Next-gen fermented food: Harnessing gut microbiome diversity and functions

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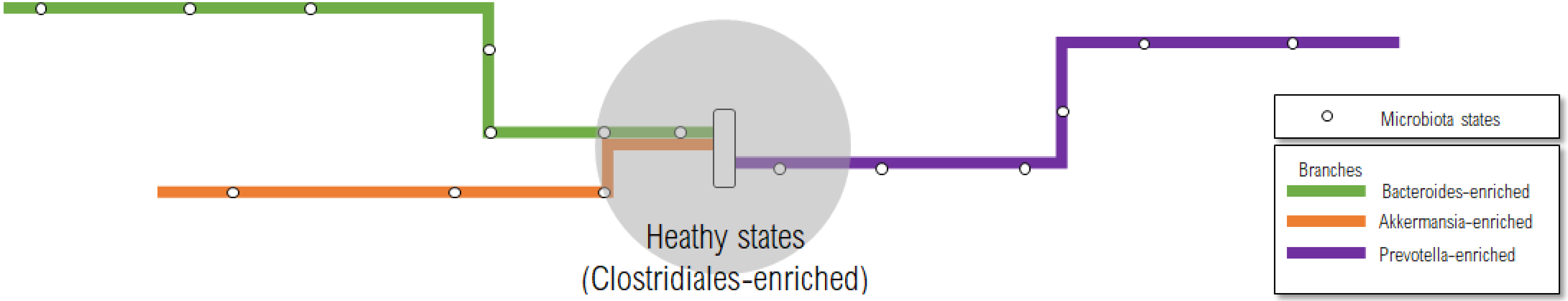
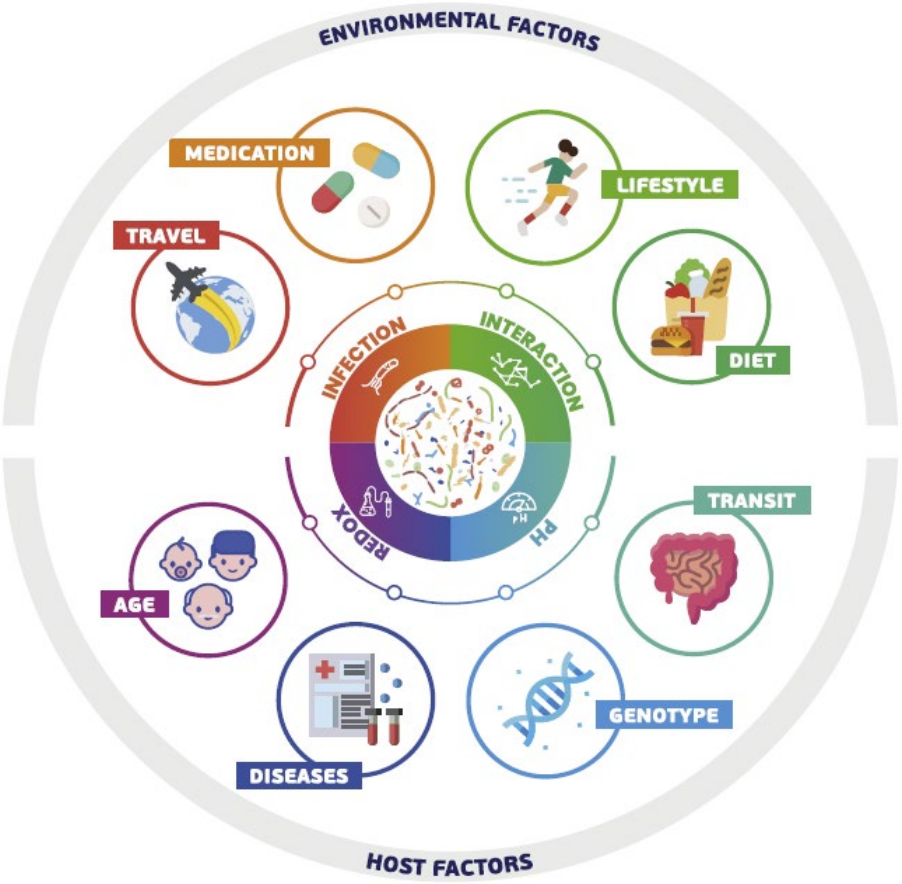
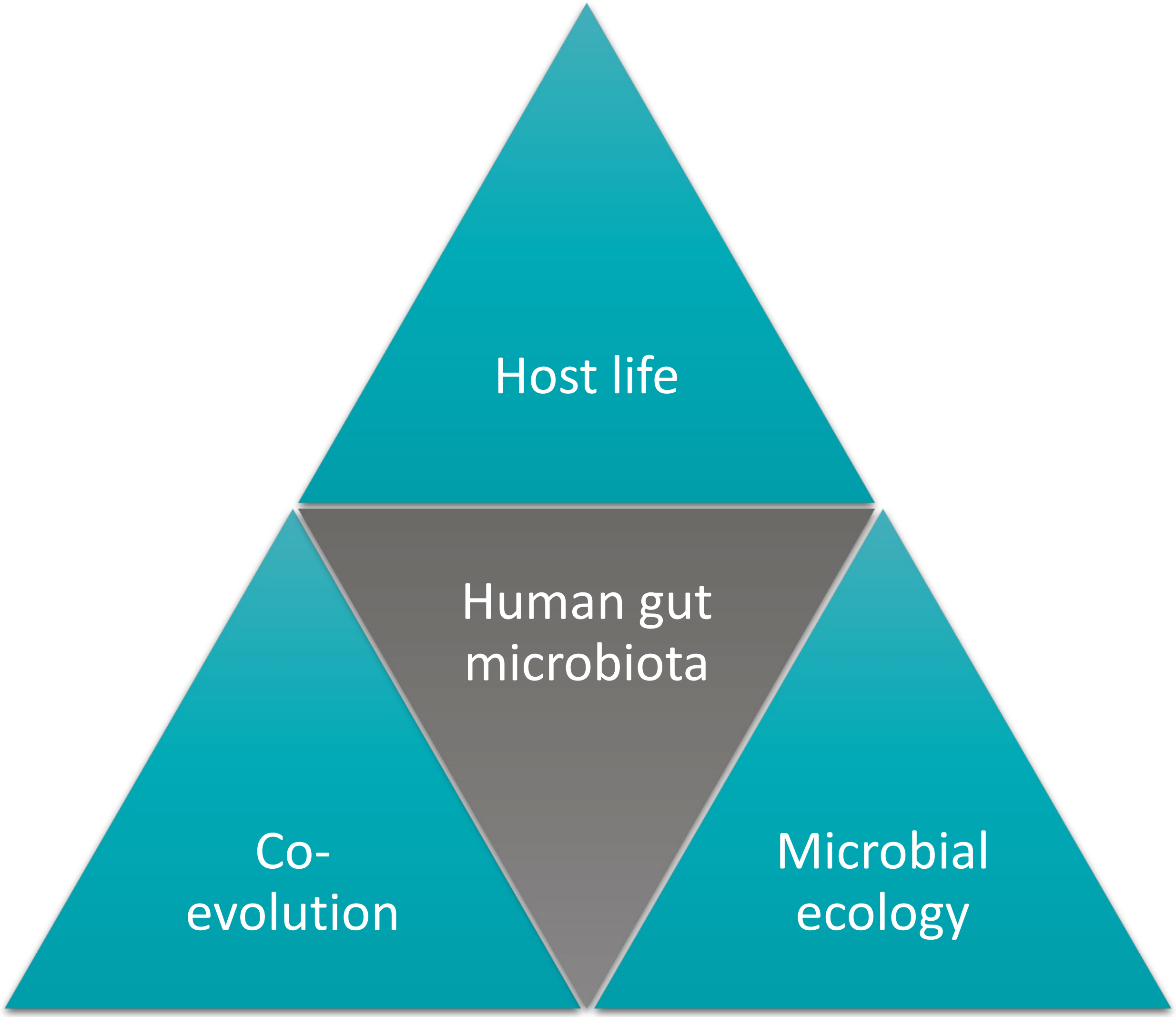
Next-gen fermented food: Harnessing gut microbiome diversity and functions.

Julien Tap
INRAE MICALIS
NMC Utrecht 2024



Different factors shapes the human gut microbiome





Host life

Human gut microbiota

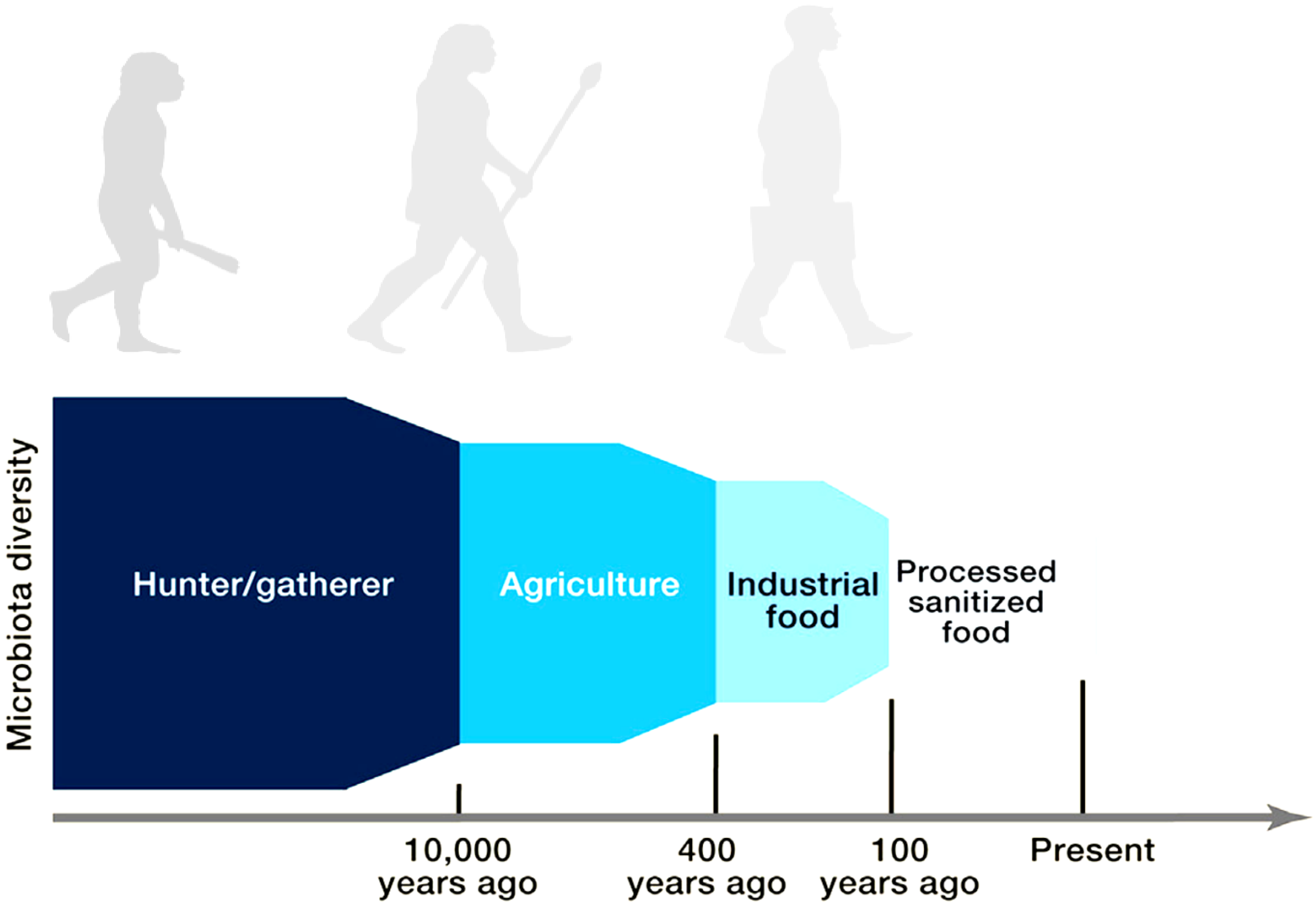
Co-evolution

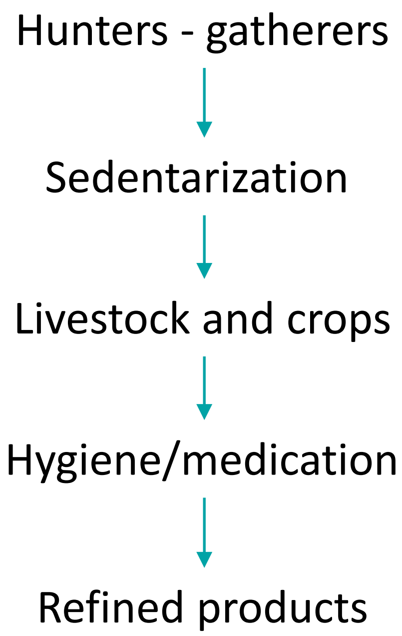
Microbial ecology

Tap et al., 2022

Diet and lifestyle effect host microbiome symbiosis

Are we uncoupling our metagenome and our genome?





