

**1st International Congress on Science and Faith:
Incompatible or Complementary?**

November 7-9, 2018

Universal Common Ancestry: Arguments for and Against

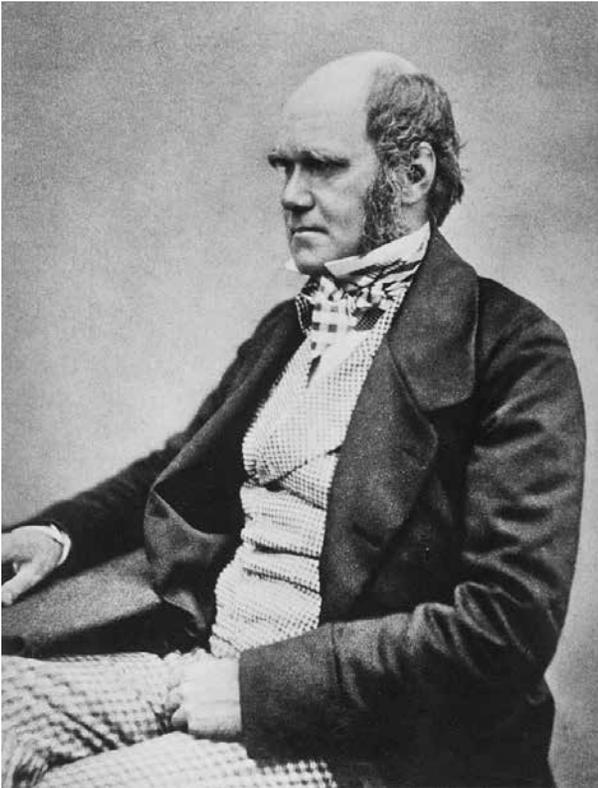
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Universal Common Ancestry

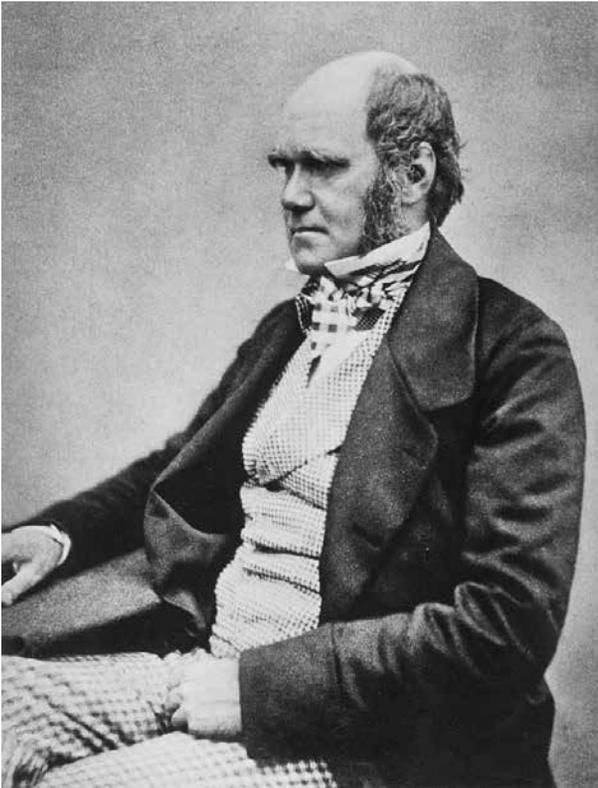


Charles Darwin

The Origin of Species (1859)

In *The Origin of Species*, Charles Darwin wrote that genealogy is “the only known cause of the similarity of organic beings.”

Universal Common Ancestry

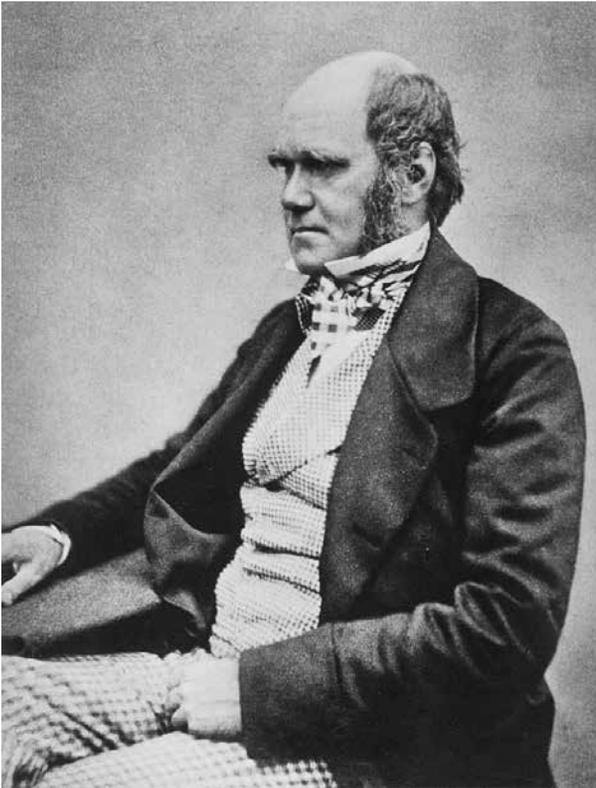


Charles Darwin

The Origin of Species (1859)

In *The Origin of Species*, Charles Darwin wrote that genealogy is “the only known cause of the similarity of organic beings.” Thus “I view all beings not as special creations, but as the lineal descendants of some few beings” that lived in the distant past.

Universal Common Ancestry

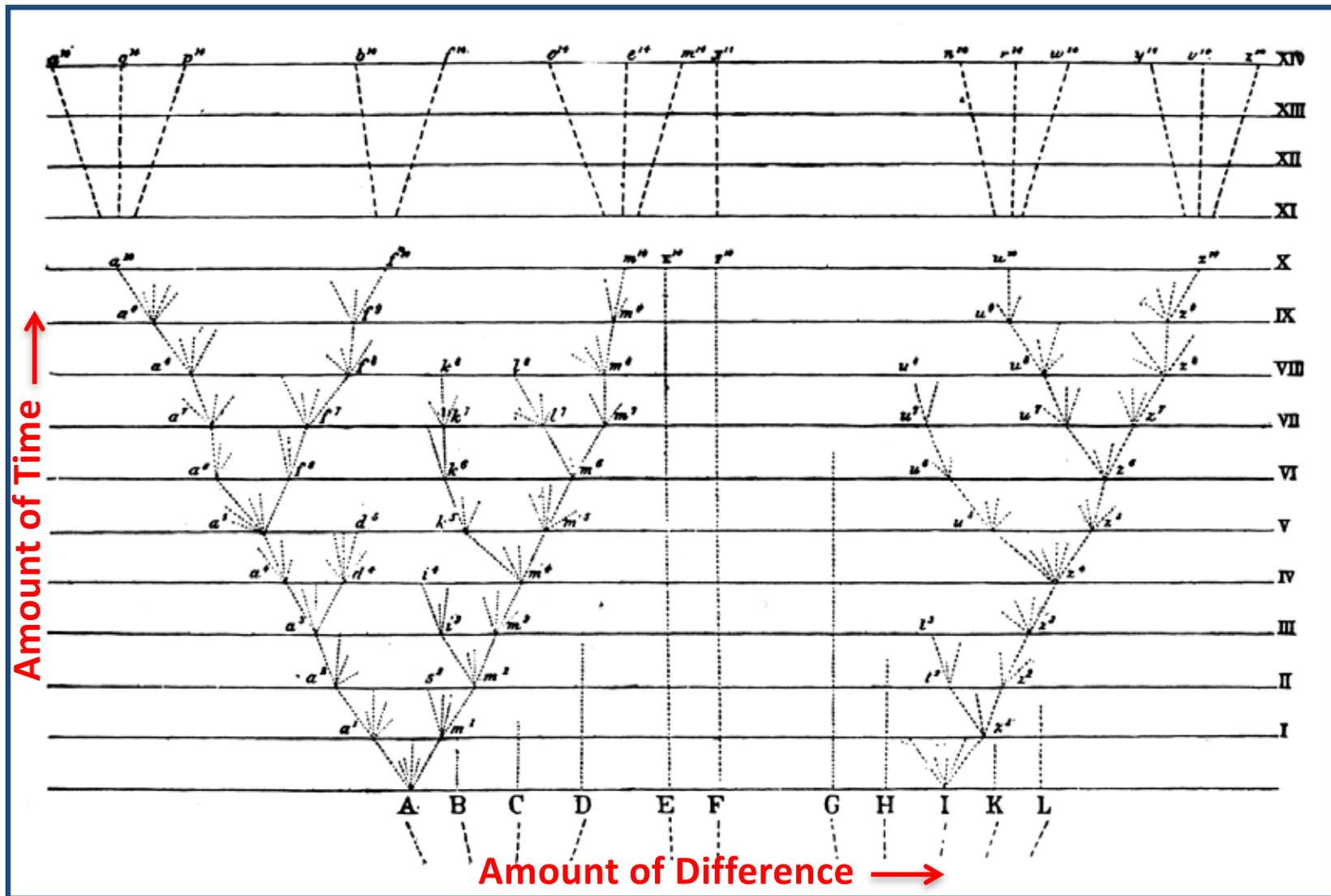


Charles Darwin

The Origin of Species (1859)

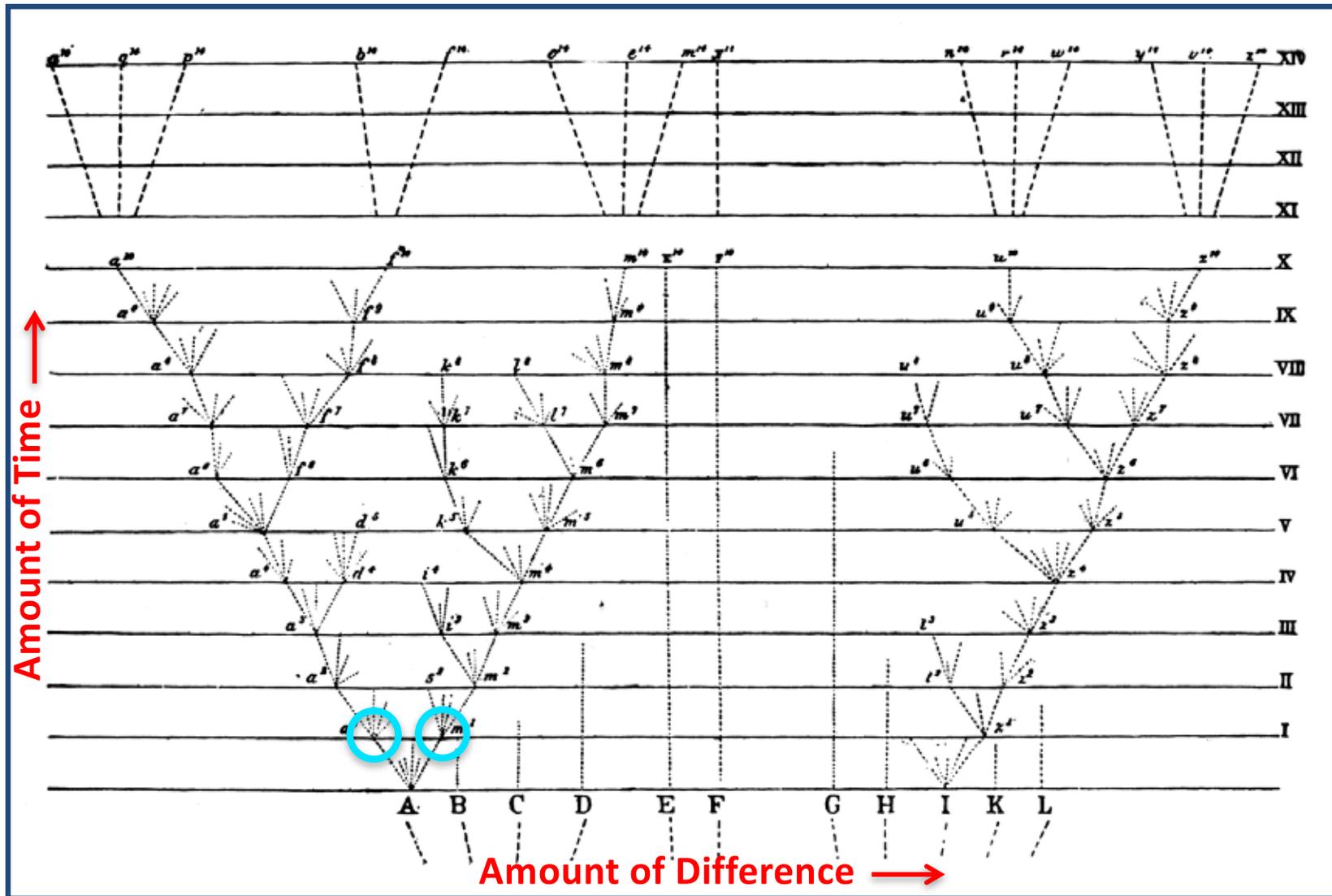
So “all living species have been connected with the parent-species of each genus, by differences not greater than we see between the varieties of the same species at the present day; and these parent-species, now generally extinct, have in their turn been similarly connected with more ancient species; and so on backwards, always converging to the common ancestor of each great class. So that the number of intermediate and transitional links, between all living and extinct species, must have been inconceivably great.”

Darwin's Tree of Life



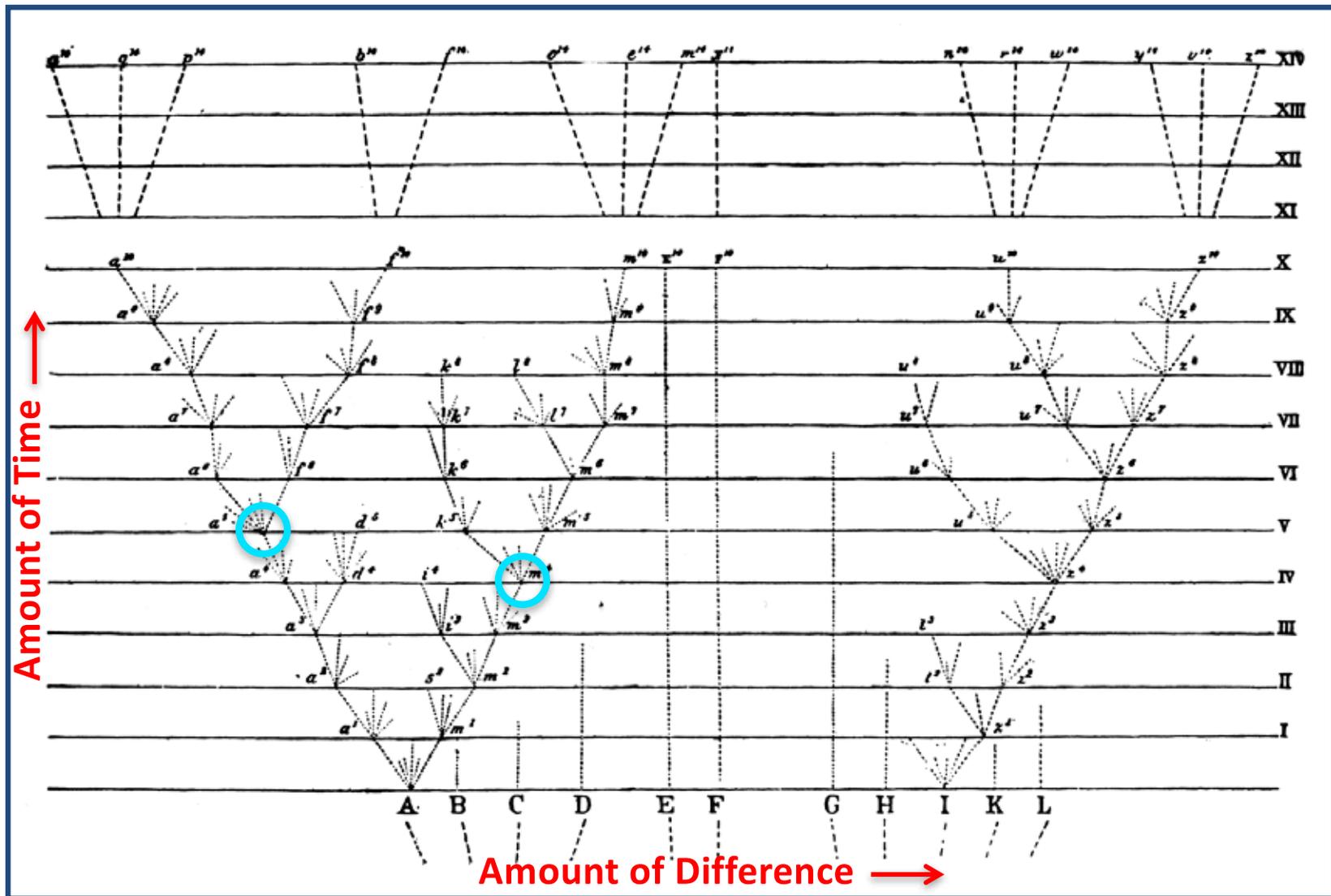
In *The Origin of Species*, Darwin sketched the branching-tree pattern that would result from descent with modification from common ancestors.

