IPS-164 Introduction to phylogenetics

Lectures 10-12 (preliminary program) room 4617

31.x. Mon history, phylogenetic trees, characters
1.xi. Tue parsimony, homology, homo

3.xi. Thu characters, optimizatio
4.xi. Fri direct optimization

7.xi. Mon tree search algo
8.xi. Tue monophyly, consensus & compromise, introduction to models

ZOOM

room 6201

IPS-164 Introduction to phylogenetics

Lectures 10-12 (preliminary program) Biocenter III room 4617

31.x. Mon history, phylogenetic trees, characters
1.xi. Tue parsimony, homology, homoplasy

3.xi. Thu characters, optimization
4.xi. Fri direct optimization

7.xi. Mon tree search algorithms
8.xi. Tue monophyly, consensus & compromise,

10.xi. Thu intro to statistical phylogenetics I
11.xi. Fri intro to statistical phylogenetics II

14.xi. Mon reconstructing phylogenies I
15.xi. Tue. reconstructing phylogenies II

room 6201

17.xi. Thu tree dating
18.xi. Fri trait evolution & diversification I

21.xi. Mon trait evolution & diversification II

Sergei Tarasov

Computer demonstrations
Biocenter I room 1401.3

14.xi. Mon 14-16 Cladistic Primer
15.xi. Tue 14-16 data repositories
17.xi. Thu 14-16 datamatrices
18.xi. Fri 14-16 TNT

21.xi. Mon 14-16
22.xi. Tue 14-16
28.xi. Thu 14-16
29.xi. Fri 14-16

IPS-164 Introduction to phylogenetics

10 ECTS

Lectures 10-12 (preliminary program)

31.x. Mon history, phylogenetic trees, charac
1.xi. Tue parsimony, homology, homoplasy

3.xi. Thu characters, optimization

8.xi. Tue monophyly, consensus & compromise,

lecture slides available in pdf-format AFTER the lectures

www.helsinki.fi/~jhyvonen/IPS-164

independent exercise due by 31.v.2023

- choose a topic
- we provide tasks for your exercise (based on the use of programs demonstrated)
- have to include a two page summary of the article(s) used

Computer demonstrations
Biocenter I room 1401.3

14.xi. Thu 14-16 Cladistic Primer
15.xi. Fri 14-16 data repositories
17.xi. Thu 14-16 winclada
18.xi. Fri 14-16 TNT

21.xi. Mon 14-16
22.xi. Tue 14-16

28.xi. Mon 14-16
29.xi. Tue 14-16

attendance required

31.x.

1. introduction, history

2. phylogenetic trees

3. taxonomic characters

4. summary

SOUND basic principles

nuts & bolts of phylogenetic analysis

PHYLOGENETICS

phulon, phulē — *Greek* race, tribe

gignesthai — *Greek* be born/produced

TAXONOMY

systematics

description

nomenclature

CLASSIFICATION of organisms

enables our navigation in the ocean of biodiversity

UPPSALA UNIVERSITET

Listen

På svenska

- Introduction
- The Life of Linnaeus
- Linnaeus and Pharmacy
- Plants and Animals
- Physics and the Cosmos
- The History of Ideas
- Linnaeus and Ecology
- Mathematics in Linnaeus' time
- Linnaeus as a Physician

Linné on line

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Linné on line

Welcome!

www.linnaeus.uu.se/online/index-en.html

On this website Uppsala University presents results of research relating to the work of one of the most famous professors throughout its history, namely Carl Linnaeus (Carl von Linné) (1707–1778).

You can learn more about

God created,
Linnaeus classified

The Life of Linnaeus
– childhood, schools, career and family

Linnaeus and Pharmacy
– a journey among the pharmaceuticals of Nature

Plants and Animals
– biological diversity in the 18th century and today

Physics and the Cosmos
– what Linnaeus did not know about the Cosmos

www.iapt-taxon.org/nomen/main.php

The History of Ideas
– Linnaeus, his epoch, his view of nature and a journey through the history of ideas

Linnaeus and Ecology
– Linnaeus' thoughts of "The Economy of Nature"

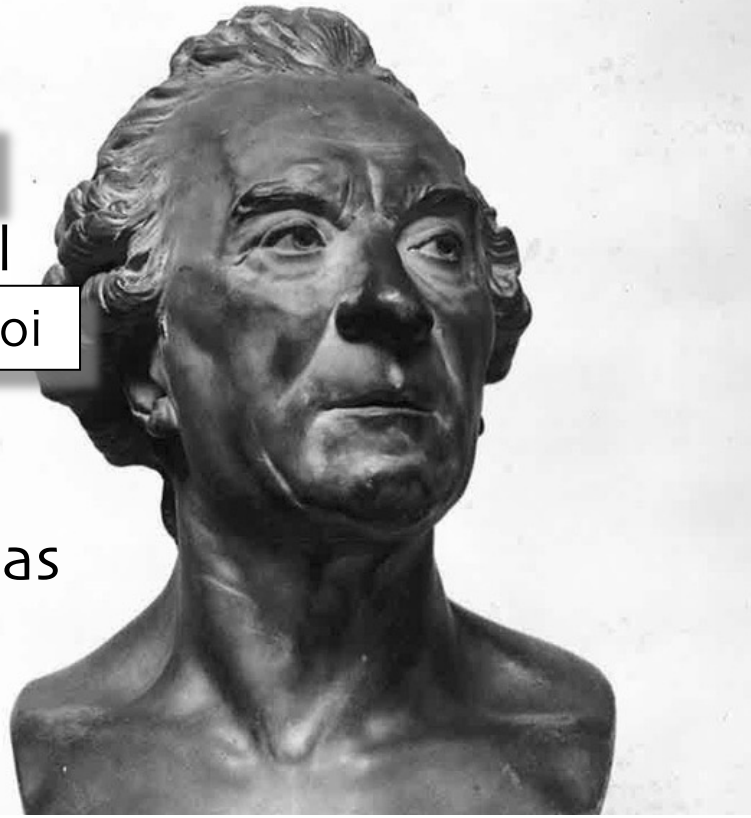
Mathematics in Linnaeus' time
– Mathematics and mathematicians of the 18th century, with a special focus on Linnaeus' professorial colleague Samuel Klingenstierna

… meanwhile in France

Georges Louis Leclerc 1707-1788

Comte de Buffon

- director of the Royal Botanical Garden in Paris — Jardin de Roi
- Histoire naturelle, générale et particulière 1749-1804
- opposed Linné´s classification as artificial



Buffon's point …. the species …. are not the abstract universals of logic of the taxonomists but are rather systems of *concrete* relationship between real creatures at the level of physical truth.

Sloan, P.R. 1976. The Buffon-Linnaeus controversy. Isis 67: 356-375

Jean-Baptiste de Lamarck

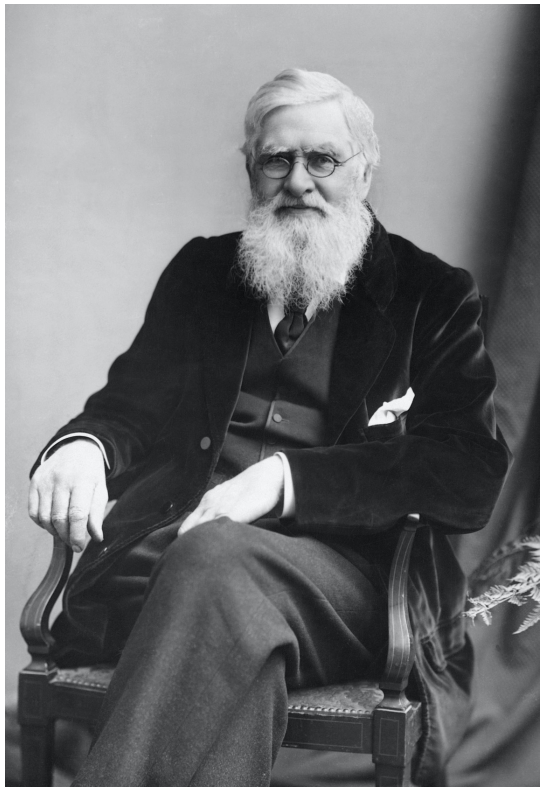
1744-1829

- 1st broad theory of evolution
- inheritance of acquired characters
- theory disproved but stimulated large no. of later studies

CHARLES DARWIN 1857

… the time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (*phylogenetic*) trees of each great kingdom of nature…

letter to Thomas Huxley



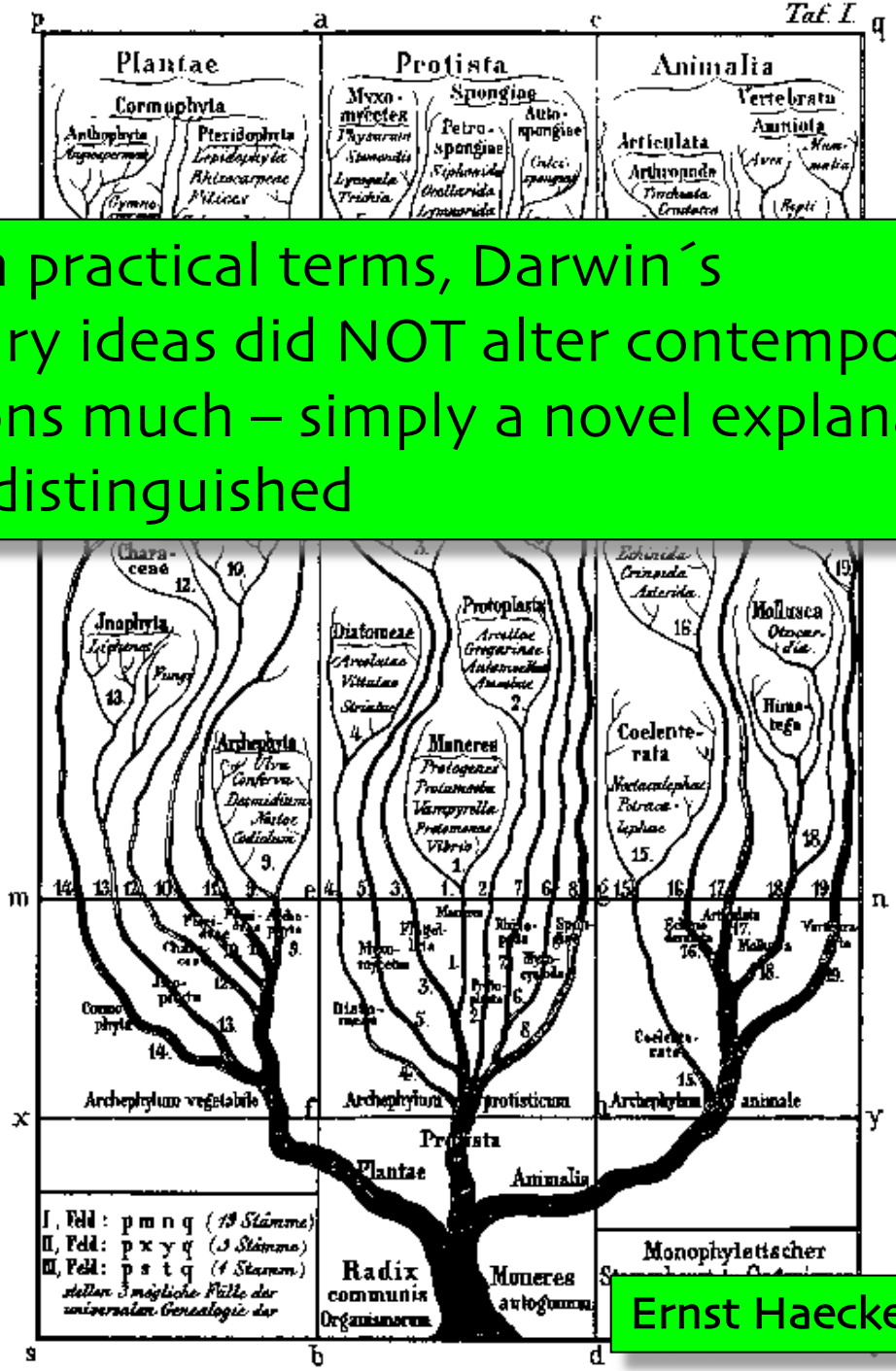
CHARLES DARWIN 1857

… the time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (*phylogenetic*) trees of each great kingdom of nature…

