Stichting NIOC en de NIOC kennisbank

Stichting NIOC (www.nioc.nl) stelt zich conform zijn statuten tot doel: het realiseren van congressen over informatica onderwijs en voorts al hetgeen met een en ander rechtstreeks of zijdelings verband houdt of daartoe bevorderlijk kan zijn, alles in de ruimste zin des woords.

De stichting NIOC neemt de archivering van de resultaten van de congressen voor zijn rekening. De website www.nioc.nl ontsluit onder "Eerdere congressen" de gearchiveerde websites van eerdere congressen. De vele afzonderlijke congresbijdragen zijn opgenomen in een kennisbank die via dezelfde website onder "NIOC kennisbank" ontsloten wordt.

Op dit moment bevat de NIOC kennisbank alle bijdragen, incl. die van het laatste congres (NIOC2025, gehouden op donderdag 27 maart 2025 jl. en georganiseerd door Hogeschool Windesheim). Bij elkaar zo'n 1500 bijdragen!

We roepen je op, na het lezen van het document dat door jou is gedownload, de auteur(s) feedback te geven. Dit kan door je te registreren als gebruiker van de NIOC kennisbank. Na registratie krijg je bericht hoe in te loggen op de NIOC kennisbank.

Het eerstvolgende NIOC vindt plaats in 2027 en wordt dan georganiseerd door HAN University of Applied Sciences. Zodra daarover meer informatie beschikbaar is, is deze hier te vinden.

Wil je op de hoogte blijven van de ontwikkeling rond Stichting NIOC en de NIOC kennisbank, schrijf je dan in op de nieuwsbrief via

www.nioc.nl/nioc-kennisbank/aanmelden nieuwsbrief

Reacties over de NIOC kennisbank en de inhoud daarvan kun je richten aan de beheerder:
R. Smedinga kennisbank@nioc.nl.
Vermeld bij reacties jouw naam en telefoonnummer voor nader contact.

Versiedatum: 02-04-2023

Bioinformatica, competentiegericht onderwijs en toetsing

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http://ibivu.cs.vu.nl

This talk

- What is Bioinformatics and what is special about it?
- Why is it currently seen as so important?
- What is the picture for students?
- How can we use all this in competence-based teaching and testing?
- What Bioinformatics training do we do at the VU?

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Gathering knowledge

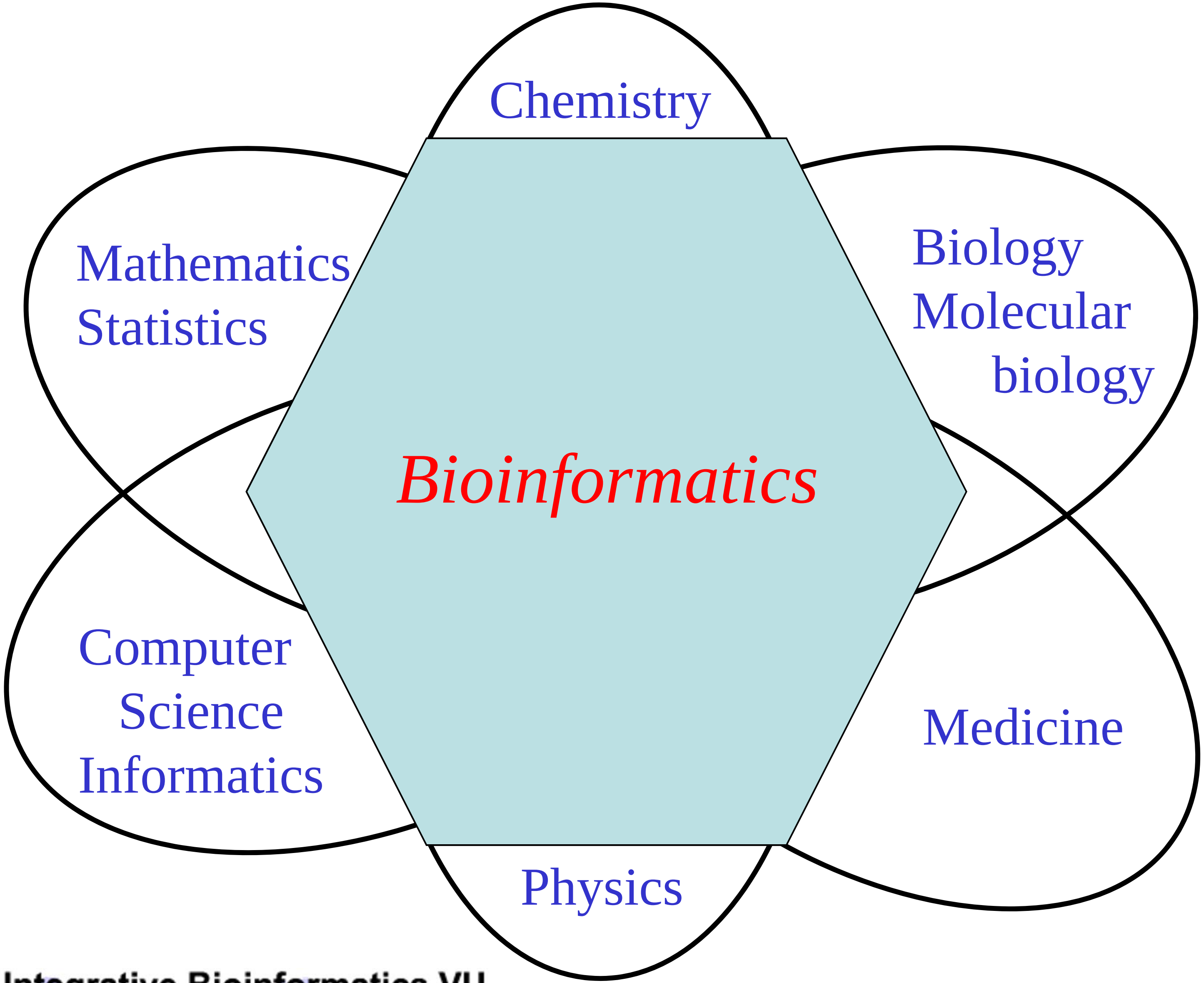
Rembrandt,
1632

- Anatomy, architecture
- Dynamics, mechanics

Newton,
1726

- Informatics
  (Cybernetics – Wiener, 1948)
  (Cybernetics has been defined as the science of control in machines and animals, and hence it applies to technological, animal and environmental systems)
- Genomics, bioinformatics
  “The science of this century”

Bioinformatics



Chemistry

Mathematics
Statistics

Biology
Molecular
biology

Bioinformatics

Computer
Science
Informatics

Medicine

Physics

Bioinformatics

“Studying informational processes in biological systems” (Hogeweg, early 1970s)

- No computers necessary
- Back of envelope OK

“Information technology applied to the management and analysis of biological data” (Attwood and Parry-Smith)

Applying algorithms with mathematical formalisms in biology (genomics); setting up computers

Bioinformatics in the olden days

- Close to Molecular Biology:
  - (Statistical) analysis of protein and nucleotide structure
  - Protein folding problem
  - Protein-protein and protein-nucleotide interaction
- Many essential methods were created early on:
  - Protein sequence analysis (pairwise and multiple alignment)
  - Protein structure prediction (secondary, tertiary structure)

Bioinformatics in the olden days (Cont.)

- Molecular evolution was studied and methods created
  - – Phylogenetic reconstruction (clustering – NJ method

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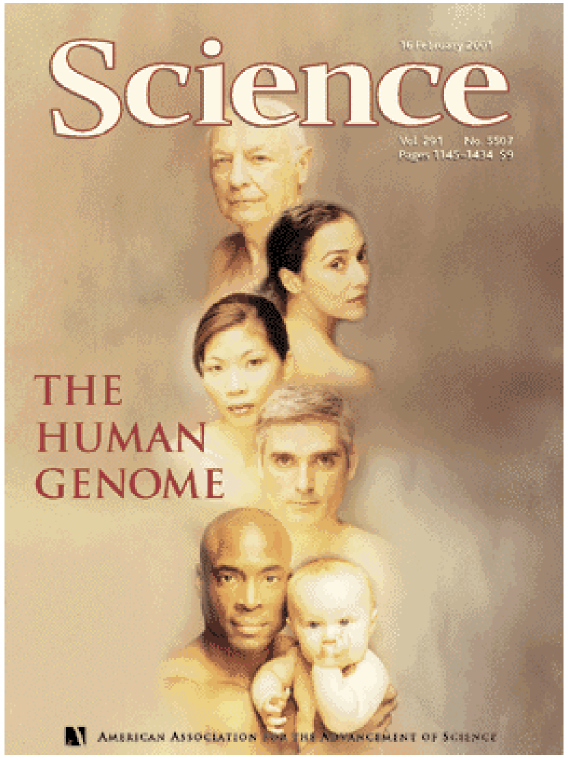
But then the big bang….

The Human Genome -- 26 June 2000



Dr. Craig Venter

Celera Genomics

Shotgun method

Sir John Sulston

Human Genome Project

Human DNA

- There are about 3bn (3×10^9) nucleotides in the nucleus of 3.5 trillion (3.5×10^{12}) cells of a human body – a total of $\sim 10^{22}$ nucleotides!
- Many DNA regions code for proteins, and are called genes (1 gene codes for 1 protein in principle)
- Human DNA contains ~26,000 expressed genes
- Deoxyribonucleic acid (DNA) comprises 4 different types of nucleotides (bases): adenine (A), thiamine (T), cytosine (C) and guanine (G).

