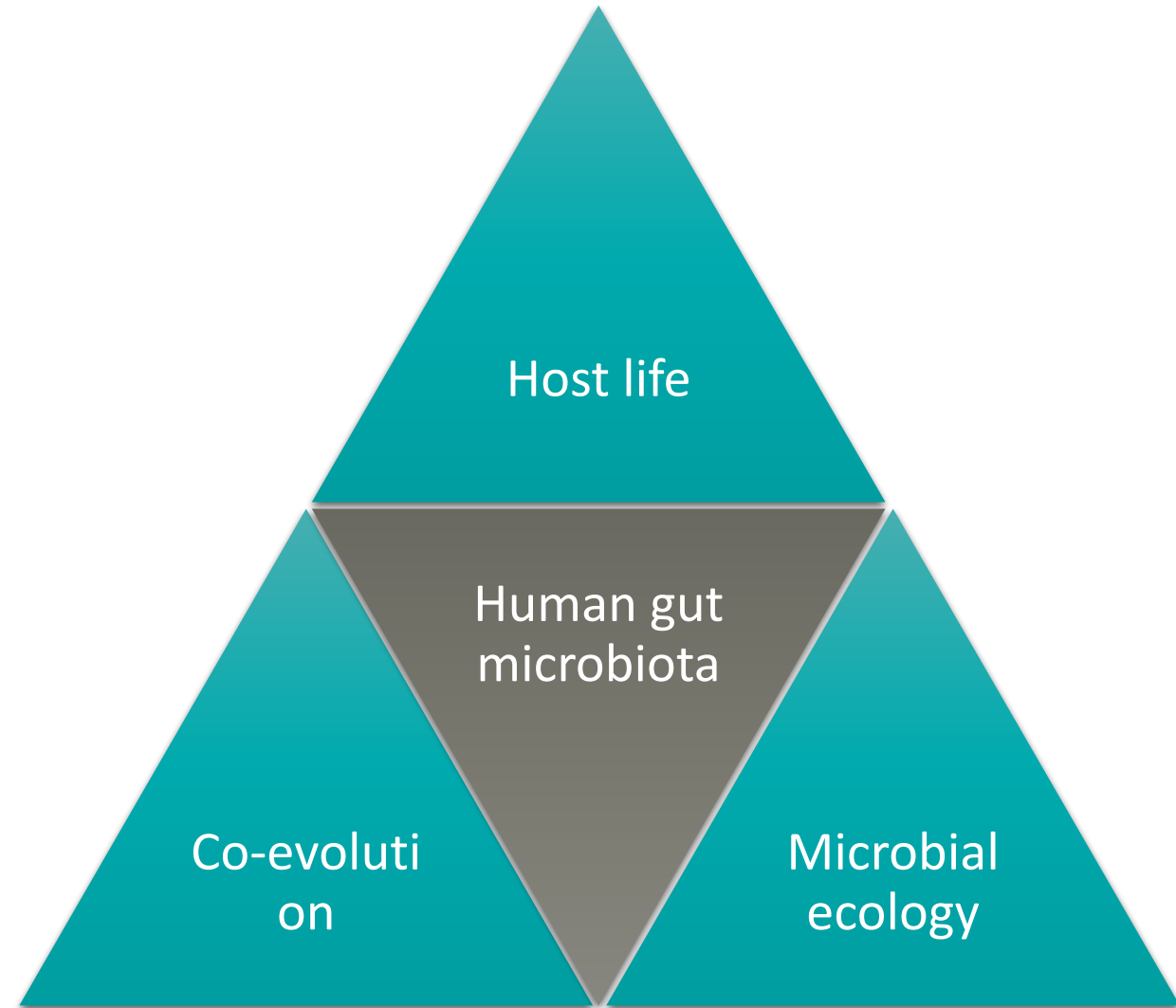
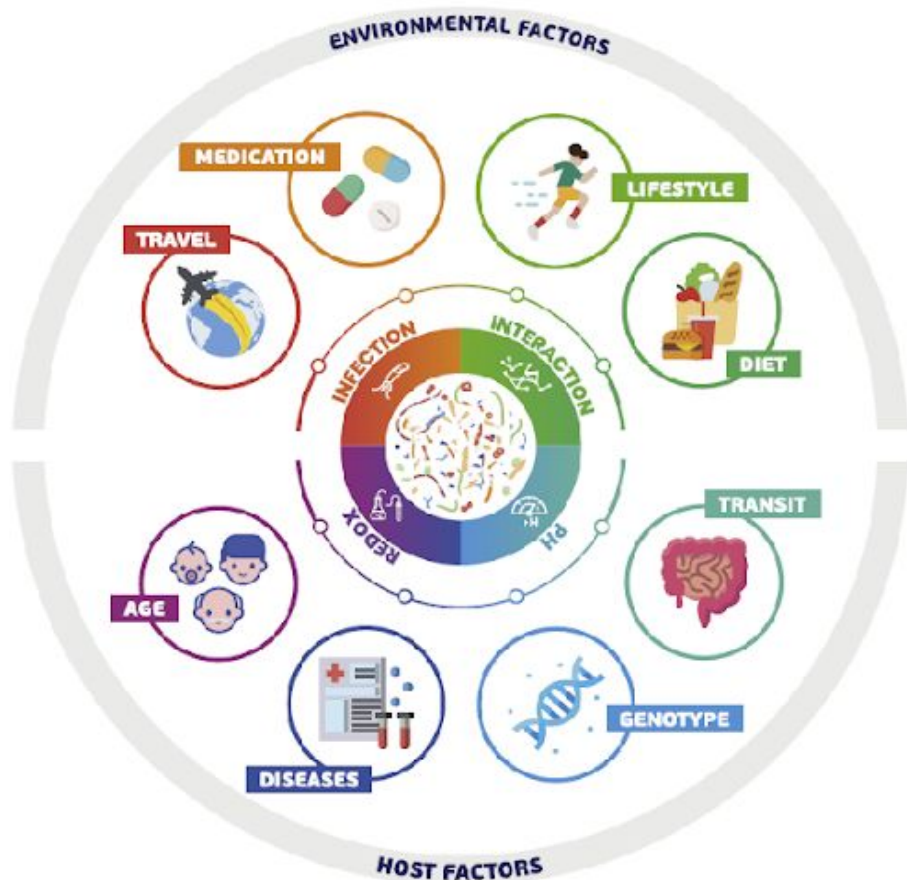


- Next-Gen Fermented Food: Harnessing Gut Microbiome Diversity and Functions

Julien Tap
INRAE MICALIS
FERMENT'IA

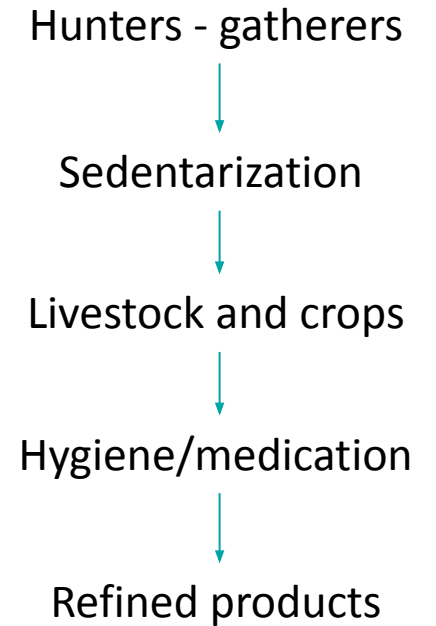
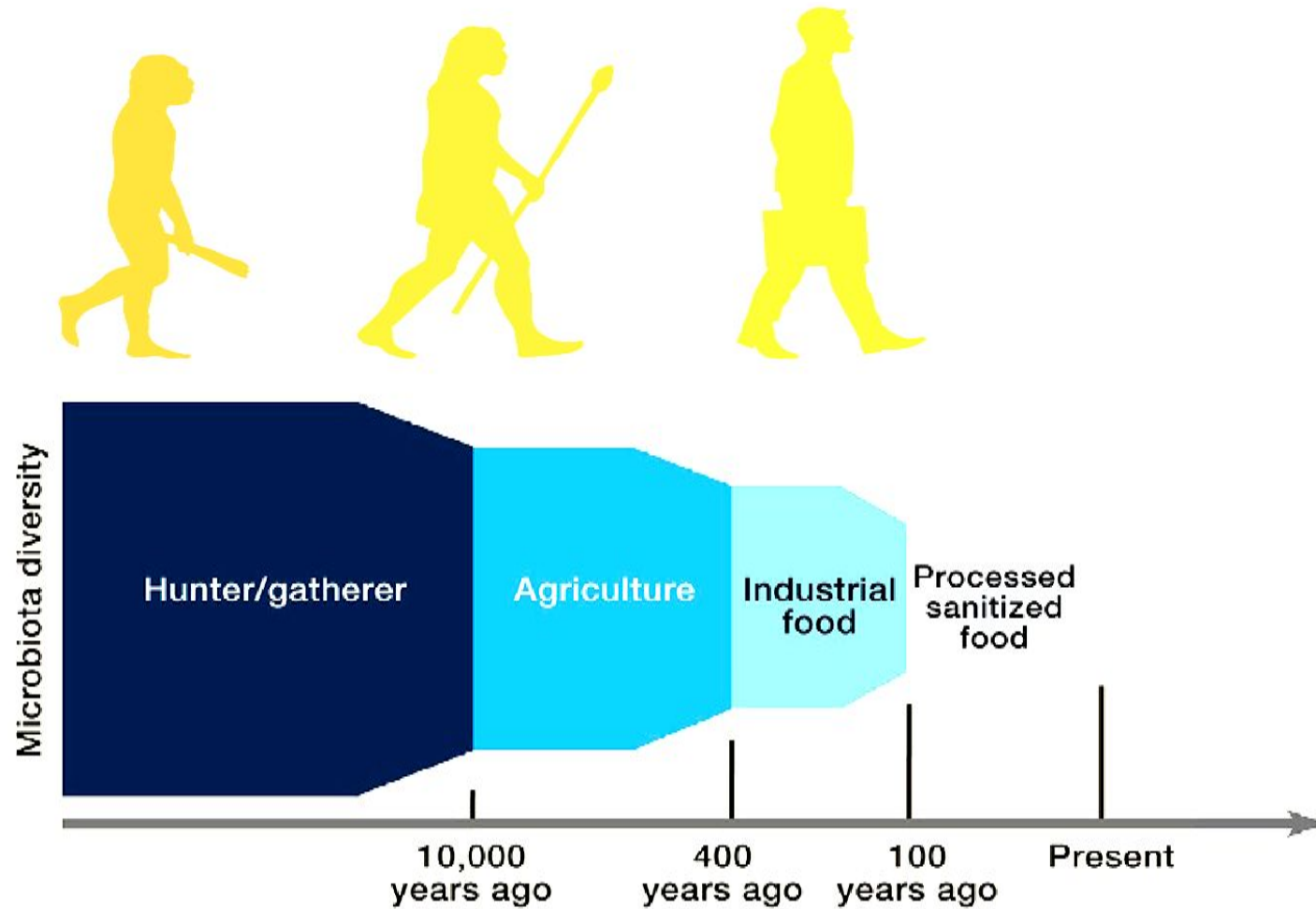


