BIOINFORMATICS

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Montefiore Institute - Systems and Modeling

GIGA - Bioinformatics

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Administration

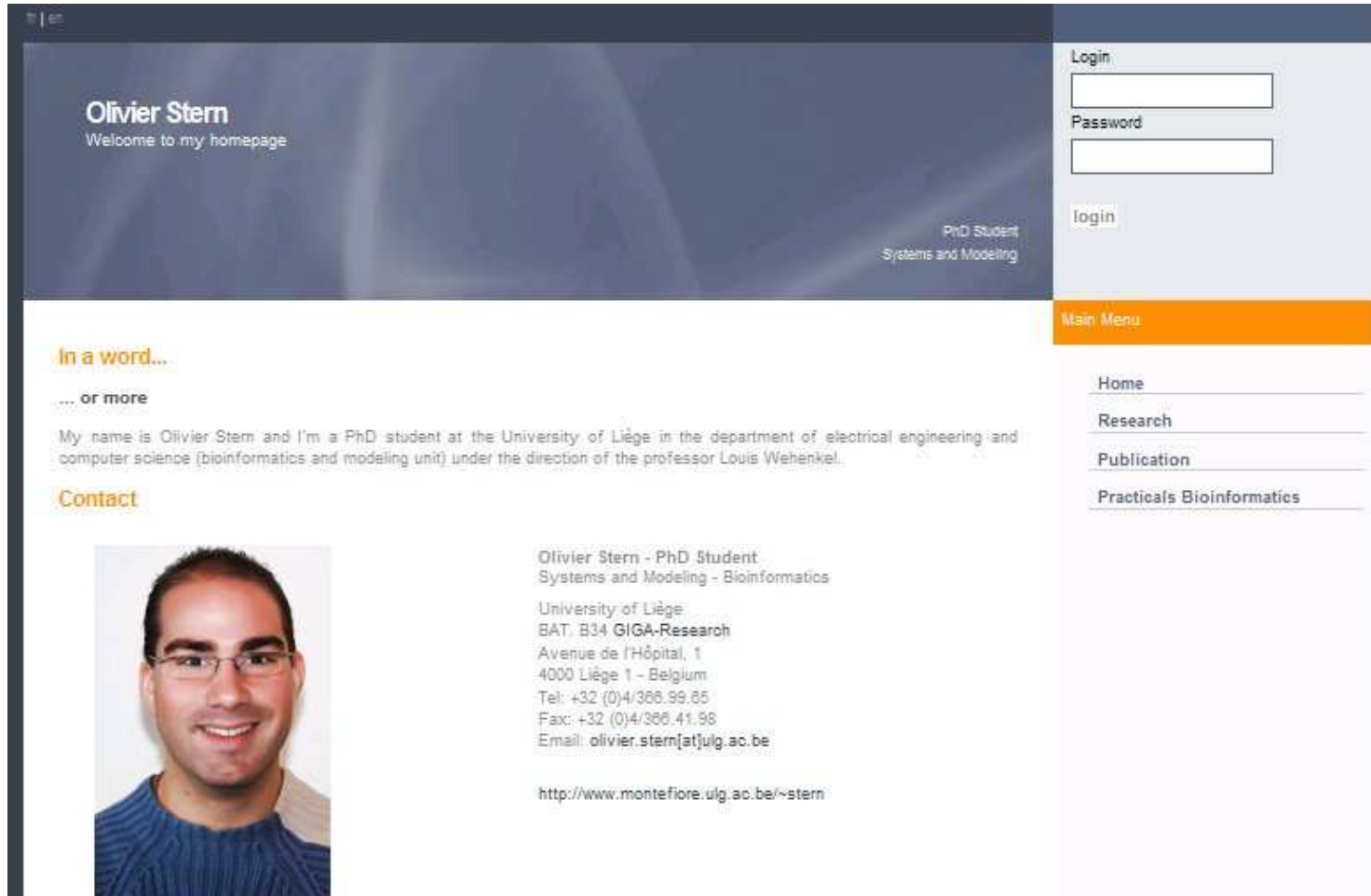| Contenus du cours	Course contents
Ce cours est une introduction au bioinformatics et peut inclure les matières suivantes : gestion de base de données et recherches de base de données des bioinformaticians, statistiques pour le bioinformatics, alignement d'ordre, identification de modèle, phylogenetics, génétique statistique et analyse microarray	This course is an introduction to bioinformatics and may include the following topics : data base management and data base searches for bioinformaticians, statistics for bioinformatics, sequence alignment, pattern recognition, phylogenetics, statistical genetics and microarray analysis
Acquis d'apprentissage (objectifs d'apprentissage) du cours	**Learning outcomes of the course**
A la fin de ce cours, les étudiants auront un goût de différents domaines couverts par bioinformatics, de connaissance pratique au sujet des recherches de base de données, de l'alignement d'ordre, de la comparaison d'expression de gène et du genomewide screening.	At the end of this course, students will have a taste of different areas covered by bioinformatics, with practica knowledge about data base searches, sequence alignment, gene expression comparison and genomewide screening.
Prérequis et corequis / Modules de cours optionnels recommandés	**Prerequisites and co-requisites/ Recommended optional programme components**
/	/
Activités d'apprentissage prévues et méthodes d'enseignement	**Planned learning activities and teaching methods**
Travail personnel par l'intermédiaire des tâches de lecture, homeworks et plus grands projets, à l'aide principalement des outils de Bioconductor dans le logiciel libre R.	Personal work via reading assignments, homeworks and larger projects, mainly using Bioconductor tools in the free software R.
Mode d'enseignement (présentiel ; enseignement à distance)	**Mode of delivery (face-to-face ; distance-learning)**
Mardi après-midi, entre 14h-18h (contrôle avec le corps enseignant), Institut Montefiore, premier	Tuesday afternoon, between 14h-18h (check with teaching staff), Institut Montefiore, first semester.