On the origin of species by means of natural selection

DESCENT WITH MODIFICATION

however, in practical terms, Darwin´s revolutionary ideas did NOT alter contemporary classifications much – simply a novel explanation for groups distinguished



Ernst Haeckel, Jena, 1866

Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

Hennig, W. 1950. Grundzüge einer Theorie der phylogenetischen systematik

Hennig, W. 1966. Phylogenetic systematics

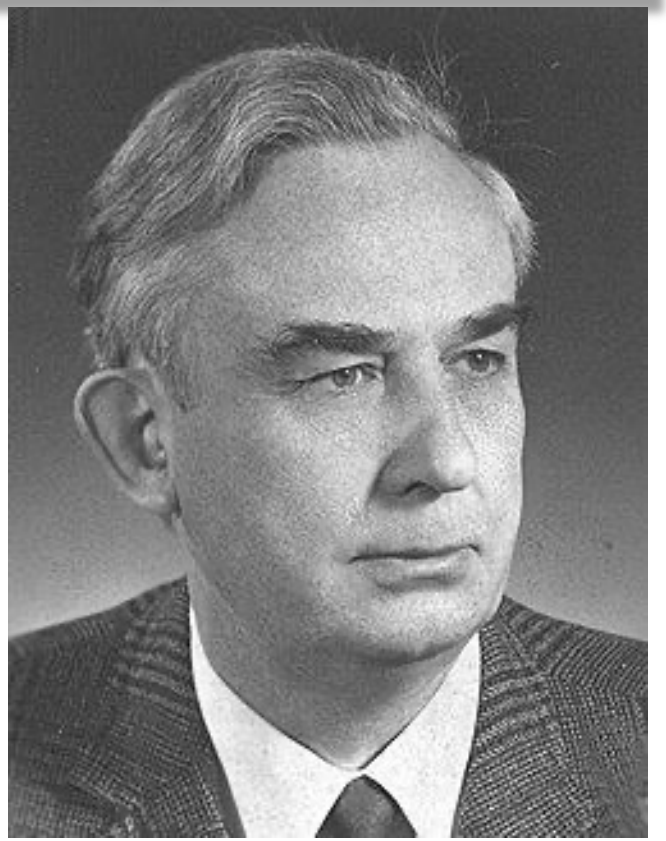
CLADISTIC REVOLUTION

CLEAR, EXPLICIT & LOGICAL presentation of basic principles of phylogenetic analysis

SYNAPOMORPHY

MONOPHYLY

PARAPHYLY



Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

http://rapinidep1.webs.com/origin/Hennig_1965.pdf

Hennig´s (1965) 3 primary questions:

1. What is phylogeny?
2. How is it established?
3. How to describe it explicitly?

Emil Hans WILLI HENNIG

*20.4.1913 †5.11.1976

Hennig´s (1965) 3 primary questions:

1. What is phylogeny?
2. How is it established?
3. How to describe it explicitly?

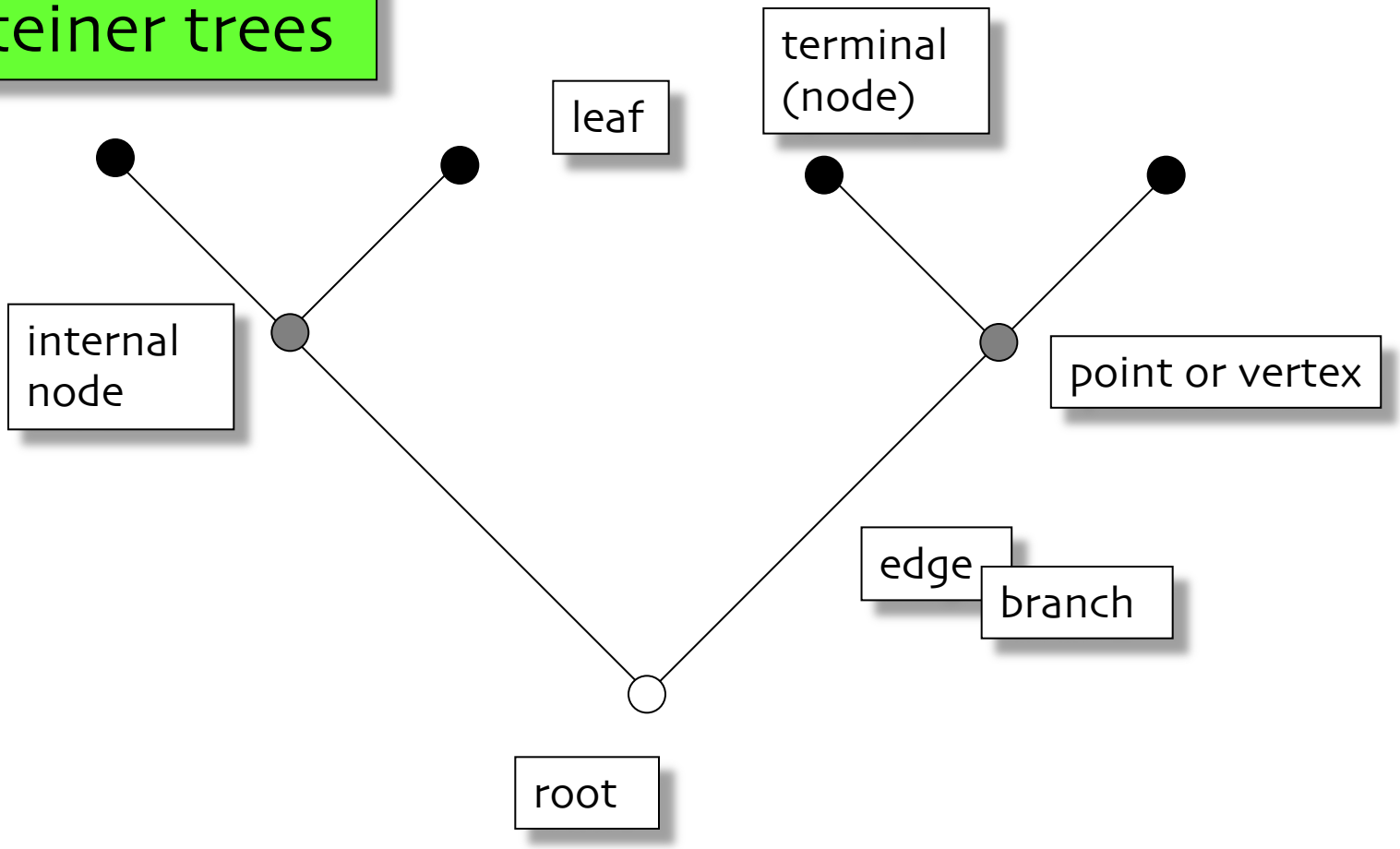
and his 3 precise answers:

1. Phylogeny is GENEALOGICAL relationship where two taxa are more closely related to each other than they are to a third one
2. Relationships are established by SYNAPOMORPHIES
3. Relationships can be presented using branching diagrams (=cladograms)

What are trees?

