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

Julien Tap, Vincent Hervé, Sophie Landaud, Dalal Werner, Marie-Helene Desmonts, Stéphane Chaillou

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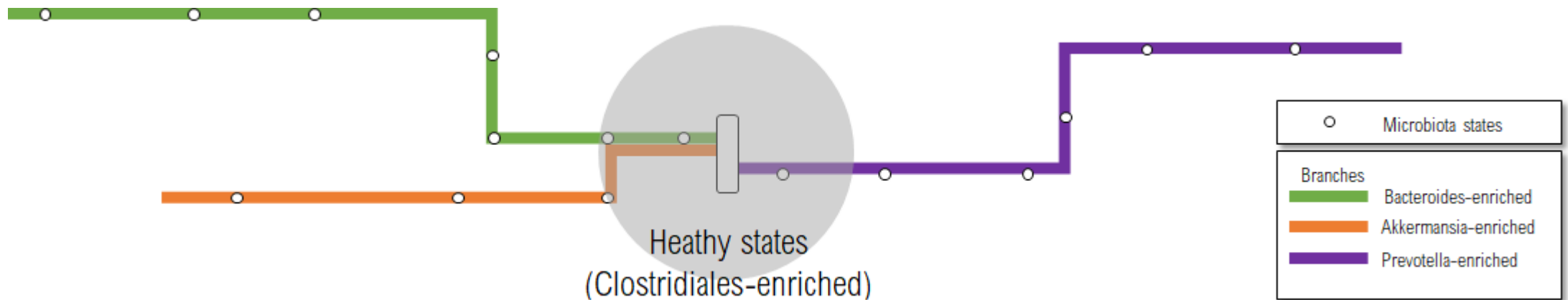
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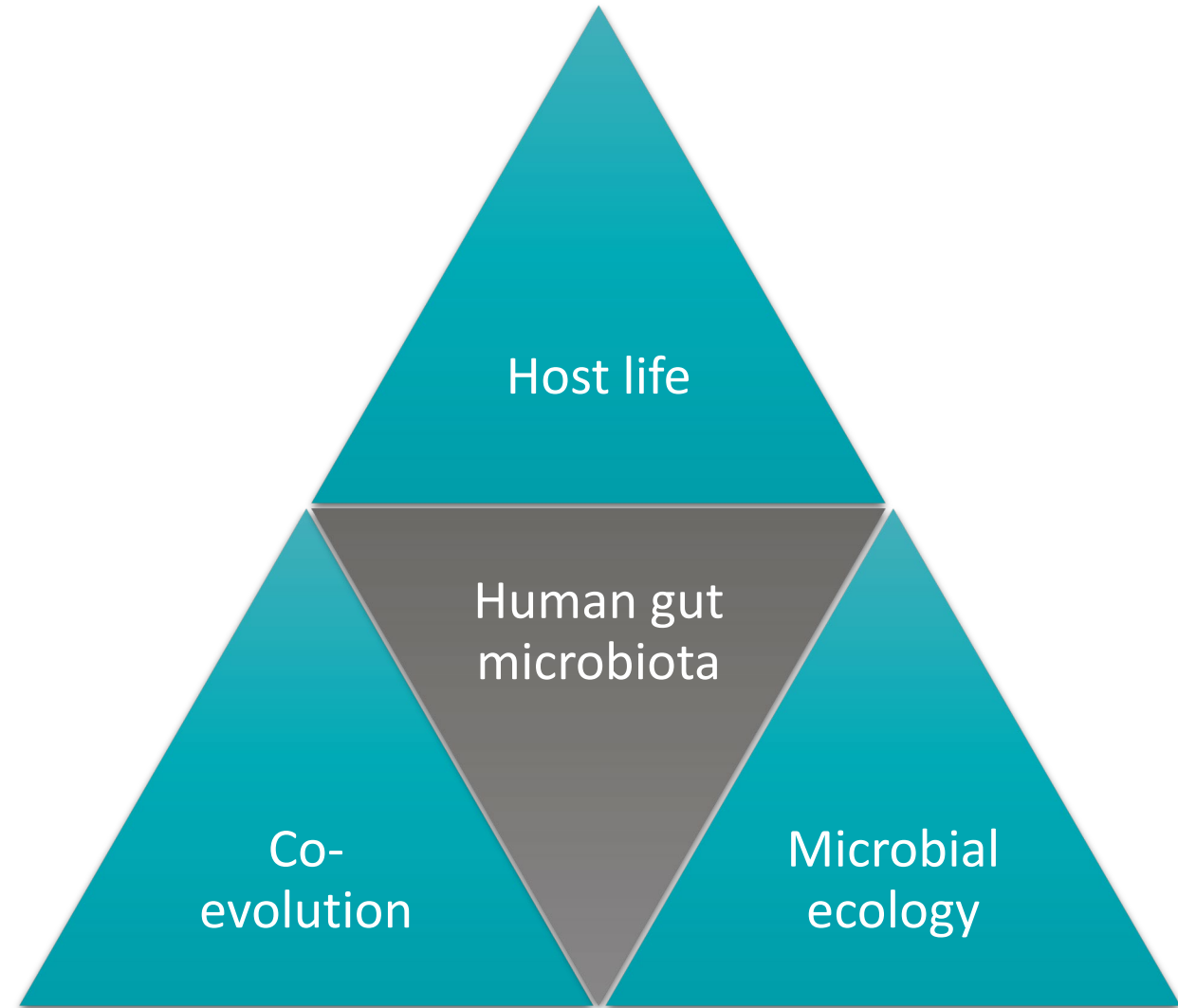
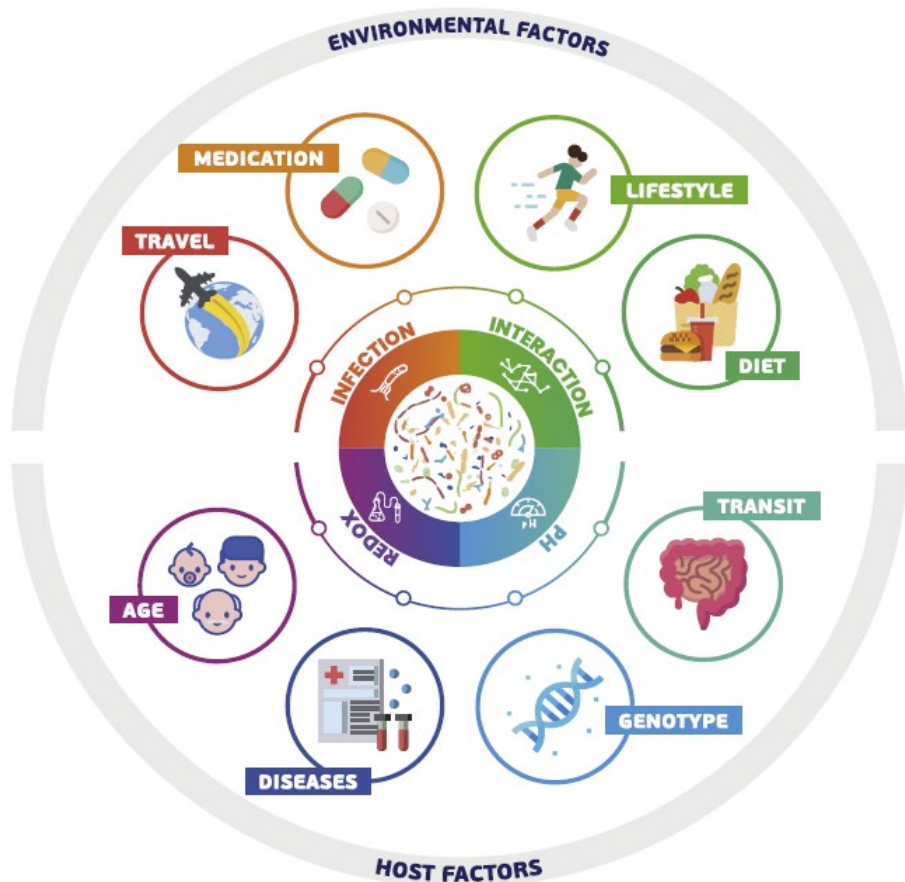
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> Next-gen fermented food: Harnessing gut microbiome diversity and functions.

Julien Tap
INRAE MICALIS
NMC Utrecht 2024

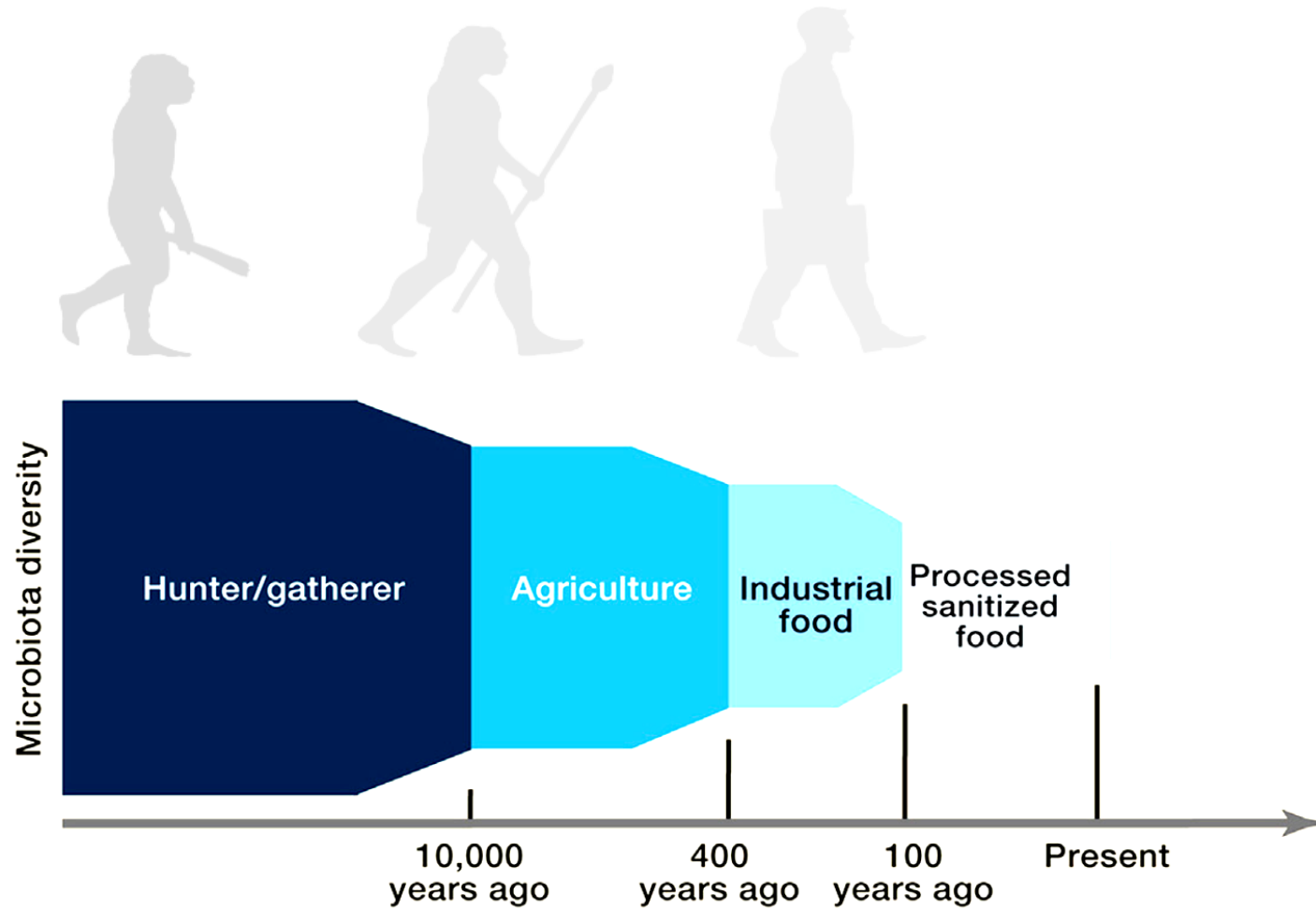


➤ Different factors shapes the human gut microbiome



> Diet and lifestyle effect host microbiome symbiosis

Are we uncoupling our metagenome and our genome?



