

Welcome to Comparative Genomics!

The purpose of this course is to familiarize informatics students with methods and theories behind comparative genomics.

- We will focus on the analysis of genomic sequences, including sequencing technologies, genome assembly, functional and structural predictions, and comparisons at macroevolutionary timescales in a phylogenetic context
- Special emphasis is on building practical skills in computational biology.

Course webpage: <https://github.com/marctollis/INF415-515-Comparative-Genomics/>

Class Hours: MoWeFri@ 12:40-1:30pm, FrankeCollBusiness Rm 345

Tollis Office Hours: TMoWeFri 2:00-2:30pm

<https://nau.zoom.us/j/88304470430>

Meeting ID: 883 0447 0430

Password: 816204

In-person format, NAU Flex-enabled.

The work

Readings

- Primary literature, assigned for most classes
- Everyone does one 10 min Presentation, lead class discussion
- If there are too many students, I can assign papers

Lectures

- Based on the module topics

Quizzes

- Based on both lectures and readings
- 12 total (low stakes), drop lowest two grades

Labs

- Focusing on computing and commonly used tools in genomics

Projects and Presentations

- Present a project based on course topics that will help your thesis
- When it's your turn to present, upload your PP to the assignment in the Content Area

Course logistics

Class time will be for:

- Lectures, presentations, discussion
- Labs - instructor goes line by line with the code, you emulate, we work on troubleshooting
 - Schedule is somewhat open, to add some breathing room
 - Labs are due a few weeks so you have time to go back and work on them.

Resources: computing

- Bring laptop to each class (duh)
- Terminal, command line, Monsoon
- Fill out computing survey
- Consider software carpentry link if you have no experience

Prerequisites and Resources

Prerequisites

- No course requirements
 - but general BIO, genetics/evolution will help
- Access to a laptop
- Familiarity with UNIX commands, but we will help

Texts

- no textbooks, we will study primary literature

Other resources:

- Google, SEQanswers, Biostars, StackOverflow
- <https://github.com/quinlan-lab/applied-computational-genomics>
- <http://www.langmead-lab.org/teaching-materials/>

INF 515

Assignment	Weight	Assignment Points (1000 total)
Attendance	10%	100
Participation	10%	100
Paper Discussion	10%	100
Computational Labs	30%	300
Project Proposal	2%	20
Quizzes	20%	200
Final Project	18%	180

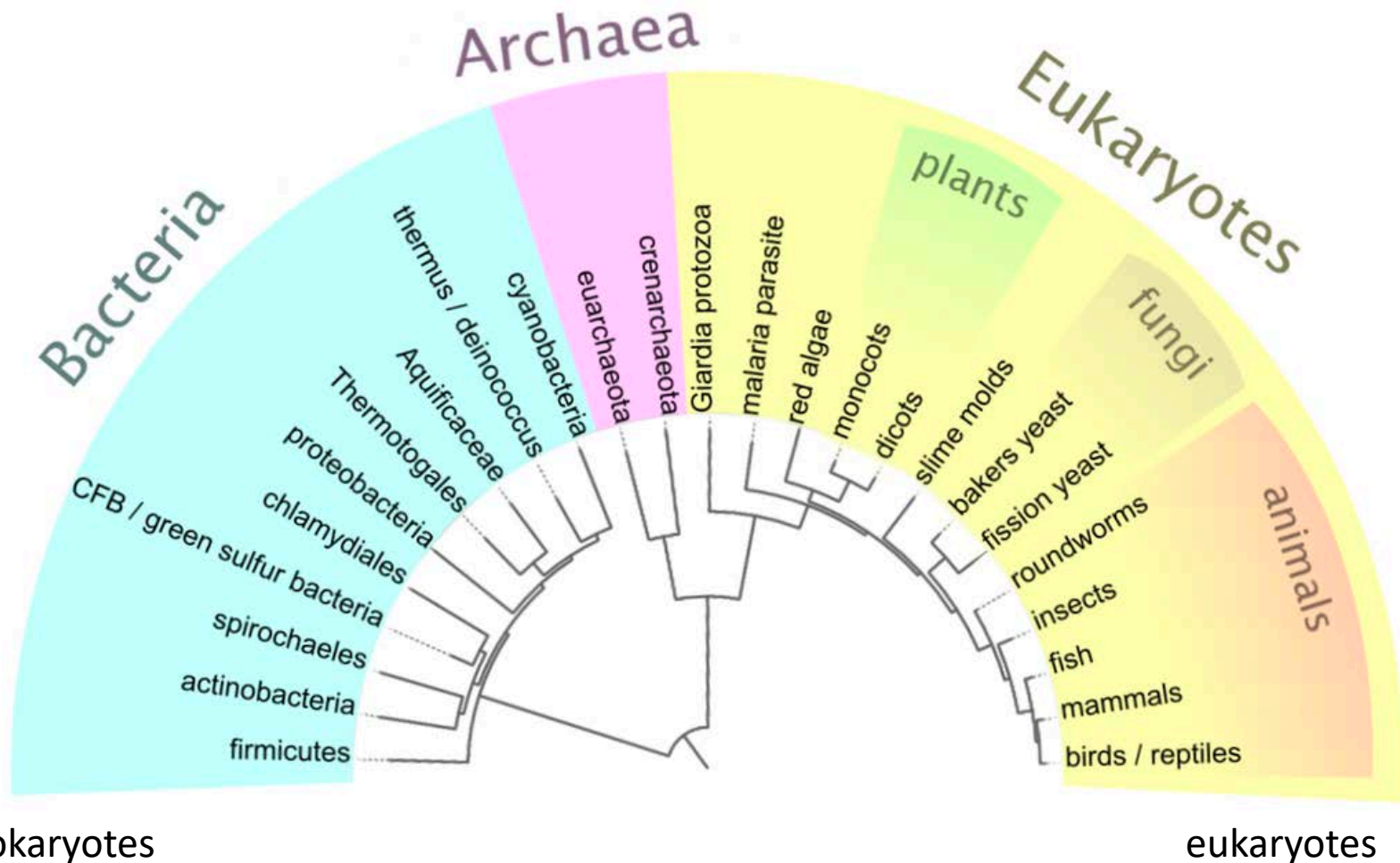
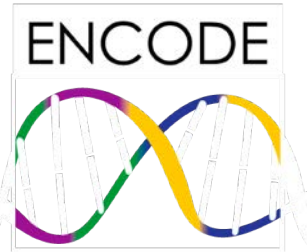
DNA: The Building Blocks of Life

DNA combines with
environment to shape
who you are

- Height, hair, eye color, skin color, shape
- Disease susceptibility and response to treatment
- Life and death: longevity, cognition



Across the Tree of Life







“Nothing makes sense in biology except in the light of evolution”
--Theodosius Dobzhansky



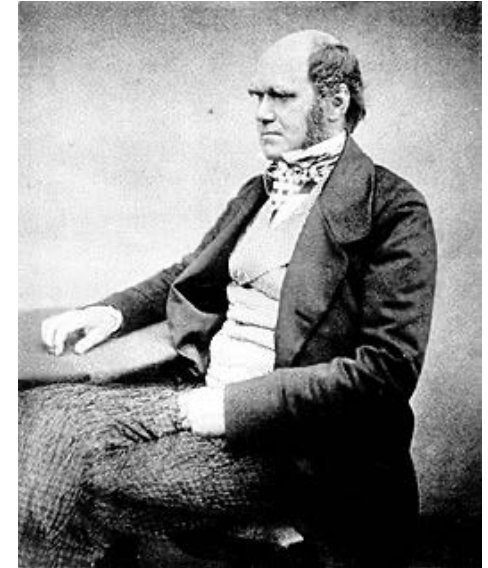
Evolution by Natural Selection

On the tendency of species to form varieties; and on the perpetuation of varieties and species by natural means of selection.

Darwin CR, Wallace AR. 1858. *Journal of the Proceedings of the Linnean Society of London.*

On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life.

Darwin, CR. 1859. Londn, John Murray.



