

Chapter 1

Introduction, History of molecular Evolution

Welcome to the 2011 class

Chau-Ti Ting

ctting@ntu.edu.tw



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Course description:

This course is to introduce the fundamentals and methodology on research of molecular evolution. The topics include evolutionary changes and patterns of sequences and methods for phylogenetic analyses. Topics on recent advances of molecular evolution studies will be offered at the end, on phylogenomics, horizontal gene transfer, and genome evolution. Students are highly recommended to take evolution, genetics or equivalent subjects before taking this course. There are three laboratory practices for students being familiar with data retrieving and analyses. Several homework assignments will be distributed during the semester, which require substantial extra work time after the class.

Lecture

Wednesday 10:20~12:10, Life Science 419

Instructors

Chau-Ti Ting (丁照棣)

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Phone: 3366 2522

Jer-Ming Hu (胡哲明)

E-mail: jmhu_at_ntu.edu.tw

Phone: 3366 2472

Course website:

<http://ceiba.ntu.edu.tw/1002molevo>

Official language: English

Prerequisite: Biology; Evolutionary
Biology; Genetics or equivalent
preferred

Office hour: Wed 12:00-13:00, or with
appointments

Laboratory practice

We will have computers available to use on the class, but you are welcome to bring your own laptop computer. In the later case, you should download the corresponding softwares before the class. You are welcome to use your own data for the homework assignments.

TA

Grading

Midterm exam 25%

Final exam 30%

Homework 35%

Classroom performance 10%

Textbook

There is no required textbook for this class. Most of the lectures are based on selected chapters from the following books.

Suggested reading

Graur, D. and W.-H. Li. 2000. *Fundamentals of Molecular Evolution*. 2nd ed., Sinauer Assoc., Sunderland, MA, USA.

Hall, B. G. 2011. *Phylogenetic trees made easy: a how-to manual*, 4th ed. Sinauer Assoc., Inc., Sunderland, MA, USA.

Li, W.-H. 1997. *Molecular evolution*. Sinauer Associates, Sunderland, MA, USA.

Lynch, M. 2007. *The origins of genome architecture*. Sinauer Associates, Sunderland, MA, USA.

Fundamentals of Molecular Evolution

by Dan Graur and Wen-Hsiung Li, 2nd Edition (1999, Sinauer)

<http://www.sinauer.com/detail.php?id=2666>

Hall, B. G. 2011. Phylogenetic trees made easy: a how-to manual, 4th ed. Sinauer Assoc., Inc., Sunderland, MA, USA.

<http://www.sinauer.com/detail.php?id=6069>

Li, W.-H. 1997. *Molecular evolution*. Sinauer Associates, Sunderland, MA, USA.

http://books.google.com.tw/books/about/Molecular_evolution.html?id=2mPGQgAACAAJ&redir_esc=y

Lynch, M. 2007. The origins of genome architecture. Sinauer Associates, Sunderland, MA, USA.

<http://www.sinauer.com/detail.php?id=4843>

Molecular Evolution and Phylogenetics
by Masatoshi Nei, Sudhir Kumar
Oxford University Press (2000)

<http://www.oup.com/us/catalog/general/subject/LifeSciences/EvolutionaryBiology/?view=us0195135855>

Molecular Evolution : A Phylogenetic
Approach
by Roderic D. M. Page, Edward C. Holmes
Blackwell Science Inc. (1998)

<http://as.wiley.com/WileyCDA/WileyTitle/productCd-0865428891.html>

Integrated Molecular Evolution by
Scott O. Rogers (Jul 27, 2011)

http://www.crcpress.com/product/isbn/9781439819951;jsessionid=43hickpiklcWh5SL-z17dQ**

More reference book

Bioinformatics and Molecular Evolution by Paul Higgs and Teresa Attwood (Wiley-Blackwell, 2005)

*Computational Molecular Evolution by Ziheng Yang (Oxford University Press, 2006)

*Inferring Phylogenies (Paperback) by Joseph Felsenstein (Sinauer, 2003)

*Statistical Methods in Molecular Evolution by Rasmus Nielsen (Springer, 2005)

The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny Ed. by Marco Salemi and Anne-Mieke Vandamme (Cambridge University Press, 2003)

Journals

Cladistics (

http://www.blackwell-synergy.com/toc/cla/21/3;jsessionid=bfrbf_x_Qdkn8)

BMC Evol Biol (<http://www.biomedcentral.com/bmcevolbiol/>)

Evolution (<http://www.blackwell-synergy.com/loi/EVO>)

Evol Dev (<http://www.blackwell-synergy.com/loi/ede>)

Evol Bioinformatics (

http://la-press.com/journal.php?journal_id=17&issue_id=103)

Genome Biology (<http://genomebiology.com/home/>)

J Evol Biol (http://www.blackwellpublishing.com/jeb_enhanced/)

J Mol Evol (<http://www.springer.com/life+sci/cell+biology/journal/239>)

Mol Biol Evol (<http://mbe.oxfordjournals.org/>)

Mol Ecol (<http://www.blackwell-synergy.com/loi/MEC>)

Mol Phyl Evol (<http://www.sciencedirect.com/science/journal/10557903>)

Syst Biol (<http://www.informaworld.com/smpp/title~db=bisc~content=...uestlist>)



Related courses and workshops

NTU campus

Mathematical Molecular Evolution (221 U4730)

Molecular Evolution Laboratory (B44 U1630)

