# Network analysis - HANDS ON !

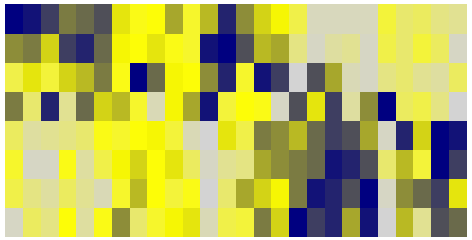
GDC: Microbiota Data Analysis Workshop; January 24th, 2020

Klaus Schlaeppi – Institute of Plant Sciences, University of Bern

Network analysis ~ research question

# Network analysis ~ research question

**Data** → **Correlation** → **Network**




| from | to | cor | p |
|---|---|---|---|
| bOTU86 | bOTU62 | 0.8923925 | 9.095391e-10 |
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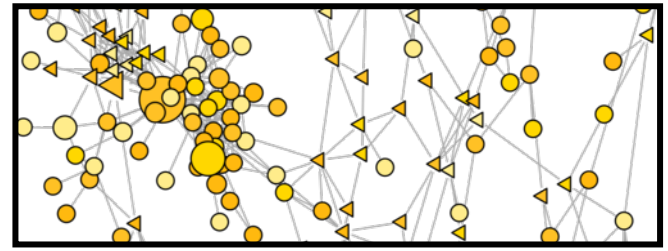


Structure?

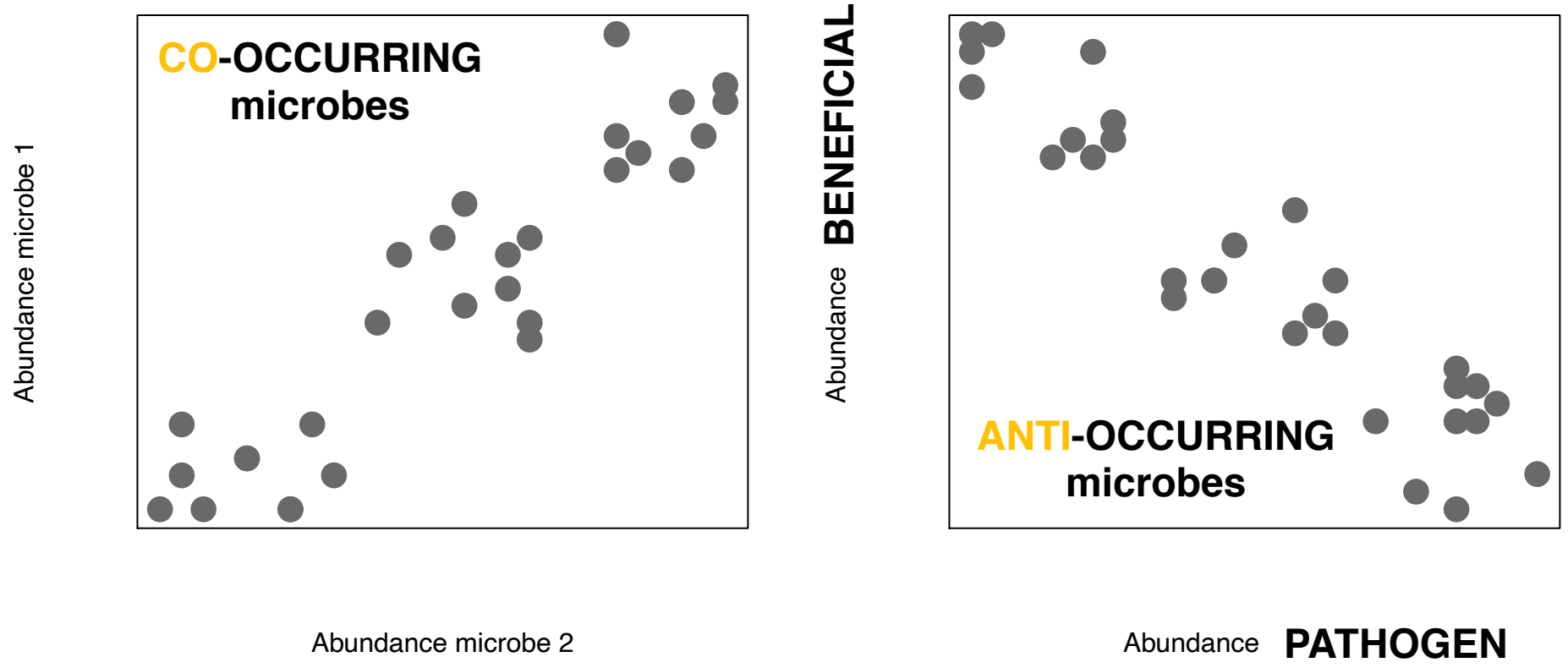
Type of correlations?

Disclaimer:

A network does not depict the **microbial interactions**, but groups microbes by their **abundance "behaviour"**.

