Community Tropicalisation Explorer: An Interactive Application to Monitor Thermal Shifts in Marine Communities

# Abstract

Shifts in species distributions driven by climate change are causing profound restructuring of ecological communities. In marine systems, warm-affinity species often expand poleward while cold-affinity species contract or decline, a phenomenon known as tropicalisation. Understanding and monitoring these changes is essential for biodiversity conservation, resource management, and climate adaptation.  
  
The Community Tropicalisation Explorer is an open-source R Shiny application that allows users to compute and visualise temporal trends in the Community Temperature Index (CTI) and decompose these trends into underlying processes: tropicalisation, detropicalisation, borealisation, and deborealisation. By automating data preparation, statistical modelling, and visualisation, the app supports both technical and non-technical stakeholders in tracking the thermal dynamics of marine biological communities.  
  
We describe the structure and core functionality of the app, including its support for flexible input formats, species-level trend analysis, process decomposition logic, and spatial summarisation. We demonstrate its use through a sample dataset and discuss its relevance for ecological monitoring in the context of global climate change.

# 1. Introduction

Climate change is reshaping ecological communities around the globe (reference). In marine ecosystems, increasing sea surface temperatures have been linked to the poleward shift of warm-affinity species, changes in community composition, and declines in cold-adapted taxa (reference). These biological responses can lead to what is termed tropicalisation: the growing dominance of species adapted to warmer thermal regimes (reference).  
  
Tracking these changes over time requires integrating species occurrence or abundance data with environmental temperature records. A widely used indicator for this purpose is the Community Temperature Index (CTI), defined as the average thermal preference of species in a community, weighted by their relative abundances (reference). CTI has been employed in terrestrial, freshwater, and marine systems to monitor biodiversity responses to warming (reference). However, calculating CTI trends, decomposing them into ecological processes (e.g. species gains or losses), and visualising results typically require advanced programming skills. This can limit the capacity of environmental agencies or NGOs to make use of their own data. To address this, we developed the Community Tropicalisation Explorer, an interactive R Shiny application that enables any user - without needing to write code - to:  
  
- Upload species-by-sample matrices with minimal formatting requirements  
- Use temperature data provided in the file, or extract temperatures automatically from satellite raster layers  
- Compute CTI values across time and space  
- Quantify whether changes are driven by gains or losses of warm or cold-affinity species  
- Generate report-ready plots and tables  
  
By making these tools more accessible, the application empowers stakeholders to independently and quickly assess climate impacts on marine biodiversity using their own monitoring data.

# 2. Software Description

The Community Tropicalisation Explorer is implemented in the R language using the shiny framework for web applications. It combines geospatial functionality (via terra, leaflet), statistical modelling (nlme, ggeffects), data wrangling (dplyr, tidyr), and visualisation (ggplot2, leaflet.minicharts) to deliver an interactive, responsive experience.  
  
The app can be launched locally from RStudio, deployed on a Shiny Server, or bundled as a standalone app. No command-line interface is required for the end-user.

## 2.1 Input Requirements

The primary input is a .csv file containing:  
  
- A unique SampleID per sample  
- StationID: a categorical site identifier  
- year: numeric or integer value (e.g., 2005, 2010,5 for summer of 2010)  
- lat and long: sample coordinates  
- temperature: in °C, representing in situ or interpolated temperature for the sample (optional)  
- Species columns: all other columns are interpreted as species, with numeric values representing either abundance or presence/absence  
  
Flexible options:  
- If the temperature column is missing, the app will assign values automatically using MODIS SST data (reference).  
- Users may upload a folder of .tif rasters (one per year) and an average SST raster if they wish to use their own high-resolution temperature time series.  
- A checkbox allows switching between abundance and presence/absence analysis.

## 2.2 App Structure and Workflow

The user interface is organised into collapsible panels and tabs that guide the user through:  
  
1. Data upload: With format checks and example data to download to help the user to format their data adequately.  
2. CTI analysis:  
 - Computation of species-level thermal preferences (STI)  
 - Calculation of sample-level CTI values  
 - Estimation of trends using both linear and mixed-effects models  
3. Process decomposition: Assigning each species’ abundance trend to one of four processes  
4. Visual outputs: Including interactive maps, trend plots, and species scatterplots  
5. Export: Tables (CTI, STI, trends) and plots (species, trends, maps) can be downloaded as .csv or .pdf

# 3. Methods

This section describes the analytical pipeline embedded in the Community Tropicalisation Explorer. The app translates species-by-sample matrices into ecological indicators of community-level warming responses, using the Community Temperature Index (CTI) and its decomposition into thermal processes. It is based on the study by reference.

## 3.1 Species Thermal Index (STI)

The Species Thermal Index (STI) reflects each species’ thermal affinity based on the temperatures at which it occurs. STIs are computed as follows:  
  
Let *Ti* be the temperature recorded for sample *i*, and *Aij* the abundance (or presence: 1/0) of species *j* in sample *i*. For each species *j*, we extract all values of *Ti* where *Aij* > 0, and define:

*nj* is the number of samples in which species *j* was present. The STI thus provides a central tendency of temperatures where a species is observed, assuming these reflect its realised thermal niche at the local scale.

## 3.2 Community Temperature Index (CTI)

The Community Temperature Index (CTI) is calculated for each sample based on the species it contains and their thermal affinities. Specifically, for sample *i*:

, the relative abundance (or occurrence frequency) of species *j* in sample *i* composed of *k* species,  
- is the thermal index of species *j*  
  
This yields a community-level index representing the weighted average of species’ thermal preferences in each sample.

