A Population Viability Analysis Modelling Tool for Seabird Species

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Report details

Natural England commission a range of reports from external contractors to provide evidence and advice to assist us in delivering our duties. The views in this report are those of the authors and do not necessarily represent those of Natural England.

Please be advised that users should refer to the most recent guidance on the GitHub site prior to running the tool. The guidance in the appendices of the original version of this report, published in July 2019, is now superseded and should no longer be used. This version of the report has been updated to reflect this (April 2022) and the appendices removed. For the updated guidance please visit the Seabird_PVA_Tool documentation page on GitHub.

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Background

Offshore renewable energy developments (ORDs), such as offshore windfarms, have the potential to impact on birds via a number of pathways. For example, individual birds are at risk of mortality from collisions with turbine blades, while others may be displaced from important habitat as a consequence of avoiding such structures. While it is individual birds that are subject to these impacts, the combined effects across individuals could lead to changes at a wider population level, particularly when the individuals within a population may experience impacts across a number of developments, spanning a wide spatial and temporal scale.

The consenting process for ORDs requires an assessment of the anticipated population consequences on seabirds at a variety of population and geographical scales (from the population within an individual Special Protection Area (SPA) colony, to wider regional population scales). This requires a method for determining the impact of marine developments on populations of seabirds across a range of scales.

Population Viability Analysis (PVA) is considered best practice to understand the population-level consequences of predicted effects of ORDs on seabirds. PVA provides a framework that uses estimated demographic rates for a population (typically survival and productivity information) in a mathematical model to forecast future levels of a population, either under currently prevailing circumstances or as a consequence of some impact applied to the population.

PVA models can be used to forecast future population levels under different scenarios, and can be used to compare baseline "no impact" conditions with "impact" scenarios based on actual or predicted impacts from ORDs (or other activities) that may affect bird numbers via changes to the survival or productivity of individual birds. Population metrics that are derived from comparisons of "baseline" and "impacted" predictions generated by PVAs can then be used to assess the "significance" of the anticipated additional mortality associated with planned developments.

However, our ability to assess the population significance of impacts from development proposals is often hampered by a lack of appropriate PVA models for the key risk species, populations and SPA colonies, and a lack of transparency and flexibility in the models available.

The aim of this project was to develop a PVA modelling framework, applicable to seabirds at a variety of scales, with a front-end, interactive web application user interface to allow users to set-up and run their own PVA models for seabird species without the need for access to specific software.

A key objective of the tool is to allow users the flexibility to explore population management-oriented objectives (e.g. assessment of impacts, evaluation of management options etc.), as well as being able to explicitly highlight the effects on model predictions of different assumptions about the model, data, species and populations concerned.

The tool can be used to assess any type of impact that changes survival or productivity rates, or as a cull or harvest of a fixed size per year. Impacts may also be positive, meaning

that mitigation or conservation measures aimed at increasing demographic rates may also be modelled. The tool also allows users to conduct PVAs at a range of scales (breeding colony to SPA or region).

The tool produces a range of tabular and graphical outputs for interpreting outputs from PVAs, and a facility for using pre-set demographic rates for 15 species of seabirds based on currently available demographic data.

While the main project objective was to develop a tool that can be used to model populations of a range of seabird species, the generic nature of the tool is such that it can potentially be applied to other groups of birds.

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1   Project background

Offshore renewable developments (ORDs) have the potential to affect seabird populations through direct collisions with infrastructure, displacement from foraging habitat, barrier effects whereby birds must fly around infrastructure to reach foraging grounds, and by noise, light and contamination. These processes affect individuals, but the cumulative effects within and across populations in terms of changes to demographic rates and population trends, are key to assessing how ORDs impact upon seabirds and protected populations. The consenting process for proposed ORDs requires an assessment of the anticipated population consequences on seabirds at a variety of population and geographical scales (from the population within a single Special Protection Area (SPA) colony under HRA to wider regional population scales under EIA). This means that a method is required for determining the impact of marine developments on populations of seabirds across all of these scales.

