

# Metagenomic Microbiome Disruption Indices

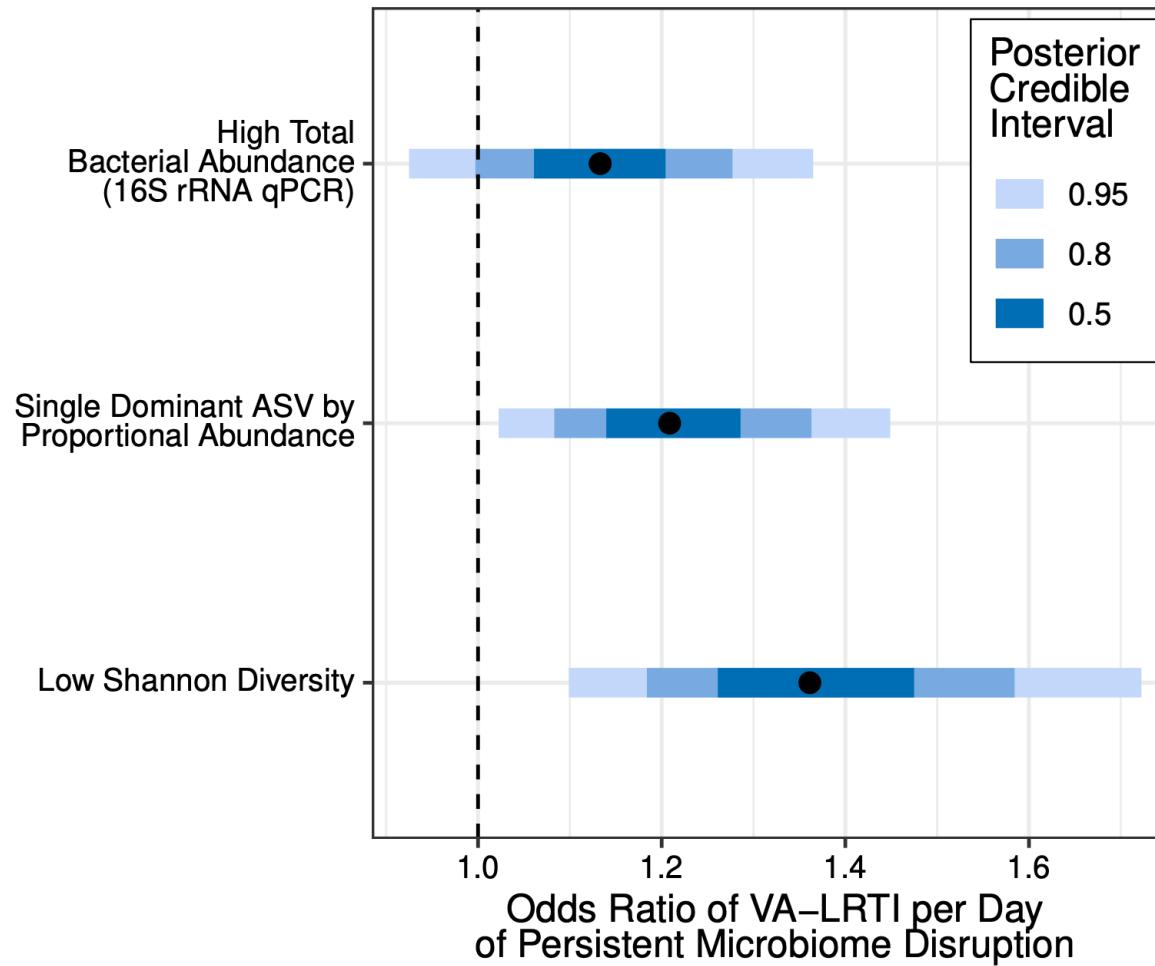