Population Genetics (B44 U1570)

Seminar in Molecular Evolution (B41 M0310)

Summer course on molecular phylogeny

Workshop on Computational Molecular Evolution (
<http://homepage.ntu.edu.tw/~ctting/CMB.html>)

Elsewhere

Summer Institute in Statistical Genetics

(<http://www.biostat.washington.edu/node/1020>)

Workshop on Molecular Evolution (

<http://workshop.molecularrevolution.org/mb/>)

Molecular Evolution

The evolution of macromolecules

- The rates and patterns of changes in the genetic material and its encoded products during evolutionary time
- The mechanisms responsible for such changes

Molecular phylogeny

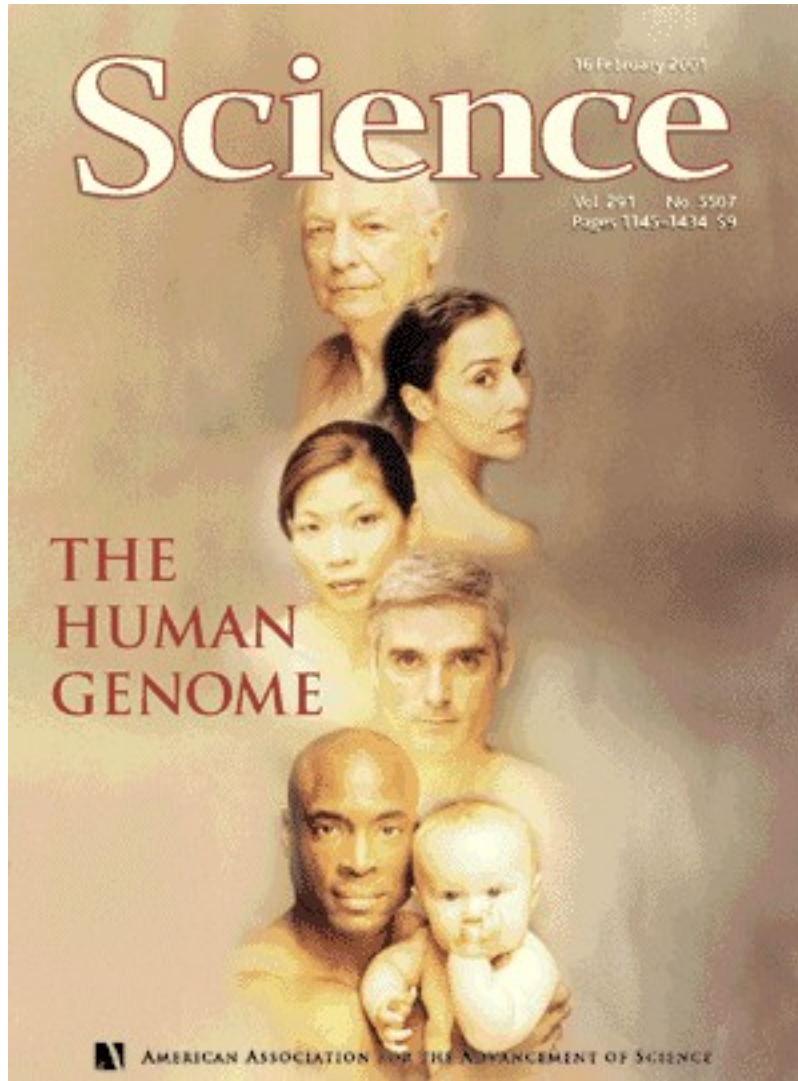
- The reconstruction of the evolutionary history of genes and organisms

Source: M. Prakash

2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 42. Discovery Publishing House. India.

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 Science /AAAS

Source: 2001. Science. Vol. 291. Issue 5507.

<http://www.sciencemag.org/content/291/5507.cover-expansion>

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The study of human evolution begins with your DNA.



 Carolina Biological Supply Company

Source: Carolina Biological Supply Company

<http://www.geneticorigins.org/>



1904

Nuttall conducted precipitin tests of serum proteins to infer the phylogenetic relationship among various groups of animals.

 Source: M. Prakash
2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 42. Discovery Publishing House. India.

George H. F. Nuttall
1904. Blood immunity and blood relationship. University press. Cambridge, England.

