

Microbial Community Dynamics

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Problem background

- What is the problem domain?
 - Microbiomes are communities of microbes living in a shared environment (human gut, lake water, ...).
 - They are interesting for basic science as well as their clinical and industrial applications.
- Researchers care mostly about ecological and medical questions.
 - Ecological: What is the community structure of microbes, and how does it respond to environmental perturbations?
 - Medical: Are any subcommunities related to disease? Which change after treatment?

Information visualization tasks

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Review

Progress

Feedback?

- **Navigation** of hierarchical time series.
 - Each microbe contributes a time series of abundances, and they can be arranged along an evolutionary tree.
 - For real-world use, need to view ≈ 500 microbes for ≈ 25 patients across ≈ 30 time points.
- **Comparisons** across sets of trees.
 - Which (sets of) microbes have different abundances in treatment and control?

Literature review

- Microbiome science has a few popular workflows.
 - QIIME, phyloseq, and ANVI'O [1, 2, 3].
- Visualization community has tackled many subtasks.
 - Degree-of-interest trees [4]: Navigation of large trees.
 - TreeVersity [5]: Comparison between pairs of trees.
 - Some methods for hierarchical time series visualization [6, 7].
 - Timeboxes and generalized selection [8, 9]: Exploring many time series, and relating to contextual information.
- What's my contribution?
 - I want to put myself out of work.

Linking time + tree

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Review

Progress

Feedback?

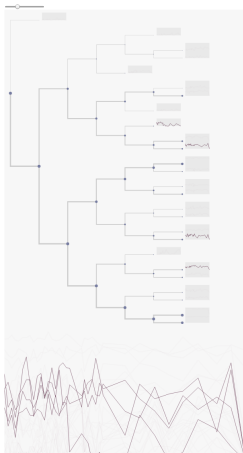


Figure: I've tried incorporating timeboxes and sparklines into visualization for a single sample.

Navigating trees

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Review

Progress

Feedback?

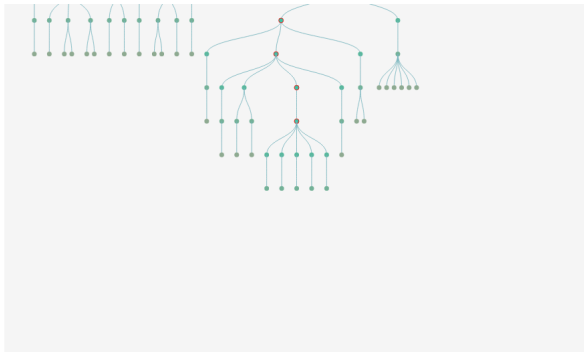


Figure: I've written a basic version of DOI trees, which doesn't include microbial abundance information.

Comparing trees

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Review

Progress

Feedback?

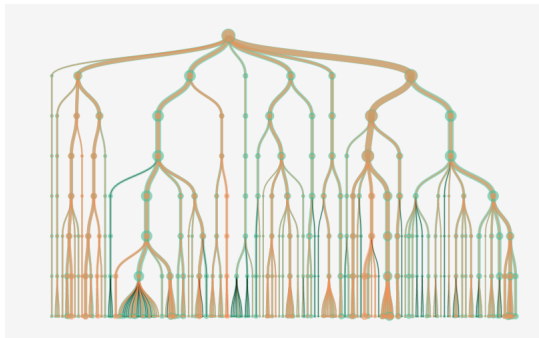


Figure: I've run preliminary experiments with TreeVersity-style comparison.

Feedback

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Review

Progress

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- The next step is to synthesize different experiments into one visualization, how would you approach this?
- How would you compare more than 2-3 samples in a single tree?
- I actually collaborate with microbiome scientists, and it might be interesting to design a study – what would be the important points to keep in mind?
- Any ideas for names? (I don't really like the ones I came up with: phyloSparklines, or treelapse, or ChronoTree, ...)



J Gregory Caporaso, Justin Kuczynski, Jesse Stombaugh, Kyle Bittinger, Frederic D Bushman, Elizabeth K Costello, Noah Fierer, Antonio Gonzalez Pena, Julia K Goodrich, Jeffrey I Gordon, et al.

Qiime allows analysis of high-throughput community sequencing data.

Nature methods, 7(5):335–336, 2010.



Paul J McMurdie and Susan Holmes.

phyloseq: an r package for reproducible interactive analysis and graphics of microbiome census data.

PLoS one, 8(4):e61217, 2013.



A Murat Eren, Özcan C Esen, Christopher Quince, Joseph H Vineis, Hilary G Morrison, Mitchell L Sogin, and Tom O Delmont.

Anvio: an advanced analysis and visualization platform for omics data.

PeerJ, 3:e1319, 2015.



Jeffrey Heer and Stuart K Card.

Doitrees revisited: scalable, space-constrained visualization of hierarchical data.

In Proceedings of the working conference on Advanced visual interfaces, pages 421–424. ACM, 2004.



John Alexis Guerra-Gómez, Audra Buck-Coleman, Catherine Plaisant, and Ben Shneiderman.

Treeversity: Interactive visualizations for comparing two trees with structure and node value changes.

In Proc. Conference of the Design Research Society-DRS2012, volume 1, page 10. Citeseer, 2012.



Spyros Makridakis, Steven C Wheelwright, and Rob J Hyndman.

Forecasting methods and applications.

John Wiley & Sons, 2008.



Yumiko Uchida and Takayuki Itoh.

A visualization and level-of-detail control technique for large scale time series data.

In Information Visualisation, 2009 13th International Conference, pages 80–85. IEEE, 2009.



Harry Hochheiser and Ben Shneiderman.

Interactive exploration of time series data.

In Discovery Science, pages 441–446. Springer, 2001.



Jeffrey Heer, Maneesh Agrawala, and Wesley Willett.

Generalized selection via interactive query relaxation.

In Proceedings of the SIGCHI Conference on Human Factors in Computing Systems, pages 959–968. ACM, 2008.