

Code for **Capturing Complex Interactions in Disease Ecology with Simplicial Sets**

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Files uploaded:

NewFig1_Code.R

R code used to generate Figure 1 in the accepted version of the paper

Author: Matthew Silk

NewFig2_Code.R

R code used to generate Figure 2 in the accepted version of the paper

Author: Matthew Silk

NewFig3_Code_Plots (zipped folder)

Python code used to generate Figure 3 in the accepted version of the paper. The folder contains a readme for the use of this set of files.

Author: Mark Wilber

CoexistenceHoles_Code_Fig4.txt

Julia code to calculate coexistence holes for Figure 4 in the accepted version of the paper.

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NewFig4_Code.R

R code to generate Figure 4 in the accepted version of the paper.

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SimplicialSetsDiseaseEcology_Appendix3.Rmd

SimplicialSetsDiseaseEcology_Appendix3.pdf

The Rmarkdown used to generate Appendix 3 from the paper and a pdf of its output (converted from html).

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