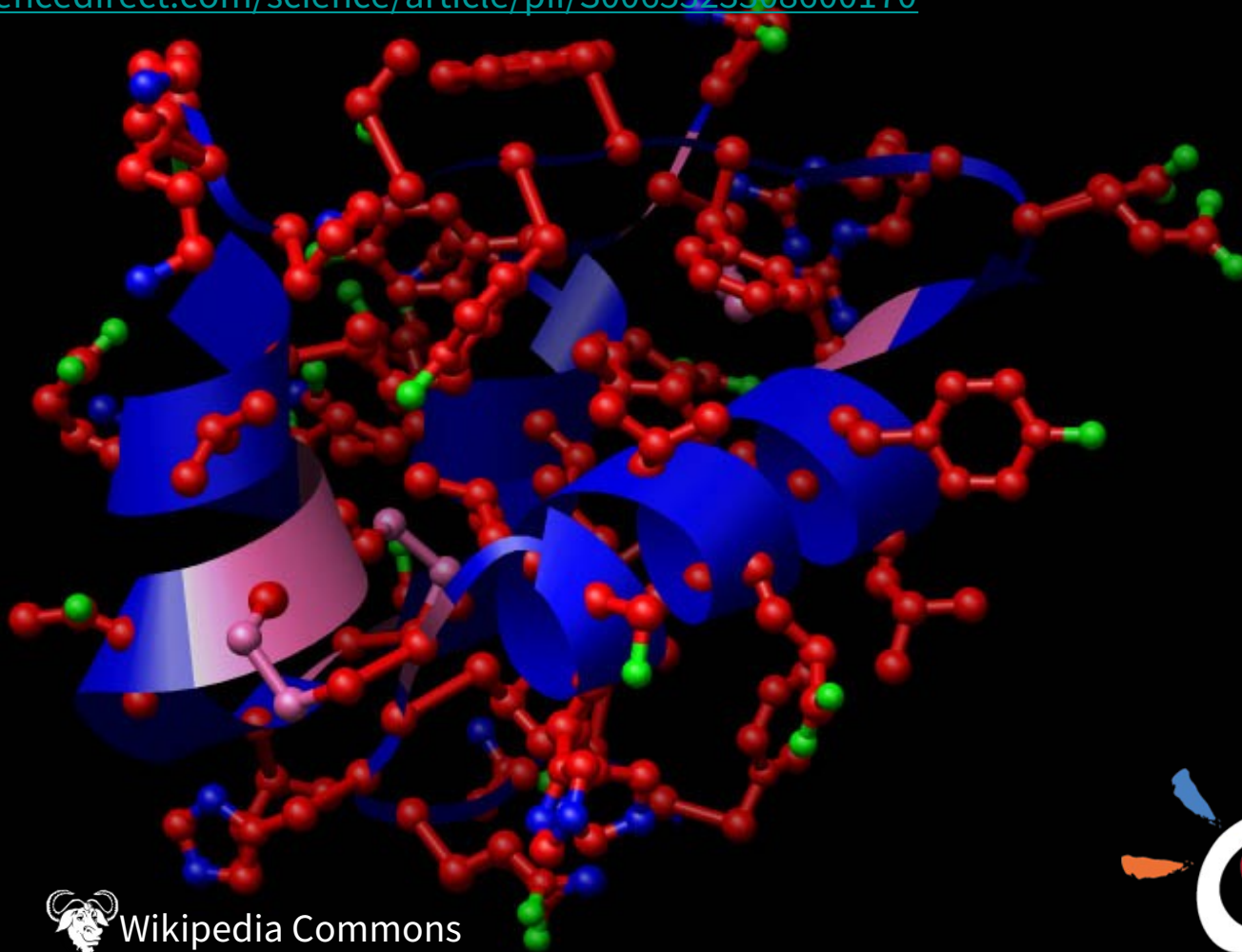
<http://www.biodiversitylibrary.org/title/8418#page/7/mode/1up>

1952

Sanger and colleagues complete first protein sequence – insulin

Sanger, F. 1952. The arrangement of amino acids in proteins. *Advances in Protein Chemistry*. 7: p.1-66.

<http://www.sciencedirect.com/science/article/pii/S0065323308600170>



Wikipedia Commons



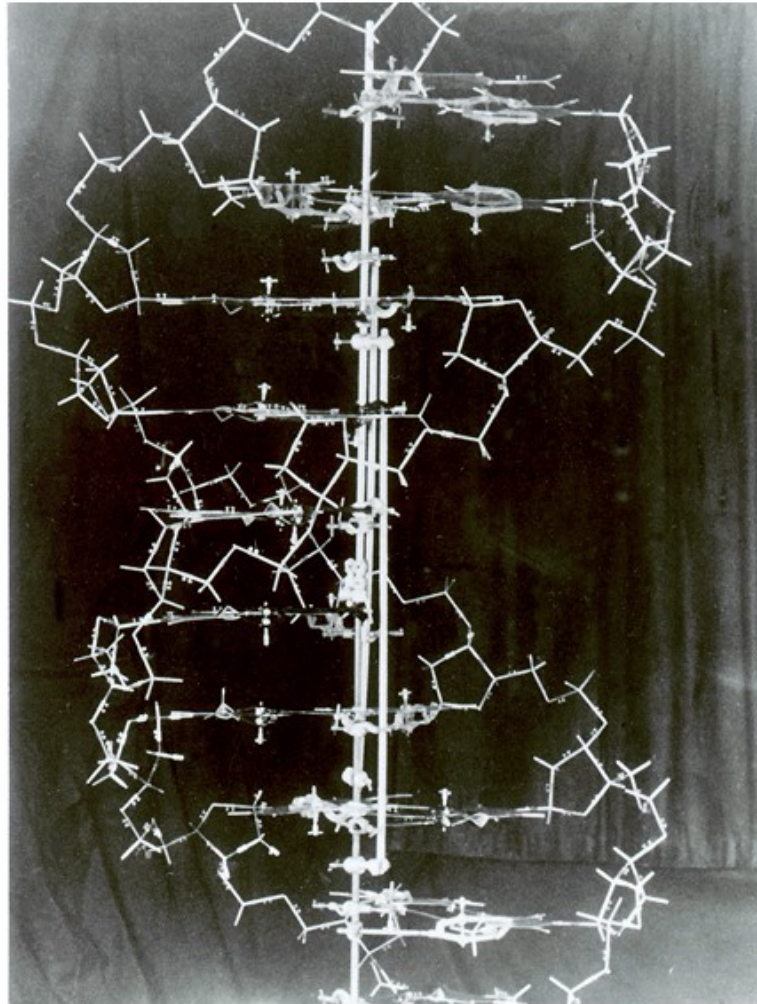
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1953



