

# Epidemiological stability of the human gut microbiome and associated factors

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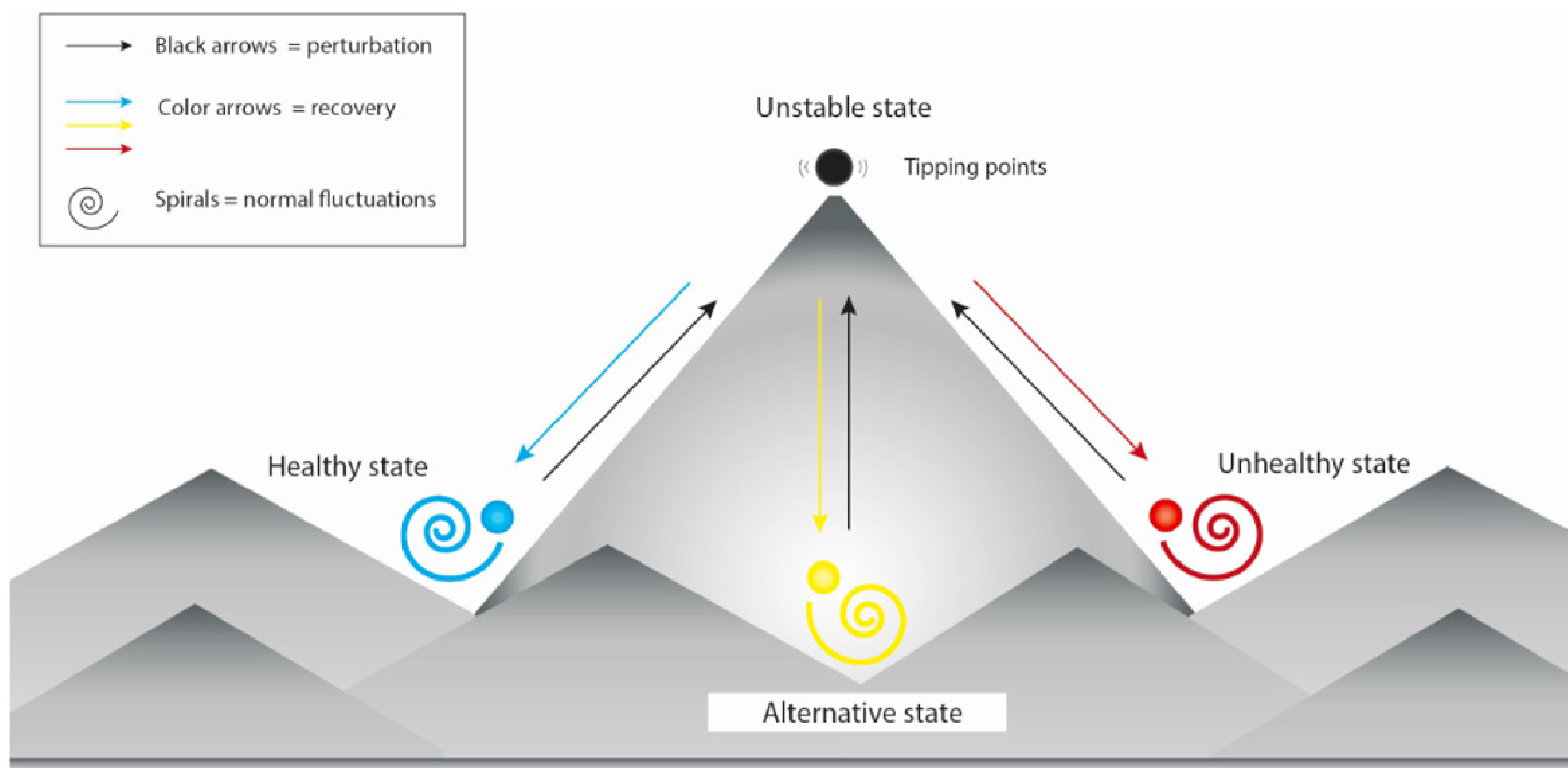
