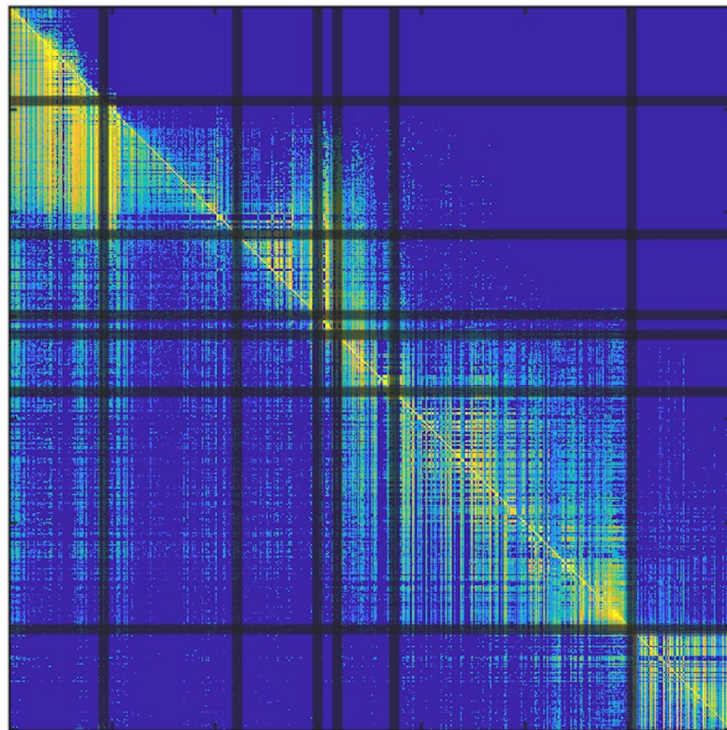

**Extending biophysical and epidemiological simulations of
larval connectivity and SCTL spread to inform mitigation
and restoration**



Extending biophysical and epidemiological simulations of larval connectivity and SCTL spread to inform mitigation and restoration

Final Report

Prepared By:

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6/14/2022

Completed in Fulfillment of PO# BA29D7 for

**Florida Department of Environmental Protection
Coral Protection and Restoration Program
1277 N.E. 79th Street Causeway
Miami, FL 33138**

This report should be cited as follows:

Holstein, D.M., Dobbelaere, T., Gramer, L., Hanert, E., McEachron, L., Muller, E. and S. Williams. 2022. Extending biophysical and epidemiological simulations of larval connectivity and SCTL spread to inform mitigation and restoration. DEP Report. Miami, FL. Pp.15.

This report was prepared for the Florida Department of Environmental Protection, Office of Resilience and Coastal Protection. Funding was provided by the Florida Department of Environmental Protection Award No. BA29D7. The views, statements, findings, conclusions, and recommendations expressed herein are those of the authors and do not necessarily reflect the views of the State of Florida or any of its sub-agencies.



Management Summary

The dispersal of propagules from restored populations is an important component of any coral reef restoration activity that hopes to have lasting demographic or metapopulation effectiveness. For this reason, biophysical models that describe larval dispersal and population connectivity have become a critical tool in coral restoration and conservation planning. However, coastal and ocean currents have the potential to transfer disease between populations, in addition to larval organisms. On Florida's Coral Reef (FCR), just such a disease, termed stony coral tissue loss disease (SCTLD) has severely degraded the health of coral reef communities as it has dispersed southward from the upper keys on ocean currents. Here we've extended dispersal simulations of the larvae of five coral species and of SCTLD disease agents in a high-resolution coastal ocean circulation model in the FCR. We've further developed nested coupled hydrodynamic-epidemiological models to incorporate the coral community with a range of susceptibilities and mortalities associated with SCTLD. This model successfully predicts the transmission of disease to the Dry Tortugas in late 2020, with local outbreaks extending throughout 2021. The model will benefit from further optimization and comparison with empirical observations of disease prevalence and coral mortality.

Executive Summary (max 1 page)

In the effort to mitigate and understand the ongoing and prolonged outbreak of Stony Coral Tissue Loss Disease (SCTLD) on Florida's Coral Reef (FCR) and throughout the Caribbean, it has become widely understood that the disease is capable of dispersal on ocean currents which has resulted in infection between otherwise isolated coral reef patches. Here we've extended coupled hydrodynamic-biological-epidemiological models of the larvae of five coral species and of SCTLD disease agents in a high-resolution coastal ocean circulation model on FCR. We have updated the hydrodynamic and dispersal models, and further developed nested coupled hydrodynamic-epidemiological models to assess how varied species' susceptibilities and mortalities associated with SCTLD has and will influence the trajectory of the disease on FCR.

Hydrodynamics remain highly explanatory for patterns of disease transmission. Species with lower but non-negligible susceptibility and mortality to SCTLD in the model appear to prolong the local and FCR-wide durations of the outbreak and enhance the probability of dispersal between distinct coral communities. Notably, the model predicts well the observed timing of disease transmission/observation at the Dry Tortugas. Aspects of this complex and multiscale model require further optimization, and the inclusion of environmental parameters such as water and environmental quality would undoubtedly improve predictions. That said, the model currently provides one of the best mathematical and holistic descriptions of the multiscale dispersal and transmission of SCTLD, and the coral mortality associated with the disease.

Also included are updated metrics that provide an estimation of coral reef restoration value at FCR locations for the five modeled species of coral. These metrics weigh both the presumed value of coral connectivity and the risk of disease exposure, and are potentially useful in the management and restoration of coral communities affected by disease, coral bleaching, and physical disturbance.

Acknowledgements

The goals of this project were shaped by input from Florida's Disease Advisory Committee (DAC).

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Figure 4. Spatial modeling in QGIS. A) The spatial extent of FCR used in the SLIM connectivity model with the survey points for NCRMP 2014 overlaid. B) Interpolation of the percent cover for the high susceptibility group. C) Interpolation of the percent cover for the intermediate susceptibility group. D) Interpolation of the percent cover for the low susceptibility group.

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Table 2. Datasets sourced for determining coral communities in the Florida Keys.
NCRMP = National Coral Reef Monitoring Program, DRM = Disturbance Response Monitoring, SCREAM = Submerged Coral Reef Ecological Monitoring.

List of Acronyms

Florida’s Coral Reef (FCR)

Stony Coral Tissue Loss Disease (SCTLD)

Disease Advisory Committee (DAC)

Second-generation Louvain-la-Neuve Ice-ocean Model (SLIM)

Gulf of Mexico (GOM)

Hybrid Coordinate Ocean Model (HYCOM)

National Coral Reef Monitoring Program (NCRMP)

Disturbance Response Monitoring (DRM)

Submerged Coral Reef Ecological Monitoring (SCREAM)

Minutes after sunset (MAS)

File transfer protocol (FTP)

1. DESCRIPTION

Here we've extended dispersal simulations of the larvae of five coral species and of Stony Coral Tissue Loss Disease (SCTLD) disease agents in a high-resolution coastal ocean circulation model on Florida's Coral Reef (FCR). We've further developed nested coupled hydrodynamic-epidemiological models to incorporate a range of species-specific susceptibilities and mortalities associated with SCTLD. Also included are updates to coral restoration value metrics that consider both coral connectivity and the risk of disease transmission.

