

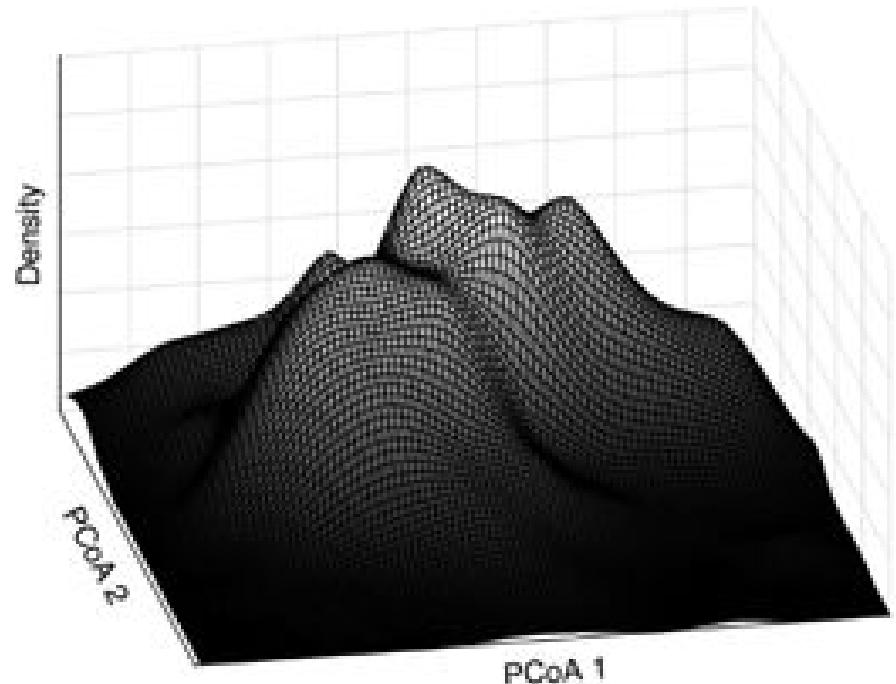
The dynamic landscape of human gut microbiota: a population-level view

Leo Lahti

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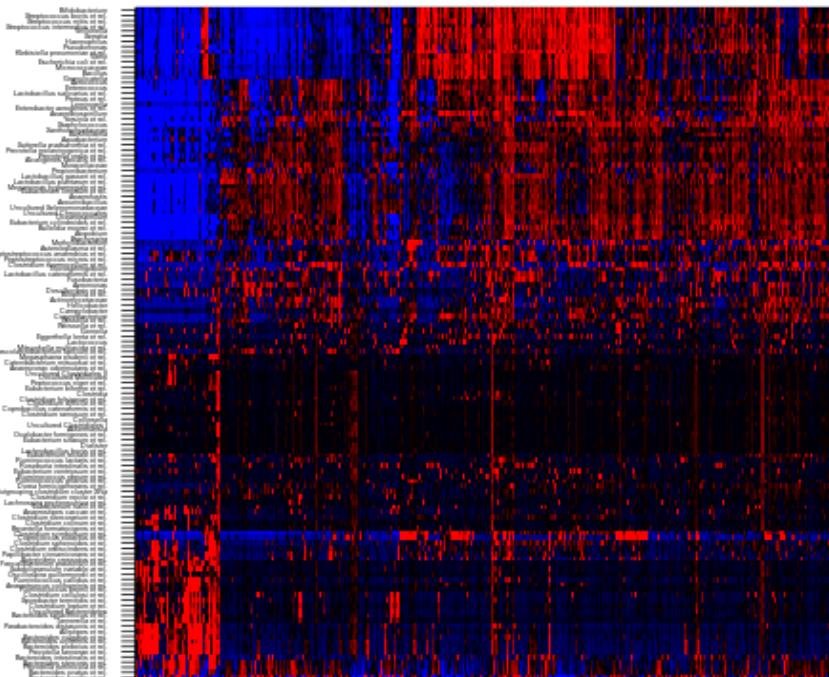


Turun yliopisto
University of Turku



Accumulating population cohorts

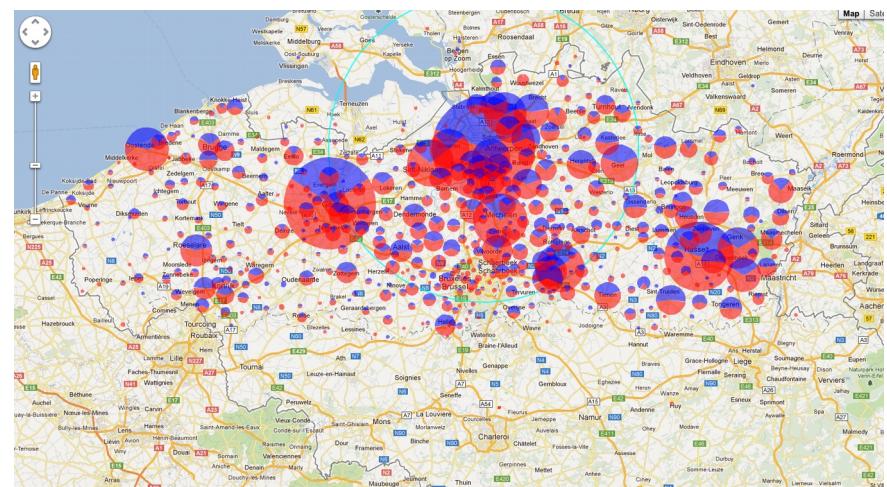
HITChip Atlas / Wageningen
N 10,000+
20+ nationalities
Highly standardized
Phylogenetic microarrays



