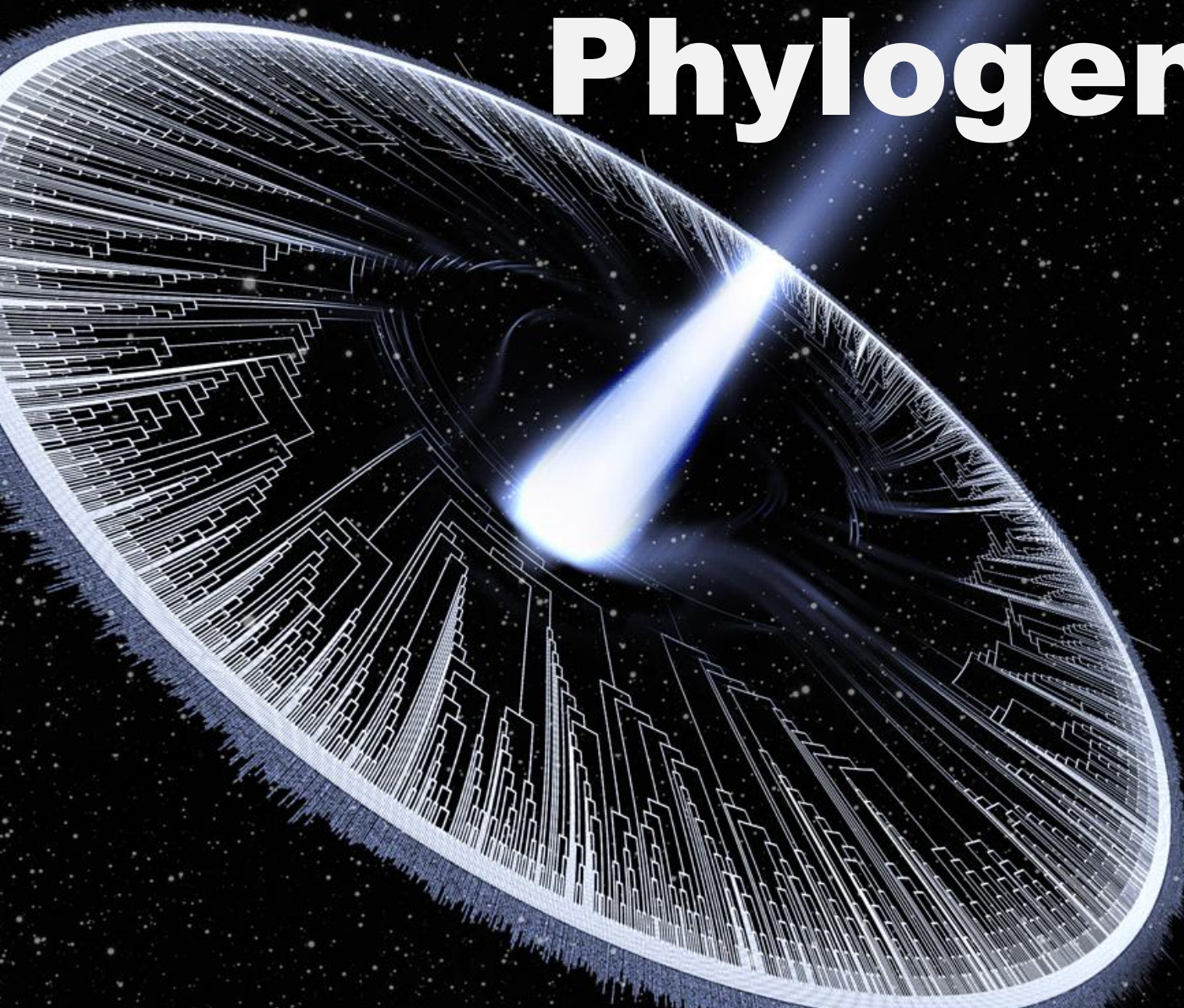


Macroevolution & Phylogenetics



Goals of the course:

1. Learn how to estimate trees
2. Learn how to use trees
3. Learn about the big questions in macroevolution
4. What are your goals?

Syllabus

Subject to change

Introductions

In the chat:

1. Your name, department, year, program
2. Research topic (1 Sentence)
3. A hobby or interest outside your job

Breakout groups

1. Introduce yourselves.

2. Why do we care about phylogenies? Have each person answer why it matters for their work (or future work) and why phylogeny matters (e.g. why you are taking this course).