Darwin's Tree of Life



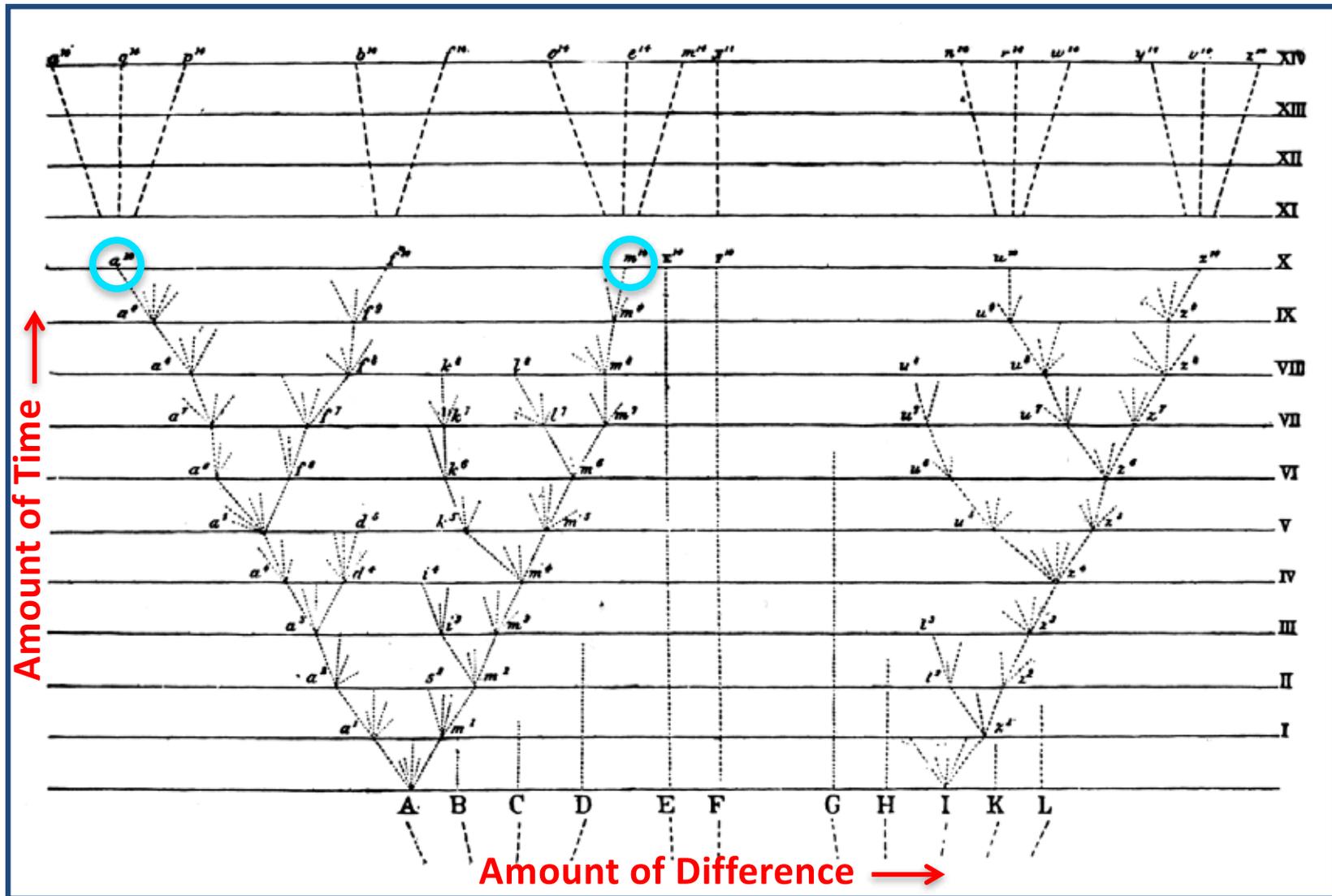
Eventually, two of the varieties become sufficiently different from each other to qualify as separate species.

Darwin's Tree of Life



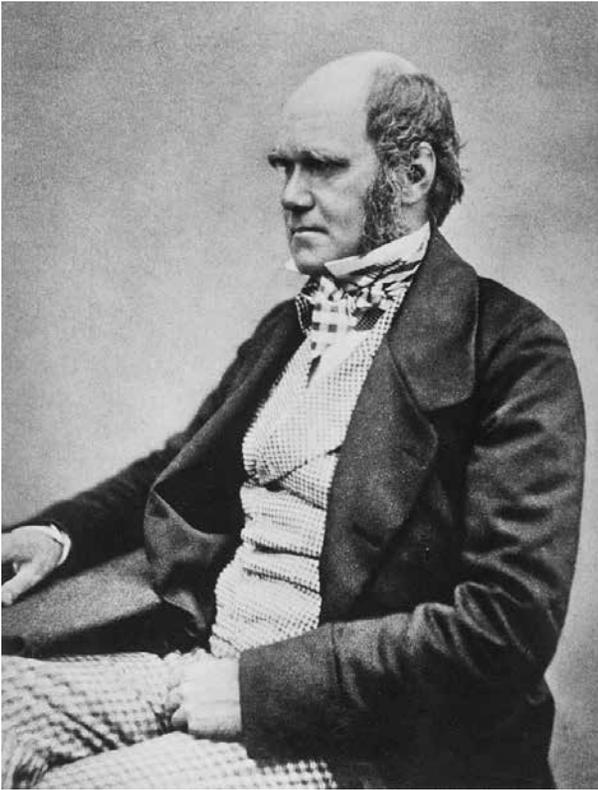
Those two species may continue to diverge, and may even split into other species, some of which may die out (become extinct).

Darwin's Tree of Life



Over a very long time the differences between the two species may accumulate until they become separate classes (such as mammals and birds).

Universal Common Ancestry



Charles Darwin

The Origin of Species (1859)

Although Darwin was not sure whether there were separate ancestors for “each great class” or a single common ancestor for all living things, he inclined toward the latter. Indeed, he wrote that “probably all the organic beings which have ever lived on this earth have descended from some one primordial form.”

A Modern Statement of the Same Idea

“All living things are fundamentally alike. At the cellular and molecular level living things are remarkably similar to each other. These fundamental similarities are most easily explained by evolutionary theory: Life shares a common ancestor.”

“Understanding Evolution,” University of California at Berkeley
https://evolution.berkeley.edu/evolibrary/article/lines_08

In my talk I will focus just on animals.

Animals certainly share many similarities:

- All are composed of membrane-bound cells.

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Animals certainly share many similarities:

- All are composed of membrane-bound cells.
- Most of their cells have nuclei.
- All use DNA as a template to make proteins.
- All obtain energy by consuming food.
- All are capable of motion at some stage in life.

Subsets of animals share many similarities:

Mammals

- All have internal skeletons.
- All have backbones.
- All nourish their young with milk.
- Most have hair.
- Most are warm-blooded.

Insects

- All have external skeletons.
- All have 3 pairs of legs.
- All have 3 body segments: head, thorax, & abdomen.
- All have antennae.
- Most have wings.

**How can we determine
whether all animals are
descended from a
common ancestor?**

Five Main Sources of Evidence

- **Fossils**
- **Embryos**
- **Homology**
- **Biogeography**
- **Molecules**

Five Main Sources of Evidence

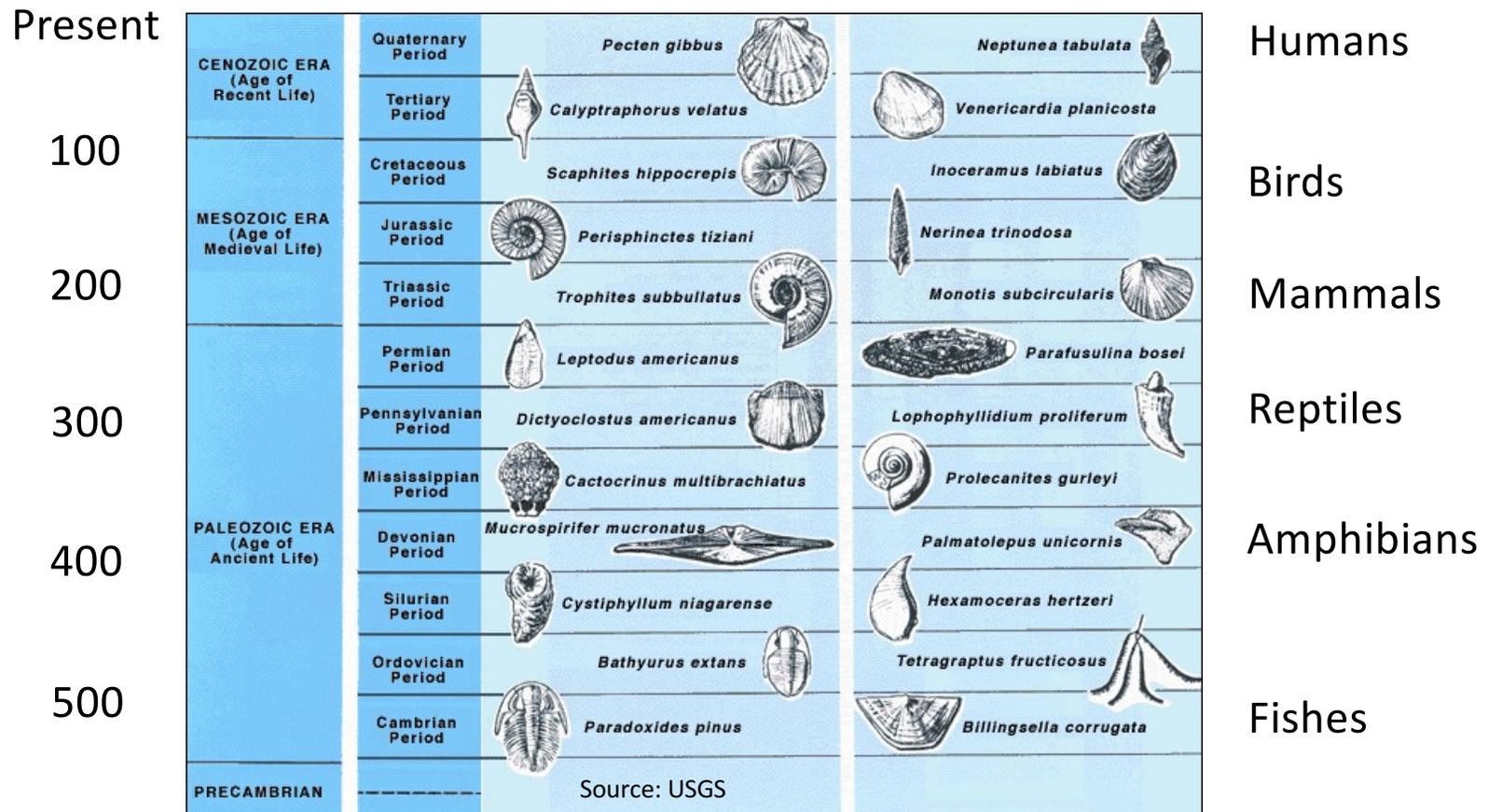
- **Fossils**

The Animal Fossil Record

Standard Geological
Time Scale
(in millions of years ago)

Index Fossils

First Appearance of
Vertebrate Classes
(animals with backbones)



The fact that the fossil record of vertebrates shows a progression from fishes to humans has been taken as evidence for Darwin's theory.

Several dozen different “body plans” occur in animals. For example, mammals have a skeleton on the inside, while insects have a skeleton on the outside. Animals with similar body plans (such as mammals and reptiles, or insects and crabs) are grouped in what biologists call a “phylum.” There are several dozen different “phyla.”

Five Major Phyla



Echinoderms (starfish, sea urchins)



Chordates (fish, reptiles, mammals)



Mollusks (clams, snails, octopuses)



Arthropods (crabs, centipedes, insects)



Annelids (leeches, earthworms)

Source: Wikipedia

Five Major Phyla

1

Echinoderms (starfish, sea urchins)

2

Chordates (fish, reptiles, mammals)

3

Mollusks (clams, snails, octopuses)

4

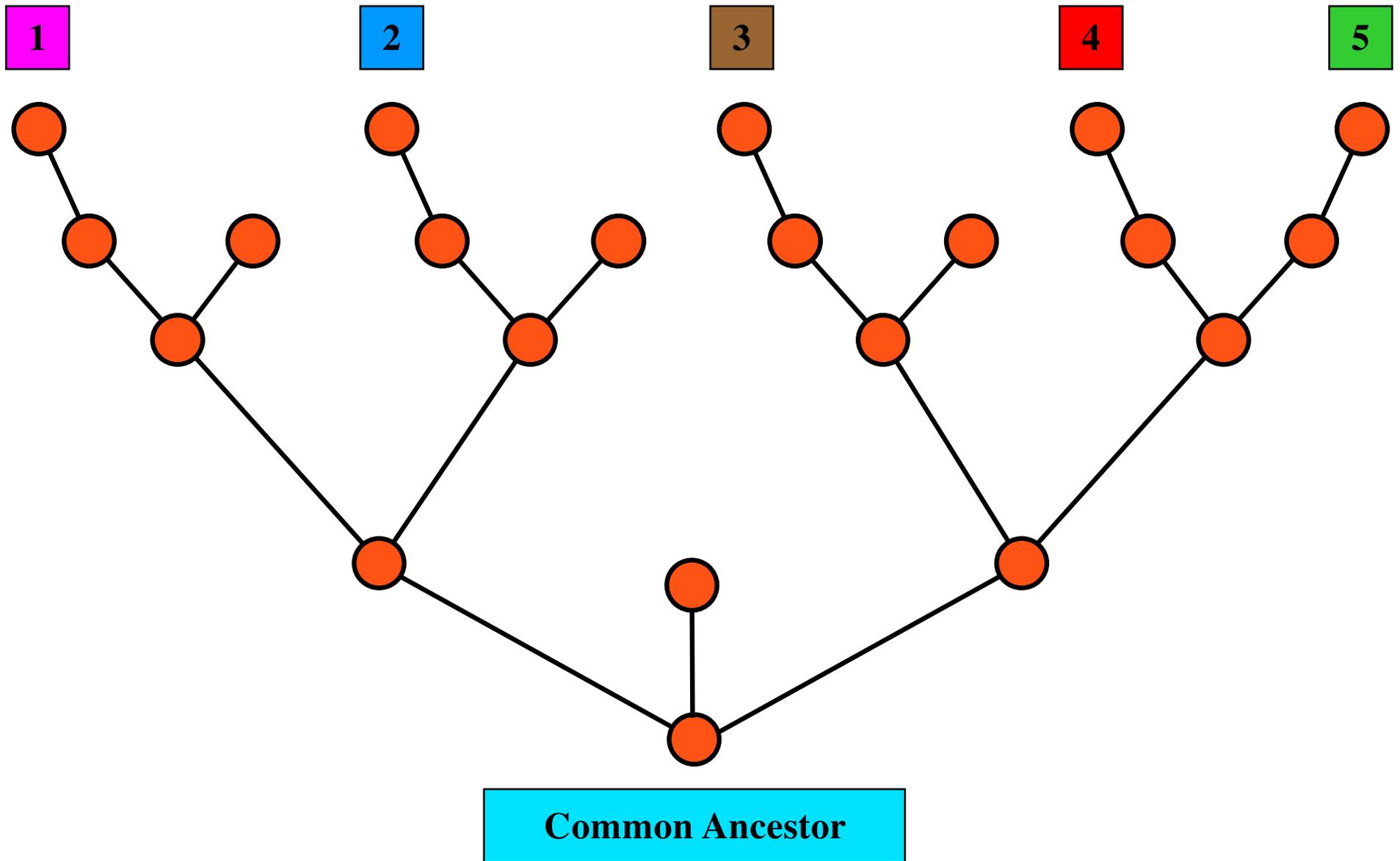
Arthropods (crabs, centipedes, insects)

5

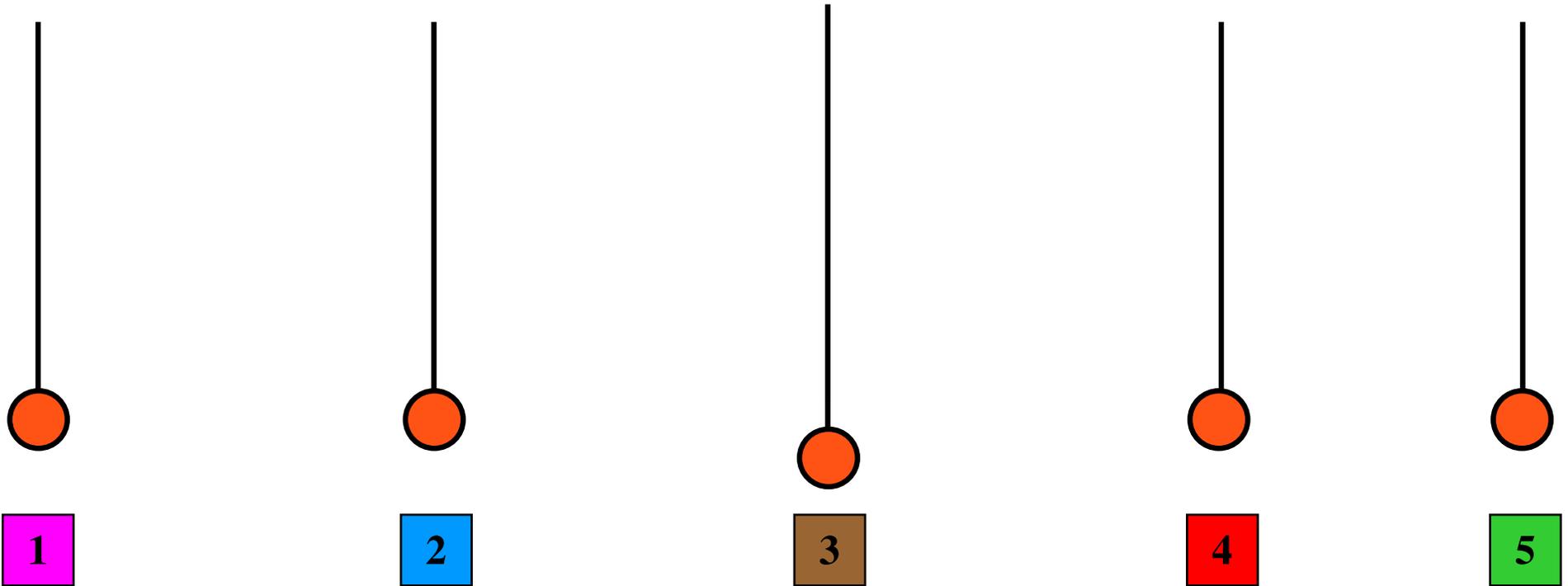
Annelids (leeches, earthworms)

If all animals were descended from a common ancestor, major (phylum-level) differences would appear *LAST* in the fossil record, after a long accumulation of smaller differences in a large number of transitional forms.

