



MicrobTiSDA: a flexible R package for inferring interspecies interactions and abundance dynamics in microbiome time-series data

Shijia Li¹, Remco Kort², Tim G.J. de Meij³, Stanley Brul¹,
Meike T. Wortel^{1*}, Johan A. Westerhuis^{1*}

¹Swammerdam Institute for Life Sciences, University of Amsterdam

²Amsterdam Institute for Life and Environment, Vrije Universiteit Amsterdam

³Amsterdam Gastroenterology Endocrinology Metabolism Research Institute,
Amsterdam UMC

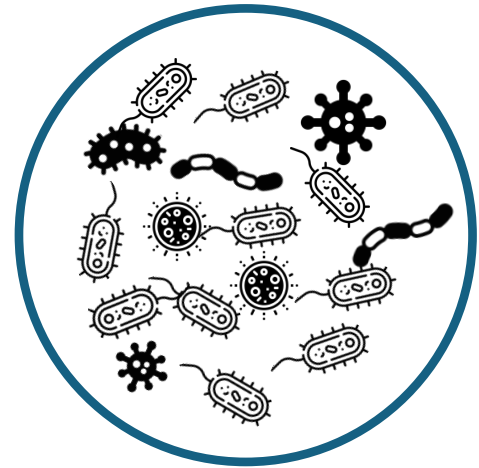
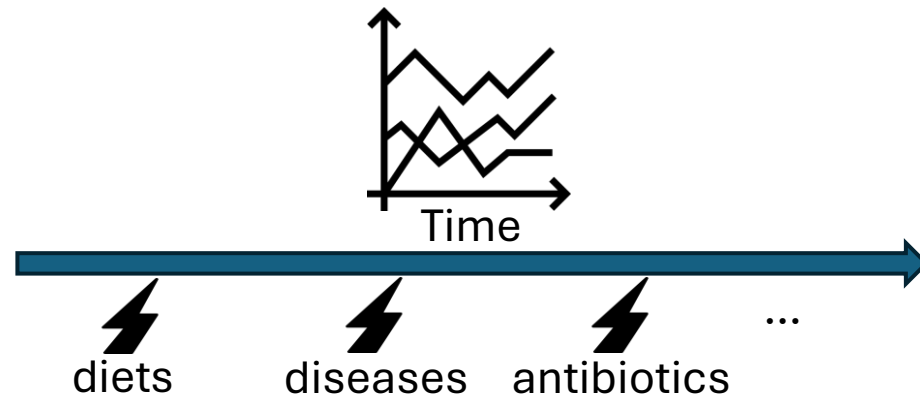


Shijia Li, Remco Kort, Tim G.J. de Meij, Stanley Brul, Meike T. Wortel, Johan A. Westerhuis. 2025. MicrobTiSDA: a flexible R package for inferring interspecies interactions and abundance dynamics in microbiome time-series data. *iMetaOmics* 2: e70067. <https://doi.org/10.1002/imo2.70067>



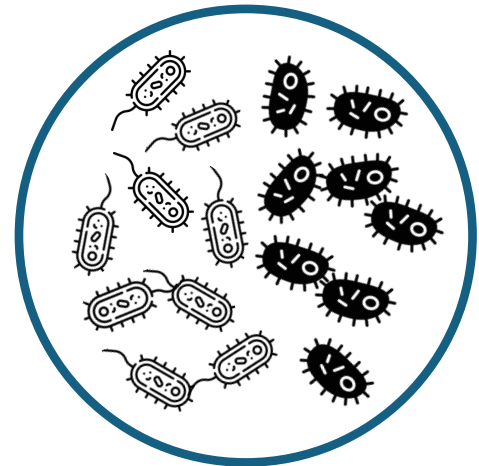
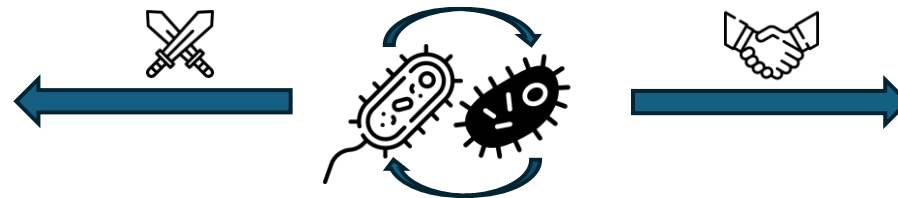
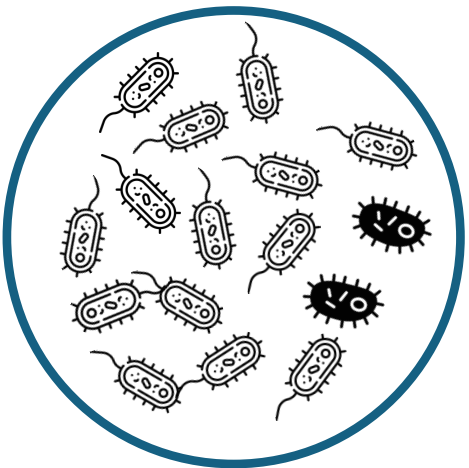
Background

