Sequence Analysis
Syllabus - FRSHWTR 512 – Fall 2017

Instructor: Dr. Ryan Newton, Ph.D., newtonr@uwm.edu, School of Freshwater Sciences

Class Meeting time & location: Monday & Wednesday from 3:30 – 4:45 PM, GRLF Room 3097. This is a face-to-face formatted course. Students will meet in the classroom all weeks at the scheduled times. Students can expect some lecture material will be posted online (UWM D2L), so that more discussion and hands-on activities can take place in the classroom.

Most weeks, Mondays will be used for lectures of new material, presentations by students, and discussion of programs used to analyze sequence data, while Wednesday class time will be spent with hands-on activities and data analysis for student final projects.

Prerequisites: Graduate student standing or undergraduate students that have a junior standing or greater and have completed classes in Biology: UWM Bio Sci 152 (Foundations) & 325 (Genetics) and Chemistry: UWM Chem 104 (General Chemistry & Qualitative Analysis) or equivalent, or obtain consent of the instructor.

Course Description: This course is designed to give students an understanding of the molecular biology underlying nucleic and amino acid based analyses and the ways nucleic acid sequence analysis is used to interrogate biological systems. Emphasis will be placed on the fundamentals of nucleic acid sequence comparison and how modern approaches use these principles to study organisms, populations, and communities (e.g. phylogeny, genomics, RNA-seq, community composition). Examples will draw more heavily from studies of microorganisms.

Required for Course Interactions: Students must have weekly access to a computer with an Internet connection to participate fully in this course. Some lectures, readings, and study materials will be posted and explained in the Desire to Learn (D2L) platform hosted by UW-Milwaukee (At the UWM homepage http://uwm.edu, click on the D2L link under the Current Students menu). To interact with the online material, students will need a computer with audio capabilities and software that can open voice-over PowerPoint (VOP) lectures posted on D2L.

Voiceover PowerPoint lectures will be posted on D2L and will require Windows Media Player (for *.wmv files on PC), QuickTime (for .M4V files playable on iOS devices) or VLC (for PC & Mac – available at http://www.videolan.org/vlc/index.html). Content and course instructions will be posted on D2L as .pdf files. Software such as Adobe Reader (free at http://get.adobe.com/reader/) capable of reading these files is necessary. It is recommended that students check e-mail and the D2L course homepage several times each week for notifications. Most of the course material will be posted in the Content area and discussions will be facilitated through the Discussions area of the D2L course site. For technical help and technical contact information, see the UWM Help Desk (help@uwm.edu; 414-229-4040), http://www4.uwm.edu/technology/help/campus/gettechhelp.cfm, or go to Bolton Hall room 225 for an in-person consultation.

Sequence Analysis 1
COVERED TOPICS
This class will cover the molecular basis of nucleic and amino acid sequence comparisons and why and how sequence analysis is used to understand a wide range of life characteristics. This basic understanding will be the foundation from which the class will then explore a variety of modern sequence analysis techniques. Students will learn the molecular structures that make up nucleic and amino acids and how this relates to sequence analysis options, how nucleic acid information is generated with sequencing platforms, the basis of scoring used in sequence comparison and alignments, using online databases for sequence analysis, basic phylogenetic reconstruction, and modern techniques for analyzing sequence information.

Learning Outcomes:
This course is designed so that students will learn:

A Molecular Biology Background for Sequence Analysis
- The molecular structure of DNA & RNA
- The basis of base pairing
- Nucleic acid sequence orientation and nomenclature
- Principles of the genetic code and open reading frames
- The impact of mutations on the genetic code & sequence comparison
- The properties, code, and functional grouping of amino acids
- Why the structure of proteins matter to sequence analysis

Sequencing platforms
- The basis for how sequence information is generated
- How sequencing platforms differ in input DNA, information generation, & data output
- Typical nucleic acid file formats and their use in sequence analysis

Comparative sequence analysis
- The difference between sequence similarity and identity and homologs/paralogs/analogs
- The basics of comparative sequence scoring matrices
- The difference between global and local alignments
- Multiple sequence alignment methods
- Online resources for conducting multiple sequence alignments
- The principles of BLAST and other comparative programs
- Basic theory and use of phylogenetic reconstruction

Modern Sequence Analysis Methods & Associated Resources
- Common sequence assembly approaches
- Basic genomic analysis and platforms to conduct genome interrogation
- The theory and practice of RNA-seq
- Microbial community composition analysis and available research tools
- Microbial metagenomics/metatranscriptomics theory and applications
**Course Structure:**

Note while effort has been taken to make this syllabus an accurate reflection of the course material, changes to its content are possible throughout the semester.