Hunters - gatherers

↓
Sedentarization

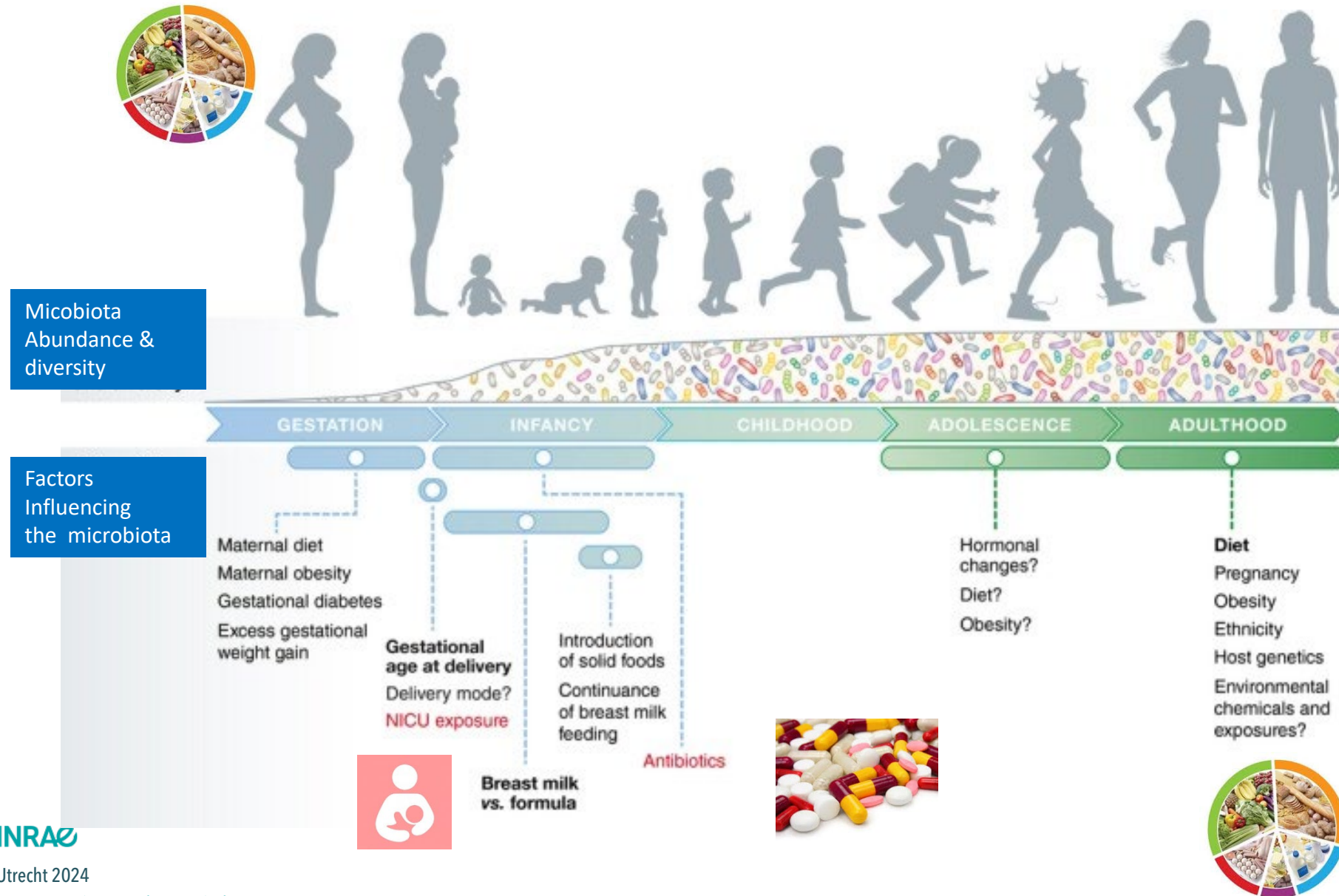
↓
Livestock and crops

↓
Hygiene/medication

↓
Refined products



> Gut microbiome throughout life span



➤ Microbiome states resilience as key factor



Healthy state



Resistance



Recovery

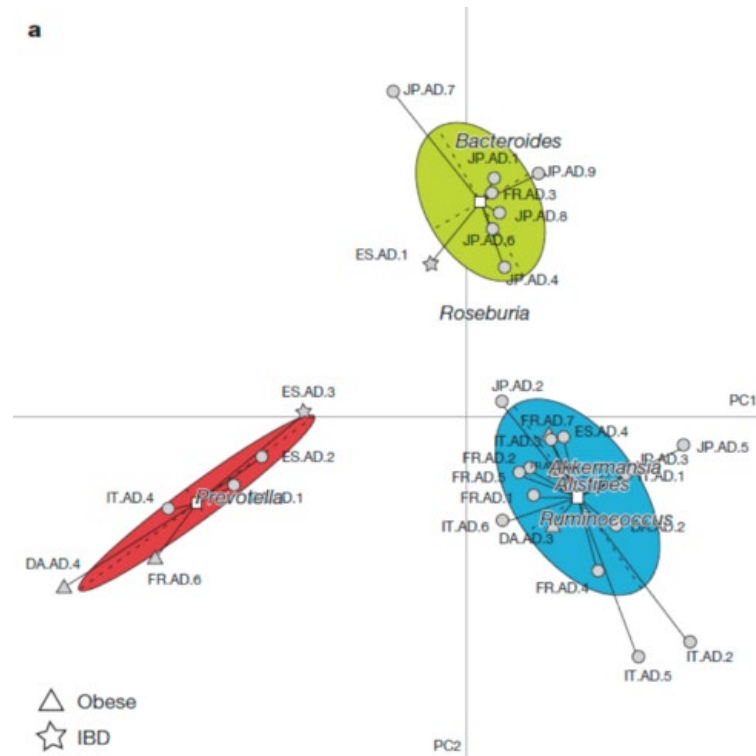
Resilience

Healthy state

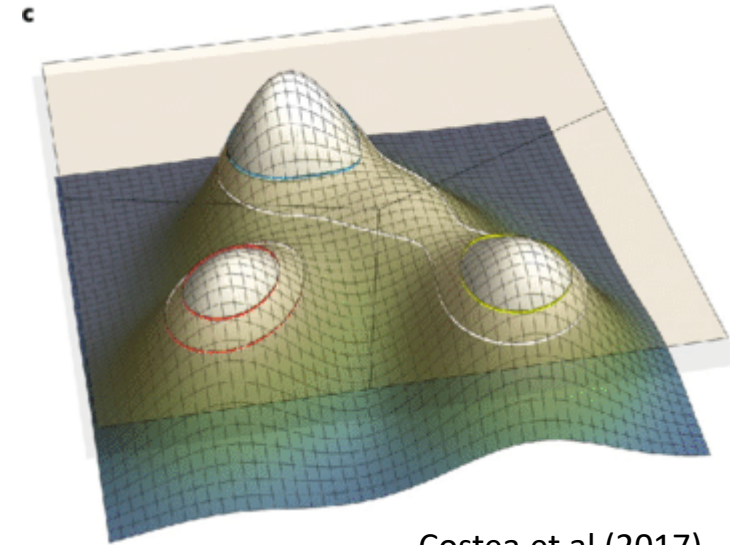


Degraded state

➤ Several attempts to decipher the gut microbiome structure



Arumugam, Raes et al (2010)



Costea et al (2017)

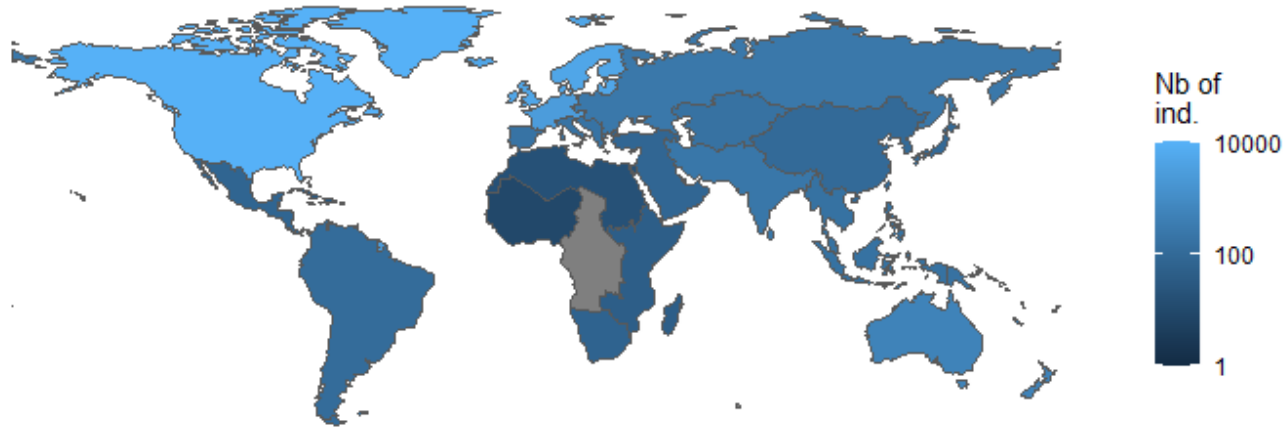
Dirichlet Multinomial Mixture (DMM) modeling

Limits:

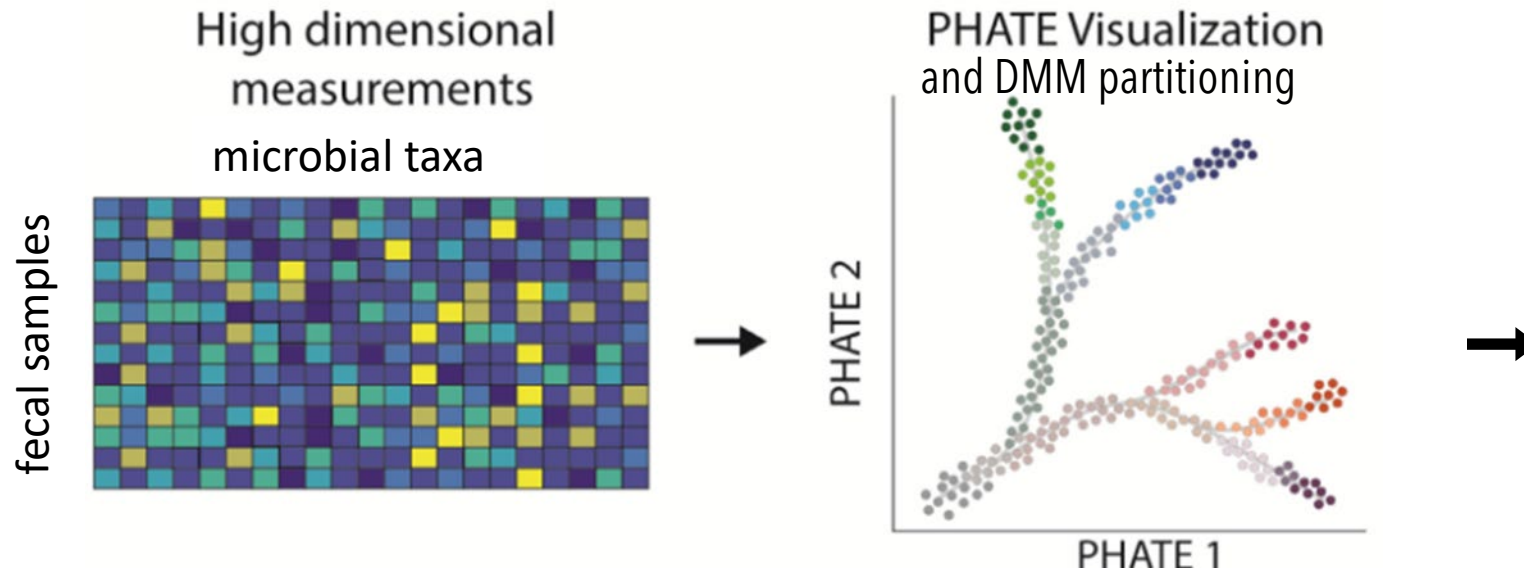
Few association with diet

Few stability assessment (e.g. with time-series)

