Seminar

Lichuang Huang

Wie-Biotech
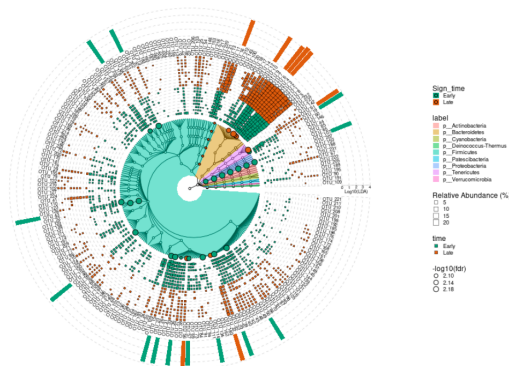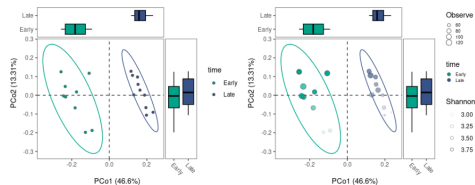
2023-09-13

Last Month

16s rRNA

Qiime2 and MicrobiotaProcess.

- importing data
- . . .
- Alpha and beta diversity analysis
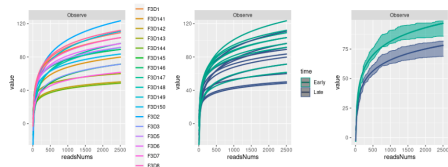- Alpha rarefaction plotting
- Taxonomic analysis
- . . .

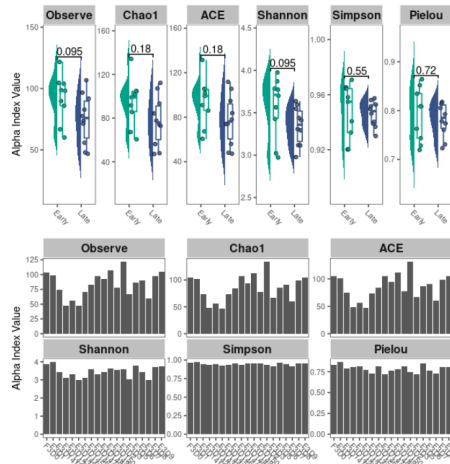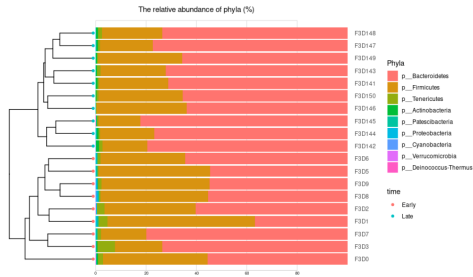The different species and the abundance of sample
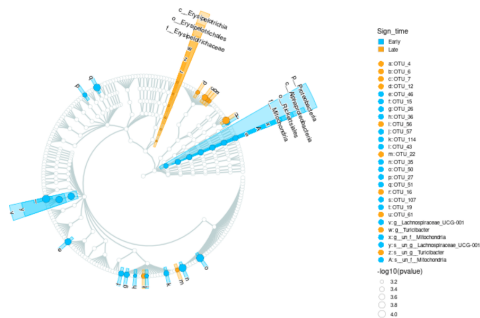
16s rRNA

The PCoA result

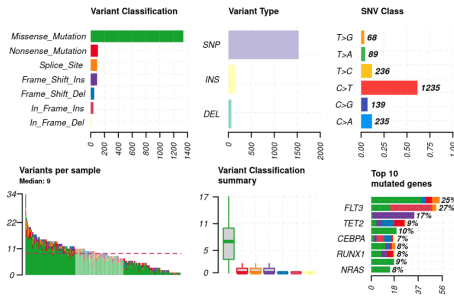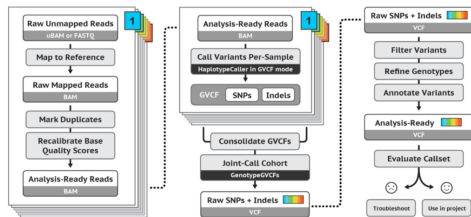The rarefaction of samples or groups

