



# MicrobTiSDA: 一个用于纵向微生物组数据分析的灵活R包

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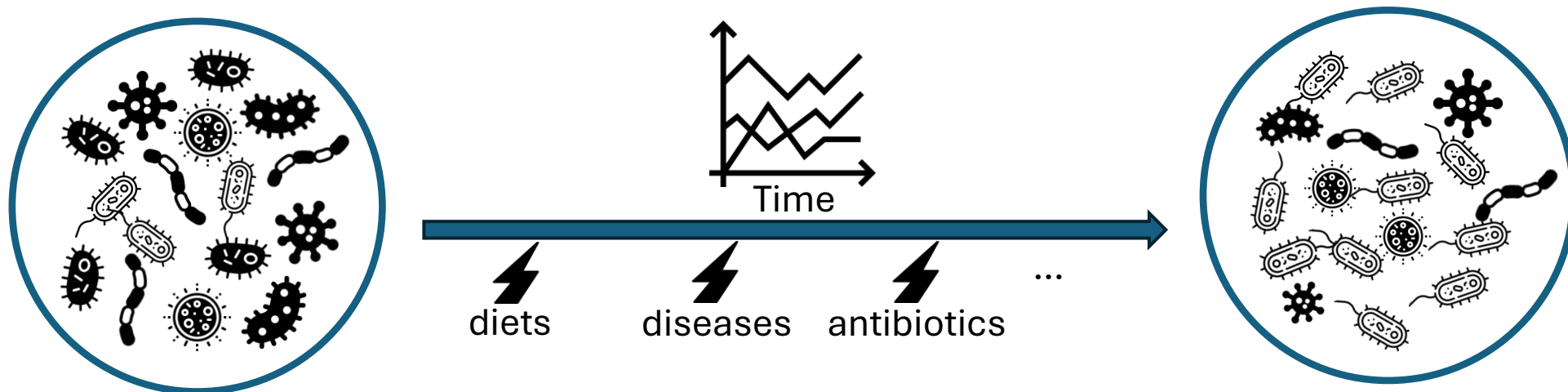


Shijia Li, Remco Kort, Tim G.J. de Meij, Stanley Brul, Meike T. Wortel, Johan A. Westerhuis. 2025. MicrobTiSDA: a flexible R package for inferring interspecies interactions and abundance dynamics in microbiome time-series data. *iMetaOmics* 2: e70067. <https://doi.org/10.1002/imo2.70067>



