Machine learning prediction of *C. difficile* colonization based on

microbiota composition on day of challenge

• We now see that microbiota are sufficient for colonization susceptibility/resistance

· Some taxa are suggestive of being protective vs unprotective (they have cropped

up multiple times; think Lachno and Porphyro vs Entero and Lacto)

Goal for this section: Generate a model through which to predict susceptibility based

on microbiota

Samples:

16S sequences from all experiments.

- Determine whether susceptible based on who was colonized at any point

throughout experiment

* Random Forest

* Taxa that were predictive

• This is a hypothesis generating step to computationally identify relevant taxa to

advance future biological/mechanistic investigations.

performance measured by the area under the receiver-operator characteristic curve

(AUROC) and the area under the precision-recall curve (AUPRC).

Mean AUROC 0.95 (s.d. 0.05)

Mean AUPRC 0.84 (s.d. 0.065)

TODO feature importance

1

Machine learning methods

TODO describe pipeline (1)

mikropml version 1.2.1 (2)

The workflow used to perform the machine learning analysis is available at https://github.com/SchlossLab/Barron_IBD-CDI_2022

References

- Topçuolu BD, Lesniak NA, Ruffin MT, Wiens J, Schloss PD. 2020. A
 Framework for Effective Application of Machine Learning to Microbiome-Based
 Classification Problems. mBio 11. doi:10.1128/mBio.00434-20.
- Topçuolu BD, Lapp Z, Sovacool KL, Snitkin E, Wiens J, Schloss PD. 2021.
 Mikropml: User-Friendly R Package for Supervised Machine Learning Pipelines.
 JOSS 6:3073. doi:10.21105/joss.03073.

Figure 5

TODO caption

