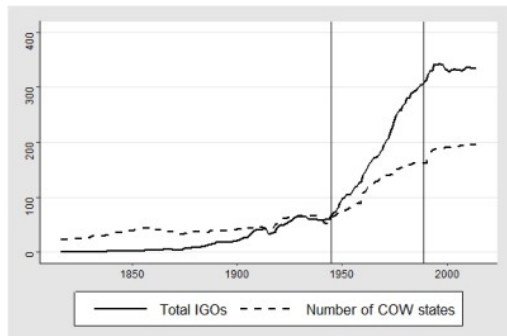


Data

igoR v0.1.1: Provides tools to extract information from the Intergovernmental Organizations ('IGO') Database , version 3, provided by the [Correlates of War Project](#). See [Pevehouse et al. \(2020\)](#) for information from 1815 to 2014, and get started with the [vignette](#).



OTrecord v0.1.0: Uses optimal transportation theory as described in [Gares, Guernec & Savy \(2019\)](#) and [Gares & Omer \(2020\)](#) to solve recoding problems. Given two databases that share a subset of variables, package functions assist users in obtaining a unique synthetic database with complete information. See the [vignette](#) for examples.

pwt10 v10.0-0: Interfaces to the [Penn World Table 10.x](#) which provides information on relative levels of income, output, input, and productivity for 183 countries between 1950 and 2019.

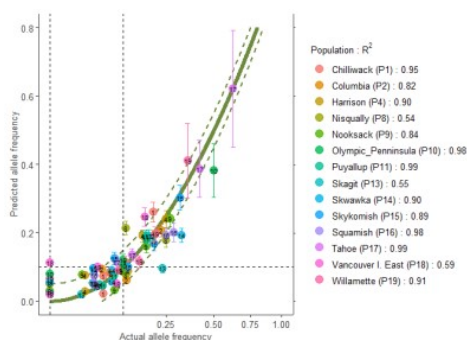
trainR v0.0.1: Interfaces to the [National Rail Enquiries](#) systems, including Darwin which provides real-time arrival and departure predictions, platform numbers, delay estimates, schedule changes and cancellations. Look [here](#) for examples.

Finance

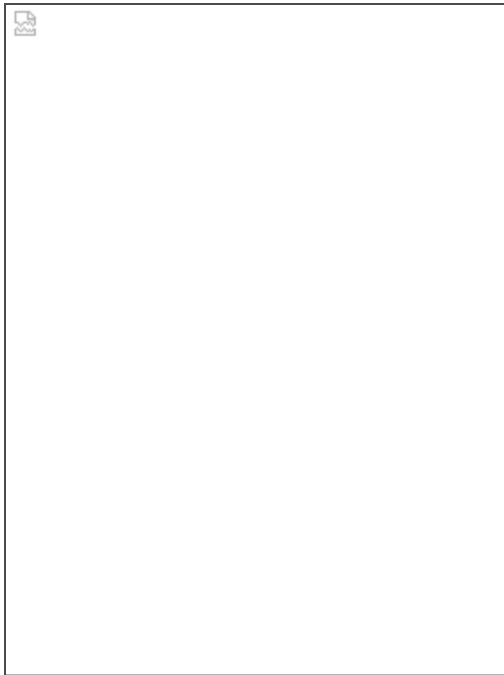
LSMRealOptions v0.1.0: Provides an implementation of the [least-squares Monte Carlo](#) simulation method to value American option products and capital investment projects through real options analysis. Cash flows are modeled as being dependent upon underlying state variables that evolve stochastically. See the [vignette](#) for examples.

Genomics

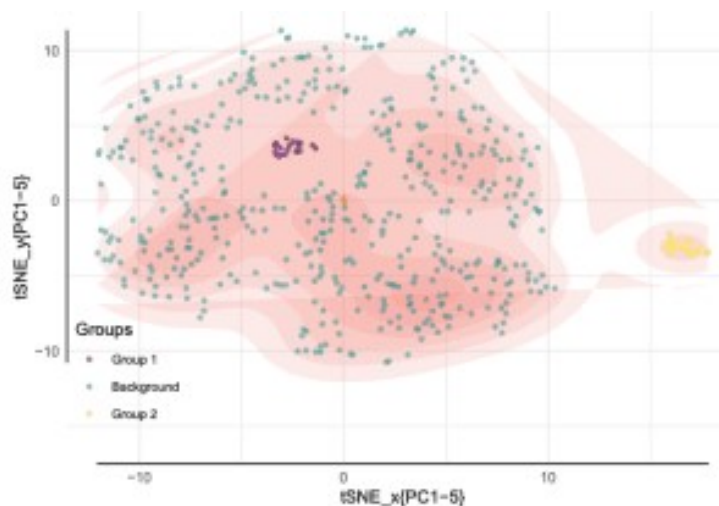
AlleleShift v0.9-2: Provides methods for calibrating and predicting shifts in allele frequencies through redundancy analysis (`vegan::rda()`) and generalized additive models (`mgcv::gam()`) and functions to visualize the predicted changes in frequencies. See [README](#) for examples.