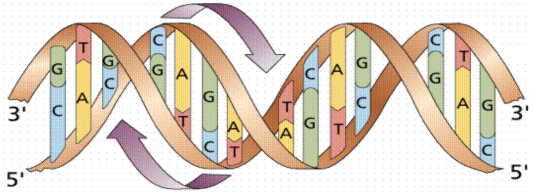
Human DNA (Cont.)

- People are different, but the DNA of different people only varies for 0.2% or less. So, only 2 letters in 1000 are expected to be different. Over the whole genome, this means that about 5 million letters would differ between individuals.
- The Human Genome has recently been announced complete (in 2004): >99% has been sequenced reliably.
- *Compact information:* 1 gram of DNA contains the information provided by a billion CDs!

Genome size

Organism	***Number of base pairs***
ϕX-174 virus	5,386
Epstein Bar Virus	172,282
Mycoplasma genitalium	580,000
Hemophilus Influenza	1.8×10^6
Yeast (*S. Cerevisiae*)	12.1×10^6
Human	$\mathbf{3.2 \times 10^9}$
Wheat	16×10^9
Lilium longiflorum	90×10^9
Salamander	100×10^9
Amoeba dubia	670×10^9

A gene codes for a protein



DNA

CCTGAGCCAACTATTGATGAA

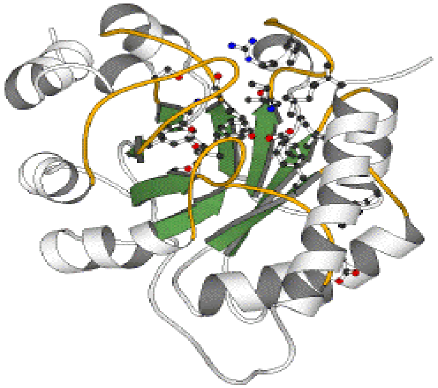
transcription

mRNA

CCUGAGCCAACUAUUGAUGAA

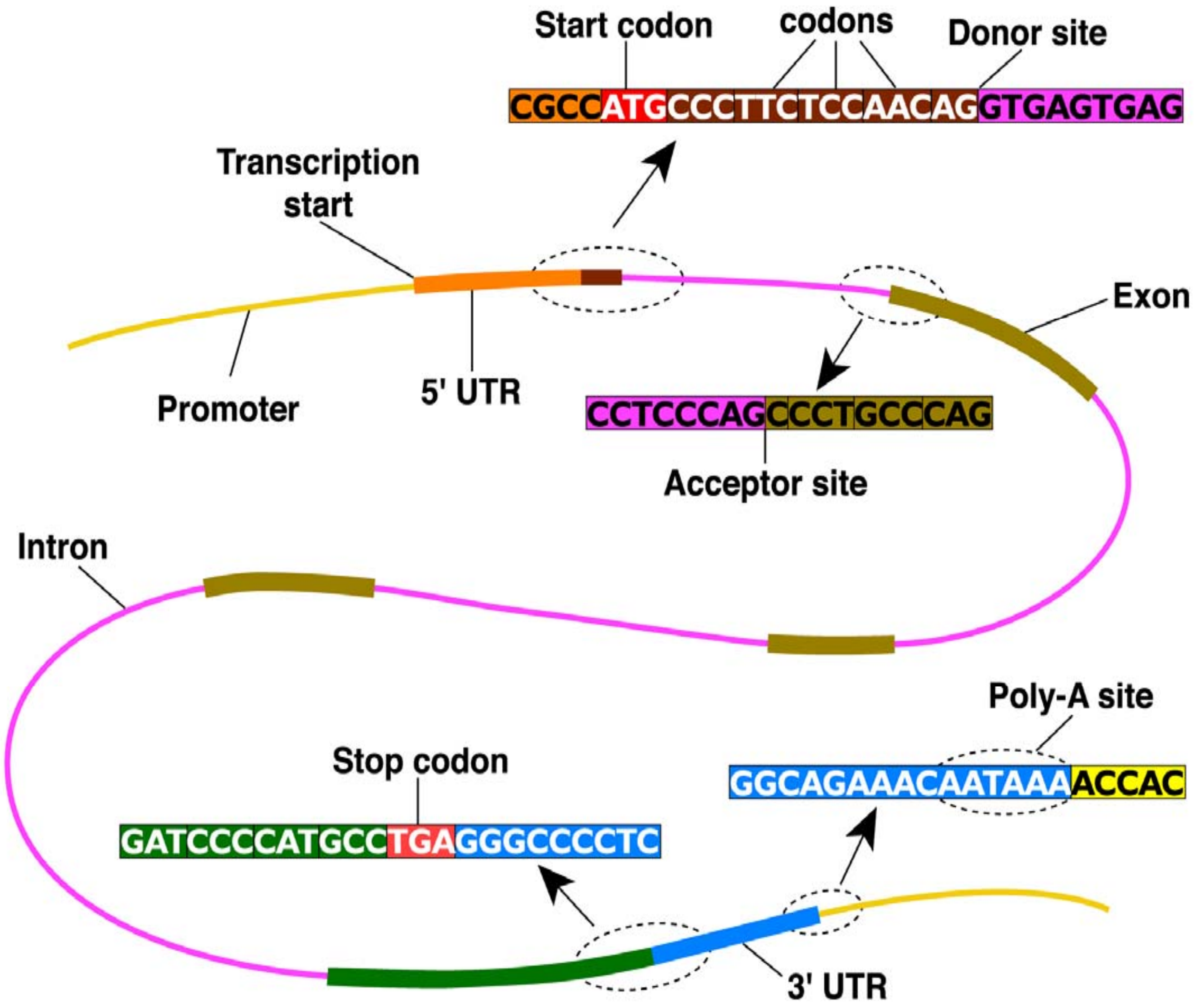
translation

Protein



PEPTIDE

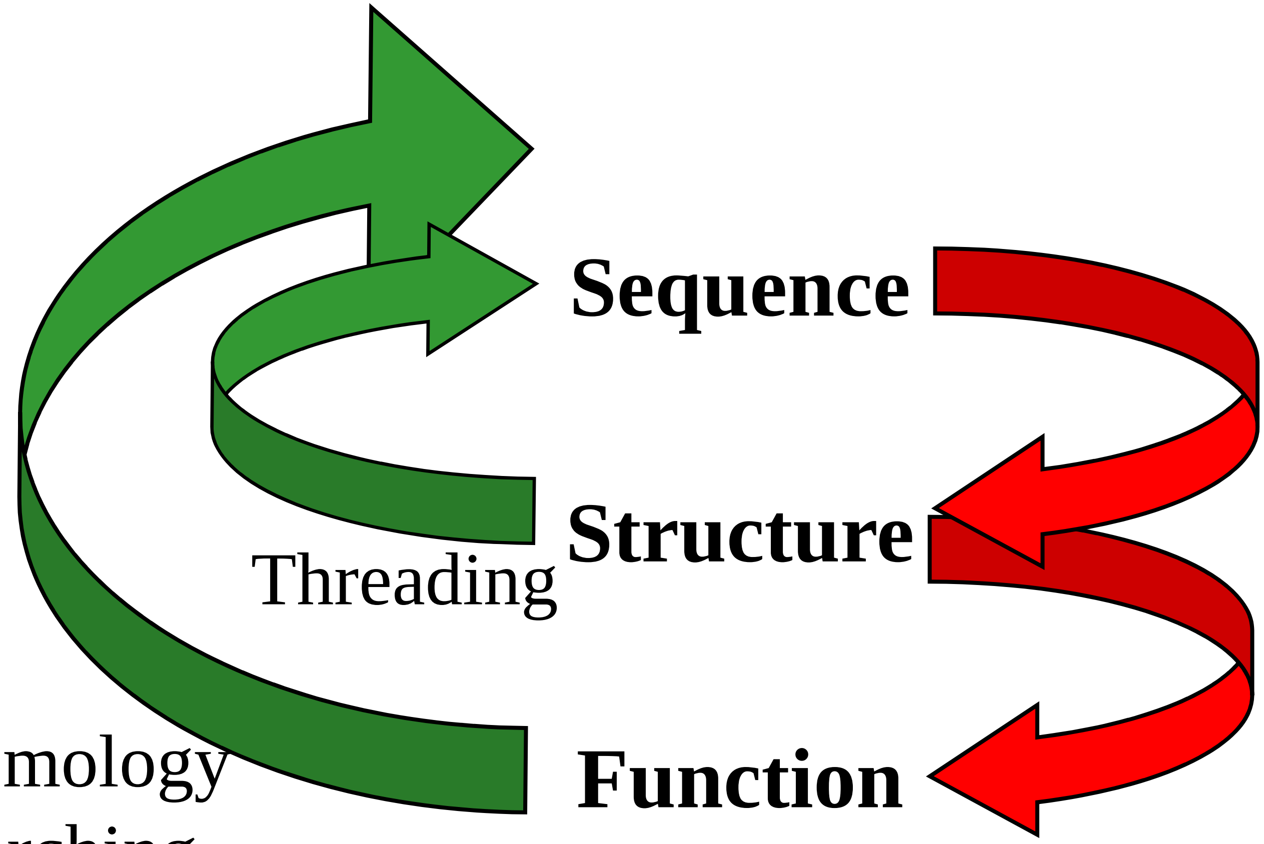
Humans have spliced genes…



Genome information has changed bioinformatics

- More high-throughput (HTP) applications (cluster computing, GRID, etc.)
- More automatic pipeline applications
- More user-friendly interfaces
- Greater emphasis on biostatistics
- Greater influence of computer science (machine learning, software engineering, etc.)
- **More integration of disciplines, databases and techniques**