Hunters - gatherers

Sedentarization

Livestock and crops

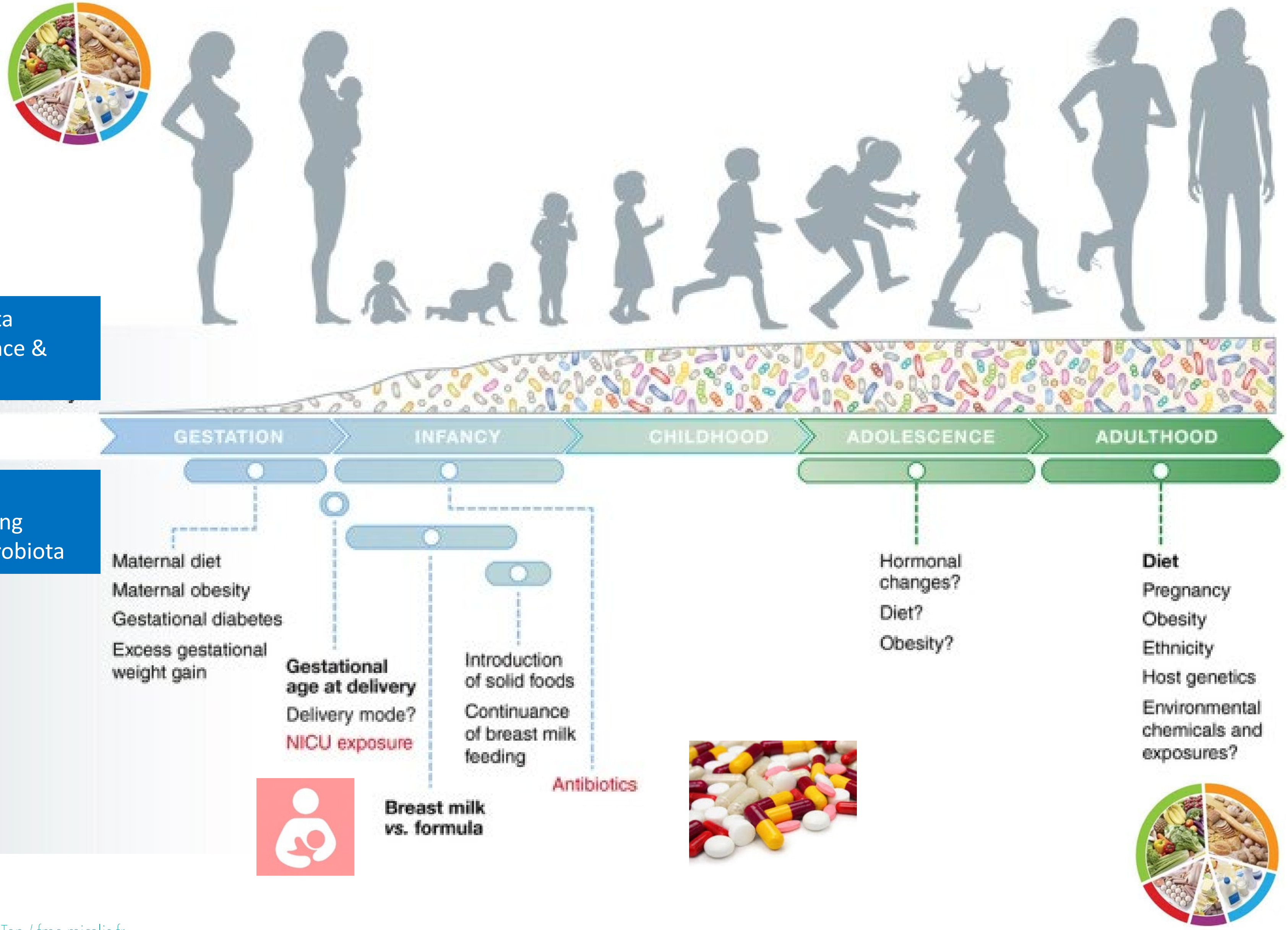
Hygiene/medication

Refined products

Gut microbiome throughout life span

Micobiota Abundance & diversity

Factors Influencing the microbiota



Microbiome states resilience as key factor

Healthy state

Resistance

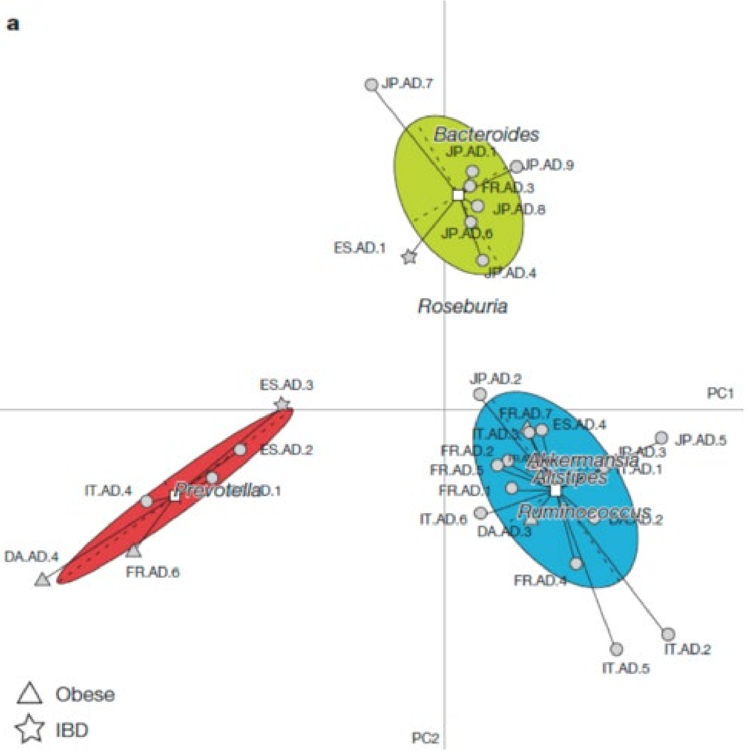
Recovery

Resilience

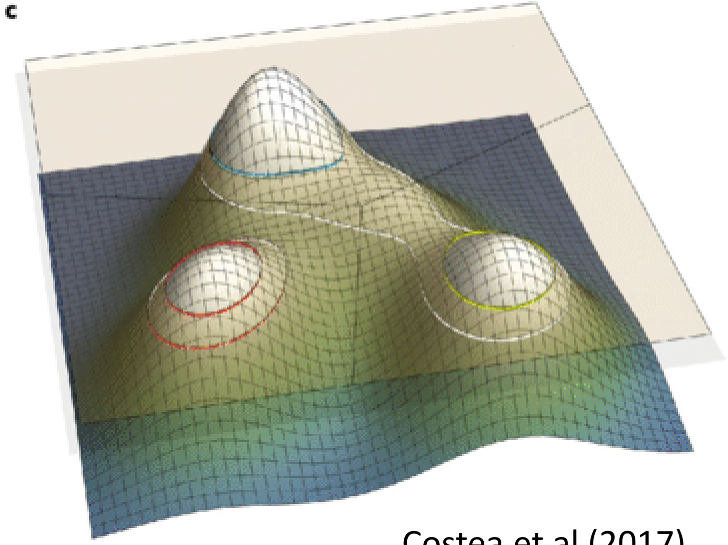
Healthy state

Degraded state

Several attempts to decipher the gut microbiome structure



Arumugam, Raes et al (2010)

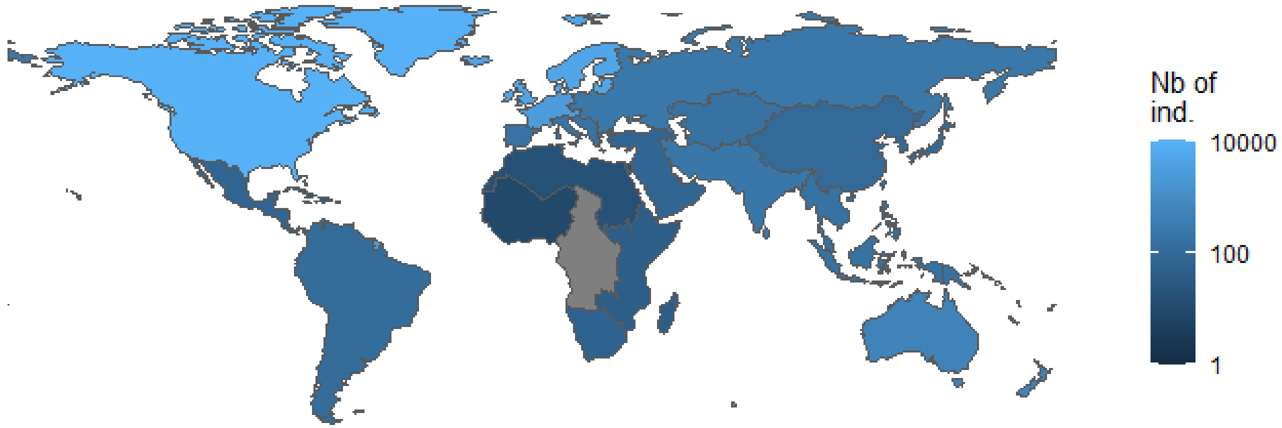


Costea et al (2017)

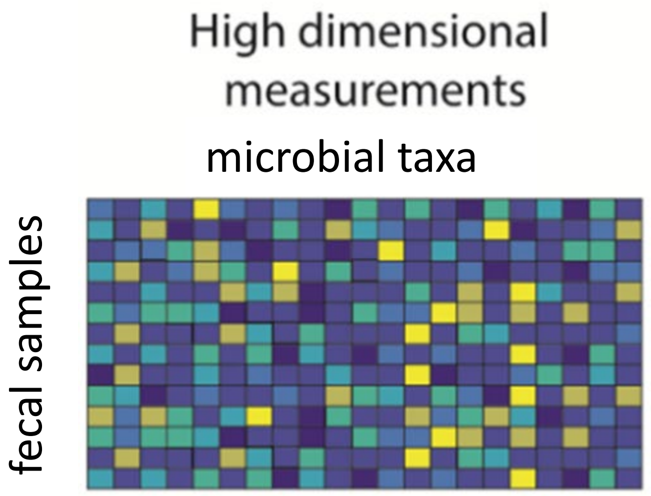
Dirichlet Multinomial Mixture (DMM) modeling

Limits:
Few association with diet
Few stability assessment (e.g. with time-series)

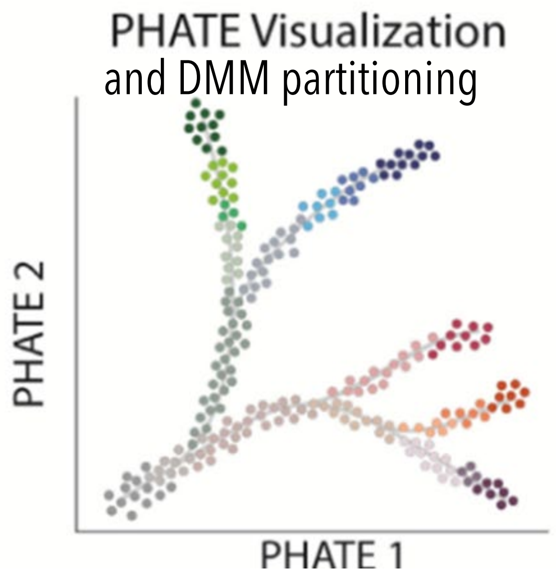
35,000 human gut microbiome samples analyzed



