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

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► To cite this version:

Julien Tap, Vincent Hervé, Sophie Landaud, Dalal Werner, Marie-Helene Desmonts, et al.. Next-gen fermented food: Harnessing gut microbiome diversity and functions. *Metabolomics & Fermented Foods*, Netherlands Metabolomics Centre, Feb 2024, Utrecht, Netherlands. hal-04489205

HAL Id: hal-04489205

<https://hal.inrae.fr/hal-04489205>

Submitted on 4 Mar 2024

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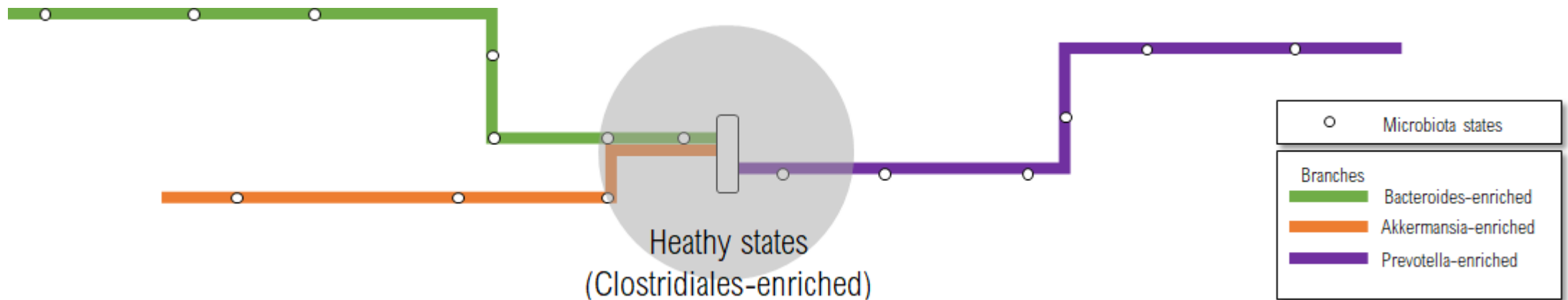
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> Next-gen fermented food: Harnessing gut microbiome diversity and functions.

Julien Tap
INRAE MICALIS
NMC Utrecht 2024

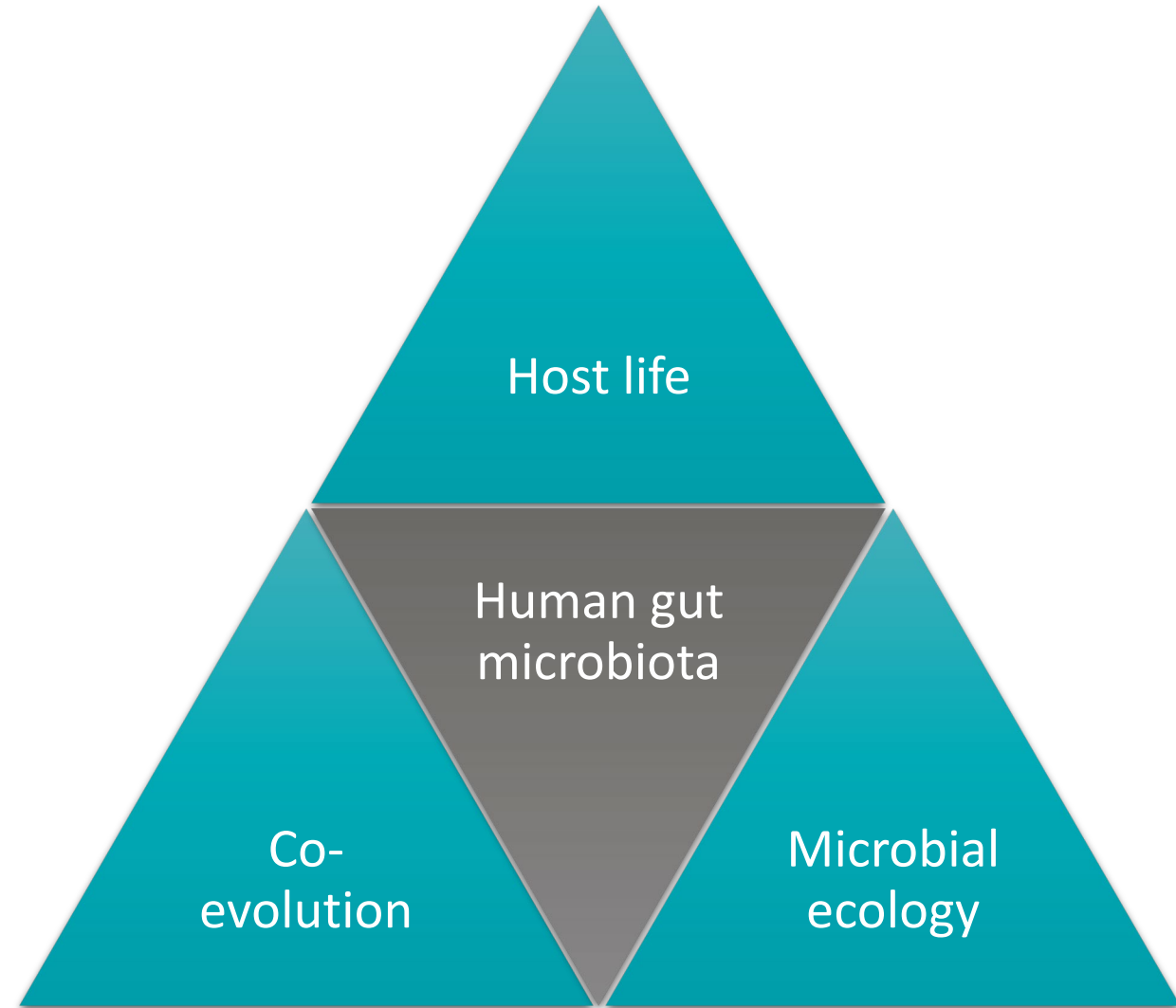
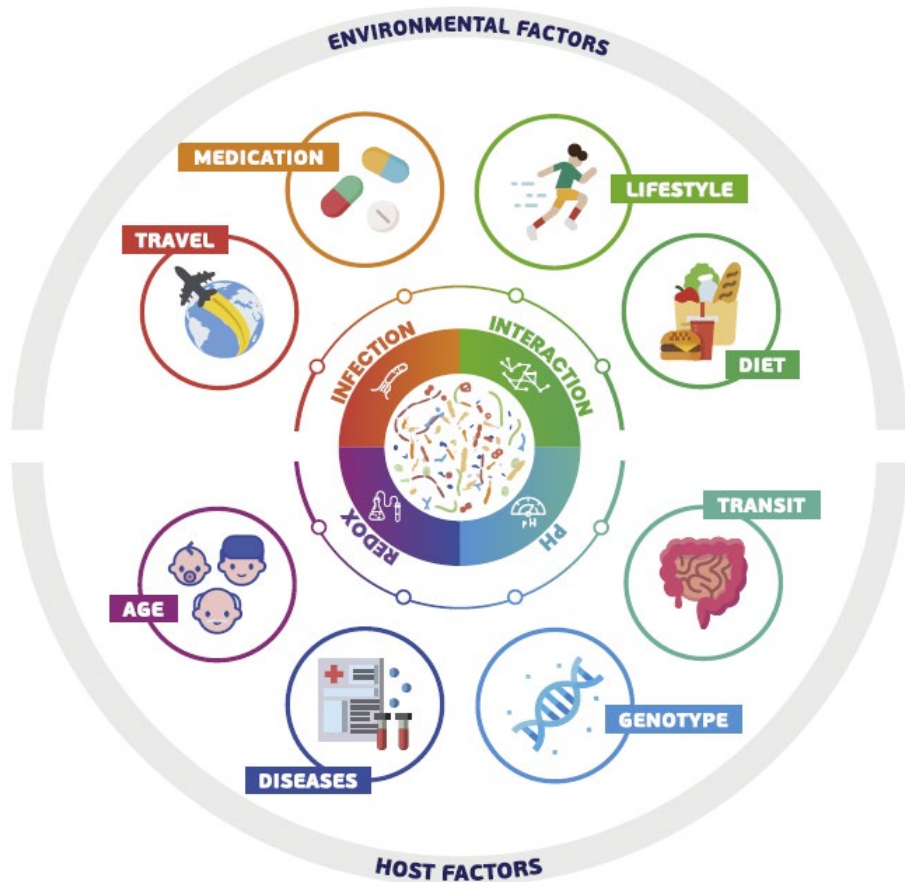


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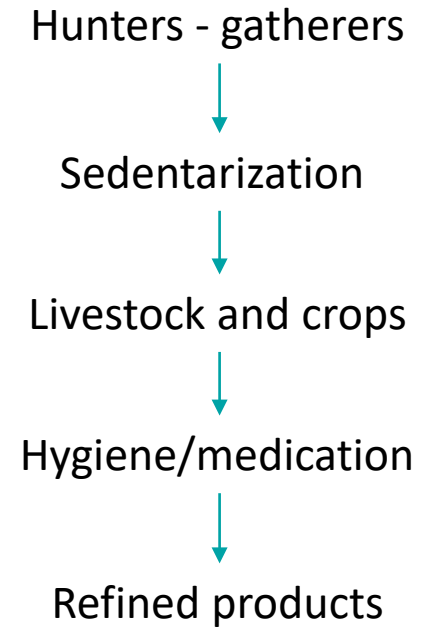
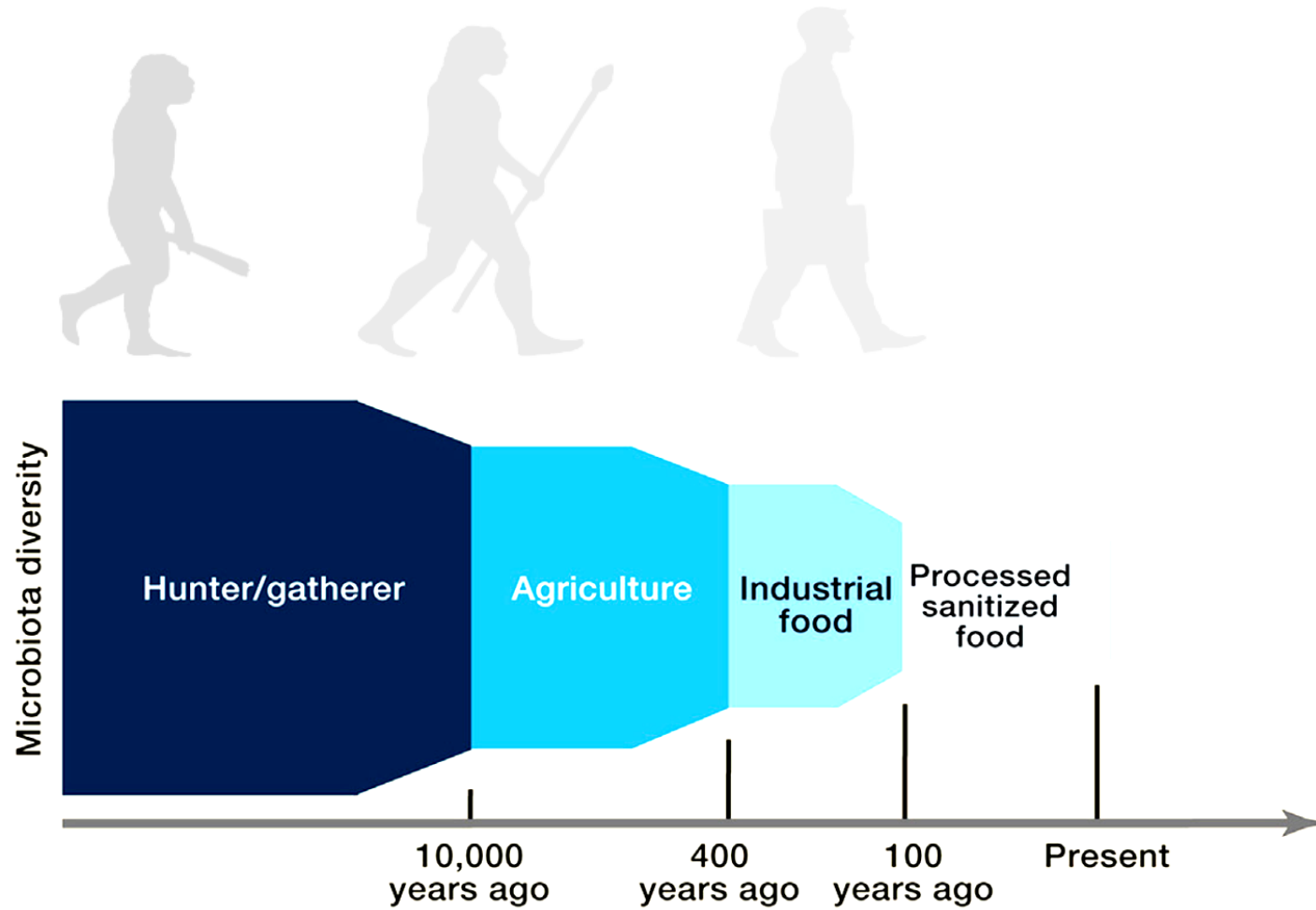
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➤ Different factors shapes the human gut microbiome

