Severe CDI manuscript

Kelly L. Sovacool[1], **Sarah E. Tomkovich**[2], **Megan L. Coden**[3], **Vincent B. Young**[2,4], **Krishna Rao**[4], **and Patrick D. Schloss**[2,5,†]

[1]Department of Computational Medicine & Bioinformatics, University of Michigan
[2]Department of Microbiology & Immunology, University of Michigan
[3]Department of Molecular, Cellular, and Developmental Biology, University of Michigan
[4]Division of Infectious Diseases, Department of Internal Medicine, University of Michigan
[5]Center for Computational Medicine and Bioinformatics, University of Michigan

Compiled November 29, 2022
[†]Correspondence: pschloss@umich.edu.

1   **ABSTRACT**   TODO

2   **IMPORTANCE**   TODO

3   **KEYWORDS:** *C. difficile* infection, supervised machine learning

INTRODUCTION

TODO

RESULTS

TODO

DISCUSSION

TODO

MATERIALS AND METHODS

TODO ([1], [2], [3])

ACKNOWLEDGEMENTS

TODO

REFERENCES

1. **Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber CF**. 2009. Introducing Mothur: Open-source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Appl Environ Microbiol 75 (23):7537–7541. doi:10.1128/AEM.01541-09.

2. **Topçuoğlu BD, Lapp Z, Sovacool KL, Snitkin E, Wiens J, Schloss PD**. May 2021. Mikropml: User-Friendly R Package for Supervised Machine Learning Pipelines. JOSS 6 (61):3073. doi:10.21105/joss.03073.

3. **Sovacool K, Lesniak N, Schloss P**. 2022. Schtools: Schloss Lab Tools for Reproducible Microbiome Research. doi:10.5281/zenodo.6540687.