Darwin's Theory

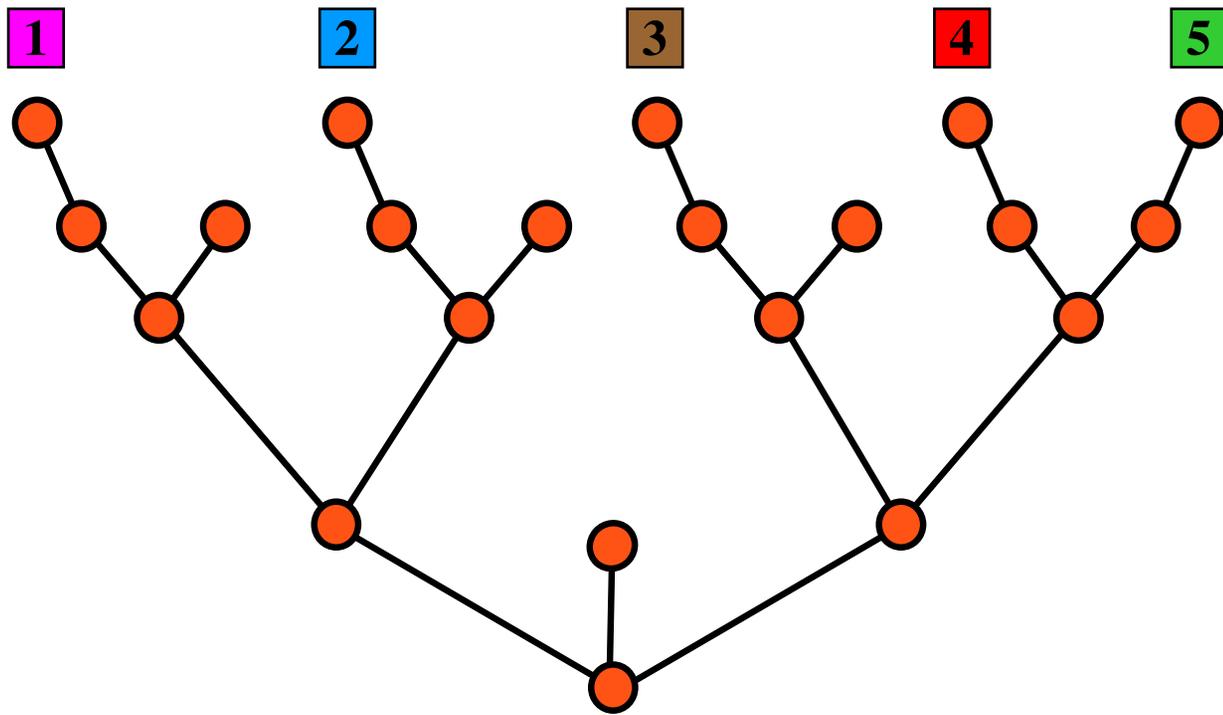


Fossil Evidence



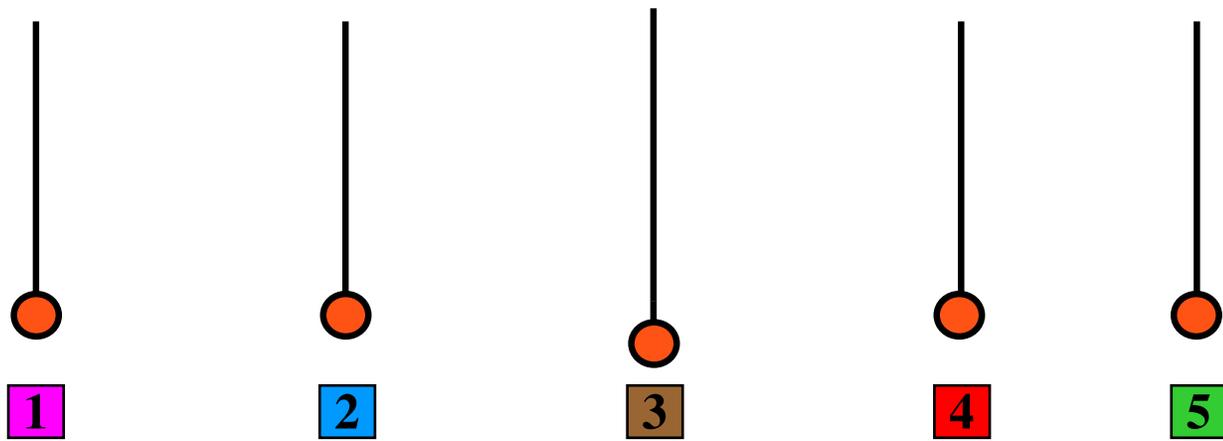
THE CAMBRIAN EXPLOSION:

These phyla appear at about the same time, fully formed, with no fossil evidence of common ancestry.



**Darwin's
Theory**

VS.



**Fossil
Evidence**

Darwin himself knew that the ancestral fossils had not been found. He wrote, “The case at present must remain inexplicable; and may be truly urged as a valid argument against the views here entertained.”

The Origin of Species (1859)

Defenders of Darwin's theory have suggested two main explanations:

- (1) The ancestors left fossils, but the fossil record is flawed or incomplete because the oldest fossils were destroyed by pressure and heat or by subsequent erosion.
- (2) The ancestors were too small or too delicate to have left fossils in the first place.

(1) Is the fossil record flawed or incomplete?

- Many Precambrian fossils have been found since Darwin's time.
- The Cambrian explosion is now well documented from several locations around the world.

(1) Is the fossil record flawed or incomplete?

The Cambrian Explosion “is real; it is too big to be masked by flaws in the fossil record.” In fact, we now know it “was even more abrupt and extensive than previously envisioned.”

James W. Valentine, Stanley W. Awramik, Philip W. Signor
& Peter M. Sadler, *Evolutionary Biology* (1991)

(2) Were ancestors too small or soft to fossilize?

- Microfossils have been found in rocks billions of years older than the Cambrian explosion.
- Many Precambrian fossils are soft-bodied.
- About 70% of the fossils in the Cambrian explosion are soft-bodied.

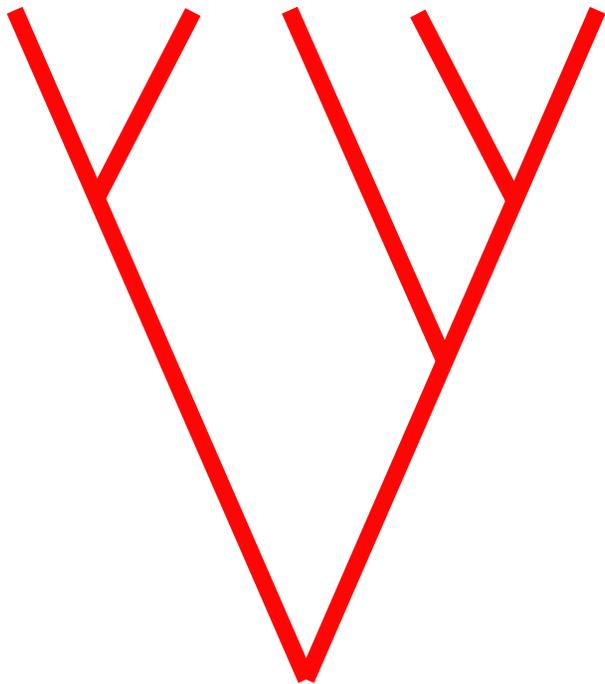
(2) Were ancestors too small or soft to fossilize?

“The long-held notion that Precambrian organisms must have been too small or too delicate to have been preserved in geologic materials...[is] now recognized to be incorrect.”

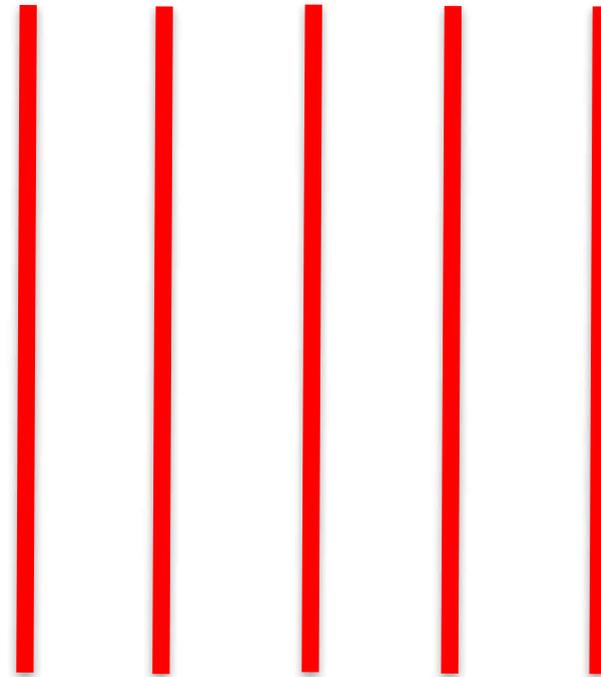
J. William Schopf, American paleontologist and expert on Precambrian fossils, *Trends in Ecology and Evolution* (1994)

Fossil Records of 5 Major Animal Phyla

Darwin's Theory



The Evidence



The fossil experts I'm about to quote are not creationists. They are merely stating what the evidence shows.

“It is consistent with the fossil record that all of the characteristic animal body plans had evolved by the close of [the Cambrian] period, but none of them can be traced through fossil intermediates to an ancestral group.”

James Valentine, American paleontologist and expert on Cambrian fossils, *On the Origin of Phyla* (Chicago: The University of Chicago Press, 2004)

“I look skeptically upon diagrams that show the branching diversity of animal life through time, and come down at the base to a single kind of animal.... Animals may have originated more than once, in different places and at different times.”

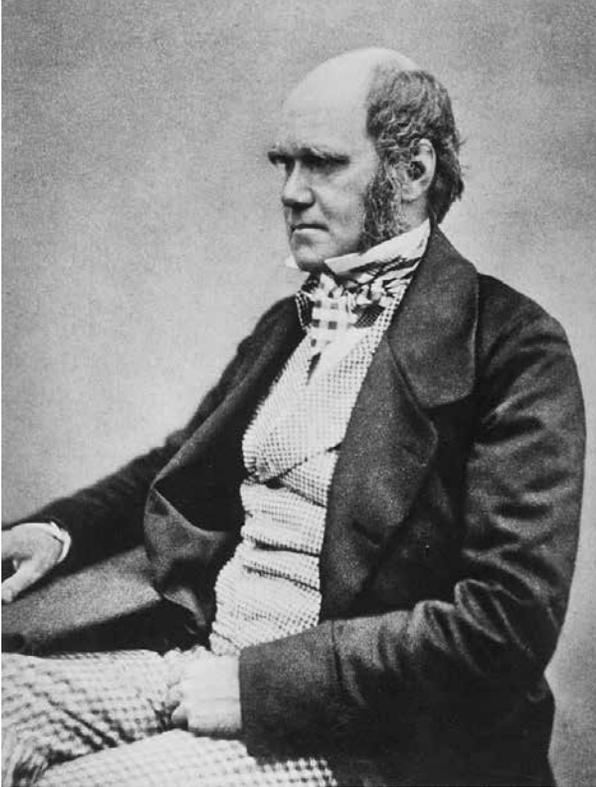
Harry Whittington, British paleontologist and expert on Cambrian fossils, *The Burgess Shale* (1985)

“The Cambrian Explosion stands
Darwin’s theory on its head.”

Jun-Yuan Chen, Chinese paleontologist and expert on
Cambrian fossils, in a lecture at the University of
Washington, 1999.

Five Main Sources of Evidence

- Fossils
- Embryos



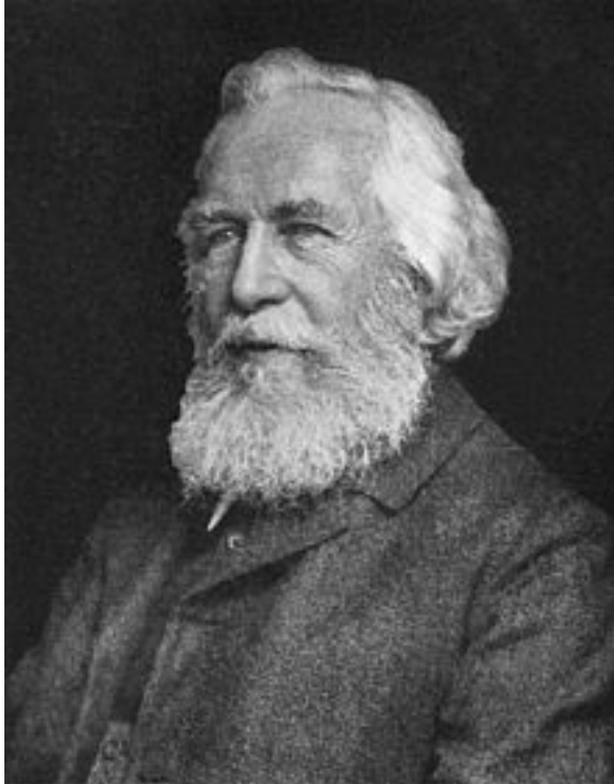
Charles Darwin

The Origin of Species (1859)

Letter to Asa Gray (1860)

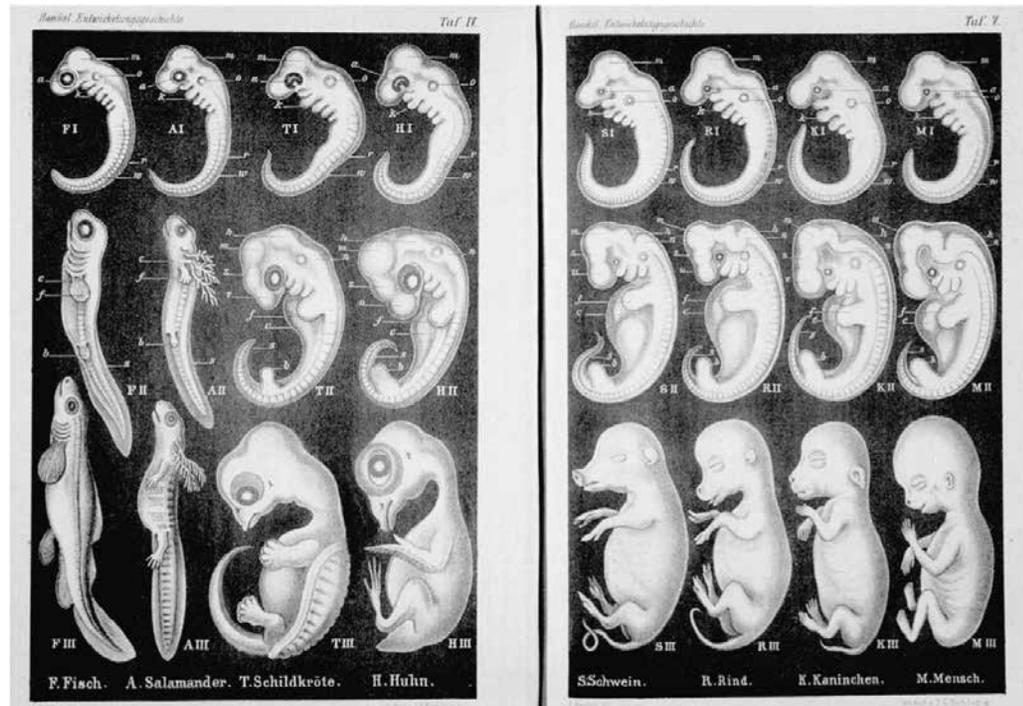
“The embryos of the most distinct species belonging to the same class are closely similar, but become, when fully developed, widely dissimilar.” Since “community in embryonic structure reveals community of descent,” early embryos “show us, more or less completely, the condition of the progenitor of the whole group in its adult state.”

This is “**by far the strongest single class of facts in favor of** common ancestry.”



Ernst Haeckel
Anthropogenie (1874)

Darwin's German supporter, Ernst Haeckel, made drawings of the embryos of vertebrates (animals with backbones) to illustrate Darwin's idea.