Protein Sequence-Structure-Function



Sequence

Structure

Function

Threading

Homology searching (BLAST)

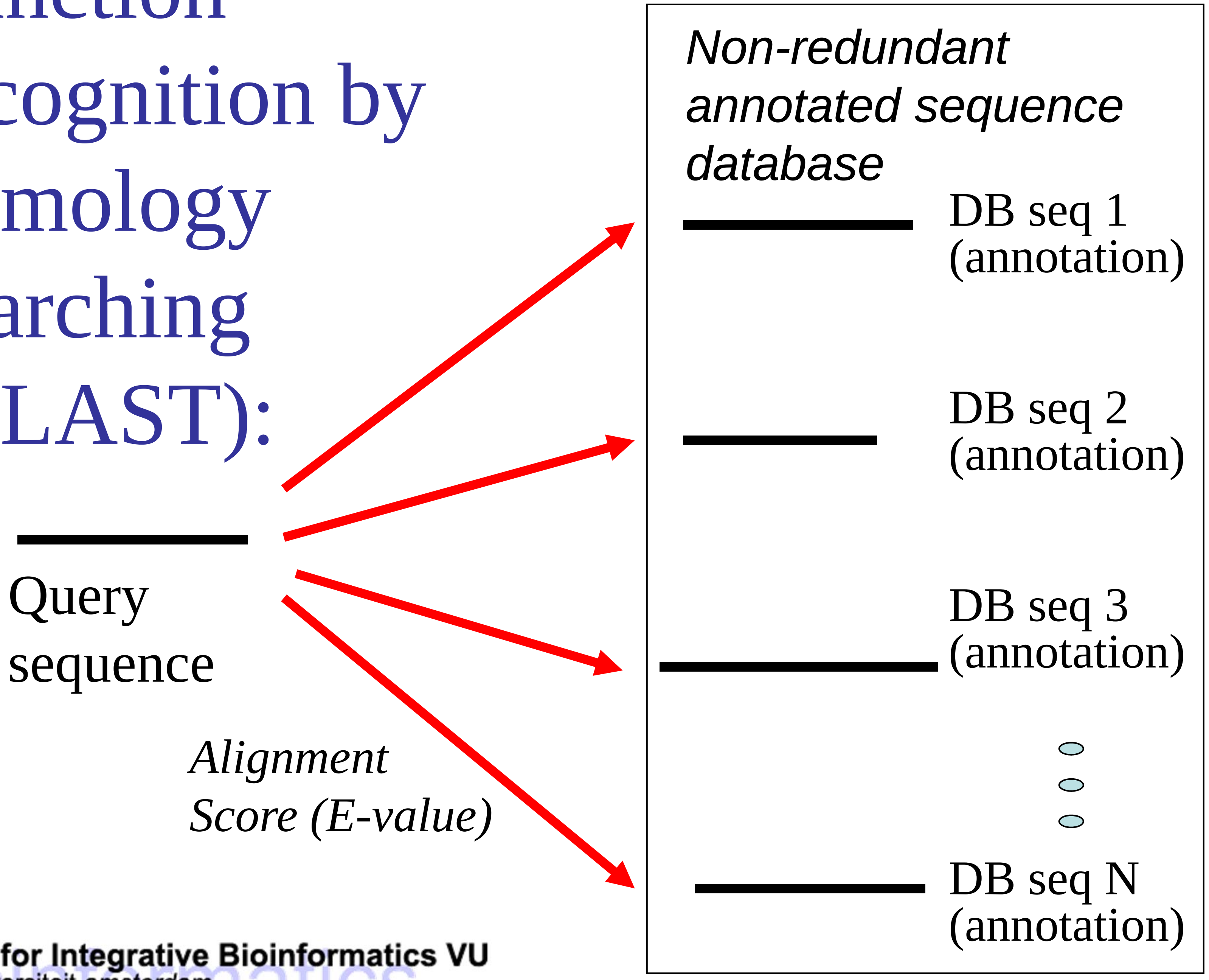
Ab initio prediction and folding

Ab initio Function prediction from structure

Luckily for bioinformatics…

- There are many annotated databases (i.e. DBs with experimentally verified information)
- *Comparative analysis:* We can relate biological macromolecules using evolution and then “steal” annotation of “neighbouring” proteins or DNA in the DB
- This works for sequence as well as structural information
- Problem: how do we score the evolutionary relationships; i.e. we need to develop a measure to decide which molecules are (probably) neighbours and which are not

Function recognition by homology searching (BLAST):



Query sequence

Alignment Score (E-value)

Non-redundant annotated sequence database

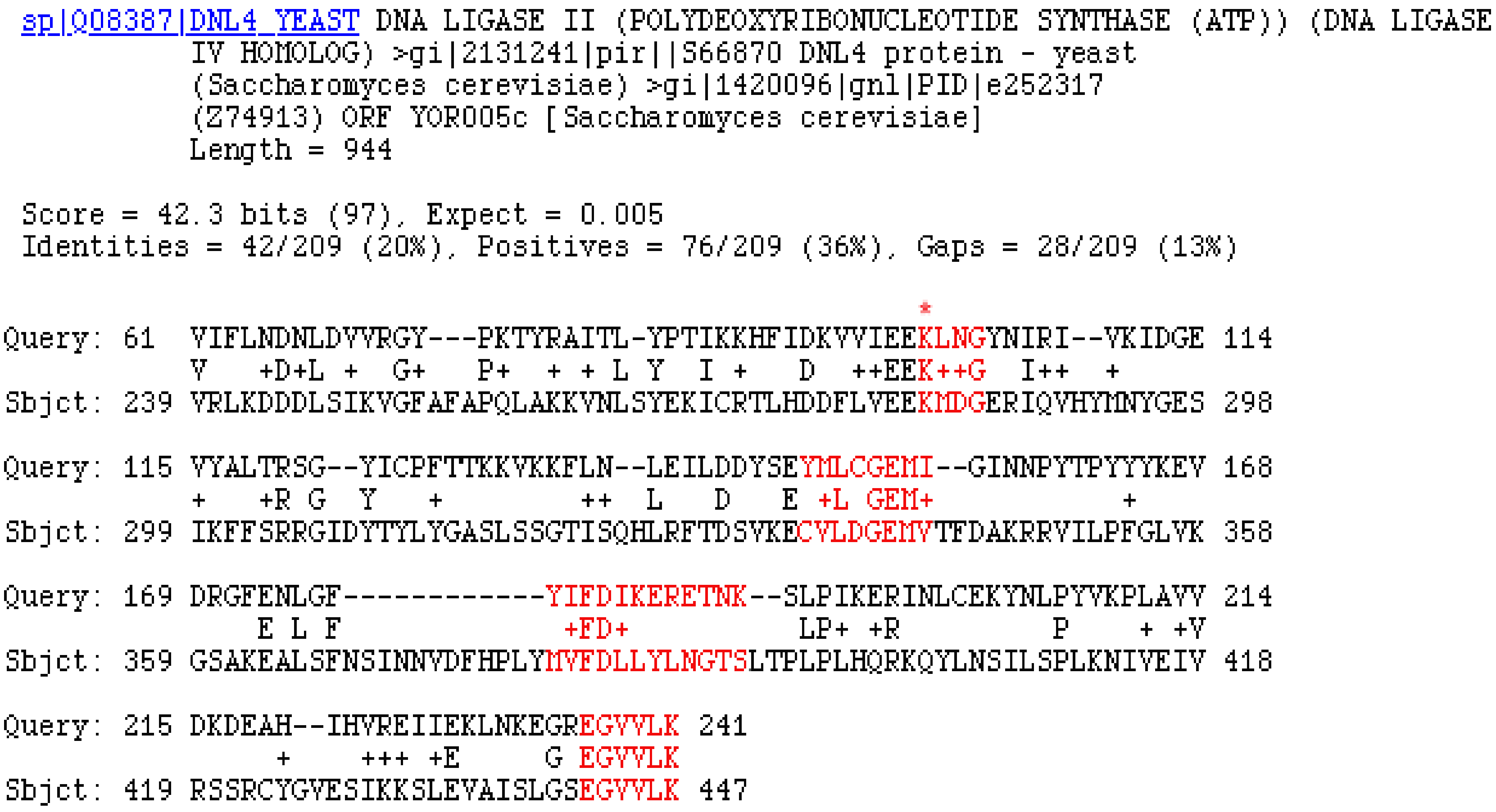
DB seq 1 (annotation)

DB seq 2 (annotation)

DB seq 3 (annotation)

DB seq N (annotation)

