

QCMi: 定量群落水平下假定的微生物生物关联的方法

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² 中国科学院大学

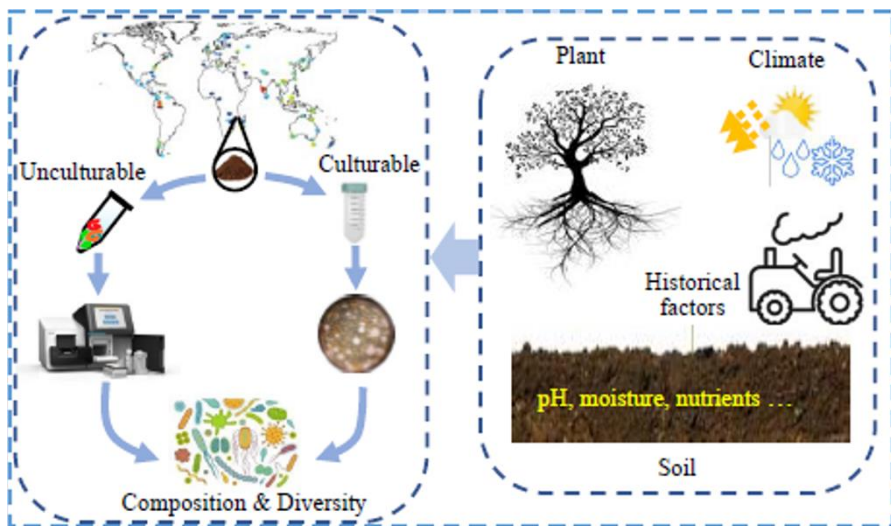
³ 河南大学生命科学学院作物逆境适应与改良国家重点实验室



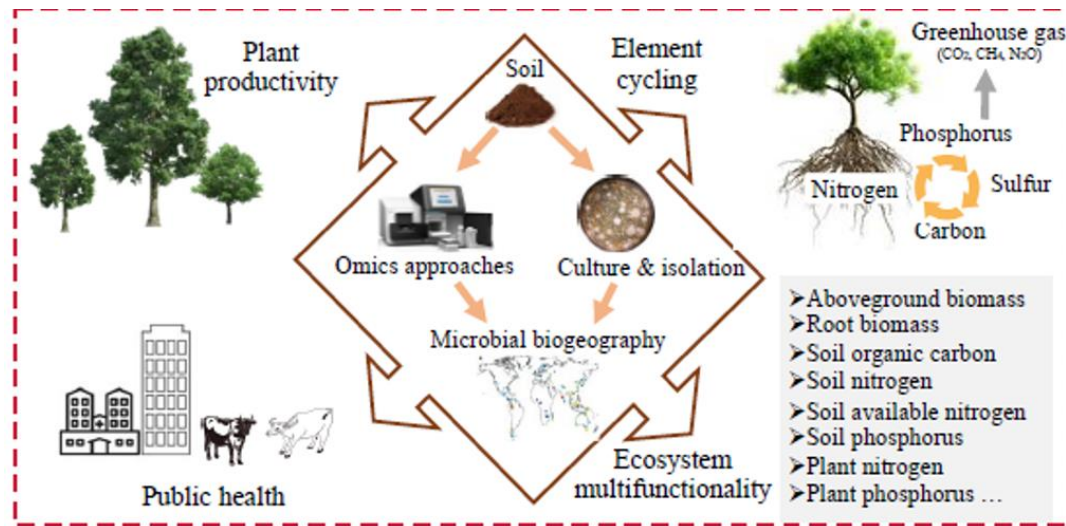
Xu Liu, Yu Shi, Teng Yang, Gui-Feng Gao, Haiyan Chu. 2023. *QCMi*: A method for quantifying putative biotic associations of microbes at the community level. *iMeta*: e92. <https://doi.org/10.1002/imt2.92>