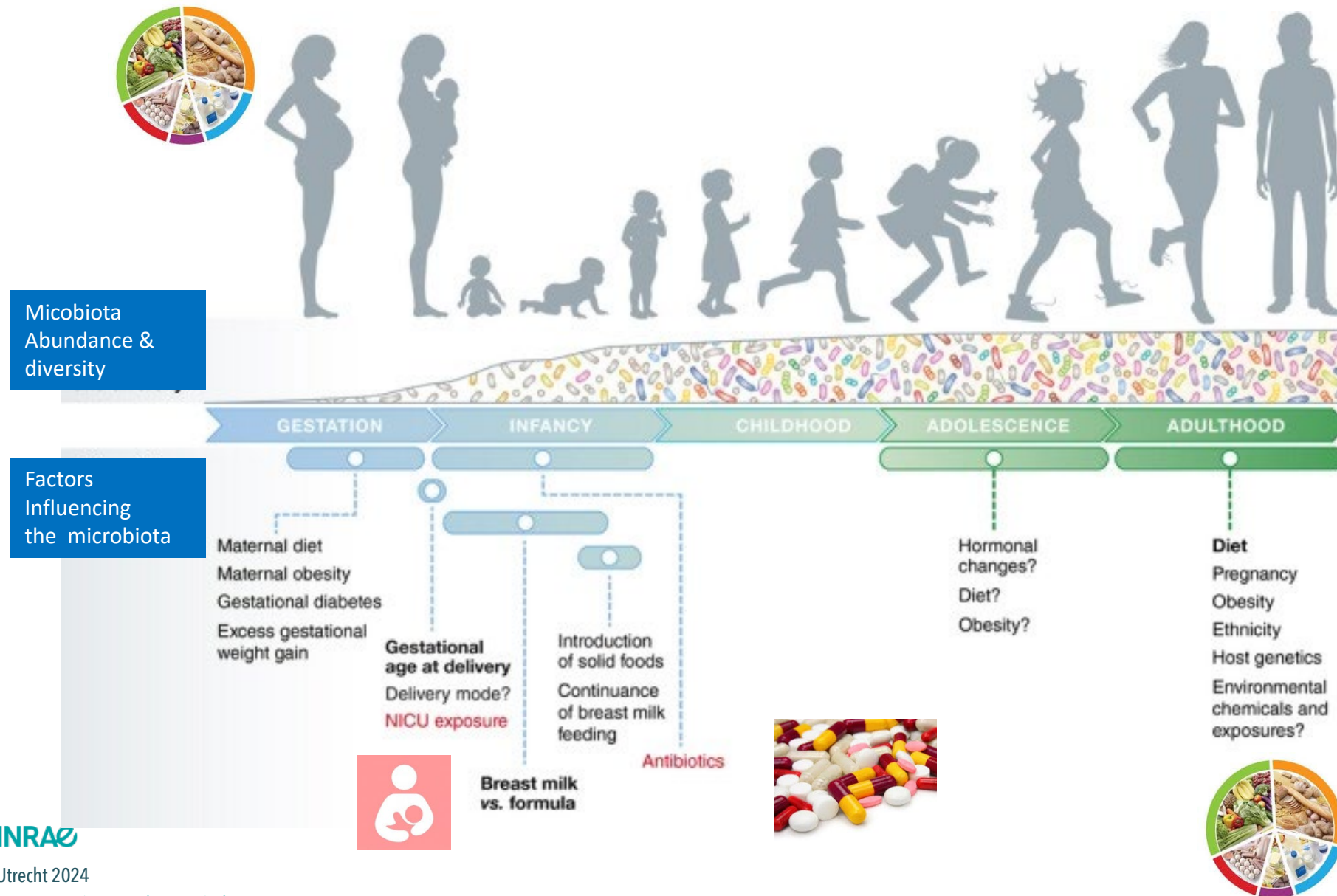


> Diet and lifestyle effect host microbiome symbiosis

Are we uncoupling our metagenome and our genome?



> Gut microbiome throughout life span



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➤ Microbiome states resilience as key factor



Healthy state



Resistance



Recovery

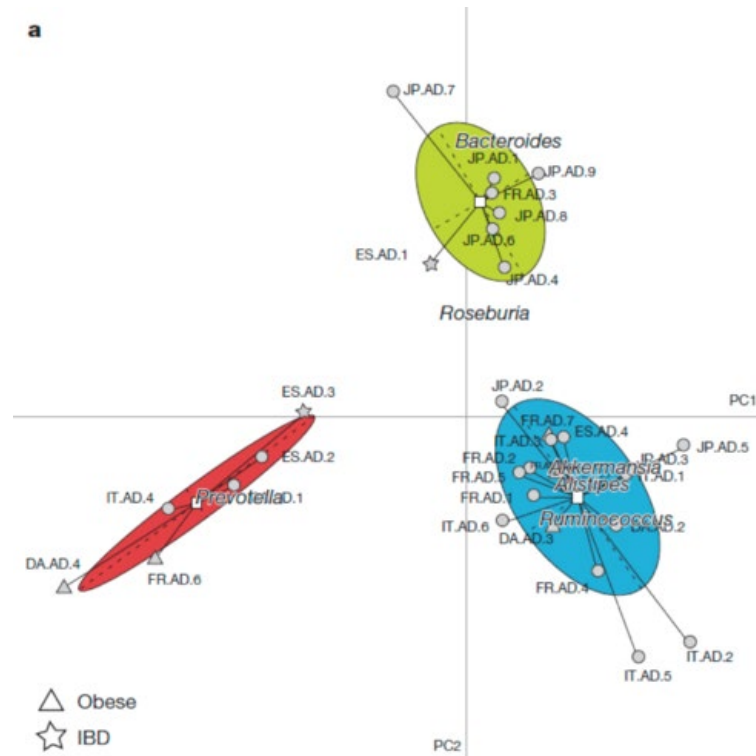
Resilience

Healthy state

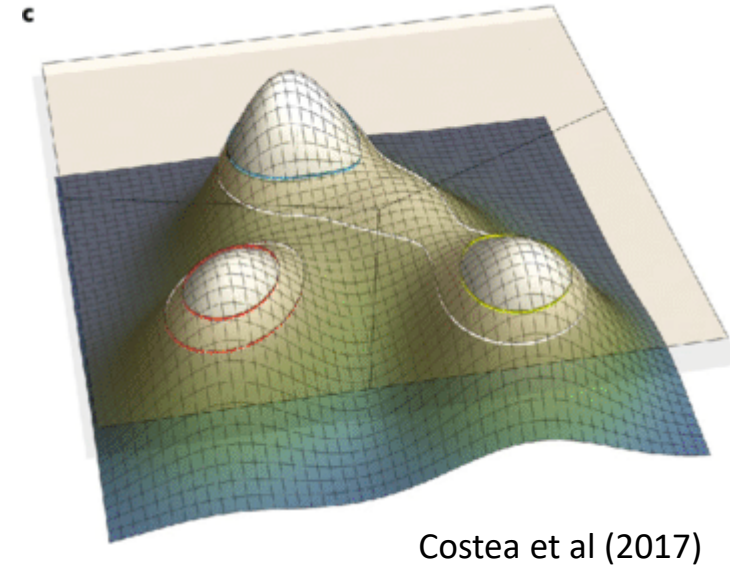


Degraded state

➤ Several attempts to decipher the gut microbiome structure



Arumugam, Raes et al (2010)



Costea et al (2017)

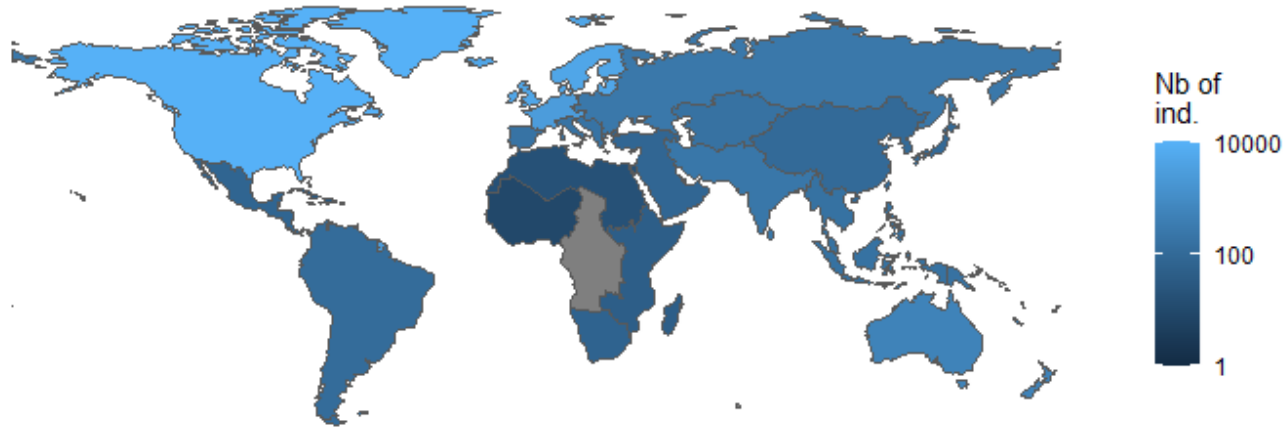
Dirichlet Multinomial Mixture (DMM) modeling

Limits:

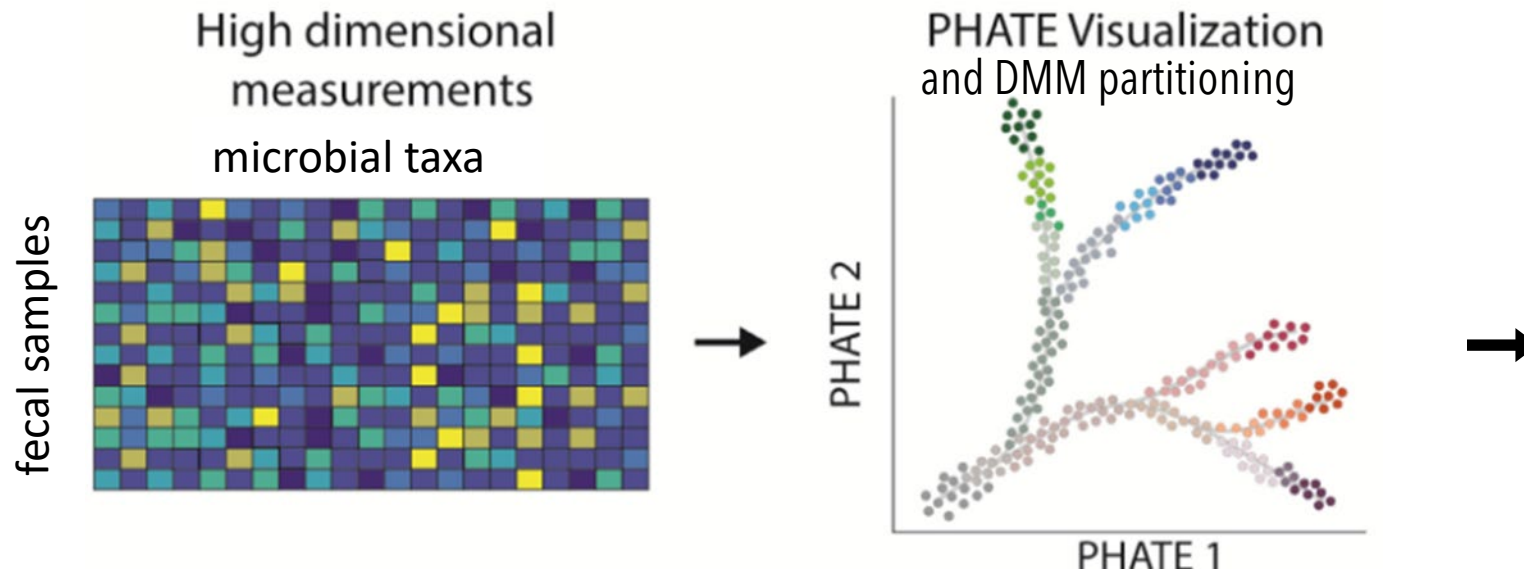
Few association with diet

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

➤ 35,000 human gut microbiome samples analyzed



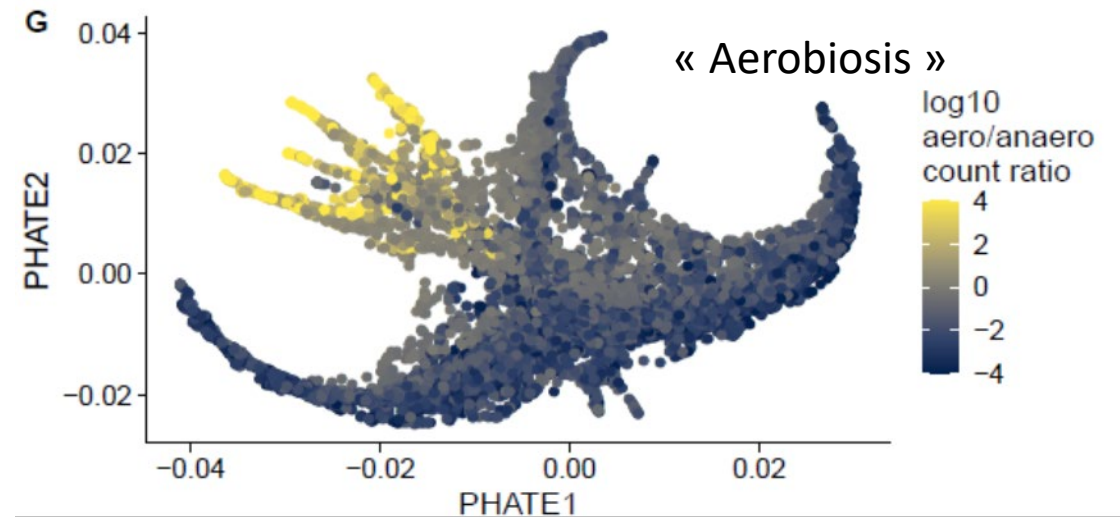
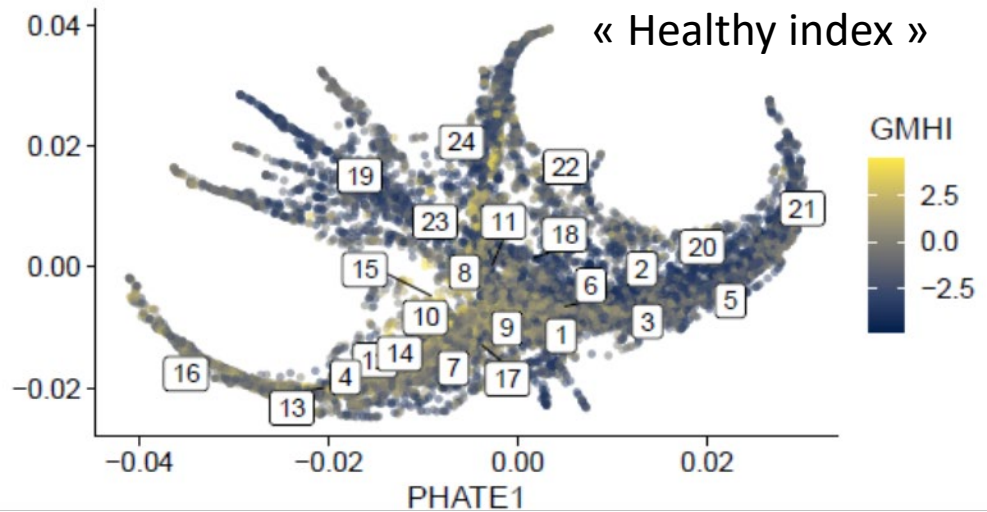
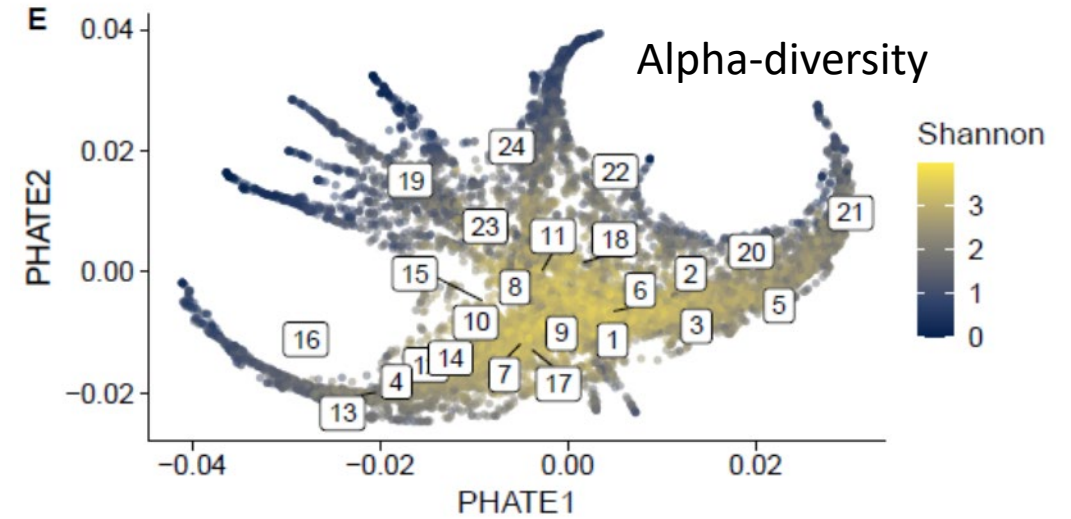
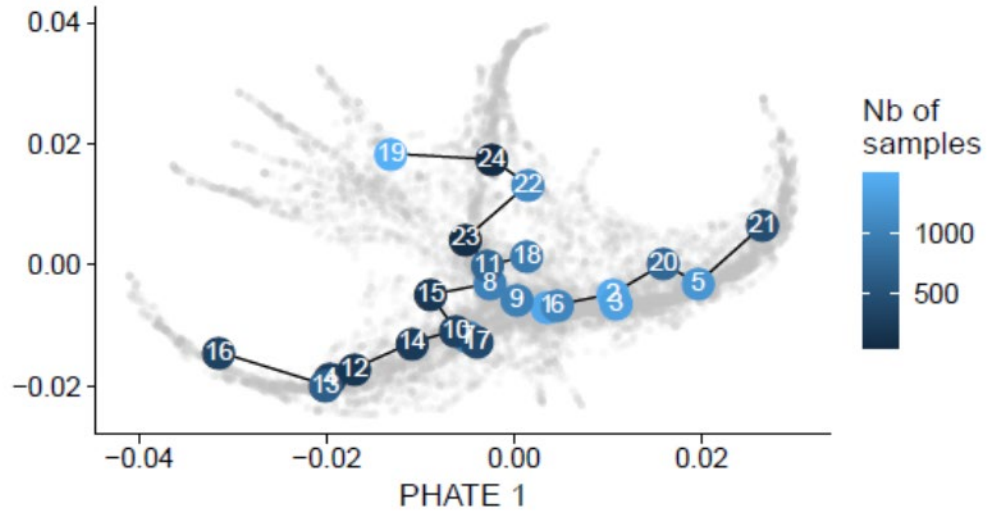
New computational method that help observe **global and local structure** at the same time



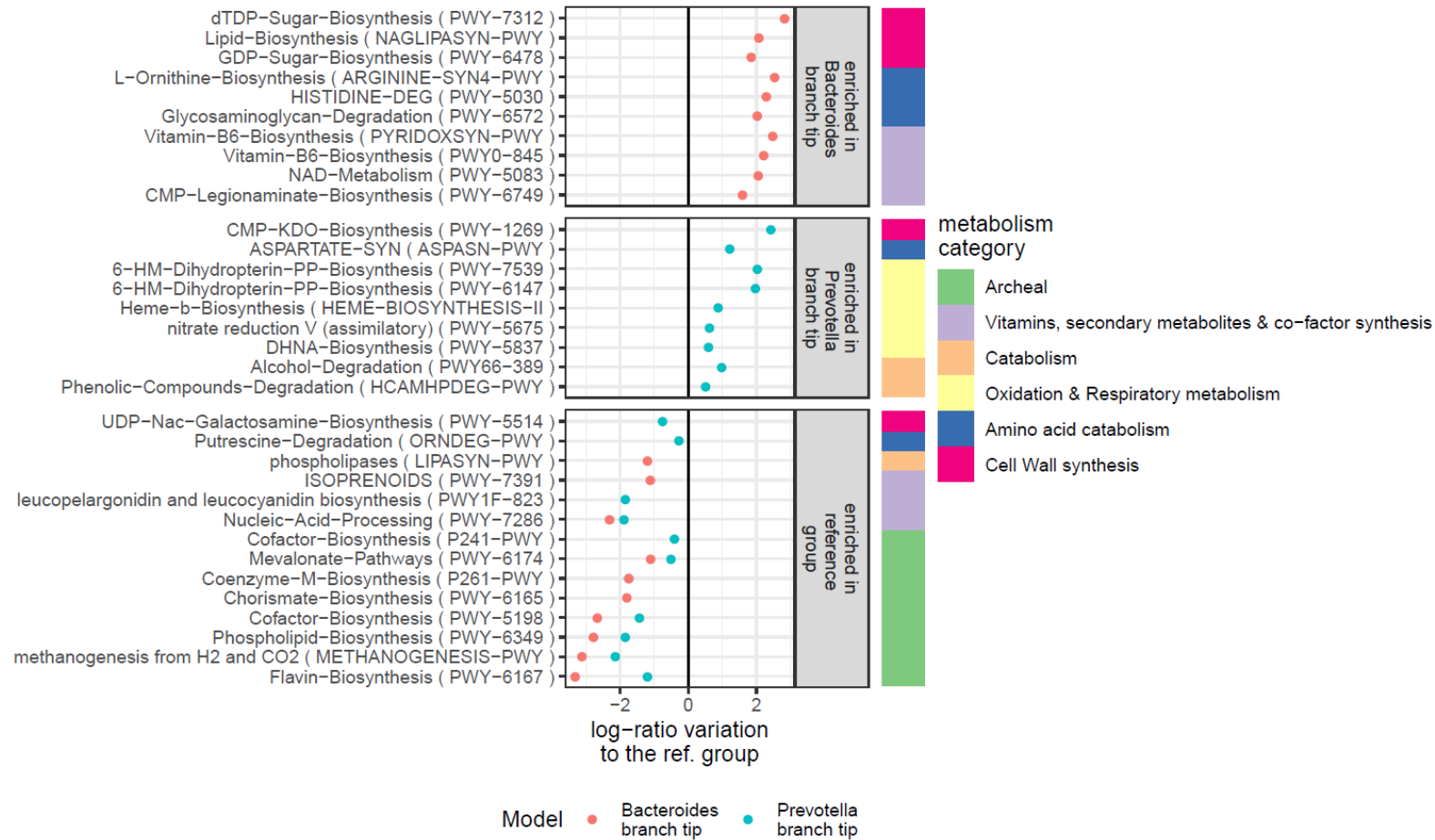
Time-series analysis to detect microbiome states