➤ 35,000 human gut microbiome samples analyzed



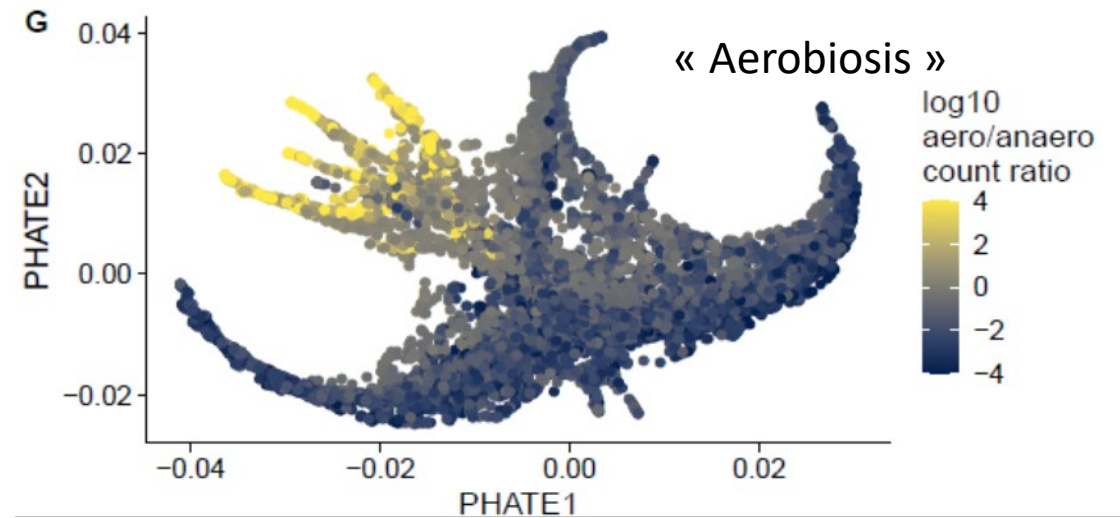
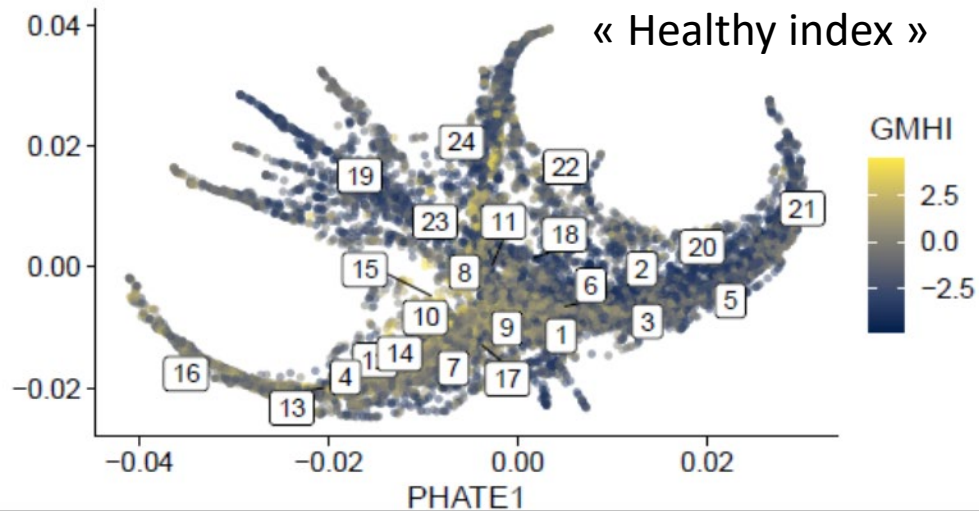
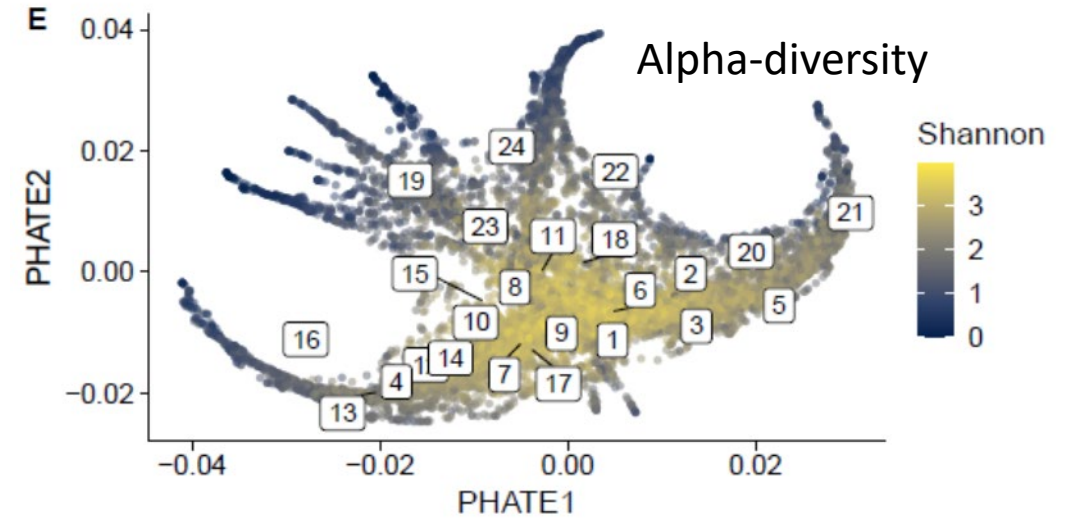
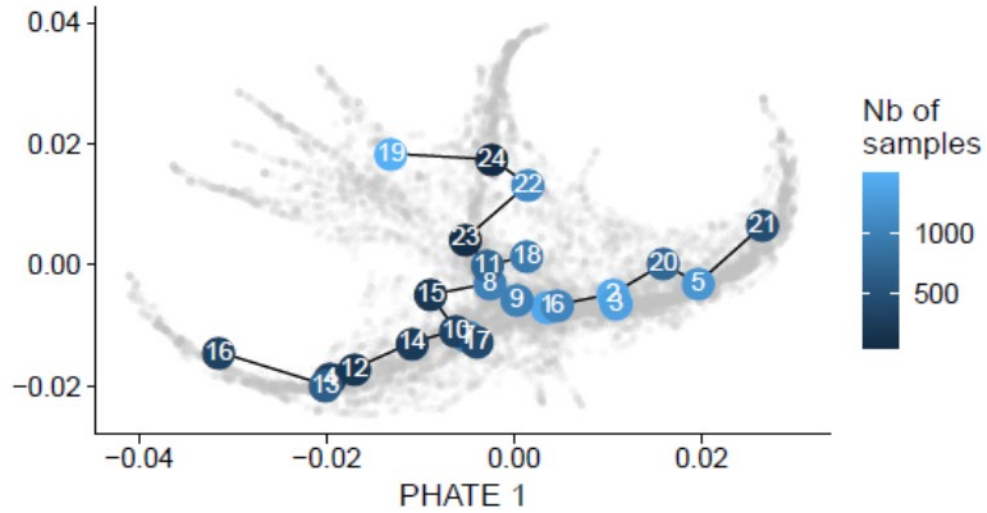
New computational method that help observe **global and local structure** at the same time



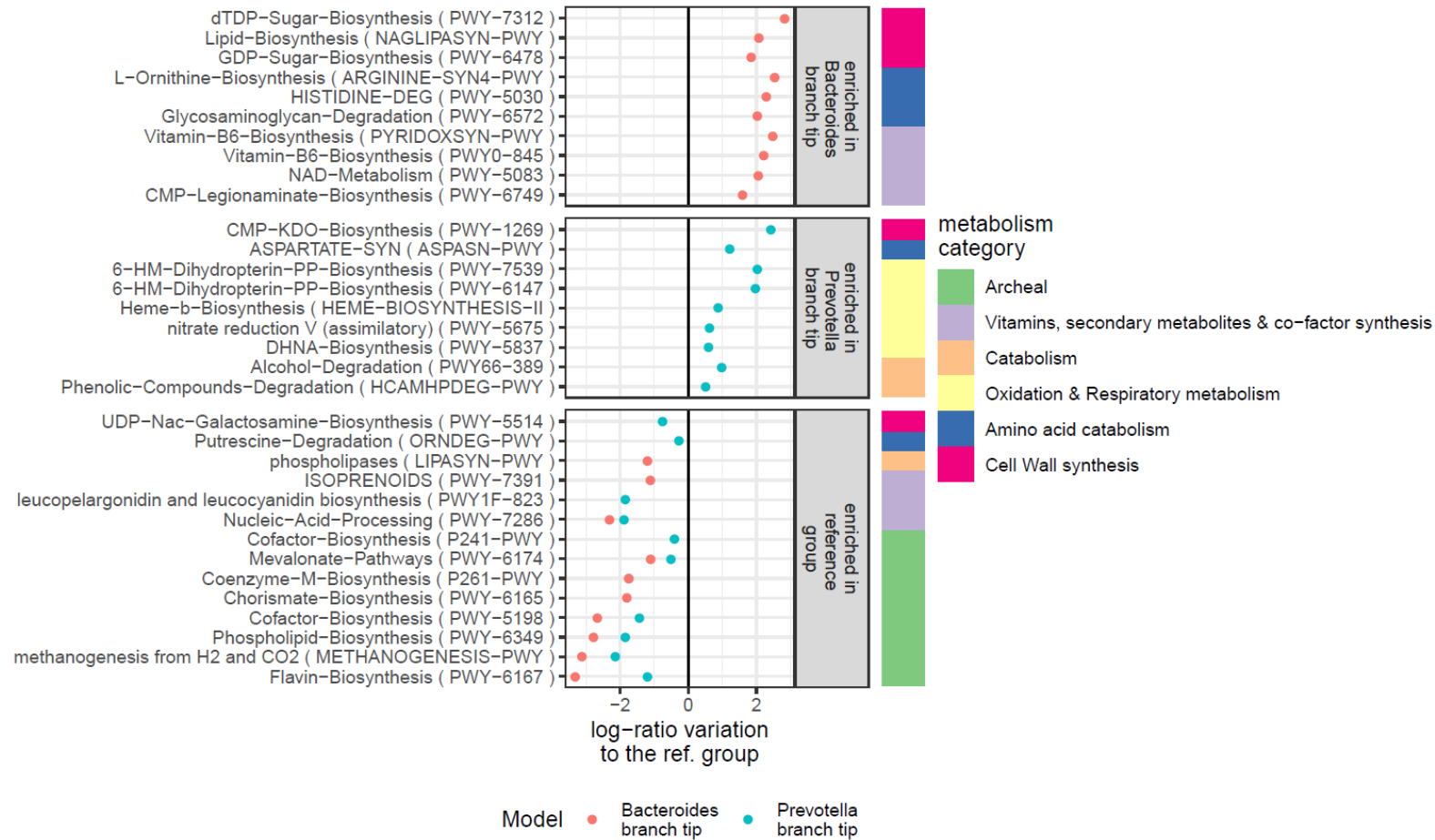
Time-series analysis to detect microbiome states