Population Viability Analysis (PVA) is considered best practice in order to understand the population-level consequences of predicted effects of renewable energy developments on seabirds because it provides a robust framework that uses demographic rates to forecast future population sizes, either under baseline conditions or under scenarios of change resulting from, for example, an offshore energy development (Maclean et al. 2007; Freeman et al. 2014). PVAs essentially employ mathematical and statistical population models to forecast future population change, and can be undertaken using methods of varying complexity. Within the PVA framework, population models are used to forecast into the future under so-called 'baseline' conditions with no impact present, and under 'scenario' conditions where an impact is applied to a population, usually via one or more of a set of demographic rates. Comparisons are then made using a range of PVA metrics to assess differences between the baseline and scenario population trajectories.

This project aimed to develop a modelling framework within the R statistical programme (R Core Team, 2017) based on a stage/age structured demographic model with a Shiny App (https://shiny.rstudio.com/) front-end tool to allow users to run PVA models for a range of seabird species, in the context of assessing impacts from ORDs. The tool is capable of assessing any type of impact in terms of a change to demographic rates, or as a cull or harvest of a fixed size per year. Impacts may also be positive, meaning that mitigation or conservation measures aimed at increasing demographic rates may also be modelled. The tool we have developed allows users to conduct PVAs at a range of scales (breeding colony to SPA or region). More specifically, users may

- define the number of years to project the population over, and the period of impact;
- specify model runs with or without an impact added, including impacts associated with multiple scenarios of change, so that these can be compared directly against each other;

- specify the impact on the population in several ways: e.g., as a change in productivity or survival rates (for either adults or immatures, or both), or as a fixed harvest of individuals;
- carry out sensitivity/elasticity testing;
- validate models against observed data using historical population projections.

The tool produces a range of tabular and graphical outputs for interpreting outputs from PVAs, and a facility for using pre-set demographic rates for 15 species of seabirds based on currently available demographic data (Arctic skua, Atlantic puffin, common guillemot, common tern, northern fulmar, great black-backed gull, great cormorant, Herring gull, black-legged kittiwake, lesser black-backed gull, little tern, northern gannet, razorbill, Sandwich tern and European shag). The current version of the tool, produced within this project, has been developed a fully functioning proof-of-concept tool for PVA analysis. It is envisaged that further development and iterations of the tool will be produced in the future.

2   R package

The **nepva** R package is designed to undertake population viability analysis (PVA) for seabird species. The development of the package constitutes part of project (NE: ITT_4555); the R package underpins the functionality of the user-friendly web-based Shiny tool that has been being developed within this project. The technical functionality of the Shiny tool has a subset of the functionality within the R package: the Shiny tool provides an interactive web-based mechanism for users to provide inputs to the R package, and to display and save the results obtained by running the R package. The R package also has some functionality that is not available within the Shiny interface (e.g. for running global sensitivity analyses, which are too computationally intensive to usefully run within Shiny).

The R package is motivated by the use of PVAs to assess the impacts of proposed offshore renewable energy developments (ORDs) upon seabird populations, but the functionality within the package is sufficiently general that the package could also be used for assessing the population-level consequences of other anthropogenic activities that impact on population demographic rates, and for assessing impacts upon non-seabird species. Note that the tool can be used to assess the impact of interventions that are likely to increase, rather than reduce, survival or productivity (e.g. removal of bycatch mortality).

The **nepva** R package documentation outlines the methodology used within the R package that underpins the functionality of the user-friendly web-based Shiny tool, the inputs that the tool requires, and the outputs that it produces.

Note that the Shiny tool has been designed for release on a server, meaning that users do not need to access to the R software on their own computer, or to be familiar with R to use the tool. Users can access the tool via a user-friendly Graphical User Interface (GUI) using a standard web browser.

3   Shiny Tool

This project aimed to develop a user-friendly tool allowing Population Viability Analysis (PVA) to be performed using two broad types of population model: (a) deterministic Leslie matrix models, and (b) stochastic Leslie matrix models. The developed tool allows users to specify the model structure, and model inputs, in a fully flexible way – in particular, providing functionality to allow users to specify survival rates (either age class, or pooled across ages), breeding success, age at first breeding, presence and extent of density dependent feedbacks on demographic rates, and the form and levels of inter-annual variability arising from demographic and environmental stochasticity.