Week 1, Sep 05: Intro to the Course, Structure of DNA & RNA, Nucleic Acid Nomenclature  
Week 2, Sep 12: Lecture: Principles of the genetic code, mutations  
Week 3, Sep 19: Lecture: Amino acids properties, code, and connection to protein structure  
Week 4, Sep 26: Lecture: Technologies for generating sequence information & Seq. Platforms I  
Week 5, Oct 03: Lecture: Sequencing platforms II & sequence file formats  
Week 6, Oct 10 Lecture: Comparative sequence analysis, similarity/identity/homology, etc.  
Week 7, Oct 17: Lecture: Scoring matrices, global vs. local alignments, & multiple seq. alignments

Exam 1

Week 8, Oct 24: Lecture: Principles of BLAST & online resources for comparative analysis  
Week 9, Oct 31: Lecture: Phylogenetic reconstruction  
Week 10, Nov 7: Lecture: Sequence assembly approaches & genomic analysis resources  
Week 11, Nov 14: Lecture: RNA-seq and eukaryotic genomics  
Week 12, Nov 21: Lecture: Microbial community composition analysis and research tools  
Week 13, Nov 28: Lecture: Microbial metagenomics/metatranscriptomics  
Week 14, Dec 5: Lecture: Review and work on research projects

Exam 2

Week 15, Dec 12: Lecture: Review and present research projects

Finals Week – Dec 18-22: Final project Due

**Credits & Time Commitment:**

This is a 3 credit-hour course. Students are expected to devote approximately 9 hours per week to the course over the semester. This time commitment will include:

- In-class time – lectures and class discussions/activities (45 hours)
- Listening/Watching online lectures & exploring online material (10 hours)
- Reading & study of assigned materials/lectures (30 hours)
- Preparation for and completion of exams (15 hours)
- Completion of learning assessment questions (12 hours)
- Topics presentations (10 hours, grad students only)
- Data analysis and write-up (35 hours)
- Exploring supplemental materials for topics to improve fundamental knowledge (as needed)
Evaluation:
Final course grade will be a result of participation in class activities, performance on exams, problem/question sets, an independent project mini-review article (grad only) and presentation. No Makeup assignments are anticipated.

<table>
<thead>
<tr>
<th>Assessment</th>
<th>Undergraduate</th>
<th>Graduate</th>
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<tbody>
<tr>
<td>Class Participation/Discussion</td>
<td>150</td>
<td>150</td>
</tr>
<tr>
<td>Exam 1</td>
<td>210</td>
<td>220</td>
</tr>
<tr>
<td>Exam 2</td>
<td>210</td>
<td>220</td>
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<tr>
<td>Topics Presentations</td>
<td>150</td>
<td>300</td>
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<tr>
<td>Final Project Technical Report</td>
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<td>290</td>
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<tr>
<td>Final Project Presentation</td>
<td>280</td>
<td>150</td>
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<tr>
<td>Total Points in Class</td>
<td>1000</td>
<td>1330</td>
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Course Grade Scale:
93-100% A; 90-92% A-; 87-89% B+; 83-86% B; 80-82% B-
77-79% C+; 73-76% C; 70-72% C-; 67-69% D+; 63-66% D; 60-62% D-; <60% F

Participation and Discussion - grades will be a result of student engagement in online and in-class materials. Participation during in-class group and lab work, completing questions for in-class tutorials, engaging in class discussions, and posting to the discussion forums will be used to calculate the participation grade (see Sticky Subjects Forum document for posting in the online forum and associated requirements).

Exams – two exams will be given in the class. The exams will cover material covered up to that point in the class.

Topics Presentations – on one (undergraduate) or two (graduate) occasions in the semester, each student will present the theory and methods related to a particular analysis, and the information in associated peer-reviewed articles related to the topic. Students will choose individual topics at the beginning of the semester. Students will present (visual based presentation, e.g. powerpoint) their researched information in a ~30-40 min lecture to the class and develop questions for class discussion and/or a tutorial for working through online tools.

Final Project – all students will be required to select a data analysis project from the datasets provided. During the semester, the students will work to analyze these data in a meaningful way using one of the techniques learned in the class or a related technique that was not covered in the class. Students will be required to come up with their own hypotheses about the data and analyze the data to address those hypotheses.

Final Project Presentation – During the last week of class, all students will present their identified question, hypothesis, data analysis procedures, and results/conclusions. Presentations should be ~12-15 min long, with 3 min for questions related to the work. I expect students will have processed the data in a meaningful way and have interpretable results to discuss.
Final Project - Technical Report (grad student only), during finals week, graduate students will turn in a technical report describing their final project analysis. These reports will include an introduction to the topic/ question (why it is relevant, including background literature), a description of the procedures used, and a results section with associated interpretation in the context of the literature. See the Technical Report help document for further information.

