

Learning microbial networks from meta-barcoding data

Application to biocontrol

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Study system: *Vitis vinifera* and *Erysiphe necator*

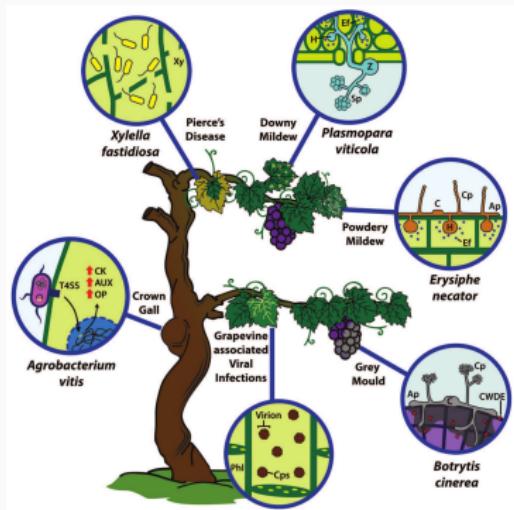
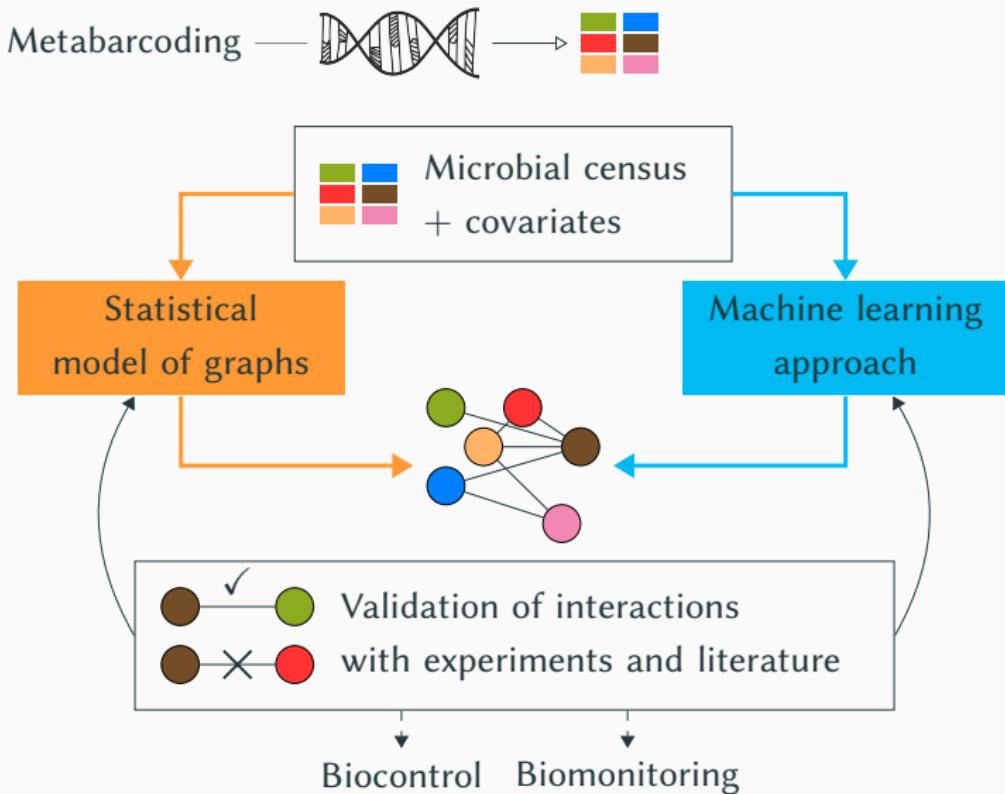


Fig. 1: Grape is vulnerable to multiple diseases such as powdery mildew (caused by *Erysiphe necator*) or downy mildew (caused by *Plasmopara viticola*) (Armijo et al. 2016)

Project Learn-Biocontrol summary

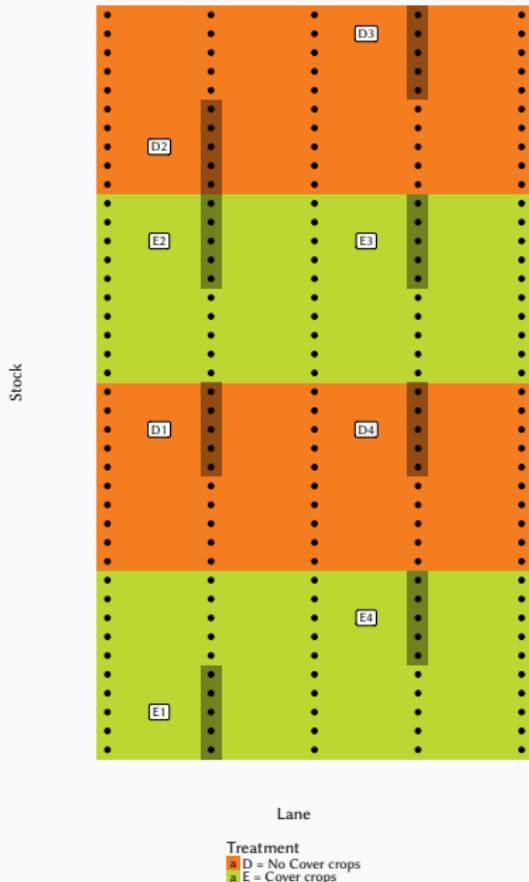


Sampling leitmotiv

→ Leaves with varying degree of infection by *Erysiphe necator*

1. Inoculation of the pathogen on an untreated vineyard
2. Sampling of leaves:
 - at different time
 - in different conditions
 - at replicated locations

Sampling design in the vineyard



- Each dot is a vine plant
- Sampled vines are highlighted by a rectangle
- Labels corresponds to each replicate within each treatment

3 dates

× 2 alley types (cover crop or not)

× 4 spatial replicates

× 2 leaf state (symptomatic or not)

× 4 leaves



= 192 sampled leaves

Different microbial habitat sampled

- Healthy leaves ($\times 4$)
- Infected leaves: Healthy part ($\times 4$) + Disease spot ($\times 4$)

→ 12 microbial habitat $\times 2 \times 3 \times 4 = 288$ samples

Sample naming scheme

Sample name example

1.D2.S3.39

1	Sampling Date
D2	Treatment and Replicate
S3	Leaf status and number
39	PCR well number

- Leaf status corresponds to the visual assessment of infection level by powdery mildew.
- The PCR well number was added to ensure uniqueness of sample names.

Thank you

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