

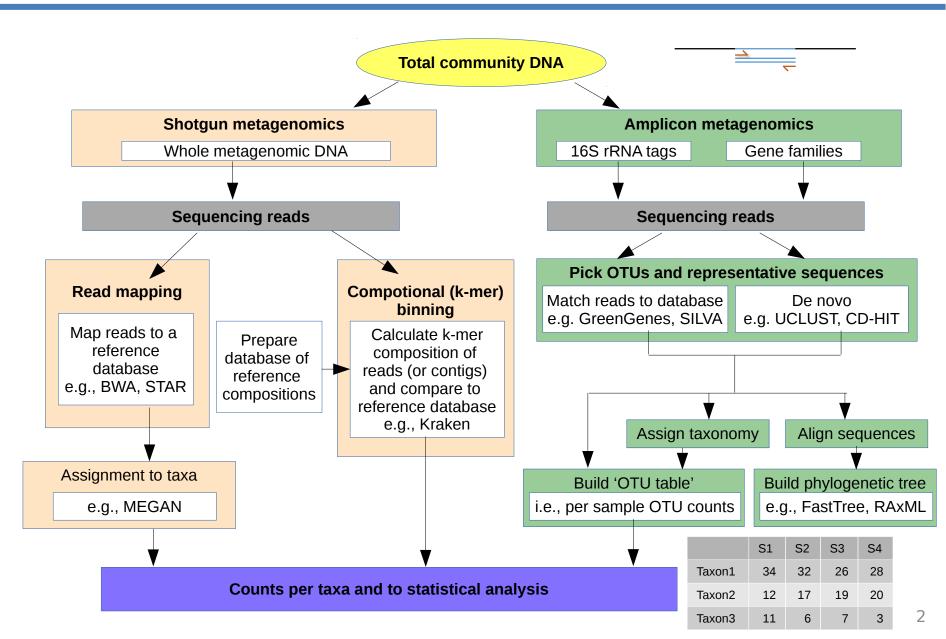
Bioinformatics approaches for Taxonomic and Functional Annotation of Metagenomes