# Research question ~ type of correlation(s)

**positive** and/or **negative** correlations?



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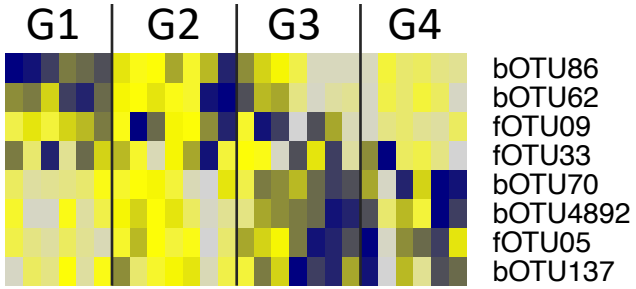


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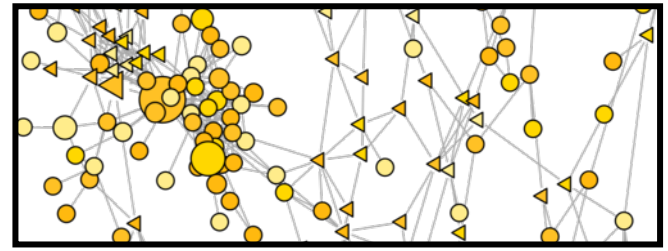

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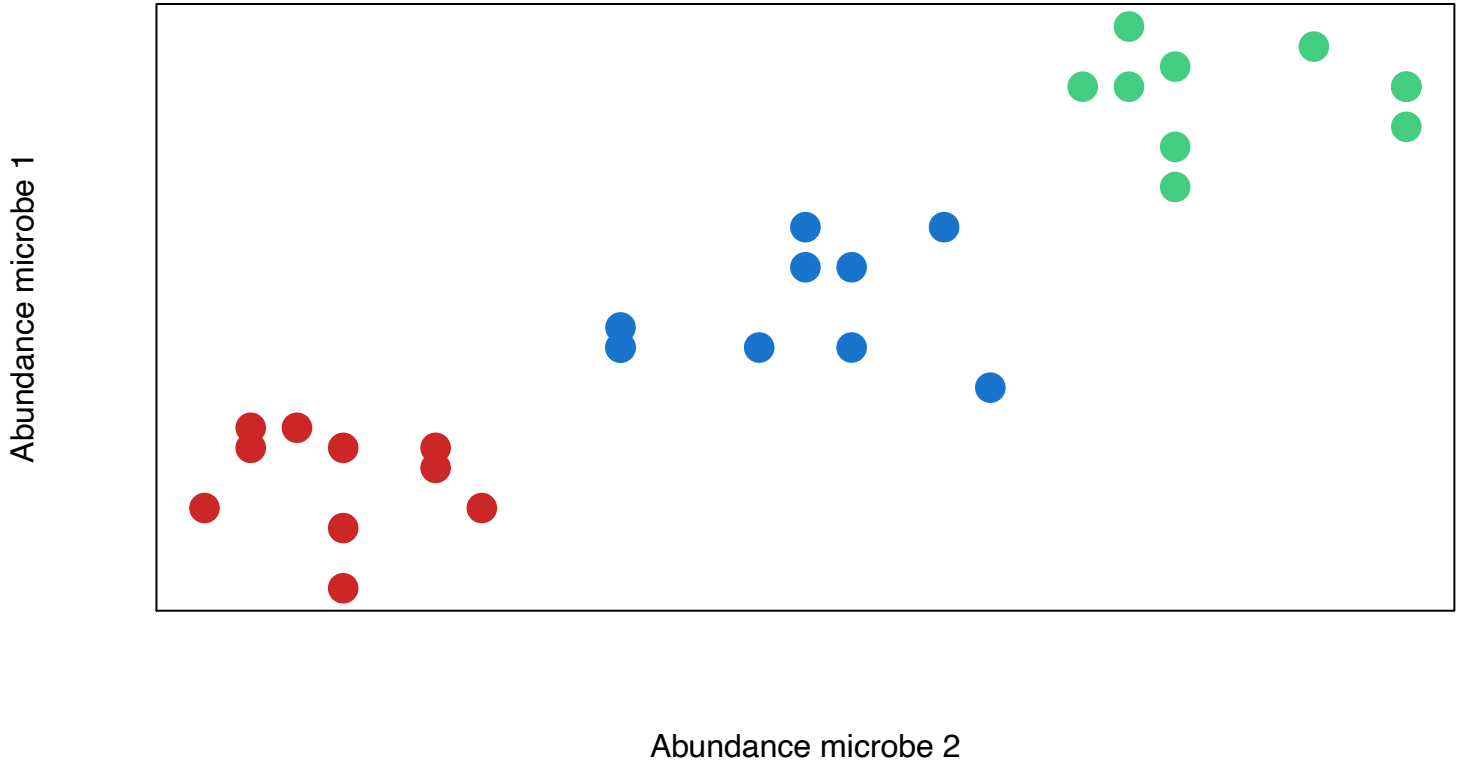
# Data structure (Network analysis ~ research question)

**Within** or **between** sample groups?



# Example for '**within** vs. **between** sample groups'

The ISME Journal
https://doi.org/10.1038/s41396-019-0383-2

ISME

ARTICLE

## Agricultural intensification reduces microbial network complexity and the abundance of keystone taxa in roots

Samiran Banerjee[1] · Florian Walder[1] · Lucie Büchi[2,3] · Marcel Meyer[1] · Alain Y. Held[1] · Andreas Gattinger[4,5] · Thomas Keller[1,6] · Raphael Charles[2,7] · Marcel G. A. van der Heijden[1,8]

Received: 21 September 2018 / Revised: 4 February 2019 / Accepted: 17 February 2019
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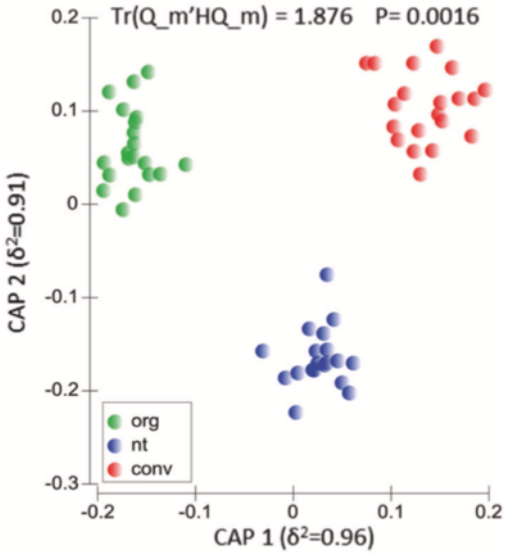
# Example for '**within** vs. **between** sample groups'