Haeckel's Embryo Drawings

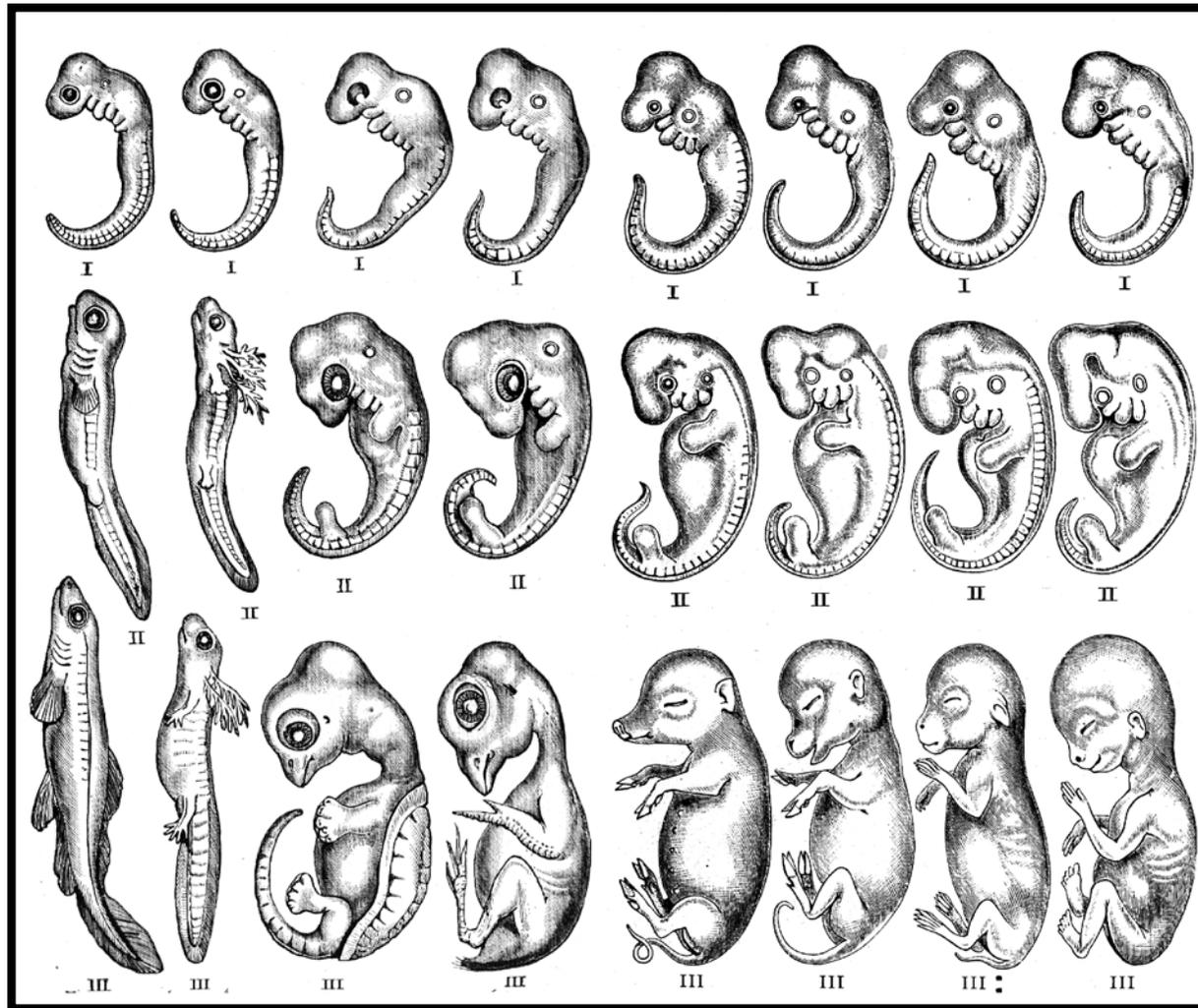
Earliest stages
Are most similar



Like the
common ancestor

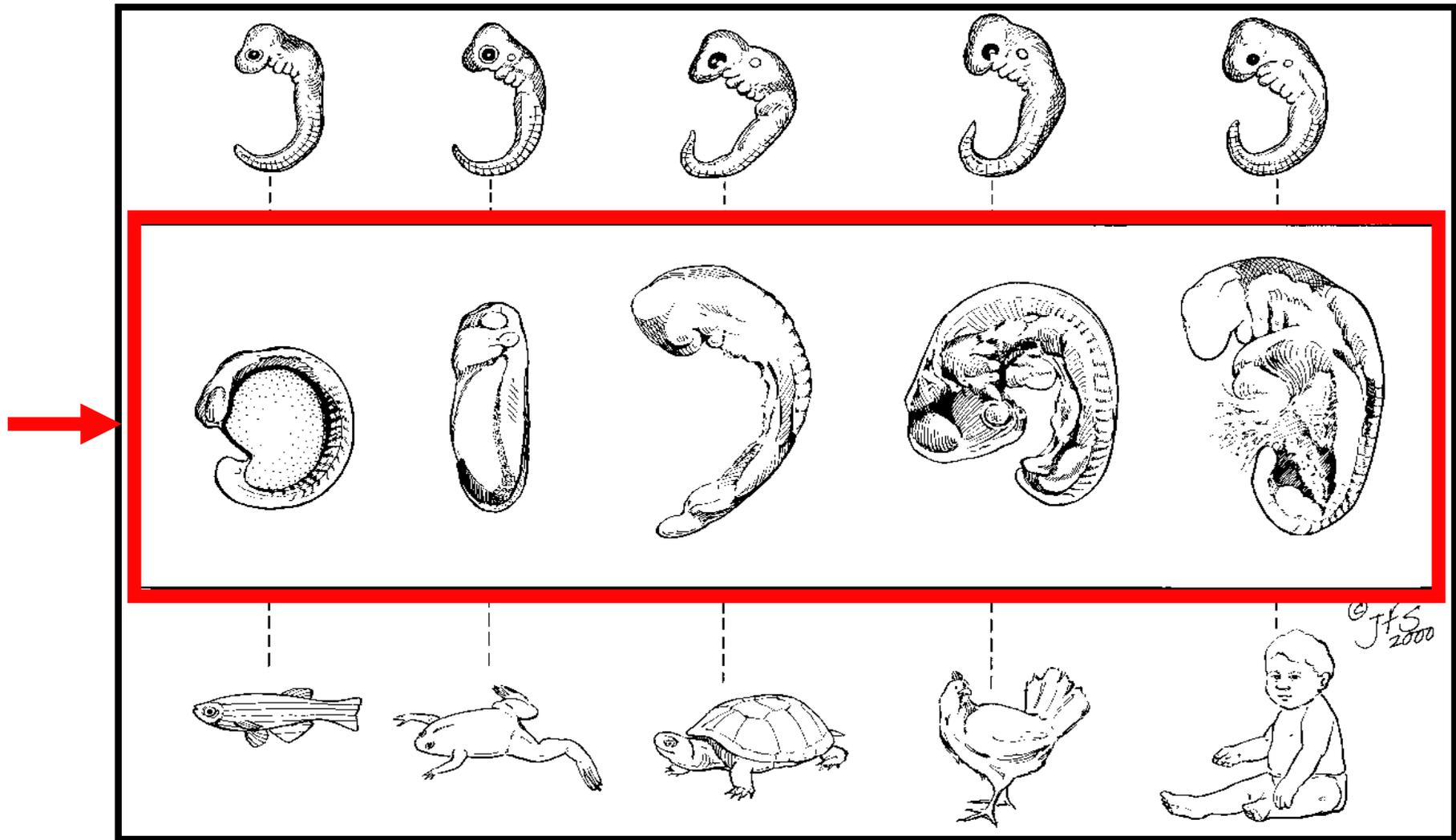
Adult features
develop later

Evolved forms



Fish Salamander Turtle Chicken Pig Cow Rabbit Human

But Haeckel exaggerated his drawings to make the early embryos look more similar than they really are. Here is a comparison of Haeckel's drawings (top) with drawings made from real embryos (red arrow and box).



Haeckel's Embryo Drawings

“It looks like it's turning out to be one of the most famous fakes in biology.”

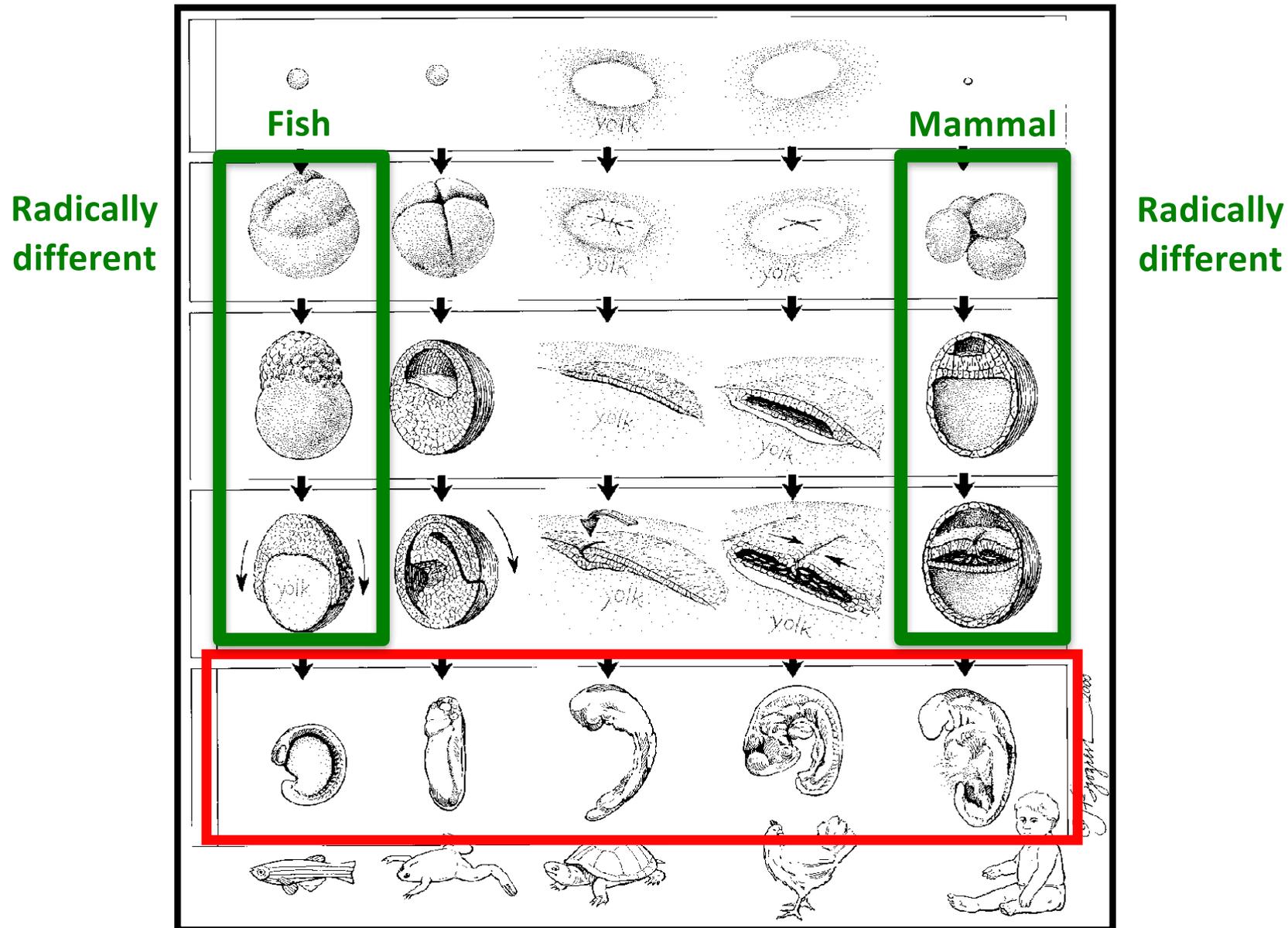
Embryologist Michael Richardson
Science (1997)

Haeckel's Embryo Drawings

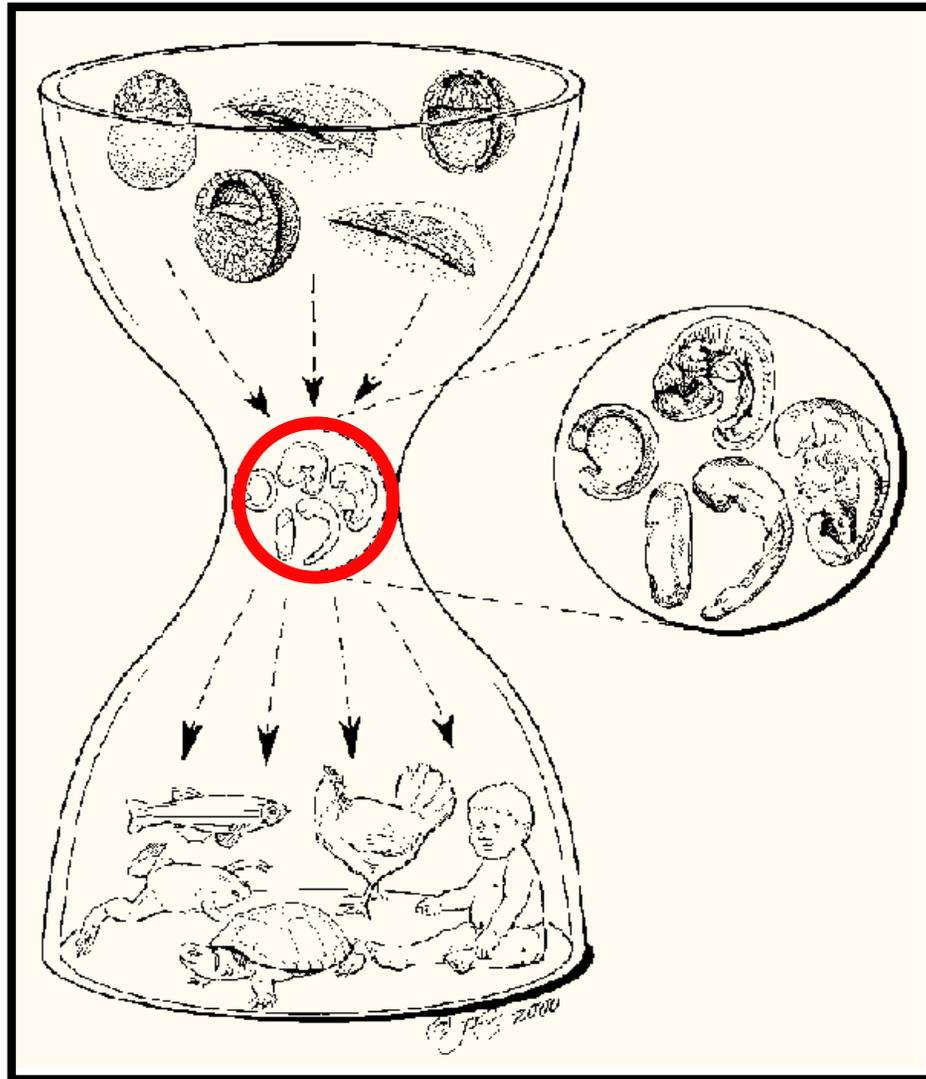
“We do, I think, have the right to be both astonished and ashamed by the century of mindless recycling that has led to the persistence of these drawings in a large number, if not a majority, of modern textbooks.”

Evolutionary Biologist Stephen Jay Gould
Natural History (2000)

Even worse, Haeckel completely omitted the earliest stages in vertebrate development. The **green rectangles** highlight some of the dramatic differences in earlier stages.



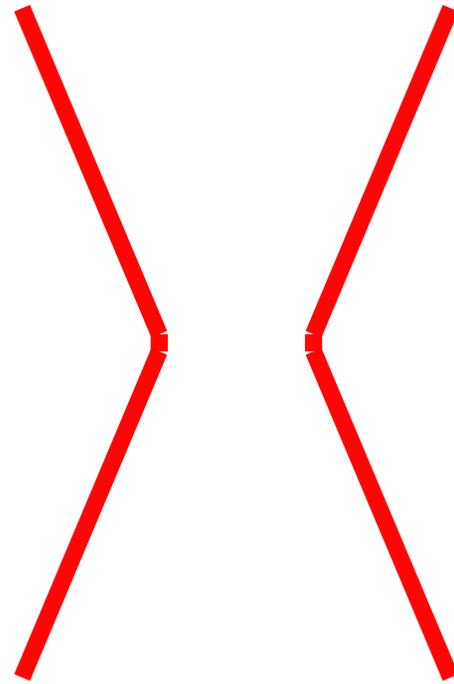
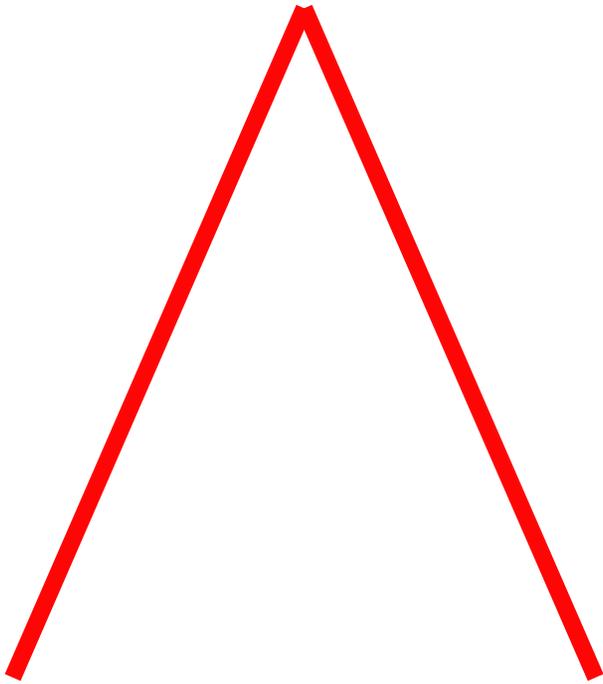
In what's now known as the “developmental hourglass” pattern, vertebrate embryos start out very different, then become somewhat similar before becoming very different again.