Jiabin Huang

Clinical Metagenomics Meeting 20.12.2018

Taxonomic analysis of metagenomes

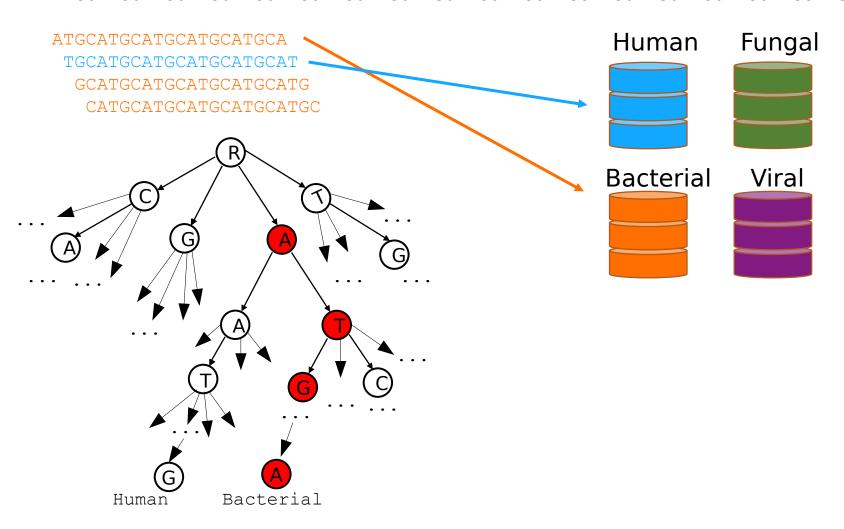




Kmer Count-based Binning



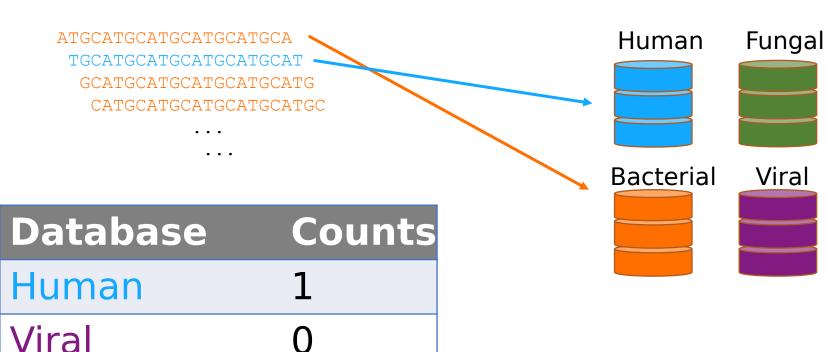
Sequencing Read



Kmer Count-based Binning



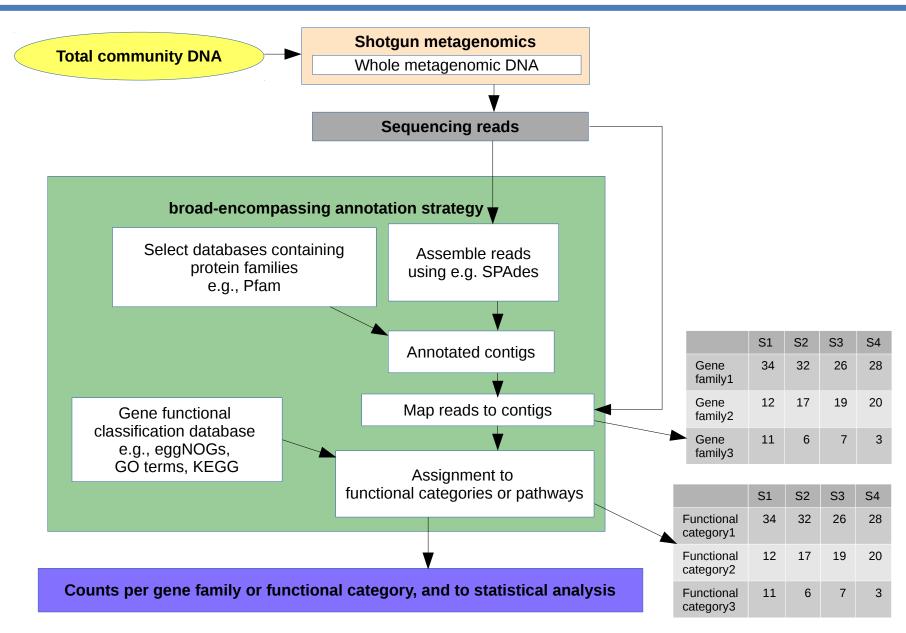
Sequencing Read



Bacterial Bacterial	123
ungal	6

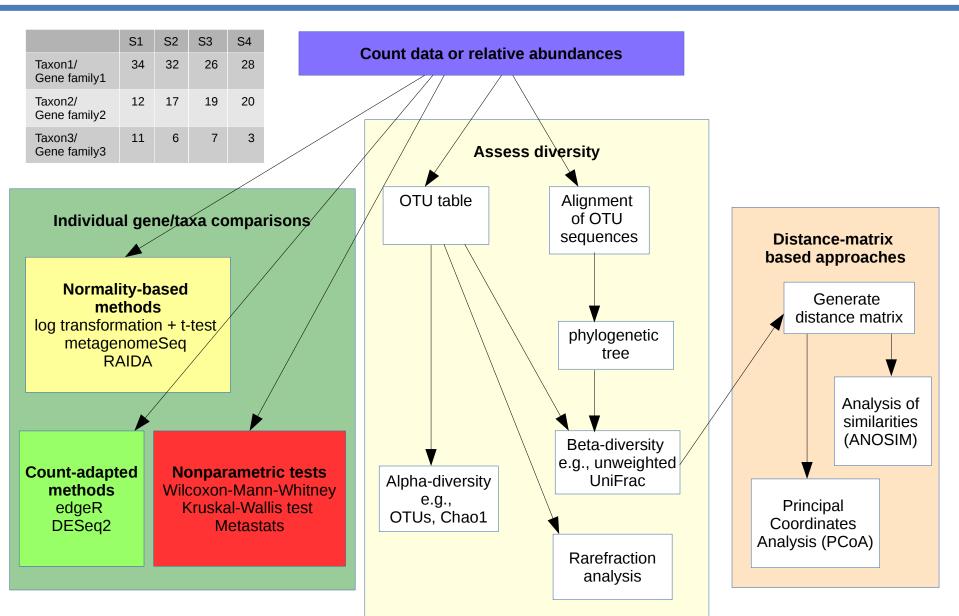
Functional analysis of metagenomes





Statistical analysis of metagenomes

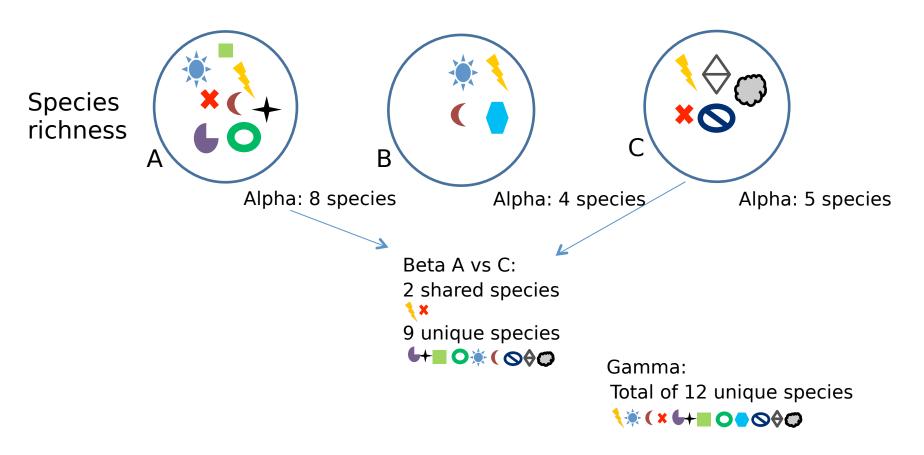




