

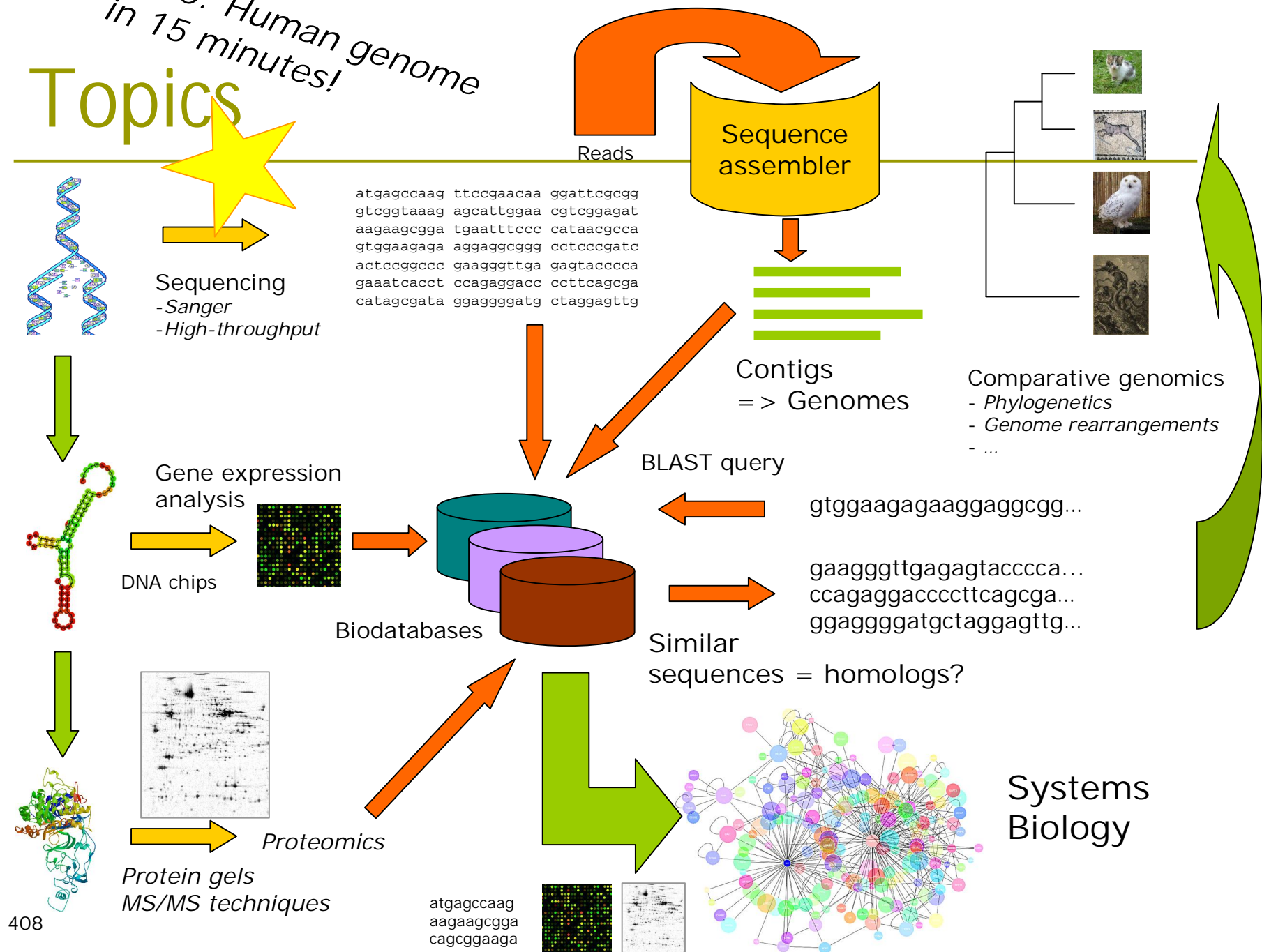
Introduction to Bioinformatics



Wrap-up

2010: Human genome
in 15 minutes!

Topics



Exams

- p Course exam Wednesday 15 October
16.00-19.00 Exactum A111
- p Separate exams
 - n Tue 18 November 16.00-20.00 Exactum A111
 - n Fri 16 January 16.00-20.00 Exactum A111
 - n Tue 31 March 16.00-20.00 Exactum A111
- p Check exam date and place before taking
the exam! (previous week or so)

Exam regulations

- ⌞ If you are late more than 30 min, you cannot take the exam
- ⌞ You are not allowed to bring material such as books or lecture notes to the exam
- ⌞ Allowed stuff: blank paper (distributed in the exam), pencils, pens, erasers, calculators, snacks
- ⌞ Bring your student card or other id!