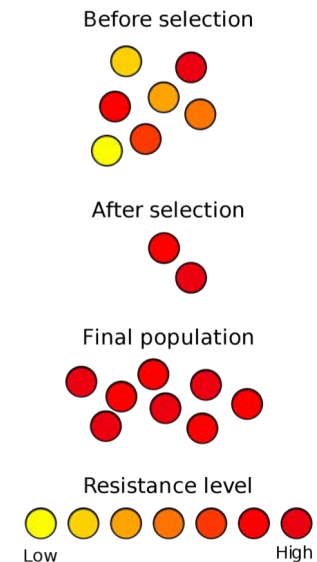
Charles Darwin, age 51

Variations in form are heritable and result in ***differential reproductive success.***

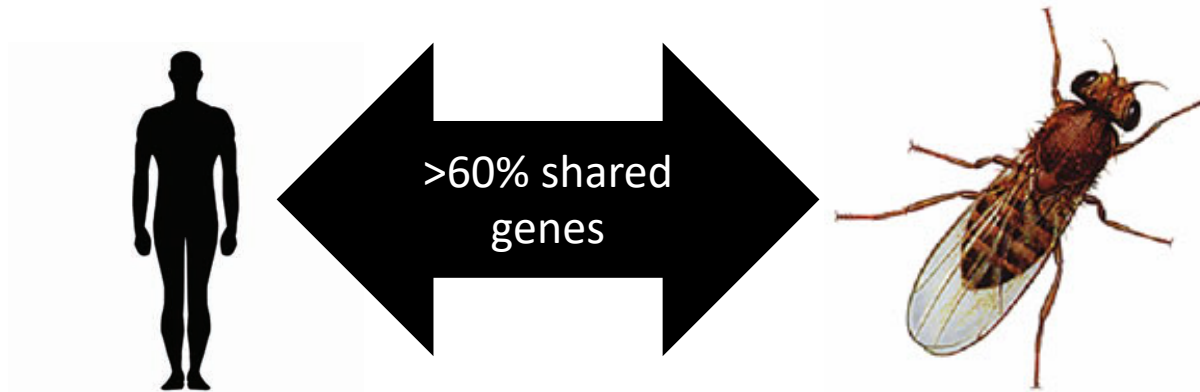
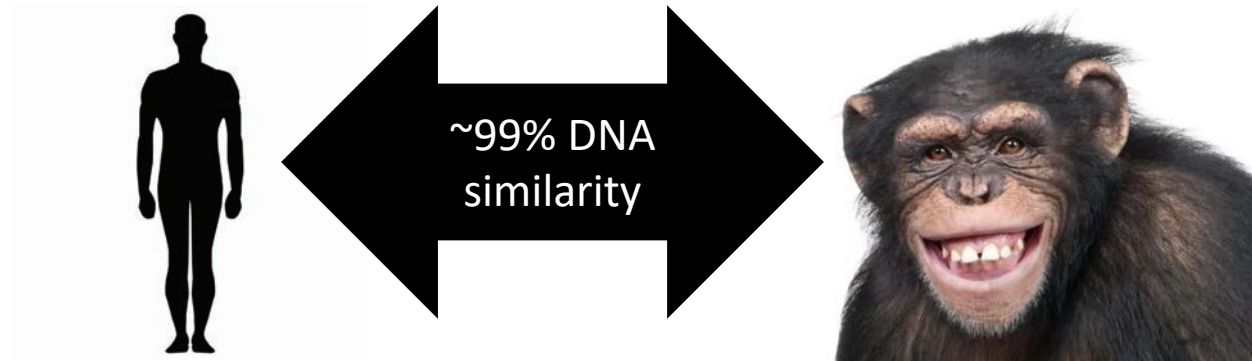
These successful variations are perpetuated and increase in frequency with each subsequent generation.

Differences between populations grow over time until they are reproductively isolated – ***forming new species.***

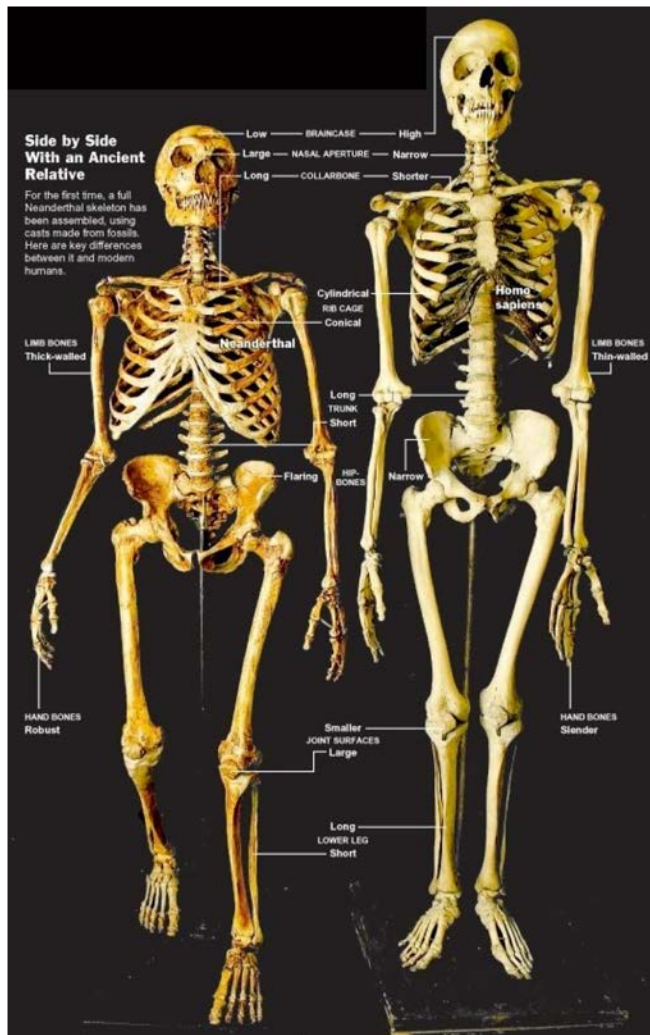
Also key: all lifeforms have descended from a ***common ancestor.***



What is Comparative Genomics?

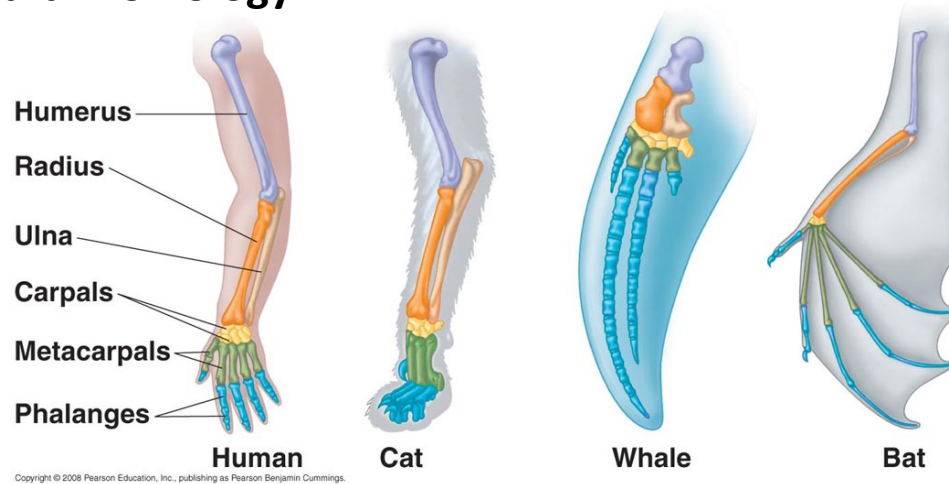


From Morphology to Genomics



Homology and Bioinformatics

Structural Homology:

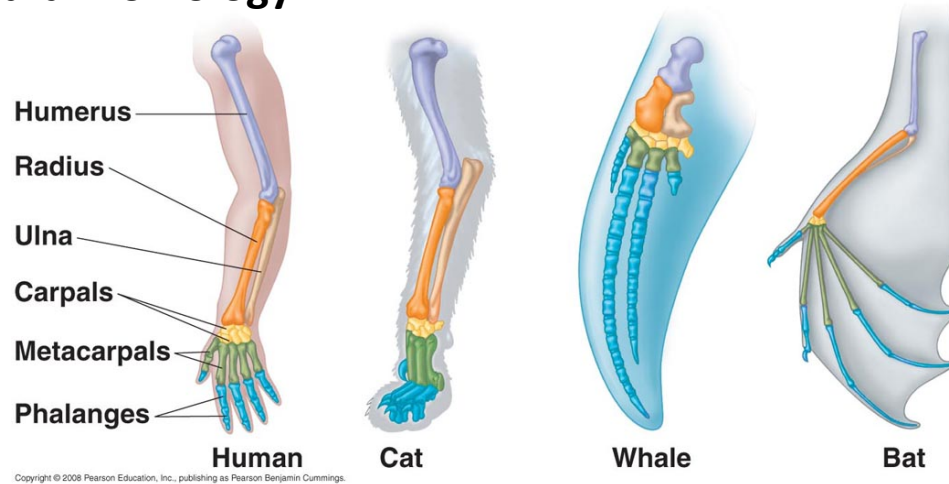


Sequence Homology (Alignment):

```
Human  KKASKPKKAASKAPTKKPKATPKATPVKKAKKKLAAT
Mouse  KKAAKPKKAASKAPSKKPKATPKATPVKKAKKKPAAT
Rat    KKAAKPKKAASKAPSKKPKATPKATPVKKAKKKPAAT
Cow    KKAAKPKKAASKAPSKKPKATPKATPVKKAKKKPAAT
Chimp  KKAAKPKKAASKAPSKKPKATPKATPVKKAKKKLAAT
      ***:*****:*****
```

Homology and Bioinformatics

Structural Homology:

