

“Thus, from the war of nature, from famine and death, the most exalted object which we are capable of conceiving, namely, the production of the higher animals, directly follows. There is grandeur in this view of life, with its several powers, having been originally breathed into a few forms or into one; and that, whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved.”

Charles Darwin, 1859

“Nothing in Biology makes sense except in the light of Evolution.”

Theodosius Dobzhansky, 1973



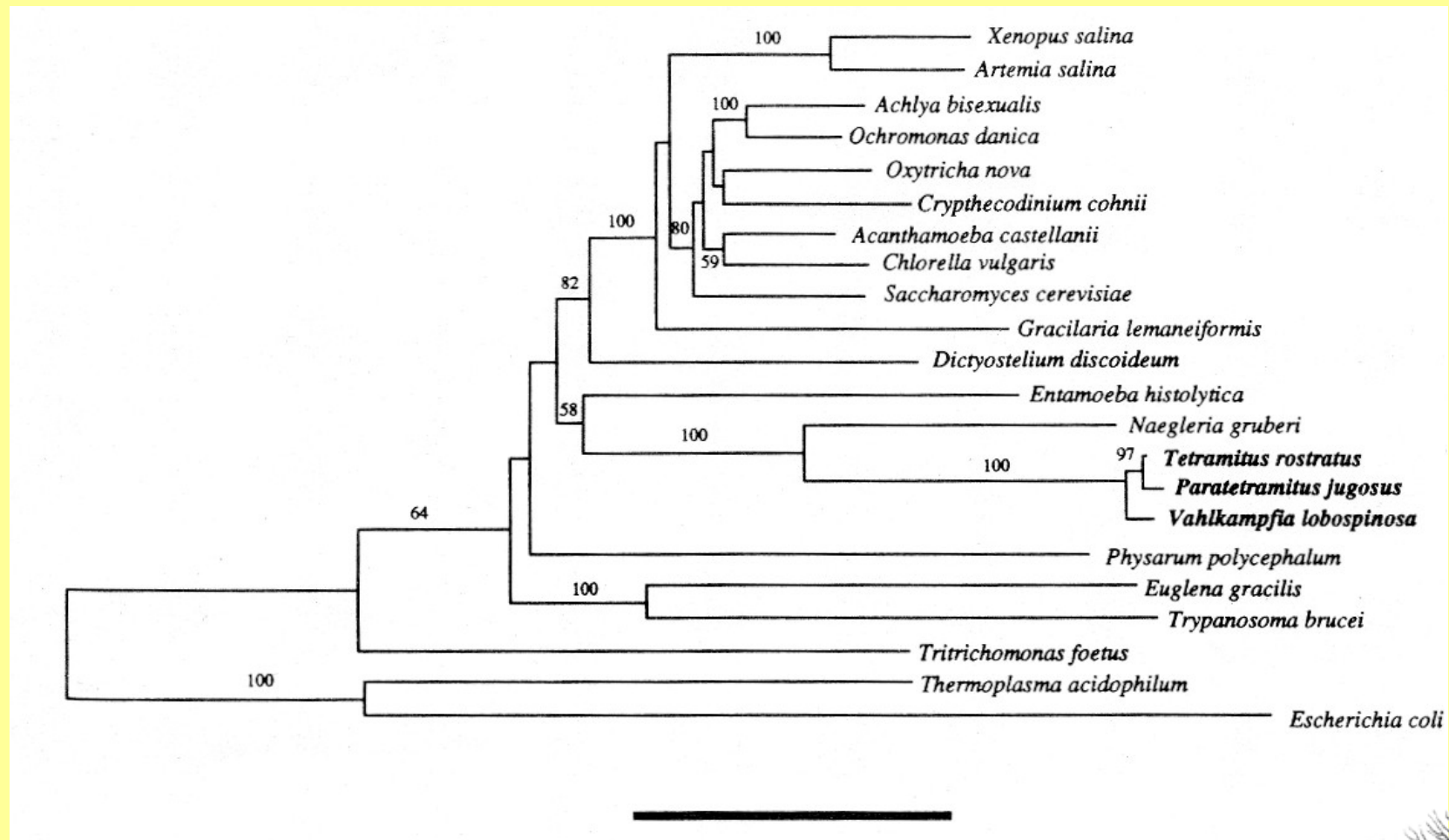
Filogenia...

...nada mais é que tentar estimar, usando dados de hoje, o passado das linhagens de organismos, mostrando suas relações “genealógicas” em uma árvore filogenética

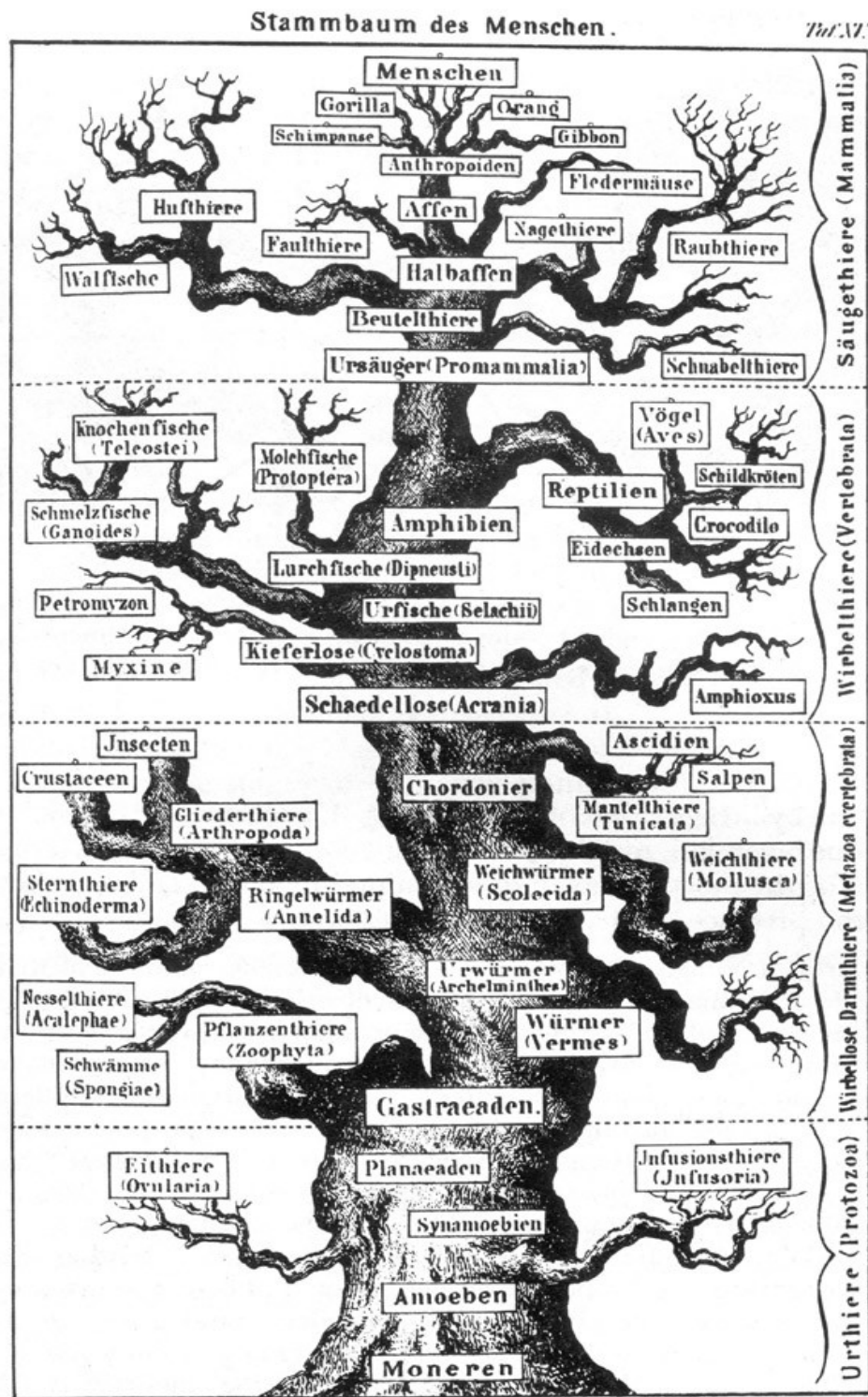




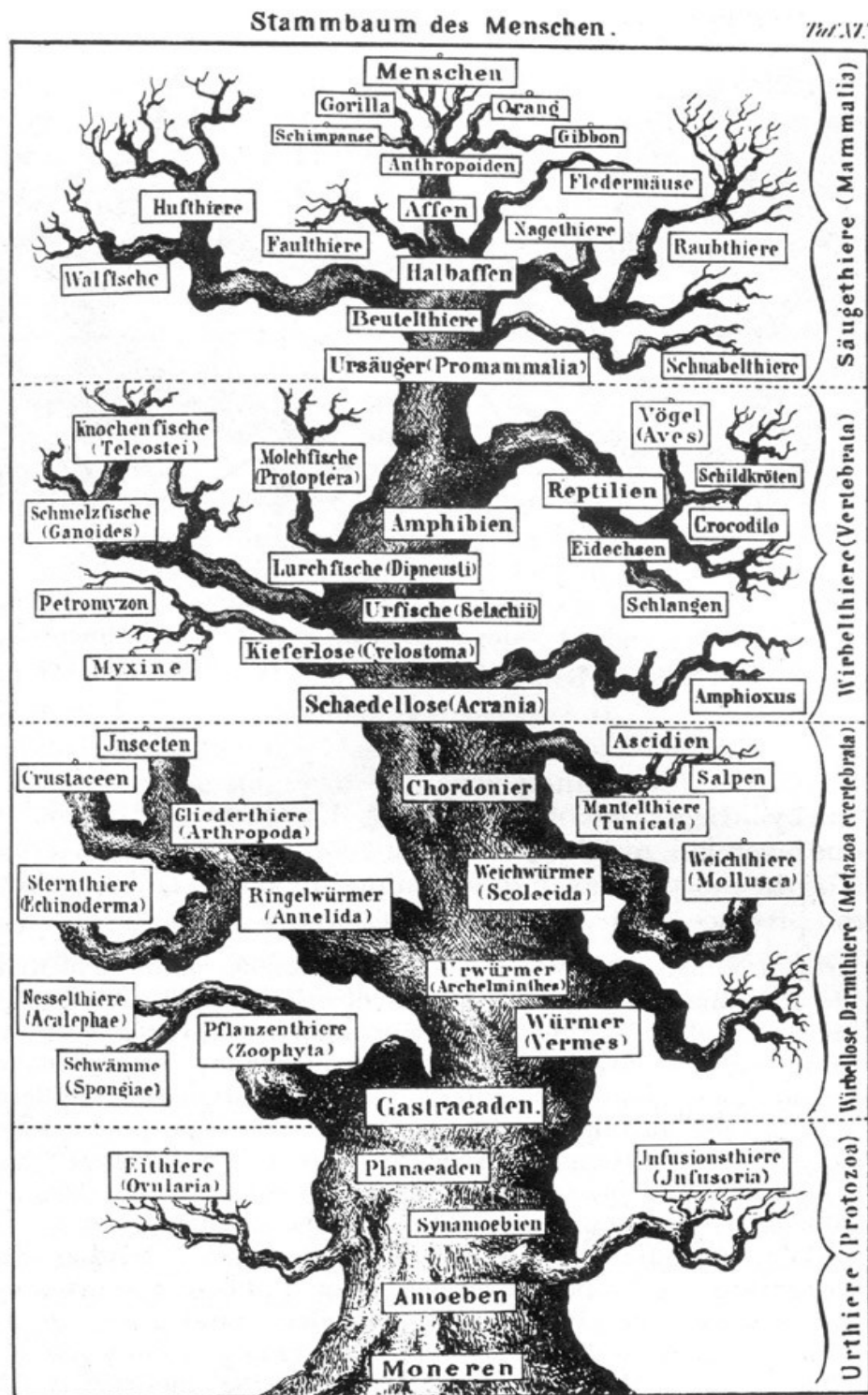
Filogenia...



Desde Darwin...



Desde Darwin...



