

Hands-on tutorial: R tools for microbial ecology

Leo Lahti. Leuven Summer School on Ecological Network Analysis. Sep 13, 2017.

- Example data: HITChip Atlas
- Data structures: phyloseq class
- Tools for analysis: microbiome R package
- Reproducible document generation: Rmarkdown

Tutorial on-line:

<http://microbiome.github.io/microbiome/Tutorial.html>



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Example data: HITChip Atlas

Gut microbiota high-throughput profiling

1006 Western adults ~ 130 genera

Highly standardized & reproducible platform

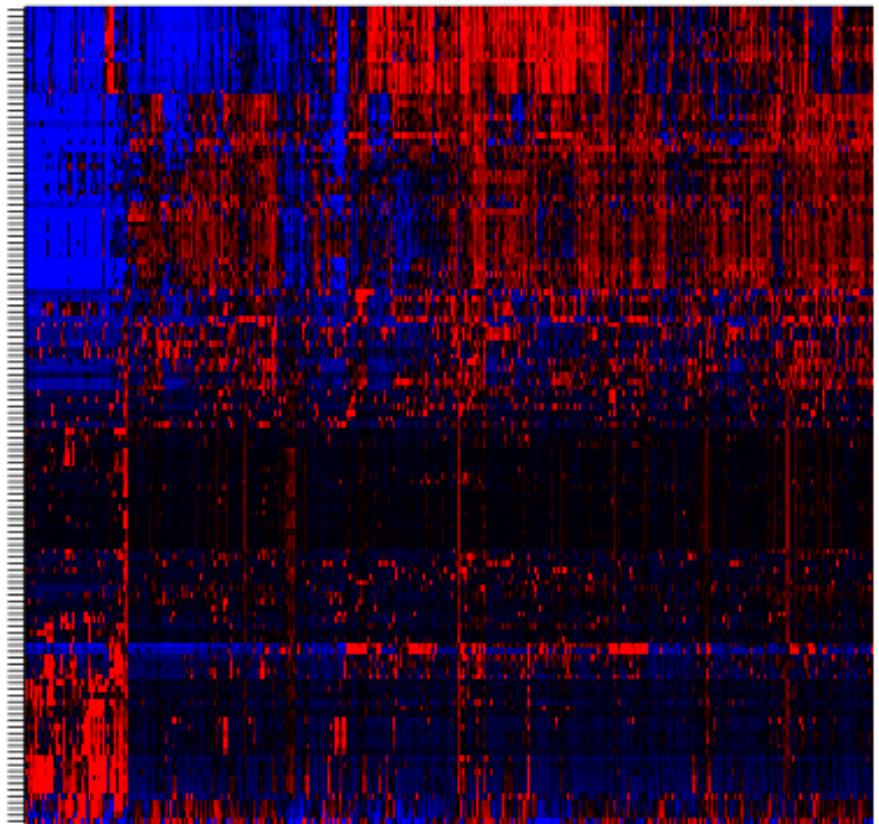
Deep phylotype level profiling

Open data & source code:
Lahti et al. Nature Comm.
2014

1000 bacterial phylotypes

Mitochondria
Bacteroides
Ruminococcus
Prevotella
Lachnospiraceae
Enterobacteriaceae
Bacteroidales
Pseudobacteroides
Ruminococcaceae
Lachnospiraceae
Enterococcus
Uncultured Bacteroidetes
Dorea
Desulfovibrionales
Desulfovibrionaceae
Desulfovibrionaceae
Escherichia
Enterococcaceae
Peptococcaceae
Peptococcus
Leptotrichaceae
Corynebacteriales
Corynebacteriaceae
Corynebacterium
Coprococcaceae
Coprococcus
Unassigned C. coccoides
Desulfovibrionaceae
Desulfovibrionaceae
Lachnospiraceae
Fusobacteriales
Fusobacteriaceae
Fusobacterium
Pseudobacteroides
Ruminococcaceae
Ruminococcus
Uncultured Ruminococcaceae
Uncultured Ruminococcaceae
Uncultured Ruminococcaceae