3. Collapse & split your collective answers into distinct ideas, and enter each unique idea at:

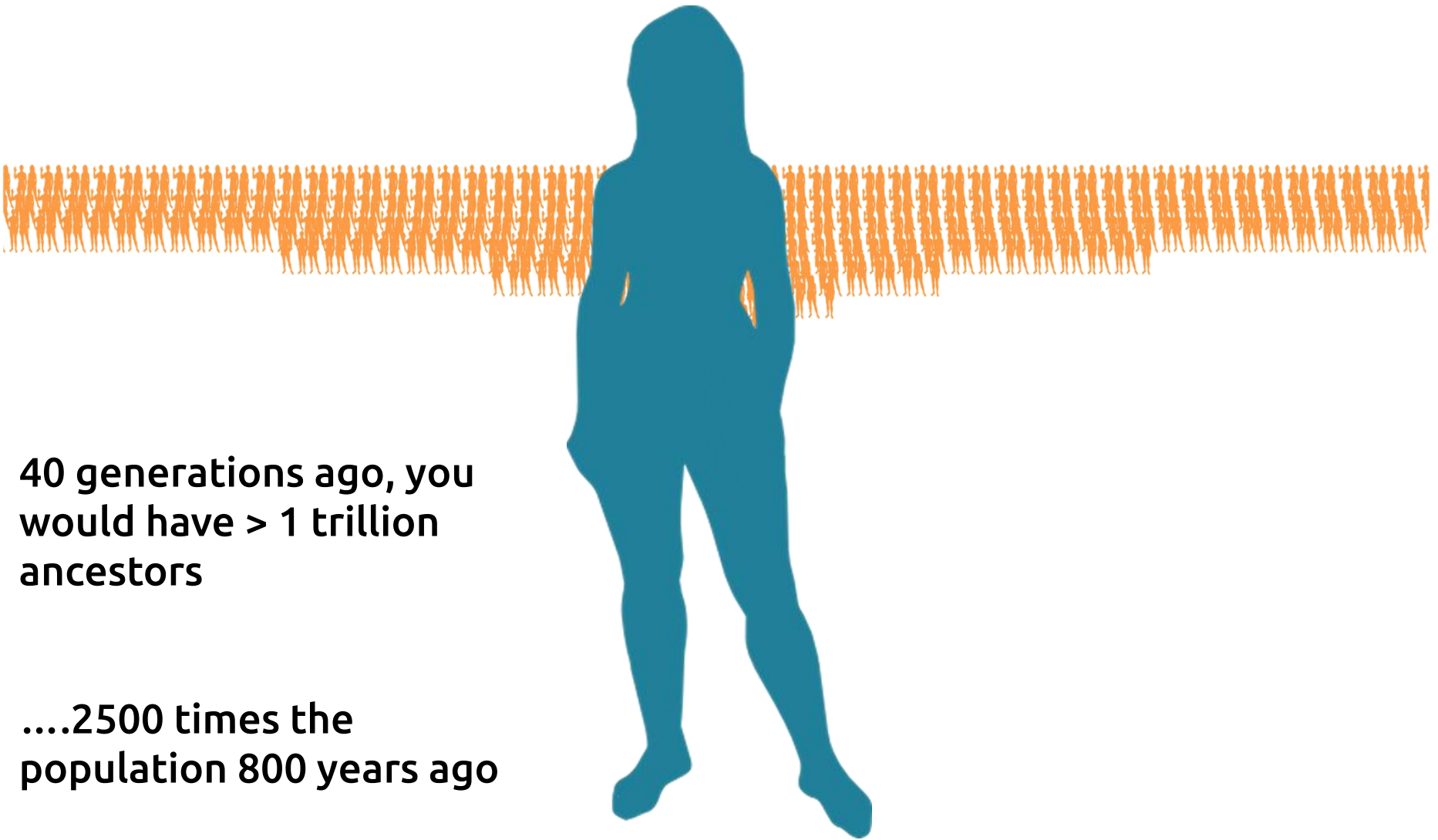
www.pollev.com/josefuyeda941

4. What's the unifying theme?

Why phylogeny?

What does a phylogeny represent?

