

Extracting ecological signal from noise: an introduction to tools for the analysis of high throughput sequencing data from microbial communities

PROGRAMME

Wednesday 8th September

08:30 – 09:30	Coffee and registration
09:30 – 10:00	Introduction/welcome (Lise Øvreås/Knut Olav Daasvatn?)
10:00 – 12:00	Presentation of participants datasets
12:00 – 13:00	Lunch
13:00 – 14:00	Noise removal from Pyrosequenced Amplicons (Christopher Quince)
14:00 – 15:00	OTU construction, total diversities and sampling efforts (Christopher Quince)
15:00 – 15:30	Coffee
15:30 – 17:30	Computer setup

Thursday 9th September

08:30 – 09:30	Taxonomic classification of reads (HIB:LA) (Anders Lanzén)
09:30 – 10:00	Dipping into the rare biosphere: features of rare and abundant bacterial taxa (HIB:LA) (Carlos Pedrós Alió)
10:00 – 10:30	Coffee
10:30 – 12:00	Practical session (Christopher Quince and Anders Lanzén)

12:00 – 13:00	Lunch
13:00 – 14:00	A short introduction to Mothur (Christopher Quince)
14:00 – 15:00	Fitting Neutral distributions (Bill Sloan)
15:00 -15:30	Coffee
15:30 – 16:30	The Qiime pipeline for analysing microbial communities (Greg Caporaso)
16:30 – 18:00	Practical session (Christopher Quince, Anders Lanzén, Greg Caporaso, Bill Sloan)

Friday, 10th September

09:00 – 10:00	Future directions in microbiology; exploring microbial community diversity, gaining new insights from massive parallel sequencing (HIB:SA) (Tom Curtis)
10:00 – 10:30	Coffee
10:30 – 11:30	Multivariate statistics for microbial communities (Christopher Quince)
11:30 – 12:30	Practical session (Chris Quince, Anders Lanzén, Greg Caporaso, Bill Sloan)
12:30 – 13:30	Lunch
13:30 – 14:30	Practical session (cont) (Christopher Quince, Anders Lanzén, Greg Caporaso, Bill Sloan)
14:30 – 15:30	Roundtable discussion: future directions in development of software and statistical tools for genomics
15:30	Formal close