N ~ 10,000

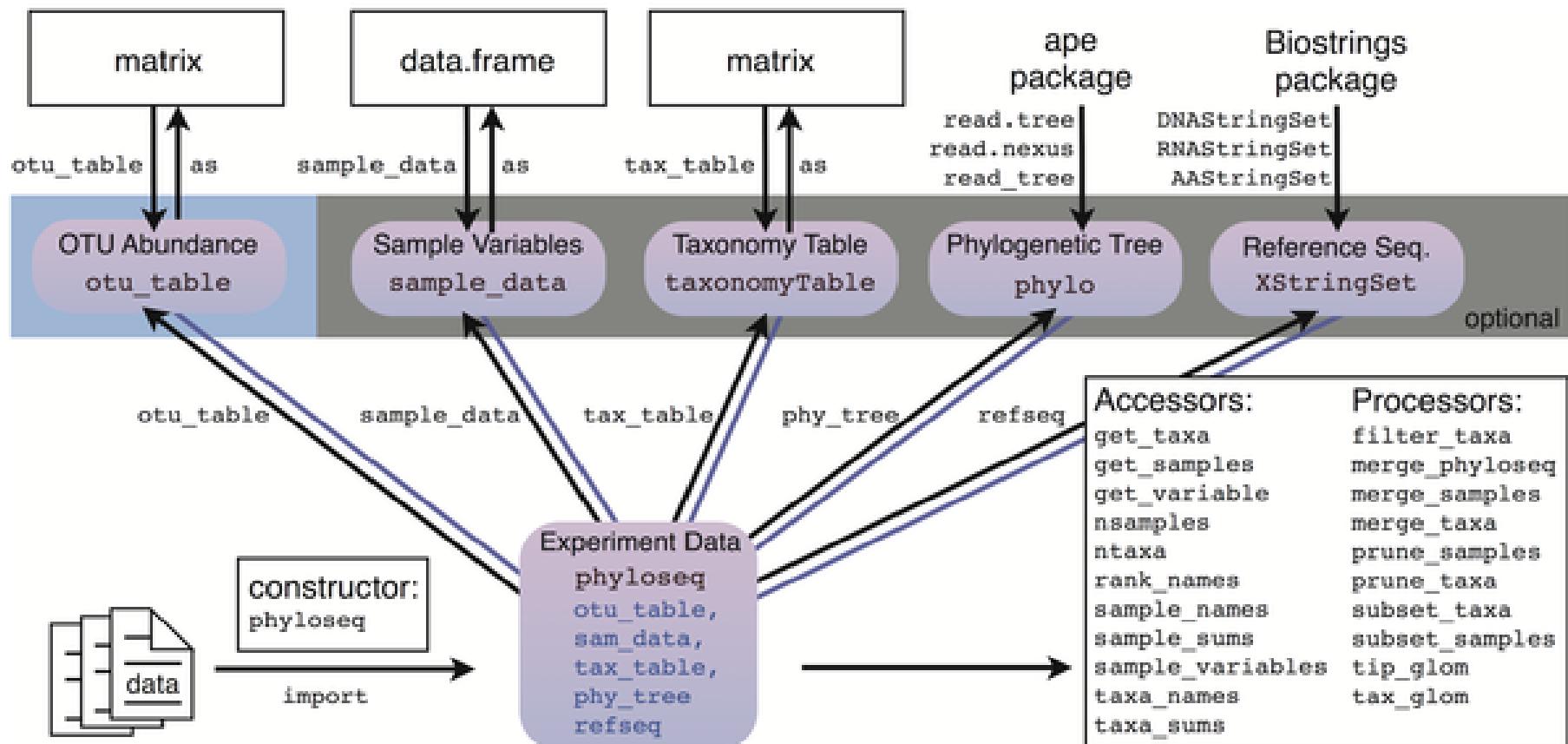


<http://microbiome.github.io>

Standardized – cost efficient – accurate at 0.1% relative abundance
Rajilic-Stojanovic et al. Env. Microbiol. 2009