Region of birth, Lifestyle, diet, and health modelization

➤ Human Gut microbiome structured as branches



➤ Low-diversity tips of branches display functional shifts

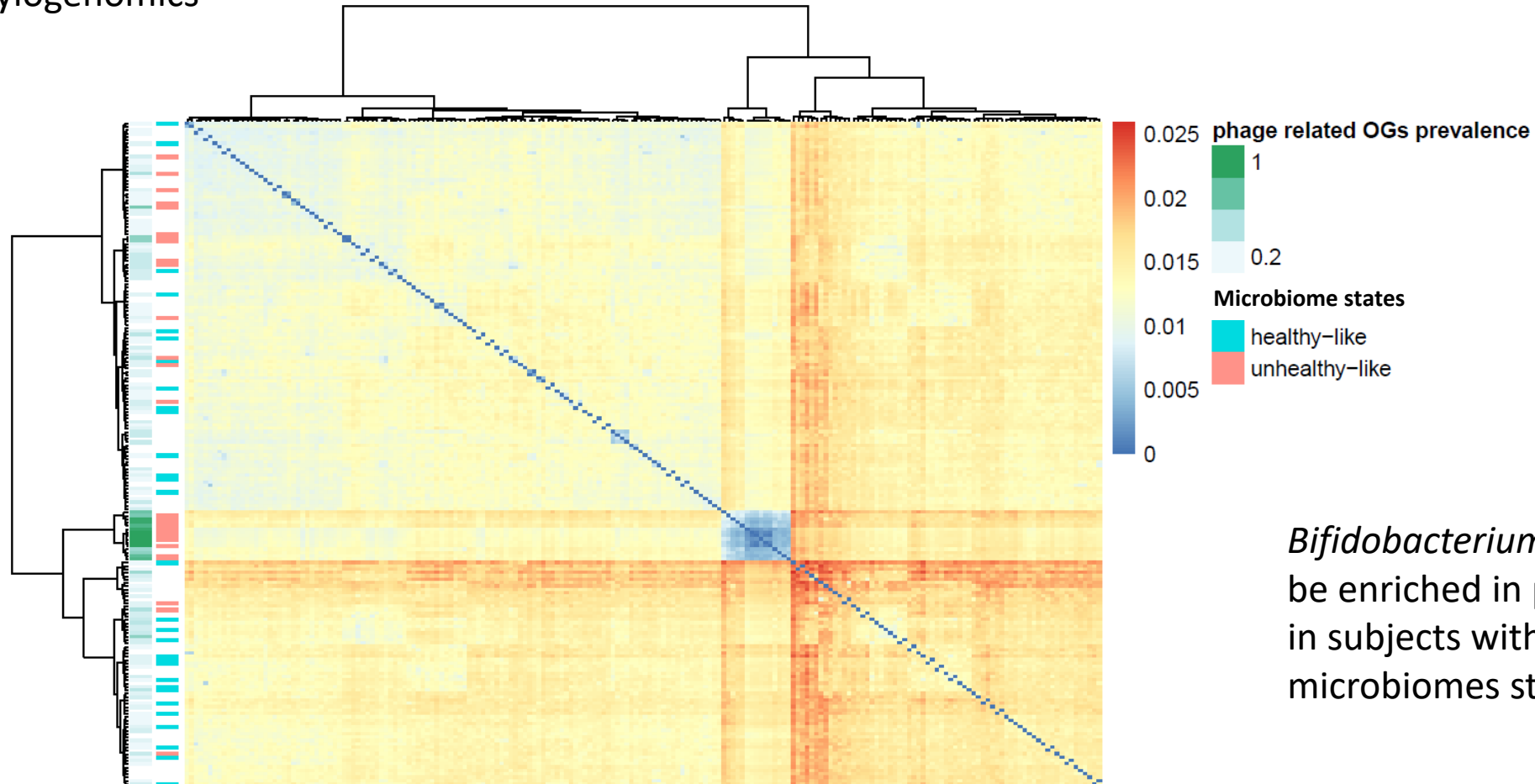


amino acid catabolism increase
in *Bacteroides* branch tip

oxidative stress response increase
in *Prevotella* branch tip

➤ Altered states showed functional differences within species

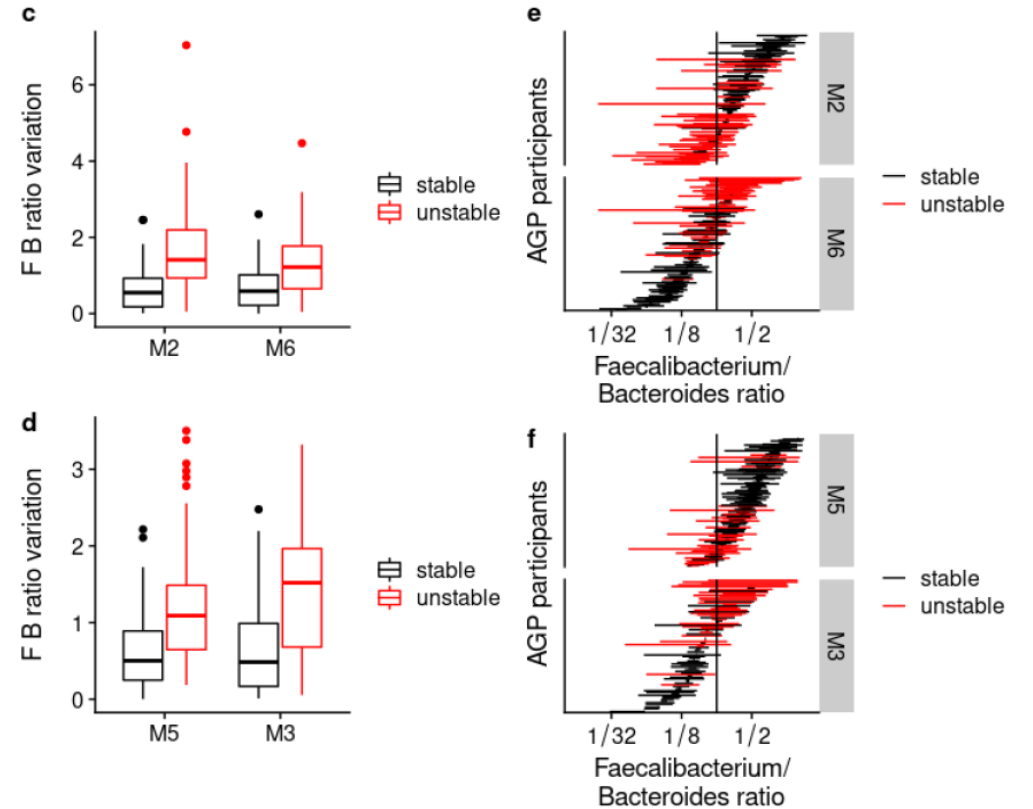
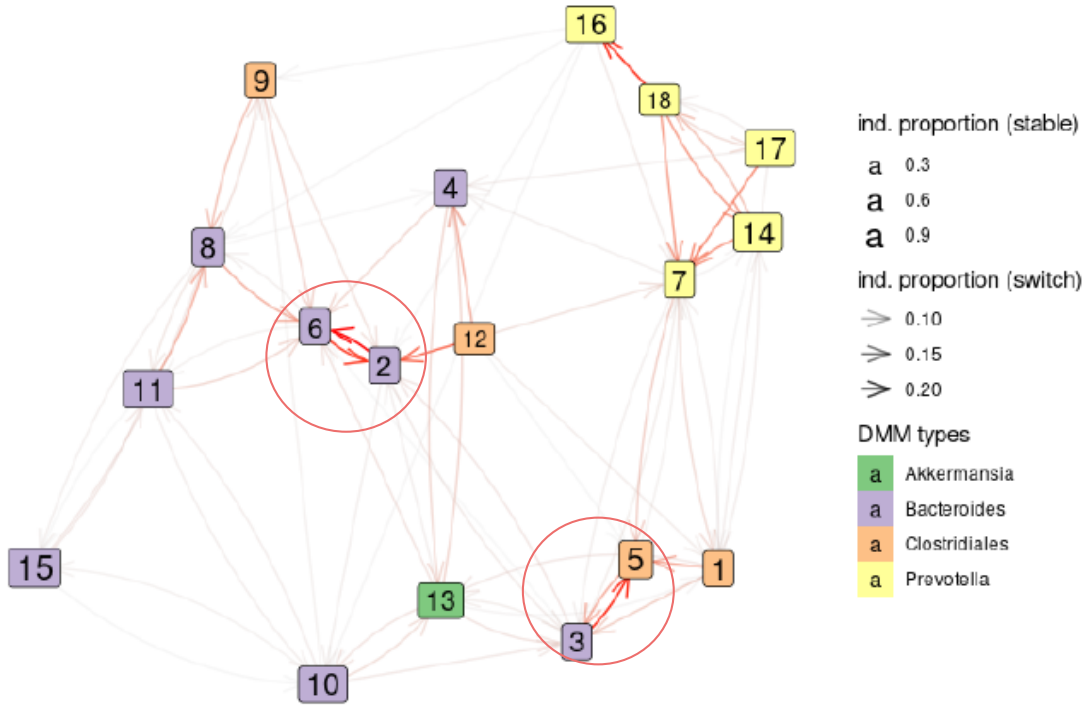
400 *B. bifidum* MAGS
phylogenomics



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

➤ Dynamics between partitions are associated to branches

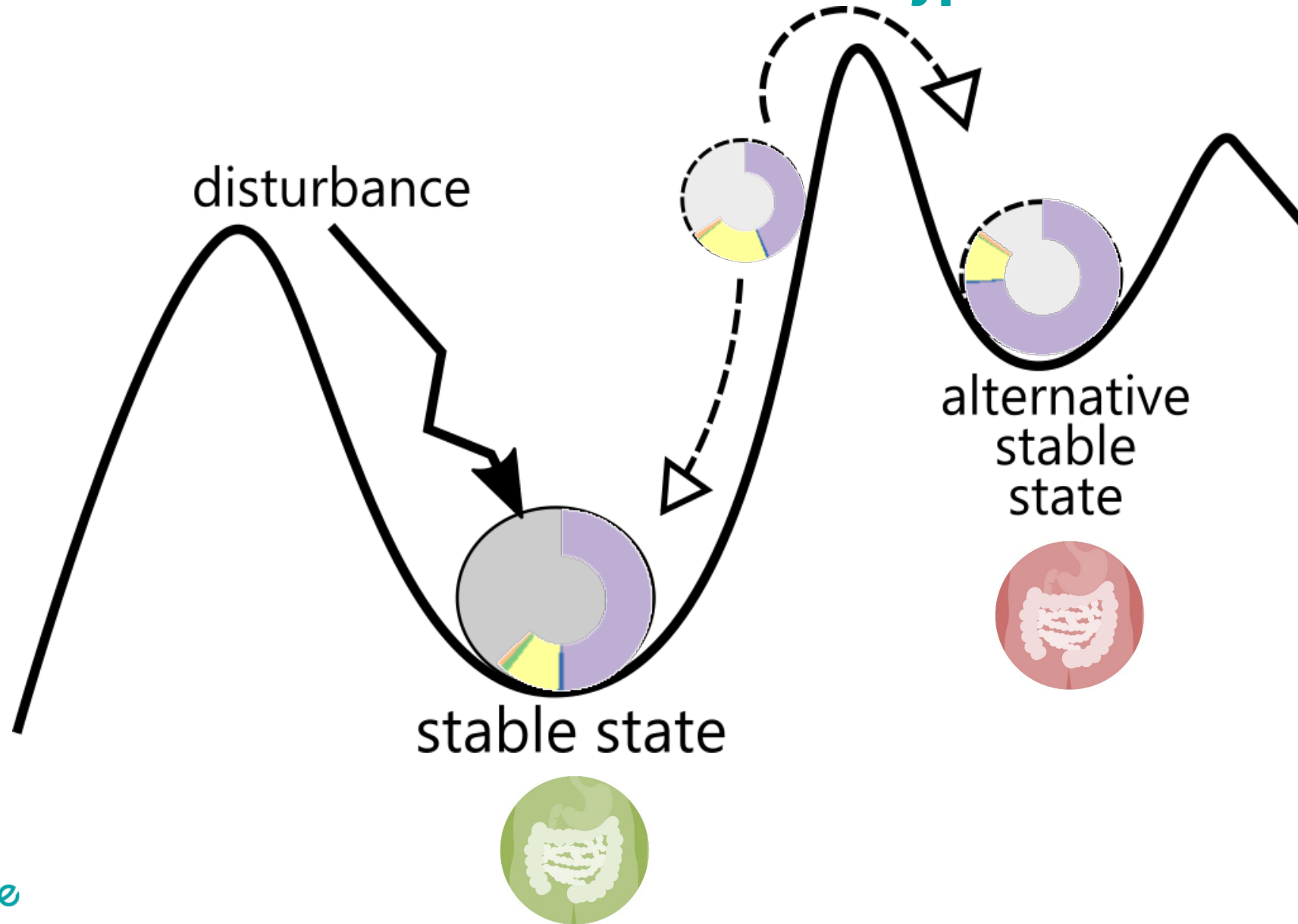
827 participants 2,998 samples 2,171 time-pairs



