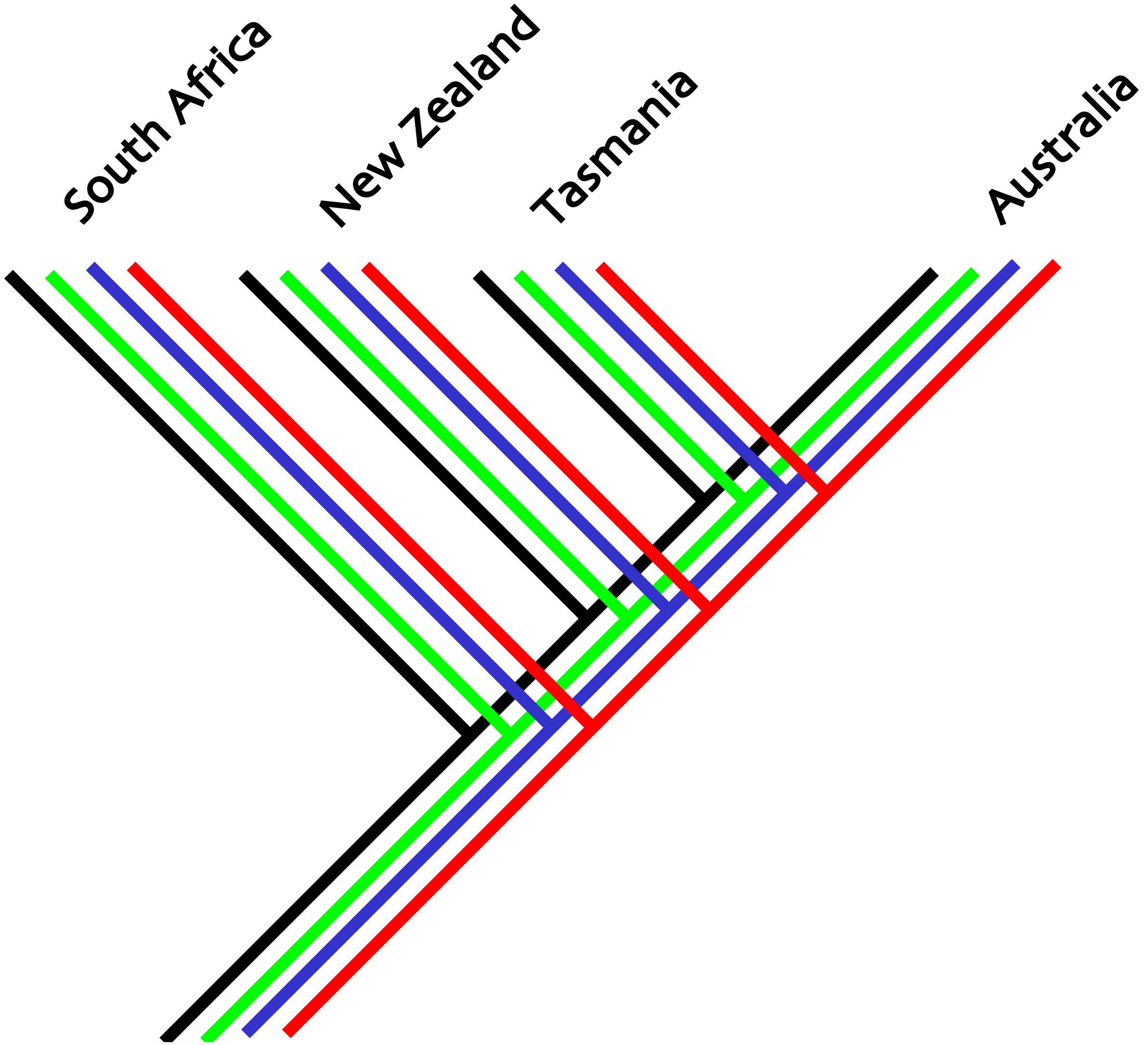


FIG. 1. Distribution of extant *Nothofagus* species showing the southern Pacific area. ASE, Southeast Australia; NCA, New Caledonia; NGU, New Guinea; NZE, New Zealand; SAM, South America; TAS, Tasmania.

plantbiology.siu.edu

Historical biogeography

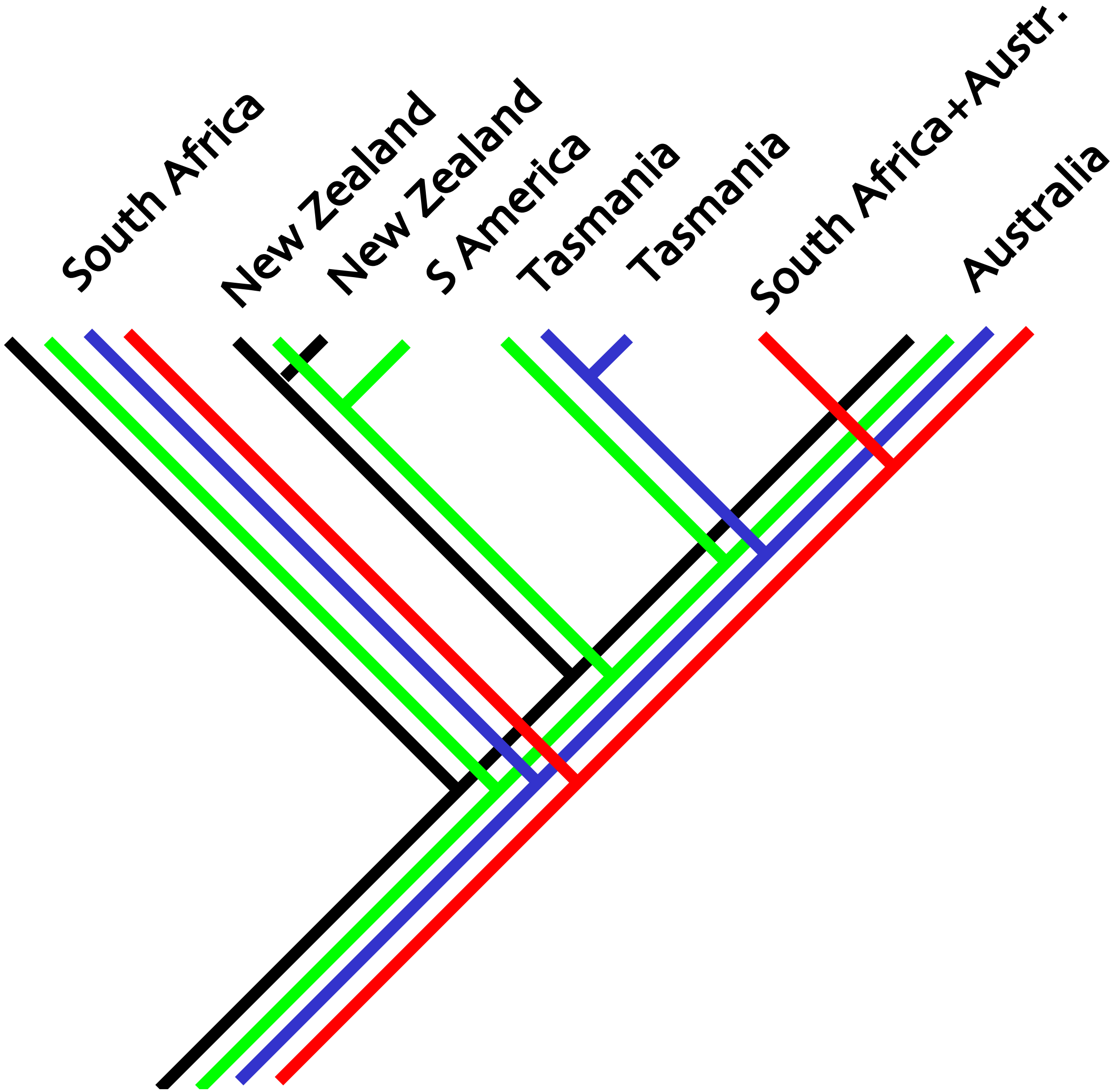


Historical biogeography

all cladograms combine geographical regions in a same way

in practice impossible, always missing, WIDELY spread taxa present & speciation WITHIN areas