acyclic connected GRAPH

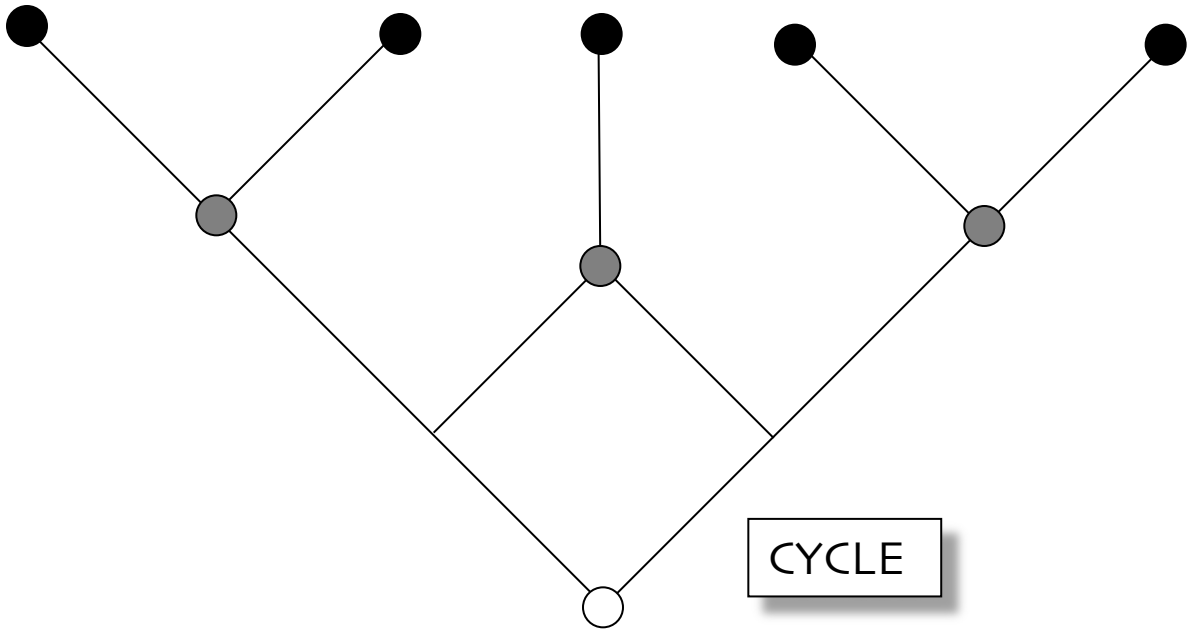
rectilinear Steiner trees



Page & Holmes 1998. Molecular evolution

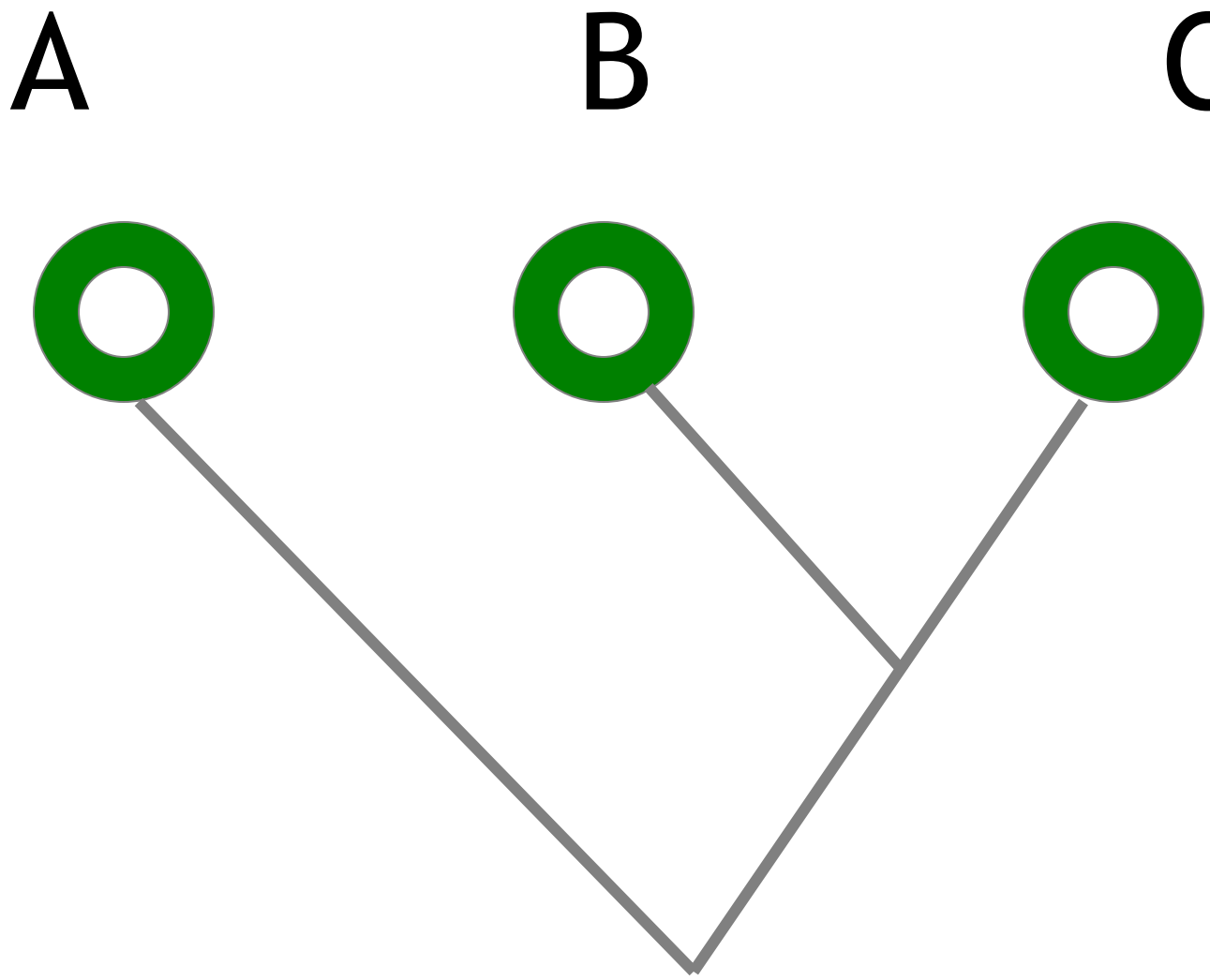
Network

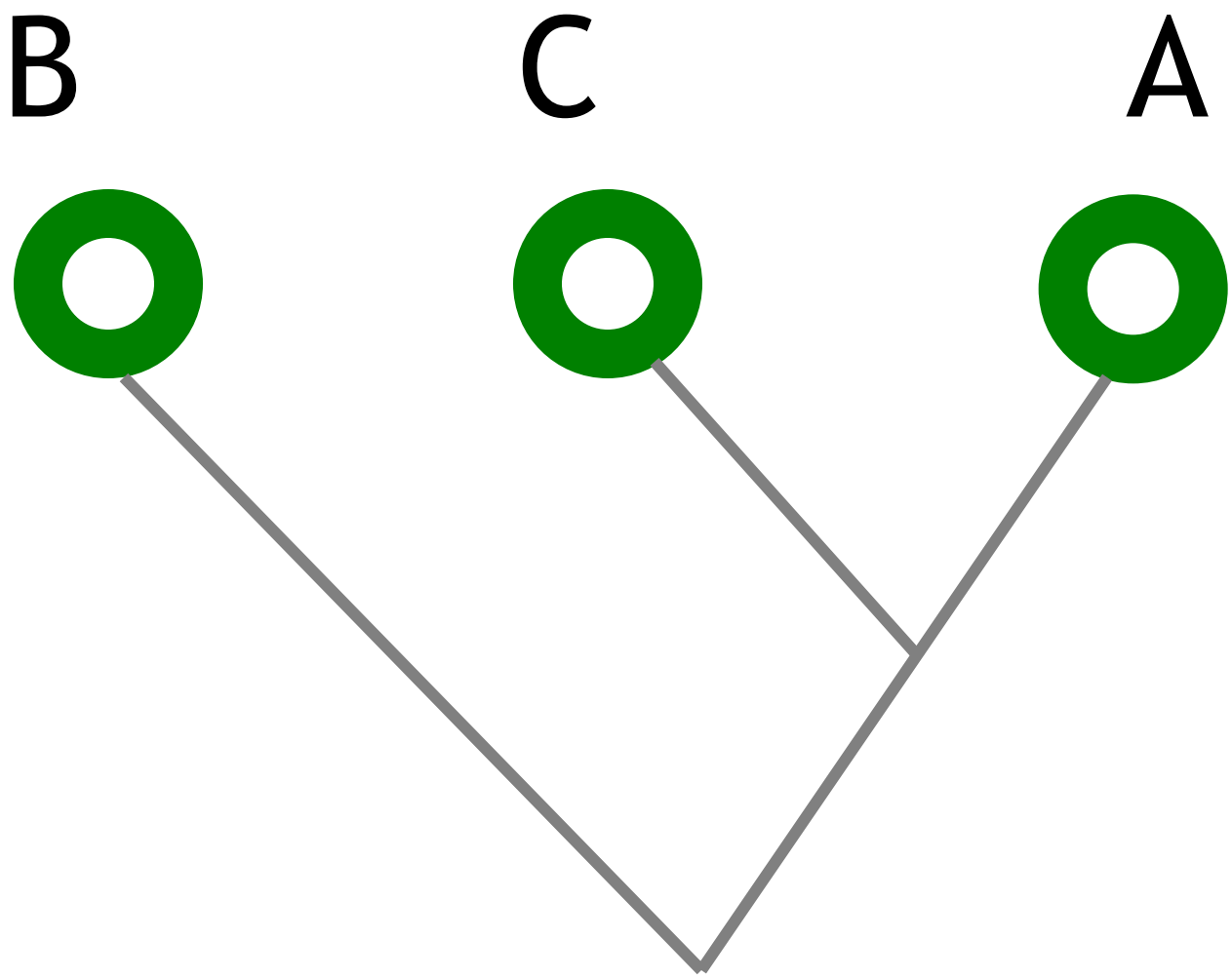
cyclic connected GRAPH

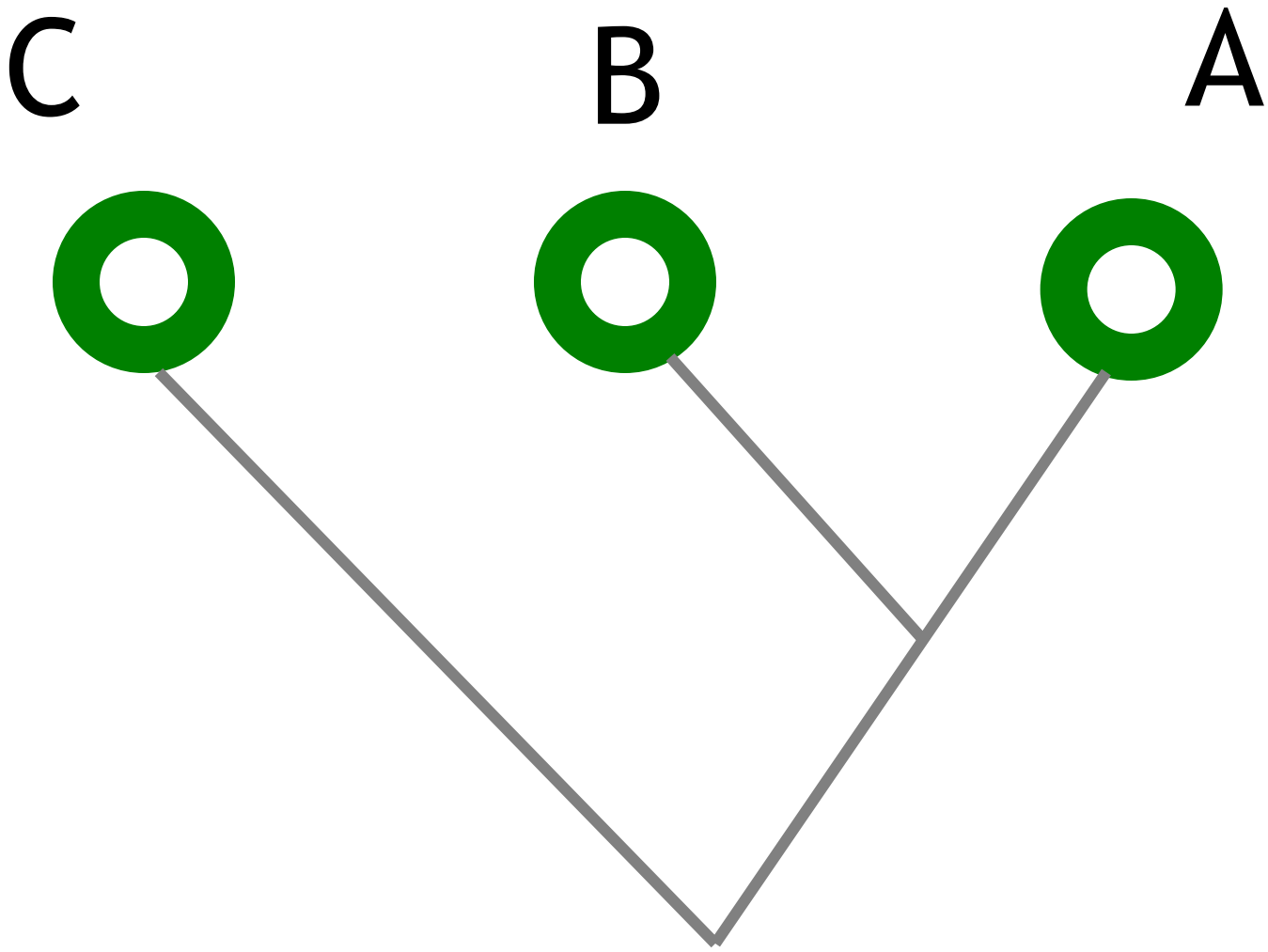


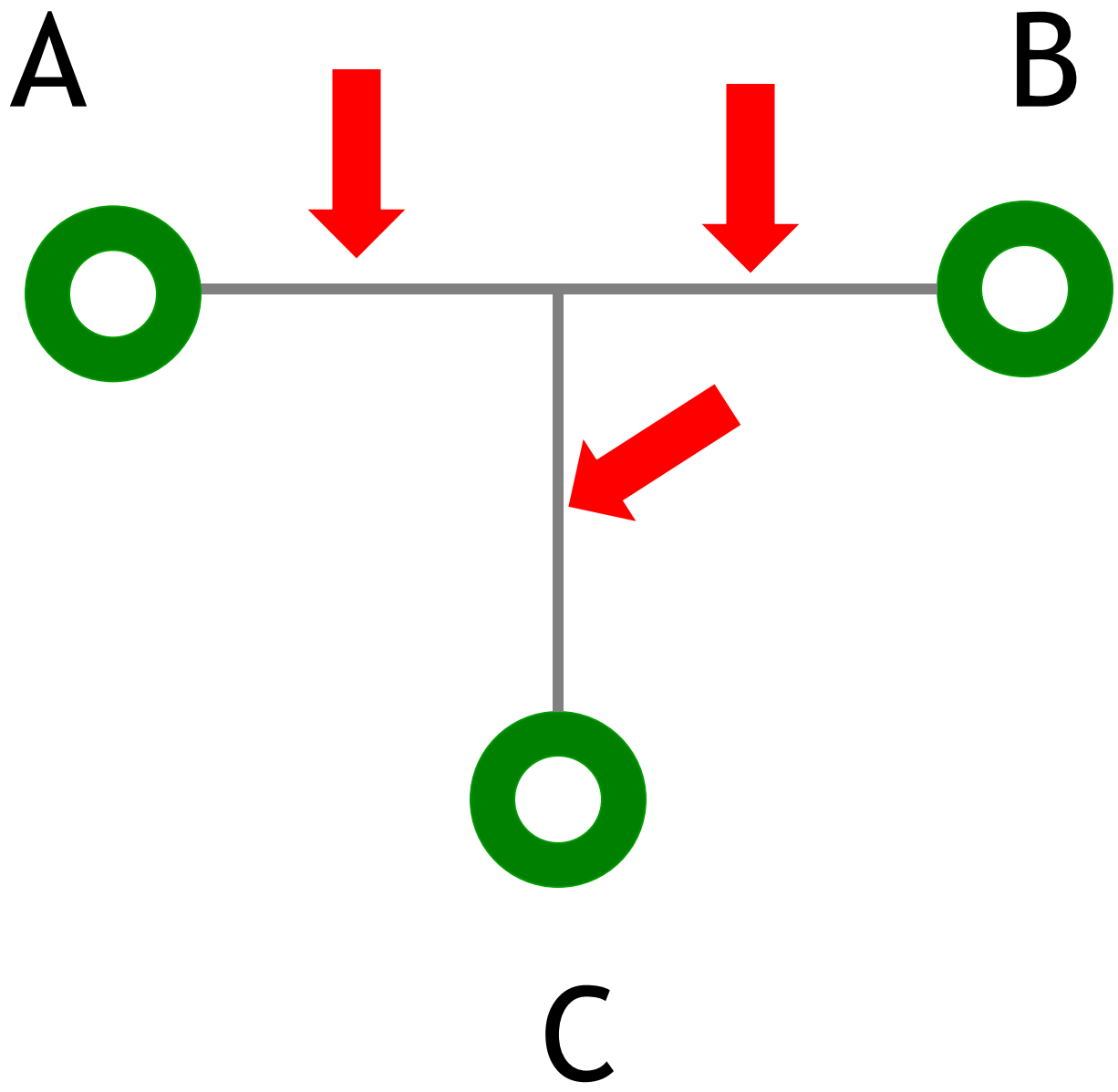
Page & Holmes 1998.
Molecular evolution

Number of possible trees?


