

Environmental Biotechnology and –Omics

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Earth and Environmental Sciences

Rutgers Newark

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Course Time: 6-9PM Location: Smith 127 Instructor: Adam Kustka
Phone: 973-353-1966 Email kustka@andromeda.rutgers.edu (preferred)
Office: Smith 140 Tuesdays and Thursdays 3-5PM
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Course Description: Environmental biotechnology describes the use of organisms to improve environmental quality, either through remediating contamination, producing goods with lower environmental impacts, or as sensitive monitors of environmental processes. All of these pursuits have rapidly progressed largely due to so-called “-omic” approaches, which involve the analysis of biomolecules and their interactions in an organism or in the environment (meta-omics). For example, genomics, proteomics and metabolomics involve the analysis of expression patterns and interactions among the totality of genes, proteins and metabolites. Principles and environmental applications of genomic and proteomic approaches will be discussed and critically evaluated, and -omic datasets will be analyzed.

Learning Objectives:

- Review the metabolic flexibility of microbes and how this is harnessed to address environmental problems.
- Understand the inter-relationships among microbial growth, biomass production, substrate (i.e., contaminant) concentration and removal rate through lecture materials and problem sets.
- Understand how molecular methods are developed and utilized to detect environmental contamination or monitor the effectiveness of remediation measures.
- Understand the various -omic approaches and current platforms, evaluate strengths and limitations as applied towards specific environmental applications.
- Handle ribosomal and protein/peptide datasets to determine species and protein identities, through in class / after class computer exercises, and homework assignments.
- Enhance skills for critically evaluating and discussing the appropriate peer reviewed scientific articles assigned throughout the course.

Course rationale:

Although –omic tools, born out of biotechnology, have exploded in their utility to address questions of environmental relevance (as evidenced by articles published in high impact journals such as Environmental Sciences and Technology, Science and Nature), many environmental science programs (at both undergraduate and graduate levels) still do not offer this kind of exposure. As a result, often only students who actively use molecular methods in their research are exposed and many graduate with only a vague idea of what these methods can offer. Through the learning objectives outlined above, including hands on experience with DNA and peptide sequence data, students will complete the course with a keen appreciation and understanding of the exciting opportunities that environmental biotechnology and –omics offers towards answering

environmental questions.

Required reading:

Rapid advances in these fields render any one textbook obsolete in at least some aspects. Some textbook materials will be used for general background (on reserve) but course materials will primarily be derived from peer reviewed literature. These are listed on last page.

Assignments:

Homework assignments will be given throughout the semester to reinforce concepts and exercises covered in class. At least one week will be allowed to complete the assignments. Late assignments will be subject to 20% per day point reductions.

Class format:

The course will consist of lecture-based teaching and learning only to provide background information on key concepts necessary for future discussions. Otherwise, our time will be spent working on data sets and having critical, and hopefully insightful, discussions on the assigned readings and student presentations.

Presentation / discussion leader:

I will meet with each of you to discuss candidate articles that you will present later in the semester. These articles should be seminal ones in the field and ideally will be ones you have chosen out of personal interest in the topic. I find it is best to start perusing literature long before the time when “the” article is decided. Often, you may find an article that was initially interesting to be a “dud”- you may have to sift through several to find the gem. One way find a good article is through web of science (available from any Rutgers terminal)... once you have a list of pertinent articles you can sift through these by sorting by “times cited” (the duds won’t be cited often). However, you can miss important new papers in this way, as cutting edge 2014 publications will not yet be cited. Another imperfect way to screen articles is to stay away from obscure journals.

Each student will present the article and open the floor for discussion. The discussion could include questions from the students to the presenter to clarify some aspect of the methods, a critical evaluation of the methods or conclusions, or a discussion of the implications of the work.

Grading Policy:

Final grades for the course are calculated based on the following breakdown:

Mid-term	20
Final exam	20
Homework assignments	35
Presentation / discussion leader	15
Class participation	10

Class schedule:

Week	Lecture topic	Homework	Tentative Readings*				
1	Introduction to Environmental Biotechnology- review of microbiology and environmental biotechnology. Stoichiometry and bacterial energetics of substrate utilization.	Kinetic / bioenergetic homework assigned.	Handout.				
2	Overview of genetic basis for life; genetic tools in environmental sciences.	Kinetic / energetic homework due	Handout.				
3	Introduction to on-line tools for sequence manipulation; fundamentals of PCR and Q-PCR; primer design.	PCR homework assigned.	Handout.				
4	High throughput genomic/transcriptomic sequencing; pyrosequencing and single molecule approaches.	PCR homework due.	Loman et al., 2012; Weckwerth 2011				
5	Applications towards environmental issues and questions. Ribosomes, phylogeny, and RNA/DNA ratios.		McLean 2013.				
6	Ribosomal based microbial community analysis; introduction to QIIME; MIDTERM	QIIME homework assigned.	Pace 2009 ; Kemp et al. 1993, Caporaso et al. 2010				
7	Analysis of ribosomal datasets using QIIME.	Candidate article list due.					
8	Proteins in environmental science- from western blots to modern mass spectrometry. Proteomics and mass spectrometry; survey, strengths and weaknesses of available technologies.	QIIME homework due.	Aebersold and Mann 2003, Abdallah et al. 2012,				
9	Introduction to MALDI-TOF and peptide mass fingerprinting	Agreement on articles by today.	Henzel et al. 2003; others TBA				
10	Peptide identification using Data Explorer and MASCOT	Biomarker homework assigned.	http://www.matrixscience.com/help.html ;				
11	Introduction to MS/MS approaches.		Jonscher 2005				
12	MS/MS continued; Environmental applications of proteomics	Biomarker homework due; MS/MS worksheet assigned	Campos et al. 2012				
13	Integrated metagenomics, stable isotope probing and metaproteomics. Tying it all together.	MS/MS worksheet due.	Benndorf et al. 2011; Taubert et al. 2012.				
14	Student presentations on articles.		TBD.				
	* Subject to supplementation (posted a week or more before class)						

Textbooks drawn upon during the course.

- Environmental Biotechnology: Principles and Applications. 2001. Rittman and McCarty. ISBN-13: 978-0071181846
- OMICS: Applications in Biomedical, Agricultural, and Environmental Sciences. 2013. Barh et al. ISBN-13: 978-1466562813.
- Brock Biology of Microorganisms. 13th Ed. 2010. Madigan et al. ISBN-13: 978-0321649638.
- An Introduction to Genetic Engineering. 3rd Ed. 2008. Nicholl. ISBN-13: 978-0521615211
- Mass Spectrometry of Proteins and Peptides: Methods and Protocols, 2nd Edition. 2008. ISBN-13: 978-1934115480.

Peer reviewed literature covered in course (subject to change prior to start of semester)

- Abdallah C, Dumas-Gaudot E, Renaut J, Sergeant K** (2012) Gel-based and gel-free quantitative proteomics approaches at a glance. *International journal of plant genomics* **2012**: 494572
- Aebersold R, Mann M** (2003) Mass spectrometry-based proteomics. *Nature* **422**: 198–207
- Benndorf D, Balcke GU, Harms H, Von Bergen M** (2007) Functional metaproteome analysis of protein extracts from contaminated soil and groundwater. *The ISME journal* **1**: 224–34
- Campos A, Tedesco S, Vasconcelos V, Cristobal S** (2012) Proteomic research in bivalves: towards the identification of molecular markers of aquatic pollution. *Journal of proteomics* **75**: 4346–59
- Caporaso J et al** (2010) QIIME allows analysis of high- throughput community sequencing data. *Nature Publishing Group* **7**: 335–336
- Henzel WJ, Watanabe C, Stults JT** (2003) Protein identification: the origins of peptide mass fingerprinting. *Journal of the American Society for Mass Spectrometry* **14**: 931–42
- Jonscher, K.** (2005) Validating sequence alignments for peptide fragmentation patterns: a primer in MS/MS sequence identification. http://proteome-software.wikispaces.com/file/view/validating_sequence_assignments.pdf
- Keller M, Hettich R** (2009) Environmental proteomics: a paradigm shift in characterizing microbial activities at the molecular level. *Microbiology and molecular biology reviews* : *MMBR* **73**: 62–70
- Loman NJ, Constantinidou C, Chan JZM, Halachev M, Sergeant M, Penn CW, Robinson ER, Pallen MJ** (2012) High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. *Nature reviews Microbiology* **10**: 599–606
- McLean TI** (2013) “Eco-omics”: a review of the application of genomics, transcriptomics, and proteomics for the study of the ecology of harmful algae. *Microbial ecology* **65**: 901–15
- Pace NR** (2009) Mapping the tree of life: progress and prospects. *Microbiology and molecular biology reviews* : *MMBR* **73**: 565–76
- Taubert M** (2012) Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. *ISME Journal* **6**: 2291–2301
- Weckwerth W** (2011) Green systems biology - From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. *Journal of proteomics* **75**: 284–305