The tool has been designed to give users the flexibility to create a custom PVA using their own data, or alternatively to pre-populate baseline demographic rates for one of 15 species based on a range of regional definitions for breeding success data, and either colony-specific or national estimates for survival rates. Some of the underlying functionality in the R package is not currently available within the Shiny tool; however we envisage iterative development of the tool over time to meet the requirements of users, and expect that the tool will progressively incorporate more functionality over time as needed. PVAs can be run for multiple subpopulations where a subpopulation is a breeding colony; this enables users to generate a PVA for an SPA or region that consists of multiple breeding colonies, generating a summed PVA at the aggregated level. In addition, the tool provides users with options to:

- define the number of years to project the population over, and the period of impact;
- specify model runs with or without an impact added, including multiple impacts, so that these can be compared directly against each other
- specify the impact on the population in several ways: e.g., as a change in productivity or survival rates (for either adults or immatures, or both), or as a fixed harvest of individuals;
- carry out sensitivity/elasticity testing;
- validate models against observed data using historical population projections.

The tool is built using Shiny as a user-friendly interface for functions within an R package (**nepva**).

The Shiny app is available as an online tool which can be accessed from:

https://github.com/naturalengland/Seabird_PVA_Tool

The **nepva** R package and full documentation for the R package is also available as a download from the above link.

The documentation for the Shiny tool and underlying **nepva** R package is included in this report. We advise that users consider both the Shiny tool guidance document and the **nepva** R package documentation for a full understanding of the inner workings and functionality of the tool.

3.1 Updating the tool

Various aspects of the Shiny tool (the user interface) may be updated with simple changes to a few of the files:

The file "shiny-helptext.R" contains the text that appears under the tooltip (i) buttons. Minor text changes to the help text can be made by changing this file.

On lines 48-56 at the top of the file "app.R" there are some global values that may be changed

- **maxnpop <- 10** : the maximum number of subpopulations that could be included (reducing this number will make the interface more responsive)
- **maxnscen <- 10** : the maximum number of scenarios that could be included (reducing this number will make the interface more responsive)
- **minyr <- 1950** : Sets the earliest year that can be used throughout the tool
- **maxyr <- 2100** : Sets the maximum year that can be used throughout the tool
- **maxyr_ini <- 2050** : Sets the maximum year for the initial population size field
- **startyr <- 2000** : sets the default impact year for the slider position
- **maxbs <- 10** : Maximum brood size
- **maxage <- 10:** Maximum age at first breeding

Edits or additions to the lookup tables, which are used to set the default values used within the R package and tool, can now easily be made directly, because the values are stored in three CSV files (which are loaded by the R package and tool). Some guidance on making edits or additions to these files is provided in the following section.

3.2 Guidance on updating the "lookup" tables associated with the NEPVA R package (& associated Shiny tool)

3.2.1 Overview

The **nepva** R package, and associated Shiny tool, include the option for "default" values of baseline demographic rates (age at first breeding, maximum brood size, productivity, adult survival and immature survival) to be selected for some species.

The values used by the package and Shiny tool when the "default" values are selected are stored in three CSV files, so if users wish to update the "default" values (e.g. should updated demographic data become available for a species) this can be achieved by directly editing these files.

Each of these files is edited in a slightly different way:

Species meta-data

Within the file **lookup-spmeta.csv** the values in the columns "AFB" (age at first breeding) and "MBS" (maximum brood size) can be changed, and the file re-saved.

Survival data

In order to change this, edit the file **lookup-surv.xlsx**, and then, when you have finished editing, go to "Save as > comma separated CSV file", and over-write the file **lookup-surv.csv**. Within **lookup-surv.xlsx** the values in all columns can be edited; note, however, that only the following six columns are actually used in the tool:

> Species; Source; Age.lo; Age.hi; Surv.mean; Surv.SD

All other columns are purely for reference (i.e. to aid anyone updating the file).

Breeding success

This file (**lookup-BS.csv**) can be edited directly by the user. Note that seven columns are actually used in the tool: "Regclass" (regional classification system), "Species", "Region" (region name), "nsites" (number of sites within the region that the outputs are based upon), "nyears" (total number of site-by-year combinations used in deriving the rates), "BS.mean" (mean breeding success) and "BS.sd" (standard deviation of breeding success).