**FAQs:**

- Wheat roots
- Fungal community profiles by *PacBio(ITS1F---ITS4)*
- Data structure: 3 types of fields (conventional, organic and no-till), 20 replicates each
- Research question: root microbiome NW ~ farming practices

beta-diversity

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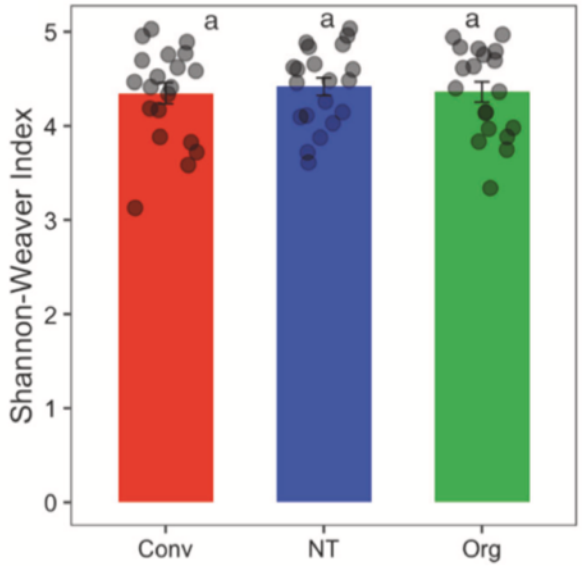
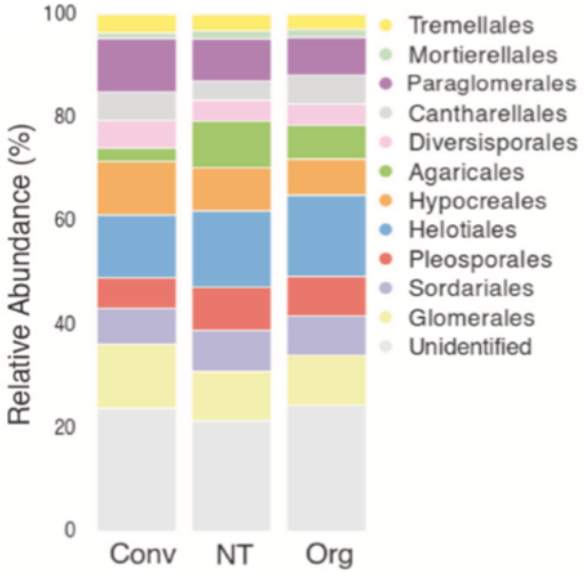



taxonomy




Banerjee *et al.* (2019), ISME J

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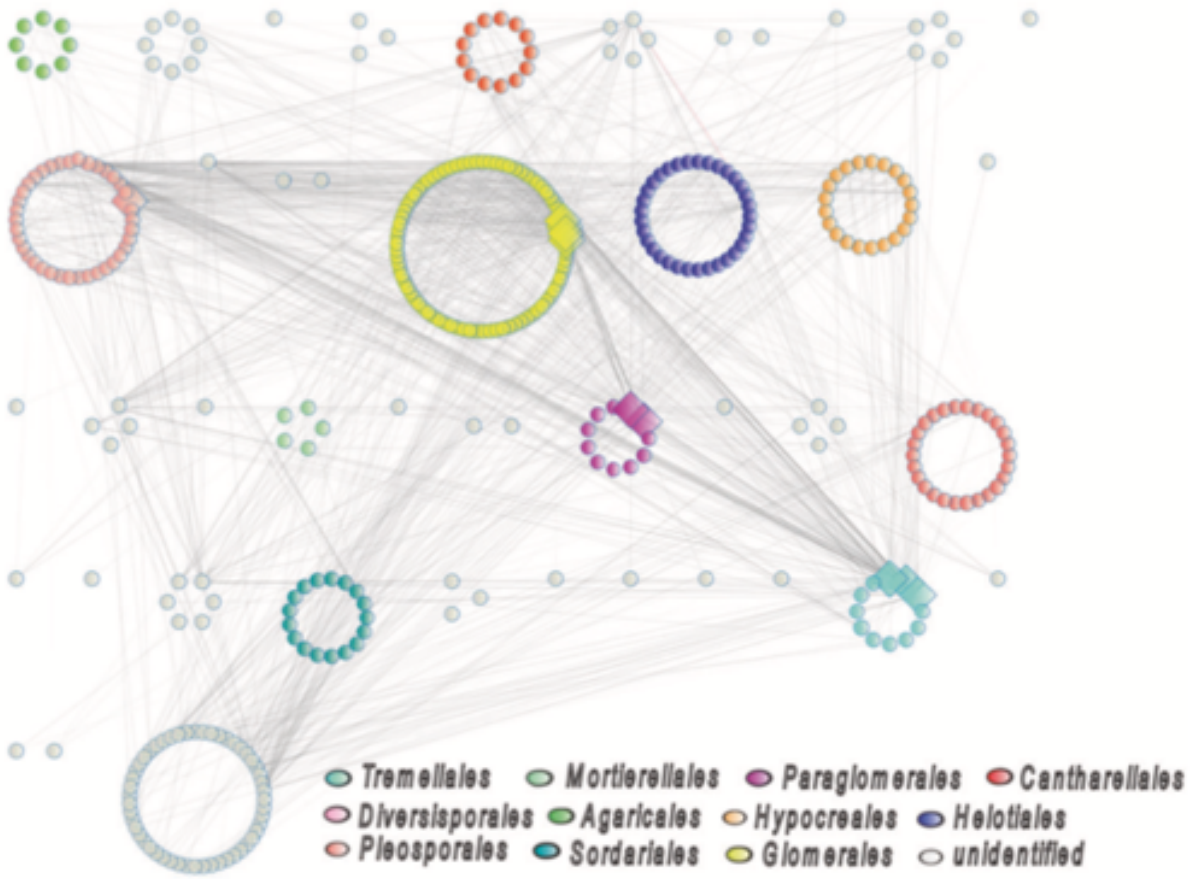
**Network analysis:**
- maximal information coefficient (MIC)
  (see Reshef et al. 2011, Science)
- MIC associations with $P < 0.05$ after FDR correction
- Plotting with Cytoscape

