

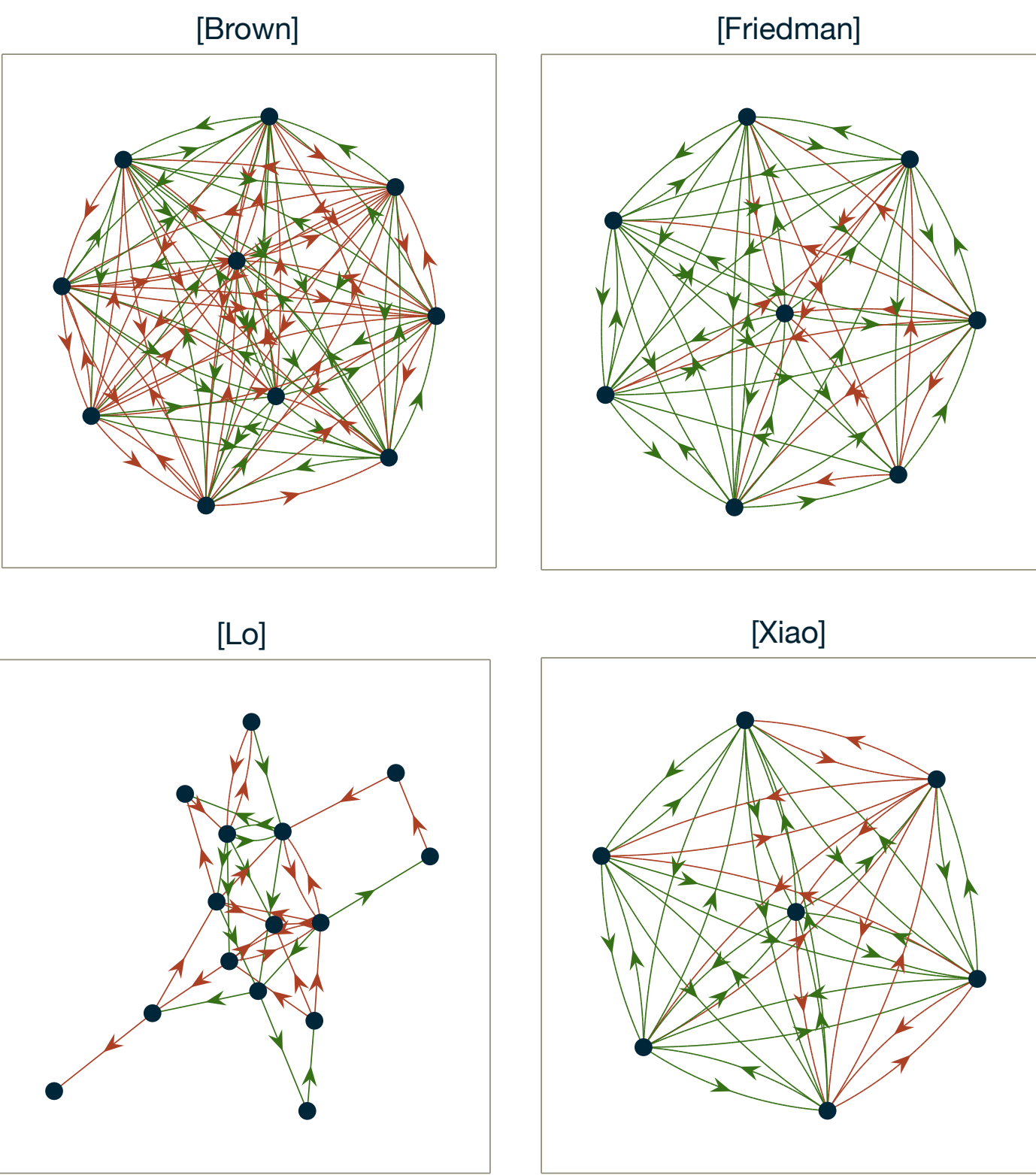
Introduction

Can tools and techniques for the analysis of human social networks offer insights on polymicrobial communities? Stable social networks, for example, often exhibit *structural balance*. Do bacterial interaction networks suggest that evolution also favors structural balance?