- Different factors shapes the human gut microbiome

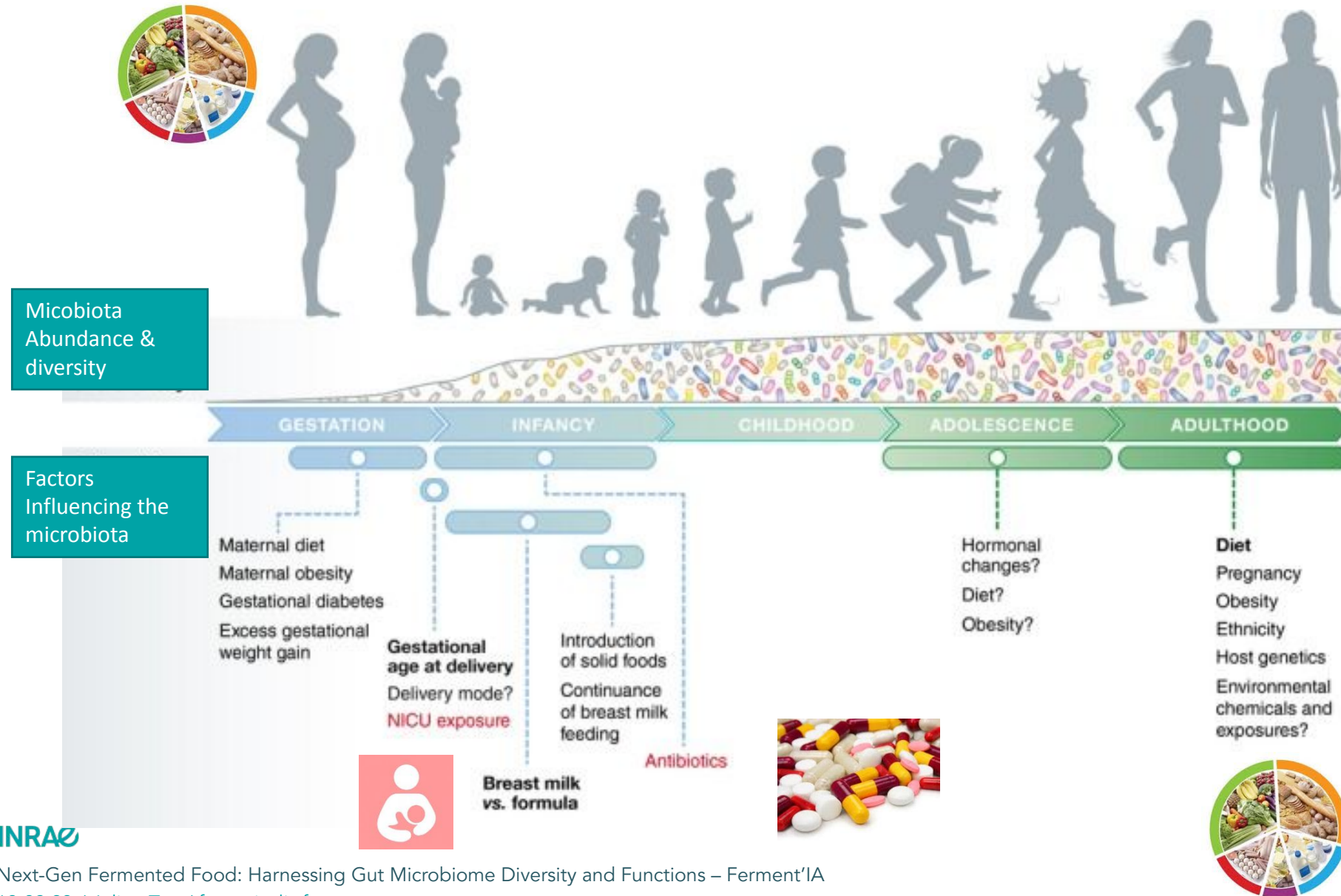


• Diet and lifestyle effect host microbiome symbiosis

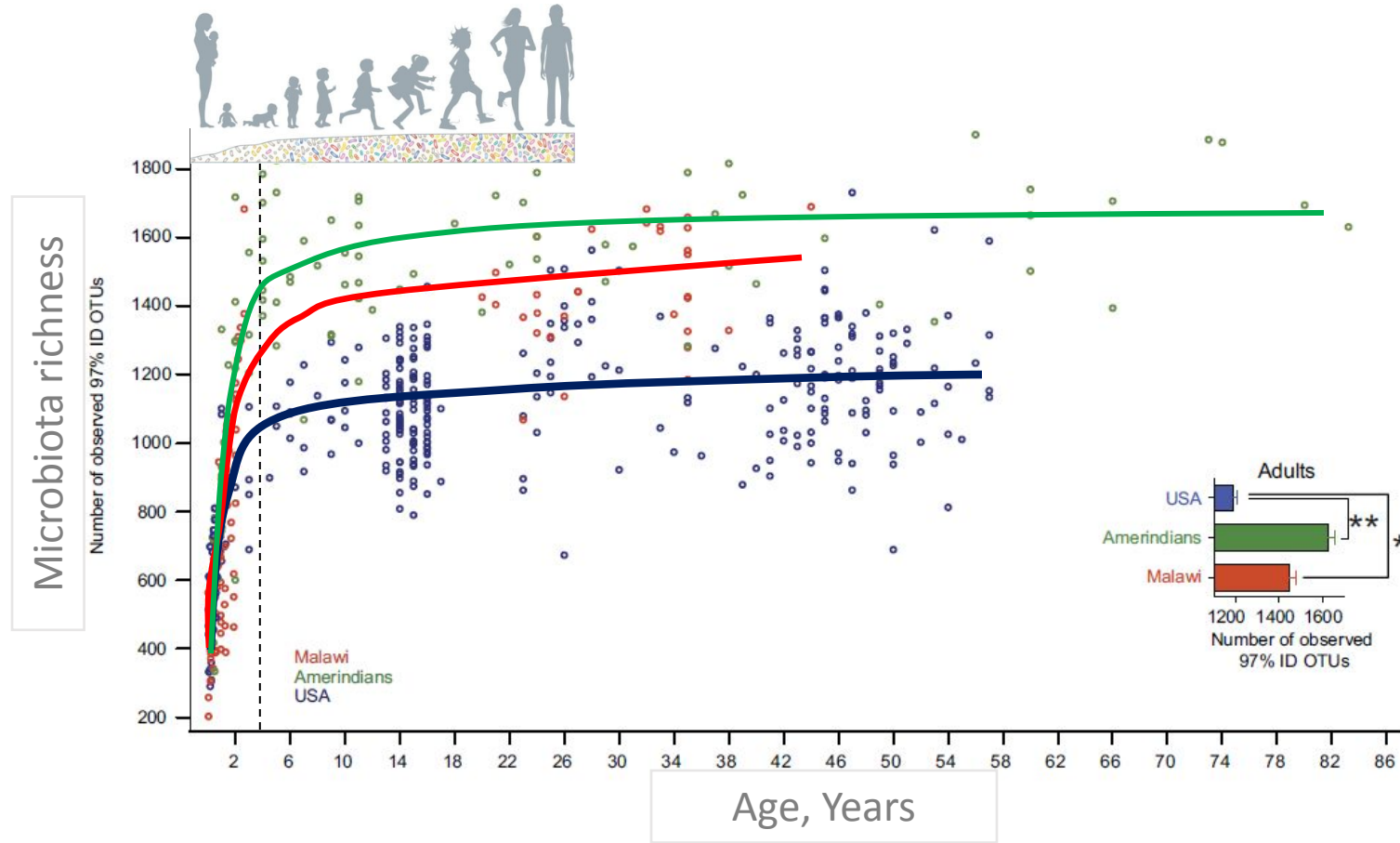
Are we uncoupling our metagenome and our genome?



• Gut microbiome throughout life span



- Gut Microbiome diversity associated with the region of birth during the lifespan



- Microbiome states resilience as key factor



Healthy state



Resistance



Recovery

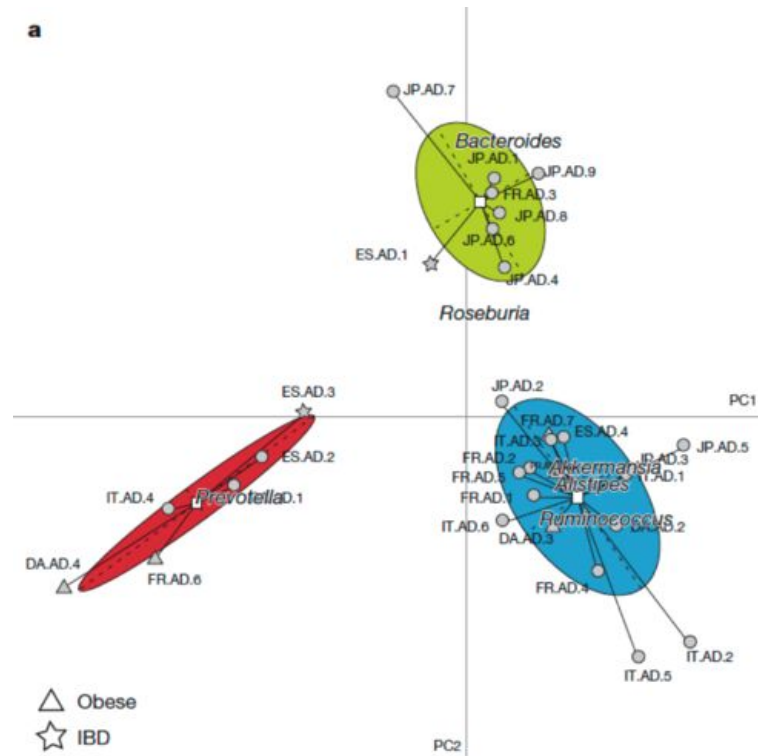
Resilience

Healthy state

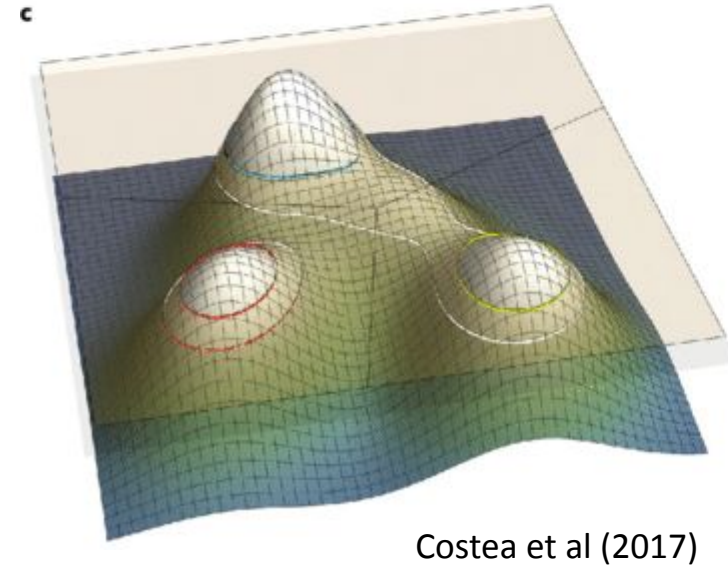


Degraded state

- Several attempts to decipher the microbiome structure



Arumugam, Raes et al (2010)



Costea et al (2017)