New computational method that help observe **global and local structure** at the same time


High dimensional measurements

→

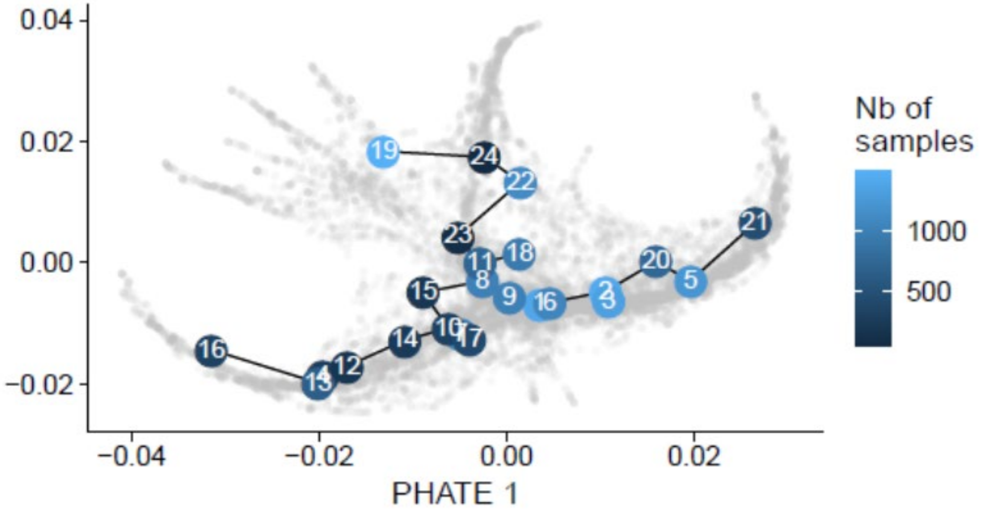

PHATE Visualization and DMM partitioning

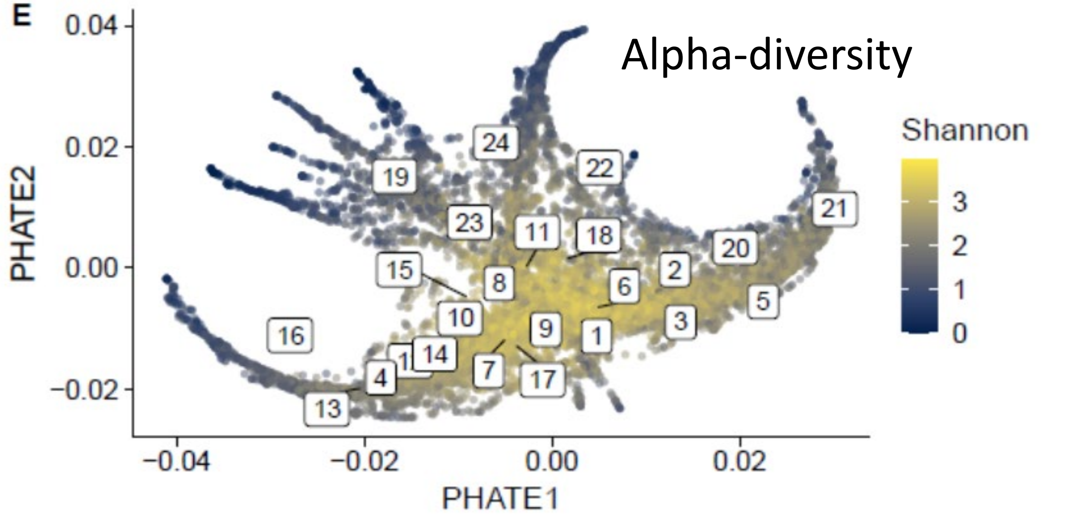
→

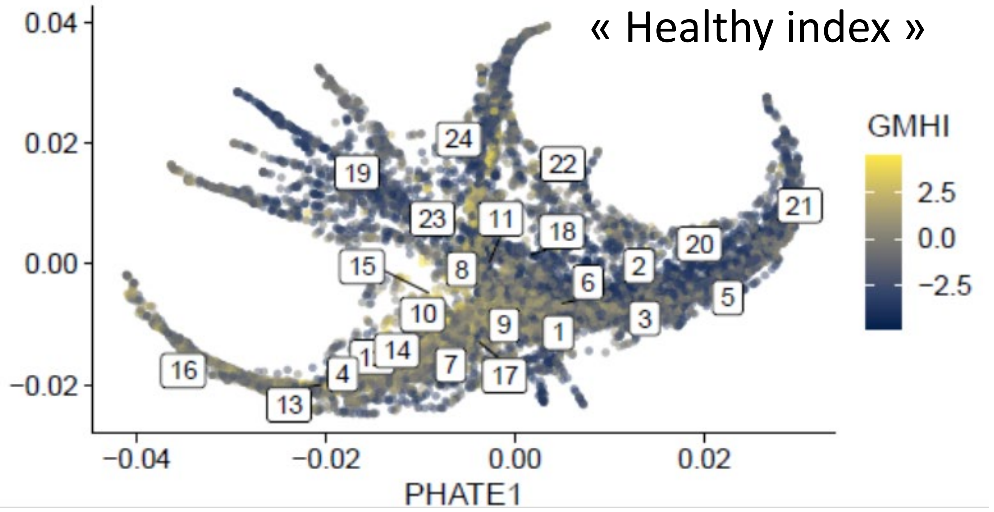
Time-series analysis to detect microbiome states

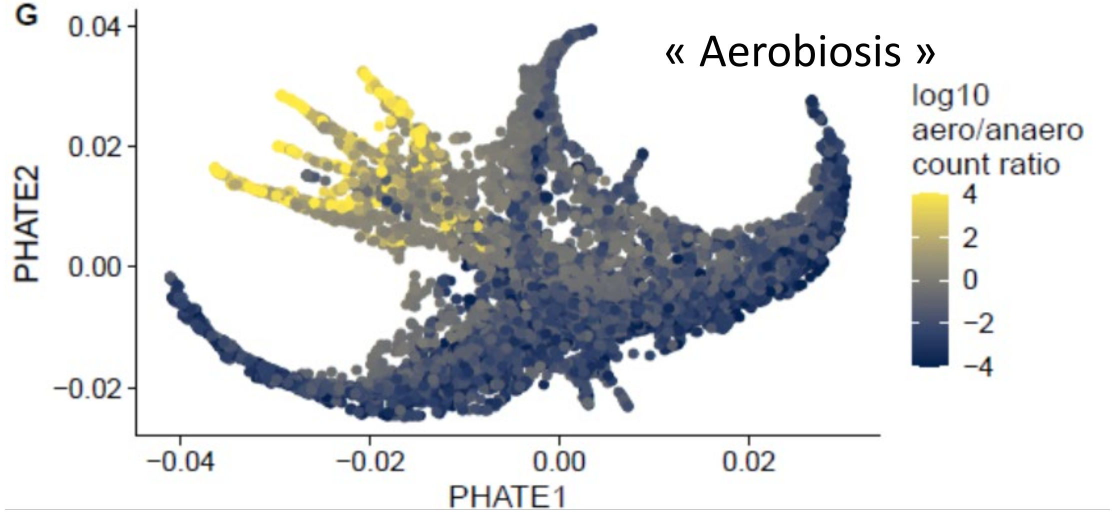
Region of birth, Lifestyle, diet, and health modelization

Human Gut microbiome structured as branches

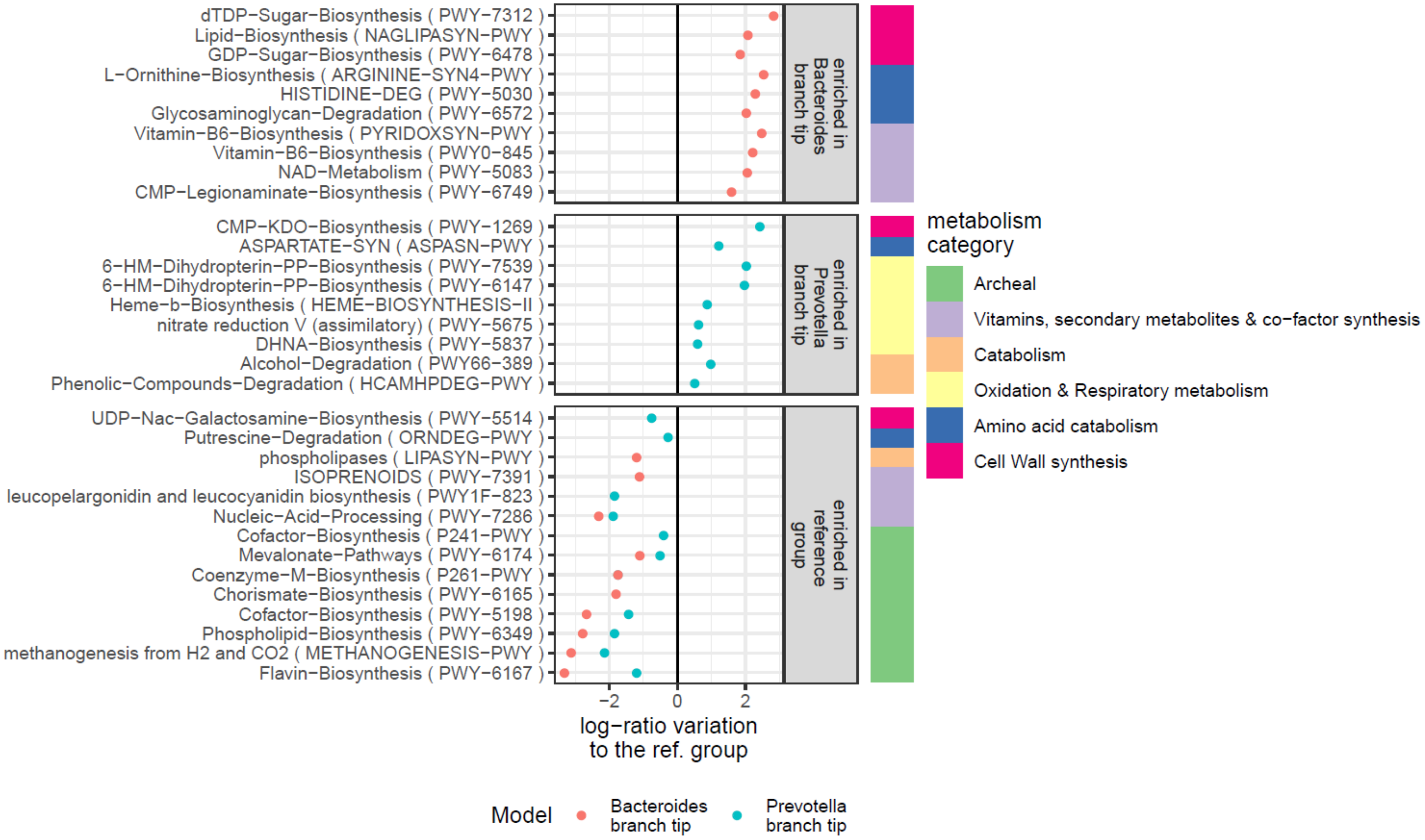



Alpha-diversity


« Healthy index »


« Aerobiosis »