Blue: Low abundance
Red: High abundance

Lahti et al. Nat. Comm. 2014

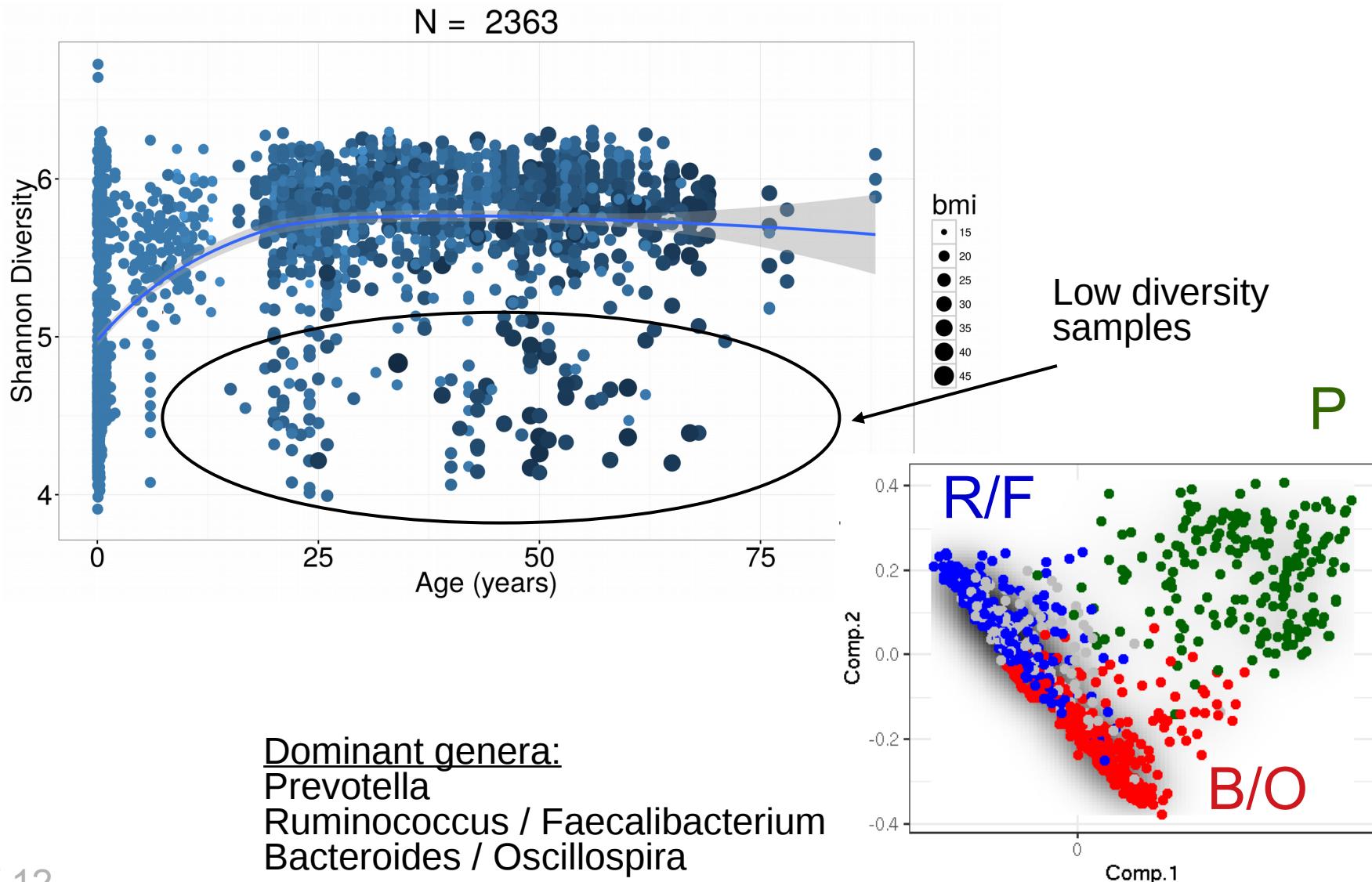
Flemish Gut Flora Raes Lab, VIB/KU
Leuven
Cross-sectional & longitudinal
Comprehensive metadata
Focused geographical coverage



Falony et al. Science 352, 2016

Software: microbiome.github.io
HMP, MetaHIT, LLDeep, TwinsUK,
American Gut..

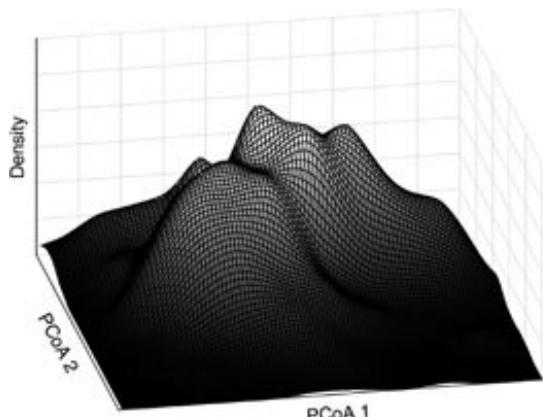
Microbiome diversity and age: healthy & normal obese subjects (HITChip Atlas)