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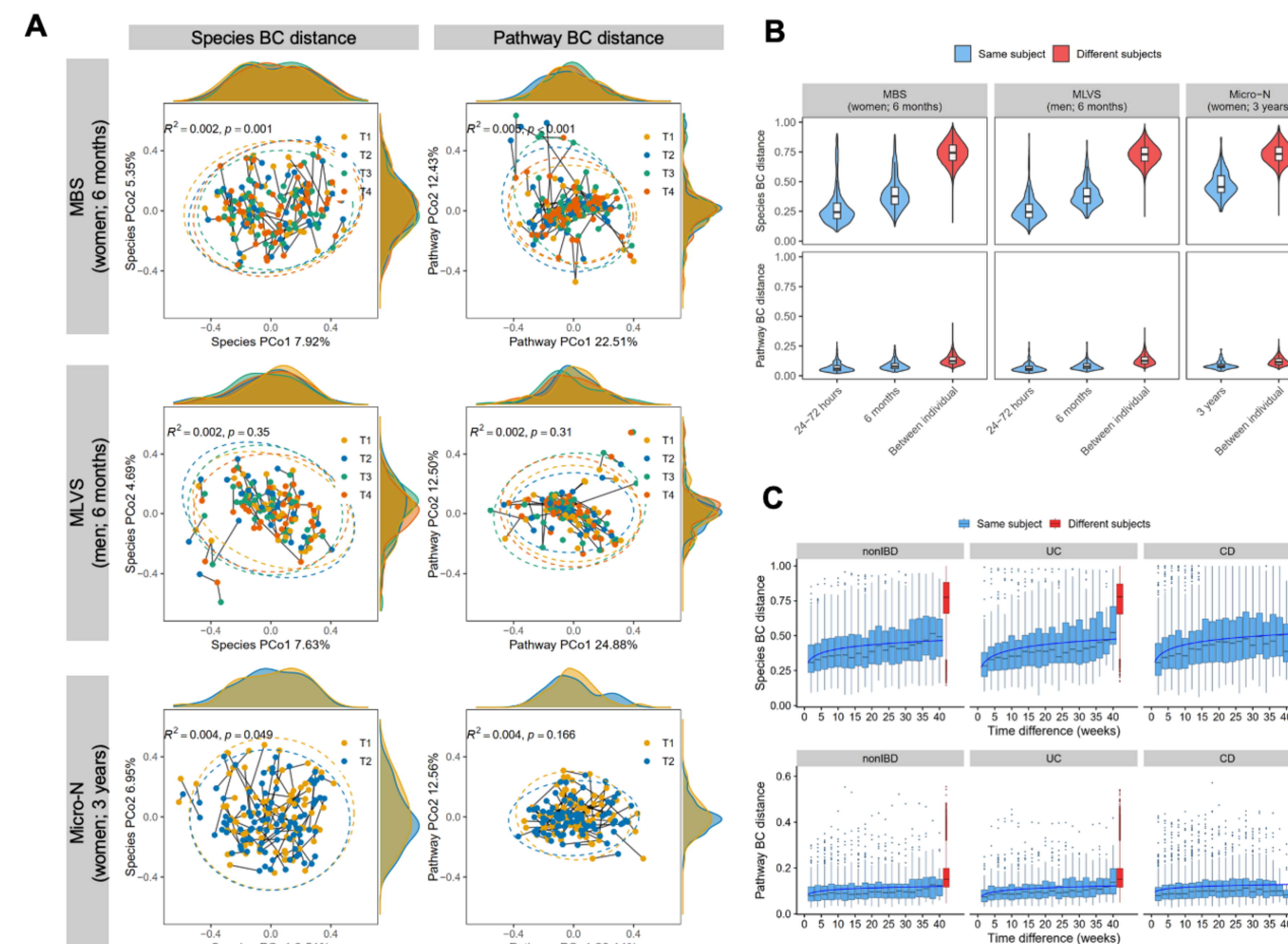
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## Background