Low-diversity tips of branches display functional shifts

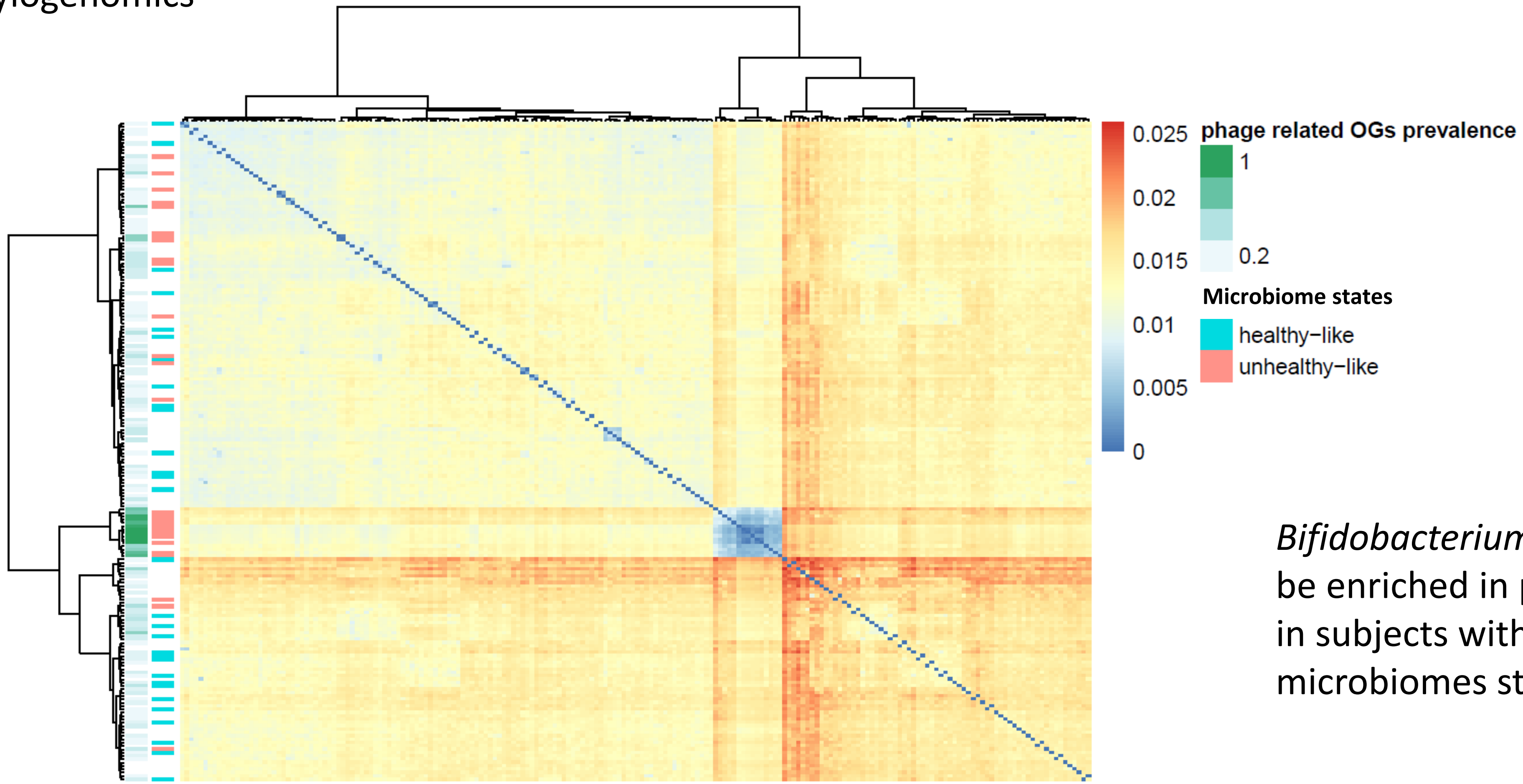


amino acid catabolism increase in *Bacteroides* branch tip

oxidative stress response increase in *Prevotella* branch tip

Altered states showed functional differences within species

400 *B. bifidum* MAGS
phylogenomics

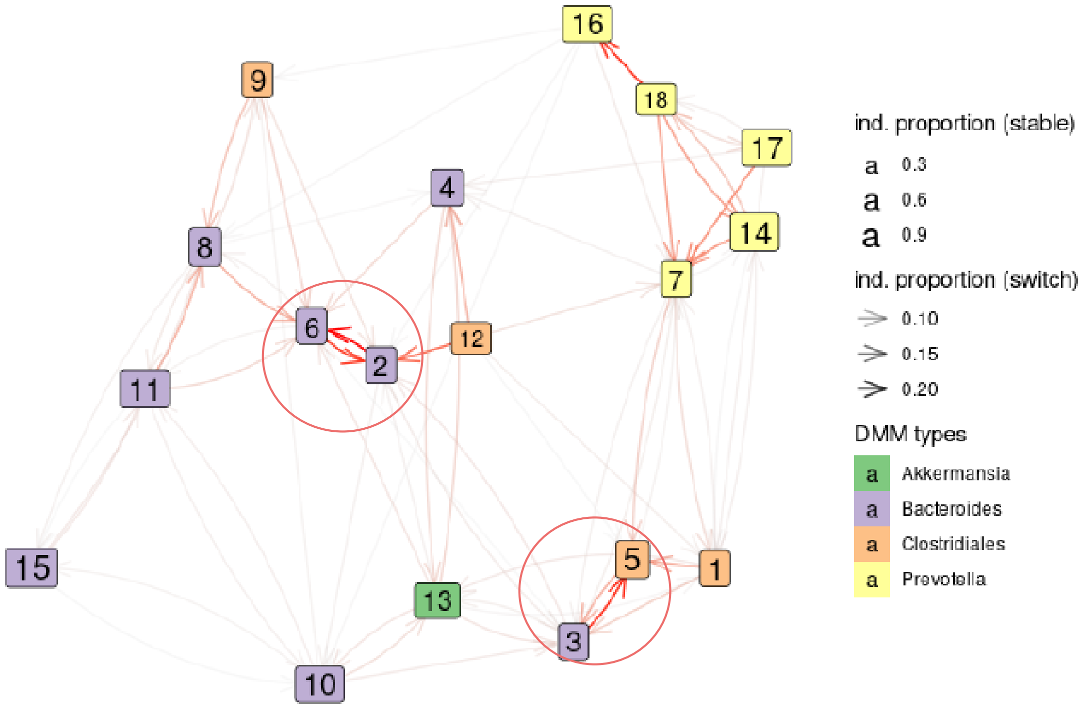


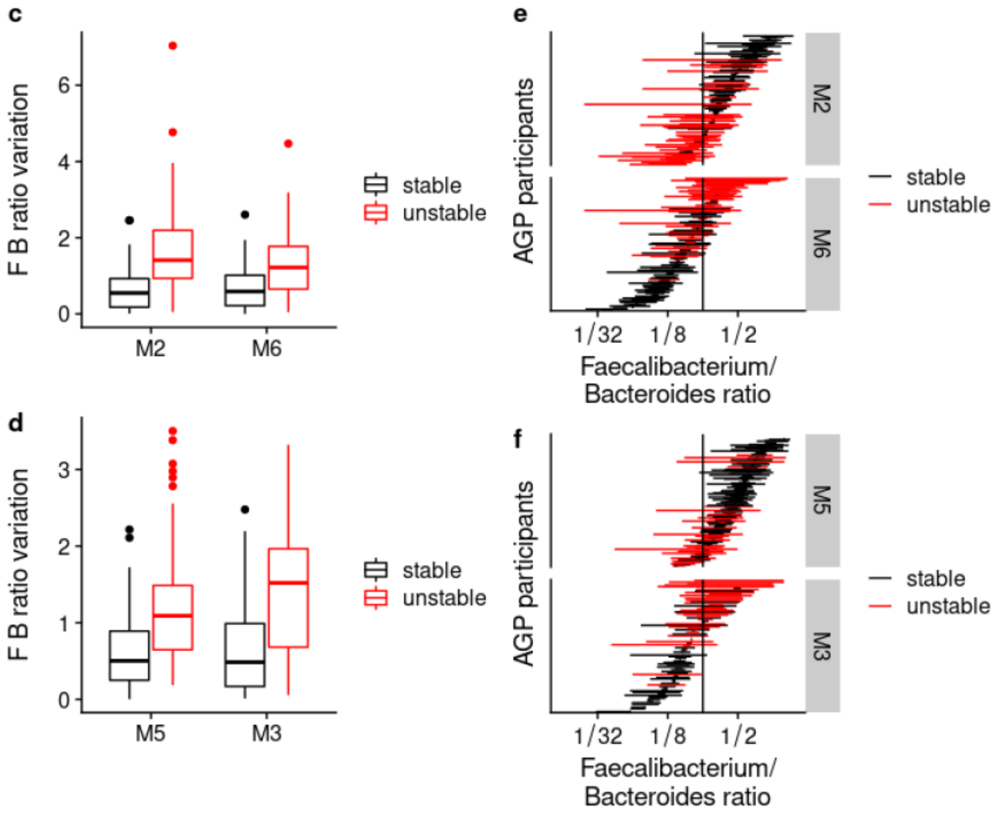
Bifidobacterium bifidum strains may be enriched in phage-related genes in subjects with altered gut microbiomes states

Ladeira *et al*, 2023

Dynamics between partitions are associated to branches

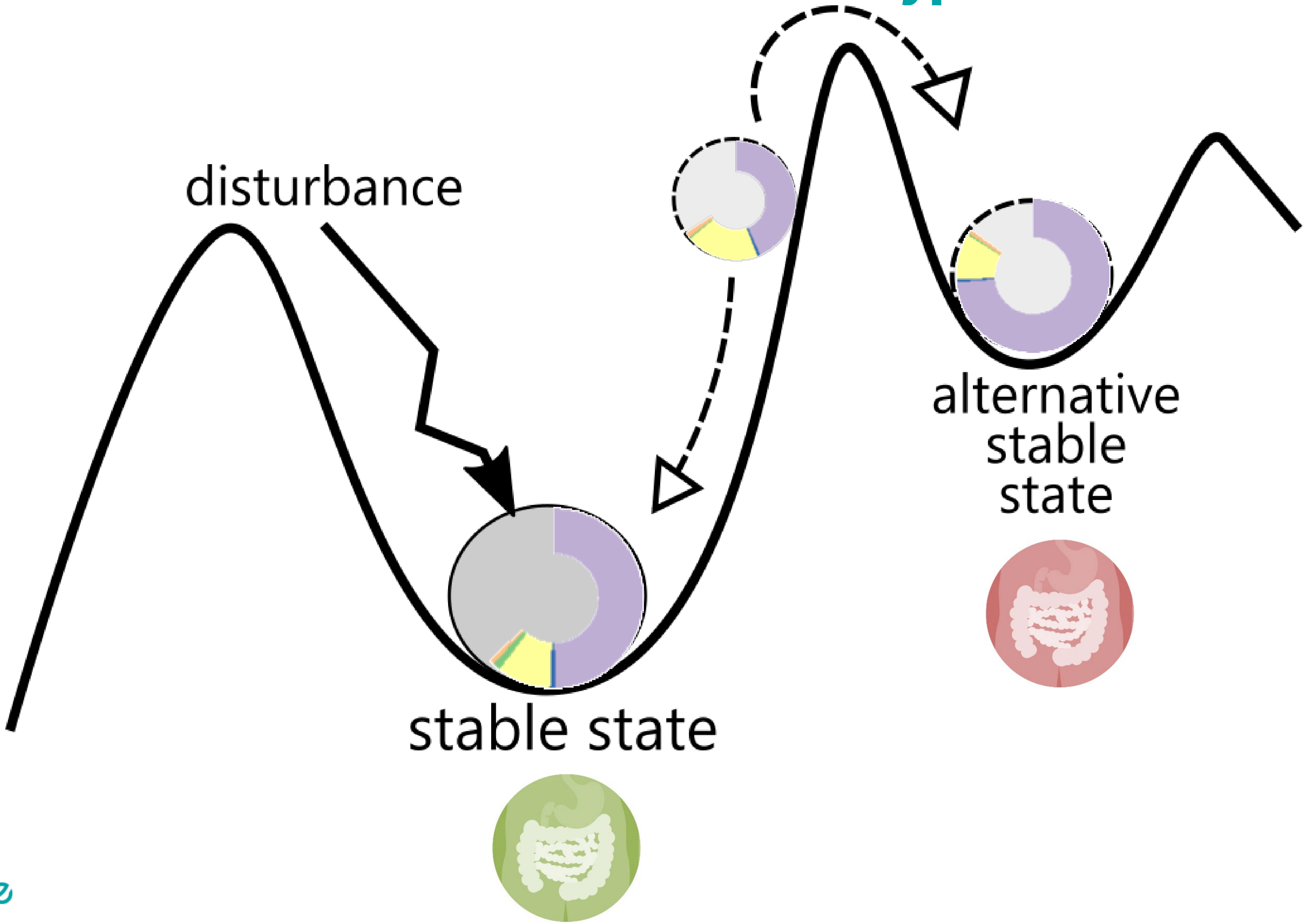
827 participants 2,998 samples 2,171 time-pairs