GenomeAdmixR v1.1.3: Provides tools to simulate how patterns in ancestry along the genome change after admixture. Se [Janzen \(2020\)](#) for the details and the vignettes [Isofemales](#), [Joyplot](#), [Visualization](#), and [Walkthrough](#).



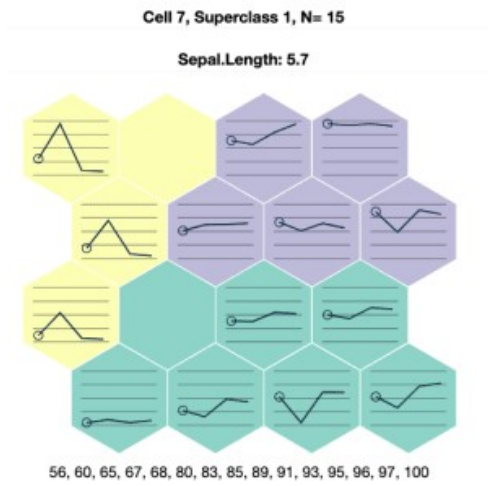
[MOSS](#) v0.1.0: Implements an omics integration method based on sparse singular value decomposition to deal with the challenges of high dimensionality, noise and heterogeneity among samples and features in omics data. See [\(Gonzalez-Reymundez & Vazquez, 2020\)](#) for background and the [vignette](#) for examples.



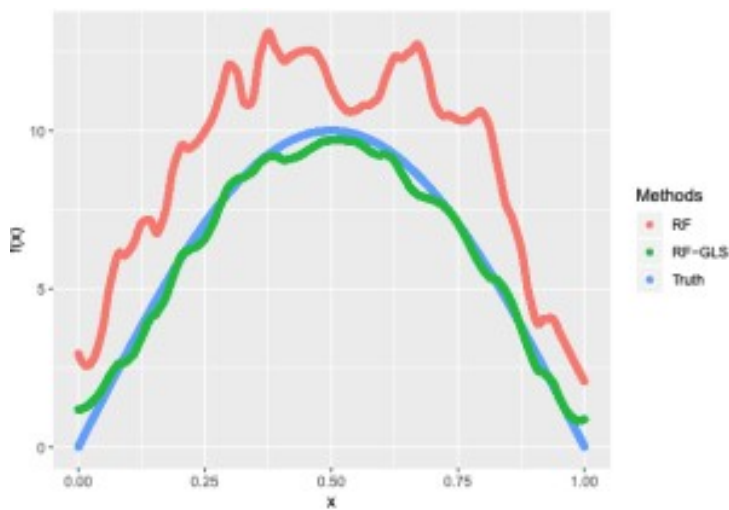
Machine Learning

[autoMrP](#) v0.98: Implements a tool that improves the prediction performance of multilevel regression with post-stratification (MrP) by combining a number of machine learning methods. For information on the method, refer to [Broniecki, Wüest, Leemann \(2020\)](#) and the [vignette](#).

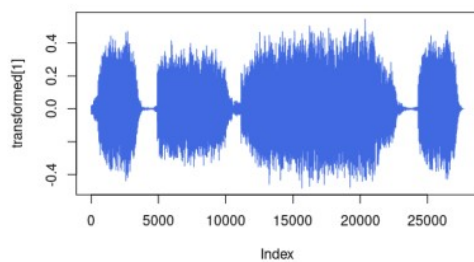
[aweSOM](#) v1.1: Implements Self-organizing maps, a method for dimensionality reduction and clustering of continuous data, as well as interactive graphics to assist analysis. See [Kohonen \(2001\)](#) for background and the [vignette](#) for an overview of the package.