Historical biogeography



Historical biogeography

all cladograms combine geographical regions in a same way

in practice impossible, always missing, WIDELY spread taxa present & speciation WITHIN areas

conflict between cladograms, conflicting hypotheses about history of areas

search for most parsimonious way to combine information provided by conflicting cladograms

diverse techniques

Historical biogeography

1) Brooks parsimony analysis

2) component analysis

3) reconciling cladograms

HOST &	ASSOCIATE
organism	gene
host	parasite
area	taxon

Historical biogeography

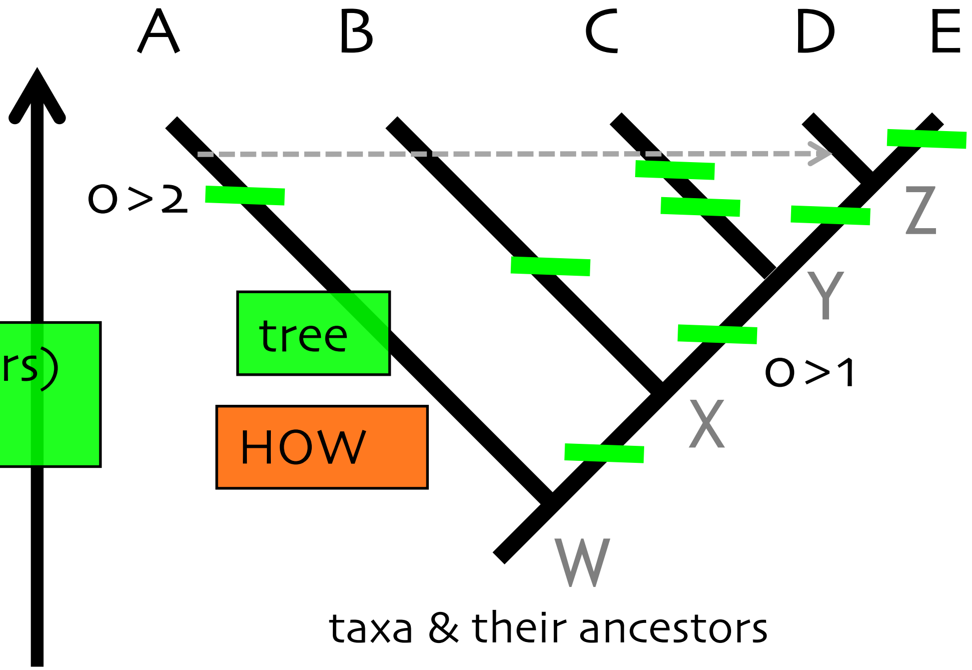
1) Brooks parsimony analysis

2) component analysis

3) reconciling cladograms

also in biogeographical analyses *different* types of parsimony or models are used

genetic information (= characters)
PREDOMINANTLY vertical

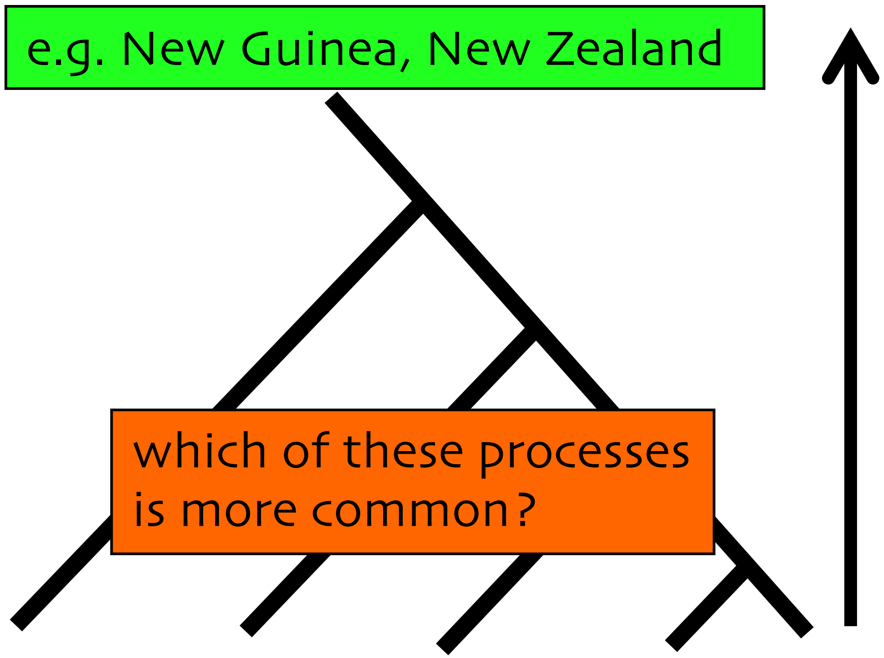


tree

HOW

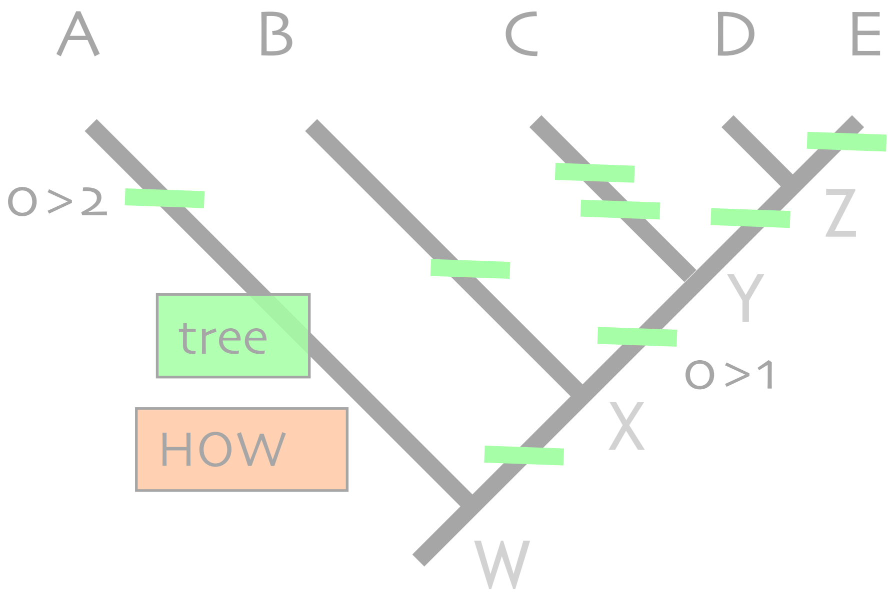
taxa & their ancestors

<u>CHANGES from ch. state to another</u>



e.g. New Guinea, New Zealand

which of these processes is more common?



tree

HOW

taxa & their ancestors

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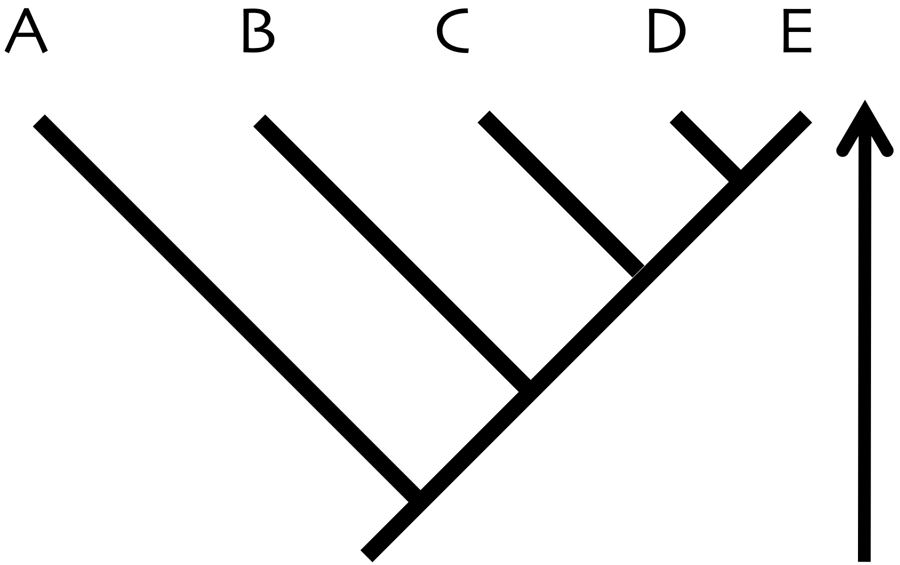


geographical areas

BOTH divide & merge

Historical biogeography

there is no reason to assume geological history to be HIERARCHIC in the same way as organismal history

organisms ARE mobile & able to spread to new areas

contemporary range does not necessarily tell about former distribution

Hovenkamp, P. 1997. Vicariance events, not areas, should be used in biogeographical analysis. *Cladistics* 13: 67–79.
Hovenkamp, P. 2001. A direct method for the analysis of vicariance patterns. *Cladistics* 17: 260–265.

