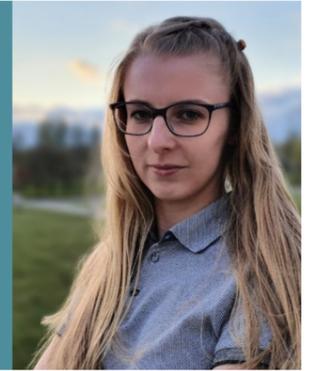


Comparing Differential Abundance (DA) methods for mycobiome in organic cultivation of strawberry

Dominika Siegieda*, Jacek Panek, Magdalena Frąć

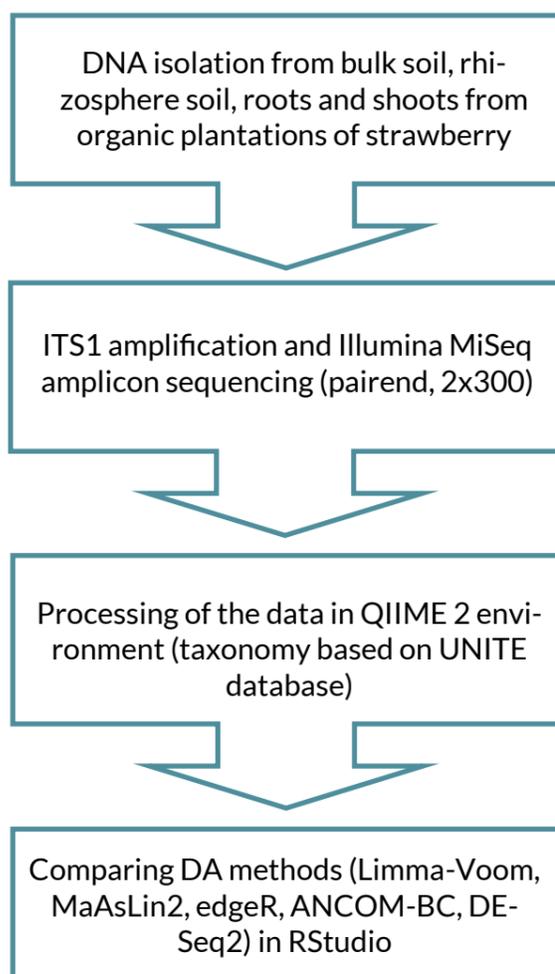
Institute of Agrophysics, Polish Academy of Sciences, Doświadczalna 4 Street, 20-290 Lublin
e-mail: d.siegieda@ipan.lublin.pl



INTRODUCTION

Organic agriculture is gaining popularity globally in recent years. European Union's initiative EU Biodiversity Strategy for 2030 focuses on increasing the area of organic farming and reducing pesticide use. Analyzing the differences and finding differentially abundant taxa between healthy and unhealthy mycobiome of plants can help to understand which fungi are the most connected with plant health. This, in result, can help to improve pesticide-reduced and sustainable agriculture. Multiple methods are used in the literature for DA (differential abundance) analyses, yet, there is no consensus on which method is optimal for microbiome and mycobiome data in particular sample type and dataset.

METHODS



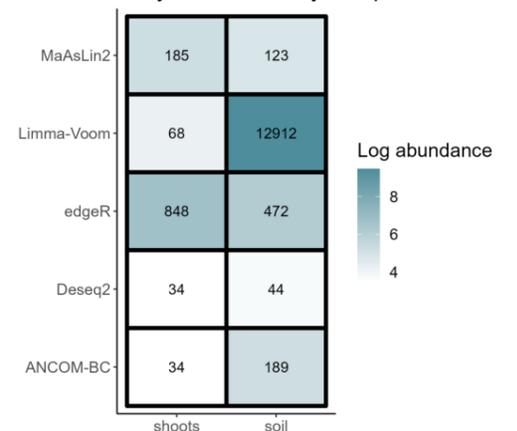
CONCLUSION

Different methods of DA testing between healthy and unhealthy samples yielded various number of taxa in both, soil and shoot samples. It is important to remember, that using only one method can find true associations, but also false positives. For DA analysis, it might be reasonable to use two or more methods in order to reduce the impact of false positives on analysis results.

RESULTS

Different methods of DA analysis harvested different number of significantly different ASVs between healthy and unhealthy bulk soil and shoots of strawberry samples. **DESeq2** found the smallest number of ASVs in both sample types, and **Limma-Voom** and **edgeR** found the biggest number of ASVs in soil and shoot samples, respectively. Limma-Voom found 86% of ASVs significantly different in soil samples—it has been known for poorly controlling false-discovery rate in some studies.

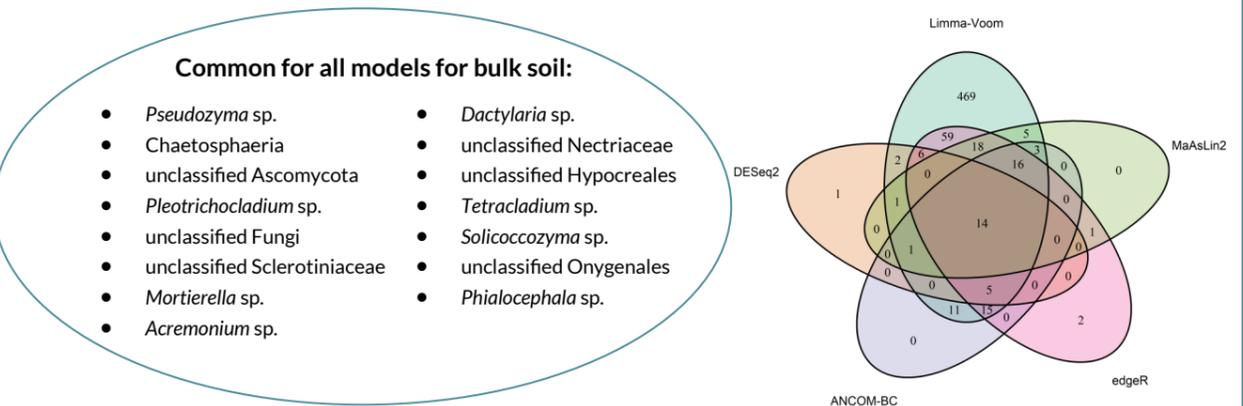
Differentially Abundant ASVs between healthy and unhealthy samples



After collapsing identification to genus level, we identified 15 genera that were Differentially Abundant between healthy and unhealthy samples of bulk soil that were common for all 5 models.

Common for all models for bulk soil:

- *Pseudozyma* sp.
- *Chaetosphaeria*
- unclassified Ascomycota
- *Pleotrichocladium* sp.
- unclassified Fungi
- unclassified Sclerotiniaceae
- *Mortierella* sp.
- *Acremonium* sp.
- *Dactylaria* sp.
- unclassified Nectriaceae
- unclassified Hypocreales
- *Tetracladium* sp.
- *Solicoccozyma* sp.
- unclassified Onygenales
- *Phialocephala* sp.



Only 2 genera were Differentially Abundant between healthy and unhealthy samples of shoots for all 5 models.

Common for all models for shoots:

- unclassified Mycosphaerellaceae
- *Sporobolomyces* sp.