Diversity calculation



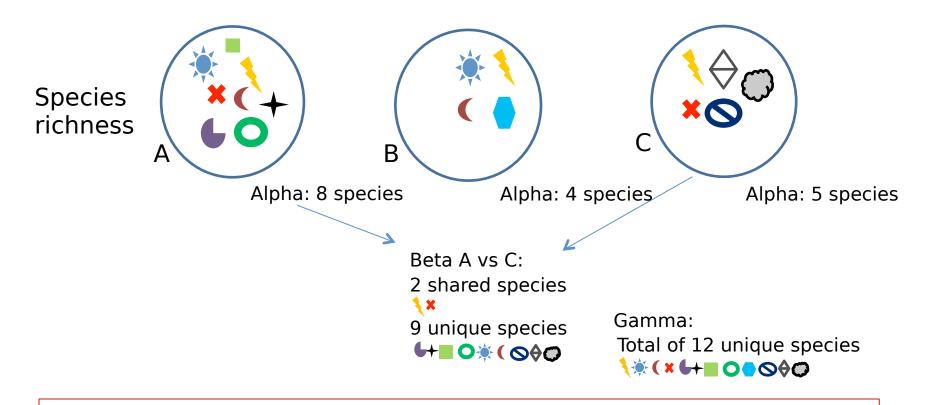
- Alpha diversity: Diversity within a single sample (Alone)
- Beta diversity: Diversity between samples
- Gamma diversity: total diversity in a landscape



Diversity calculation



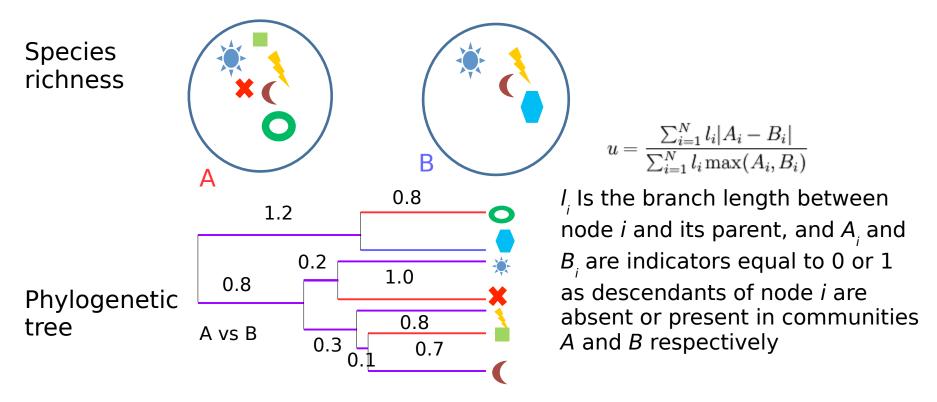
- Alpha Diversity = richness and evenness of individuals within a habitat unit.
- Beta Diversity = expression of diversity between habitats.
- Gamma Diversity = landscape diversity or diversity of habitats within a landscape or region.



