Course Description

SYBB 311/411A is a 5-week course that introduces students to the high-throughput technologies used to collect data for bioinformatics research in the fields of genomics, proteomics, and metabolomics. In particular, we will focus on genotyping, DNA/RNA sequencing, mass spectrometry-based proteomics, and mass spectrometry-based metabolomics. This is a lecture-based course that relies heavily on out-of-class readings. Students will be assigned three research papers for writing reports, two of which will be used also for paper presentations in teams. Graduate students will be expected to give an oral presentation on an article related to the subjects of this course at the end of the course.

SYBB 311/411A is part of the SYBB survey series which is composed of the following course sequence: (1) Technologies in Bioinformatics, (2) Data Integration in Bioinformatics, (3) Translational Bioinformatics, and (4) Programming for Bioinformatics. Each standalone section of this course series introduces students to an aspect of a bioinformatics project - from data collection (SYBB 311/411A), to data integration (SYBB 311/411B), to research applications (SYBB 311/411C), with a fourth module (SYBB 311/411D) introducing basic programming skills.

Classroom Times and Location

August 25th - September 22nd Tuesday & Thursday, 10:00-11:15 AM
Thwing 101

Undergraduate students

Prerequisites: BIOL 214 and 215; OR BIOL250
Undergraduate students must register for all four modules (SYBB 411A, B, C and D).

Graduate students

Prerequisites: Graduate standing OR Prerequisites not met permission
Graduate students have the option of enrolling in all four courses or choosing the individual modules most relevant to their background and goals with the exception of SYBB411D, which must be taken with SYBB411A.

Instructors:  Masaru Miyagi, PhD
Center for Proteomics and Bioinformatics
Office: BRB 928
Email: mxm356@case.edu
Office Hours: Mon 3:00 to 5:00 PM

Thomas LaFramboise, Ph.D.
Department of Genetics and Genome Sciences
Office: BRB 625
Email: txl80@case.edu

Michelle Puchowicz, PhD
Department of Nutrition
Office: BRB 924
Email: map10@case.edu
Grading
The overall grading scheme of the course will consist of in-class participation, and written reports; graduate students have the additional requirement of an in-class final presentation.

<table>
<thead>
<tr>
<th>Graded Item</th>
<th>Undergraduate %</th>
<th>Graduate %</th>
</tr>
</thead>
<tbody>
<tr>
<td>In-class participation &amp; class attendance</td>
<td>30%</td>
<td>30%</td>
</tr>
<tr>
<td>Writing Report on Journal Articles</td>
<td>50%</td>
<td>20%</td>
</tr>
<tr>
<td>Paper Presentation</td>
<td>20%</td>
<td>20%</td>
</tr>
<tr>
<td>Final Presentation for Graduate Students</td>
<td>--</td>
<td>30%</td>
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</table>

Final grade will be computed based on the grading scheme above. Final letter grades will be issued out of the possible 100 points. Tentative scale A = ≥ 90, B = 80 – 89, and etc. However, these ranges may be adjusted (“curved”), at the discretion of the instructor, based on class performance.

Academic Integrity
No form of academic dishonesty including cheating, plagiarism, misrepresentation, or obstruction will be tolerated in this class. Plagiarism in any form will result in a failing grade. If you have questions regarding this matter, please see: [http://studentaffairs.case.edu/office/judicial](http://studentaffairs.case.edu/office/judicial)
<table>
<thead>
<tr>
<th>Week #</th>
<th>Date</th>
<th>Lecture</th>
<th>Topics</th>
</tr>
</thead>
</table>
| 1      | Aug 25  | Genomics | • Introduction to systems biology and bioinformatics  
                                  • Sanger sequencing  
                                  **Recommended readings:**  
|        |         |         | **Assign Students Papers for Writing a Report and Presentation**                            |
| 2      | Sep 1   | Genomics | • Introduction to genotyping arrays  
                                  • Highly parallel genotyping platforms  
                                  • “Next generation” sequencing (NGS)  
                                  • NGS file formats  
                                  • Mapping/alignment/variant calling  
                                  • Introduction to transcriptomics  
                                  • Transcriptome assessment platforms  
                                  • RNA-sequencing (RNA-Seq)  
                                  • RNA-Seq data analysis  
                                  **Recommended readings:**  
|        |         |         | **Student paper presentations in teams**                                                    |
|        | Sep 3   | Proteomics | • Introduction to proteomics  
                                    • Fundamentals of mass spectrometry  
                                    • Protein/peptide identification  
                                    • Protein/peptide quantification  
                                    **Recommended readings:**  
|        |         |         | **Assign Students Papers for Writing a Report and Presentation**  
                                    **Due date for the first report** |
<table>
<thead>
<tr>
<th>Week</th>
<th>Date</th>
<th>Lecture</th>
<th>Instructor</th>
<th>Topic</th>
<th>Details</th>
</tr>
</thead>
</table>
| 3    | Sep 8 | 5 Proteomics | Masaru Miyagi | Applications of proteomics | • Expression proteomics  
• Interaction proteomics  
• Post-translational modification proteomics  
• Drug-target identification  
**Recommended readings:**  
• Principles of proteomics, 2nd Edition (2014), by Richard M. Twyman, Garland Science, Chapter 4, 7, 8 and 10  
• Introducing Proteomics: From concepts to sample separation, mass spectrometry and data analysis, 1st Edition (2011), by Josip Lovrić, Wiley |
|      | Sep 10 | 6 Proteomics | Masaru Miyagi | Student paper presentations in teams | |
| 4    | Sep 15 | 7 Metabolomics | Michelle Puchowicz | Targeted metabolomics | • Introduction to metabolomics  
• Quantification of metabolites  
• Flux analysis of metabolites  
**Recommended readings:**  
**Assign Students Papers for Writing a Report**  
**Due date for the second report** |
|      | Sep 17 | 8 Metabolomics | Masaru Miyagi | Untargeted metabolomics | • Separation and detection of metabolites  
• Identification and quantification of metabolites  
• Pathway and network analysis of metabolic data  
**Reading material:**  
<p>| 5    | Sept 22 | 9 Graduate Student paper presentations in teams | Masaru Miyagi | Both the undergraduate and graduate students will receive extra credit for asking questions and comments during the final presentations. |
|      | Sept 22 | | | <strong>Due date for the third report</strong> |</p>
<table>
<thead>
<tr>
<th>Section</th>
<th>Description</th>
<th>Undergraduate Grading Scale</th>
<th>Graduate Grading Scale</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Introduction</strong></td>
<td>This section of the review should state the research question and explain why it is interesting, state the hypotheses tested.</td>
<td>10%</td>
<td>10%</td>
</tr>
<tr>
<td><strong>Methods</strong></td>
<td>Briefly describe the methods (design, participants, materials, procedure, what was measured), how data were analyzed.</td>
<td>40%</td>
<td>30%</td>
</tr>
<tr>
<td><strong>Results</strong></td>
<td>Describe the results. Discuss whether they were significant or not? Explain the key implications of the results.</td>
<td>40%</td>
<td>30%</td>
</tr>
<tr>
<td><strong>Discussion</strong></td>
<td>Briefly describe why the study did or did not produce significant results. Did anything unexpected influence the findings? Suggest a future line of research or &quot;next steps&quot; to improve the body of knowledge.</td>
<td>10%</td>
<td>30%</td>
</tr>
</tbody>
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**Graduate students must also address:** what other methods might have been appropriate to address the research question; why did the authors not choose an alternative method (discuss at least 2 alternatives)