## 3.3 Temporal Trend Estimation

To detect whether CTI changes significantly over time, the app fits two types of models:  
  
- Per-station linear model: for each site s, a model is fitted:

where *t* is the sampling year, and ​ is the estimated trend.

- Mixed-effects model: a global model including all stations as random intercepts:

where is a station-level intercept.

Estimates are produced using the nlme::lme function. A confidence interval and p-value for the global slope β\_1 are shown. The significance of the trend is reflected in the colour of the main CTI trend line.

## 3.4 Species Trend Analysis and Process Decomposition

### 3.4.1 Species Trend Estimation

For each species at each station, we fit a model to the (log-transformed) abundance or presence/absence over time:  
  
log(A\_j,t + 1) = α + δ\_j \* t + ε\_t  
  
The slope δ\_j indicates whether the species is increasing or decreasing over time.

### 3.4.2 Thermal Process Classification

Each species trend is then compared to the mean CTI of its station. We define:  
  
Δ\_j = STI\_j - mean(CTI\_s)  
  
A species is classified into one of four thermal processes:  
- Increase & Δ\_j > 0 → Tropicalisation  
- Increase & Δ\_j < 0 → Borealisation  
- Decrease & Δ\_j > 0 → Deborealisation  
- Decrease & Δ\_j < 0 → Detropicalisation

### 3.4.3 Process Strength

To quantify how much each process contributes to change, the app computes the absolute contribution per species as:  
  
|δ\_j \* Δ\_j|  
  
These are then summed and normalised across all species at a station to yield relative strength (%). The result is a profile per station showing which processes dominate.

# 4. Discussion

## 4.1 Bridging Ecological Science and Usability

One of the central motivations for the Community Tropicalisation Explorer is the growing recognition that ecological research must extend beyond academic circles to be impactful. Although statistical tools for monitoring biodiversity exist in R and other languages, they often remain inaccessible to those responsible for practical conservation and management: marine station operators, government agencies, NGOs, and local monitoring networks. The app responds directly to this challenge by embedding established ecological theory and statistical models into a graphical user interface. This removes the technical burden of scripting and modelling from the user, while preserving the rigour and reproducibility of the underlying analyses. The result is a tool that enables any stakeholder, regardless of coding expertise, to independently process, interpret, and visualise their biodiversity data. This focus on accessibility is not a simplification—it is a translation. The app doesn't "dumb down" the methods; rather, it packages them responsibly in a format that aligns with how stakeholders work. This aligns with calls in the ecological community to develop usable science—science that is not only credible and salient, but also legitimate and convenient for decision-makers (reference).

## 4.2 Promoting Reproducibility and Openness

The application is fully open-source, distributed under a permissive license, and built entirely in R using widely used packages. This openness is crucial for:  
  
- Transparency: Users can inspect and audit the exact logic used in the analysis.  
- Extensibility: Future contributors can adapt the app to other systems or taxa.  
- Longevity: Institutions are not locked into black-box software with unclear dependencies or licensing issues.  
  
Moreover, because the app can be run locally and all computations happen on the client’s machine, data privacy is preserved—a common concern in governmental or sensitive biodiversity contexts.  
  
The app also aligns with the principles of FAIR data (Findable, Accessible, Interoperable, Reusable), not only by consuming FAIR-compliant inputs but by allowing users to produce clearly structured outputs that can be archived or shared.

## 4.3 Addressing Knowledge Retention and Staff Turnover

In many monitoring projects, there is a recurrent issue of institutional knowledge loss: analyses are coded by a student or temporary researcher, who then moves on. Their custom scripts, stored in personal folders or half-maintained GitHub repositories, become brittle or unusable over time.  
  
By encapsulating the full workflow—from data upload to interpretation—in an interactive tool, this app offers a buffer against staff turnover. Agencies or institutions can continue their monitoring efforts even as personnel change, without losing analytical continuity.  
  
This is not just a convenience—it’s a matter of data equity. Communities and institutions that lack dedicated data scientists should still be able to derive insight from the biodiversity data they collect.

## 4.4 The Role of Design in Ecological Tools

The design of ecological software often prioritises power over usability. This app tries to rebalance that, recognising that a tool’s impact is shaped not only by what it can do, but by who can use it. The addition of elements such as:  
  
- collapsible info boxes with plain-language explanations  
- use of icons and visual metaphors (e.g., pie charts, trend colours, emojis)  
- real-time feedback during analysis  
- exportable, publication-quality figures  
  
…is not cosmetic. It is part of a deliberate effort to communicate science more clearly, to more people, without requiring specialist interpretation.  
  
Good design, in this context, is not a luxury—it is a form of accessibility.

## 4.5 Remaining Limitations

Despite its strengths, the app is not a one-size-fits-all solution:  
  
- CTI is a useful but coarse indicator. It cannot capture all ecological nuance (e.g., community turnover without thermal change).  
- STI estimates may be unreliable for rare species or taxa with unclear thermal affiliations.  
- Station-level trends can be noisy with short time series; caution is advised when fewer than 5 years of data are available.  
- Presence–absence mode is more robust to sampling bias but less sensitive to abundance trends.  
  
Nonetheless, the app encourages critical exploration rather than passive consumption. Users are encouraged to download and explore intermediate tables and plots, and to use the app as a launching point for deeper questions, not a final answer.

## 4.6 Toward a Broader Culture of Usable Science

This app is just one piece of a growing movement to make ecological science more usable, modular, and collaborative. As species distributions shift and climate risks escalate, the need for tools that translate complex data into actionable insight becomes urgent.  
  
The Community Tropicalisation Explorer was designed not only to fill a methodological gap—but also to signal a cultural shift: from isolated scripts to shareable workflows, from passive data reporting to active data interpretation, and from knowledge gatekeeping to knowledge empowerment.