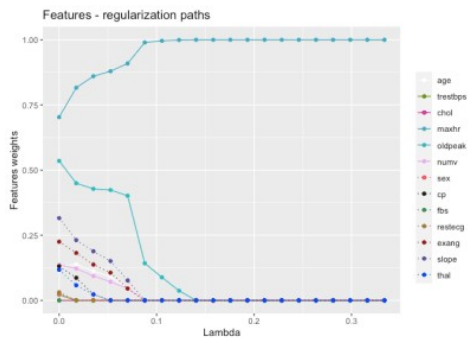
[RandomForestsGLS](#) v0.1.2: Fits non-linear generalized least square regression models with Random Forests as described in [Saha, Basu & Datta \(2020\)](#).



[torchaudio](#) v0.1.1.0: Provides access to datasets, models and preprocessing facilities for deep learning in audio. See the [vignette](#).

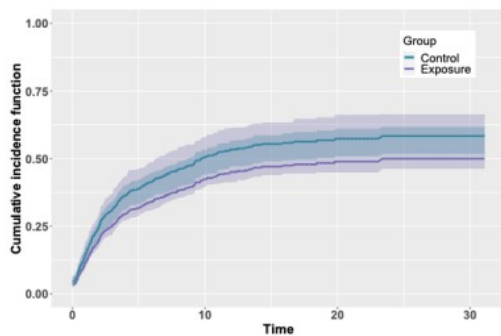


[vimpclust](#) v0.1.0: Implements functions to perform sparse k-means clustering with a group penalty and variable selection on mixed categorical and numeric data. See [Chavet et al. \(2020\)](#) for background. There are vignettes on [numeric](#) and [mixed data](#) sparse k-means clustering.

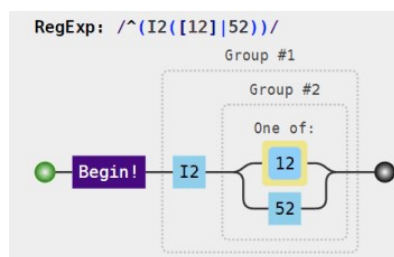


Medicine

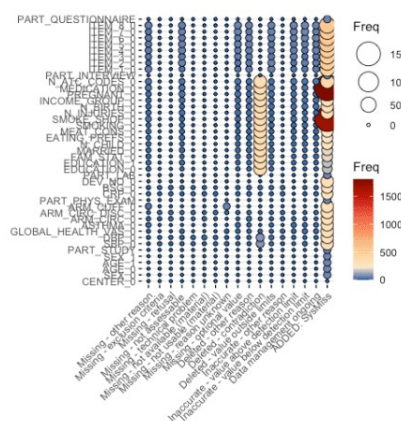
[cmprskcoxmsm v0.2.0](#): Provides functions to estimate treatment effect a under marginal structure model for the cause-specific hazard of competing risk events. Functions also estimate the risk of the potential outcomes, risk difference and risk ratio. See [Hernan et al. \(2001\)](#) for the theory and the [vignette](#) for examples.



[coder v0.13.5](#): Provides functions to classify individuals or items based on external code data identified by regular expressions. A typical use case considers patients with medically coded data, such as codes from the International Classification of Diseases. There is an [overview](#) and vignettes on [class codes](#), [interpreting regular expressions](#), and [example data](#).



[dataQuieR v1.0.4](#): Provides functions to assess data quality issues in studies. See the [TMF Guideline](#) and the [DFG Project](#) for background, and the [vignette](#) for examples.



[NHSDDataDictionary v1.2.1](#): Provides a common set of simplified web scraping tools for working with the [NHS Data Dictionary](#). This package was commissioned by the [NHS-R community](#) to provide this consistency of lookups. See the [vignette](#) to get started.

Science

LPDynR v1.0.1: Implements methods that use phenological and productivity-related variables derived from time series of vegetation indexes to assess ecosystem dynamics. Functions compute an indicator with five classes of land productivity dynamics. Look [here](#) for background. See the [vignette](#) for an example.

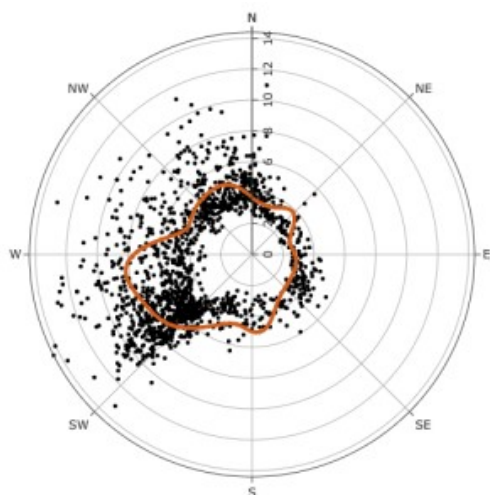
rgee v1.0.8: Provides an [Earth Engine](#) client library for R that includes all [Earth Engine](#) API classes, modules, and functions, as well as additional functions for importing spatial objects, extracting time series, and displaying metadata and interactive maps. Look [here](#) for further details. Read the [Introduction](#) and the vignette on [Best Practices](#) to get started.



