

UNWEAVING DNA STRANDS from the TREE of LIFE

A C G T

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WHY DNA ?

Advancements in studying complete genomes or their segments revolutionized contemporary biology and society at large.

Easy access to information, genetic and historical, written in the linear order of DNA letters: A, T, C, G, has illuminated relatedness across all levels of biological hierarchy. Ancient DNA opened a spectacular window on our extinct kin, Neanderthals and Denisovans.

In this course rationale for using DNA sequences in studying relationship of life forms, or phylogeny, will be presented in the introductory lecture, followed by two hours hands on exercise in the lab to demonstrate basic principles of data acquisition and analyses.

Knowing phylogeny not only generates testable hypotheses on trait evolution and history of life on Earth but also has broad practical application in medicine, agriculture and conservation biology.

INTRODUCTION

DNA - Just a fashion or the key to unlock the workings of an overwhelming diversity of ever changing life forms ?

Homo sapiens as a model species

Variation in DNA

How often the same DNA stretches are dissimilar ?

Hypervariable segments allow easy identification of individuals

“Zróbcie mi DNA!” - Practical applications of hypervariable STR loci in paternity assessment, forensic science and identification of human remains

Global perspective and justification

- Geographic patterns in distribution of genomic variants provide clues to the past history, human demography and migrations
- Thanks Mum! mtDNA a circular maternal molecule with great potential, and pitfalls
- Processes behind geographic patterns of variation within and between populations are well understood and founded on solid theory of population genetics.

Universal molecule, methods and theory

- DNA variation can be studied in all organisms, because DNA is omnipresent

Likewise theoretical principles can be applied to its interpretation

- **Genealogical history of organisms, can be recovered from patterns of mutations recorded in DNA to build dendrograms, phylogenetic trees**

Here the practical part begins:

Wet Lab

Studying variation in DNA

- PCR and downward procedures
- *Sacra simplicitas* - what does exactly the DNA polymerase do?
sequencing DNA - homage to Frederick Sanger

You will set up PCR reactions, amplify DNA segments and visualize amplicons on a gel.

Analysing sequence similarity – inferring phylogeny

- aligning sequences
- distance measures
- simple algorithms of tree construction

Using BioEdit you will align sequences, identify polymorphic sites, indels, calculate divergence, and run simple algorithms to obtain phylogenetic trees. More complicated model based inferences will be explained.

A virtual visit to GenBank, repository of DNA sequences, is also planned

She/He Participants:

- The lab can accommodate 8 students at a time.
Two groups are planned for this term in January 2014,
and additional two in the Summer term, in February/March.
- Bring your laptop. You will be provided with lab protocols,
chemicals, consumables etc.
- A lab coat is a must; we can fit you one, if you ask in advance.
For the blessed with overproliferating hair root cells a pony tail
coiffure is advised.