2. METHODS

2.1. Task 1: Hydrodynamic and dispersal modeling

1.1.1. **Goals:** We will extend hydrodynamic and dispersal models to include 2021/2022, and additional coral species (*Colpophyllia natans* and *Pseudodiploria strigosa*). Simulations will be completed by UCLouvain, and analyses will be completed by LSU and Mote.

1.1.2. **Deliverable(s):** Model outputs (hydrodynamic fields for SE FL available as netcdf files; monthly coral and disease connectivity matrices for FCR available as CSV and MAT files, connectivity analyses). All deliverables will be available for download for one year, unless another file sharing method is preferred. SLIM is available on a Git, complete with Wiki and support documentation (<https://git.immc.ucl.ac.be/slim/slim/-/wikis/home>).

2.2. Task 2: Epidemiological modeling and restoration metrics

1.1.3. **Goals:** We will incorporate patch-specific coral community information into multispecies models of disease spread and persistence. As a part of our previous and ongoing work, we have developed spatially realistic metrics and indices of both the restoration value and disease risk of habitats on FCR. These metrics are missing important epidemiologic information on disease spread and susceptibility. Environmental and community data will be collated and modeled by Mote. Epidemiological modeling and analyses will be completed by LSU.

1.1.4. **Deliverable(s):** Model outputs (Patch metrics describing coral larval and disease connectivity, and restoration value available as CSV files). All deliverables will be available for download for one year, unless another file sharing method is preferred.

3. RESULTS

3.1. Task 1: Coupled hydrodynamic and propagule dispersal modeling

We used the unstructured-mesh depth-integrated coastal ocean model SLIM to simulate ocean currents over an area that includes FCR but also the Florida Strait and part of the Gulf of Mexico. The hydrodynamic simulations span May 2018 to February 2022. By using an unstructured mesh, we increased the model resolution only over FCR and hence concentrated computational resources where they were most needed. SLIM, being a depth-averaged model, is well-suited to shallow-water flows. On the shelf break and in deeper areas, it might however not be able to model more complex processes such as

mesoscale eddies that are observed along the southern flank of FCR and the thermally-driven Florida Current. This issue has been partly circumvented by relaxing SLIM's velocity toward the depth-averaged velocity obtained with the HYbrid Coordinate Ocean Model (HYCOM, Chassignet et al., 2007) implemented over the Gulf of Mexico, when the water depth exceeds a certain threshold.

The mesh has been updated for this project to extend further west on the Western Florida Shelf, which mitigates some questionable boundary forcing from the GOM HYCOM. The mesh resolution depends only on the distance to the coast but we distinguish between the coastlines along FCR where we impose a maximum resolution of 50 m and the other coastlines along which the maximum resolution is 1 km. The mesh has been generated with the open-source mesh generator seamsh (<https://pypi.org/project/seamsh/>) and is shown in Figure 1. It has about 7×10^5 elements. The coarsest elements, far away from FCR, have a size of about 13 km.

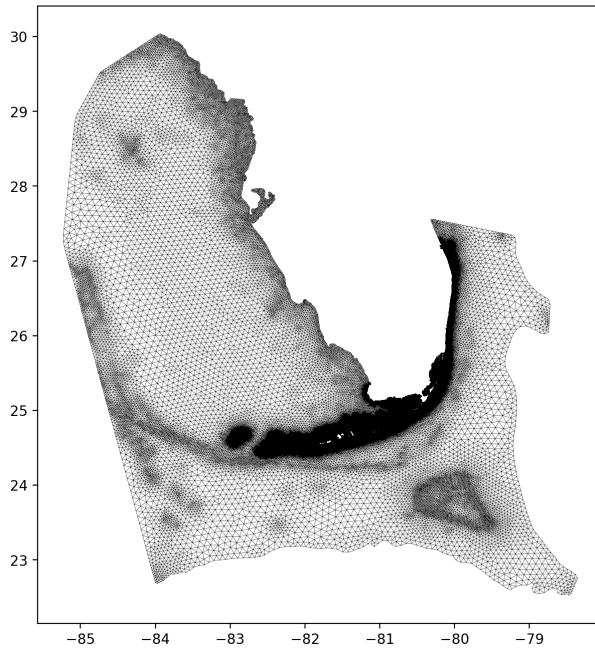


Figure 1. Model computational domain. This illustrates the benefits of unstructured meshes to represent the fine-scale details of the topography and hence simulate currents down to the scale of individual reefs and islands. The mesh has been updated to incorporate more of the Western Florida Shelf.

3.2. Task 1: Dispersal modeling

The simulated currents were then used to model the dispersal of both disease agents and coral larvae. Simulations were completed through February 2022 for disease (monthly), extended through the 2021 spawning seasons for *Orbicella faveolata* and *Acropora cervicornis*, and run for four spawning seasons (2018-2021) for *Colpophyllia natans* and *Pseudodiploria strigosa* following the approach of Dobbelaere et al. (2020). To simulate the physical processes driving larval dispersal, we used a depth-averaged Lagrangian particle tracker. The deterministic advection term is modeled with a 4th-order Runge-Kutta and the stochastic diffusion term is modeled as a Wiener process whose diffusivity is calculated using Okubo (1971)'s formula. Biological processes representing the larval life history traits were included in the particle tracker. These included mortality, competence, and settlement. Table 1 provides a summary of the spawning dates for each coral species. For all species, after a latency period of 5.12 days, larvae acquired competency at a rate of 0.063 day^{-1} and lost competency with a rate 0.016 day^{-1} . Mortality was implemented using a standard Weibull survival model with scale parameter 0.06 day^{-1} and shape parameter 0.641.

Table 1. Species specific spawning dates and times used in larval dispersal modeling. MAS = minutes after sunset.

Year	<i>A. cervicornis</i> (125-200 MAS)	<i>C. natans</i> (30-60 MAS)	<i>D. cylindrus</i> (60-120 MAS)	<i>O. faveolata</i> (100-275 MAS)	<i>P. strigosa</i> (215-260 MAS)
2018	07/28-08/11 08/27-09/10	09/01-09/03 10/01-10/03 10/30-11/01	08/01-08/05 08/31-09/05	07/29-07/30	09/01-09/03 10/01-10/03 10/30-11/01
2019	08/16-08/30	08/21-08/23 09/20-09/22 10/19-10/21	08/20-08/24	08/17-08/18	08/21-08/23 09/20-09/22 10/19-10/21
2020	08/04-08/18	08/09-08/11 09/08-09-10 10/07-10/09	08/08-08/12	08/05-08/06	08/09-08/11 09/08-09-10 10/07-10/09
2021	08/23 09/06	08/28-08/30 09/27-09/29 10/26-10/28	08/24-08/25	08/27-08/31	08/28-08/30 09/27-09/29 10/26-10/28

The output of the Lagrangian particle tracker is a potential connectivity matrix whose entries are denoted M_{ij} . The matrix rows correspond to the source reefs and the columns correspond to the destination reefs. Hence M_{ij} represents the number of virtual larvae or disease agents originating from reef i that have settled on reef j . The ~14,000 (sub-)reefs in FCR yield a connectivity matrix with 196 million entries. While the majority of these entries are zero, it remains challenging to extract useful information from such a large matrix. The connectivity matrix can be more easily handled by interpreting it as a large graph. Graph nodes will be all the reefs of FCR. Node i will be connected to node j if the corresponding entry in the connectivity matrix (M_{ij}) is non-zero. The strength of a connection corresponds to the number of larvae or disease agents traveling from one node to the other. These connectivity matrices are then normalized by the number of larvae or

disease agents released on each (sub-)reef to compute the weights w_{ij} , that give the probability of connection between (sub-)reefs.

