

**Microbiome Data Analysis Workshop Course Outline**

This data analysis workshop will cover the fundamentals of microbiome analysis. In brief, it will cover the basics of sequencing using the Illumina platforms, including the methodology for generating libraries, the data files and their structure. Following this, the basics of the commandline interface with simple commands, followed by a more in-depth look at the Qiime software package and its use for analysing microbiome datasets. Finally, the attendees will be introduced to two different software tools: LefSe (biomarker analysis) and PiCrust (metabolomic analysis). Furthermore, to put microbiome studies into context, several Scottish researchers will present their microbiome research, while providing a valuable networking opportunity for the attendees and the researchers.

Learning objectives:

1. Understand the next generation sequencing process and the resultant datafiles

2. Be competent in basic commandline commands (cd, mv, rm, mkdir etc)

3. Understand what the Qiime package is and how it is used

4. Be able to use a simple Qiime pipeline to analyse a training dataset

5. Be proficient in using LefSe and PiCrust to produce biomarker graphs and an initial metabolomic analysis based on the microbiome differences between factors

**Day 0**

* Attendees arrive

**Day 1**

Session 1

* Welcome Address Prof Paul Garside
* Cindy Smith “Investigation of the microbial community in various aquatic ecosystems”
* Christine Edwards “Microbiome colonisation of the infant gut and its links with diet and metabolism”

Session 2

* Katarina Oravcova “Nosocomial infections – investigating the cause”.
* Brief Introduction from Students
  + 1 slide introduction, who are you, where are from and what is your research interest
* Networking lunch
* University of Glasgow Tour

Session 3

* Introduction to sequencing – how it all works (lecture)
  + Covering Illumina sequencing (the machines and their capabilities), the basic structure of a sequencing library – with particular reference to 16S libraries
* Introduction to 16S sequencing (lecture)
  + the microbiome and how we determine its content
  + What we target and why it is important
  + An overview of other possibilities (i.e. other target regions and metagenomic shotgun sequencing)
  + Generating good quality samples and general pitfalls to avoid

**Day 2**

Session 1

* Data Output (lecture)
  + Introduction to FastQ files, their structure, barcoding.
* Commandline introduction basic commands (practical workshop)
  + The commandline, what it is, and how we use it
  + Practical workshop covering the basic commands used to navigate through the filesystem, and manipulate files.
* Networking lunch



Session 2

* Speaker 1 – Lauren Carruthers “The microbiota pro-files: are schistosomes and anti-helmithic drugs influential agents?”
* Data QC and manipulation (practical workshop)
  + Practical workshop covering data QC (FastQC), trimming using cutadapt, combining reads with overlap using Pandaseq.

Networking Dinner

**Day 3**

Session 1

* Qiime (practical workshop)
  + Overview of the Qiime package, what it is, and what it does
  + Overview of Qiime2 - differences and similarities
  + Why use Qiime and not Qiime2 – Qiime is more open and easier to follow/breakdown into components, it provides a better platform for teaching basic bioinformatics simultaneously with metagenomic analysis
  + How to install Qiime or Qiime2 on an Amazon AWS instance
  + Qiime workshop walkthrough all day
* Lunch

Session 2

* Speaker 2– Adrian Muwonge “Microbiome in humans and pigs in Uganda”
* Description and discussion on summary figures and top-level results
* Overview of alpha and beta diversity and figures produced

Networking Dinner

**Day 4**

Session 1

* LefSe – biomarker analysis
* Lunch

Session 2

* Speaker 3 – Richard Burchmore “The effects of antibiotic treatment on the gut microbiome”
* Further analyses – PiCrust

Farewell Dinner

**Day 5**

Session 1

* Alternative analysis pipelines
  + Different options within Qiime
  + Online platforms
  + Mothur (an alternative to Qiime)
  + Qiime 2
* Open discussion
* Lunch
* Session from local Engagement team to discuss KI strategies e.g. facilitate presentation of future research findings to communities that provided samples or are most affected.

Course ends - Attendees fly home

*Please note: speakers and titles may be subject to change due to other commitments.*