Data structure for taxonomic profiling: phyloseq

<https://github.com/joey711/phyloseq>



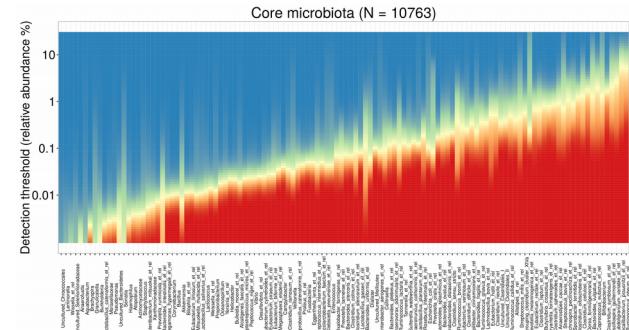
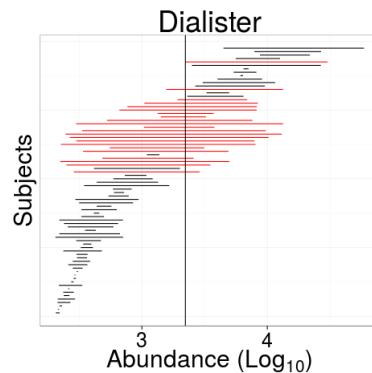
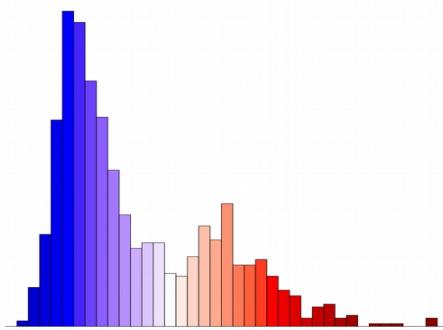
McMurdie PJ, Holmes S (2013) phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. PLOS ONE 8(4): e61217. <https://doi.org/10.1371/journal.pone.0061217>
<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0061217>

Analysis tools: microbiome R package

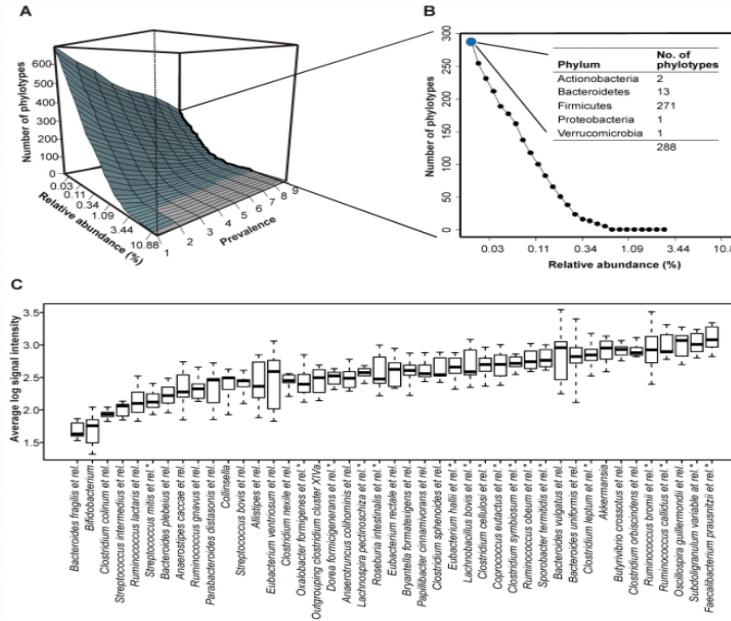
R/Bioconductor package for the analysis of 16S microbiome profiling data (Lahti, Shetty et al.).

Github: <http://microbiome.github.io/microbiome/>

- Diversity, Stability, Core, Visualization..
- Extending the phyloseq data format & tools