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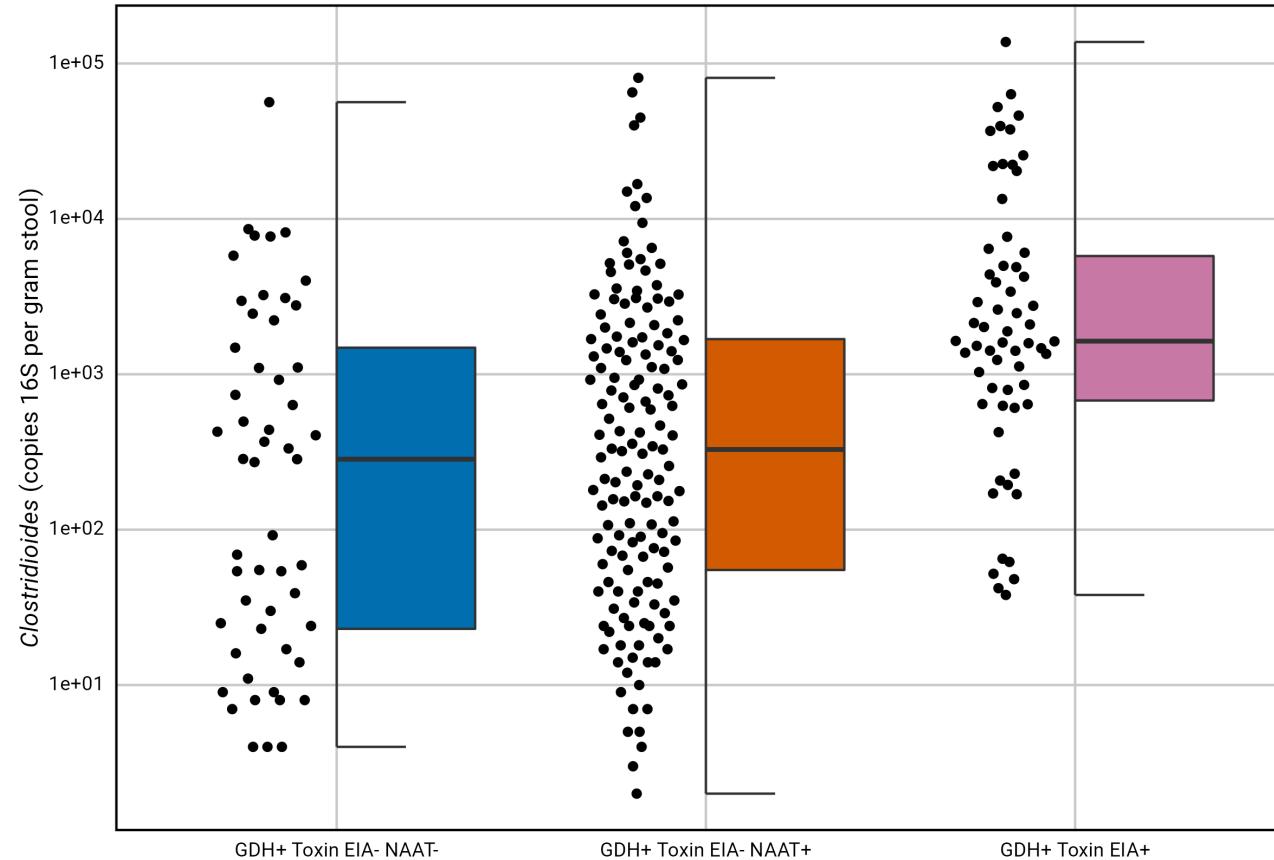
University of Pennsylvania

