Papers in Methods in Ecology and Evolution Journal that document Shiny Apps

Reading these to get an idea of how my report might look/sound.

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| Reference | Date | Info |
| (Pascal *et al.*, 2020) | 27/5/22 | **A Shiny r app to solve the problem of when to stop managing or surveying species under imperfect detection**  **Abstract**  Partially observable Markov decision processes solvers are useful to find optimal sequential decisions under imperfect detection. However, POMDPs remain inaccessible to most applied ecologists.  Our Shiny r app also allows users to run simulations of optimal management and graphically represent the optimal solution.  **Intro**  Third, POMDP solutions are difficult to represent, interpret and explain (Dujardin et al., 2015, 2017). Fourth, like many academic fields, interactions between end-users and researchers are often lacking limiting the potential impact of research.   * MMA results could be difficult to explain – shiny app can help * Increases impact of research due to the interactivity   **Methods**  Our r package smsPOMDP provides a set of functions (Supporting Information 1) to help solve the SMS problem with a Shiny r app (Chang et al., 2018). Shiny is an r package that enables the user to build interactive web applications with r.  The smsPOMDP package and documentation are hosted at https://github.com/conse rvation-decisions/smsPOMDP. The online version of the app is also available at <https://conservation-decisions.shinyapps.io/smsPOMDP/>   * Include this in mine   Figure 3 presents the flowchart illustrating the different functionalities of the app. The user starts by setting the parameters of the problem—default values corresponds to the original Sumatran Tiger problem (Figure 3a). Once the parameters of the problem are provided, the user interface of the app provides interactive graphs Figure 3b). The user can then set a history of past actions and observations (Figure 3c). Next, the app solves the POMDP (Figure 3d), derives the optimal policy graph from the user's inputs and runs several simulations of management (Figure 3e). The interactive plots are updated consequently (Figure 3f).  **They have a case study where results section would normally be.** |
| (Johnson, 2022) | 27/5/22 | **PhycoCanopy: An R Shiny tool for exploring primary production in macroalgal canopies**  **Abstract**  PhycoCanopy offers a way of exploring how different algal parameters and environmental settings can affect net canopy photosynthesis.  A total of 23 parameters can be varied to investigate the consequences of changes in key processes such as the tidal cycle, position of algae relative to the low tide mark and photosynthesis in air.  **Intro**  Estimates of canopy photosynthesis form an important part of the debate around the contribution of macroalgae to local and global carbon budgets and the potential associated value of algae as Blue Carbon.   * Estimates of how agricultural systems impacts BD impacts the debate on how we use our land.   While models are useful for integrating various influences on macroalgal photosynthesis, no widely available tool exists. PhycoCanopy is intended to fill this gap: providing an accessible means to visualize changes in net photosynthesis over different time periods under different conditions. The interactive nature of R Shiny (Chang et al., 2021) facilitates sensitivity tests for individual parameters and allows the user to tune simulations to particular environmental conditions.  **Model**  Sliders are used in the R Shiny implementation to allow users to select 23 parameters affecting algal traits, photosynthesis rates and environmental conditions.  Model output is summarized by plots of frond water content, surface irradiance, instantaneous net photo-synthetic rate and the height of water above the shore level where the algae are attached. To aid interpretation, the TAI generated by the chosen frond parameters is given, along with the estimated net photosynthesis over the chosen time period of simulations (g C m−2).  **Usage**  Phycocanopy differs from other macroalgal models (e.g. Bordeyne et al., 2020; Rogers & Shears, 2016) by including explicit processes of canopy shading and desiccation mitigation. |
| (Silva *et al.*, 2022) | 28/5/22 | **treetop: A Shiny-based application and R package for extracting forest information from LiDAR data for ecologists and conservationists**  **Abstract**  However, advanced computational skills and specialized knowledge have been normally required to extract forest information from LiDAR.  This paper introduces the treetop application, an open-source web-based and R package LiDAR analysis tool for extracting forest structural information at the tree level, including cutting-edge analyses of properties related to forest ecology and management.  **TREETOP: An open-source tool**  The aim of this paper is to present treetop, a freely available, open access web-based LiDAR analysis tool, and a standalone R package (treetop).  **Background and model formation**  treetop is both an interactive online tool as well as a standalone R package (Silva et al., 2021) that puts complex ITD and crown delineation procedures easily within reach of any non-specialized user, allowing the visualization of forest information promptly and the ability to download generated results in a variety of file formats.  The tool was developed using RStudio, a free and open-source integrated development environment for R (R Core Team, 2018), and the Shiny package in R (Chang et al., 2019).  