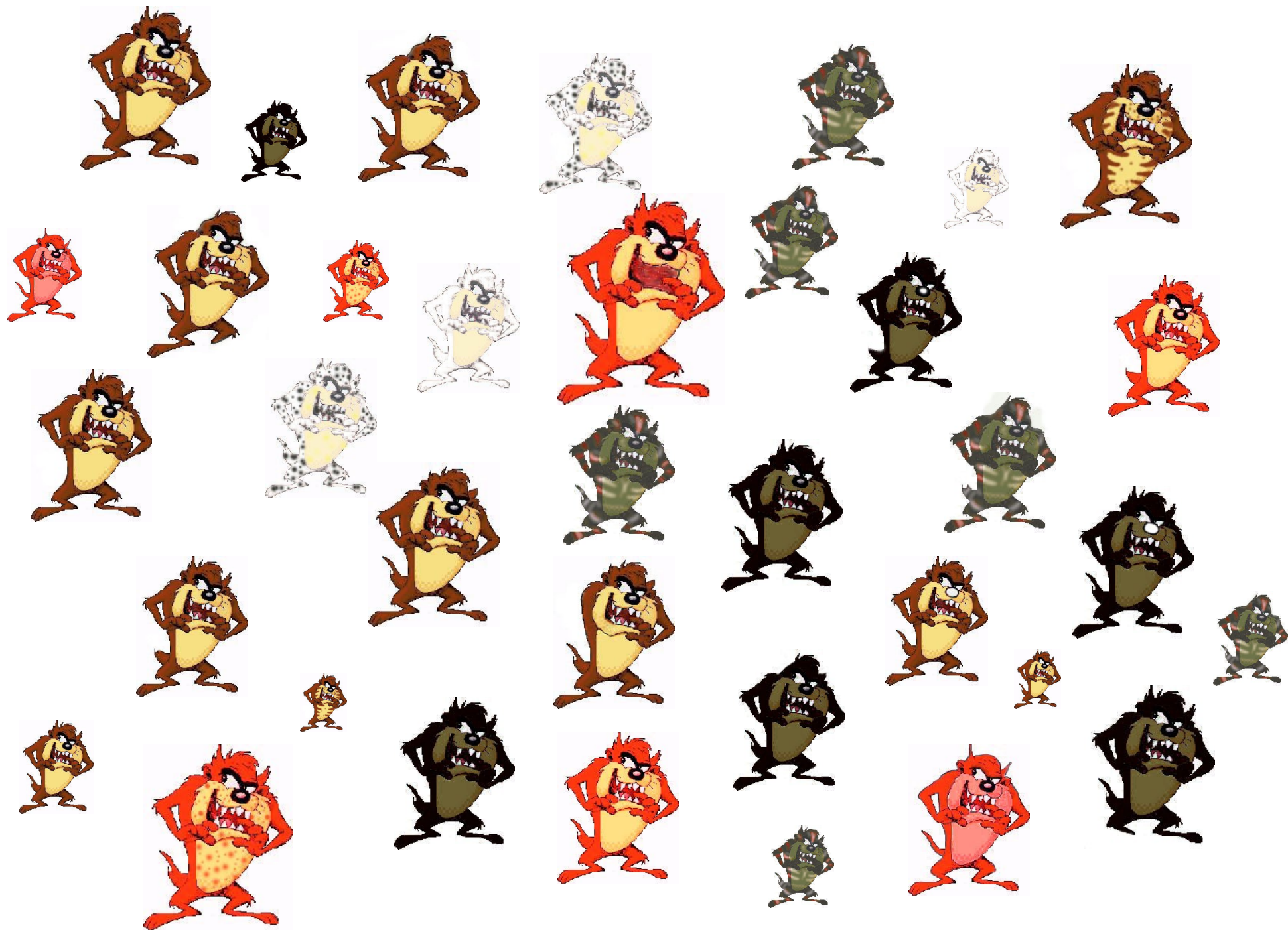
Descent with modification...

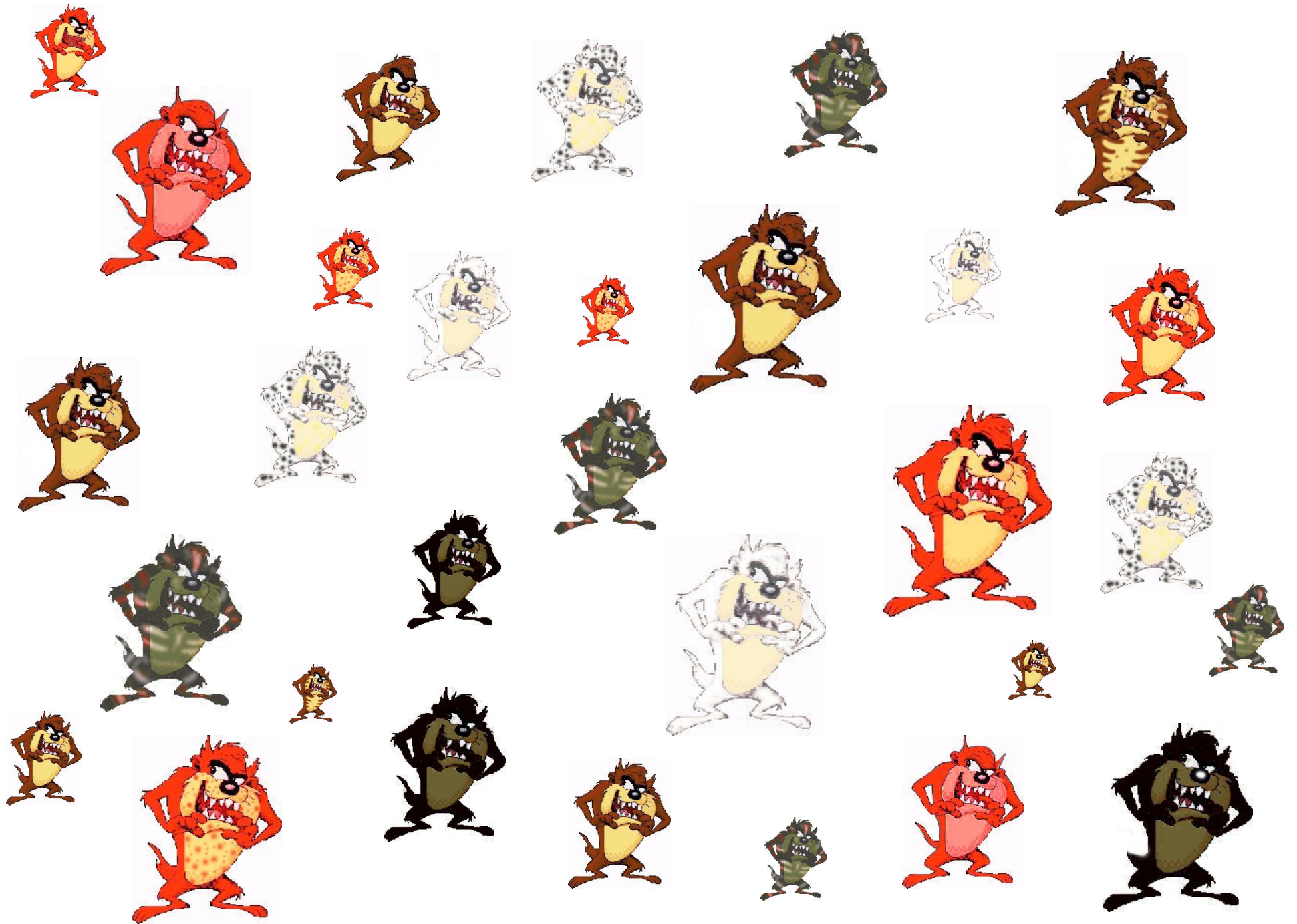
Survival of the fittest...

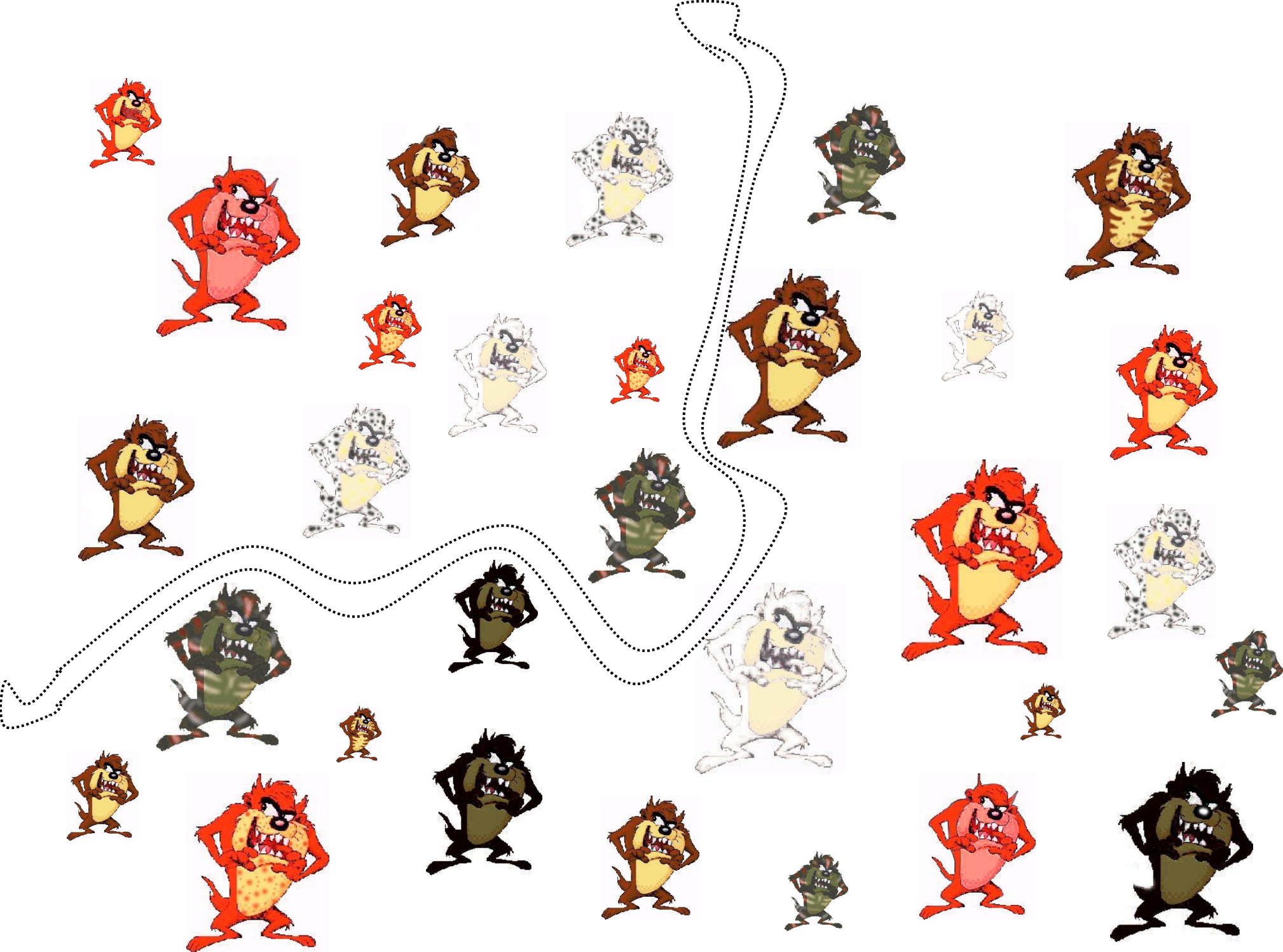
Differential reproduction...

