

**INTER AMERICAN UNIVERSITY OF PUERTO RICO
METROPOLITAN CAMPUS
SCHOOL OF SCIENCE AND TECHNOLOGY
NATURAL SCIENCE DEPARTMENT
MASTER'S IN SCIENCE IN MOLECULAR MICROBIOLOGY**

SYLLABUS

I. GENERAL INFORMATION

Course Title	:	Microbial Genomics
Code and number	:	MOMI 6320
Credits	:	3
Academic term	:	
Instructor	:	
Office hours and location	:	
Office telephone	:	
E-mail	:	

II. DESCRIPTION

Analysis of molecular organization, information, and genomic products. Emphasis on sequencing, assembly, and annotation. Description of genes in genomes and metagenomes of clinical and environmental origin. It requires 30 hours of conference-laboratory.

III. OBJETIVES

It is expected that at the end of the course, the student will be able to:

1. Appreciate the use of genomics as a tool for detecting genes in genomes and metagenomes.
2. Contrast different mechanisms of microbial metabolism by reviewing scientific literature.
3. Apply computational platforms for next-generation sequence analysis.
4. Characterize microbial communities using variable regions of the 16S gene.

Competencies of the graduate profile addressed in this course:

1. To establish the importance of Microbiology in the genomic era, in aspects related to human health and the balance of ecosystems.
2. Evaluate the most useful platforms for analyzing molecular microbiology data using emerging tools.
3. Evaluate scientific information from diverse sources.

IV. CONTENT

- A. Introduction to Microbial Genomics
 - 1. Properties of nucleic acids
 - 2. DNA replication
 - 3. Genetic information flow and Central Dogma
 - 4. Gene transcription and translation
 - 5. Proteins: structure and function
- B. DNA sequences: More than just protein-coding genes
 - 1. Omics
 - 2. Importance of genomic information
 - 3. Introduction to Bioinformatics: Analyzing DNA, RNA and Protein Sequences protein sequences
 - 4. Introduction to PubMed (NCBI)
- C. Sequencing and Quality Control Platforms
 - 1. Sanger
 - 2. 454
 - 3. Illumina
 - 4. PacBio
- D. Access to sequencing data and related information
 - 1. NCBI
 - 2. EMBL-EBI
- E. Sequence alignment
 - 1. BLAST
 - 2. Pairwise
 - 3. Mega-BLAST
 - 4. BLAT
- F. Multiple Sequence Alignment (MSA)
- G. MSA analysis
 - 1. MEME
 - 2. GenDoc
- H. Molecular Phylogeny and Evolution
 - 1. Properties of phylogenetic trees
 - 2. Types of phylogenetic trees
 - 3. Construction and analysis of phylogenetic trees phylogenetic trees from MSA
- I. Next Generation Sequencing (NGS) analysis of genomic DNA
 - 1. Workflow for NGS Experiments
 - 2. Quality assessment
 - 3. Assembly
 - 4. Annotation
 - 5. Biological database
- J. Completed microbial genomes
 - 1. Bacteria
 - 2. Archaea
 - 3. Viruses
 - 4. Fungi
 - 5. Parasites
- K. Characterization of microbiological communities

1. Variable regions of 16sRNA ribosomal gene
 2. Sequence analysis
 3. Case studies (presentation of scientific)
 4. Human microbiome
 5. Microbiome in the environment
 6. Microbiome in other niches and ecosystems
- L. Metagenomics
1. Metadata
 2. Sequence processing
 3. Gene assembly, mapping and annotation.
- M. Microbial genomics research (presentation of scientific papers)
1. Mosaicism and horizontal transfer of virulence genes
 2. Whole genome sequencing (WGS) for identification and annotation of virulence genes
 3. Antibiotic resistance and virulence
 4. Adaptive (directed) evolution and bioengineering.
 5. Biofuels and bioremediation
 6. Vaccine production
- N. Tools for genomic data interpretation

V. LEARNING ACTIVITIES

1. Illustrated lectures in power point format
2. Invited speakers
3. Computer lab
4. Exercises and computer simulations

VI. EVALUATION

The evaluation of the course will be based on:

	Score	% of Final Grade
Research article discussion	200	20
Proposal written and presentation	200	40
Assignments/Quizzes	100	20
Written projects	100	20
Total	600	100

Class Attendance and Exams

Class attendance is mandatory. A student who needs to be absent from class should contact the professor before the class by phone or email. There will be no make-up exams, except for reasons of illness. In such case, make-ups will be offered with a doctor's excuse during the final exam period during the professor's office hours.