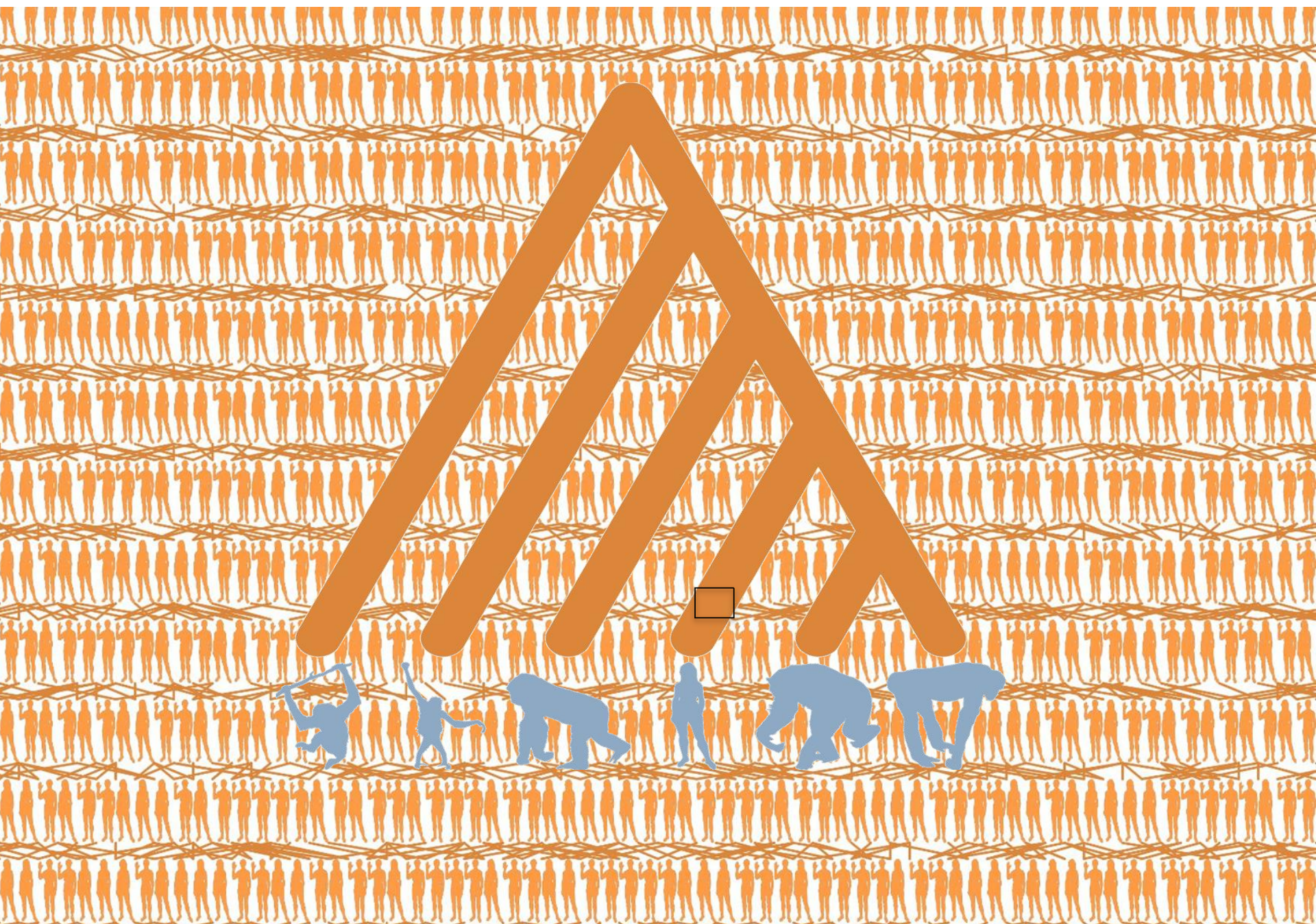
www.OneZoom.org/life/

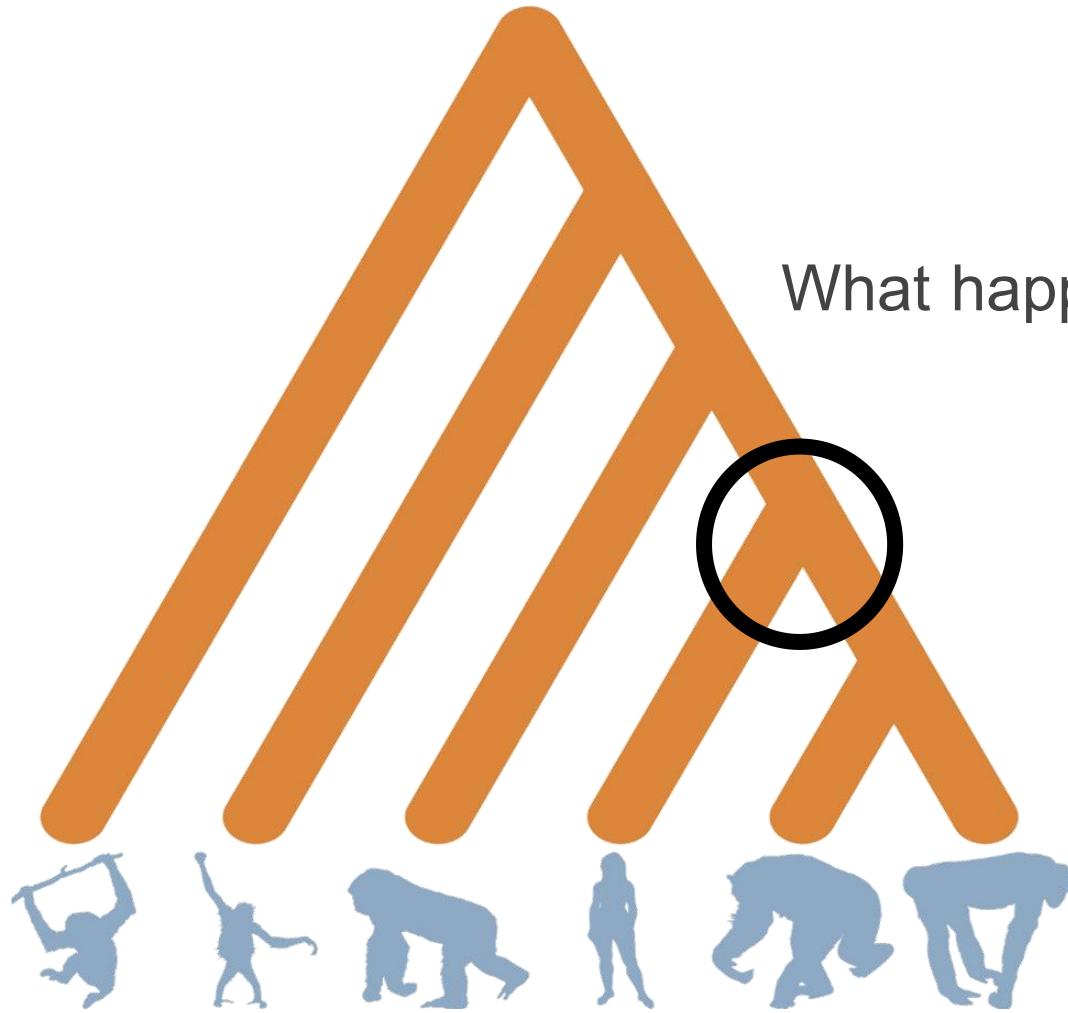


**40 generations ago, you