①



Q1: Species temporal dynamic patterns

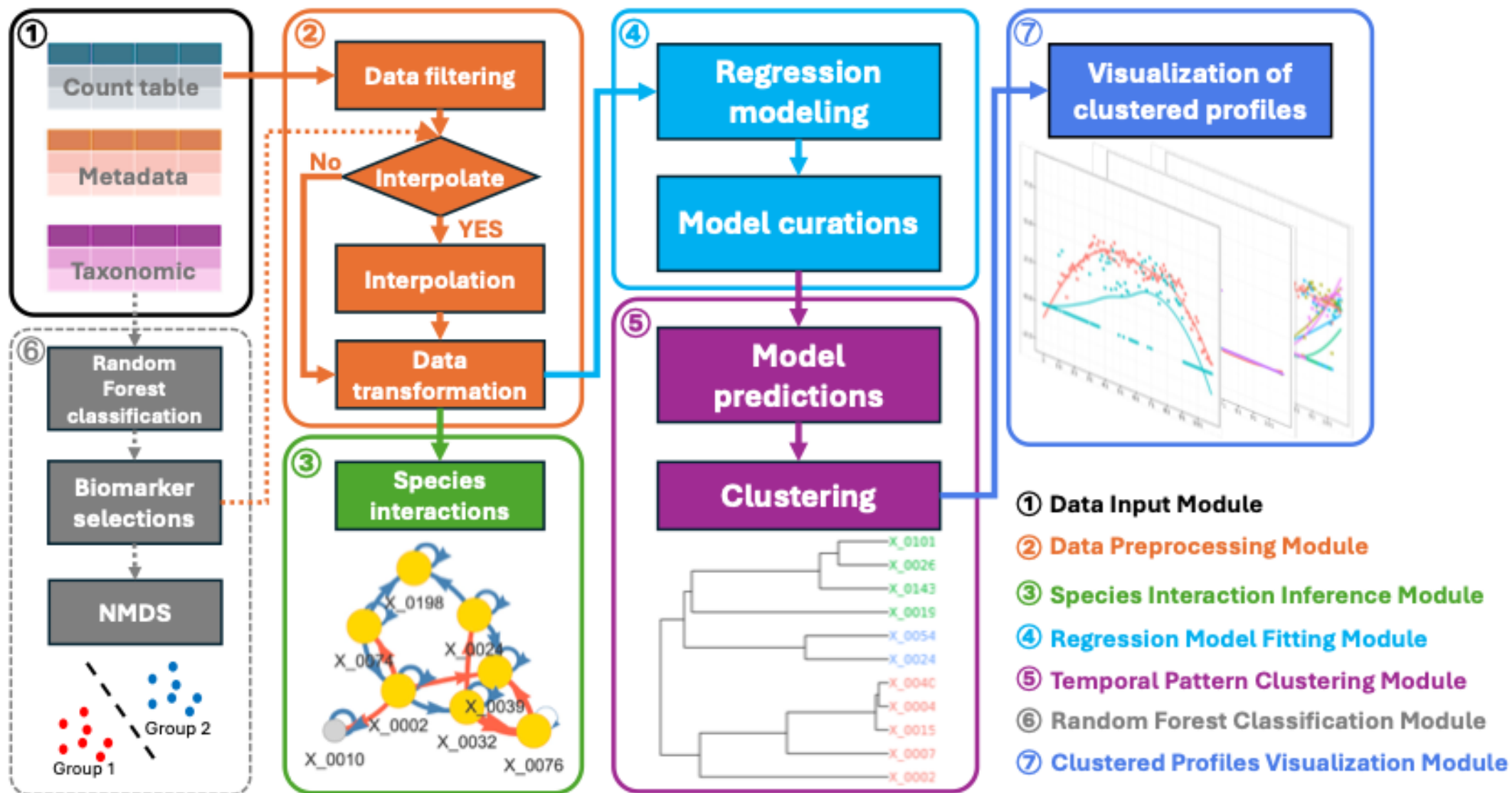
②



Q2: Species interaction relationships



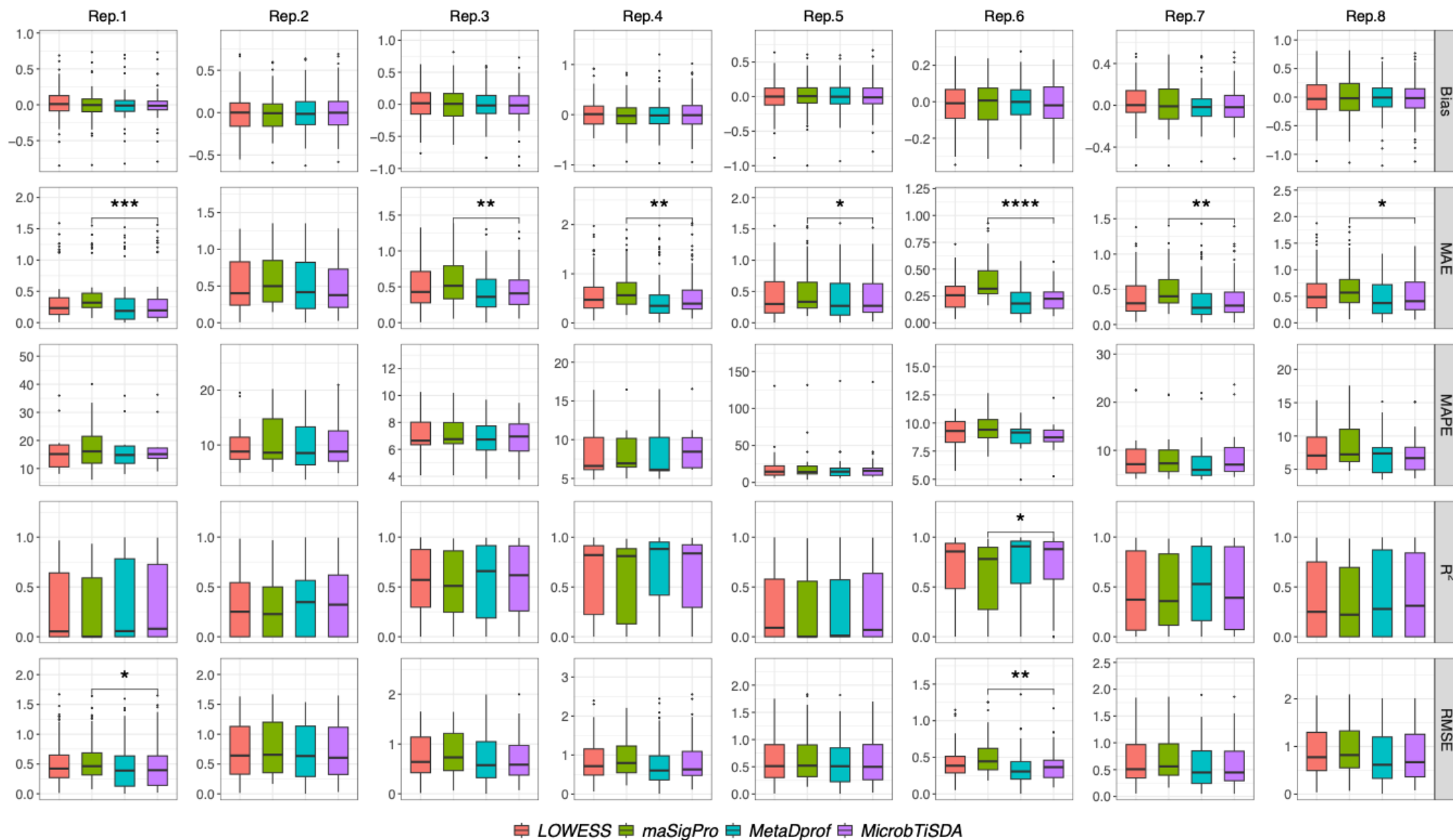
Methods