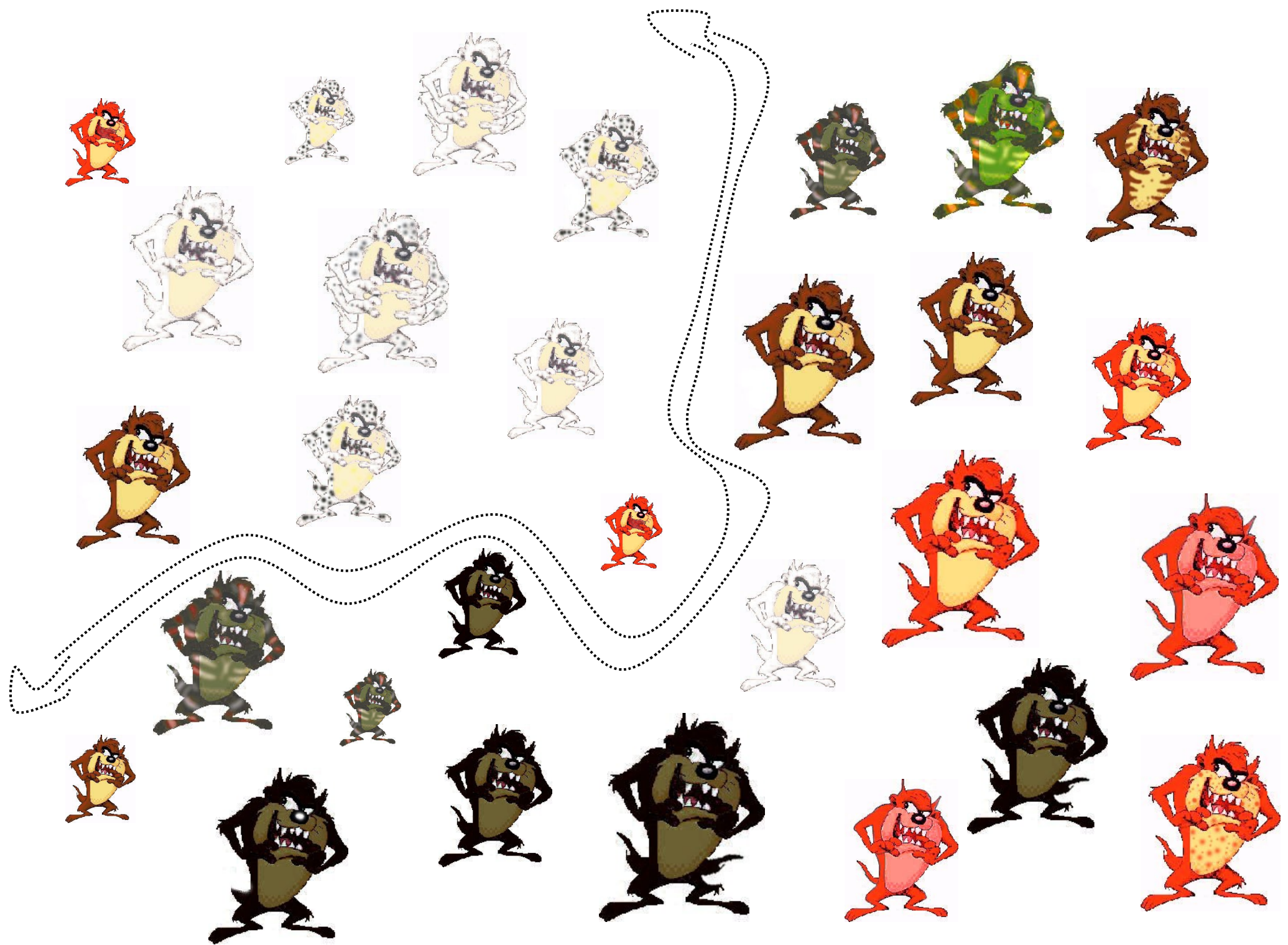
Tree of Life...

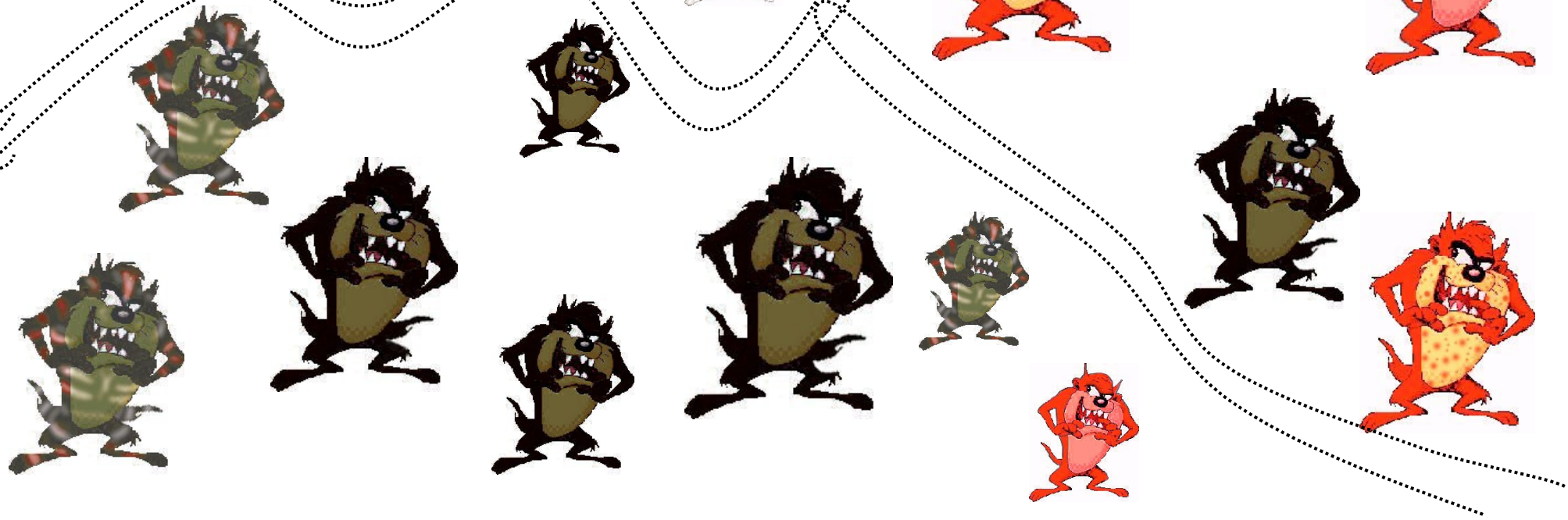
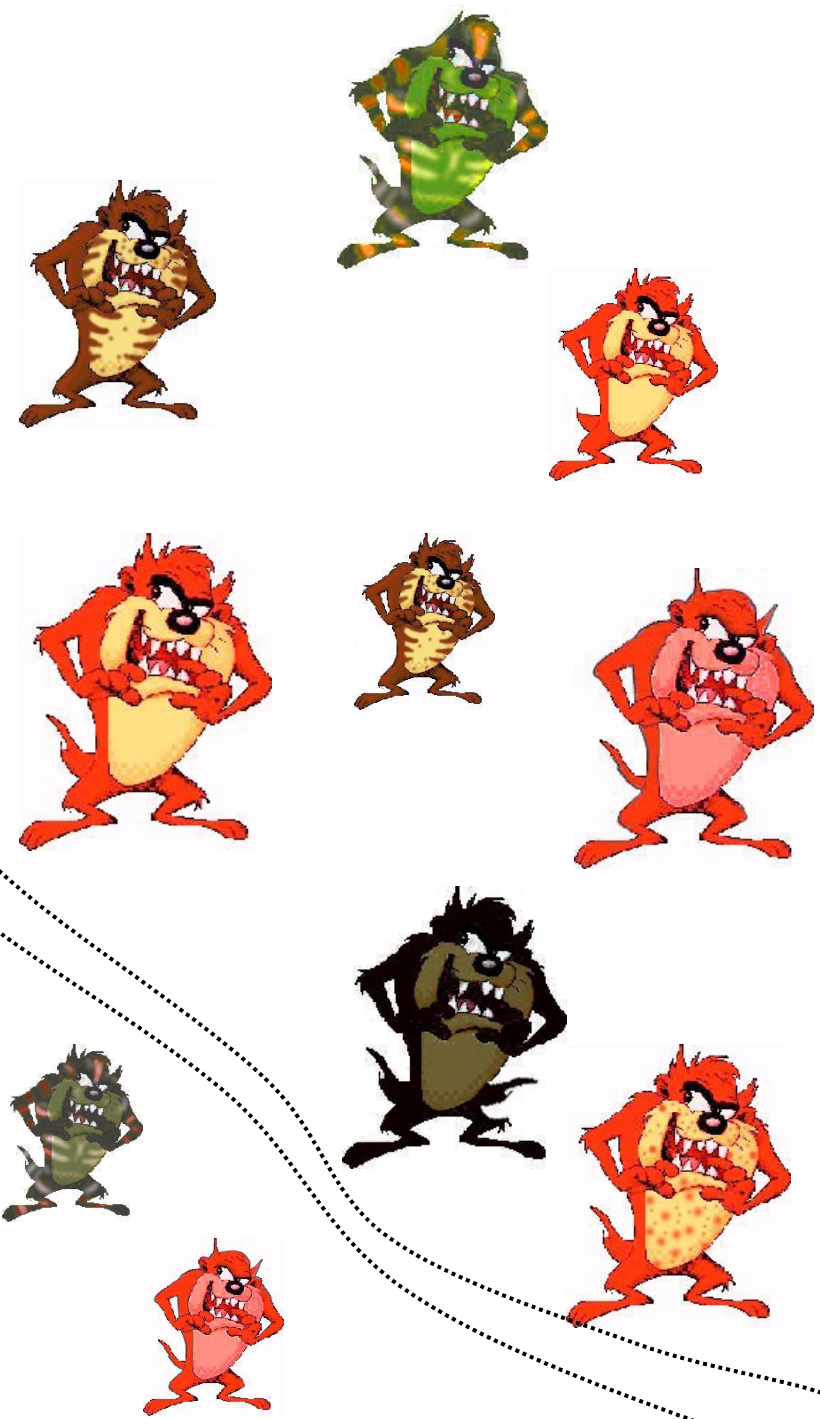
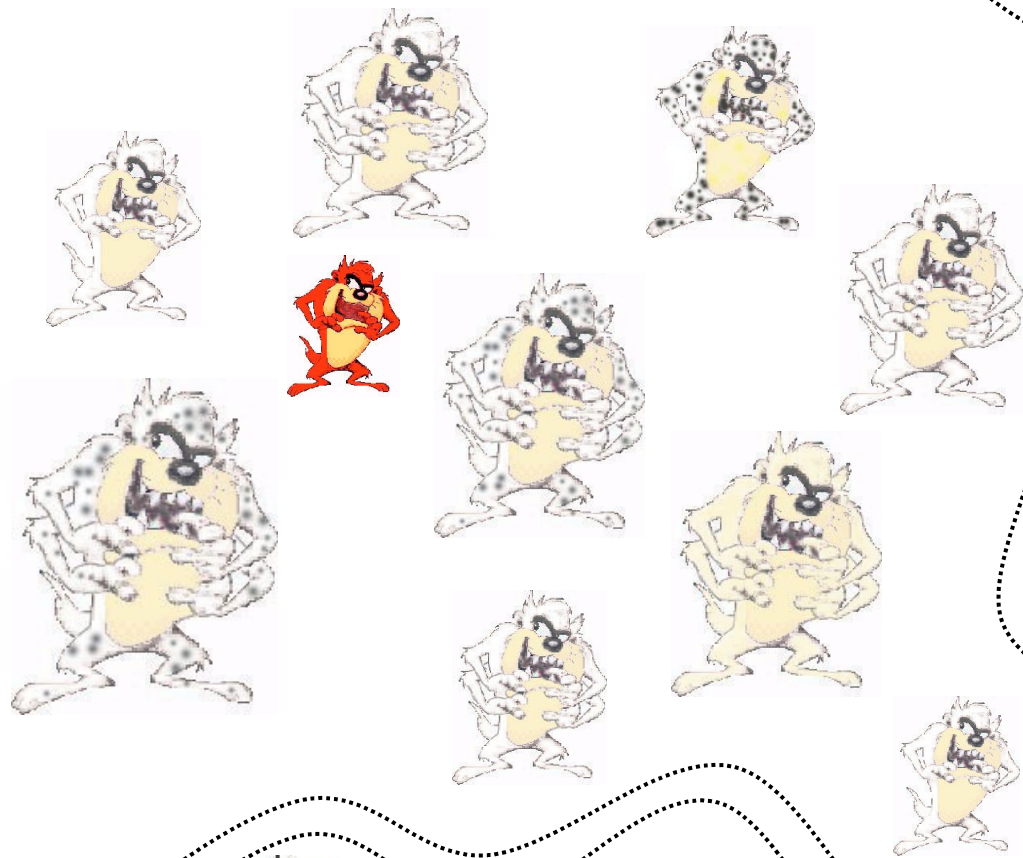