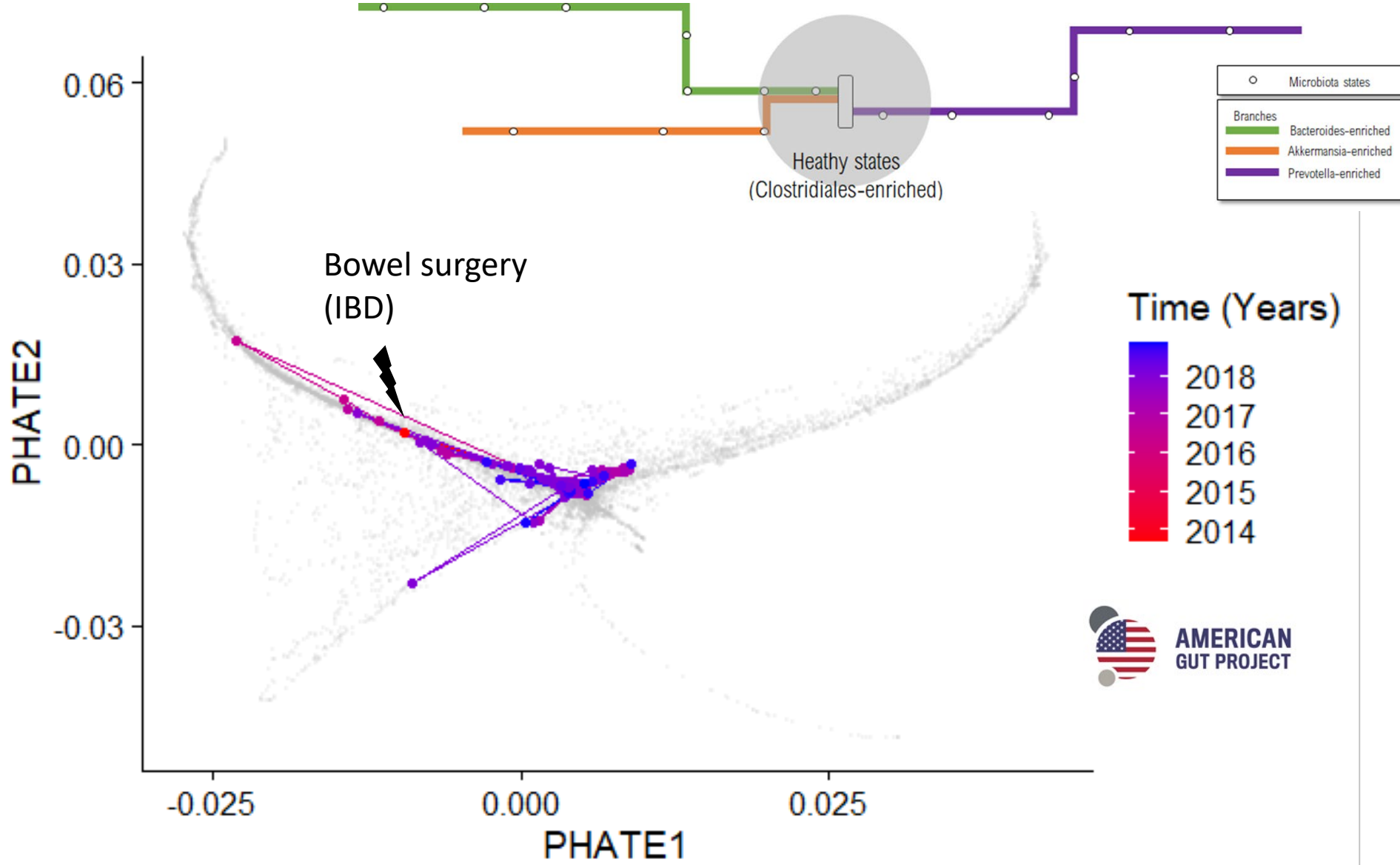
Faecalibacterium/Bacteroides as a tipping element explaining the switch between some states



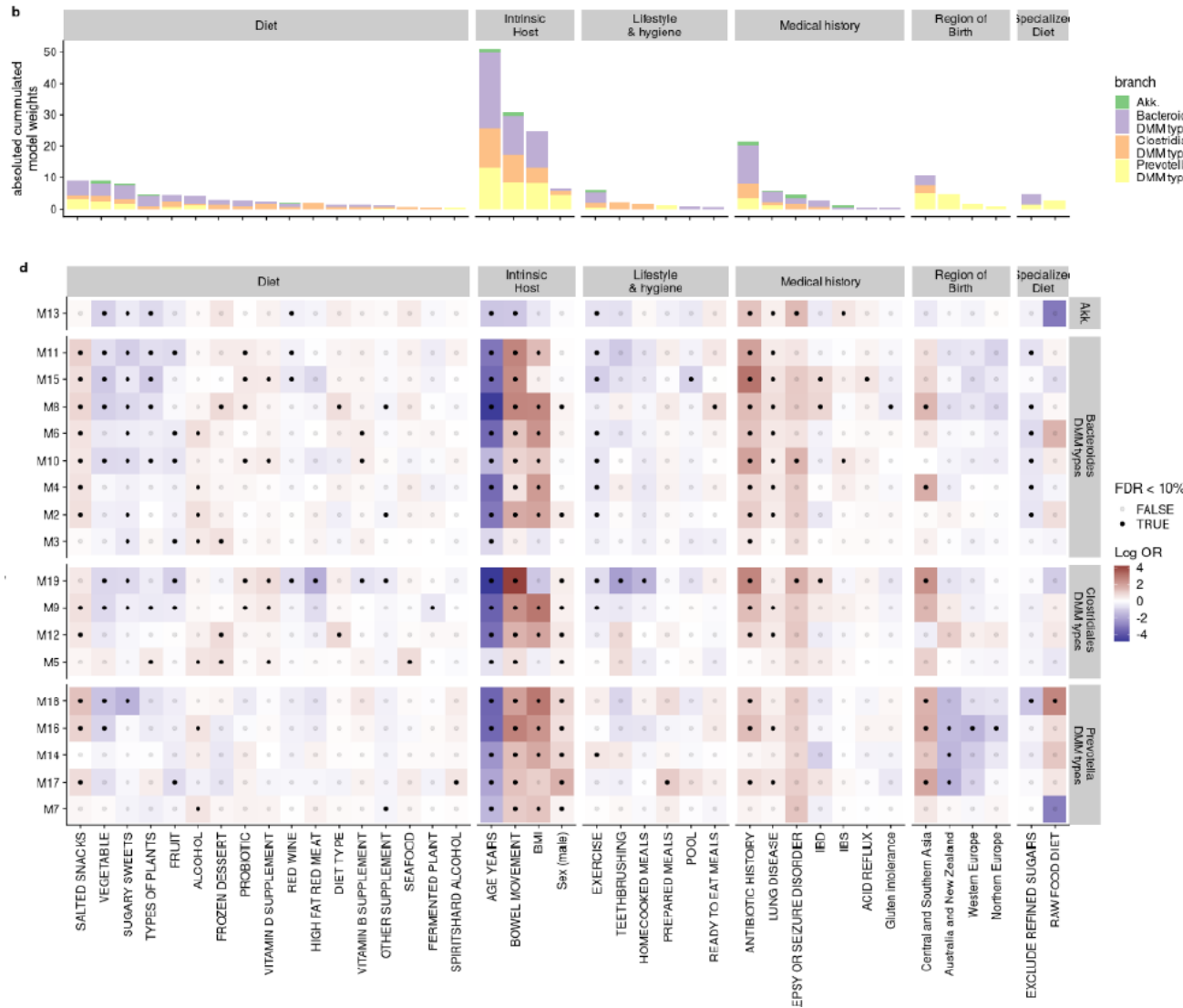
> Gut microbiome alternative stable states hypothesis



> Branches help to monitor gut microbiome recovery



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



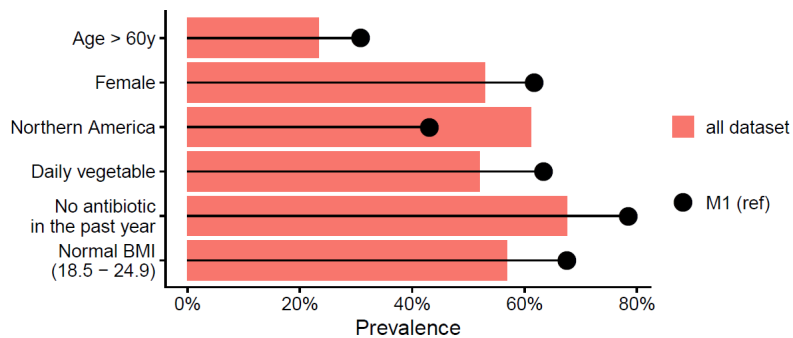
Sex, exercises frequency and **region of birth** associated differentially between branches

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

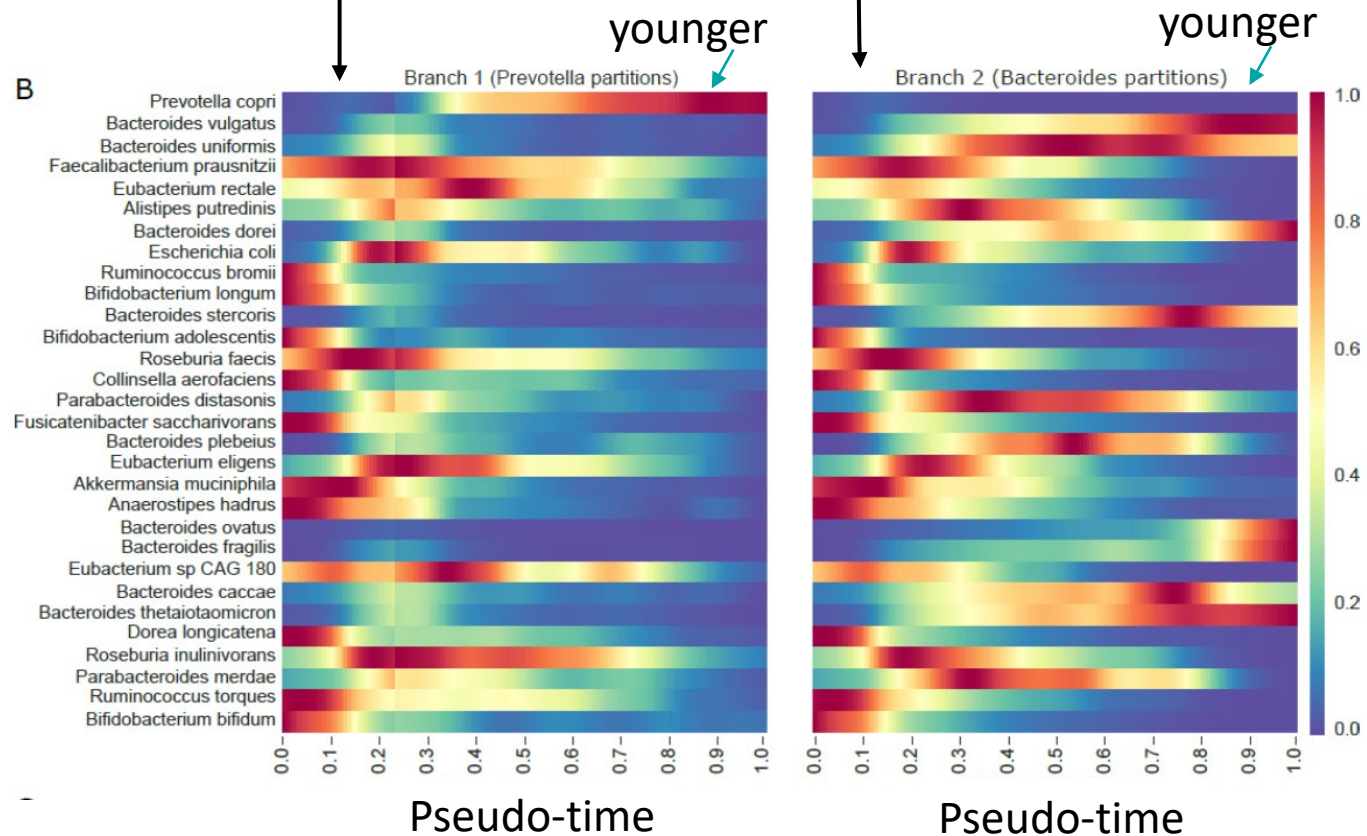
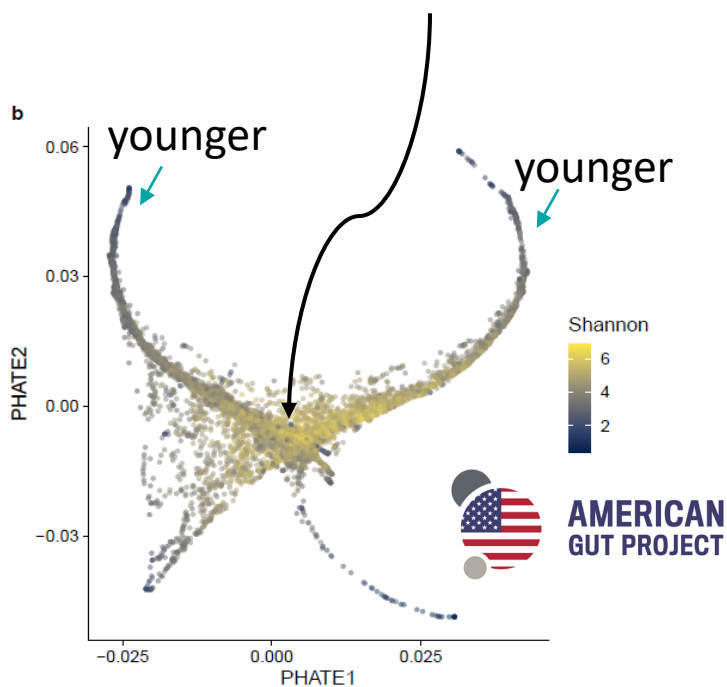
Specialized diet associated with altered state within *Prevotella* branch



