



AVS 454/554: DNA Sequencing Analysis Lab

Instructor

Dr. Sue Ishaq (she/her); sue.ishaq@maine.edu,

I do not have pre-scheduled office hours, but I am always happy to meet to help you navigate your project.

Time

Fall 2023: live sessions are held on zoom on Mondays from 2 – 3 pm, and Wednesdays from 9 – 10 am. All sessions are recorded and made available on Brightspace for asynchronous students.

Location and mode of instruction

Online over Zoom, but students who need in-person accommodations may contact me.

Class format: Short lectures followed by guided computer laboratory time and discussions on bioinformatics and theory. Various outputs from the analysis will be submitted online for assignments. This course requires access to a computer.

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Description of course and prerequisites

This course will take students from raw DNA sequencing data through quality assurance, through to data interpretation, statistical analysis, and presentation of the results as a mock scientific article. A background in

microbiology, microbial ecology, or genetics would be beneficial. No programming or data analysis experience is required. Students who are performing research may bring their own sequencing data to process in class. Students will become familiar with command-line programs and basic computer programming techniques; understand bioinformatics methods such as quality trimming, assembling contigs, sequence alignment, using reference databases, and statistical comparisons; gain hands-on experience in bioinformatic analysis of DNA sequences using the R platform and its packages; primarily, DADA2, phyloseq, vegan, ggplot2; and be able to apply the knowledge gained in class to other sequence types and programs. Students may bring their own data, or some can be provided. AVS 454 and 554 cannot both be taken for credit.

Credit hours: 2

Prerequisites: AVS 254 or BIO 319 or Bio 350 or BMB 280 or WLE 200 or SMS 300, and STS 232 or MAT 215; or graduate student standing

Course materials and digital services used

- Textbook and readings: There is no required textbook for this class. Reading material will be provided as electronic journal articles or readings.
- Lecture slides: All lectures are provided at the beginning of the semester as pdfs with annotated speaker notes included as comments in the document. These will be updated as needed with corrections.
- Lecture recordings: All lectures are recorded, and video files are added to Brightspace after class.
- Software: All software used in the course is free and can be downloaded to a personal computer.
- Assignments: All assignments can be submitted through Brightspace, and each assignment portal has more detailed instructions, grading rubrics, and the proposal assignment has an optional document template.
- Brightspace Online Learning Software
 - [Log into Brightspace](#). Read the [tutorial](#). Download the [Pulse app](#).
 - Brightspace is the online learning management system used at the University of Maine. In our course Brightspace site, you will be able to access course materials, assignment descriptions, this syllabus, and the course schedule. You will submit your work through Brightspace and will be able to access your grades and feedback as well. You can download a "Brightspace Pulse" app for most mobile devices from your regular app store. Be aware: Some functions in Brightspace work better when accessed through a laptop/desktop than through a mobile device. Support for the website and mobile apps includes video tours, IT Help Desk, and other resources. If you continue to have problems with Brightspace, please let me know as soon as possible.
 - If you wish to retain a personal copy of course materials, please do so before the end of the semester. **You will not have access to a course's Brightspace site after you complete the course.** You can store copies of material you wish to retain on Google Drive, your hard drive, or other media of your choosing. Other materials posted by your faculty may be found at the library.
- Zoom Online Conferencing Software
 - Read the [UMaine tutorial](#).
 - Zoom is an online conference software that students can use to attend class remotely as needed. Students may invite friends and family to watch their presentation using Zoom.

I am happy to provide accommodations to the way course materials are formatted or provided to make them easier to access and understand. Please let me know if you have suggestions to improve the course materials.

Student learning outcomes and objectives to meet them:

After completion of the course, students will be able to:

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1. Use an understanding of bioinformatics methods, such as quality trimming, assembling contigs, sequence alignment, using reference databases, and statistical comparisons, to curate a data processing and analysis workflow. This may include bioinformatic analysis of DNA sequences, using the R platform and its packages, MEGA, NCBI genome assembly, MG-RAST, etc. (Quantitative Literacy)
2. Demonstrate proficiency in taking raw DNA sequence data through quality control steps to interpretation, and summation of the workflow and results into mock scientific journal article manuscripts. (Quantitative Literacy)
3. Demonstrate scientific writing skills, specific to manuscript preparation, including incorporating instructor and peer-review comments and revisions. Submit multiple drafts and progression the ideas with each draft.
4. Demonstrate skills in peer-reviewing manuscripts, including reviewing, editing, and scientific critique.