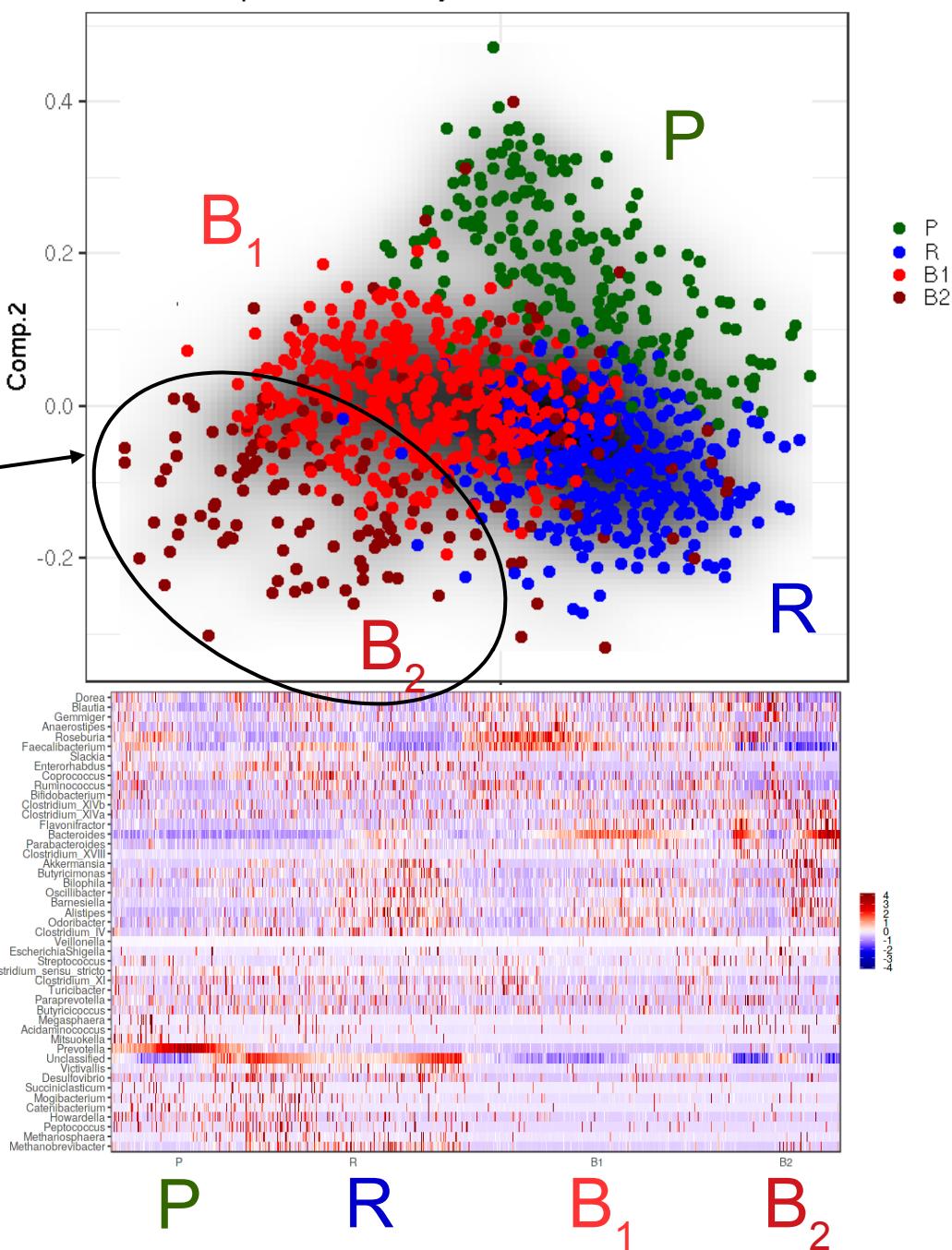
Broad community types (Flemish Gut Flora)

Bacteroides splits in
two subtypes

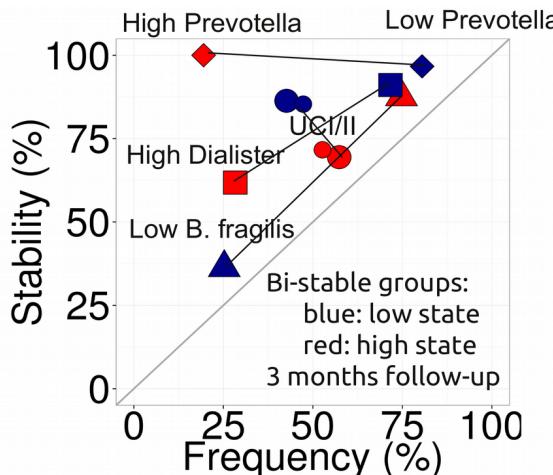
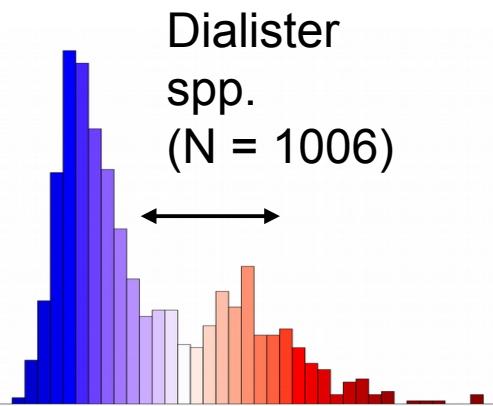
B_2 subtype associated
with IBD & low cell
count
(Vandepitte et al. Nature 2017)