Performance evaluation

- Evaluation of natural spline regression model performance

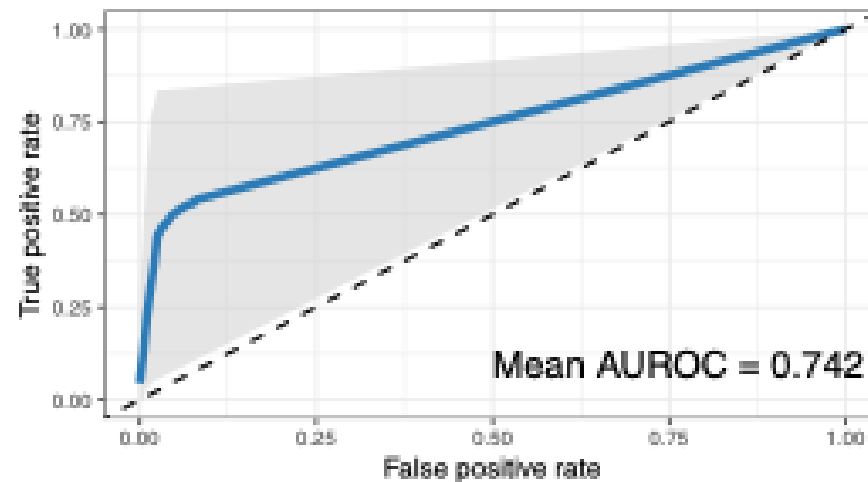




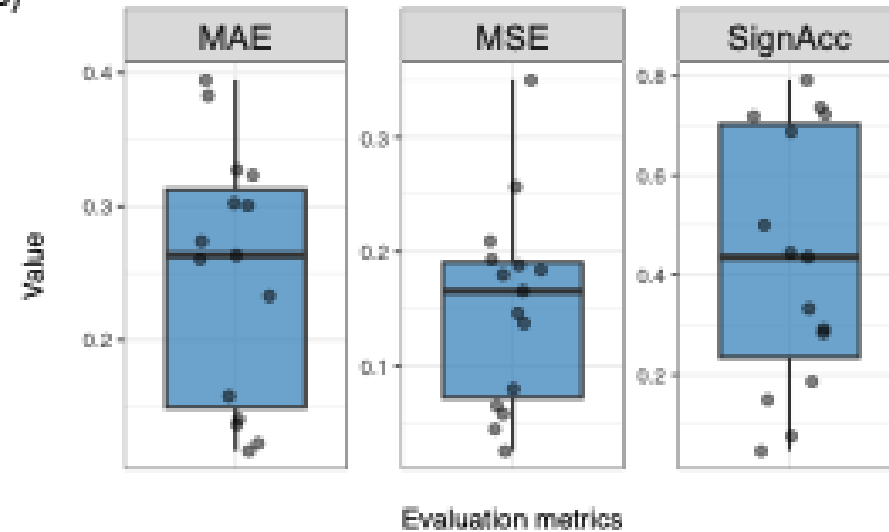