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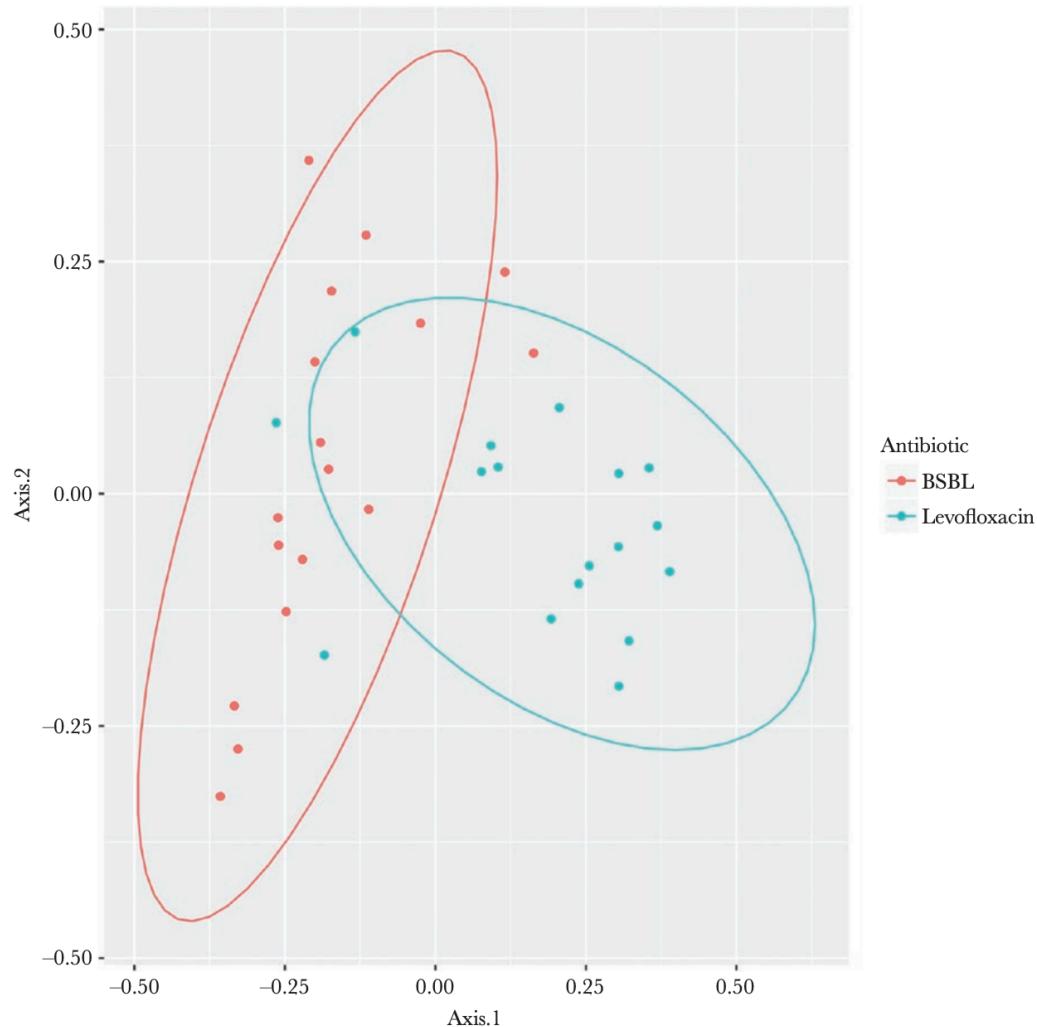
# Microbiome Disruption Indices



