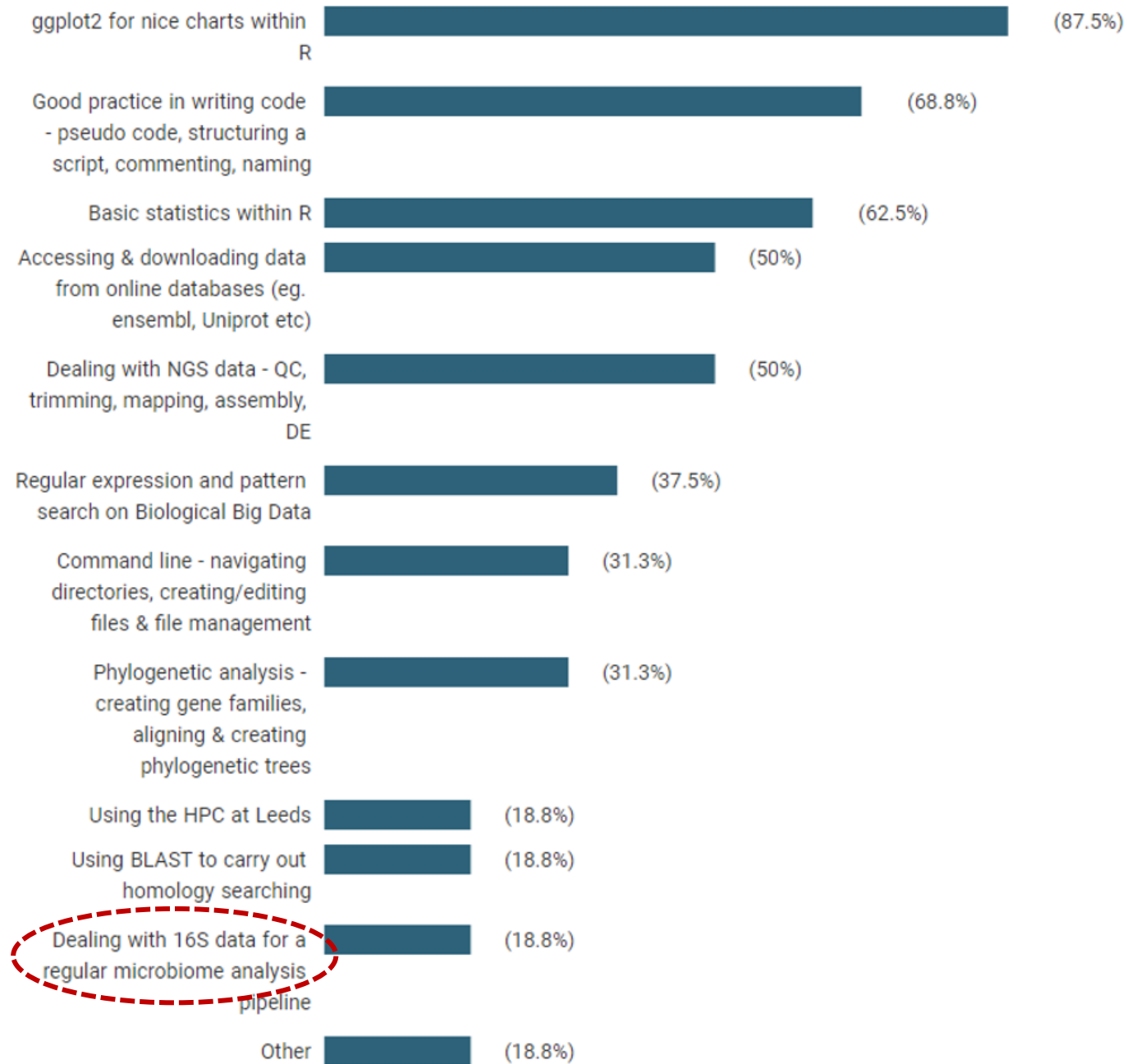


Dealing with 16S data for Microbiome Analyses

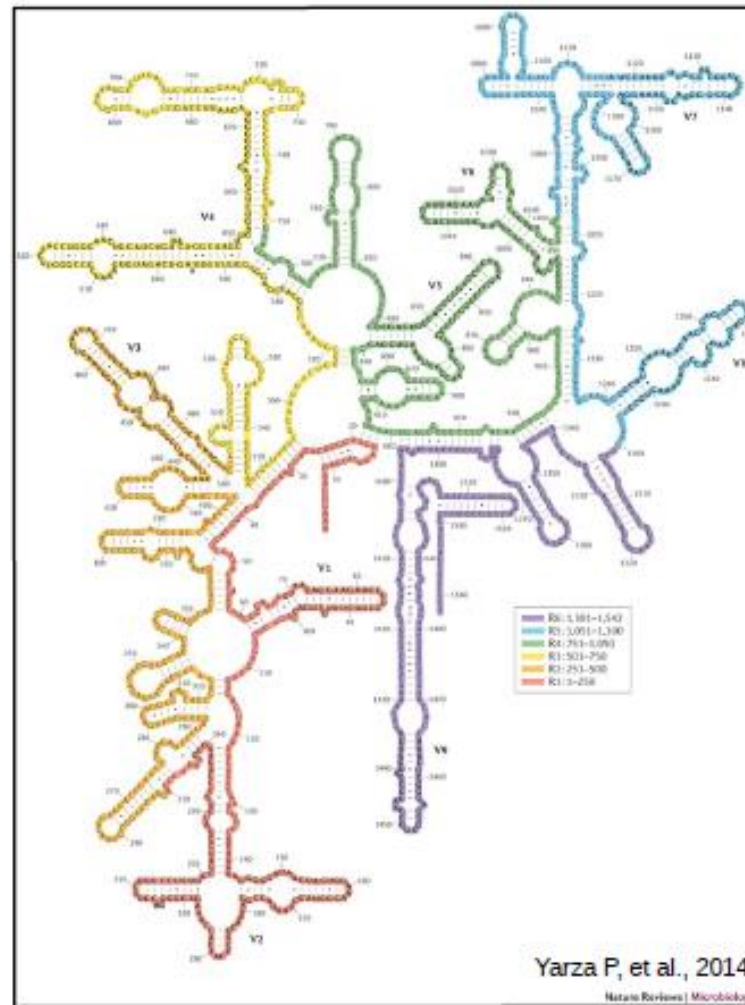
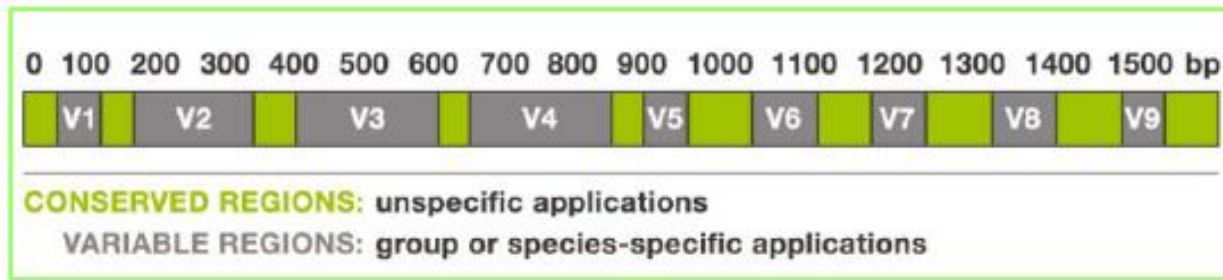
Club Moderators: Elton Vasconcelos, Peter Mulhair, Euan McDonnell, Chew Cheng, and Dapeng Wang

Topics to be addressed - Survey Result



- 16S rRNA gene architecture

- The most frequently used gene for microbial community assessment/characterization