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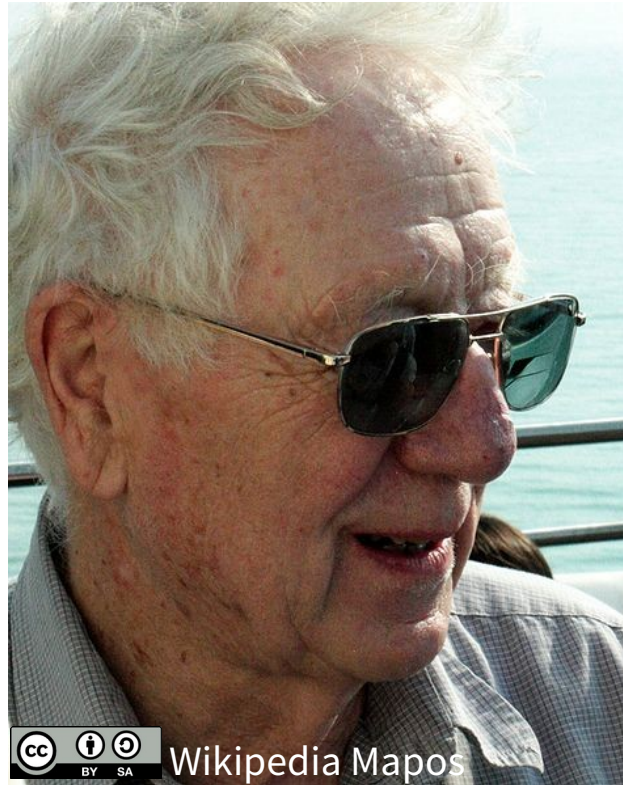
Watson and Crick in 1953. Cold Spring Harbor Laboratory

1955

Smithies uses starch-gel electrophoresis to identify protein polymorphisms

 John C. Avise

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1215845/>



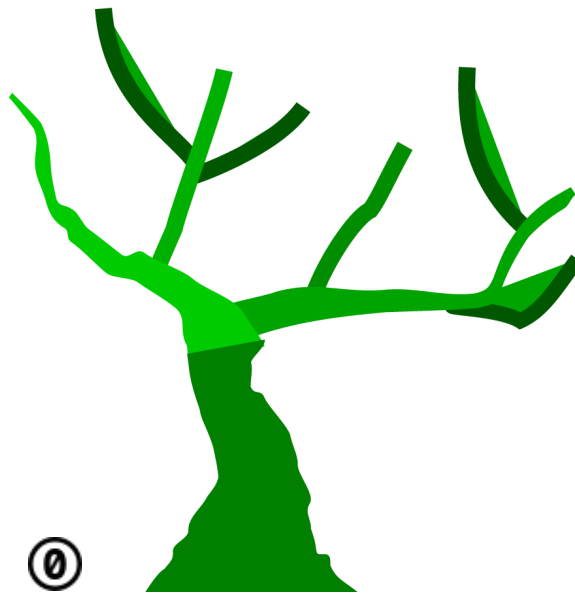
1963

Margoliash determines amino acid sequences for cytochrome c in several taxa and generates the first phylogenetic tree for a specific gene product.



John C. Avise

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC221244/>

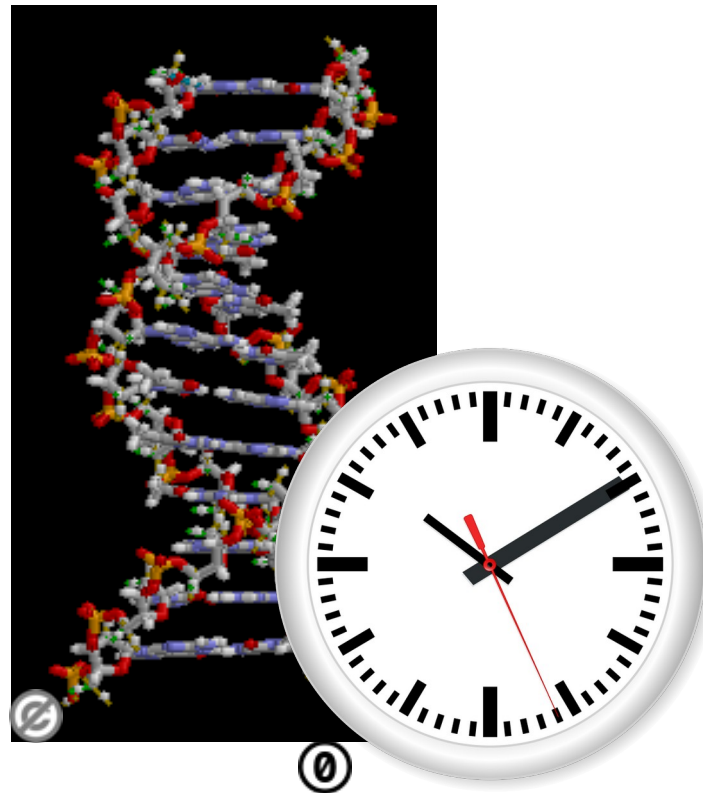


①

1965

Zuckerkandl and Pauling
• “molecular clock” hypothesis.