These results (May 2018-January 2021) are described in this group's previous final report. Thus, these deliverables (May 2018-February 2022) are provided without further discussion. Images are available in Appendix I. Hydrodynamic output are available as netcdf files through FTP. Lagrangian particle tracking and connectivity outputs are available as text and shapefiles.

3.3. Task 2: Connectivity and restoration value

Coral weighted in- and out-degree:

Simple in- and out-degree (k_i) is an integer count of the number of incoming or outgoing connections from any single node, respectively:

$$k_i = \sum_j^N x_{i,j}$$

Where x is the logical $\{0,1\}$ extracted from a connectivity adjacency matrix that indicates whether a connection exists between any i and j pair. In an undirected graph, in- and out-degree are identical, whereas in a directed graph, such as in the current case, they can be distinct. Further, in our coral and disease dispersal networks, edges have weights which indicate their probability (higher edge weights indicate a higher biophysical probability of connection, or arrival from i to j). Weighted (in- or out-) degree is a relative measure that incorporates both the number of incoming or outgoing connections and the weight ($w_{i,j}$) of those connections (*sensu* Opsahl et al. 2010):

$$s_i = \sum_j^N w_{i,j}$$

Where $w_{i,j}$ is the weight $[0,1]$ extracted from the connectivity matrix C_{ij} that indicates the probability of arrival from i to any j . The weighted in- and out-degree are estimated as:

$$C_{out}^{coral}(i) = k_i^{out} \times \left(\frac{s_i^{out}}{k_i^{out}} \right)^\alpha$$

$$C_{in}^{coral}(i) = k_i^{in} \times \left(\frac{s_i^{in}}{k_i^{in}} \right)^\alpha$$

Where α is a positive tuning parameter that tunes the relative importance of the number of connections versus the weight of those connections. An α of 0.5 is typical (Opsahl et al. 2010).

Disease weighted in-degree:

Similarly, we have used weighted in-degree to describe each node's incoming disease connectivity, or risk:

$$C_{in}^{dis}(i) = k_i^{dis,in} \times \left(\frac{s_i^{dis,in}}{k_i^{dis,in}} \right)^{\alpha_{dis}}$$

Theoretically, since dispersing pathogenic material and its implications for coral reefs are fundamentally different from dispersing larvae, the tuning parameter, α_{dis} , could or should be distinct from that for coral larval dispersal. For example, if a very small amount or likelihood of connectivity (e.g., low edge weight) can result in disease transmission between habitats, it is possible that α should be set low, close to 0, to indicate that edge weight is less important than the number of incoming connections. Conversely, if high amounts of incoming infectious material are necessary to initiate disease onset, α could be set high to prioritize the importance of strong connections. For our purposes, we have kept at α_{dis} at 0.5 for simplicity.

Combined weighted restoration metric:

A weighted restoration metric (R_i) penalizes coral weighted out-degree by disease weighted in-degree at each location:

$$R_i = \frac{C_{out}^{coral}(i)}{\max_{i=1, \dots, n} C_{out}^{coral}} \times \left(\frac{C_{out}^{coral}(i) - \beta C_{in}^{dis}(i)}{C_{out}^{coral}(i)} \right)$$

Where β is a tuning parameter $[0, \infty]$ which indicates the relative importance of disease risk for the restoration value of a location for a given species. Disease outbreaks vary in both space and time, and have different implications for different coral species. β allows the impact of disease risk for restoration value to range from zero ($\beta = 0$) to equal to the impact of coral weighted out-degree ($\beta = 1$) and beyond as necessary. Note that β may vary by species.

These results (May 2018-January 2021) are described in this group's previous final report. Thus, these deliverables (May 2018-February 2022) are provided without further discussion. Images are available in Appendix II, and model output is available as text and shapefiles.

3.4. Task 2: Coral cover estimations

Coral cover was estimated throughout FCR based on records of coral cover for coral species that were grouped into one of three SCTLTD susceptibility categories (low susceptibility "LS", medium susceptibility "MS", and high susceptibility "HS"). These data were acquired from multiple sources (Table 2).

Table 2. Datasets sourced for determining coral communities in the Florida Keys. NCRMP = National Coral Reef Monitoring Program, DRM = Disturbance Response Monitoring, SCREAM = Submerged Coral Reef Ecological Monitoring.

Data Source	Time Period	Metric
NCRMP	2014, 2016, & 2018	Percent Cover
NCRMP DRM	2014-2018	Abundance & Density
DRM SCREAM	1999-2013	Abundance & Density
SCREAM	1999-2009	Percent Cover

All data exploration and filtering was done in R version 4.1.1. Only the NCRMP 2014 data was used to model the coral communities on Florida's Coral Reef (FCR) prior to the onset of SCTLTD as percent cover provided the best metric to integrate into the

transmission model. The 2014 subset of NCRMP was further filtered to only include hard coral species with 15 or more entries (Figure 2).