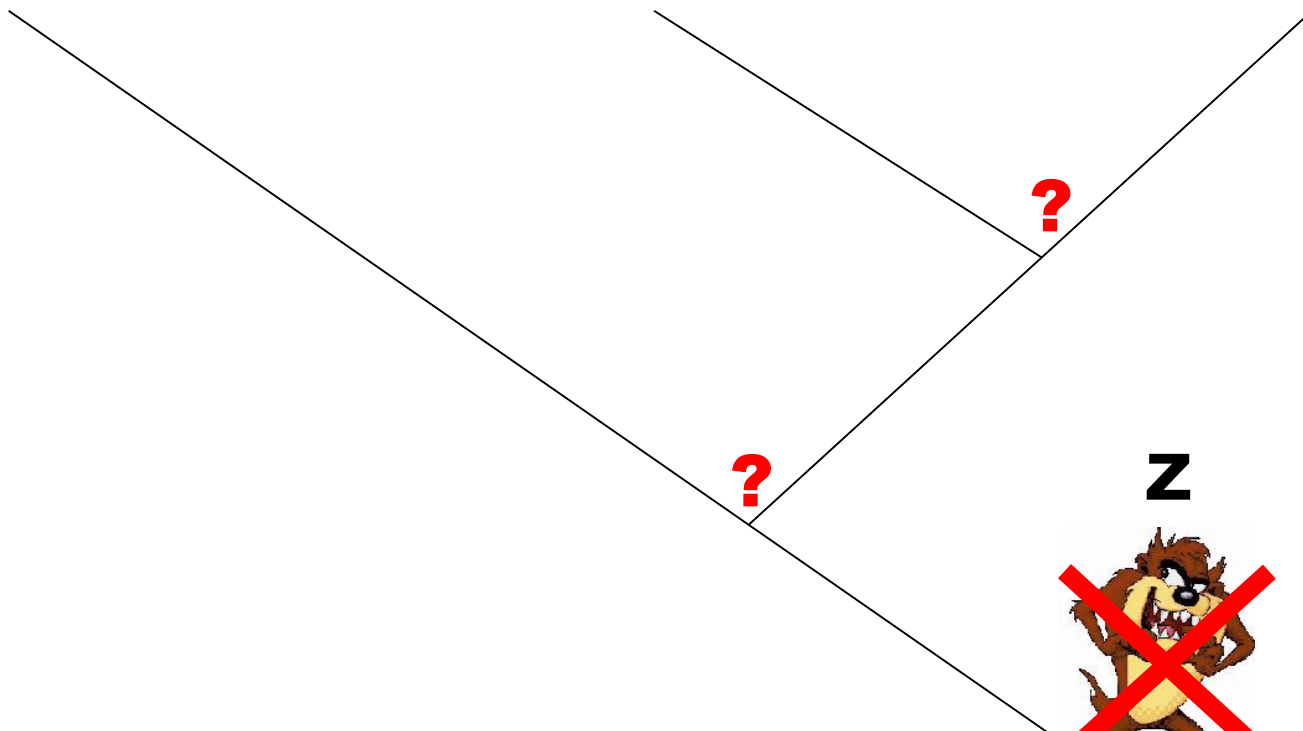


A

B

C

Presente



?

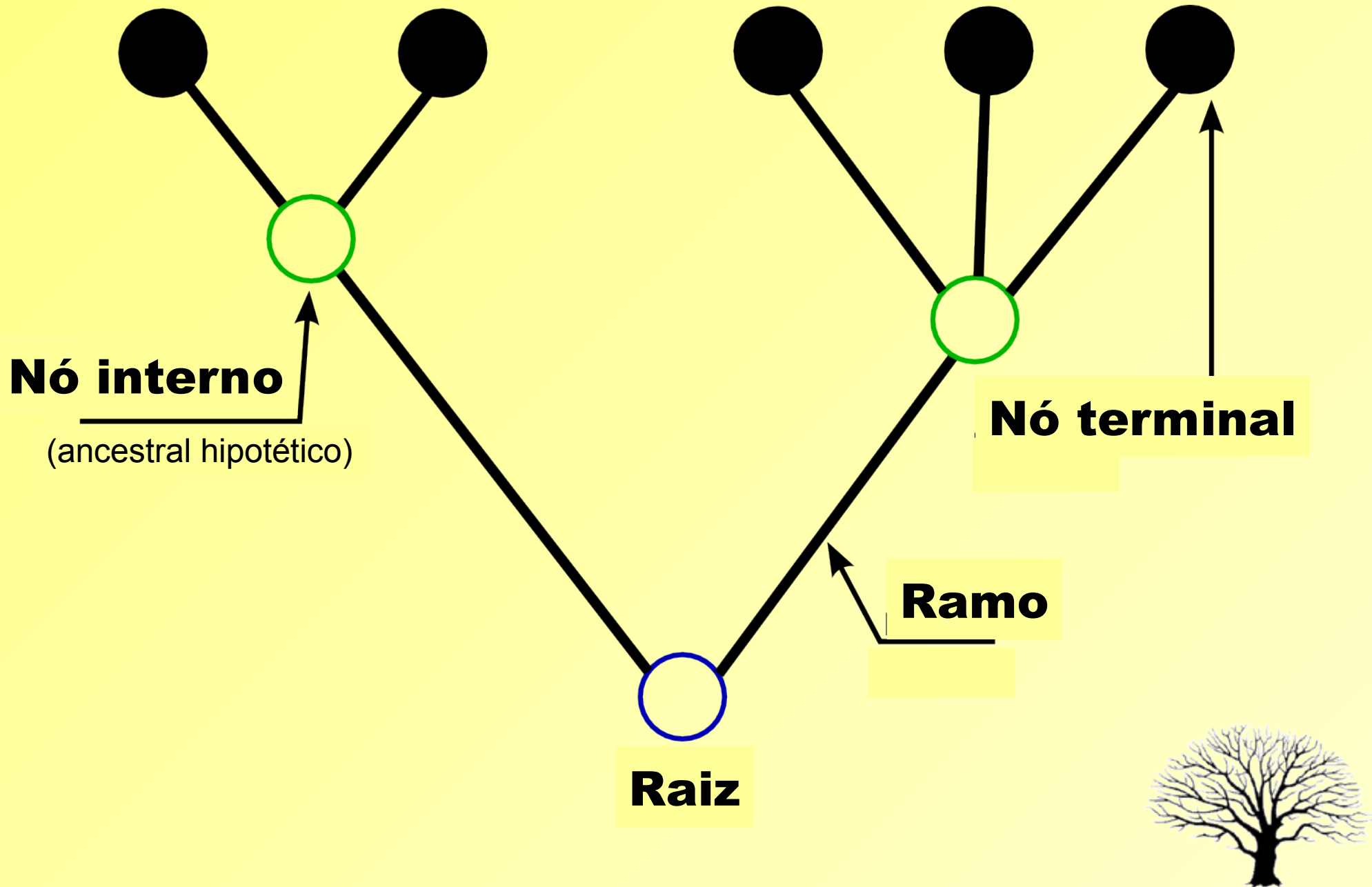
?