Undergraduates may produce the final project technical report for extra credit.

Course Policies:
Attendance: With the exception of extreme emergencies, which require official documentation, class attendance is compulsory. Each missed class will result in a 5% decrease to the student’s final grade. If an absence is anticipated or in the case of an extreme event, then contact the instructors as soon as possible to discuss the problem.

Late assignments will be downgraded by 5% for each day past the due date.

Missed Exam Policy: There are no make-up exams, except for extreme emergencies, which require official documentation. In such an event, contact us as soon as possible to discuss the problem. Class presentations are considered examinations. An un-excused absence will result in lost points for that exam. Policies regarding final examinations can be found at the following: http://www.uwm.edu/Dept/SecU/acad%2Badmin_policies/S22.htm.

Suggested Learning Objective Resources:
Learning in this course will rely heavily on reading of scientific literature. There is no assigned textbook. Required reading material for individual topics will be posted on D2L. Students may find any of the following textbooks as useful resources:


List of Required Reading:
Below is a list of the primary journal articles that students will be expected to read and discuss over the semester. Journal article readings will be assigned each week according to the learning objectives and material covered during that time. Note: this list is incomplete and subject to change as new materials become available.


Koren & Phillippy. 2015. One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. Current Opinion in Microbiology 23:110-120.


Other Class Resources:
Class notifications. The course will be coordinated through e-mail and D2L. Reading material, class feedback and assignment delivery must be submitted by the due date using an official UWM email address. Please ensure that you check your official UWM e-mail and D2L frequently because you are responsible for all announcements and course changes posted there.

It is recommended that students use a high-speed internet connection to access D2L from off campus. If D2L content is not opening, examine the settings of your internet browser “pop-up-blocker” or switch internet browsers. Also be aware that timed assignments (e.g. quizzes/exams) do not stop if an internet connection is lost, so it is advised that students use a trusted internet connection and if possible a hardline connection.

The Library. Library work/access will be an important part of the course. In particular, the course will make use of the primary scientific literature (i.e. journal articles) so students will need to understand how to access this literature through library resources. See http://www4.uwm.edu/libraries/ (Specific Journal Titles dropdown menu for journal access). Google Scholar also may be of use to search for articles of interest (http://scholar.google.com).

Class Notes: You are responsible for your own note taking: taking notes is an essential part of the learning process.

General Course/Campus Policies:
Students with Special Needs: Students with special needs should arrange to speak with the instructor(s) during the first week of classes so we can best accommodate your learning style. Note University Policies: Students with disabilities. Verification of disability, class standards, the policy on the use of alternate materials and test accommodations can be found at the following: http://www.uwm.edu/Dept/DSAD/SAC/SACltr.pdf

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Religious observances. Policies regarding accommodations for absences due to religious observance are found at the following: http://www.uwm.edu/Dept/SecU/acad%2Badmin_policies/S1.5.htm

Students called to active military duty. Accommodations for absences due to call-up of reserves to active military duty should be noted. http://www3.uwm.edu/des/web/registration/militarycallup.cfm

Incompletes. The conditions for awarding an incomplete to graduate and undergraduate students can be found at the following:

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Discriminatory conduct (such as sexual harassment). Definitions of discrimination. Harassment, abuse of power, and the reporting requirements of discriminatory conduct are found at the following:
http://www.uwm.edu/Dept/SecU/acad%2Badmin_policies/S47.pdf

Academic misconduct. In this course, you are expected to perform to the best of your ability in an honest manner. Cheating, plagiarism, or other acts of misconduct will result in a severe penalty to you, as per University of Wisconsin System Chapter 1.
http://www.uwm.edu/Dept/OSL/DOS/conduct.html Plagiarism is a particular concern: many students seem unclear about what it involves. I recommend that you read:
http://www.plagiarism.org/learning_center/what_is_plagiarism.html because ignorance is not acceptable as an excuse.

Complaint procedures. Students may direct complaints to the head of the academic unit or department in which the complaint occurs. If the complaint allegedly violates a specific university policy, it may be directed to the head of the department or academic unit in which the complaint occurred or to the appropriate university office responsible for enforcing the policy.

Grade appeal procedures. Procedures for student grade appeal appear at the following:
http://www.uwm.edu/Dept/SecU/acad%2Badmin_policies/S28.htm

Final examination policy. Policies regarding final examinations can be found at the following:
http://www.uwm.edu/Dept/SecU/acad%2Badmin_policies/S22.htm