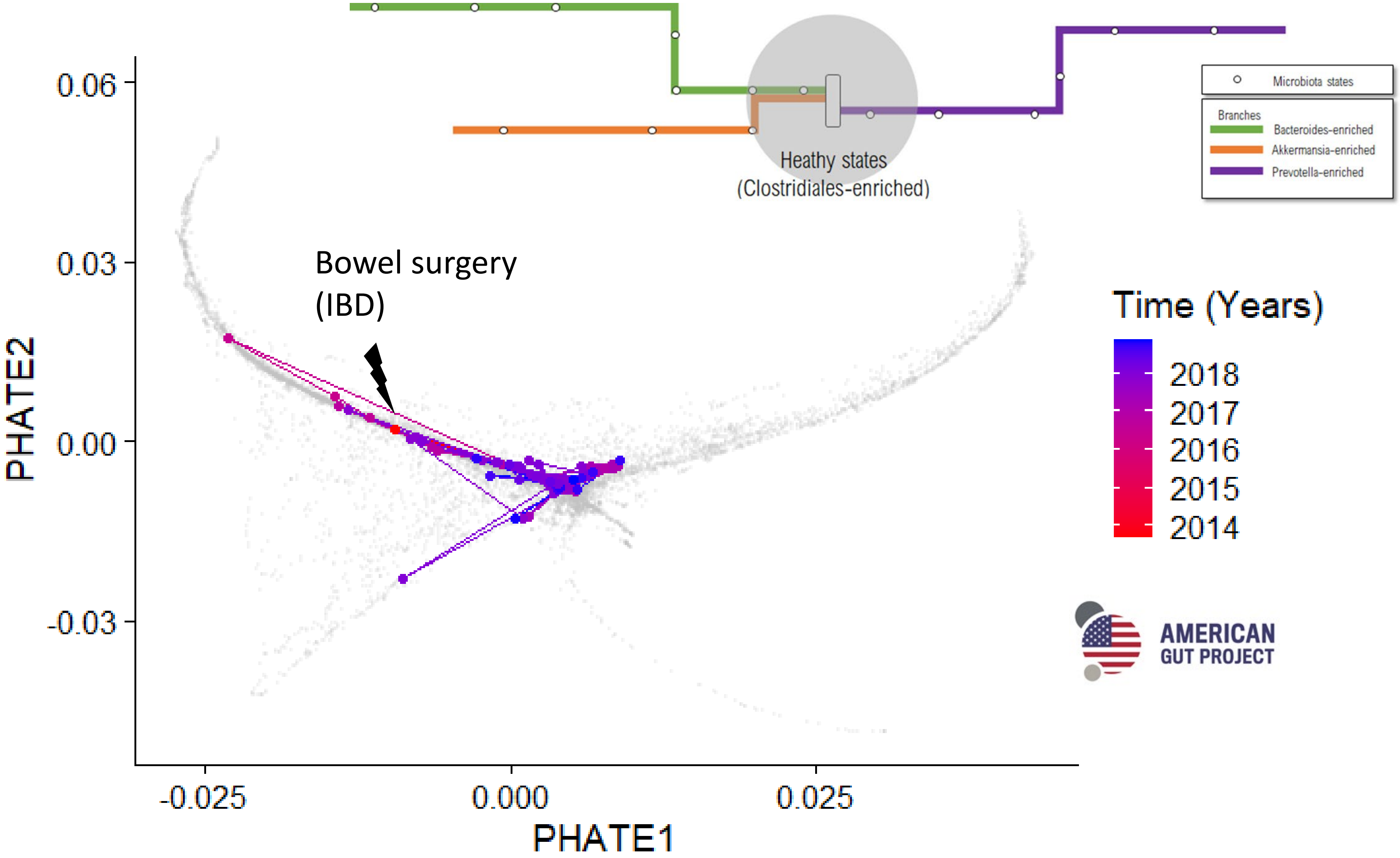


Feacalibacterium/Bacteroides as a tipping element explaining the switch between some states

Gut microbiome alternative stable states hypothesis

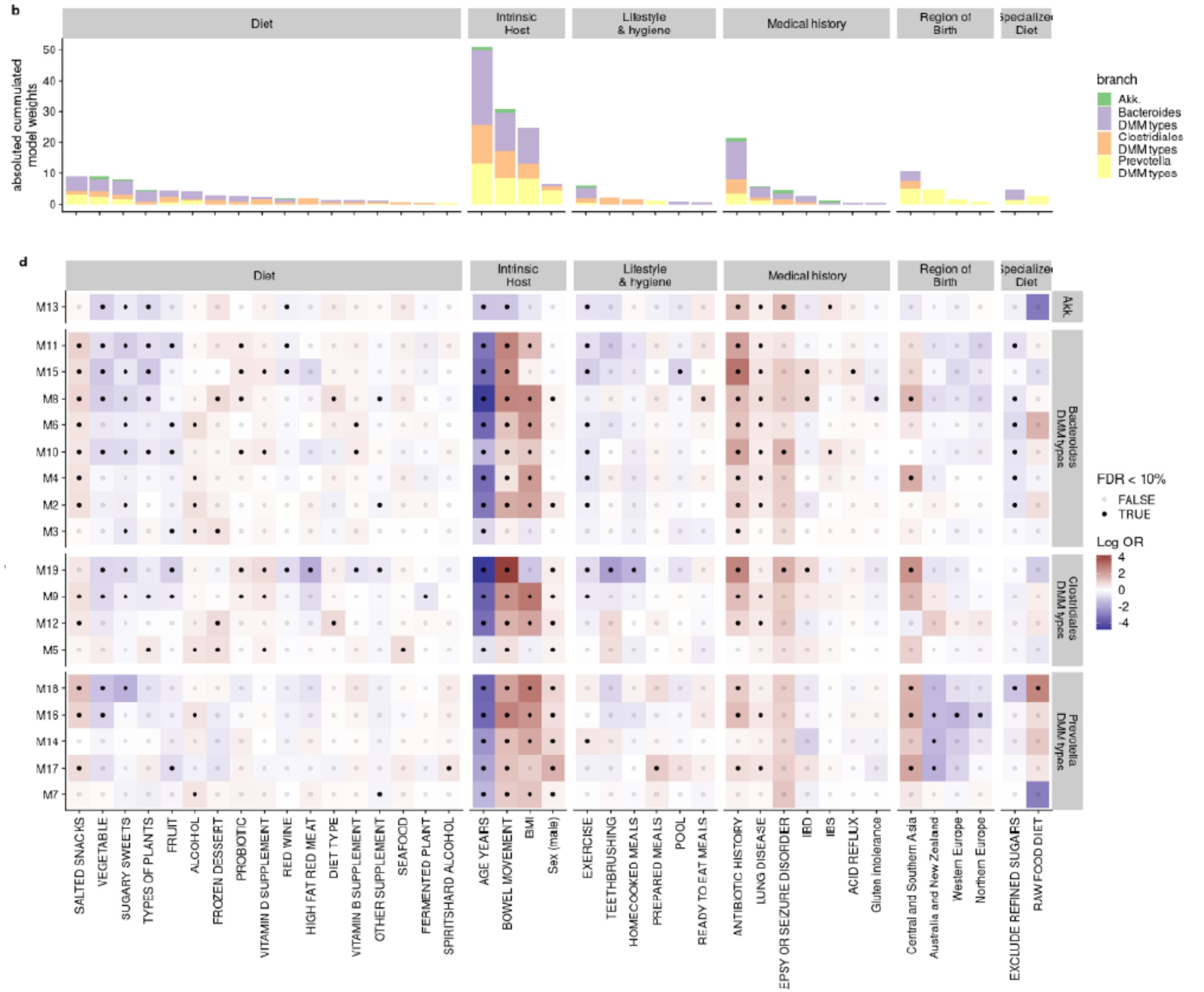


Branches help to monitor gut microbiome recovery



AMERICAN GUT PROJECT

Gut microbiome states are differentially associated with host and env factors

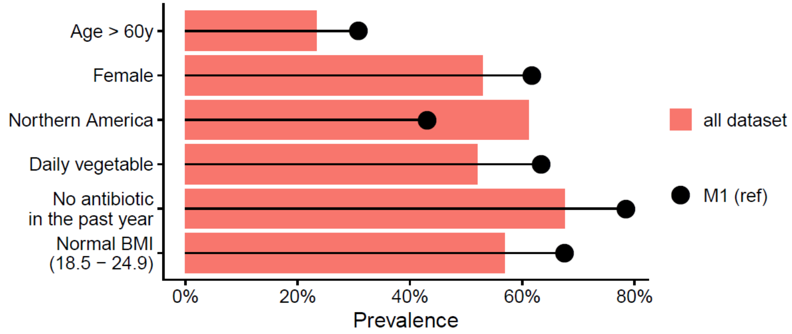


Sex, exercises frequency and **region of birth** associated differentially between branches

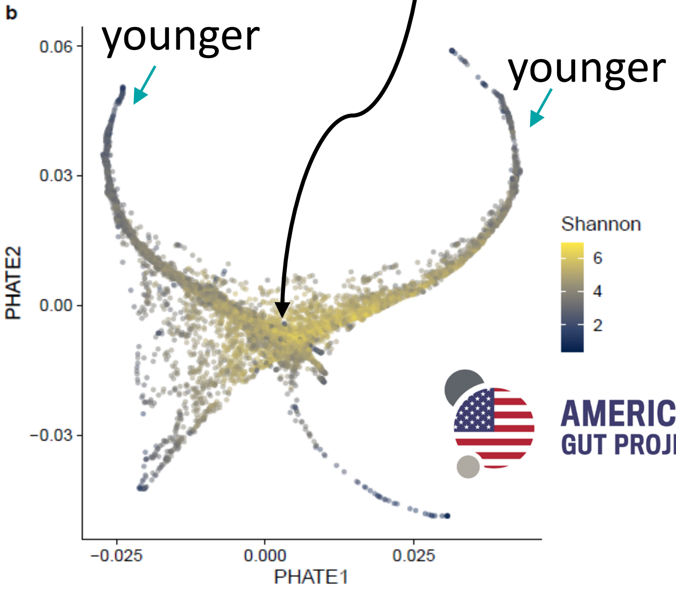
Lifestyle and hygiene associated with altered state within *Bacteroides* branch

Specialized diet associated with altered state within *Prevotella* branch

Do we already observe a intergenerationally mass extinction ?