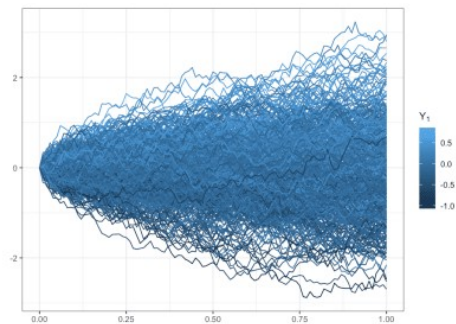
SAMtool v1.1.1: Provides tools for simulating the **MSEtool** operating model to inform data-rich fisheries. It includes a conditioning model, tools for assessing models of varying complexity and comparing models, and diagnostic tools for evaluating assessments inside closed-loop simulations. There is a [User Guide](#) and a series of seven more vignettes including an [overview](#) of the Rapid Conditioning Model (RCM) for conditioning **MSEtool** operating models, and a [mathematical description](#) of RCM.

Statistics

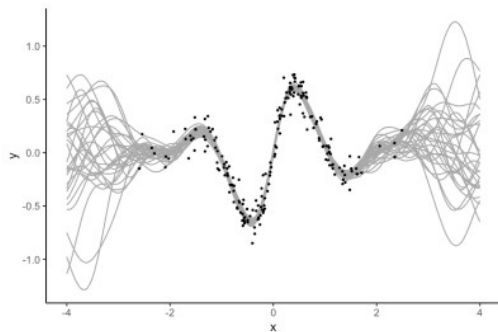
circularEV v0.1.0: Provides functions for performing extreme value analysis on a circular domain. See the [local methods example](#) and the [spline example](#).



ghcm v1.0.0: Implements a statistical hypothesis test for conditional independence which can be applied to both discretely observed functional data and multivariate data. See [Lundborg et al. \(2020\)](#) for details and the [vignette](#) for an overview of the generalized Hilbert Covariance measure with examples.



[gplite](#) v0.11.1: Implements the most common Gaussian process models using Laplace and expectation propagation approximations, maximum marginal likelihood inference for the hyperparameters, and sparse approximations for larger datasets. See the [vignette](#) for a quick start.



[multibridge](#) v1.0.0: Implements functions to evaluate hypotheses concerning the distribution of multinomial proportions using bridge sampling. Functions are able to compute Bayes factors for hypotheses that entail inequality constraints, equality constraints, free parameters, and mixtures of all three. See [Sarafoglou et al. \(2020\)](#) for background and the examples: [Memory of Lifestresses](#), [Mendelian Laws of Inheritance](#), and [Prevalence of Statistical Reporting Errors](#).




[partR2](#) v0.9.1: Provides functions to partition the variance explained in generalized linear mixed models (GLMMs) into variation unique to predictors and variation shared among predictors. This can be done using semi-partial R^2 and inclusive R^2 . See [Nakagawa & Schielzeth \(2013\)](#) and [Nakagawa, Johnson & Schielzeth \(2017\)](#) for the theory and the [vignette](#) for examples.