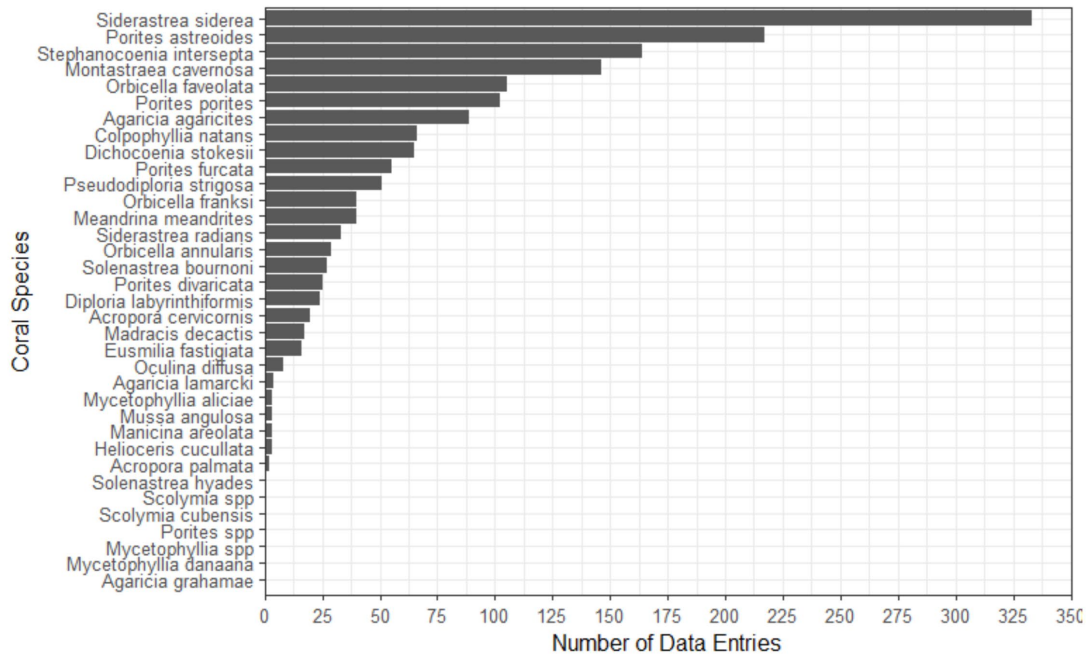


Figure 2. Number of data entries per coral species during 2014 in the NCRMP dataset.

The remaining 21 species were grouped into susceptibility categories for SCTLD (low susceptibility “LS”, medium susceptibility “MS”, and high susceptibility “HS”) based on the case definition (NOAA, 2018). Species with intermediate, or medium susceptibility to SCTLD were most abundant across FCR in 2014 (Figure 3). Percent cover was summed for each susceptibility group at each sampling unit (point) and subsets were created for each group to be used as individual layers in QGIS (V. 3.24.1; QGIS 2022; Figure 4 A). In QGIS, the percent cover of each susceptibility group was interpolated using the inverse distance weighted (IDW) method (Figure 4 B-D). IDW interpolation weights sampled points so that the influence of one point in relation to another decreases with distance from the interpolated point being created (QGIS, 2022). The interpolation created ‘heatmaps’ of percent cover for each susceptibility group (Figure 4 B-D). Average percent cover for each susceptibility group was then calculated for each reef patch (same spatial extent used in the SLIM connectivity model) and extracted to a ‘csv’ file for use in the transmission model. Importantly, the model scenario described below utilizes a coral cover interpolation that has since been updated. Future epidemiological model simulations will utilize the updated coral cover interpolation.

Figure 3. Percent living coral cover of the 21 most recorded species across all sampling units in 2014 (summed percent cover divided by total number of sampling units) colored by susceptibility group.

Figure 4. Spatial modeling in QGIS. A) The spatial extent of FCR used in the SLIM connectivity model with the survey points for NCRMP 2014 overlaid. B) Interpolation of the percent cover for the high susceptibility group. C) Interpolation of the percent cover for the intermediate susceptibility group. D) Interpolation of the percent cover for the low susceptibility group.

3.5. Task 2: Epidemiological modeling

These estimates were then utilized in a spatially and temporally realistic epidemiological model that describes the transmission and severity of SCTL on FCR from May 2018-February 2022. This model is an extension of the model described in Dobbelaere et al. 2020, and shares many of its characteristics. Where it differs is that it integrates coral cover (abundance) and community (susceptibility categories). This model is a nested susceptible-infectious-recovered (SIR) compartment model, where recovery is currently assumed to indicate mortality.

The basis of the SIR compartment model is a system of differential equations. Transmission of SCTLD within a patch is controlled by the transmission rate, β , (Eqs. 1 and 2). The proportion of infected individuals, βSI , is influenced by transmission from local infectious colonies, and also by disease entering the patch from upstream patches at any time, $C_{j,t}$ (Eq. 5), and “recovery”, σI . Coral tissue entering the recovered compartment are no longer diseased, but transition immediately into the dead compartment, according to the mortality rate m , currently set at 1. There is capacity in the model to transition recovered corals into resistant and then susceptible compartments according to the loss of protection rate, r , which is currently set to 0.

$$\begin{aligned}\frac{dS}{dt} &= -\beta S((I_{Comm} + C_{jt})/(1 + C_{jt})) + rR \\ \frac{dI}{dt} &= \beta S((I_{Comm} + C_{jt})/(1 + C_{jt})) - \sigma I \\ \frac{dR}{dt} &= \sigma I(1 - m) - rR \\ \frac{dD}{dt} &= \sigma mI\end{aligned}$$

The transmission probability between patches is derived from a dispersal model of passive particles in high-resolution hydrodynamic fields, and the probability of dispersal between any two patches at any time of the year. Transmission probabilities between patches are described in a three-dimensional matrix of disease dispersal probability (P) with source and destination (i, j) on two axes, and time (t) on the third. The dispersal probability is then scaled by the total diseased tissue at each source location (I_i), and accumulated at each destination (j) to arrive at the transmission of disease from upstream habitats at any given time ($C_{j,t}$).

$$C_{j,t} = 1 - \prod_i^n 1 - P_{i,j,t} * I_{i,t}$$

Within-patch disease dynamics are distinct for three categories of corals, those with low-, medium-, and high-susceptibility and mortality to SCTLD. For most compartment transmissions, these categories remain distinct; however, transmission can occur *between* any category of coral, although at category-specific rates, from a within-patch multi-host disease pool, based on the total diseased coral tissue (I_{comm}). Thus, each variable described above has coral category-specific sub-variables. This coupling of numerical models of biophysical dispersal and community epidemiology results in a highly dynamic spatially and temporally explicit modeling framework.

This system of differential equations was solved in Matlab software using ode45. Initial modeling conditions mirrored those of Dobbelaere et al. (2020). By 2018 SCTLD had already been infecting corals for several years. Dobbelaere et al. (2020) estimated the amount of time between first documentation of disease at sites on the FCR and model initiation (May 2018), and used the SIR model *sans* connectivity to approximate the state of the outbreak at sites with disease at May 2018. Those methods were repeated here, and represent the initial conditions of the coupled model.