PSI-BLAST output example



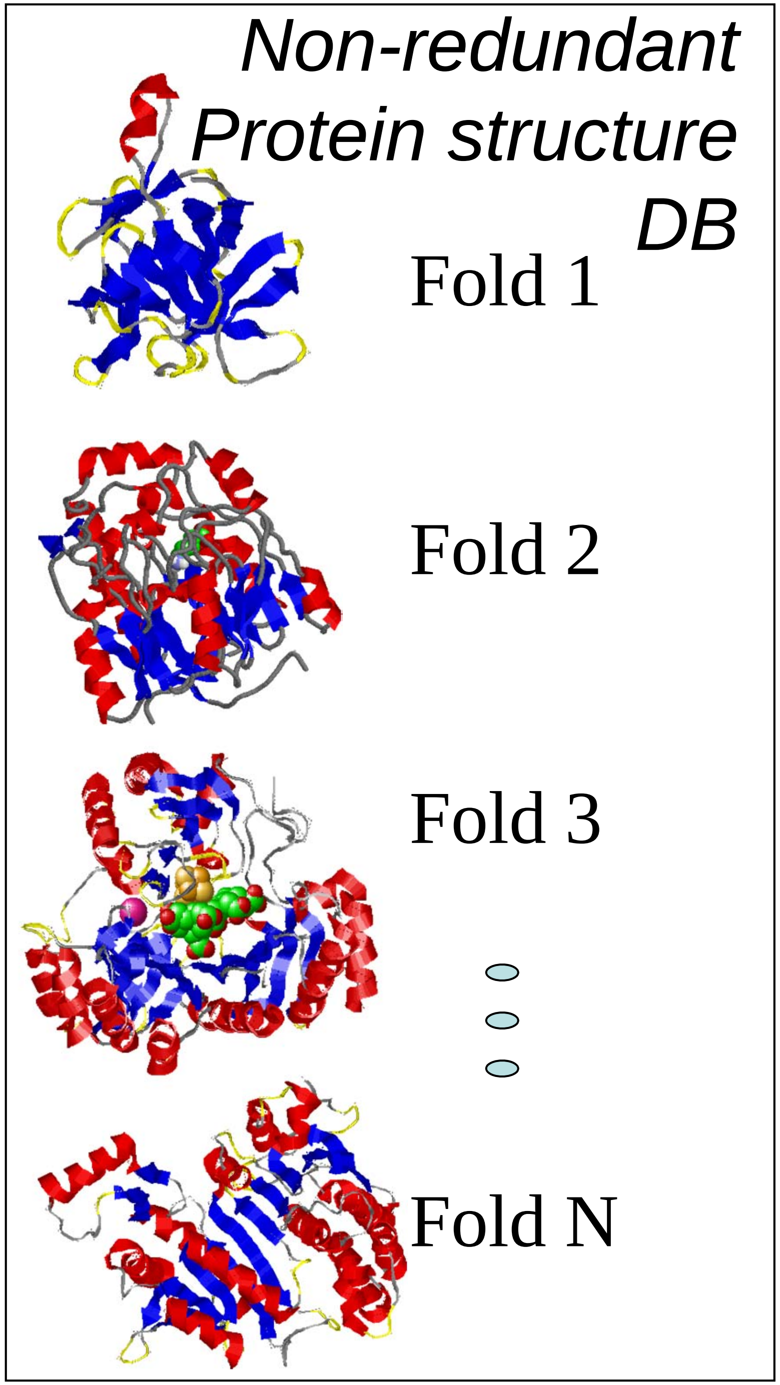
```
 sp|Q08387|DNL4_YEAST DNA LIGASE II (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) (DNA LIGASE
          IV HOMOLOG) >gi|2131241|pir||S66870 DNL4 protein - yeast
          (Saccharomyces cerevisiae) >gi|1420096|gnl|PID|e252317
          (Z74913) ORF YOR005c [Saccharomyces cerevisiae]
          Length = 944

 Score = 42.3 bits (97), Expect = 0.005
 Identities = 42/209 (20%), Positives = 76/209 (36%), Gaps = 28/209 (13%)

                                                        *
Query: 61  VIFLNDNLDVVRGY---PKTYRAITL-YPTIKKHFIDKVVIEEKLNGYNIRI--VKIDGE 114
           V   +D+L +  G+   P+  + + L Y  I +   D  ++EEK++G  I++   +
Sbjct: 239 VRLKDDDLSIKVGFAFAPQLAKKVNLSYEKICRTLHDDFLVEEKMDGERIQVHYMNYGES 298

Query: 115 VYALTRSG--YICPFTTKKVKKFLN--LEILDDYSEYMLCGEMI--GINNPYTPYYYKEV 168
           +   +R G  Y   +        ++  L   D   E +L GEM+           +
Sbjct: 299 IKFFSRRGIDYTYLYGASLSSGTISQHLRFTDSVKECVLDGEMVTFDAKRRVILPFGLVK 358

Query: 169 DRGFENLGF------------YIFDIKERETNK--SLPIKERINLCEKYNLPYVKPLAVV 214
               E L F             +FD+          LP+ +R         P    + +V
Sbjct: 359 GSAKEALSFNSINNVDFHPLYMVFDLLYLNGTSLTPLPLHQRKQYLNSILSPLKNIVEIV 418

Query: 215 DKDEAH--IHVREIIEKLNKEGREGVVLK 241
                +    +++ +E     G EGVVLK
Sbjct: 419 RSSRCYGVESIKKSLEVAISLGSEGVVLK 447
```

Fold recognition by threading:

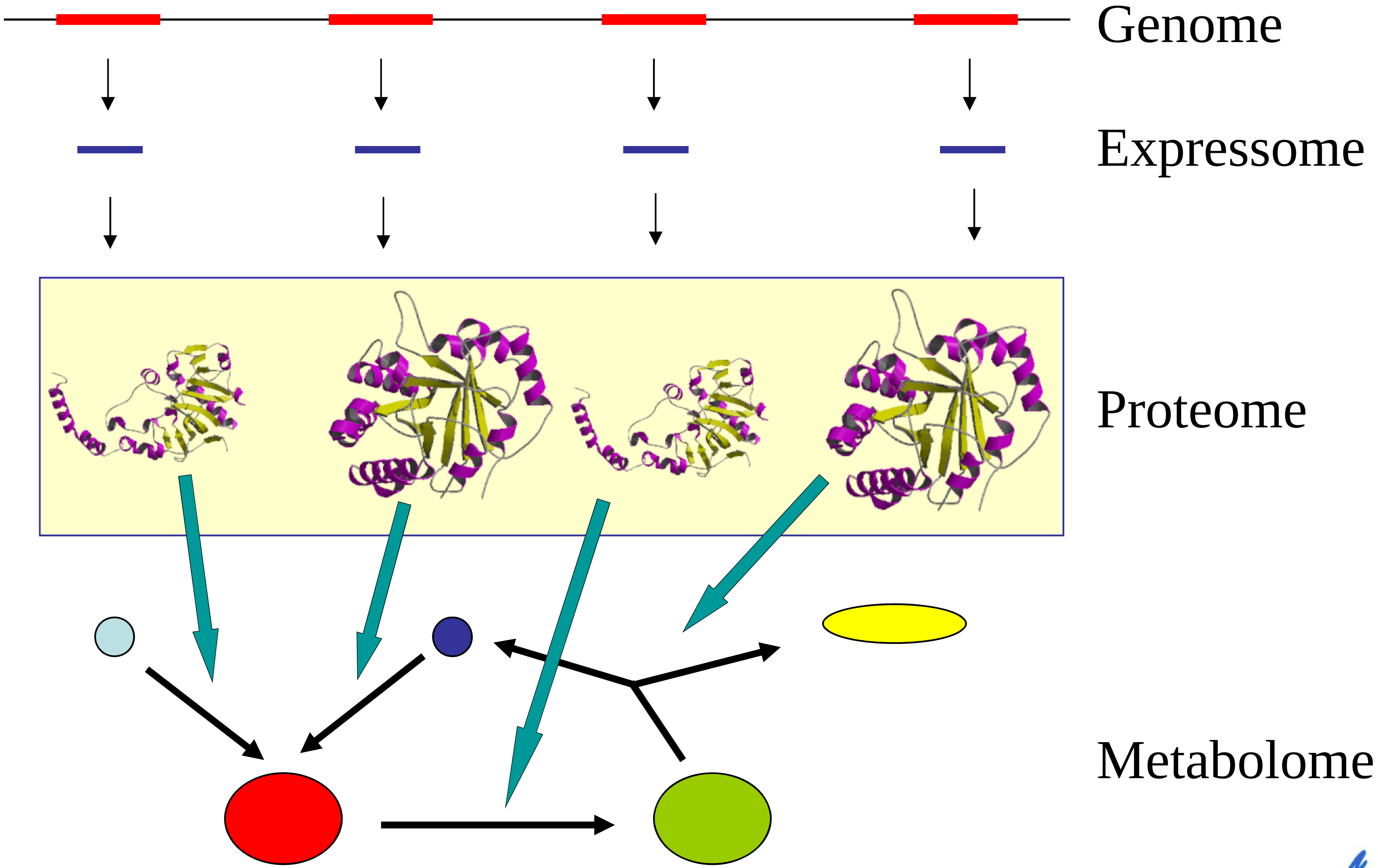
THREADER and GenTHREADER

Query sequence

Compatibility scores



Functional Genomics



Genome

Expressome

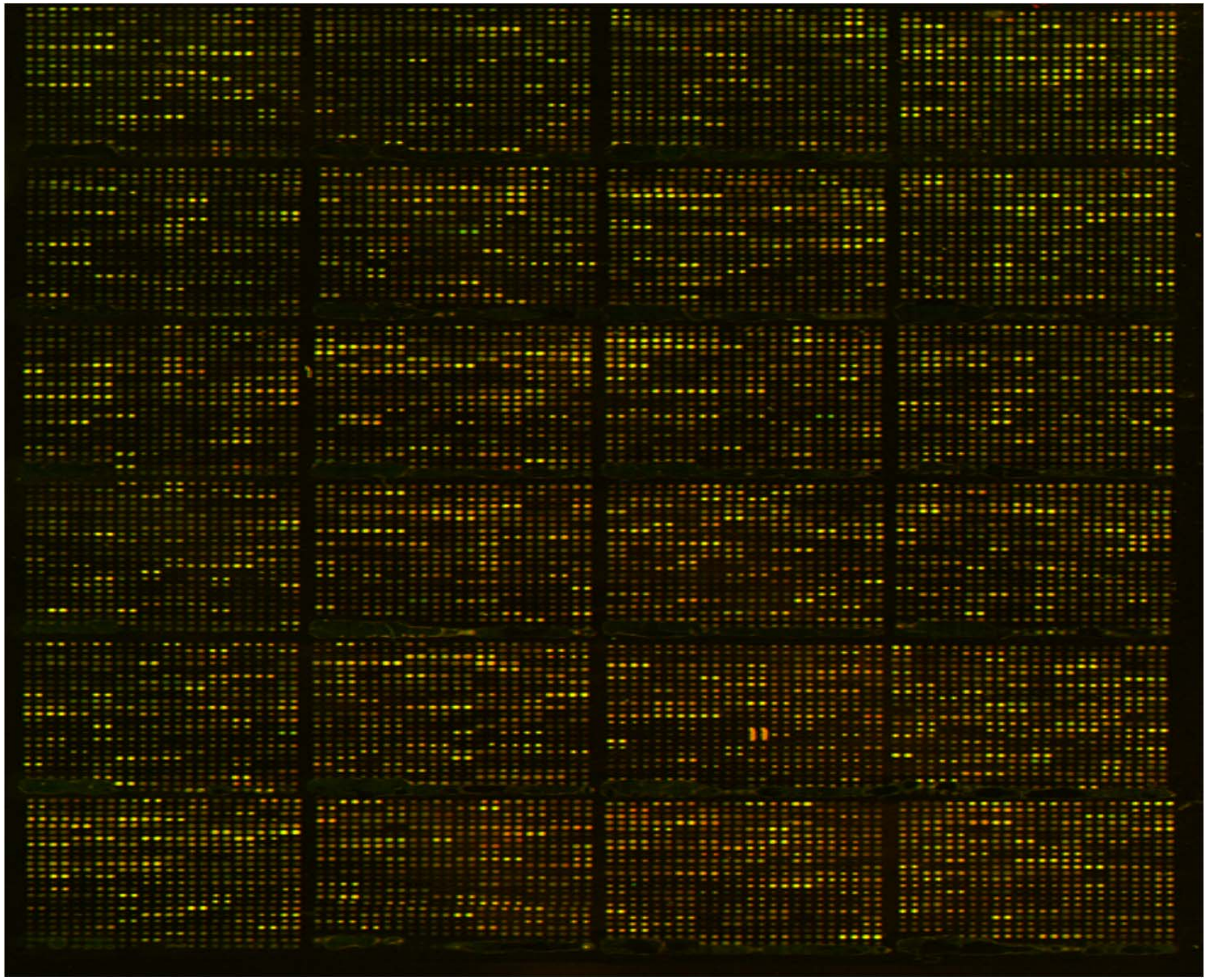
Proteome

Metabolome

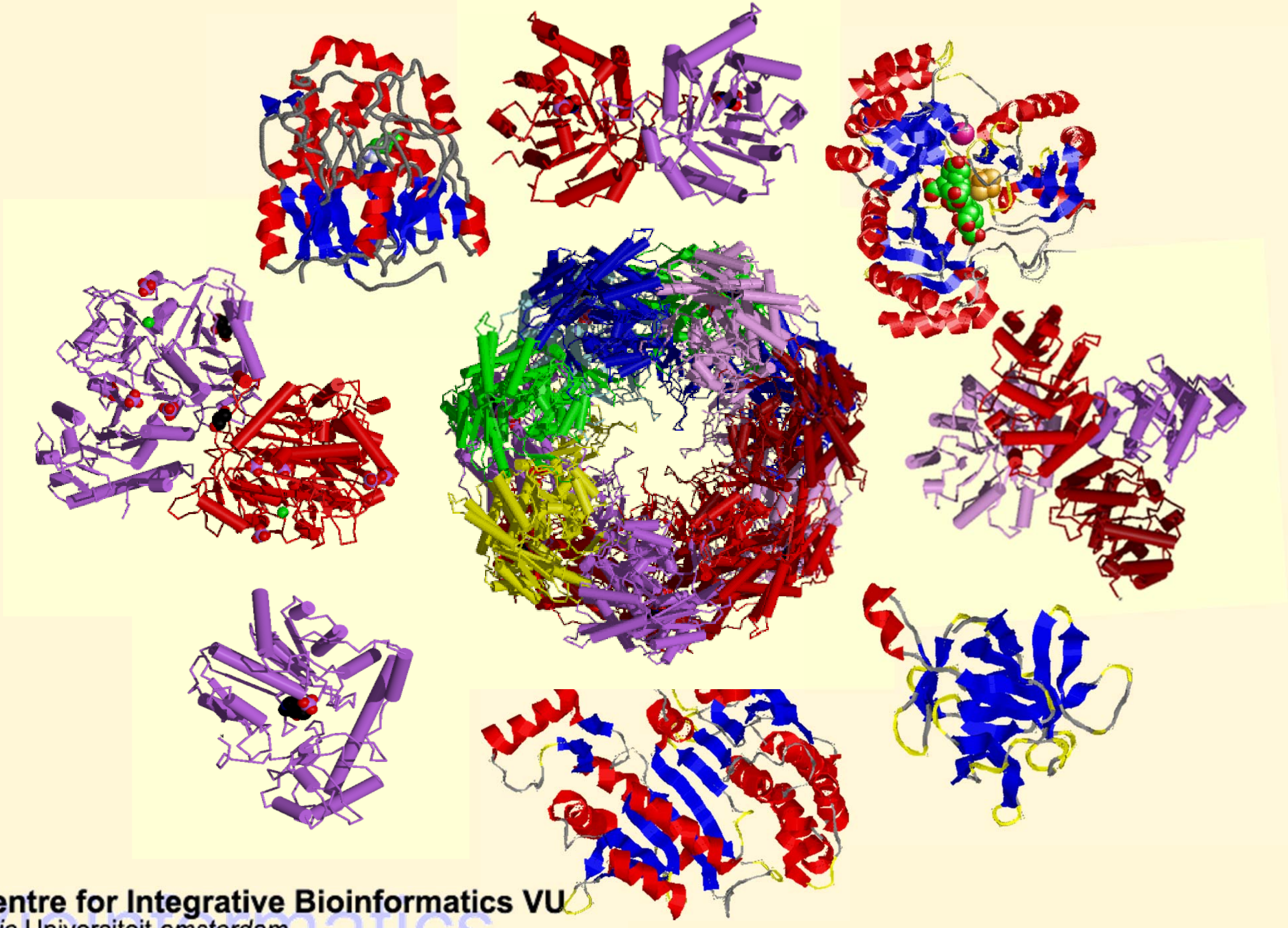
Genomics data

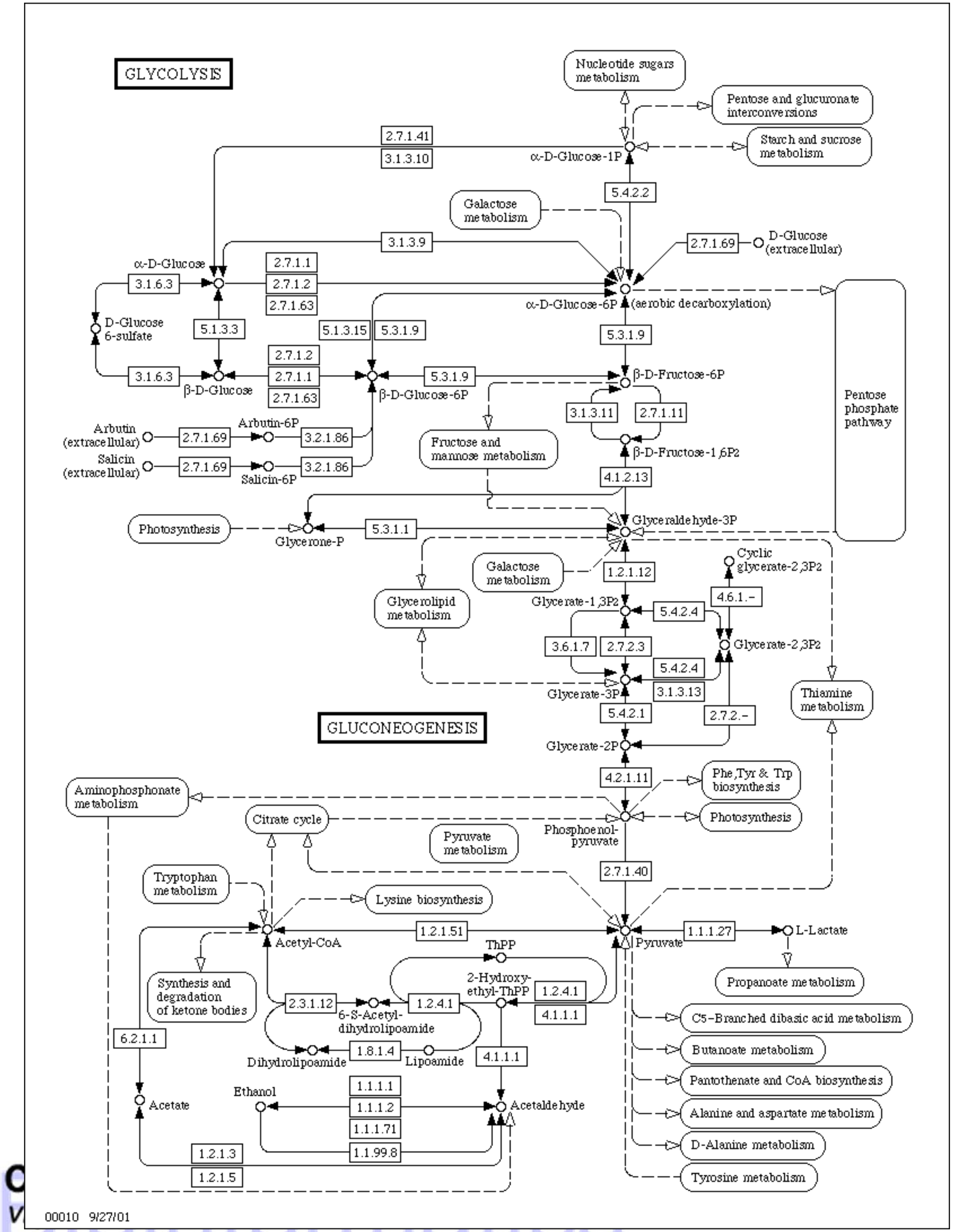
- Sequence data, Expression data, Regulation networks, Signalling cascades, Translation, etc.
- Proteomics, Metabolomics, Physiomics
- Databases
  - DNA, EST
  - Protein sequence (UniProt)
  - Protein structure (PDB)
  - Microarray data
  - Proteome
  - Metabolome
  - Protein-protein interactions (PPI)
  - Mass spectrometry/NMR/X-ray

Microarrays



Proteome





Metabolic networks

Glycolysis and Gluconeogenesis

Kegg database (Japan)

Modern bioinformatics is closely associated with genomics

- The aim is to solve the genomics information problem and understand cellular processes and disease
- Ultimately, this should lead to biological understanding how all the parts fit (DNA, RNA, proteins, metabolites) and how they interact (gene regulation, gene expression, protein interaction, metabolic pathways, protein signalling, regulation, etc.)

Algorithms in bioinformatics

- String algorithms
- Dynamic programming
- Machine learning (Neural Netsworks, k-Nearest Neighbour, Support Vector Machines, Genetic Algorithms, ..)
- Markov chain models
- hidden Markov models
- Markov Chain Monte Carlo (MCMC) algorithms
- Stochastic context free grammars
- EM algorithms
- Gibbs sampling
- Clustering, tree algorithms
- Text analysis
- Hybrid/combinatorial techniques and more…

Bioinformatics

- Offers an ever more essential input to
  - Molecular Biology
  - Pharmacology (drug design)
  - Agriculture
  - Biotechnology
  - Clinical medicine
  - Anthropology
  - Forensic science
  - Chemical industries (detergent industries, etc.)

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Studentenevaluatie

“De docent is wel goed maar het is een idioot vak”

2de jaars VU student(e) Medische Natuurwetenschappen

Bioinformatica onderzoek

De laatste jaren is in Nederland toenemend geïnvesteerd in onderzoek en onderwijs in de Bioinformatica. Dit is in belangrijke mate het gevolg van ontwikkelingen in het genomics- en biomedisch onderzoek, waarbij Bioinformatica steeds meer een centrale plaats inneemt. Bioinformatica is een zeer breed en multi-disciplinair vak, waar informatici, statistici, biologen en medici zeer nauw moeten samenwerken. Algoritme ontwikkeling (machine learning) en high-throughput data mining (grootschalige analyses van genomics datasets) is een essentiele component van het bioinformatica onderzoek. Daarbij is het onderzoek toenemend toegepast en grootschalig, veroorzaakt door de beloften die genomics onderzoek biedt en de reusachtige datasets die door genomics onderzoekers worden gegenereerd. De breedte/diepte van het vak, de snelle ontwikkelingen en het feit dat er nauwelijks uitgewerkt lesmateriaal is, maakt dat het opzetten van bioinformatica-onderwijs een enorme uitdaging is.

Bioinformatica onderwijs

Uitdagingen:

- de omvang (breedte/diepte) van het vak
- snelle ontwikkelingen
- weinig uitgewerkt lesmateriaal
- studententoestroom in Master vanuit zeer verschillende disciplines (biologie, medicijnen, chemie, informatica, natuurkunde, etc.)

Het opzetten van bioinformatica-onderwijs is een flinke uitdaging.