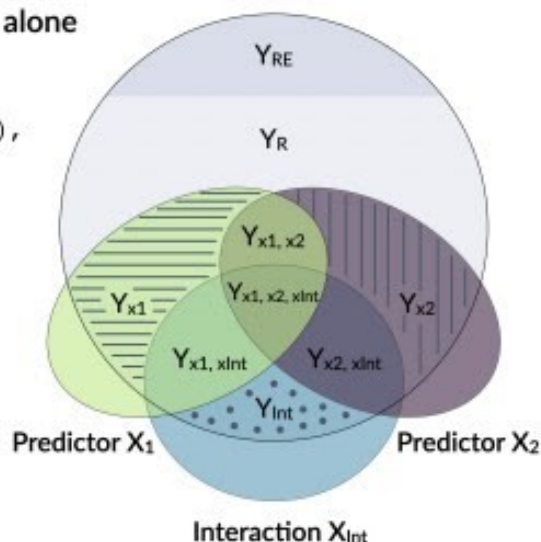
(A) Main effect and interaction alone

Generic syntax

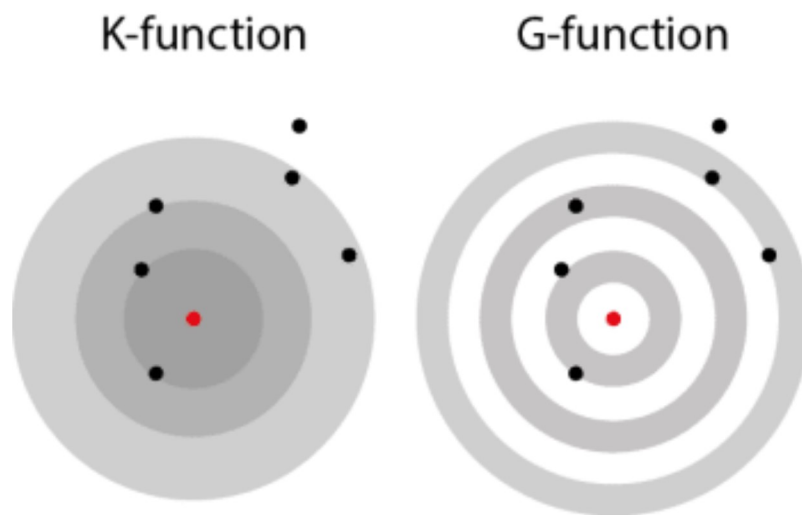
```
mod <- lmer(Y ~ X1 * X2 + (1|RE),
            data)
partR2(mod, partvars = c('X1',
                          'X2', 'X1:X2'), data)
```

Components estimated

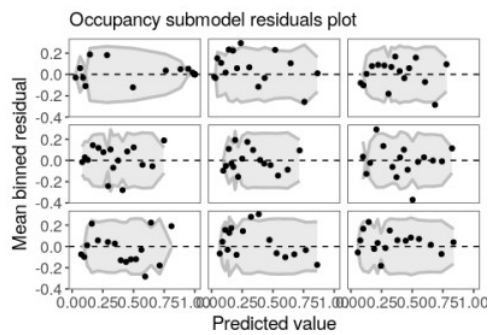
-  X_1
-  X_2
-  $X_1 : X_2$



[spNetwork](#) v0.1.1: Provides tools to perform spatial analysis on network including estimating network kernel density, building spatial matrices. See [Okabe et al. \(2019\)](#) for background and the vignettes: [Network k Functions](#), [Network Kernel Density Estimate](#), [Details about NKDE](#), and [Spatial Weight Matrices](#).



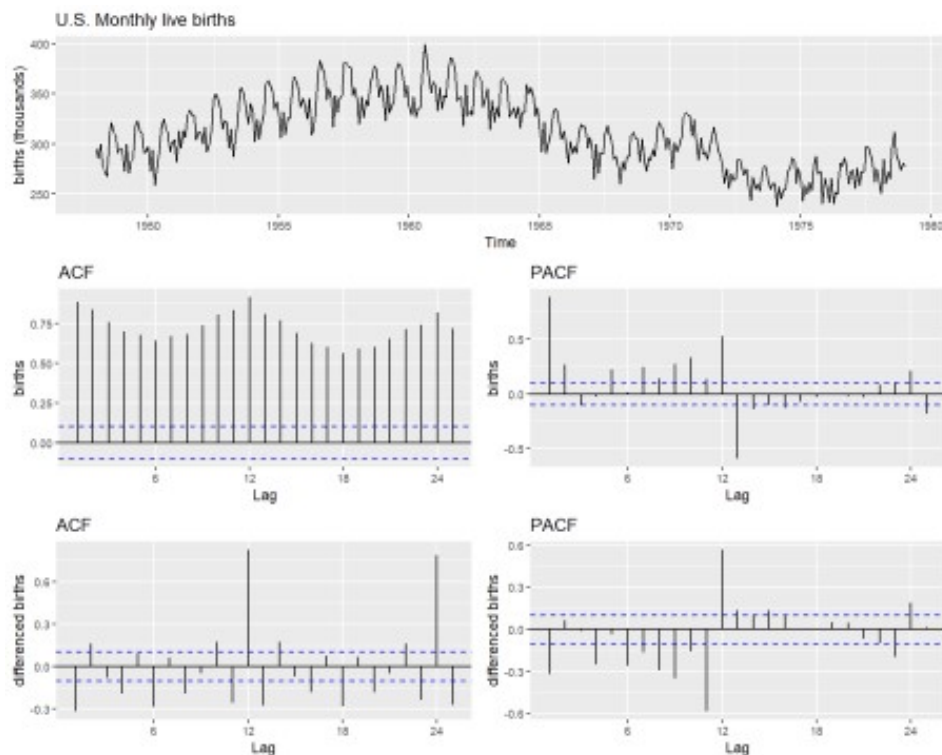
ubms v1.0.2: Provides functions to fit Bayesian hierarchical models, including single-season occupancy, dynamic occupancy, and N-mixture abundance models, of animal abundance and occurrence with the `rstan` package. See [Carpenter et al. \(2017\)](#) and [Fiske and Chandler \(2011\)](#) for background. There is a package [Overview](#), a vignette on [Random Effects](#), and another on [Comparing ubms with JAGS](#).