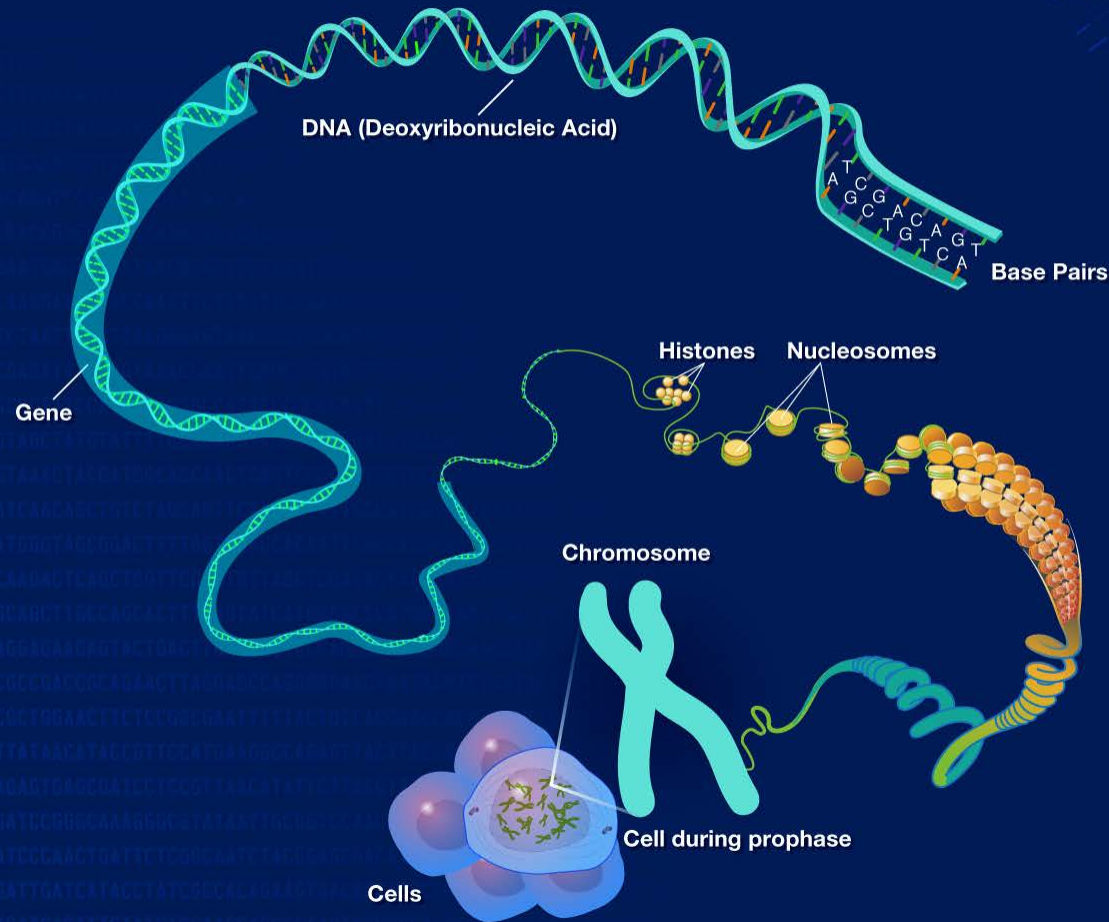


Sequence Homology (Alignment):

Human	KKAS	KPKKAASKAP	T	KKPKATPKATPVKKAKKK	L	AAT
Mouse	KKAA	KPKKAASKAP	S	KKPKATPKATPVKKAKKK	P	AAT
Rat	KKAA	KPKKAASKAP	S	KKPKATPKATPVKKAKKK	P	AAT
Cow	KKAA	KPKKAASKAP	S	KKPKATPKATPVKKAKKK	P	AAT
Chimp	KKAA	KPKKAASKAP	S	KKPKATPKATPVKKAKKK	L	AAT
	***	:	*****	:	*****	***

A Brief Guide to Genomics

NHGRI FACT SHEETS
genome.gov



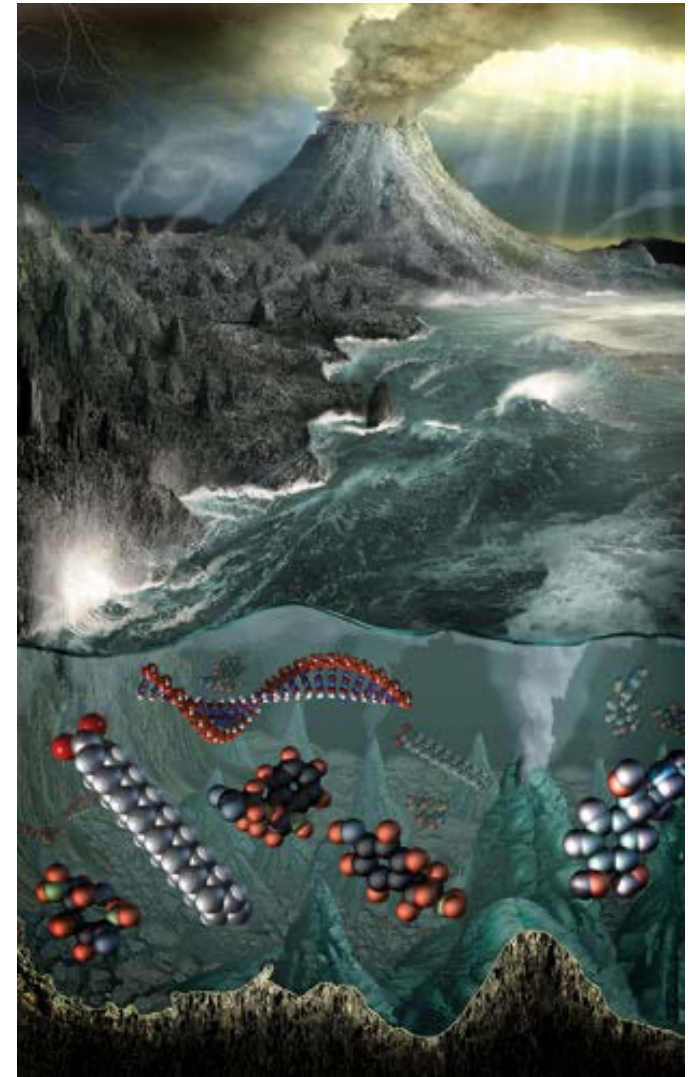
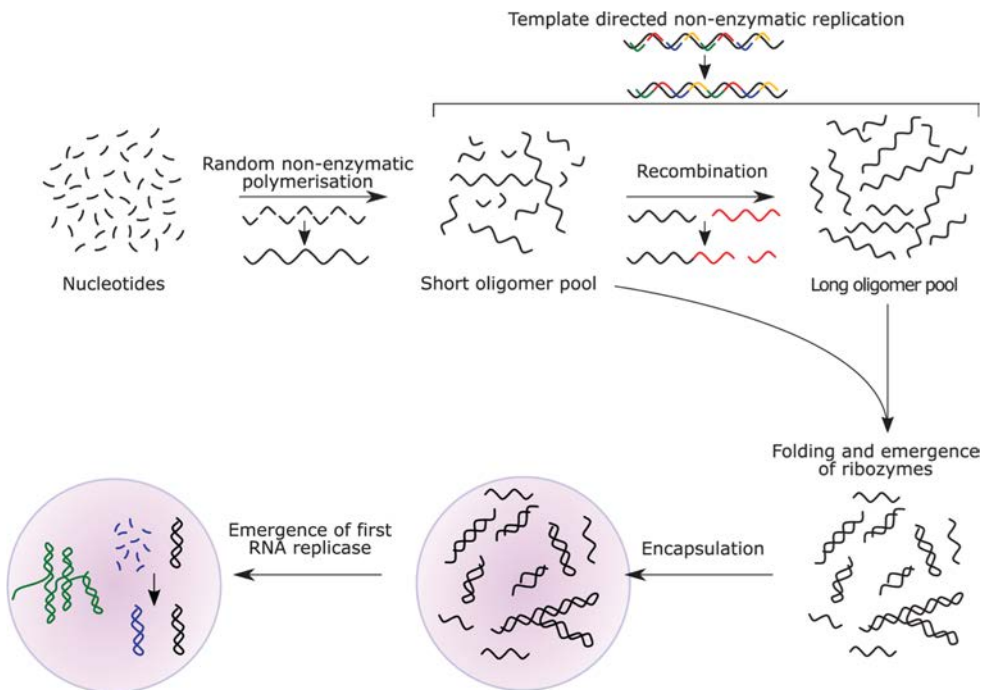
NIH National Human Genome Research Institute

- **genome**: all the genetic material of an organism
- 1920 by Hans Winkler
- Combination of gene and chromosome

The origins of the genome

RNA World (Rich, 1962)

- RNA stores information
- behaves as a catalyst
- possible to transfer DNA to RNA viruses
- this may have stimulated the move to a DNA world