Dirichlet Multinomial Mixture (DMM) modeling

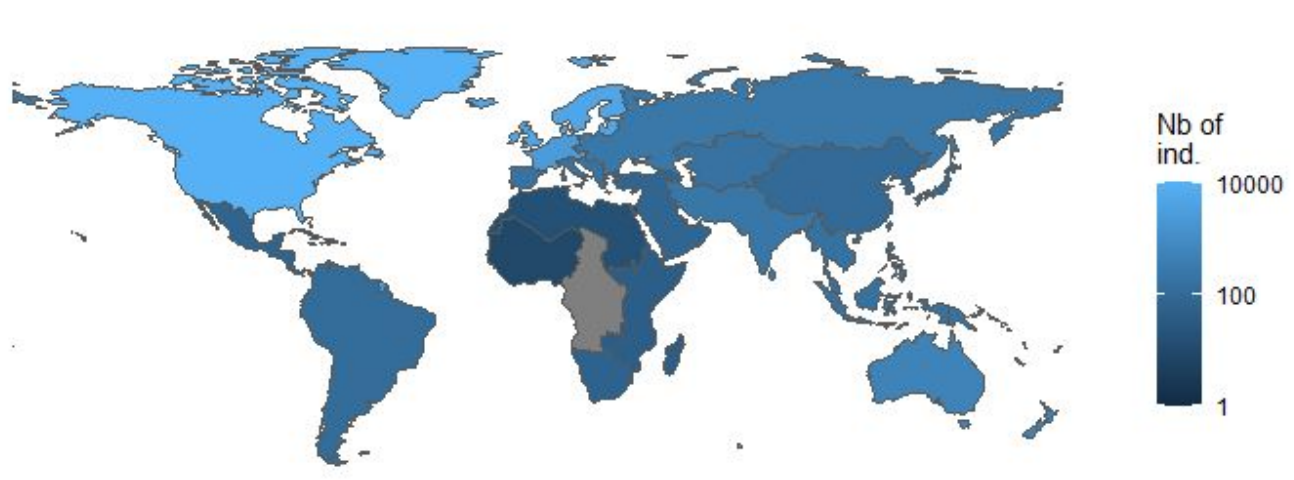
Limits:

Few association with diet

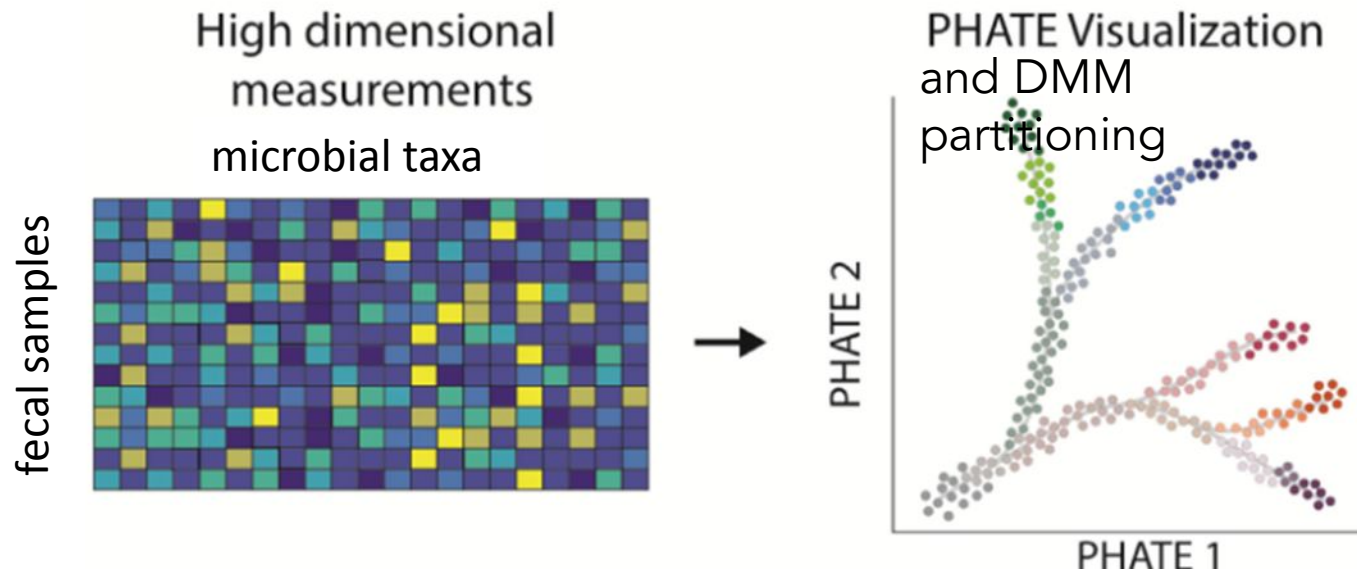
Few stability assessment (e.g. with time-series)



- 35,000 human gut microbiome samples analyzed



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

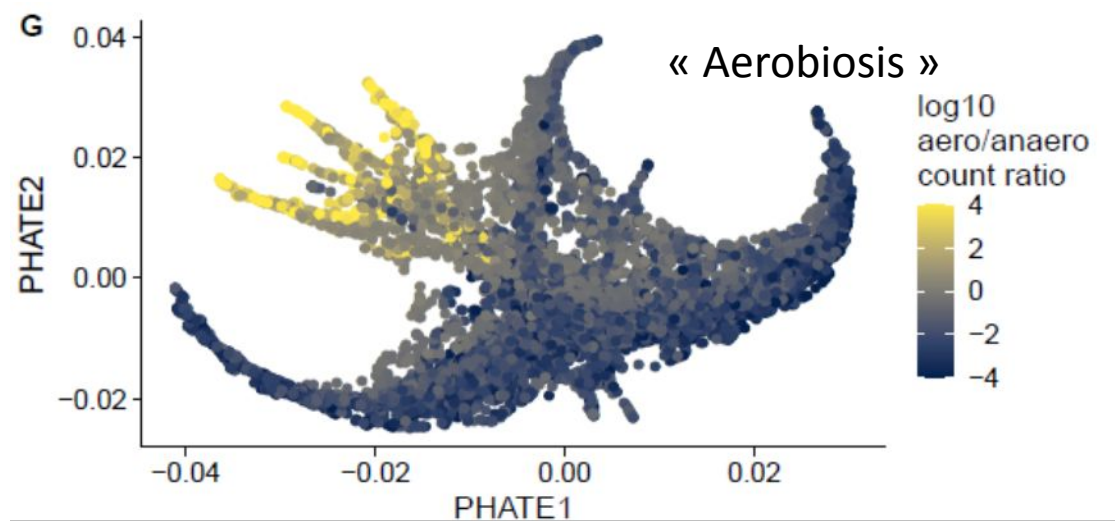
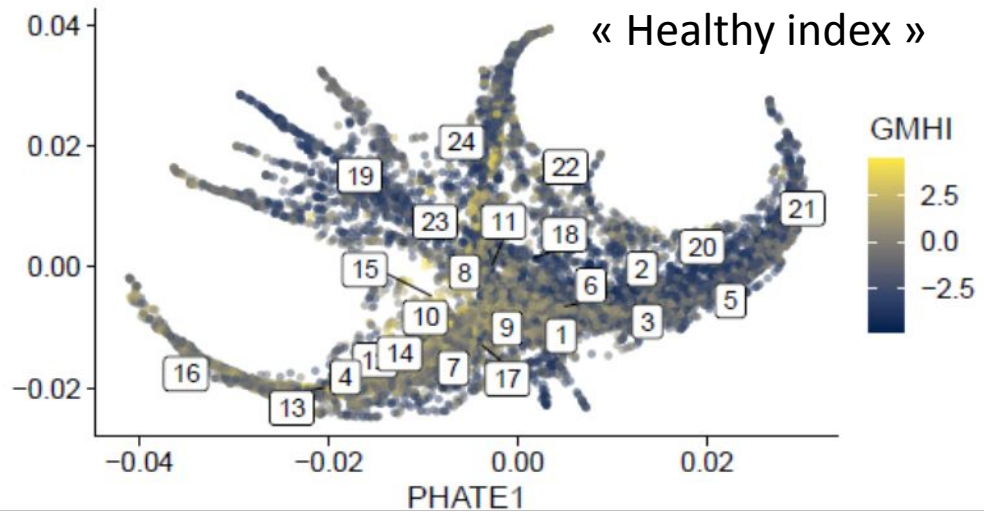
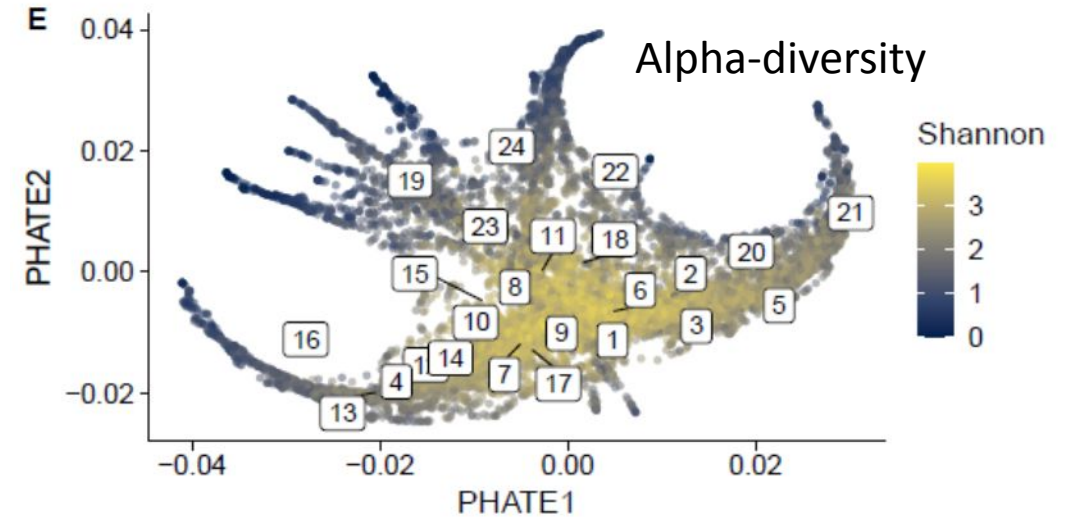
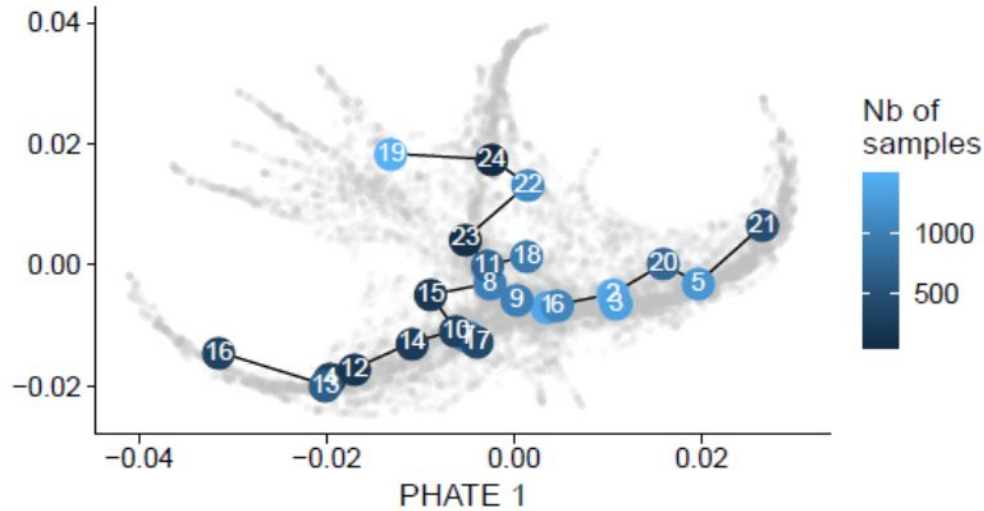