A
B
C


B
C
A


C
B
A


A
B
C

n	B(n)
3	1
4	3
5	15
6	105
7	945
8	10 395
9	135 135
10	2 027 025
15	7 905 853 580 625
20	221 643 095 476 699 771 875
50	3×10^{74}

number of undirected trees

$B(n) = (2n-5)!!$

$$B(n) = (2n-5)!!$$

$$(2 \times 9 - 5)!!$$

$$(18 - 5)!!$$

$$13!!$$

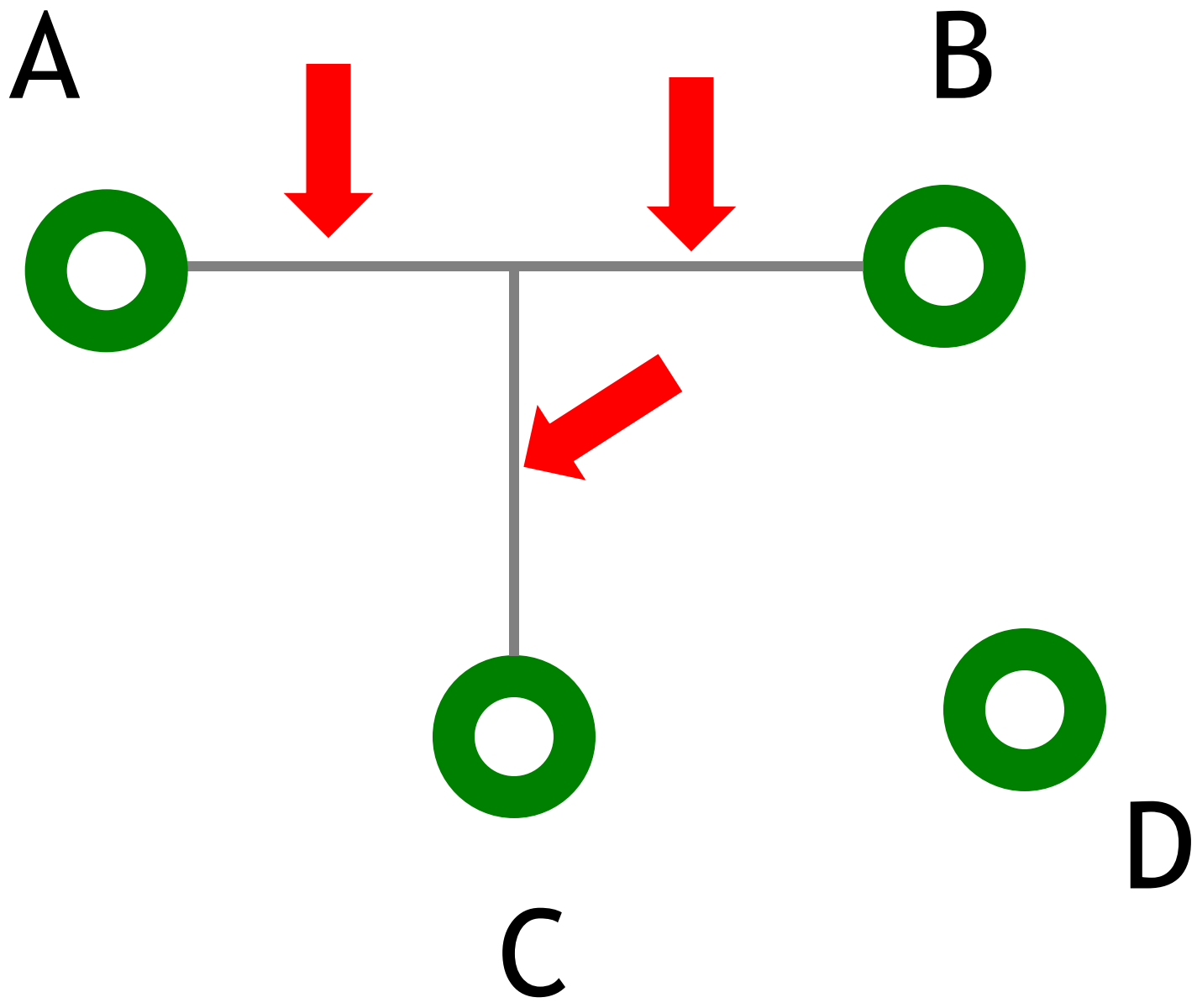
$$13 \times 11 \times 9 \times 7 \times 5 \times 3 \times 1$$

