Hot Science Cool Talks

UT Environmental Science Institute

49

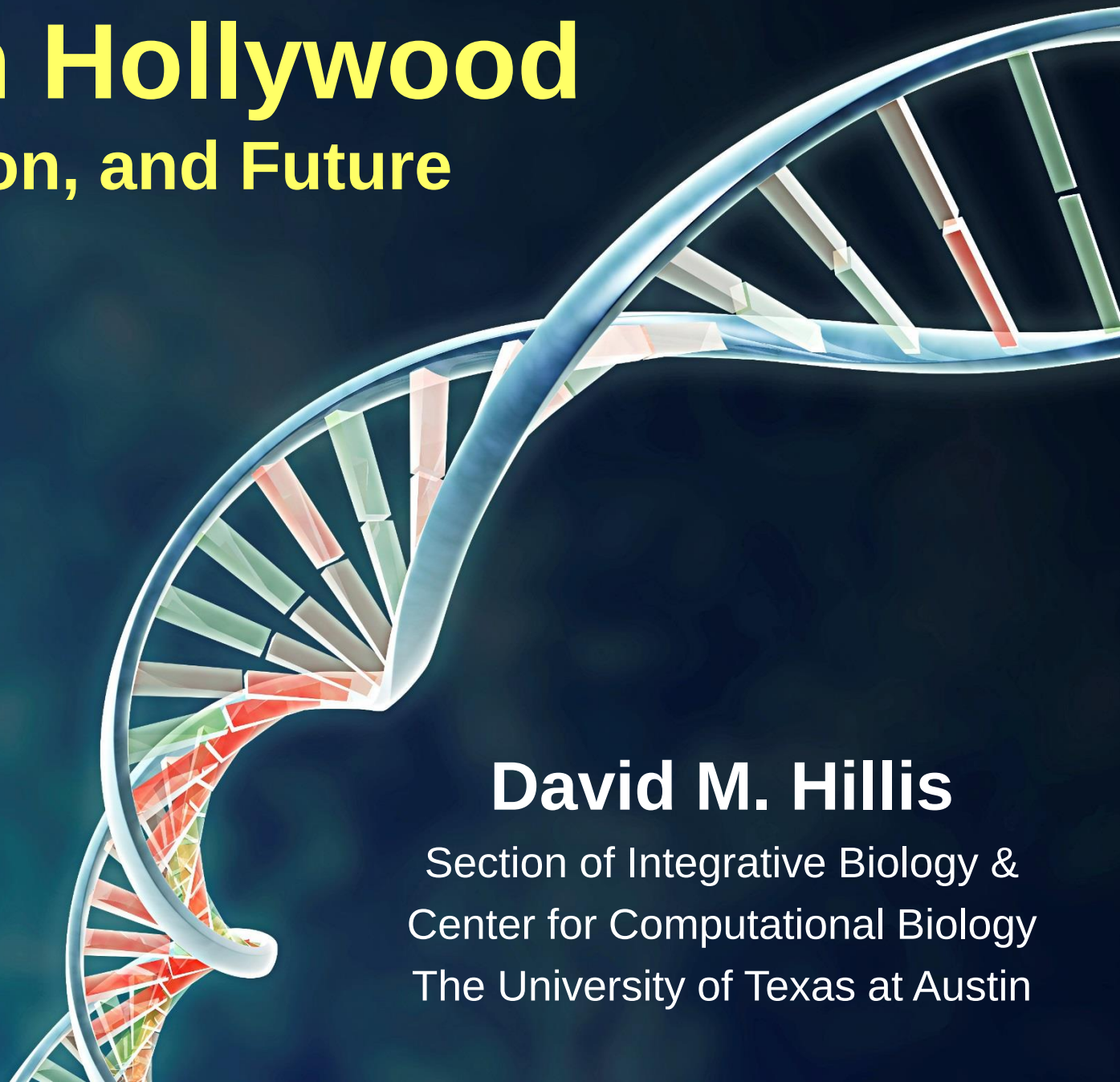
DNA in Hollywood: Fact, Fiction and Future

Dr. David Hillis

September 14, 2007

DNA in Hollywood

Fact, Fiction, and Future



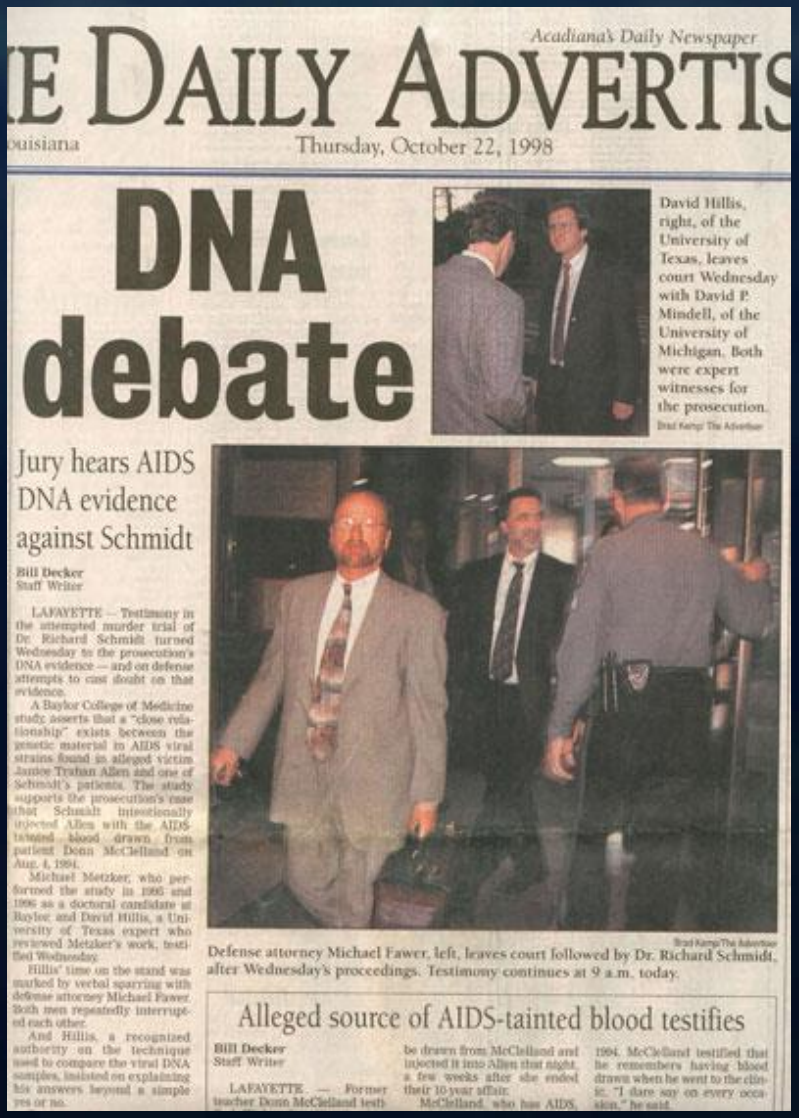
David M. Hillis

Section of Integrative Biology &

Center for Computational Biology

The University of Texas at Austin


CSI clip



Acadiana's Daily Newspaper

E DAILY ADVERTIS

uisiana Thursday, October 22, 1998

DNA debate

David Hillis, right, of the University of Texas, leaves court Wednesday with David P. Mindell, of the University of Michigan. Both were expert witnesses for the prosecution.

Brad Kemp/The Advertiser

Jury hears AIDS DNA evidence against Schmidt

Bill Decker
Staff Writer

LAFAYETTE — Testimony in the attempted murder trial of Dr. Richard Schmidt turned Wednesday to the prosecution's DNA evidence — and on defense attempts to cast doubt on that evidence.

A Baylor College of Medicine study asserts that a "close relationship" exists between the genetic material in AIDS viral strains found in alleged victim Janice Trahan Allen and one of Schmidt's patients. The study supports the prosecution's case that Schmidt intentionally injected Allen with the AIDS-tainted blood drawn from patient Donn McClelland on Aug. 4, 1994.

Michael Metzker, who performed the study in 1995 and 1996 as a doctoral candidate at Baylor and David Hillis, a University of Texas expert who reviewed Metzker's work, testified Wednesday.

Hillis' time on the stand was marked by verbal sparring with defense attorney Michael Fawer. Both men repeatedly interrupted each other.

And Hillis, a recognized authority on the technique used to compare the viral DNA samples, insisted on explaining his answers beyond a simple yes or no.

Brad Kemp/The Advertiser

Defense attorney Michael Fawer, left, leaves court followed by Dr. Richard Schmidt, after Wednesday's proceedings. Testimony continues at 9 a.m. today.

Alleged source of AIDS-tainted blood testifies

Bill Decker
Staff Writer

LAFAYETTE — Former teacher Donn McClelland testi

be drawn from McClelland and injected it into Allen that night, a few weeks after she ended their 10-year affair.

McClelland, who has AIDS,

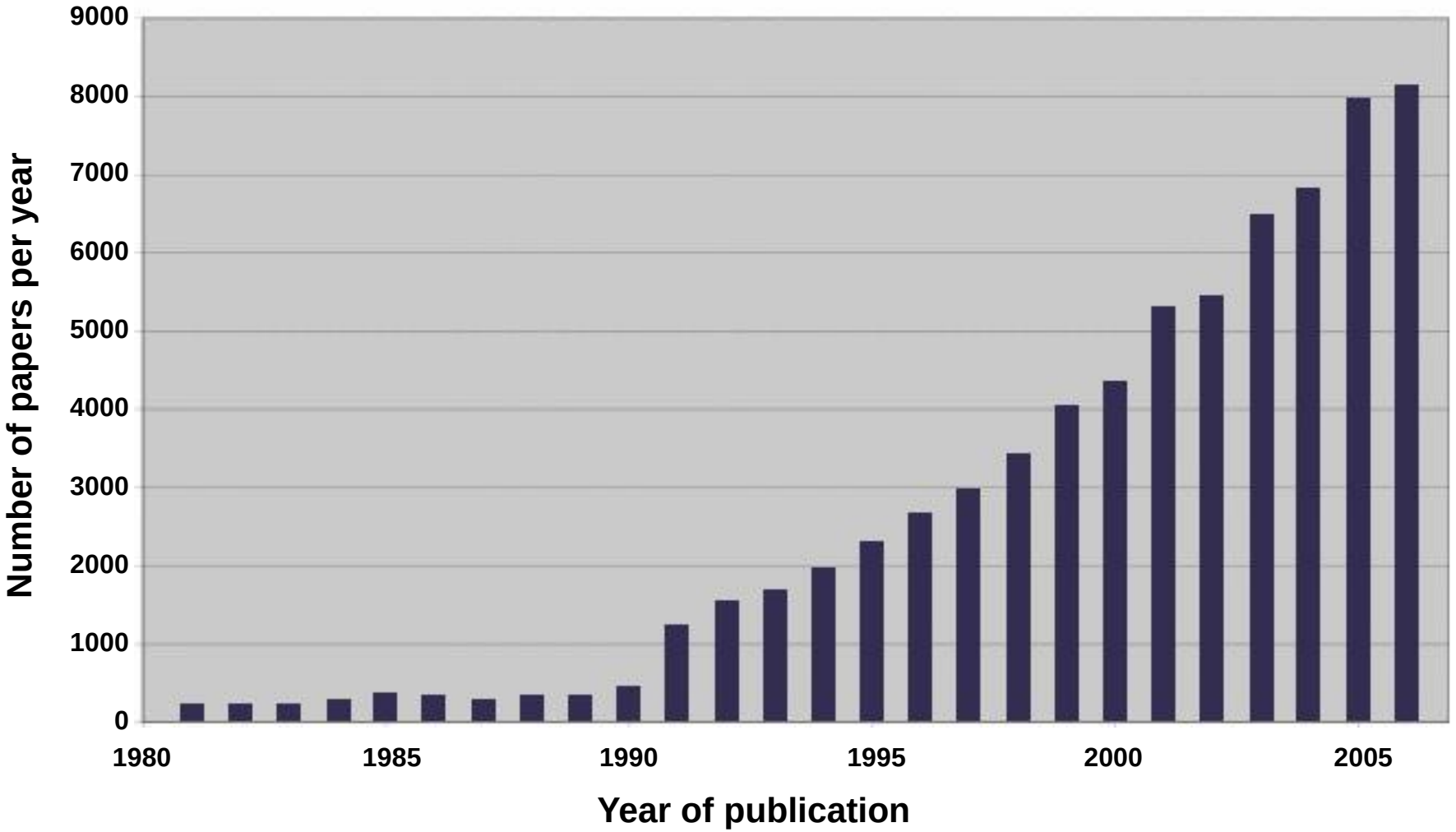
1994. McClelland testified that he remembers having blood drawn when he went to the clinic. "I dare say on every occasion," he said.

Phylogenetic analysis can be used to trace viral infections through a human population

- **Origins of HIV, SARSand other viruses transmitted between animals and humans**
- **Global virus diversity for vaccine trials**
- **Epidemiological studies**
- **Identification of new diseases**
- **Forensic uses**

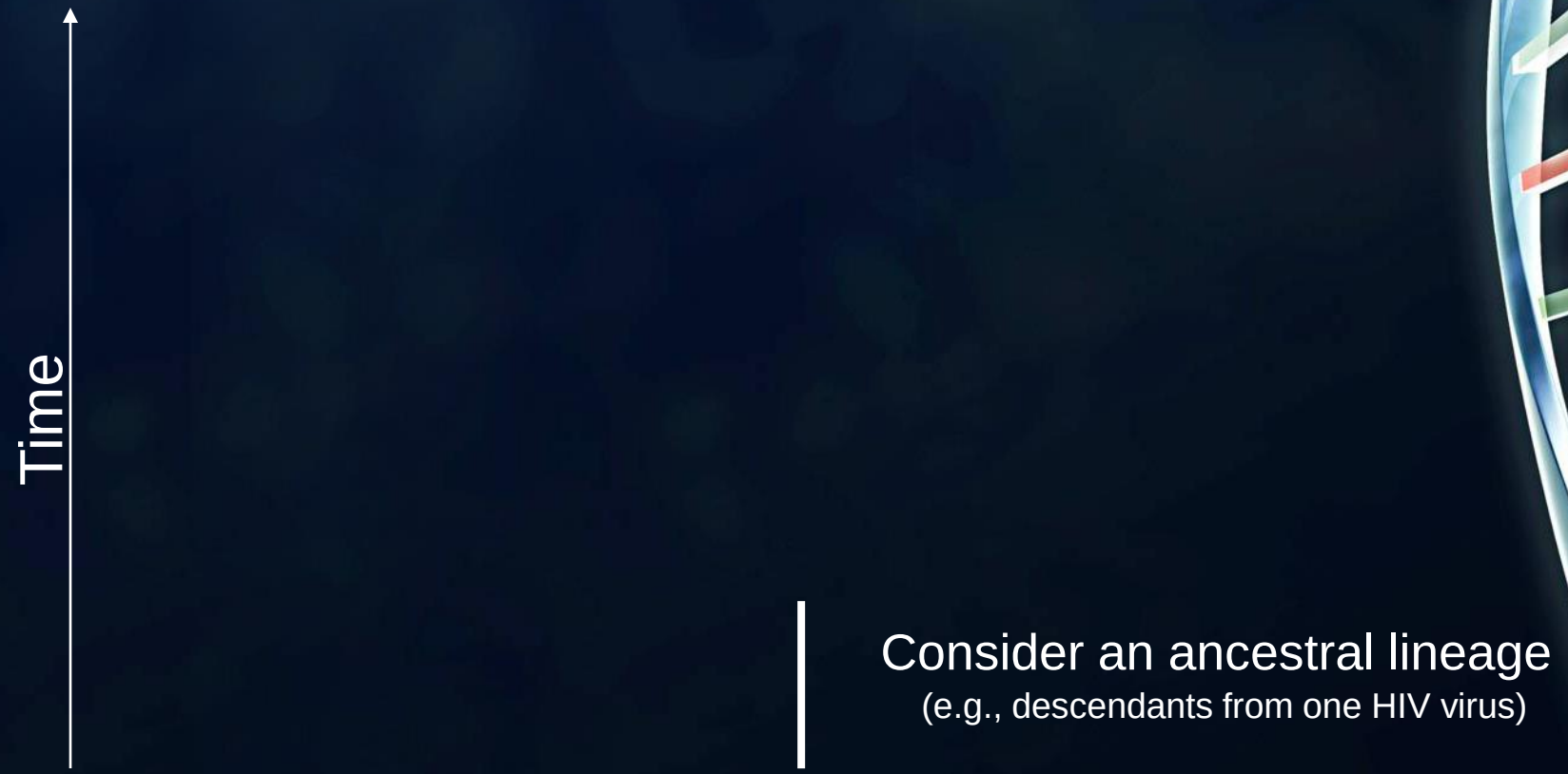
Phylogeny Papers, 1981-2006

(with “phylogeny” or “phylogenetic” in title or abstract)



Phylogeny

Evolutionary relationships among lineages, such as genes, individuals, populations, species, etc.