Time-series analysis to detect microbiome states

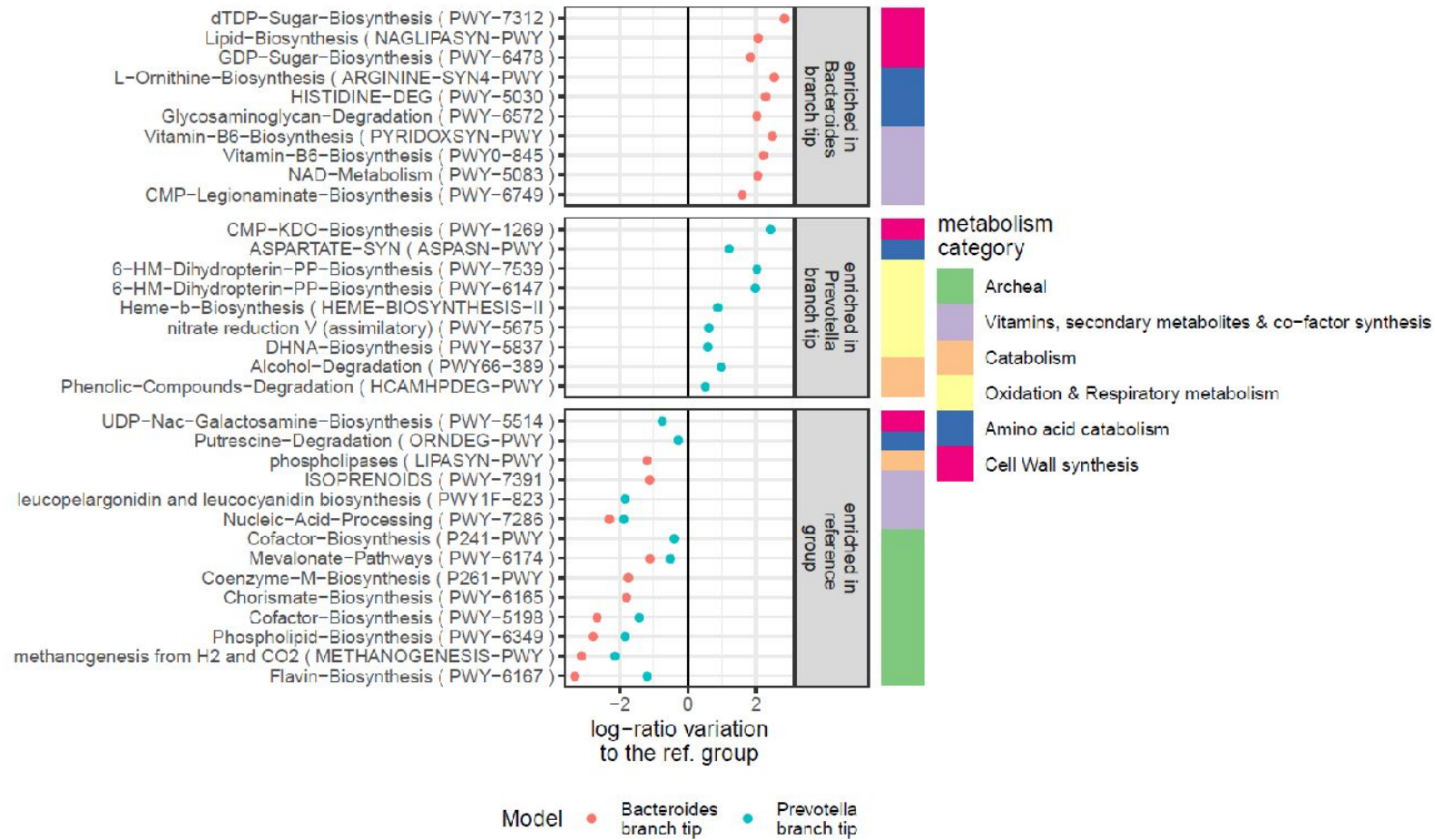
Region of birth, Lifestyle, diet, and health modelization



- Human Gut microbiome structured as branches



• Low-diversity tips of branches display functional shifts



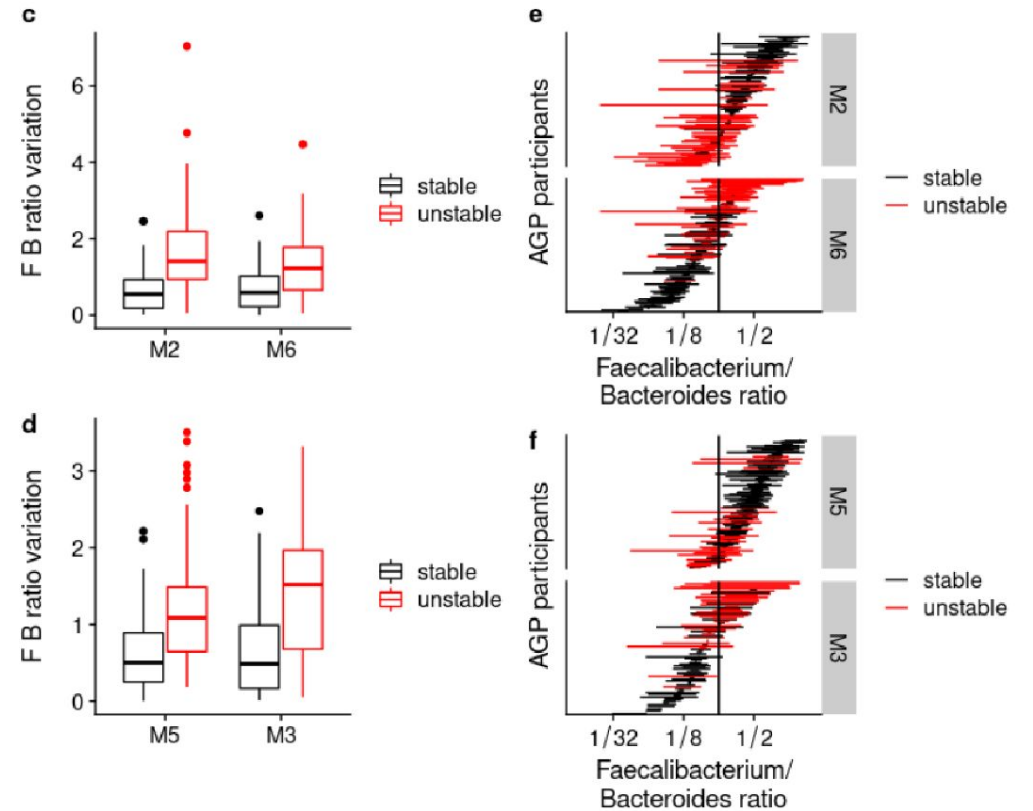
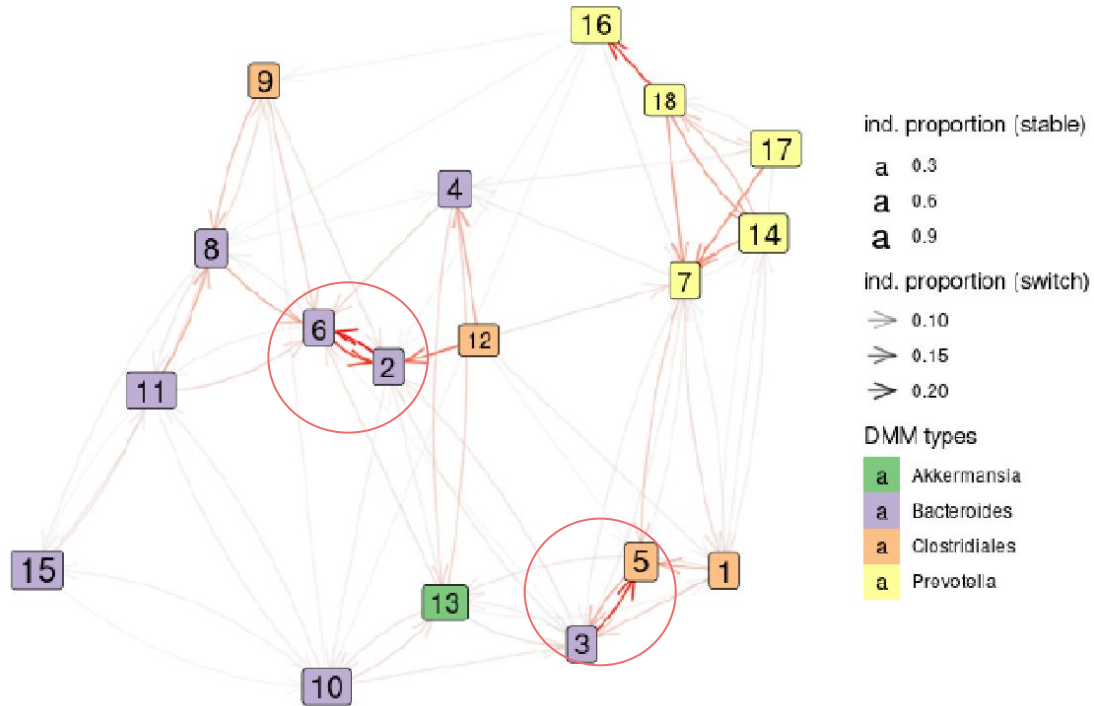
amino acid catabolism increase
in *Bacteroides* branch tip

oxidative stress response increase
in *Prevotella* branch tip



• Dynamics between partitions are associated to branches

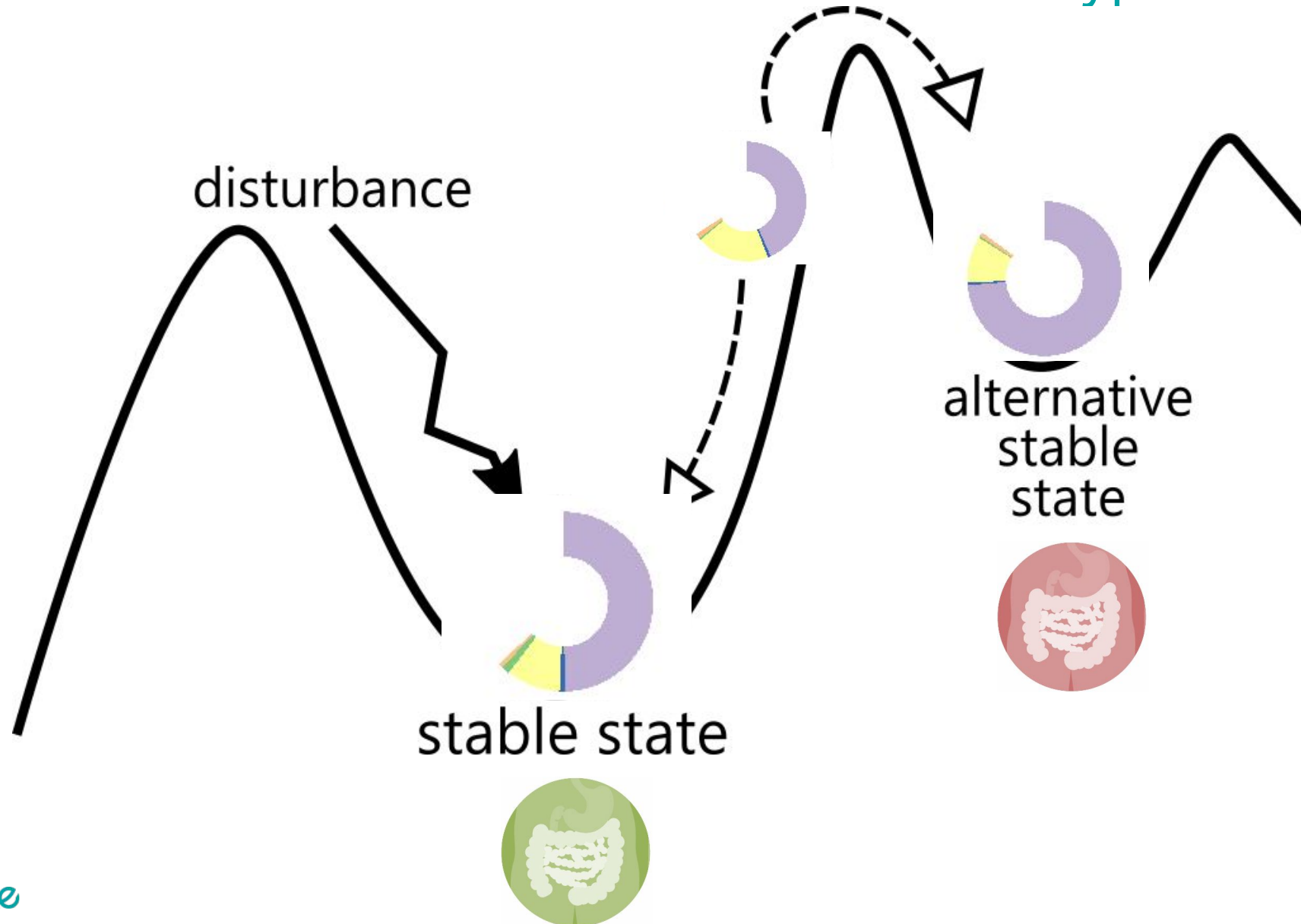
827 participants 2,998 samples 2,171 time-pairs