Workshops

Personal work via

- reading assignments,

- homeworks and

- one large final project

mainly using Bioconductor tools in the free software R.

Practicals and additional help (1) - GIGA

(http://www.montefiore.ulg.ac.be/~stern/)

Practicals and additional help (1) – Montefiore

(http://www.montefiore.ulg.ac.be → personnel scientifique)

Organization: tentative course layout

Room	Date	In Class Time	Course Topic
1.21 (B28)	20-sept	16-18	CH1: Bioinformatics - what it means and does not mean
1.21 (B28)	4-oct	16-18	Intro to R
1.21 (B28)	11-oct	16-18	CH2: A primer on genetics
1.21 (B28)	18-oct	16-18	CH3: Sequence analysis
1.21 (B28)	25-oct	14-16	CH3: Sequence analysis (continued)
		16-18	Sequence analysis in practice - **HMW1 Assignment**
1.21 (B28)	8-nov	14-16	CH4: Comparison of sequences
		16-18	Comparing sequences in practice - **HMW2 Assignment**
1.21 (B28)	15-nov	14-17.30	CH5: Genome-wide association analysis
		17.30-18.00	Genome-wide association analysis in practice - **HMW3 assignment**
1.21 (B28)	22-nov	14-18	CH6: A world of interactions
1.21 (B28)	29-nov	14-16	Data mining with Random Jungle - **HMW4 assignment**
		16-18	Opportunity to ask questions about the HMWs to the assistents
1.21 (B28)	6-déc	14-17	CH7: Family relationships - an advantage or disadvantage?
		17-18	Showcase of FAMMDR (no exam material)
TBA	TBA	14-16	GUEST SPEAKER: a case study
		16-18	Project assignment: combining HMW3-4

- Interested in a particular bioinformatics application?
- Let me know, and I can incorporate it as separate section of the course…

Organization

- The course will be interactive in English/French.

    o All course notes are in English.

    o Homeworks can be handed in in French.

    o Examination will be in French (or in English if requested for).

# Passing the course successfully

- You can obtain a maximum of 100 points

  - Written exam in French: maximum of 60 points

    - Multiple choice questions – closed book (discussable)

  - Practicals: maximum of 40 points (4 homeworks)

    - Homeworks are handed in electronically unless mentioned otherwise. You can choose the language

    - Homeworks 3 and 4 are actually part of a larger project and will have several components. A presentation presenting this homework can be part of a supporting oral exam (discussable)

- **When practicals are not handed in in time (without acceptable reason) → ZERO**

Course notes materials

- Main course book:

  - Richard C. Deonier, Simon Tavare & Michael S. Waterman:
    Computational Genome Analysis – an Introduction, Springer 2005
  - Check with campus facilities for good rates
  - The book is recommended as complement to the course slides, but is
    not mandatory. It is a nice reference book

- Course slides are obtained via the course website at:

  http://www.montefiore.ulg.ac.be/~kvansteen/

Motivation for course book
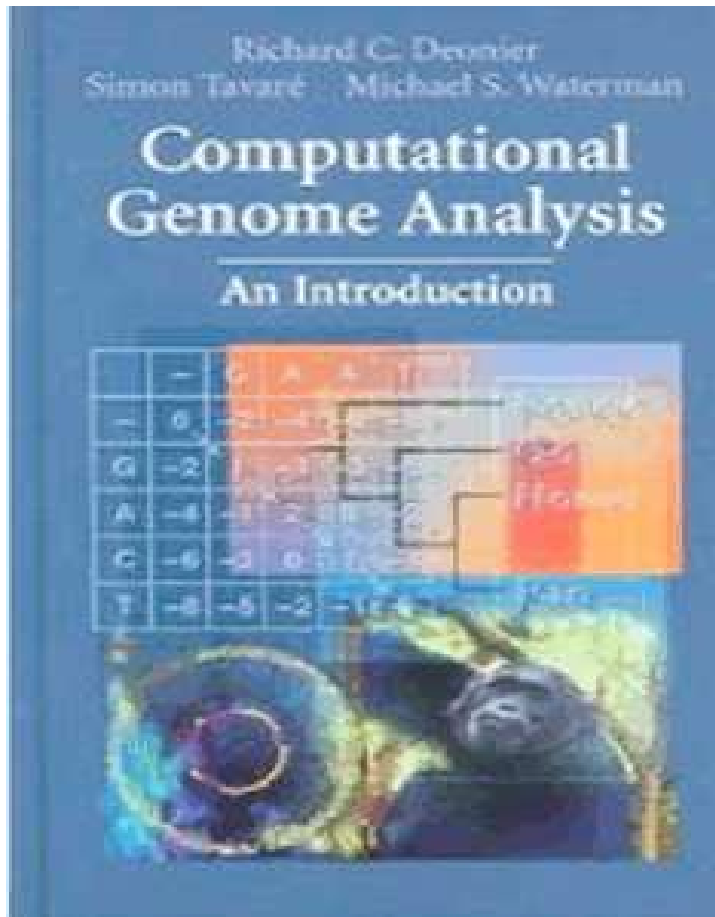
- Biological background (ch 1)

- Probability calculus (ch 2 and 3)

- Sequence alignment (ch 6)

- Rapid alignment methods;
  FASTA and BLAST (ch 7)

- Phylogenetic trees (ch 12)

- Expression data analysis (ch 11)

Good supporting books

Course website   www.montefiore.ulg.ac.be/~kvansteen

Course notes materials

Questions?