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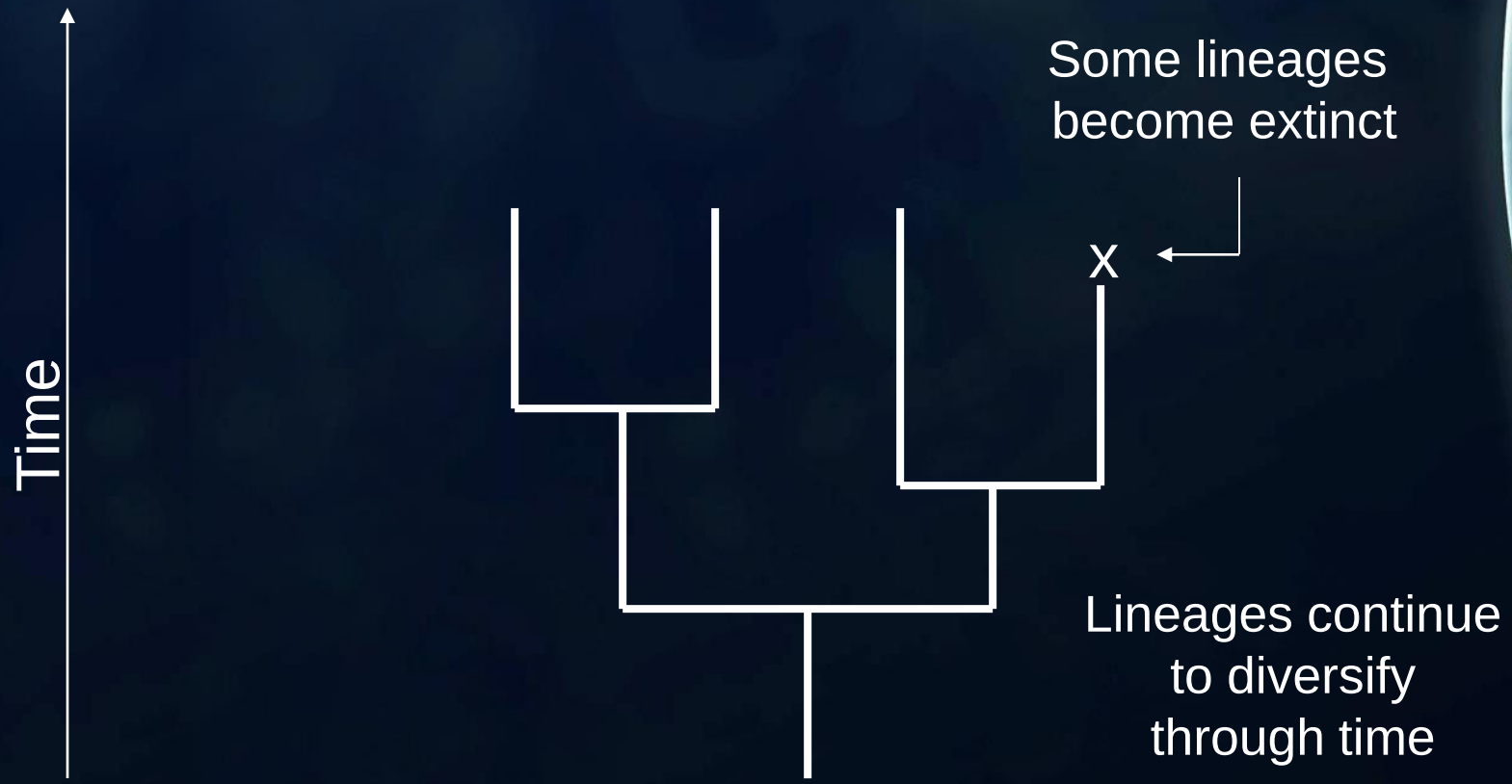


Phylogeny

Evolutionary relationships among lineages, such as genes, individuals, populations, species, etc.

The relationships among lineages produce a phylogenetic tree

Phylogeny

Evolutionary relationships among lineages, such as genes, individuals, populations, species, etc.

If samples are taken at this point in time…

X

…then the reconstructed phylogenetic tree will look like this

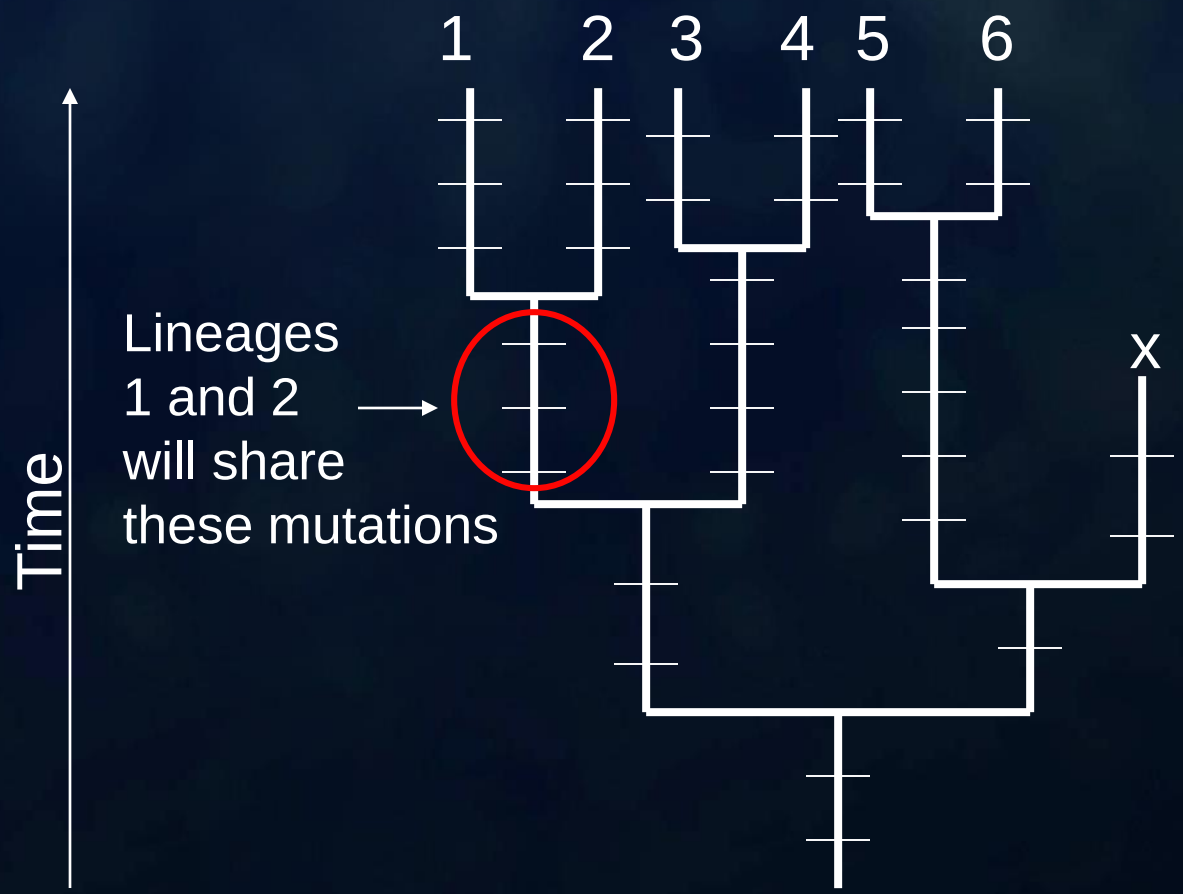
Phylogeny

How is evolutionary history reconstructed?

Each of these tick marks represents a new mutation in the genome of the respective HIV lineage

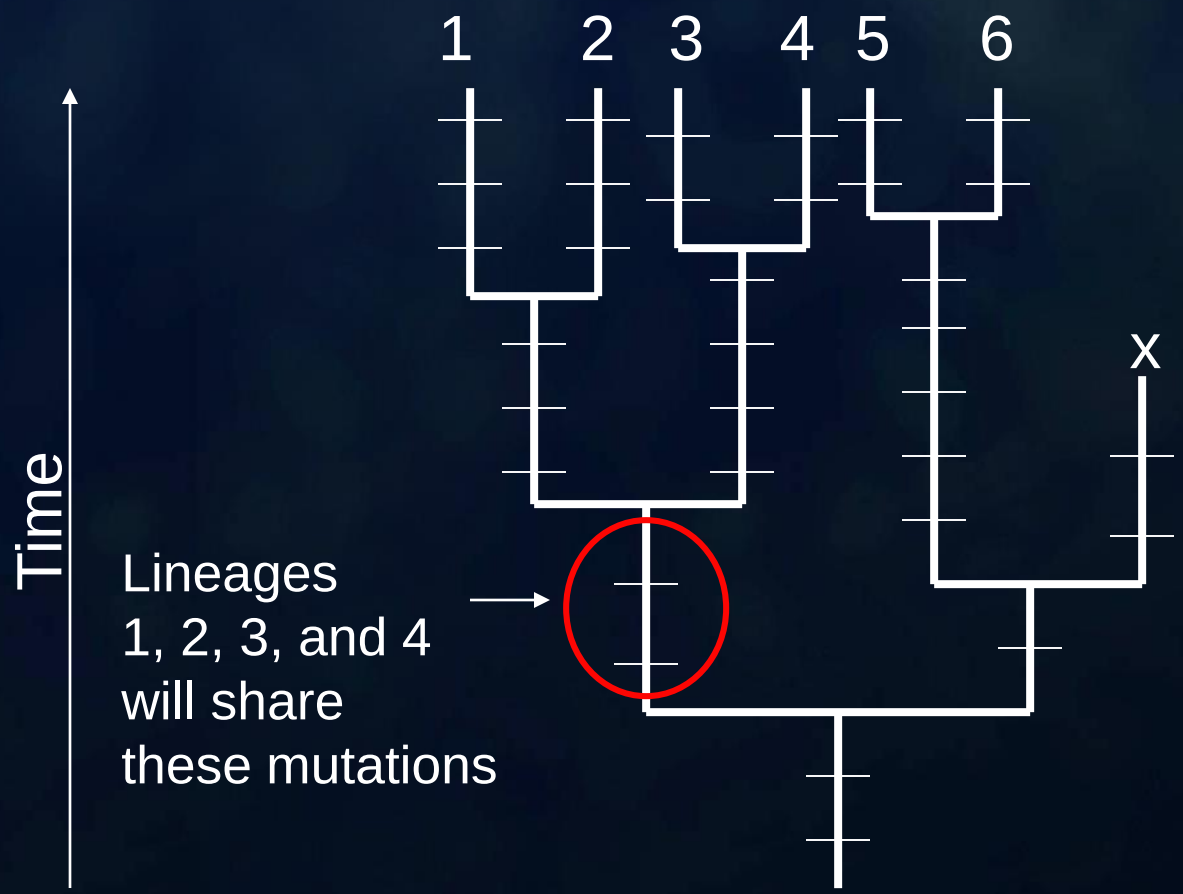
Phylogeny

How is evolutionary history reconstructed?



Phylogeny

How is evolutionary history reconstructed?



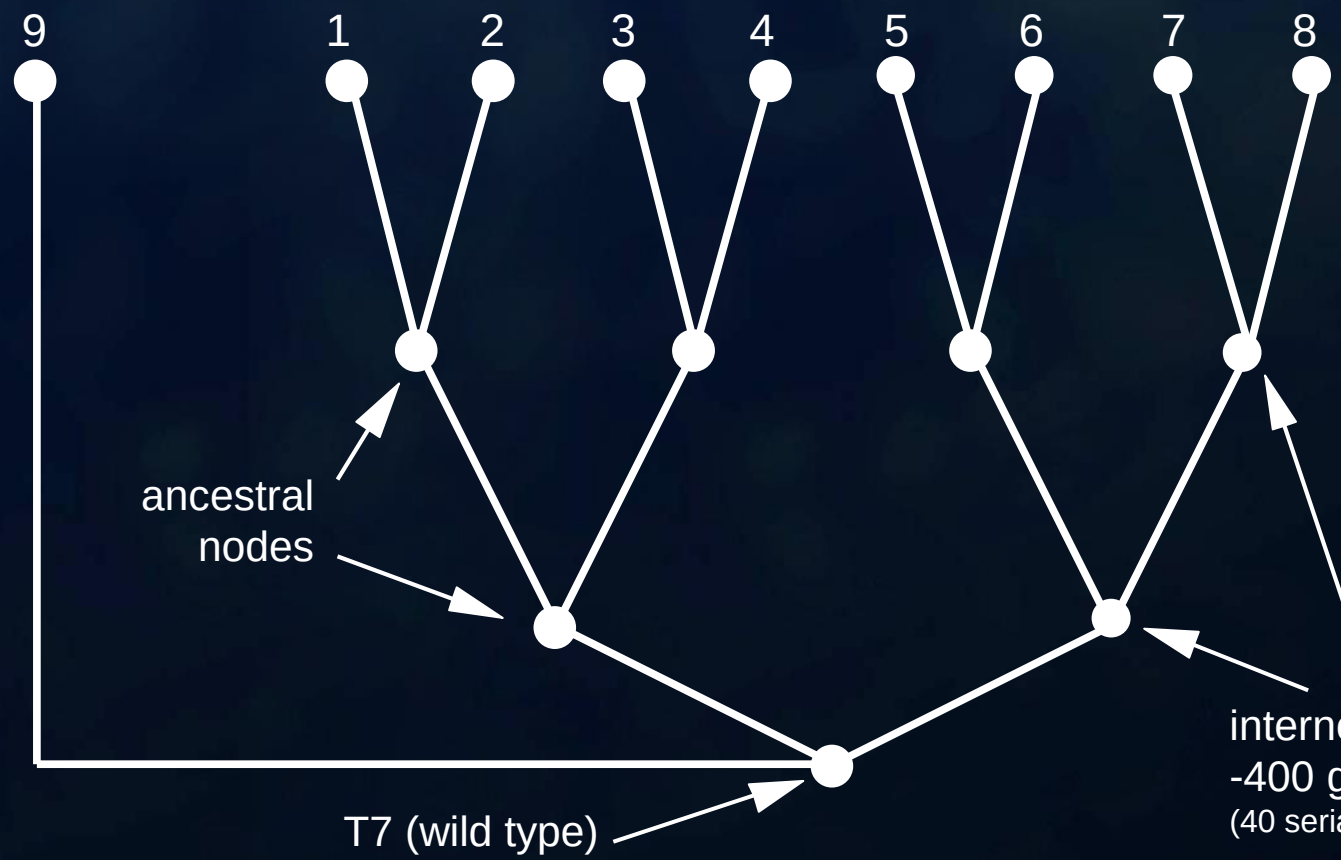
Phylogeny

How is evolutionary history reconstructed?

A model of HIV evolution
is used to account for multiple changes to the same sites on a genome, different rates of changes among sites, and other details of HIV evolution

How do we know phylogenetic analysis works?

Experimental evolution to test phylogenetic methods



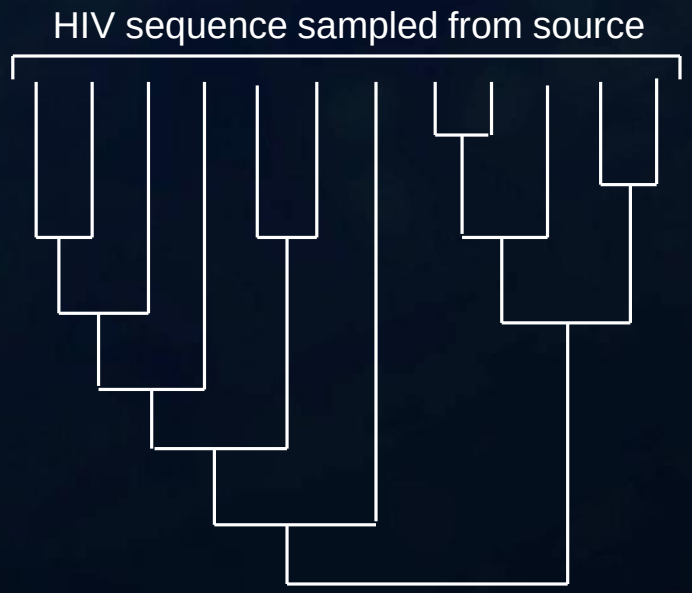
Hillis et al., 1992 (Science 255:589-592)3

HIV transmission

Viral transmission events may be traced back through time among individuals in a population.