研究背景

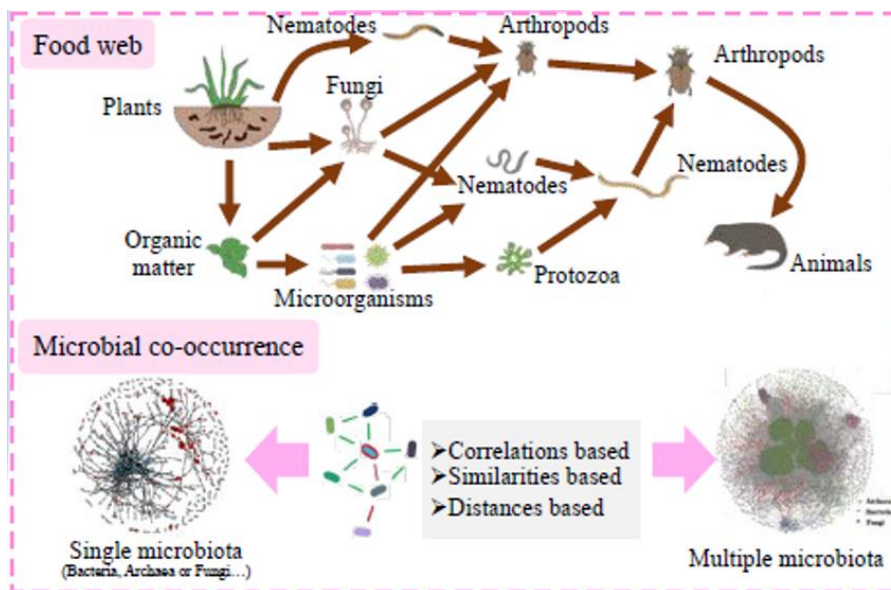
分布



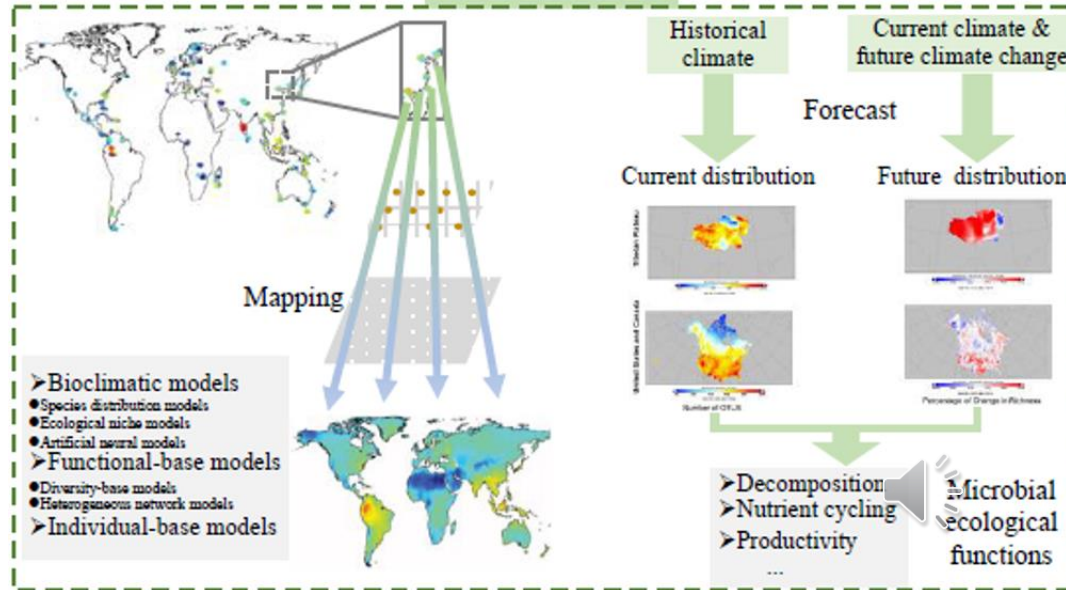
功能



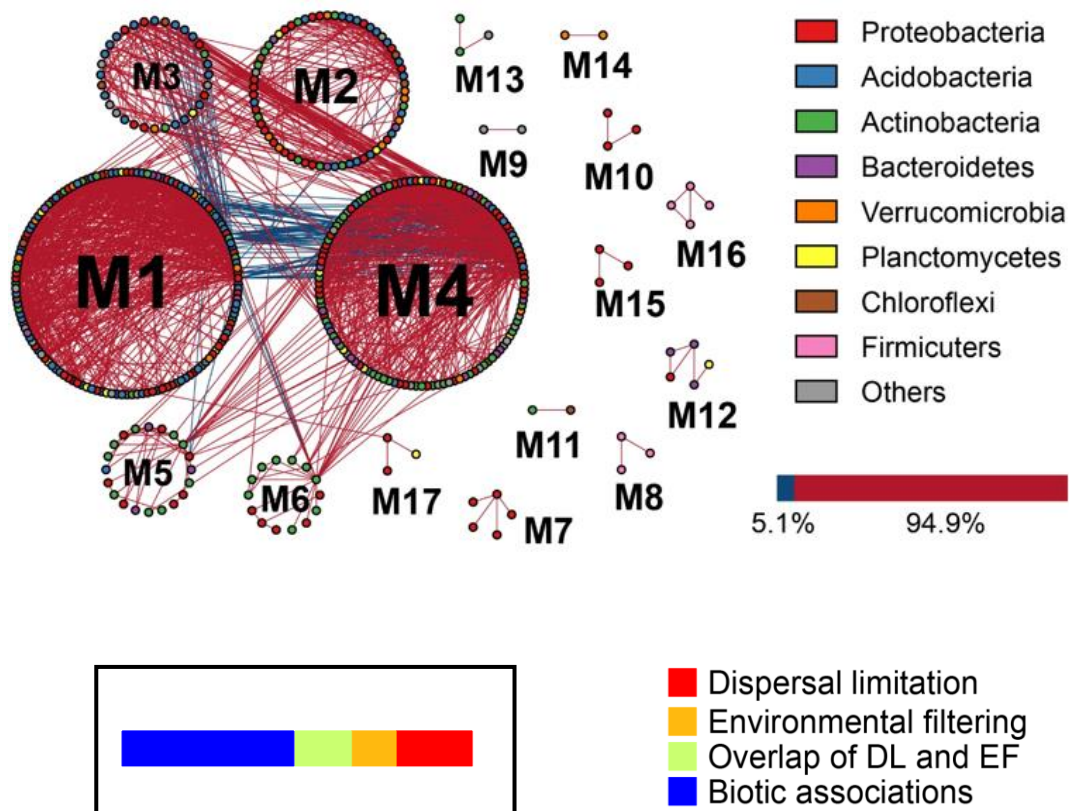
互动



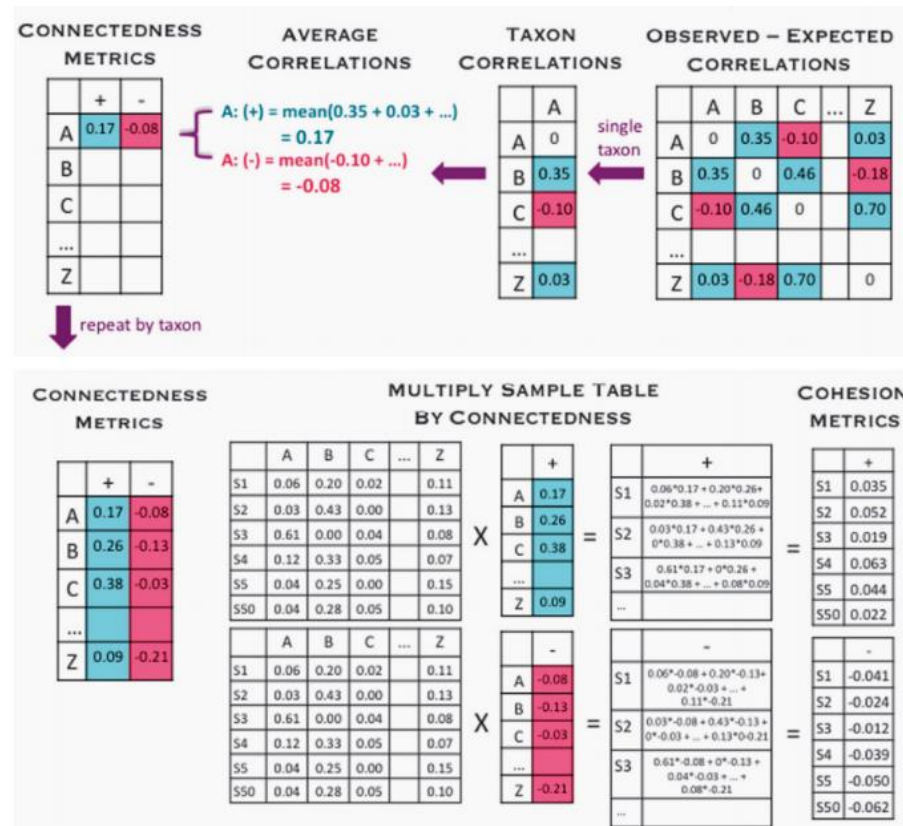
预测



研究背景



Goberna, 2019. *Mol. Eco. Res.*

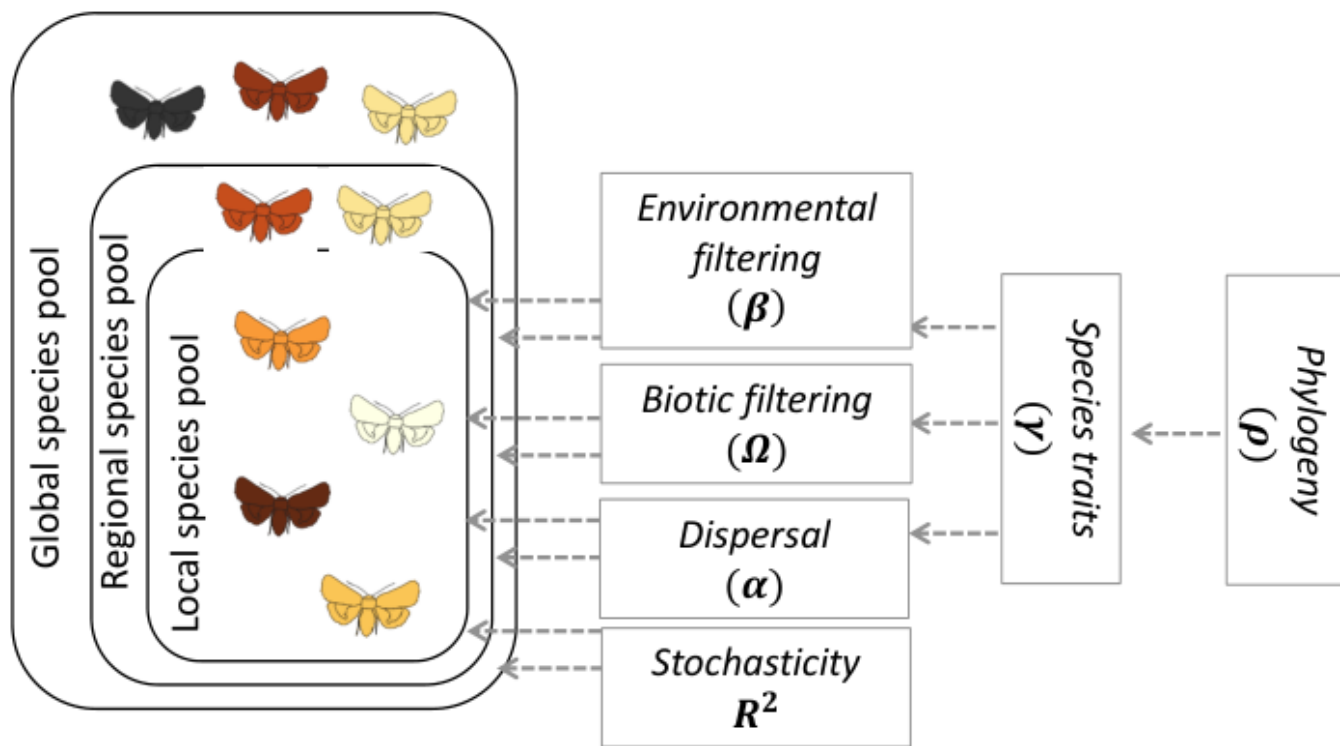


Herren, 2017. *ISME J*

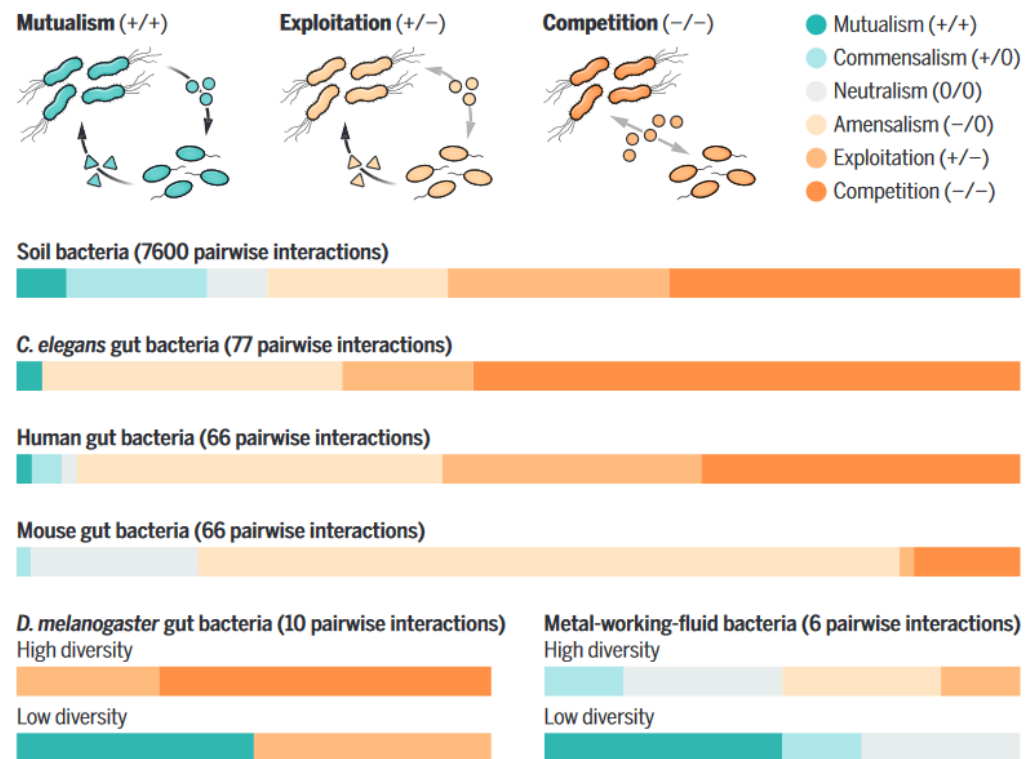
共存网络关系中包含复杂的生物与非生物关联

网络凝聚力反映微生物关联的群落复杂性

研究背景



Tikhonov, 2020. *Methods in Ecology and Evolution*

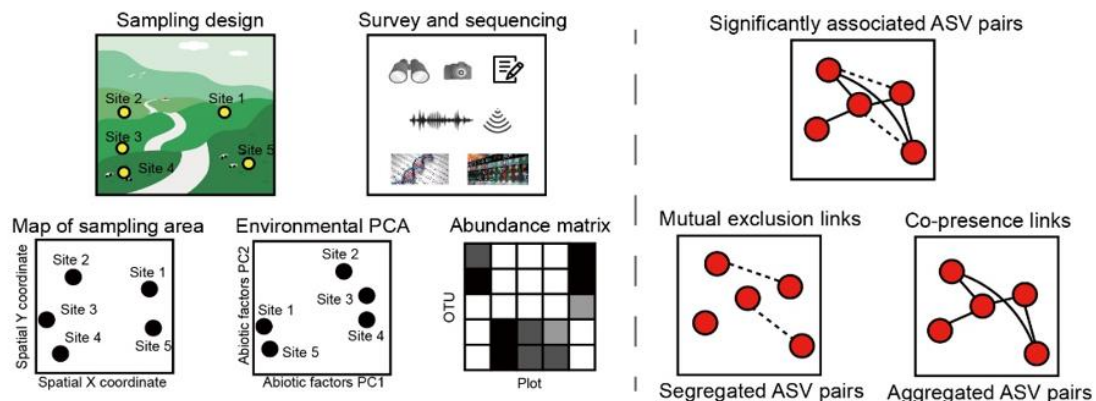


Palmer, 2022. *Science*

Vellend过程理论表明，生态群落构建过程不仅受中性过程影响，还受到环境选择和生物过滤作用共同驱动