Region of birth, Lifestyle, diet, and health modelization

➤ Human Gut microbiome structured as branches



➤ Low-diversity tips of branches display functional shifts

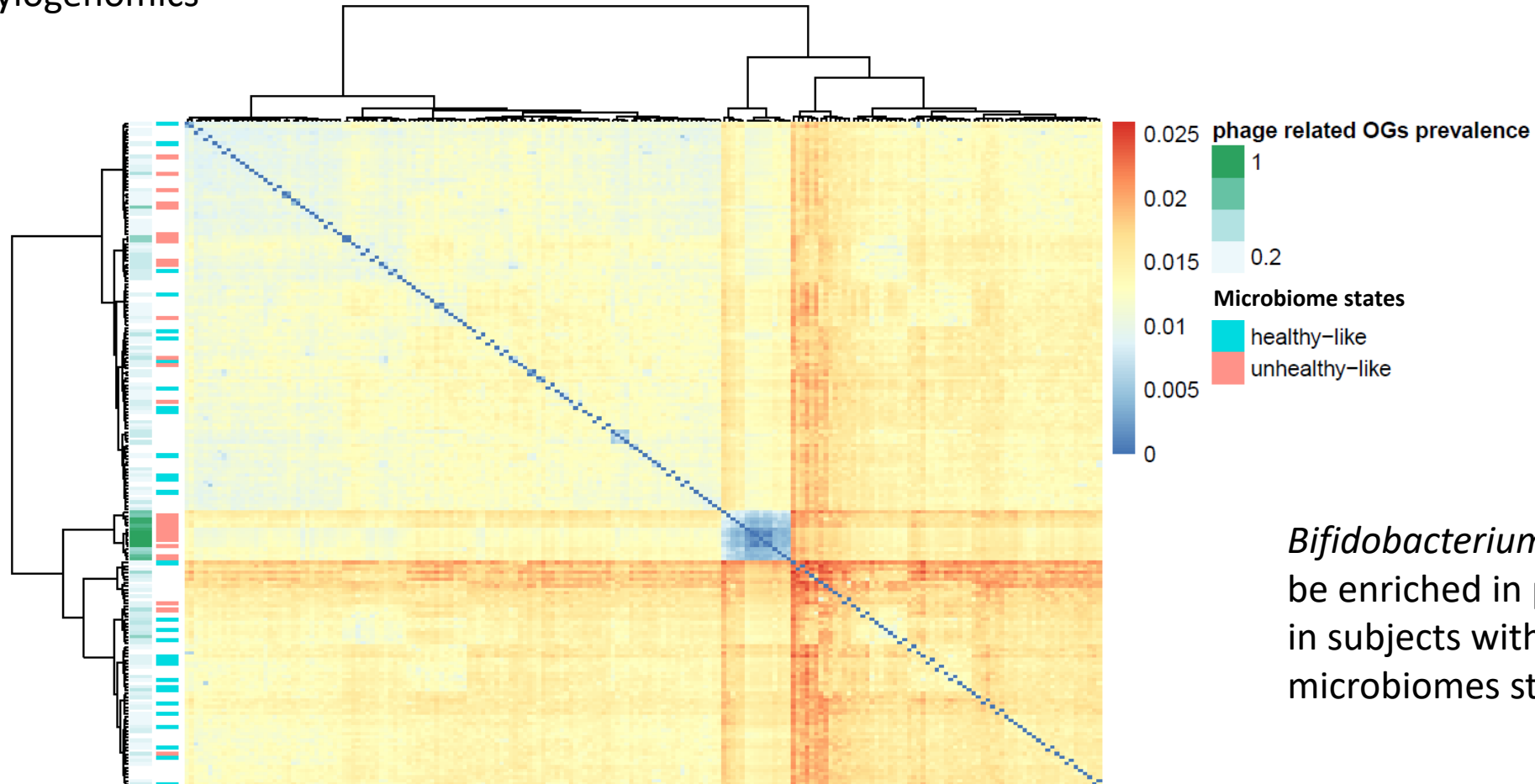


amino acid catabolism increase
in *Bacteroides* branch tip

oxidative stress response increase
in *Prevotella* branch tip

➤ Altered states showed functional differences within species

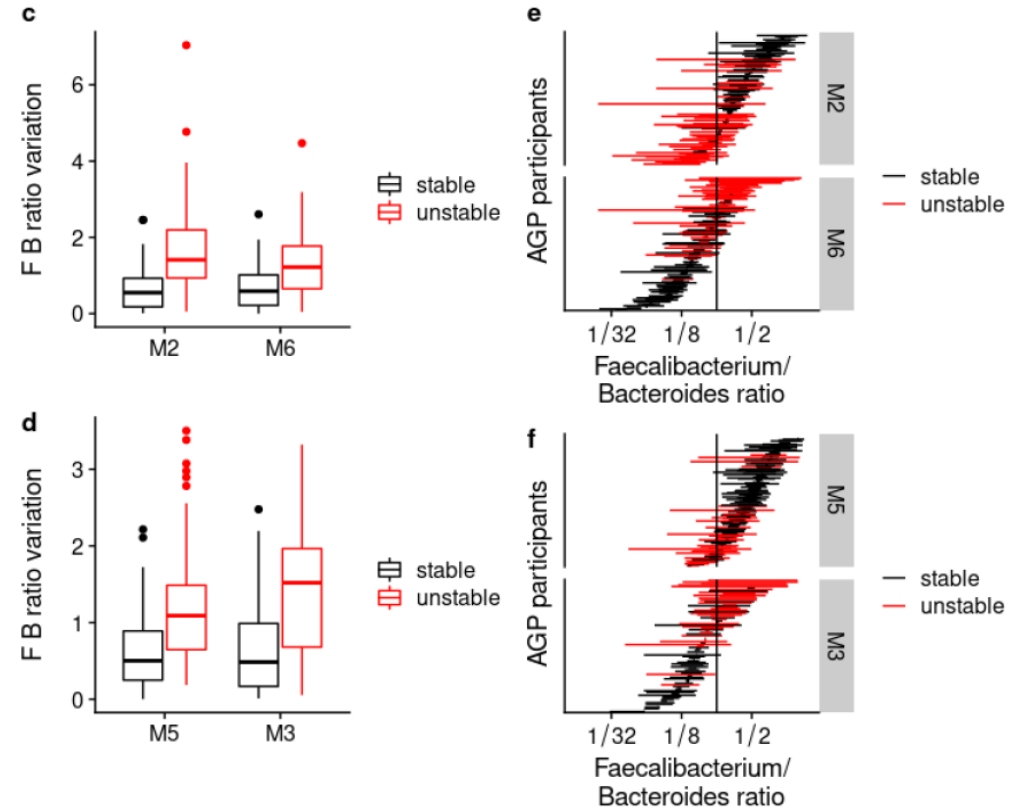
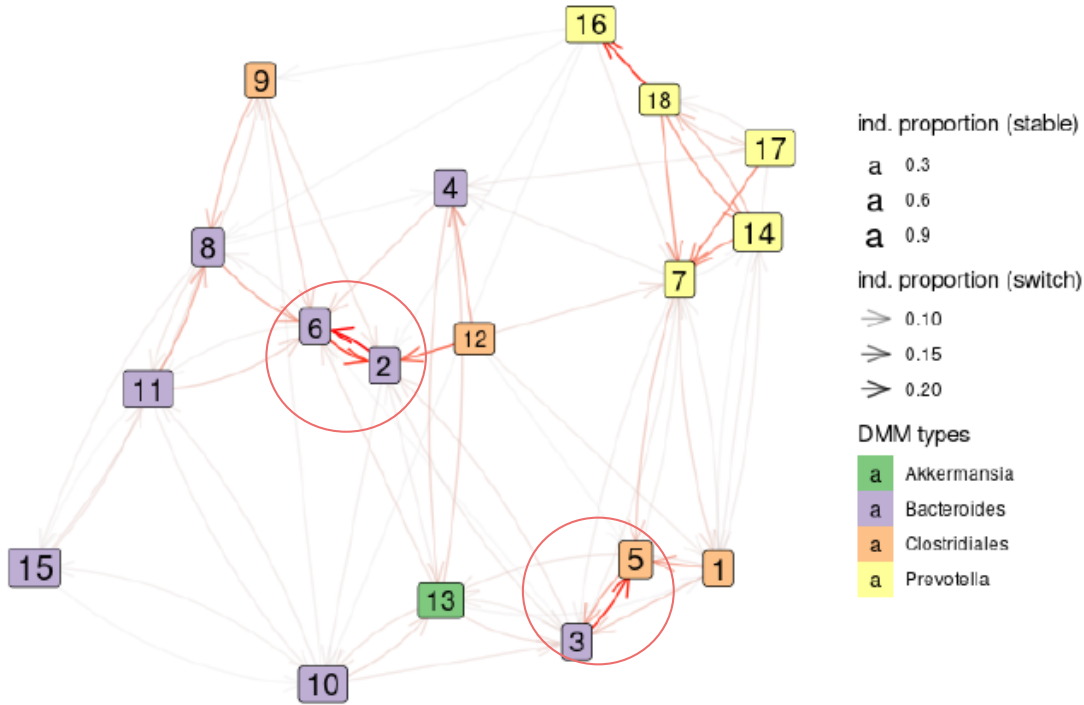
400 *B. bifidum* MAGS
phylogenomics



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

➤ Dynamics between partitions are associated to branches

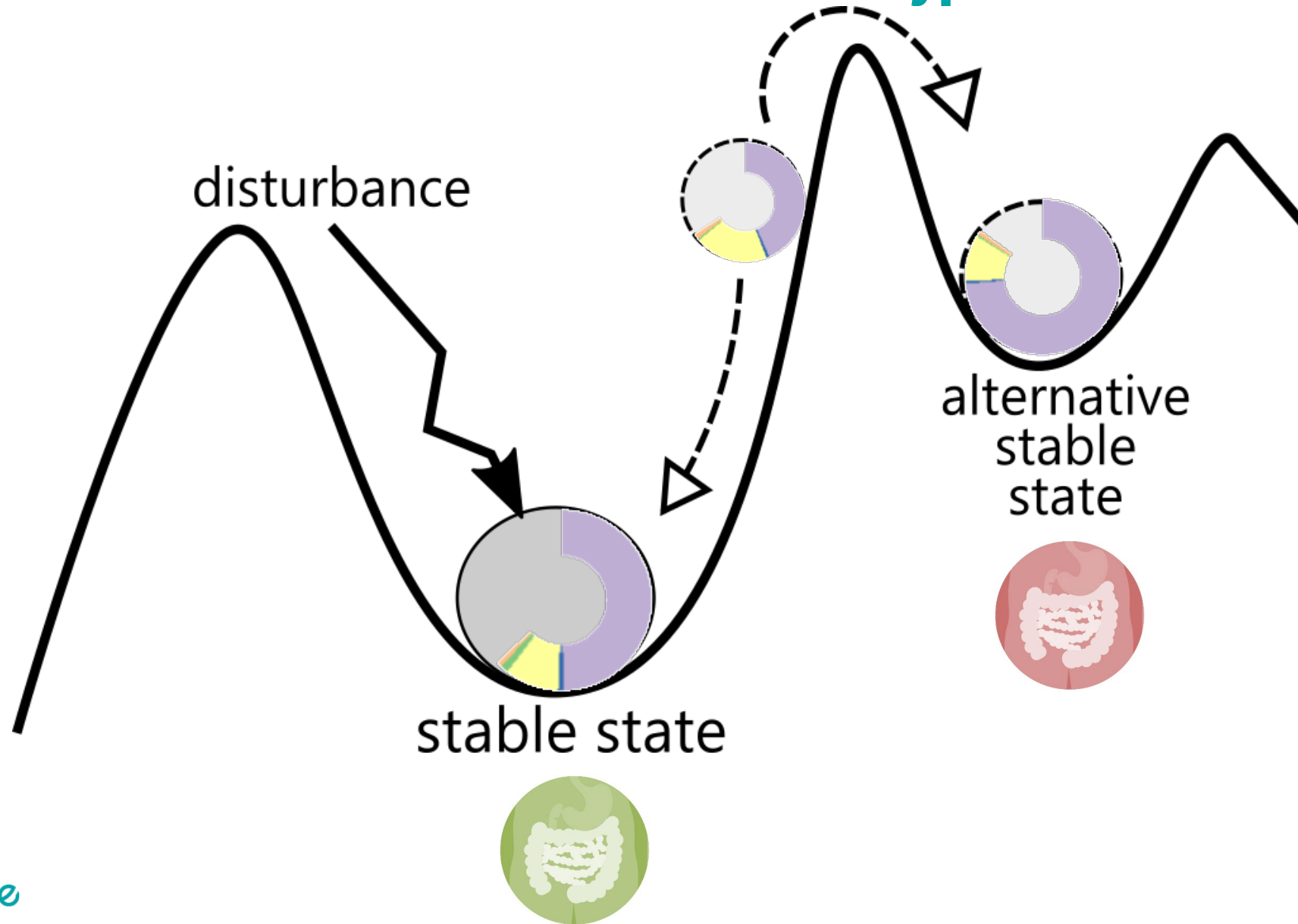
827 participants 2,998 samples 2,171 time-pairs