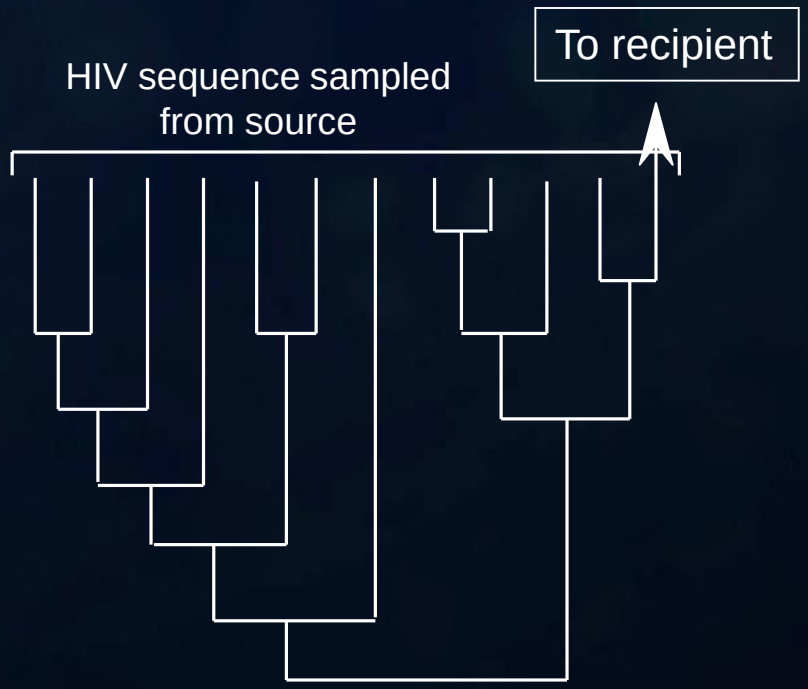
To imagine how this is possible, start by considering the diversity of HIV within one infected individual:

Time 1: Prior to Transmission event



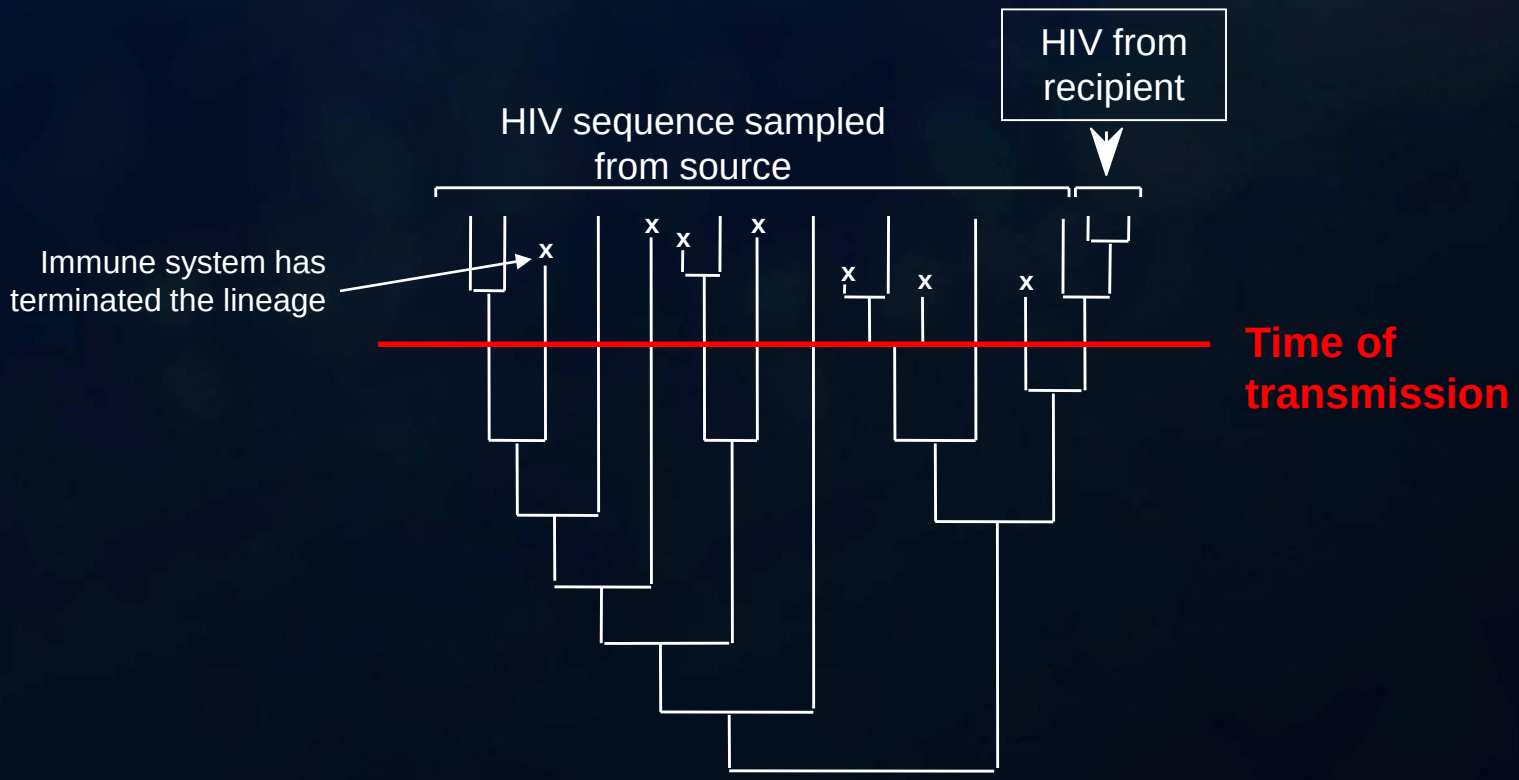
At the transmission event, the HIV in the recipient represents a small subset of the HIV in the source:

Time 2: The transmission event



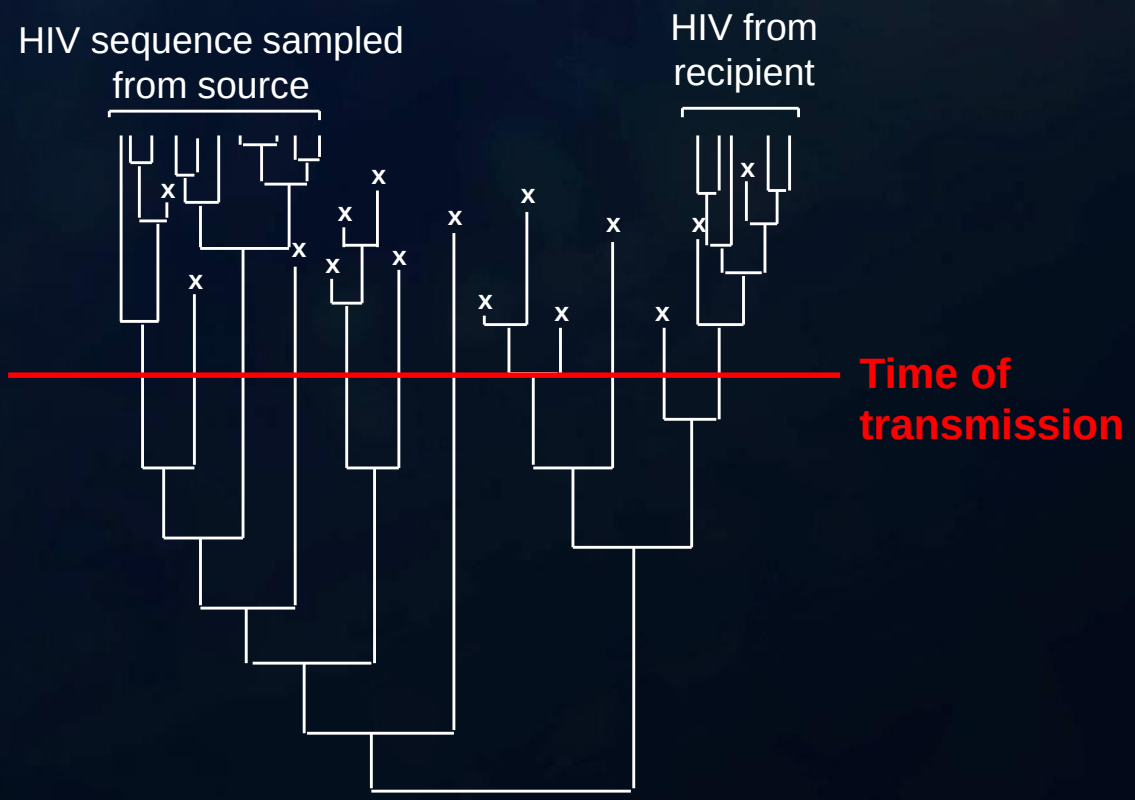
As time passes, HIV lineages in the source and recipient diversify, and other lineages become extinct.

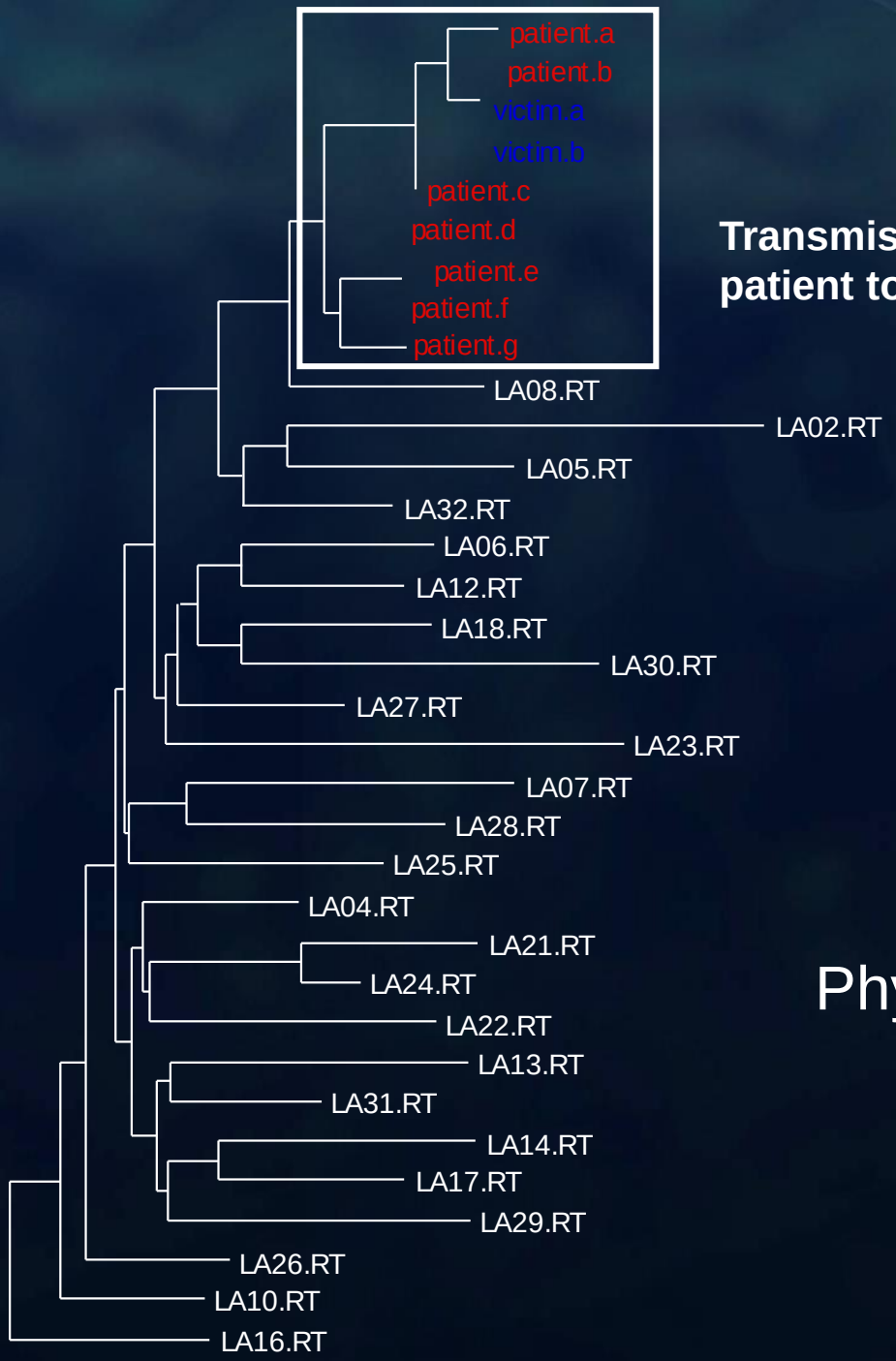
Time 3: Shortly after transmission event



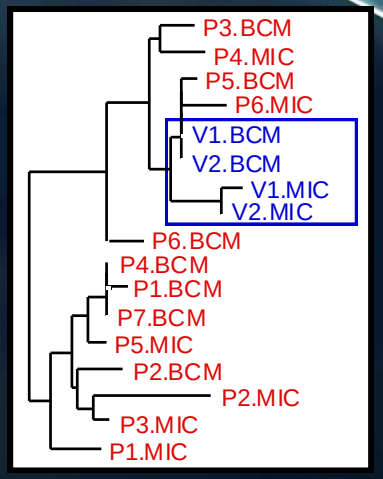
After enough time has passed, immunoselection will result in an apparent sister-group relationship among the HIV lineages in the source and recipient:

Time 4: Further after transmission event





Transmission from patient to victim



New sequences added

Phylogenetic evidence: *pol* sequences

Metzker et al., 2002
(PNAS 99:14292-14297)

Acadiana's Daily Newspaper

E DAILY ADVERTIS

Saturday, October 24, 1998

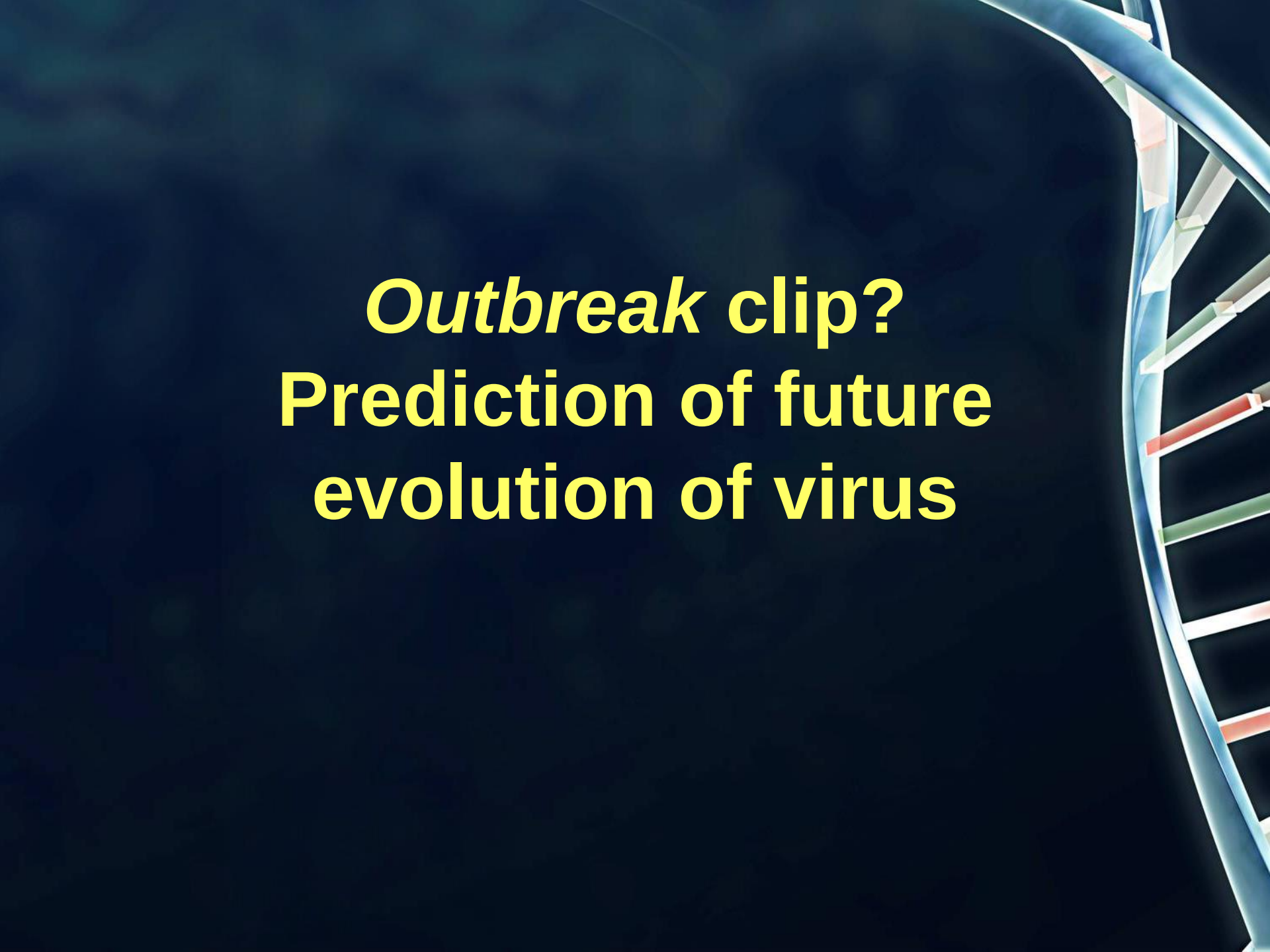
Schmidt guilty

Doctor faces 50-year jail sentence

Dr. Richard Schmidt, center, leaves the Lafayette Parish Courthouse Friday night with his despondent wife, Barbara, after being convicted of attempted second-degree murder. Schmidt is accompanied by courthouse security and defense attorney Gerald Block, left.