Expectations of students and university policies

Attendance and Participation

Students are expected to attend lectures, but it is understood that life often precludes this and that students may be performing field work or are located off-campus. Students may attend class virtually, through Zoom, which will be offered for each class. Students who will miss a significant number of classes, or who require additional accommodations, may contact me to make alternate arrangements. Students who are lactating or caring for young children may bring them to class (see section on Pregnancy, lactation, and parenting).

Students are expected to participate in discussions in class, or on Brightspace. I strive to create inclusive discussions, but if students still find it challenging to participate, please notify me and I will alter the discussion format as needed. Supporting inclusion and community is an active process that involves both invitation, and support to ensure that the learning community is and remains an equitable and inclusive place. Students are expected to conduct themselves in a professional, courteous manner and abide by university policies.

Course Schedule Disclaimer (Disruption Clause): In the event of an extended disruption of normal classroom activities (due to COVID-19 or other long-term disruptions), the format for this course may be modified to enable its completion within its programmed time frame. In that event, you will be provided an addendum to the syllabus that will supersede this version.

Late Assignments

I will accept assignments for a certain period of time after the due date, however, the assignments in this class build on one another and their due dates are specifically set to help you achieve the end goals of this class. You will not receive a grade reduction for late assignments, but you waive the right to receive feedback which might impact the quality of successive drafts and your next grade. **After 28 hours of lateness on manuscript assignments, a more difficult rubric will be applied to your submission.** Regular assignments will not be accepted after the last day of class and the final draft will not be accepted after the finals period. If you cannot complete all assignments within the semester, please contact me about taking an Incomplete instead of a letter grade and setting up deadlines to complete the coursework after the semester in order to receive a letter grade.

Campus Policies

“The University of Maine is an EEO/AA employer, and does not discriminate on the grounds of race, color, religion, sex, sexual orientation, transgender status, gender expression, national origin, citizenship status, age,

disability, genetic information or veteran’s status in employment, education, and all other programs and activities.” Follow the links for more information.

[Academic Honesty Statement*](#)

[Students Accessibility Services Statement*](#)

[Course Schedule Disclaimer*](#)

[Observance of Religious Holidays/Events*](#)

[Sexual Discrimination Reporting \(Long\)*](#)

[Sexual Discrimination Reporting \(Short\)*](#)

[UMaine Land Acknowledgement](#)

Students Accessibility Services (SAS) Statement

All students may request an accommodation for this course without a letter, and I will do my best to comply. If you need an accommodation letter for another course or to have it on file for this course: please [contact SAS](#), 121 East Annex, (207) 581-2319, as early as possible in the term.

Note on authorship

If you are pursuing a manuscript for publication in this class, the work you generate is your intellectual property. I do not expect to be an author on your manuscript, or to have ownership over any materials you generate. I would like me/the class to be mentioned in the Acknowledgments section. I will help you facilitate authorship roles with the full research team (i.e. the people that generated these data).

Assignments and Assessment: Detailed instructions and rubrics on Brightspace.

Not graded	<i>Discussion boards</i> – After some classes, there will be a discussion board to complete on Brightspace. These are not graded but will help you generate ideas and items that you can use to form your other graded assignments.
5 points	<i>Quiz</i> – Read a short document provided in the quiz and answer a few questions to test your understanding. Quiz is on Brightspace, <u>is not timed, and may be taken twice</u> . Quiz is auto-graded, contact me if you feel there has been an error.
5 points	<i>Assignments</i> Assorted small assignments to help build other skills
Undergrad: 2 reviews, 25 points Graduates: 4 reviews, 25 points	<i>Peer review</i> – Students will perform reviews of other students’ manuscript draft one and two. Details on performing a review will be provided in class, but generally reviewers should comment on how well the information is presented: if the proposal makes sense, if the objectives of the study are clear, if the scientific approach is easy to understand, and if you notice spelling, grammatical, or formatting errors.
5 points	<i>Elevator Speech</i> – Give a 2-3 min (timed), non-technical summary of your project or topic. You can use notes, but do not prepare slides or visuals. The goal of the elevator speech is to describe your project conversationally, to get someone interested.
60 points (3 drafts at 10, 20, and 30 points)	<i>Mini scientific manuscript</i> Lab work output will be used to write one scientific manuscript using amplicon sequencing data, which will be submitted with successive revisions 3 times during the semester. We will generate the Methods and Results section in lab, and students will be responsible for generating the Introduction and Discussion sections independently. Students may work collaboratively with up to three students per group, but the manuscript length, depth of information, and quality of the writing should reflect the