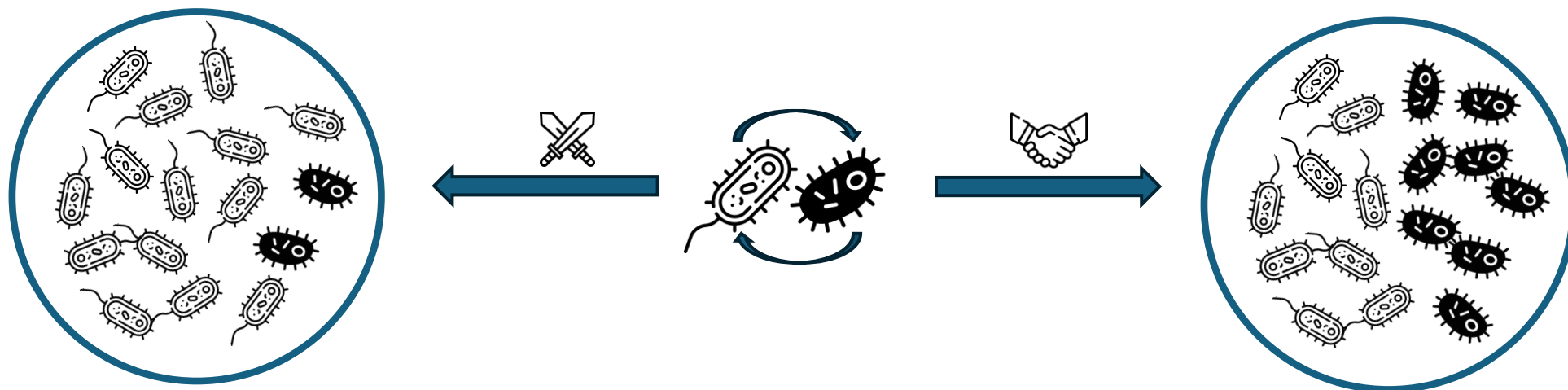
# 背景

①



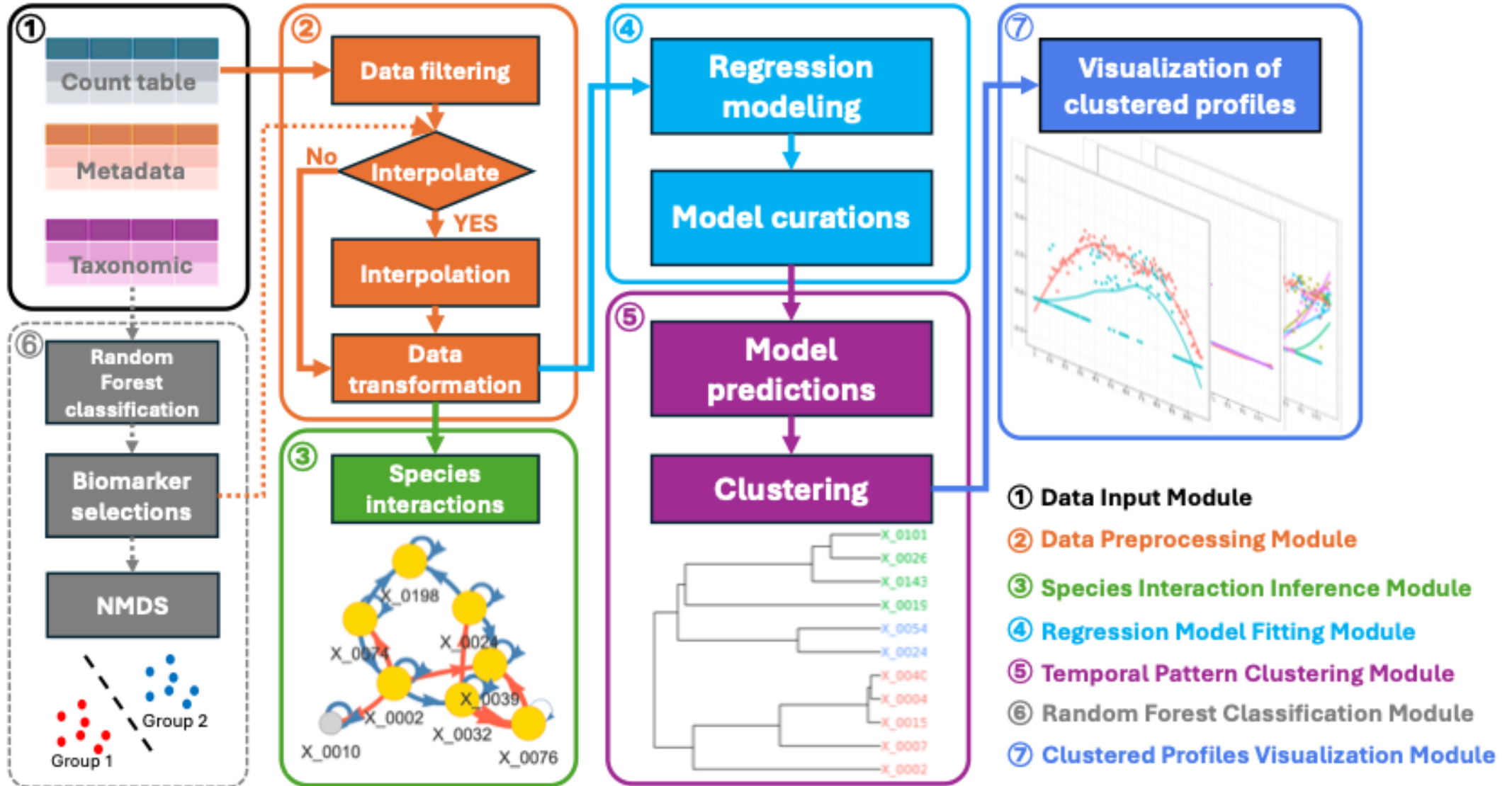
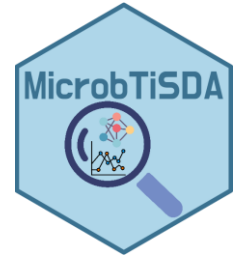
Q1: 微生物群落中的微生物丰度如何随时间发生变化?