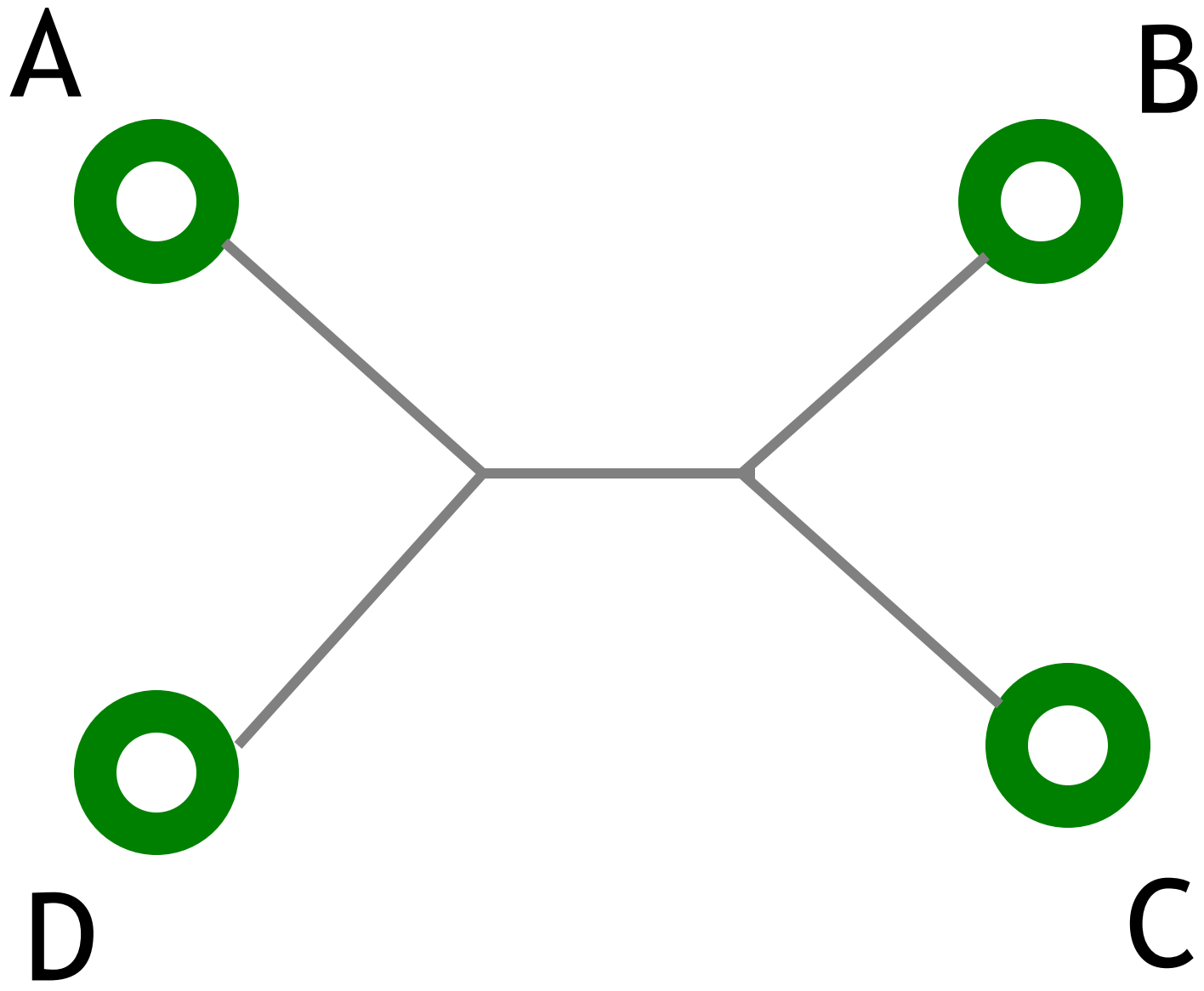
$$135\ 135$$

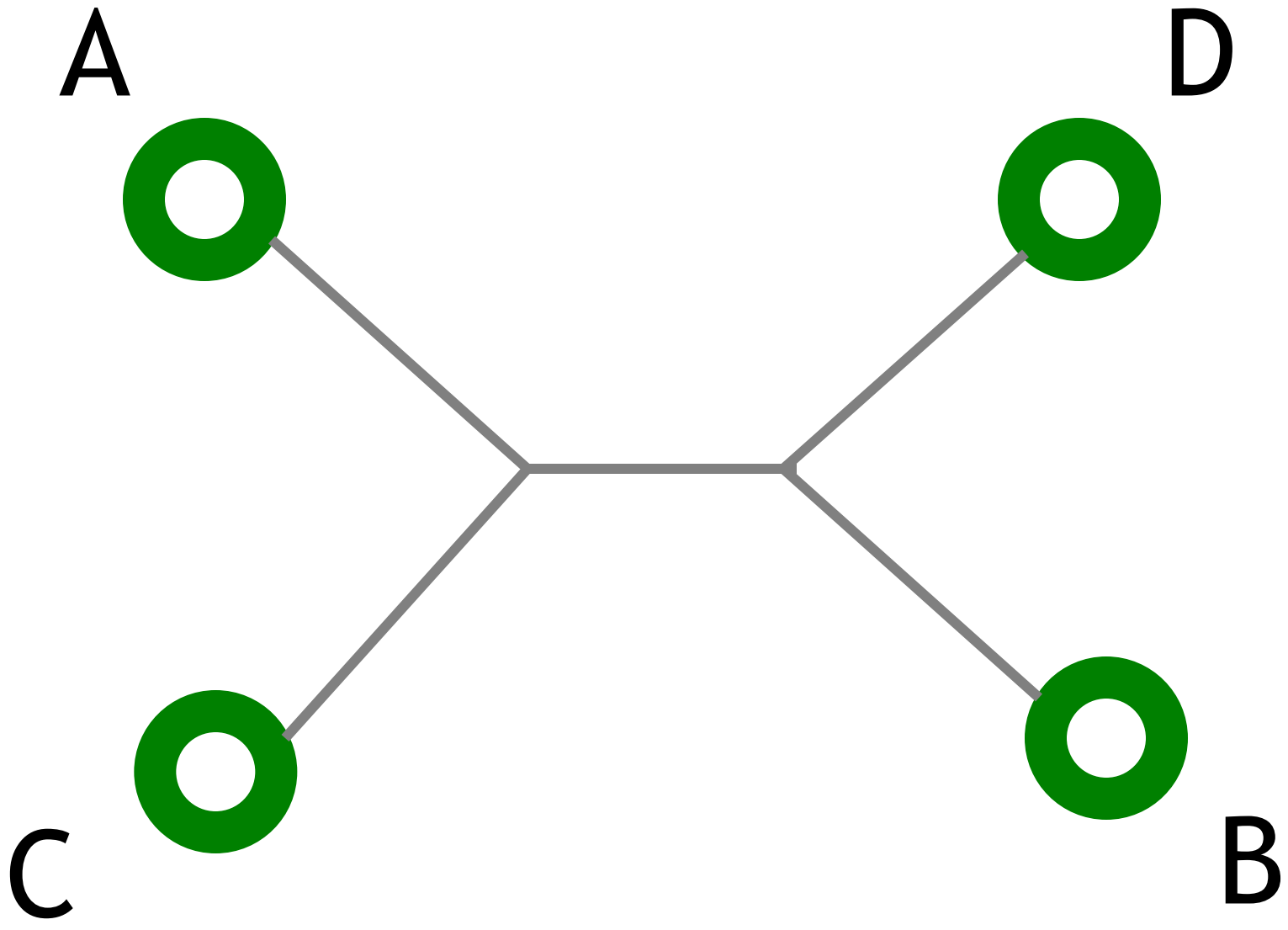
n	B(n)
3	3
4	15
5	105
6	945
7	10 395
8	135 135
9	2 027 025
10	34 459 425
15	213 458 046 676 875
20	8 200 794 532 637 891 559 375

