

Degree	Type	Year	Semester
4313473 Bioinformatics	OB	0	1

Contact

Name: Antonio Miguel Espinosa Morales

Email: AntonioMiguel.Espinosa@uab.cat

Use of languages

Principal working language: english (eng)

Teachers

Juan Carlos Moure Lopez

Raquel Egea Sánchez

Prerequisites

For the general development of the course, it is recommended to have a B2 level, or equivalent, of English language.

For this module, it is very recommended to have basic notions of computer usage in Linux, knowledge of common user tools and basic statistics.

Objectives and Contextualisation

General objectives of this module are the application of the core tools and basic techniques for development in this area of knowledge. Provide skills to successfully assume the adaptation to changing technologies and new paradigms emerging in this interdisciplinary field.

Skills

- Design and apply scientific methodology in resolving problems.
- Identify the biocomputing needs of research centres and companies in the biotechnology and biomedicine sectors.
- Possess and understand knowledge that provides a basis or opportunity for originality in the development and/or application of ideas, often in a research context.
- Student should possess the learning skills that enable them to continue studying in a way that is largely student led or independent.
- Use operating systems, programs and tools in common use in biocomputing and be able to manage high performance computing platforms, programming languages and biocomputing analysis.
- Work individually and as part of a team in an international and multidisciplinary context.

Learning outcomes

1. Design, analyse and evaluate the performance of parallel infrastructures and large volumes of data.
2. Design and apply scientific methodology in resolving problems.

3. Identify the advantage and limitations of biocomputing and the importance of applying new computer technology in omic research.
4. Manage parallel platforms and biocomputing databases according to needs.
5. Master programming language in R and Perl Biocomputing.
6. Possess and understand knowledge that provides a basis or opportunity for originality in the development and/or application of ideas, often in a research context.
7. Student should possess the learning skills that enable them to continue studying in a way that is largely student led or independent.
8. Use algorithms and statistical calculation techniques to manage large volumes of data.
9. Use the main molecular databases, the main standard formats for molecular data and integrate data from different sources
10. Work individually and as part of a team in an international and multidisciplinary context.

Content

Introduction to Module

Professor Juan Carlos Moure

Computational Thinking

Professor Juan Carlos Moure

- Why computers and biology?
- Computational workflows
- Computer Programs
- Computer Architecture
- Programming concepts
- Algorithms and data structures

Programming languages: R

Professor Toni Espinosa

- R programming
- Bioconductor

Linux (commands and shell scripting)

Professor Toni Espinosa

- Basic linux: basic commands and editors, user management, software management, file system
- Shell scripting: terminal tools, variables and execution environment, examples and exercises

Programming Languages and Algorithms

Professors Toni Espinosa and Juan Carlos Moure

- Overview of programming languages in Bioinformatics
- Data types and contexts
- Data manipulations and operations
- Input/Output
- Code reutilization: modules and subroutines
- Regular expressions
- Third party code integration

Database management with MySQL

Professors Toni Espinosa

- Introduction to databases
- DBMS structure, MySQL
- Creation of biological Databases
- Query analysis of biological databases

Methodology

The methodology will combine classroom work, supervised problem solving in class, unsupervised work in the computing lab, homework from recommended readings and independent study student. It will use the virtual platform and asked for papers related to the thematic blocks

Activities

Title	Hours	ECTS	Learning outcomes
Type: Directed			
Classroom work	20	0.8	
Problem solving (in class)	14	0.56	
Work in the computing lab	12	0.48	
Type: Supervised			
Performing lab work from recommending reading	15	0.6	
Type: Autonomous			
Regular general work on the deliverables definition and materials given	83	3.32	

Evaluation

The methodology will combine classroom work, problem solving in the classroom, unsupervised work done in the computing lab and individual work from recommended readings. It will make use of the virtual platform and will make references to selected publications related to the thematic blocks.

Evaluation activities

Title	Weighting	Hours	ECTS	Learning outcomes
Evaluation of work done during the module, presented by the user	10%	1	0.04	2, 5, 7, 9, 10
Final Exam	10%	1	0.04	2, 10
Individual theoretical and practical tests	50%	2	0.08	1, 2, 3, 4, 10
Laboratory work, possibly in groups	30%	2	0.08	2, 4, 5, 6, 8, 9, 10

Bibliography

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- Bell, Charles; Kindahl, Mats; Thalmann, Lars. "MySQL High Availability". O'Reilly, 2010.
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- GenBank. Nucl. Acids Res., 30(1):17-20. URL <http://nar.oupjournals.org/cgi/content/abstract/30/1/17>.
- Berman, H. M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T. N., Weissig, H., Shindyalov, I. N. & Bourne, P. E. (2000).The Protein Data Bank. Nucleic Acids Res., 28(1):235-242.
- Bessant, C., Shadford, I., Oakley, D. "Building Bioinformatics Solutions with Perl, R and MySQL", Oxford University Press, 2009
- Boeckmann, B., Bairoch, A., Apweiler, R., Blatter, M.-C., Estreicher, A., Gasteiger, E., Martin, M. J., Michoud, K., O'Donovan, C., Phan, I., Pilbout, S. & Schneider, M. .The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Res., 31(1):365-370.
- Christiansen, P., Wall, L., Orwant, J., "Programming Perl". 4th Edition, O'Reilly, 2012
- Mäkinen et al., Genome-Scale Algorithm Design: Biological Sequence Analysis in the Era of High-Throughput Sequencing. Cambridge Univ. Press, 2015.
- Matloff, N., "The Art of R Programming". No Starch Press Inc., 2011
- Lutz, M., "Learning Python", O'Reilly, 5th edition, 2013
- Siever, E., Figgins, S., "Linux in a nutshell" O'Reilly 2009.
- Sobell, M., "A Practical Guide to Linux. Commands, editors and shell programming". Prentice Hall, 2009.
- Tindall, James., Begining Perl for Bioinformatics. O'Reilly 2012.

Recommended websites

- <http://mscbioinformatics.uab.cat>
- <https://cv.uab.cat>

Search for bioinformatics and computer science topics in UAB library e-book resources:

- <http://www.uab.cat/biblioteques/trobador>
- <http://sfx.cbuc.cat/uab/azbook>
- <http://pagines.uab.cat/bctdigital/>
- [http://cataleg.uab.cat/search~S1*cat/I?SEARCH=\(02.034\)57](http://cataleg.uab.cat/search~S1*cat/I?SEARCH=(02.034)57)

Linux manual: http://materials.cv.uoc.edu/continguts/PID_00148368/index.html