②



Q2: 微生物群落中的物种之间存在什么样的交互作用模式?

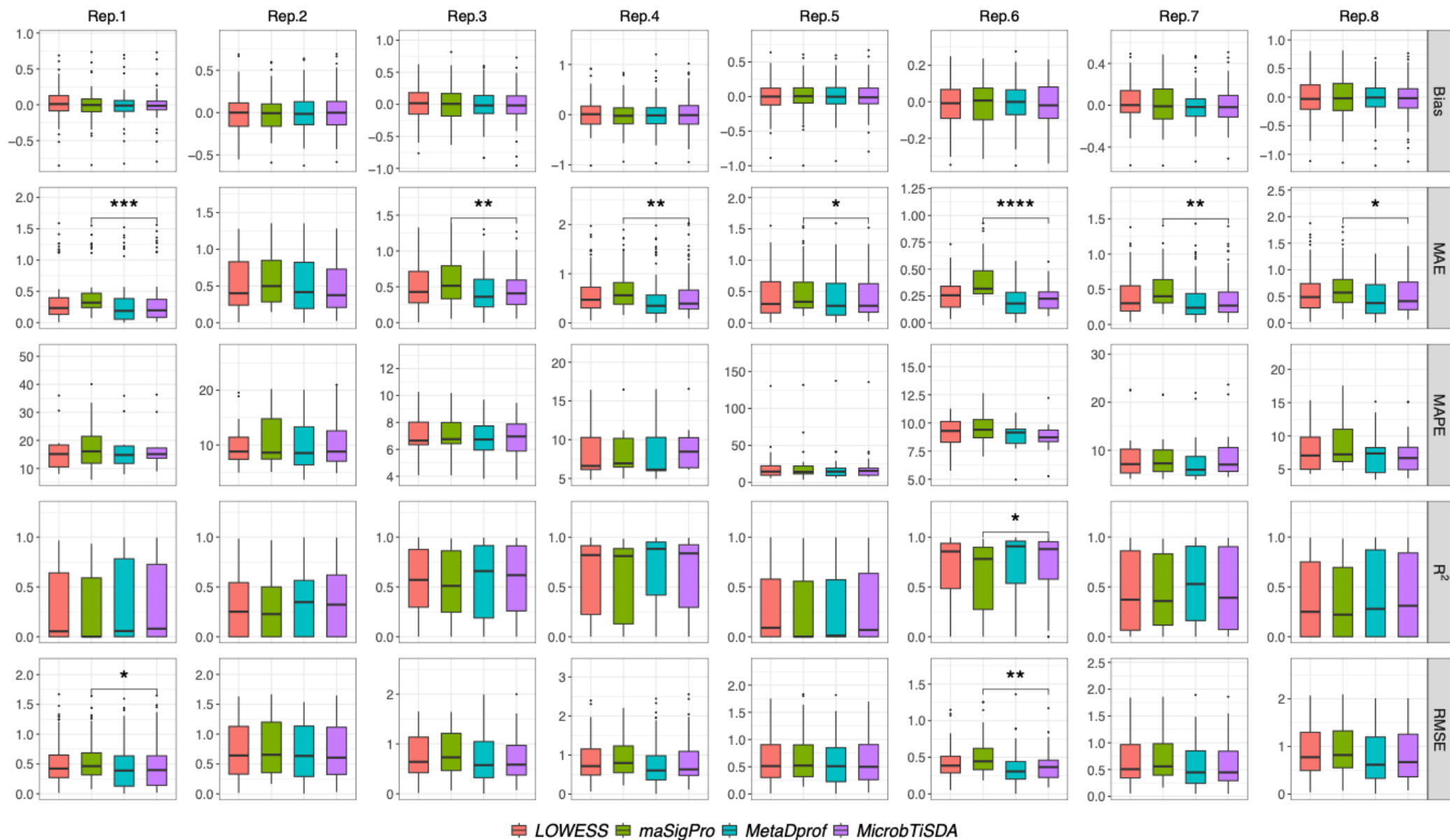
# 方法





# MicrobTiSDA性能测试

- MicrobTiSDA拟合的物种时间序列丰度回归模型的性能评估

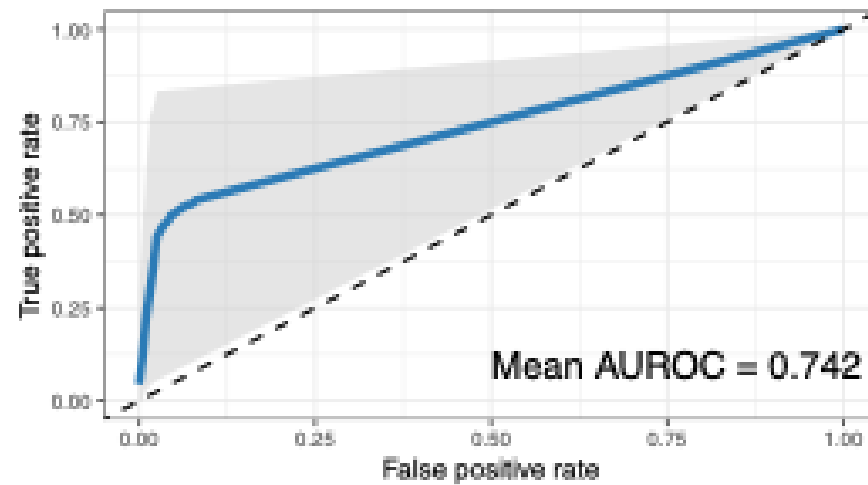