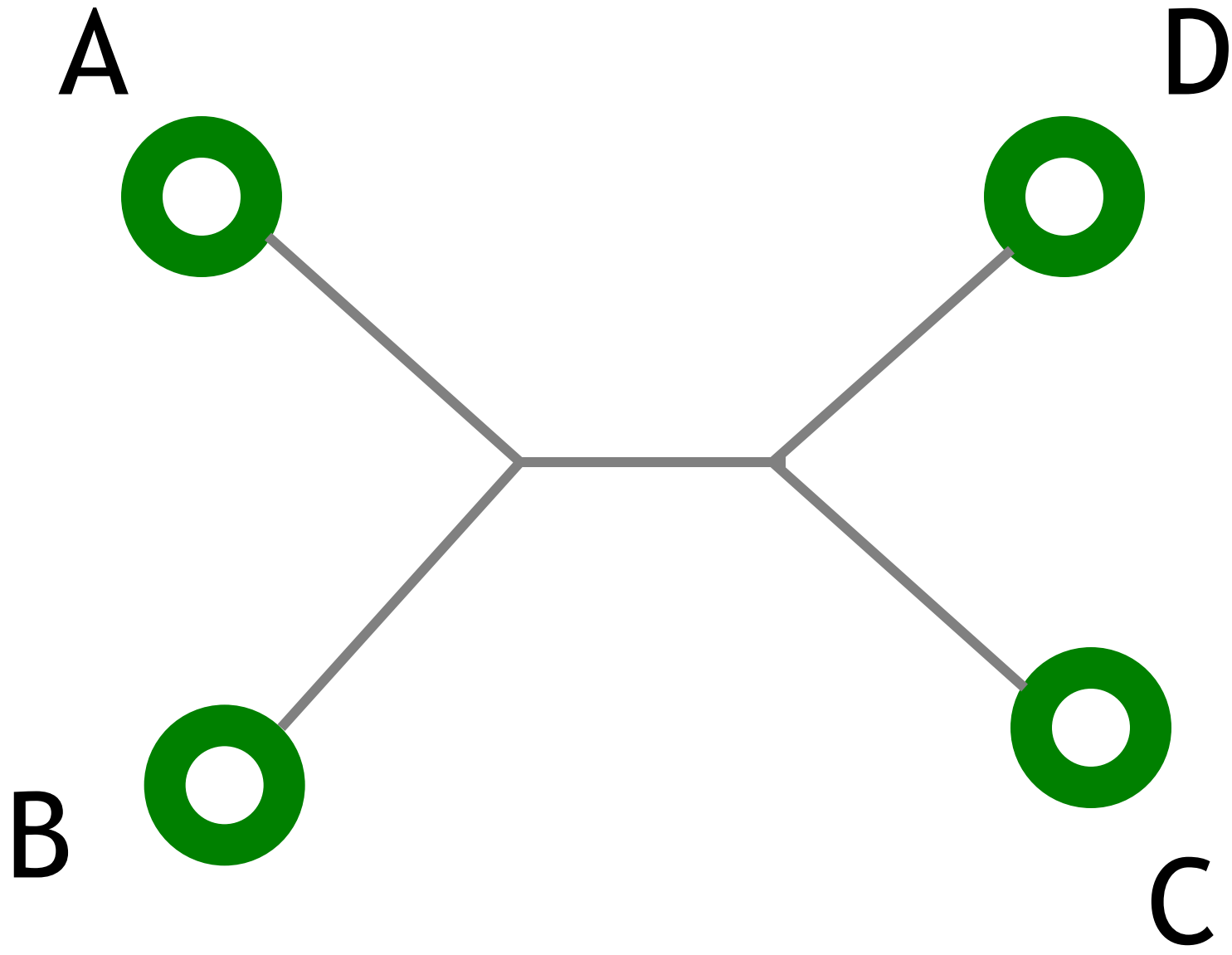
number of directed trees

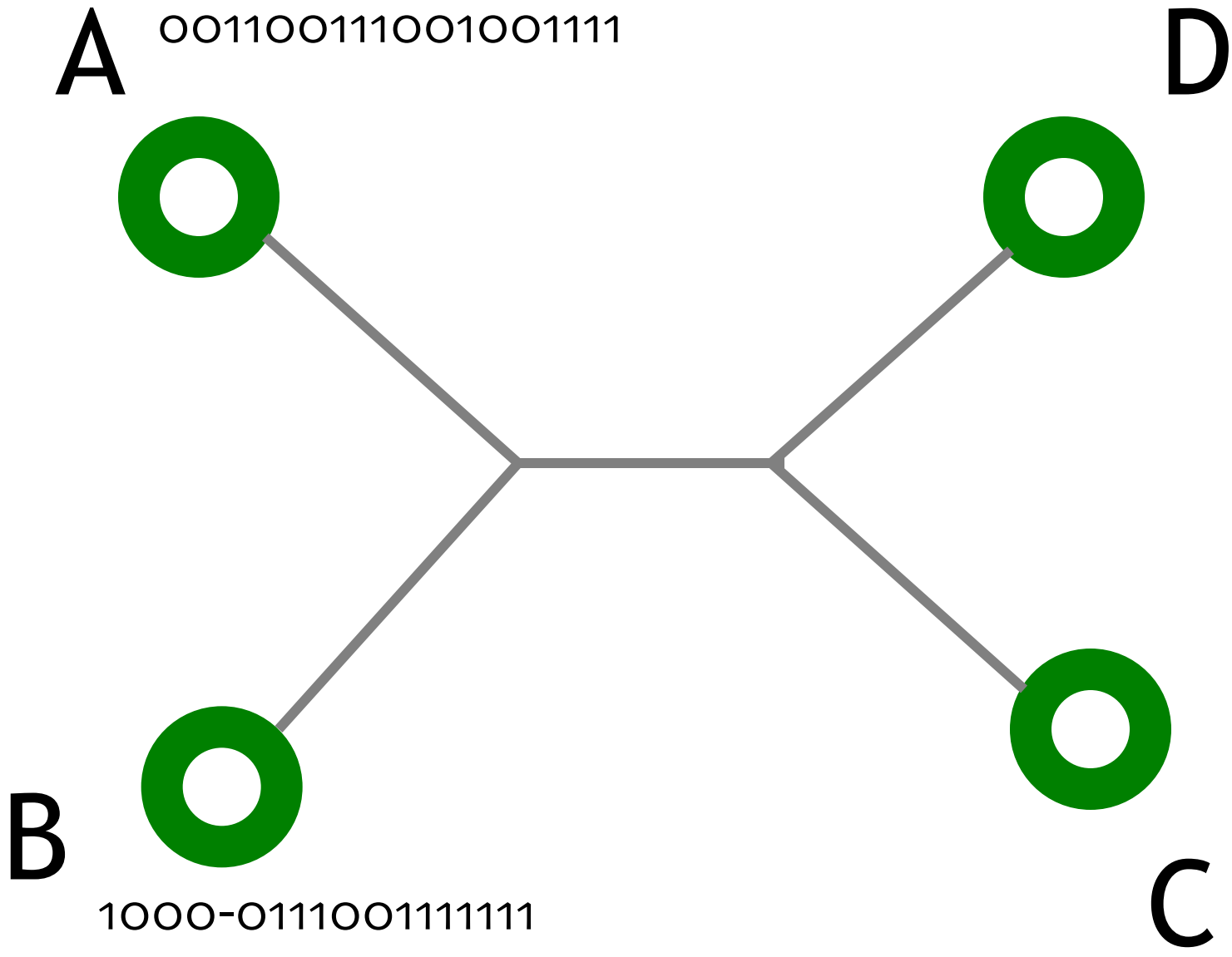
$B(n) = (2n-3)!!$


A
B
C
D


A
B
D
C


A
D
C
B


A
D
B
C


A
00110011100100 1111
D
B
1000-01110011111111
C

characters	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
terminals A	1	0	0	0	0	1	0	0	0	0
B	1	0	1	1	1	1	1	1	1	1
C	0	1	1	0	0	1	1	1	1	0
D	1	0	0	0	0	1	1	0	0	0
E	1	0	1	0	1	1	1	1	1	0

TAXONOMIC CHARACTERS

= potentially useful for phylogenetic analysis

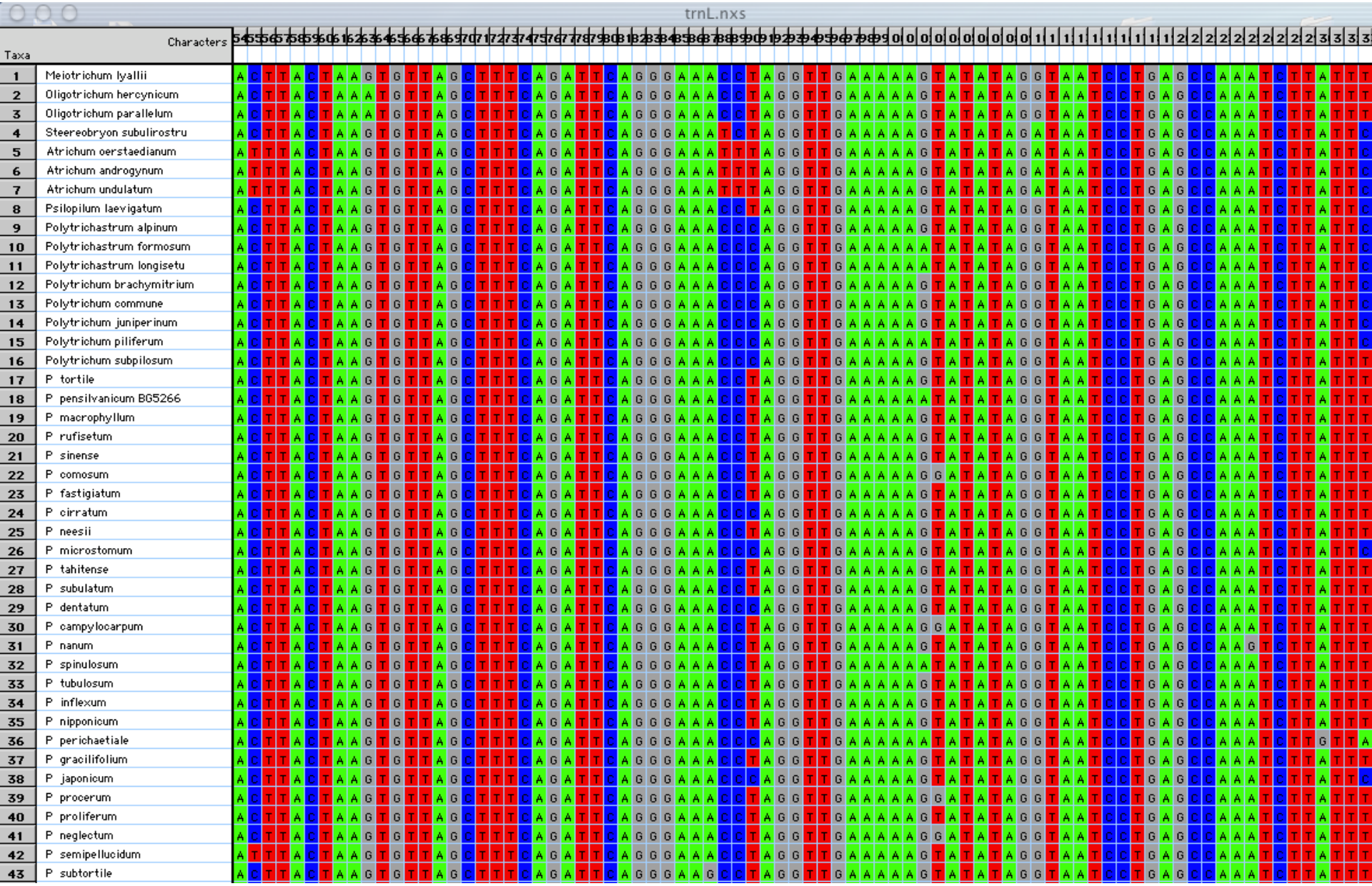
COMPARATIVE STUDY OF CHARACTERS










trnL.nxs
Taxa
Characters
1 Meiotrichum lyallii
2 Oligotrichum hercynicum
3 Oligotrichum parallelum
4 Steereobryon subulirostru
5 Atrichum oerstaedianum
6 Atrichum androgynum
7 Atrichum undulatum
8 Psilopilum laevigatum
9 Polytrichastrum alpinum
10 Polytrichastrum formosum
11 Polytrichastrum longisetu
12 Polytrichum brachymitrium
13 Polytrichum commune
14 Polytrichum juniperinum
15 Polytrichum piliferum
16 Polytrichum subpilosum
17 P tortile
18 P pensilvanicum BG5266
19 P macrophyllum
20 P rufisetum
21 P sinense
22 P comosum
23 P fastigiatum
24 P cirratum
25 P neesii
26 P microstomum
27 P tahitense
28 P subulatum
29 P dentatum
30 P campylocarpum
31 P nanum
32 P spinulosum
33 P tubulosum
34 P inflexum
35 P nipponicum
36 P perichaetiale
37 P gracilifolium
38 P japonicum
39 P procerum
40 P proliferum
41 P neglectum
42 P semipellucidum
43 P subtortile

observations about compared organisms

interpretation

coding as characters and their states

TAXONOMIC CHARACTERS

transformation series, character
character, character state

Wiley´s 3 conditions for characters to be useful in cladistic analysis:

1. variation between compared terminals

2. observed variation shows regularity

3. variation controlled genetically, not induced by environment

from the level of single nucleotides to macromorphology

ALL assumedly homologous characters that show VARIATION between terminals are POTENTIALLY useful for infering phylogeny

TAXONOMIC CHARACTERS

we can use for example the following when trying to find potential homologies:

1. topology (position)

2. external similarity

3. "continuum" between character states

TAXONOMIC CHARACTERS

1. PRELIMINARY hypothesis about homology

   observed similarities between compared terminals are interpreted as HOMOLOGIES (NULL hypothesis)

2. distinguish character STATES
3. with cladistic analysis we "test" these preliminary hypotheses against those made for other characters-->

TAXONOMIC CHARACTERS

hypothesis about homology either accepted or rejected

HOMOLOGY = shared feature inherited from common ancestor

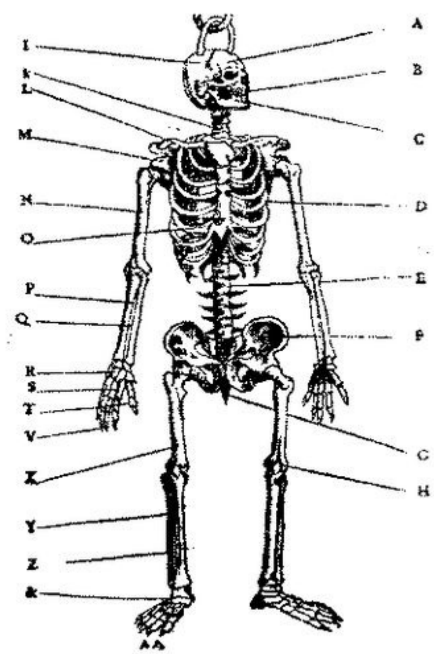
HOMOLOGY

Richard Owen (1804-1892) originally presented (1848) concept of HOMOLOGY for
similar structures of organisms that represent ARCHETYPE

Pierre Belon (1517-1564)

LIVRE I. DE LA NATVRE

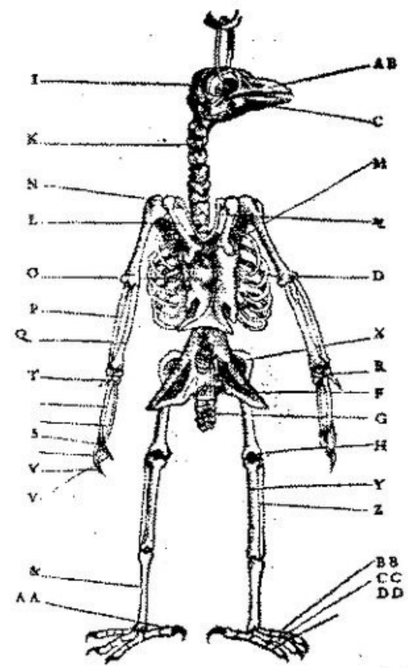
Portraict de l'amas des os humains, mis en comparaison de l'anatomie de ceux des oyseaux, faisant que les lettres d'icelle se raporteront à ceste cy, pour faire apparoistre combien l'affinité est grande des vns aux autres.