http://en.wikipedia.org/wiki/History_of_molecular_evolution



1966

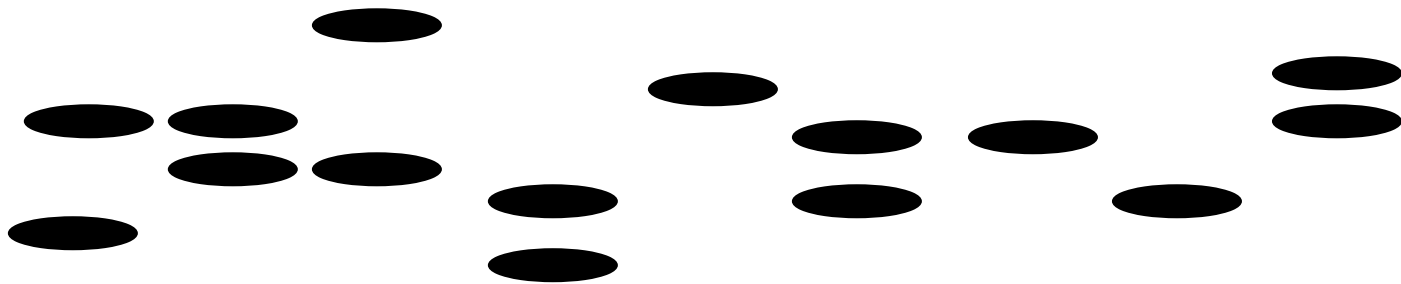
Harris, Lewontin and Hubby

- electrophoresis and histochemical enzyme stains
- examined level of genetic variability in natural populations.

http://en.wikipedia.org/wiki/Richard_Lewontin

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1211186/?tool=pmcentrez>

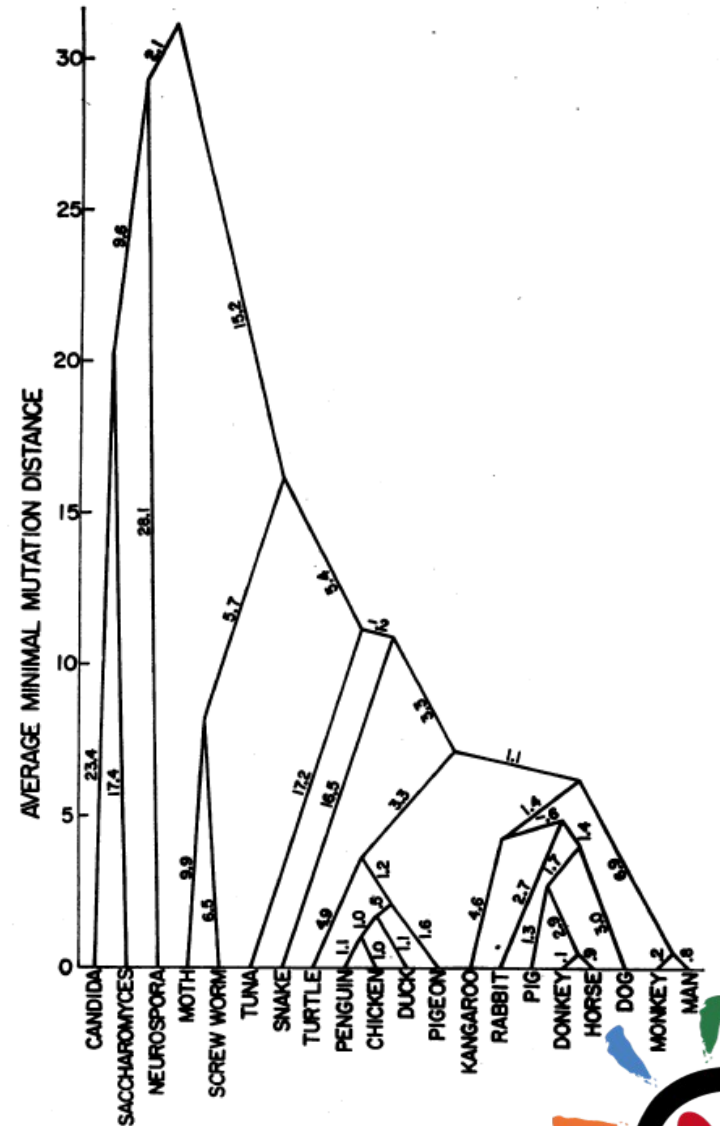
<http://www.jstor.org/stable/75451>



1967

Fitch and Margoliash •“Construction of phylogenetic trees” published in Science.

Walter M. Fitch and Emanuel Margoliash
1967. Construction of phylogenetic trees.
Science Vol. 155: p. 279-284



Source: Walter M. Fitch and Emanuel Margoliash
1967. Construction of phylogenetic trees. Science Vol. 155: p.
279-284

<http://www.sciencemag.org/content/155/3760/279.full.pdf>

CC/NUMBER 27
JULY 4, 1988

This Week's Citation Classic®

Fitch W M & Margoliash E. Construction of phylogenetic trees.
Science 155:279-84, 1967.

[University of Wisconsin Medical School, Madison, WI and Protein Section, Department of Molecular Biology, Abbott Laboratories, North Chicago, IL]

This paper provided a way to construct an evolutionary tree using a measure of genetic distance obtained from amino acid sequence differences interpreted in terms of the genetic code. [The *SCI*® indicates that this paper has been cited in over 670 publications.]