- Fecal microbiome has been widely investigated as a predictive biomarker and potential diagnostic tool in epidemiological studies.
- However, the human gut microbiome is **dynamic** rather than static, which undergoes continuous fluctuations both autonomously as well as in response to short-term disruptions and long-term habitual factors.
- **Repeated stool sampling** is still challenging in large population-based cohort studies, highlighting the importance to characterize temporal dynamics of the gut microbiome in epidemiological settings.
- There is little evidence on how **modifiable risk factors** shape the temporal stability of human gut microbiome.

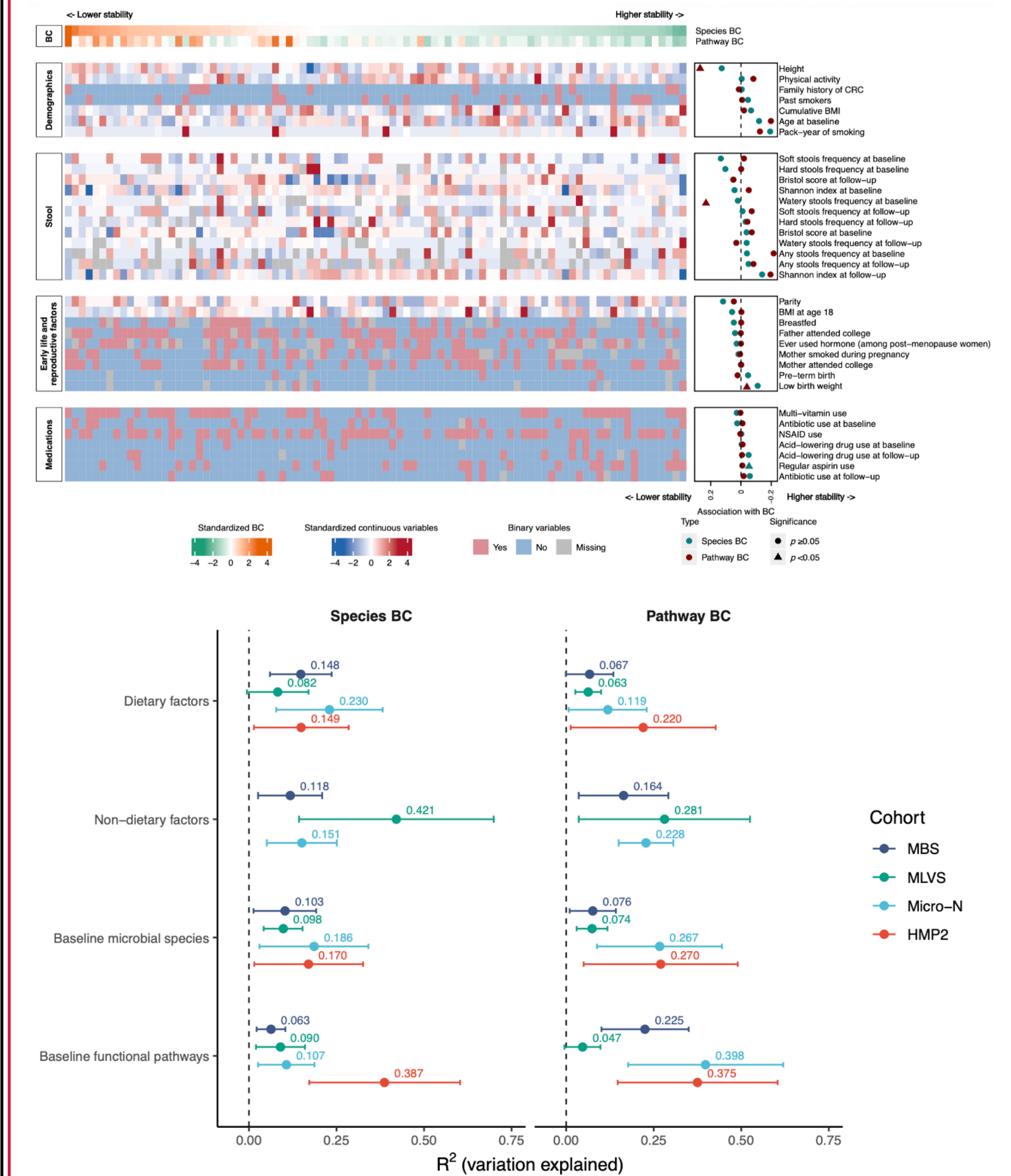


## Within-individual variation increases over time but remain substantially lower than between-individual variation

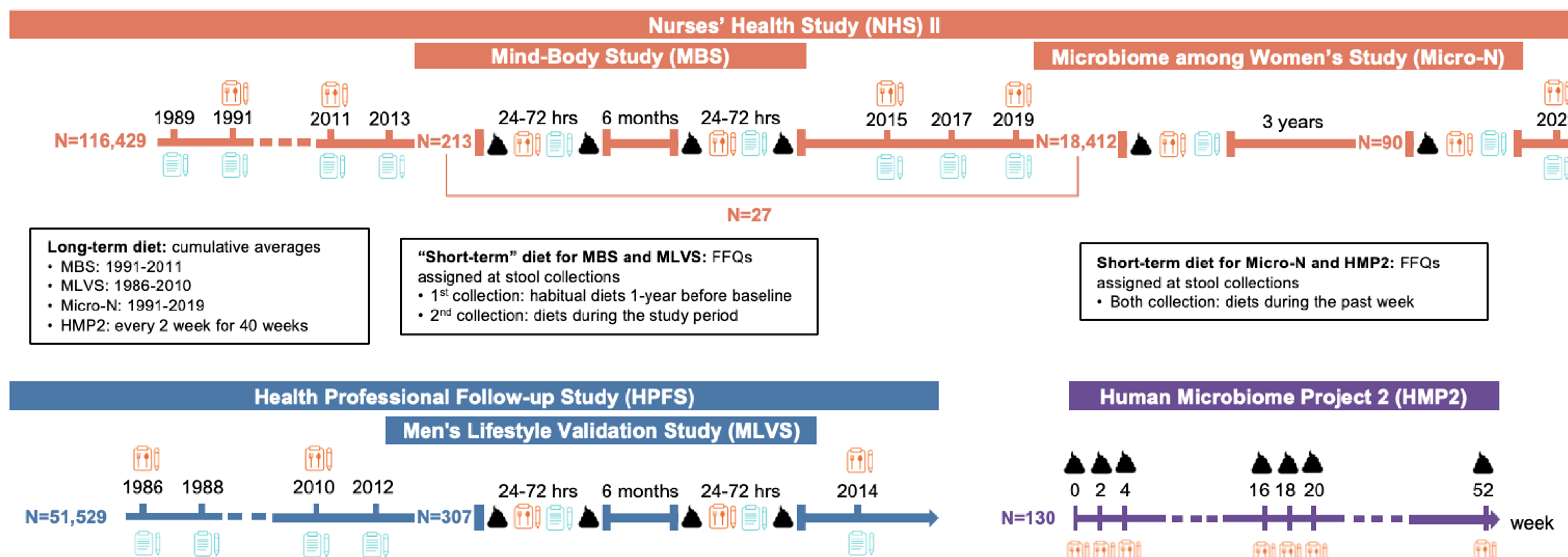


- Collection timepoint explained only a **minimal** proportion (0.2–0.5%) of the variation in BC distances of microbial composition, both at the species and pathway level
- **Functional** profiles tend to be more stable than **species** profiles

## Weak and inconsistent associations of diet and lifestyle factors with stability



## Study design



- Shotgun metagenomics sequencing
- MetaPhlan4 for taxonomic and HUMAnN4 for functional profiling
- Minimum prevalence (10% of samples) and relative abundance (taxa: >0.01%; pathways: >0.001%) thresholds

- In epidemiological settings, the human gut microbiome is relatively stable over time intervals ranging from days to years.
- Determinants of gut microbiome stability appear to vary across different time scales
- Provide context for future population-based research using fecal microbiome data.

## Acknowledgments & Contact

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