DES OYSEAVX, PAR P. BELON. 41

La comparaison du susdit portraict des os humains monstre combien cestuy cy qui est d'vn oyseau, en est prochain.

Portraict des os de l'oyseau.



A B Les Oyseaux n'ont dents ne levres, mais ont le bec tranchant fort ou foible, plus ou moins selon l'affaire qu'ils ont eu à mettre en pieces ce dont ils vivent.

M Deux palerons longs & estroicts, vn en chascun costé.

K L'os qu'on nommé la Lunette ou Fourchette n'est trouvé en aucun autre animal, hors mis en l'oyseau.

D Six costes, attachees au coffre de l'estomach par devant, & aux six vertebres du dos par derriere.

F Les deux os des hanches sont longs, car il n'y a aucunes vertebres au dessoubs des costes.

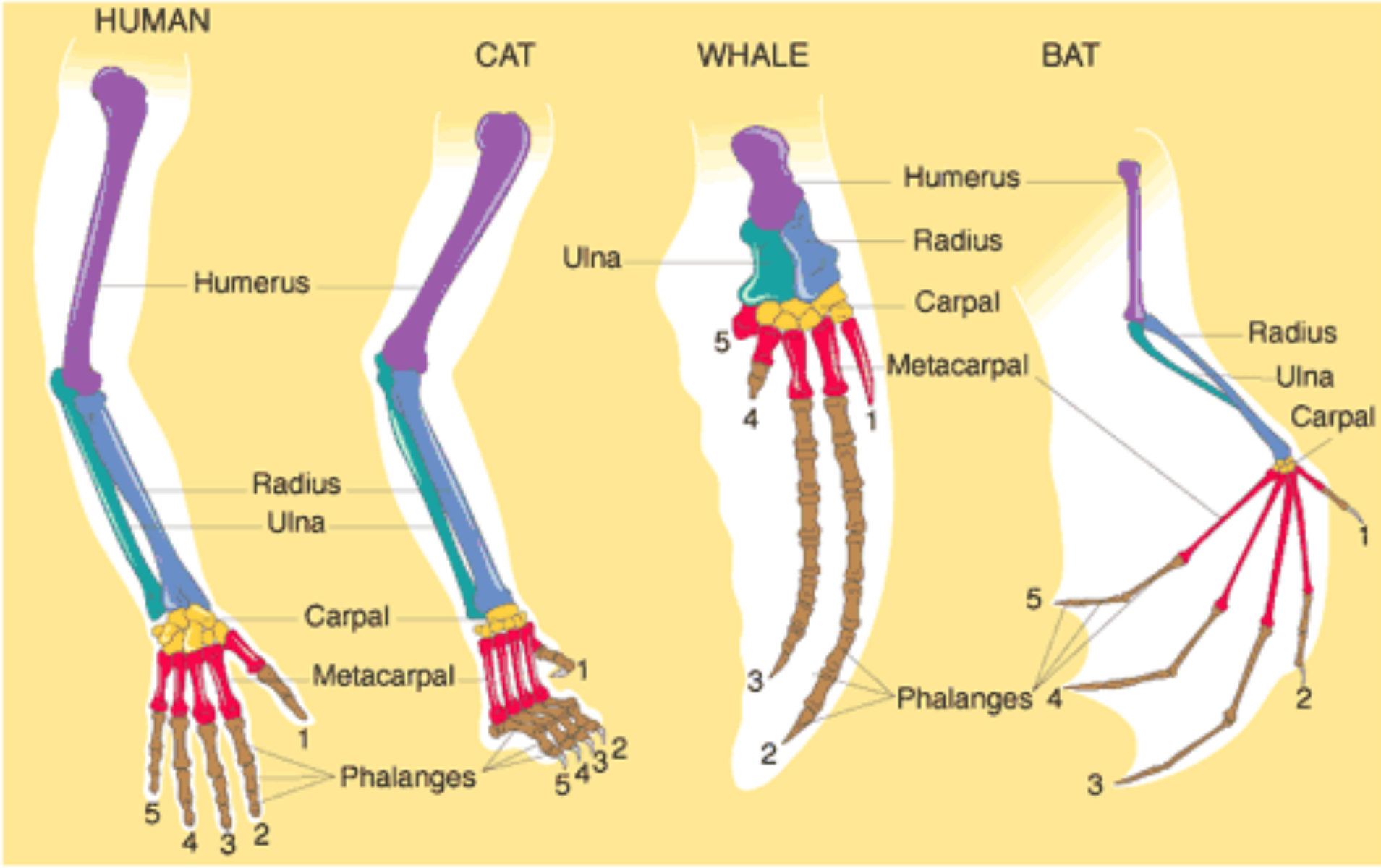
G Six osselets au croupion.

H La rouelle du genoil.

I Les sutures du test n'apparoissent guere sinon qu'il soit bouilly.

k Douze vertebres au col, & six au dos.

d iii



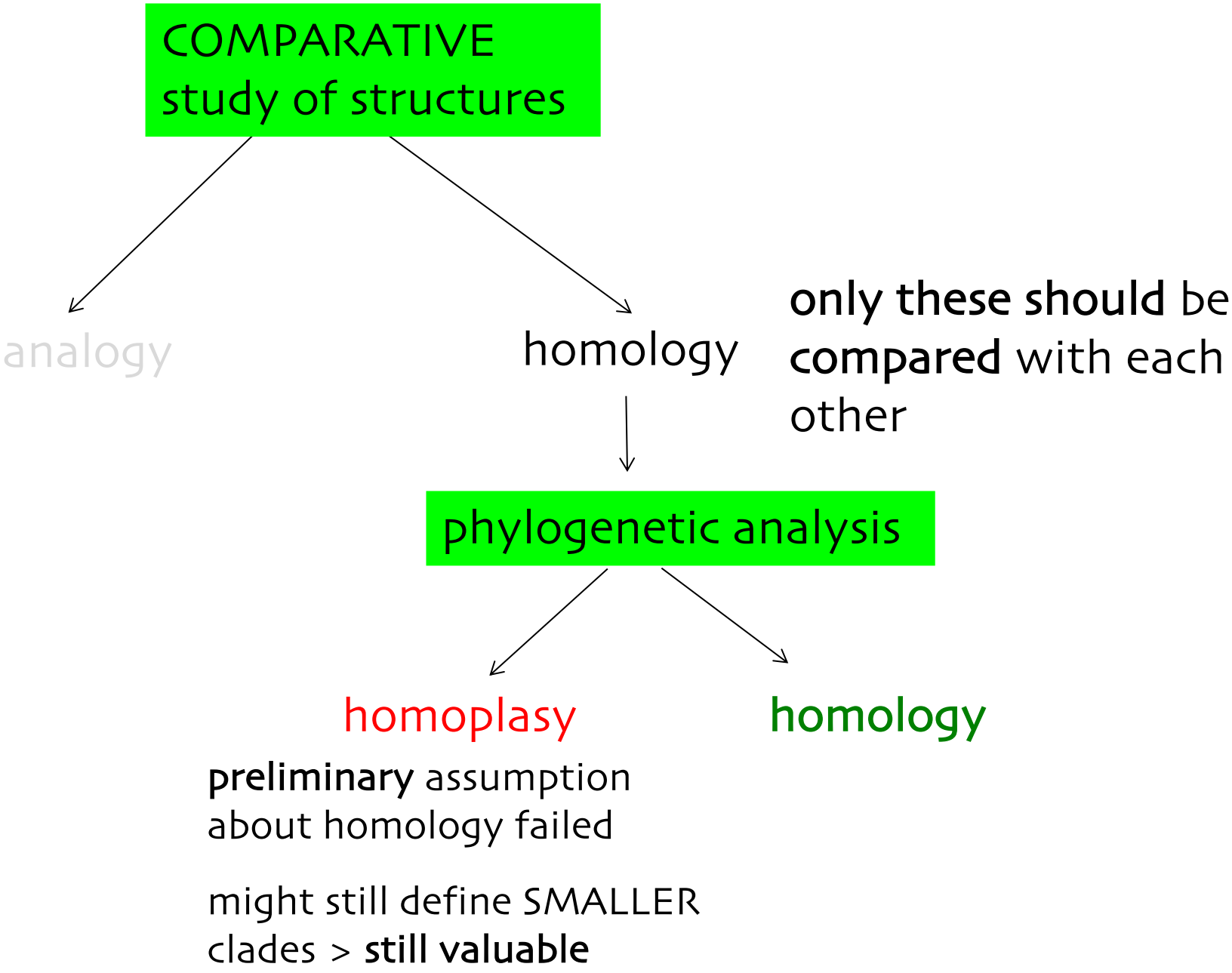
HOMOLOGY & ANALOGY

HOMOLOGY
same organ in different animals under every variety of form and function

ANALOGY
a part or organ in one animal which has the same function as another part or organ in a different animal

HOMOLOGY & ANALOGY

homology informs about history, part of historical signal,
ANALOGY does NOT


COMPARATIVE
study of structures
analogy
homology
only these should be compared with each other
phylogenetic analysis
homoplasy
homology
preliminary assumption about homology failed
might still define SMALLER clades > still valuable

TAXONOMIC CHARACTERS

binary characters (only 2 character states)
coded 0 & 1

teeth by lf margins : present (0), absent (1)

in many characters numerous character states can be distinguished , coded 0, 1, 2, 3, 4, etc.