> Do we already observe a intergenerationally mass extinction ?



Older and healthy diet and lifestyle

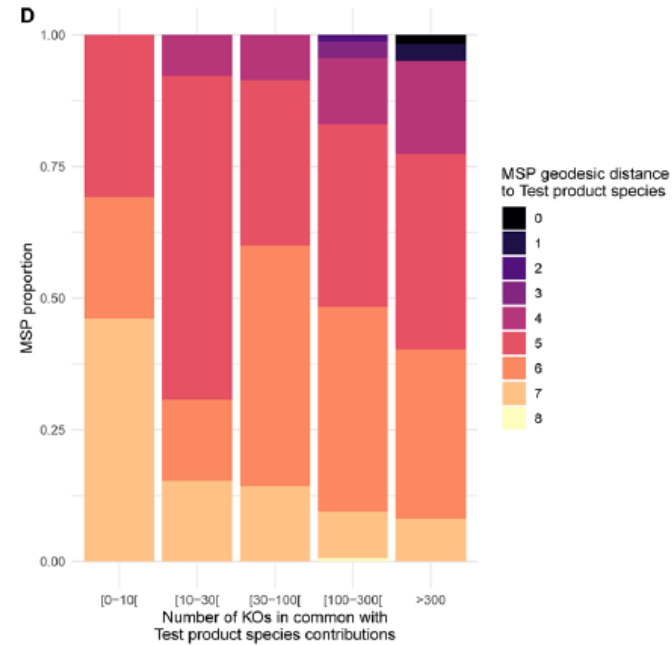
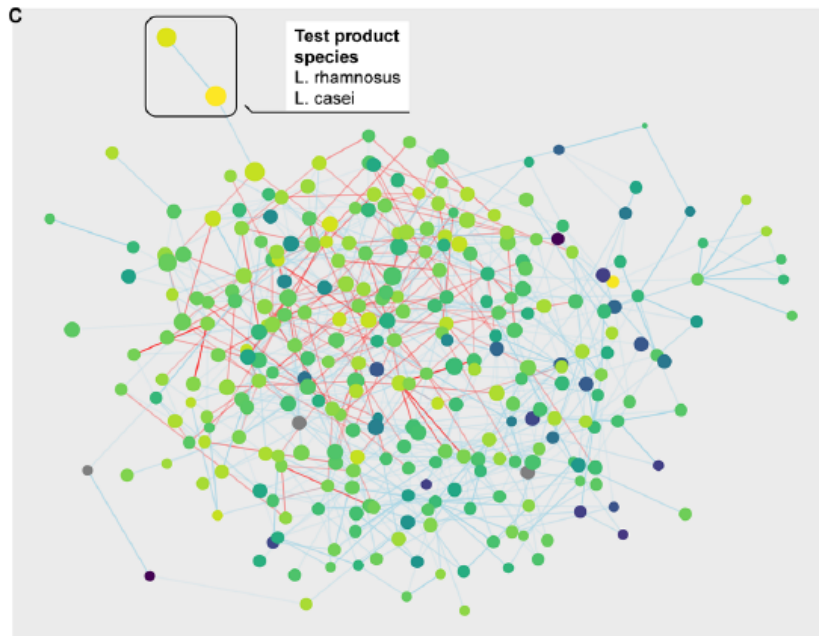


➤ Harnessing the microbial potential of fermented foods to avoid the point of no return



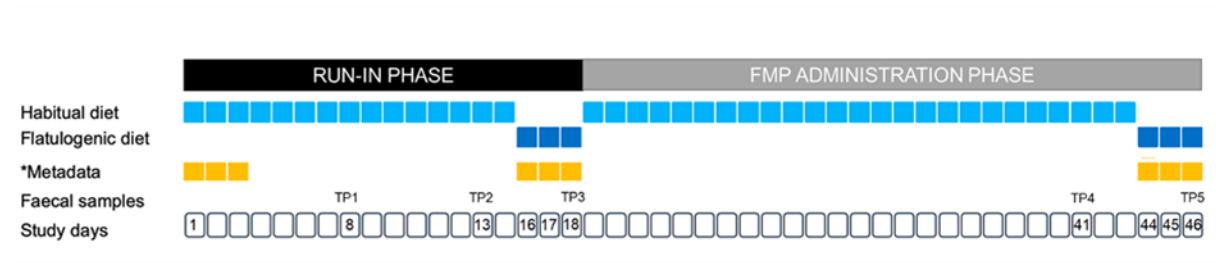
➤ Food microbiome engraftment is gut microbiome baseline dependent

Modular coalescence between gut and biotics species

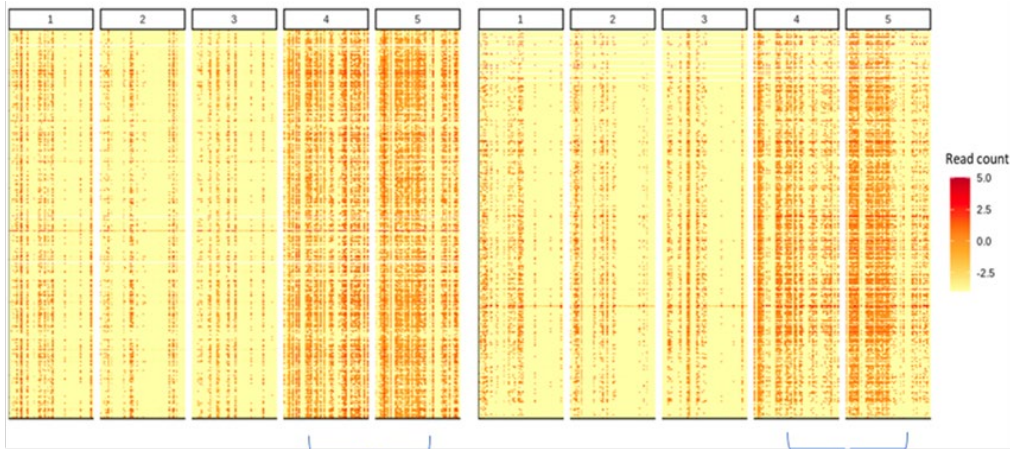


“Engraftment” as function of existing niche and metabolic pathway

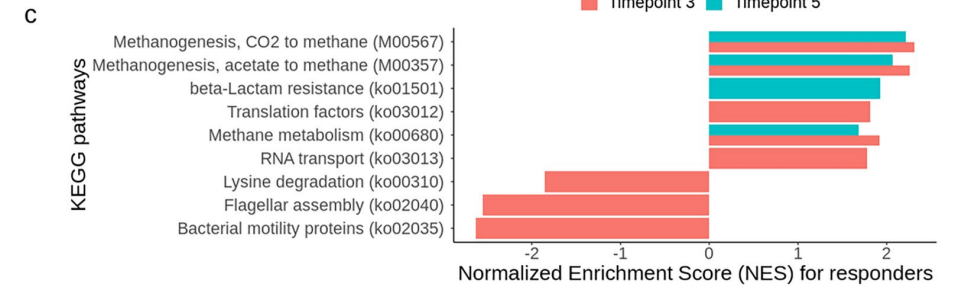
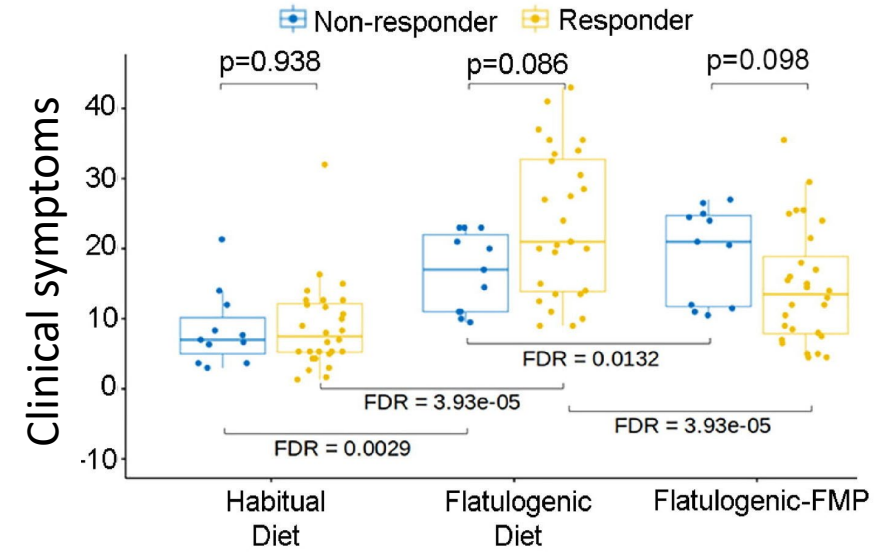
➤ Food microbiome clinical effect is gut microbiome baseline dependent