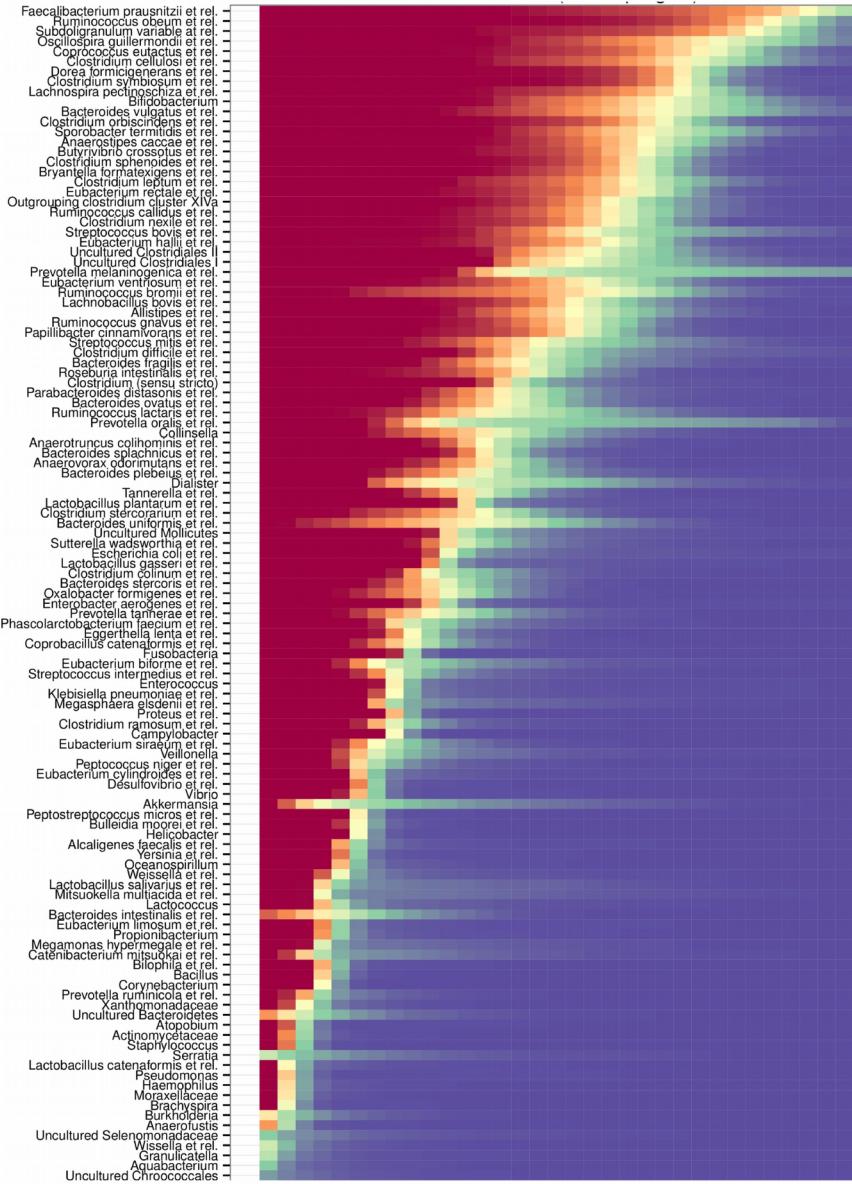
Core microbiota, healthy western adults (n=456)



Jalanka-Tuovinen et al. (2011) PLoS One 6:e23035
 Salonen et al. (2012) Clinical microbiology and infection 18:16–20.



Code: microbiome.github.com



Detection threshold (abundance)

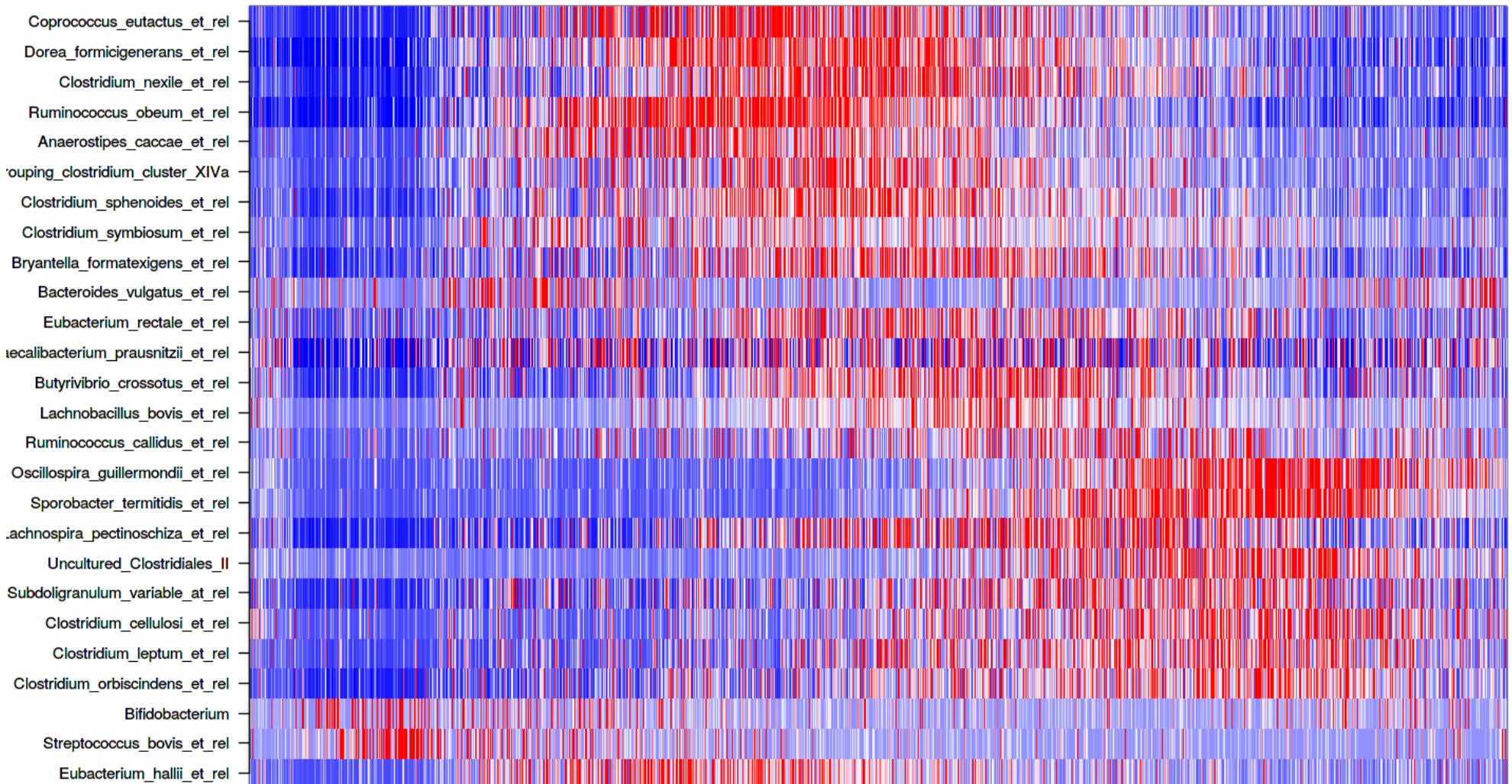
HITChip Atlas Core. Shetty et al. FEMS Microbiol. Reviews 2017, fuw045.
 Data from Lahti et al. Nat Comm, 2014.