A C G T

petal color: white (0), yellow (1), orange (2)
red (3), blue (4)

TAXONOMIC CHARACTERS

continuous characters & landmark data

QUANTITATIVE characters, ch. state distinction impossible/problematic

VARIATION still observed between terminals

TAXONOMIC CHARACTERS

transformation series, character character, character state

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TAXONOMIC CHARACTERS

continuous characters & landmark data

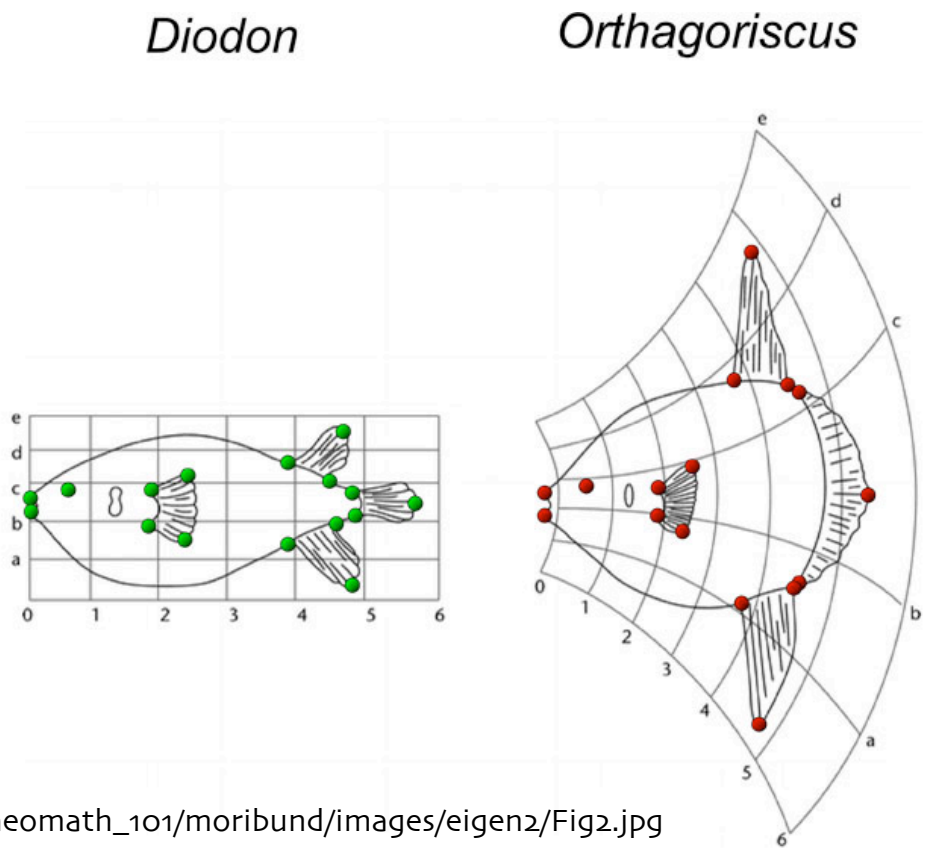
QUANTITATIVE characters, ch. state distinction impossible/problematic

VARIATION still observed between terminals

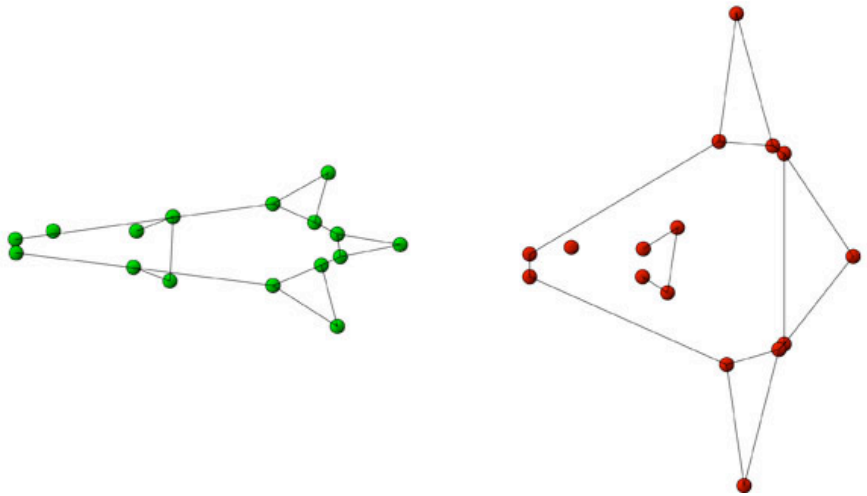
numerous case studies have shown that also these kind of characters DO include valuable phylogenetic information

most advanced applications allow use of these characters directly & together with other kind of characters

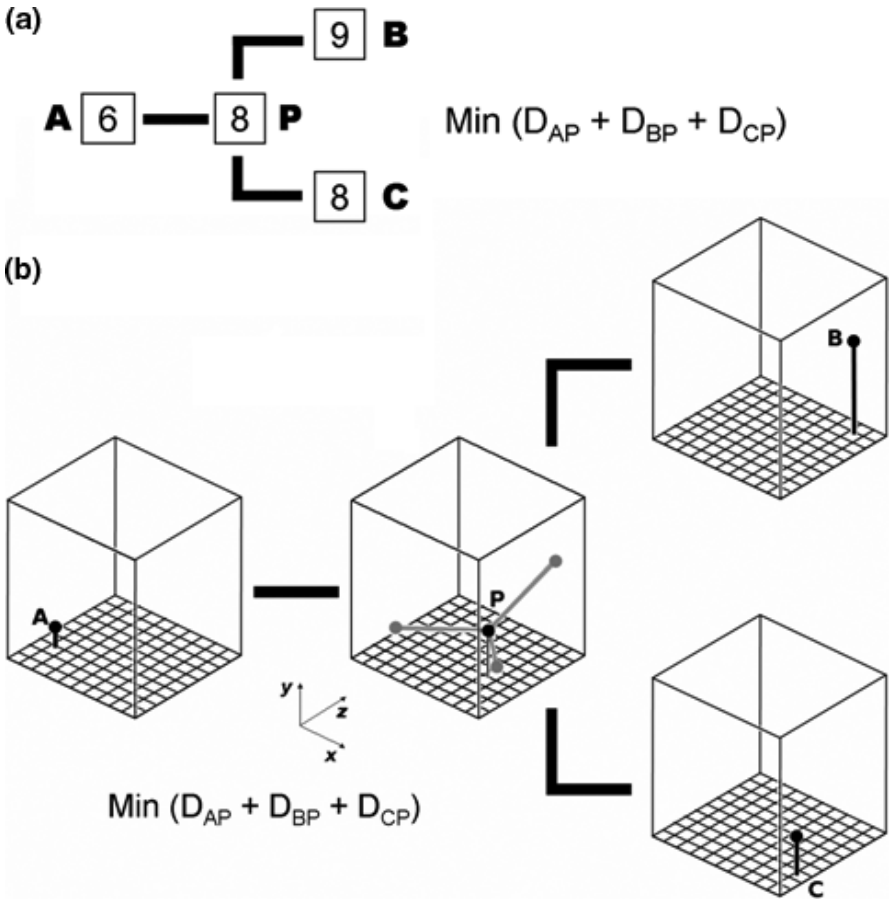
e.g. with program TNT



http://cdn.palass.org/palaeomath_101/moribund/images/eigen2/Fig2.jpg



Catalano, S.A. & al. 2010. Phylogenetic morphometrics (1): the use of landmark data in a phylogenetic framework. Cladistics 26: 539-549.



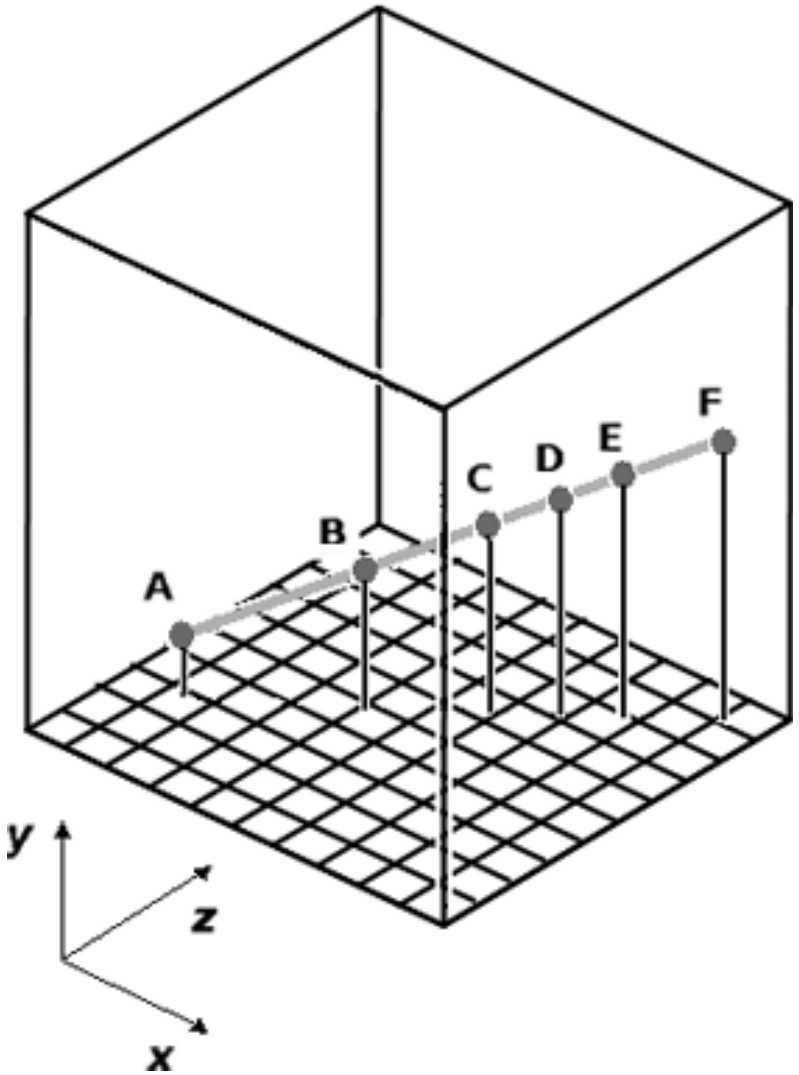


Fig. 1. Comparison between (a) Farris optimization and (b) 3D landmark optimization. In Farris optimization, the sum of the numerical differences between states is minimized. In landmark optimization, the distances between landmark positions are minimized.

SUMMARY

ALL organisms share common ancestor

descent with modification

hypotheses about evolutionary history can presented as branching diagrams

phylogenetic **trees**

number of trees grows EXPONENTIALLY when number of studied organisms increase

for phylogenetic analyses basically ALL characters that show variation between terminals can be used

compiled as matrices

character states are distinguished within characters

some programs with algorithms that are able analyze also continuous & landmark data