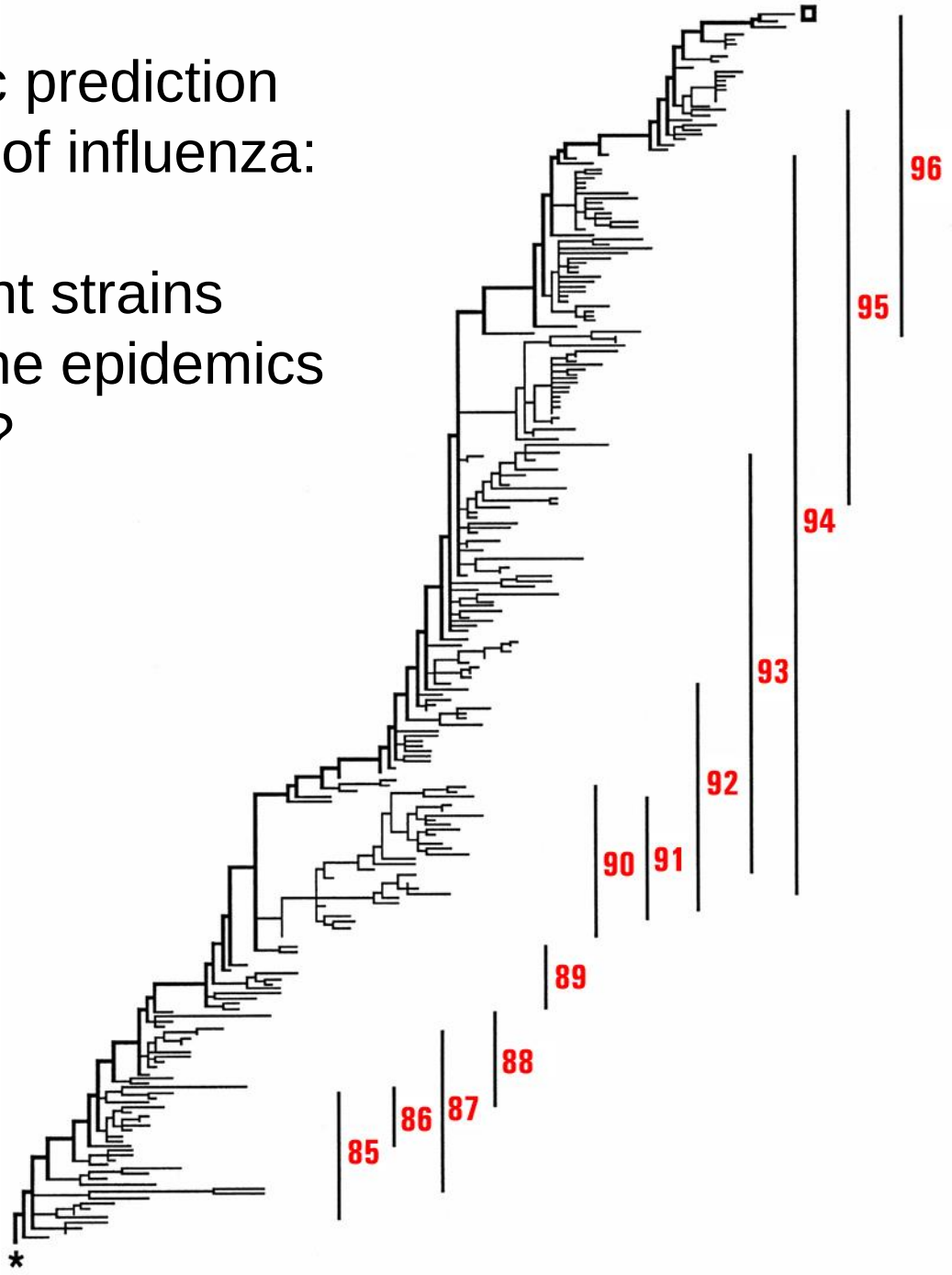
Claps, sobs, fainting spell greet verdict

- Schmidt was convicted of attempted murder; currently serving term of 50 years of hard labor
- First use of phylogenetic analysis in U.S. criminal case
- Phylogenetics can be used to trace infections of human pathogens among individuals


Outbreak clip?
Prediction of future evolution of virus

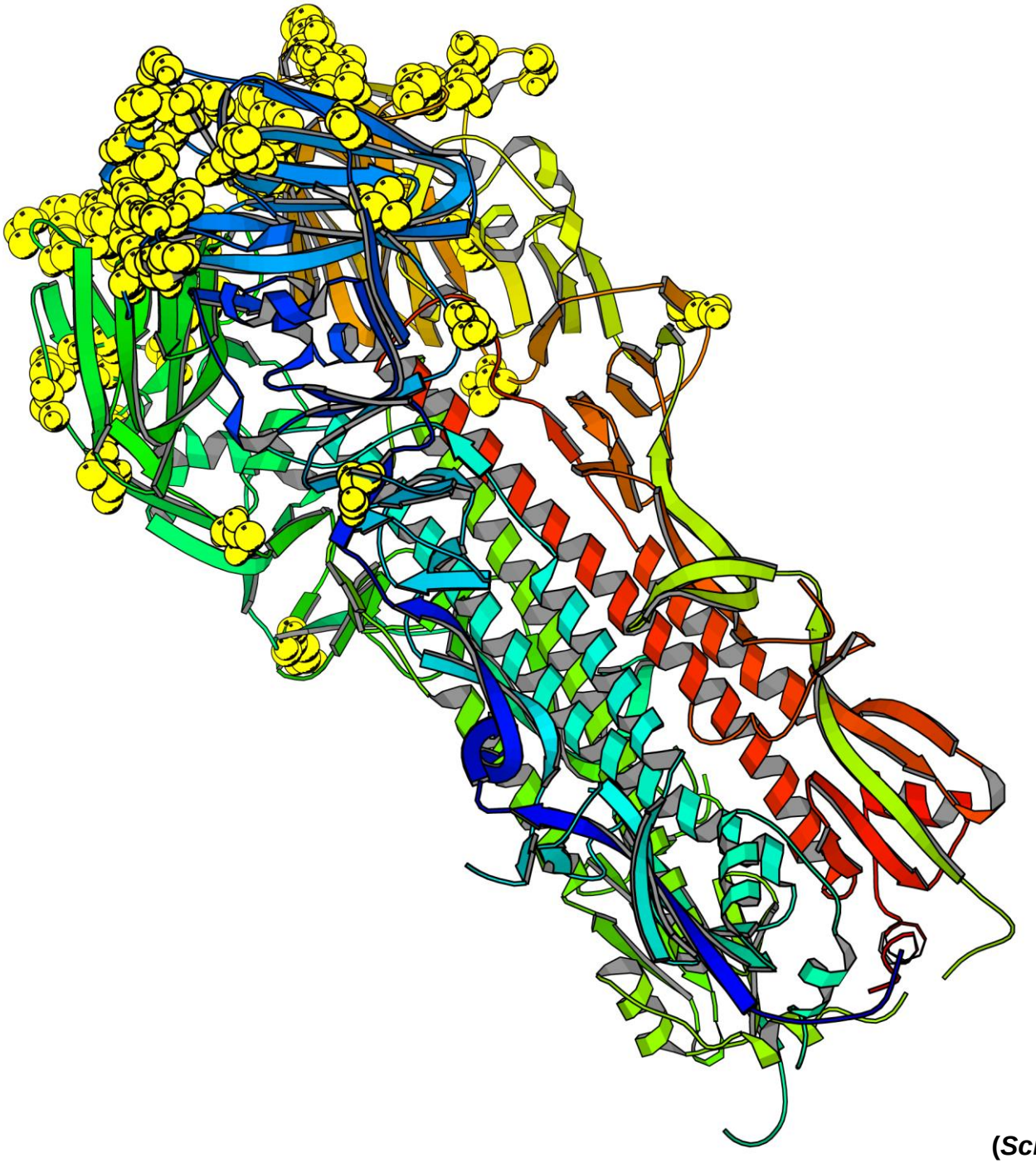
Phylogenetic prediction
of the future of influenza:

Which current strains
will lead to the epidemics
of tomorrow?

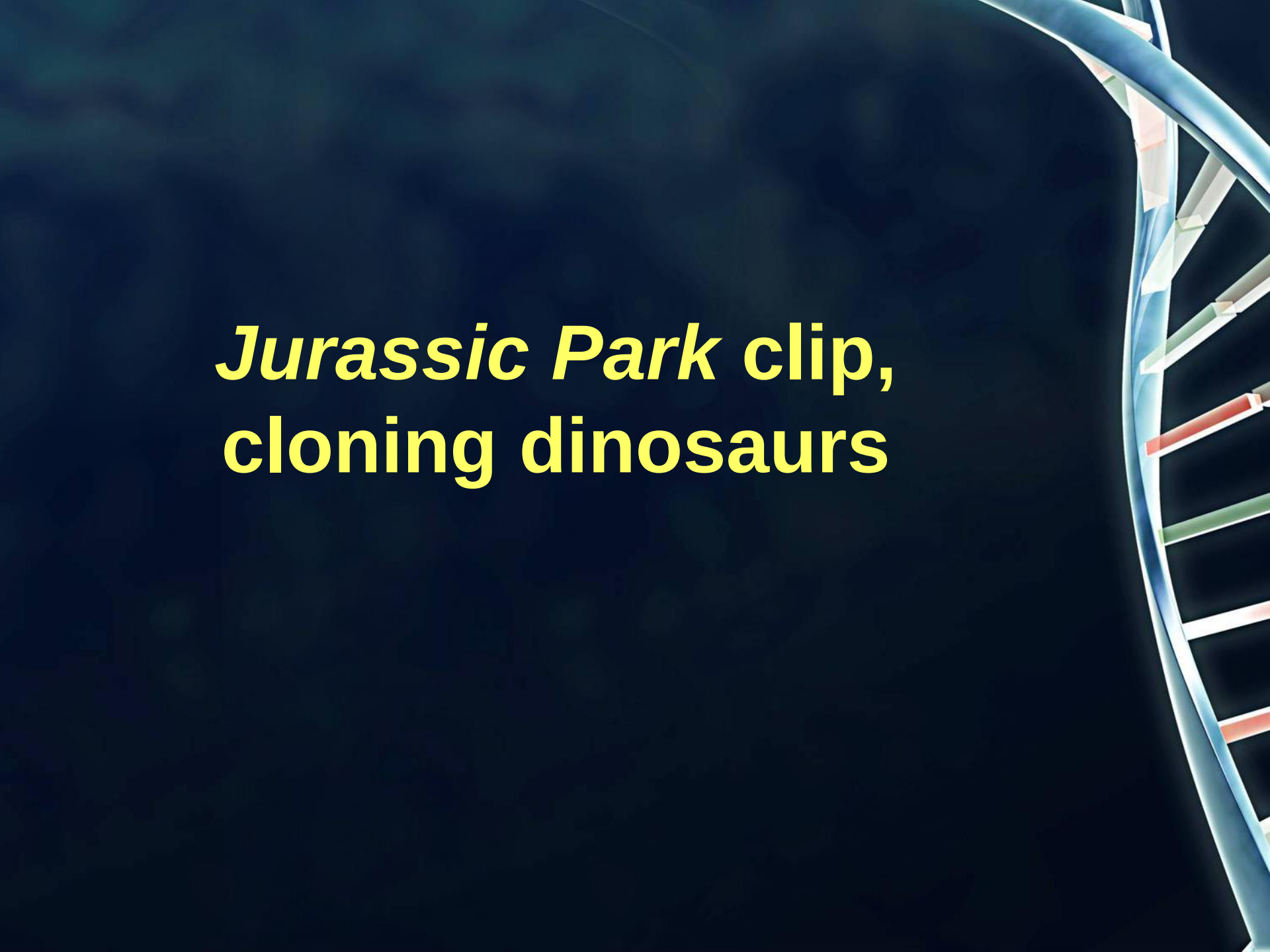


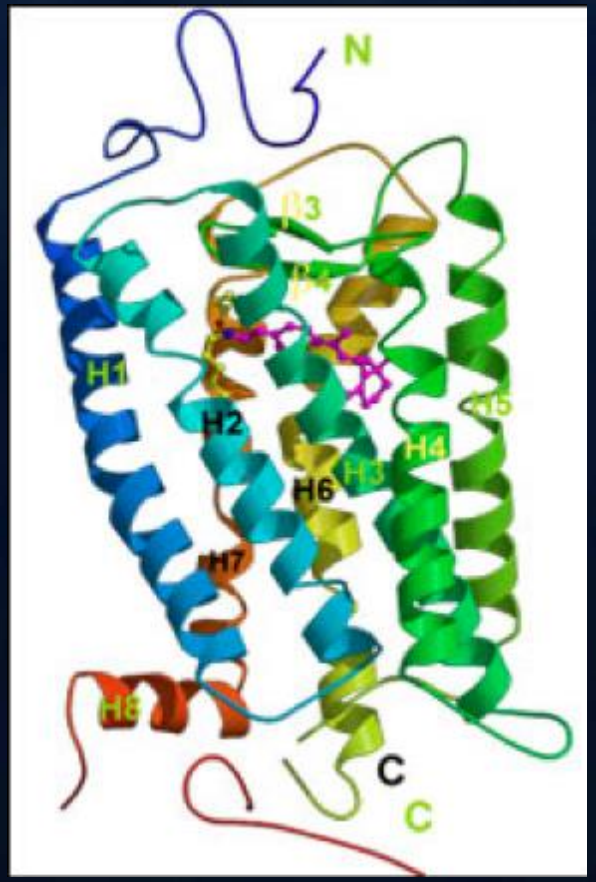
years samples were taken

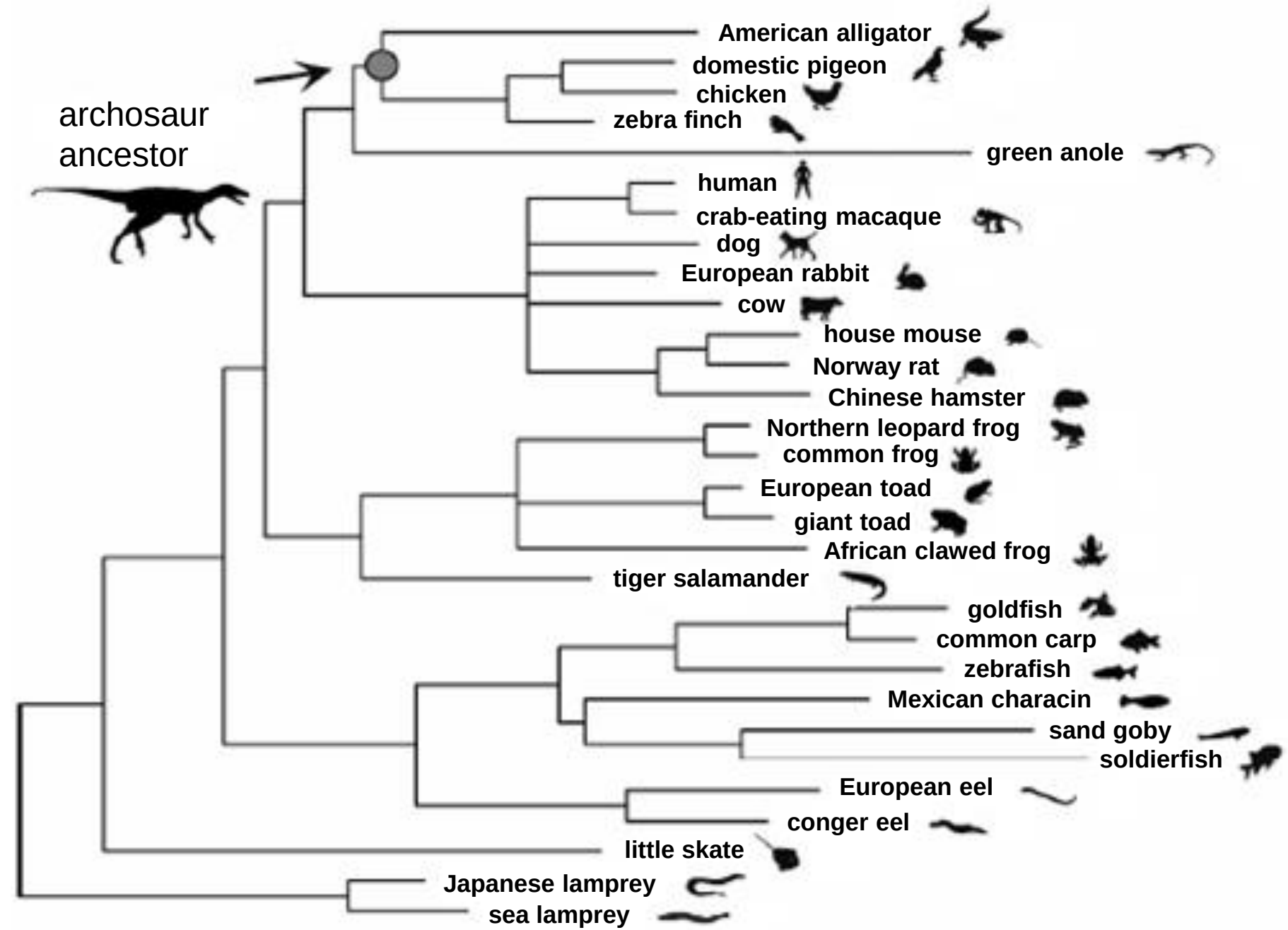
Bush et al., 1999
(*Science* 286:1921-1925)