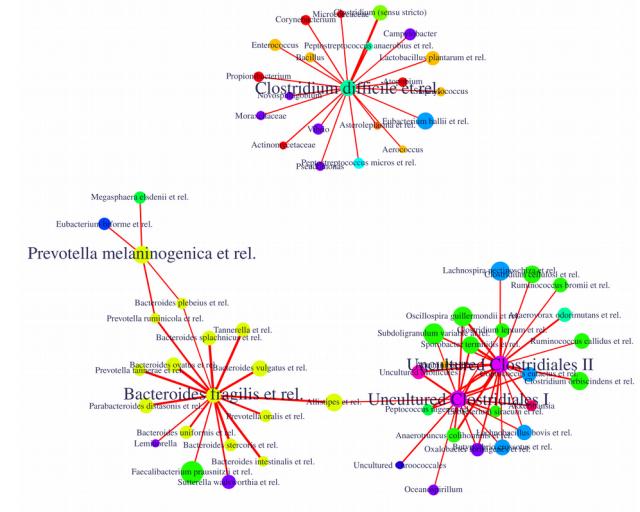
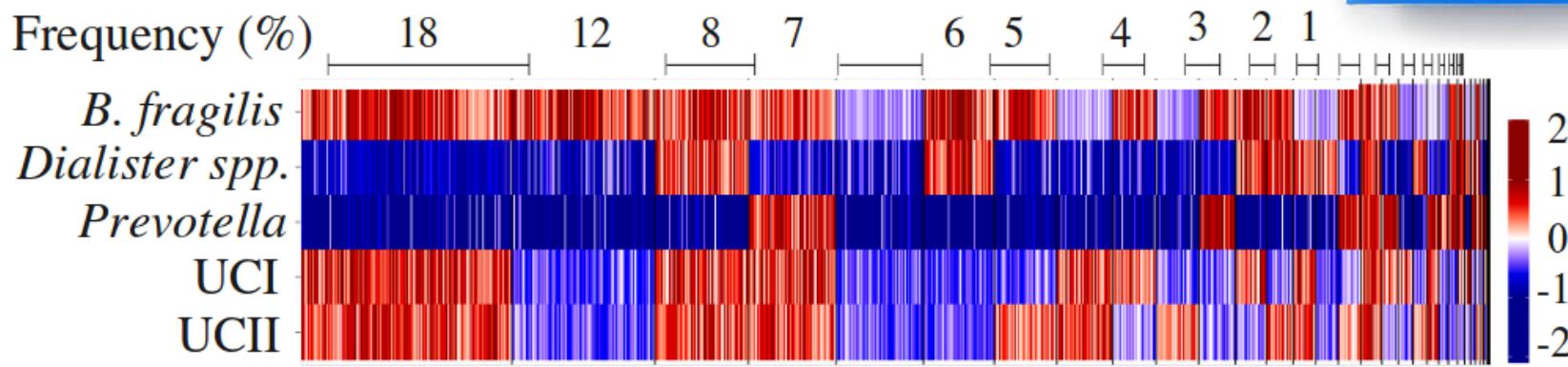
PCoA/compositional/bray/N=1106



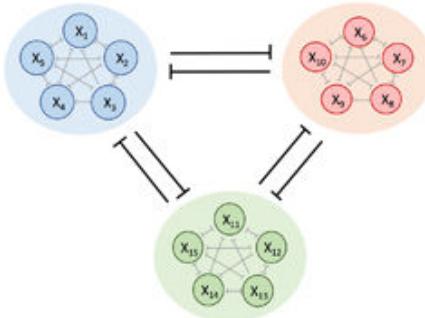
Bi-stable tipping elements & community substructure (potential analysis & Fokker-Planck dynamics)



Ecosystem states rich combinations of independent tipping elements ?



Mechanisms of microbial community assembly?



b

$$\frac{dX_i}{dt} = X_i(b_i f_i(\{X_k\}) - k_i X_i)$$

$$f_i(\{X_k\}) = \prod_{\substack{k=1 \\ k \neq i}}^N \frac{K_{ik}^n}{K_{ik}^n + X_k^n}$$

X_i	X_1	X_2	X_3	b_i	k_i
X_1	-	0.1	0.1	1	1
X_2	0.1	-	0.1	0.95	1
X_3	0.1	0.1	-	1.05	1

Multi-stability and the origin of microbial community types

Didier Gonze, Leo Lahti, Jeroen Raes & Karoline Faust

The ISME Journal (2017) **11**, 2159–2166 (2017)

doi:10.1038/ismej.2017.60



nature
COMMUNICATIONS

Tipping elements in the human intestinal ecosystem

Leo Lahti , Jarkko Salojärvi, Anne Salonen, Marten Scheffer & Willem M. de Vos

Nature Communications **5**, Article number: 4344 (2014)

Intestinal microbiome landscaping: insight in community assemblage and implications for microbial modulation strategies