PROBLEM: Doesn't take relatedness of each species into account!

Beta-diversity: UniFrac





- Branches unique to A are red, unique to B are blue, in common are purple
- UniFrac Distance Measure = Branch length of red or blue branches / Branch length of all colors = (0.8+0.8+1.0+0.7)/ (1.2+0.8+0.8+0.8+0.2+1.0+1.0+0.3+0.8+0.1+0.7+0.7) = 0,39
- Weighted Unifrac takes abundance into account branch lengths weighted by relative abundance

Case study amplicon metagenomics





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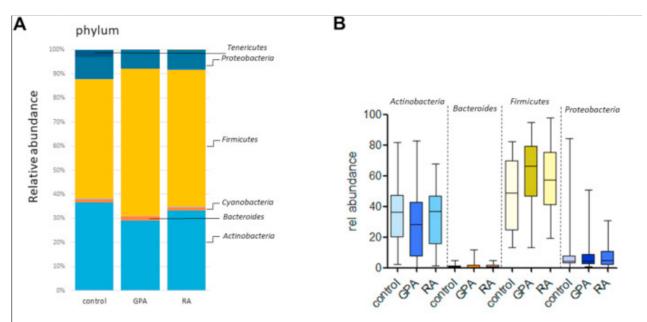
Journal of Autoimmunity

journal homepage: www.elsevier.com/locate/jautimm



Changes in the composition of the upper respiratory tract microbial community in granulomatosis with polyangiitis

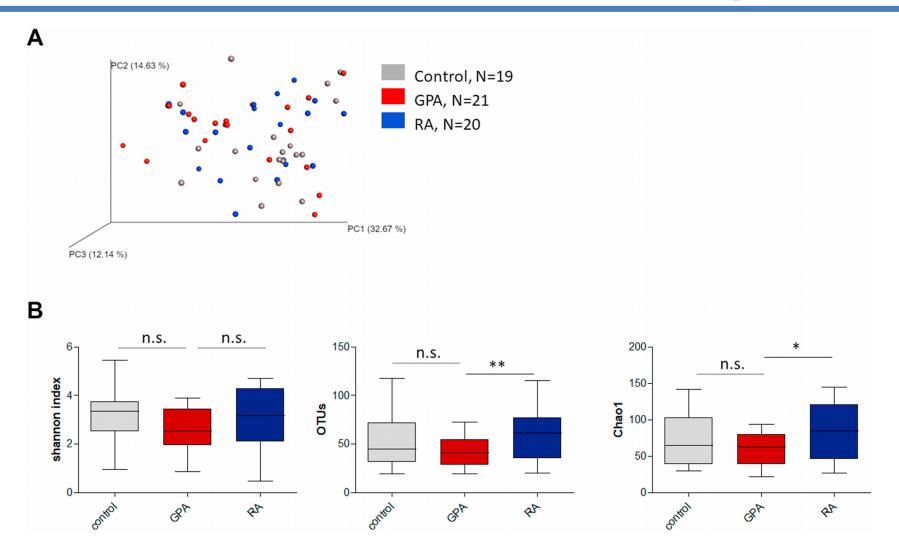
Peter Lamprecht^{a,*,1}, Nicole Fischer^{b,c,1}, Jiabin Huang^b, Lia Burkhardt^d, Marc Lütgehetmann^b, Fabian Arndt^e, Ida Rolfs^f, Anja Kerstein^a, Christof Iking-Konert^g, Martin Laudien^f



Bacterial community composition of the microbial upper respiratory tract in patients with granulomatosis with polyangitis (GPA) and rheumatoid arthritis (RA) and healthy controls.