-> Overall meta-network (all 60 samples)

From the caption:
- across three farming systems
- by fungal orders
- White = positive, red = negative and …
  … wavy lines = nonlinear relationships
- Diamonds = keystone taxa […]

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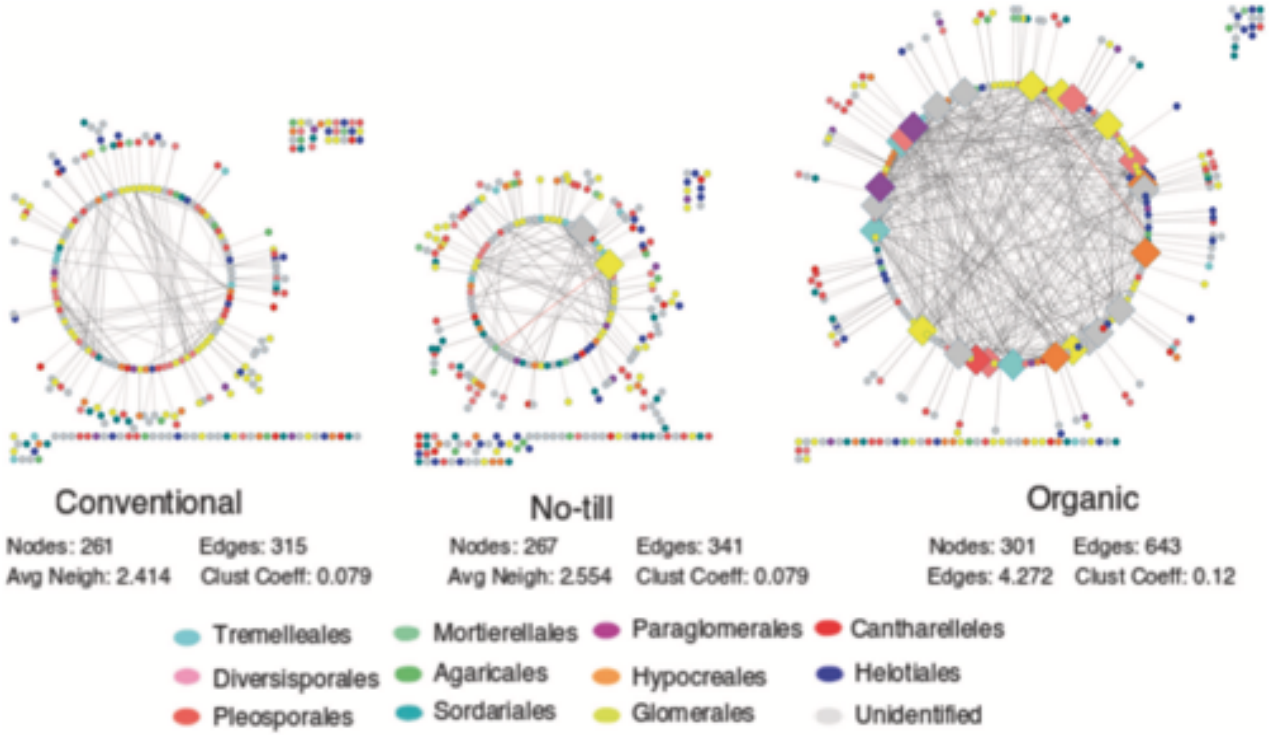
-> 3 farming-specific networks (20 samples each)

COMPARISON of network topology:
- same parameters for calc.
- similar number of nodes in analysis
- BUT: different network patterns