would have > 1 trillion
ancestors**

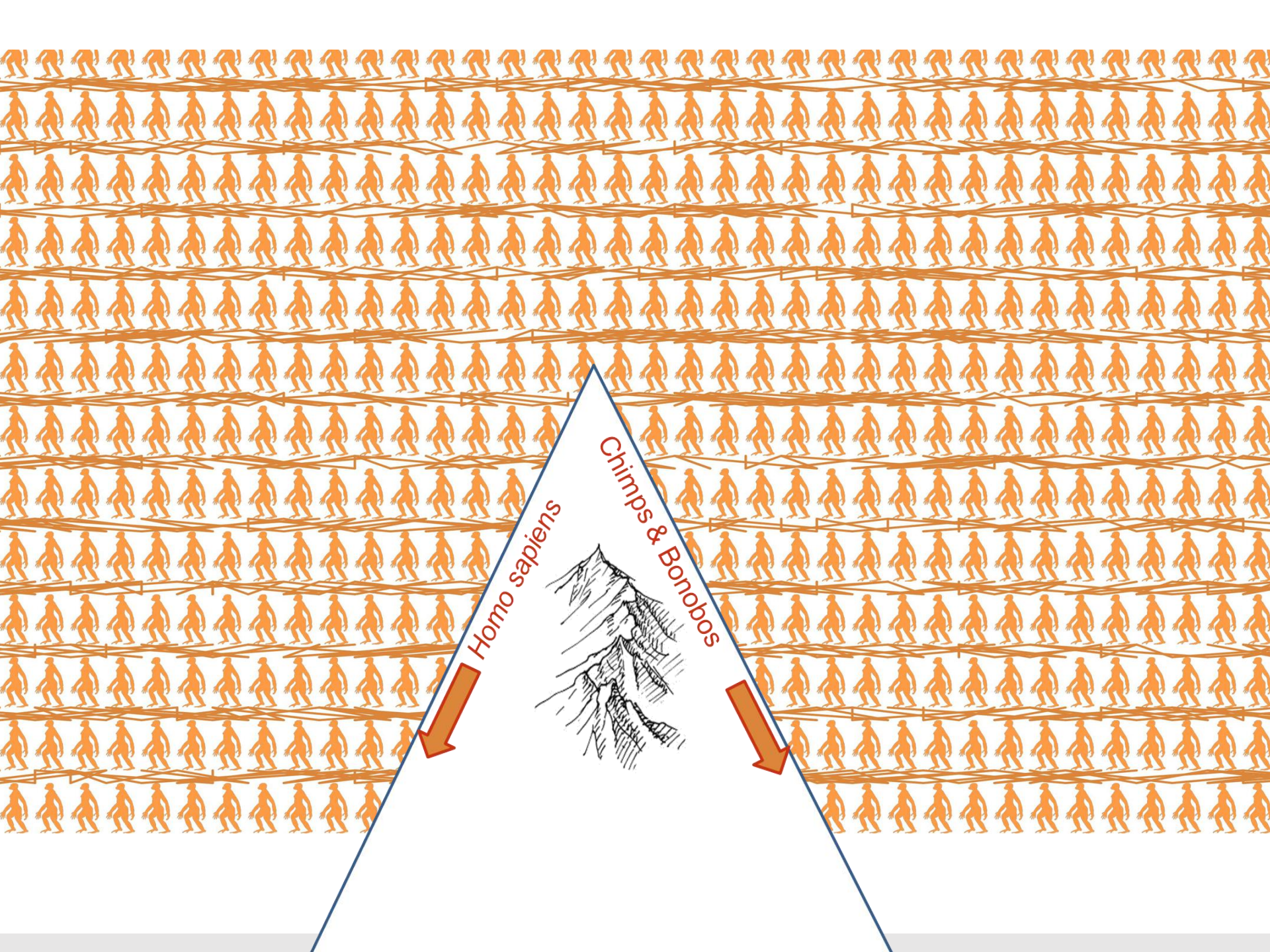
**....2500 times the
population 800 years ago**