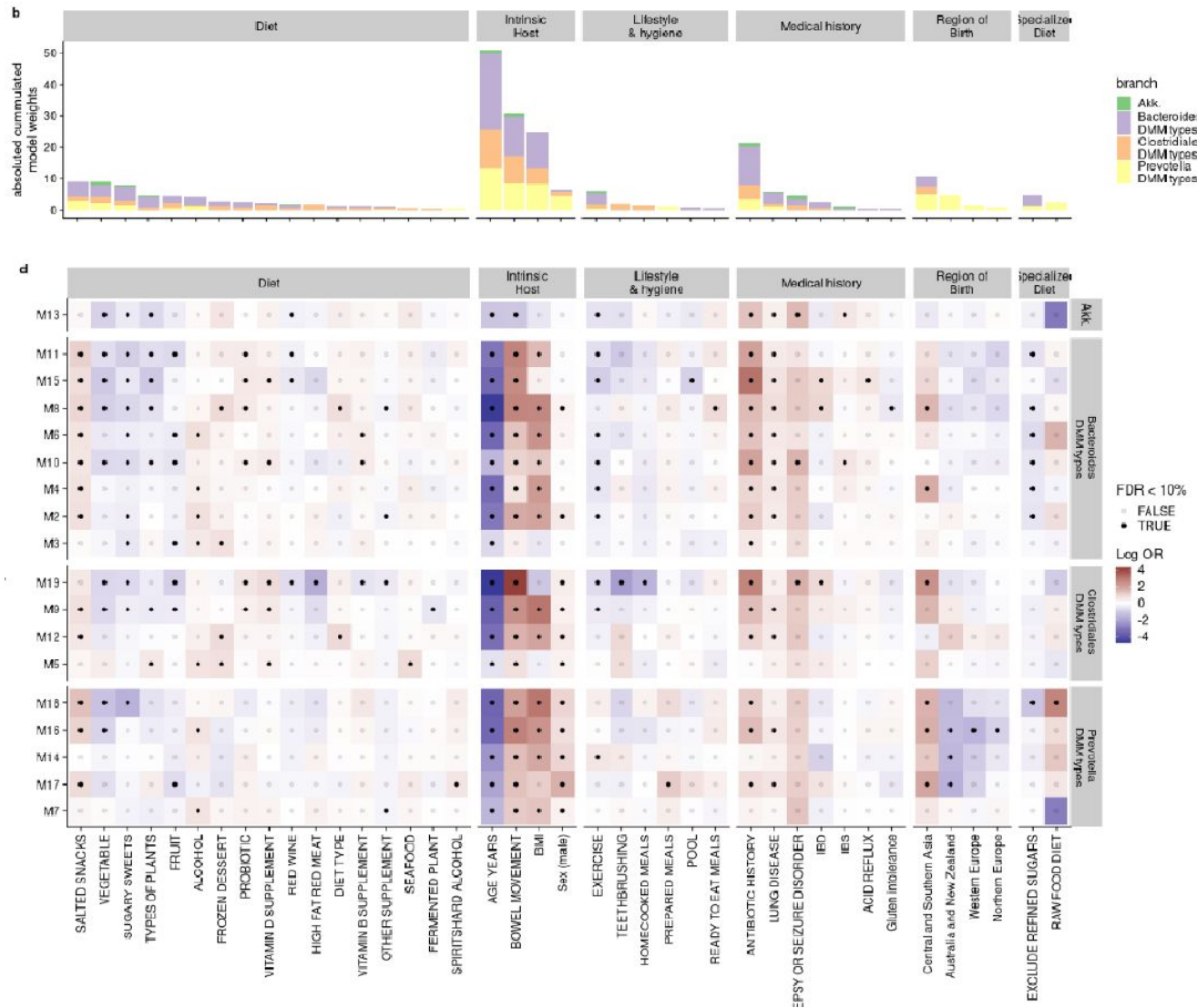
Faecalibacterium/Bacteroides as a tipping element explaining the switch between some states



- Gut microbiome alternative stable states hypothesis



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



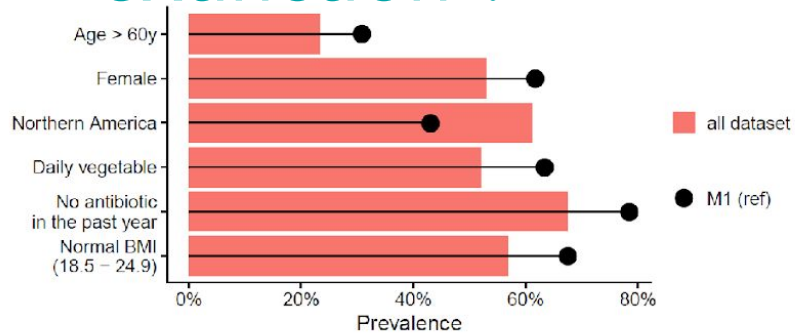
Sex, exercises frequency and **region of birth** associated differentially between branches

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

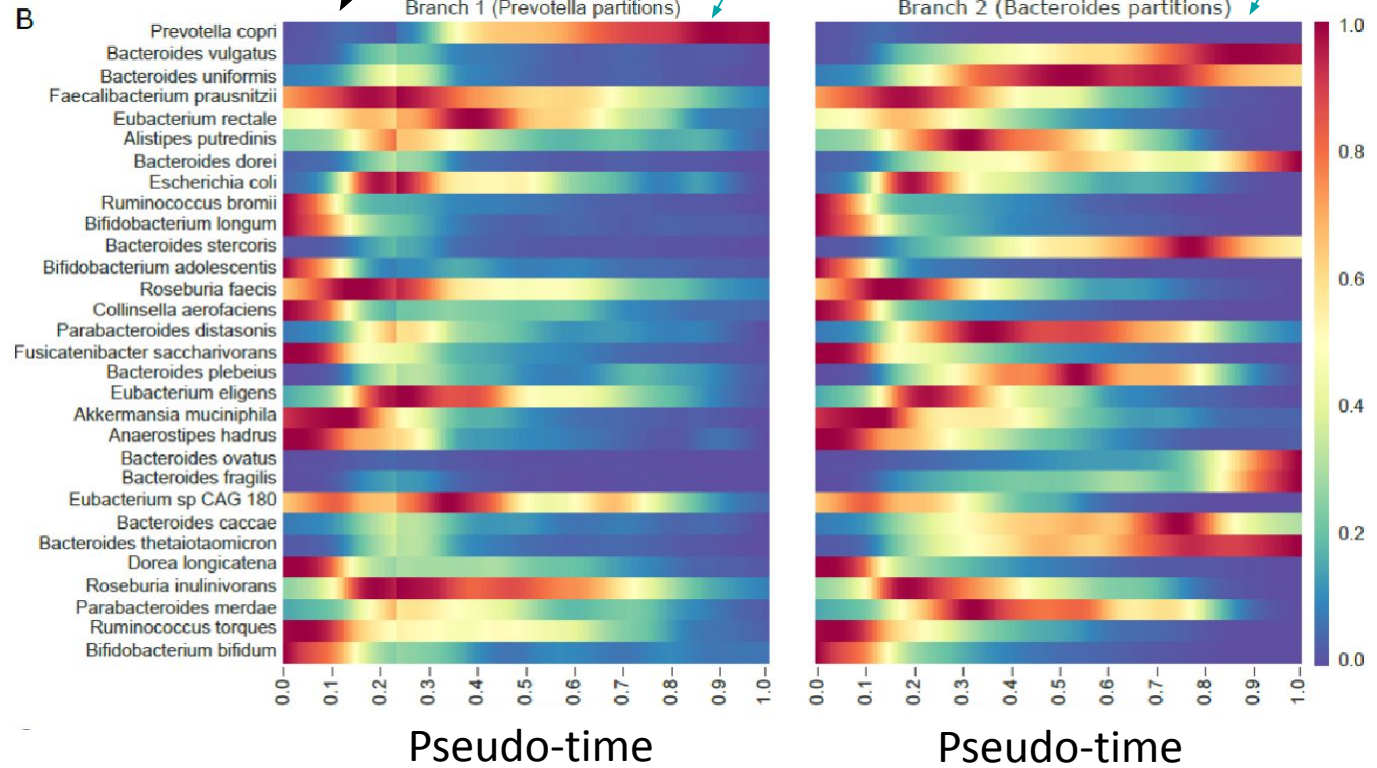
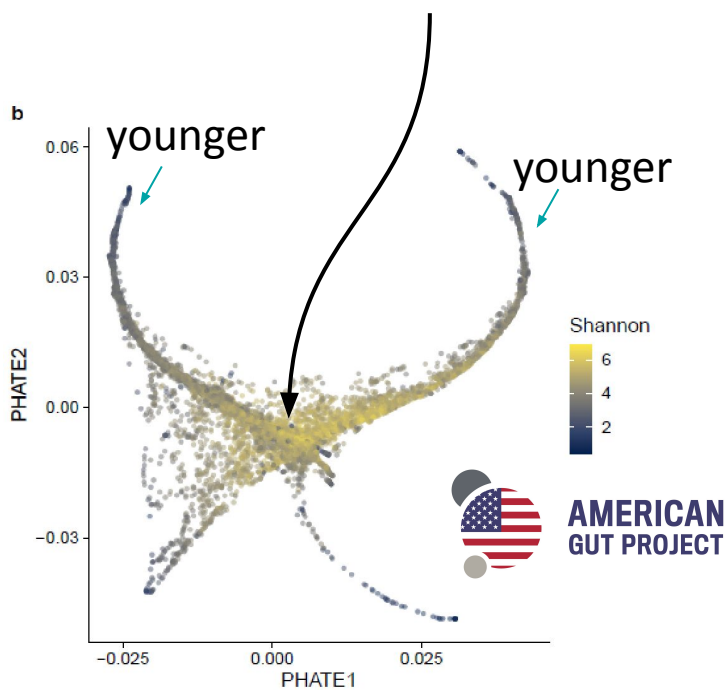
Specialized diet associated with altered state within *Prevotella* branch



Do we already observe a intergenerationally mass extinction ?