Z



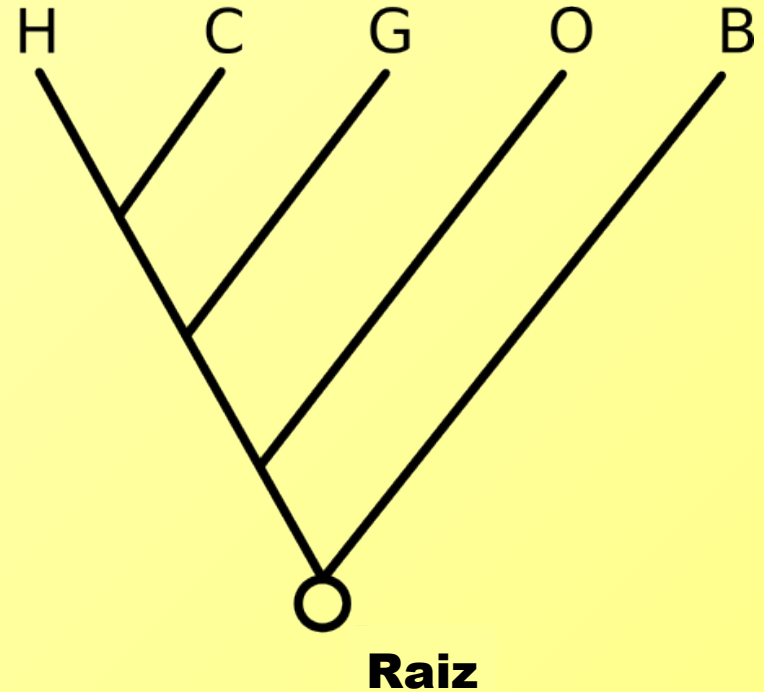
Passado

Terminologia básica



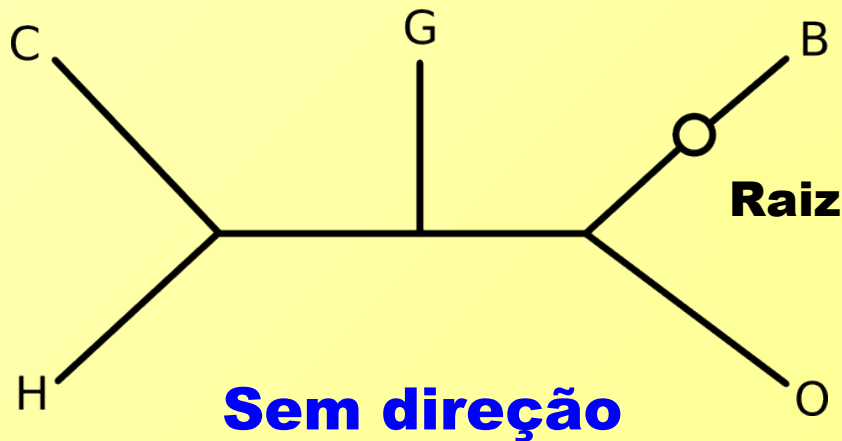
Roots, bloody roots

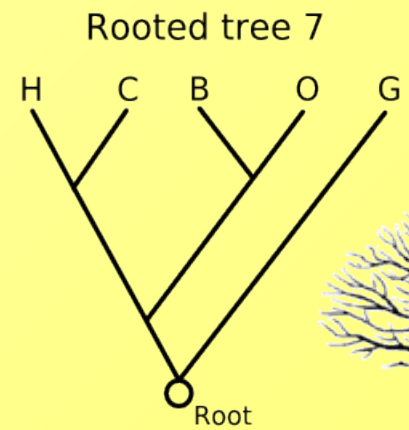
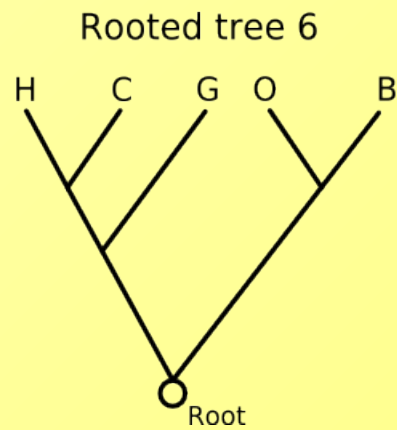
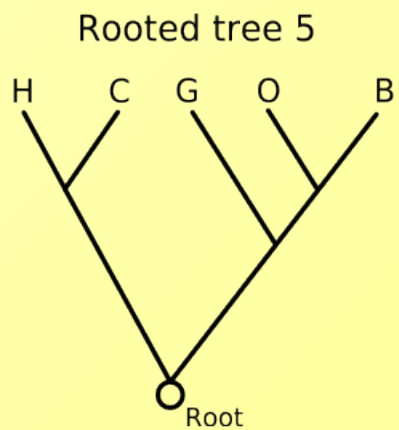
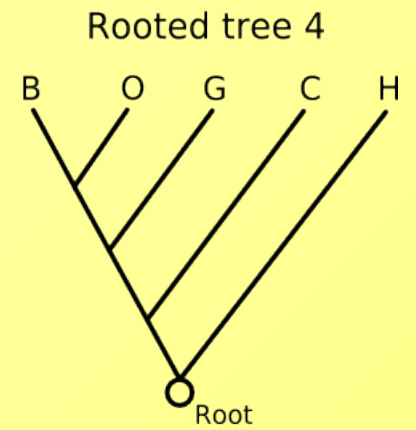
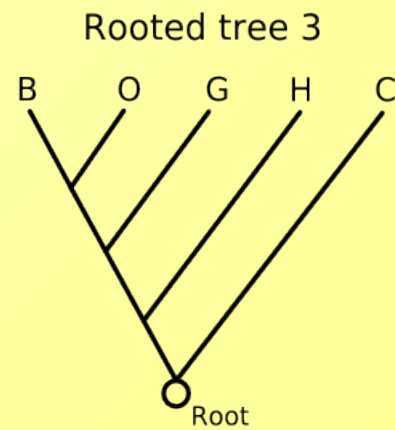
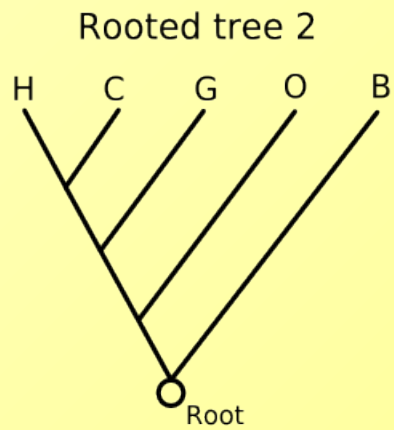
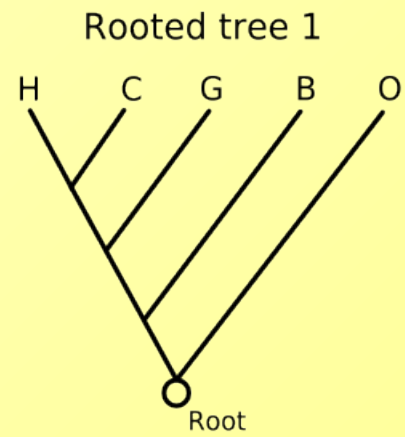
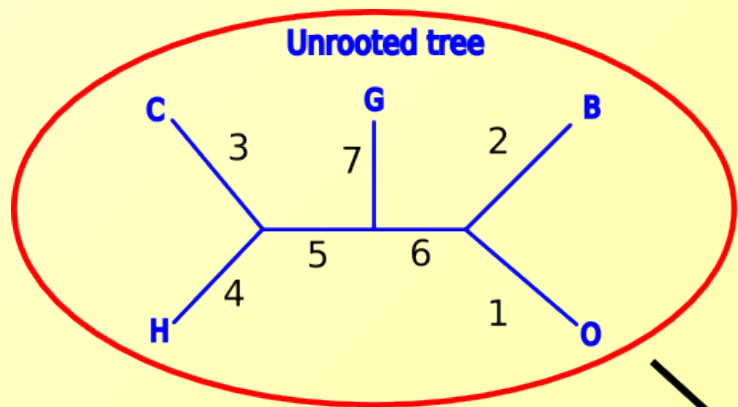
Árvore enraizada



Tempo

Árvore não-enraizada





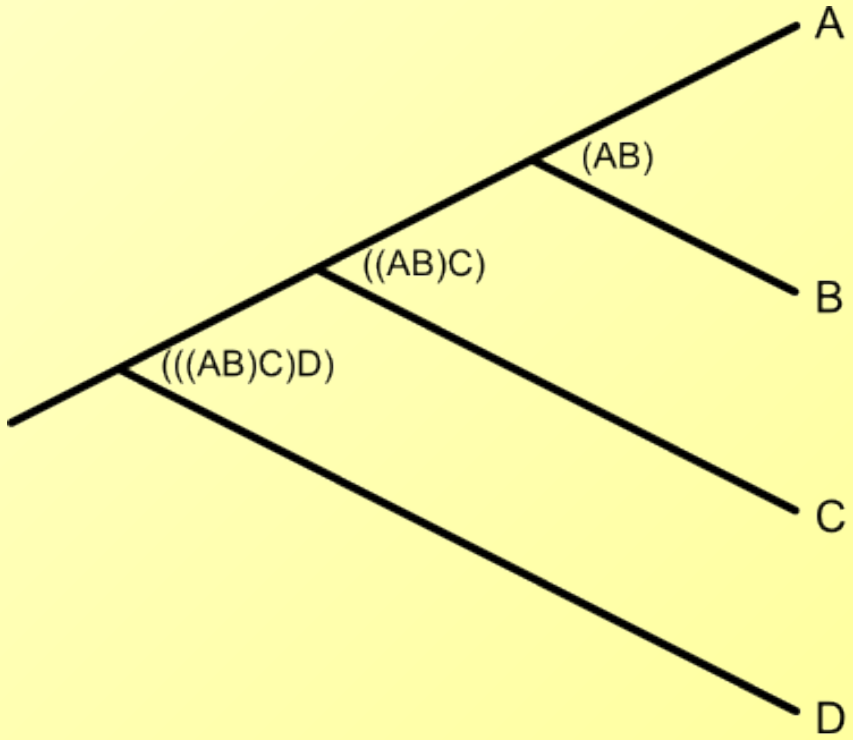
The number of evolutionary trees (Joseph Felsenstein, 1978)

número de organismos	número de árboles enraizadas
2	1 (10^0)
3	3 (10^0)
4	15 (10^1)
5	105 (10^2)
6	945 (10^3)
7	10.395 (10^4)
8	135.135 (10^5)
9	2.027.025 (10^6)
10	34.459.425 (10^7)
11	654.729.075 (10^8)
12	13.749.310.575 (10^{10})
13	316.234.143.225 (10^{11})
14	7.905.853.580.625 (10^{12})
15	213.458.046.676.875 (10^{14})
16	6.190.283.353.629.375 (10^{15})
17	191.898.783.962.510.625 (10^{17})
18	6.332.659.870.762.850.625 (10^{18})
19	221.643.095.476.699.771.875 (10^{20})
20	8.200.794.532.637.891.559.375 (10^{22})
21	319.830.986.772.877.770.815.625 (10^{23})
22	13.113.070.457.687.988.603.440.625 (10^{25})

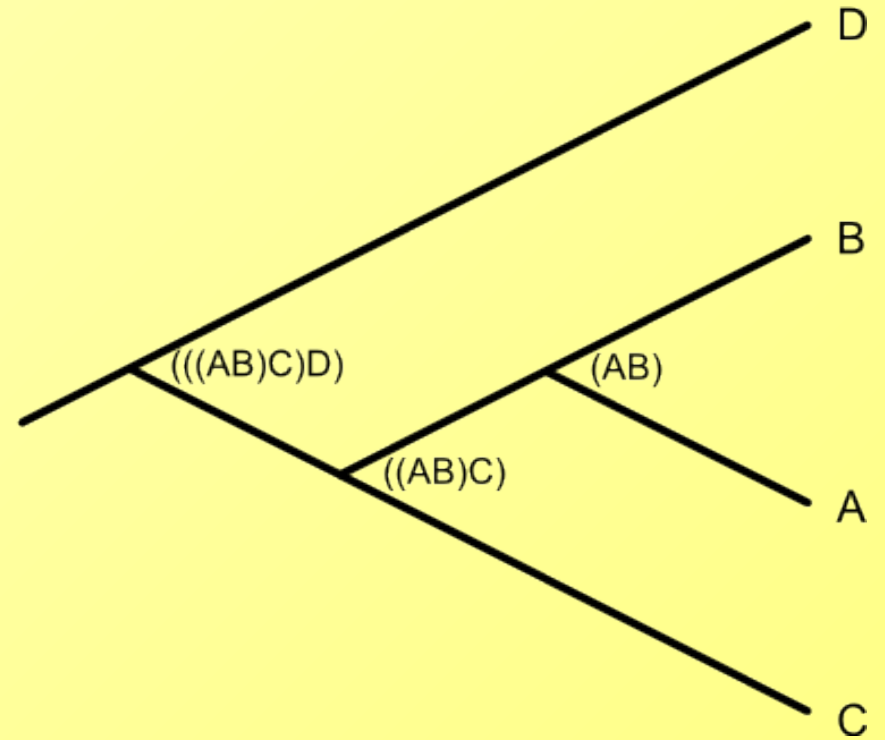
(binárias apenas, essa nem é uma dessas $\sim 10^{100}$ árvores!)