What happened here ?



Terminology

Root

Branch/edge

Node

Tip

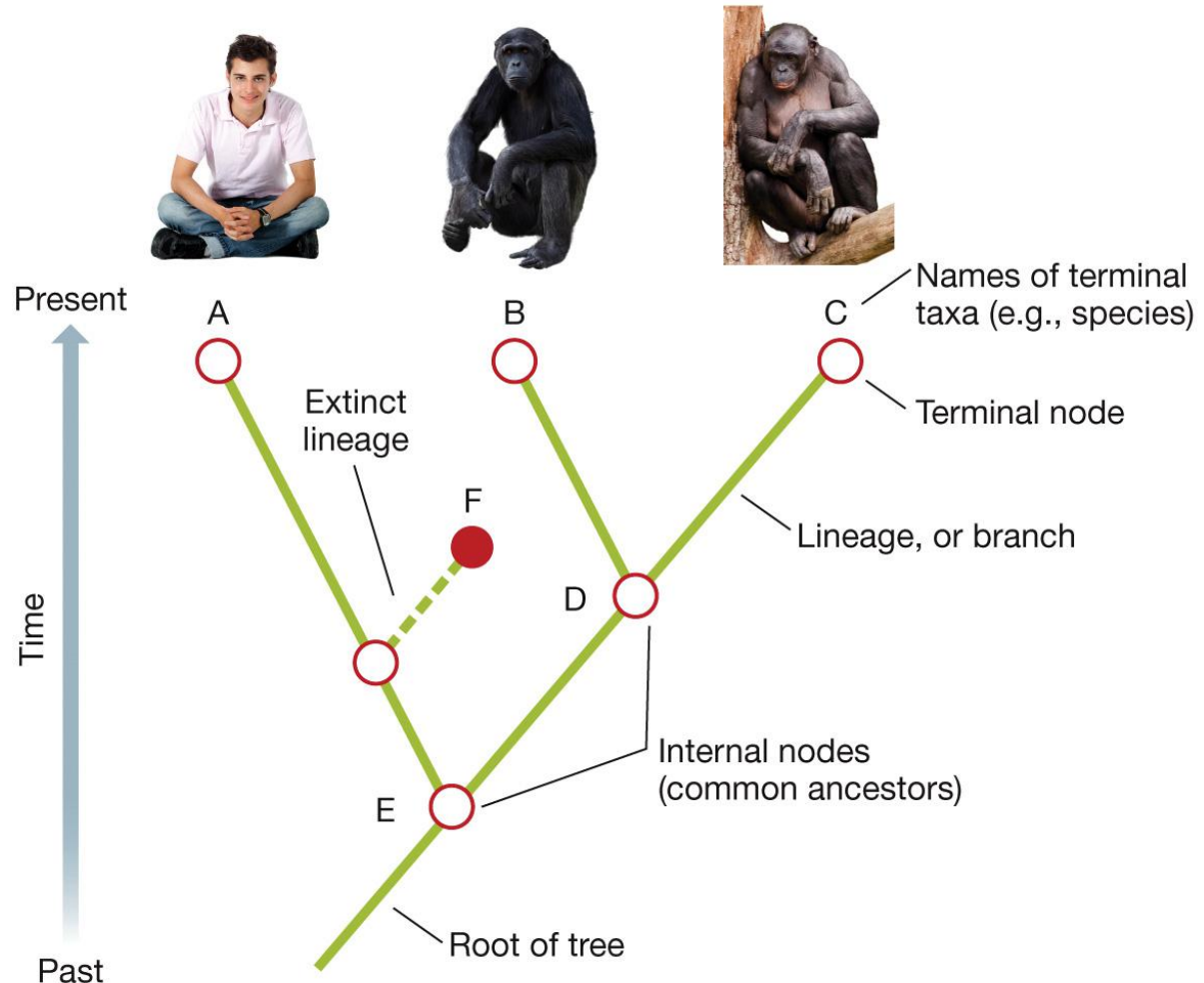
Outgroup

Clade

Monophyletic

Paraphyletic

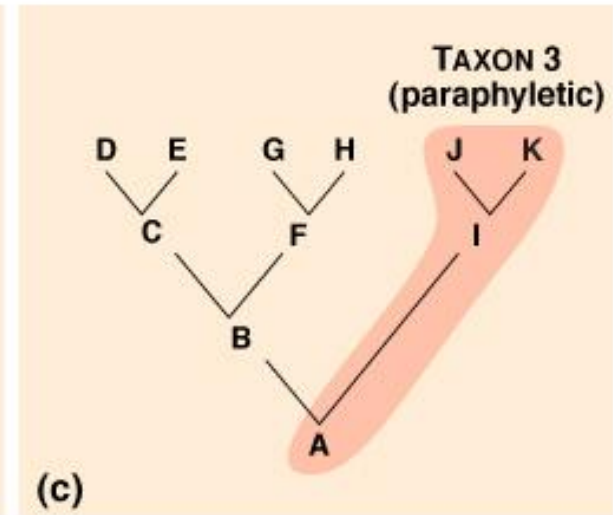
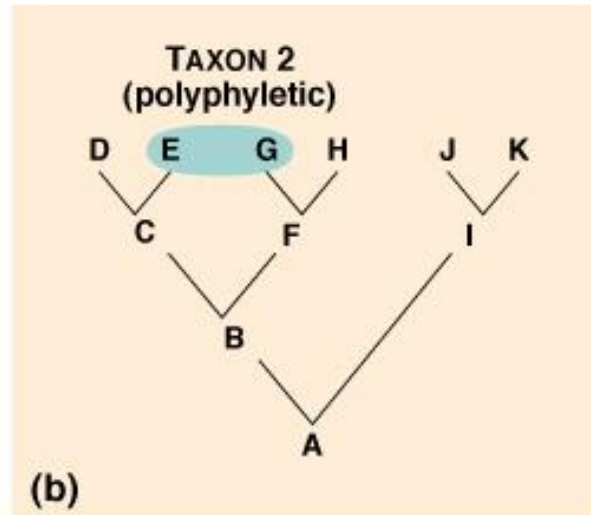
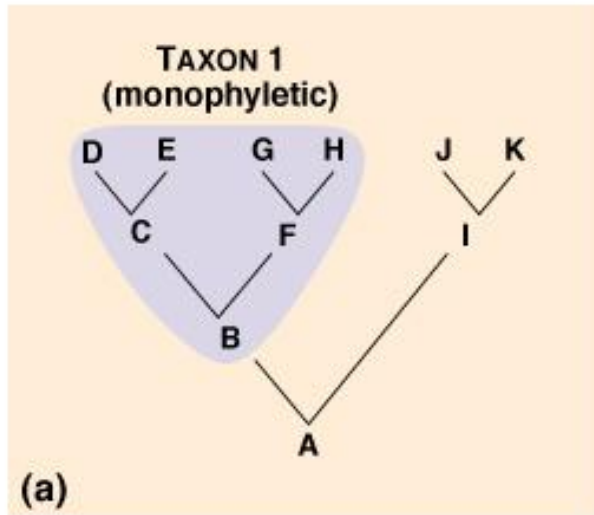
Polyphyletic



EVOLUTION 4e, Figure 2.6
© 2017 Sinauer Associates, Inc.

Taxonomy & Systematics

Goal: Monophyly



Other terminology:

split

bipartition

binary

polytomy

multifurcation/bifurcation

stem

crown

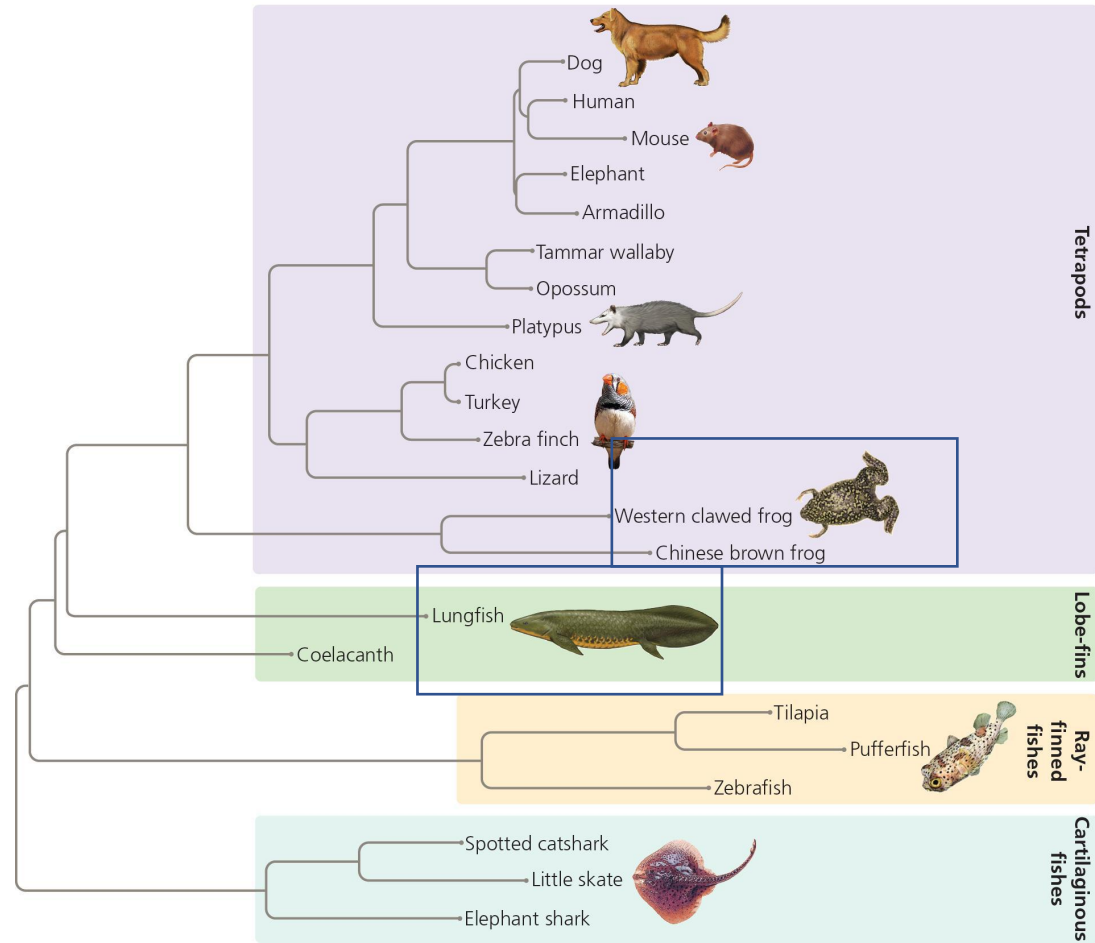
rooted

unrooted

ultrametric/nonultrametric

The phylogeny depicted clearly demonstrates that Lungfish are basal to /more primitive than frogs