VII. SPECIAL NOTES

A. Auxiliary services or special needs

All students who require auxiliary services or special assistance must request these at the beginning of the course or as soon as they know that they need them, through the proper registry, in the Office of Orientation with Sr. José Rodríguez.

B. Honesty, fraud, and plagiarism

Dishonesty, fraud, plagiarism and any other inappropriate behavior in relation to academic work constitutes major infractions sanctioned by the General Student Regulations. The major infractions, as stated in the General Student Regulations, may have as a consequence, suspension from the University for a definite period greater than one year or the permanent expulsion from the University, among others sanctions.

C. Use of electronic devices

Cellular telephones and any other electronic device that could interrupt the teaching and learning processes or alter the environment leading to academic excellence will be deactivated. Any urgent situation will be dealt with, as appropriate. The handling of electronic devices that allow students to access, store or send data during evaluations or examinations is prohibited.

D. Compliance with the Provisions of Title IX

The Federal Higher Education Act, as amended, prohibits discrimination because of sex in any academic, educational, extracurricular, and athletic activity or in any other program or function, sponsored or controlled by a higher education institution, whether or not it is conducted within or outside the property of the institution, if the institution receives federal funds.

In harmony with the current federal regulation, in our academic unit an Assistant Coordinator of Title IX has been designated to offer assistance and orientation in relation to any alleged incident constituting discrimination because of sex or gender, sexual harassment or sexual aggression. The Assistant Coordinator, Sr. George Rivera, can be reached by phone at 787-250-1912, extension 2262 o 2147, or by e-mail griverar@metro.inter.edu.

The Normative Document titled Norms and Procedures to Deal with Alleged Violations of the Provisions of Title IX is the document that contains the institutional rules to direct any complaint that appears to be this type of allegation. This document is available in the Web site of Inter American University of Puerto Rico (www.inter.edu).

VIII. EDUCATIONAL RESOURCES

Electronic Resources

1. MG-RAST (the Metagenomics RAST): metagenomics.anl.gov
2. Integrated Microbial Genomes (IMG) -img.jgi.doe.gov/

3. The Galaxy Project: Online bioinformatics analysis for everyone: galaxyproject.org

IX. BIBLIOGRAPHY

Textbooks

Jonathan Pevsner (2015) *Bioinformatics and Functional Genomics*, 3rd edition, Wiley-Blackwell.

Robert F. Weaver (2012). *Molecular Biology*, Fifth Edition. McGraw-Hill, NY.

Bernard R. Glick, Jack J. Pasternak, & Cheryl L. Patten (2010) *Molecular Biotechnology: Principles and Applications of Recombinant DNA* 4th Edition. ASM Press, Washington DC.

Encyclopedia of Metagenomics SpringerReference. Springer-Verlag Berlin Heidelberg
<https://link.springer.com/referencework/10.1007%2F978-1-4614-6418-1>

Supplementary readings

During the semester students will be assigned independent readings of scientific articles to complement the course material. Students will choose two scientific articles related to microbial genomics to discuss in the classroom. The following are some of the recommended articles:

1. *The Science and Applications of Microbial Genomics: Workshop Summary* (2013). Institute of Medicine (US) Forum on Microbial Threats. Washington (DC): National Academies Press (US).
2. *The New Science of Metagenomics Revealing the Secrets of Our Microbial Planet*. (2007) National Research Council (US) Committee on Metagenomics: Challenges and Functional Applications. Washington (DC): National Academies Press (US).
3. Loman N. J. & Pallen M. J. (2015). *Twenty years of bacterial genome sequencing*. *Nature Reviews Microbiology* 13, 787–794.
4. Land M. *et al.* (2015) *Insights from 20 years of bacterial genome sequencing*. *Funct Integr Genomics*. 15(2),141-61.
5. Pearson W.R. (2001). *Protein sequence comparison and Protein evolution*. Tutorial - ISMB2000. Department of Biochemistry and Molecular Genetics, University of Virginia, Charlottesville, VA 22908, USA.
6. Pallen M. J. (2016). *Microbial bioinformatics 2020*. *Microb Biotechnol*. 9(5), 681–686.
7. Blainey P. C. (2013). The future is now: single-cell genomics of bacteria and archaea. *FEMS Microbiol Rev*. 37(3), 10.1111/1574-6976.12015.
8. Relman D.A. (2012). Microbial Genomics and Infectious Diseases. *N Engl J Med*. 365(4), 347–357.
9. Zhou J. *et al.* (2015). High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. *mBio*. 6(1), e02288-14.
10. Narihito T. & Kamagata Y. (2017). Genomics and Metagenomics in Microbial Ecology: Recent Advances and Challenges. *Microbes Environ*. 2017 Mar; 32(1), 1–4.

11. Nikolaki S. and Tsiamis G. (2013). Microbial Diversity in the Era of Omic Technologies. *Biomed Res Int.* 2013, 958719.
12. Miller R.R. et al. (2013). Metagenomics for pathogen detection in public health. *Genome Med.* 5(9), 81.
13. Morgan X. C. et al. (2013) Biodiversity and Functional Genomics in the Human Microbiome. *Trends Genet.* 29(1), 51–58.
14. Olson N.D., et al. (2015) Best practices for evaluating single nucleotide variant calling methods for microbial genomics. *Front Genet.* 6, 235.
15. Lasken R. S. (2014) Recent advances in genomic DNA sequencing of microbial species from single cells. *Nat Rev Genet.* 15(9), 577–584.
16. Köser C.U. et al. (2012) Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. *PLoS Pathog.* 2012 Aug; 8(8): e1002824.
17. Oulas A. et al. Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. *Bioinformatics and Biology Insights* 2015:9 75–88.
18. Lee D. et al. (2007). Predicting protein function from sequence and structure. *Nature Reviews Molecular Cell Biology* 8, 995-1005.
19. Dudley JT, Butte AJ (2009) A Quick Guide for Developing Effective Bioinformatics Programming Skills. *PLoS Comput Biol* 5(12): e1000589.

Electronic resources

During the semester you will be recommended WEB resources to supplement with course material or to do bioinformatics work. The following are some of the recommended articles:

1. The National Center for Biotechnology Information (NCBI) - <https://www.ncbi.nlm.nih.gov/>
2. NCBI PubMed - <https://www.ncbi.nlm.nih.gov/pubmed/>
3. Nucleic Acids Research, Oxford Academic -<https://academic.oup.com/nar>
4. DOE Joint Genomics Institute, Microbial Genome Projects: <http://www.jgi.doe.gov/>
5. ExPASy Molecular Biology Server: <http://www.mrc-lmb.cam.ac.uk/genomes/madanm/pres/swiss1.htm>
6. Proteomics webpage - <http://www.mcponline.org/>
7. MG-Rast - Argonne National Laboratory - <http://metagenomics.anl.gov/> (MG-RAST: Metagenomics RAST Server) - www.anl.gov/mcs/project/mg-rast-metagenomics-rast-server
8. The Institute for Genomic Research(TIGR) – (JCVI) <http://www.jcvi.org/> (Comprehensive Microbial Resource) - <http://cmr.jcvi.org/cgi-bin/CMR/CmrHomePage.cgi>
9. Nature.com: Bacterial Genomics https://www.nature.com/search?article_type=protocols,research,reviews&subject=bacterial-genomics
10. Genome research <http://genome.cshlp.org/> (Microbial Genomics) - <http://genome.cshlp.org/search?fulltext=microbial+genomics&submit=yes&x=5&y=10>
11. Microbial Genomics - Microbiology Society Journals
12. <http://mgen.microbiologyresearch.org/content/journal/mgen>
13. JGI IMG Integrated Microbial Genomes & Microbiomes - <https://img.jgi.doe.gov/>
14. The Galaxy Project - <https://galaxyproject.org/>
15. Biostars online bioinformatics forum <https://www.biostars.org/>

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