	<p>number of students in the group. Graduate students are expected to present a higher quality of writing, > 15 citations, more nuanced statistical analysis or graphical representation, and more in-depth discussion sections.</p> <p>Specific instructions are provided on Brightspace, and guidelines may be found in the “writing manuscripts” reading. For each successive submission, students will incorporate revisions from instructor and (when available) peer review to progress the complexity of the scientific content and the maturity of the writing style.</p> <p>At the end of the semester, students may opt to use their analysis and manuscript and pursue submission in a scientific journal along with the research team who provided their dataset. Not all datasets may be applicable, and the final decision will rest with the student and with the Principal Investigator who owns the data. Submission for journal review is <u>completely elective</u> and is not considered in the grading of this class in any way.</p>
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Grading (out of 100 points): A = 93–100; A- = 90–92; B+ = 87–89; B = 83–86; B- = 80–82; C+ = 77–79; C = 73–76; C- = 70–72; D+ = 67–69; D = 63–66; D- = 60–62; F = 0–59.

Schedule of lectures and assignments.

Each row is one class, and all the associated materials (lecture notes, readings, assignments, assessments, links) are included in a Brightspace module which correspond to the name and order of the lab.

Day	Title, Description, Assignments for each module
	<p>**Prior to the first class** Download and install R (the program candy): https://www.r-project.org/ and Rstudio (the fancy wrapper): https://rstudio.com/products/rstudio/download/</p> <ul style="list-style-type: none"> • Suggested software for viewing/editing files: Sublime 3 text editor: https://www.sublimetext.com/3 • Suggested resources for new R users: <ul style="list-style-type: none"> ○ PDF on Brightspace: AVS454 Basic Info on Command Line and R ○ http://www.r-tutor.com/r-introduction ○ R tutorial, https://www.statmethods.net/r-tutorial/index.html <p>**After every class**</p> <p>Update/clean up your code, annotate with notes, add to your methods or results section of your manuscript by describing what you did that day.</p>

Week 1	
M 8/28	<p><i>"Intro to the class"</i>, syllabus and course expectations, finding course materials. Students will introduce themselves, their major, and what they hope to get out of the class.</p> <p><i>Lab 1: Introduction to R and getting started for beginners</i> The rest of the first class will be spent helping first-time R users make sure they have everything sorted. Experienced R users are welcome to leave class early. We will practice installing R and packages, keeping good notes and workflow files, basic file import and data entry.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action Item: Make sure you have the sequencing files for your project (or the example files) on your computer. Fastq.gz is the preferred file format, but fastq and fasta also work. <input type="checkbox"/> Reading 1: Read/watch a lecture on Brightspace on a sequencing technology of your choice: Illumina, PacBio, Ion Torrent, Roche, Sanger. Available as pdf and recorded slides. <input type="checkbox"/> Reading 2: Read/watch a lecture on Brightspace, AVS454 <u>Data_files_and_quality</u>
W 8/30	<p><i>Lab 2: How to assess amplicon data quality and trim</i> Check in from last class, then we will assess raw data quality in R for our samples, and decide whether to use contigs or single reads. We will choose parameters to use for filtering and trimming, which you may complete in class or on your own time before the next class.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action Item in R: Complete the "filter and trim" step with DADA2 by next class. <input type="checkbox"/> Action Item in R: Continue personalizing your copy of the workflow, including file and folder names, notes to yourself, and summaries of each step. <input type="checkbox"/> Discussion on Brightspace: Make one aggregate quality plot for the Forward reads, and one for the Reverse reads (if you have any). Summarize the quality of each in a sentence, and why you continued with Forwards only, or F+R. List the trimming parameters you chose and why/what they accomplished.
Week 2	
M 9/4	Labor day, no class
W 9/6	<p><i>Lab 3: How to calculate error rates and pick sequence variants</i> Check in from last class, then we will use DADA2 in R to estimate the error rates in the dataset. While that is running, we will talk about how DADA2 uses the error rates to pick SVs, and briefly how that compares to OTUs.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: Complete the dada (slow) and makeSequenceTable (quick) commands in R by next Tuesday <input type="checkbox"/> Discussion on Brightspace: List the number of bases you used for the error rate picking, the number of total SVs that were created, and the lowest and highest SVs in a sample. <input type="checkbox"/> Reading: Callahan_2016_DADA2 <input type="checkbox"/> Reading: Callahan_2017_ASVs_over_OTUs <p>We'll go over these papers as a group next class, bring thoughts and questions</p>
Week 3	
M 9/11	<p><i>Lab 3.1 Journal club day: DADA2 and the Great ASV Debate</i> Let's go over the two Callahan papers assigned in the previous class, define terms we didn't understand, and share our thoughts on ASV vs. OTU debate. Please read Callahan_2016_DADA2, and Callahan_2017_ASVs_over_OTUs prior to the class period.</p>