Time Series

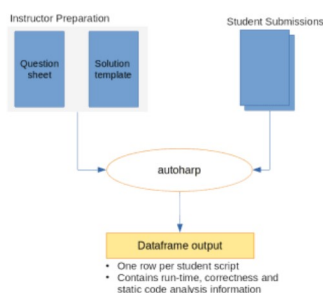
autostsm v1.2: Provides functions to automate the decomposition of structural time series into trend, cycle, and seasonal components using the Kalman filter. See [Koopman et al. \(2012\)](#) for the theory and the [vignette](#) for an overview with examples.

bayesforecast v0.0.1: Provides functions to fit Bayesian time series models using `Stan` for full Bayesian inference. It includes seasonal ARIMA, ARIMAX, dynamic harmonic regression, GARCH, t-student innovation GARCH models, asymmetric GARCH, random walks, stochastic volatility models for univariate time series. See [Hyndman \(2017\)](#) and [Carpenter et al. \(2017\)](#) for background and [README](#) for examples.



Utilities

[autoharp](#) v0.0.5: Implements customizable tools for assessing and grading R or R-markdown scripts from students which allow for checking correctness of code output, runtime statistics and static code analysis. There is a [User Manual](#) and a vignettes on the S4 class [treeharp](#).



[cachem](#) v1.0.4: Provides functions to cache R objects with automated pruning. Caches can limit either their total size or the age of the oldest object (or both), automatically pruning objects to maintain the constraints. See [README](#) for examples.

[eList](#) v0.2.0: Provides list compression functions to convert for loops into vectorized `lapply()` functions which support loops with multiple variables, parallelization, and loops across non-standard objects. See the [vignette](#) for examples.

[Microsoft365R](#) v1.0.0: Builds on `AzureGraph` to implement and interface to [Microsoft365](#) and enables access to data stored in SharePoint Online and OneDrive. See the [vignette](#) to get started.

[rtables](#) v0.3.6: Provides a framework for declaring complex multi-level tabulations and then applying them to data. Tables are modeled as hierarchical, tree-like objects which support sibling sub-tables, arbitrary splitting or grouping of data in row and column dimensions, cells containing multiple values, and the concept of contextual summary computations. There is a [Introduction](#) and a series of vignettes on [comparing](#) against baseline or control, a clinical trials [example](#), constructing tables [manually](#), [pruning and sorting](#) tables, [subsetting](#) tables, [Tabulation concepts](#), and a [comparison with dplyr](#) tabulation.

	ARM A (N=134)	ARM B (N=134)	ARM C (N=132)
Responders	114 (85.07%)	90 (67.16%)	120 (90.91%)
Non-Responders	20 (14.93%)	44 (32.84%)	12 (9.09%)
Unstratified Response Analysis			
Difference in Response Rates (%)		-17.91	5.83
95% CI (Wald, with correction)		(-27.89, -7.93)	(-1.94, 13.61)
p-value (Chi-Squared Test)		0.0006	0.1436
Odds Ratio (95% CI)		0.36 (0.2 - 0.65)	1.75 (0.82 - 3.75)
Complete Response (CR)	78 (58.21%)	55 (41.04%)	97 (73.48%)
95% CI (Wald, with correction)	(49.38, 66.67)	(32.63, 49.87)	(65.1, 80.79)
Partial Response (PR)	36 (26.87%)	35 (26.12%)	23 (17.42%)
95% CI (Wald, with correction)	(19.58, 35.2)	(18.92, 34.41)	(11.38, 24.99)
Stable Disease (SD)	20 (14.93%)	44 (32.84%)	12 (9.09%)
95% CI (Wald, with correction)	(9.36, 22.11)	(24.97, 41.47)	(4.79, 15.34)
Progressive Disease (PD)	0 (0%)	0 (0%)	0 (0%)
95% CI (Wald, with correction)	(0, 2.72)	(0, 2.72)	(0, 2.76)
Not Evaluable (NE)	0 (0%)	0 (0%)	0 (0%)

