# **GBIO0009 – Topics in Bioinformatics**

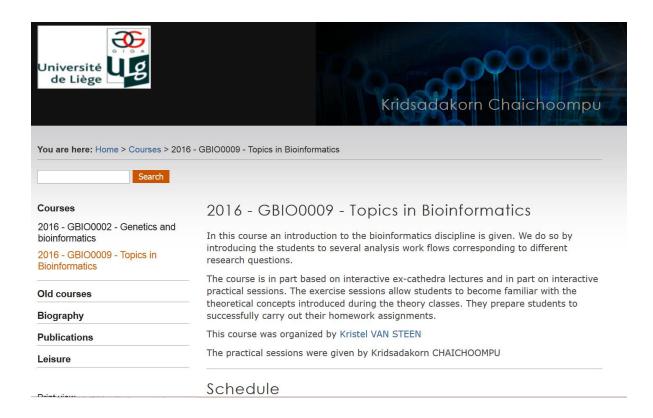
Montefiore Institute - Systems and Modeling
GIGA - Bioinformatics
ULg

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#### **Administration**

Course website:

http://www.montefiore.ulg.ac.be/~chaichoompu/CK/?Courses\_\_\_2016\_-GBIO0009\_-\_Topics\_in\_Bioinformatics



# Kristel Van Steen, PhD<sup>2</sup>

Home

CV (Long - Updated)

Synopsis of activities

**Consultancy Charter** 

FNRS CR Rita Brandão References

#### Links to affiliations

- ULg homepage
- Institut Montefiore
- GIGA-R
- Center for Medical Genetics Ghent (at UG)
- <u>Center for Human Genetics (at K.U.Leuven)</u>
- ----X Marie Curie ITN: Machine Learning for Personalized Medicine
- ----X Pancreas COST Action: An integrated European platform for pancreas cancer research: from basic science to clinical and public health

#### **Contact Information**

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

K Van Steen

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#### **Administration**

#### Course instructors

#### Prof. Kristel Van Steen

- Office: level +1, B34 (GIGA tower)
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- http://www.montefiore.ulg.ac.be/~kvansteen



#### **Teaching Assistant**

- Kridsadakorn (Kris) Chaichoompu
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#### **Administration**

Tutor-student commitments (progcours.ulg.ac.be)

#### Activités d'apprentissage prévues et méthodes d'enseignement

Le cours est basé en partie sur des lectures interactives ex-cathedra et en partie sur des sessions pratiques interactives. Les sessions d'exercices permettent aux étudiants de se familiariser avec les concepts théoriques introduits pendant les cours théoriques. Ils préparent les étudiants à réaliser avec succès leurs travaux à domicile. A propos des travaux à domicile, 3 types de travaux peuvent être présentés: 1) basé sur la littérature (i.e. discuter un article lié au sujet du cours); 2) basé sur la programmation (i.e. vise les étudiants avec un fort bagage informatique); 3) style classique (i.e., travail de type questions-réponses). Les étudiants peuvent travaille en groups mais doivent sélectionner au moins 2 types au travers du cours et au moins un travail basé sur la littérature. Ces derniers sont présentés et discutés en classe pour clarifier de manière plus approfondie les concepts couverts pendant les sessions de cours

#### Planned learning activities and teaching methods

The course is in part based on interactive ex-cathedra lectures and in part on interactive practical sessions. The exercise sessions allow students to become familiar with the theoretical concepts introduced during the theory classes. They prepare students to successfully carry out their homework assignments. Regarding the homework assignments, three homework styles may be presented: 1) literature-based (i.e., discussing a paper related to the class topic); 2) programming-based (i.e., targeting students with a strong informatics background); 3) classic style (i.e., questions-answers type of homework). Students can work in groups but should select at least 2 styles throughout the course and at least once a literature-based homework. The latter are presented and discussed in class, to further clarify concepts covered during the theoretical or practical course sessions.

# What will we be doing?

General course content

In this course an introduction to the bioinformatics discipline is given. We do so by introducing the students to several analysis work flows corresponding to different research questions.

Typical topics that are covered in this course include:

- Genome-wide association screening using SNP chip arrays
- DNA sequence association analysis
- Genomic patient/population substructure
- Biological networks
- Case study: cognitive genetics

# What will we be doing?

- General course content
  - Analytics
  - Focus on
    - Theoretical underpinnings of analysis types
    - Informatics / Software (what? Context? How?)

#### How will we do it?

# "Theory" classes

- Course notes are in English
- Main instructor: K Van Steen
- Guest speakers on particular subtopics (e.g., biological networks and cognitive genetics)

- The "theory" course will be interactive in English/French:
  - In-class discussion papers
  - Analysis frameworks: discussing different viewpoints
  - Slides and course website information as supporting docs ("syllabus")

#### How will we do it?

#### "Practical" classes

- "Homework assignments" constitute an important part of this class and make links to the theory and practical classes.
- Main tutor: K Chaichoompu (who will provide details)
- Homeworks:
  - Reading assignment with presentation and in-class discussions (graded)
  - Computing project with guiding Questions (graded)
- Homework assignments result in a "group" report and should be handed in electronically in English (K Chaichoompu: step by step guide)
- See documentation on course website + next slide

# Organization of GBIO0009 Homework Assignments Topics in Bioinformatics

- Form groups and select a "type of homework" (see below: different types imply different rules). Same group for all assignments!
- All homework types need to be represented. Hence, every group should have chosen a
  programming-style homework assignment, and a literature-based project assignment,
  before the end of the course.