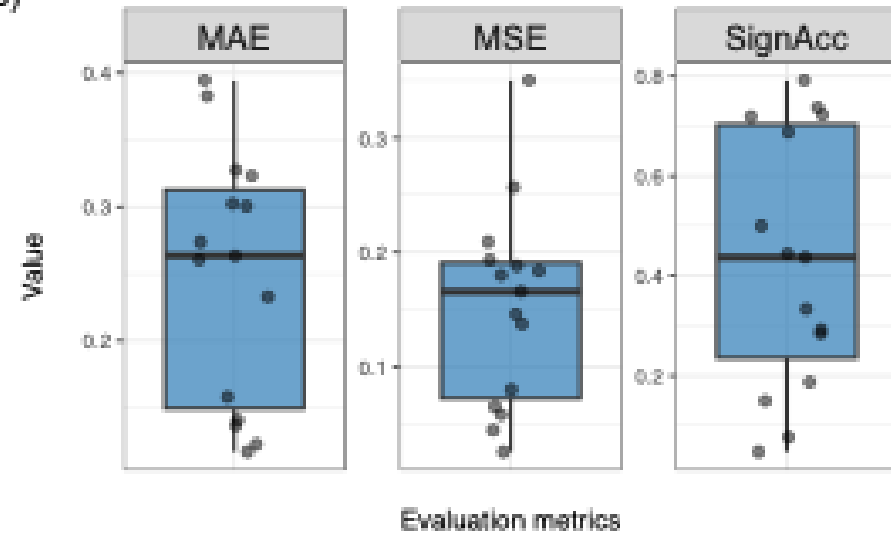
# MicrobTiSDA性能测试

- MicrobTiSDA推断物种交互作用的性能评估以及运算速率评估

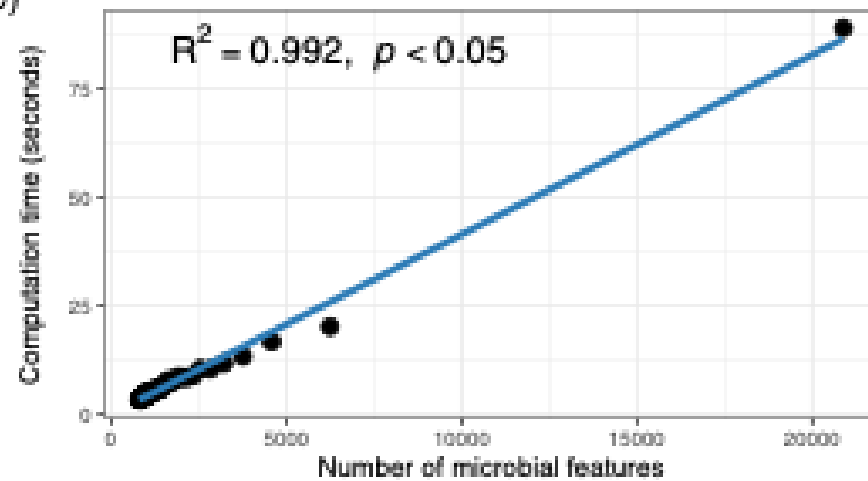
(A)



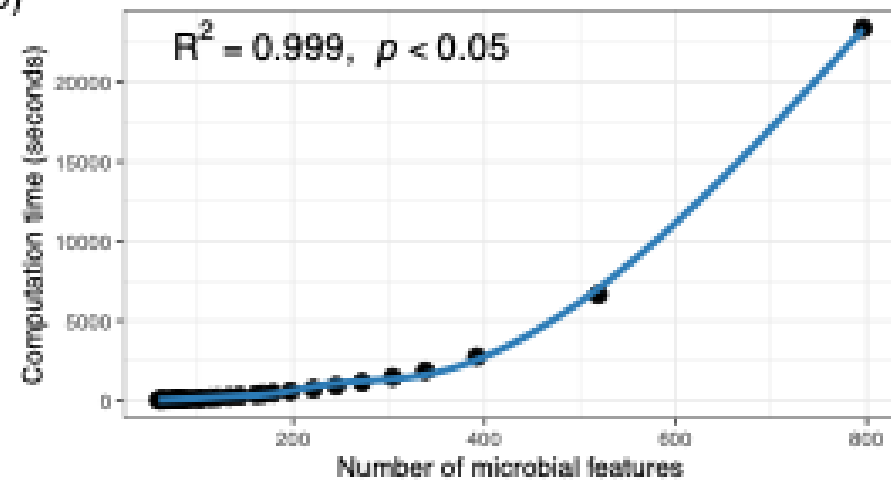
(B)



(C)