Sudarshan A. Shetty , Floor Hugenholtz, Leo Lahti, Hauke Smidt, Willem M. de Vos

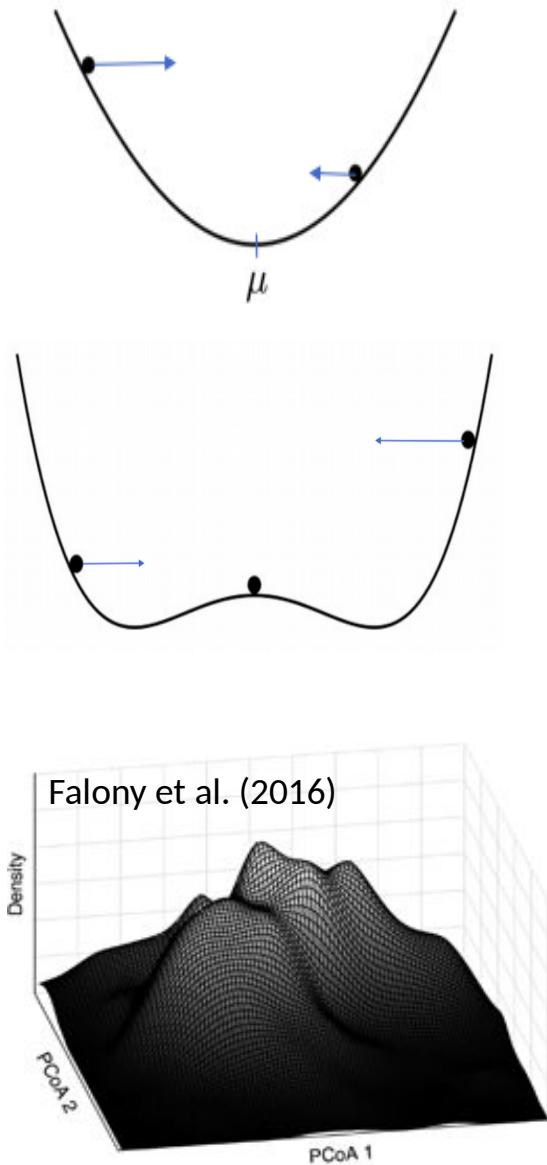
FEMS Microbiology Reviews, Volume 41, Issue 2, 1 March 2017, Pages 182–199, <https://doi.org/10.1093/femsre/fuw045>

Published: 09 February 2017 Article history

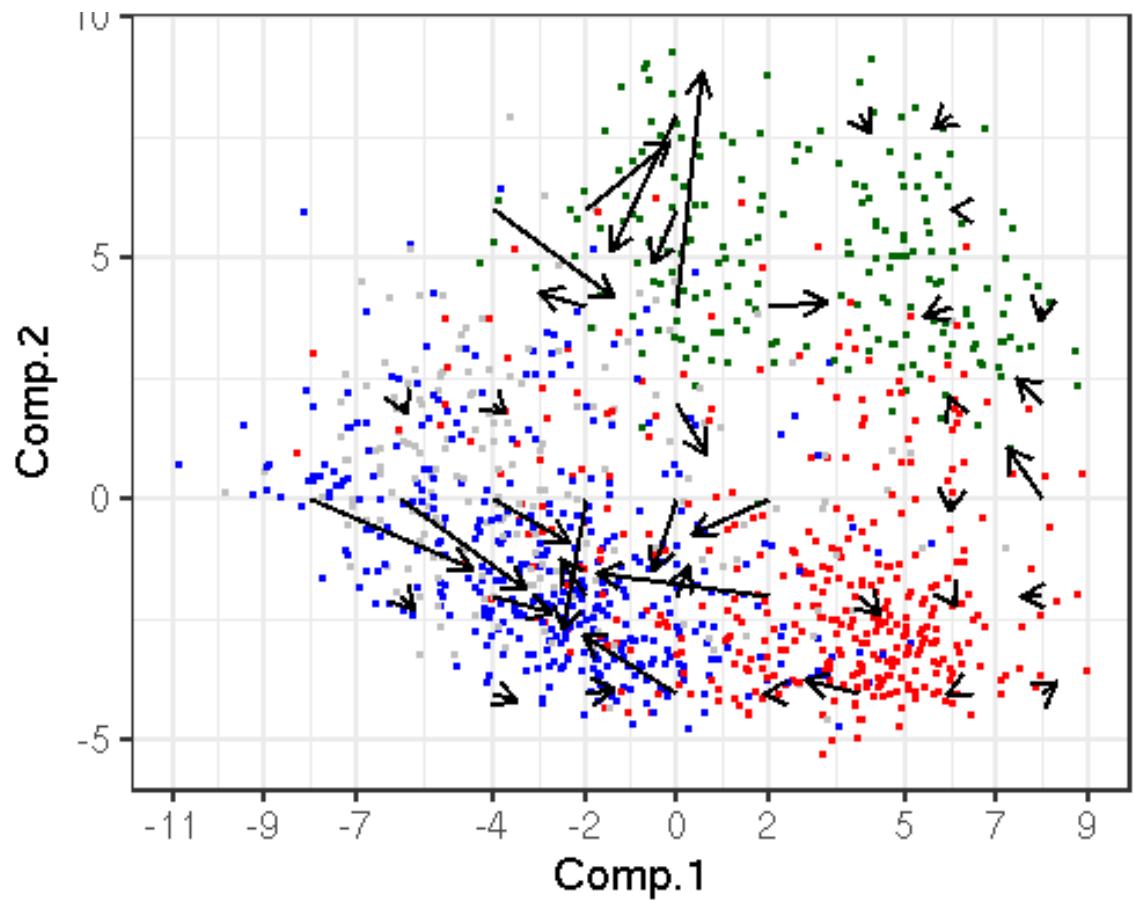


Linking statistical and ecological theory: Hubbell's unified neutral theory of biodiversity as a hierarchical Dirichlet process 1
Keith Harris¹, Todd L Parsons², Umer Z Ijaz³, Leo Lahti⁴, Ian Holmes⁵, Christopher Quince^{6,*}