The origins of the genome

Informational genes process protein synthesis and RNA transcription

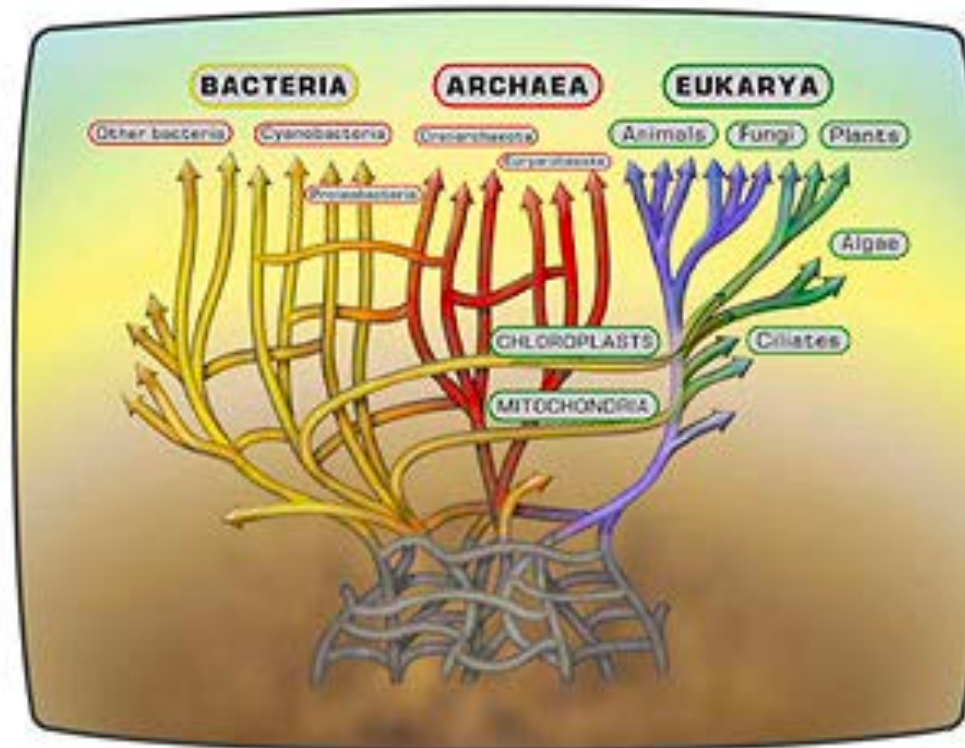
- They may have originated in an RNA world

Operational genes perform cellular functions such as making cell walls and synthesizing amino acids

Both of these types of genes are found in all eukaryotes and prokaryotes

Rivera et al. 1998 Genomic evidence for two functionally distinct gene classes. *PNAS*

The origins of the genome

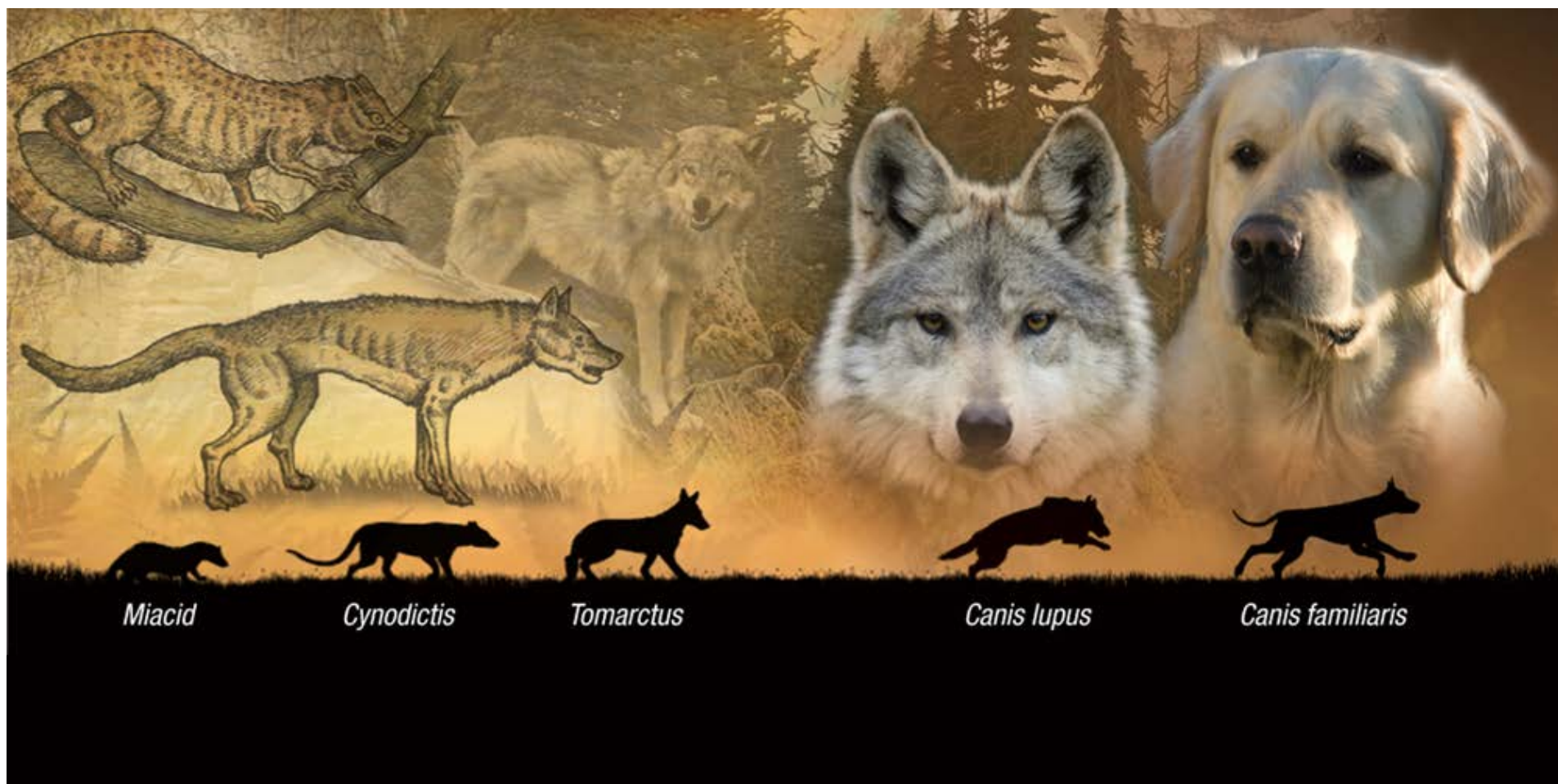


Lateral gene transfer at the base of the tree of life
Is there even a tree of life?

Earliest Genomics Experiments

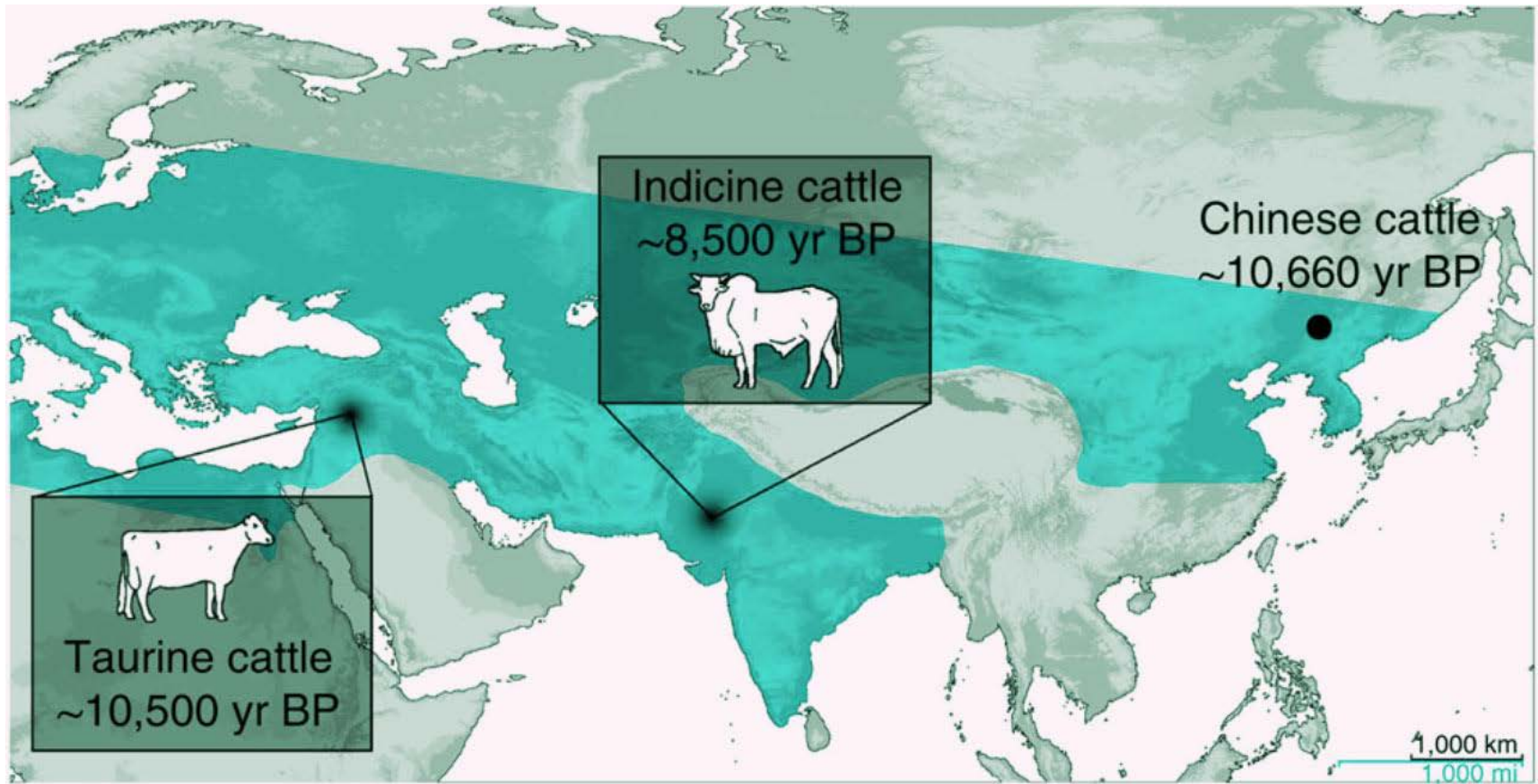
?