Microbiome investigation on samples of interest in Vet Med



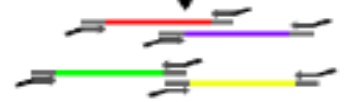
Sample collection



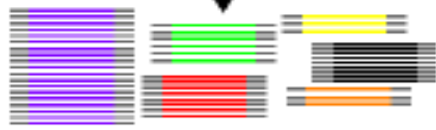
DNA prep



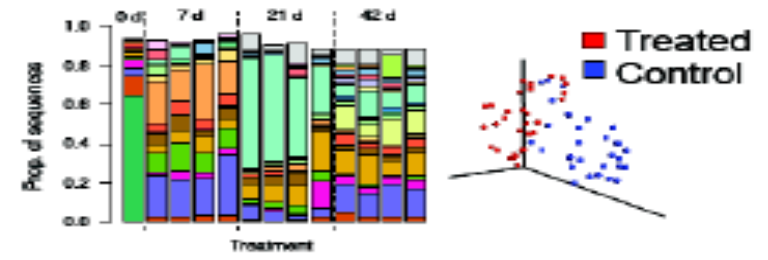
PCR



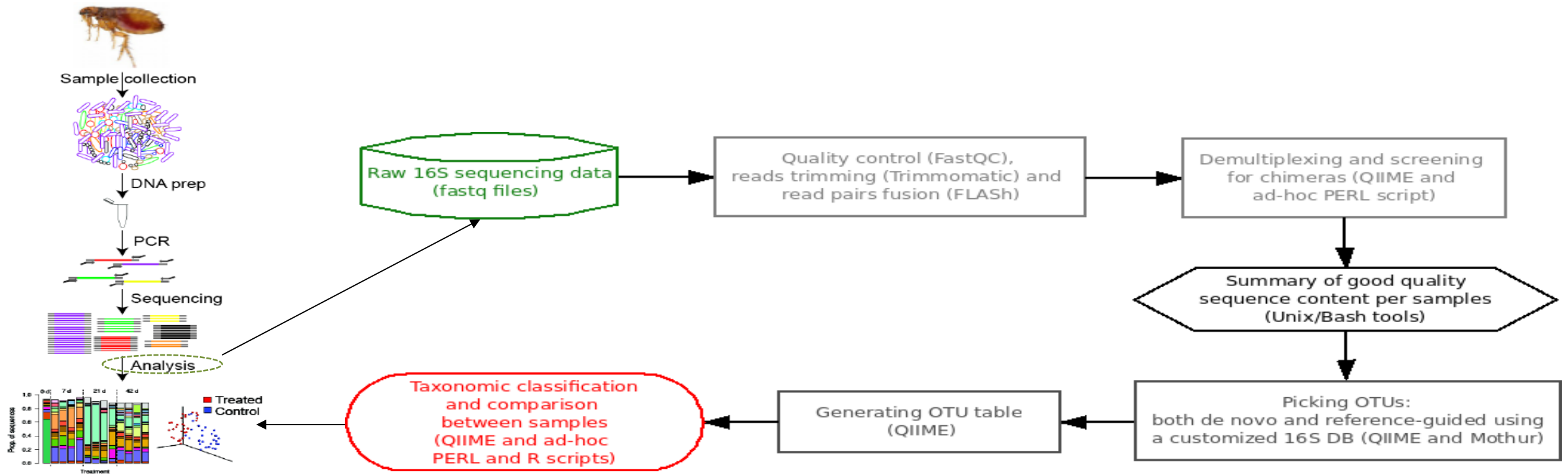
Sequencing



Analysis



■ Computational Workflow (pipeline) for Microbiome Analysis



Typical computational workflow combining *ad-hoc* scripts to several different available tools in order to define **operational taxonomic units (OTUs)** for each sample and accurately classify and compare them.

Bring your issues on!

Discussion on new topics to be addressed
prior launching a second survey.