	<ul style="list-style-type: none"> <input type="checkbox"/> Assignment (5 pts): Plagiarism quiz on Brightspace, ~ 40 min of time, can take twice, have one week to complete <input type="checkbox"/> Reading: Read lecture on Brightspace, AVS454_concept_Genetic_distance <input type="checkbox"/> Reading (optional, suggested for anyone using 16S data): AVS454_rRNA_sequencing_theory
W 9/13	<p><i>Lab 4: How to remove chimeras and verify workflow</i></p> <p>Check in from last class, then we will use DADA2 in R for removing chimeras, and counting our reads in previous steps to make sure we like what we did before moving on. Looking into positive and negative controls.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: complete some/all of the workflow verification steps by next class <input type="checkbox"/> Reading: AVS 454_sources_of_sequencing_contaminants <input type="checkbox"/> Reading: Prosser_2010_need_for_replication <input type="checkbox"/> Prep for next class: If you have the DNA quantification data (nanodrop) for your libraries, you can use that next class for further QC. If you don't, don't worry about it.
Week 4	
M 9/18	<p><i>Lab 5: How to remove contaminants</i></p> <p>Check in from last class, then we will revisit data quality discussion and the wet-lab and dry-lab contaminants you are likely to find in sequencing data, and setting up code to use sequenced negative controls to clean up your data. Together in R we will use negative controls or DNA quantification data to remove contaminating sequences from data using Dr. Ishaq's code or <i>decontam</i>. If you don't have negative controls, this time will be used to catch up, revise, or write. Either way, you can remove unwanted taxa by name.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: complete either Ishaq method or the decontam method by next class <input type="checkbox"/> Discussion on Brightspace: Describe how you used negative controls to remove possible contaminants, and if you will be removing any taxa by name and why (ex. Mitochondrial matches). Include ordination plots of the 'before' and 'after'. <input type="checkbox"/> Reading: Nearing_2021_microbiome_processing_yields_different_results
W 9/20	<p><i>Lab 6: How to make taxonomy databases and/or assign taxonomy</i></p> <p>This concept-only day involves talking about sequencing databases, and strategies for finding or making a database for non-microbial amplicons. The homework will be to make a 10-sequence database, but you are not required to make your own database to use for the data analysis in the next class.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Assignment (5 pts): Complete the "DIY taxonomic reference database" exercise on creating reference databases using MEGA, due by next class. Instructions on Brightspace. This is a demo assignment, and will not be used in your data analysis workflow. <input type="checkbox"/> Reading (choose 1): <ul style="list-style-type: none"> ➤ Balvociute_2017_comparing_taxonomic_databases ➤ Smith_2020_database_choice_rumen_microbiome ➤ Collins_2021_Meta-Fish_database_12S ➤ Weigand_2019_reference_libraries_aquatic_biota
Week 5	