Data

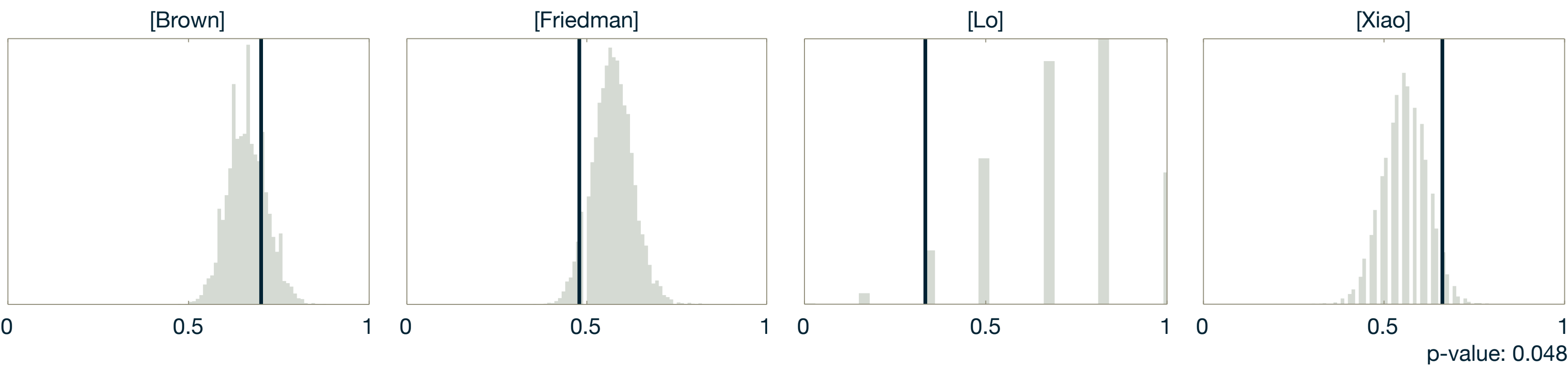
Brown Lab and published research.

	Nodes	Edges	$\langle k \rangle$	Frac(+)	
[Brown]	10	88	8.8	0.45	Cystic Fibrosis lung microbiome
[Friedman]	8	53	6.6	0.74	Synthetic soil microbiome
[Lo]	15	35	2.3	0.40	Human gut microbiome
[Xiao]	7	41	5.9	0.68	Synthetic maize root microbiome

