

# Supplementary Materials

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September 23, 2020

## 1 Simulation Design

We simulated microbiome relative abundance data using the NorTA similar to [?]. Using this method, we can generate synthetic microbial counts that incorporates a complex correlation structure and multiple types of marginals. Specifically, we chose our marginals to be the zero-inflated negative binomial distribution based on results by Kurtz et al. [1]

We benchmark the parameters to our model based on the

## References

- [1] Zachary D. Kurtz, Christian L. Müller, Emily R. Miraldi, Dan R. Littman, Martin J. Blaser, and Richard A. Bonneau. Sparse and Compositionally Robust Inference of Microbial Ecological Networks. *PLOS Computational Biology*, 11(5):e1004226, May 2015.