Grading

- p Grading: on the scale 0-5
 - n To get the lowest passing grade 1, you need to get at least 30 points out of 60 maximum
- p Course exam gives you maximum of 48 points
- p Note: if you take the first separate exam, the best of the following options will be considered:
 - n Exam gives you max 48 points, exercises max 12 points
 - n Exam gives you max 60 points
- p In second and subsequent separate exams, only the 60 point option is in use

Exercise points

- ρ Max. marks: 31
- ρ 80% of 31 \sim = 24 marks -> 12 points
- ρ 2 marks = 1 point

Topics covered by exams

- ⌘ Exams cover everything presented in lectures (exception: biological background not covered)
- ⌘ Word distributions and occurrences (course book chapters 2-3)
- ⌘ Genome rearrangements (chapter 5)
- ⌘ Sequence alignment (chapter 6)
- ⌘ Rapid alignment methods: FASTA and BLAST (chapter 7)
- ⌘ Sequencing and sequence assembly (chapter 8)

Topics covered by exams

- ρ Similarity, distance and clustering (chapter 10)
- ρ Expression data analysis (chapter 11)
- ρ Phylogenetic trees (chapter 12)
- ρ Systems biology: modelling biological networks (no chapter in course book)

Bioinformatics courses in 2008

- ⌞ Biological sequence analysis (II period, Kumpula)
 - ⌞ Focus on probabilistic methods: Hidden Markov Models, Profile HMMs, finding regulatory elements, ...
- ⌞ Modeling of biological networks (20-24.10., TKK)
 - ⌞ Biochemical network modelling and parameter estimation in biochemical networks using mechanistic differential equation models.

Bioinformatics courses in autumn 2008

- ρ Bayesian paradigm in genetic bioinformatics (II period, Kumpula)
 - η Applications of Bayesian approach in computer programs and data analysis of
 - ρ genetic past,
 - ρ phylogenetics,
 - ρ coalescence,
 - ρ relatedness,
 - ρ haplotype structure,
 - ρ disease gene associations.

Bioinformatics courses in autumn 2008

- p Statistical methods in genetics (II period, Kumpula)
 - n Introduction to statistical methods in gene mapping and genetic epidemiology.
 - n Basic concepts of linkage and association analysis as well as some concepts of population genetics will be covered.

Bioinformatics courses in Spring 2009

- ρ Practical Course in Biodatabases (III period, Kumpula)
- ρ High-throughput bioinformatics (III-IV periods, TKK)
- ρ Phylogenetic data analyses (IV period, Kumpula)
 - η Maximum likelihood methods, Bayesian methods, program packages
- ρ Metabolic modelling (IV period, Kumpula)

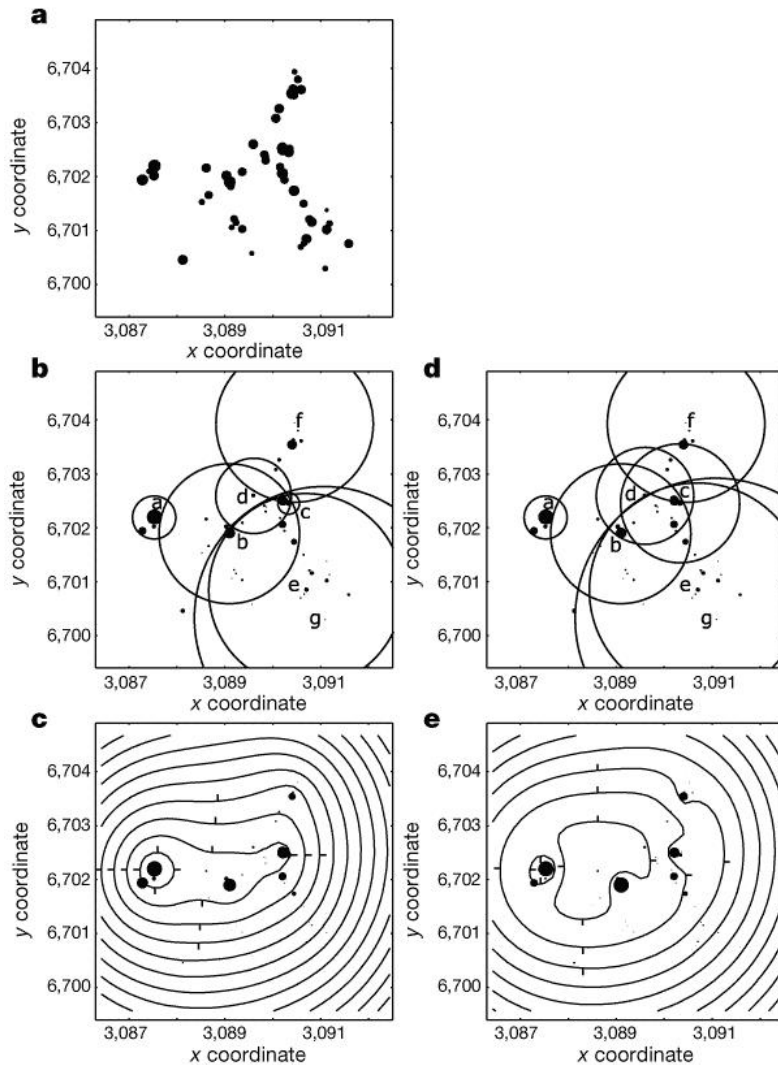
Genomes sequenced – all done?

