Electronic supplements for CARMMHA's pelagic injury paper

August 11, 2022

Preamble

This is an Electronic Supplement to the manuscript Marques et al. "Quantifying Deepwater Horizon oil spill induced injury on pelagic cetaceans" submitted to Marine Ecology Progress Series (MEPS).

There are 7 Electronic Supplements to the paper. The master file containing links to all the other 6 additional Electronic Supplements related to this paper is ES0_ElectronicSupplements.

You might be reading this file as a pdf or as an html. The links on this file only work if you are using the html version of it, available via the github repository or if you compiled it yourself as html and you have all the 7 html files in the same folder. Otherwise, as a pdf distributed as an Electronic Supplement to the MEPS paper, the links might not work. ***They might work. If it is possible, we can work with the MEPS Editorial Office such that we can add links below that will link to actual files, say the pdfs of each of these 7 files, on the publisher server***.

Version history

- 1.0 [date] Version included as a pdf Electronic Supplement in the MEPS original submission - *note to co-authors: this note will be deleted when we submit and we are not tracking versions prior to submitting to MEPS, so that will be version 1.0 by definition*

Introduction

This document is a master file that presents a full list of Electronic Supplements available.

All these files are created as dynamic reports using RMarkdown.

The source .Rmd files are provided in the github repository:

https://github.com/TiagoAMarques/CARMMHApapersSI

The above repository also includes all the code required for readers to reproduce independently the paper results. Below is a quick description of how all the results in the paper might be recreated by the reader, within a framework of reproducible research.

This means also that it should be straightforward for a reader to update the results with new information, be it new data that becomes available or different assumptions about the populations, allowing to explore both the consequences of new knowledge or the impact of the assumptions we made on the results presented.

List of Electronic Supplements

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There are 6 other main Electronic Supplements files submitted as such to MEPS. We labeled these ES1 to ES6 to help readers locating them in the repository and refer to them in the paper as such. Names and brief content descriptions follow:

- ES1_ExpertElicitation – Supplementary material about the expert elicitation exercises, which includes information about
  - the density dependence scale parameter,
  - the probability of an animal exposed to oil recovering, and
  - the survival reduction.
- ES2_InitialPopulationSizes – Supplementary material about the initial population sizes and proportion of animals exposed to oil. Includes point estimates of the spatial models used to estimate the stock size, the oil footprint considered to have an impact on survival, and hence the delineation of the area including the proportion exposed for each of the species considered; Note that the initial population sizes and proportion exposed are provided as data. The reason we do not provide the code that allows the user to reproduce the objects is because the model and objects used to do so are not ours to distribute. For all taxonomic units these come from models reported by Roberts et al. (2015). This supplementary material also includes the code required to generate the paper tables 1 and 2 as well as a table used in `getInjury.Rmd`.
- ES3_GestationDuration - Supplementary material with details about how we obtained gestation duration for each taxonomic unit considered, which gets used to scale survival and fecundity/reproduction related parameters with respect to *Tursiops truncatus*.
- ES4_ComparingSurvivalsAcrossStocks – Supplementary material about the stock specific survival probabilities given the scaling by gestation duration. Includes code to work with files containing the Siler model posterior parameters and for obtaining the proportion of animals alive at a given age and age specific survival for *Tursiops truncatus*.
- ES5_GetInjury - the code for the production of all the injury measures presented on the paper;
- ES6_ModelEvaluation - the code for the production of all the sensitivity and uncertainty results presented on the paper.

A couple of additional files regarding *Tursiops truncatus* used in Schwacke et al. (2021) might also be relevant, since we build on values and parameters on these to get components of the model parametrization of the different taxonomic units in the pelagic paper:

- AgeOfSexualMaturity - Supplementary material with details about how we obtained the age at sexual maturity for *Tursiops truncatus*.
- SurvivalReduction – Supplementary material about how we obtain the survival reduction factor for *Tursiops truncatus*. This combines baseline survival probability with post-spill survival probability obtained by spatial capture recapture (SCR). For the baseline survival probability we describe the analysis that integrates the different components required. The post-spill survival for Barataria Bay bottlenose dolphins is obtained in a separate paper, Glennie et al (2021).

How to reproduce the paper results

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All the results in the paper can be recreated by the reader by running the code provided. Having the code also facilitates extending and using the code under different scenarios, species and locations. This is considered the most convenient way to share the results, since all the outputs would be too large to share in the github repository.

All the results

The results shown in the paper tables are produced by different bits of code from the supplementary material:

- Table 1 and 2 are produced within ES2_InitialPopulationSizes.pdf; In fact, we recommend you run this first as it also creates a table (`Table4GetInjury.txt`) required to run the code in `GetInjury.pdf` that creates Table 3 below.
- Table 3 is produced within ES5_GetInjury.pdf. This can only be run after you have created the results. Note that it is fundamental that there is an object `ns` that defines in `ES5_GetInjury.Rmd` the correct number of iterations you used to run the code.

To produce the results in Table 3 the user would have to run the code chunk `getresults` (in file ES5_GetInjury.pdf) that runs the actual simulations. That chunk is set to not run by default when you compile ES5_GetInjury.pdf.

Running that code is safer to be done directly on a console. If you compile ES5_GetInjury.pdf after turning the argument `eval=FALSE` into `eval=TRUE` you will also get as a bonus the `ES5_GetInjury` document, which has summary tables of all the results.

The code chunk `getresults` loops over all the 15 taxonomic units, defined by the right 4 letter code inside the object `Sps`, going into the right folders for each taxonomic unit to find the required inputs and creating outputs (R workspaces) with simulation results in the corresponding species folders.