The remaining two columns ("BS.sd1" and "BS.sd2") are solely included in order to assist in calculating "BS.sd", and can safely be left blank. BS.sd1 is the mean of the within-site standard deviations, and BS.sd2 is the standard deviation across the mean BS values for the sites. BS.sd is equal to the maximum of these two quantities.

3.2.2 Guidance on making specific changes

Updating values

The values contained within the following columns can safely be updated, so long as logically invalid values (e.g. negative survival rates) are avoided:

lookup-spmeta.csv : AFB, MBS

lookup-surv.csv : Age.lo, Age.hi, Surv.mean, Surv.SD

lookup-bs.csv : nsites, nyears, BS.mean, BS.sd

Adding or removing data

It is possible to add additional populations, regions, regional classifications and/or species to the files, or to delete existing selections for these.

When doing this, however, note that:

- Note that whole columns should never be deleted from any of the lookup files. Additional columns may be added, but will not be used by the R package/tool
- If a species is removed from **lookup-spmeta.csv** it cannot be used in the R package/tool, even if it appears in the other two lookup files
- If data for a species is added to **lookup-surv.csv** or **lookup-bs.csv** it is essential that the species also has an entry in **lookup-spmeta.csv**
- Species names must be consistent across the three files. R is case-sensitive, and sensitive to spacing; so, for example, if a species is labelled as "Great cormorant" in one file but "Great Cormorant" in another this will lead the R package/tool to crash.
- Values of the following columns cannot be left blank:

    lookup-spmeta.csv : Species, AFB, MBS

    lookup-surv.csv : Species; Source; Age.lo; Age.hi

    lookup-bs.csv : Regclass, Species, Region, nsites, nyears

4   Validation

To validate the implementation of the Leslie Matrix calculations within the **nepva** R package, and therefore within the Shiny tool, we derived an analytical growth rate from a simple, deterministic Leslie Matrix and compared this to the growth rate estimated by the equivalent model in the R package.

Note that this can only be done for purely deterministic models, because it is not possible to derive an analytical solution from the Leslie Matrix for a stochastic model, where in effect the Leslie Matrix is changing in every year. However, we can introduce small amounts of stochasticity in the simulated population, and compare to the analytical growth rate derived from a corresponding deterministic model, and would expect the estimated growth rate to be similar.

To find the analytical solution to the growth rate – which is the asymptotic growth rate – we create the Leslie matrix in R, and then find its dominant eigenvalue, which is equivalent to the asymptotic population growth rate (commonly expressed as lambda) for that population.

```r
calc.pgr <- function(demobase.prod, demobase.survadult, demobase.survimmat = NULL, afb=5){

  if(is.null(demobase.survimmat)){

    demobase <- c(demobase.prod, rep(demobase.survadult, afb + 1))
  }
  else{

    demobase <- c(demobase.prod, demobase.survimmat, demobase.survadult)
  }

  lm <- make.leslie.matrix(demobase, afb = afb)

  as.numeric(eigen(lm)$values[1])
}
```

We set parameter values for baseline productivity (per pair), baseline adult survival rate and age at first breeding, and then output the dominant eigenvalue for the resulting Leslie matrix to get the corresponding asymptotic population growth rate ('analytical GR').

We then use the R package to set up the same suite of parameters, and project forwards for a number of years (in the examples below, 35 years). We then use the predicted population sizes in the first and final output years (technically, this is the 'impact.start' year and the 'output.final' year in the 'Simulation Mode' of the tool, or 'nepva.simplescenarios' function in the R package) to calculate the population growth rate over that period ('Simulated GR'). We then compare the analytical GR and simulated GR to check that the R package produces an estimate of population

growth rate very similar to the analytical solution derived entirely from the Leslie matrix. Note, however, that we would not expect an identical result because the analytical GR is the asymptotic growth rate, whilst the simulated GR is the growth rate calculated over a number of projected years. There will also be rounding differences in the number of individuals at each time step that will result in slightly different estimates for the two growth rates (particularly when populations start to get very small).