#### Type 1: Literature-based project

This involves choosing a paper from the literature that extends or provides additional background on the material of the course (chapter) and then summarizing the paper, its objectives, results.

When drafting your slides, do not copy the paper, but show you have understood the main ideas of the paper and "discuss" the paper. Such a discussion could include thoughts on what was the key idea, strengths or weaknesses of the methods/experiments, comments on the writing, ways to extend the work, flaws in the argument/data/experiments, etc. Anything is fine, as long as it demonstrates some real thought.

A selection of papers will be provided, but if you have another interesting paper to discuss, please send your suggestion to the TA. The course instructors will then decide whether the paper is eligible or not.

#### Type 2: Computing project (with guiding questions)

You will be given a data and a real-life bioinformatics data problem. Using software that will be explained in class (TA), you will be asked to solve the problem. Guiding questions and supporting documents will be presented to you, to help you in achieving this goal.

#### Format and report

All assignments (Type 1/ Type 2) will be presented and discussed in class. Slides and slides presenting should be in English.

Only for Type 2 projects, a report is needed. This report reflects the process you adopted in solving the problem that was presented to you and should be no more than the equivalent of 5 single-spaced typed pages of text, excluding figures, tables and bibliography. It should contain an abstract (e.g., description of the problem), a methods part (e.g., how did you solve the problem), a results part (e.g., what are your findings) and a discussion part (e.g., how other people in the scientific community solve such a problem). If citations are made to other papers, there should be a bibliography! Only one report per group is needed.

#### **Evaluation**

Homeworks count for 60% of your final score ... Opportunities will be created to discuss the homeworks (homework assignments) in class or in private.

#### What will be evaluated?

• At the end of the course, you have an idea about what bioinformatics entails as a profession.

- Since this course is an introductory course, you will be evaluated about key concepts related to each subtopic, rather than in-depth understanding of each subfield (analytics)
- Pros and cons of certain practical implementations and their motivations may be evaluated as well

## How will be evaluated?

HW1	HW2	Examination	
30	30	40	

- No final grade without homeworks
- Homeworks not handed in in time: 0
- Exam in January ("open book")

#### How will be evaluated?

## Literature style homeworks

[1 homework = discuss 1 paper – or a section, indicated by the instructors, when the paper is too large]

- Discuss the paper and make a group report
- Make links
  - between the paper and the course,
  - between the paper and additional info outside the course

# **Evaluation criteria – presentation**

Criterium	Key words			
	Concepts, slides content, slides composition, fellow			
	students do not have questions regarding "new"			
Clarity	statements (i.e., not covered in class) made on the			
	slides or during the presentation			
Illustrations	ns Not too much; not only copy and paste from course			
on slide	but novel illustrations; supportive			
Presentation	Eager beaver (a person who is very enthusiastic about			
Skills	doing something)			
	Presentation content as presented is understood:			
Understanding	adequate reply to questions and comments (incl. those			
	from fellow students)			
Group	Scoring will be done on an individual basis; balanced			
dynamics	partitioning of tasks			

## **Evaluation criteria – report (programming-style)**

- Ability to formulate the research problem and to sketch the context (introductions, data description, tool description, etc)
- Presentation summary of the analysis workflow (methods, analysis section)
- Discussion (of the analysis tools, of the quality of the analysis, validity of results – when put in a broader context, ...)
- Correct and creative input (stuffing, conclusion section)
- General structure of the report (sectioning)

# **Tentative course layout**

## [changes will be communicated via the course website]

Bioinforma	atics (room	n R75, B28)				
2016						
Sep-21	KVS	Intro**				
Sep-28	KVS	GWA				
Oct-05	KC	Software a	vailability (R basics) and data formats / handlin	HW1a: pa	pers + prg (	(R)
Oct-12	KVS	GWA				
	KC	Tutorial A	GWA in PLINK	HW1b: papers + prg (PLINK)		
Oct-19	FA	Tutorial M	B-MDR	HW2		
Oct-26	KVS	GWAI				
Nov-09	KVS	Presentation assignment 1				
Nov-16	KC	Tutorial B Clustering (patient stratification in IBD, pop stra HW2				
Nov-23	GUEST1	Biological networks (Kathleen Marchal Lab)				
Nov-30	GUEST2	Cognitive genetics (Frank Kooy)				
Dec-07	ALL	Q & A				
Dec-14	ALL	Presentation assignment 2				

#### **Course references**

Computational Genome Analysis - an introduction

http://www.tok.ro/toksite/downloads/Bioinformatika/Konyvek/konyvek%20 bioinfo%20fejezetekkel%20+%20bioinfo%20konyvek/Computational%20Gen ome%20Analysis.pdf

• Applied Statistics for Bioinformatics using R

https://cran.r-project.org/doc/contrib/Krijnen-IntroBioInfStatistics.pdf

# Questions?