Earliest Genomics Experiments

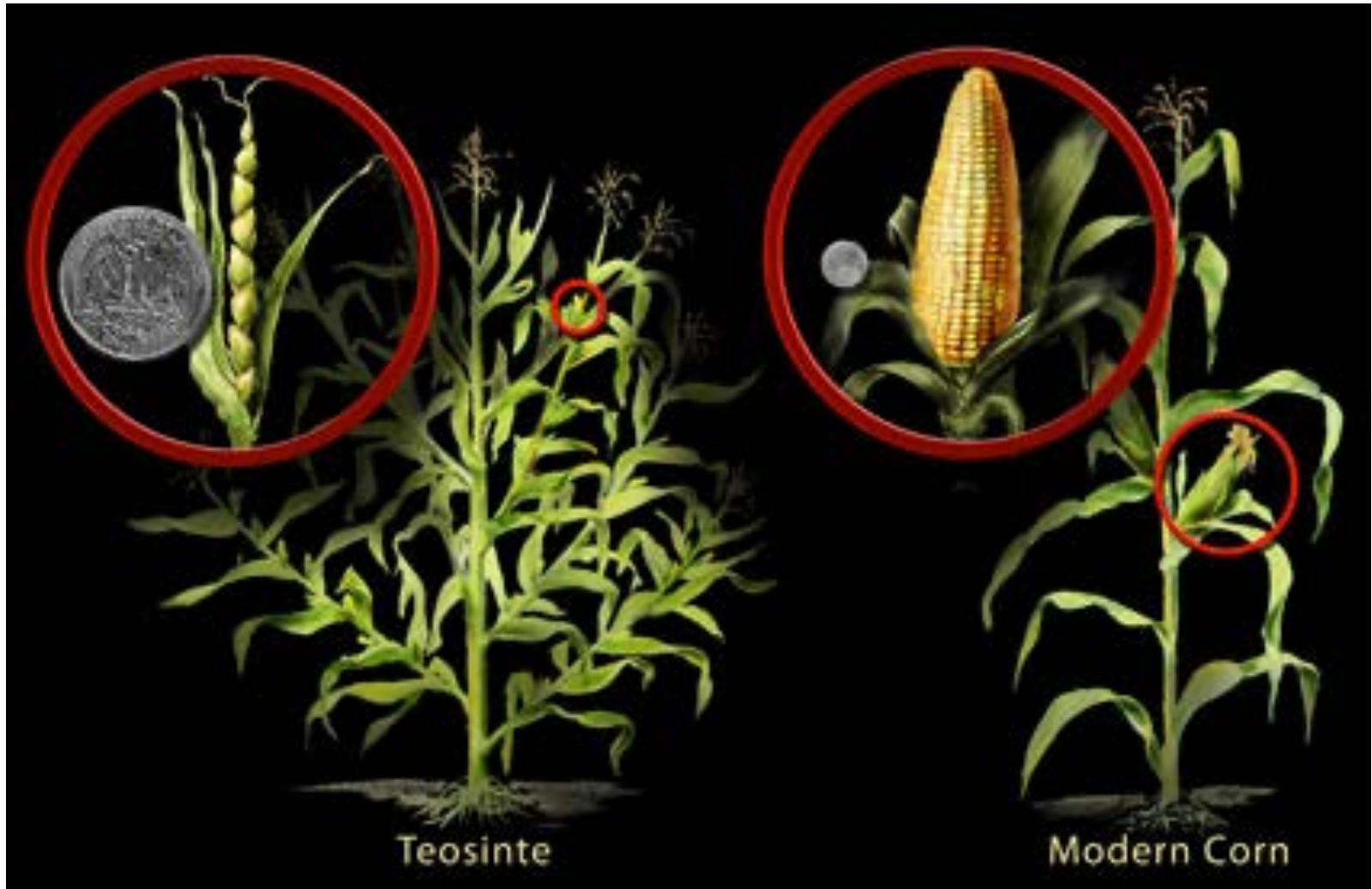


15,000 to 35,000 years before present

Earliest Genomics Experiments



Earliest Genomics Experiments

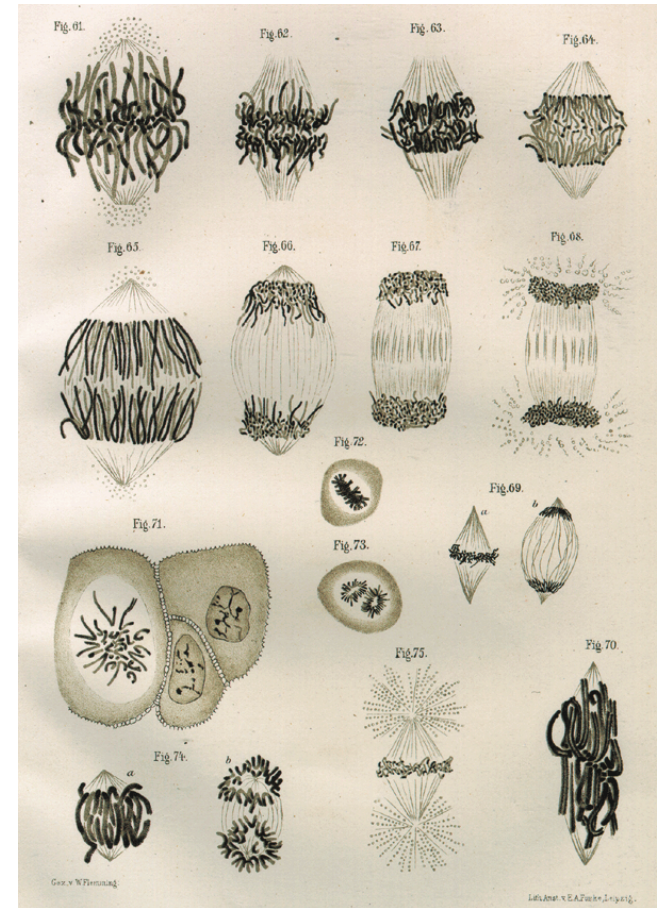


6,000 to 10,000 year before present

Discovery of chromosomes

Mid-19th century: with proper staining techniques, microscopes could observe structures that were involved in cell division.

‘Chromosome’ comes from the Greek words for ‘colored body’

















Drawing of mitosis, Walther Flemming.

Flemming. 1882. *Zellsubstanz, Kern und Zelltheilung* (Cell Substance, Nucleus and Cell Division)







Laws of inheritance

1. Law of Dominance
2. Law of Segregation
3. Law of Independent Assortment

Characteristics of pea plants Gregor Mendel used in his inheritance experiments							
Seeds		Flower colour	Pod		Stem		size
form	cotyledons		form	colour	position of inflorescences	size	
 round roundish	 yellow	 white	 full	 yellow	 axial	 long	
 wrinkled	 green	 violett-red	 constricted between the seeds	 green	 terminal	 short	

Versuche über Pflanzen-Hybriden. Verh. Naturforsch (Experiments in Plant Hybridization)

Mendel, G. (1866). Ver. Brünn 4: 3–47 (in English in 1901, J. R. Hortic. Soc. 26: 1–32).

		 pollen ♂	
		B	b
 pistil ♀	B	 BB	 Bb
	b	 Bb	 bb

First genetic maps

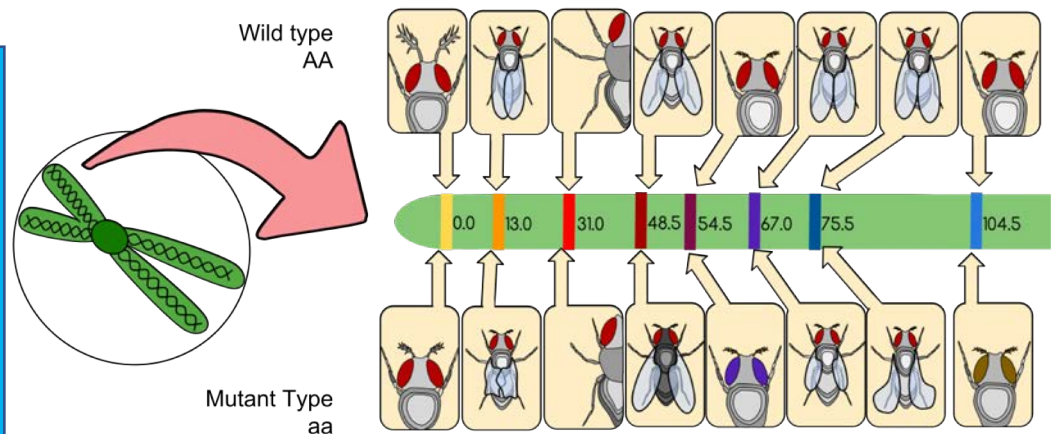
Mendel's Law of Independent Assortment states that alleles of a gene sort into gametes independently of other genes

Sturtevant and Morgan discovered that the probabilities of co-occurrences of traits are due to the distance between the genes along the chromosome – ***the genes are linked***.