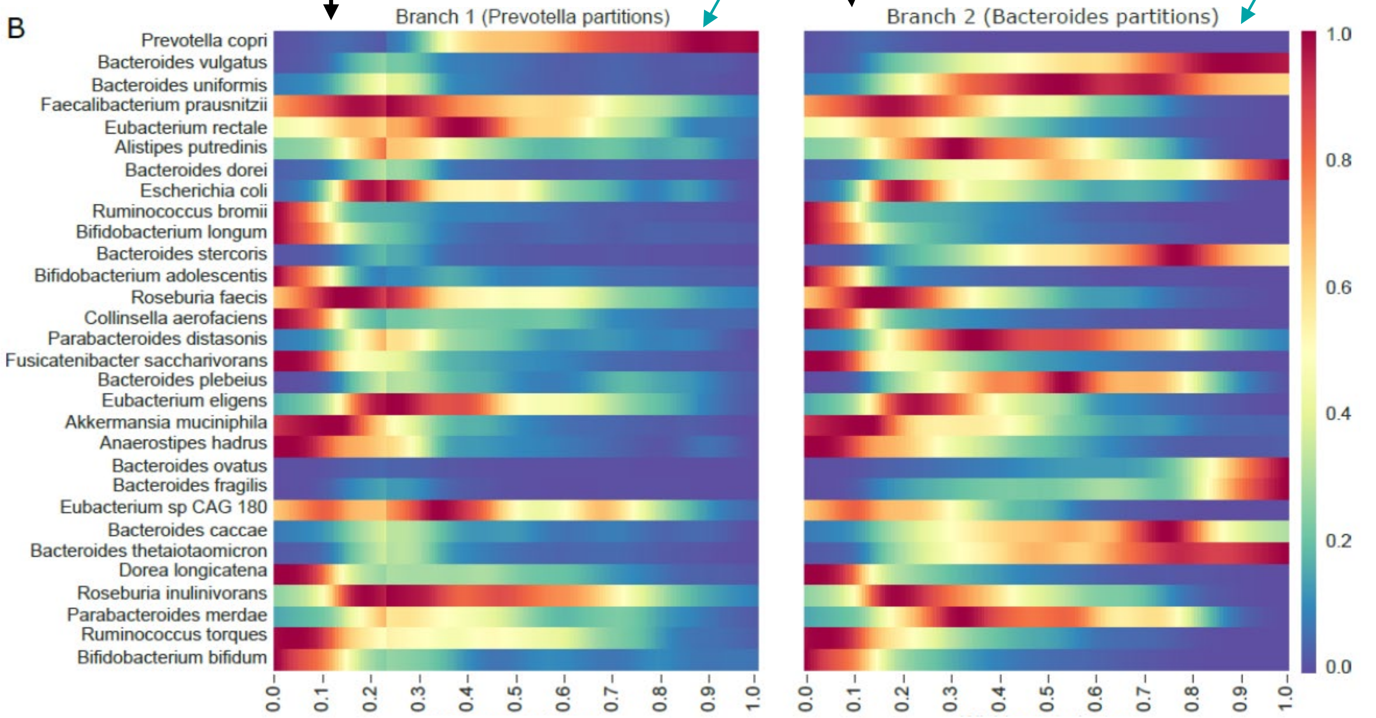
Older and healthy diet and lifestyle



younger

younger

AMERICAN GUT PROJECT



younger

younger

Pseudo-time

Pseudo-time

SABRINA WEISS SCIENCE 04.01.2023 12:00 PM

A Mass Extinction Is Taking Place in the Human Gut

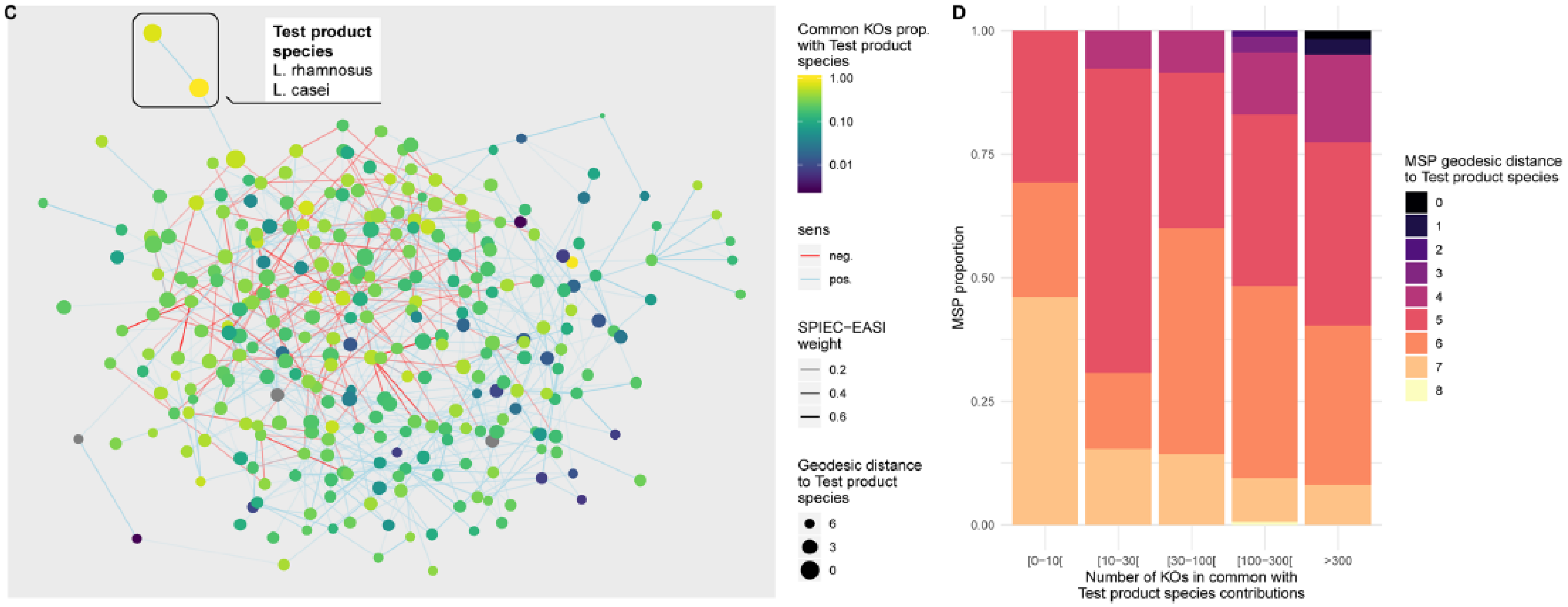
To preserve humankind's diverse bacteria, scientists are harvesting, freezing, and storing poop from around the world.

Tap et al., Nature Comm. 2023

Harnessing the microbial potential of fermented foods to avoid the point of no return

Food microbiome engraftment is gut microbiome baseline dependent

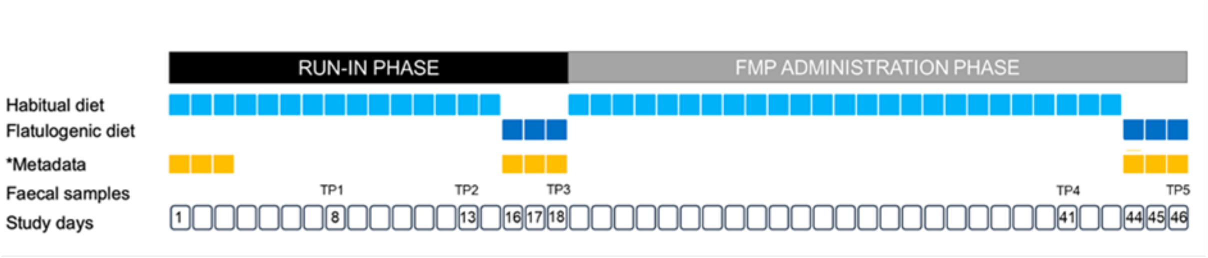
Modular coalescence between gut and biotics species



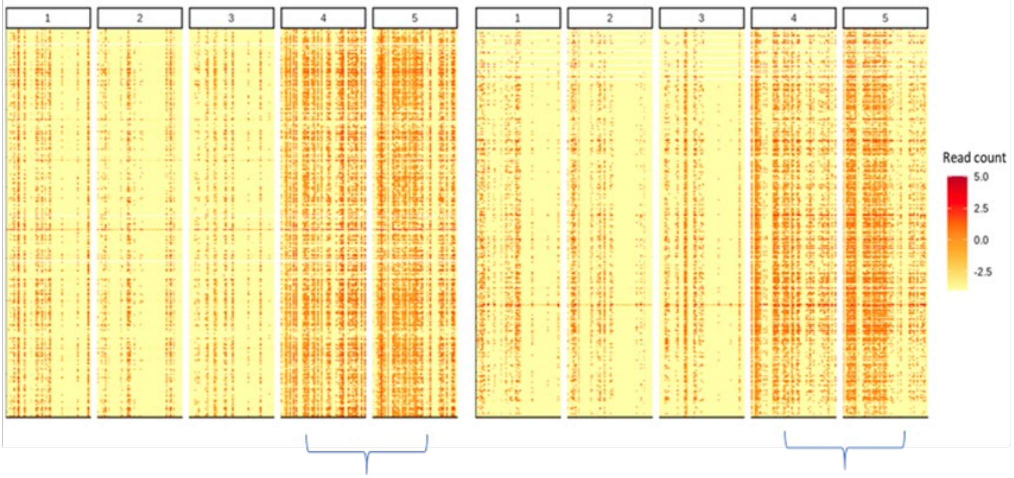
“Engraftment” as function of existing niche and metabolic pathway

Alvarez et al., 2020

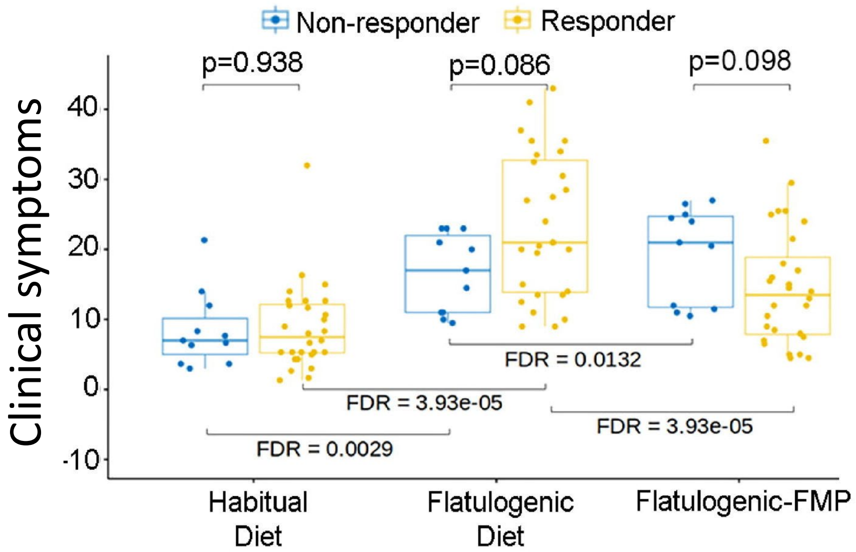
Food microbiome clinical effect is gut microbiome baseline dependent

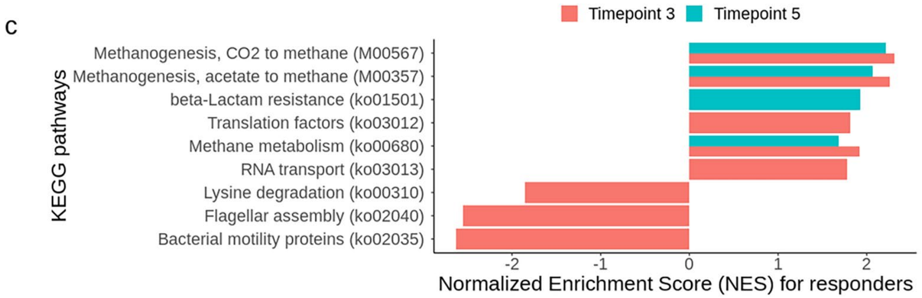


flatulogenic diet (61% carbohydrates, 25% proteins and 14% fat, 27 g of fiber per day)



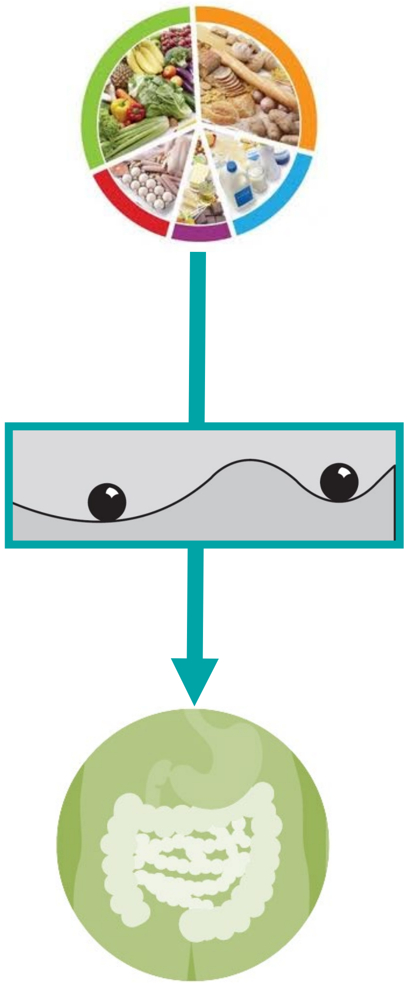
After FMP consumption, FMP active strains detected by metatranscriptomics