Hoe zit dit voor studenten

- Studenten kunnen moeite hebben met de oplossingsgerichte en heuristische aanpak die vaak nodig is in bioinformatica onderzoek.
- Vaak is een bioinformatisch probleem ill-defined, zijn er veel verschillende aanpakken mogelijk, en is er geen gouden standaard om de aanpak te testen.

Hoe zit dit voor studenten

- Van antwoord naar vraag terugredeneren is vaak moeilijk voor jongerejaars studenten

Bioinformatics practioners

- Need to have a well-developed concept of the art of doing science
- Need a high ability for (mathematical) abstraction
- Need a broad developed knowledge
- Need an ability to quickly absorb and integrate novel concepts
- Need well-developed engineering and practical skills in the area of computer science.

Bioinformatics students

- Should have knowledge concerning all neighbouring disciplines
- Should have an ability to deal with incomplete knowledge and mental pictures, while still being able to ask appropriate (research) questions
- Biology is the science area of complexity and inconsistency, where mathematical and physical concepts seem to derail frequently. Students should be trained to deal with these complexities.

Bioinformatica studenten

- Moeten met inconsistenties en complexiteit om kunnen gaan.
- Moeten kennis hebben van o.a. biologie, genomics, statistiek, modelleringstechnieken en -formalismen, en multivariate statistiek.
- Moeten bioinformatica methoden kunnen gebruiken en begrijpen.
- Moeten bioinformatica methoden kunnen ontwikkelen (en kunnen programmeren)

Bioinformatica studenten

- Sydney Brenner: “Bioinformatics research ranges from book-keeping to real art”.

  Students need to develop the skills and mentality to allow this full range of activities.

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Competentiegerichte vraagstelling (voorbeeld 1)

B.2. Een moleculaire biologe heeft een reguliere expressie waarmee zij de functionaliteit van een eiwit kan vaststellen:

`[AS]-D-[IVL]-G-x4-{PG}-C-[DE]-R-[FY]2-Q,`

waarbij [XY] betekent dat X en Y voor kunnen komen op de positie, x4 betekent ieder aminozuur voor 4 posities, en {PG} = *not* (P *or* G).

Ook heeft zij een multiple alignment van 30 orthologe sequenties met 150 posities waarin gaps voorkomen.

Zij wil graag weten of de sequenties in haar multiple alignment de functie hebben zoals beschreven in de reguliere expressie, d.w.z. of de sequenties voldoen aan het functionele motief zoals gegeven in de bovenstaande reguliere expressie.

Competentiegerichte vraagstelling (voorbeeld 1)

Vraag: geef een procedure met een *scoring function* waarop zij dat zou kunnen doen. Bedenk dat het functionele motief op meerdere posities in het multiple alignment zou kunnen passen. Gebruik voor de scoring functie de index x voor de positie in de reguliere expressie ($1 \leq x \leq 15$), i voor de sequenties in het alignment ($1 \leq i \leq 30$) en j voor de posities in het multiple alignment ($1 \leq j \leq 150$). **Hint:** de procedure en score moeten de best mogelijke *fit* weergeven.

Competentiegerichte vraagstelling (voorbeeld 2)

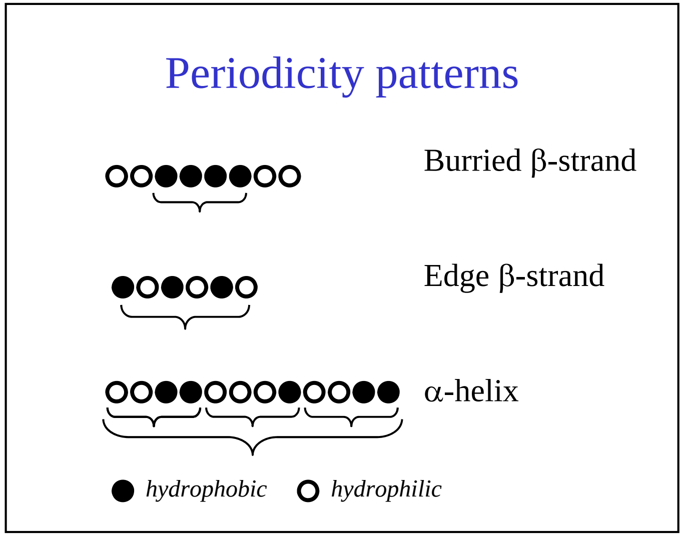
B4. De biologe van vraag B.2. en B.3. heeft nog een multiple alignment waarvoor zij graag de secundaire structuur zou willen bepalen. Onderstaand zijn twee segmenten van het multiple alignment: voorspel hiervoor de secundaire structuur.