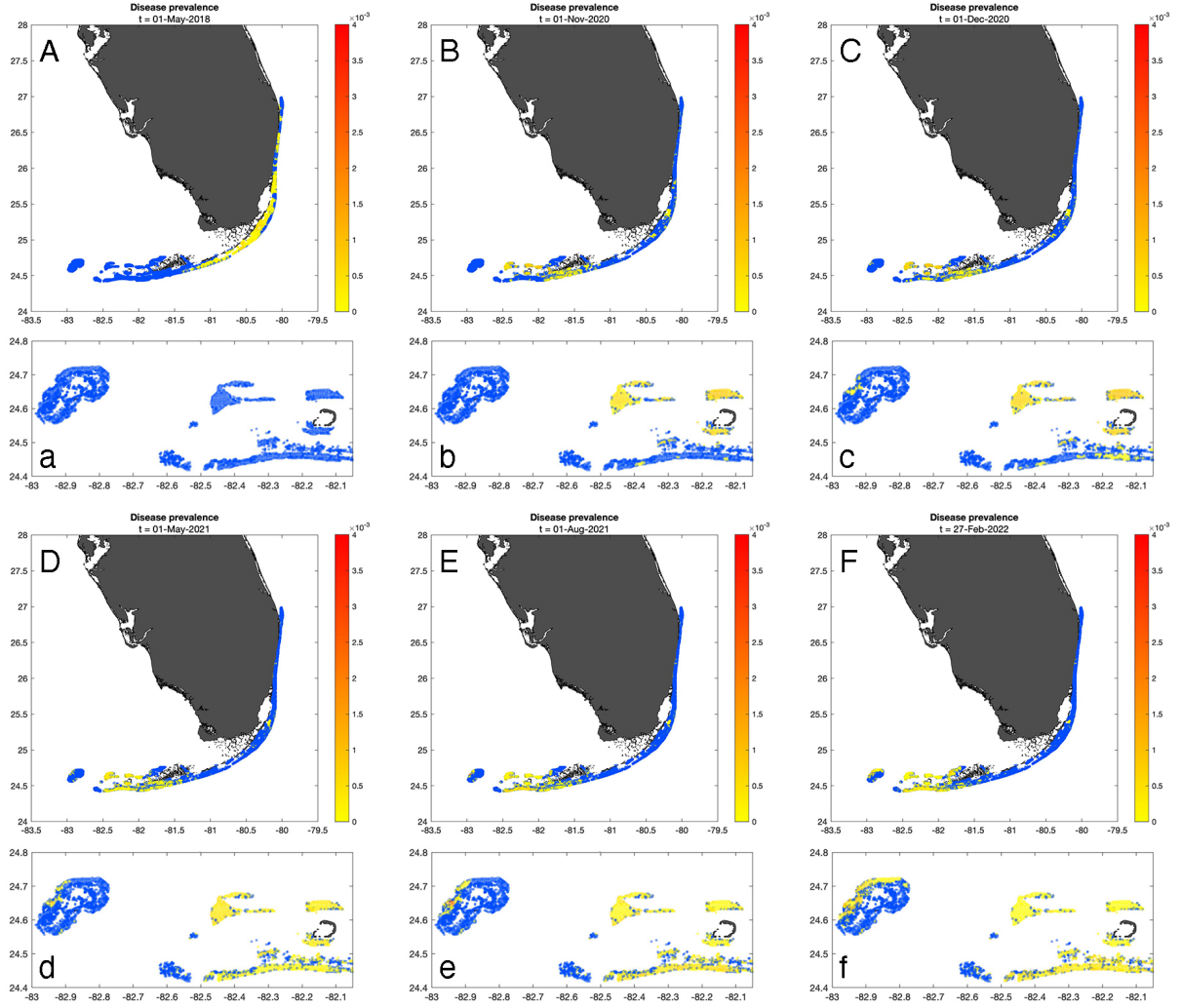


Figure 5. Disease prevalence at locations on the entire FCR (capital letters) and the Marquesas/Dry Tortugas (lower case) at representative times. The first panels (A and a) are at model initiation. B and b are just prior to transmission to the Dry Tortugas, and C and c are just after. D-F show the progression of the disease over the following $\sim$ year.

Dobbelaere et al. (2020) estimated β and m from an approximated R_0 that resulted in approximately 85% removal (mortality) throughout the model initialization period. This resulted in a $\beta \approx 0.155$ and $\sigma \approx 0.143$. These species-averaged rates were used to approximate rates of β and σ for each susceptibility category, so that the mean rates remained near those estimated in Dobbelaere et al. (2020). Ultimately, rates that were used were: $\beta_{LS} = 0.07/d$; $\beta_{MS} = 0.15/d$; $\beta_{HS} = 0.40/d$; $\sigma_{LS} = 0.07/d$; $\sigma_{MS} = 0.14/d$; $\sigma_{HS} = 0.30/d$. These values were used to reproduce an acceptable local outbreak duration, total coral mortality, and an R_0 greater than one (which indicates community transmission). In the future, we intend to continue to test the model's sensitivity to these parameters.

In the coupled model, a threshold T controls the minimum amount of disease pathogen transition between patches that initiates disease locally at previously unaffected sites. The model is very sensitive to this parameter, as shown in Dobbelaere et al. (2020). In this study we ran the model with a range of T values to assess the model's sensitivity and to

estimate which values produced spatial and temporal patterns of infection that were consistent with observations and our previous work (e.g., Dobbelaere et al. 2022). When a previously unaffected patch receives disease transmission above T , disease is initiated in that patch in the high susceptibility coral category at 0.01% prevalence (Dobbelaere et al. 2020 set this initial prevalence at $\sim 0.07\%$). A major observed pattern used to optimize T was the timing of infections in the Dry Tortugas (spring/summer 2021) and the timing of disease dispersal to the Dry Tortugas predicted in Dobbelaere et al. (2022) (late 2020).

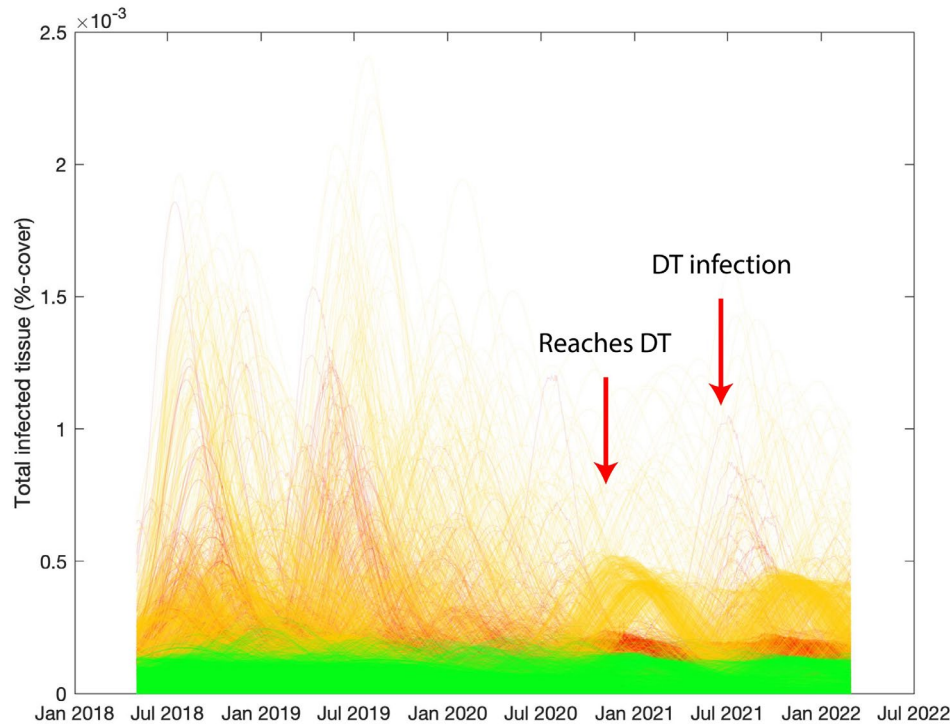


Figure 6. Total infected coral tissue at each location throughout the model duration. Each location has three curves; red = high susceptibility; orange = medium susceptibility; green = low susceptibility. Arrows show approximate timing of transmission to the Dry Tortugas and curves associated with community transmission within the Dry Tortugas.