Historical biogeography

in MOST applications PREDEFINED areas are used that do NOT correspond perfectly with ranges of organisms

Arias, J.S. & al. 2011. Spatial analysis of vicariance: a method for using direct geographical information in historical biogeography. *Cladistics* 27: 617–628.

material is composed of CONCRETE observations of occurrence of organsims, NOT predefined areas

aim is to find DIVISIONS that are SHARED by numerous taxa

www.lillo.org.ar/phylogeny/GEM/

Evolutionary biology

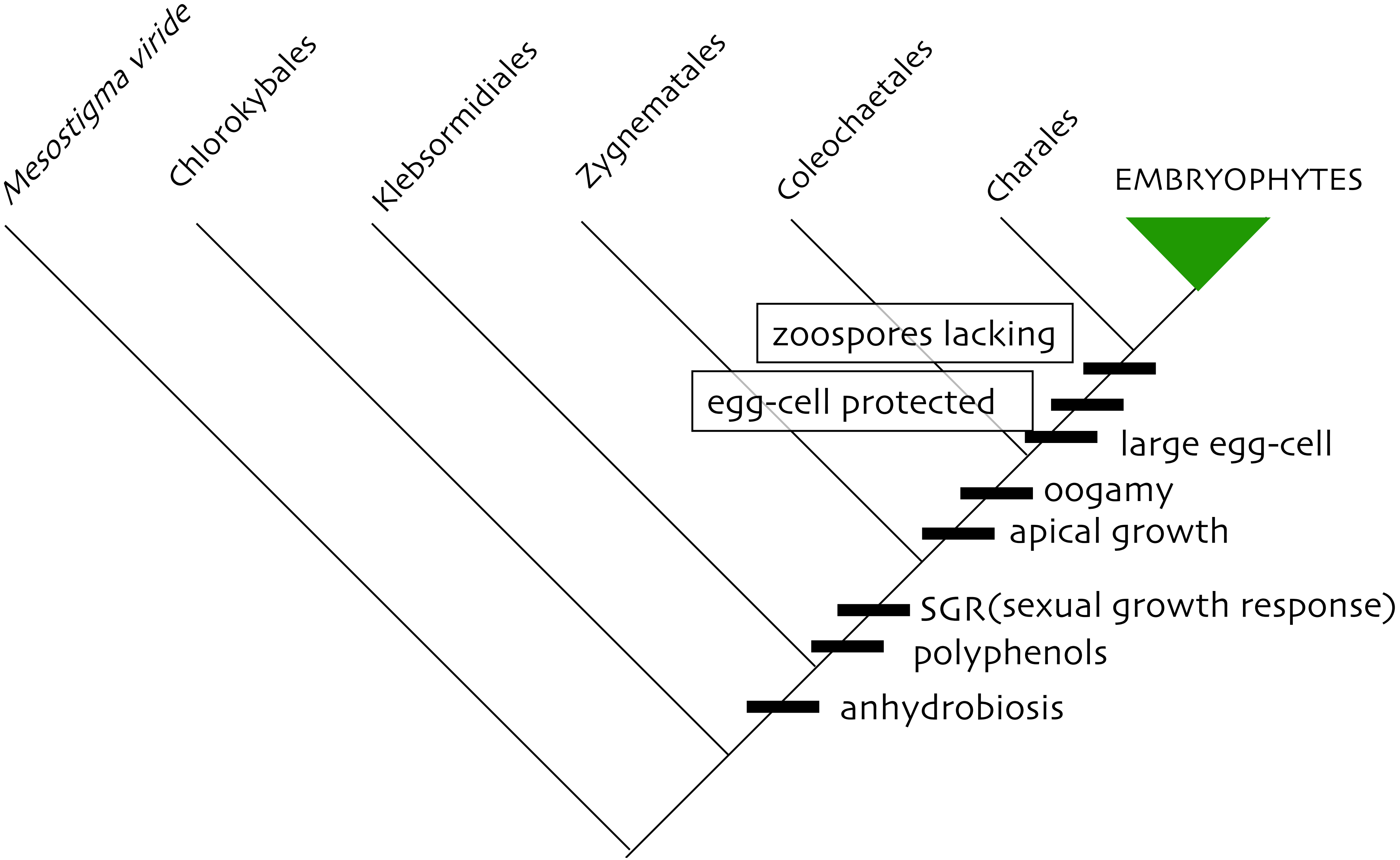
cladograms provide information about SEQUENCE of evolutionary events

e.g. in the lineage leading to embryophytes biochemical changes preceded those of morphology

previously developed characters enabled those developed later

changes that proved to be of uttermost importance in novel & harsh environment

EMBRYOPHYTES



HILIFE – HELSINKI INSTITUTE OF LIFE SCIENCE /

VIIKKI MONDAY SEMINARS

Twitter #viikkimon

Organizer: Juha Saarikangas, juha.saarikangas@helsinki.fi, tel. +358 40 539 5894

29.4. Charles F. Delwiche (Univ. Maryland, USA)
Colonizing the land: basal streptophyte transcriptomes and fundamental plant biology

Evolutionary biology

sexual dimorphism

~~dwarf males~~

spider genus *Nephila*

♀ 18-36 mm

♂ 3-10 mm

sister groups ♂ **5-6 mm**

GIGANTIC females

in some spider groups males ARE smaller than those found in outgroups

DIFFERENT reasons for sexual dimorphism

Ecology

JUST SO –stories
refutation of unfounded hypotheses

cladograms enable comparison of ecological hypotheses

common assumption: natural selection favors better adaptation > main reason for evolutionary changes

spiders have 2 major web-types:

1) small & irregular (cobweb)

2) large & regular (orb-web)

automatically assumed that the latter have developed from the former

phylogenetic analysis --> cobwebs have developed from ord-webs

http://entomology.si.edu/StaffPages/coddington.htm

Home › Research & Collections › Entomology › Staff ›

SI Entomology Staff

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  National Museum of Natural History
  10th & Constitution NW
  Washington, DC 20560-0105
- **Education:**
  1975 B.S. Yale University
  1978 M.A. Harvard University
  1984 PhD. Harvard University