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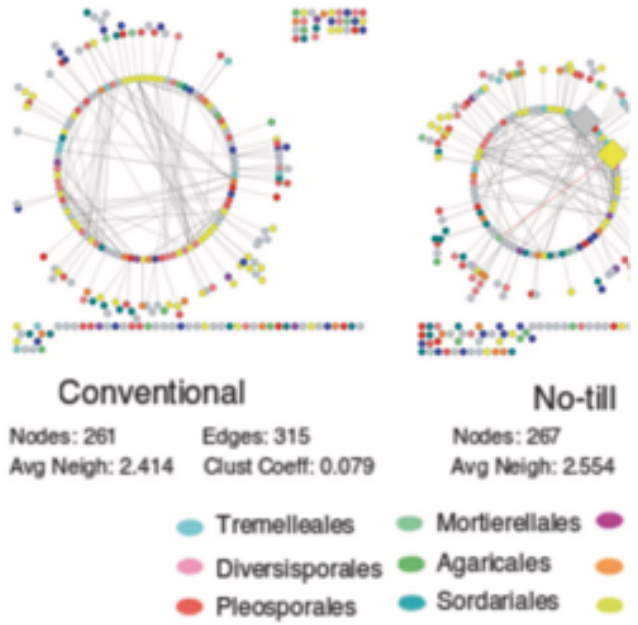
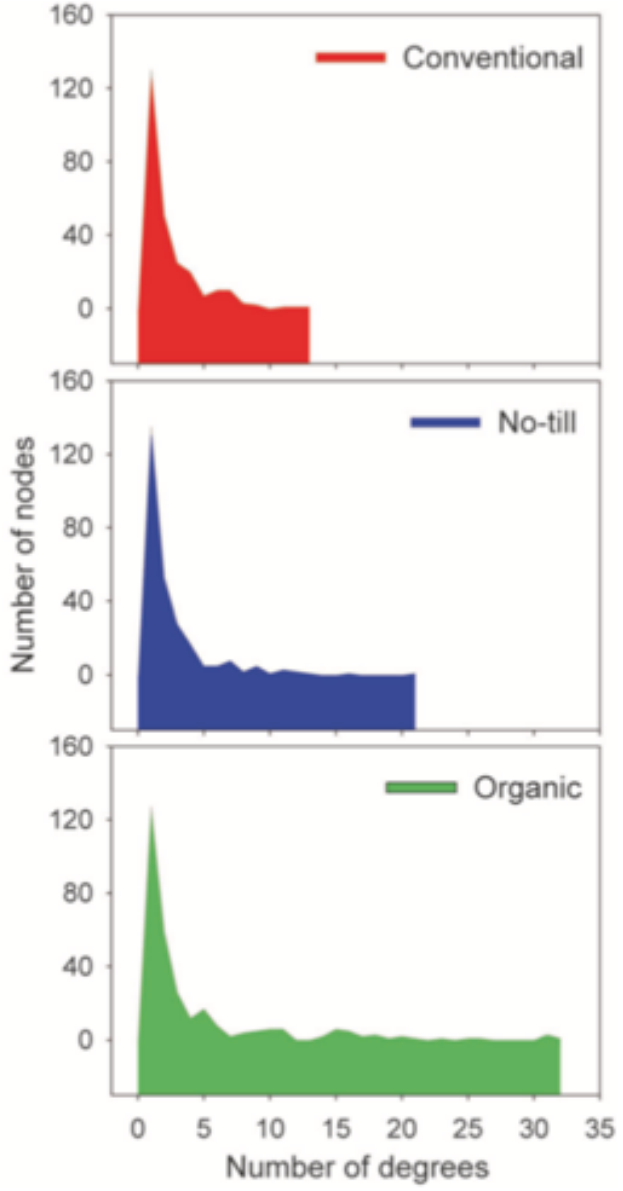
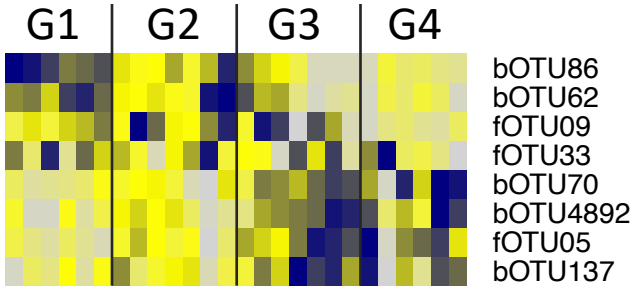



Banerjee *et al.* (2019), ISME J

# Network analysis ~ research question

**Data**

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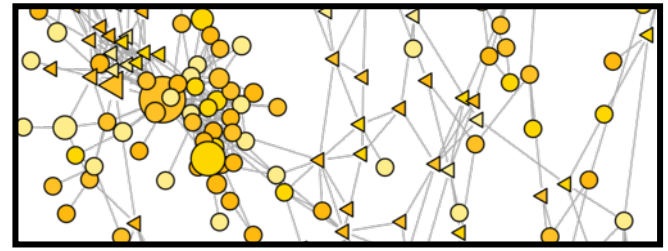
**Network**



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# Study: Root microbiota ~ P fertilization

Phytobiomes Journal • 2019 • 3:112-124 https://doi.org/10.1094/PBIOMES-12-18-0057-R

OPEN ACCESS

Phytobiomes Journal

phytobiomesjournal.org APS

A Transdisciplinary Journal of Sustainable Plant Productivity

RESEARCH

e-Xtra*

## Petunia- and Arabidopsis-Specific Root Microbiota Responses to Phosphate Supplementation

**Natacha Bodenhausen,[1,2] Vincent Somerville,[1] Alessandro Desirò,[3] Jean-Claude Walser,[4] Lorenzo Borghi,[5] Marcel G. A. van der Heijden,[1,6,7] and Klaus Schlaeppi[1,8,†]**

