

Williams, S.D., and M.R. Patterson. 2020. Resistance and robustness of the global coral–symbiont network. Ecology.

Data S2

Data S2 contains code and data files needed to run the network bleaching model, null network models, and robustness removal models. All code was written in Python 2.7.16 using a jupyter notebook or R version 3.5.1 using R studio. The code is also available via a GitHub repository, DOI: 10.5281/zenodo.3595582.

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File list

`Resistance.csv`: Results of bleaching model simulations and resistance calculations.

First column – Row number (ignore)

Spatial.Scale – Location/Spatial scale of network

R – Mean resistance value from 100 simulations of bleaching model

R_std – Standard deviation of resistance values from 100 simulations of bleaching model

Simulation – Which network type, natural network or null network models (Network = natural network, Shuffled Tolerances, Random Bipartite Degree Conserved, Random Bipartite Not-Degree Conserved)

Group – Used for plotting convenience

Statlab – statistical significance label from randomization test results

`Robustness.csv`: Results of the robustness analyses

Network – Which location/spatial scale (abbreviated names)

Mean – Mean R50 value from 100 simulations

Std – Standard deviation of R50 value from 100 simulations

Model – Which removal model (Bleach = bleaching model, LT_BH = average link tolerance high to low, LT_BL=susceptible links, LT_HL= susceptible host links, LT_SL=susceptible symbiont links, Random_link=random links, Degree_high= high to low degree, Degree_low=low to high degree, Random_node=random nodes, Tolerance_low=susceptible nodes)

Removed – links, both type of nodes, hosts, or symbionts

Type – link or node removal model

R50_who – Which robustness scenario (both=total, hosts=host, symbms=symbiont)

Group2 – Used for plotting convenience

Group – Used for plotting convenience

Statlab – statistical significance label from randomization test results

Connectance – connectance of network

Hosts – number of hosts in network

Symbionts – number of symbionts in network

Links – number of links in network

TEST_resistance_perms.csv: For testing the statistics code in the R markdown file.

Net_dtemp – resistance values from each bleaching model simulation of the natural network

hsrand_dtemp – resistance values from each bleaching model simulation of the shuffled tolerances null network

rand_dtemp – resistance values from each bleaching model simulation of the random tolerances null network

rbndc_dtemp – resistance values from each bleaching model simulation of the RBNDc null network

rbdc_dtemp – resistance values from each bleaching model simulation of the RBDC null network

Resistance_RandomizationTest_results.csv: Results of randomization tests of significance for the resistance results, details in Appendix S2.

Spatial Scale – Which network (abbreviations for Global, ocean-basins, or subregions)

Dif_means – Difference in observed means

Obt_p – Obtained P value

Obt_f – Obtained F statistic

Pval –P value based on difference in F statistic; (number of permutations that resulted in a F.stat > obtained F.stat + 1)/(1+number of permutations)

Type1 –which network is being compared to type2 (natural or null models)

Type2—which network is being compared to type1 (natural or null models)

p_adjust_holm – holm adjusted p value

`Robustness_RandomizationTest_results.csv`: Results of randomization tests of significance for the robustness results, details in Appendix S2.

Spatial Scale – Which network (abbreviations for Global, ocean-basins, or subregions)

RobustnessType – Total, host, or symbiont robustness scenario

Dif_means – Difference in observed means

Obt_p – Obtained P value

Obt_f – Obtained F statistic

Pval –P value based on difference in F statistic; (number of permutations that resulted in a F.stat > obtained F.stat + 1)/(1+number of permutations)

Type1 –which network is being compared to type2 (natural or null models)

Type2—which network is being compared to type1 (natural or null models)

p_adjust_holm – holm adjusted p value

`SwainSymsR.csv`: Swain et al. (2017) thermal tolerance ranks that are adapted for the symbiont node thermal tolerances. See Swain et al. (2017) for file description.

`BleachingModel_Resistance_Py27.ipynb`: Jupyter notebook for simulating the bleaching model (Eq. 1), calculating resistance, degree distribution fitting, the host-specific network, and the generalized network.

`BleachingModel_Resistance_Py27.pdf` – PDF of Jupyter notebook above.

`RemovalModels_Robustness_Py27.ipynb`: Jupyter notebook for the removal models and robustness analyses

`RemovalModels_Robustness_Py27.pdf`: PDF of Jupyter notebook above.

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`StatisticsAndVisualization_R35.rmd`: Rmarkdown for visualizing the model results, statistics described in Appendix S2, and code for symbiont node tolerances.

`StatisticsAndVisualization_R35.nb.html`: html of Rmarkdown above.