Non-mechanistic models of microbiome dynamics



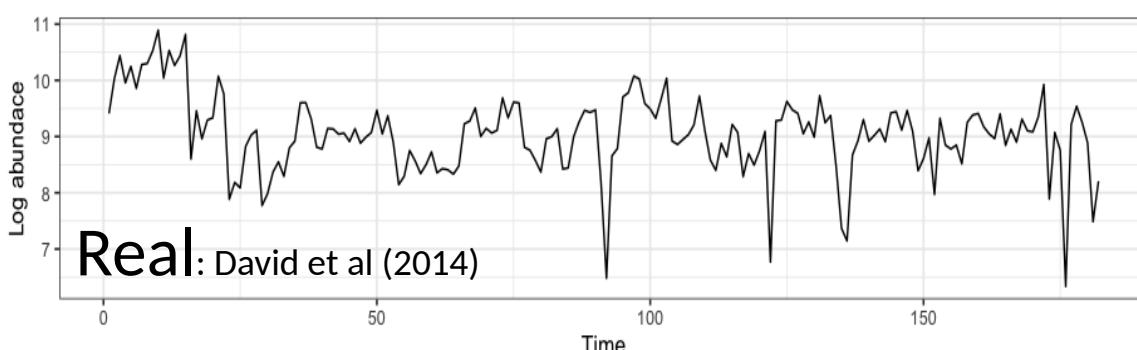
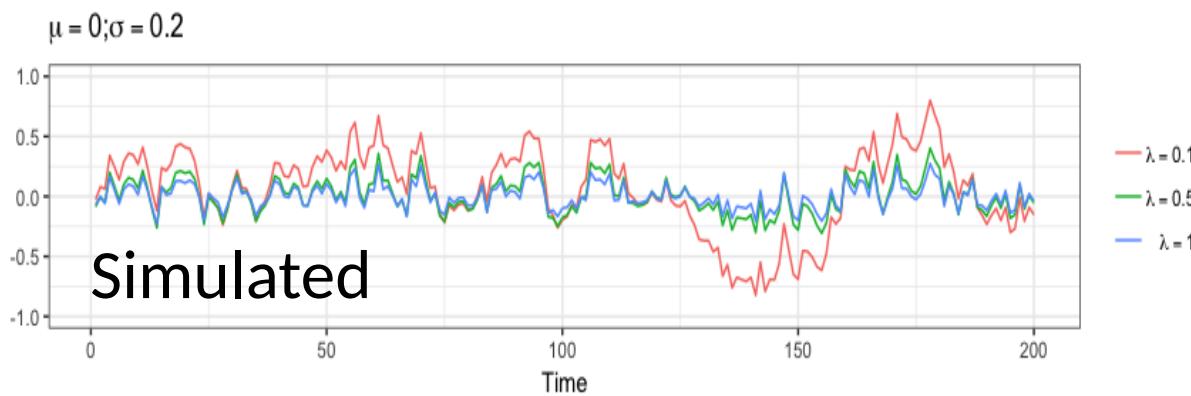
HITChip Atlas – PCA with CLR-transformed genus abundances (1006 cross-sectional + 78 longitudinal profiles combined)



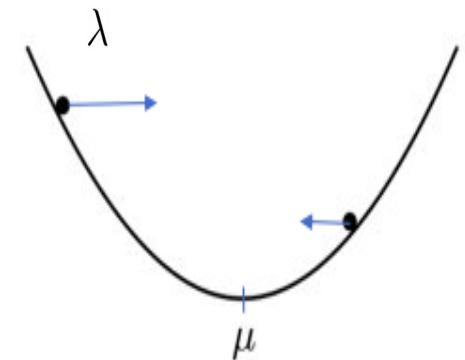
State resilience, stochasticity, and OU Process

Ornstein-Uhlenbeck Process (OUP) quantifies key properties of a stable state

$$dX = \lambda(\mu - X)dt + \sigma dS$$

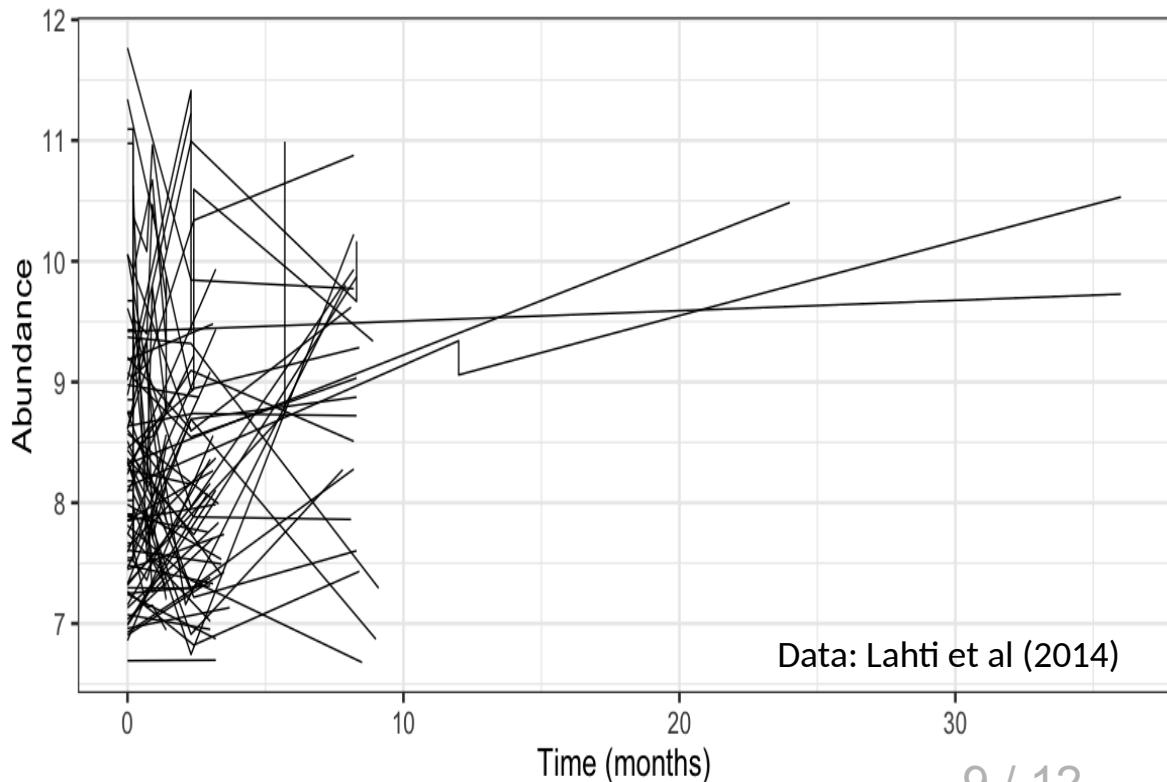
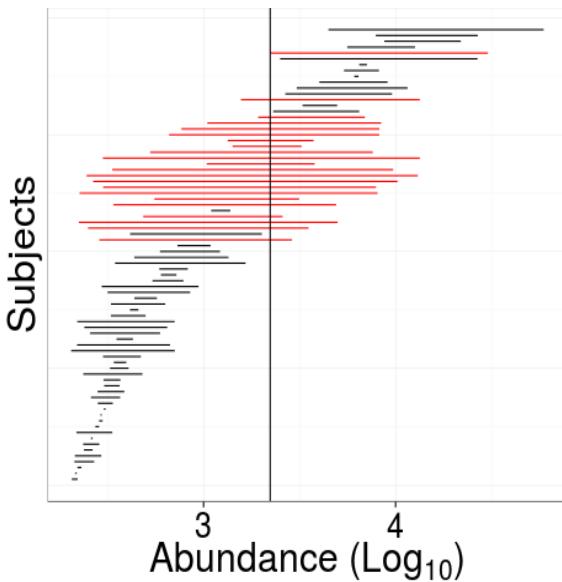