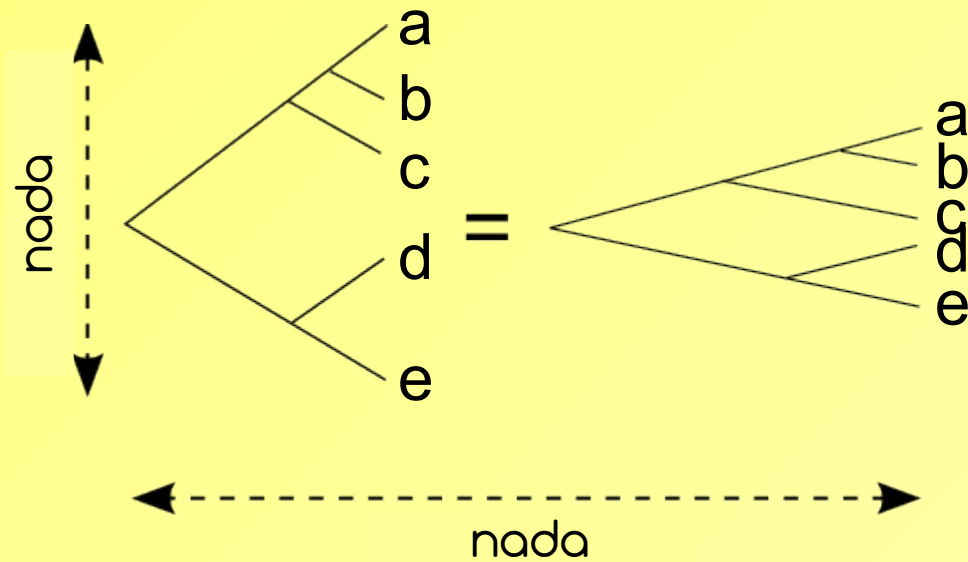
Acanthamoeba tree



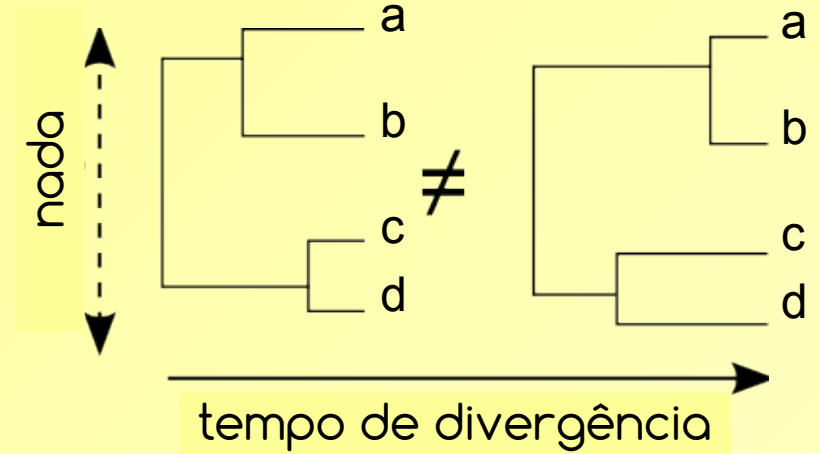
=



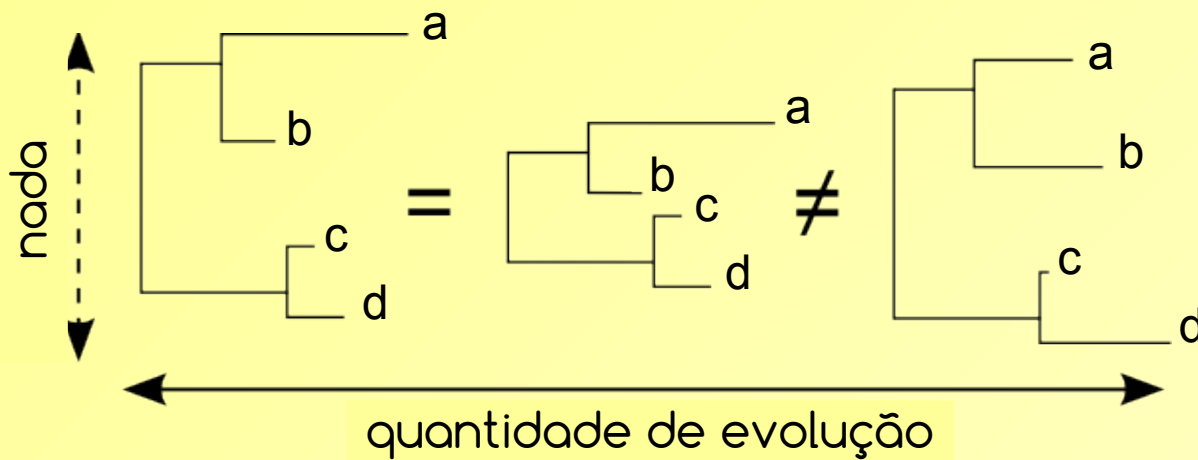
Cladograma



Árvore ultramétrica



Árvore aditiva



Bootstrap

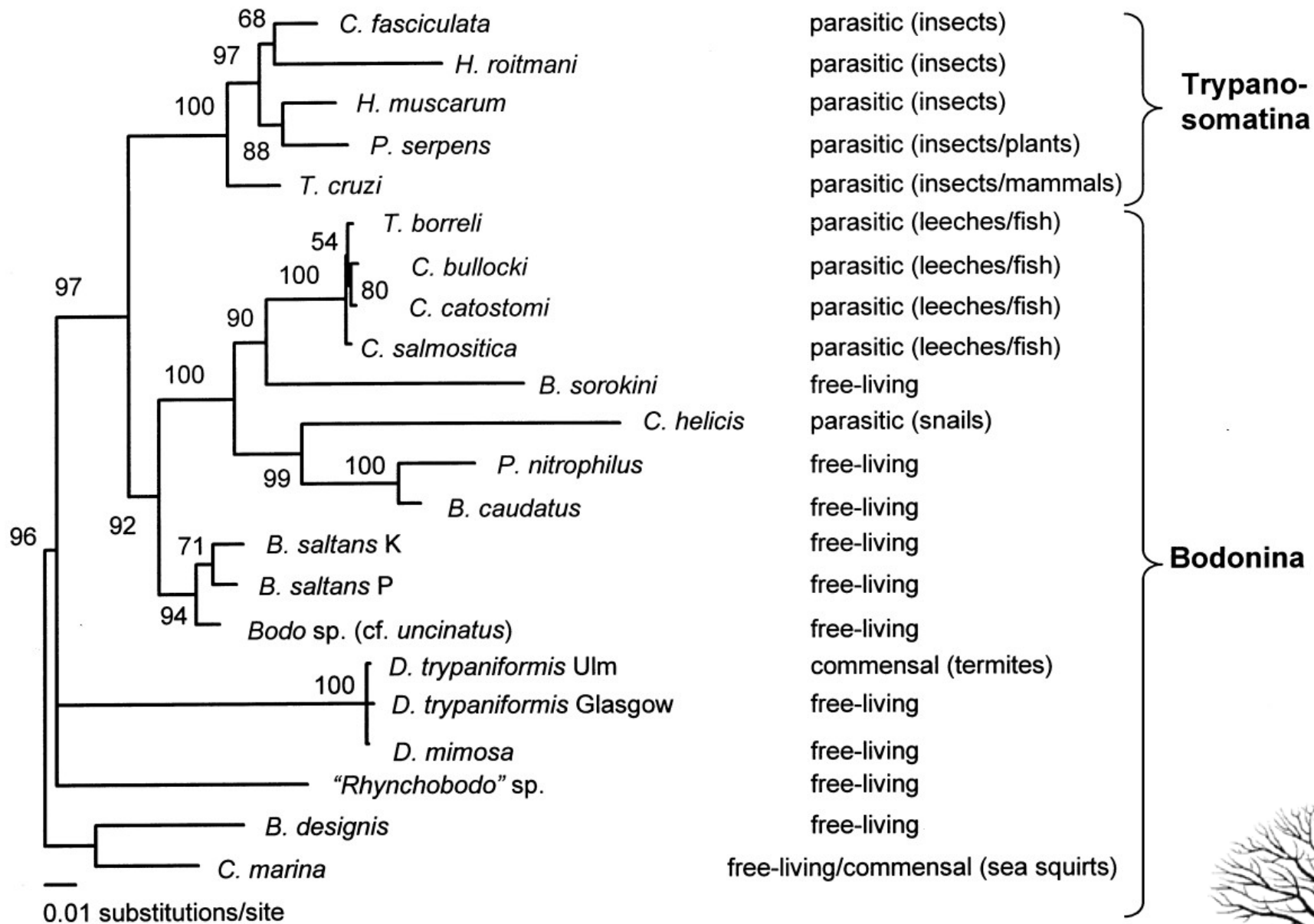


Bootstrap

Medida de robustês estatística dos grupos inferidos na árvore, com certos dados e metodologia.



Bootstrap



A**B****C****Presente****Pergunta!**

**Quem é mais próximo,
filogeneticamente, de **A**?**

Passado**?****?****Z**

Homologia é...

... resultado de herança
a partir de um ancestral comum



Homologia segundo Richard Owen, 1843

Homólogo:

o mesmo órgão, mesmo em diferentes variedades de forma e função
(correspondência real ou em essência)

Analogia:

similaridade superficial ou enganosa

Richard Owen, 1843



Depois de Darwin...

“The natural system is based upon descent with modification (...) the characters that naturalists consider as showing true affinity (i.e. **homologies**) are those which have been **inherited from a common parent**, and, in so far as **all true classification is genealogical**; that community of descent is the common bond that naturalists have been seeking.”

Charles Darwin, 1859



Homologia é...

... resultado de herança
a partir de um ancestral comum

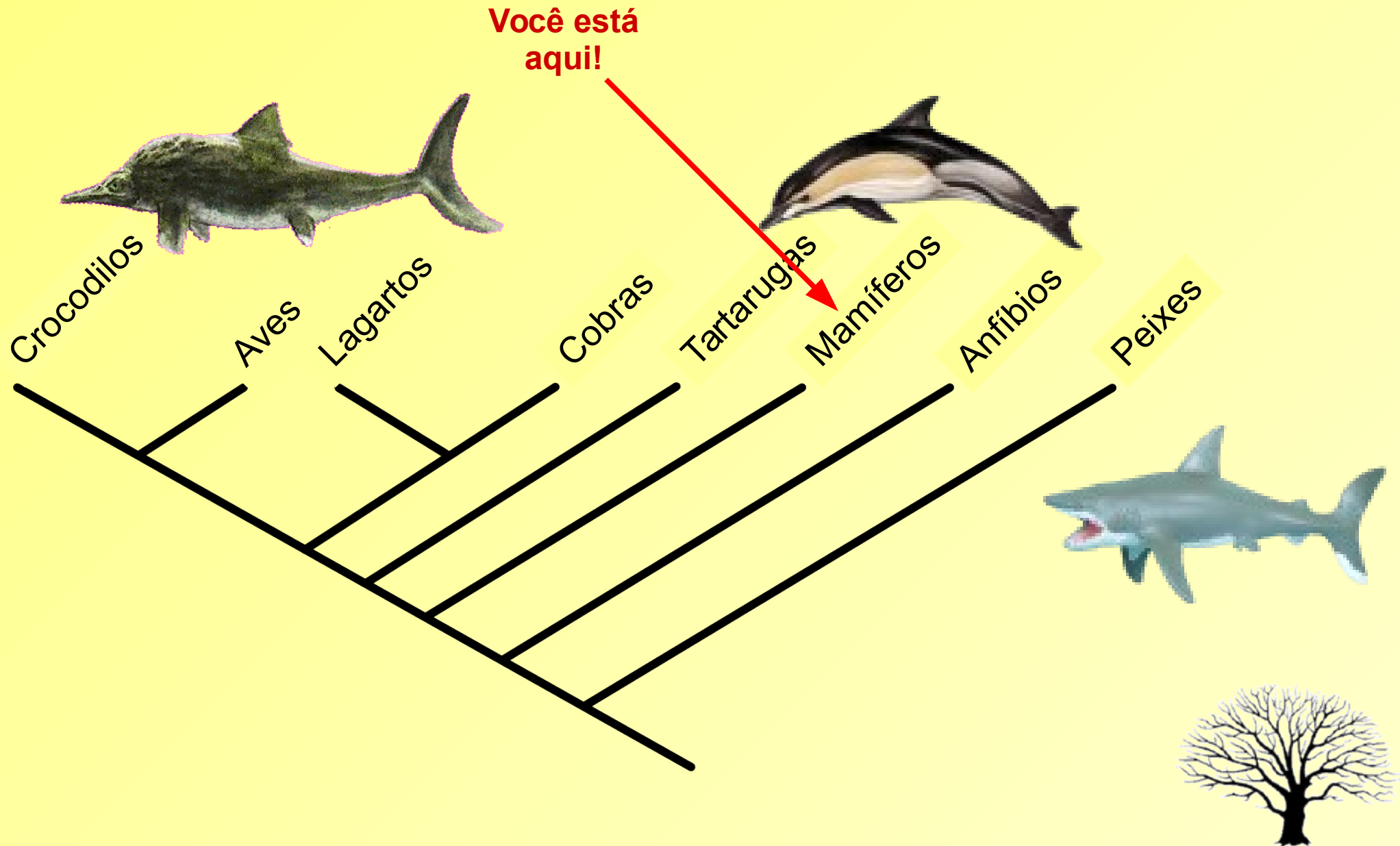


Homologia NÃO é...

Analogia (ou homoplasia, convergência, paralelismo, etc.), que é similaridade resultante de pressão seletiva para uma função.



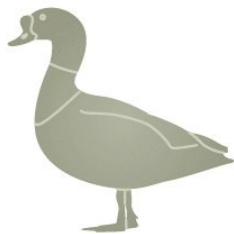
Por que homologia é importante?



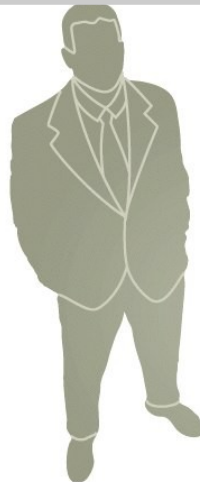
Por que homologia é importante?

Pergunta:

**As asas de morcegos, insetos e aves
são homólogas entre si?**



Asas



Sem asas



Asas

Figure 19-2a Genomes 3 (© Garland Science 2007)



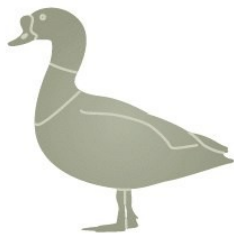
Por que homologia é importante?

Pergunta:

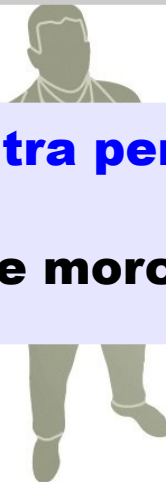
**As asas de morcegos, insetos e aves
são homólogas entre si?**

Outra pergunta:

E só as de morcegos e aves?