方法流程

★ Step1. Construct ecological networks



★ Step2. Assign assembly processes

1. Are spatial distance significantly different between sites with different ASV states?

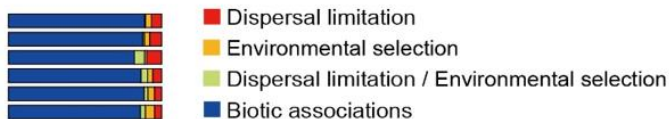


2. Are environmental factors significantly different between sites with different ASV states?



Putative biotic associations

- Positive associations (Aggregated pairs)
- Negative associations (Segregated pairs)



★ Step3. Quantify the strength of biotic associations

	SP 1
SP 1	0
SP 2	0.35
SP 3	-0.1
SP 4	0.03

Average correlation

SP 1: (+) = $\text{mean}(0.35+0.03+\dots)$
=0.17

SP 1: (-) = $\text{mean}(-0.10+\dots)$
=-0.08

	Connectedness	
	+	-
SP 1	0.17	-0.08
SP 2		
SP 3		
SP 4		

Repeat

	Connectedness	
	+	-
SP 1	0.17	-0.08
SP 2	0.26	-0.13
SP 3	0.38	-0.03
SP 4	0.09	-0.21

Species abundance table				
	SP1	SP2	SP3	SP4
Si1	0.06	0.20	0.02	0.11
Si2	0.03	0.43	0	0.13
Si3	0.61	0	0.04	0.08
Si4	0.04	0.25	0	0.15
Si5	0.04	0.28	0.05	0.10

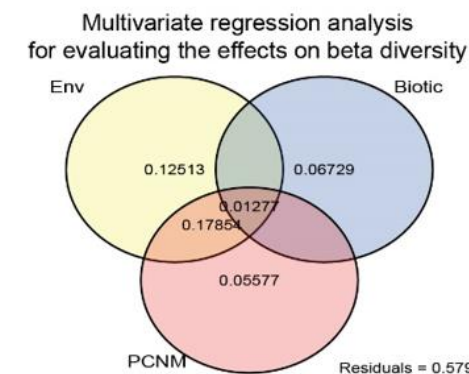
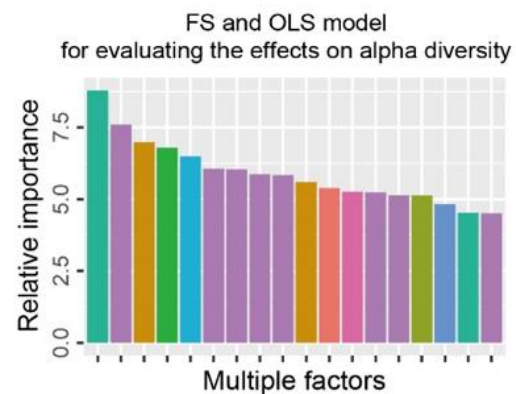
%*%
matrix multiplication