This is also the code inside the file `RunAllSims.R`, that could be sourced to produce the same effect, and shown below for completeness:

```
#this runs all the simulations and produces outputs for all species
source("Functions/reqfuns.R")          # most functions are here
source("Functions/SilerFuns.R")        # Siler model functions are here
source("Functions/runSims.R")          # To run the simulations for all species
#define the species we run simulations for
Sps <- c("Bwsp", "Fatt", "Ggri", "Gmac", "Kosp", "Pele", "Pmac",
"Satt", "Sbre", "Scly", "Scoe", "Sfro", "Slon", "Ttro", "Ttrs","Ttru")
#define the number of iterations to run
ns <- 5
# define the number of years each iteration is run for
ny <- 150
for (i in Sps){
runSims(Sp = i, nsims = ns, nyears = ny)
}
```

The folder structure and all files required to successfully run the code is in the above github repository (under folder `FolderArchitecture2runCode`). The recommended procedure is to download this entire folder into a local folder and then run `RunAllSims.R`.

At a bare minimum running the code requires the following folders and the material provided in them:

- `InputFiles`: this folder includes a number of files that are treated as data, inputs required to run the code, including the key file `SpeciesDefinitionFile.xlsx` that contains all the details for all the different taxonomic units
- `InOutBySp`: a folder that also contains a specific set of subfolders with inputs per species, namely `N_boot.csv` and `N_boot_in_oil.csv`, a distribution of initial population sizes of both all animals and exposed animals. This is also the folder where results for each taxonomic unit are outputted into
- `Functions`: folder containing all the R code including functions required to run the simulations

Note that the chunk `getresults` (in file ES5_GetInjury.pdf) could take a considerable amount of time to run. The consequence of running said chunk will be to populate the folders inside `InOutBySp` with the R workspaces holding the results that the rest of the code in ES5_GetInjury.pdf uses to produce the tables with injury metrics.

A single taxonomic unit

If one wants to run a simulation for a single taxonomic unit it might be simpler to use simply the following code.

As an example, this would run a simulation for the sperm whale, for 50 years, with 3 iterations,

```
#define species
sp <- "Pmac"
#define number of years
years <- 50
#define number of iterations
# Warning: starting with a small number of iterations is highly recommended.
sims <- 3
# this is also inside "RunAllSims.R"
source("Functions/reqfuns.R")          # most functions are here
source("Functions/SilerFuns.R")        # Siler model functions are here
source("Functions/runSims.R")          # function to run the simulations for all species
runSims(Sp = sp, nsims = sims, nyears = years)
```

This code will nonetheless require the corresponding taxonomic unit specific part of the above folder architecture to run smoothly.

References

Glennie, R.; Thomas, L.; Speakman, T.; Garrison, L.; Takeshita, R. & Schwacke, L. 2021. Estimating spatially-varying density and time-varying demographics with open population spatial capture-recapture: a photo-ID case study on bottlenose dolphins in Barataria Bay, Louisiana, USA arXiv:2106.09579

Roberts, J. J.; Best, B. D.; Mannocci, L.; Fujioka, E.; Halpin, P. N.; Palka, D. L.; Garrison, L. P.; Mullin, K. D.; Cole, T. V. N.; Khan, C. B.; McLellan, W. A.; Pabst, D. A. & Lockhart, G. G. 2016 Habitat-based cetacean density models for the U.S. Atlantic and Gulf of Mexico *Scientific Reports* **6**: 22615 DOI: 10.1038/srep22615

Schwacke, L. H.; Marques, T. A.; Thomas, L.; Booth, C.; Balmer, B. C.; Barratclough, A.; Colegrove, K.; Guise, S. D.; Garrison, L. P.; Gomez, F. M.; Morey, J. S.; Mullin, K. D.; Quigley, B. M.; Rosel, P.; Rowles, T. K.; Takeshita, R.; Townsend, F. I.; Speakman, T. R.; Wells, R. S.; Zolman, E. S. & Smith, C. R. 2021 Modeling population impacts of the Deepwater Horizon oil spill on a long-lived species with implications and recommendations for future environmental disasters *Conservation Biology* **36**: e13878 DOI: 10.1111/cobi.13878

Reproducible research

We have invested a considerable amount of time to make our analysis fully transparent and reproducible (Figure ES0_1). This means also that it should be relatively straightforward for a reader to update the results with new information, be it new data that becomes available or different assumptions about the populations consider, allowing to explore both the consequences of new knowledge that becomes available in the future or the impact of the assumptions we made, and potentially changing them, on the results presented.

If you make use of any of this material in your own work, it would be appreciated if you would contact Tiago Marques to let him know. Suggestions or comments for improvements will also be greatly appreciated.

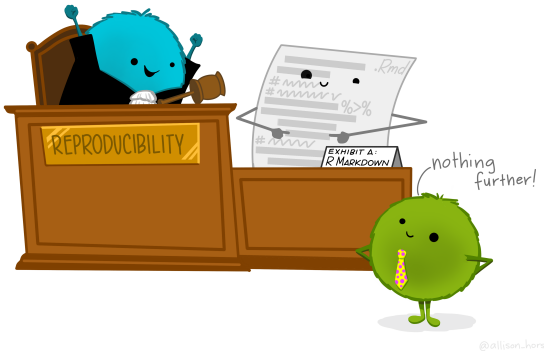

Figure 1: Figure ES0.1: Artwork by @allison_horst at available at https://github.com/allisonhorst/stats-illustrations. This image illustrates the concept of reproducible research and is a tribute to Allison's work on combining art and science.