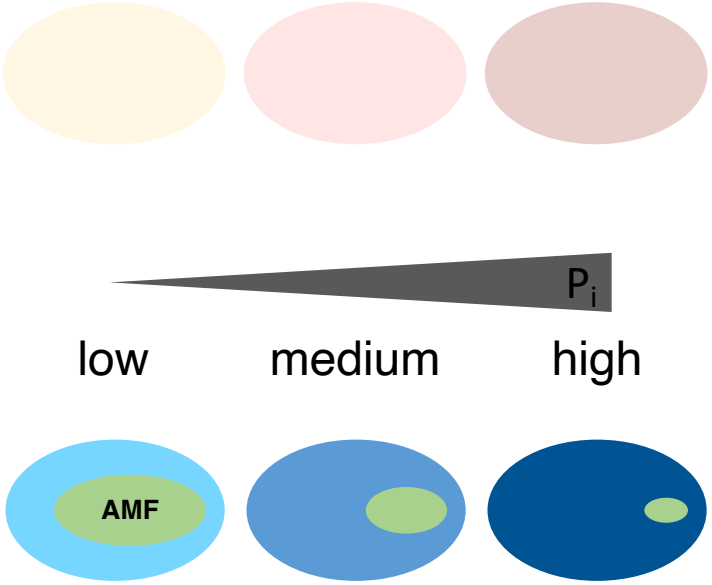
[1] Division of Agroecology and Environment, Agroscope, Zurich, Switzerland
[2] Department of Soil Sciences, Research Institute of Organic Agriculture FiBL, Frick, Switzerland
[3] Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, U.S.A.
[4] Genetic Diversity Centre, ETH Zurich, Zurich, Switzerland
[5] Institute of Plant and Microbial Biology, University of Zurich, 8008 Zurich, Switzerland
[6] Institute for Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland
[7] Plant-Microbe Interactions, Institute of Environmental Biology, Faculty of Science, Utrecht University, Utrecht, The Netherlands
[8] Institute of Plant Sciences, University of Bern, Switzerland

Accepted for publication 27 March 2019.

Bodenhausen *et al.* (2019), Phytobiomes J

# Study: Root microbiota ~ P fertilization

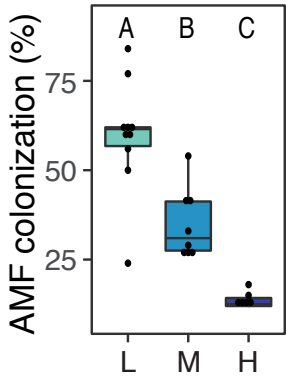
The root microbiota of mycorrhizal plants enriches for AMF(=Glomeromycotina) under low-P



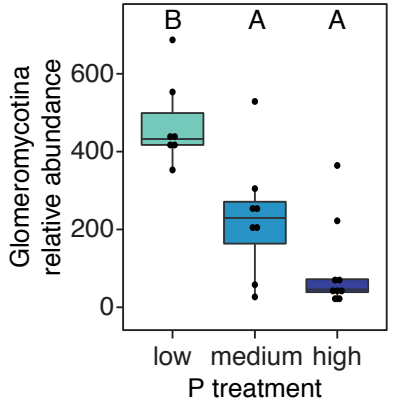

Arabidopsis

Petunia

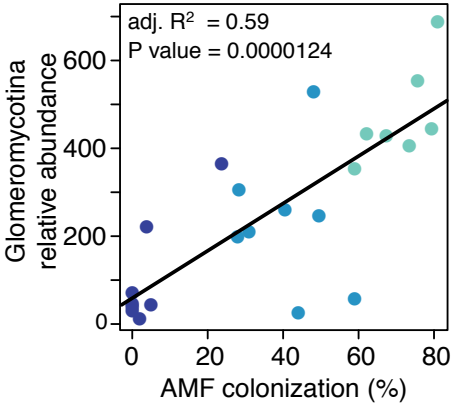
Microscopy




Sequencing

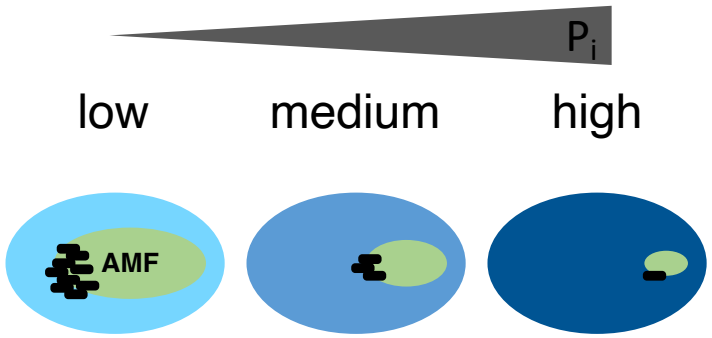



Correlation

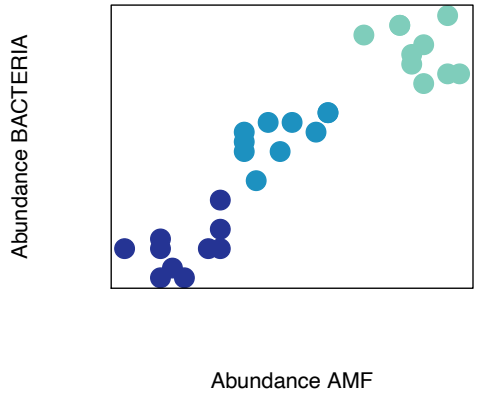


# Study: Root microbiota ~ P fertilization

Can we find bacteria that share the **same abundance behavior** as AMF along a P gradient?