Performance evaluation

- Evaluation of interspecies interaction inference performance

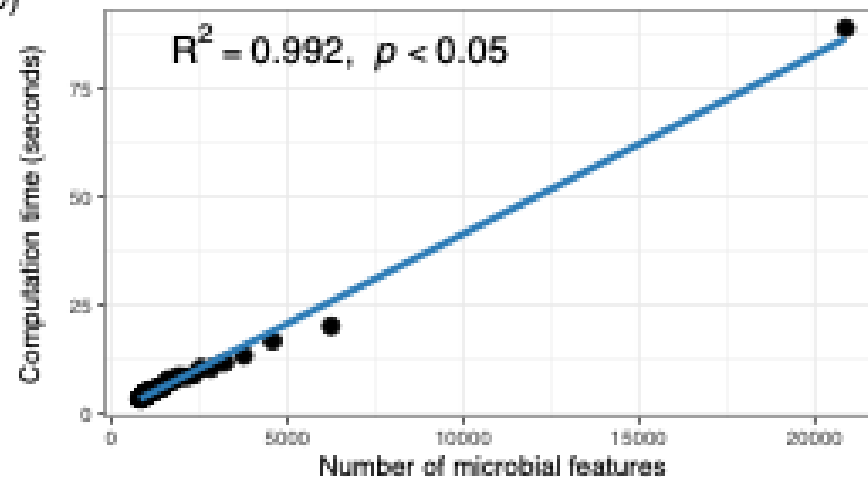
(A)



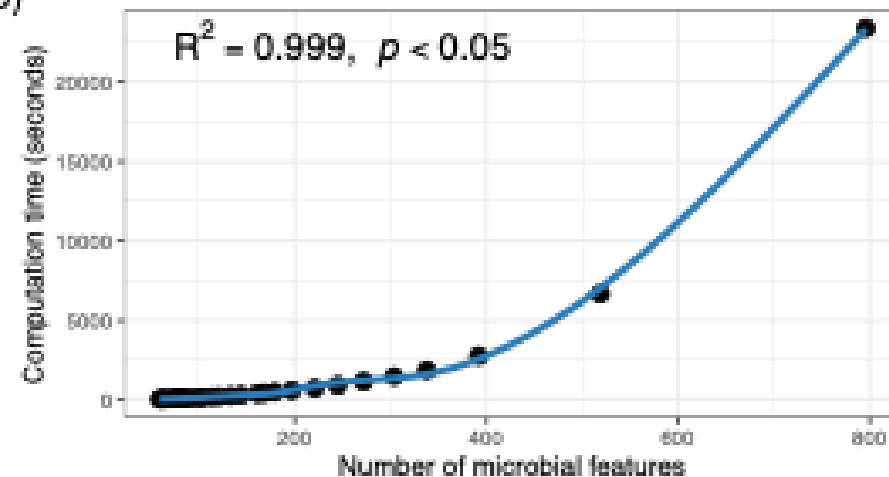
(B)



(C)



(D)