Asas



Sem asas

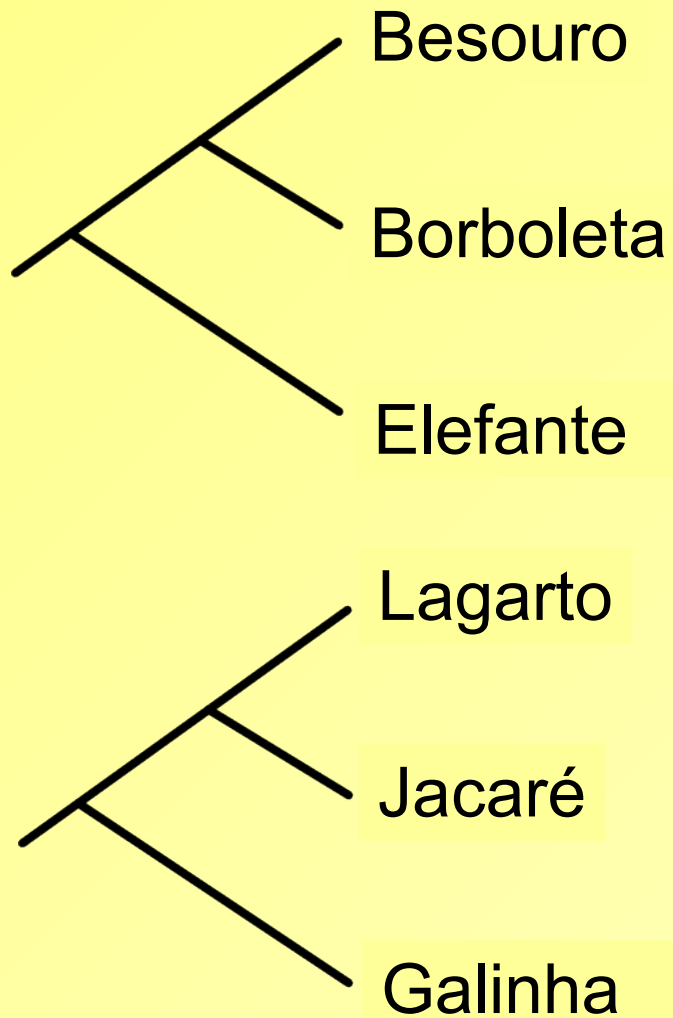


Asas

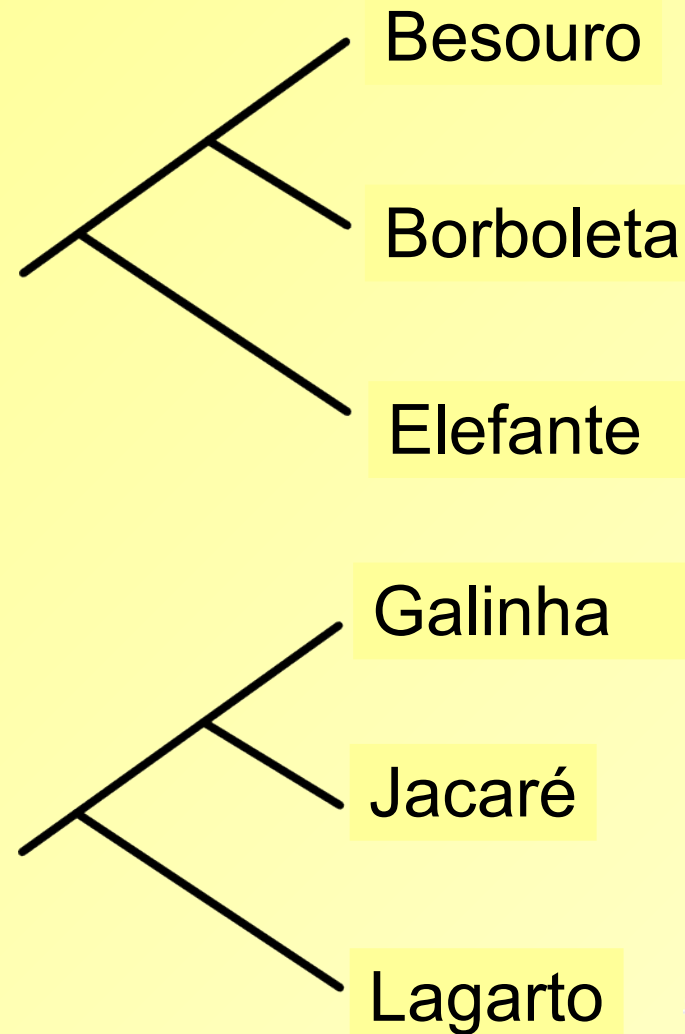


Por que homologia é importante?

Similaridade



Homologia





Anos 1960: filogenia molecular

J. Theoret. Biol. (1965) 8, 357–366

Molecules as Documents of Evolutionary History

EMILE ZUCKERKANDL AND LINUS PAULING

*Gates and Crellin Laboratories of Chemistry,
California Institute of Technology, Pasadena, California, U.S.A.*

(Received 17 September 1964)

Different types of molecules are discussed in relation to their fitness for providing the basis for a molecular phylogeny. Best fit are the “semantides”, i.e. the different types of macromolecules that carry the genetic information or a very extensive translation thereof. The fact that more than one coding triplet may code for a given amino acid residue in a polypeptide leads to the notion of “isosemantic substitutions” in genic and messenger polynucleotides. Such substitutions lead to differences in nucleotide sequence that are not expressed by differences in amino acid sequence. Some possible consequences of isosemanticism are discussed.

Zuckerkandl, E. & Pauling, L. Molecules as documents of evolutionary history. *J. Theor. Biol.* 8, 357–366 (1965).

Construction of Phylogenetic Trees

A method based on mutation distances as estimated from cytochrome *c* sequences is of general applicability.

Walter M. Fitch and Emanuel Margoliash

Biochemists have attempted to use quantitative estimates of variance between substances obtained from different species to construct phylogenetic trees. Examples of this approach include studies of the degree of interspecific hybridization of DNA (1), the degree of cross reactivity of antisera to purified proteins (2), the number of differences in the peptides from enzymic digests of purified homol-

ogous proteins, both as estimated by paper electrophoresis-chromatography or column chromatography and as estimated from the amino acid compositions of the proteins (3), and the number of amino acid replacements between homologous proteins whose complete primary structures had been determined (4). These methods have not been completely satisfactory because (i) the portion of the genome examined

20 JANUARY 1967

Fitch, W. M. & Margoliash, E. Construction of phylogenetic trees. *Science* 155, 279–284 (1967).





Molecules as documents of evolutionary history

“We may ask the question **where** in the now living systems the greatest amount of information of their past history has survived and how it can be extracted”

“Best fit are the different types of macromolecules (sequences) which carry the **genetic information**”

Zuckerlandl & Pauling, 1965

Journal of Theoretical Biology, 8: 357-366.



Anos 1960: filogenia molecular

J. Theoret. Biol. (196

Molecules

EM

Gat
California Ins

Different types of
providing the b
"semantides", i.e.
genetic informati
more than one co
polypeptide leads
and messenger pe
nucleotide sequen
sequence. Some p

Zuckerkandl,
documents c
Biol. 8, 357-36

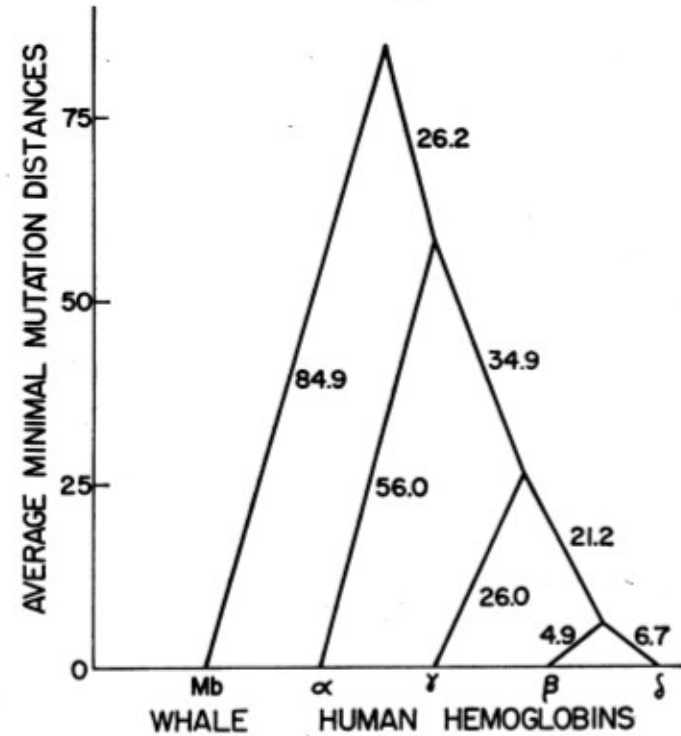
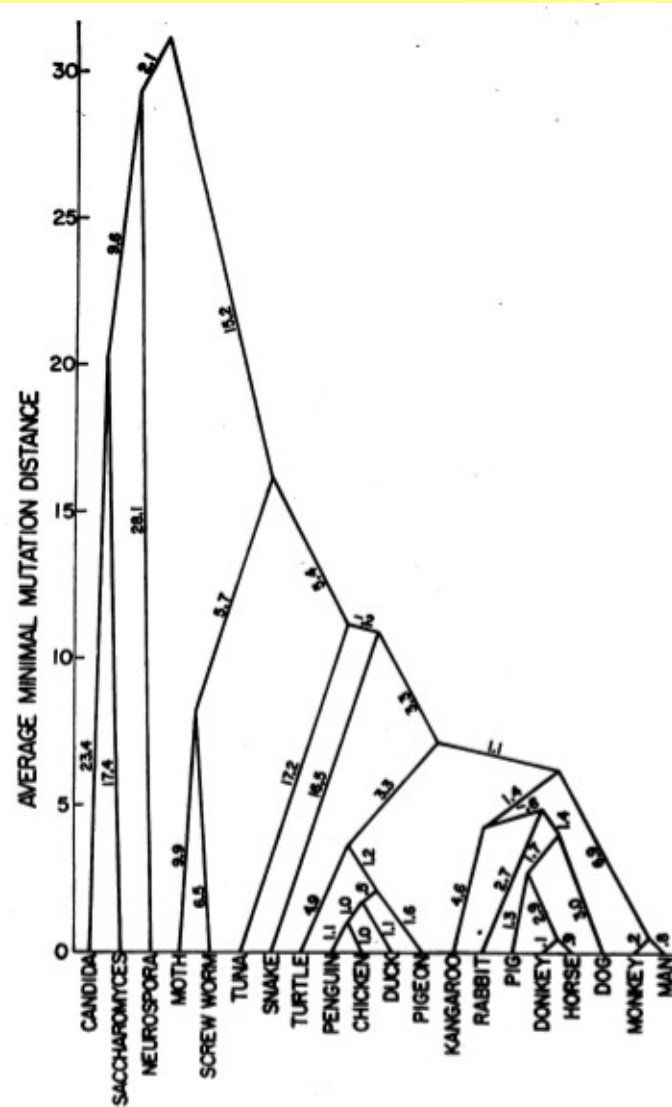


Fig. 2 (left). Phylogeny as reconstructed from observable mutations in the cytochrome c gene. Each number on the figure is the corrected mutation distance (see text) along the line of descent as determined from the best computer fit so far found. Each apex is placed at an ordinate value representing the average of the sums of all mutations in the lines of descent from that apex.

Fig. 3 (right above). A gene phylogeny as reconstructed from observable mutations in several heme-containing globins. See Fig. 2 for details. The percent "standard deviation" (7) for this tree is 1.33.

Trees

estimated
ability.

argoliash

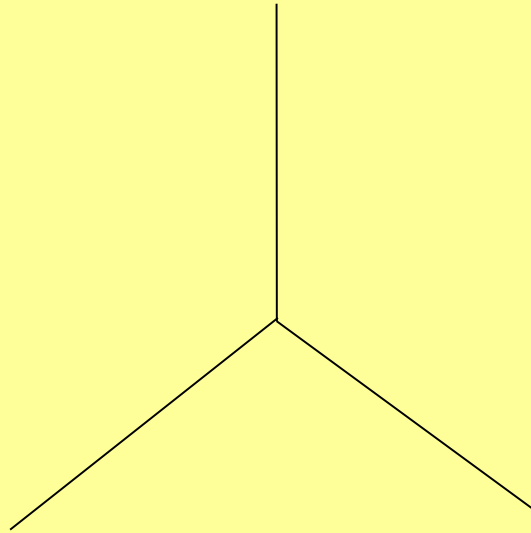
both as estimated by
resis-chromatography
tography and as es-
amino acid composi-
teins (3), and the
acid replacements
ous proteins whose
structures had been
These methods have
y satisfactory because
he genome examined

on of
4 (1967).