λ = mean reversion rate
 μ = long-term mean
 σ = stochasticity level
 S = stochastic process



Real time series: short, sparse, noisy

Aggregate information across many
individuals and time series → Hierarchical models

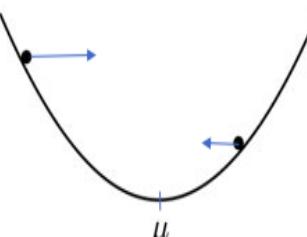
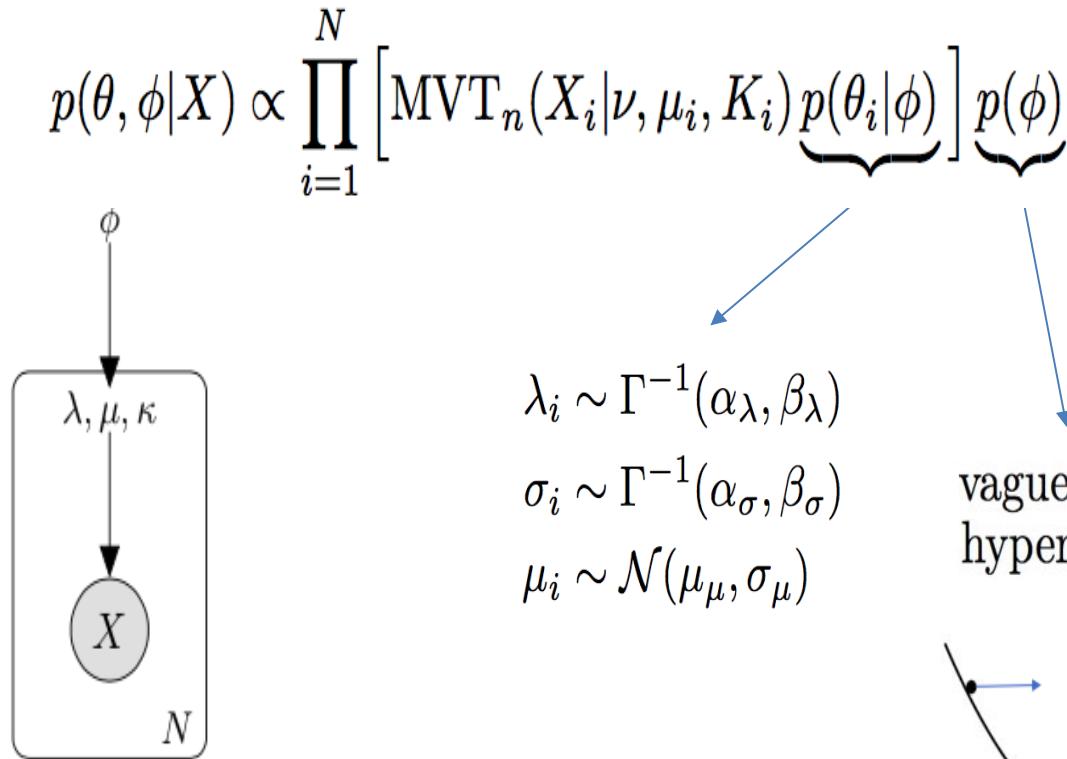


Hierarchical OU Process to aggregate many short, sparse, irregular & stochastic time series

