

MSc Bioinf: **Metagenomics Module** – Timetable

Location: Boyd Orr room 1006

The aim of this course is to give a complete overview of the algorithms and software available for microbial metagenomics. The course will cover both 16S rRNA gene analysis (first week) and shotgun metagenome sequencing (second week).

Monday 27th January:

10:00am – 10:30am: **Introduction to the bioinformatics of microbial metagenomics** (Dr Christopher Quince)

- What is metagenomics?
- Difference between 16S rRNA gene sequencing and shotgun metagenomics
- Course overview and assessment

10:30am – 11:00am: **Sequencing platforms and errors** (Dr Christopher Quince)

- Major NGS platforms relevant to metagenomics
- Sequencing and PCR error rates in 16S rRNA amplicons

11:00am – 11:30am: **Taxonomic profiling and OTU construction from 16S rRNA genes** (Dr Christopher Quince)

- Classification vs. clustering
- Algorithms for OTU construction
- Choice of 16 rRNA databases
- Taxonomic classification
- Biases

11:30am – 12:00am: **Noise removal for accurate determination of OTU richness** (Dr Christopher Quince)

- Impact of errors on OTU estimation
- AmpliconNoise for 454 sequences

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: **Practical**

- Introduction to the linux command line
- AmpliconNoise tutorial for 454 pyrosequence data

Tuesday 28th January:

10:00am – 11:00am: **Diversity estimation for microbial communities** (Dr Christopher Quince)

- Alpha diversity metrics
- Rarefaction
- Extrapolating to total diversities
- Multiple samples

11:00am – 11:30am: **Introduction to Python programming** (Dr Umer Ijaz)

- Basic data types
- Flow control

11:30am – 12:00am: **Sequence file formats** (Dr Umer Ijaz)

- File formats: fasta, fastq (including quality scores), genbank, clustalw, blast, and sam

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: **Python programming practical** (Dr Umer Ijaz)

Wednesday 29th January:

10:00am – 11:00am: **Multivariate statistics for microbial community analysis** (Dr Christopher Quince)

- Community comparison metrics
- Ordination
- Hypothesis testing
- Power calculations

11:00am – 11:30am: **Brief introduction to R and R programming** (Dr Umer Ijaz)

11:30am – 12:00am: **Class discussion on plans for individual data analysis**

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: **Practical** (Dr Christopher Quince and Dr Umer Ijaz)

- Multivariate statistics in R

Thursday 30th January

10:00am – 12:00am: **The QIIME pipeline for microbial community analysis + online tutorials**

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: **QIIME tutorials continued**

Friday 31st January

10:00am – 11:00am: **SeqEnv: Annotating sequences with environmental information** (Dr Christopher Quince)

11:00am – 12:00pm: Practical: **Illumina amplicon analysis** (Dr Umer Ijaz)

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 2:00pm: Practical: **Illumina amplicon analysis cont.** (Dr Umer Ijaz)

2:00pm – 4:00pm: Practical: **Individual data analysis**

Monday 3rd March:

10:00am – 10:30am: **Introduction to shotgun metagenomics** (Dr Christopher Quince)

10:30am – 11:30am: **Read based metagenomics profiling** (Dr Christopher Quince)

- Taxonomic profiling
- Functional analysis

11:30 – 12:00am: **Overview of webservers for metagenomics analysis** (Dr Umer Ijaz)

- MGRast, IMG, WebMG, EBI etc.

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: Practical: **Read based metagenome analysis** (Drs Christopher Quince, Umer Ijaz, Melanie Schirmer)

- Megan
- MetaPhlann

Tuesday 4th March:

11:00am – 12:00am: **Introduction to Biopython programming** (Dr Umer Ijaz)

- Accessing databases
- Processing BLAST output

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: **Biopython programming practical** (Dr Umer Ijaz)

Wednesday 5th March:

10:00am – 11:00am: **Metagenome assembly** (Dr Christopher Quince)

11:00am – 12:00am: **Contig annotation** (Dr Christopher Quince)

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: Practical: **Metagenome assembly and annotation** (Drs Christopher Quince and Umer Ijaz)

- Ray, MetaVelvet, etc.

Thursday 6th March:

10:00am – 11:00am: **Taxonomic classification and clustering of contigs** (Dr Christopher Quince)

11:00am – 12:00am: Practical: **Annotation, taxonomic classification and clustering of contigs** (Drs Christopher Quince and Umer Ijaz)

12:00am – 1:00pm: Lunch (not provided)

1:00pm – 3:00pm: Practical: **Annotation, taxonomic classification and clustering of contigs** (Drs Christopher Quince and Umer Ijaz)

Friday 7th March:

10:00am – 12:00am: Practical: **Individual data analysis**