...AAT CGC TTC GAT CGA TTA GCT AAA TGC TCG GAT CGA AC...



...AAA CGC CCC GAT CGG TTA GCT AAA TGC TCG GAG GAT CGA AC...

...AAT CGC CCC GAT CGA TTC GCT AAA TGC --G GAT CGA AC...

...A-- CGC TTC AGC TAG TTA GCT AGA TGC TCG GAT CGA AC...

...AAT CGC TTC GAC CGA TTA GCT AGA TGC TCG GAT CGA AC...

...AAT CGC TTC GAT CGA TTA GCA TCT AAA TGC TCG GAT CGA AC...

...AAT CGC TTC GGG CGA TTA GCA TCT AAA TGC TCG GAT CGA AC...





Homologia: alinhamento

**Colocar todos resíduos homólogos
na mesma coluna**





Colocar todos resíduos homólogos na mesma coluna

	1	5	10	15	20	25	30	35	40																															
1	GCATTACTTTCGGTAGCGCGGAAAGGCGACGGGACTTATA																																							
2	C...C.....C.....A.....																																							
3	T.....																																							
4	.T.....T.....																																							
5	T.....																																							
6	T.....C.....G.....																																							
7	T.....G.....																																							
8	C.....G.....																																							

Figure 19-17a Genomes 3 (© Garland Science 2007)

Figure 19-17a Genomes 3 (© Garland Science 2007)



NUNCA

fale em porcentagem de homologia!

(ou algo do tipo)



Homologia NÃO é... similaridade ou identidade

O que se quer dizer geralmente é IDENTIDADE
(ou às vezes similaridade)

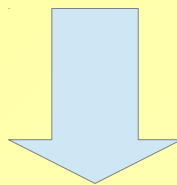
Aliás: falta de similaridade
nem sempre é falta de homologia!





Alguns problemas com a filogenia de um só marcador

- O gene tem de refletir o organismo, mas nem sempre isso acontece
- Perda diferenciada de membros de uma família gênica ancestral
- Falhas na amostragem (técnica)
- Muitos genes são muito curtos para dar suporte estatístico significativo a suas filogenias

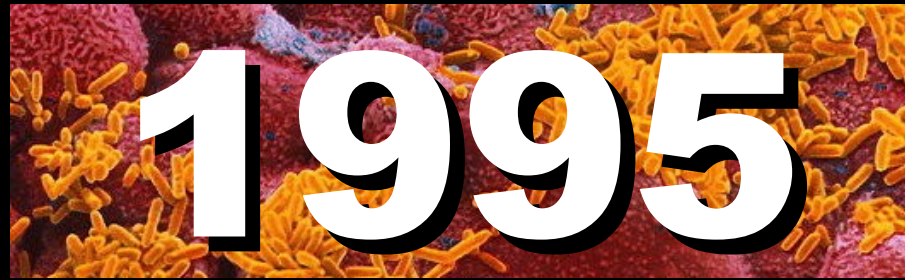


Incongruência



Genomas

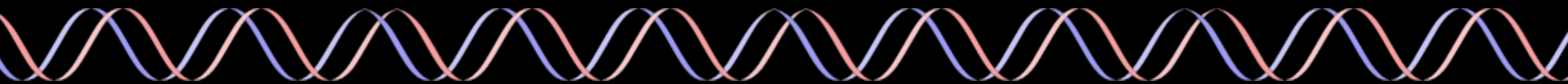
GATCGATCGCGCTAGCTAACTCGATAAATATG
CTAGCTTAGCTAGCTCTAGAGCGCGCTAGCAT
GCATCGATGGATATCGATCGAAAATCGCTCGT
GCTAGCTGCTAGAAATAGCTTCGATCGTTTGCTA
CGCGCTAGCTATATATCGATGCCCGCGGATGCT
GCATCGATCGCGATAGCGAGTATCGGCTTTATA
CATGAGCTATATAGCGCGCTAGCTGATGCATC
GCTAGCTTAGCTAGCTAGCTTAGCTTCTTCGAC
ACTCGCATAGCTCTCTAGACTAGAGATCGATT

A scanning electron micrograph (SEM) showing numerous yellow, rod-shaped bacteria (Haemophilus influenzae) clustered together on a textured, reddish-brown surface. The bacteria are oriented in various directions, some appearing as individual rods while others are in small groups.

1995

***Haemophilus influenzae* Rd KW20**

www.genomesonline.org



37.687 completos

Archaea: 745

Bacteria: 31.452

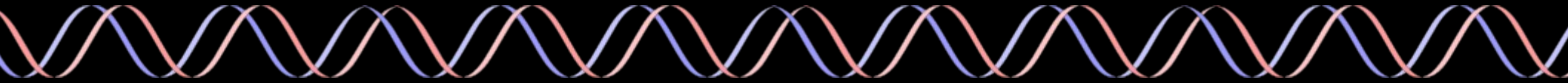
Eukarya: 5.490

17.322 em progresso

Archaea: 346

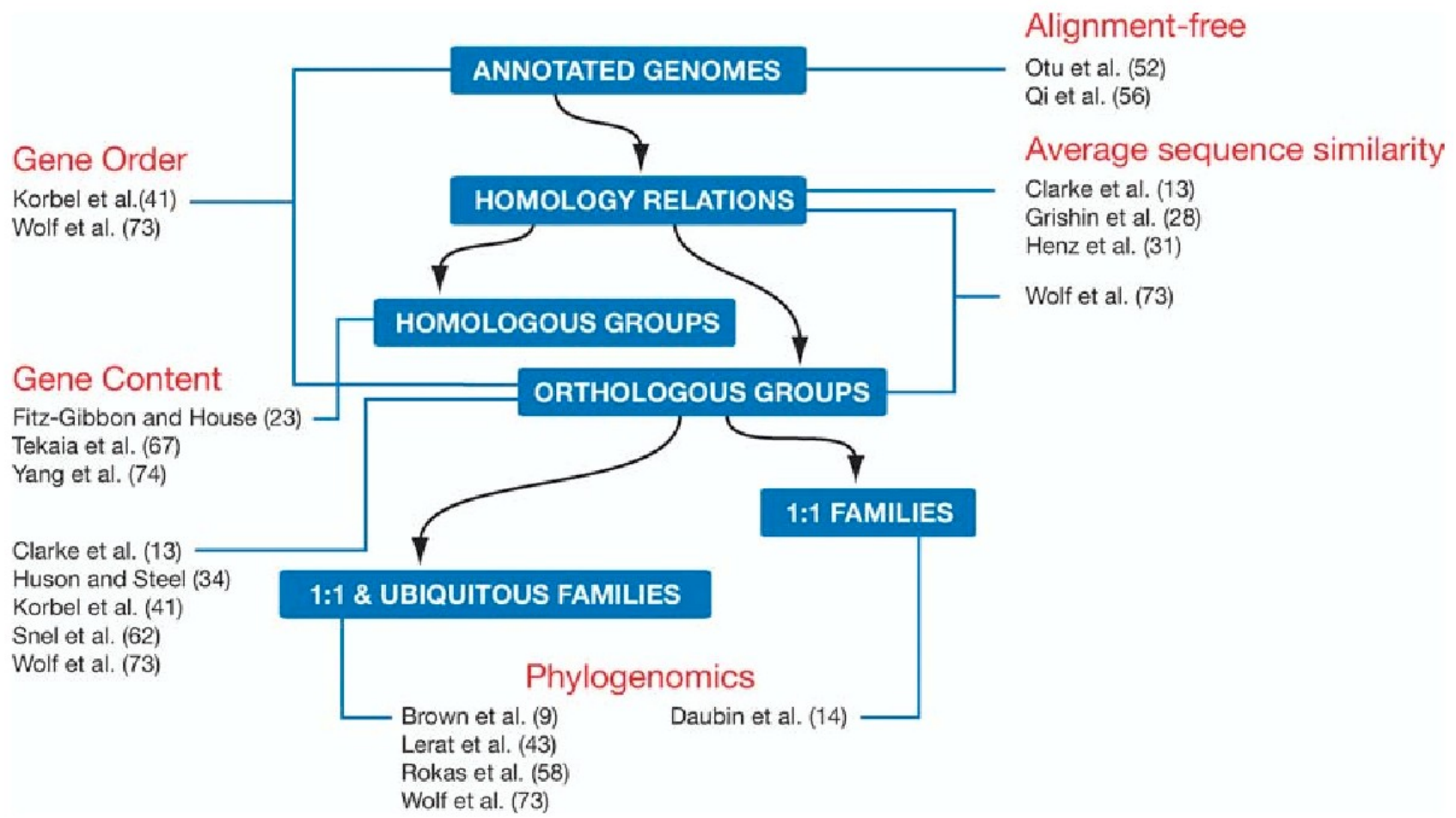
Bacteria: 11.485

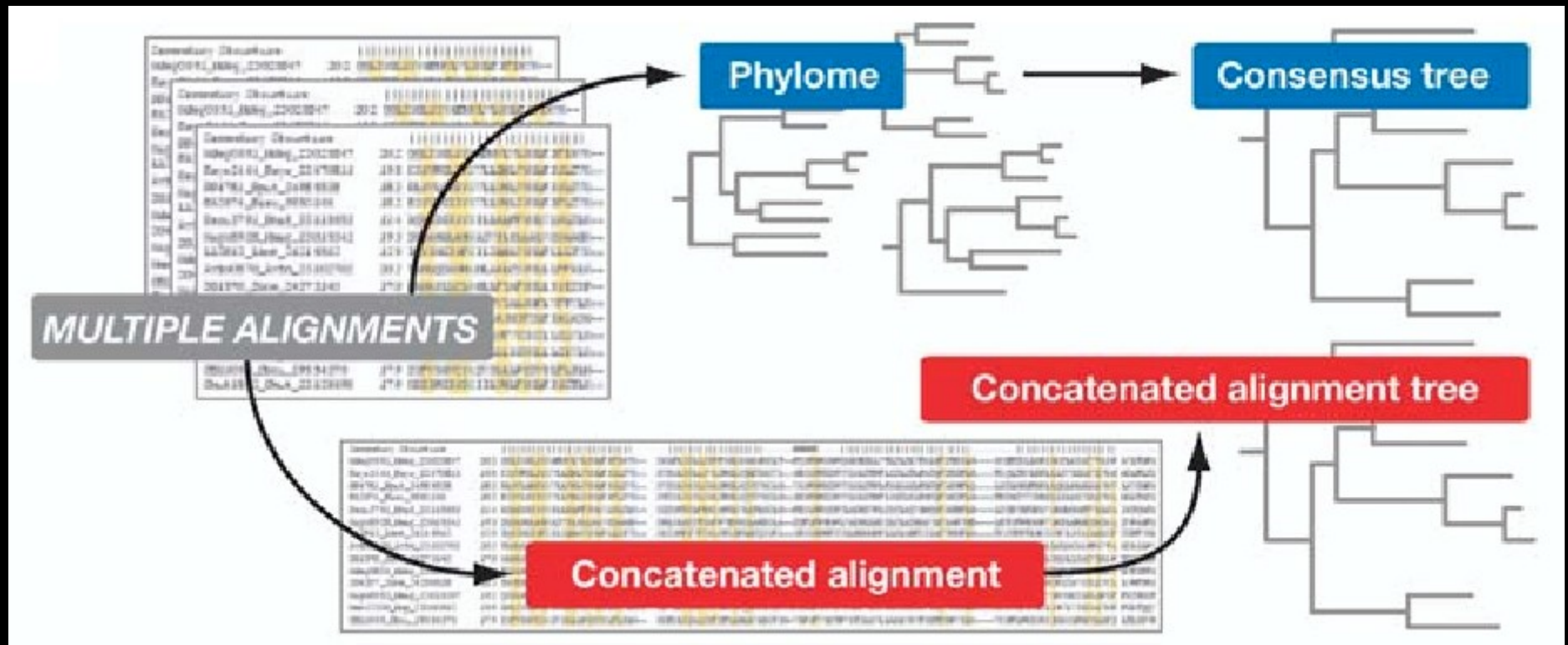
Eukarya: 5.491



Filogenômica







Supermatriz



Alinhar

Filtrar



Concatenar

Analisar

Superárvore



Alinhar

Filtrar



Analisar

Combinar