The online version of treetop is publicly available on the shinyapps.io, a service platform for hosting Shiny web apps, at https://carlosasilva.shinyapps.io/weblidar-treetop/ and has limited size for input (30 Megabytes).  The R package version of treetop can run natively on a user's computer and can be downloaded via the Comprehensive R Archive Network (CRAN) (https://cran.r-project.org/web/packages/treetop/index. html). In addition, it can be installed directly in R install.packages (treetop) and launched by the single command line launchApp(). The R package launches a native Shiny-based app identical to the treetop web-based tool.  TABLE 1 Features of the web-LiDAR tree top application  **TREETOP applications and case studies**  **Final considerations**  We have provided an overview of the design and usage of treetop, the first web-based application and R package for ecologists and conservationist to automatically extract and analyse forest information from LiDAR-CHM data. The tool provides five panels which were described in detail, and functionality exemplified with three case studies using LiDAR datasets collected from disparate forest ecosystems, illustrating the ecological meaning of the analyses included in the application. The paper presents case studies.  treetop is open-source software and the source code as well as the datasets used in this study are available on the treetop GitHub repository (https://github.com/carlos-alberto-silva/weblidar-treetop). |
| (Kearney *et al.*, 2021) | 28/5/22 | **Modelling the joint effects of body size and microclimate on heat budgets and foraging opportunities of ectotherms**  **Abstract**  All functions are now integrated into the biophysical modelling r package NicheMapR and as a Shiny app, which should provide new insights and avenues for investigation into functional interactions between body size and habitat structure for ectotherms.  **Intro**  Evaluating when, where and for how long an ectotherm can safely forage in the open without overheating is a fundamental question in physiological and behavioural ecology.  Here we develop a generic, transient heat-budget model for the R programming environment. The model is suitable for small to moderate-sized organisms and captures heat-flow via radiation and convection for different geometries.  **Discussion**  The Shiny app we have created to run the simulations via a graphical user interface (Supporting Information Appendix S4, http://bioforecasts.science.unimelb.edu.au/ectotherm\_transient/) includes tools for visualising the results in comparison with satellite imagery and will facilitate applied use of the approach in managing and accessing thermal aspects of habitat connectivity. |
| (Doser *et al.*, 2021) | 28/5/22 | **spOccupancy: An R package for single-species, multi-species, and 2 integrated spatial occupancy models**  **Abstract**  We introduce the spOccupancy R package designed to fit single-species and multi-species 19 spatially-explicit occupancy models.  spOccupancy provides user-friendly functions for data simulation, model fitting, model 27 validation (by posterior predictive checks), model comparison (using information criteria 28 and k-fold cross-validation), and out-of-sample prediction. We illustrate the package’s 29 functionality via a vignette, simulated data analysis, and two bird case studies.  The spOccupancy package provides a user-friendly platform to fit a variety of single and 31 multi-species occupancy models, making it straightforward to address detection biases 32 and spatial autocorrelation in species distribution models even for large data sets.  **Intro**  Here we present spOccupancy, an R package that fits SSOMs, MSOMs, and IOMs that can 95 accommodate spatial autocorrelation in potentially massive data sets. We fit spatial SSOMs, 96 MSOMs, and IOMs in a point-referenced framework using either Gaussian processes or Nearest 4 97 Neighbor Gaussian Processes (NNGPs; Datta et al. 2016; Finley et al. 2019).  **Models**  **Implementation and usage**  Here we briefly describe functionality for the five main tasks performed by spOccupancy.  **Case studies**  We demonstrate spOccupancy functionality with two case studies on forest breeding birds in 244 the eastern USA.  **Conclusions and future directions**  Our spOccupancy R package fits spatially-explicit single-species, multi-species, and integrated 289 occupancy models for potentially massive data sets. The package includes functions for data 290 simulation, model fitting, model validation, model comparison, and out-of-sample prediction.  We are currently working on including the following extensions within the package…  We expect spOccupancy will serve as a user-friendly tool for ecologists and 297 conservation practitioners to account for detection biases and spatial autocorrelation using large 298 data sets (e.g., hundreds of thousands of locations) in assessments of species distributions and 299 community patterns across broad spatial regions, an increasingly important objective in species 300 distribution modeling applications. |