De fragmenten van het multiple alignment zijn:

```
DKRSVLMICKTG   en      MVDRLIKEFYTSDNQ
DRRTGLMIIRTG           MIDRLLREFYTTDDQ
EKRDILVILDTG           MIERLLRDYYSTNDQ
EKKDILMLIRTS           VIDKILRDFFGSNNN
DKKEVIMILDTS           PAAKIIDDAFGSDEE
```

Neem als hydrofiele aminozuren: D, E, G, H, K, N, Q, R, S, en T.
Neem als hydrofobe aminozuren: A, C, F, I, L, M, P, V, W, en Y.
Hieronder staan de *periodicity patterns* zoals verwacht voor de α-helix en twee soorten β-strand:

Competentiegerichte vraagstelling (voorbeeld 2)



Vraag: voorspel de secundaire structuur van de twee bovenstaande stukken multiple alignment met gebruikmaking van de *periodicity patterns*. Gebruik de letters ‘H’ voor helix, ‘B’ voor burried β-strand, ‘E’ voor edge β-strand, en ‘C’ voor coil.

Hint: Let op de conserveringspatronen in de multiple alignments.

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Bioinformatics teaching @ IBIVU

Introduction to Bioinformatics

26 two-hour course blocks

Medical Natural Sciences 2nd year

2-year international Bioinformatics master's

International 2-year Master Bioinformatics @ VU

Target group:

- Students with Bachelor Physics, Chemistry, Mathematics, Computer Science, Biology, or Medical Natural Sciences
- *Students from Medicine or Health sciences?*
- *Computer science students don't know the biology and biology students don't know the computer science*

Remarks:

1. We require programming experience for some courses.
2. VU master teaching is moving towards *pre-master* of 6 months maximally, to fill in deficiencies and to aim at students coming from non-academic higher education.

International 2-year Master Bioinformatics @ VU

Centre for Integrative Bioinformatics (IBIVU)

Faculty of Sciences/Faculty of Earth & Life Sciences

Free University Amsterdam

http://www.ibivu.cs.vu.nl

Outline: 45 ECTS courses, 75 ECTS practical work (120 ECTS total):

- Compulsory courses 30 credits
- Optional courses 16-18 credits
- First traineeship 30-60 credits (Major)
- Second traineeship 15-30 credits (Minor)
- Optional third traineeship 15-30 credits

International 2-year Master Bioinformatics @ VU

Compulsory courses (6 ECTS each):

Course 1. Sequence Analysis
Course 2. DNA/Protein structure-function analysis and prediction
Course 3. Bioinformatics data analysis and tools
Course 4. Genome analysis: structural and functional genomics
Course 5. Integrative bioinformatics

International 2-year Master Bioinformatics @ VU

Compulsory courses (6 ECTS each):

- 2-hour lectures
- practical assignments (mini-projects)
- most assignments offer various complexity options
- all information on-line (IBIVU website)
- students can get individual help from teachers
- students work on real open-ended research questions, select approach themselves, and have own responsibility

International 2-year Master Bioinformatics @ VU

Optional courses (3-6 ECTS each):

Are provided by the IBIVU mainly through the Biology, Mathematics and Computer Science Departments. Students may also choose courses at other departments in consultation with your mentor.

A range of optional courses is available, including Introduction to Bioinformatics, Statistical Genetics, Statistical Models, Machine Learning, Evolutionary Methods, Neural Networks, Data Mining Techniques, Scientific Visualization and Parallel Programming (Department of Computer Science).

International 2-year Master Bioinformatics @ VU

Traineeships:

- Can be carried out VU-wide:
    - The Centre for Neurogenomics and Cognitive Research (CNCR)
    - The Institute for Molecular Cell Biology (IMC)
    - The IBIVU
    - The Centre for Complex Molecules
- Embedded in national initiatives in which the IBIVU participates:
    - Ecogenomics
    - Center for Medical Systems Biology (CMSB)
- Other national or international institutes (VU Internationalisation)

Visualisation and Teaching

The ICwall @ VU

4096 x 1536
pixels

A cheap scalable solution: multiple beamers (from the back), stereo viewing.

Challenges: alignment, porting software

Bioinformatics Masters in The Netherlands

“Core” masters:

- CMBI, University of Nijmegen (Gert Vriend) – *classical, general*
- Wageningen University (Peter Schaap), in collaboration with CMBI – *genomics oriented*
- IBIVU, Free University of Amsterdam (Jaap Heringa) – *classical, general, tool creation*

Bioinformatics Masters in The Netherlands

“Combination” masters:

- Master *Life Sciences,* Groningen University (Ritsert Jansen) – Bioinformatics courses
- *Major Bioinformatics in Master Life Science & Technology*, University of Leiden (Joost Kok)
- Master *Molecular Cell Biology and Bioinformatics*, University of Amsterdam, starting 2005
- *Major Bioinformatics in Master Life Sciences*, University of Maastricht (Robert Vlietinck)
- Master *Theoretical Biology & Bioinformatics*, University of Utrecht (Paulien Hogeweg) - *modelling*
- Master *Genomics and Bioinformatics,* University of Utrecht (Albert Heck)

Netherlands BioInformatics Centre (NBIC)

- Bioinformatics Application Service Provider (BioASP)
- BioRANGE – National collaborative bioinformatics integrated project
- Biowise – National bioinformatics training initiative
  - Biotune
    - Software for categorising and storing teaching materials
    - Software for course development

name	**Sequence Analysis**
aim	A theoretical and practical bioinformatics course about biological sequence analysis. The course provides an introduction to the algorithmic and biological principles of sequence analysis, as well as practical implications. *Goals:* •At the end of the course, the student will be aware of the major issues, methodology and available algorithms in sequence analysis. •At the end of the course, the student will have hands-on experience in tackling biological problems in sequence analysis.
contents	*Theory*: •Dynamic programming, database searching, pairwise and multiple alignment, probabilistic methods, pattern matching, evolutionary models, and phylogeny. *Practical*: Assignment programming own alignment software based on dynamic programming Assignment homology searching and pattern recognition using biological and disease examples Assignment multiple alignment of biological sequences
methodology	13 Lectures (2 two-hour lectures per week); Assignment introductions; Computer practicals; Hands-on support
literature	E-course material: *http://ibivu.cs.vu.nl* Books: Richard Durbin, Sean R Eddy, Anders Krogh, Graeme Mitchison (1998). Biological Sequence Analysis. Cambridge University Press, 350 pp., ISBN 0521629713.
teaching	Active participation (November/December 2004).
test	Assignment results and oral or written exam (depending on number of course students)
target group	Students with Bachelor Physics, Chemistry, Mathematics, Computer Science, Biology, or Medical Natural Sciences, with a strong interest in Bioinformatics
remarks	The course is taught in English
required knowledge	Some experience in programming is required.

name	**DNA/Protein Structure-Function Analysis and Prediction**
aim	A theoretical and practical bioinformatics course on the analysis and prediction of structure-function relationships of DNA and protein molecules. The course provides an introduction to the molecular principles of structure and function, available bioinformatics analysis and prediction techniques, and biological databases. *Goals:* •At the end of the course, students will be aware of the major issues, methodology and . •At the end of the course, the student will have hands-on experience in molecular modeling and studying structure-function relationships.
contents	*Theory*: •Protein folding and energetics, experimental structure determination, protein fold families, protein structure databases, protein secondary structure prediction, fold prediction, molecular modeling, protein-protein interactions, DNA/RNA structure/function, DNA/RNA structure prediction *Practical*: Assignment homology modelling Assignment immunocomplex modelling
methodology	13 Lectures (2 two-hour lectures per week); Assignment introductions; Computer practicals; Hands-on support
literature	E-course material: http://ibivu.cs.vu.nl Books: Carl Branden & John Tooze (1998). Introduction to Protein Structure. 2nd Edition or higher. Garland Science, 410 pp., ISBN 0815323050.
teaching	Active participation (January/February 2005).
test	Assignment results and oral or written exam (depending on number of course students)
target group	Students with Bachelor Physics, Chemistry, Mathematics, Computer Science, Biology, Medical Natural Sciences or Medicine, with a strong interest and some basic knowledge in Bioinformatics
remarks	The course is taught in English.
required knowledge	A completed course *Sequence Analysis* is a strong advantage.

Name	**Bioinformatics data analysis and tools**
aim	A theoretical and practical bioinformatics course on the fundamentals of bioinformatics tools and tool creation for biological data mining. Goals: •At the end of the course, students will be aware of the issues, methodology and available bioinformatics tools for •At the end of the course, students will have hands-on experience in molecular modeling and studying structure-function relationships.
contents	*Theory:* •Inverse protein folding, introduction to statistical thermodynamics of soft and biological matter (5 lectures), genetic algorithm, repeat recognition tools and concepts (e.g. transitivity), molecular mechanics simulations, (hidden) Markov models, pattern recognition, machine learning techniques *Practical:* Assignment Statistical Thermodynamics Assignment hidden Markov modelling
methodology	13 Lectures (2 two-hour lectures per week); Assignment introductions; Computer practicals; Hands-on support
literature	E-course material (slides, assignment material, papers): http://ibivu.cs.vu.nl Books: Biological Physics. Energy, Information, Life. Philip Nelson. 600 pages , W H Freeman & Co., (July 2003), ISBN: 0716743728
teaching	Active participation (April/May 2005).
test	Assignment results and oral or written exam (depending on number of course students)
target group	Students with Bachelor degree in Physics, Chemistry, Mathematics, Computer Science, Biology, Medical Natural Sciences or Medicine, with a strong interest and some basic knowledge in Bioinformatics
remarks	The course is taught in English.
required knowledge	A completed course *Sequence Analysis* and *DNA/Protein Structure-Function Analysis and Prediction* is a strong advantage. Some experience in programming is required.