A. True
B. False

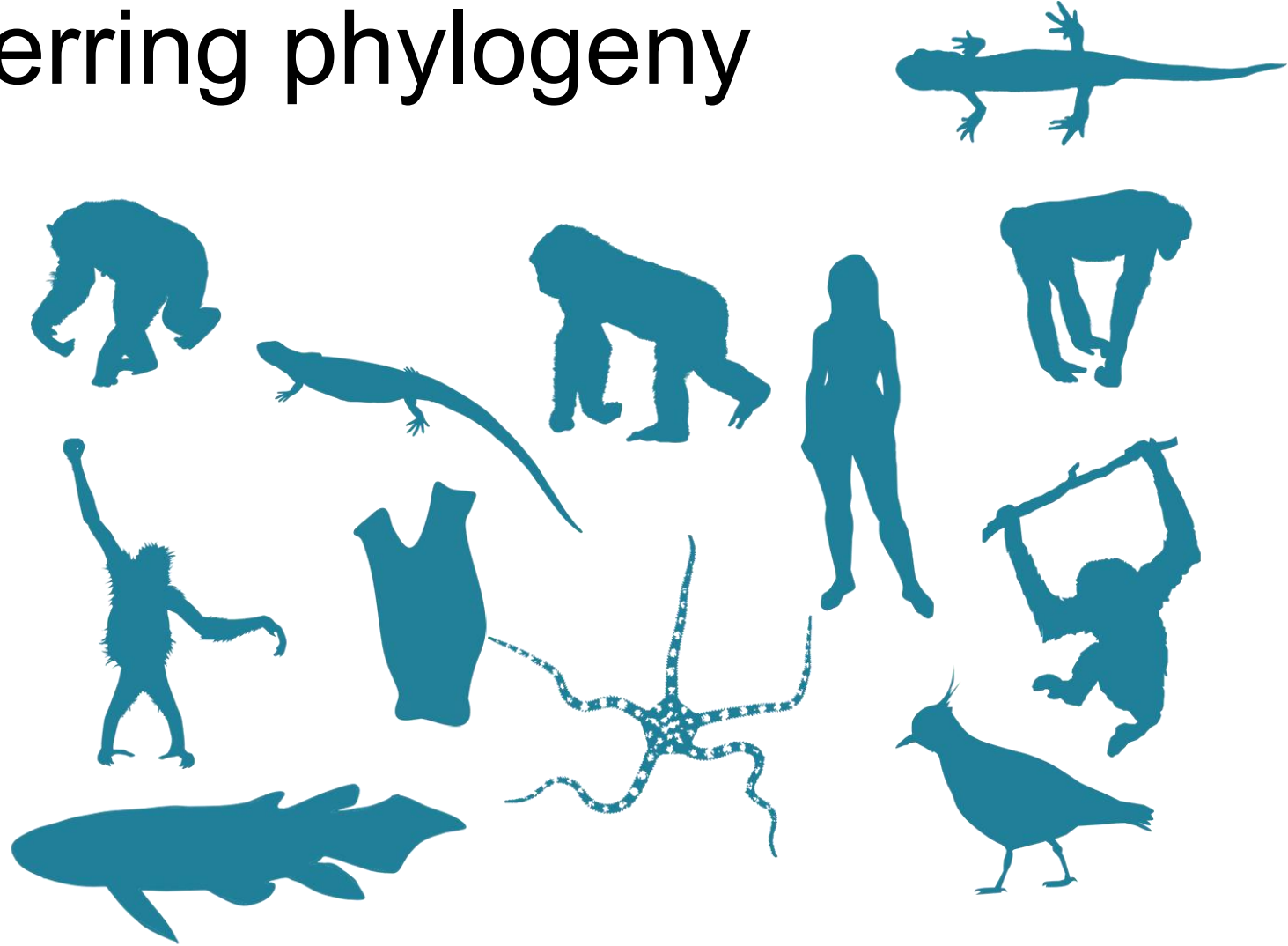


Assignment I: Canvas self-assessment

Read Baum & Smith, and complete the questions in Assignment I.

I'm going to assume you understand basic terminology and can read & interpret trees going forward. So if you don't understand any of the questions, bring your questions to class.

Going backwards- Inferring phylogeny



How many possible trees for 4 taxa?

Tree space is huge!!