Vertebrate Embryo Development

Darwin's Theory

The Evidence

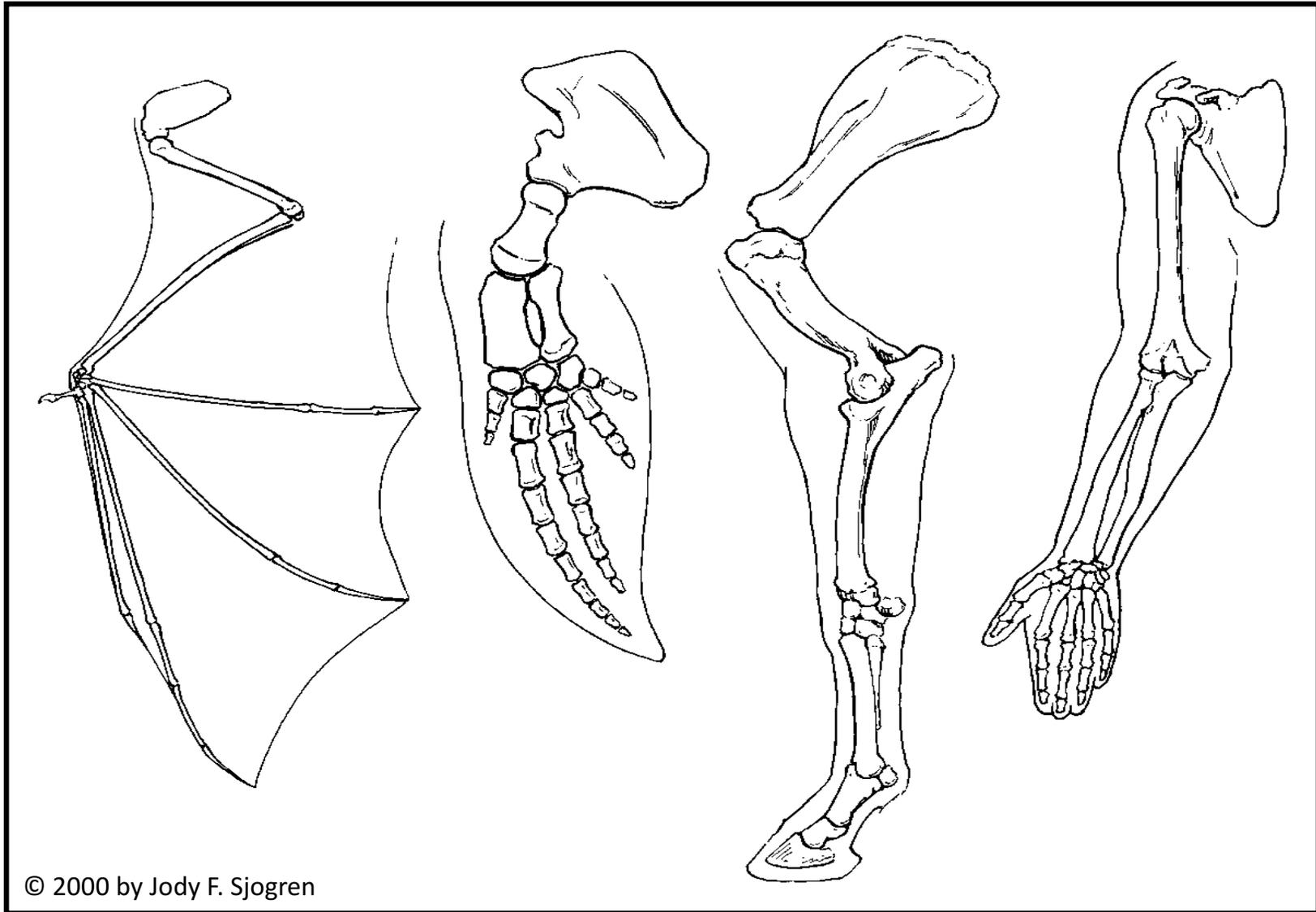


So the “facts” that Darwin considered “by far” the best evidence for common ancestry turn out not to be facts at all.

Five Main Sources of Evidence

- Fossils
- Embryos
- **Homology**

Homology in Vertebrate Limbs



Bat

Porpoise

Horse

Human

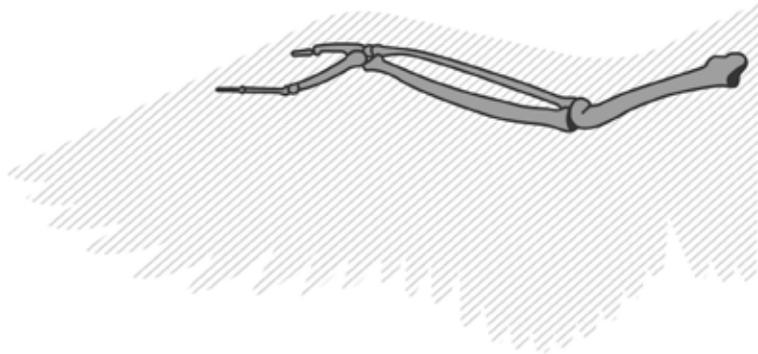
Even before Darwin, biologists noticed that the forelimbs of vertebrates had similar bones, though they served different functions (flying, swimming, walking, grasping). In particular, the bones were similar in **structure** and **position**.

British biologist Richard Owen (like others before him) called this “homology,” and he distinguished it from similarity due to **function**, which he called “analogy.”

Bat



Bird



Insect

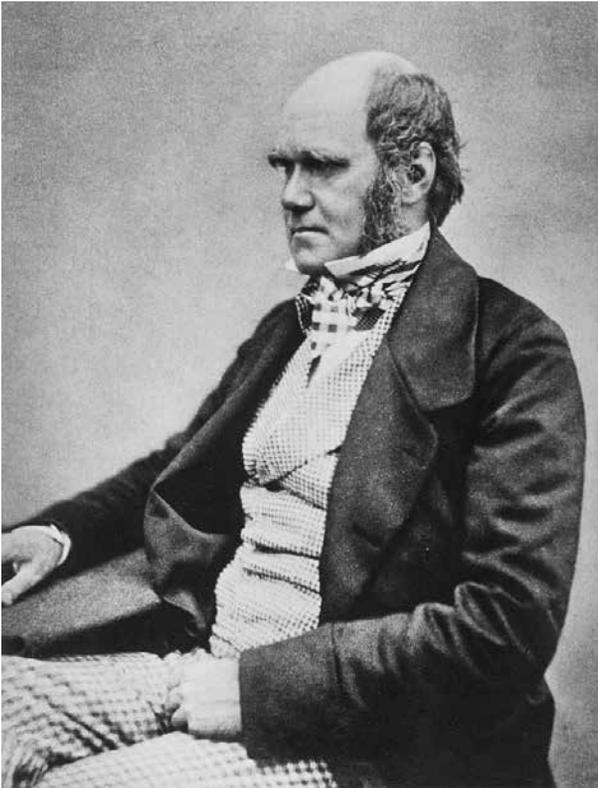


Because the bat's wing and the bird's wing have bones with similar structure and position (even though the bird has fewer "fingers"), they are **homologous**.

Although the insect's wing is similar in the sense that it is used for flying, it has a pattern of veins instead of bones. Because there is no similarity of structure and position, the insect's wing is **analogous**.

According to Owen, homologies were constructed according to an archetype or idea.

Homology



Charles Darwin

The Origin of Species (1859)

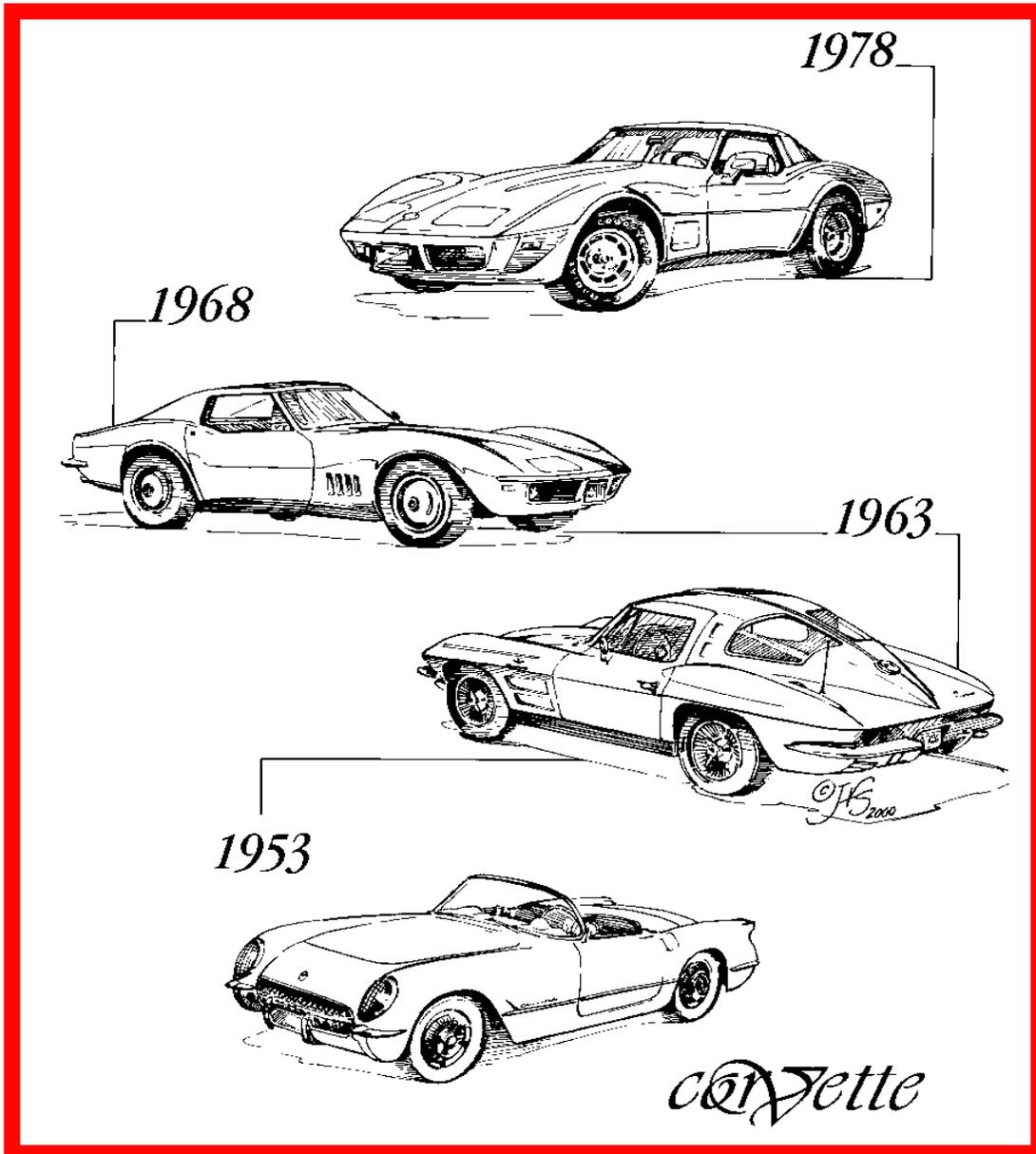
For Darwin, however, homology was due to common ancestry. He wrote that homologous features are among the facts that “proclaim so plainly, that the innumerable species, genera and families of organic beings, with which this world is peopled, have all descended, each within its own class or group, from common parents.”

Homology



In 1990, biologist Tim Berra published a book titled *Evolution and the Myth of Creationism*. In it, he illustrated how biologists use a series of homologies to establish common ancestry, “and the evidence is so solid and comprehensive that it cannot be denied by reasonable people.”

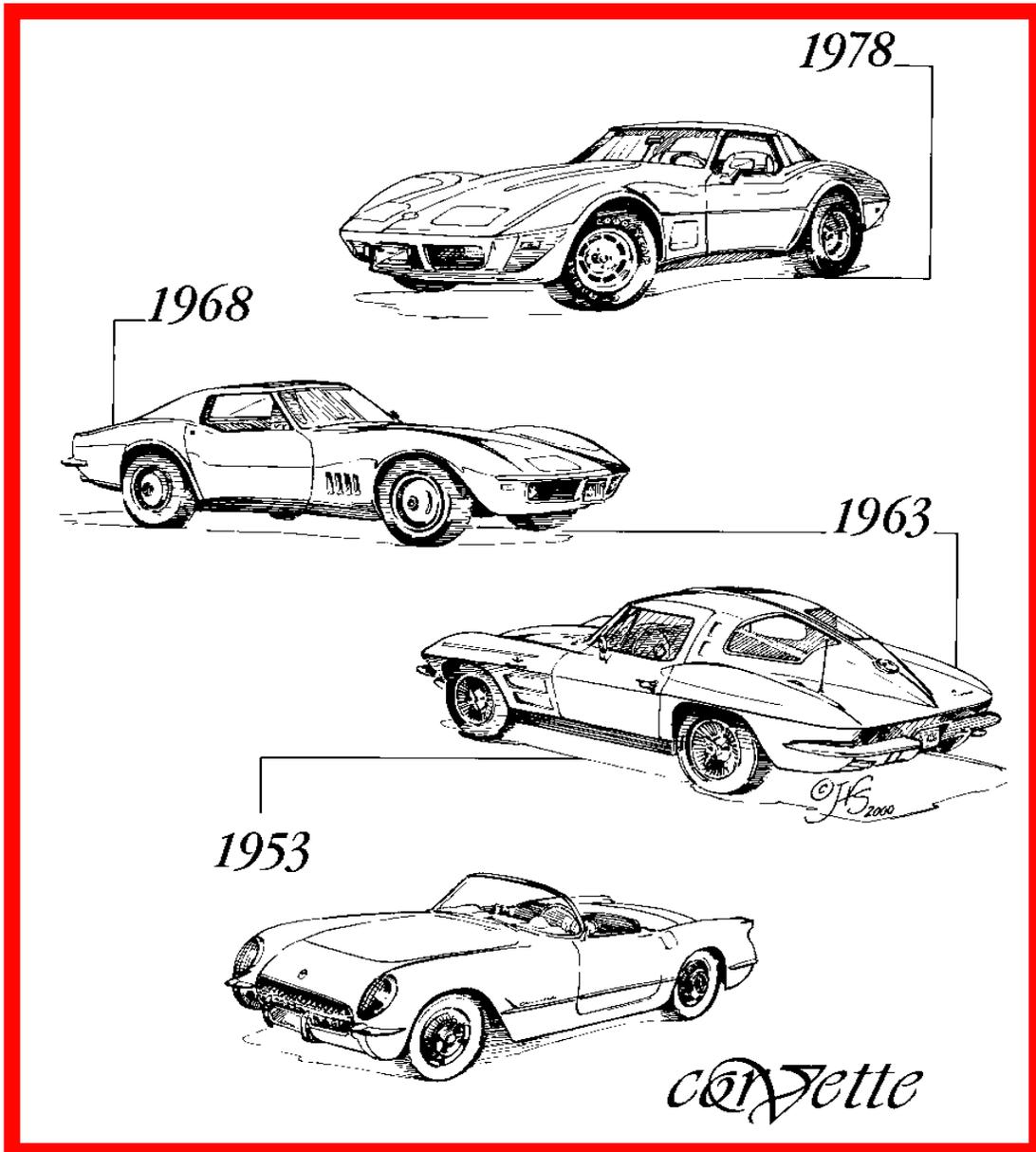
Homology



This was Berra's illustration: "If you compare a 1953 and a 1954 Corvette, side by side, then a 1954 and a 1955 model, and so on, the descent with modification is overwhelmingly obvious."

But Corvettes are designed.

Homology



Phillip Johnson called this “Berra’s blunder.” The lesson of it is that a series of homologies isn’t necessarily due to common ancestry. It could equally well be due to common design.

In order to show that homologies are due to common ancestry instead of common design, it is important to show how ancestors produce homologies. The bones of vertebrate limbs are not present in the fertilized egg. Where do they come from?

With the rise of genetics after 1900, biologists attributed features such as bone structure to “genes,” which were thought to contain a program for embryo development.

For decades, most biologists thought that homologous features were caused by similar genes.

But more and more evidence showed that similar genes could not explain homologies.

In 1971, British embryologist Gavin De Beer wrote: “Because homology implies community of descent from... a common ancestor it might be thought that genetics would provide the key to the problem of homology. This is where the worst shock of all is encountered [because] characters controlled by identical genes are not necessarily homologous, and homologous structures need not be controlled by identical genes.”

Gavin de Beer, *Homology: An Unsolved Problem* (1971)

De Beer concluded that “the inheritance of homologous structures from a common ancestor... cannot be ascribed to identity of genes.”

Gavin de Beer, *Homology: An Unsolved Problem* (1971)

So the mechanism that produces homology remains unknown.

To make things clearer, evolutionary biologists changed the definition of homology from “similarity of structure and position” to “similarity due to common ancestry.”

“After 1859 there has been only one definition of homologous that makes biological sense.... Attributes of two organisms are homologous when they are derived from an equivalent characteristic of the common ancestor.”

Evolutionary biologist Ernst Mayr,
The Growth of Biological Thought (1982)

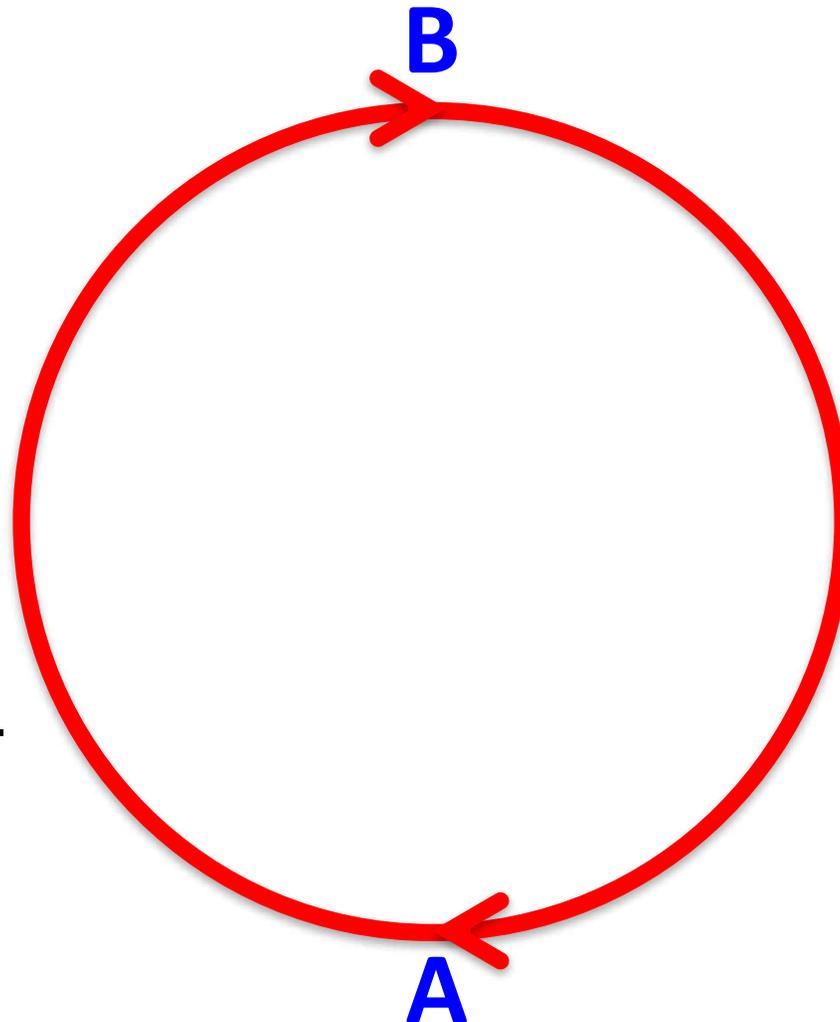
But once homology is **defined** as similarity due to common ancestry, it can't be used as **evidence** for common ancestry. That would be arguing in a circle.