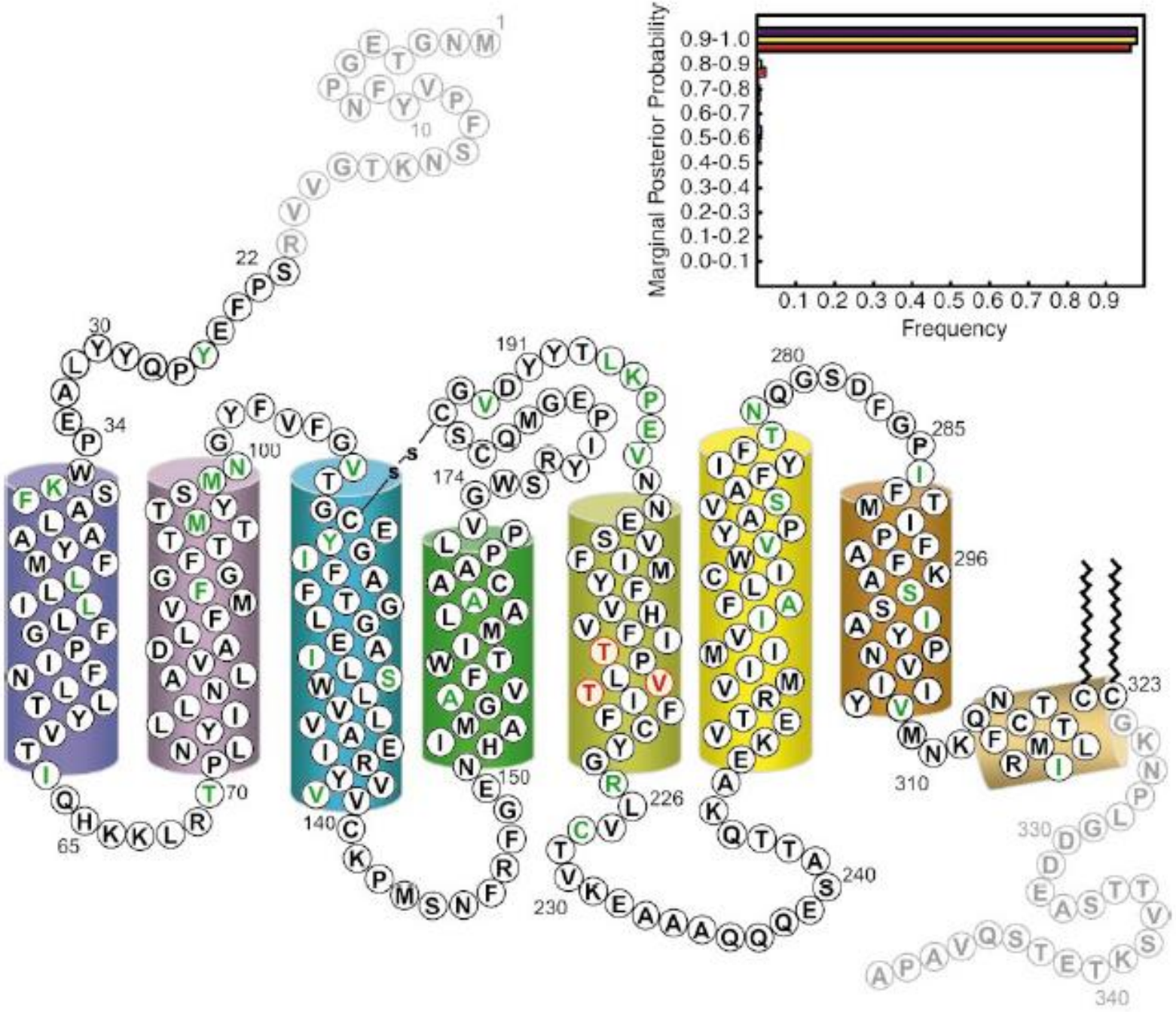
Hillis, 1999
(*Science* 286:1866-1867)


Jurassic Park clip,
cloning dinosaurs


N
H1
H2
H3
H4
H5
H6
H7
H8
C
C



Chang et al., 2002 MBE 19:1483-1489


Marginal Posterior Probability
0.9-1.0
0.8-0.9
0.7-0.8
0.6-0.7
0.5-0.6
0.4-0.5
0.3-0.4
0.2-0.3
0.1-0.2
0.0-0.1
0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Frequency

Star Trek clip, showing Tricorder


-DATA SENSE-
ALPHA
BETA
GAMMA
DELTA
LIBRARY
DEVICE INPUT
COM TRANSMISSION
INTRSHP
TRICRDR
ACPT
POOL
EMRG
IMAGE RECORD
FWD
INPUT
RVS
ERASE
LIBRARY
ID
TR-590 TRICORDER X


Gallus gallus
Turdus migratorius
Rattus norvegicus
Mus musculus
Homo sapiens
Heterodon platyrhinos
Sceloporus undulatus
odon punctatus
emys scripta
yctolagus cuniculus
tor mississippiensis
phlonectes natans
phis bannanicus
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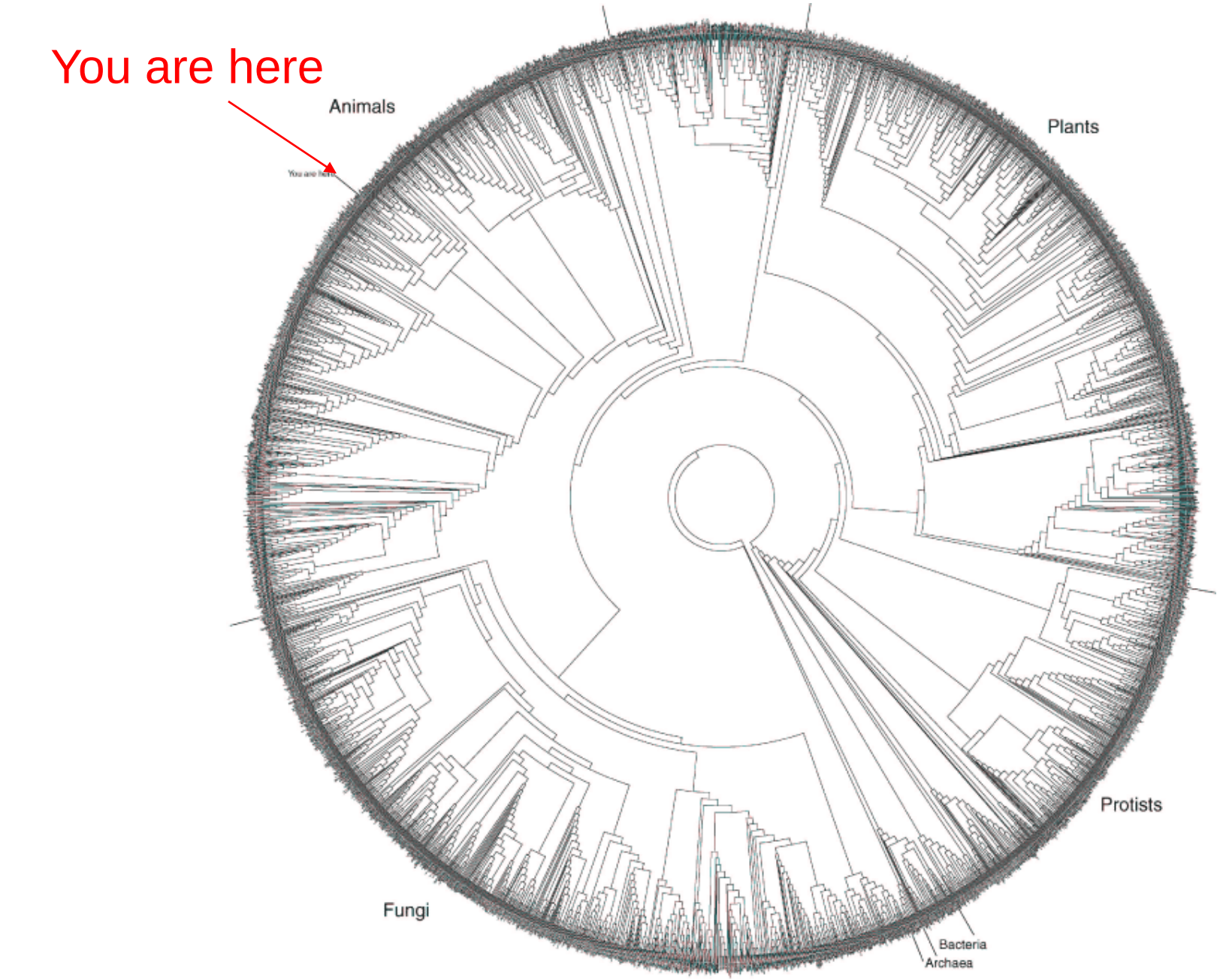
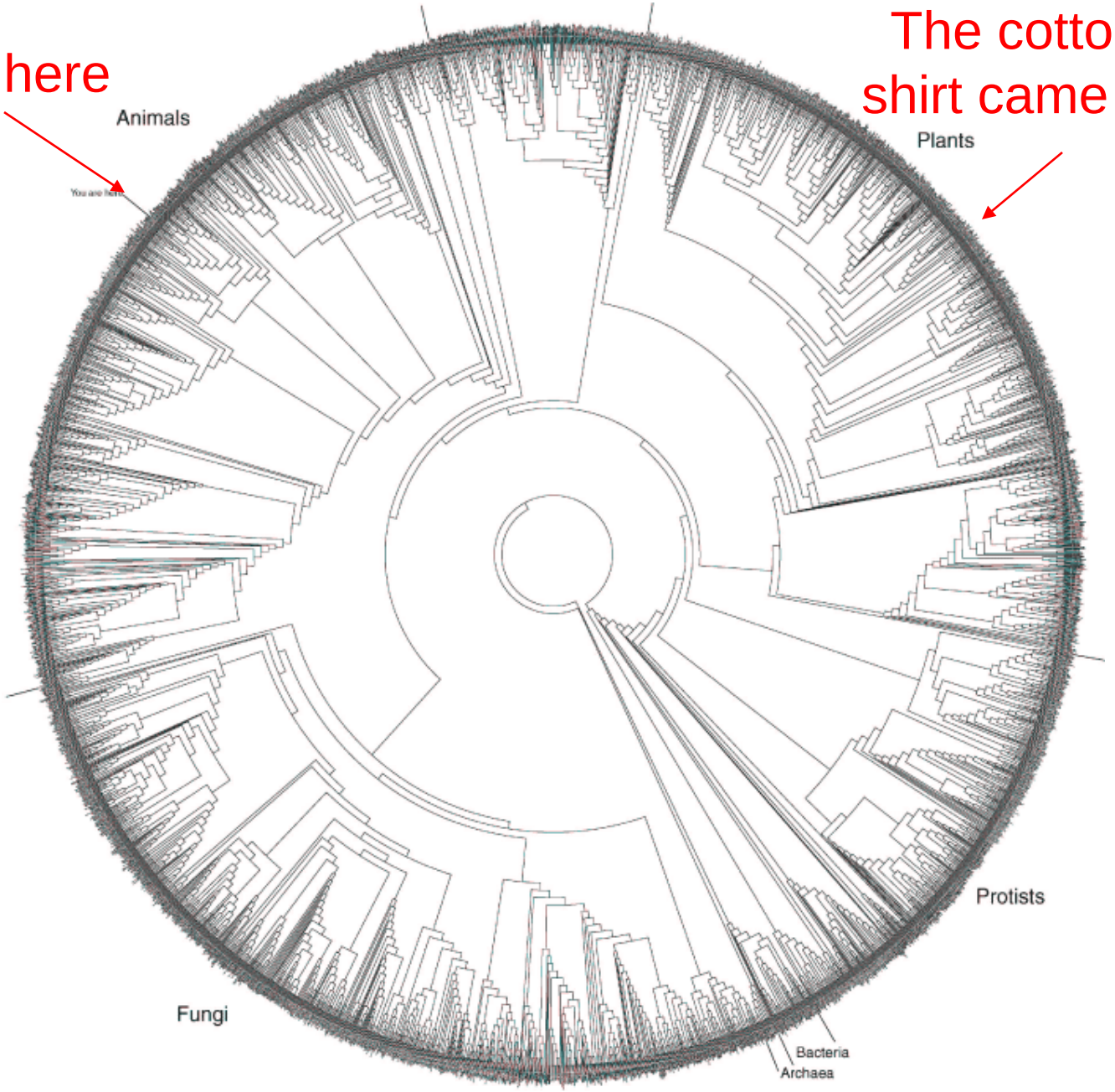
nia alternans
ssus pictus
holbrooki
s laevis



Download wall poster from: http://www.zo.utexas.edu/faculty/antisense/DownloadfilesToL.html (see *Science* 300:1692-1697)

You are here

The cotton in your shirt came from here



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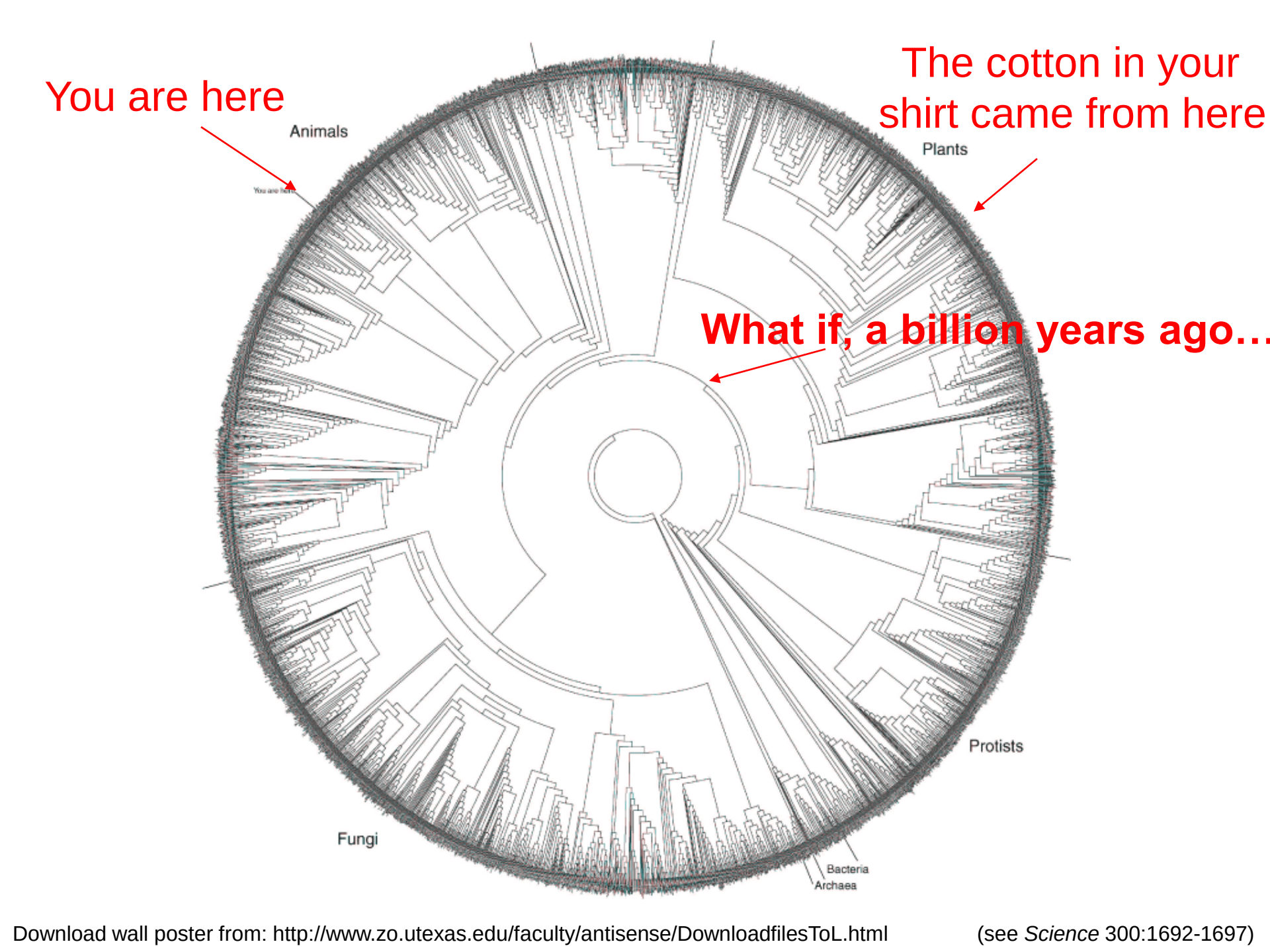

