# Timeline for "Applied Bioinformatics"

*[Version 2.0: September 14, 2022]*

***Warning: This course requires a significant amount of work outside of class!*** It is a 5 ECTS credit unit course, which translates to ~150 hours of semester work, but we only meet for 14 lectures and 14 exercise sessions, for a total of ~56 hours of face-to-face time. The remainder (~6-7 hours each week!) will be spent doing readings, tutorials, practice, homework, and group semester project work *outside of class*.

**NOTE: assigned readings for each week should be completed *before* coming to class that week. All reading is REQUIRED unless if otherwise noted.**

**V**: lecture and group discussion
**P**: group hands-on analysis (practical session)

| Week | Date | Topic and assigned reading *(to be completed before class)* |
|---|---|---|
| **Module 1: Introduction to microbiomes and microbial bioinformatics toolkit** | | |
| **1** | 20.09 | **V**: Introduction and overview of bioinformatics, microbiomes, and their relevance to food/agro/health. Discuss!<br>**Reading (before class!)**: (1) Berg 2020; (2) choose one: Zmora, Blaser, Trivedi. Prepare to discuss in class.<br>**P:** Intro to scientific computing "toolkit": python, Jupyter, and GitHub. Read before class: (1) JupyterHub introduction (on Moodle); (2) Git and GitHub (Moodle); (3) Data Carpentry Python Tutorial (Moodle). In this week we do not yet look at microbial datasets, but learn about the software toolkit we will use, taking a simple dataset from (non-microbial) ecology. The Data Carpentry tutorial starts with basic python and moved on to intermediate topics, so enter at the point appropriate for your level.<br>● Recommended for python learners: Google Python Course |
| **2** | 27.09 | **V:** DNA sequencing and overview of microbiome "omics" technologies.<br>**P:** Metadata! Managing and visualizing dataframes with pandas.<br>**Reading**: Week 2 exercises (see Moodle) and 1. Heather and Chain 2015.<br>Week 2 exercise due before class<br>Module 1 homework is due at the end of the week. |
| **Module 2: Analysis of microbial *sequence data*** | | |
| **3** | 4.10 | **V:** Microbiome analysis methodology: marker-genes and their analysis.<br>*Assemble term project groups based on interests*.<br>**P**: Sequence alignment, clustering, and comparison.<br>**Reading**: 1. Woese and Fox 1977. 2. Bolyen 2019. 3. Callahan 2017. 4. Scan the QIIME 2 docs, incl. "what is QIIME 2" and "Core Concepts"* and **QIIME 2 tutorials***: overview tutorial through "Denoising and clustering"; "Clustering sequences" tutorial; "Importing" tutorial.<br>Week 3 exercise due before class |
| **4** | 11.10 | **V/P:** Sequence search methods and taxonomy classification<br>**Reading**: 1. Parks 2018. 2. **QIIME 2 tutorials***: overview tutorial through taxonomy<br>Week 4 exercise due before class |
| **5** | 18.10 | **V/P:** Taxonomy, phylogeny, and function<br>**Reading**: 1. skim Zhu 2019. 2. Baldauf 2003. 3. **QIIME 2 tutorials***: overview tutorial through phylogeny building<br>Week 5 exercise due before class<br>Module 2 homework is due at the end of the week. |
| **Module 3: Analysis of microbial *community data*: diversity, function, and ecology** | | |
| **6** | 25.10 | **V/P:** Measuring and comparing diversity: alpha diversity |

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| | | **Reading**: 1. Hughes 2001. 2. Thompson 2017. 4. **QIIME 2 tutorials***: rarefaction and diversity sections.<br>Week 6 exercise due before class<br>Midterm reports due for group projects by the end of the week. |
| **7** | 01.11 | V/P: Measuring and comparing diversity: beta diversity<br>**Reading**: 1. Lozupone and Knight 2005<br>Week 7 exercise due before class |
| **8** | 08.11 | **V/P:** Data normalization and differential abundance<br>**Reading**: 1. Gloor 2017. 2. McMurdie and Holmes 2014. 3. Weiss 2017.<br>Week 8 exercise due before class |
| **9** | 15.11 | **V/P**: Metagenomics vs. "metabarcoding"<br>**Reading**: 1. Quince 2017. 2. Eloe-Fadrosh 2016. 3. Nayfach 2019. 4. Paez-Espino 2016.<br>Week 9 exercise due before class |
| **10** | 22.11 | **V/P:** Functional redundancy and stability. Interactive discussion of reading!<br>**Reading**: 1. Louca 2018. 2. Yachi and Loreau 1999. 3. Relman 2012<br>Week 10 exercise due before class<br>Module 3 homework is due at the end of the week. |
| **Module 4: Advanced topics in microbial bioinformatics.** | | |
| **11** | 29.11 | **V/P**: Advanced data visualization with Python<br>**Reading**: Week 11 exercises (see Moodle)<br>Week 11 exercise due before class |
| **12** | 06.12 | **V/P**: Machine learning. Group discussion of reading.<br>**Reading**: 1. Wastyk 2020. 2. Subramanian 2014. 3. Lloyd-Price 2019. 4. **QIIME 2 tutorials***: Predicting sample metadata values with q2-sample-classifier.<br>Week 12 exercise due before class |
| **13** | 13.12 | **V/P:** No lecture or exercises! We will spend the day working on group projects.<br>**Suggested Reading**: (purely for inspiration this week!) 1. Niccum 2020. 2. Rao 2021. 3. Blasche et al 2021 4. Goldford 2018 |
| **14** | 20.12 | **Group presentations.** *Prizes for the best presentation!*<br>*Group projects are due **by the end of the day**.* |

***Note on QIIME 2 documentation and tutorials**. The core documentation and tutorials can be found online at https://docs.qiime2.org/. I list the topics that need to be learned, and usually mention specific document titles when it is important for reading more about a specific method or process. However, ***I do not link to specific pages, because the meta-objective here is for you to learn how to navigate software documentation websites!*** In addition to reading the listed tutorials, you should explore some of the links in those tutorials (including to other tutorials, external websites, or literature references) to gain a better understanding of the methods and their applications. Whenever you learn about a specific QIIME 2 action (in a tutorial or in class), you should also check out the "plugins" section of the documentation to learn more about that action, its usage, and any parameters that modify its behavior. You are welcome to also run through the tutorials (e.g., copy over the commands into your own Jupyter notebooks), but this is not necessary as it is redundant with the notebooks that we have already created.