**UCA Biodiversity Workshop, May16-18 2016**

Monday morning

**Introduction** – workshop overview and learning objectives. (20 mins)

**Barcoding** – methodology and utility. Martin (30 mins)

**Barcoding** – sequence analysis, putting your sequences in the context of a reference tree. Dave (30 mins)

**Microbial diversity** — Libusha and Martin (60 mins total)

**16S tag sequencing** — methodology, utility and limitations, discussion of microbial mat 16S dataset that will be used in the tutorial. Libusha (60 mins)

Monday afternoon

Install Qiime and R (Libusha, Fatima, Dave)

Unix tutorial (Libusha, Fatima, Dave)

Tuesday morning

**Research overview** – 30 mins each (Martin, Fatima, Dave, Libusha)

Tuesday afternoon

**Qiime tutorial** -- 16S microbial mat analysis (Libusha, Fatima, Dave)

Wednesday morning

**Stats lecture and integrated R tutorials** (Fatima, Dave)

* Introduction to R
* Data Visualization, Descriptive and Inferential Statistics, Multiple comparisons

Wednesday afternoon

**Sampling Bias and Diversity tutorial** (Fatima, Dave)

* Overview of diversity measures
* Introduction to the vegan package in R
* Interactive Activity!

**Recap discussion and feedback** (All)