targets v0.1.0: Brings together function-oriented programming and `make`—like declarative workflows in toolkit for building statistics and data science pipelines in R. The methodology borrows from [GNU make](#) and [drake](#). See the [vignette](#) and the [reference website](#).

Visualization

ggmulti v0.1.0: Provides tools such as serial axes objects, Andrew's plot, various scatter plot glyphs to visualize high dimensional data. There are vignettes on visualizing [high dimensional data](#), [adding glyphs to scatter plots](#), and creating [histograms with density](#).

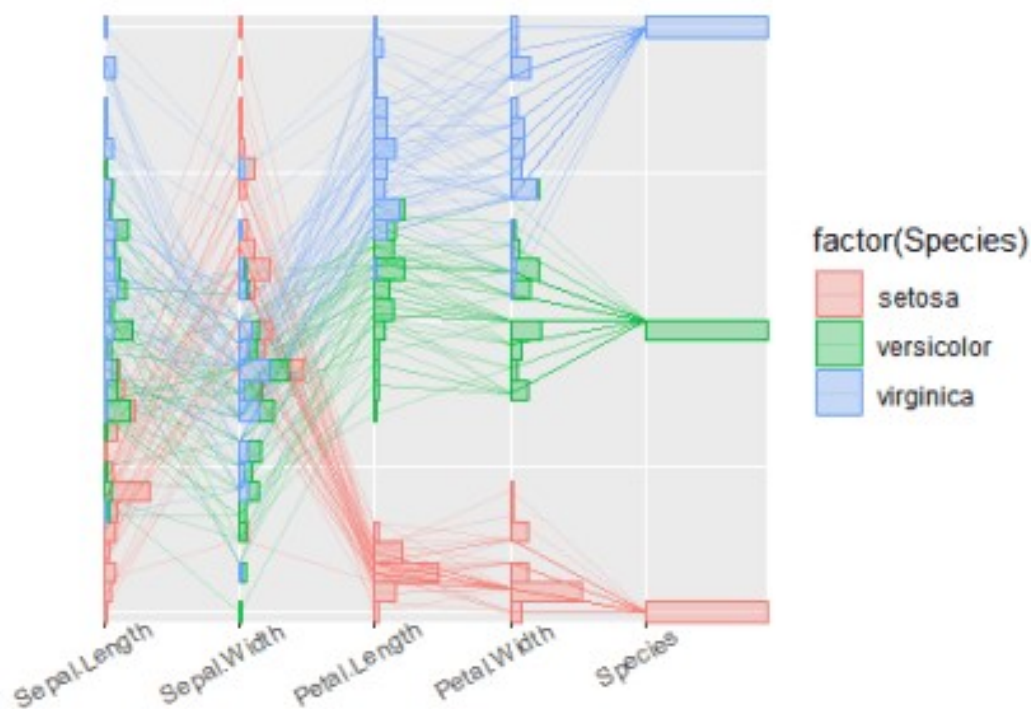
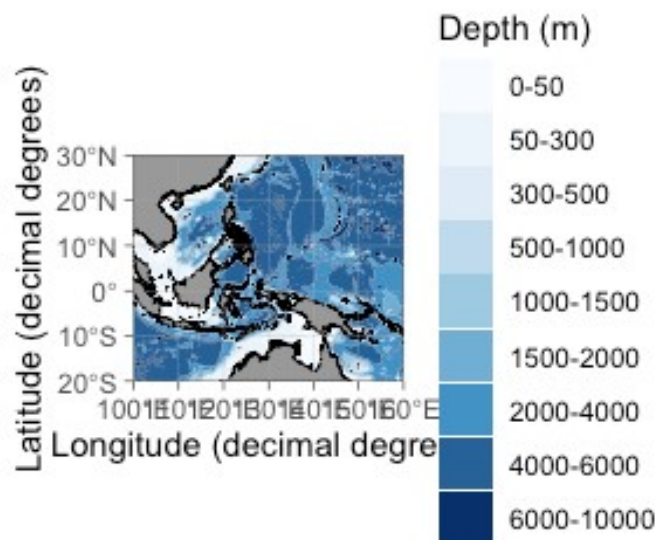
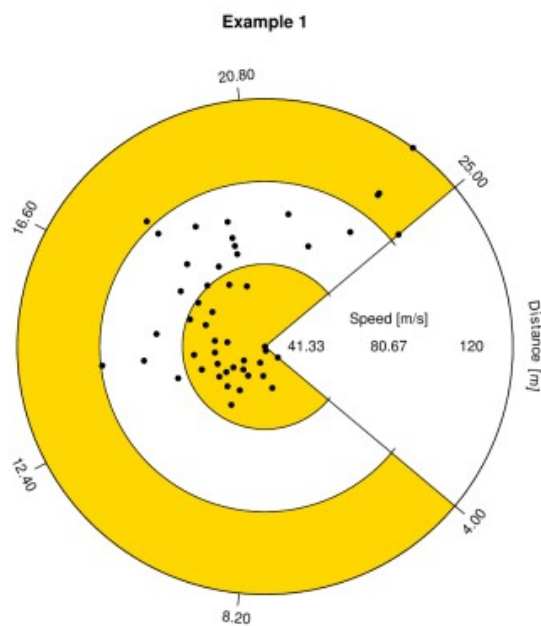


