UNIVERSIDADE FEDERAL DE SANTA CATARINA
CENTRO DE CIÊNCIAS BIOLÓGICAS
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Programa de Pós-Graduação em
BIOTECNOLOGIA &
BIOCIÊNCIAS
mestrado & doutorado

SEMESTER 2020.1

I. COURSE

CODE	CORUSE	CREDITS		HOURS SEMESTRE	
		Theoretical	Practical	Theoretical	Practical
	Genome Analysis	1	1	15	15

II. CLASS INFORMATION

CLASS MEETS	N° APPLICANTS	HOUR	LOCAL
09 a 13 de march de 2020 (Morning and afternoon)	20	9:00 – 12:00 14:00 – 17:00	Check schedule

III. PROFESSOR(S)

Prof. Rodrigo Baptista, PhD (Universty of Georgia / USA)
Prof. Dr. Glauber Wagner (Coordinator) – (Email: glauber.wagner@ufsc.br, Sala: CCB/MIP – 3° andar, n° 318A)

IV. Prerequisite

Prior requisites are not required.

V. COURSE(S) FOR WHICH DISCIPLINE IS OFFERED

Graduate Program in Biotechnology and Biosciences/UFSC and participants of the CAPES-PRINT projects associated with PPG in Biotechnology and Biosciences

Level (×) Master's degree and/or (×) Doctorate

VI. MENU

Critical study of classic and recent genome literature and hands on computational exercises with real data from a genome project. Genome sequence assembly, automated annotation and searching molecular databases. SNP analysis and comparative genomics will. This class will have a "hands-on" laboratory component with an emphasis on how to use and interpret genomics software results. Emphasis will be placed on understanding the approaches and algorithms used to generate, store and analyze very large data sets including the strengths and limitations of genome-scale analyses

VII. GOALS

Making the jump from analyzing a single gene or pathway to analyzing an entire genome requires a shift not only in technique, but perspective. When is a whole genome analysis appropriate? What type of analysis should it be? What are the computational options? What are the controls? How do you install and run the programs? How to keep track of your codes? This class will focus on a critical study of classic and recent genome literature and hands on computational exercises with real data from a genome project on campus.

VIII. TEACHING/PROGRAM DEVELOPMENT

This class will have a "hands-on" laboratory component with an emphasis on how to use and interpret genomics software results. Emphasis will be placed on understanding the approaches and algorithms used to generate, store and analyze very large data sets including the strengths and limitations of genome-scale analyses. Detailed instruction on how to use particular software programs is not the focus of this course. Students will work on genome analysis projects from several organisms. Prior bioinformatics experience beyond the use of internet resources and the ability to program are not required.

IX. EVALUATION

Skills development along the course (3,0)
Oral Presentations at the end of the course (3,0).
Attendance and interest (4,0).

X. SCHEDULE

Data		Time / Local	Hrs	Tipo*	Topic	Professor
09/03	Mon	9:00 – 12:00 – SIPG08	3	TP	Introduction to UNIX (basic knowledge)	Prof. Baptista Prof. Glauber
09/03	Mon	14:00 – 17:00 – SIPG08	3	TP	UNIX (awk)/parsing big datasets	Prof. Baptista
10/03	Tue	9:00 – 12:00 – SIPG08	3	T	Sequencing Technologies	Prof. Baptista
10/03	Tue	14:00 – 17:00 – SIPG08	3	TP	Putting the puzzle together: Genome Assembly	Prof. Baptista
11/03	Wed	9:00 – 12:00 – SIPG08	3	TP	Finding genes - Introduction to Genome Annotation	Prof. Baptista
11/03	Wed	14:00 – 17:00 – SIPG08	3	TP	Exploring gene functions – Introduction to Gene Ontology	Prof. Baptista
12/03	Thu	9:00 – 12:00 – SIPG08	3	TP	Comparative genomics – Orthology and Phylogenomics	Prof. Baptista
12/03	Thu	14:00 – 17:00 – SIPG08	3	TP	Detecting variation – Introduction to SNPs	Prof. Baptista
13/03	Fri	9:00 – 12:00 – SIPG08	3	TP	Designing a Genome project	Prof. Baptista
13/03	Fri	14:00 – 17:00 – SIPG08	3	T	Oral presentations	Prof. Baptista Prof. Glauber

XI. BIBLIOGRAPHY

1. Baxevanis and Ouellette. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. 2nd Edition (2004). Editora John Wiley & Sons. ISBN: 978-0471478782
2. Bradnam and Korf. Unix and PERL to the rescue!: A field guide for the life sciences (and other data-rich pursuits) (2012). Cambridge Press. ISBN 978-0-521-16982-0
3. Haddock and Dunn. Practical Computing for Biologists (2011). Sinauer associates. ISBN 978-0-87893-391-4

Web sites for the class:

http://www.ncbi.nlm.nih.gov/guide/all/#howtos_
http://www.ncbi.nlm.nih.gov/books/NBK25500/
https://wiki.gacrc.uga.edu/wiki/Software
https://www.ncbi.nlm.nih.gov/sra
https://www.ebi.ac.uk/ena
https://eupathdb.org/eupathdb/
https://rpbaptista.weebly.com/