3.6. Task 3: Florida Keys Coral Disease Early-Alert Dashboard

Goals: We will work with complementary DEP funded projects to incorporate model outcomes into existing dashboards and modeling activities. Specifically, we will work with partners at the University of South Florida (Dan Otis and Tylar Murray) and FWC (collaborator McEachron) to incorporate a time series of connectivity matrices that describe the probability of disease transmission into the Florida Keys Coral Disease Early-Alert Dashboard.

Deliverable(s): Summary of updates to the Florida Keys Coral Disease Early - Alert Dashboard in Word format (incorporated into Exhibit A and the final report).

Matrices describing monthly SCTLD transmission probabilities between FCR locations have been provided to the Florida Keys Coral Disease Early-Alert Dashboard.

4. DISCUSSION

A sensitivity analysis on threshold T demonstrated that with the current model parametrization, a maximum T of 2.5×10^{-6} is required for disease transmission to the Dry Tortugas within the model's timeframe. This value of T also resulted in the transmission of the disease to the Dry Tortugas in late 2020, which corresponds to the predictions of Dobbelaere et al. (2022) that Florida Current eddies late in 2020 would have allowed the transmission of SCTLD westward from reefs near the Marquesas. In this scenario, the Dry Tortugas outbreak intensifies throughout early 2021 and is still occurring at the end of the simulation in February 2022 (Fig. 5 & 6). We believe this implies either that the current epidemiological parameterization is reasonable, or that transmission of the disease to the Dry Tortugas is not sensitive to epidemiological parameterization so far as disease is active in the Marquesas in late 2020.

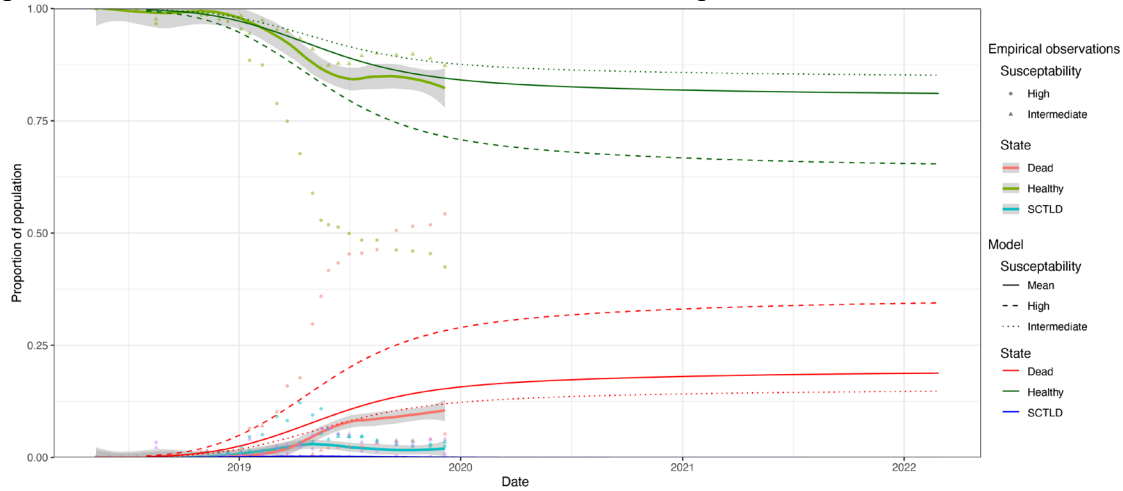


Figure 7. Comparison of FCR-wide model results with empirical observations from three monitored locations (similar to results of Dobbelaere et al. [2020]). Model results are averaged from 1,384 locations at which simulated disease outbreaks began in August 2018. Note that the model may underestimate the proportion of infected corals present at any one time and the mortality of highly susceptible species, suggesting that β_{HS} may be higher in reality, and that lower σ may be necessary – potentially in intermediately susceptible species – to produce a standing population of infected corals.

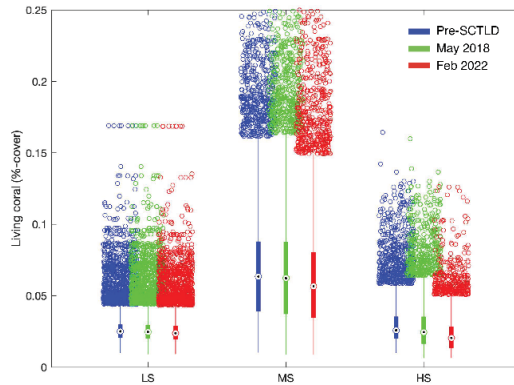


Figure 8. Simulated coral cover loss from estimated 2014 levels (blue) at model initiation in May 2018 (green) and at the end of the simulation in February 2022 (red) for each susceptibility category. Points are medians, boxes show the 25th and 75th quartiles, whiskers are 1.5 x the interquartile range, and circles are outliers. LS = low susceptibility; MS = medium susceptibility; HS = high susceptibility.

Optimization of this nested epidemiological model is ongoing, but the remainder of the results refer to the model scenario where $T = 2.5 \times 10^{-6}$ and other model parameters are left constant. Although the pattern of infection to the Dry Tortugas is a major spatiotemporal pattern to model against, and this scenario captures that pattern well, future work by this group will involve further parameter exploration. Notably, locations near the eastern margin of the Dry Tortugas where disease was first observed in May 2021 did not become diseased in the current simulation. This could indicate a number of inconsistencies between the current model and reality, including hydrodynamic conditions, initial conditions, and SIR parameterizations. The current scenario has similar results to Dobbelaere et al. (2020) that match well with observed patterns of infection and removal (death) on FCR (Fig. 7), and high vulnerability Dry Tortugas reefs predicted in Dobbelaere et al. (2022) became infected in the current simulation (notably, Dobbelaere et al. [2022] did not simulate epidemiology). However, both Dobbelaere et al. (2020) and the current study may underestimate the loss of living coral tissue due to SCTLD through February 2022 (Fig. 8). The current model predicts that for sites affected by SCTLD, the mean (SEM) loss of coral cover (% of benthos) through February 2022 is 1.28% ($\pm 0.014\%$). This translates to a mean (SEM) coral loss of 11.76% (0.097%) at affected sites. Importantly, an updated coral cover interpolation has recently become available, which is likely to influence these results. An important next step of this work is to further optimize epidemiological parameters to better match realized coral loss due to SCTLD on FCR, and this working group intends to work closely with researchers and resource managers on FCR to do so.

5. REFERENCES

1. Dobbelaere, T., Holstein, D. M., Muller, E. M., Gramer, L. J., McEachron, L., Williams, S. D. & Hanert, E. Connecting the Dots: Transmission of Stony Coral Tissue Loss Disease From the Marquesas to the Dry Tortugas. *Front. Mar. Sci.* **9**, (2022).
2. Dobbelaere, T., Muller, E. M., Gramer, L. J., Holstein, D. M. & Hanert, E. Coupled Epidemio-Hydrodynamic Modeling to Understand the Spread of a Deadly Coral Disease in Florida. *Front. Mar. Sci.* **7**, 1–16 (2020).