| (Chamberlain and Szöcs, 2013) | 1/6/22 | **taxize: taxonomic search and retrieval in R**  **Abstract**  Taxonomic data is becoming increasingly available on the web, but scientists need a way to access it in a programmatic fashion that’s easy and reproducible.  We have developed taxize, an open-source software package (freely available from http://cran.r-project.org/web/packages/taxize/index.html) for the R language.  taxize provides simple, programmatic access to taxonomic data for 13 data sources around the web.  We discuss the need for a taxonomic toolbelt in R, and outline a suite of use cases for which taxize is ideally suited.  The taxize package facilitates open and reproducible science by allowing taxonomic data collection to be done in the open-source R platform.  **Intro**  Programmatically getting taxonomic names solves the problem by looping over a list of names. In addition, doing taxonomic searching, etc. becomes reproducible. With increasing reports of irreproducibility in science4,5 , it is extremely important to make science workflows repeatable.  The goal of taxize is to make many use cases that involve retrieving and resolving taxonomic names easy and reproducible.  Table 1. Some key functions in taxize, what they do, and their data sources.  In taxize, we have written a suite of R functions that interact with many taxonomic data sources via their web APIs.  **Why do we need taxize?**  Scientists ideally need a tool that is free and can be used programmatically, thereby facilitating reproducible research. The goal of taxize is to facilitate the creation of reproducible and easy to use workflows for searching for taxonomic names, resolving them, getting higher taxonomic names, and other tasks related to research dealing with species.  **Data sources and package details**  New data sources can be added; for example, we plan to add the following sources: Wikispecies and The Tree of Life.  **Use cases**  Goes through process of how taxise can be used from installing the package, to resolving taxonomic names, to retrieving higher taxonomic names etc.  **Conclusions**  Taxonomic data are becoming more widely available on the web, yet scientists require programmatic access to this data for developing reproducible workflows. taxize was created to bridge this gap.  We hope taxize will be taken up by the community and developed collaboratively, making it progressively better through time as new use cases arise, bug reports are squashed, and contributions are merged. |
| (Shackelford *et al.*, 2021) | 14/6/22 | **Dynamic meta-analysis: a method of using global evidence for local decision making**  **Abstract**  Meta-analysis is often used to make generalisations across all available evidence at the global scale.  We show how an interactive method of meta-analysis—dynamic meta-analysis—can be used to assess the local relevance of global evidence.  We developed Metadataset (www.metadataset.com) as a proof-of-concept for dynamic meta-analysis. Using Metadataset, we show how evidence can be filtered and weighted, and results can be recalculated, using dynamic methods of subgroup analysis, meta-regression, and recalibration. With an example from agroecology, we show how dynamic meta-analysis could lead to different conclusions for different subsets of the global evidence.  In this study, we show how dynamic meta-analysis can meet an important challenge in evidence-based decision making—the challenge of using global evidence for local decisions.  We suggest that dynamic meta-analysis can be used for subject-wide evidence synthesis in several scientific disciplines, including agroecology and conservation biology.  Future studies should develop standardised classification systems for the metadata that are used to filter and weight the evidence.  Future studies should also develop standardised software packages, so that researchers can efficiently publish dynamic versions of their meta-analyses and keep them up-to-date as living systematic reviews.  Metadataset is a proof-of-concept for this type of software, and it is open source.  Future studies should improve the user experience, scale the software architecture, agree on standards for data and metadata storage and processing, and develop protocols for responsible evidence use.  **Background**  It can be difficult to use meta-analysis to make decisions about interventions in a specific context, unless the results are known to be generalizable to that specific context. What is needed is a method of meta-analysis that enables decision makers to answer the question, “How effective is this intervention in my specific context?”  It has been suggested that “research cannot provide an exact match to every practitioner’s circumstances, or perhaps any practitioner’s circumstances because environments are dynamic and often changing, whereas completed research is static” [5]. A partial solution to this problem could be to make research more dynamic, by enabling decision makers to interact with it.  For example, decision makers could filter a database of research publications, to find studies that are more relevant to their circumstances, or they could weight these studies by relevance to their circumstances.  We developed a tool for this purpose, and here we show how this tool could be used to assess the local relevance of a global meta-analysis in agroecology.  As we define it here, dynamic meta-analysis is a method of interactively filtering and weighting the data in a meta-analysis. The diagnostic feature of a dynamic meta-analysis is that it takes place in a dynamic environment (e.g. a web application), not a static environment (e.g. a print publication), and this enables users to interact with it.  We developed Metadataset [24] as a proof-of-concept for dynamic meta-analysis. Metadataset is a website that provides two methods of interactive evidence synthesis: (1) browsing publications by intervention, outcome, or country (using interactive evidence maps) (Fig. 1) and (2) filtering and weighting the evidence in a dynamic meta-analysis (Fig. 2).  We plan to expand Metadataset to other subject areas, and we welcome collaborations. Here we focus on cover crops in Mediterranean climates as an example of dynamic meta-analysis.  **Results**  Goes through how you use the app using a case study.  **Discussion**  Dynamic meta-analysis provides a partial solution to an important problem in evidence-based decision making— lack of access to relevant evidence [7–9]—not only by helping users to find locally relevant evidence in a global evidence base, but also by helping them to use this evidence to reach locally relevant conclusions.  For example, we showed how a hypothetical user could reach a different conclusion when using the global evidence (cover crops have no effect on cash crop yields) instead of the locally relevant evidence (brassicas have negative effects on cash crop yields in California).  Metadataset compared to other tools   * Compare differences * Highlights exclusive benefits of Metadataset e.g. option for recalibration via weighting studies based on relevance   Dynamic scoping could also provide a partial solution to the “apples and oranges” problem in meta-analysis [34], since users could decide for themselves which “apples” and which “oranges” should be compared (e.g. deciding which interventions and/or outcomes should be analysed together).  There is an important distinction between a dynamic meta-analysis, as we have defined it here, and a living review. As we see it, the diagnostic feature of a living review is that it is updated as soon as possible after a new study is published, whereas the diagnostic feature of a dynamic meta-analysis is that it is interactive. However, a dynamic meta-analysis could use data from a living review, and thus it could be part of a living review. Metadataset already uses data from an online database that can be easily updated, and so it is already possible to use Metadataset for living reviews. When new studies are added to the database, they are immediately available for dynamic meta-analysis. A traditional meta-analysis is static and cannot easily be updated without reanalysis and republication. In contrast, a dynamic meta-analysis can be easily updated, and therefore it could be ideal for the meta-analytic component of a living review.  Dynamic meta-analysis could lead to a rebalancing of power and responsibility in evidence-synthesis, since evidence users would be able to make decisions that are typically made by researchers.   * There are some disadvantages to this as well e.g. If a user does multiple analyses, and selects only one of these analyses as the basis for their decision (perhaps because it supports their political agenda), then it will be difficult to defend the credibility of their conclusions (the problem of “cherry picking”). * Our objective here is only to show how dynamic meta-analysis could be used, as a proof-of-concept, and not how it should be used. Protocols for evidence use would need to be developed together with stakeholders   Dynamic meta-analysis is limited by the quantity and quality of data and metadata that are available for each study.  It has often been suggested that standards of data reporting need to be improved (e.g. [41]), but here we suggest that standards of metadata reporting also need to be improved, and standardised systems for classifying metadata need to be developed for use in evidence synthesis.  There are several challenges that will need to be met, before dynamic meta-analysis can be scaled up and used more widely.  We would welcome collaborations with other researchers and software developers to improve this proof-of-concept and/or to develop alternative software packages for dynamic meta-analysis.  Among the technical challenges, the software for dynamic meta-analysis will need to handle larger datasets and larger numbers of users than our proof-of-concept can handle.  This software will also need to be better tested with users (both researchers and decision makers), to improve the user experience. For example, different versions of the software could be developed for different types of user (e.g. researchers with experience of meta-analysis vs decision makers without any experience of data analysis).  The software will also need to provide other analytical options. For example, Metadataset calculates the log response ratio, but many researchers may want other measures of effect size (e.g. the standardised mean difference) and other options for data processing (e.g. other methods of imputing missing data).   * Mine currently does LRR and percentage change   Among the philosophical challenges, standardised classification systems for metadata will need to be developed, and so will protocols for evidence use.   * This is being done by Daero for mine   **Methods**  The code is open source (Django app: https://github.com/ gormshackelford/metadataset), Shiny app: https://github. com/gormshackelford/metadataset-shiny), and the data is open access (the data can be downloaded in CSV files via the Shiny app).  Methods for dynamic meta-analysis on Metadataset. The Shiny app uses the methods from Shackelford et al. [25] to calculate the mean effect size of an intervention as the log response ratio. The response ratio is the numerical value of an outcome, measured with the intervention, divided by the numerical value of an outcome, measured without the intervention. The natural logarithm of the response ratio (the log response ratio) is typically used for meta-analysis [44]. Using the rma.mv function from the metafor package in R [45], the Shiny app fits a mixed-effects meta-analysis that accounts for non-independence of data points.   * Describe the models that are run   Also describes what the users can do e.g. what filters are available.  Describe warnings that can occur? E.g. If one or more of the filters were not included in the meta-regression model, then we show a warning. |
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