16s rRNA

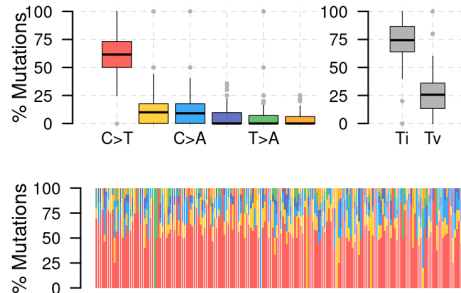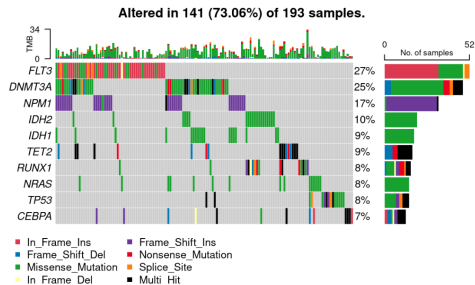The hierarchical cluster result of samples and the abundance of Phylum

The cladogram of differential species

WES

GATK4 ~~elprep~~ elprep, ANNOVAR and maftools

WES

Repetition of Technology

Article

Article

BugSigDB captures patterns of differential abundance across a broad range of host-associated microbial signatures

Ludwig Geistlinger[1], Chloe Mirzayi[2,3], Fatima Zohra[2,3], Rimsha Azhar[2,3], Shaimaa Elsafoury[2,3], Clare Grieve[2,3], Jennifer Wokaty[2,3], Samuel David Gamboa-Tuz[2,3], Pratyay Sengupta[4,5,6], Issac Hecht[7], Aarthi Ravikrishnan[8], Rafael S. Gonçalves[1], Eric Franzosa[9,10,11], Karthik Raman[4,5,6], Vincent Carey[12], Jennifer B. Dowd[13], Heidi E. Jones[2,3], Sean Davis[14], Nicola Segata[15,16], Curtis Huttenhower[9,10,11] & Levi Waldron[2,3,15]✉

A wide range of data sources
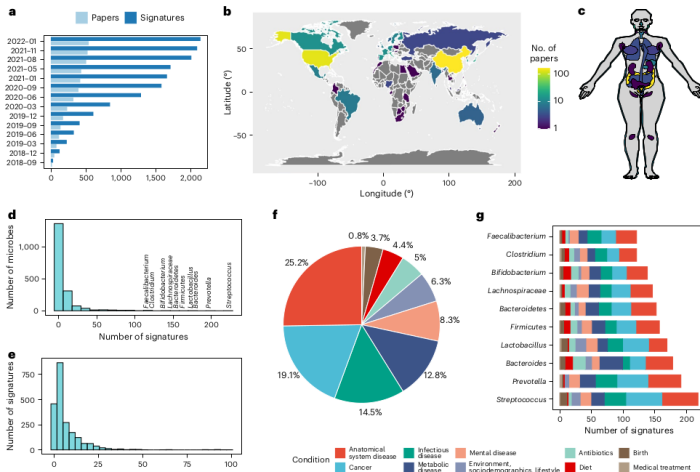
Microbe co-occurrence
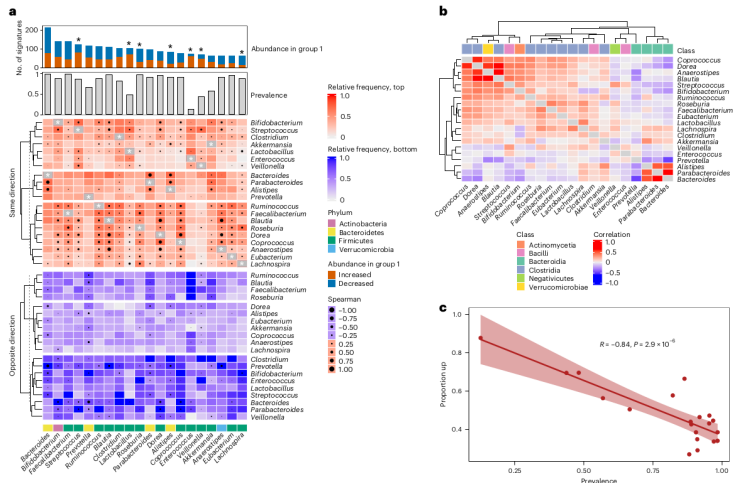
Microorganisms and disease