M 9/25	<p>Lab 6.1 No class, Sue is traveling, but you should try to perform the taxonomy assignment step in R before next class</p> <ul style="list-style-type: none"> <input type="checkbox"/> Due: DIY database on Brightspace <input type="checkbox"/> Action item: complete taxonomy assignment in R by next class. Assigning species-level is optional. Use the Silva database for 16S if using example data from class. It is recommended to let this run overnight. <input type="checkbox"/> Discussion on Brightspace: Which database did you select and why. Find the citation for the paper which presents the database, so you can include that in your methods section. Most databases will have this information on their webpage.
W 9/27	<p>Lab 6.2 <i>Catch up on analysis day</i> Let's go over where we are at, trouble shoot, and spend some time letting our code run.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Discussion on Brightspace: what are the research questions you want to try and answer? Draw and describe your experimental design, what groups or factors are you looking at? Are any factors nested within another? Do you have samples from the same host or source over time (repeated measures)? Do you have biological or technical replicates? <input type="checkbox"/> Reading: Hong_2022_to_rarefy_or_not_to_rarify <input type="checkbox"/> Reading: Schloss_2023_preprint_rarefy_still_best <p>We'll go over these papers as a group next class, bring thoughts and questions</p>
Week 6	
M 10/2	<p>Lab 6.3 Journal club day: To rarefy or not, and why we inevitably rarefy Let's go over the Hong and Schloss papers assigned in the previous class, define terms we didn't understand, and share our thoughts on rarefication step debate. Please read Hong_2022_to_rarefy_or_not_to_rarify, and Schloss_2023_preprint_rarefy_still_best prior to the class period.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Reading: Read a lecture on Brightspace, AVS454_experimental design and models. <input type="checkbox"/> Reading: AVS454_alpha_diversity_nitty_gritty
W 10/4	<p>Lab 7: <i>How to rarefy and graph alpha diversity</i> Check in from last class, then we will use phyloseq in R to rarefy our data and start making pretty graphs to quantitatively describe the microbial diversity we have.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: Fancy up at least one alpha diversity plot that you'll use for your manuscript <input type="checkbox"/> Reading: Read a lecture on Brightspace, AVS454_quick stats
Week 7	
M 10/9	No class – Fall Break
W 10/11	<p>Lab 8: <i>How to run alpha diversity stats</i> Check in from last class, then we will use phyloseq, vegan, and other packages in R to run statistics on Alpha diversity.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: complete means testing or other statistical comparison for your alpha diversity <input type="checkbox"/> Assignment due: Put whatever you have drafted so far for the amplicon analysis manuscript (includes background and quality-assurance processing steps but not much else yet) into the Google Drive folder by midnight.

	<p>Assignment (10 pts): Peer review round 1. Undergrads select 1 manuscript to read, grads select 2 manuscripts to read, make comments on in google docs, and/or revise using “suggestion mode”. Note, everyone will be able to see these comments. To obtain the grade, write 1 short paragraph for each manuscript summarizing what you liked and what you commented on, and submit to Brightspace for only me to see. Detailed instructions can be found on Brightspace. Due October 19th.</p>
Week 8	
M 10/16	<p><i>Lab 9: Other ways to graph alpha diversity – no class, lecture is pre-recorded</i></p> <ul style="list-style-type: none"> <input type="checkbox"/> Reading: Ecartot_2015_writing_scientific_article <input type="checkbox"/> Reading: Read a lecture on Brightspace, AVS454_writing_manuscripts
W 10/18	<p><i>Lab 9.1 no class, Sue is traveling</i> <i>Open class time: Catch up on alpha diversity graphs and stats</i></p> <ul style="list-style-type: none"> <input type="checkbox"/> Assignment due: Peer reviews on drive and submitted to Brightspace by 10/19. <input type="checkbox"/> Reading: Shade_2017_diversity_microbial_ecosystems
Week 9	
M 10/23	<p><i>Lab 10: Comparing changes in taxonomy</i> Lecture and lab: “Delineation of taxonomic change”; general guidelines for displaying taxonomy, as well as DESeq2, random forests, LEFSe.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: complete at least one of the graph types explored in this session <input type="checkbox"/> Reading: Read a lecture on Brightspace, AVS454_how_do_you_figure
W 10/25	<p><i>Lab 11: Beta diversity and simple ordinations</i> Check in from last class, then using phyloseq or vegan/ggplot2 we will compute community-level similarity and graph beta diversity as ordination plots.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: make at least one simple ordination to visualize beta diversity in your data <input type="checkbox"/> Assignment due (10 pts): First draft of amplicon analysis manuscript that includes background and quality-assurance processing steps. Due on Brightspace by midnight. <input type="checkbox"/> Reading: Ramette_2007_multivariate_microbial_ecology <input type="checkbox"/> Reading: Palmer_Ordination_Methods_Overview
Week 10	
M 10/30	<p><i>Lab 12: Beta diversity and ordination stats</i> Check in from last class, then using phyloseq or vegan/ggplot2 we will run stats on our beta diversity ordinations and think about other ways to graph beta diversity.</p> <p>Reading: Xia_2017_hypothesis_testing</p>
W 11/1	<p><i>Lab 13: Beta diversity component analysis</i> Lecture and Lab: “Beta diversity component analysis”. more community-level analysis. RDA, CCA, db-RDA, WTF.</p> <ul style="list-style-type: none"> <input type="checkbox"/> Action item: complete a CCA or an RDA or a db-RDA (don’t need more than one) <input type="checkbox"/> Reading: Borcard_2006_RDA_vs_CCA
Week 11	