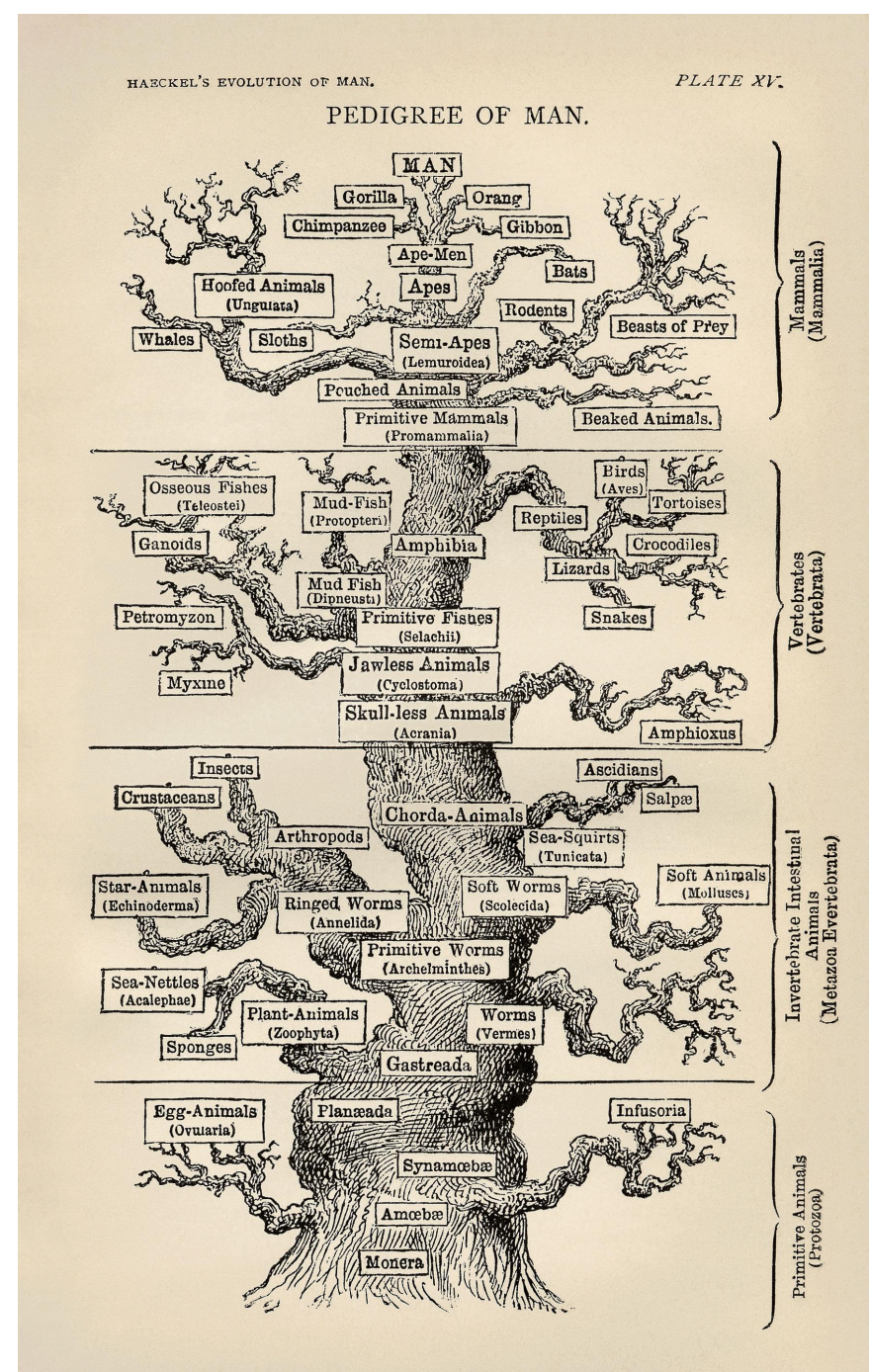
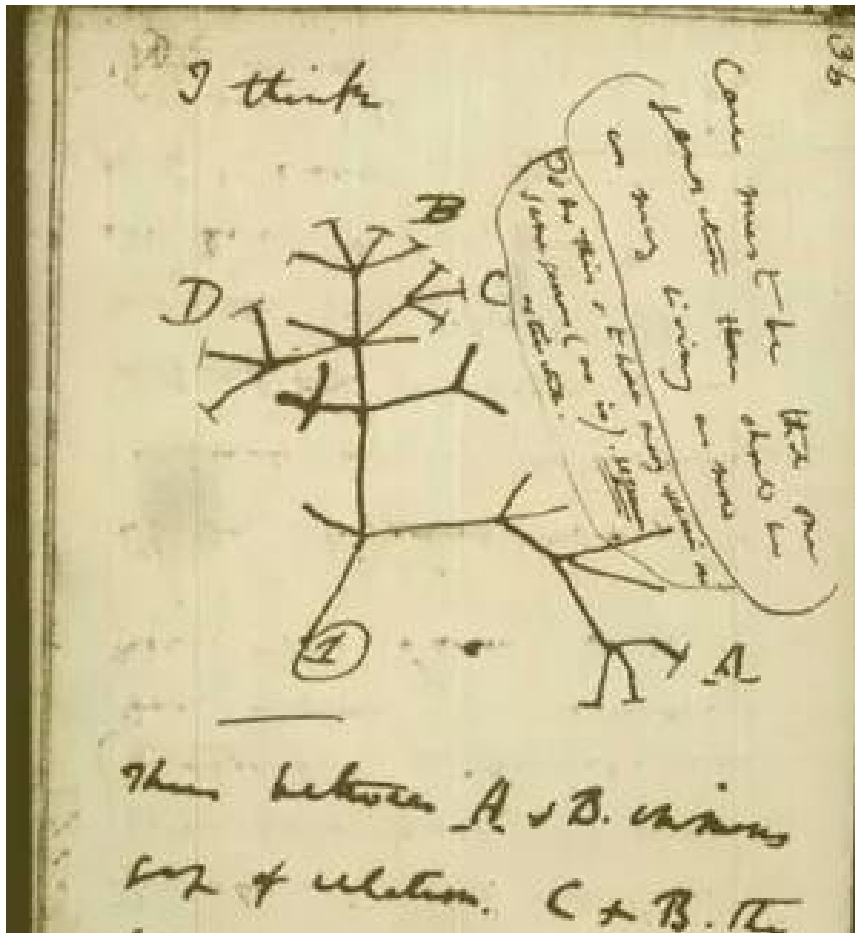
Table 3.1: The number of rooted, bifurcating, labeled trees for n species, for various values of n . The numbers for more than 20 species are approximate.