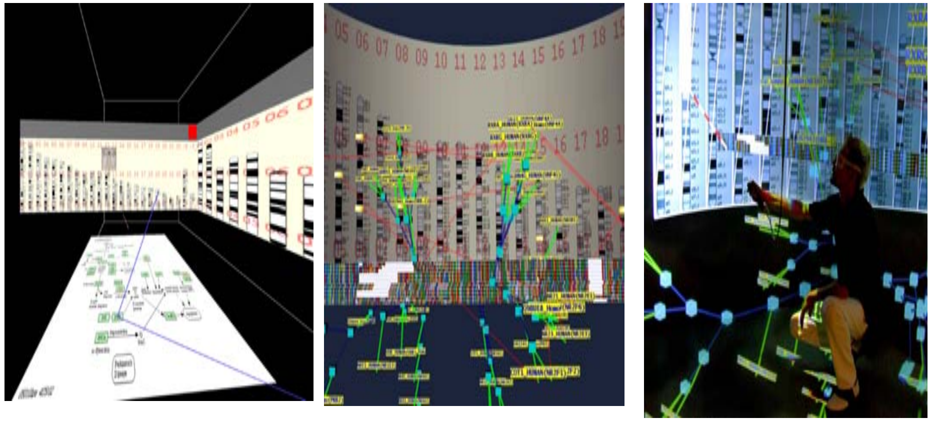
name	**Genome Analysis**
aim	A 1-month intensive course for introduction to genomics and bioinformatics techniques used to analyse and integrate genomics data sets.
contents	*Static genome analyses:* DNA, RNA and protein primary, secondary, tertiary en quaternary structures; genome sequencing, methods and annotation; genome projects (bacteria, yeast, plant, animal, human), bioinformatics and databases; COG, EST, SNP, motifs *Dynamic genome analyses:* transcriptome (arrays en clustering, QPCR, SAGE); proteomics (mass spectrometry, arrays, 2D gel electrophoresis, homology modeling); metabolomics (methods, interpretation, databases) *Functional genetics:* knock-out, reporter genes, expression vectors, promoter-probe studies; reverse genetics, RNAi, transgenese *Integrative genome analyses:* network modelling, Metabolic Control Analysis, biochemical databases; physiomics *Application areas:* medical genomics; ecogenomics; sociogenomics; pharmacogenomics; biotechnological genomics; ethical aspects
methodology	15 short modules, each including a lecture, (computer) practical and self study Tutorials/discussions of book material, lecture notes Computer practicals Lab demonstrations: Students follow and assist an experienced postdoc/Ph D student performing a key experiment. Data evaluation and interpretation on site.
literature	Powerpoint presentations via Blackboard Book: *A primer of genome science*. Gibson G and Muse, SV, Sinauer Associates Inc Publishers, 2002, ISBN 0-87893-234-8 (pbk). E-course material: http://ibivu.cs.vu.nl
teaching	Active participation
test	Exam (50%), assignments (25%) and computer analyses (25%)
target group	Students with Bachelor Physics, Chemistry, Mathematics, Computer Science, Biology, or Medical Natural Sciences, with a strong interest in Bioinformatics
remarks	The course will be taught in Dutch; provisions can be made for English speakers.
required knowledge	Bachelor Physics, Chemistry, Mathematics, Computer Science, Biology, Medical Natural Sciences.

name	**Integrative Bioinformatics - Intracellular networks**
aim	A 1-month intensive course providing an introduction to cell biological networks.
contents	*Theory*: The course gives an introduction to the behavior of intracellular networks, including metabolic pathways, signal transduction chains, gene expression pathways and their hierarchical organization. Metabolic and Hierarchical Control Analysis, Biological Non Equilibrium Thermodynamics, Genetic Network Analysis, Elementary Mode Analysis, Flux (Balance Analysis) will be explained and practiced. The levels of genomics (genome, transcriptome, proteome, metabolome and function) and their interrelationships will be clarified, both theoretically and experimentally. *Practical*: •inspection experiments performing flux and metabolite; measurements and subsequent regulation analysis; inspection experiments; designing network targeted inhibitors of parasites; flux analysis on the basis of a set of computer data; control analysis on the basis of earlier experimental results; •extra assignment integrative bioinformatics for bioinformatics master students (1 ECTS)
methodology	Lectures; Tutorials/discussions of book material; Lecture notes Web-courses (www.siliconcell.net); Computer practicals; Lab-inspection work: Students follow and assist an experienced postdoc/Ph D student performing a key experiment. Data evaluation and interpretation on site.
literature	E-course material: http://www.bio.vu.nl/hwconf/teaching/Mathbiochemie/; www.siliconcell.net Books: Chapters from:Understanding the Control of Metabolism (Fell, D) Portland Press; Metabolic Engineering in the Postgenomic Era (Kohlodenko & Westerhoff, Editors), Horizon Bioscience; Thermodynamics and Control of Biological Free-energy transduction (Westerhoff and Van Dam), Elsevier
teaching	Active participation (March/April 2005)
test	Written exam
target group	Students with Bachelor Physics, Chemistry, Mathematics, Biology, Medical Biology with a strong interest in the interface between these disciplines and bioinformatics
remarks	The course is taught in the English language and involves extensive direct contact with the professors and associate professors.
Required knowledge	Bachelor Physics, Chemistry, Mathematics, Informatics, Biology, Medical Natural Sciences, or equivalent;

Integrative Visualisation

Porting SARAgene virtual reality comparative genomics software

The CAVE @ SARA



The ICwall @ VU

SaraGene

3D visualisation important for large genomic data sets:

- Clustering and mapping genes onto location, expressome, metabolome, etc.
- Many data objects (labels): need 3D to place objects and high resolution to read labels
- CAVE has good 3D but low resolution (e.g. labels not easily readable)
- ICwall has bit less 3D capability but much higher resolution.

Problems/suggestions

- Diverse target group, how to get students up to scratch before starting masters. *Lost a (biology) student due to inability to program.*
  - Biosapiens pre-master?
  - Biosapiens driven bioinformatics bachelor?
- Standards/exams
  - Competence based learning: minimal skills/knowledge definition
  - European bioinformatics master certificate
- Structuring subjects: students don’t always appreciate where things fit in. *“Teacher was OK but subject is idiotic”*
- Lack of students in Dutch science faculties
  - Biosapiens driven Bioinformatics PR initiative (e.g. *Bioinformatics and Society*)
- Utilities
  - Bioinformatics practical course book; slides, exercises, practical, exam questions DB; E-learning; Grid-based distance learning, Visualisation/ICwall

Needs

- Quality of teaching
  - – Train the trainers (Biosapiens can help)
- Course material organized (in english (!) and accessible) (Biosapiens)
  - – Background material previous to the master courses
- Standards and reciprocal recognition
- What else do we need?

Funding possibilities

- *Erasmus mundus* and European initiatives
- BioSapiens training and general courses (“European Permanent School and Advanced workshops”)
- ESF, EMBO and FEBS possible liasons for workshop organization
- Students interchange (housing facilities)

THE END

Abstract

- De laatste jaren is in Nederland toenemend geïnvesteerd in onderzoek en onderwijs in de Bioinformatica. Dit is in belangrijke mate het gevolg van ontwikkelingen in het genomics- en biomedisch onderzoek, waarbij Bioinformatica steeds meer een centrale plaats inneemt. Bioinformatica is een zeer breed en multi-disciplinair vak, waar informatici, statistici, biologen en medici zeer nauw moeten samenwerken. Algoritme ontwikkeling (machine learning) en high-throughput data mining (grootschalige analyses van genomics datasets) is een essentiele component van het bioinformatica onderzoek. Daarbij is het onderzoek toenemend toegepast en grootschalig, veroorzaakt door de beloften die genomics onderzoek biedt en de reusachtige datasets die door genomics onderzoekers worden gegenereerd. De breedte/diepte van het vak, de snelle ontwikkelingen en het feit dat er nauwelijks uitgewerkt lesmateriaal is, maakt dat het opzetten van bioinformatica-onderwijs een enorme uitdaging is.
- Aan de Vrije Universiteit verzorgd het Centre for Integrative Bioinformatics masteronderwijs alsmede een bachelorcursus Bioinformatica voor studenten Medische Natuurwetenschappen (MNW). Onze ervaring is dat studenten moeite kunnen hebben met de oplossingsgerichte en heuristische aanpak die vaak vereist is in bioinformatica onderzoek. Naast het aanleveren van benodigde kennis (waar een selectieprobleem heerst door de breedte van het vak) staat competentiegericht onderwijs centraal.
- In mijn voordracht bespreek ik de centrale problemen en positionering van Bioinformatica-onderzoek en zal ik ingaan op de competentiegerichte elementen in onderwijs en toetsing.