Traits that are commonly observed together are literally near each other.

***The Linear Arrangement
of Six Sex-Linked Factors in
Drosophila as shown by
their mode of Association***

Sturtevant, A. H. (1913)
Journal of Experimental
Zoology, 14: 43-59



Jumping genes

Early geneticists thought genes were stable entities arranged linearly along a chromosome like beads on a string

The discovery of transposable elements showed that some genes can move or copy themselves

The movement of these elements during meiosis had an effect on many traits – ***and revealed genetic regulation for the first time.***

More than half of the human genome is comprised of transposable elements.

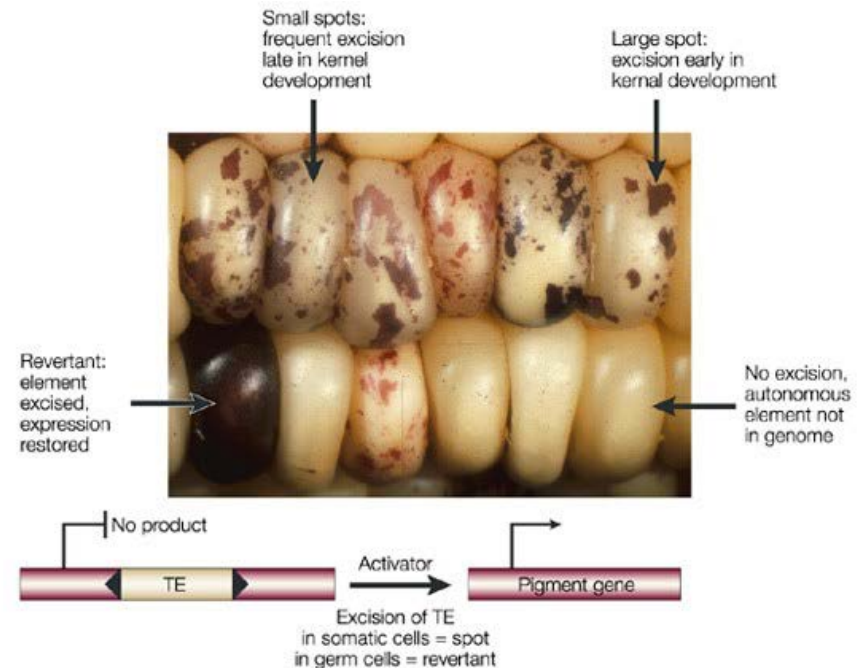
The origin and behavior of mutable loci in maize.

McClintock, B. (1950) PNAS. 36(6):344–355.



Barbara McClintock,
Winner of Nobel
Prize in Physiology or
Medicine (1983)

(wikipedia)



DNA

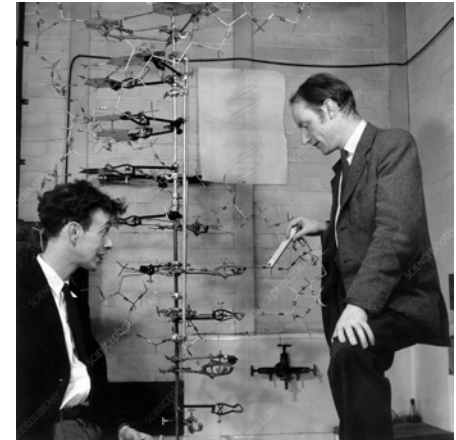
Identified in 1869 by Friedrich Miescher in human WBCs

1944 Avery – hereditary units (**genes**) are made of DNA

Chargaff (1950) described a “chemistry of heredity” – found that DNA varies across species

Watson and Crick – initially credited with discovery of the **double helix**

Rosalind Franklin took the **X-ray crystallography** photographs that proved it



Watson and Crick, 1953



Rosalind Franklin, 1958

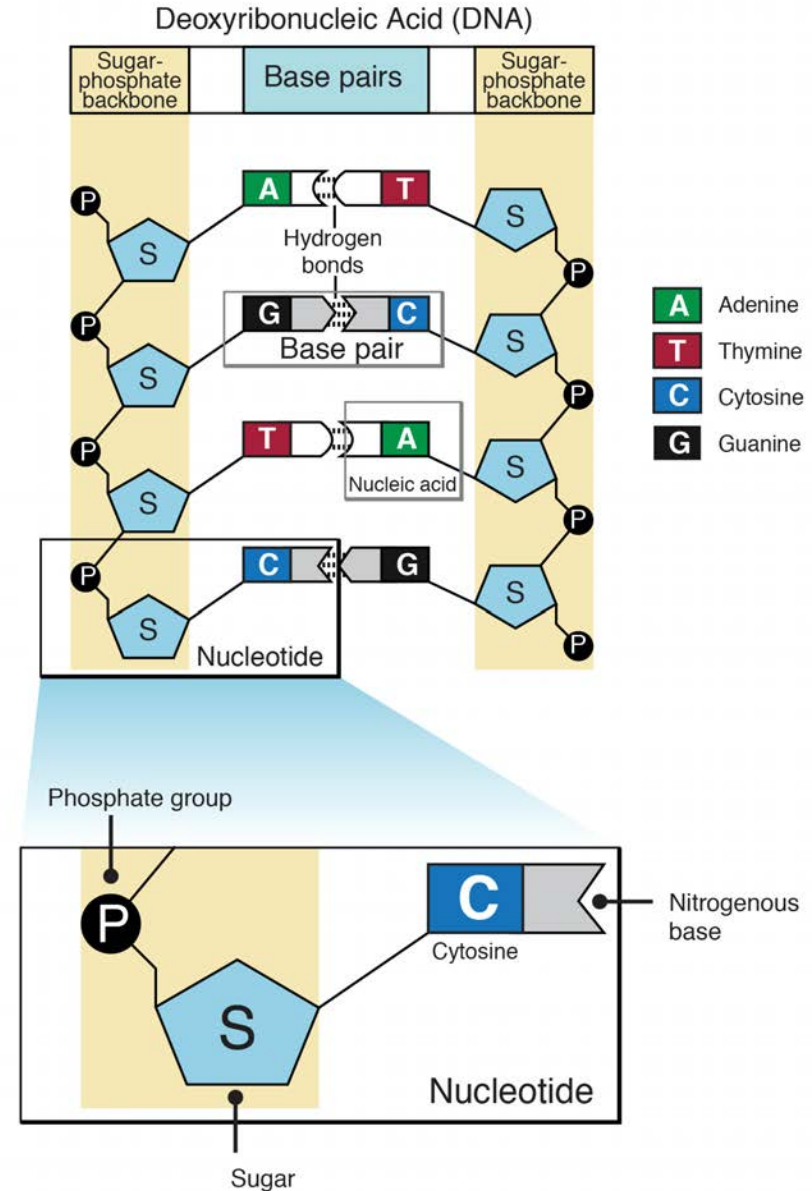
Molecular structure of nucleic acids; a structure for deoxyribose nucleic acid

Watson JD, Crick FH (1953). *Nature* 171: 737–738.

Nobel Prize in Physiology or Medicine in 1962

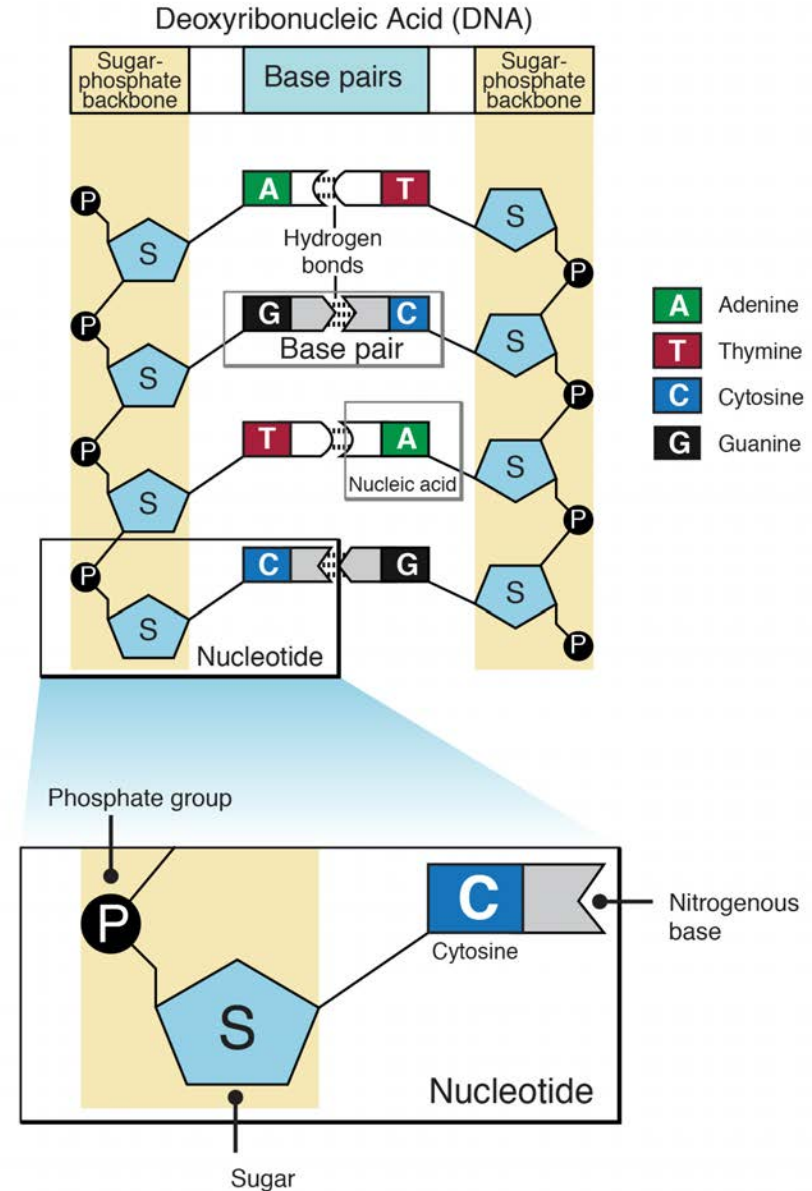
DNA

- Deoxyribonucleic acid
 - A molecule made of two nucleotide chains coiled around each other (double helix)
 - each nucleotide contains a sugar attached to a phosphate group, and a nitrogen containing base.
 - adenine (A)
 - cytosine (C)
 - guanine (G)
 - thymine (T)



