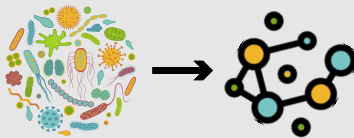
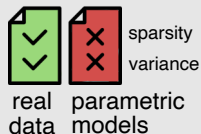


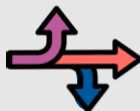
sequencing microbial communities
produces complex, high-dimensional data...



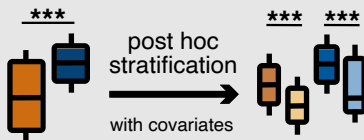
...yet existing parametric simulation frameworks **lack biological realism**



many statistical methods can model **differential abundance** between groups...



...and some are flexible enough to **model known confounders**

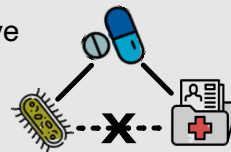


novel, validated simulation method
signal implantation

neutral benchmark
under realistic and confounded conditions



Clinical association studies have **high confounding potential** and should prioritize **covariate-aware methods**



Metagenomic simulation

DA method evaluation

MWAS application

risk of spurious association