M 11/6	<p><i>Lab 13.1 Open class time: Focus on beta diversity</i> Collaboratively work on refining our beta diversity analysis, manuscript, etc.</p> <p><input type="checkbox"/> Reading (choose 1):</p> <ul style="list-style-type: none"> ○ Escobar_2020_niche_modeling_epidemiology ○ Malard_2022_niche_modeling_soil
W 11/8	<p><i>Lab 13.2 Journal club day: niche modeling</i> Let's go over two papers that focus on ecological niche modeling, to understand how we can apply that thinking to our own papers. Please read Escobar_2020_niche_modeling_epidemiology and Malard_2022_niche_modeling_soil prior to the class period.</p> <p><input type="checkbox"/> Assignment due: Put whatever you have drafted so far for the amplicon analysis manuscript (includes background and quality-assurance processing steps but not much else yet) into the Google Drive folder by midnight.</p> <p><input type="checkbox"/> Assignment (15 pts): Peer review round 2. Undergrads select 1 manuscript to read, grads select 2 manuscripts to read, make comments on in google docs, and/or revise using "suggestion mode". Note, everyone will be able to see these comments. To obtain the grade, write 1 short paragraph for each manuscript summarizing what you liked and what you commented on, and submit to Brightspace for only me to see. Detailed instructions can be found on Brightspace. Comments due in 10 days.</p>
➤ Week 12	
M 11/13	<p><i>Lab 14: Niche versus neutral models</i> Go over some examples of niche modeling in R and online. Optional to perform on your data.</p> <p><input type="checkbox"/> Optional Reading: Fisher_Mehta_2014_niche_neutral</p> <p><input type="checkbox"/> Optional Reading: Fahimipour_Gross_2020_bacterial_metabolic_niche_mapping</p>
W 11/15	<p>No class - <i>Open time</i> to work on analysis, manuscript, etc.</p> <p><input type="checkbox"/> Assignment due: Peer reviews due, finish comments on Google docs and submit summaries to Brightspace for the grade</p>
Week 13	
M 11/20	<p><i>Lab 15: Source tracking</i> Go over some examples of source tracking in R and online. Optional to perform on your data.</p> <p><input type="checkbox"/> Reading: Pirzadian_2020_sinks_as_sources</p> <p><input type="checkbox"/> Optional Reading: Knights_2011_source_tracker</p> <p><input type="checkbox"/> Optional reading: Carter_2020_source_tracker_microbial_forensics</p>
W 11/22	<p><i>No class – Thanksgiving Break</i></p>
Week 14	
M 11/27	<p><i>Lab 16: PiCRUST function prediction</i> Go over functional prediction for microbial community 16S data. Optional to perform.</p> <p><input type="checkbox"/> Optional Reading: Douglas_2020_PiCRUST2</p> <p><input type="checkbox"/> Assignment due (20 pts): Second draft of amplicon analysis manuscript due for grading</p>

W 11/29	<p><i>Lab 17: Tree building</i></p> <p>Trees, as needed. Free time for additional analysis/writing</p> <p><i>Open class time: Graphics check-up</i></p> <p>Let's go back over the graphics and make sure they are telling the story we think they are. Time to chat about improving our graphics and making them the best we think we can.</p> <p>Assignment prep (5 pts): give elevator speeches in next class</p>
Week 15	
M 12/4	Give elevator speeches in class (5 pts) – you will be timed
W 12/6	Give elevator speeches in class (5 pts) – you will be timed. Asynchronous students will find a time to present to me between now and end of finals.
F 12/8	Last day of fall classes and last day late assignments will be accepted (not including the final draft, will be accepted during finals week)
R 12/14 (finals)	Assignment due (30 pts): Final draft of amplicon analysis manuscript due by midnight.