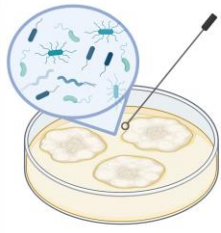
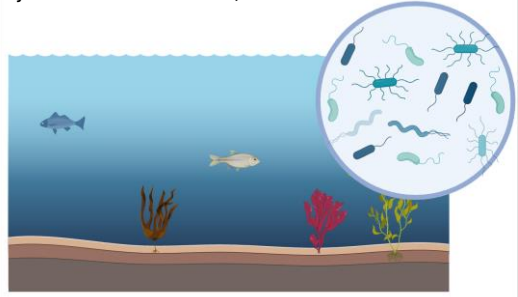
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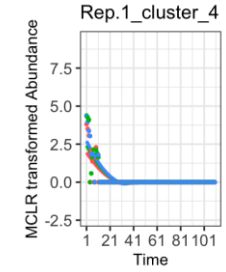
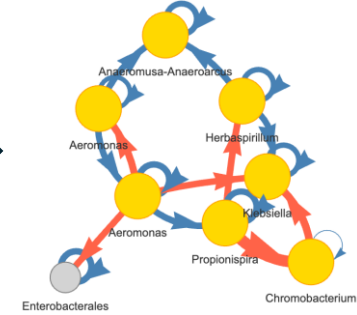
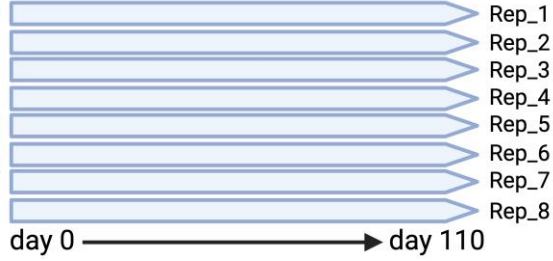
# 应用

## Dataset 1: Aquatic microbiome

Fujita et al. *Microbiome*, 2023



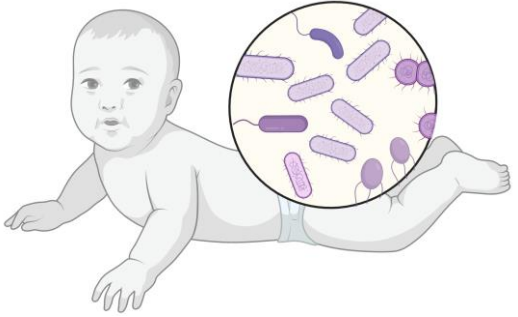
## 880 time-series samples



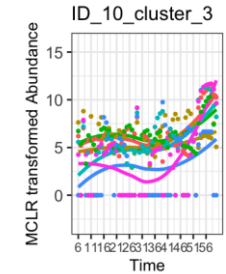
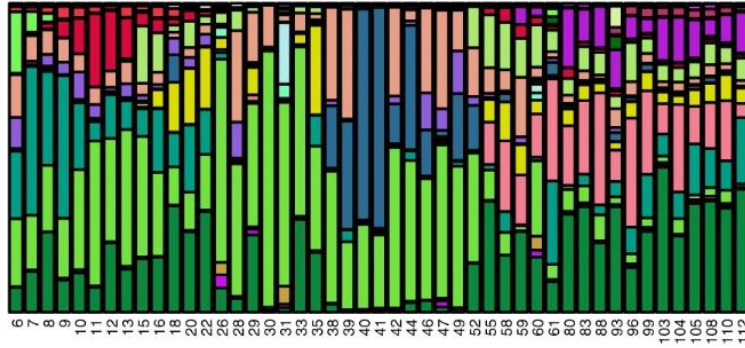
Features  
— X\_0032 (Propionispira)  
— X\_0076 (Chromobacterium)  
— X\_0198 (Anaeromusa-Anaeroarcus)