Abundances of the shared core taxa are highly individual

Z-score across subjects: **red – high abundance & blue – low abundance**

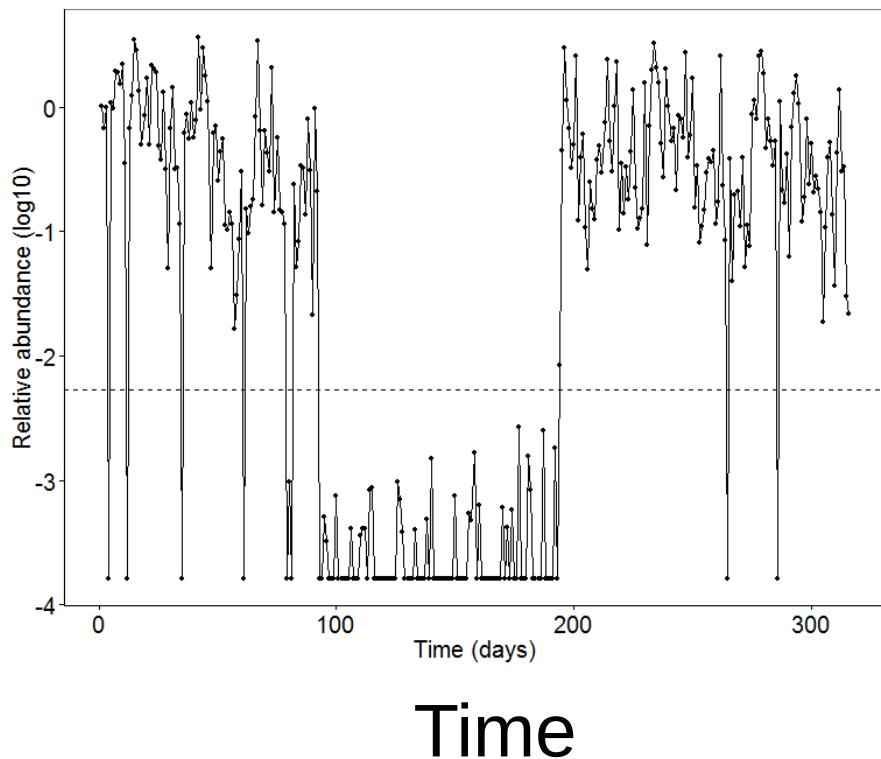
Core microbiota shows remarkable variation across population.