6. APPENDIX I – CONNECTIVITY RESULTS

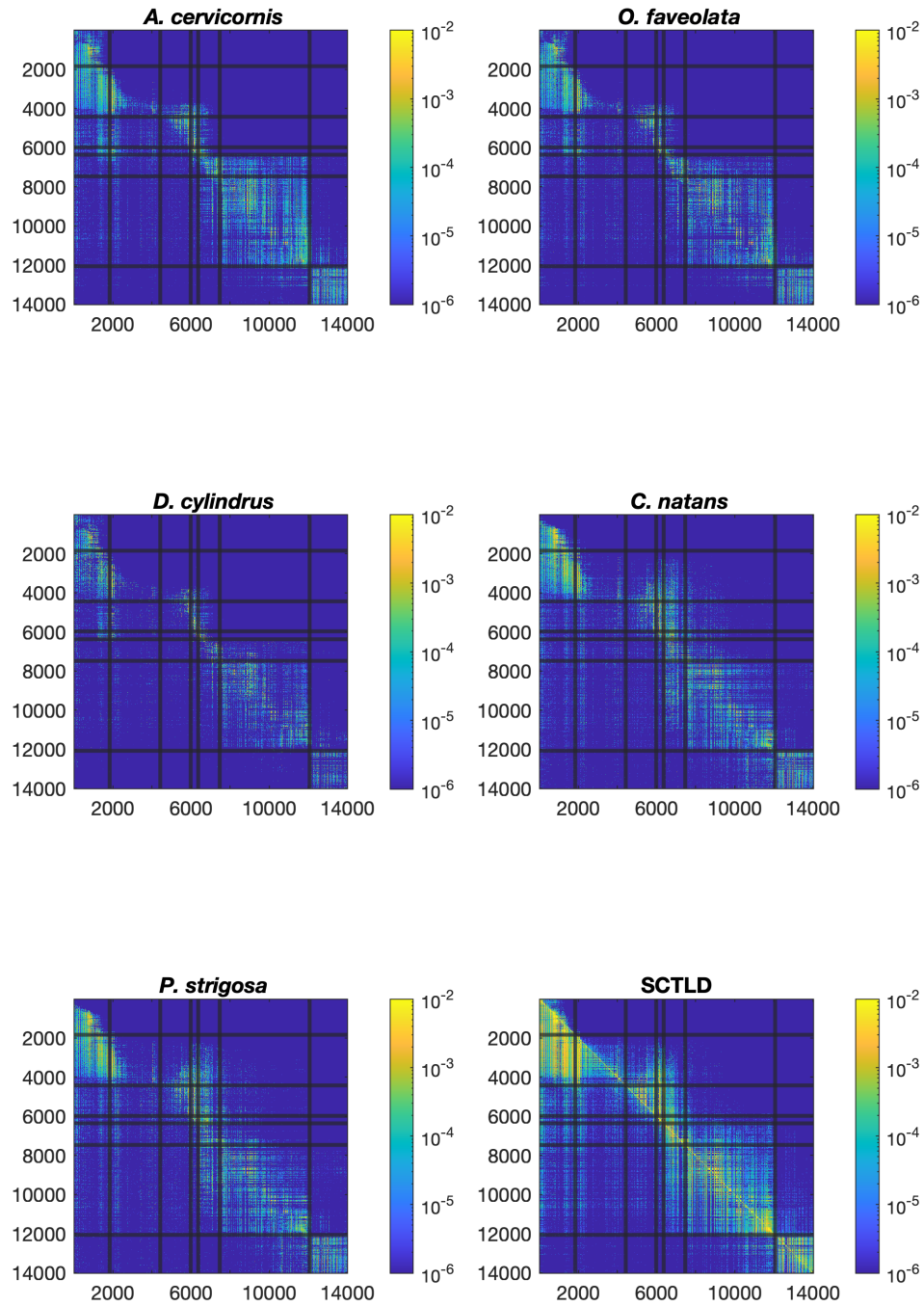


Figure A1.1. Updated connectivity matrices (probability of arrival) for the five modeled species and SCTLD. Source locations are on the y-axis and destination locations on the x-axis. Locations are arranged roughly from NE to SW. Black lines delineate, in order (low to high): SE FL, BISC, UK, UKMK transition, MK, LK, DT (shown geographically in Fig. A1.2). No thresholding is used in these matrices.

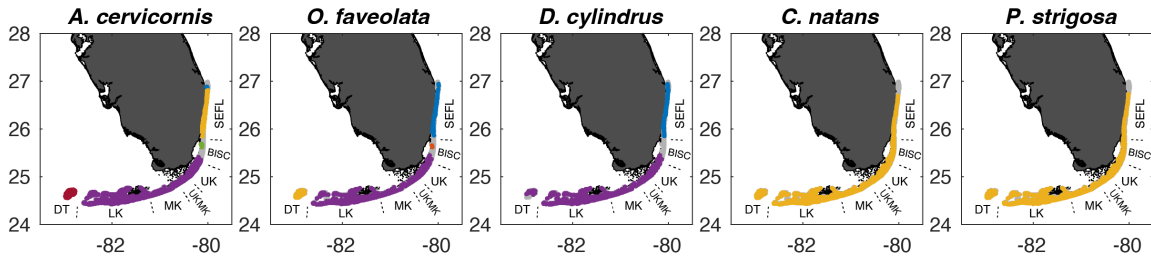


Figure A1.2. Updated strongly connected components (SCCs) for coral dispersal and connectivity. A threshold of 0.001 probability of arrival is used. Note that SCCs for *A. cervicornis*, *O. faveolata*, and *D. cylindrus* are largely unchanged with two additional years of simulation. *C. natans* and *P. strigosa* networks appear to have one large SCC. This appears due to considerably more exchange between the UK, UKMK, and MK.

APPENDIX II – Coral Restoration Metric

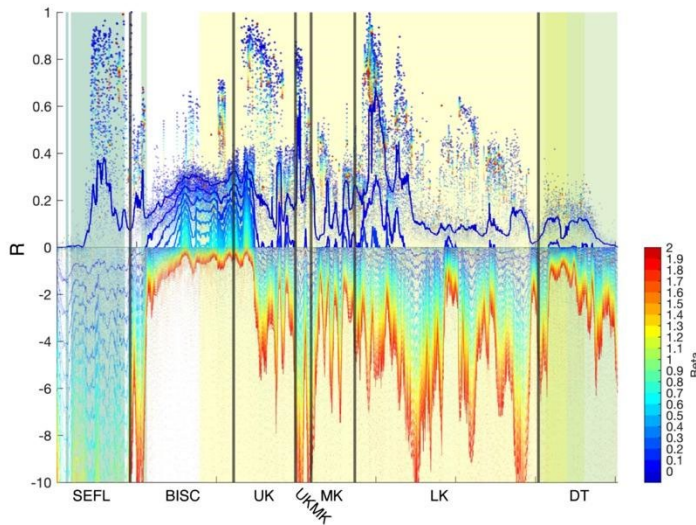


Figure A2.1. Restoration value (R) by location for *A. cervicornis* and for varying values of β . Colored lines are moving medians (NE to SW) for each β . Shaded rectangles loosely indicate the spatial extent of the major SCCs in each network graph (Fig A1.2). Vertical lines are approximate distinctions between SEFL, BISC, UK, UKMK, MK, LK and DT. Scores lower than 0 are shown with transparency to enhance readability.