B

A

How do we know
that feature B is
descended from
feature A?
Because B is
homologous to A.

But once homology is **defined** as similarity due to common ancestry, it can't be used as **evidence** for common ancestry. That would be arguing in a circle.



How do we know that feature B is homologous to feature A?
Because B is descended from A.

How do we know that feature B is descended from feature A?
Because B is homologous to A.

“Common ancestry is all there is to homology.” Thus “homology is the anticipated and expected consequence of evolution. Homology is not evidence of evolution.”

Evolutionary biologist David Wake,
Novartis Symposium on Homology (1999)

“By making our explanation into the definition of the condition to be explained, we express not scientific hypothesis but belief. We are so convinced that our explanation is true that we no longer see any need to distinguish it from the situation we were trying to explain. Dogmatic endeavors of this kind must eventually leave the realm of science.”

Philosopher of biology Ronald H. Brady,
Cladistics (1985)

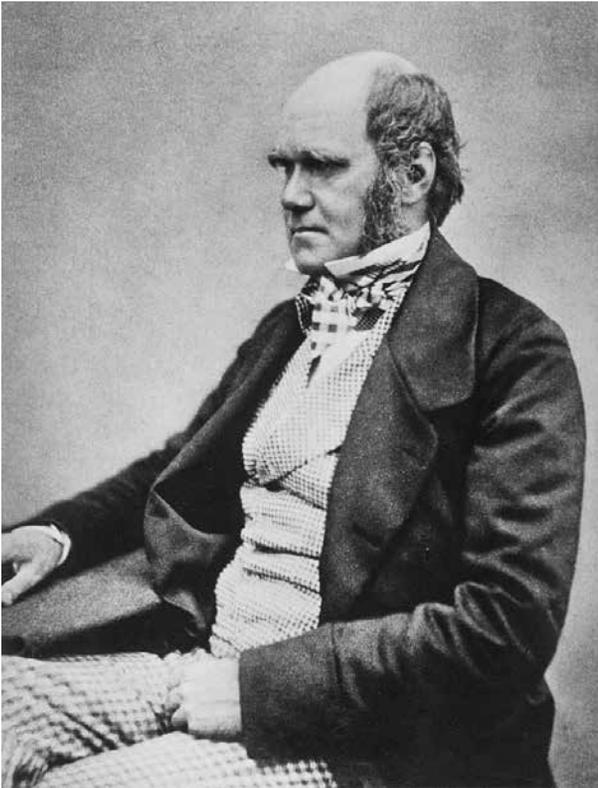
Five Main Sources of Evidence

- Fossils
- Embryos
- Homology
- **Biogeography**

Biogeography

Biogeography deals with the geographic distribution of animals and plants.

Biogeography



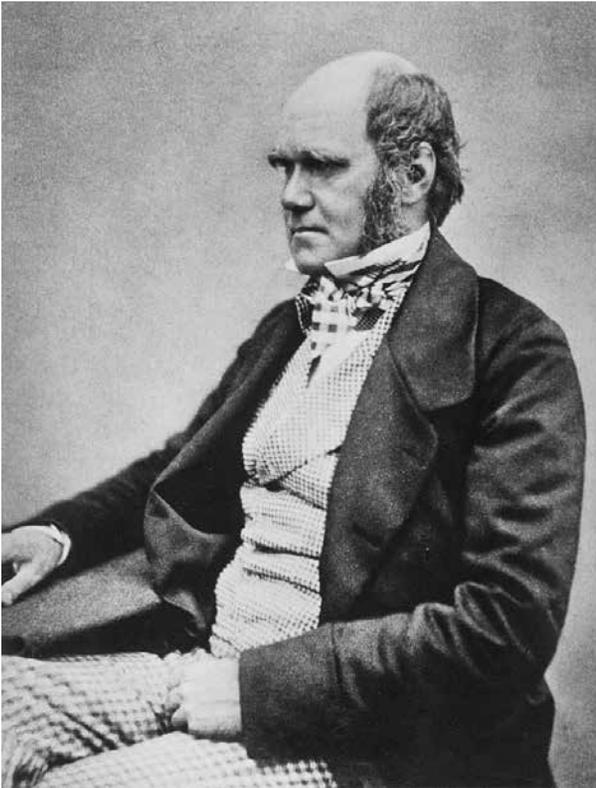
Charles Darwin

The Origin of Species (1859)

“Why, it may be asked, has the supposed creative force produced bats and no other mammals on remote islands? On my view this question can easily be answered; for no terrestrial mammal can be transported across a wide space of sea, but bats can fly across.”

These phenomena are “inexplicable on the theory of independent creation.”

But not all distributions can be explained by migration.

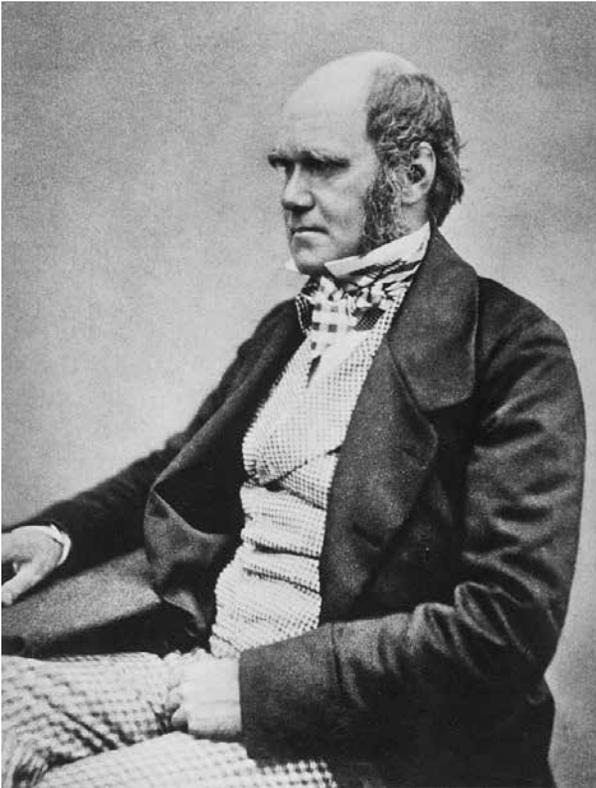


Charles Darwin

The Origin of Species (1859)

“The identity of many plants and animals, on mountain-summits, separated from each other by hundreds of miles of lowlands, where the Alpine species could not possibly exist, is one of the most striking cases known of the same species living at distant points, without the apparent possibility of their having migrated from one to the other.”

But not all distributions can be explained by migration.



Charles Darwin

The Origin of Species (1859)

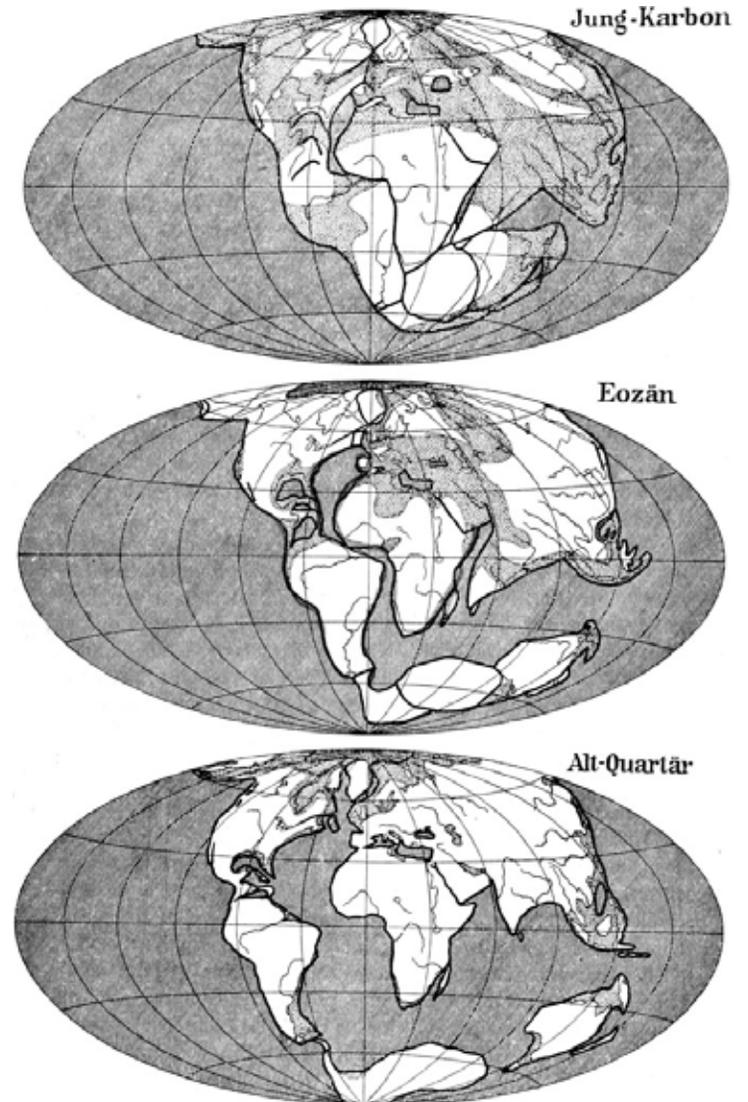
Darwin argued that animals living in the last Ice Age became stranded on cold mountain tops as the glaciers melted, isolating them in the locations they now inhabit.

Modern biologists call this fragmentation of a once-continuous population “**vicariance.**”



Alfred Wegener
*Entstehung der Kontinente und
Ozeane*
(1929)

Seventy years later,
German geo-
physicist Alfred
Wegener argued
that millions of
years ago there
was only one
continent (top).
Then it broke up
and the pieces
gradually drifted
apart (middle and
bottom).



So in addition to changes in climate, vicariance due to continental drift has been used to explain some biogeographical distributions.

Standard (Darwinian) View: Two main factors produce geographical distributions.

Migration

- Individuals from a center of origin migrate to other places and colonize them.

Vicariance

- A single population is fragmented by a radical change in climate or the emergence of major geographical barriers (such as open ocean).

Migration or Vicariance?

Flightless birds are found in Australia, South America, and Africa. Since they could not have flown across the ocean, biologists long thought that they were descended from an ancestor that lived before the continents drifted apart.



**Cassowary
(Australia)**



**Rhea
(South America)**



**Ostrich
(Africa)**

Migration or Vicariance?

But a team of biologists showed in 2008 that these birds originated **after** the continents separated and that their similarities had “independent origins.” This “removes the need to postulate vicariance by continental drift” to explain their distribution.



Source: Summerdrought (Wikipedia)

**Cassowary
(Australia)**



Source: Chucao (Wikipedia)

**Rhea
(South America)**



Source: Nevit Dilmen (Wikipedia)

**Ostrich
(Africa)**

Migration or Vicariance?

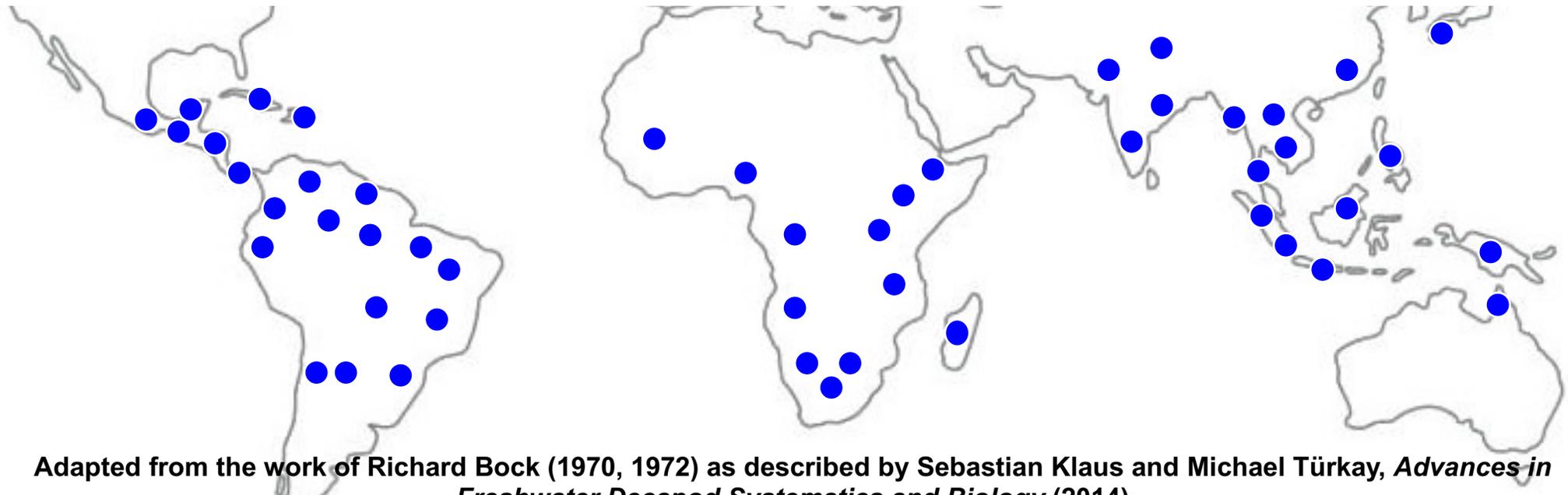
Another example: Freshwater crabs complete their life cycles exclusively in freshwater habitats and are incapable of surviving prolonged exposure to salt water. Today, very similar-looking species are found in widely separated lakes and rivers in Central and South America, Africa, Madagascar, India, Asia and Australia.



Adapted from the work of Richard Bock (1970, 1972) as described by Sebastian Klaus and Michael Türkay, *Advances in Freshwater Decapod Systematics and Biology* (2014)

Migration or Vicariance?

Evidence indicates that these freshwater crabs originated long after the continents separated, so their distribution is inconsistent with vicariance. But they could not have migrated across the oceans. So neither vicariance nor migration provides a convincing explanation for the biogeography of these animals



Adapted from the work of Richard Bock (1970, 1972) as described by Sebastian Klaus and Michael Türkay, *Advances in Freshwater Decapod Systematics and Biology* (2014)

There are many other cases of similarities in animals that are clearly NOT due to common ancestry.

**This phenomenon is called
“convergence.”**

Convergence in Animals

Mammals are vertebrates that nourish their young with milk.

Depending on how they give birth, they are classified as either monotremes, or marsupials, or placentals.

- Monotremes lay eggs, like birds.
- Marsupials give birth to fetuses that crawl into a pouch where the mother nourishes them while they complete embryo development.
- Placentals nourish their young internally and give birth to fully formed babies.

From an evolutionary point of view, such basic differences in their ways of giving birth mean that these three sub-classes must have diverged from a common ancestor long before they acquired their modern forms.

Yet convergence among their modern forms is widespread.

Convergence in Animals

Echidna
(Egg-laying **Monotreme**)



Source: JJ Harrison (Wikipedia)

Porcupine
(Live-bearing **Placental**)



Source: J Glover (Wikipedia)

Convergence in Animals

Australian Thylacines
(**Marsupial**)



American Gray Wolf
(**Placental**)



Convergence in Animals

Australian Wombat
(**Marsupial**)



American Groundhog
(**Placental**)



Convergence in Animals

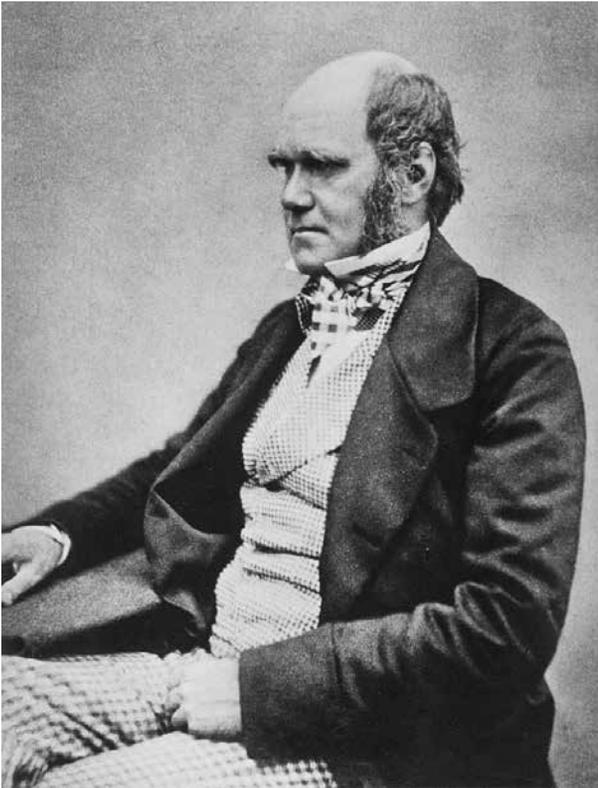
- Marsupial Mammals
 - Thylacine
 - Wombat
 - Sugar Glider
 - Kakarratul
 - Antechinus
 - Bilby
- Placental Mammals
 - Wolf
 - Groundhog
 - Flying Squirrel
 - Mole
 - Mouse
 - Rabbit

There are many more examples of convergence in animals, as well as many examples in plants.

According to Cambridge University biologist Simon Conway Morris, “**convergence is ubiquitous.**” Thus “not only is the Universe strangely fit to purpose, but so, too... is life’s ability to navigate to its solutions.”