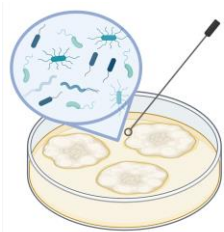
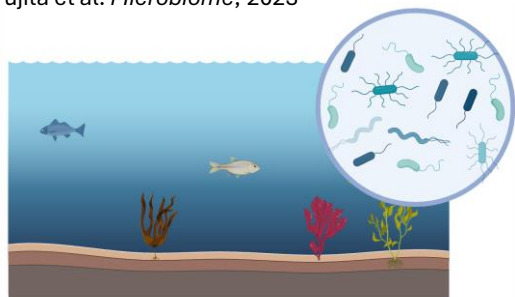




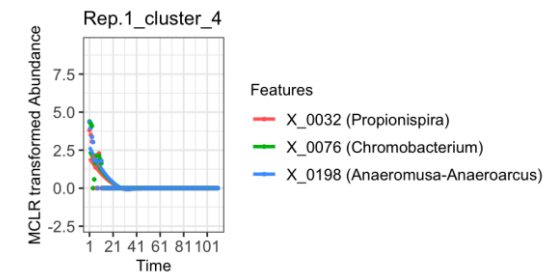
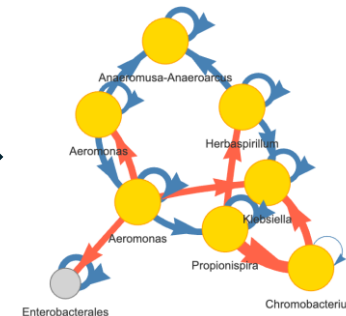
Applications