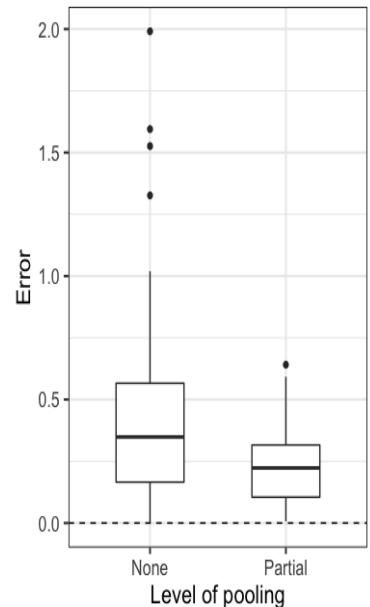


**Poster
#127**

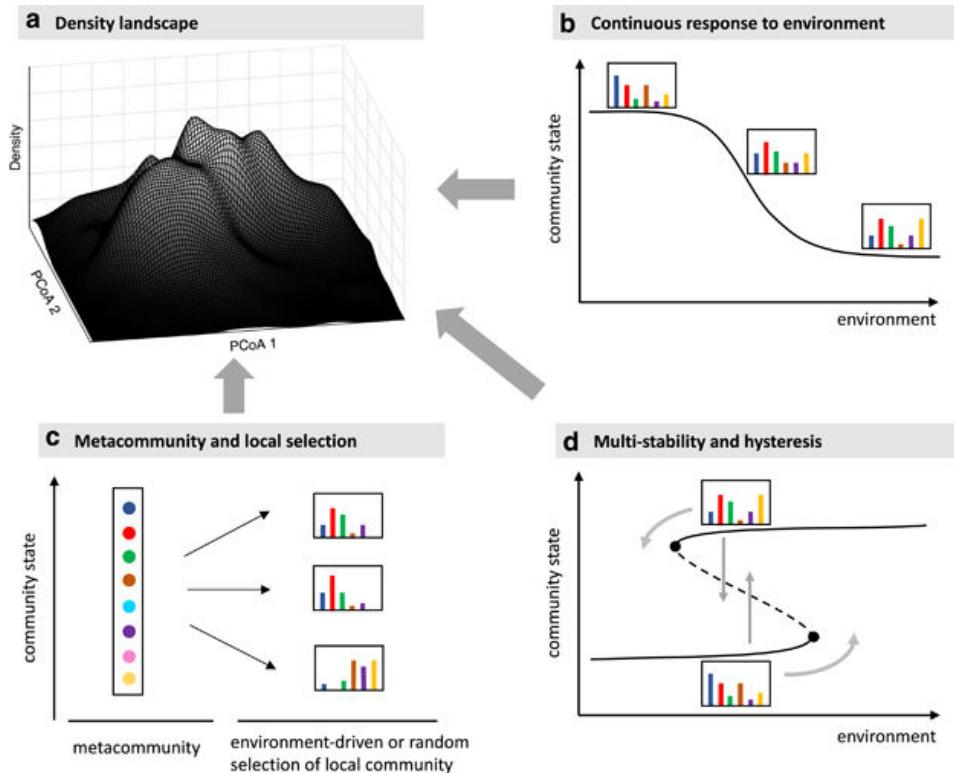
Each time series is an individual realization of underlying mean-reversible stochastic process



Pooling improves accuracy



Communities are mixtures of ecological processes .. the structure of noise can hint at dominant mechanisms

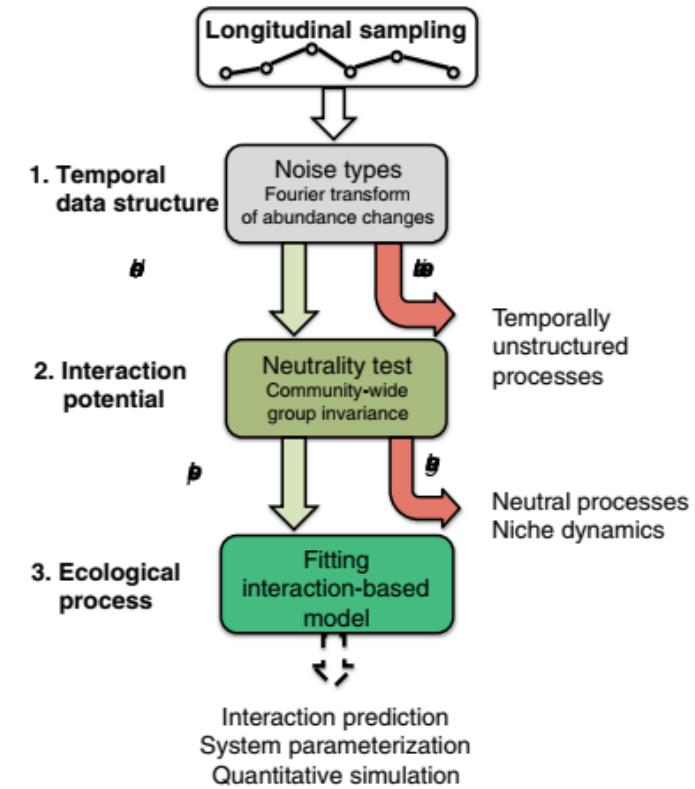


Multi-stability and the origin of microbial community types

Didier Gonze, Leo Lahti, Jeroen Raes & Karoline Faust

Signatures of ecological processes in microbial community time series

Karoline Faust^{1*}, Franziska Bauchinger², Béatrice Laroche³, Sophie de Buyl^{4,5}, Leo Lahti^{1,6,7}, Alex D. Washburne^{8,9}, Didier Gonze^{5,10} and Stefanie Widder^{1,12,13*}



Ville Laitinen
Aaro Salosensaari
Teemu Niiranen

Willem de Vos
Sudarshan Shetty

Anne Salonen
Jarkko Salojärvi

Karoline Faust
Didier Gonze

Raes Lab
Sara Vieira-Silva
Gwen Falony
Raul Tito
Marie Joossens



Thank You !

**Poster
#127**



Software: microbiome.github.io

leo.lahti@iki.fi | openresearchlabs.github.io | [@antagomir](https://twitter.com/antagomir)



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SUOMEN AKADEMIA
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