Simon Conway Morris, *Life’s Solutions* (Cambridge University Press, 2003)

Universal Common Ancestry



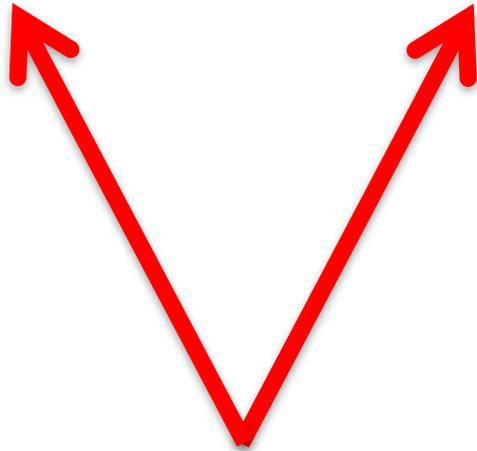
Charles Darwin

The Origin of Species (1859)

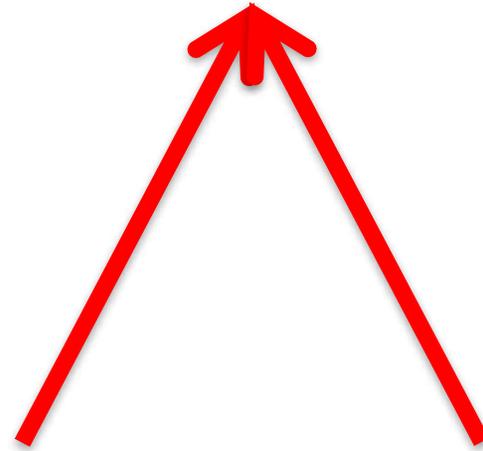
Recall that in *The Origin of Species* Darwin wrote that genealogy [i.e., common ancestry] is “the only known cause of the similarity of organic beings.”

But convergence shows that many similarities are **not** due to common ancestry.

Darwin's Theory



Convergence



Convergence stands Darwin's theory on its head.

Since the evidence from fossils, embryos, and biogeography fails to confirm Darwin's Tree of Life, modern evolutionary biologists have relied more and more on molecular evidence.

Five Main Sources of Evidence

- Fossils
- Embryos
- Homology
- Biogeography
- **Molecules**

Seven Major Phyla

(Two worm phyla that did not leave Cambrian fossil records are added here to the original five.)

- 1 **Platyhelminthes (flatworms, tapeworms)**
- 2 **Nematodes (roundworms, hookworms)**
- 3 **Echinoderms (starfish, sea urchins)**
- 4 **Chordates (fish, reptiles, mammals)**
- 5 **Mollusks (clams, snails, octopuses)**
- 6 **Arthropods (crabs, centipedes, insects)**
- 7 **Annelids (leeches, earthworms)**

All of these animals use a four-subunit molecule called “18s rRNA” to make proteins. But the sequences of subunits in them differ slightly from one phylum to another. In the simplified example below, the second sequence is slightly different from the first, and the third sequence is even more different, so we might infer that the first is more closely related to the second than it is to the third:

A	C	G	U	A	C	G	U	A	C	G	U	A	C
A	C	G	U	G	C	G	U	A	C	U	U	A	C
A	C	A	U	G	C	G	U	G	C	U	U	G	C

We can group the seven phyla into three different groups based on the similarity of sequences in their 18s rRNA molecules.

3

Echinoderms (starfish, sea urchins)

4

Chordates (fish, reptiles, mammals)

6

Arthropods (crabs, centipedes, insects)

1

Platyhelminthes (flatworms, tapeworms)

5

Mollusks (clams, snails, octopuses)

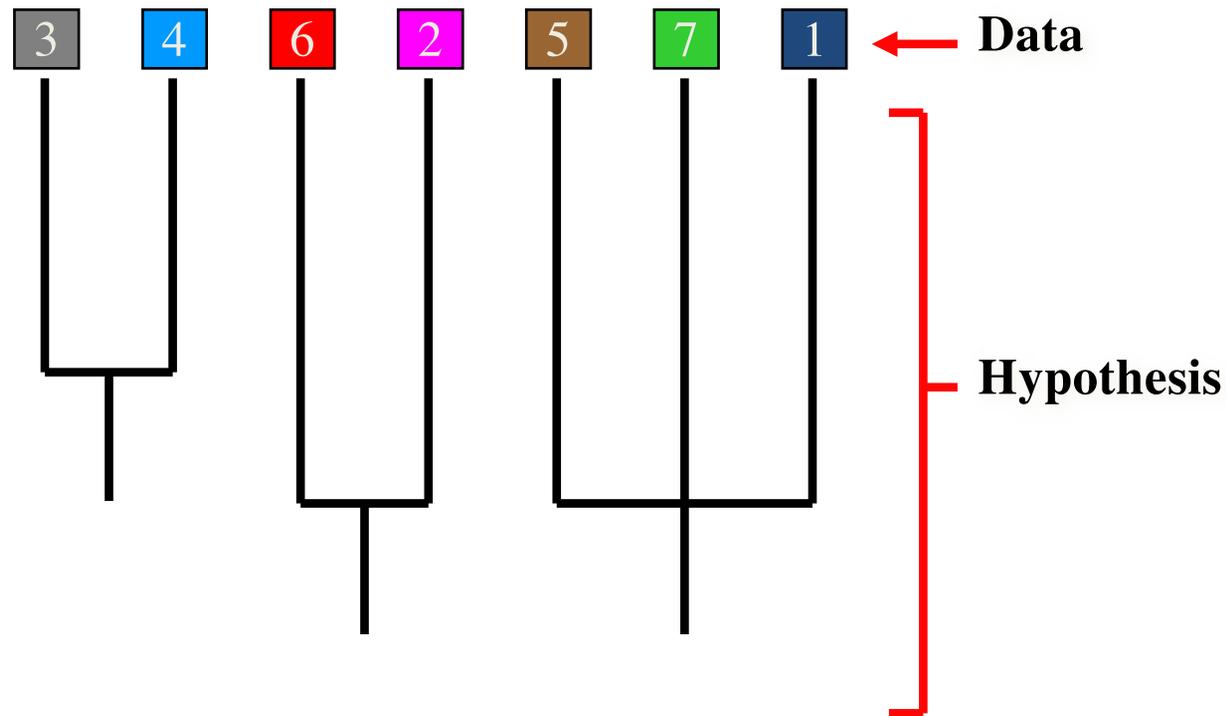
7

Annelids (earthworms, leeches)

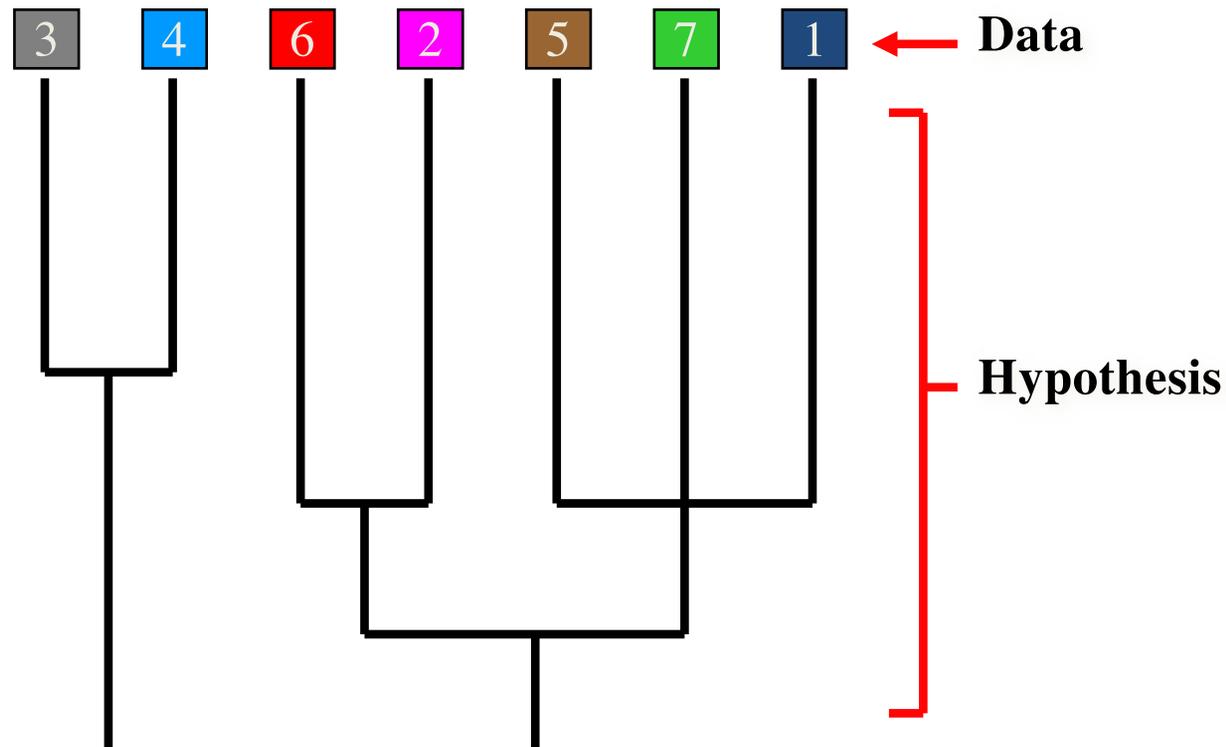
2

Nematodes (roundworms, hookworms)

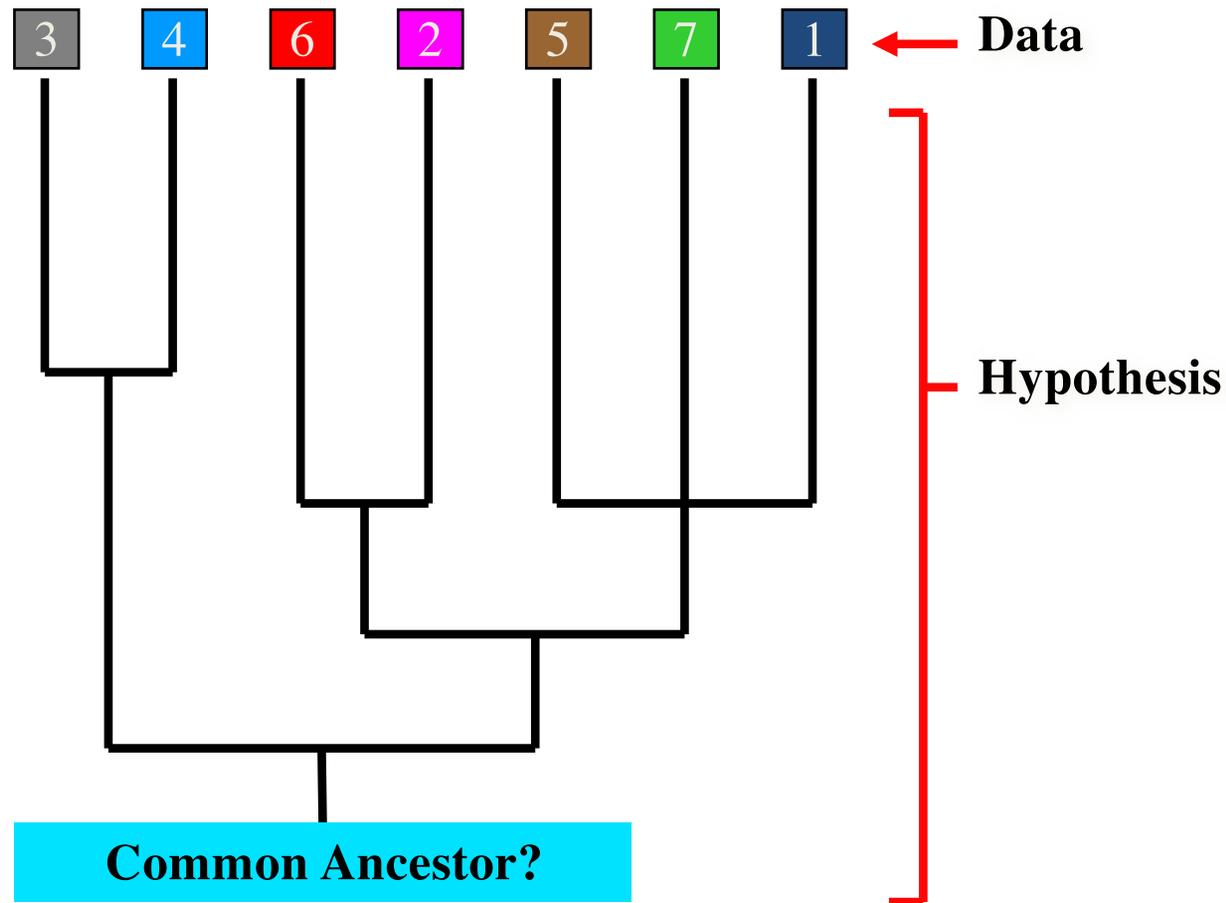
This grouping based on 18s rRNA can be used to construct a hypothetical “tree” of evolutionary relationships (called a “phylogeny”). Note that the only data are in the living phyla at the top. The lines below them are hypothetical.



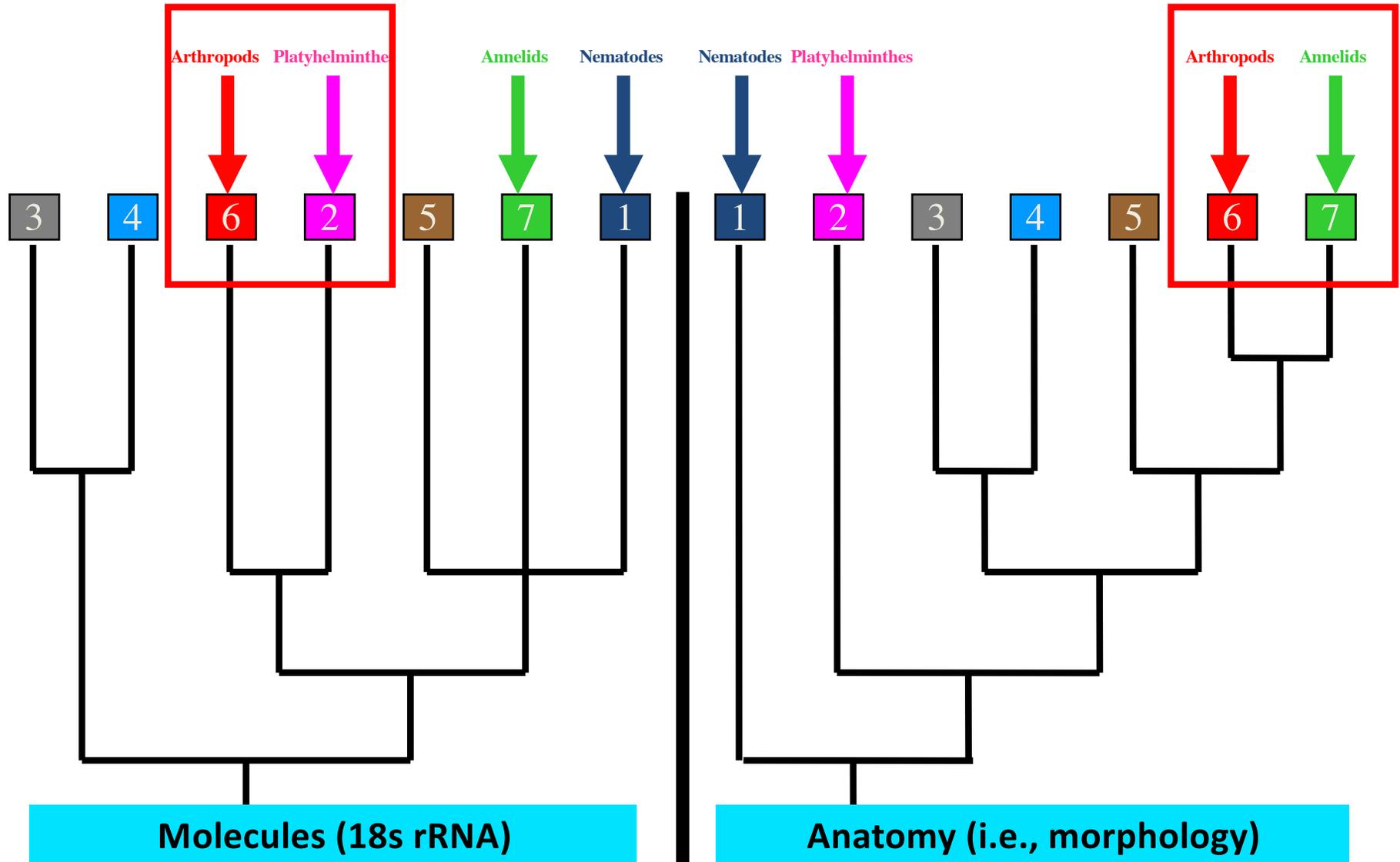
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But an evolutionary tree based on 18s rRNA can be very different from a tree based on anatomy.