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

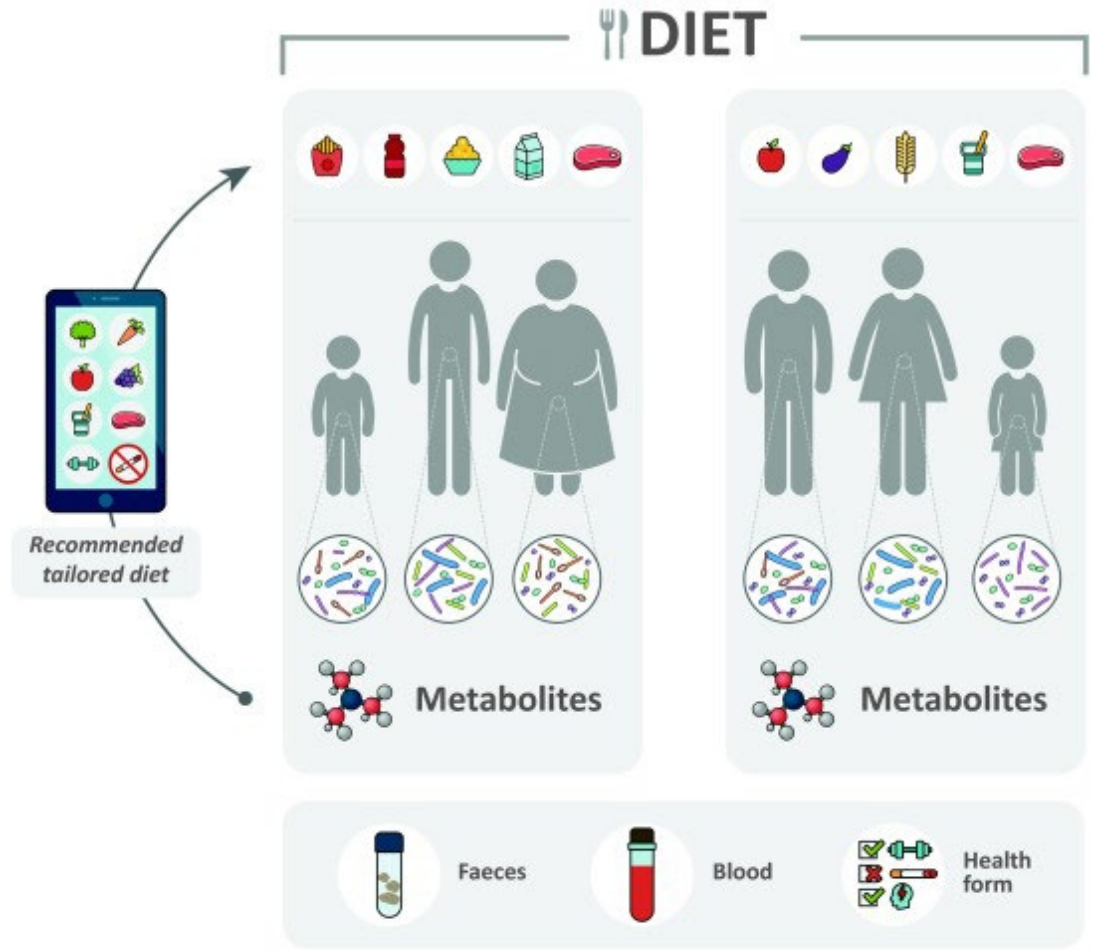
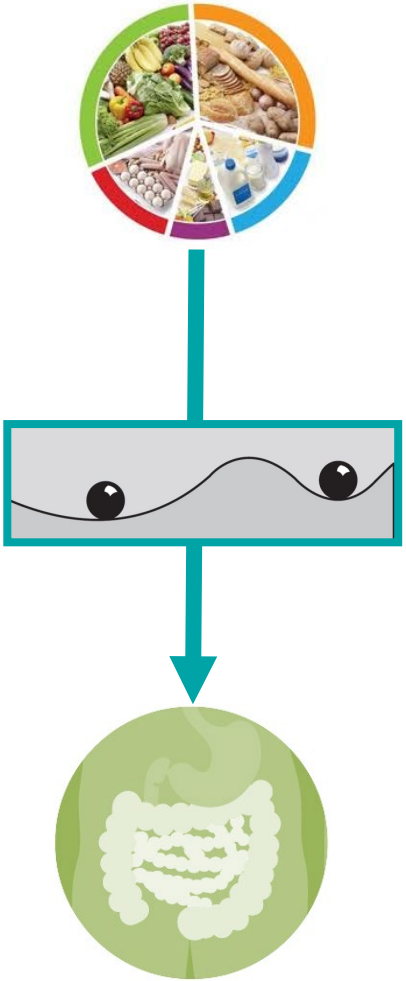


After FMP consumption, FMP active strains detected by metatranscriptomics



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

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

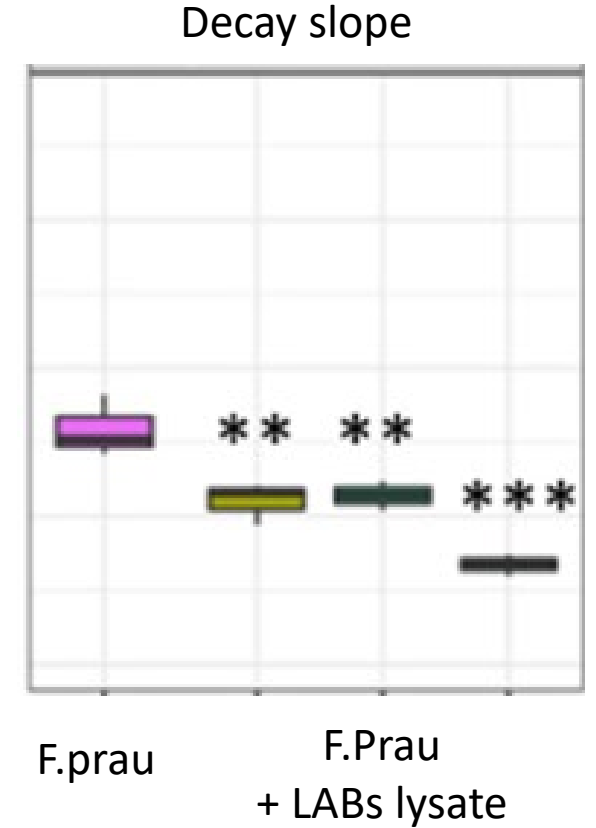
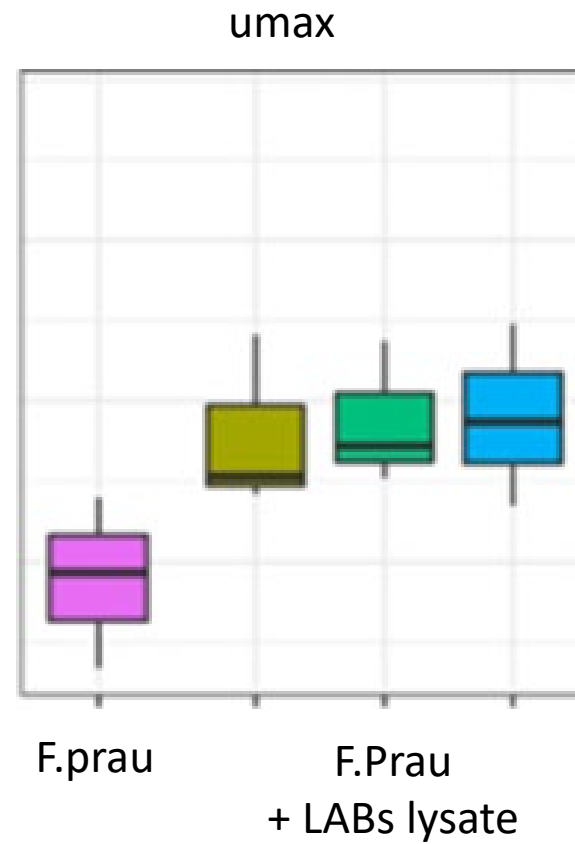
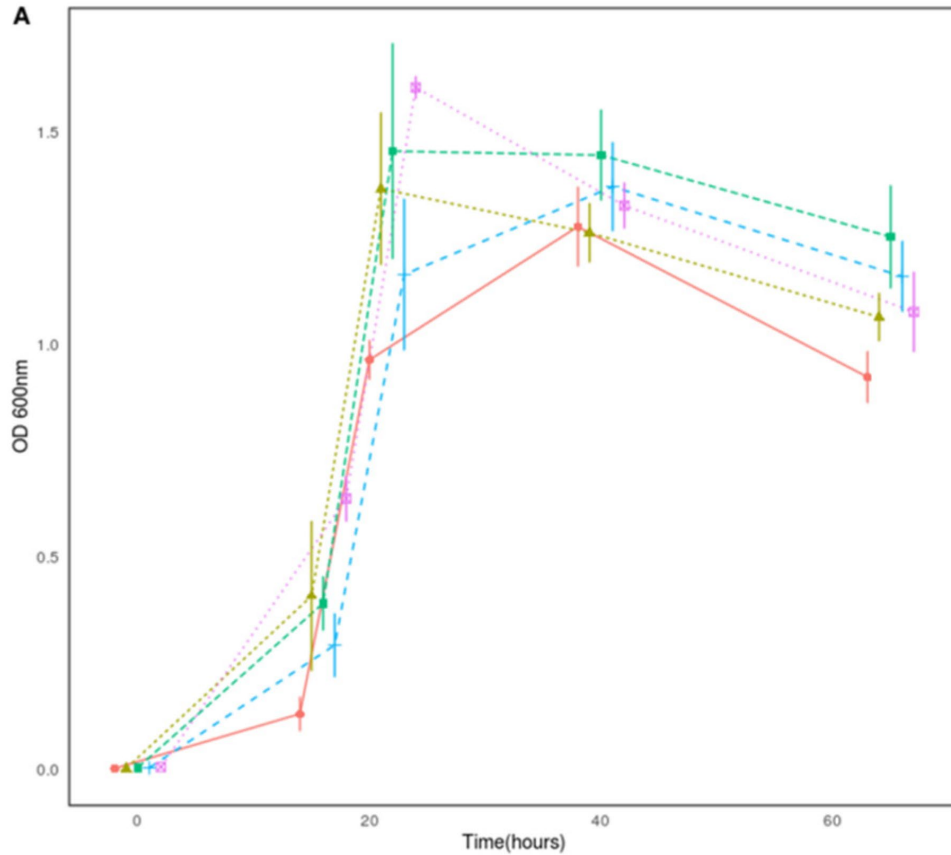


Recommended tailored diet

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



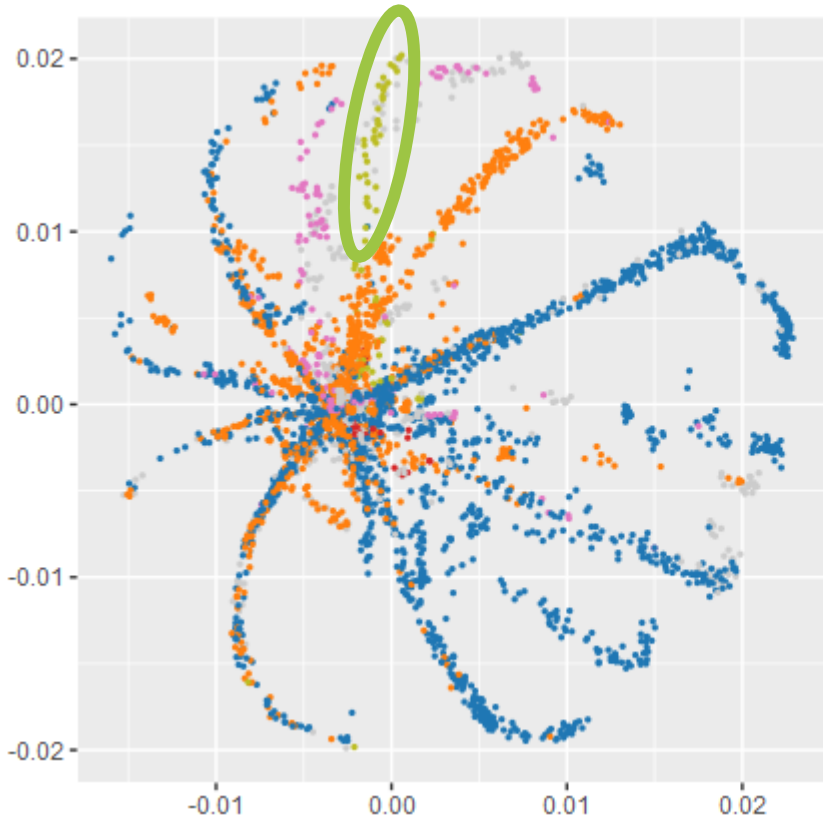
Increase of peptidoglycan levels for cell wall formation *F.prau*

Lebas, Derrien and colleagues (2020)