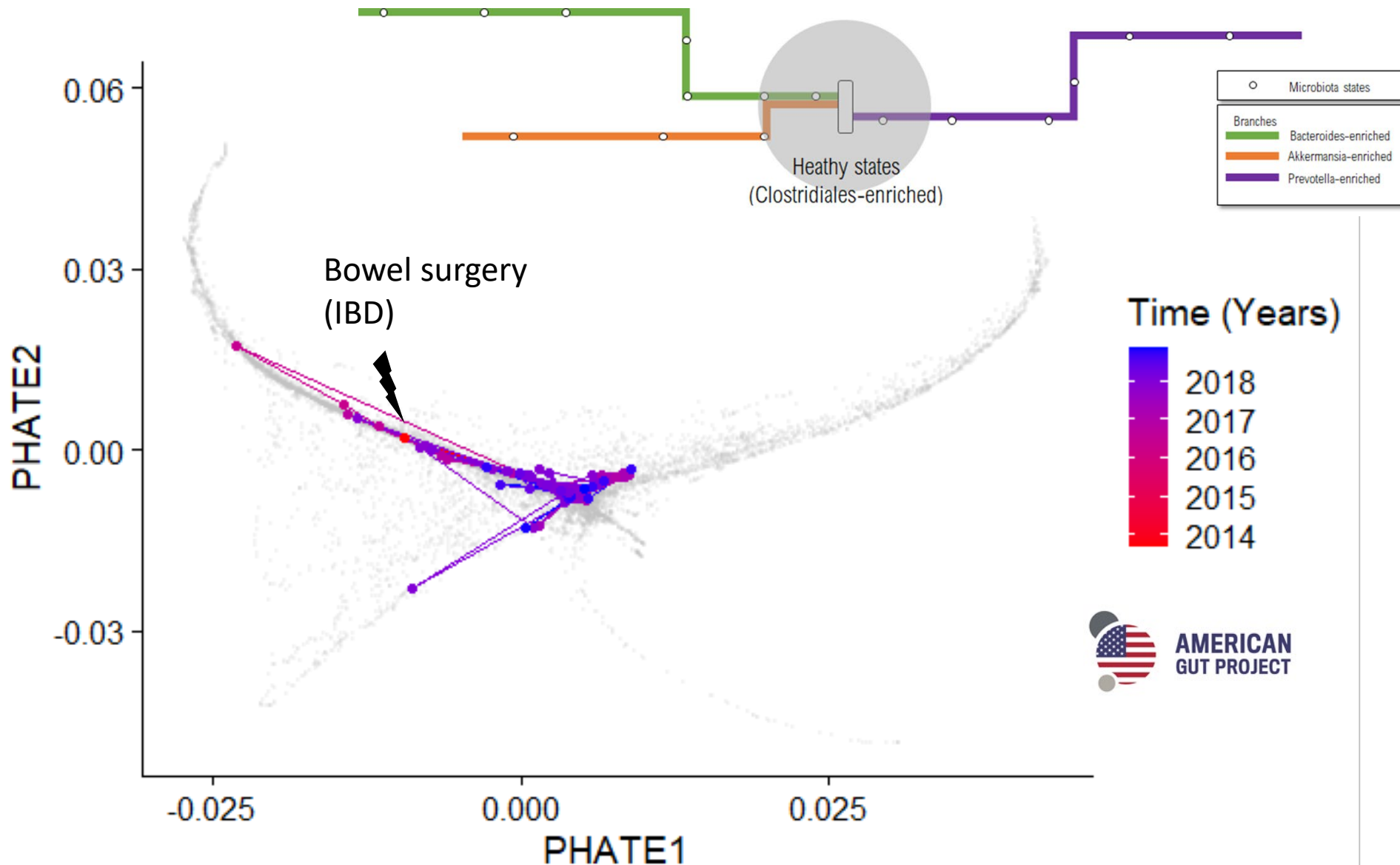
Faecalibacterium/Bacteroides as a tipping element explaining the switch between some states



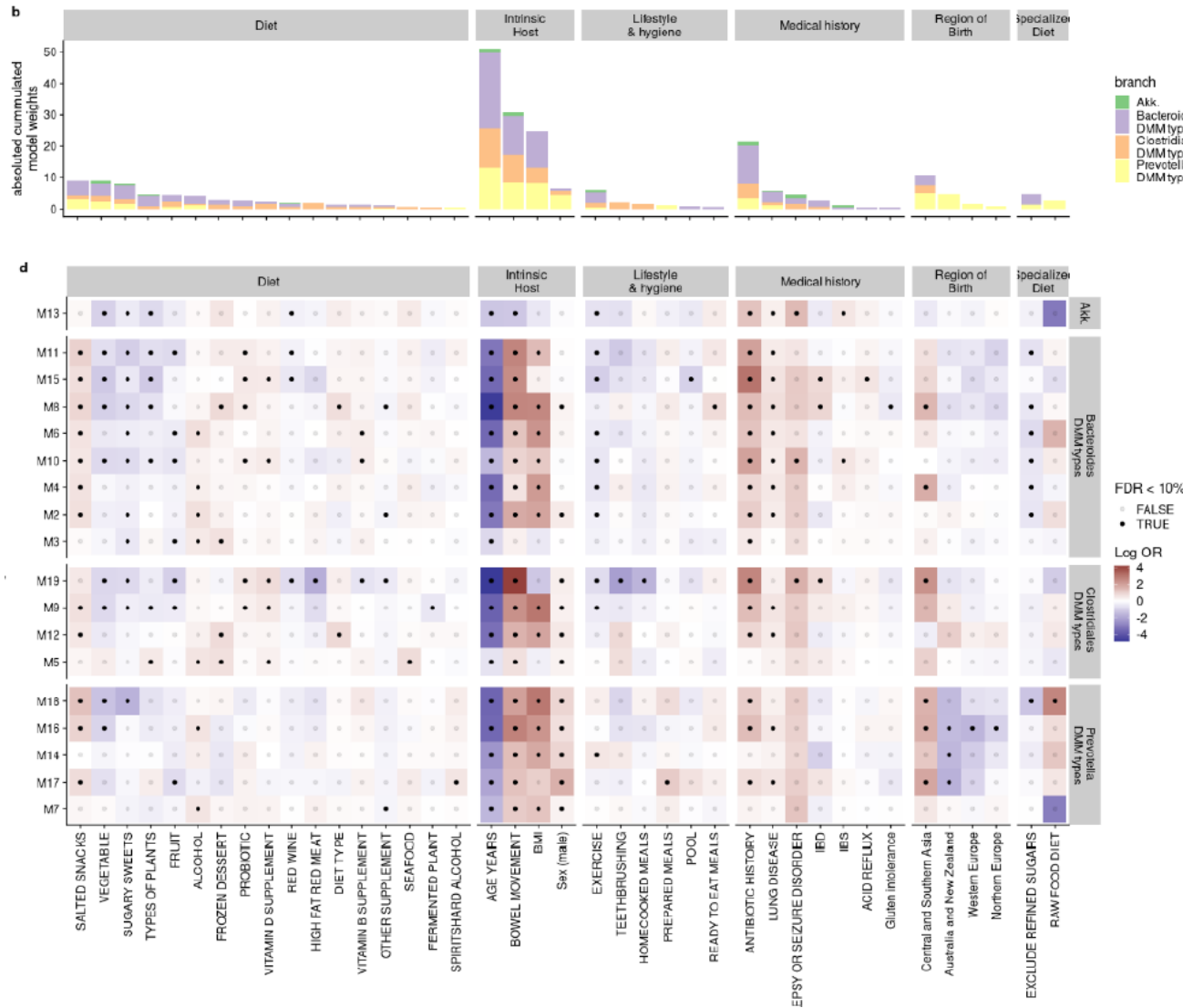
> Gut microbiome alternative stable states hypothesis



> Branches help to monitor gut microbiome recovery



➤ Gut microbiome states are differentially associated with host and env factors



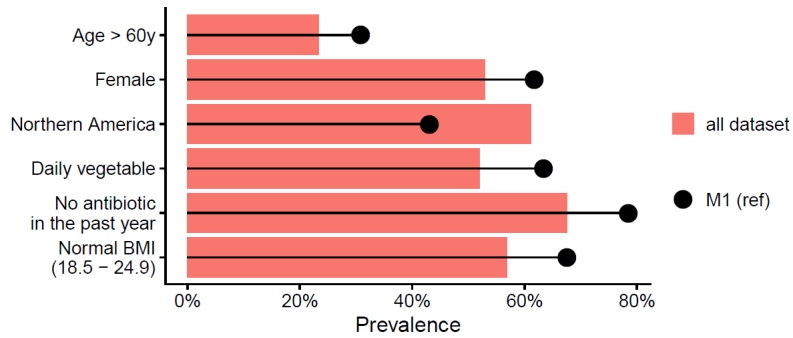
Sex, exercises frequency and **region of birth** associated differentially between branches