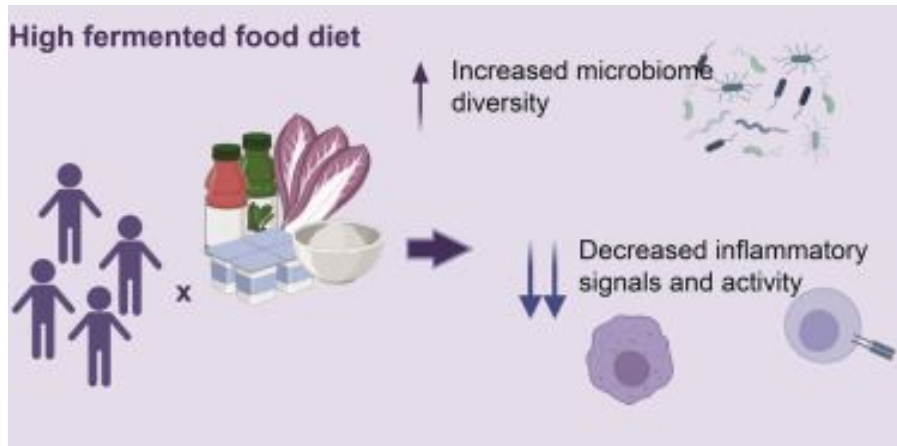
Older and healthy diet and lifestyle



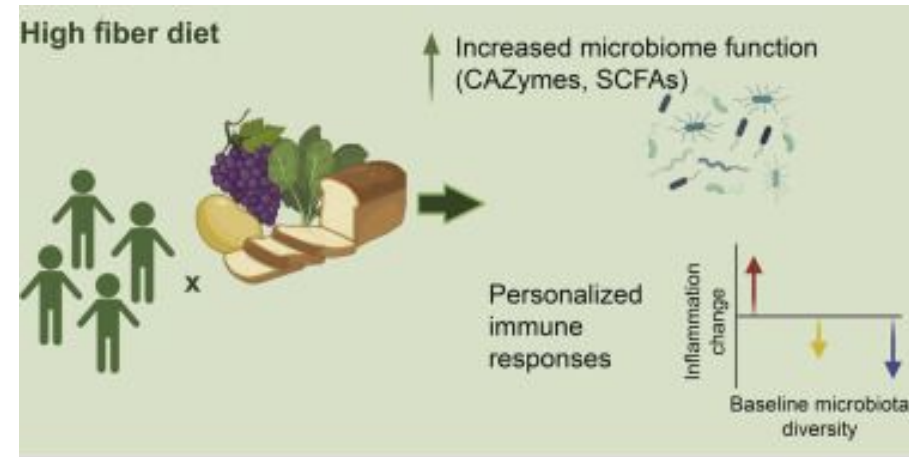
- Harnessing the microbial potential of fermented foods to avoid the point of no return



- How fermented foods can fit precision nutrition for health?



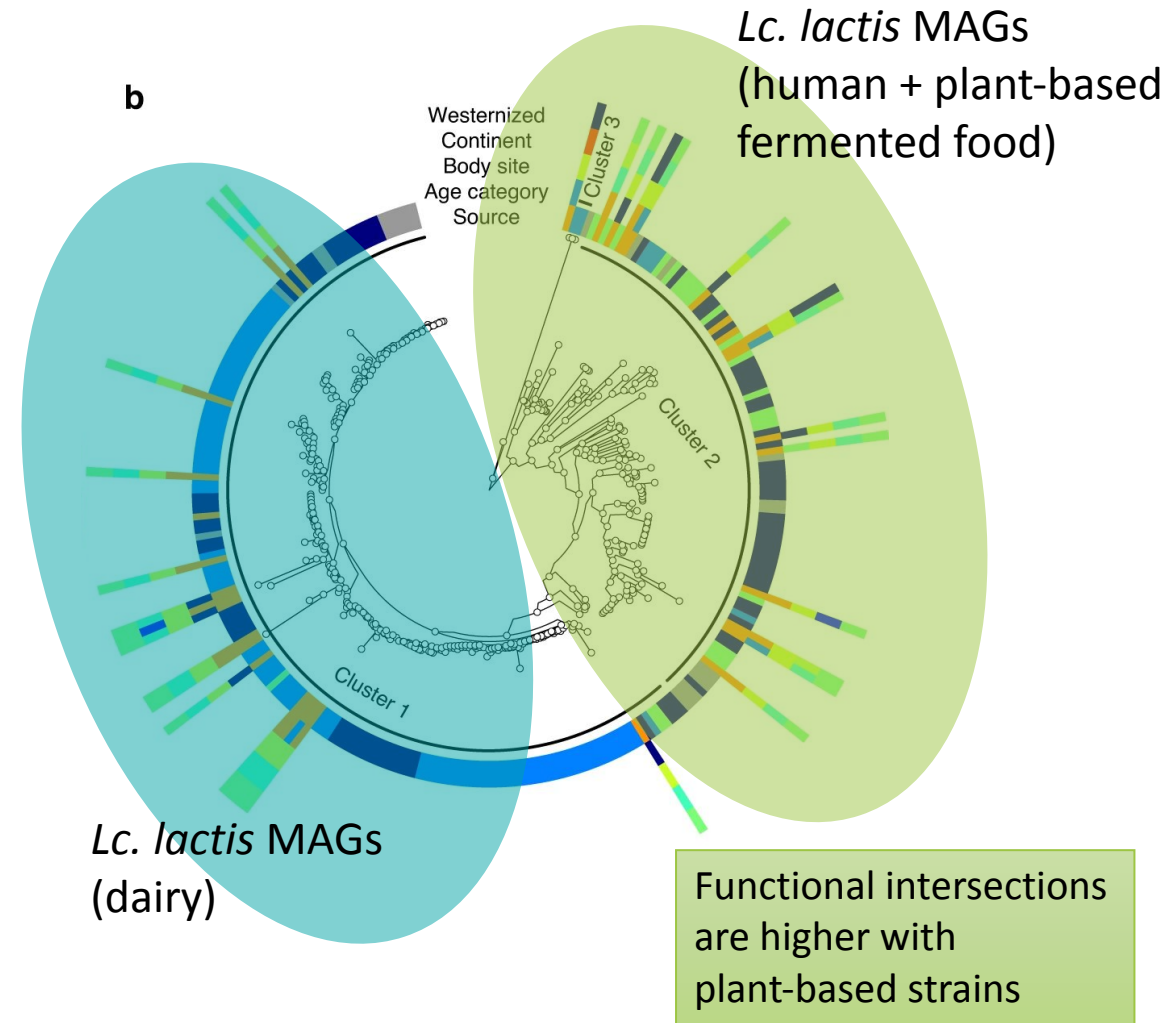
Fermented foods valuable solution in countering the decreased microbiome diversity



Personalized immune as function of gut microbiota baseline

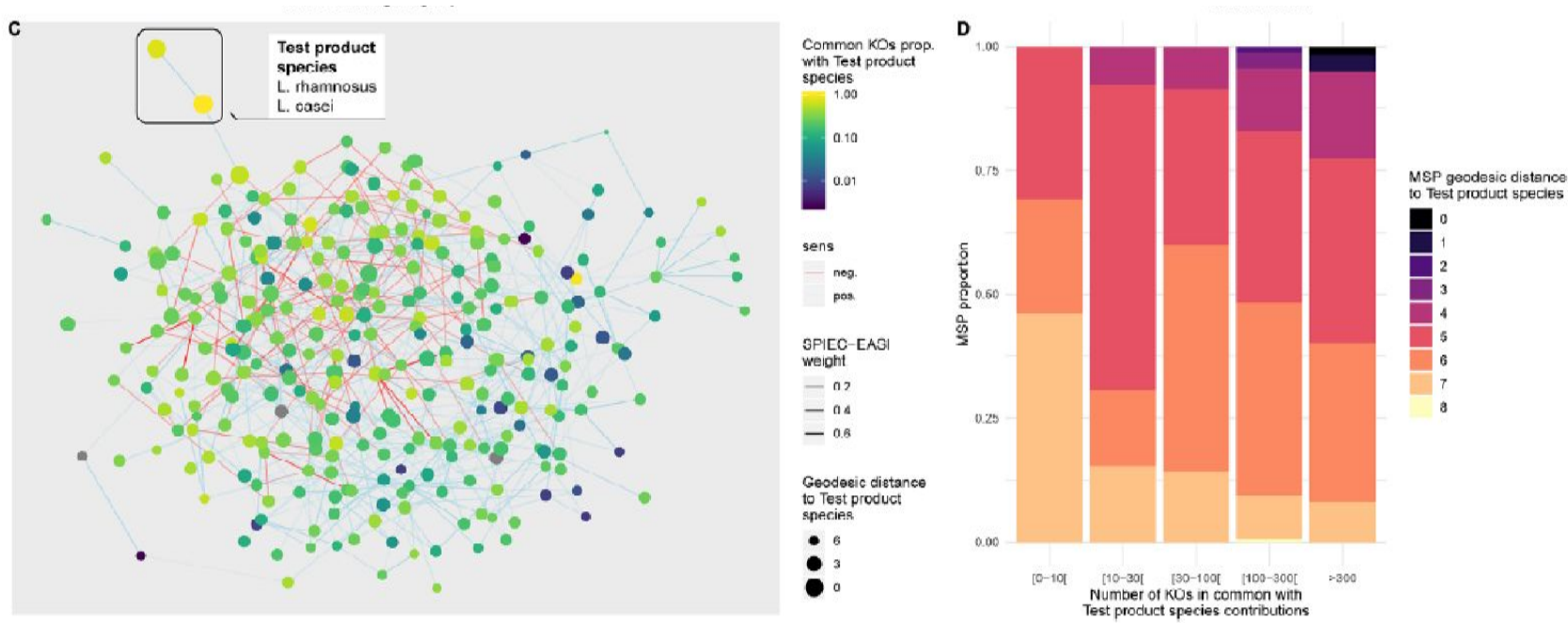
Wastyk et al., 2021

- Large intersection between food and human microbial species but subtype matters



- Gut microbiome functional enrichment by fermented food is personalized

Modular coalescence between gut and food species



“Engraftment” as function of existing niche and metabolic pathway



- Fermented food strains are active in gut microbiome

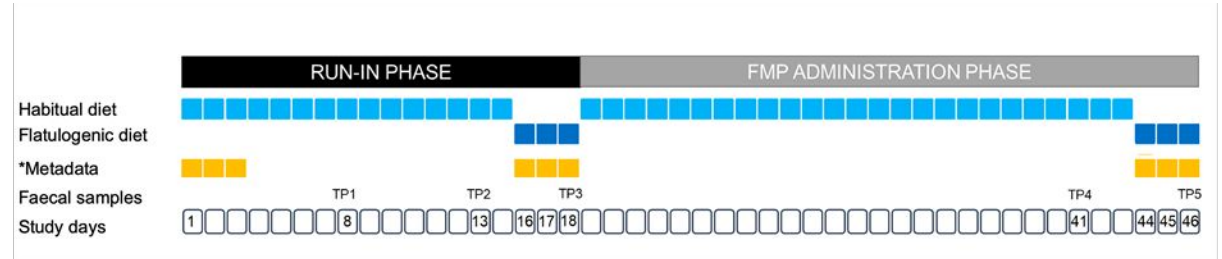
FMP product

Streptococcus salivarius subsp. *thermophilus* strains (CNCM I-2773, CNCM I-2130, CNCM I-2272),