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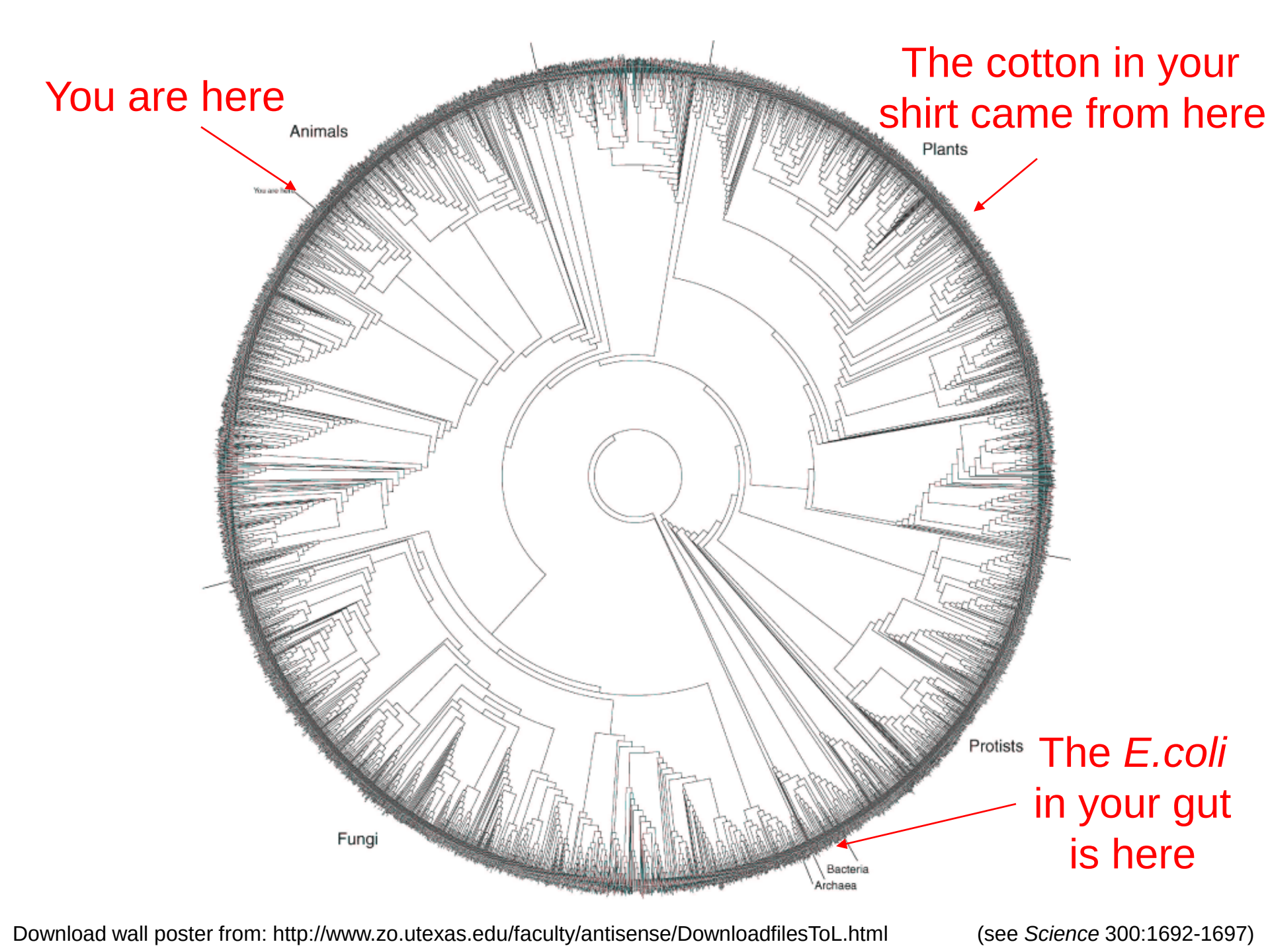

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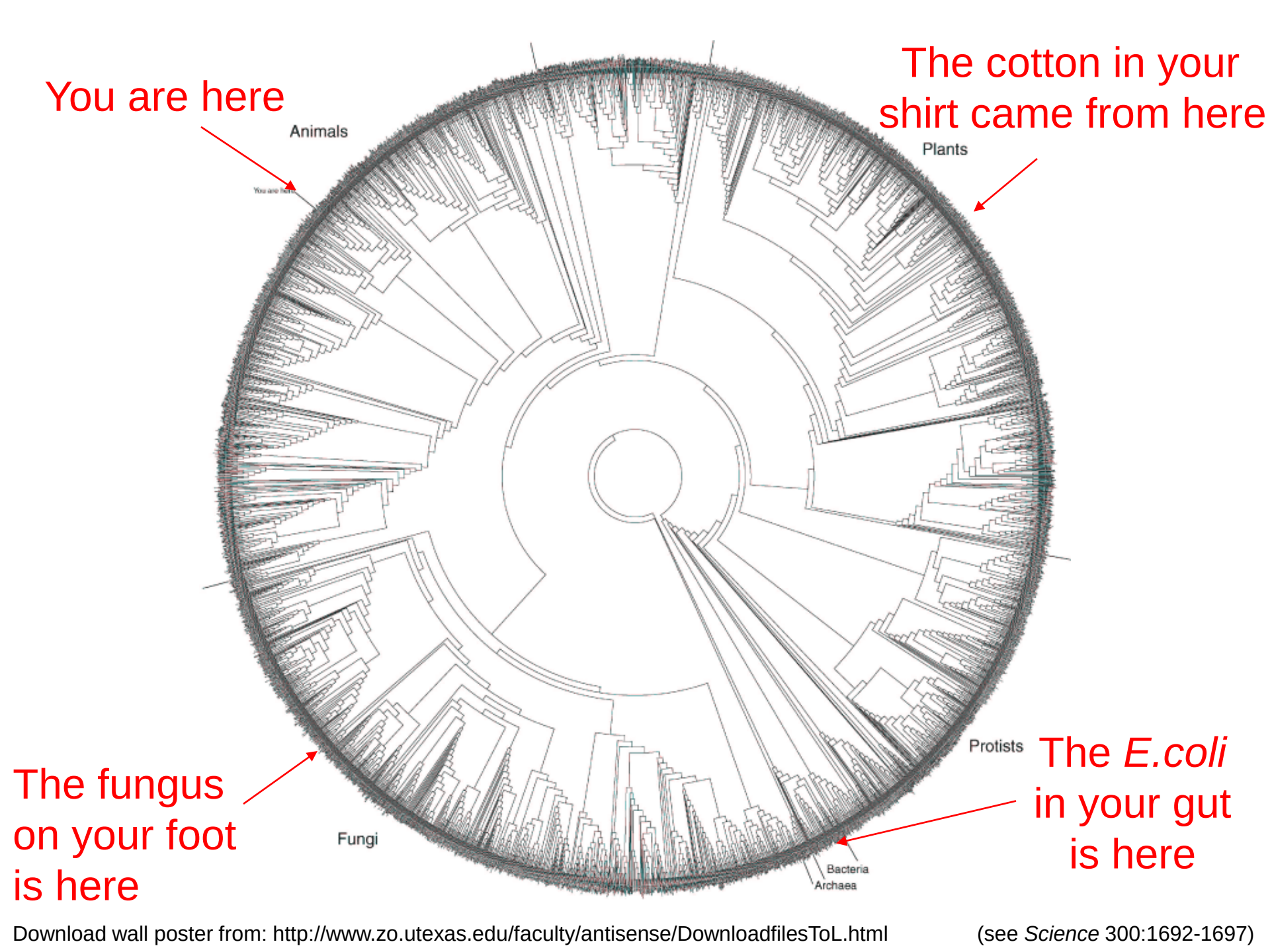
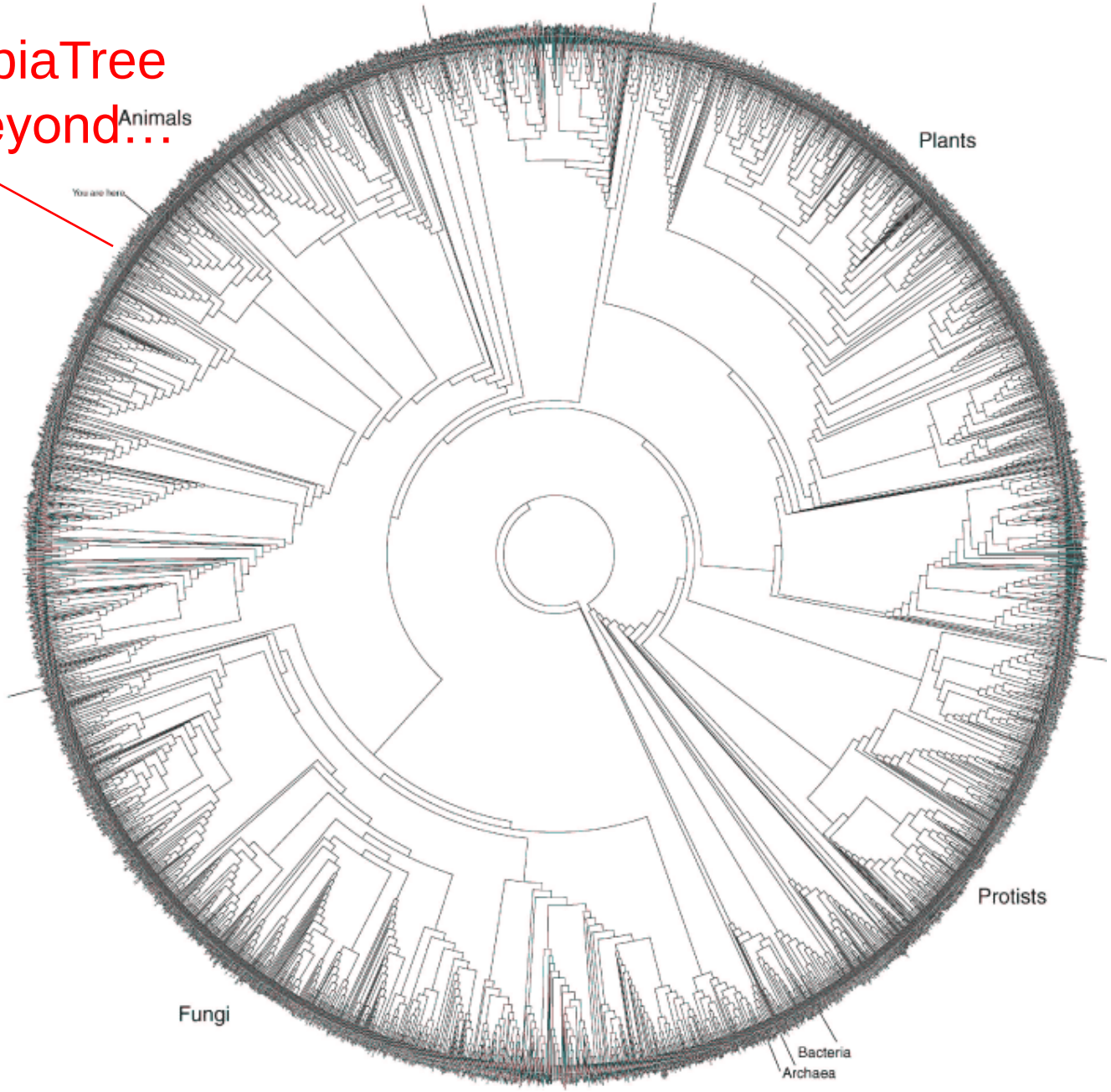


Download wall poster from: http://www.zo.utexas.edu/faculty/antisense/DownloadfilesToL.html

(see *Science* 300:1692-1697)