- p Sequencing is just the beginning
 - n What do genes and proteins do?
 - p Functional genomics
 - n How do they interact with other genes and proteins?
 - p Systems biology



Two sides of the same question!

Bioinformatics (at least mathematical biology) can exist outside molecular biology



Melitaea cinxia, Glanville Fritillary butterfly

The metapopulation capacity of a fragmented landscape
Ilkka Hanski and Otso Ovaskainen
Nature 404, 755-758(13 April 2000)

Metagenomics

p Metagenomics or environmental genomics

- n "At the last count 1.8 million species were known to science. That sounds like a lot, but in truth it's no big deal. We may have done a reasonable job of describing the larger stuff, but the fact remains that an average teaspoon of water, soil or ice contains millions of micro-organisms that have never been counted or named. "

-- Henry Nicholls

Omics

- ρ Genome
- ρ Transcriptome
- ρ Metabolome
- ρ Metallome
- ρ Lipidome
- ρ Glycome
- ρ Interactome
- ρ Spliceome
- ρ ORFeome
- ρ Speechome
- ρ Mechanome
- ρ Phenome
- ρ Exposome
- ρ Textome
- ρ Receptorome
- ρ Kinome
- ρ Neurome
- ρ Cytome
- ρ Predictome
- ρ Omeome
- ρ Reactome
- ρ Connectome

Take-home messages

- ⌘ Don't trust biodatabases blindly!
 - ⌘ Annotation errors tend to accumulate
- ⌘ Consider
 - ⌘ Statistical significance
 - ⌘ Sensitivityof your results
- ⌘ Think about the whole "bioinformatics workflow":
 - ⌘ Biological phenomenon -> Modelling -> Computation -> Validation of results
- ⌘ Results from bioinformatics tools and methods must be validated!
- ⌘ Actively seek cooperation with experts

Bioinformatics journals

- ⌘ Bioinformatics, <http://bioinformatics.oupjournals.org/>
- ⌘ BMC Bioinformatics,
<http://www.biomedcentral.com/bmcbioinformatics>
- ⌘ Journal of Bioinformatics and Computational Biology (JBCB), <http://www.worldscinet.com/jbcb/jbcb.shtml>
- ⌘ Journal of Computational Biology,
<http://www.liebertpub.com/CMB/>
- ⌘ IEEE/ACM Transactions on Computational Biology and Bioinformatics , <http://www.computer.org/tcbb/>
- ⌘ PLoS Computational Biology, www.ploscompbiol.org
- ⌘ In Silico Biology, <http://www.bioinfo.de/isb/>
- ⌘ Nature, Science (bedtime reading)

Bioinformatics conferences

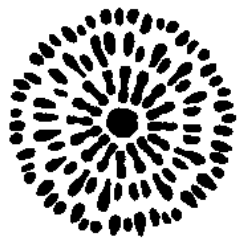
- ρ ISMB, Intelligent Systems for Molecular Biology (Toronto, July 2008)
- ρ ICSB, International Conference on Systems Biology (Göteborg, Sweden; 22-28 August)
- ρ RECOMB, Research in Computational Molecular Biology
- ρ ECCB, European Conference on Computational Biology
- ρ WABI, Workshop on Algorithms in Bioinformatics
- ρ PSB, Pacific Symposium on Biocomputing

*January 5-9, 2009
The Big Island of Hawaii*

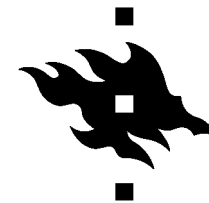


Master's degree in bioinformatics?

- p You can apply to MBI during the application period November '08 – 2 February '09
 - n Bachelor's degree in suitable field
 - n At least 60 ECTS credits in CS or mathstat
 - n English language certificate
- p Passing this course gives you the first 4 credits for Bioinformatics MSc!