(HITChip Atlas; N = 5005)



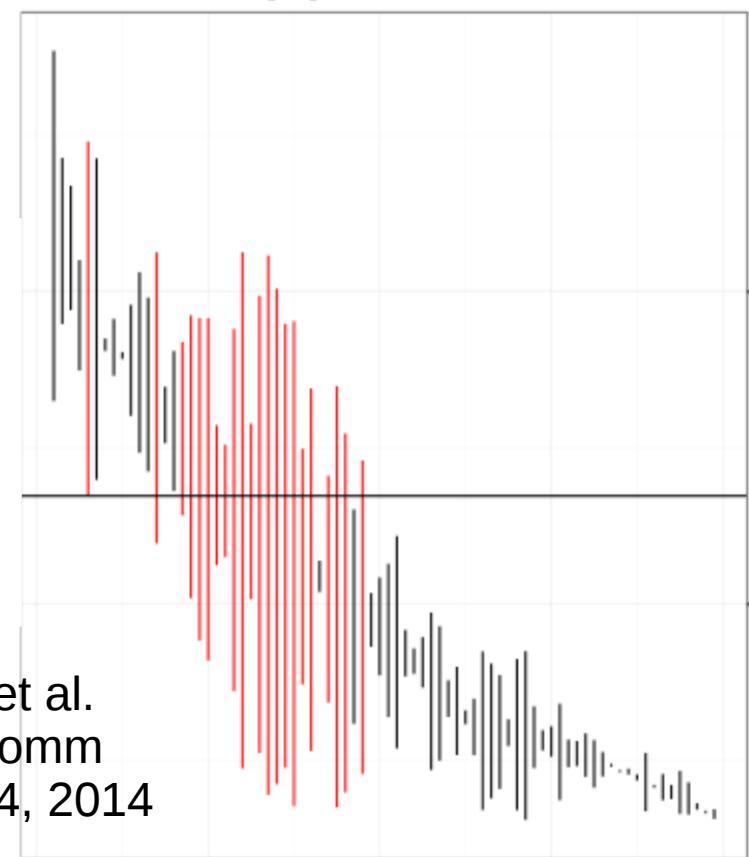
Detecting a tipping point: temporal instability at intermediate abundances is another key indicator of bistability

One long time series:
Lachnospiraceae



Many short time series:
Dialister spp.

Abundance

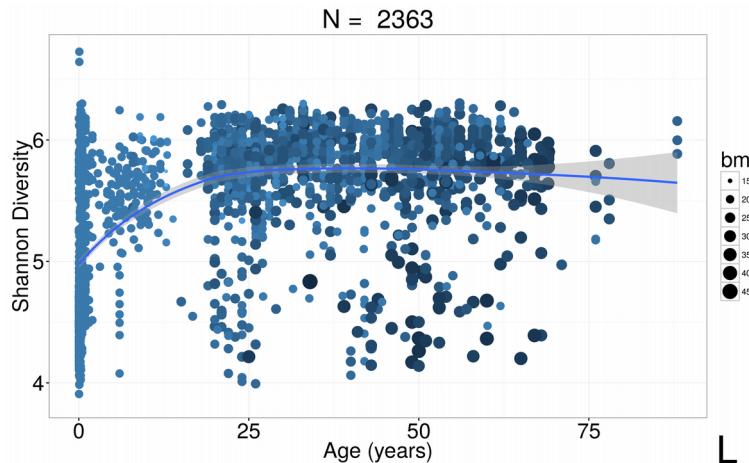


Reproducible analysis workflow

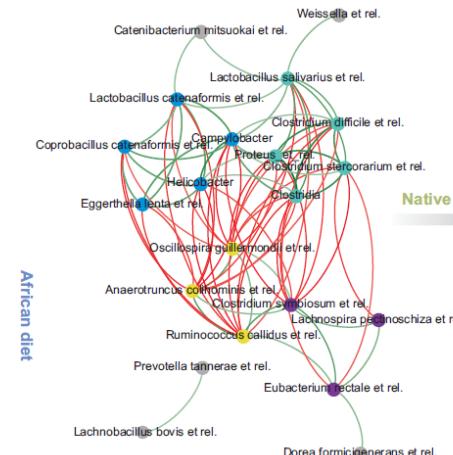
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L Lahti & WM de
Vos; Unpublished



O'Keefe et al. Nat.
Comm. 2015.