

# Application of FracMinHash to analyse the phylogenetic context of *Phytophthora*

---

Felix Seidel

[felix.seidel@student.uni-tuebingen.de](mailto:felix.seidel@student.uni-tuebingen.de)

June 5, 2024

# Overview

A short story

Background

Phylogenetic Context of *Phytophthora*

Conclusion

## A short story

---

# The setting

Picture of idyllic farms, potato, maybe avocado?

## The villain: *Phytophthora*

Picture of affected plants, maybe three bullet points (yearly damage)

# The hero?

"Unfortunately, we cannot just walk to some mountain and throw jewelrey in it to defeat the villain" Research on the modes of operation, effector genes, and **phylogeny** of that species

## Background

---

# Phylogenetic Tree



# Phylogenetic Outline<sup>1</sup>

---

<sup>1</sup>Bagci, Bryant, Cetinkaya, and Daniel H Huson, “Microbial Phylogenetic Context Using Phylogenetic Outlines”; Bryant and Daniel H. Huson, “NeighborNet”.

---

<sup>2</sup>Bagci, Bryant, Cetinkaya, and Daniel H Huson, “Microbial Phylogenetic Context Using Phylogenetic Outlines”.

I think I skip Mash, if I need more time I can add it. Need to ensure that this slide is to get some distance estimation that we can use to calculate the outlines

---

<sup>3</sup>Irber et al., *Lightweight Compositional Analysis of Metagenomes with FracMinHash and Minimum Metagenome Covers*.

# Phylogenetic Context of *Phytophthora*

---

# The implementation with `fmhdist`

Maybe some block diagram to illustrate the pipeline?

don't provide slide that discusses the big outlines, boring and not much value.  
mention it, but don't discuss this.

## Compare this to Mash

maybe put both outlines on one slide?

## Origin of the hashes in the sketch (1)

Show plot that I've used in the thesis, maybe without the complexity, then with the complexity



## Origin of the hashes in the sketch (2)

Show the plot for *P. infestans*

some genomes have those windows, some don't



## Conclusion

---

## Method works in general

## Potential next steps

Thanks!