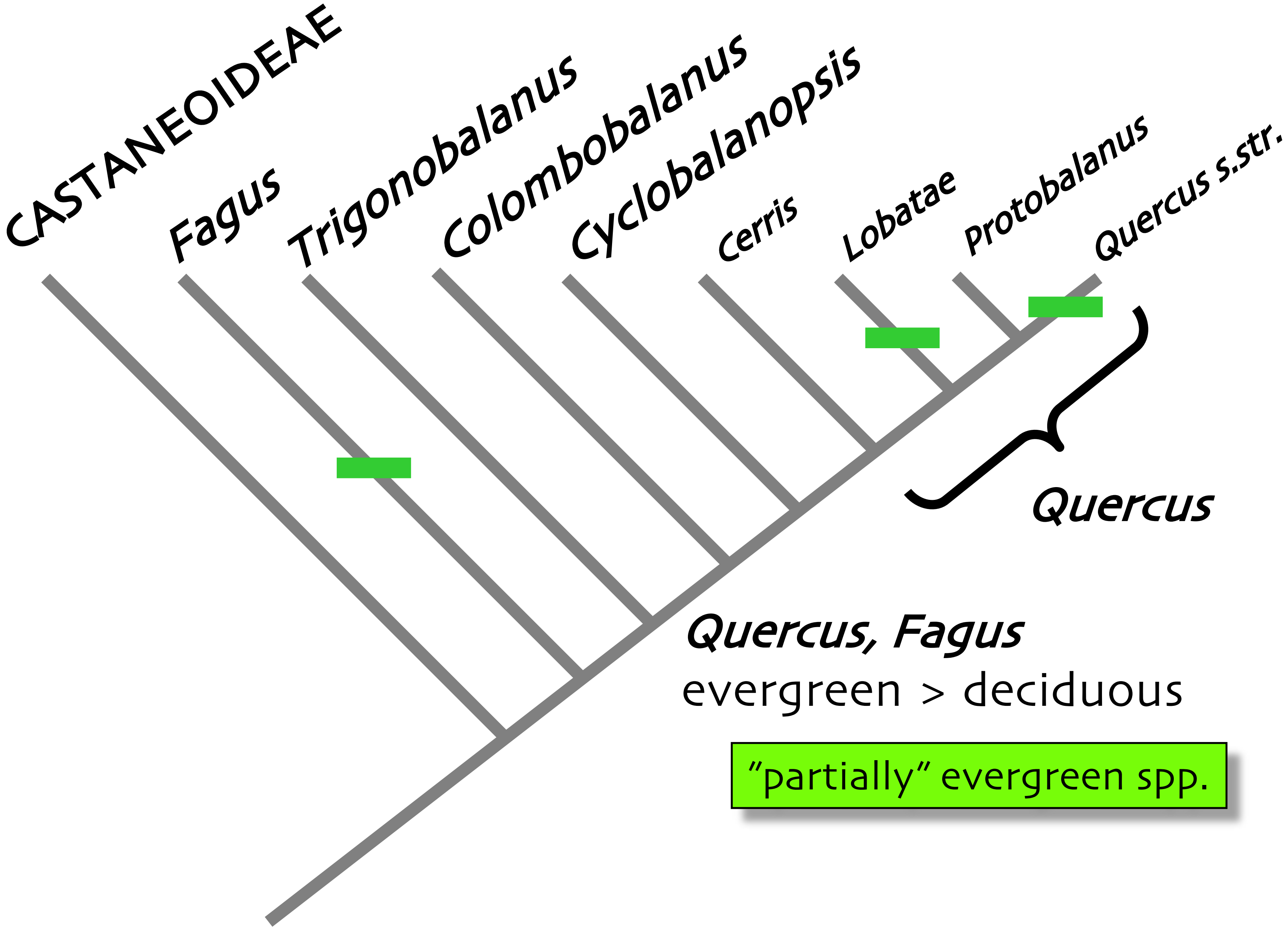
Ecology

Quercus, Fagus deciduous spp.

Wanntorp, H.-E. & al. 1990. Phylogenetic approaches in ecology. *Oikos* 57: 119-132

Quercus, Fagus

lvs deciduous > tendency to retain lvs long into winter



Quercus, Fagus
evergreen > deciduous

🟩 "partially" evergreen spp.

Applied biology

vector of destructive
curly top virus

BIOLOGICAL CONTROL

pest of sugar beet (*Beta vulgaris*) originally described as a member of S American genus *Eutettix*

phylogenetic analysis ----> *Circulifer tenellus,* originally from Mediterranean region

info.ag.uidaho.edu/keys/plates/plate10.htm

Applied biology

plant breeding

- developing cold resistant *Rhododendron*

Applied biology

plant breeding

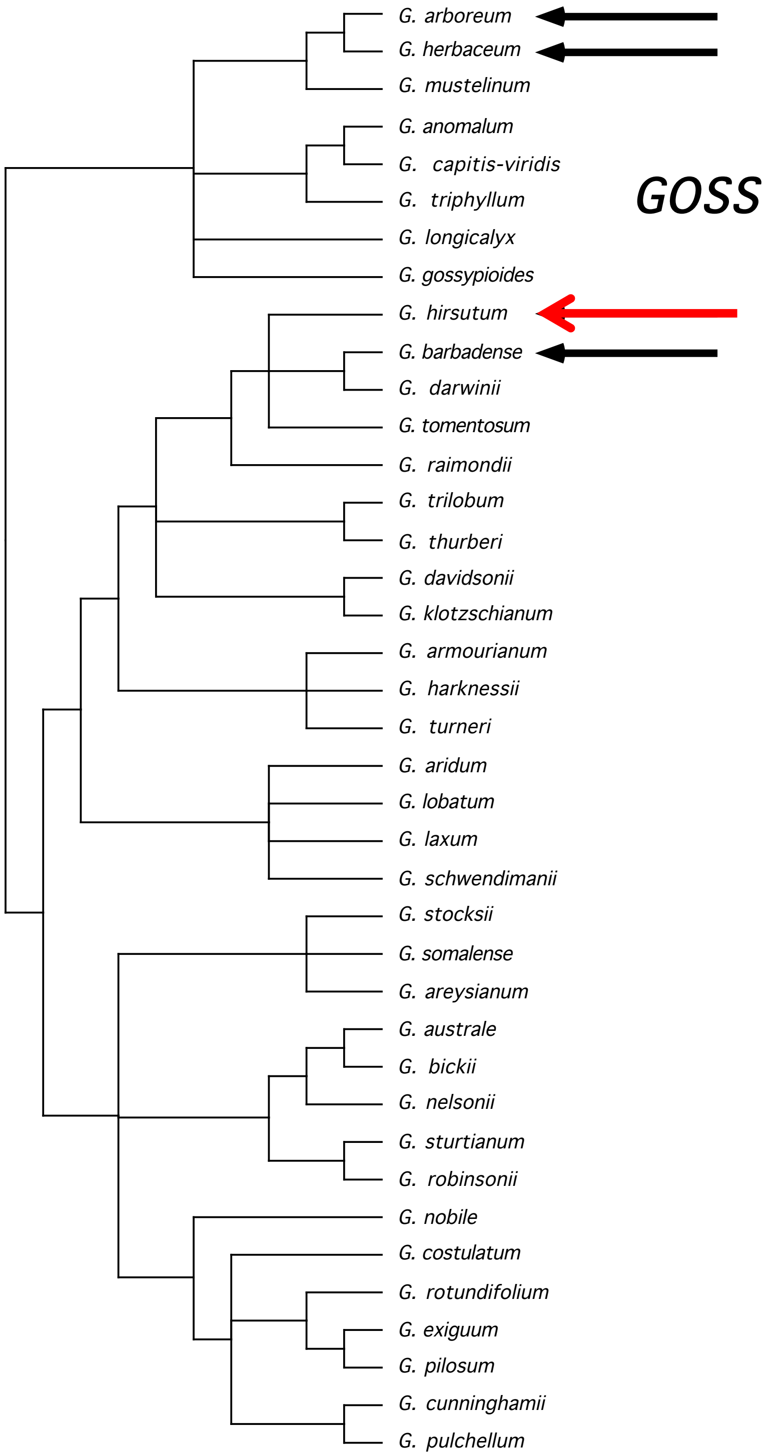
Ledum palustre

Rhododendron tomentosum

www.botany.wisc.edu/garden/db/plantimages/Gossypium_hirsutum_L.JPG

Gossypium hirsutum
Mo Fayyaz

GOSSYPIUM L.

