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| Date | Topic | Schedule |
| Wednesday  13 August 2014: | Basics/ QIIME | * 9:30 -10:00 Welcome, course introduction * 10:00-12:30 Tutorial: Introduction to Linux/command-line (Tracy) * 12:30-13:30 Lunch * 13:30-14:30 Lecture: Overview of microbial community ecology and high-throughput sequencing (Ashley) * 15:00 Tutorial Installing QIIME on your laptop (Ashley) * 15:45 Break * 16:00 Tutorial: First steps in data analysis using QIIME, including using Python scripts (Ashley) * 18:00 Break for dinner * 20:00 5-min Research Presentations 1 / Research presentations 2 |
| Thursday  14 August 2014 | Diversity / QIIME | * 09:15-10:30 Tutorial: Using resources (Amazon: how to start an instance, etc; local servers) other than your laptop for the heavy lifting of sequence analysis (Josh) * 10:30-10:45 Break * 10:45 - 12:30 Lecture: Alpha diversity in all of its glory, Tutorial: Building an OTU table and calculating alpha diversity in QIIME * 12:30 Break for lunch * 13:15 Lecture: Beta diversity and visualizing community patterns * 14:00 Tutorial: Beta diversity in QIIME, exporting data tables for R * 18:00 Break for dinner * 20:00 **Shared guest lecture w/ NGS**: Rich Lenski? Jack Gilbert? |
| Friday  15 August 2014 | MOTHUR | * Tutorial: Installing mothur (Tracy) * General mothur-ing: sequence processing, alpha diversity, beta diversity, visualization, exporting data tables for R * If there is time: Move on to lecture what can you do: hypothesis testing ecology. * **Guest Lecture: Patt Schloss** * Evening firepit |
| Saturday  16 August 2014 | Shotgun Metagenomics | * Shotgun metagenomics: annotation (Josh) * End of the day option (or complete independently): installing R / RStudio /vegan package * **Guest lecture**: Titus? Jack Gilbert? Zackee Sabree? |
| Sunday  17 August 2014 | Shotgun Metagenomics | * Brunch: J. Teidje to join us for Brunch and offer an informal Q/A perspective on Microbial Ecology * Morning: Metagenomics continued: assembly * Afternoon: Relax! Free time, Bell’s brewpub in Kalamazoo for dinner |
| Monday  18 August 2014 | Community ecology / R | * Lecture: Hypothesis testing, identifying gradients, and linking environmental and community data (Jay Lennon?) * Tutorials: Using R for community ecology analyses (Stuart Jones) * **Guest lecture**: Stuart Jones / Jay Lennon |
| Tuesday  19 August 2014 | Databases, independent study | * AM: Early PM: **Guest tutorial**: J. Cole: RDP * Mid AM: Databases for community sequences: What’s available out there? Learning activity: Split into teams for each to explore one db in-depth, report back to the group * Late AM: **Guest tutorial**: Kathryn Docherty: NEON database * Late PM: Independent study and directed trouble shooting; TAs available * **Guest lecture**: Meghan Duffy? * Last night fire pit social / BBQ celebration |
| Wednesday  20 August 2014 | Choose your own adventure | Options:  Ashley   * Networks analyses: LSA, MINE, Cytoscape (Ashley) * Analyzing individual community structure: Taxon’s contribution to community dynamics (Ashley)   Tracy   * Introduction to Python scripting for database mining and data wrangling * Data management (SQL / best practices, where to store the data)   Josh   * Using the web to pull data from databases (MG-RAST) (Josh) * Using markers other than 16S for amplicon sequencing (ITS, 18S) * KEGG Pathway / functional pathway analysis * Advanced annotation of metagenomic reads   Adina Howe?  Kathryn Docherty  Linking contextual and metadata to genomic data |