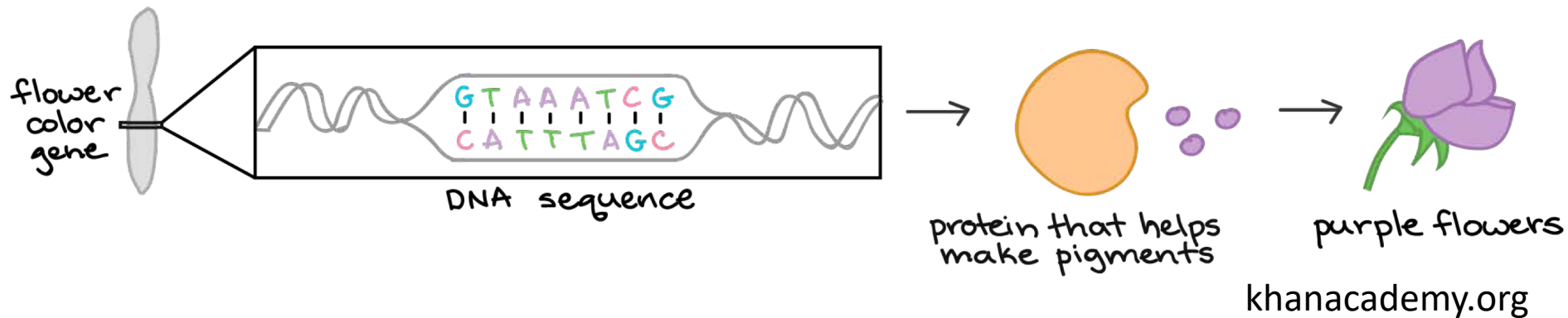
DNA

- RNA is composed of nucleotides too.
 - uracil replaces thymine
- each nucleotide has a complement that it fits into like a lock-and-key with a hydrogen bond in order to complete the double helix.
 - A \leftrightarrow T
 - G \leftrightarrow C
- This is called base pairing.
 - base vs base pair (bp)



The Central Dogma of Molecular Biology

“Once 'information' has passed into protein it cannot get out again. In more detail, the transfer of information **from nucleic acid to nucleic acid, or from nucleic acid to protein may be possible**, but transfer from protein to protein, or from protein to nucleic acid is impossible. Information means here the precise determination of sequence, either of bases in the nucleic acid or of amino acid residues in the protein”

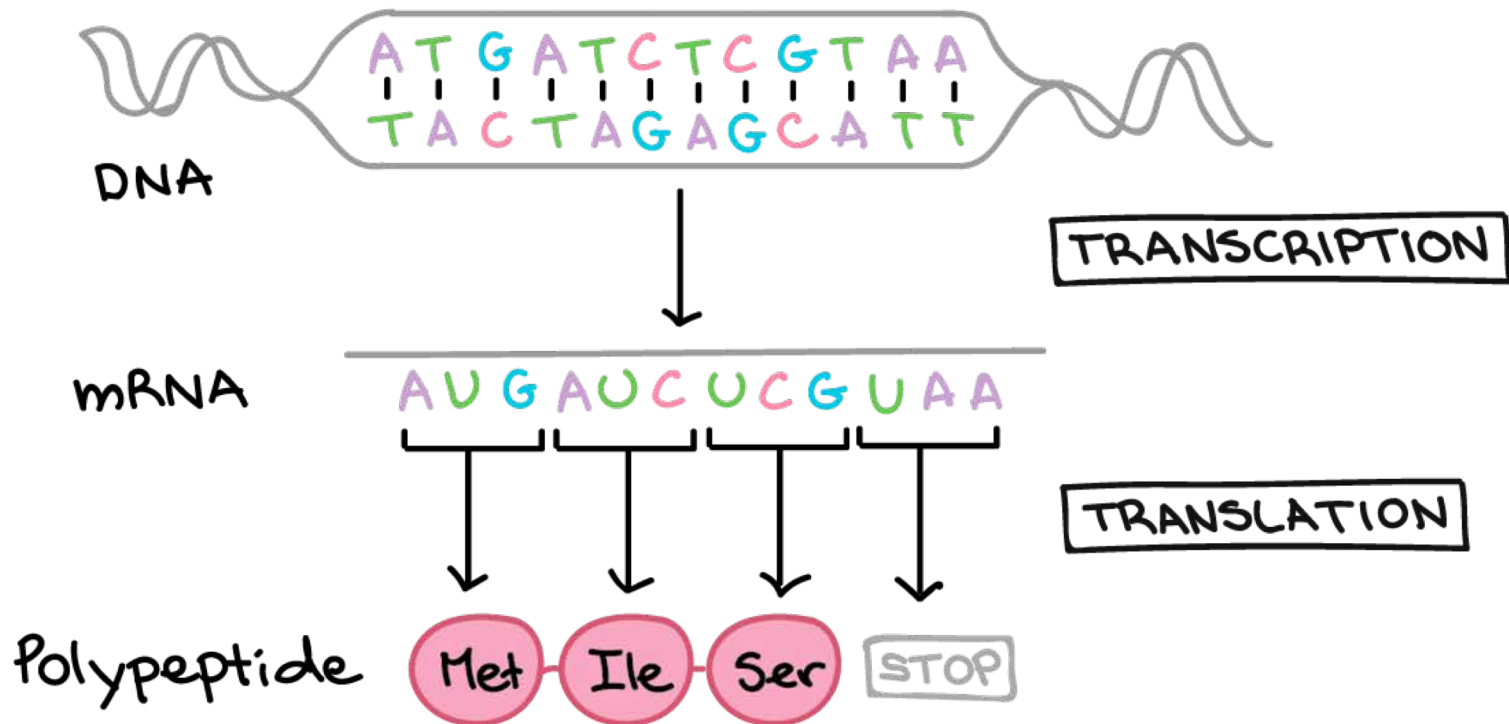


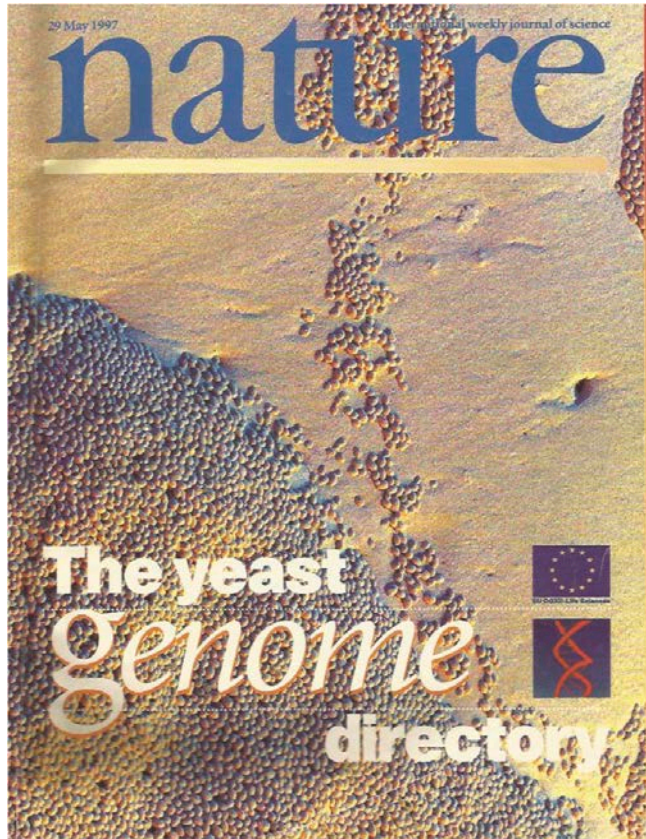
On Protein Synthesis

Crick, F.H.C. (1958). Symposia of the Society for Experimental Biology pp. 138–163.