Walter M. Fitch
Ahmanson Center for Biological Research
University of Southern California
Los Angeles, CA 90089-1481

revealed that there was some slowness in the rate of sequence publication from his laboratory and that he had another 10 completed sequences. He offered to provide them to me. What a windfall! At the stroke of a conversational noon-hour clock, the sample size was doubled to 20, permitting us to present a tree spanning the largest part of the eukaryotic kingdom, and I got a coauthor whose prose was pellucid.

The genetic code was solved (except we then thought that the methionine and tryptophan codons were twofold degenerate), the minimum base differences were plugged into the



Source: Walter M. Fitch, 1988, Citation Classic, No. 27.

<http://garfield.library.upenn.edu/classics.html>

<http://garfield.library.upenn.edu/classics1988/A1988N888200001.pdf>



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1968

Kimura proposes that the majority of molecular changes in evolution are due to random drift of neutral or nearly neutral mutations.

http://en.wikipedia.org/wiki/Motoo_Kimura#cite_note-Kimura68-1
<http://www.nature.com/nature/journal/v217/n5129/abs/217624a0.html>



Source: John C. Avise

1994. Molecular Markers, Natural History and Evolution, p. 42. Chapman & Hall. New York, USA.

1969

King and Jukes

- “Non-Darwinian evolution”
- Also proposed neutral theory .

http://en.wikipedia.org/wiki/Non-Darwinian_Evolution

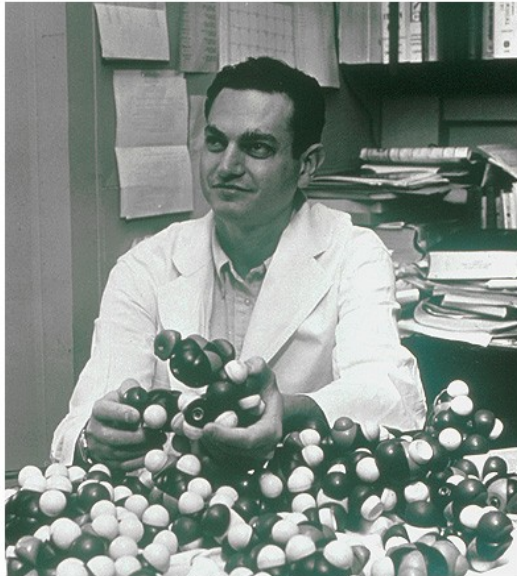
<http://www.sciencemag.org/content/164/3881/788>.

1961

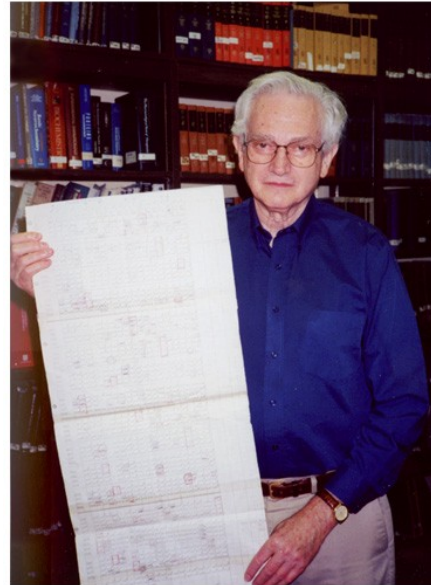
Marshall Nirenberg, a young biochemist at the National Institute of Arthritic and Metabolic Diseases, discovered the first "triplet"—a sequence of three bases of DNA that codes for one of the twenty amino acids that serve as the building blocks of proteins. Subsequently, within five years, the entire **genetic code** was deciphered.

Source: Genome News Network

http://www.genomenewsnetwork.org/resources/timeline/1961_Nirenberg.php



Courtesy of the National Library of Medicine.
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Courtesy of Dr. S. Chan, DNA Learning Center.
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1972