= Hard Problem

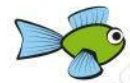
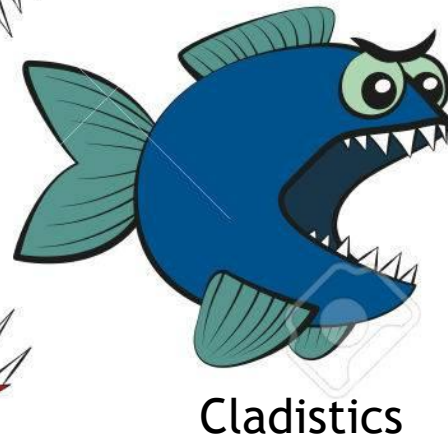
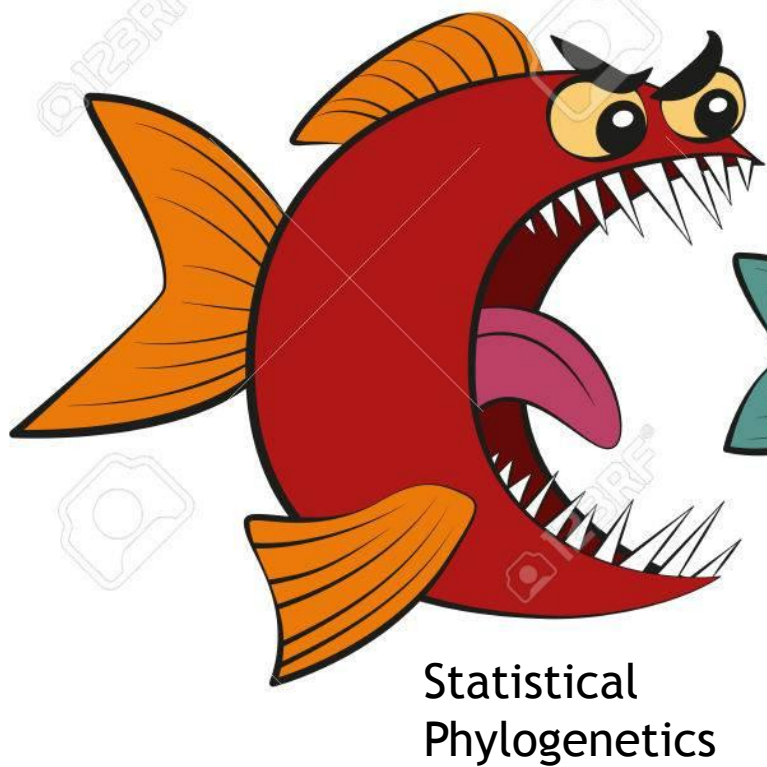
Species	Number of trees
1	1
2	1
3	3
4	15
5	105
6	945
7	10,395
8	135,135
9	2,027,025
10	34,459,425
11	654,729,075
12	13,749,310,575
13	316,234,143,225
14	7,905,853,580,625
15	213,458,046,676,875
16	6,190,283,353,629,375
17	191,898,783,962,510,625
18	6,332,659,870,762,850,625
19	221,643,095,476,699,771,875
20	8,200,794,532,637,891,559,375
30	4.9518×10^{38}
40	1.00985×10^{57}
50	2.75292×10^{76}

How can we find the “true” tree?
(Is there a true tree?!?)

History of phylogenetic inference



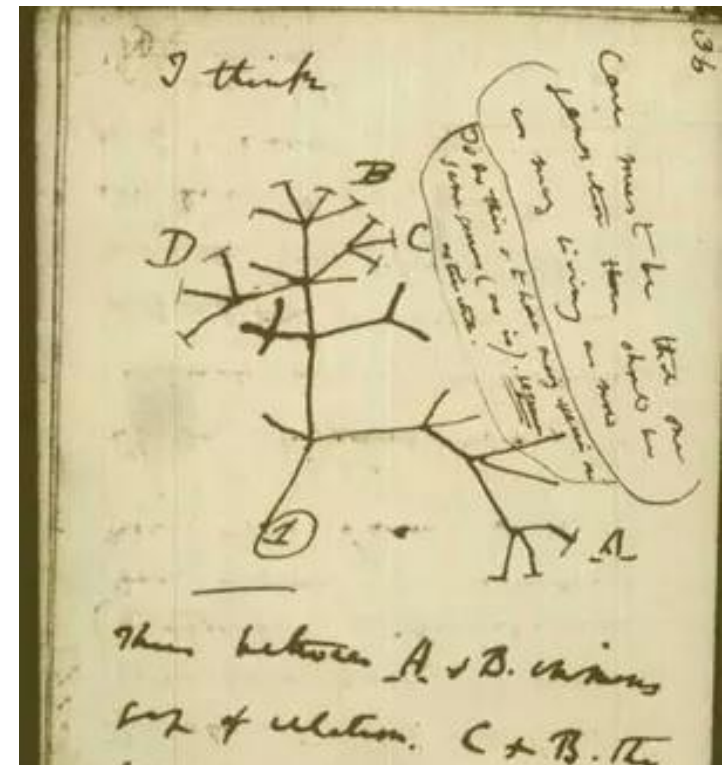
History of phylogenetic inference



History of phylogenetic inference: Evolutionary Taxonomy

No objective methodology

Relies on expert opinion & a
lifetime of study



History of phylogenetic inference: Phenetics

Numerical Taxonomy & distance methods - measure overall similarity

How do you measure similarity?

What are the drawbacks of this approach?

Sokal, Sneath & Rohlf (1960's) argued phenetics provided much needed reproducibility

Human	M	V	H	L	T	P	E	E	K	S	A	V	T	A	L	W	G	K	V	N	V	D	E	V	G	G	E	A	L	G	R	L	L	V	V	Y	P	W	T	Q	R	F	F	E	S	F	G	D	L	S					
Baboon	N
Cow	.	-	-	.	.	A	.	.	.	A	F	K	
Sheep	.	-	-	.	.	A	.	.	.	A	.	.	.	G	F	K	A	H	
Mouse	D	A	.	.	A	.	.	S	G	A	Y	.	D		
Hamster	D	A	.	.	A	L	.	.	G	A	.	A	.	.	A	H	
Chicken	.	.	.	W	.	A	.	.	.	Q	L	I	.	G	A	.	C	.	A	.	.	.	A	.	.	.	I	A	.	.	.	N		

C

```
graph LR; Root(( )) --- Node1(( )); Root --- Node2(( )); Node1 --- Human[Human]; Node1 --- Node3(( )); Node3 --- Baboon[Baboon]; Node3 --- Node4(( )); Node4 --- Cow[Cow]; Node4 --- Sheep[Sheep]; Node2 --- Node5(( )); Node5 --- Mouse[Mouse]; Node5 --- Node6(( )); Node6 --- Hamster[Hamster]; Node6 --- Chicken[Chicken];
```

Human

Baboon

Cow

Sheep

Mouse

Hamster

Chicken

Next time: Parsimony & Cladistics