Figure 2

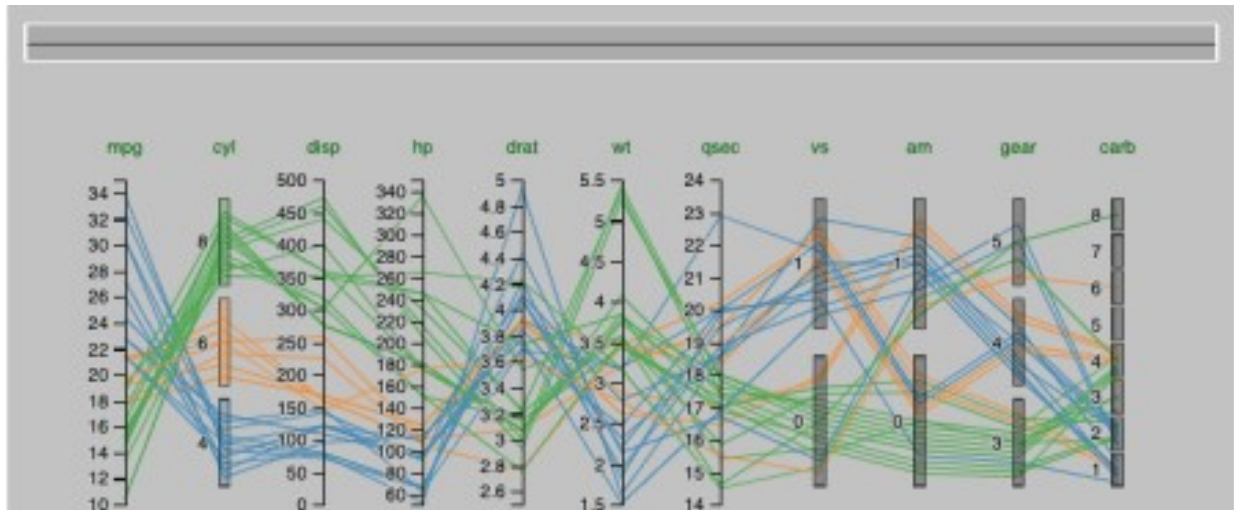
ggOceanMaps v1.0.9: Allows plotting data on bathymetric maps using `ggplot2` using data that contain geographic information from anywhere around the globe. There is a [User Manual](#) and a [vignette](#) on pre-made shape files.



[pacviz](#) v1.0.0.5: Provides functions to map data onto a radial coordinate system and visualize the residual values of linear regression and Cartesian data in the defined radial scheme. See the [pacviz documentation](#) for more information.



[parallelPlot](#) v0.1.0: Provides functions to create parallel coordinates plots using the `htmlwidgets` package and `d3.js`. The [vignette](#) provides multiple examples.



[thematic](#) v0.1.1: Provides tools to “theme” ggplot2, lattice, and base graphics using a small set of choices that include foreground color, background color, accent color, and font family. See [README](#) for examples.