In the table below, we demonstrate for a number of parameter values that the R package generates a simulated growth rate that is consistent with the analytical growth rate derived solely from the Leslie matrix.

Table 1. Estimates for population growth rate derived analytically from the corresponding deterministic Leslie Matrix (Analytical GR) or estimated from simulated model output (Simulated GR). Growth rates are shown for a range of baseline demographic parameter values, and all assume age at first breeding is five.

	Productivity rate	**Adult survival rate**
	0.8	*0.82*
Analytical GR	0.982	
Simulated GR	0.980	
	1.6	*0.82*
Analytical GR	1.051	
Simulated GR	1.059	
	1.0	*0.75*
Analytical GR	0.925	
Simulated GR	0.913	
	1.0	*0.9*
Analytical GR	1.091	
Simulated GR	1.104	
	0.4	*0.9*
Analytical GR	1.012	
Simulated GR	1.013	

We next demonstrate that adding a small amount of environmental stochasticity (using the beta/gamma option) or including demographic stochasticity (with or without a maximum brood size) also results in simulated population growth rates that match very closely with the analytical growth rate derived from the same Leslie matrix, without any environmental stochasticity included.

Table 2. Estimates for simulated growth rates when environmental stochasticity is included in the simulated model ('Env'), or for when demographic stochasticity ('Demo'; Poisson or binomial with maximum brood size equal to 3) is included in the model, or for when both environmental and demographic stochasticity are included in the model ('Both'). In all cases, model parameters were set as: productivity rate: 0.4; adult survival rate: 0.9, age at first breeding: 5 years. The analytical growth rate for the deterministic Leslie matrix with the same baseline demographic rates is **1.012**.

Type of stochasticity	Standard deviation in productivity	Standard deviation in adult survival rate	Simulated growth rate	Difference in GRs
Env	0.01	0.01	1.013	-0.001
Env	0.1	0.1	1.011	0.001
Env	0.2	0.1	1.011	0.001
Env	0.3	0.1	1.009	0.003
Env	0.4	0.1	1.008	0.004
Env	0.1	0.2	1.003	0.009
Env	0.1	0.25	0.991	0.021
Demo (Poisson)			1.013	-0.001
Demo (binomial)			1.013	-0.001
Both	0.1	0.25	0.993	0.019

In conclusion, we find that these validation tests demonstrate that the PVA model is behaving in accordance with mathematical derivations of expected output when run deterministically. In addition, when different types of stochasticity are added to the models, the results are in line with expectations, further validating the implementation of the different model forms in the R package and Shiny tool.

5 Future work

During the development of the tool, several areas where the underlying R package, and Shiny tool would benefit from further development were identified. Here, we document these developments, first for the underlying R package (5.1 – 5.4), and then for the Shiny interface (5.5).

5.1 Burn-in

The current tool assumes, by default, that the age structure in the initial year can be derived from the stable age structure associated with a deterministic Leslie matrix model. This will, in general, only be an approximation to the age structure associated with the model being used (especially if the model contains density dependence, environmental stochasticity or demographic stochasticity). As the PVA progresses through time, the age structure will tend to convergence to the age structure of the actual model, but at the start of the time series there will be a divergence between the age structure being used in the PVA and the "proper" age structure associated with the model and demographic rates.

This discrepancy can, in principle, be resolved through the use of a "burn-in" period: e.g. through the inclusion of additional "pseudo-years" (artificial years) immediately after the year associated with the initial counts. There are two potential ways to include "burn-in" in the tool:

Approach 1: this is a simple re-labelling trick. By way of a simple example: assume that the initial population count is associated with the year 2018, that we are interested in outputs for the period from 2020 until 2050, and that we decide to include a burn-in period of an additional 10 years. We can do this by including an additional 10 "pseudo-years" in between 2018 and 2019, so that the PVA is now run for 43, rather than 33, years, with the years being ordered as:

2018, pseudo1, pseudo2,…etc.,pseudo9,pseudo10, 2019,2020,…etc.…,2050.

We then ignore the pseudo-years when we report the results of the PVA. This approach is very simple to implement, but has the disadvantage that it means that the initial population size is now being allocated to the incorrect year – i.e., in practice it has the effect that the initial population count is assumed to relate to 2008, rather than 2018, and this shift may substantially alter the results of the PVA.