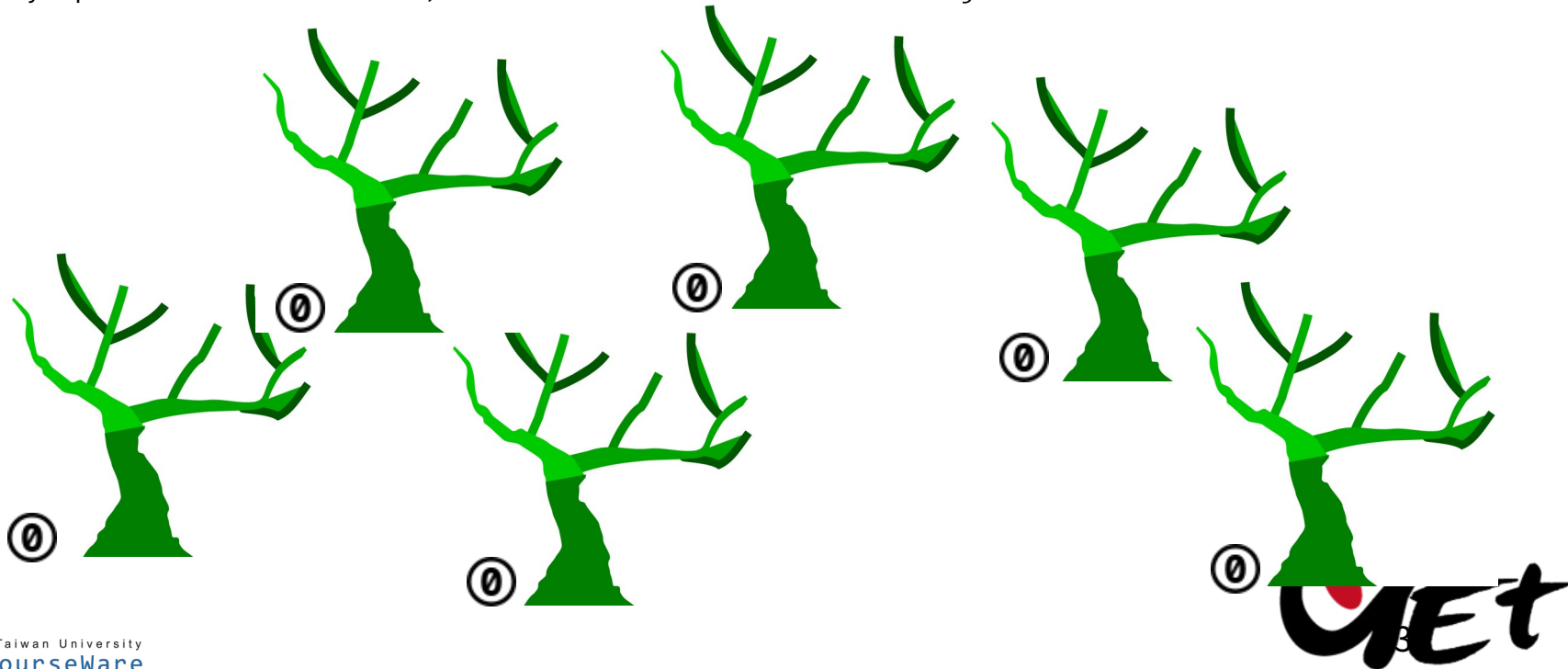
Nei's genetic distance has greatly facilitated the study of evolutionary relationships among populations or closely related species.

http://en.wikipedia.org/wiki/Masatoshi_Nei

<http://www.jstor.org/stable/2459777>

Source: M. Prakash

2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 47. Discovery Publishing House. India.



1977

Molecular biologists by the 1970s had deciphered the genetic code and could spell out the sequence of amino acids in proteins. But inability to easily read off the precise nucleotide sequences of DNA forestalled further advances in molecular genetics and all prospects of genetic engineering. Walter Gilbert (with graduate student Allan M. Maxam) and Frederick Sanger, in 1977, working separately in the United States and England, developed new techniques for rapid DNA sequencing.

 Source: Genome News Network



Courtesy of Dr. F. Sanger, MRC Cambridge.
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Cold Spring Harbor Laboratory

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1981

Palmer and colleagues begin an important series papers utilizing cpDNA for phylogenetic constructions in plants

 Source: John C. Avise
1994. Molecular Markers, Natural History and Evolution, p. 42. Chapman & Hall. New York, USA.

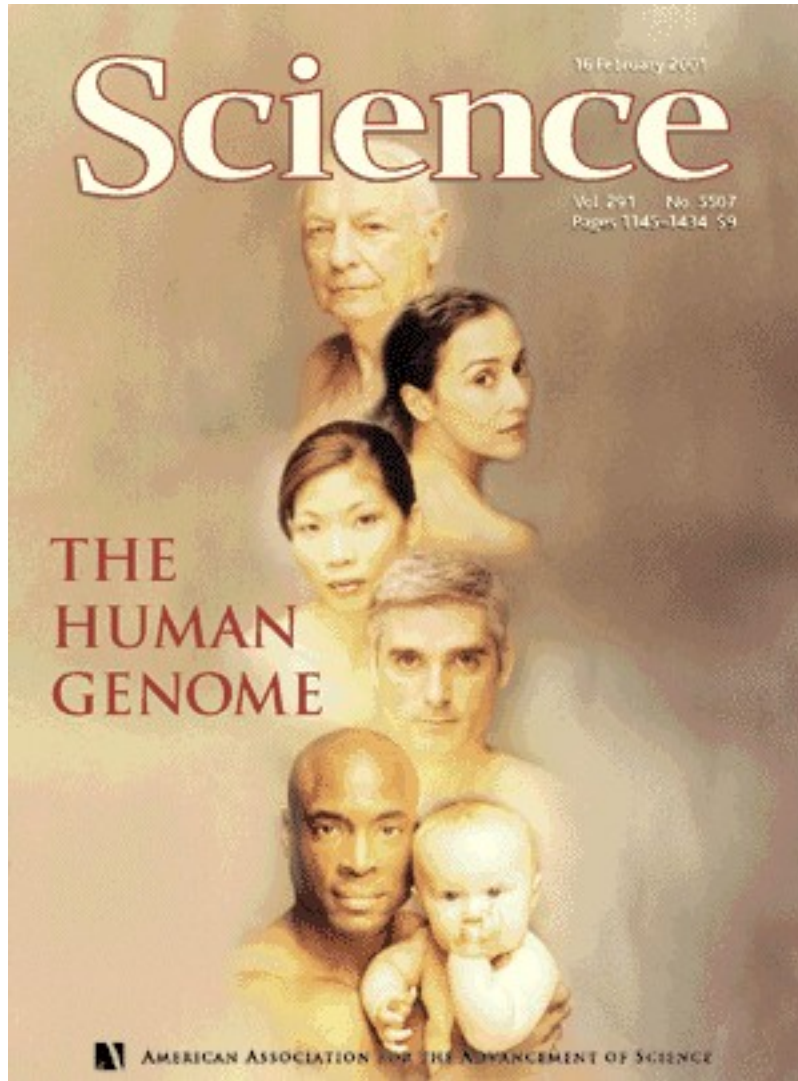
1984

Sibley and Ahlquist

- DNA-DNA hybridization
- primate evolution study.

http://en.wikipedia.org/wiki/DNA-DNA_hybridization

<http://www.springerlink.com/content/g3020651ml536640/>



 Science /AAAS

Source: 2001. Science. Vol. 291. Issue 5507.