	Connectedness	
	+	-
SP 1	0.17	-0.08
SP 2	0.26	-0.13
SP 3	0.38	-0.03
SP 4	0.09	-0.21

Repeat

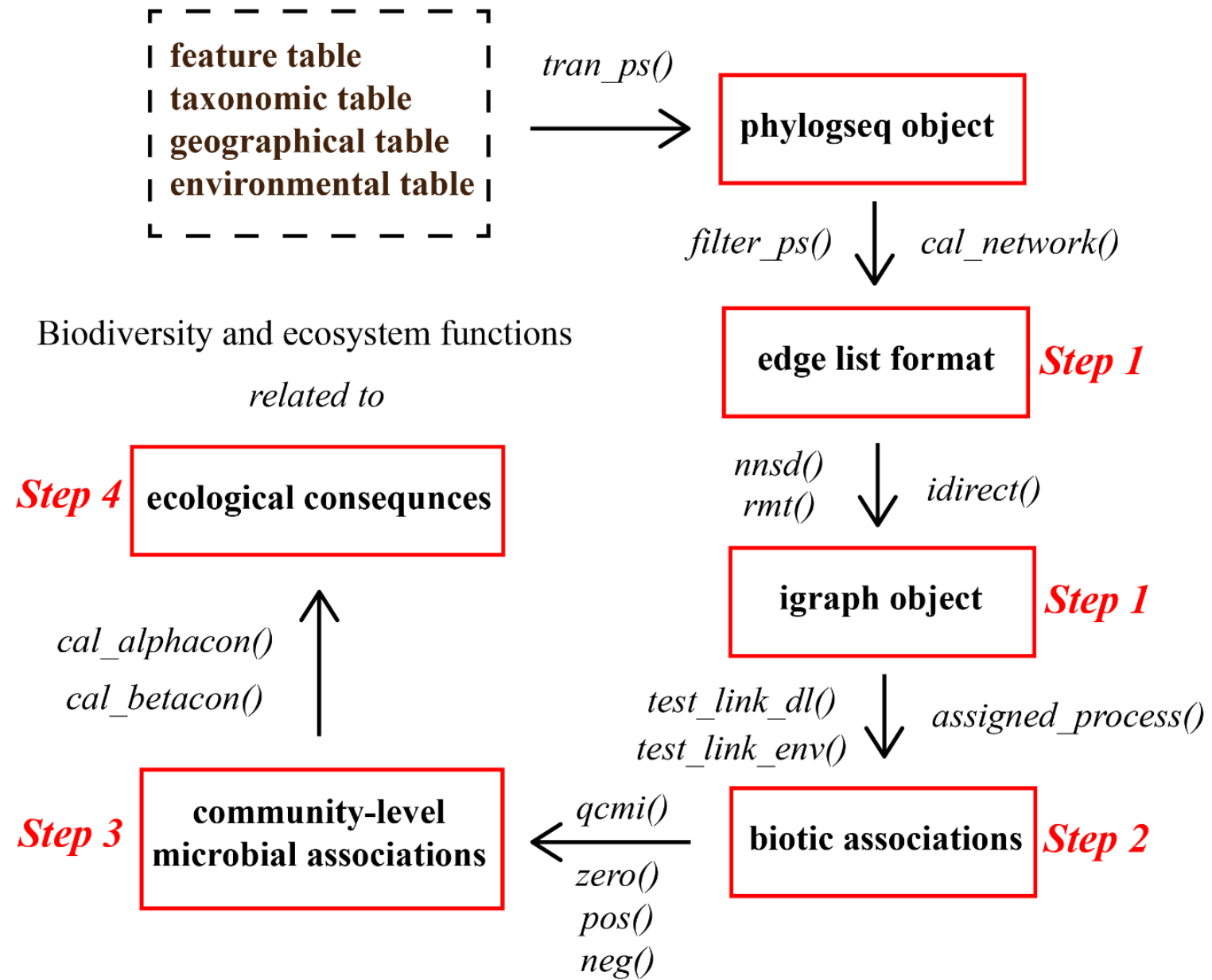
	Local strength	
	+	-
Si 1	0.035	-0.041
Si 2	0.052	-0.024
Si 3	0.019	-0.012
Si 4	0.063	-0.050
...