“DNA makes RNA makes protein”

THE CENTRAL DOGMA





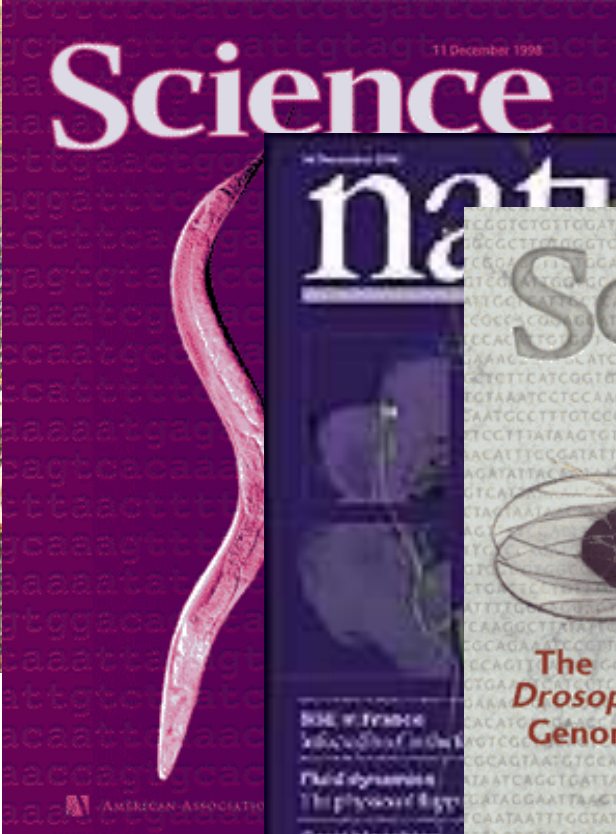
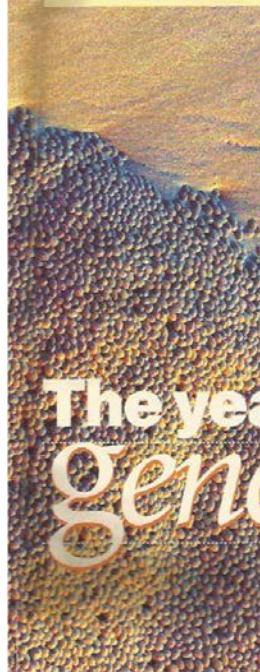
1997: *Saccharomyces cerevisiae* (12Mb)



1998: *Caenorhabditis elegans* (97Mb)



2000: *Arabidopsis thaliana* (115 Mb)



2000: *Drosophila melanogaster* (120 Mb)



Lander et al. 2001



Venter et al. 2001

CLINIC

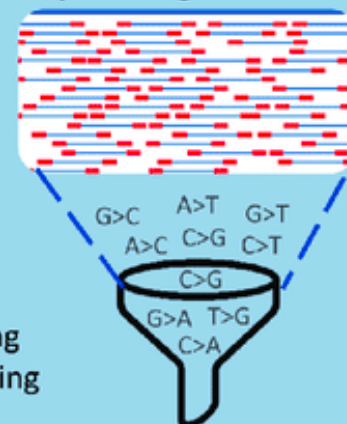
Pre-test appointment

- Medical history review
- Family history evaluation
- Physical exam
- Genetic counseling session
- Insurance considerations



LAB

Sequencing



Informatics

- Sequence alignment
- Variant calling
- Variant filtering

Variant classification

- Gene – phenotype association
- Variant analysis

Clinical genomic sequencing



Genome report

Post-test follow-up

- Medical decision making
- Re-phenotyping
- Familial segregation testing
- Input for decision support tools

Feedback to lab

- New phenotypic data
- Segregation study results



PATIENT

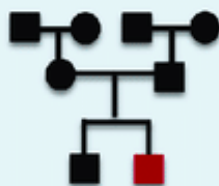
Indications

- Diagnostic
- *Family history of possible genetic disease**
- *Screening for genetic predisposition to disease or pharmacogenomics**

**Not routine clinical practice*

Applications

- Modified treatment
- Personalized disease surveillance
- Familial contextualization



CLINIC AND HEALTH CARE SYSTEM

De novo mutation discovery and validation

De novo mutations are sequences not inherited from your parents.

Reference: ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Father(1): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Father(2): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Mother(1): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Mother(2): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Sibling(1): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

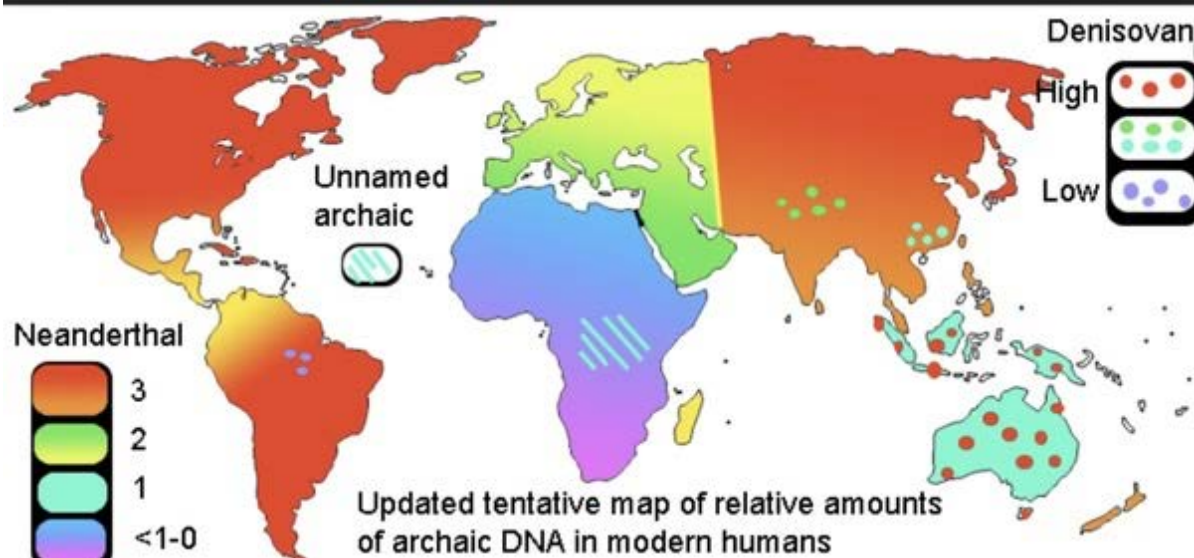
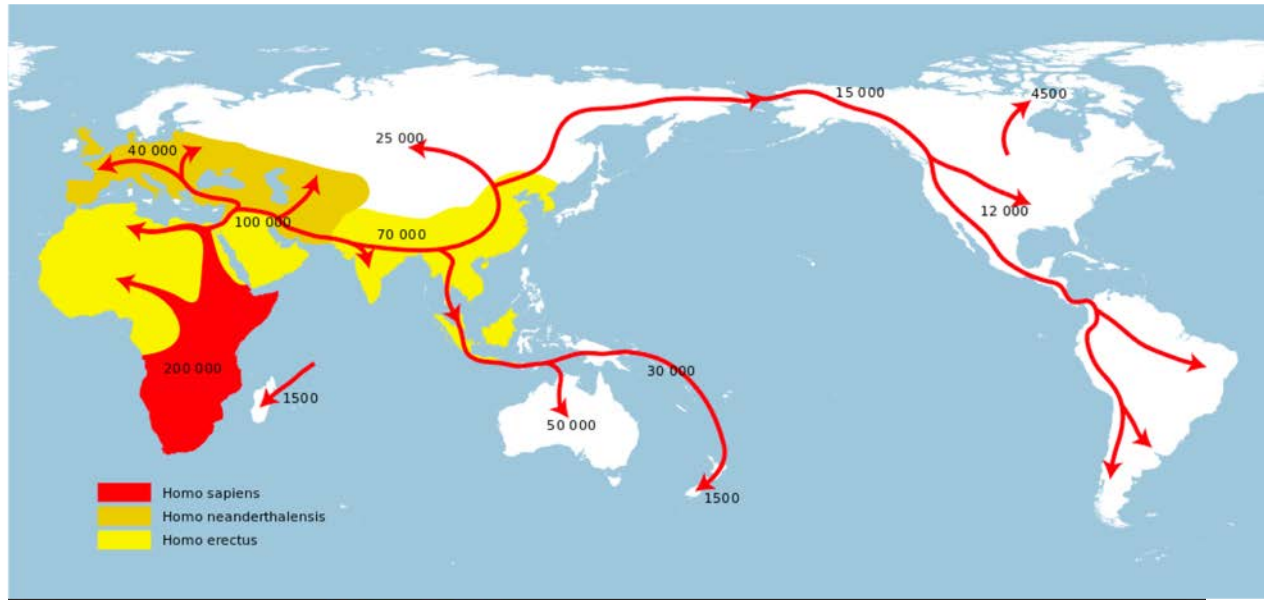
Sibling(2): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Proband(1): ...TCAAATCCTTTTAAATAAAGAAGAGCTGACA...

Proband(2): ...TCAAATCCTTTTAAAT***AAGAGCTGACA...

4bp heterozygous deletion at chr15:93524061 CHD2

Out of Africa: we contain Neanderthal DNA in our genomes



For the rest of this week

1. Reflect on the fact that we all share a bit of Earth's history within ourselves.
2. Sign up for presentation.
3. Add a thread to the Introductions Forum.
4. Fill out computing survey.
5. Read Shendure et al. 2017 – I will present.
6. Quiz 1 – will cover lecture and paper