<http://www.sciencemag.org/content/291/5507.cover-expansion>

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<http://www.geneticorigins.org/>



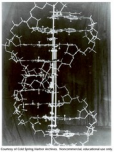
Homework Assignment I

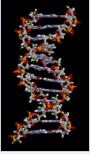
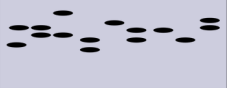
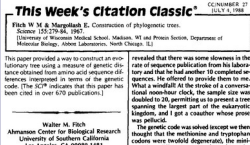
- 1) Write a paragraph about yourself (including name, background, and contact information) and your research interests.
- 2) What do you expect to learn from taking this course?

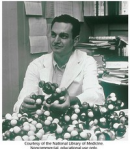
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P17. "The mechanisms responsible for such changes"		M. Prakash 2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 42. Discovery Publishing House. India. http://books.google.com.tw/books?id=OoG4_y2Q9AEC&printsec=frontcover&hl=z h-TW#v=onepage&q&f=false 2012/02/21 visited <i>It is used subject to the fair use doctrine of:</i> •Taiwan Copyright Act Articles 52 & 65	P17
P17. "The reconstruction of the evolutionary history of genes and organisms"		M. Prakash 2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 42. Discovery Publishing House. India. http://books.google.com.tw/books?id=OoG4_y2Q9AEC&printsec=frontcover&hl=z h-TW#v=onepage&q&f=false 2012/02/21 visited <i>It is used subject to the fair use doctrine of:</i> •Taiwan Copyright Act Articles 52 & 65	P17
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P22. "Smithies uses starch-gel electrophoresis to identify protein polymorphisms."		John C. Avise 1994. Molecular Markers, Natural History and Evolution, p. 42. Chapman & Hall. New York, USA. http://books.google.com.tw/books?id=aWSbZf-dRbEC&printsec=frontcover&hl=zh-TW#v=onepage&q&f=false <i>It is used subject to the fair use doctrine of:</i> •Taiwan Copyright Act Articles 52 & 65	P22
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P23. "Margoliash determines amino acid sequences for cytochrome c in several taxa and generates the first phylogenetic tree for a specific gene product."		John C. Avise 1994. Molecular Markers, Natural History and Evolution, p. 42. Chapman & Hall. New York, USA. http://books.google.com.tw/books?id=aWSbZf-dRbEC&printsec=frontcover&hl=zh-TW#v=onepage&q&f=false <i>It is used subject to the fair use doctrine of:</i> •Taiwan Copyright Act Articles 52 & 65	P23
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		Walter M. Fitch and Emanuel Margoliash. 1967. Construction of phylogenetic trees. Science Vol. 155: p.282 http://www.sciencemag.org/content/155/3760/279.extract?sid=fe0a324a-4d85-453e-b77a-8a69782df245 2012/02/21 visited <i>It is used subject to the fair use doctrine of:</i> •Taiwan Copyright Act Articles 52 & 65 • Science /AAAS Copyright Statement	P26
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P28. “Kimura proposes that the majority of molecular changes in evolution are due to random drift of neutral or nearly neutral mutations.”		John C. Avise 1994. Molecular Markers, Natural History and Evolution, p. 42. Chapman & Hall. New York, USA. http://books.google.com.tw/books?id=aWSbZf-dRbEC&printsec=frontcover&hl=zh-TW#v=onepage&q&f=false 2012/02/21 visited <i>It is</i> used subject to the fair use doctrine of: •Taiwan Copyright Act Articles 52 & 65	P28
P29. “Marshall Nirenberg, a young biochemist at the National Institute of Arthritic and Metabolic Diseases... Subsequently, within five years, the entire genetic code was deciphered”		Genome News Network http://www.genomenewsnetwork.org/resources/timeline/1961_Nirenberg.php 2012/02/21 visited <i>It is</i> used subject to the fair use doctrine of: •Taiwan Copyright Act Articles 52 & 65	P29
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P30. “Nei’s genetic distance has greatly facilitated the study of evolutionary relationships among populations or closely related species.”		M. Prakash 2007. Encyclopaedia of Gene Evolution Vol. 2, Molecular Genetics, p. 47. Discovery Publishing House. India. http://books.google.com.tw/books?id=OoG4_y2Q9AEC&printsec=frontcover&hl=zh-TW#v=onepage&q&f=false 2012/02/21 visited <i>It is</i> used subject to the fair use doctrine of: •Taiwan Copyright Act Articles 52 & 65	P30
P31. “Molecular biologists by the 1970s had deciphered... developed new techniques for rapid DNA sequencing.”		Genome News Network http://www.genomenewsnetwork.org/resources/timeline/1977_Gilbert.php 2012/02/21 visited <i>It is</i> used subject to the fair use doctrine of: •Taiwan Copyright Act Articles 52 & 65	P31 38