★ Step4. Calculate the effects of biotic associations

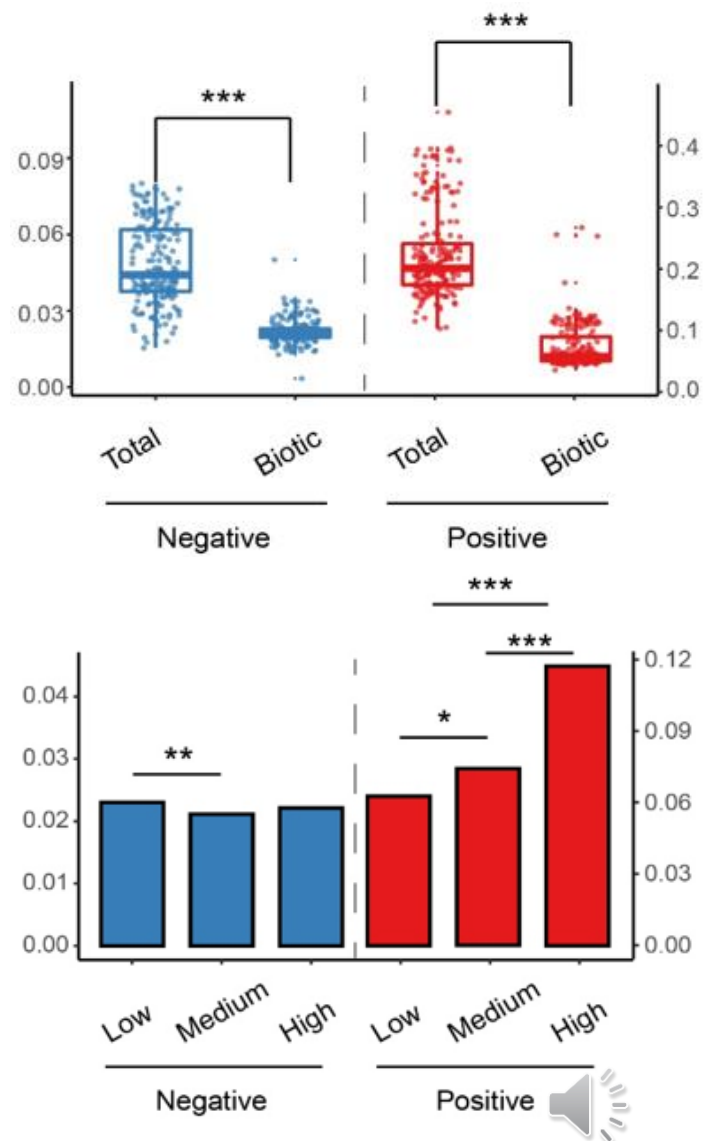
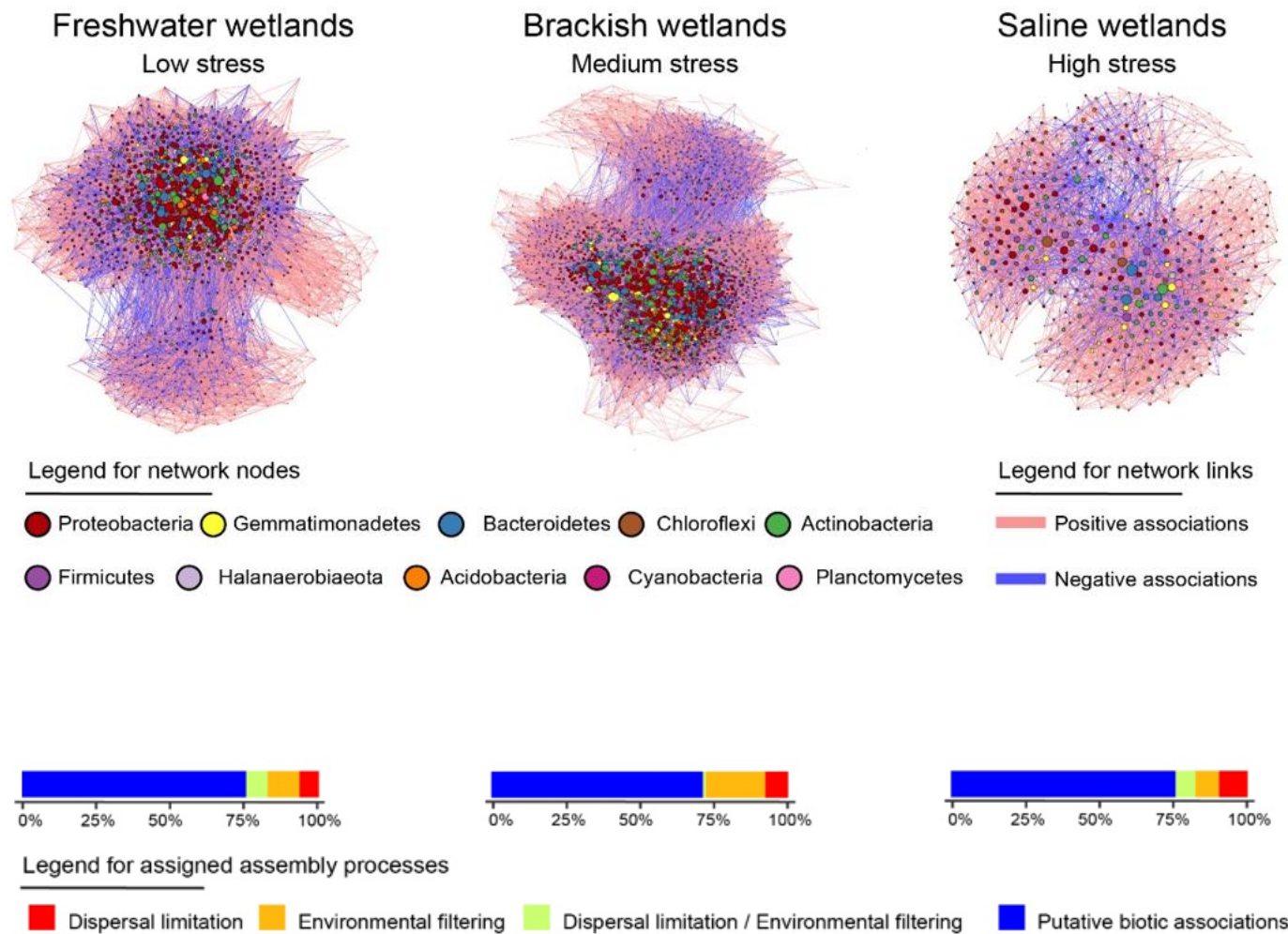