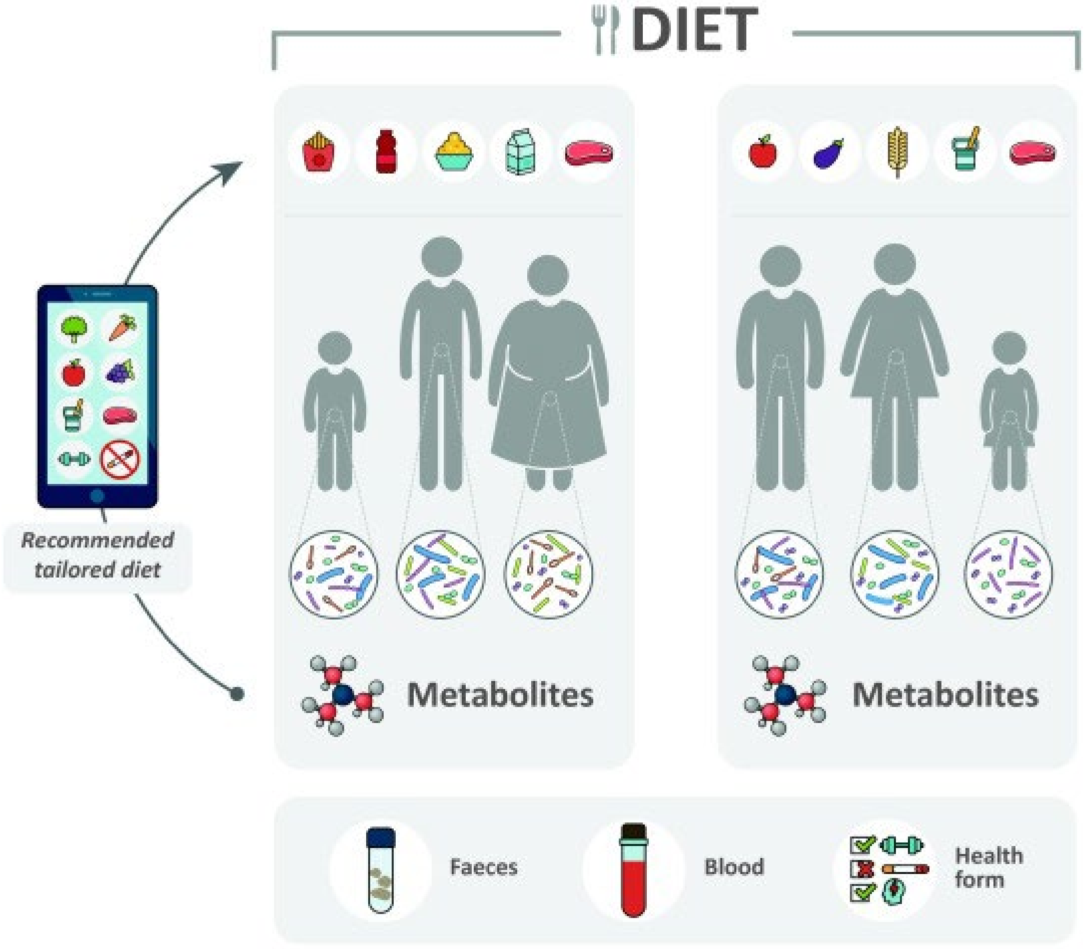




After FMP intake (TP5), higher responder group showed higher methanogenesis activity than low-responders

From gut microbiome states to next-gen fermented foods design

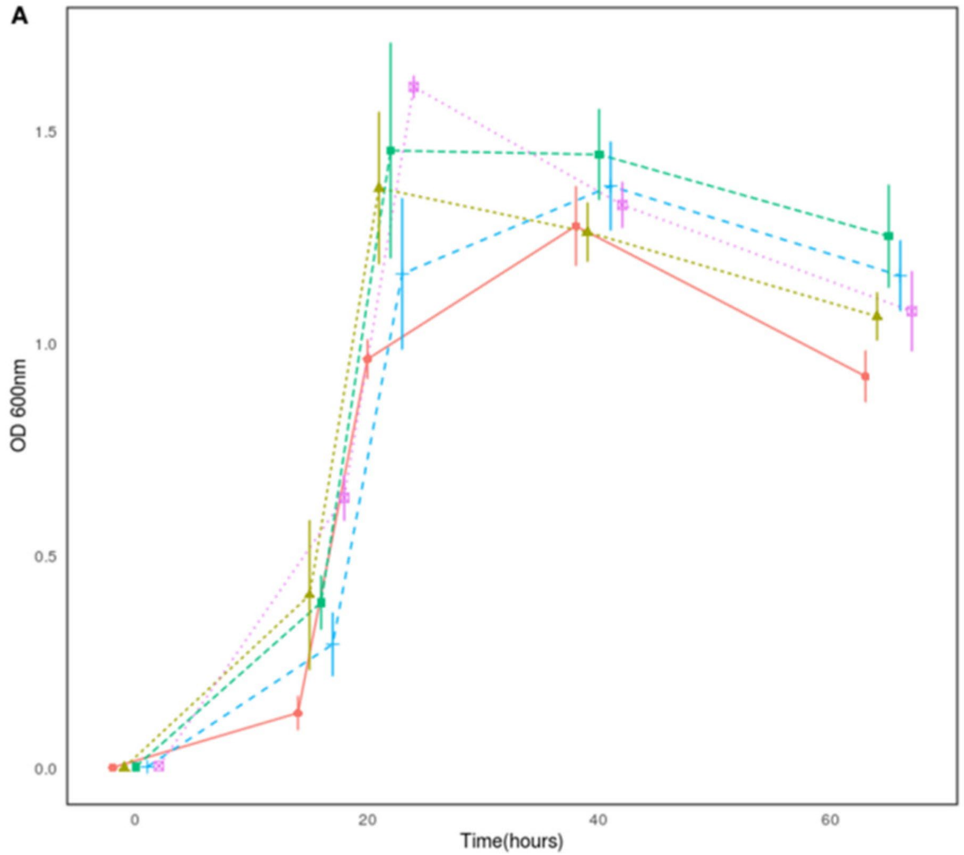




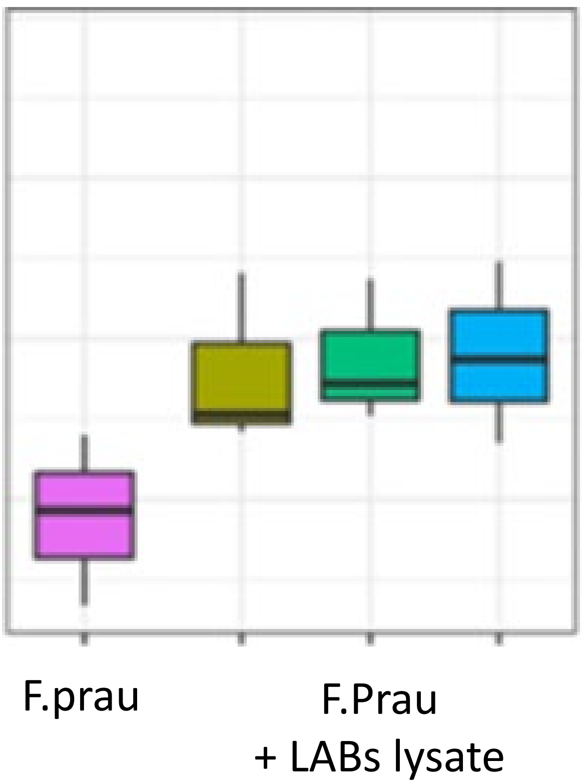
Trends in Microbiology

Prevent gut microbiome critical transition to strengthen its resilience using next-gen fermented foods

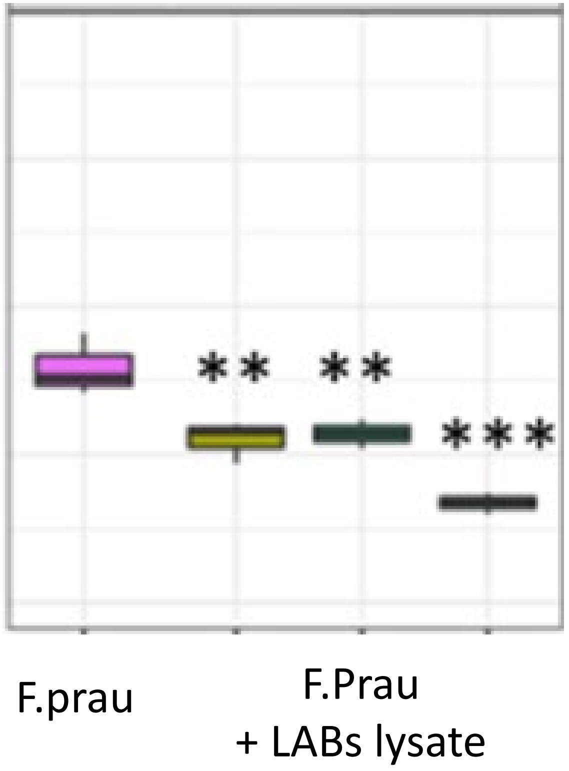
Towards selecting strains with abilities to prevent tipping point in gut microbiota