➤ Fermented food microbiome is shaped by deterministic dynamic processes

N = 4973 samples

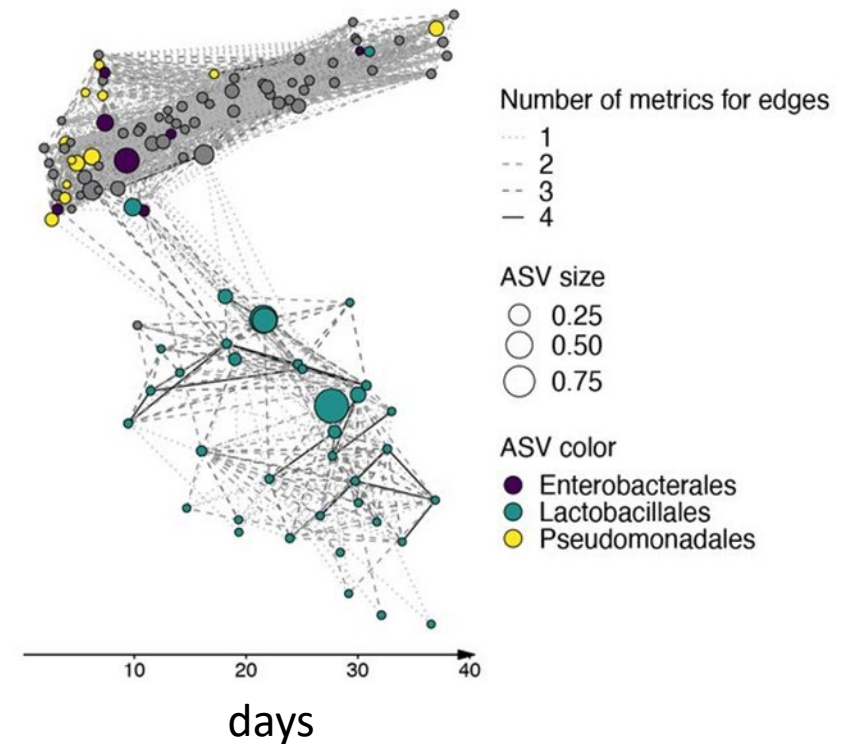


Food categories

- 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)



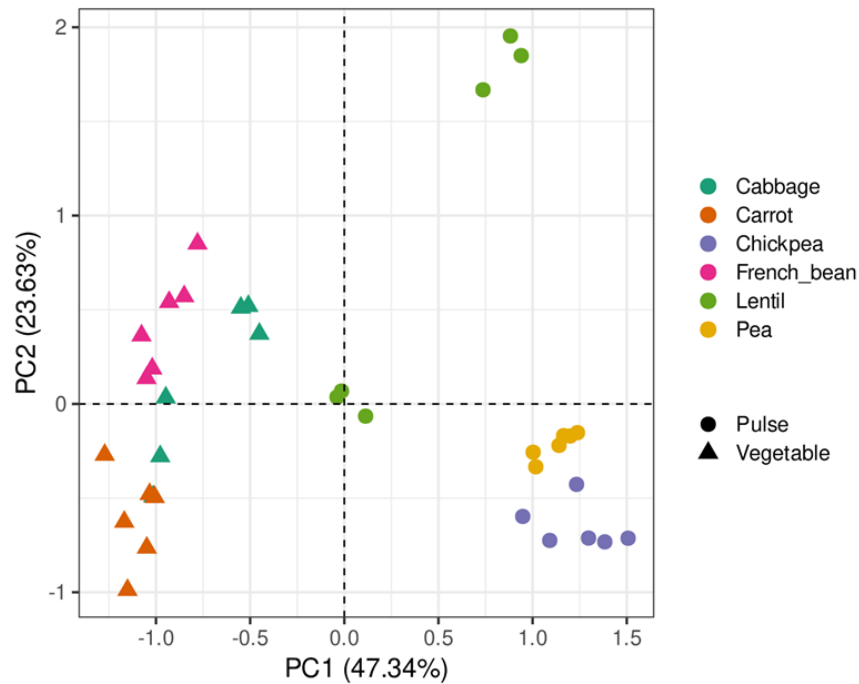
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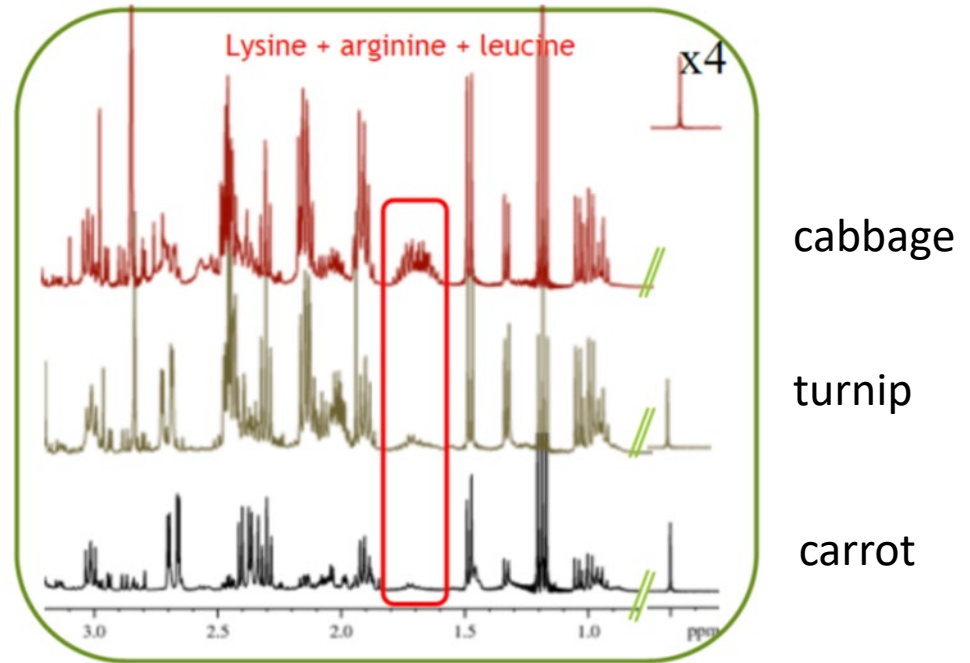
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➤ Plant-based matrices metabolome matters

Unfermented plant based matrices
LC-MS amino-acids profiles



Unfermented plant-based
NMR profiles



SayFood
Food & Bioproduct Engineering

Vincent Hervé

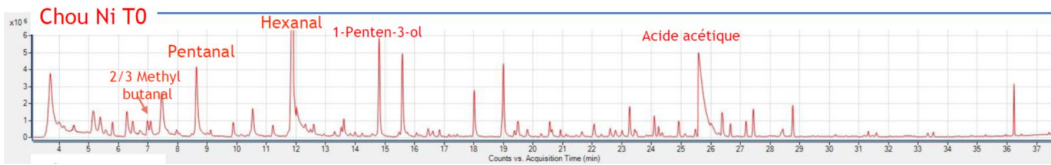


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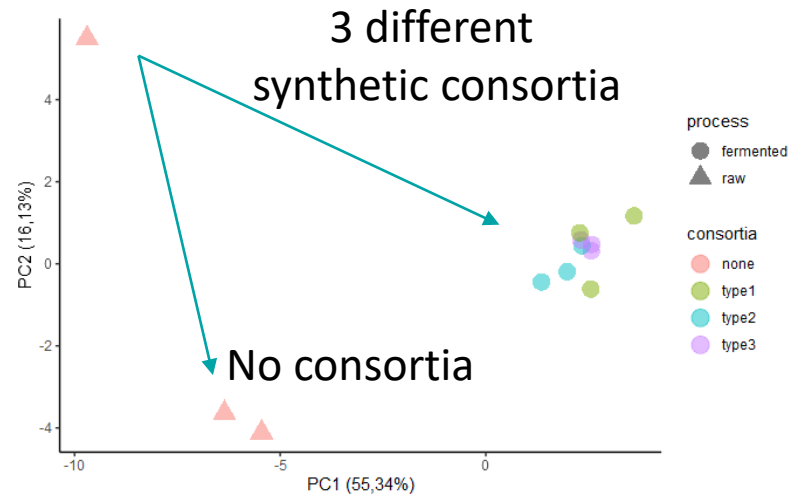
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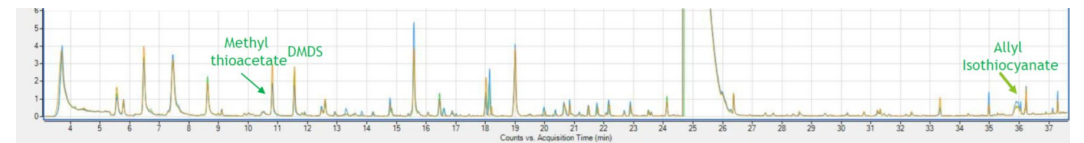
➤ Fermented plantbased food metabolome converge despite different synthetic consortia inoculation



Hexanal
Pentanal



Acetate
Esters
Volatile Sulfur Compounds



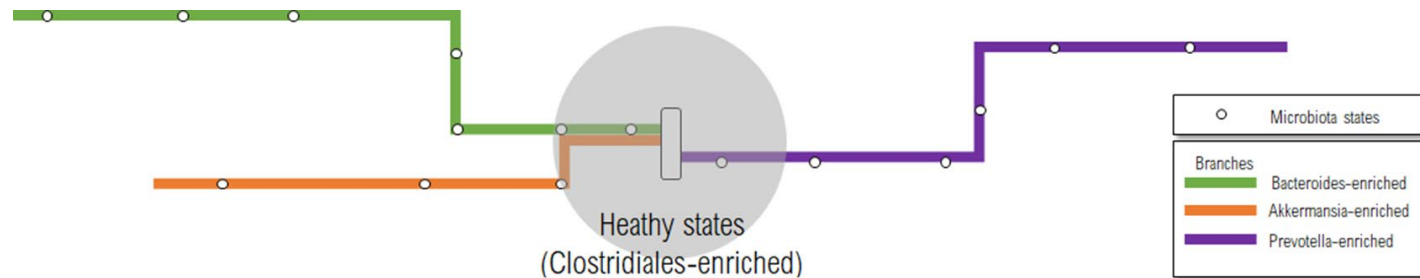
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> Take home messages

- 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



UC San Diego

Rob Knight's lab
Daniel McDonald
Franck Lejzerowicz

...



Chays Mannichanh
Fernando Azpiroz
Iñigo Oyarzun



Muriel Derrien
Patrick Veiga
Boris Le Nevé

...



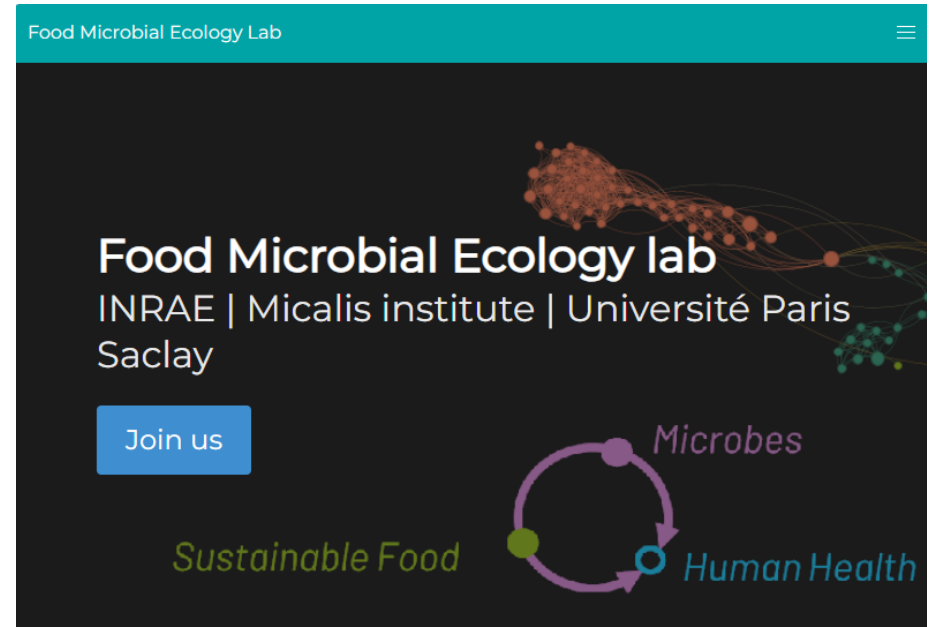
Vincent Hervé
Sophie Landaud

...



Dalal Werner
Marie Hélène Desmots

...



Marie-Christine Champomier-Vergès
Stéphane Chaillou

...



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