MBI MASTER'S DEGREE
PROGRAMME IN BIOINFORMATICS



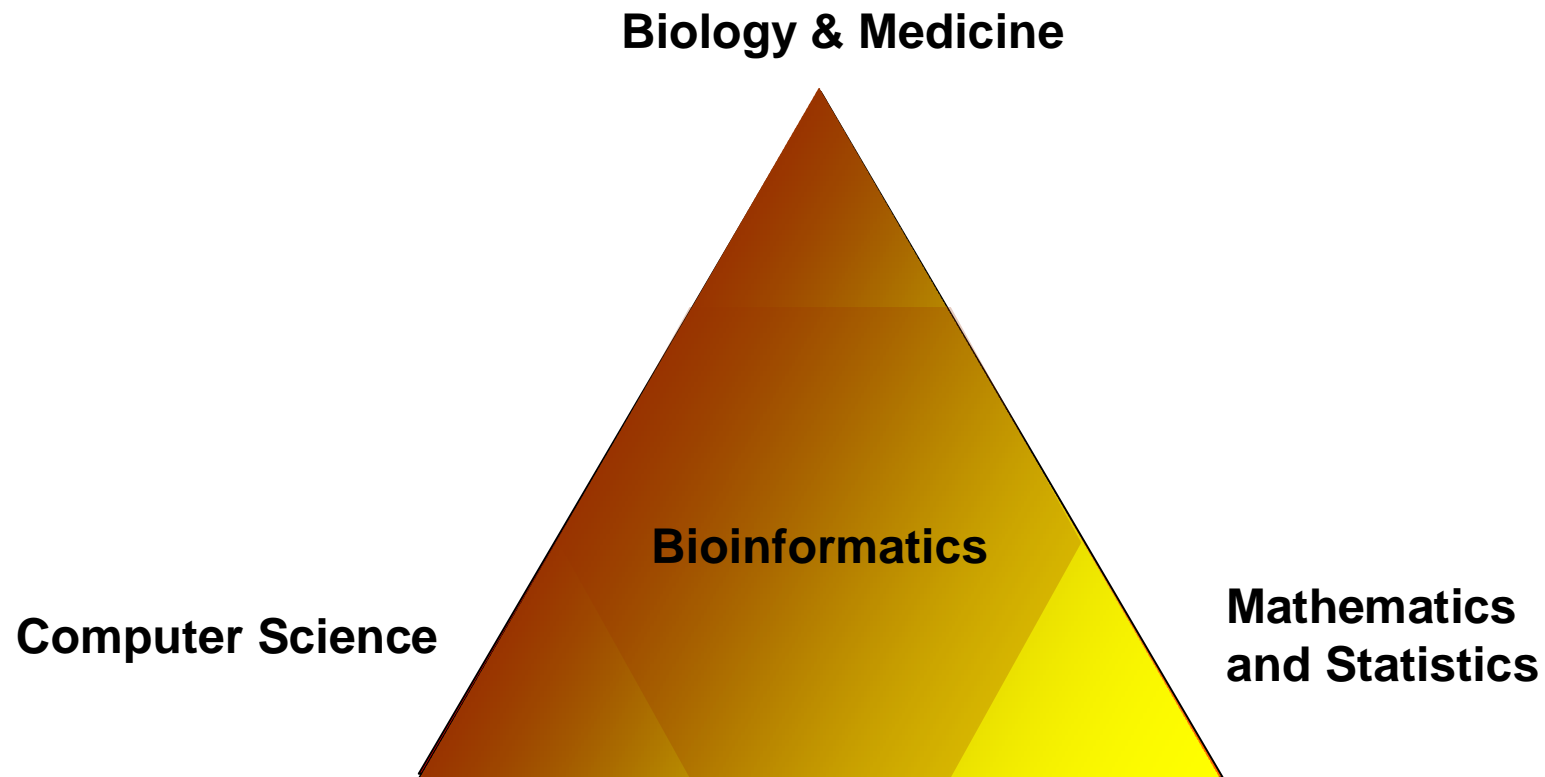
Information session on MBI

- ⌘ Wednesday 19.11. 13.00-15.00 Exactum D122
- ⌘ www.cs.helsinki.fi/mbi/events/info08
- ⌘ Talks in Finnish

Mailing list for bioinformatics courses and events

- ρ MBI maintains a mailing list for announcement on bioinformatics courses and events
- ρ Send email to bioinfo@tcs.helsinki.fi if you want to subscribe to the list (you can unsubscribe in the same way)
- ρ List is moderated

The aim of this course



Where would you be in this triangle?

Has your position shifted during the course?

Feedback

- p Please give feedback on the course!
 - n <https://ilmo.cs.helsinki.fi/kurssit/servlet/Valinta?kieli=en>
- p Don't worry about your grade – you can give feedback anonymously

Thank you!

p I hope you enjoyed the course!



Halichoerus grypus, Gray seal or *harmaahylje* in Finnish