umax



Decay slope

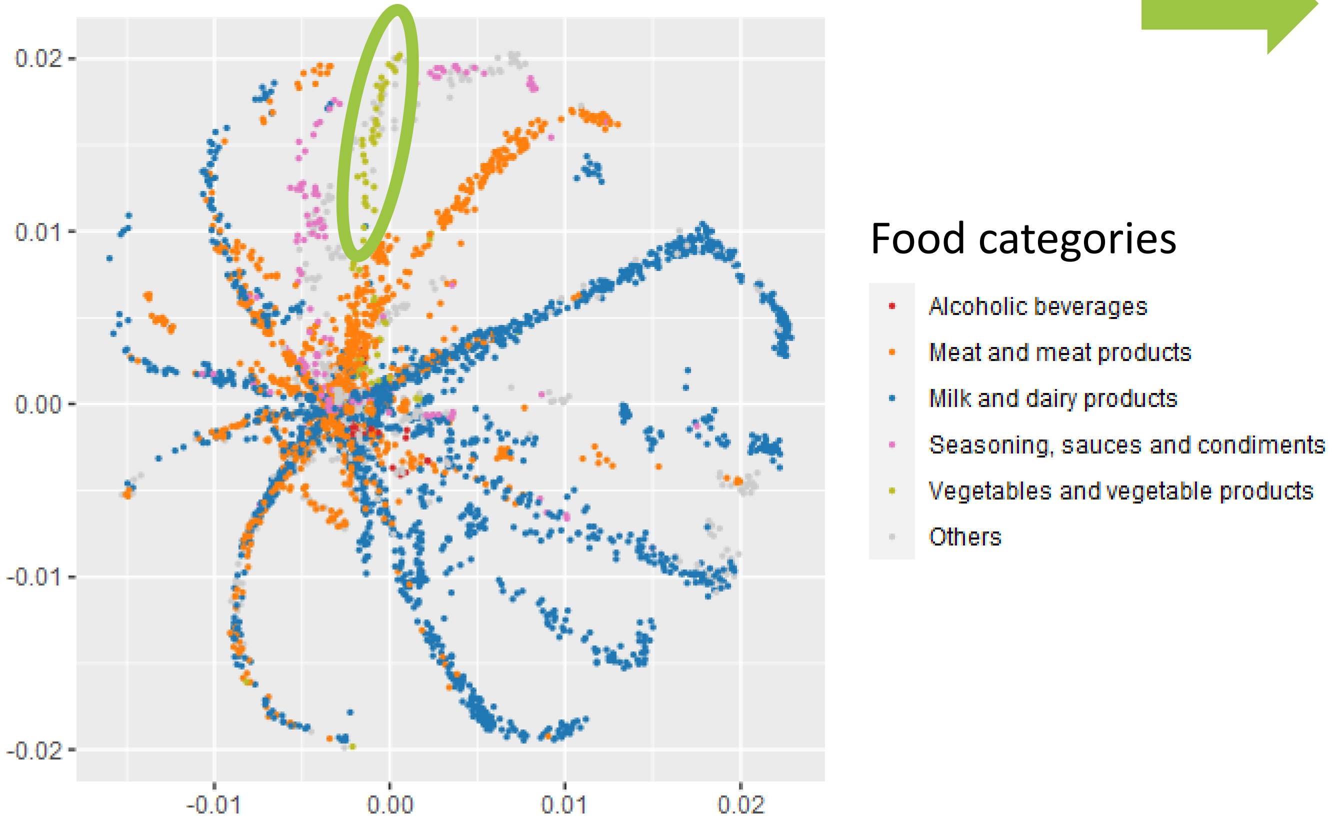


Increase of peptidoglycan levels for cell wall formation *F.prau*

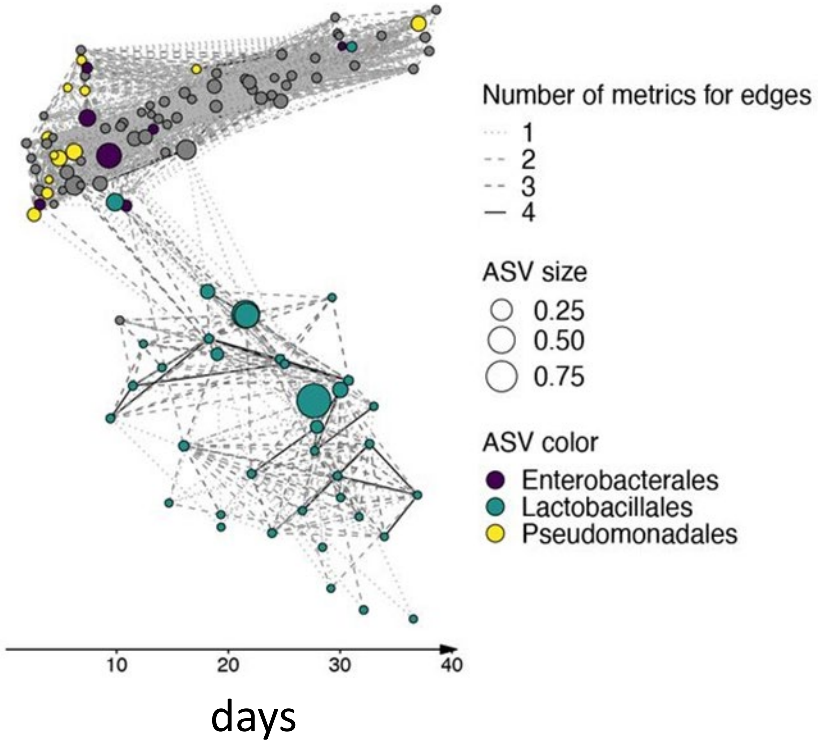
Lebas, Derrien and colleagues (2020)

Fermented food microbiome is shaped by deterministic dynamic processes

N = 4973 samples



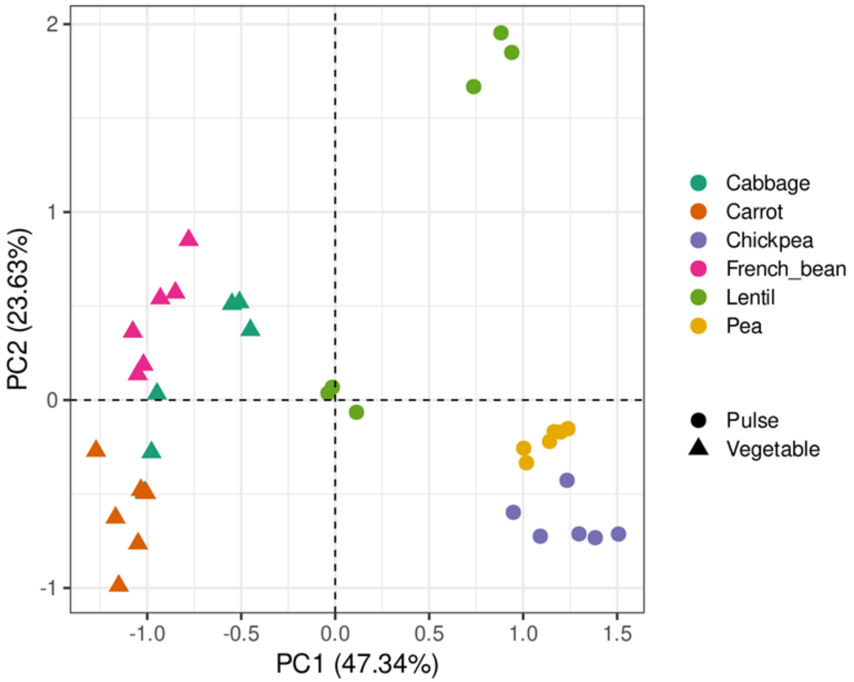
Kimchi dynamics



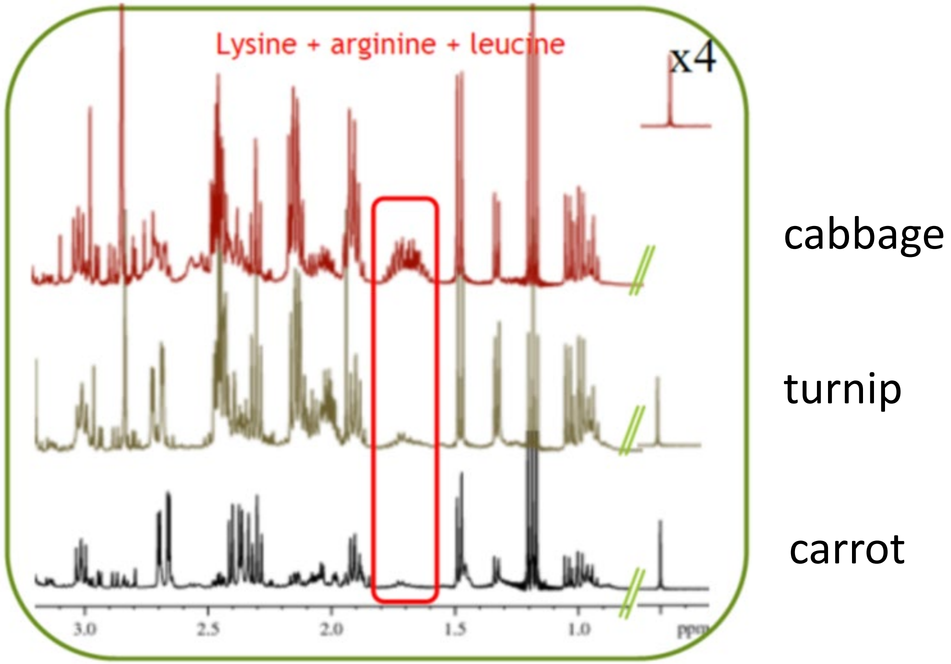
Junker *et al.* Biorxiv (2024)

Plant-based matrices metabolome matters

Unfermented plant based matrices
LC-MS amino-acids profiles



Unfermented plant-based
NMR profiles

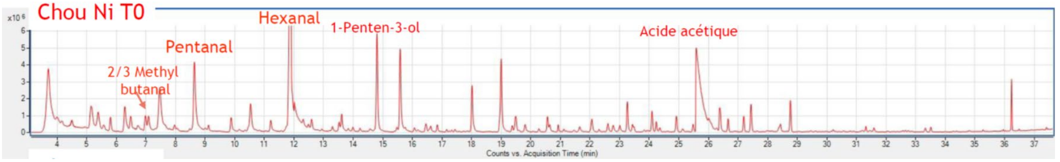


SayFood
Food & Bioproduct Engineering

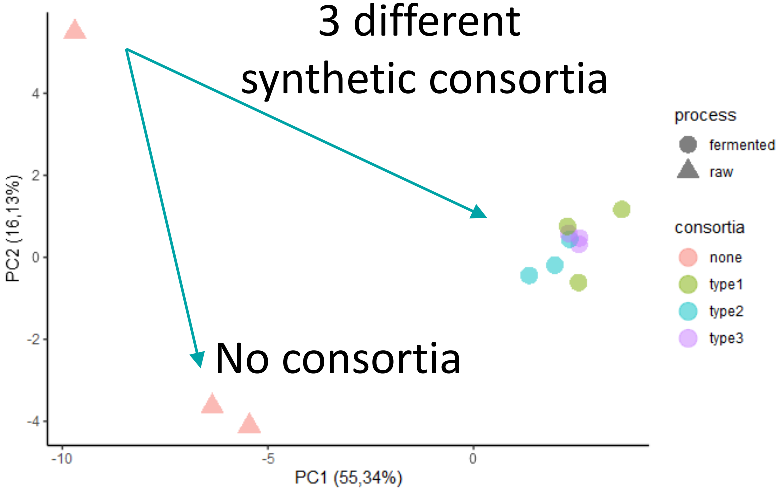
Vincent Hervé

Aerial

Fermented plantbased food metabolome converge despite different synthetic consortia inoculation



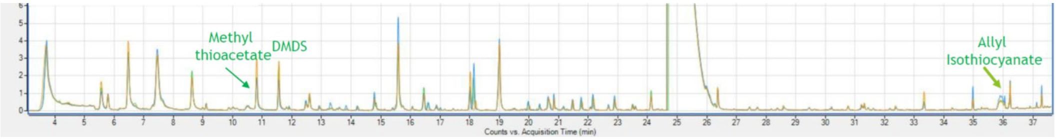
Hexanal
Pentanal



3 different synthetic consortia

No consortia

Acetate
Esters
Volatile Sulfur Compounds

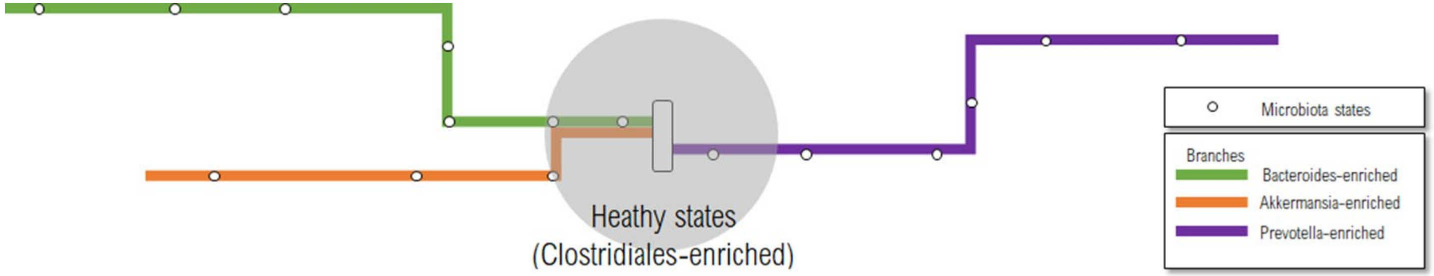


metasimfood

Take home messages

- Gut microbiome ecological landscape is made of **local states** that are dynamically linked within "**branches**" where **critical transition** occurred

- Fermented food can help but **effects may be personalized** thank to gut **microbiota states at baseline**



- Prototyping next-gen fermented food should include **gut tipping elements** and **food matrix metabolites** during screening for better **personalized and beneficial effects**.

Acknowledgments

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Dalal Werner
Marie Hélène Desmonts
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Food Microbial Ecology Lab

Food Microbial Ecology lab

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