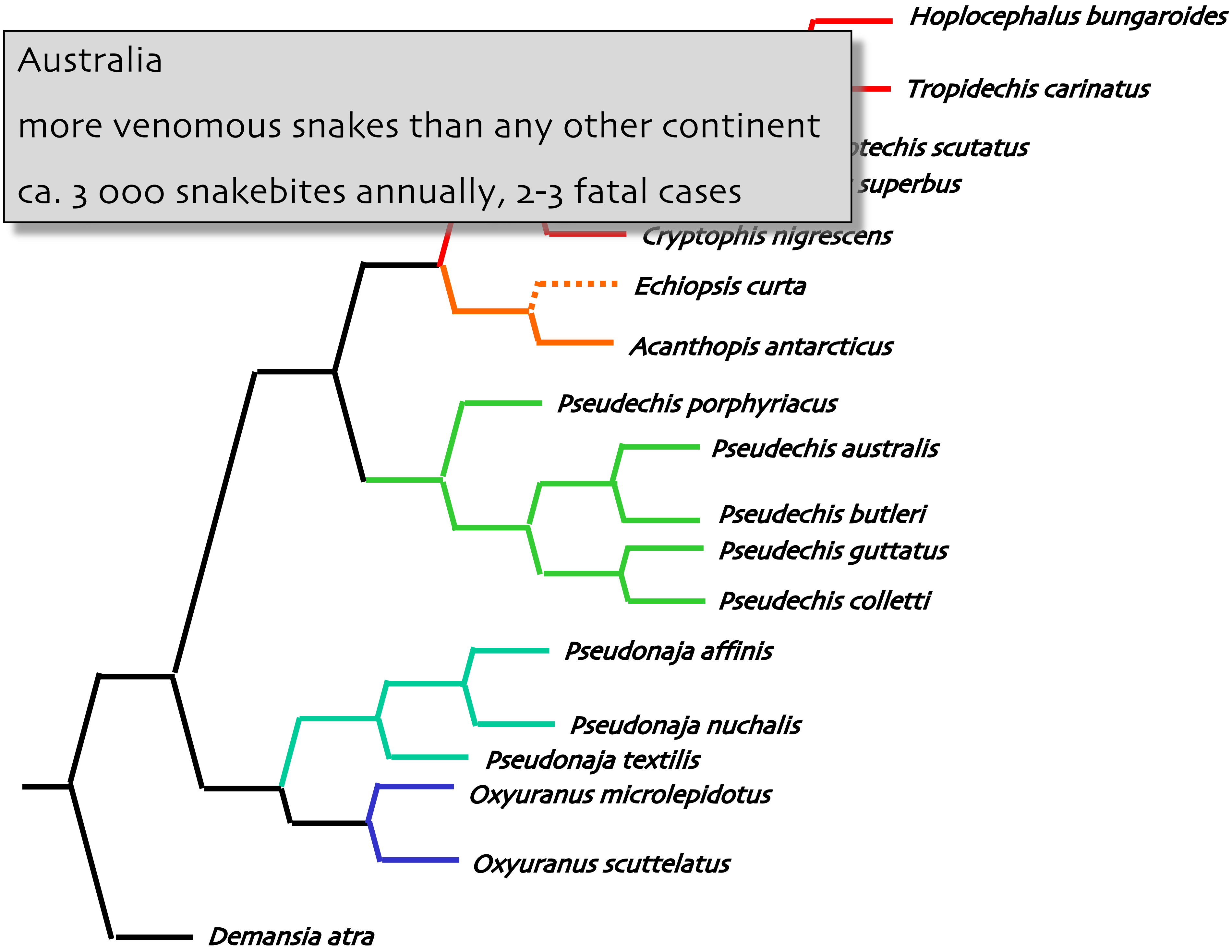


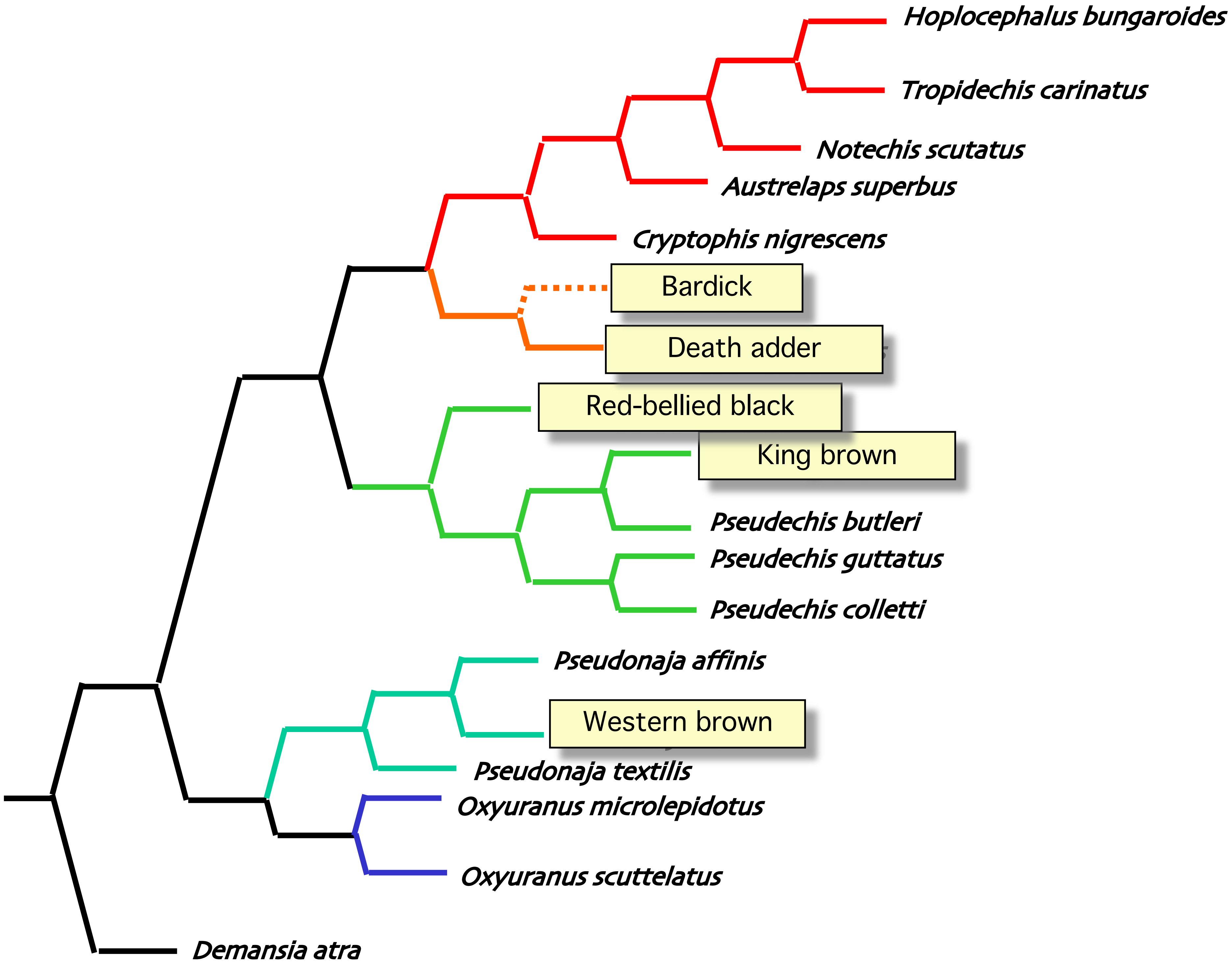
Seelenan ym. 1997. Congruence and consensus in the cotton tribe (Malvaceae). Syst. Bot. 22: 259-290

Australia

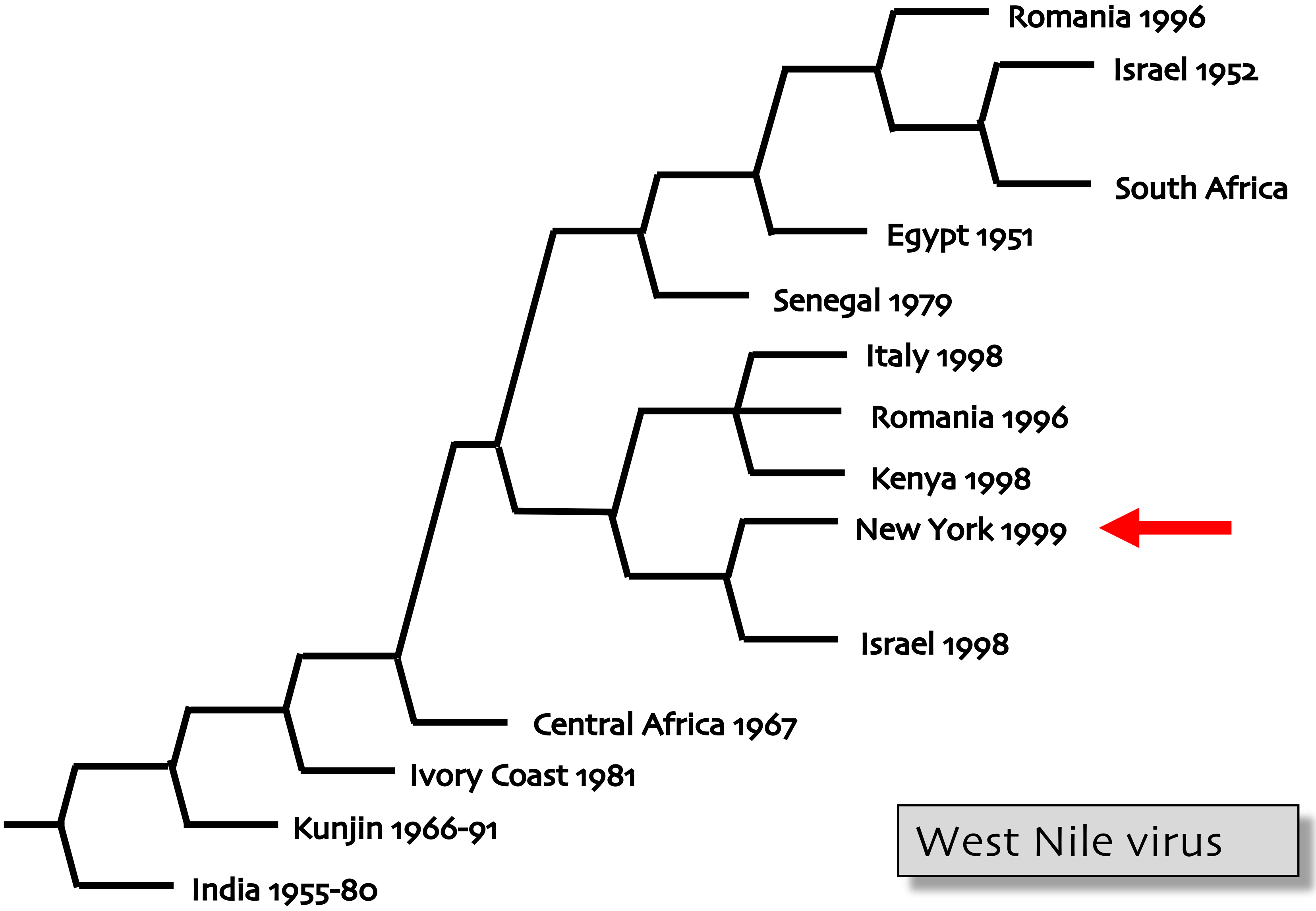
more venomous snakes than any other continent