There is bonus content on Brightspace, including overview lectures and selected readings, if you want to read more on whole-genome sequencing, metagenomics, metatranscriptomics, challenges of using 16S and how to account for genetic and sequencing-technology-based problems in the bioinformatic workflow.

UMaine resources related to research, statistics, writing, and careers:

- Fogler Library
 - OneSearch, <https://library.umaine.edu/>; find scientific literature
 - Research Data Management: <https://libguides.library.umaine.edu/datamanagement>
 - Creating a research poster: <https://libguides.library.umaine.edu/confposters>
 - Creating a research presentation: <https://libguides.library.umaine.edu/confposters/presentations>
 - Presentation Practice Room, <https://library.umaine.edu/use/presentation-practice-room/>
- Statistics Consultation, <https://umaine.edu/tasc/stats/> (may have a cost associated with this service, talk to your research mentor before setting up a consultation)
- Writing Center, <https://umaine.edu/wcenter/>; tutoring, editing, skills development

There is always someone on campus to help you

My door is always open and I am always willing to help students, however, as a university employee I am also required to keep the community safe by disclosing information on crimes. This means I am a “mandatory reporter”. If you disclose something to me, including in assignments, I am obligated to provide this information to the campus Title IX office. The Title IX Office will contact you discretely, and offer you support services, guidance, and help you choose if you want to take action.

For confidential resources on campus:

- Counseling Center: (207) 581-1392
- Cutler Health Center: (207) 581-4000.
- Rape Response Services: 1-800- 871-7741
- Partners for Peace: 1-800-863-9909.

For support services on campus which may have to report the incident to others who can help:

- (emergency and non emergency) [Title IX Student Services](#), (207) 581-1406,
- (emergency and non emergency) University of Maine Police: (207) 581-4040 or 911.
- (non emergency) Office of Community Standards: (207) 581-1409.

Support services off campus:

- [Mabel Wadsworth Center](#), Bangor: reproductive health care, abortion, addiction help, et

Free food and clothing

- [Black Bear Exchange's Food Pantry](#), Orono campus
- Old Town Crossroads Ministry

University Rainbow Resource Center

[The Rainbow Resource Center](#) located in Memorial Union, Room 224, empowers and increases the visibility of Lesbian, Gay, Bisexual, Transgender, and Queer (LGBTQ) people by promoting equality and inclusiveness. We strive to maintain an open, safe, and supportive environment for students, staff, faculty and alumni and provide educational opportunities, information, and advocacy services.

Pregnancy, lactation, and parenting

I am happy to make accommodations for students based on pregnancy, lactation, and parental needs, as well as work with the Office of Equal Opportunities (E.O.). The state of Maine and UMaine policies allows students to breastfeed in any space, including in class. If a lactation space is required, please contact E.O. for arrangements. The [Pregnant on Campus Initiative](#) provides pregnancy and parenting resources in Orono.

University Veterans Education and Transition Services (VETS)

[University of Maine's VETS Center](#) serves student veterans as they apply to, attend and advance beyond UMaine. The Veterans Center connects student veterans with the resources they need to successfully transition from combat to classroom to career. This includes help navigating the admissions process, applying for financial aid and U.S. Department of Veterans Affairs education benefits, academic assistance and preparing to re-enter the workforce. The VETS Center is located in Room 143 of the Memorial Union.

University Counseling Services

If you are experiencing a mental health emergency: Dial 911. You can also call campus Police Services at (207) 581-4040. For urgent help, please check this page for your options: <https://umaine.edu/counseling/need-urgent-help/>.

Over the course of our time at the University, we may face a variety of concerns – depressed mood, anxiety, stress, family concerns, body image, substance use, sexuality and many others – that may interfere with their ability to focus on their studies. [Counseling Services](#) provides mental health and social support for all currently enrolled students. Staff follow strict legal and ethical guidelines concerning the confidentiality of counseling. Counseling services is located in Cutler Health Center, Room 125 and can be reached by phone at (207) 581-1392.

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