Dataset 1: Aquatic microbiome

Fujita et al. *Microbiome*, 2023

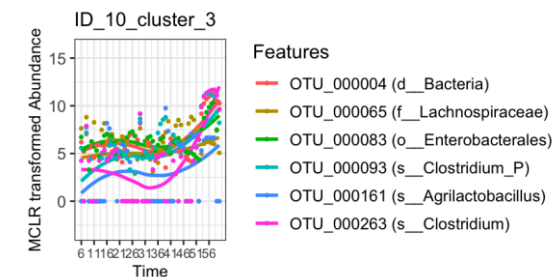
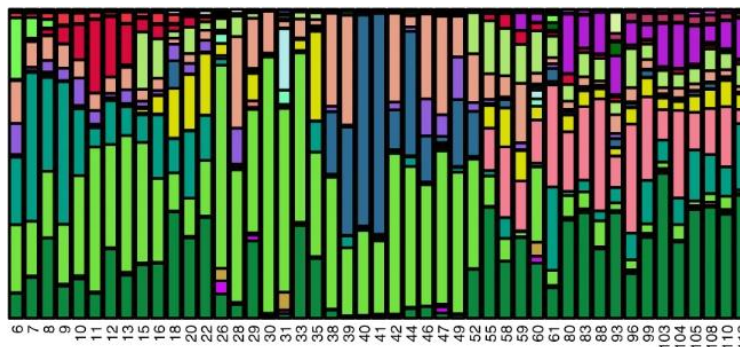
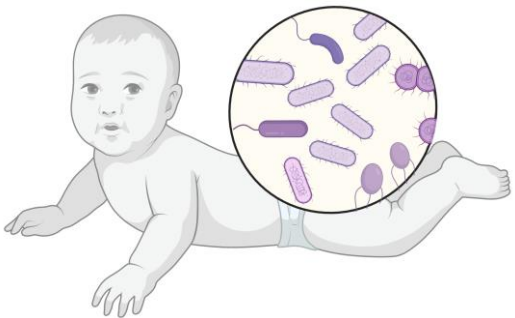


880 time-series samples



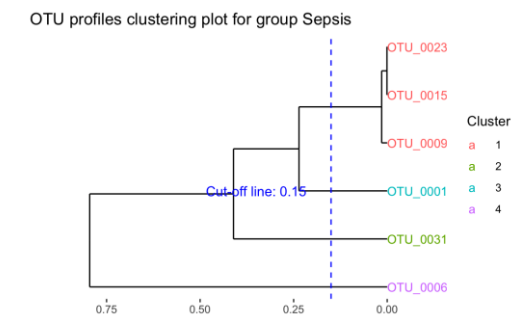
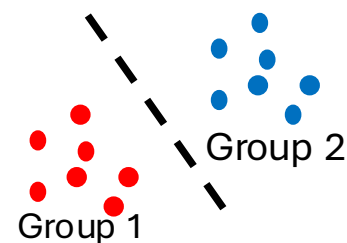
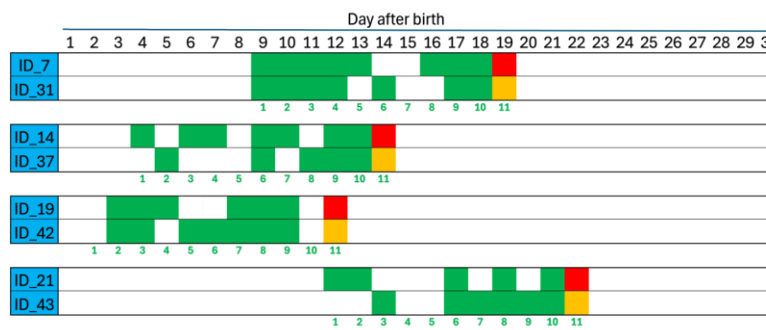
Dataset 2: Term infant gut microbiome