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

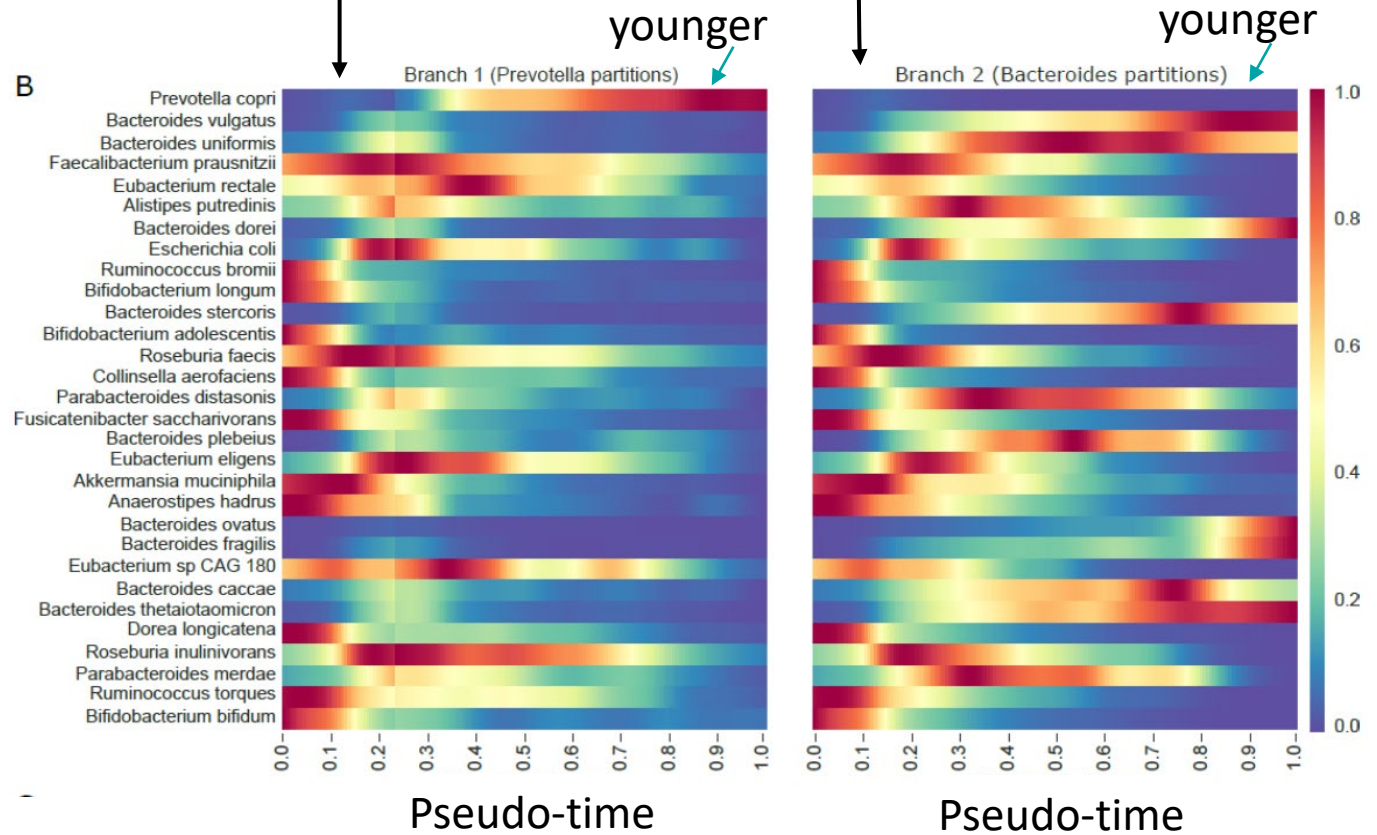
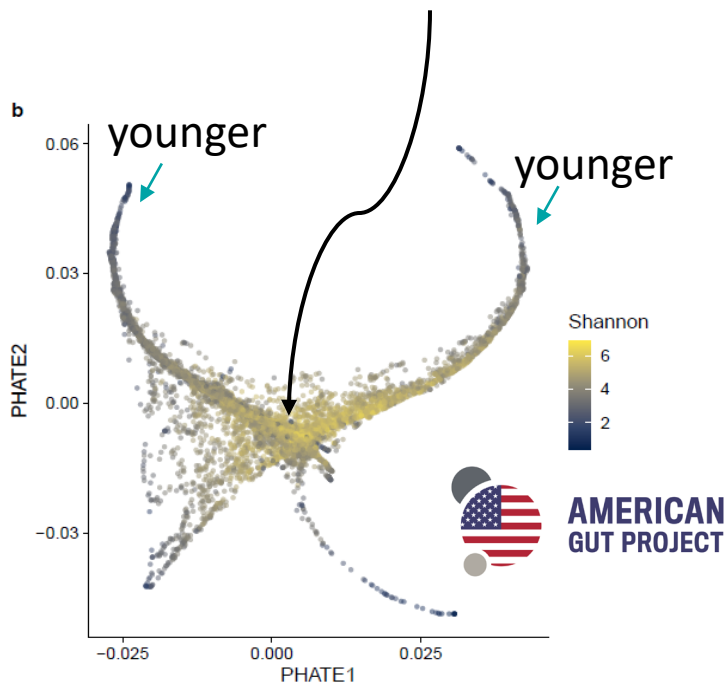
Specialized diet associated with altered state within *Prevotella* branch



> Do we already observe a intergenerationally mass extinction ?



Older and healthy diet and lifestyle

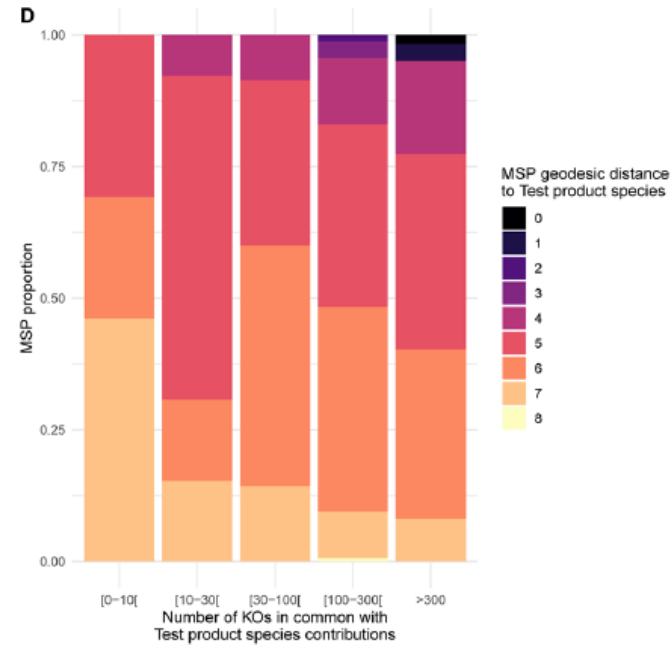
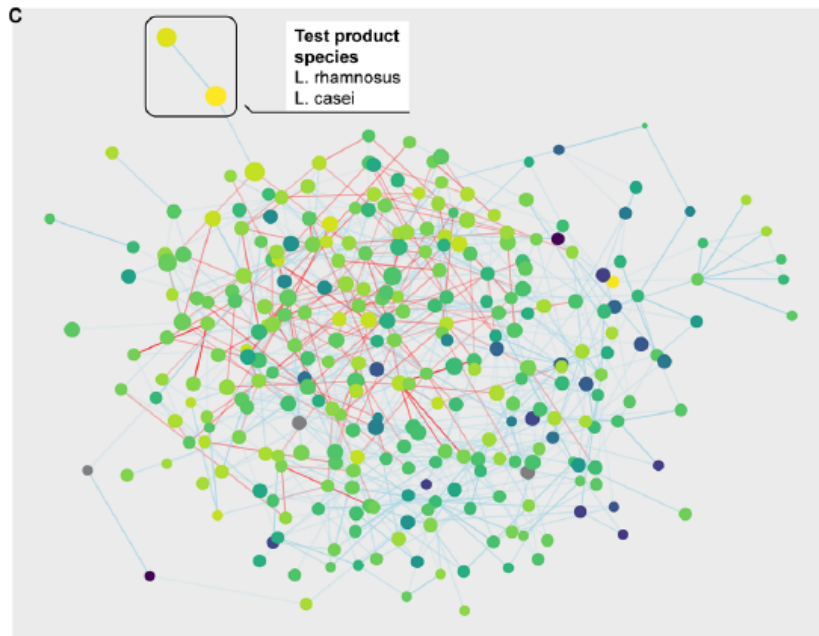


➤ Harnessing the microbial potential of fermented foods to avoid the point of no return



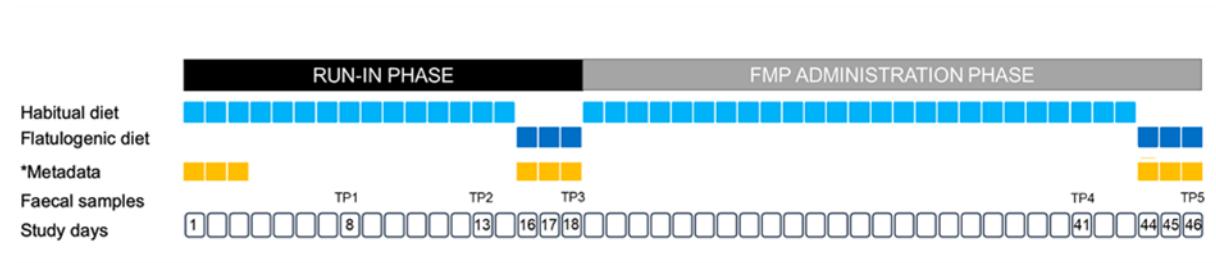
➤ Food microbiome engraftment is gut microbiome baseline dependent

Modular coalescence between gut and biotics species

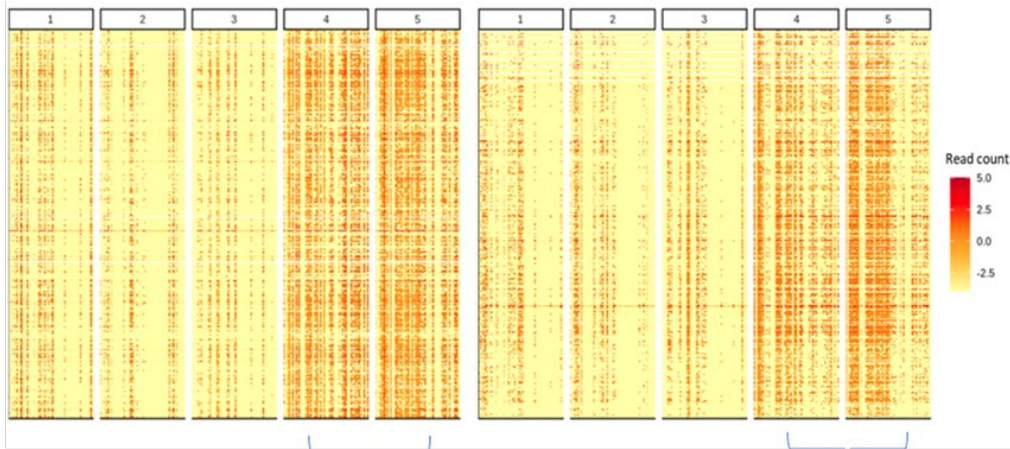


“Engraftment” as function of existing niche and metabolic pathway

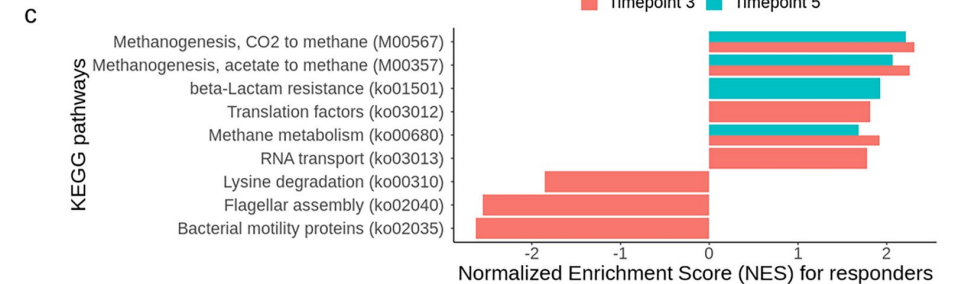
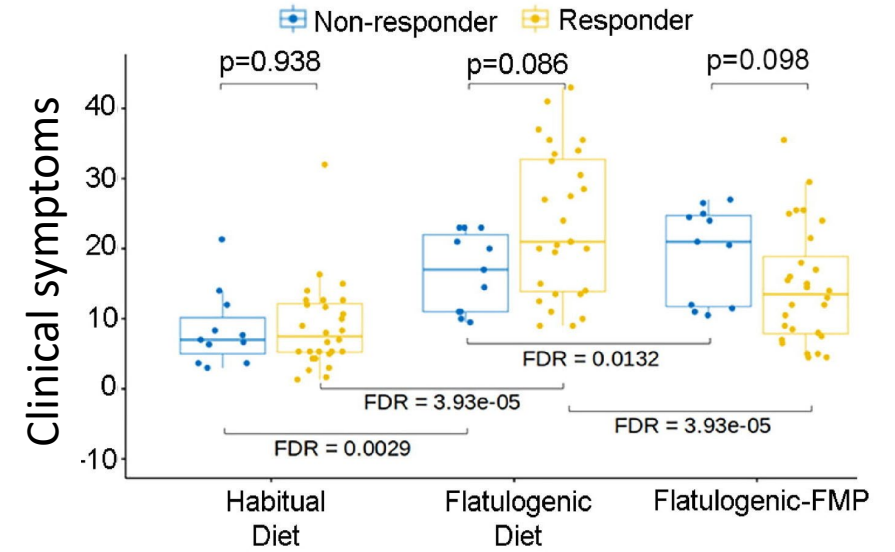
➤ Food microbiome clinical effect is gut microbiome baseline dependent