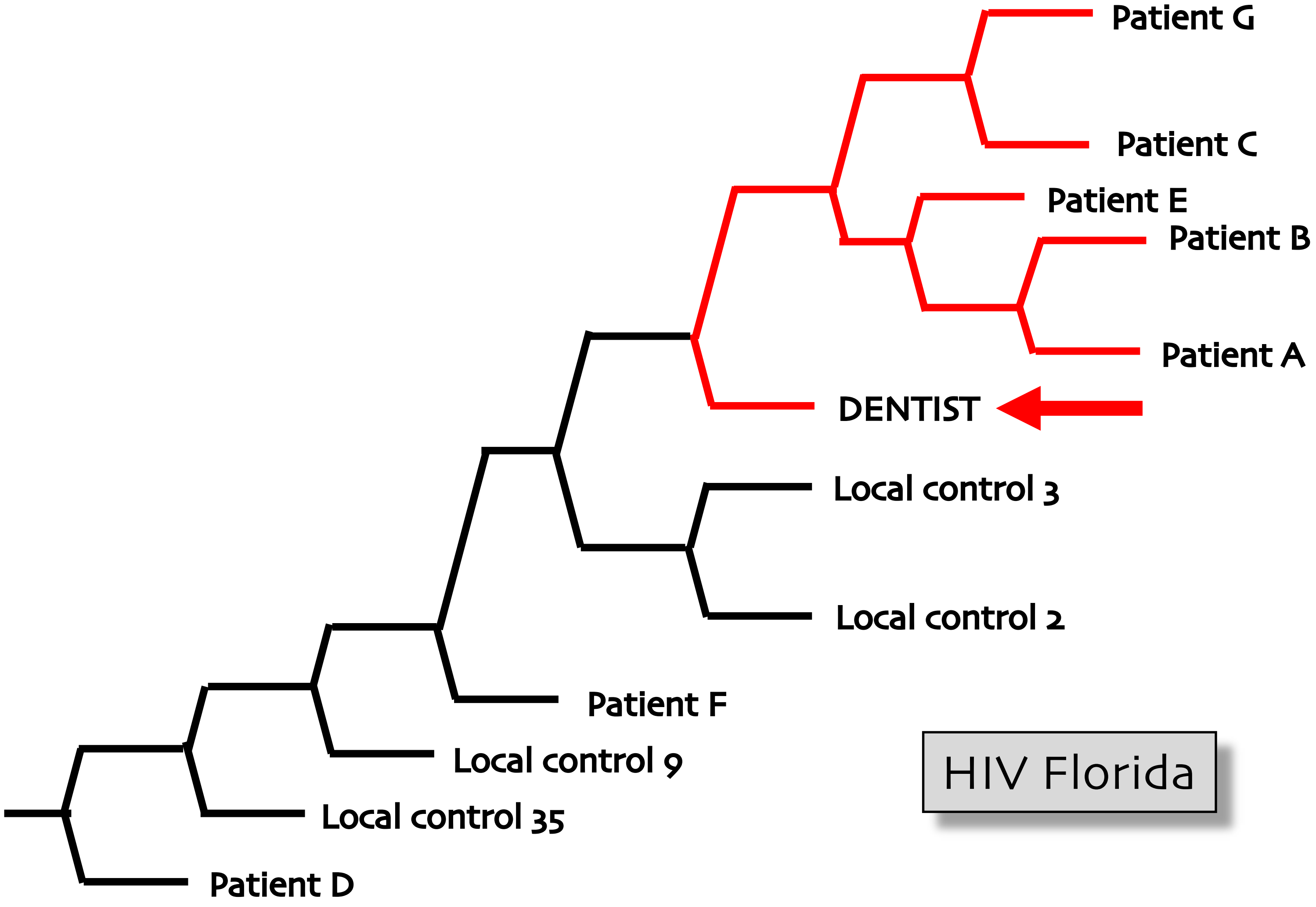
ca. 3 000 snakebites annually, 2-3 fatal cases




Hoplocephalus bungaroides
Tropidechis carinatus
Notechis scutatus
Austrelaps superbus
Cryptophis nigrescens
Bardick
Death adder
Red-bellied black
King brown
Pseudechis butleri
Pseudechis guttatus
Pseudechis colletti
Pseudonaja affinis
Western brown
Pseudonaja textilis
Oxyuranus microlepidotus
Oxyuranus scuttelatus
Demansia atra

West Nile virus





HIV Florida

Ou, C.-Y. & al. 1992. Molecular epidemiologyof HIV transmission in a dental practice. *Science* 256: 1165-1171.