## Dataset 2: Term infant gut microbiome

de Muinck et al. *Nature communications*, 2017



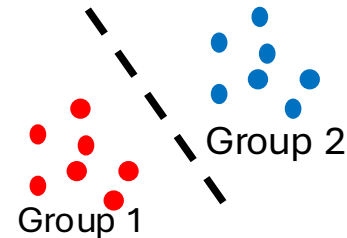
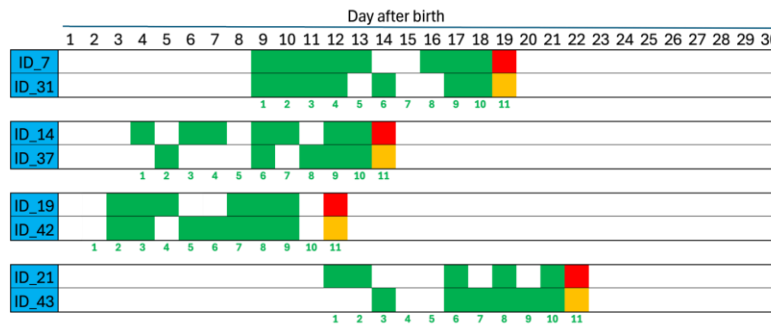
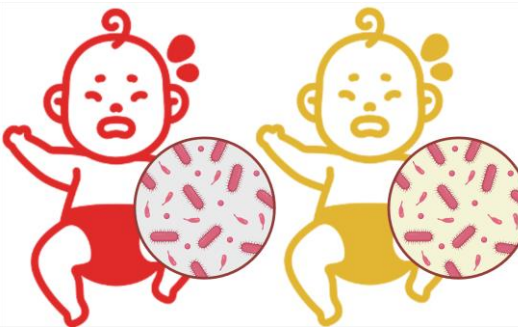
## 2684 time-series samples



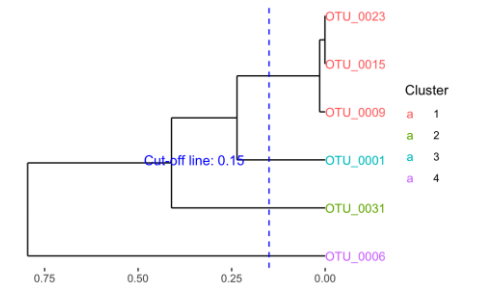
Features  
— OTU\_000004 (d\_Bacteria)  
— OTU\_000065 (f\_Lachnospiraceae)  
— OTU\_000083 (o\_Enterobacteriales)  
— OTU\_000093 (s\_Clostridium\_P)  
— OTU\_000161 (s\_Agrilactobacillus)  
— OTU\_000263 (s\_Clostridium)

## Dataset 3: Preterm infant gut microbiome

## 56 time-series samples



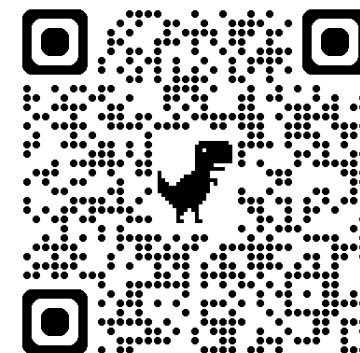
OTU profiles clustering plot for group Sepsis



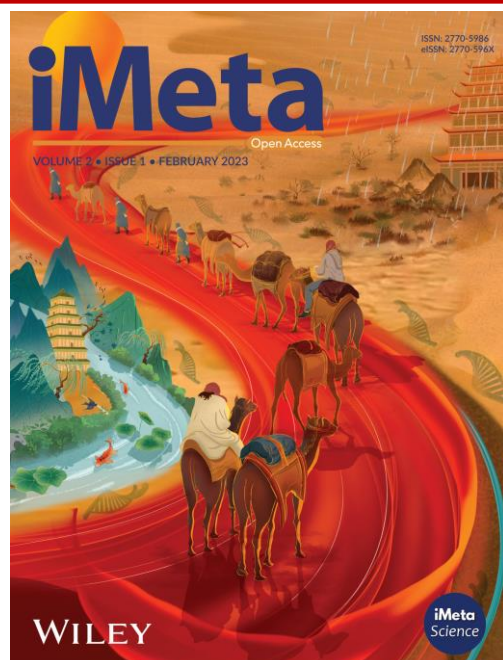


# 总结

- 在这项研究中，我们介绍了一个专门用于微生物组时间序列数据分析的R包——MicrobTiSDA;
- MicrobTiSDA为微生物组时间序列数据分析提供从数据预处理到结果可视化的流程化的解决方案;
- MicrobTiSDA与类似的工具相比具有更好的性能以及快速的运算效率;
- MicrobTiSDA具有极高的灵活性与广泛适用性;
- 网址: <https://github.com/Lishijiagg/MicrobTiSDA>



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