

Questions lecture 1: Introduction to Genomics

- 1) a. What was David Botstein's contribution to the Human Genome project, b. explain the underlying principles, and why was it crucial for the project to succeed?
- 2) Define 1 cM. What's the physical equivalent in humans? Is it the same in *Drosophila* for example?
- 3) a. What was the major difference in sequencing approach between the "public" and "private" Initiatives? Explain the underlying principles and why there was common belief that the private effort would fail.
b. Sanger sequencing revolutionized genome biology. Explain briefly how it works and which "upgrades" it required by Smith and Hunkapillar to make it useful for sequencing the human genome.
- 4) When Bill Clinton announced in June 2000 the availability of the human genome sequence, was his statement correct? Please clarify.
- 5) A. Explain the principle of Illumina sequencing. B. Name other sequencing approaches and describe the principle underlying each in 2-3 sentences.
- 6) A. How does genome size relate to complexity? B. And what about the gene number?
No correlation between complexity and number of genes.
- 7) What's the difference between homologs, orthologs, and paralogs?
- 8) What is meant when it is stated that the human FOXP2 has undergone accelerated evolution?
- 9) What are syntenic genomic regions?
- 10) Can humans and chimps interbreed?
- 11) Provide a rough proportional breakdown of the human genome in constrained, repetitive, and coding sequence.
- 12) What is the difference between LINEs, SINEs, and DNA transposons, and which constitute the largest genome portion? And what's the difference between an autonomous and non- autonomous repetitive element?
- 13) Which kind of repetitive elements enlarges the genome? Explain the mechanism.
- 14) A. What's the difference between a micro- and mini-satellite? B. Describe how they may originate.
- 15) Explain the mechanism of DNA fingerprinting and a concrete application.