To AmphibiaTree and beyond…



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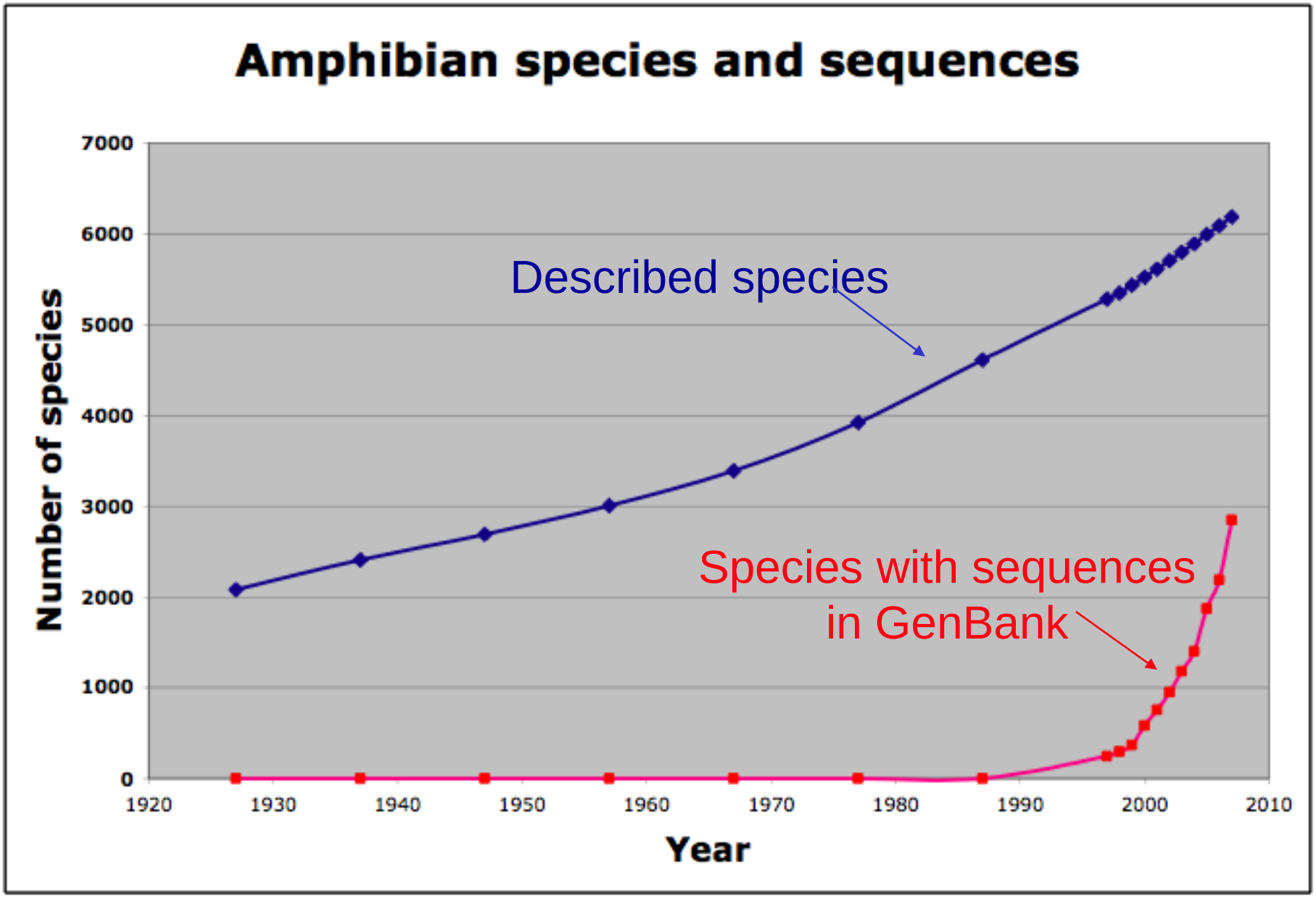
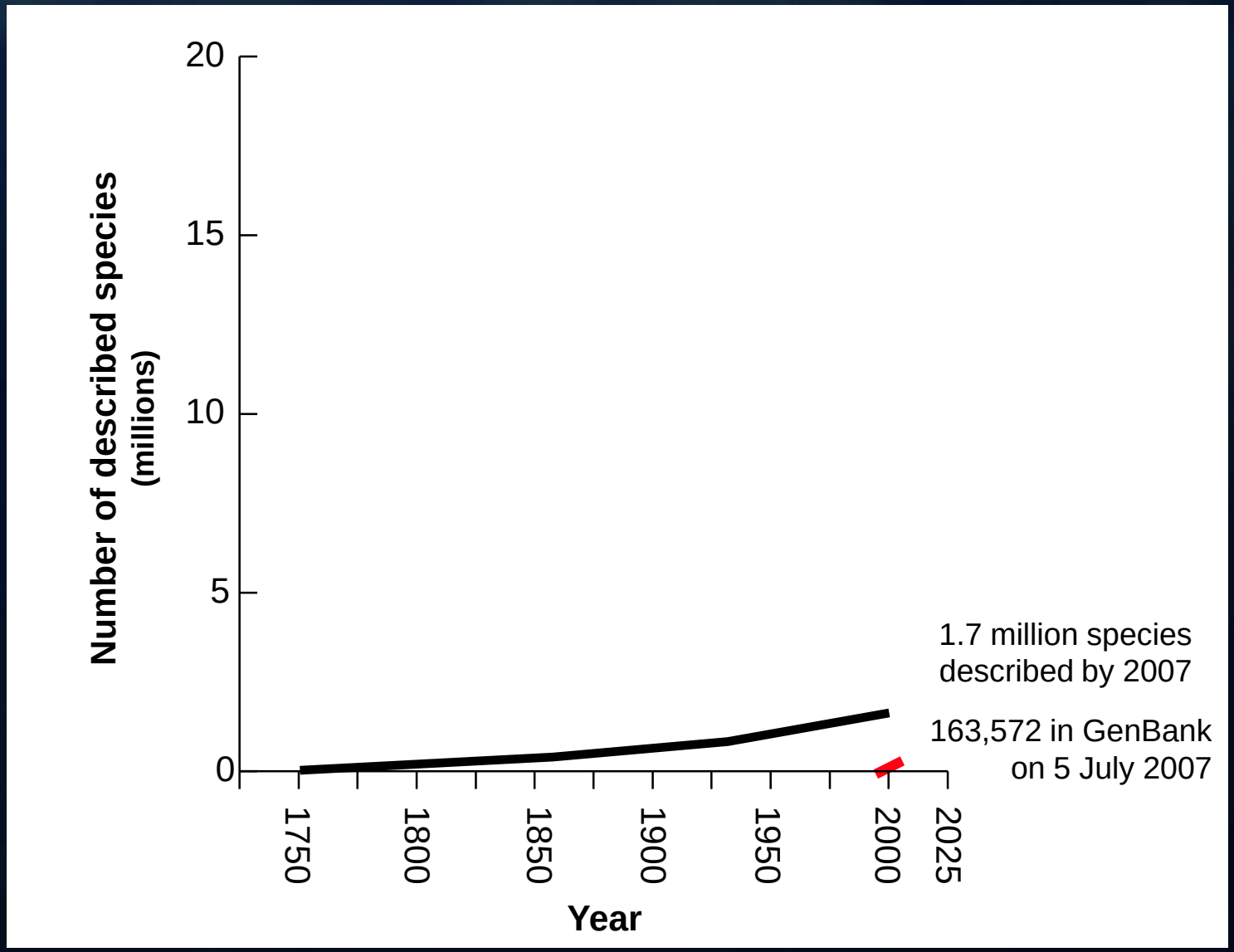
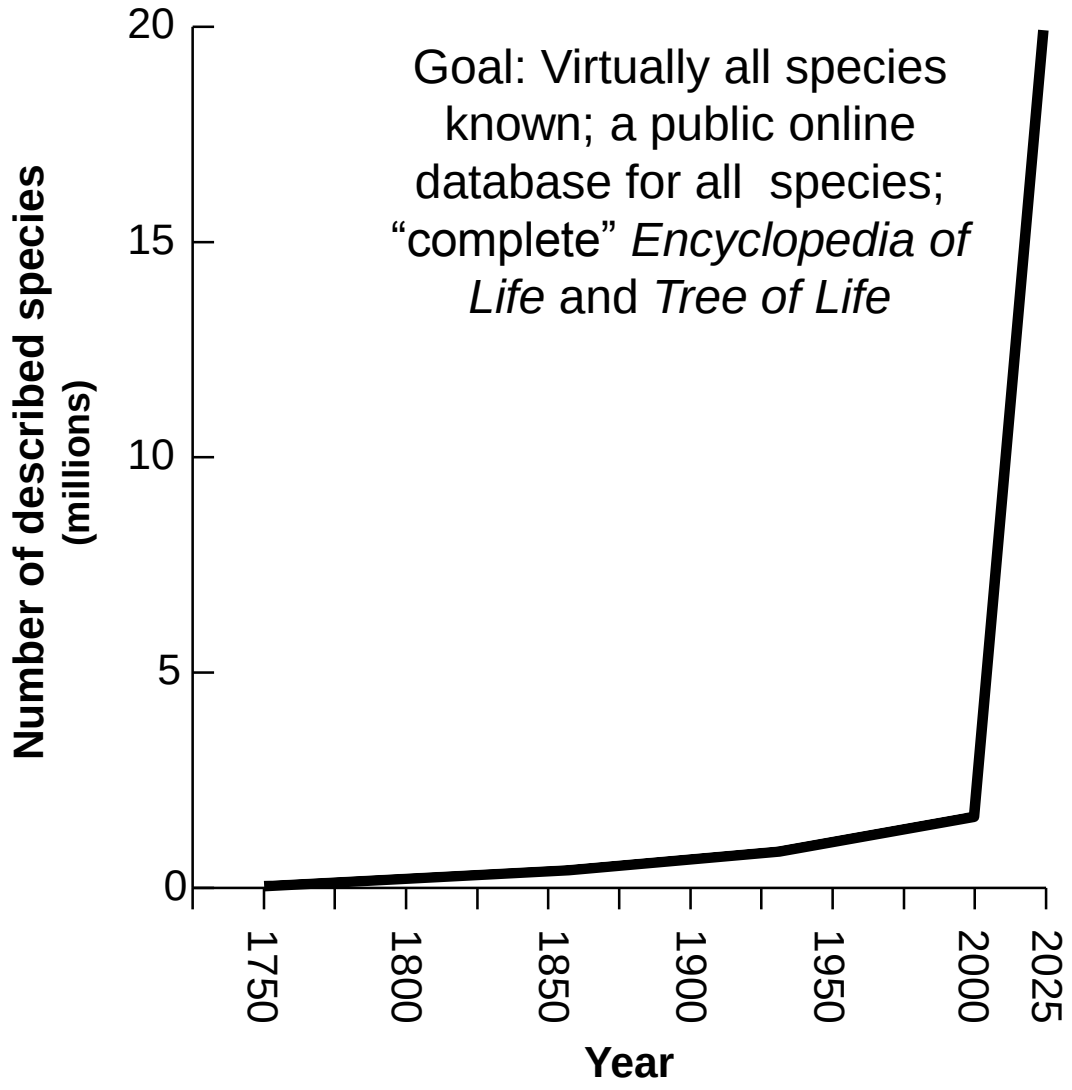

Amphibian species and sequences
Number of species
7000
6000
5000
4000
3000
2000
1000
0
1920
1930
1940
1950
1960
1970
1980
1990
2000
2010
Year
Described species
Species with sequences
in GenBank

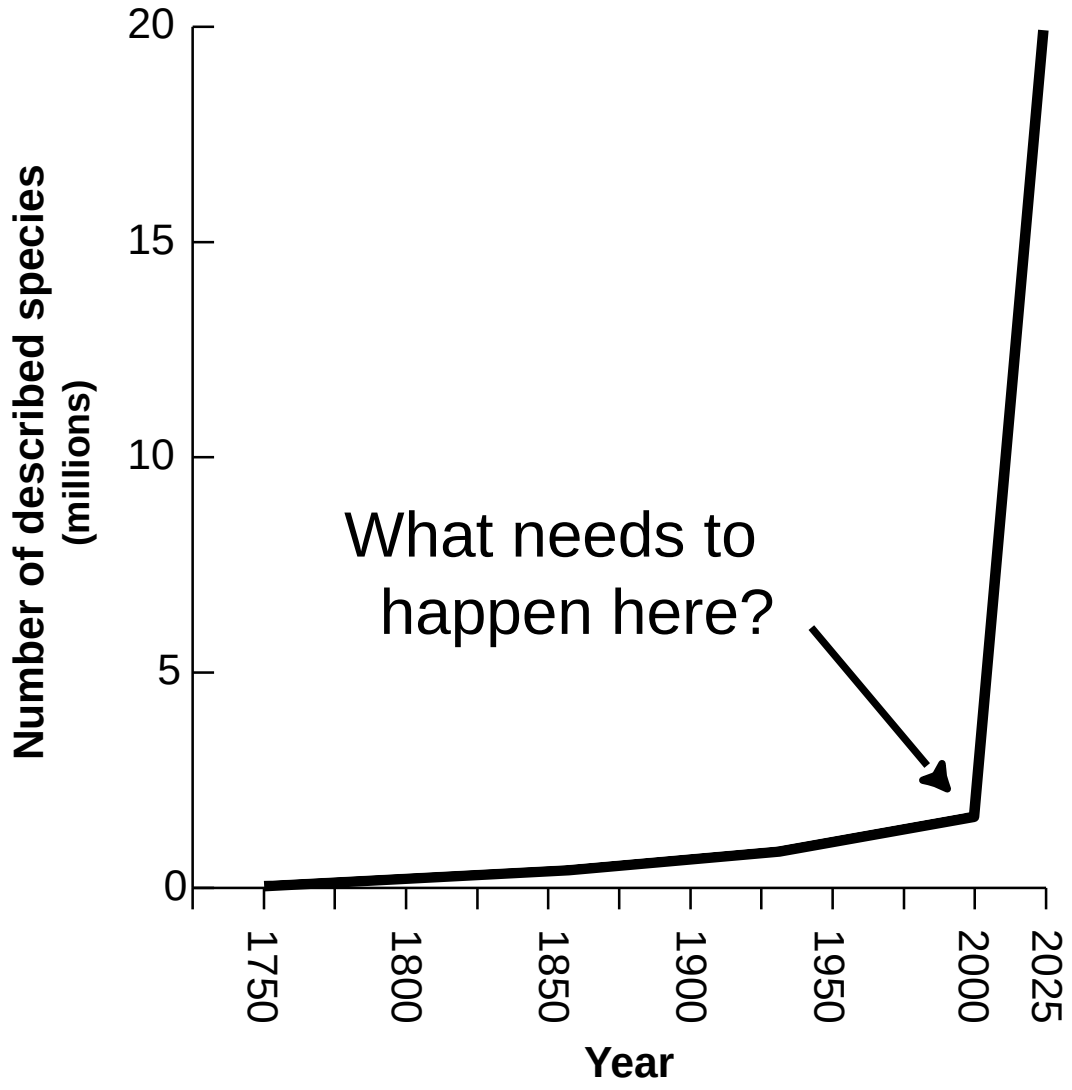
Number of Described Species



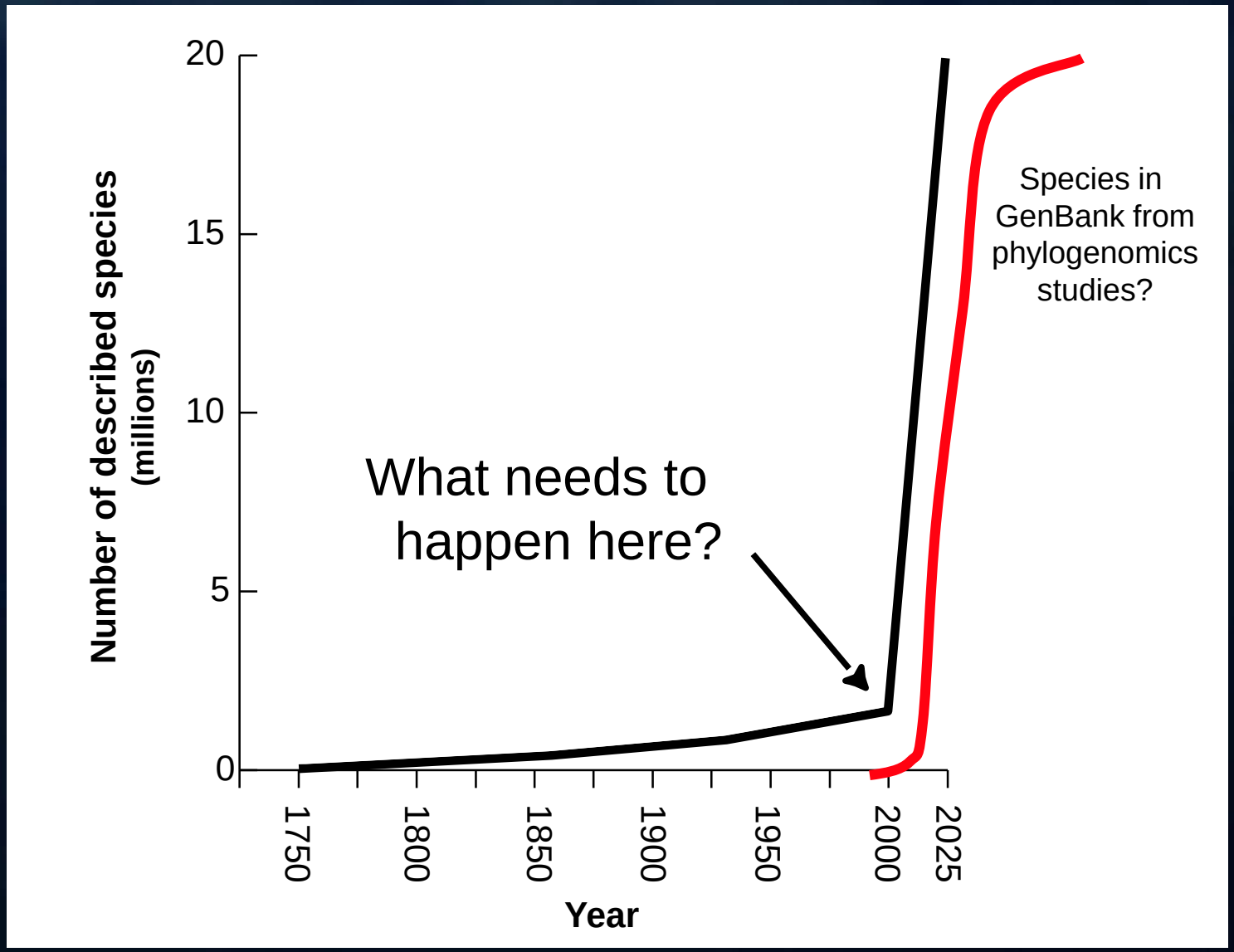
Number of Described Species



Number of Described Species



Number of Described Species



Is a “Biocorder of Life” Possible?

Step one:

DNA isolation and amplification of a series of target genes

Step two:

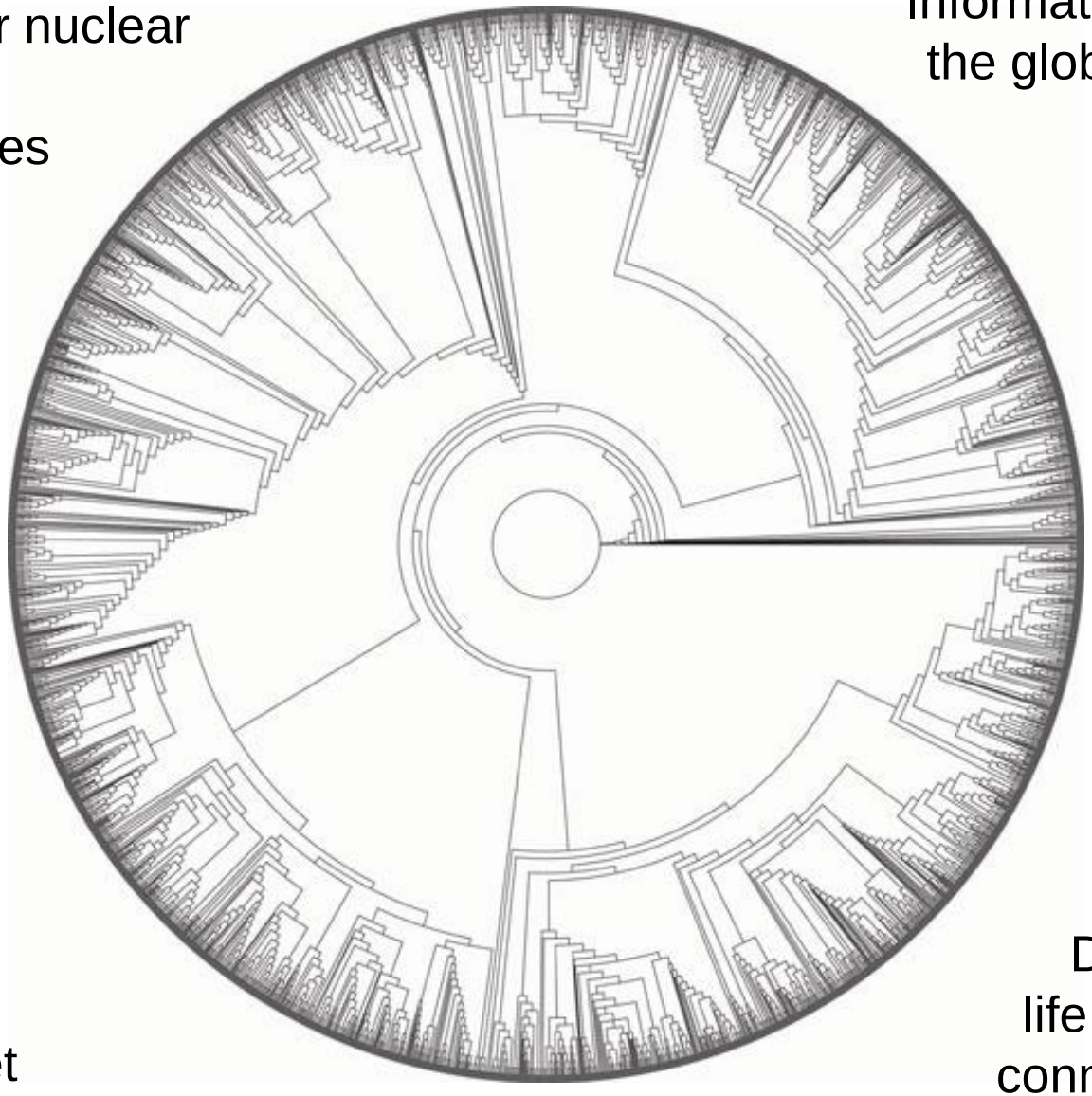
Rapid sequencing of amplified genes

Step three:

Placement of unknown within the Tree of Life

rRNA and other nuclear genes identify unknown species as a fungus

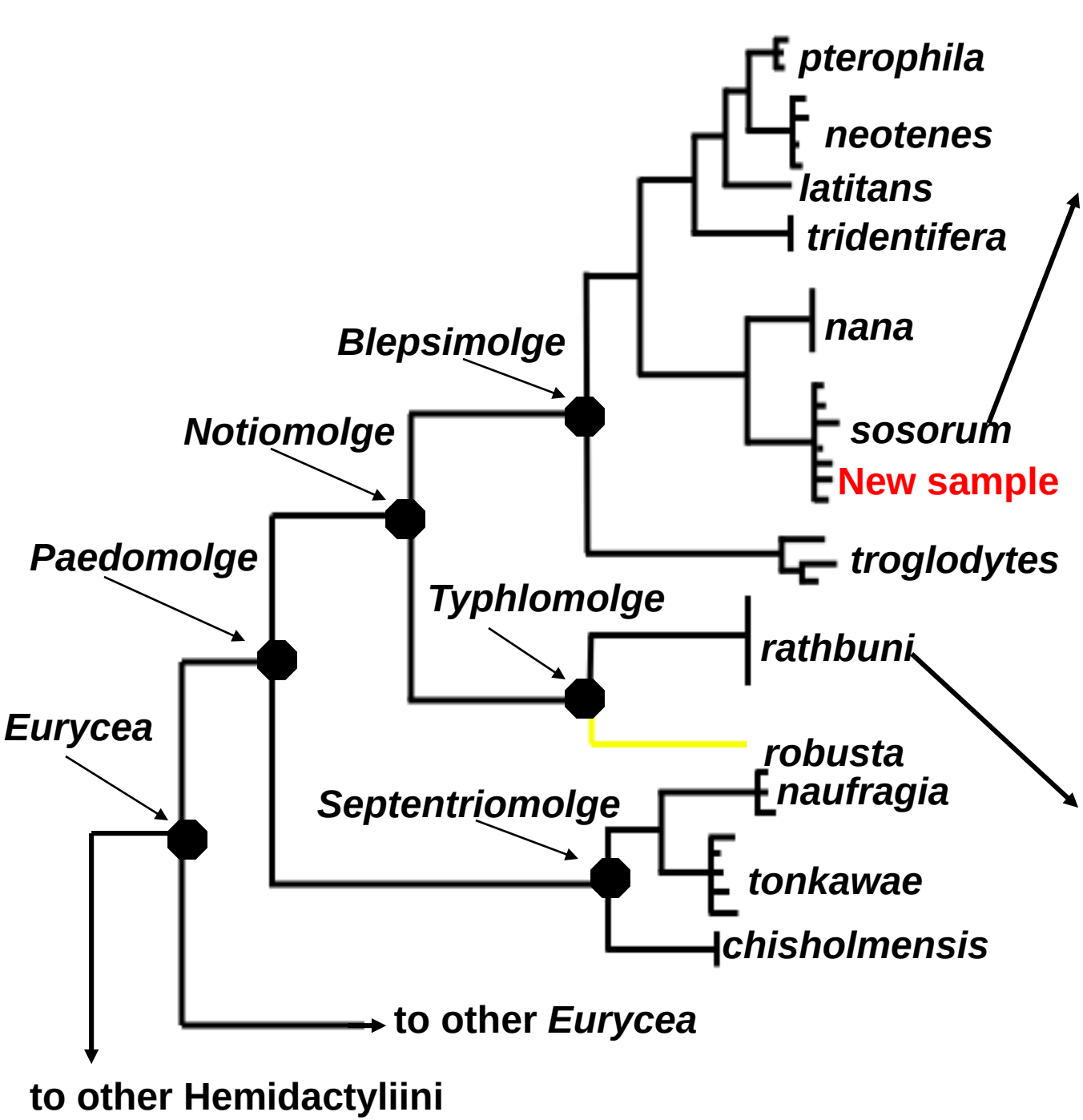
Go to Fungal Tree



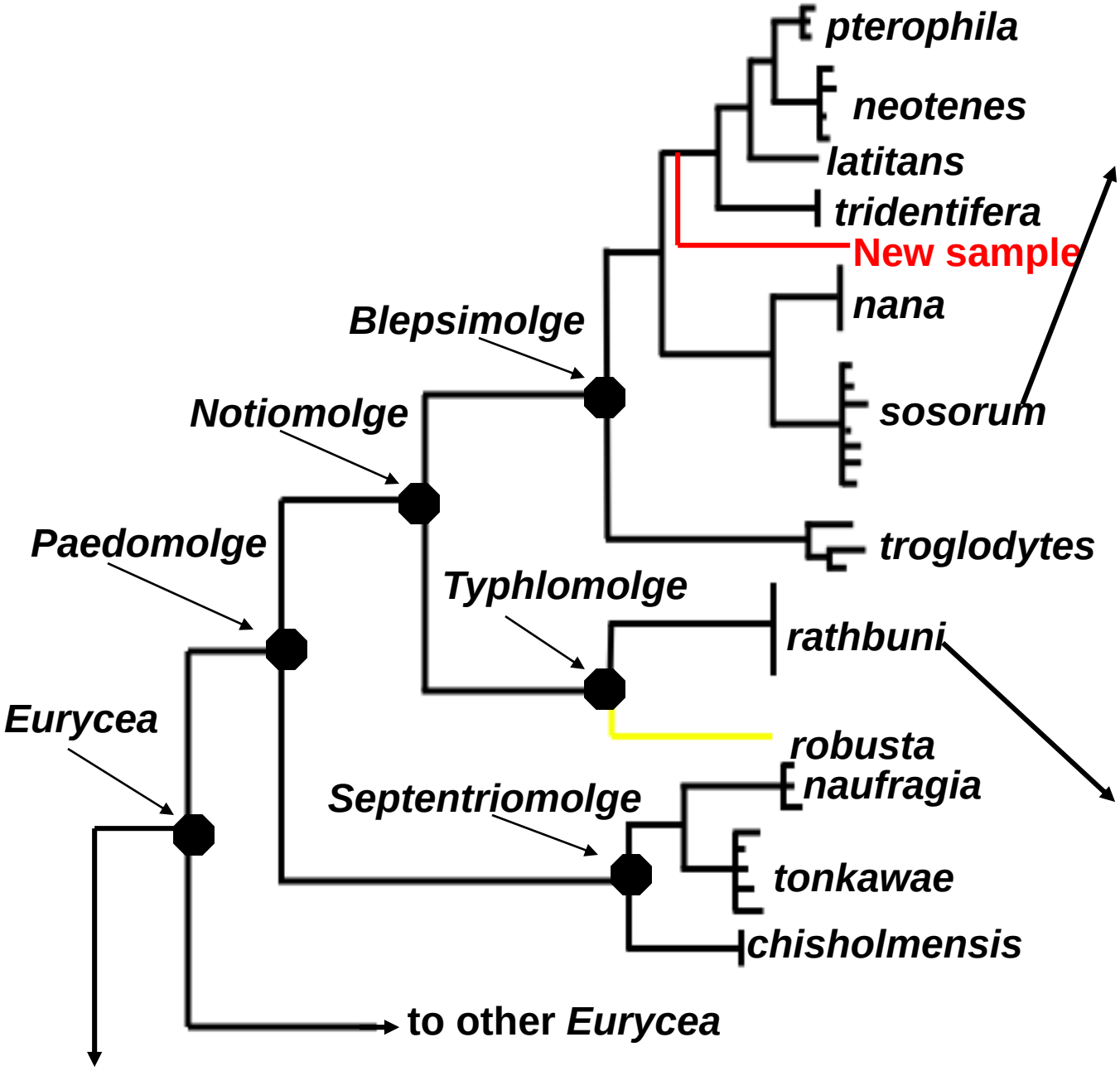
Sample of target genes identify unknown fungus as a chytrid: *Batrachochytrium dendrobatidis*

Information added to the global database of Life

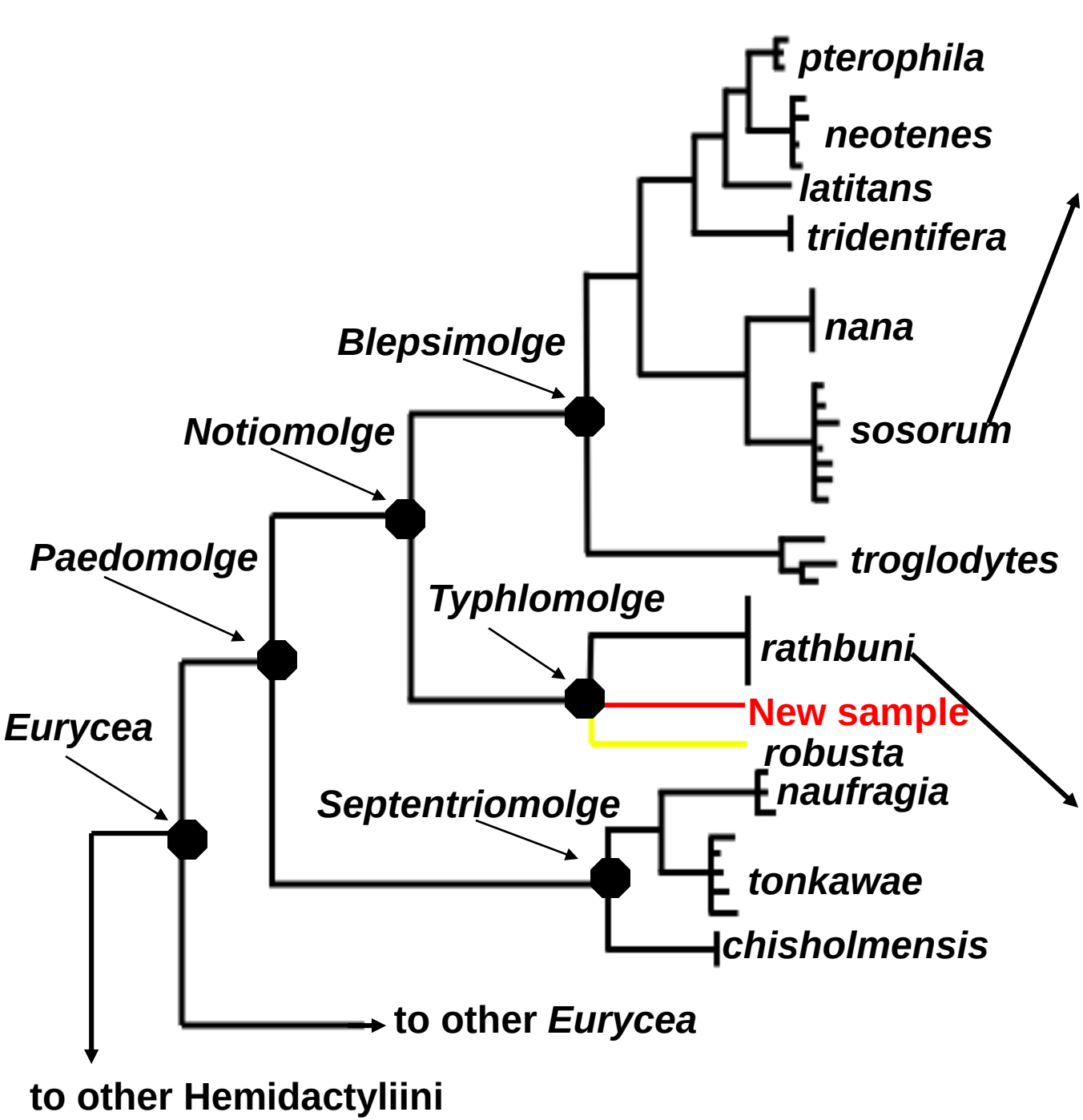
Data, locality, life history, etc. connected to the *Encyclopedia of Life*; connection to declines



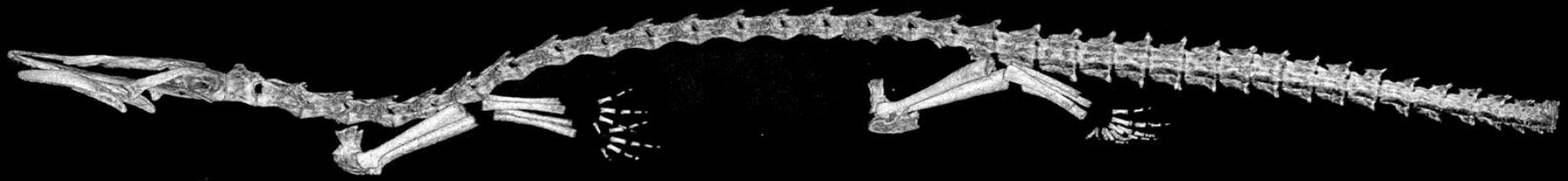
Hillis et al., 2001 (*Herpetologica* 57:266-280), and unpublished data

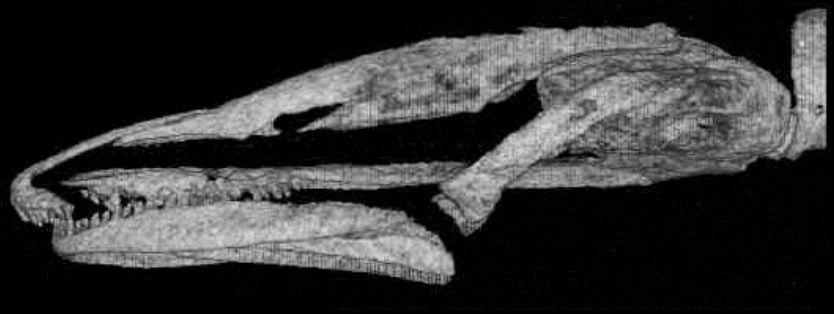


Hillis et al., 2001 (*Herpetologica* 57:266-280), and unpublished data



Hillis et al., 2001 (*Herpetologica* 57:266-280), and unpublished data





Tree of Life (Phylogenomics) Approach

Advantages:

- Can be automated; rapid rate increase
- Cost per identification of each new species less than current methods, especially assuming development of automated and portable sequencing technology
- Puts taxonomic knowledge in public databases, rather than just ephemeral human minds
- Better uses the talents of taxonomic experts, who benefit from all the new data
- Universal databases make taxonomy much more valuable and available to all biologists

Dr. David Hillis

David Hillis was born in Copenhagen, Denmark, but spent his formative years in tropical Africa and India. In this environment, Hillis learned a love of biology, entertaining himself by making collections of butterflies, amphibians, and reptiles. Hillis received his B.S. degree (with honors) from Baylor University in 1980, and M.A., M.Ph. and Ph.D. (all with honors) from The University of Kansas in 1983, 1984, and1985, respectively. After two years on the faculty at the University of Miami, he joined the Department of Zoology at UT Austin in 1987 and was awarded a prestigious National Science Foundation Presidential Young Investigator Award the same year. In1992, he was appointed to the Alfred W. Roark Centennial Professorship in Natural Sciences, and in 1998 became the first Director of the School of Biological Sciences at the University of Texas-Austin. In 1999, Hillis was one of 32 people chosen to receive a prestigious MacArthur Foundation fellowship, known informally as the "genius award".

David Hillis' research interests span much of biology, from development of statistical and computational methods for analyzing DNA sequences, to molecular studies of viral epidemiology, to studies of the diversity and phylogeny of life (particularly vertebrates), to the origin and behavior of unisexual organisms. He has published over 130 scholarly articles and two technical books, and has served as Editor or Associate Editor of a dozen scientific journals. He is an active member of many scholarly societies and national research panels, and has served as the President of the Society of Systematic Biologists. In the past decade, the 23 graduate students and 12 postdocs in his laboratory have produced an additional 120 independent scholarly articles.