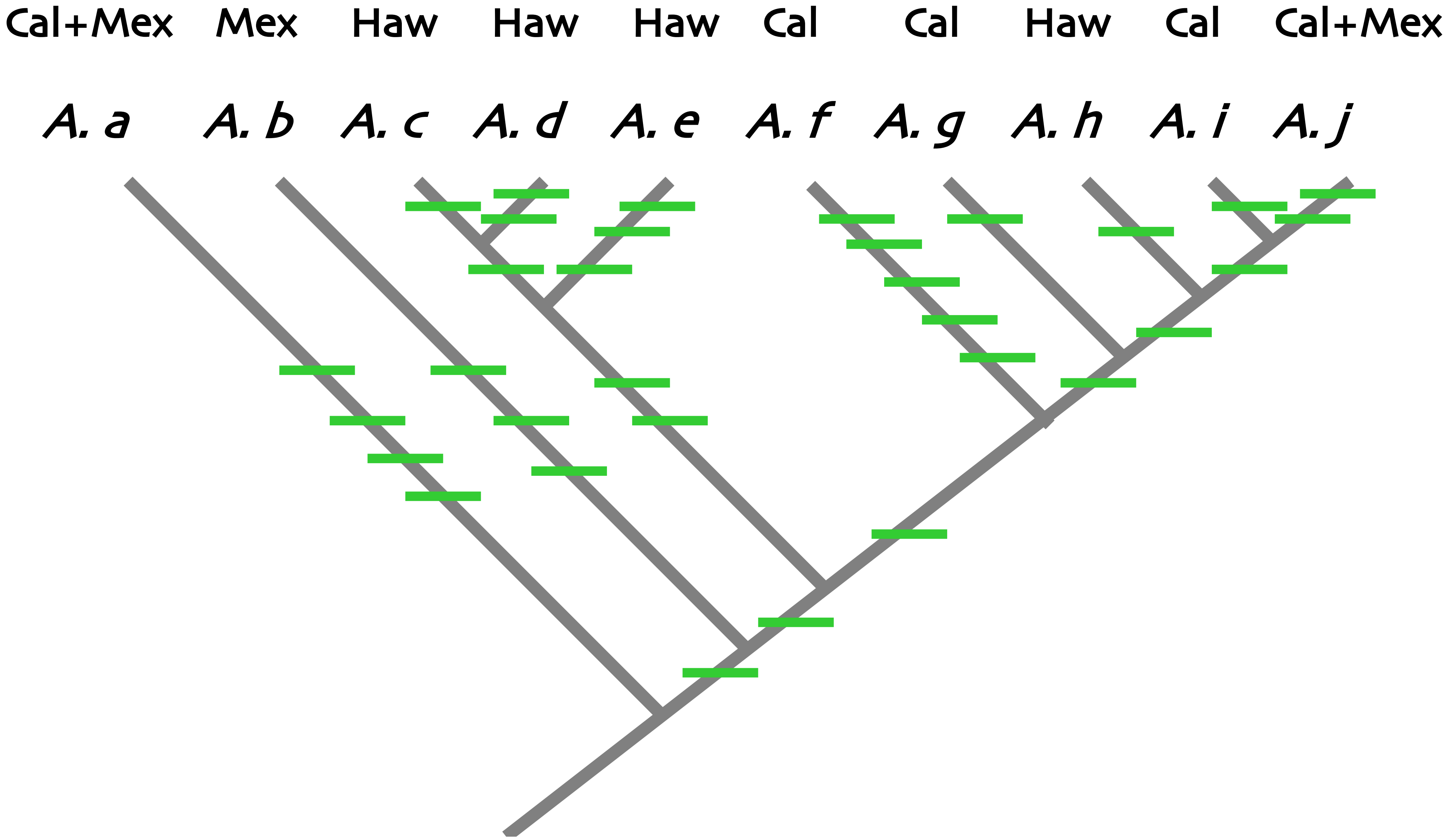
Applied biology

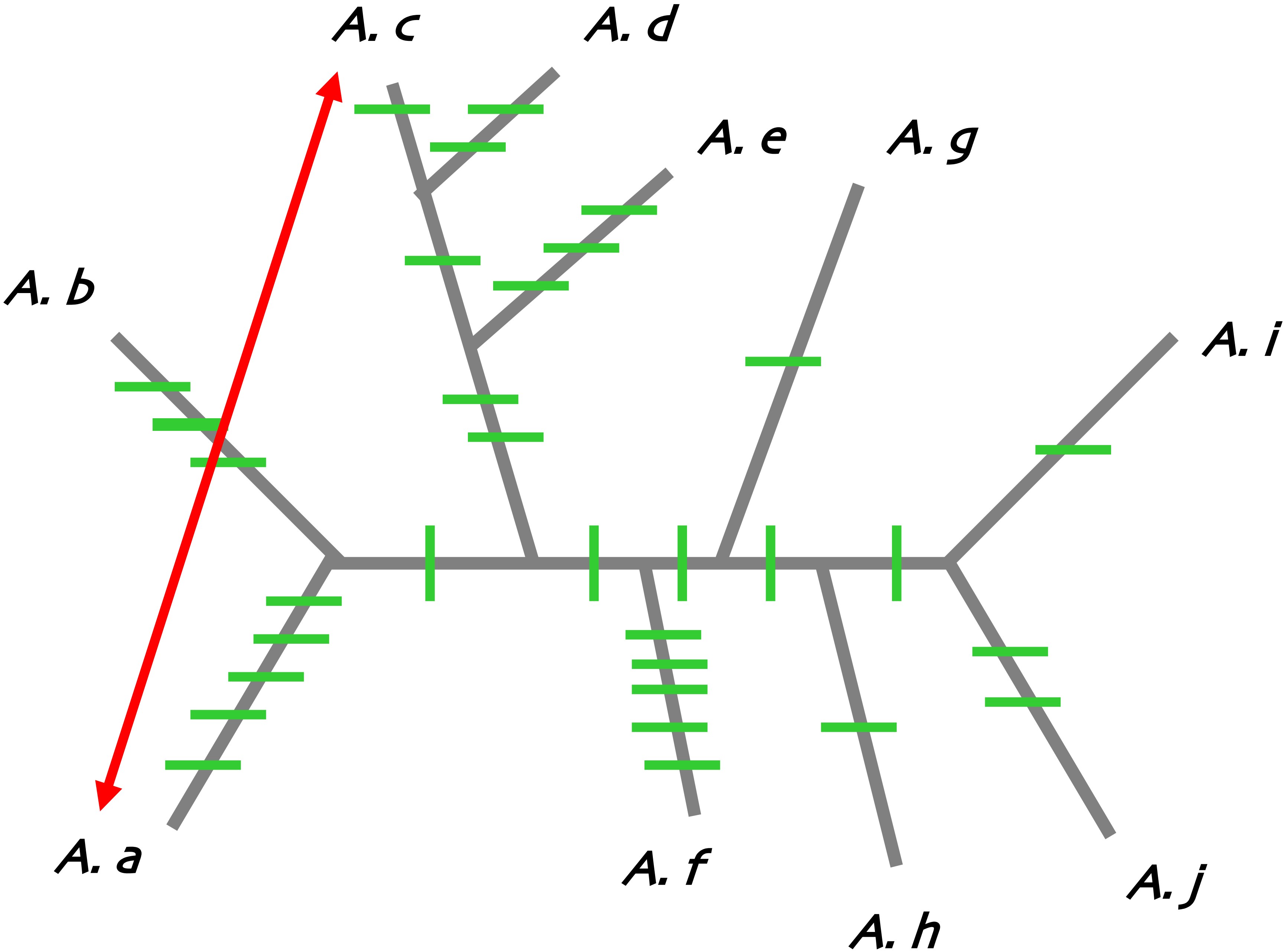
Biodiversity

bio ORIGIN from Greek ***bios* '(course of) human life.'** The sense is extended in modern scientific usage to mean ***'organic life.'***

diversity |diˈvərsitē; dī-|
noun (pl. **-ties)**
the state of being diverse; variety

Plant genus *A*




A. c
A. d
A. e
A. g
A. b
A. i
A. a
A. f
A. h
A. j

A. a -- A. b 8 evolutionary changes

A. a -- A. c 10 evolutionary changes

A. a -- A. d 11 evolutionary changes

search for LONGEST subtree
for a certain predefined
number of terminals

evolutionary changes

goal is to **MAXIMIZE** biodiversity

A. a -- A. f 12 evolutionary changes

Walker, P.A. & Faith, D.P. 1994. Diversity-PD: procedures for conservation evaluation based on phylogenetic diversity. *Biodiversity Letters* 2: 132-139.