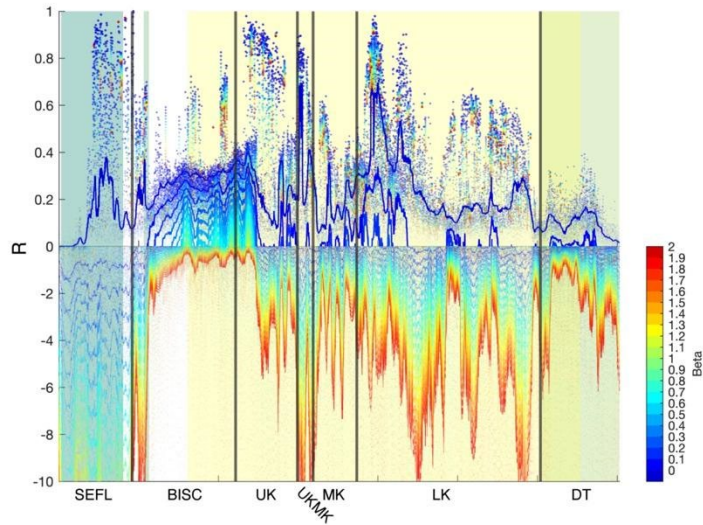


Figure A2.2. Restoration value (R) by location for *O. faveolata* and for varying values of β . Colored lines are moving medians (NE to SW) for each β . Shaded rectangles loosely indicate the spatial extent of the major SCCs in each network graph (Fig A1.2). Vertical lines are approximate distinctions between SEFL, BISC, UK, UKMK, MK, LK and DT. Scores lower than 0 are shown with transparency to enhance readability.

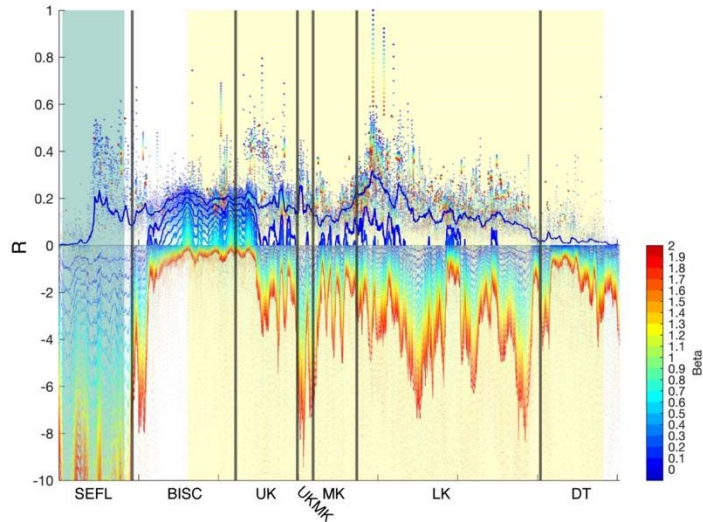


Figure A2.3. Restoration value (R) by location for *D. cylindrus* and for varying values of β . Colored lines are moving medians (NE to SW) for each β . Shaded rectangles loosely indicate the spatial extent of the major SCCs in each network graph (Fig A1.2). Vertical lines are approximate distinctions between SEFL, BISC, UK, UKMK, MK, LK and DT. Scores lower than 0 are shown with transparency to enhance readability.

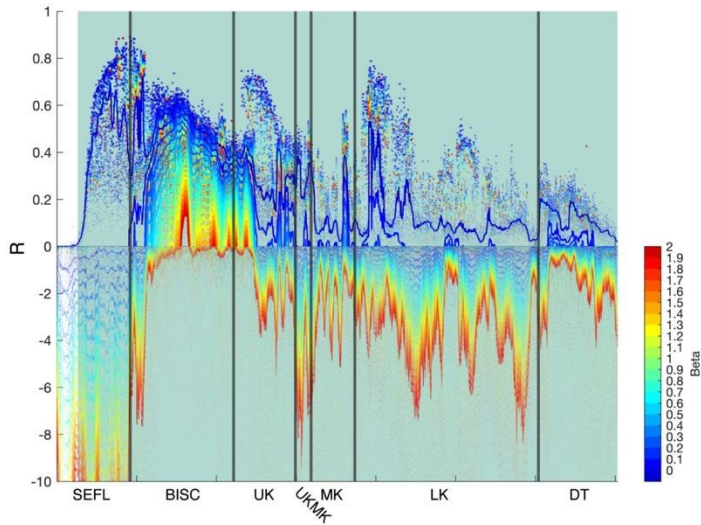


Figure A2.4. Restoration value (R) by location for *C. natans* and for varying values of β . Colored lines are moving medians (NE to SW) for each β . Shaded rectangles loosely indicate the spatial extent of the major SCCs in each network graph (Fig A1.2). Vertical lines are approximate distinctions between SEFL, BISC, UK, UKMK, MK, LK and DT. Scores lower than 0 are shown with transparency to enhance readability.

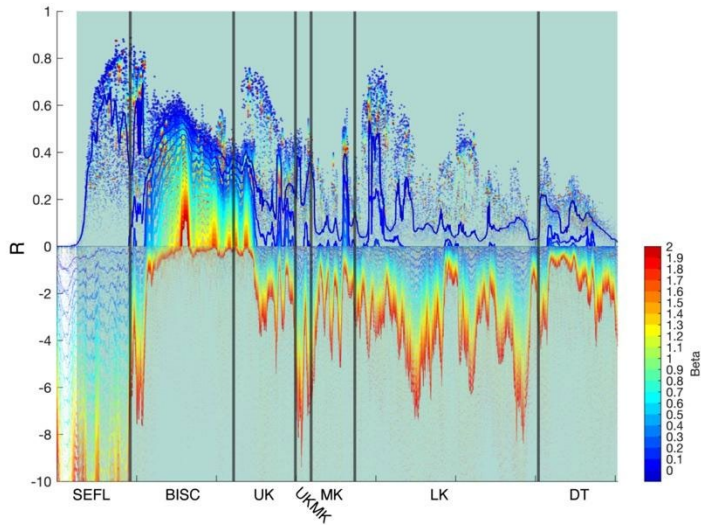


Figure A2.5. Restoration value (R) by location for *P. strigosa* and for varying values of β . Colored lines are moving medians (NE to SW) for each β . Shaded rectangles loosely indicate the spatial extent of the major SCCs in each network graph (Fig A1.2). Vertical lines are approximate distinctions between SEFL, BISC, UK, UKMK, MK, LK and DT. Scores lower than 0 are shown with transparency to enhance readability.