**co-abundant bacteria?**



# Study: Root microbiota ~ P fertilization

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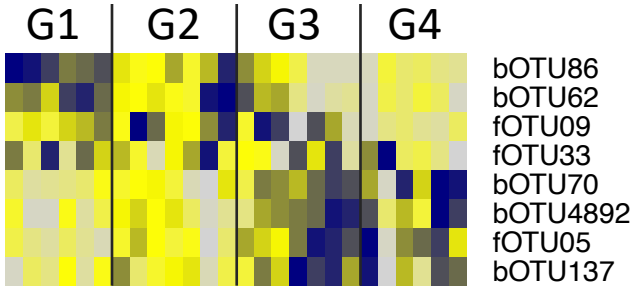


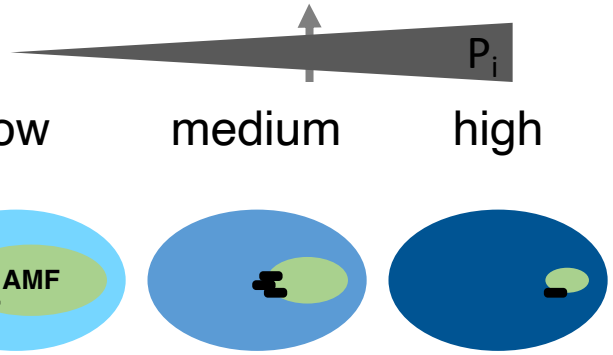


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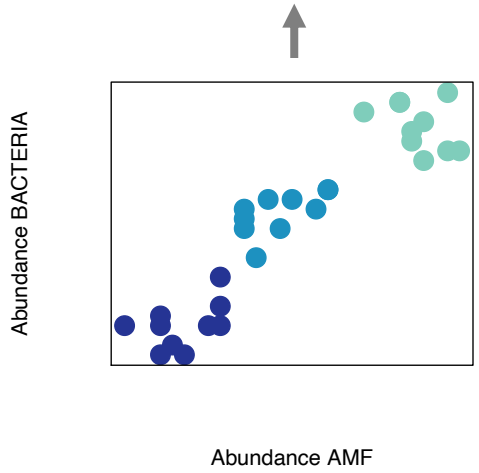
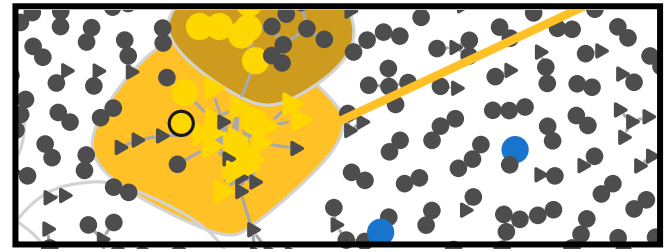



## Network



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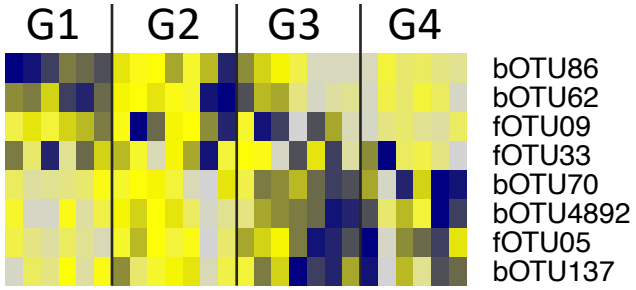


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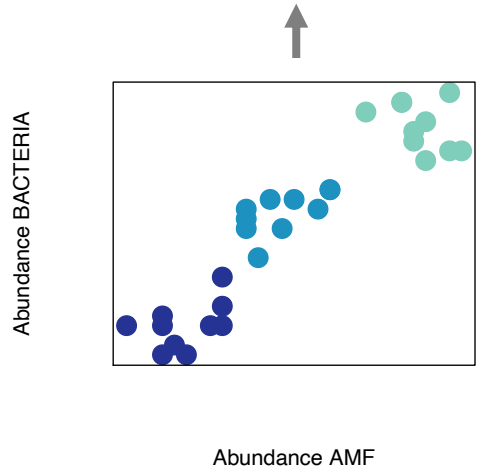


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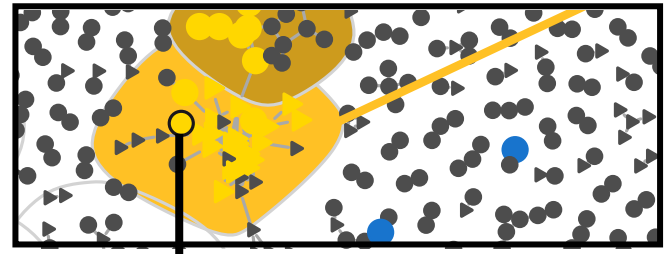
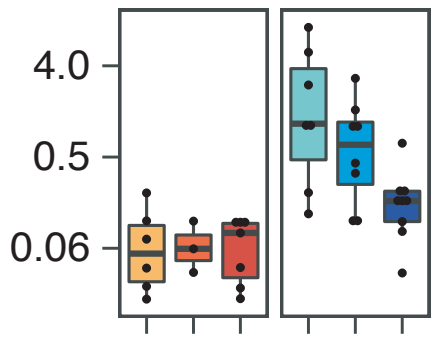
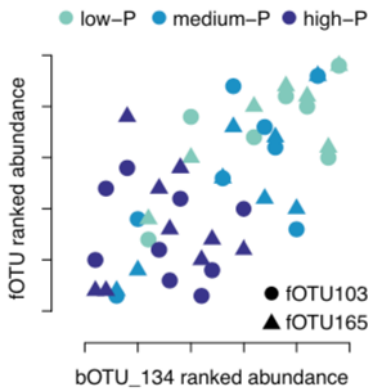