de Muinck et al. *Nature communications*, 2017



Dataset 3: Preterm infant gut microbiome

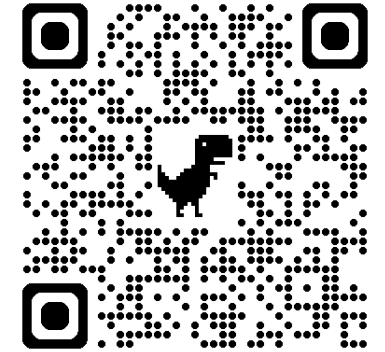
56 time-series samples





Summary

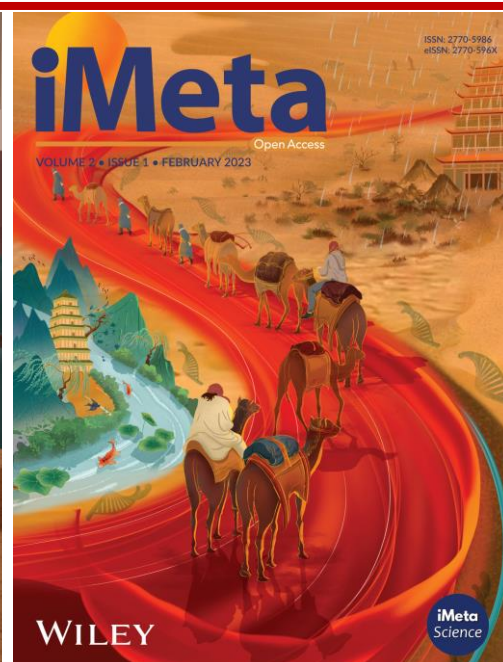
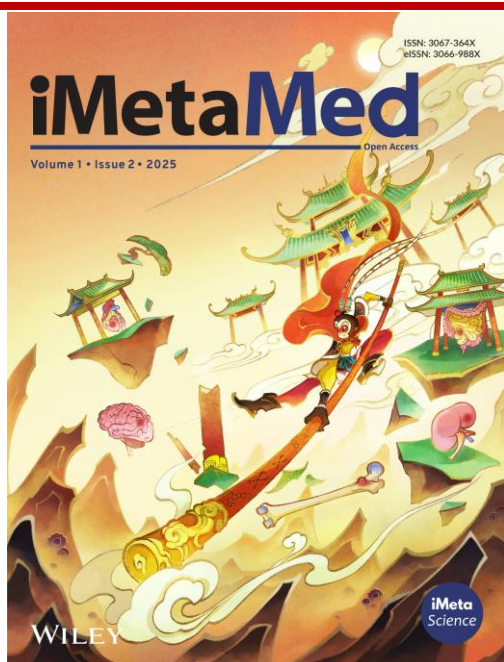
- ❑ In this study, we introduced an R package, MicrobTiSDA, specifically designed for the analysis of microbiome time-series data;
- ❑ MicrobTiSDA provides a streamlined workflow for microbiome time-series data analysis;
- ❑ Compared to similar tools, MicrobTiSDA demonstrates superior performance and rapid computational efficiency;
- ❑ MicrobTiSDA offers high flexibility and broad applicability across diverse microbiome datasets;
- ❑ Website: <https://github.com/Lishijiagg/MicrobTiSDA>



Shijia Li, Remco Kort, Tim G.J. de Meij, Stanley Brul, Meike T. Wortel, Johan A. Westerhuis. 2025. MicrobTiSDA: a flexible R package for inferring interspecies interactions and abundance dynamics in microbiome time-series data. *iMetaOmics* 2: e70067. <https://doi.org/10.1002/imo2.70067>

iMeta: To be top journals in biology and medicine

WILEY



“iMeta” launched in 2022 by iMeta Science Society, **impact factor (IF) 33.2**, ranking **top 65/22249 in world and 2/161 in the microbiology**. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Cell*, *Nature Biotechnology*/*Methods*/*Microbiology*/*Medicine*/*Food***. Its unique features include video abstract, bilingual publication, and social media with 600,000 followers. Indexed by **SCIE/ESI**, **PubMed**, **Google Scholar** etc.

“iMetaOmics” launched in 2024, with a **target IF>10**, and its scope is similar to ***Nature Communications*, *Cell Reports*, *Microbiome*, *ISME J*, *Nucleic Acids Research*, *Briefings in Bioinformatics***, etc.

“iMetaMed” launched in 2025, with a **target IF>15**, similar to ***Med*, *Cell Reports Medicine*, *eBioMedicine*, *eClinicalMedicine*** etc.



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

Submission: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



[iMetaScience](#)



[iMetaScience](#)



office@imeta.science

imetaomics@imeta.science



[Promotion Video](#)

Update
2025/7/6