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

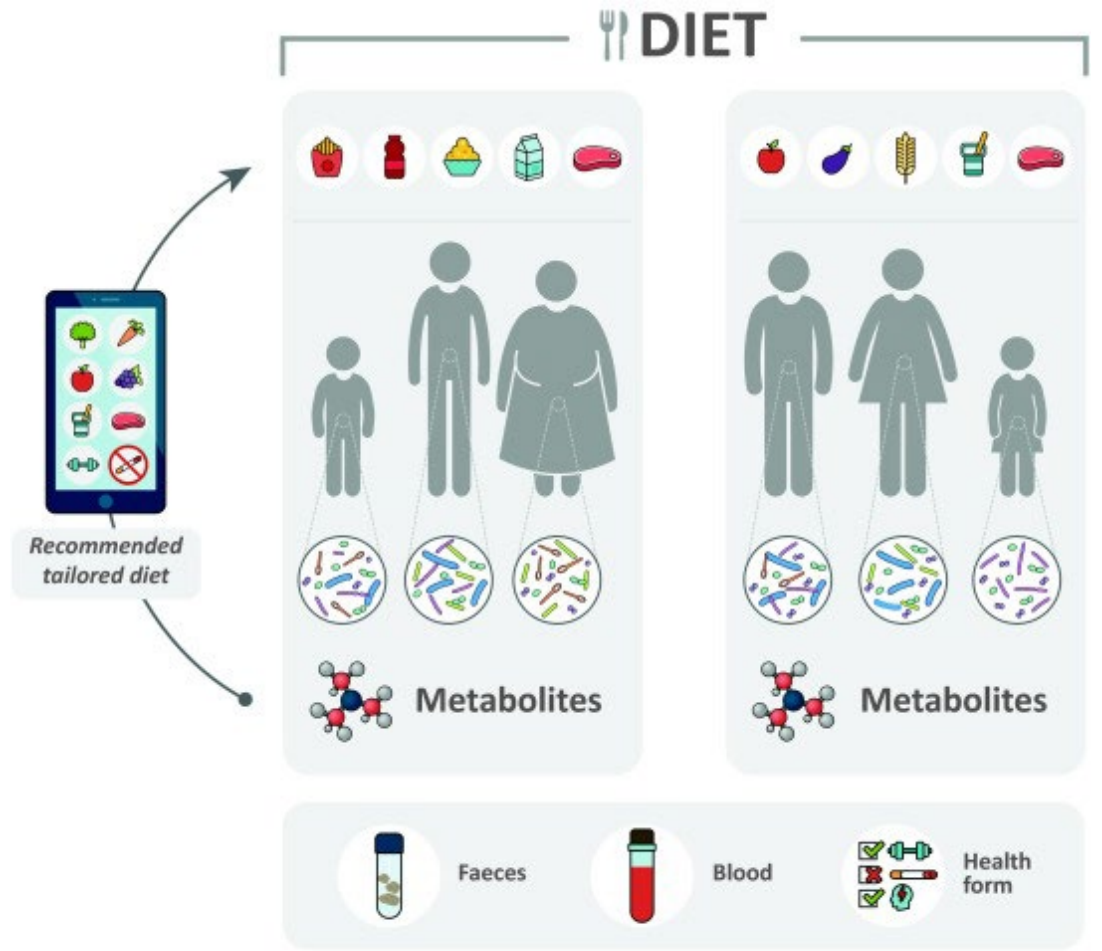
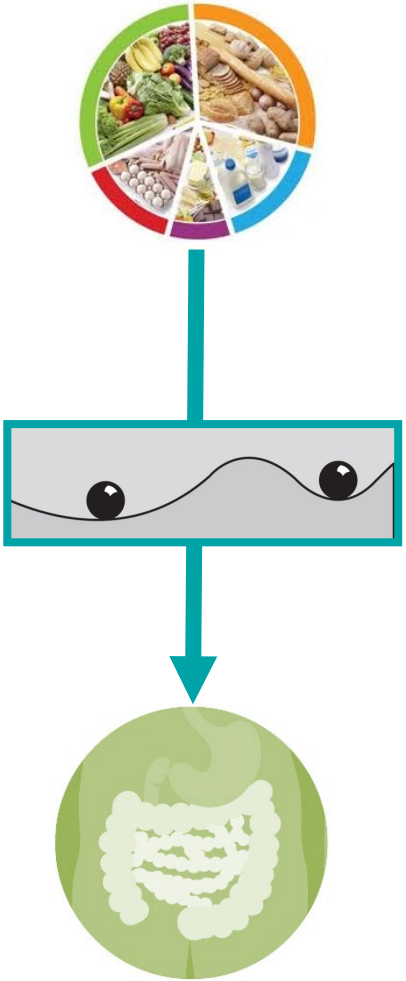


After FMP consumption, FMP active strains detected by metatranscriptomics



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

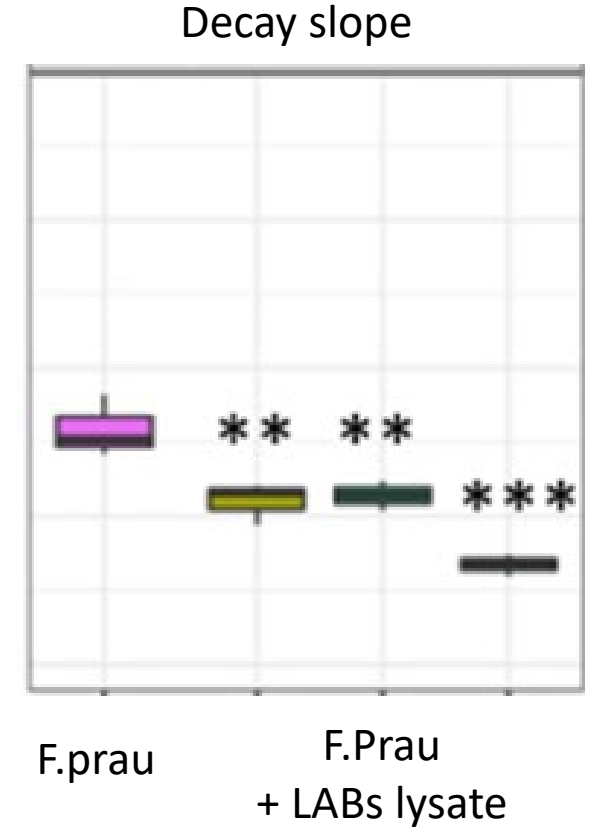
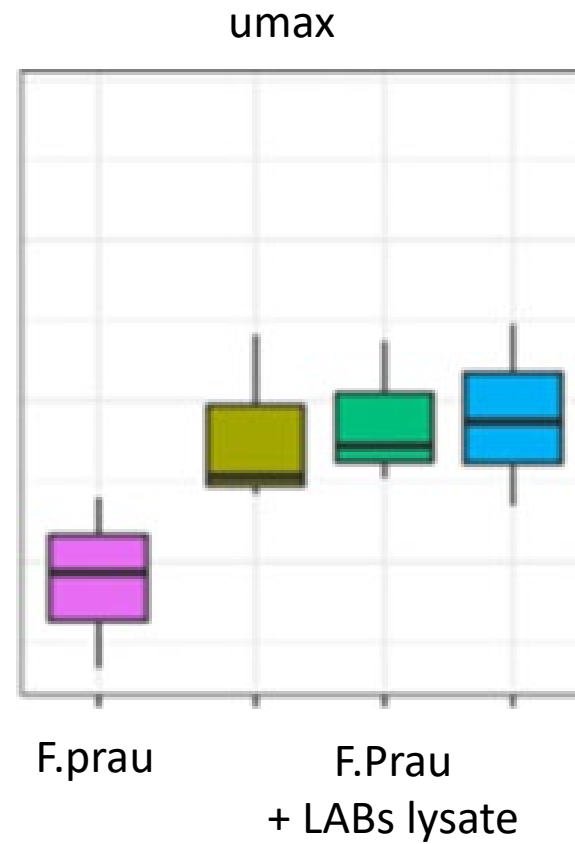
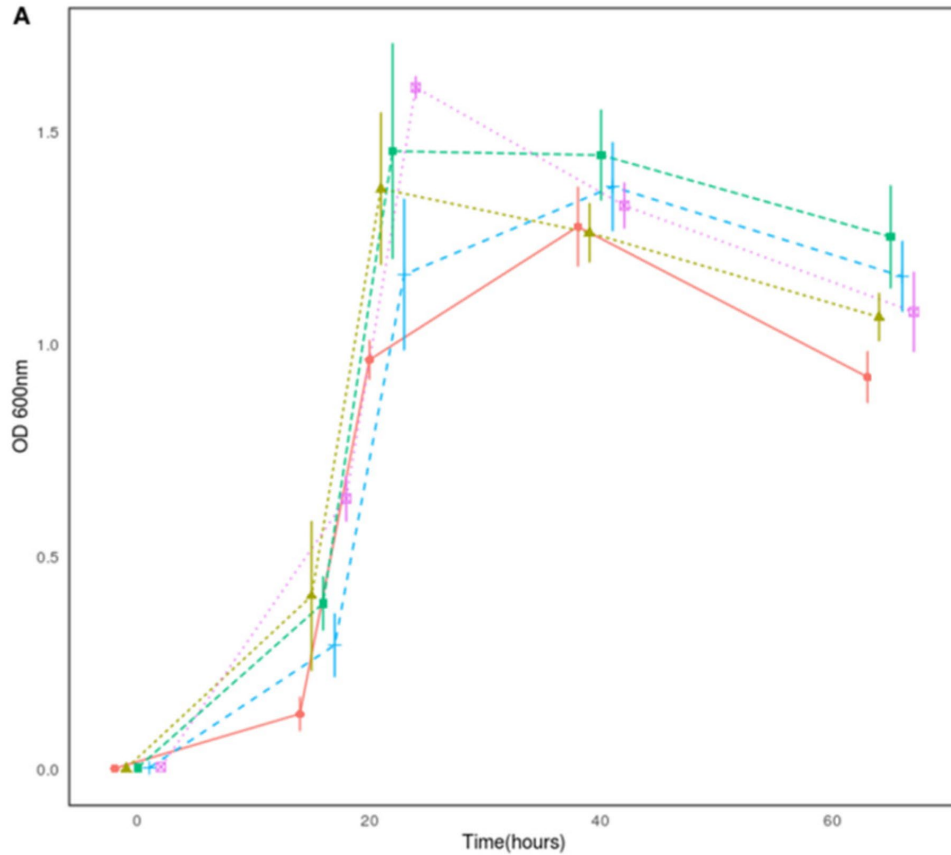
> From gut microbiome states to next-gen fermented foods design