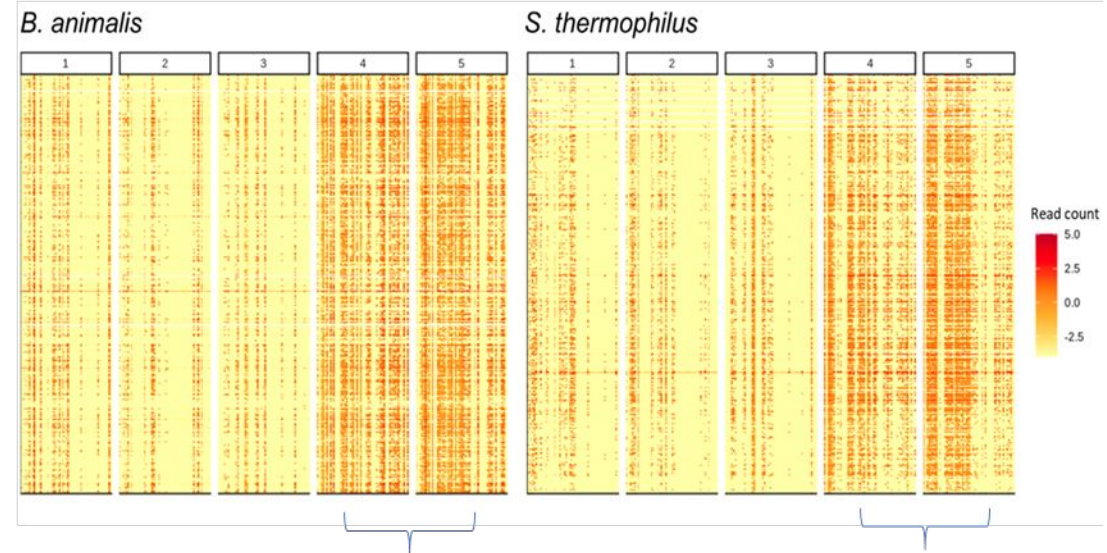
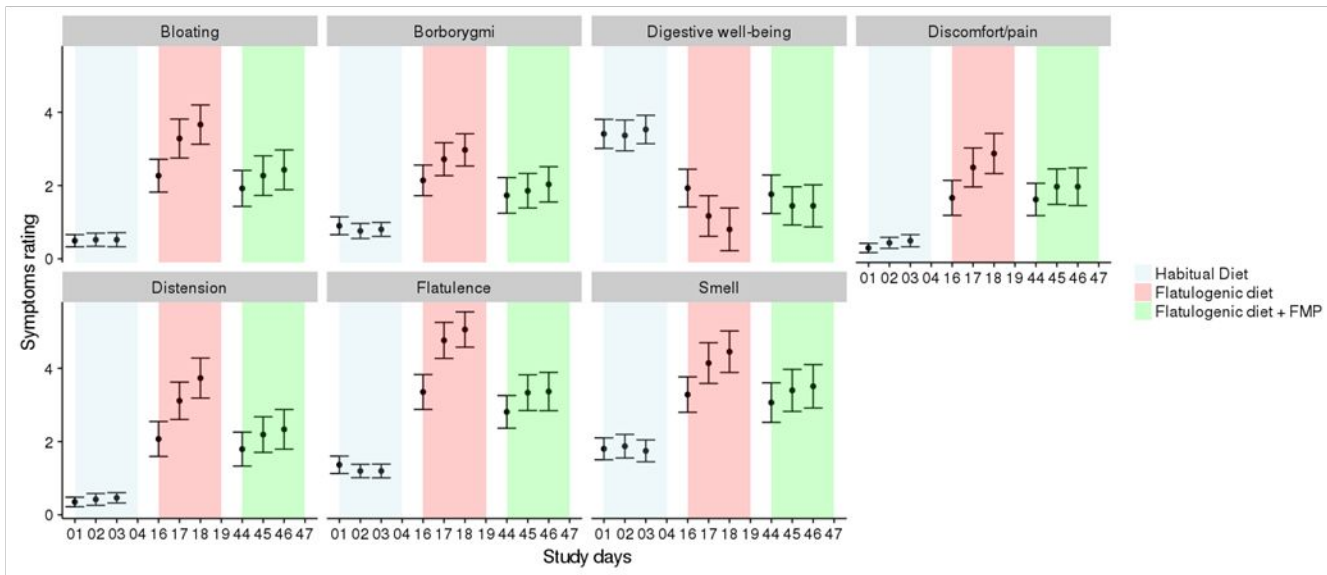
Lactobacillus delbrueckii subsp. *bulgaricus* (CNCM I-1519),

***Bifidobacterium animalis* subsp. *lactis* (CNCM I-2494)**

Lactococcus lactis subsp. *lactis* (CNCM I-1631).



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



After FMP consumption, FMP active strains detected by metatranscriptomics

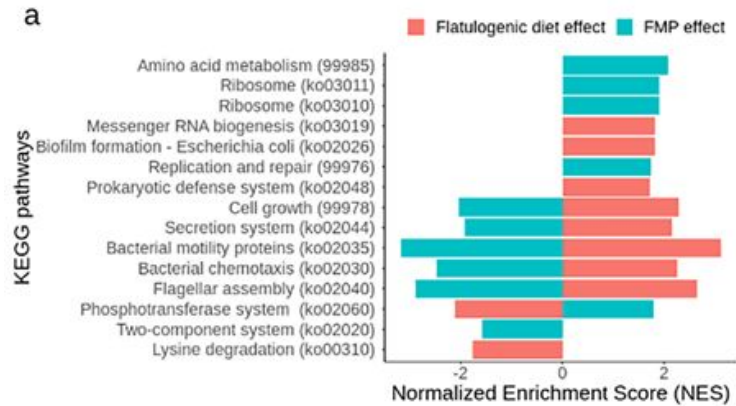


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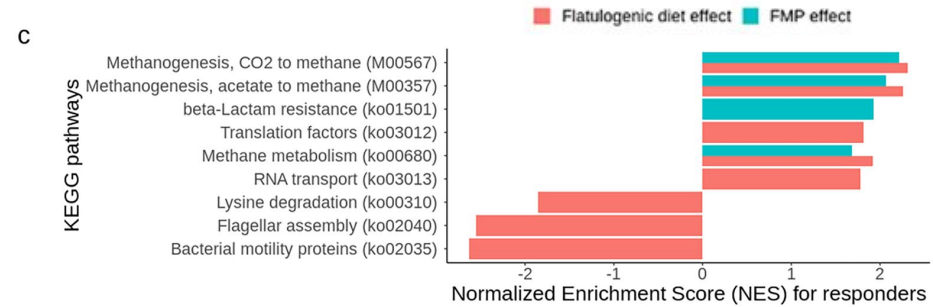
Next-Gen Fermented Food: Harnessing Gut Microbiome Diversity and Functions – Ferment'IA

13.09.23 / Julien Tap / fme.micalis.fr

- Fermented food consumption was associated with gut microbiota metabolic changes

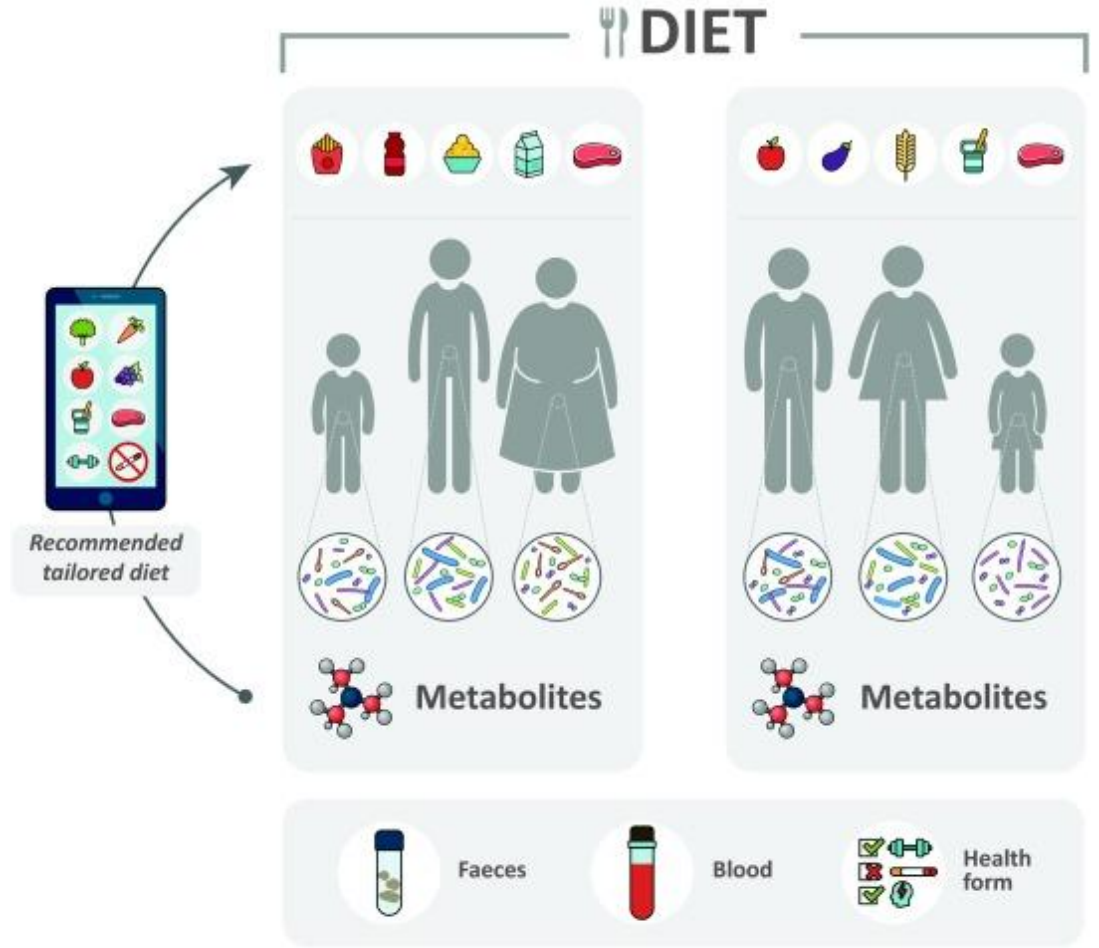
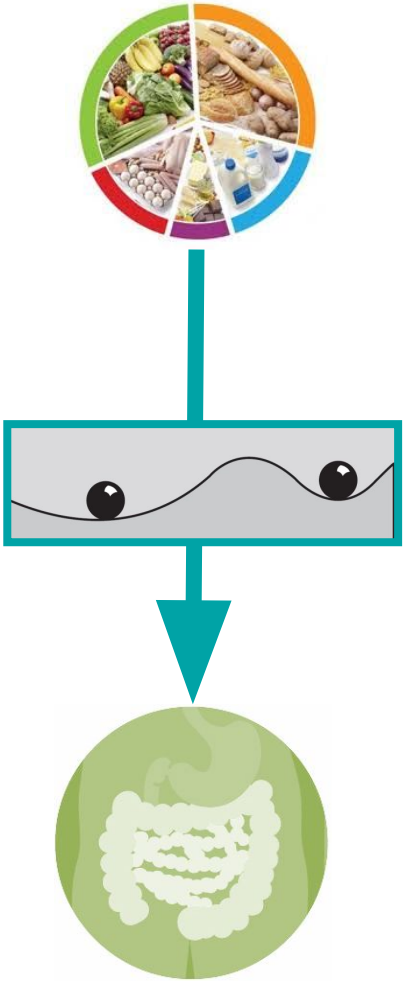


Flatulogenic diet might increase cell motility and cell growth whereas FMP consumption exhibited the opposite effect