1. 构建生态网络, 2. 分配构建过程, 3. 定量生物关联, 4. 评估生态后果

导入和输出数据类型

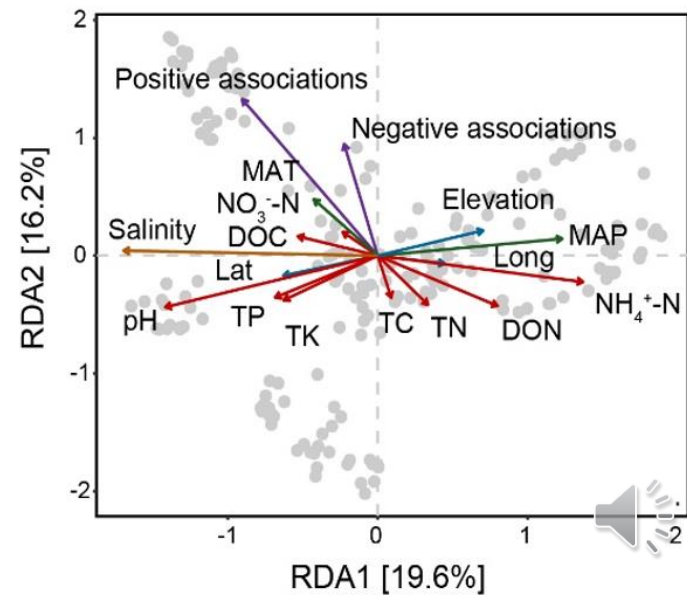
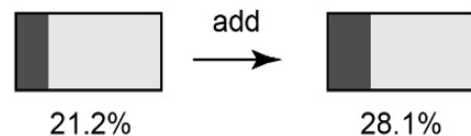
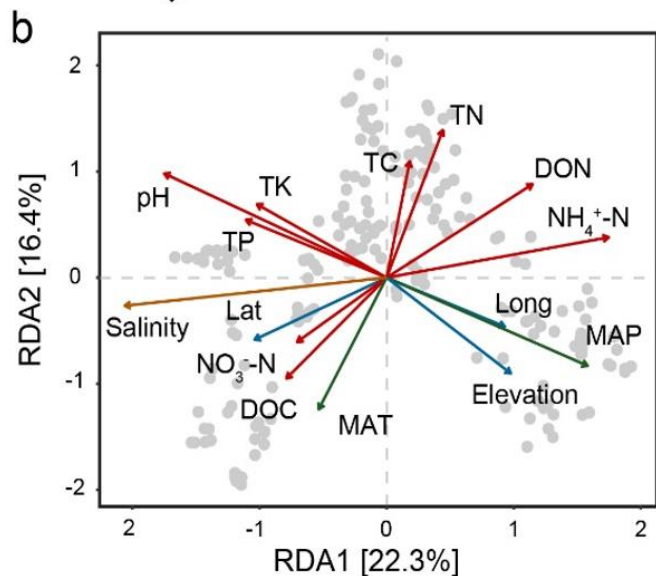
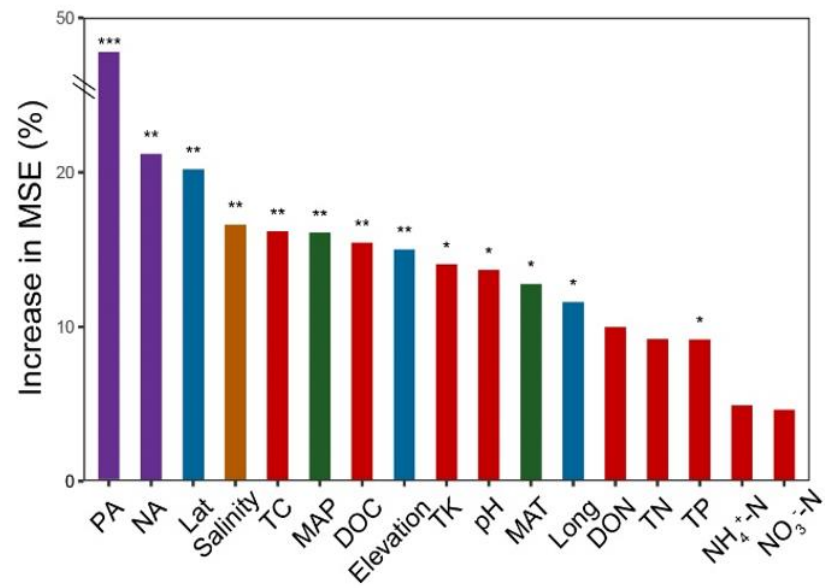
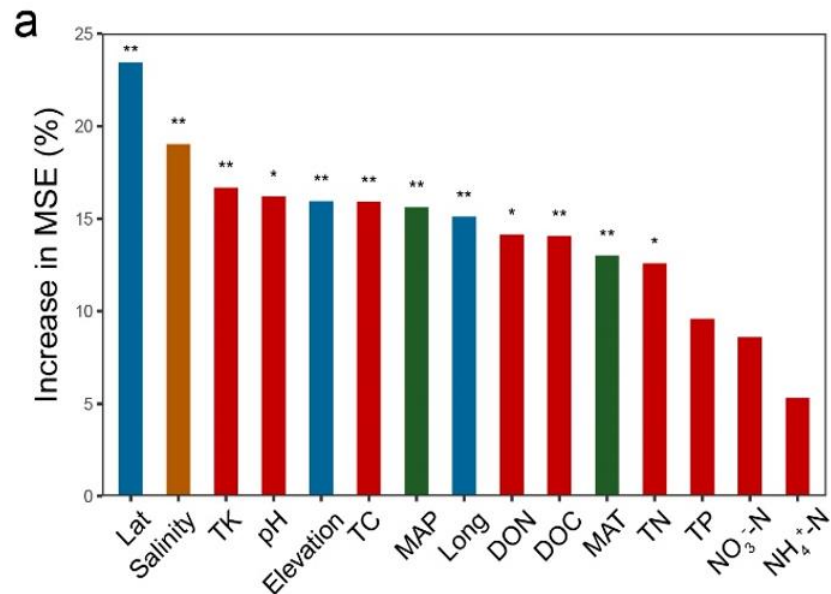