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



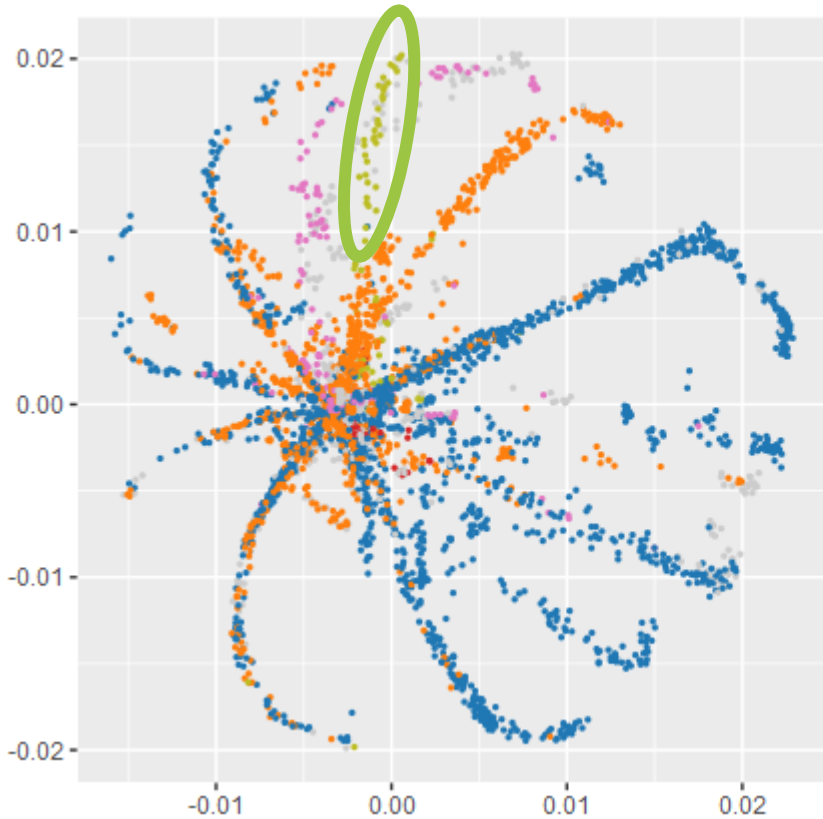
Increase of peptidoglycan levels for cell wall formation *F.prau*

Lebas, Derrien and colleagues (2020)



➤ Fermented food microbiome is shaped by deterministic dynamic processes

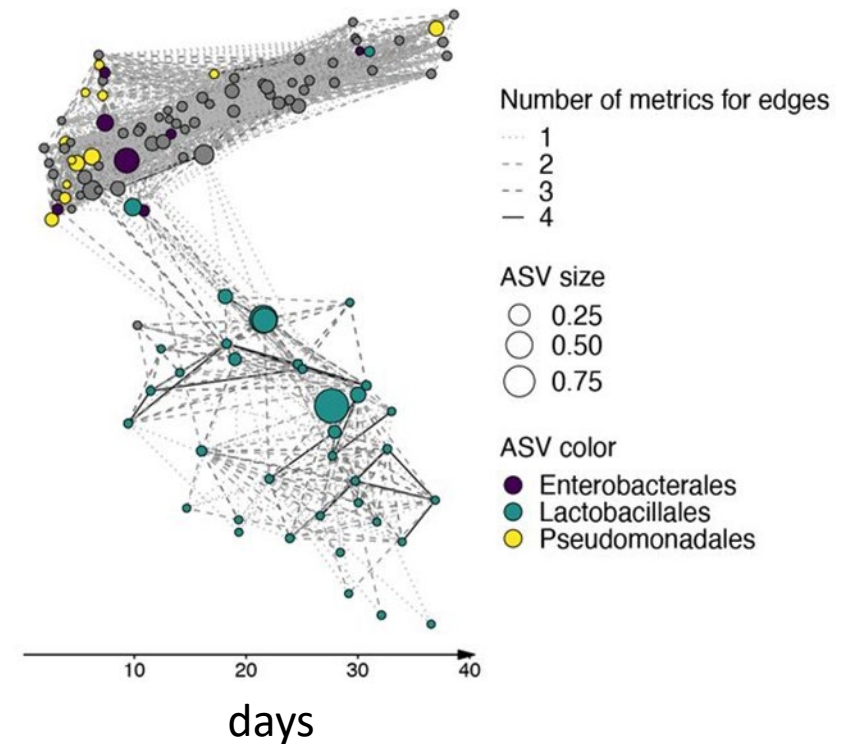
N = 4973 samples



Food categories

- Alcoholic beverages
- Meat and meat products
- Milk and dairy products
- Seasoning, sauces and condiments
- Vegetables and vegetable products
- Others

Kimchi dynamics



Junker *et al.* Biorxiv (2024)



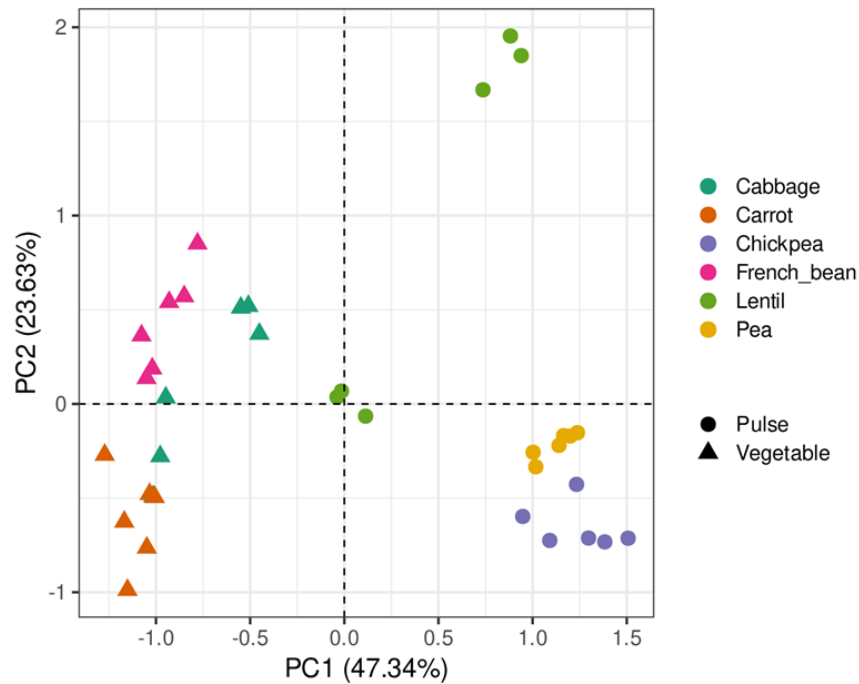
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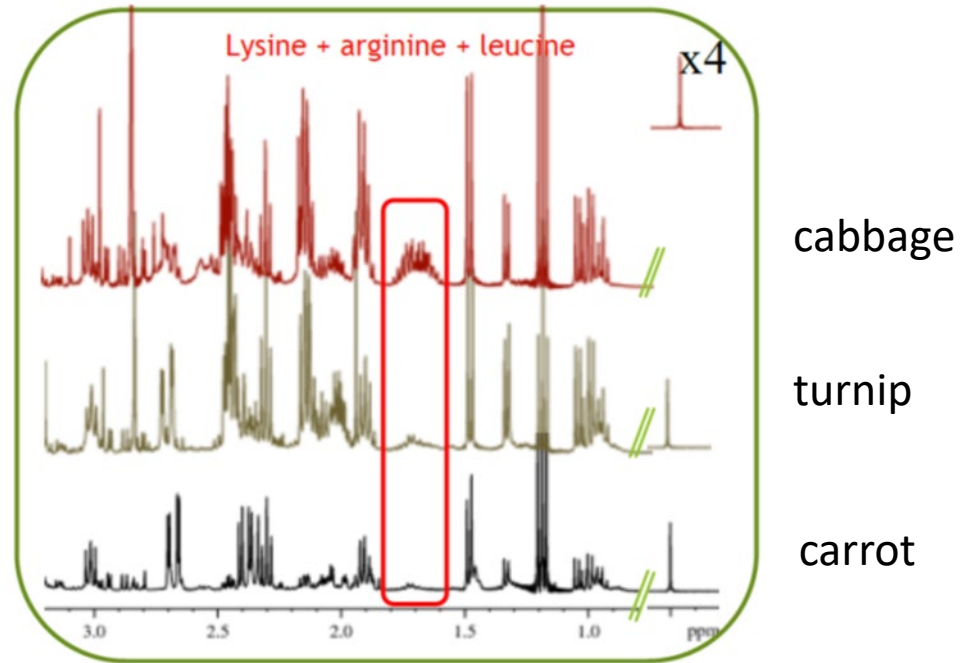
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➤ Plant-based matrices metabolome matters

Unfermented plant based matrices
LC-MS amino-acids profiles



Unfermented plant-based
NMR profiles



SayFood
Food & Bioproduct Engineering

Vincent Hervé

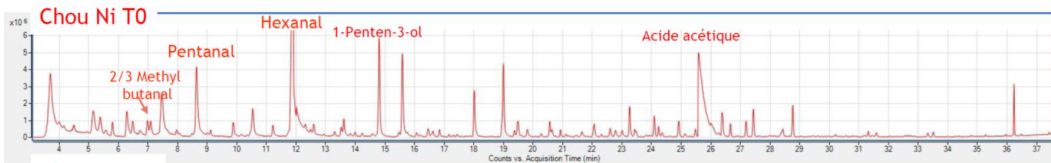


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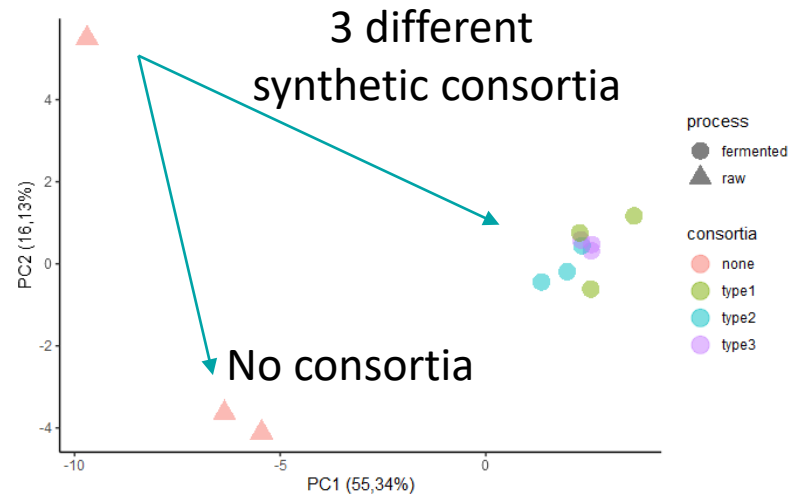
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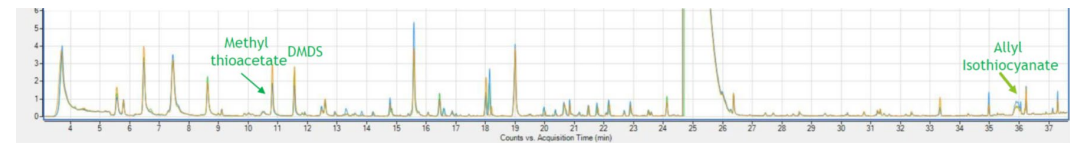
➤ Fermented plantbased food metabolome converge despite different synthetic consortia inoculation



Hexanal
Pentanal



Acetate
Esters
Volatile Sulfur Compounds



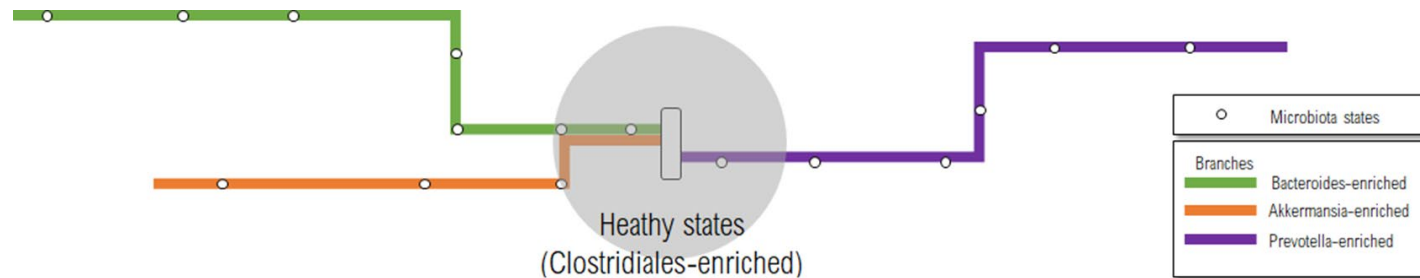
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> Take home messages

- 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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Marie Hélène Desmots

...



Marie-Christine Champomier-Vergès
Stéphane Chaillou

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