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

- Endgame : From gut microbiome states to next-gen fermented food



Trends in Microbiology

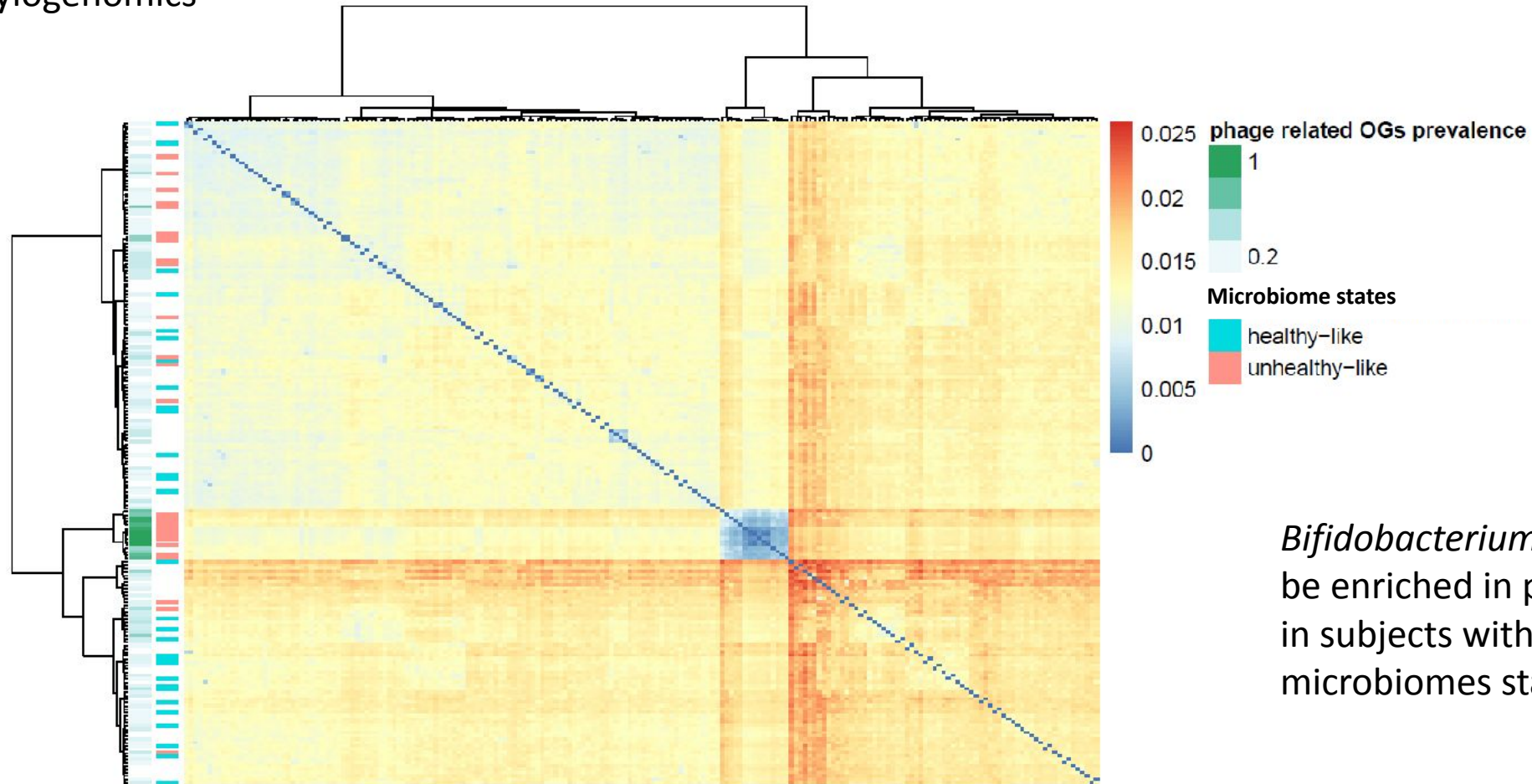
Prevent gut microbiome critical transition to strengthen its resilience using next-gen fermented food



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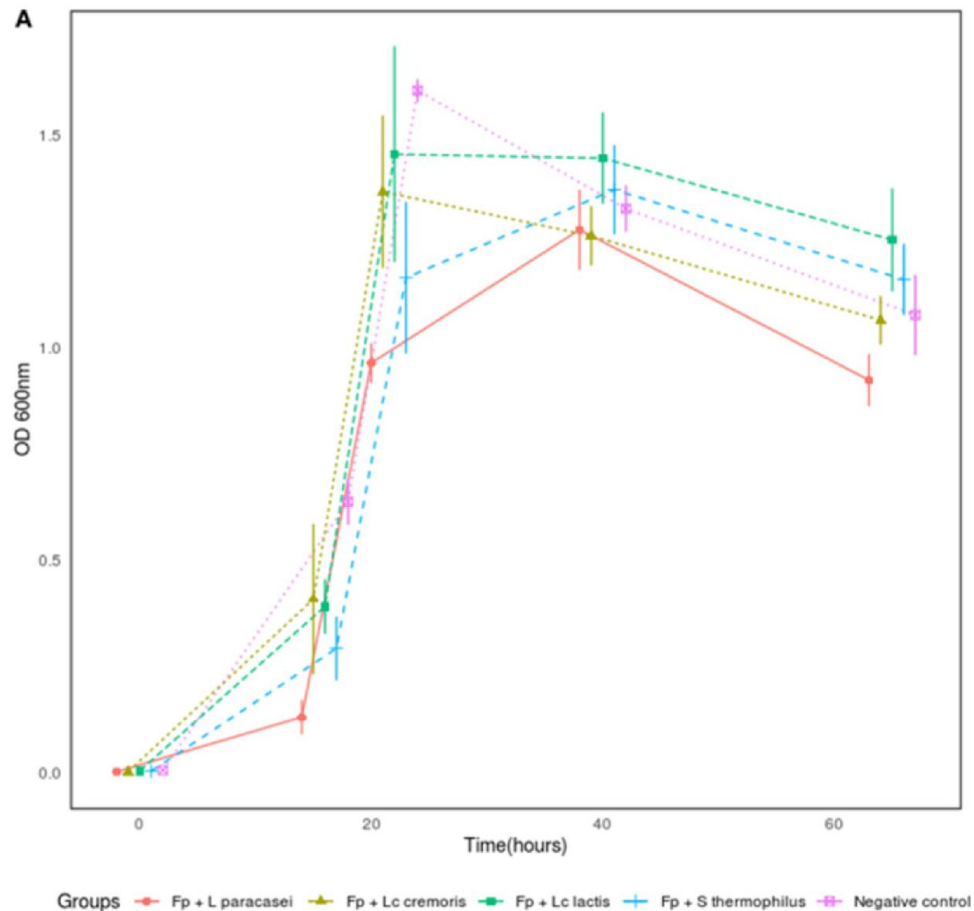
- Altered states showed functional differences within species

400 *B. bifidum* MAGS
phylogenomics

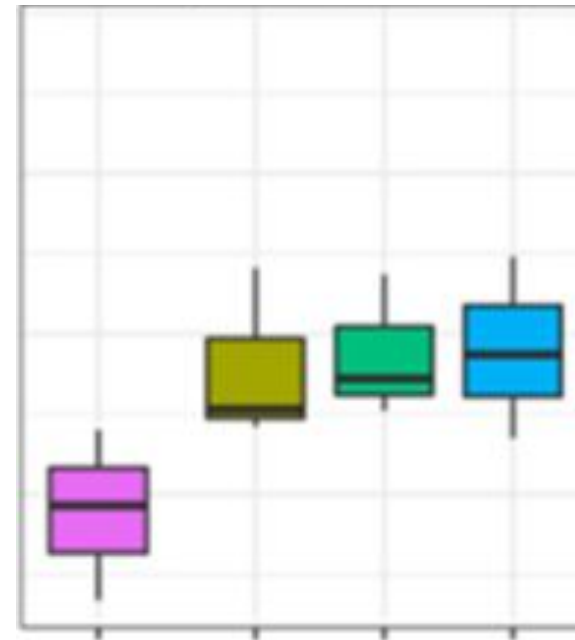


Bifidobacterium bifidum strains may be enriched in phage-related genes in subjects with altered gut microbiomes states

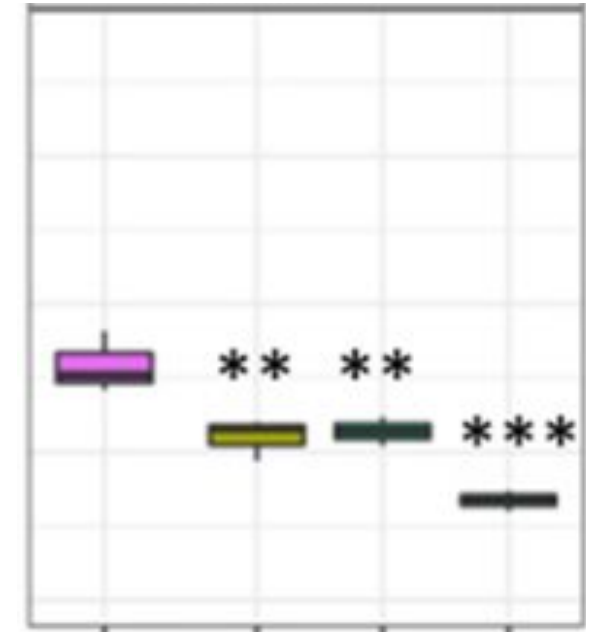
- Towards building food microbiome ecosystems with abilities to prevent catastrophic shifts in gut microbiota



umax



Decay slope

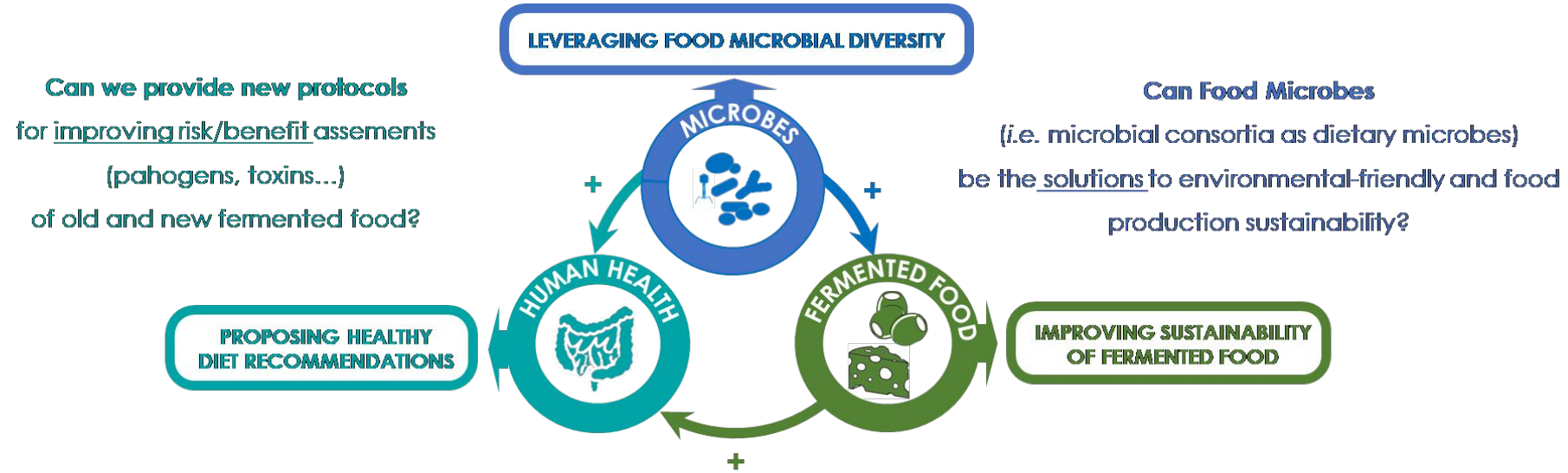


Increase of peptidoglycan levels for cell wall formation *F.prau*



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- How to design next-gen and sustainable fermented food?



Can we demonstrate that fermented food consumption improve human health and restore (maintain) human microbiome symbiotic relationship ?

What would be the impact of transition from animal- to plant-based fermented food (anti-nutritional factors, low availability of certain nutrients...) ?

Stéphane Chaillou (Coord.)



<https://www.domino-euproject.eu/>



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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 foods and biotics can help but effects may be personalized thanks to gut microbiota states and their functional contributions
- Prototyping process of next-gen fermented food should include gut tipping elements during screening for better personalized and beneficial effects.



- Acknowledgments



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...



redbionom

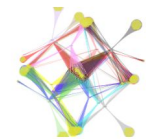
waldronlab/
curatedMetagenomicData



Curated Metagenomic Data of the Human Microbiome

16 Contributors 12 Issues 108 Stars 26 Forks

tapj/**branches**



code related to enterobranches

1 Contributor 0 Issues 0 Stars 1 Fork



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- BACK UP