案例研究及结果



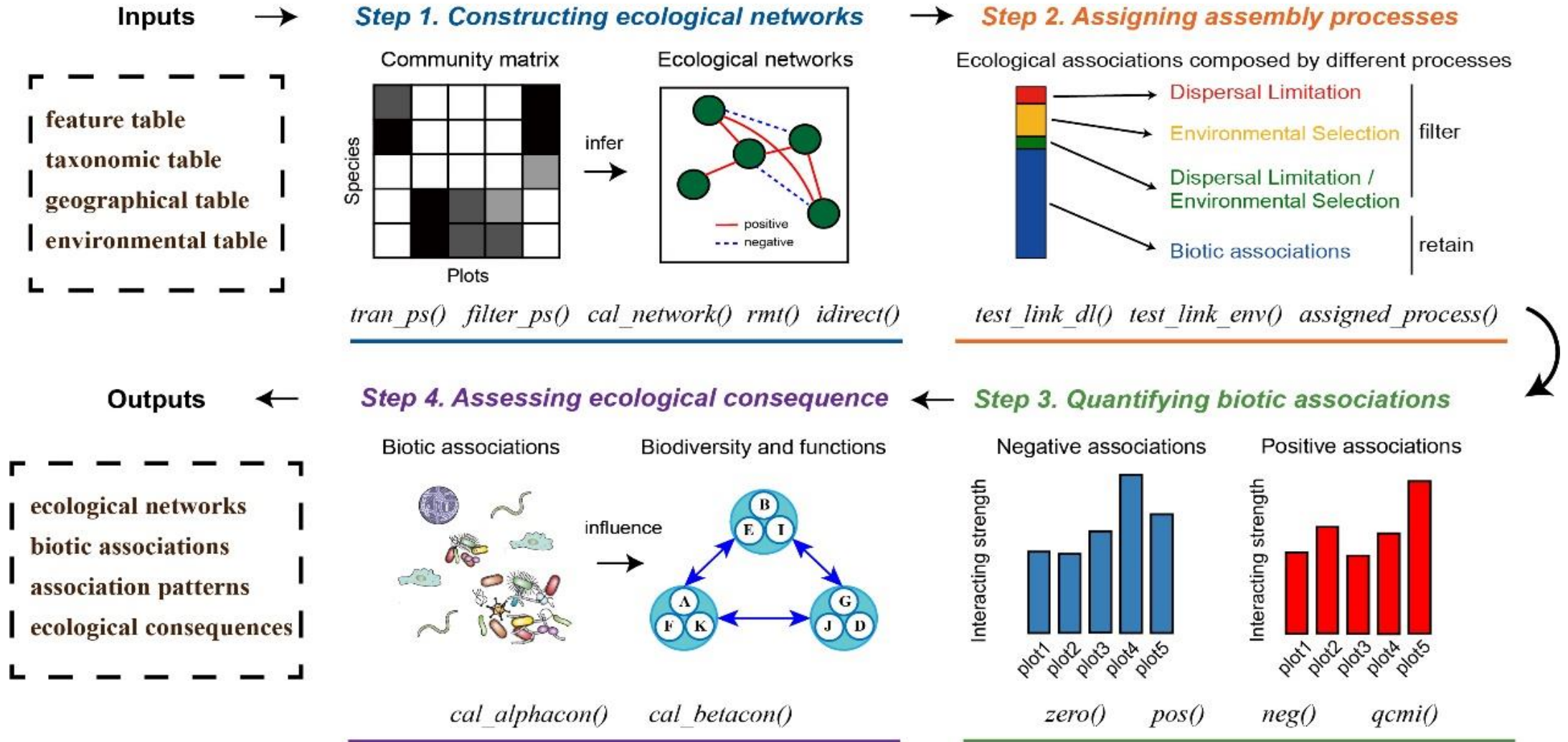
应用于实例数据的结果展示、数据比较、生态意义挖掘

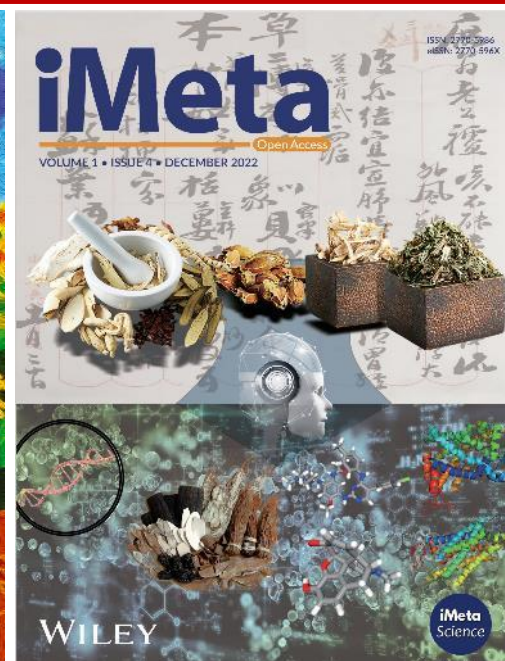
案例研究及结果



群落水平的假定生物关联对于理解微生物多样性产生和维持机制至关重要

总结





“*iMeta*”由威立、肠菌分会和华人科学家出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10%(IF > 15)的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、前3年免出版费、50万用户的社交媒体宣传等。2022年的三月、六月、九月和十二月期已正式在线出版发行，相继被[Google Scholar](https://scholar.google.com/)、[PubMed\(部分\)](https://pubmed.ncbi.nlm.nih.gov/)、[DOAJ](https://doaj.org/)、[Scopus](https://scopus.com/)等数据库收录！



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