

Mini-course Compositional Data Analysis



Mini-course CoDA



Agenda

- 1. Introduction to network learning
- 2. Association estimation
- 3. The SPIEC-EASI approach and R package
- 4. From associations to adjacencies
- 5. Network analysis



Introduction to network learning

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Networks and graphs

• The term **graph** is used in computer science and math



Graph with labeled **vertices** and **edges**





Directed graph

Undirected graph

• The term **network** is used in physics, biology, and social sciences

Network with labeled nodes and links

Networks in cell / molecular biology

- Protein-protein interaction (PPI) networks
- Gene regulatory (co-expression) networks
- Metabolic networks
- Signaling networks
- Neuronal networks
- Microbial (ecological) interaction networks

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Microbiome networks

 \rightarrow Insights into the organizational structure of a microbial community



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Network comparison

 \rightarrow Does the microbial composition change across different conditions?



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Typical network analysis workflow





From sequencing data to networks



Data characteristics:

- We observe only a **sample** of the true microbial composition
- **Compositional** (only relative information)
- Sequencing depth (total number of reads) varies across samples
- Zero-inflated
- **High-dimensional** (number of taxa p >> sample size n)



Outlook

In the remainder of this lesson, we will answer the following questions:

- Why is the sample correlation matrix not a good estimator in the high-dimensional case?
- How can we measure microbial associations?
- How can LASSO regression be useful in microbial association estimation?
- How do we get from an association matrix to the final network?
- How can the constructed network be analyzed?