Approach 2: this is a two-stage approach. If we apply this approach to the previous example it would involve:

a. running a PVA for the years 2018,pseudo1,…,pseudo10, and extracting the age structure associated with year "pseudo10";
b. running the actual PVA for the period 2018 to 2050, with the results of stage (a) (i.e. the age structure extracted from pseudo10),, rather than the stable age structure of a deterministic model, used to determine the initial age structure.

Approach 2 should be more defensible than Approach 1, but would require a more substantial revision of the current code.

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5.2 Extensions to the Leslie matrix model

The R package, and potentially also the Shiny tool, could be adapted to include a range of extensions to the Leslie matrix model, in order to ensure that the models can capture a wider range of assumptions regarding the biology of the population being modelled. These extensions would also offer the potential to apply the tool to additional species (including non-seabird species) and populations.

The simplest extensions would be the inclusion of additional parametric statistical models for density dependence, environmental stochasticity and demographic stochasticity – the tool has been set up in such a way that this would be a relatively straightforward change to make.

Some other key potential extensions, which would require more involved work, include:

   a) allowing survival and productivity rates of breeding adults to vary by age – this would, for example, allow for the incorporation of senescence effects;
   b) allow scenarios of impact to alter age at first breeding, as well as changing survival and productivity rate;
   c) allow for a proportion of breeding age birds to skip breeding – the R package already allows for this to a very limited extent, but the biological realism of the way this is represented could be improved (e.g. by allowing birds that skip breeding to have different survival rates from those that breed);
   d) allow for the effects of immigration and emigration – e.g. through the use of a meta-population model.

5.3 Parameter estimation

Some of the inputs to the current model (in particular impacts of density dependence, and the correlation matrix associated with baseline demographic rates) are difficult to estimate by extracting simple summaries from the observed data – they need to be obtained by fitting a parametric statistical model to the data. This is also true of some of the possible extensions to the model (e.g., skipped breeding, and meta-population dynamics). The R package could potentially be extended to include the functionality to do this. It is worth noting, however, that estimation is, in general, a much harder process to automate than simulation (which forms the basis for the current tool). In addition, future work could add alternative model formulations for environmental stochasticity and density dependence, particularly as more empirical studies are undertaken to provide quantitative estimates for key model parameters.

5.4 Additional functionality for specifying impacts

The tool and R package could be extended to allow impact scenarios to operate over different time periods. Currently, although different impacts may be specified, they must all operate over the same time period. This addition to allow in-combination and cumulative assessments to be conducted that incorporate different start dates and operation periods of ORDs.

5.5 Interface with other tools

The tool could potentially be extended to provide a smoother interface to existing tools for estimating the impacts of offshore renewables upon seabirds (e.g. the Stochastic Collision Risk Model (McGregor et al 2018), or SeaBORD (Searle et al 2018)).

A simpler extension would be to alter the current tool so that it is able to accept estimates of demographic rates produced using a semi-integrated population model (SIPM) (Freeman et al 2014; Jitlal et al. 2017): this would be a relatively straightforward change to the current tool, as the SIPM is based upon a stochastic Leslie matrix model. The key feature of the SIPM that is absent from the current tool is uncertainty in the initial population size.

5.6 Future developments for Shiny interface

We have identified a few modifications to the tool that could be implemented to improve future usability. These include:

- Adding a progress bar to indicate progress towards completion for a model run (once the run has been started). The **nepva** R package prints out an update on the run progress, however, it would require additional work to interface a progress update from R with the Shiny interface;

- Adding a cancel button to allow users to stop runs once started. After some research, this does not seem to be possible in Shiny at the moment – however, should it become possible in future developments for Shiny, it would be a very useful addition to the tool;

- Saving the R workspace after a run has been completed, so that users could upload a previous run and re-run it (note that the current version of the tool allows users to download a log file for each run so runs may be replicated if desired using the values from this file);

- Adding a direct link on the Shiny interface to the relevant documentation for the tool (Final report, guidance manual and **nepva** R package documentation);

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