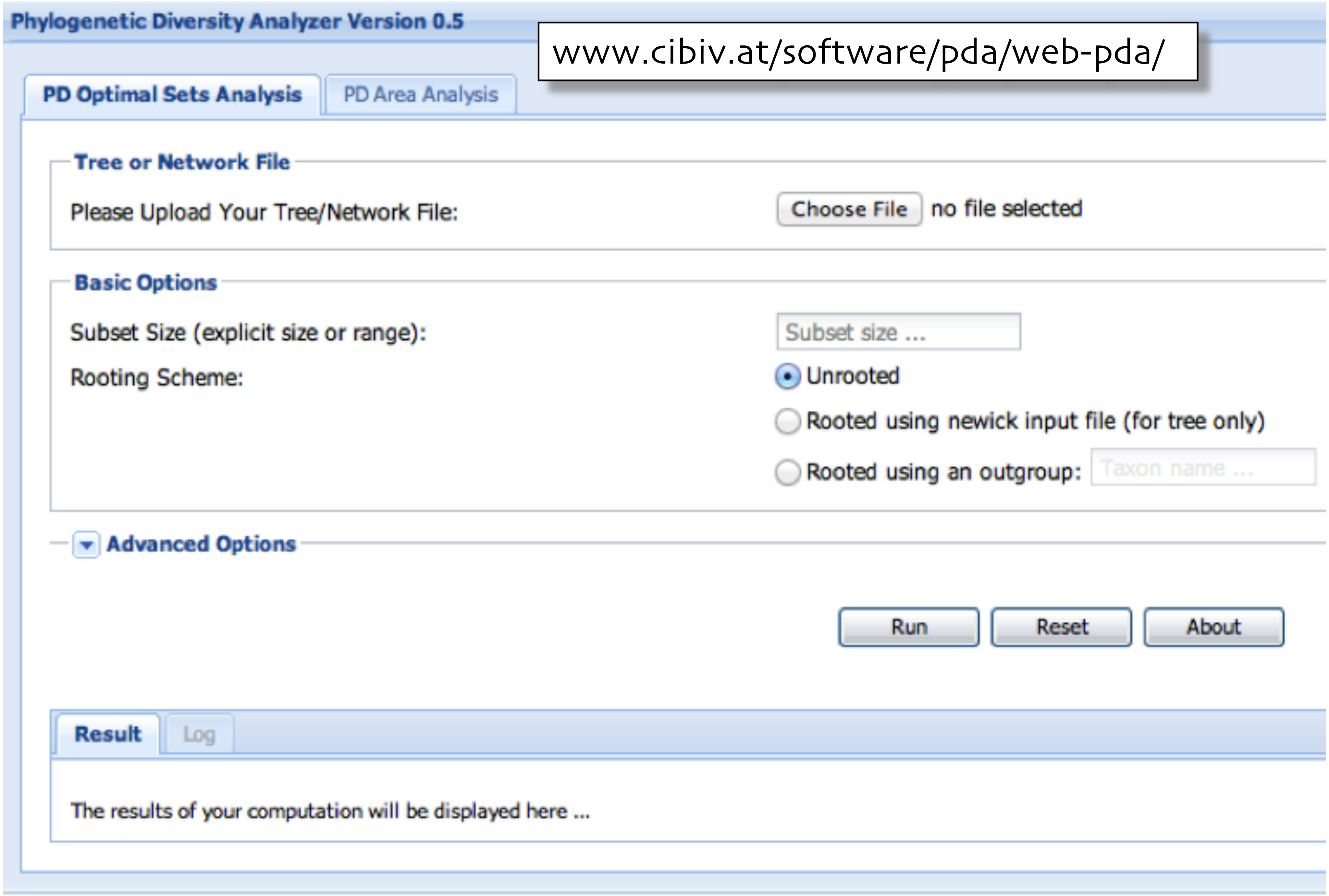
A

Minh, B.Q. & al. 2006. Phylogenetic diversity within seconds. *Systematic Biology* 55: 769-773.

A. a -- A. i

A. a -- A. j

www.cibiv.at/software/pda/web-pda/



Phylogenetic Diversity Analyzer Version 0.5

Tree or Network File

Please Upload Your Tree/Network File: no file selected

Basic Options

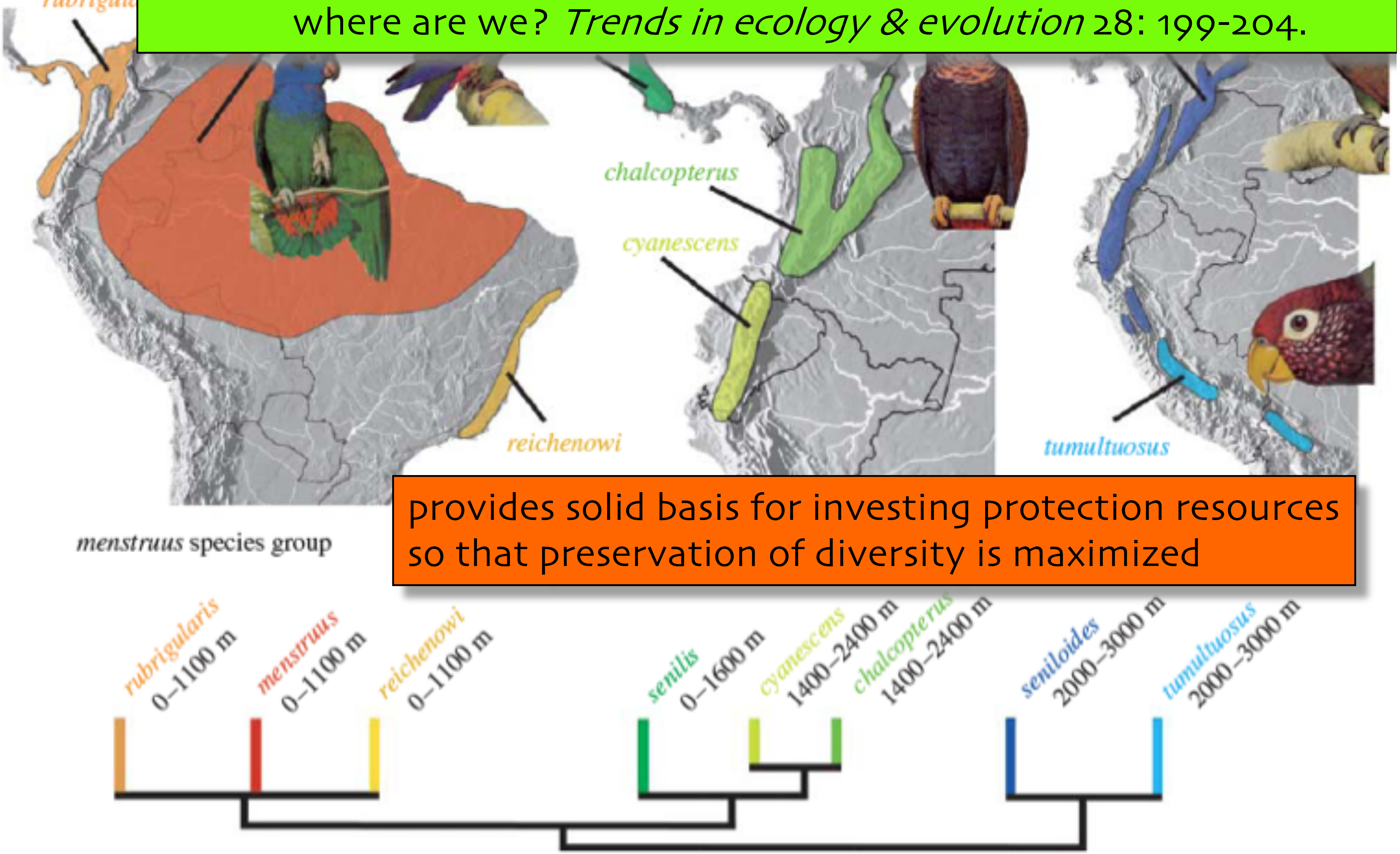
Subset Size (explicit size or range): Subset size ...

Rooting Scheme:
● Unrooted
○ Rooted using newick input file (for tree only)
○ Rooted using an outgroup: Taxon name ...

The results of your computation will be displayed here ...

Pionus

Winter, M. & al. 2013. Phylogenetic diversity and nature conservation: where are we? *Trends in ecology & evolution* 28: 199-204.



provides solid basis for investing protection resources so that preservation of diversity is maximized edgeofexistence.org

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OUR COMMUNITY

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Help support EDGE species today. See how you can help save them from extinction

ASSEMBLING THE TREE OF LIFE

www.nsf.gov/bio/pubs/reports/atol.pdf

HARNESSING LIFE'S HISTORY TO BENEFIT SCIENCE AND SOCIETY

SUMMARY

1. ALL taxa share common ancestor

Tree of Life

descent with modification

2. Signs of history can be found in ALL extant organisms

phylogenetic "signal"

from macromorphology to nucleotides

3. Comparative study of HOMOLOGIES enable hypotheses about phylogeny

4. Most reliable hypotheses are obtained by using LARGE number of characters of NUMEROUS taxa

simultaneous analysis

character CONGRUENCE

SUMMARY

5. Phylogenetic methods can be divided to 3 main groups according to optimality criteria used

distance

rich character information reduced to one number

parsimony

model based methods

6. Two latter differ in how much background knowledge is accepted

descent with modification vs.

explicitly defined models about evolution

UNIQUE events of history vs.

statistical treatment

SUMMARY

7. Fossils are NOT necessary for phylogenetic reconstruction but might be useful in many ways

8. Classification should reflect phylogeny as faithfully as possible, or at the very least, it should NOT be in conflict with it

ALL levels of hierarchy do NOT need formal name

9. Classification based on results of cladistic analysis contains maximal amount of information

minimization of exceptions

10. Reliable & easily comparable updated hypotheses about phylogeny enhance research in many fields of biology

refutation of unfounded hypotheses

and finally...

HISTORY IS PERHAPS PRODUCT OF ACCIDENTS BUT THE PATTERN THESE ACCIDENTS HAVE LEFT IS STILL OPEN FOR STUDY and this study can be systematic and reveal clear pattern despite of its accidental origin

Darwin-L internet keskusteluryhmä 1996-97

Independent exercise

BSc/MSc thesis