Case study amplicon metagenomics



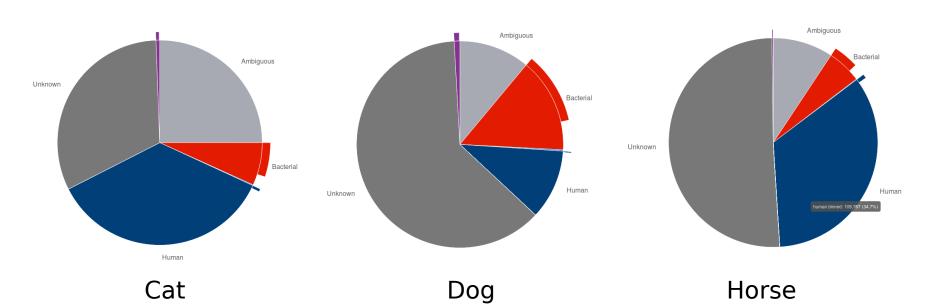


(A) PCoA plot of weighted_unifrac (B) Alpha diversities

Case study shotgun metagenomics



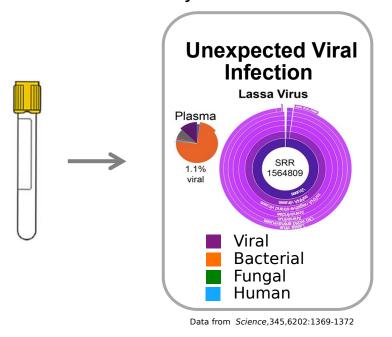
Samples	Human	Bacterial	Viral	Fungal	Ambiguous	Unknown
Cat	35.6%	6.7%	0.5%	0.1%	25%	31.8%
Dog	10.9%	14.7%	0.8%	0.1%	11%	62.1%
Horse	34.7%	5.3%	0.1%	0.0%	9.4%	51.5%



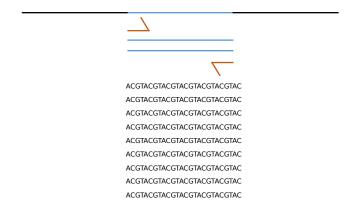
Target capture metagenomics



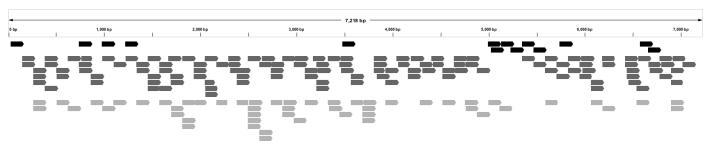
- Shotgun metagenomics
 - Fragment DNA and sequence randomly



- Amplicon metagenomics
 - PCR amplify a gene of interest
 - Tells you what types of organisms there are
 - Bacteria/Archaea (16S rRNA),
 Microbial Euks (18S rRNA), Fungi
 (ITS), Virus (no good marker)

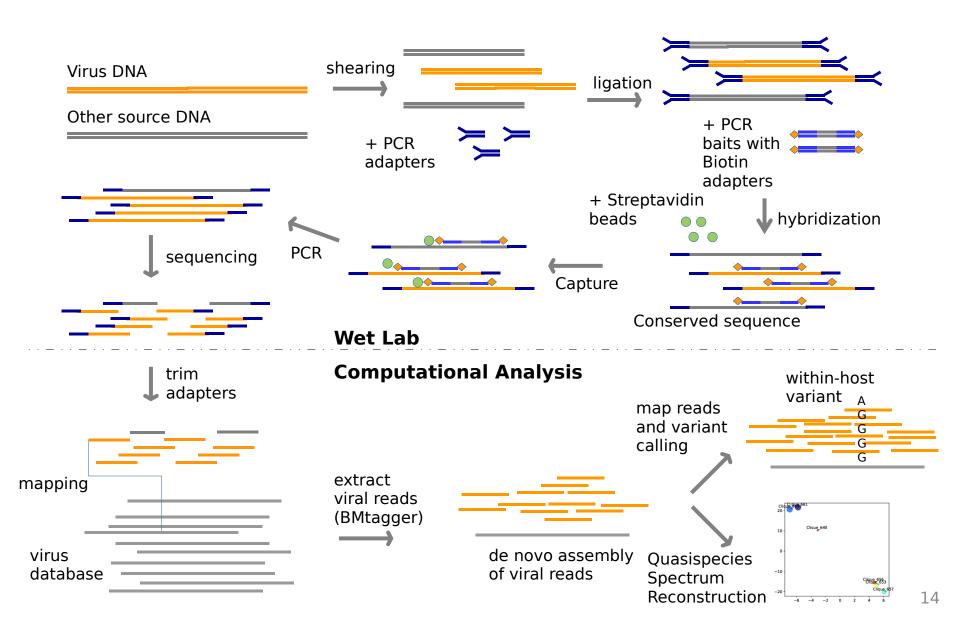


- Target capture enrichment
 - Require probes for a hybridization reaction



Virus metagenomics using target capture I





Word cloud of Metagenomics