Univariable toxin EIA model: *Clostridioides* OR 1.07 (95%CI 1.02 - 1.12)

Multivariable toxin EIA model: *Clostridioides* OR 1.05 (95%CI 1.01 - 1.16) & *Lachnospiraceae* OR 0.32 (95%CI 0.14 - 0.96)

# Antibiotics & Microbiome Disruption



# Microbiome Disruption & Bacterial Transmission

- Hypothesis: post-infection/antibiotic repopulation matters:
  - both infection & antibiotics decimate mucosal microbial communities
  - the "source" for repopulation often an MDRO-rich hospital environment
  - failed repopulation risks recurrent infection (CDI & others)
  - microbial therapeutics can restore colonization resistance
- Aim: use microbiome measures to trace bacterial transmission
  - define mechanisms of **colonization resistance**
  - features of resident mucosal microbiota that resist introduction of new species (including pathogens) via direct competition and/or host immune modulation

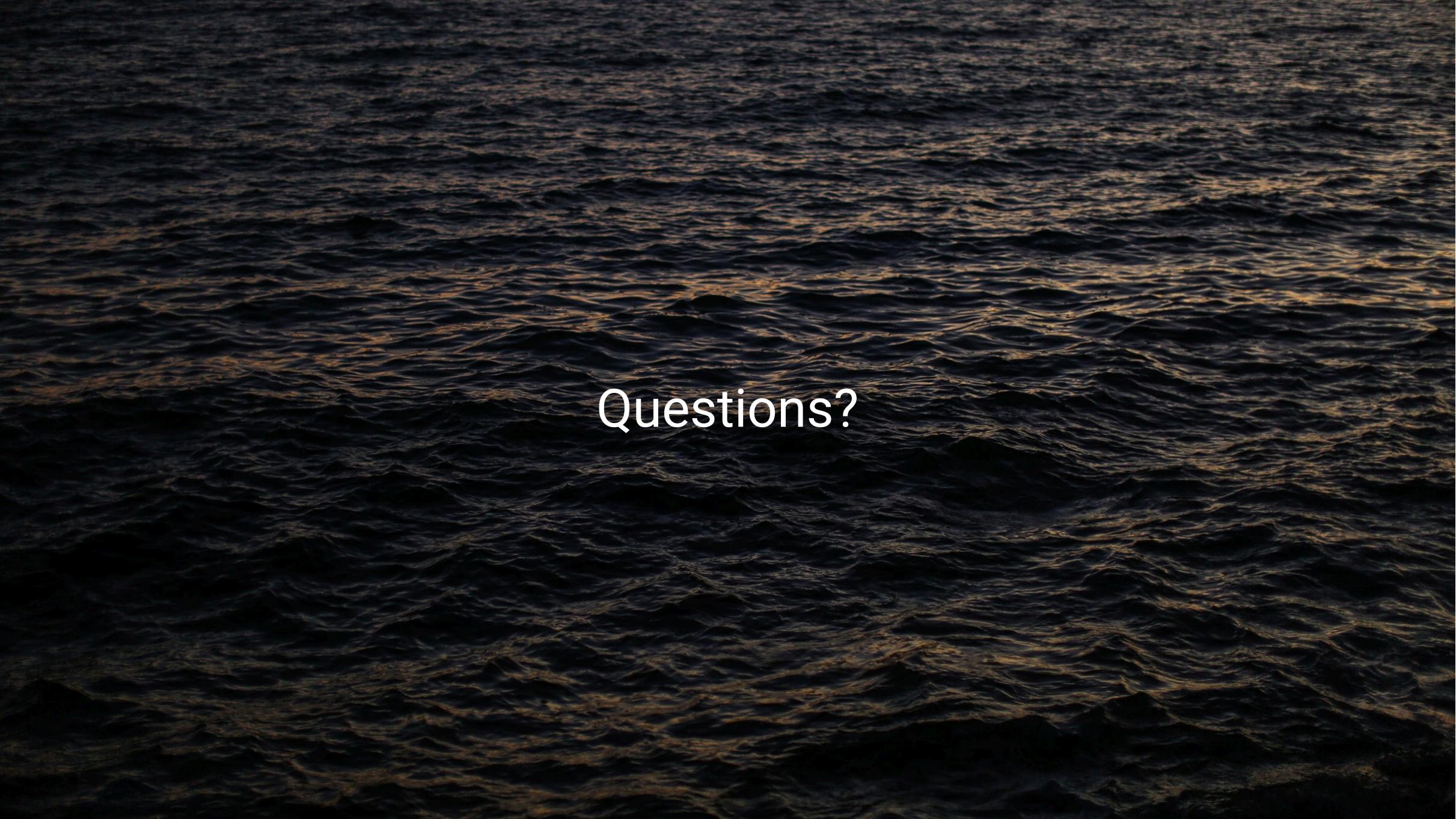
# Conclusions

- Bacterial infections are characterized by low-diversity / dominance, emphasizing the importance of post-treatment repopulation; antibiotics exacerbate low-diversity state in a class-dependent manner.
- Passive repopulation from the healthcare environment risks MDRO colonization.
- Opportunity for MBTs to engineer mucosal microbiome succession and prevent infection, but PK/PD, optimal conditioning, and optimal timing must be better defined.
- To understand the mechanisms of microbiome change and MBT effects requires novel modeling approaches, including HGAMs and phylogenetic regression.

# Acknowledgements

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The background of the image is a dark, textured surface of ocean waves. The light from the setting or rising sun is reflected off the water, creating a golden glow along the crests and in the ripples, which provides a strong contrast to the deep blues and blacks of the deeper water.

Questions?