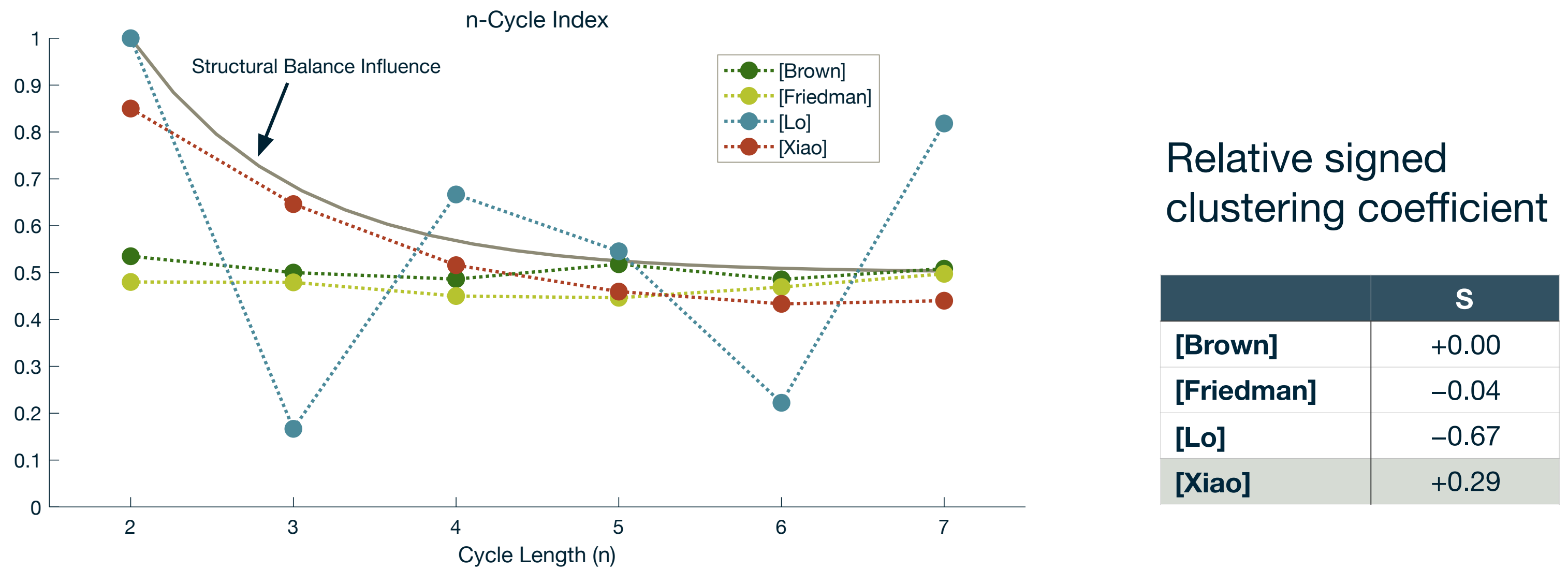


Results

Measured cycle index vs. topology-preserving random network



Behavior of n-cycle index with increasing cycle length



Methods

Generalized Lotka-Volterra interaction matrix defines a network graph G , consisting of bacterial *taxa* a, b, c, \dots with edges $a \rightarrow b$ representing interactions between *taxa*.

$$\sigma(a \rightarrow b) = \begin{cases} +1 & \text{if } a \text{ promotes } b \\ -1 & \text{if } a \text{ inhibits } b \\ 0 & \text{otherwise} \end{cases}$$
$$\Sigma(a,b,c) = \sigma(a \rightarrow b) + \sigma(b \rightarrow c) + \sigma(c \rightarrow a)$$
$$\Pi(a,b,c) = \sigma(a \rightarrow b) \cdot \sigma(b \rightarrow c) \cdot \sigma(c \rightarrow a)$$

Cycle Index

$$CI(G) = \frac{\left| \{ (a,b,c) \in G \mid (a \rightarrow b \rightarrow c \rightarrow a) \cap \Sigma(a,b,c) \neq 1 \} \right|}{\left| \{ (a,b,c) \in G \mid a \rightarrow b \rightarrow c \rightarrow a \} \right|}$$

n-Cycle Index

$$CI_n(G) = \frac{\left| \{ (a,b,\dots,z) \in G \mid \Pi(a,b,\dots,z) = 1 \} \right|}{\left| \{ (a,b,\dots,z) \in G \mid a \rightarrow b \rightarrow \dots \rightarrow z \rightarrow a \} \right|}$$

RSCC

$$S(G) = \frac{\sum_{(a,b,c) \in G} \Pi(a,b,c)}{\left| \{ (a,b,c) \in G \mid a \rightarrow b \rightarrow c \rightarrow a \} \right|}$$

Code and data available from <https://github.com/GaTechBrownLab/sbalance>

Conclusions

In general, the available data show no evidence that polymicrobial networks exhibit structural balance. One of the data sets [Xiao], however, shows strong evidence of structural balance by all available metrics: cycle index, n-cycle index, and relative signed clustering coefficient.

The inconsistency in the results may be due to:

- Different environments and time scales under which the interactions evolved.
- Different methods for analyzing data and inferring Lotka-Volterra interaction matrices.
- Irrelevance of structural balance to polymicrobial networks (i.e. coincidence).

References

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Lo C, Marculescu R (2017) Inferring Microbial Interactions from Metagenomic Time-series Using Prior Biological Knowledge. *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics*:168-177.

Xiao Y, Angulo MT, Friedman J, Waldor MK, Weiss ST (2017) Mapping the ecological networks of microbial communities from steady-state data. bioRxiv.