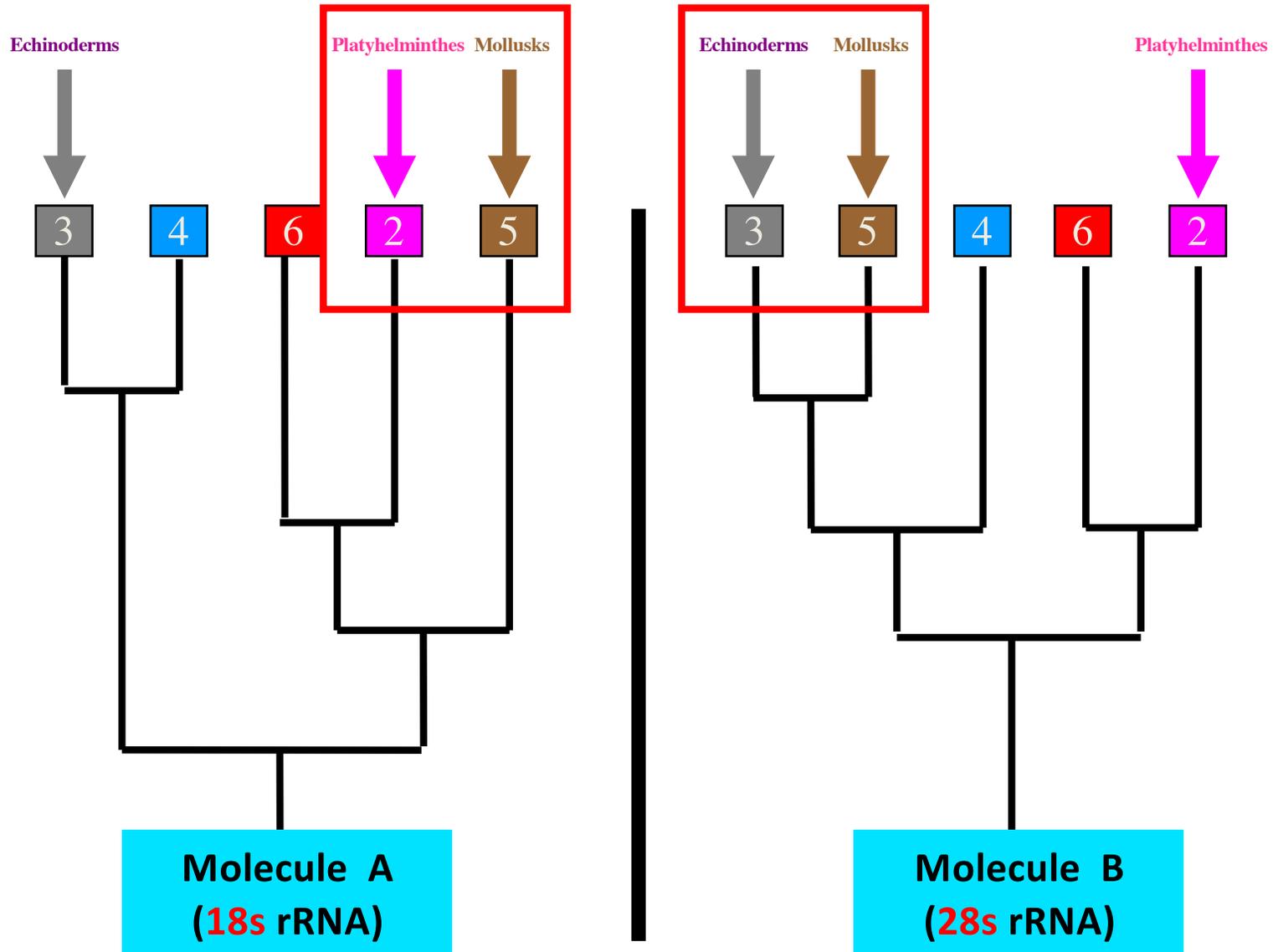


Anna Marie A. Aguinaldo & James A. Lake, *American Zoologist* (1998)

“Evolutionary trees constructed by studying biological molecules often don’t resemble those drawn up from morphology.”

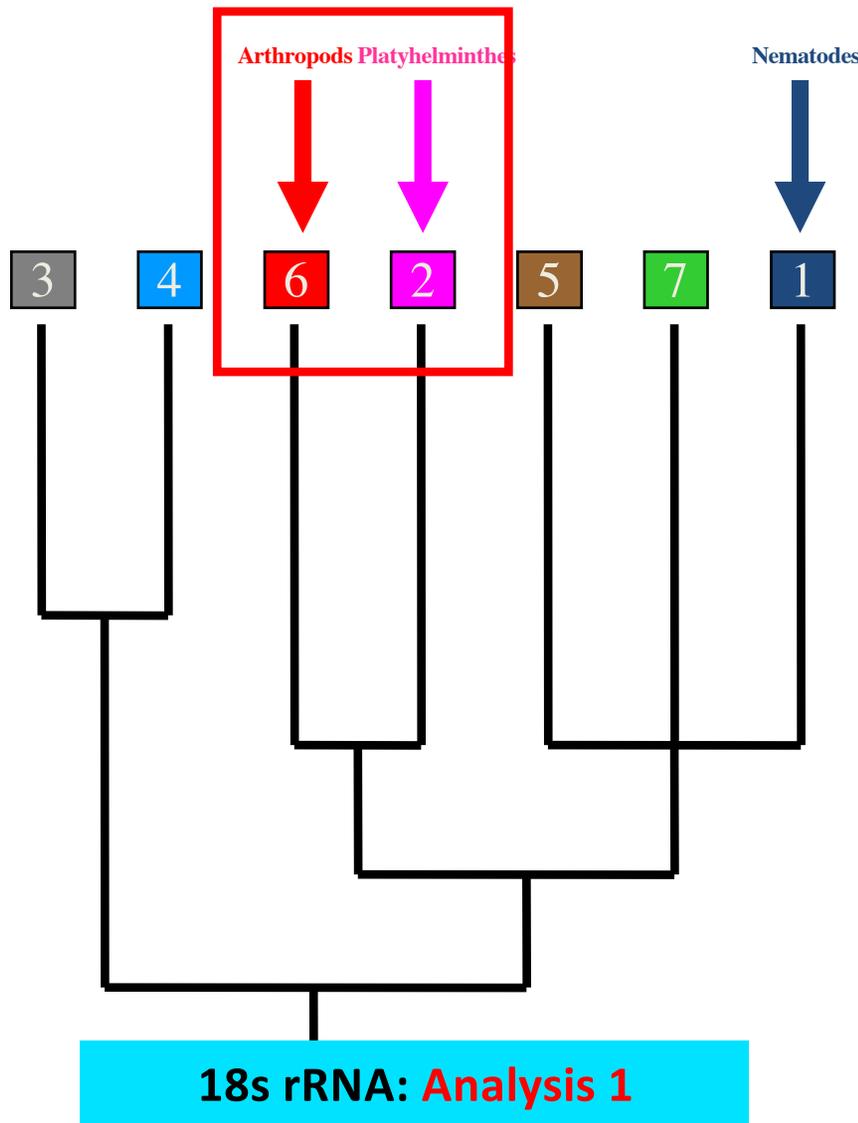
Trisha Gura, “Bones, Molecules, or Both?” (*Nature* 2000)

And evolutionary trees based on one molecule can be very different from trees based on other molecules.

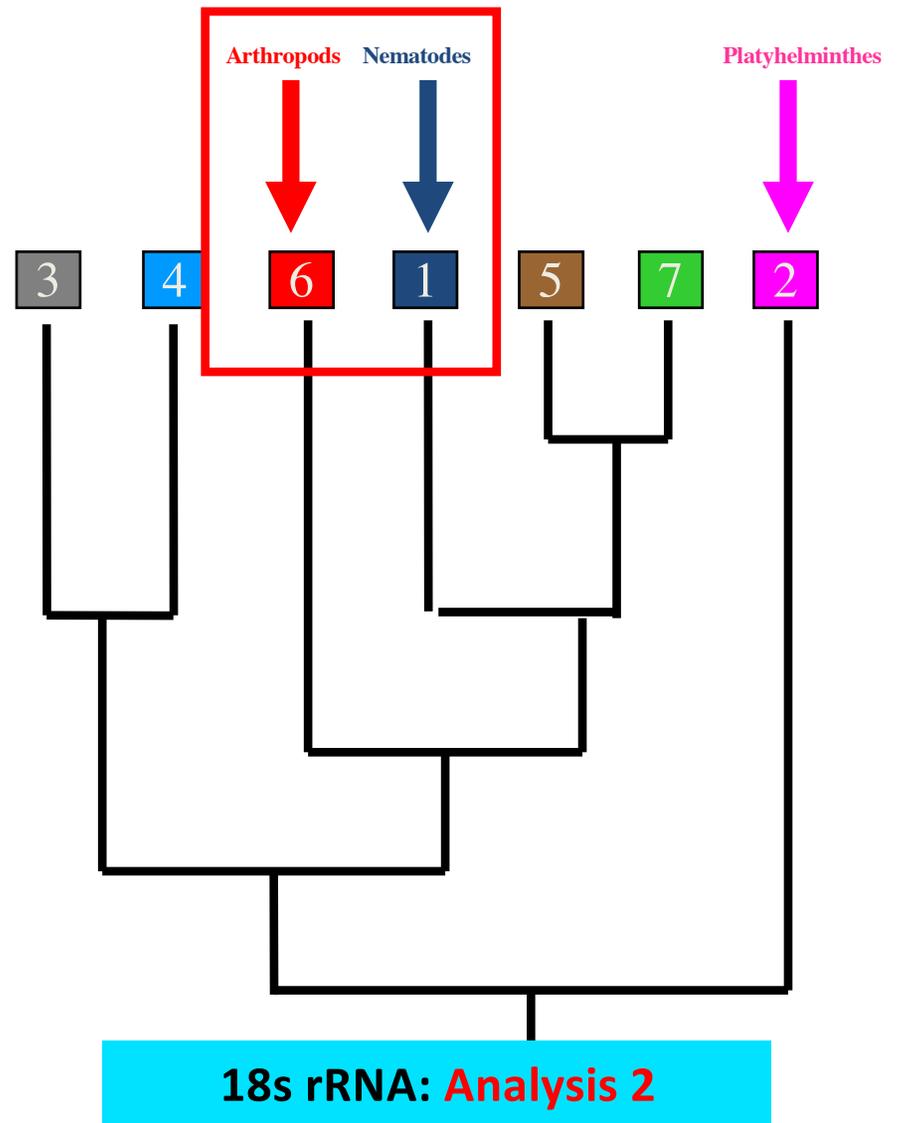


R. Christen et al., *EMBO Journal* (1991)

Even worse, analyses of the same molecule by different laboratories can produce different evolutionary trees.



Aguinaldo & Lake, *American Zoologist* (1998)

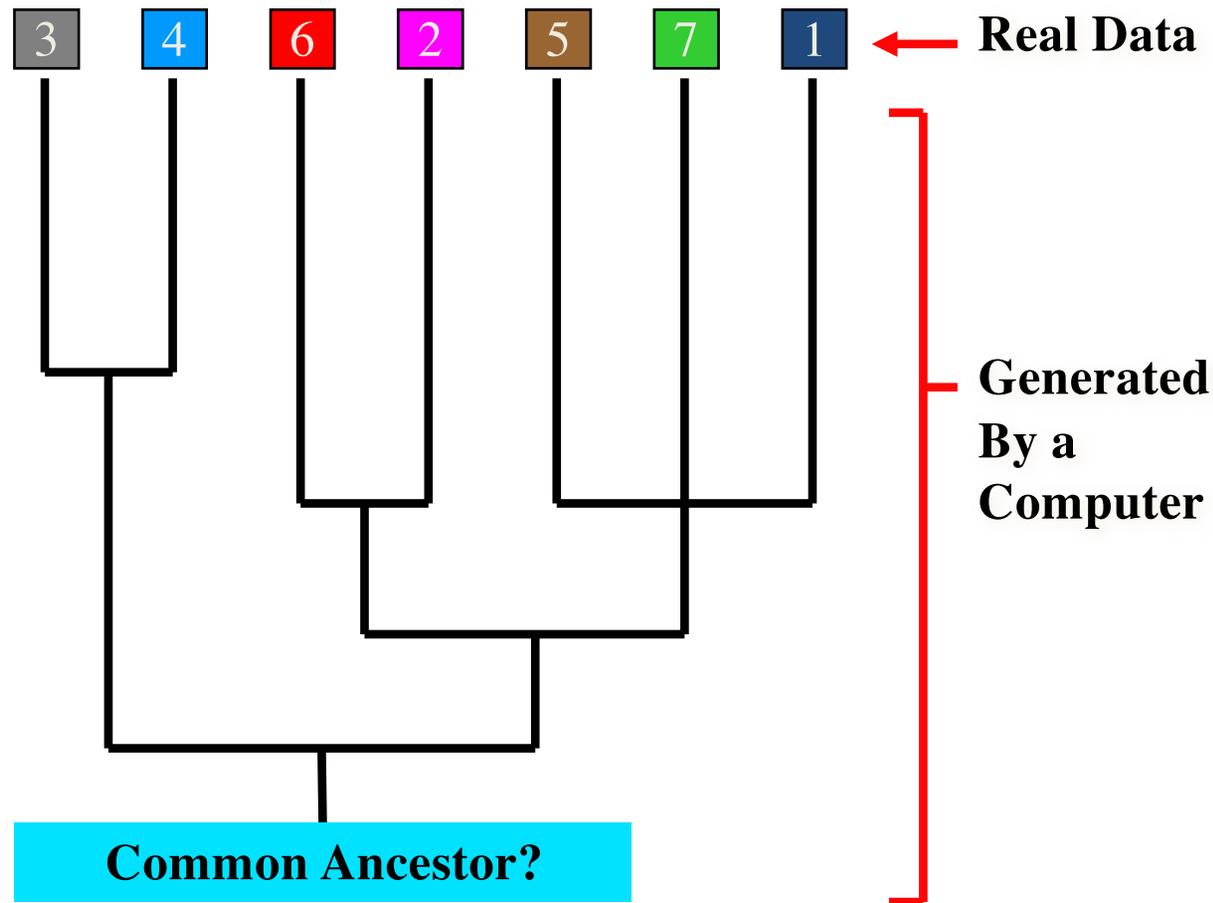


Birgitta Winnepeninckx, et al., *Molecular Biology & Evolution* (1995)

In 2012, a team of four American evolutionary biologists concluded, “Incongruence between phylogenies [evolutionary trees] derived from morphological *versus* molecular analyses, and between trees based on different subsets of molecular sequences has become pervasive.”

Liliana Dávalos, Andrea Cirranello, Jonathan Geisler and Nancy Simmons, *Biological Reviews of the Cambridge Philosophical Society* (2012)

The problem is not just incongruence. The problem is that common ancestry must be **assumed** from the start. The data are fed into a computer that has been programmed ahead of time to construct a tree.



Aggravating the problem is the recent discovery of “**orphan genes.**” (I’m using “gene” here to mean a protein-coding sequence of DNA, though as Dr. Sternberg will tell you tomorrow this definition is problematic.) An “orphan gene” is restricted to one group of organisms; it has no detectable similarity to genes in other groups.

There are “large numbers of genes that have no detectable homology outside a very small set of highly related species. Such genes are found in the [DNA] of every new species examined,” and usually make up 10% - 20% of all genes in the organism.

**Verster, Styles, Mateo, Derry, Andrews, and Fraser,
Genes, Genomes, Genetics (2017)**

“Why, if proteins in different organisms have descended from common ancestral proteins..., do so many today show no similarity to each other?”

Daniel Fischer and David Eisenberg, *Bioinformatics* (1999)

Evolutionary biologists have proposed a number of hypotheses to try to explain how orphan genes might have originated, but they are only hypotheses.

The question remains unanswered.

Then how do biologists deal with orphan genes when constructing phylogenetic trees? The authors of a 2016 article about the phylogeny of insects dealt with them by ignoring them completely, discarding 40% of the DNA sequences from the fruit fly and 80% of the DNA sequences from the water flea.

Jeffrey Rosenfeld, Jonathan Foox, and Rob DeSalle, *Molecular Phylogenetics and Evolution* 97 (2016)

Universal Common Ancestry?

**So the molecular evidence,
like the evidence from
fossils, embryos, homology,
and biogeography, fails to
demonstrate universal
common ancestry.**

Universal Common Ancestry?

My biggest problem with universal common ancestry is that, so far, we have observed common ancestry only within existing species (microevolution).

Universal Common Ancestry?

In 1997, evolutionary biologist Keith Stewart Thomson wrote: “A matter of unfinished business for biologists is the identification of evolution's smoking gun,” and “the smoking gun of evolution is speciation [the origin of new species].” Before Darwin, the consensus was that species can vary only within certain limits; indeed, centuries of artificial selection had seemingly demonstrated such limits experimentally. “Darwin had to show that the limits could be broken,” wrote Thomson, “so do we.”

Keith Stewart Thomson, *American Scientist* (1997)

Universal Common Ancestry?

Despite the title of his 1859 book, Darwin never solved the “mystery of mysteries,” as he called the origin of species. And it is still a mystery.

“The origin of species – Darwin’s problem – remains unsolved.”

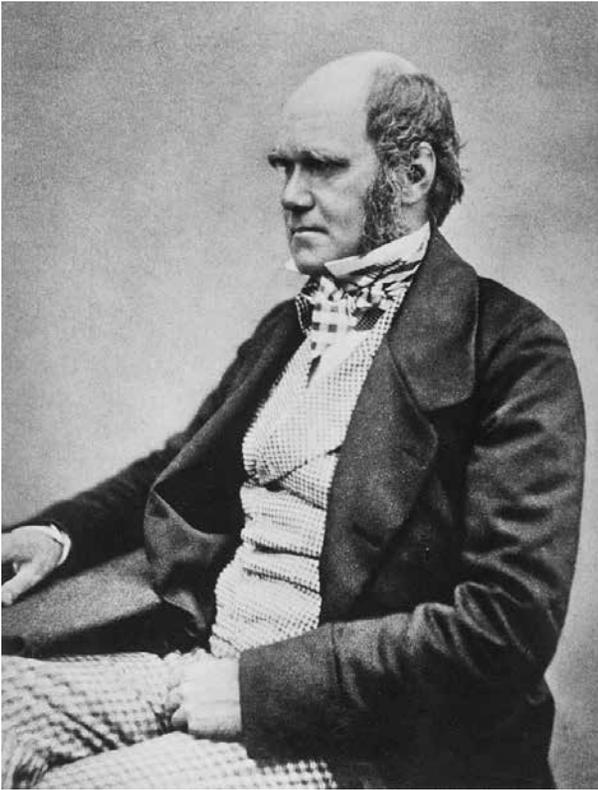
Biologists Scott Gilbert, John Opitz, and Rudolf Raff,
Developmental Biology (1996)

Universal Common Ancestry?

Since common ancestry has been observed only within existing species,* why should we assume that all species share common ancestry?

*** With the exception of speciation due to chromosome doubling, which has been observed in plants, but which cannot account for the open-ended divergence required for macroevolution.**

Universal Common Ancestry?



Charles Darwin

Letter to Charles Lyell (1859)

For Darwin, universal common ancestry was an expression of his materialistic philosophy:

“I would give absolutely nothing for [my theory], if it require miraculous additions at any one stage of descent.

CONCLUSIONS

- Neither fossils, nor embryos, nor homology, nor biogeography, nor molecules confirm universal common ancestry.

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My question is, why should we assume universal common ancestry?