**bOTU134**

*Ca*. Glomeribacter

Arabido. Petunia



# Study: Root microbiota ~ P fertilization

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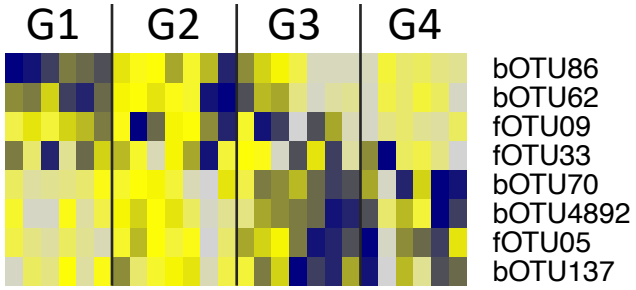


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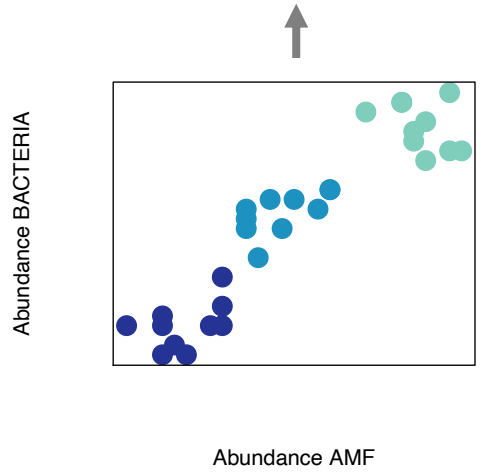


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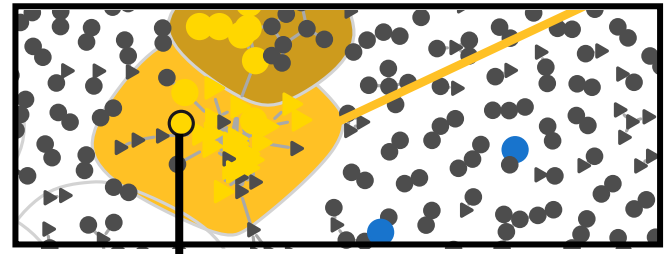

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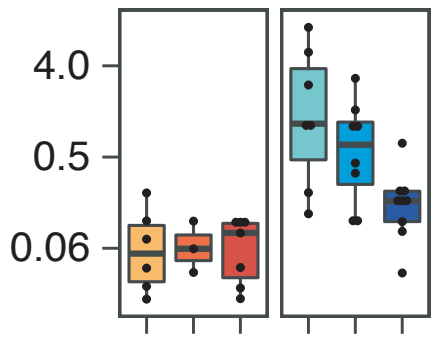
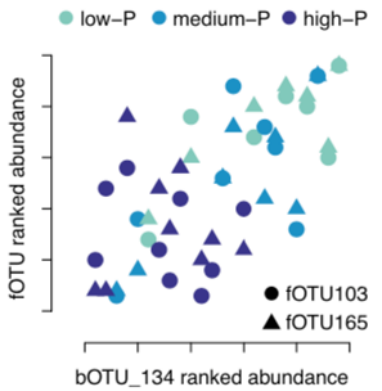
*Ca*. Glomeribacter
Arabido. Petunia




Bodenhausen *et al.* (2019), Phytobiomes J

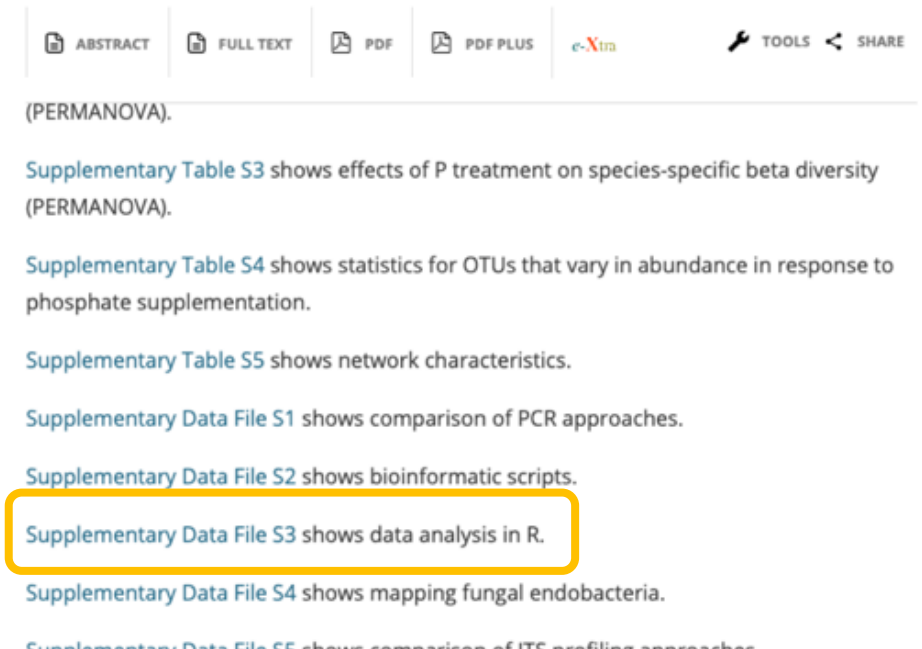
# Network analysis - HANDS ON !
# GDC: Microbiota Data Analysis Workshop, 2020

*Klaus Schlaeppi*

*2020-01-22*

## Code and data origin

Code and data are derived from the study by Bodenhausen et al. (2019) in the Phytobiomes journal. It consists of a subset of the original analysis, is more simplified and contains additional code chunks for further examples. The used data focusses only root microbiota profiles of the Petunia plants that were either grown under low-P, medium-P or high-P fertilization regimes.

# Reference to the published data

https://apsjournals.apsnet.org/doi/full/10.1094/PBIOMES-12-18-0057-R