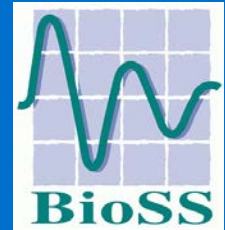# A Population Viability Analysis Modelling Tool for Seabird Species

## Guide for using the PVA tool (v2.0) user interface

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Date 18/01/2020

**Title** A Population Viability Analysis Modelling Tool for Seabird Species

**Client** Natural England & JNCC

**Client reference** ITT_4555 - C19-0287-1259 PVA tool Phase II

**UKCEH reference** NEC06986

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# Contents

# 1 User Guidance for Tool Interface

## 1.1 Background

This tool allows 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 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. 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. Note that this should not be considered a facility for running metapopulation PVAs, because the tool does not account for any movements of individuals between colonies. 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 impact scenarios, 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 on a range of input parameters;

- 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*) available on the GitHub repository Seabird_PVA_Tool[1]. Full documentation for the R package is also available as a download from the repository.

This document provides guidance for setting up and running PVAs using the Shiny Tool. It should be used in conjunction with the R package documentation for a full understanding

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[1] https://github.com/naturalengland/Seabird_PVA_Tool

of the inner workings and functionality of the tool. However, as described in the main report[2], not all of the functionality in the *nepva* R package is available via the tool interface.

## 1.2 Main menu

The PVA tool is launched via a browser (Chrome is recommended, but the tool also functions in other browsers such as Firefox and IE). The interface has a main menu panel on the left-hand side of each page. The menu panel can be hidden or revealed at any time by clicking on the three-bar icon.
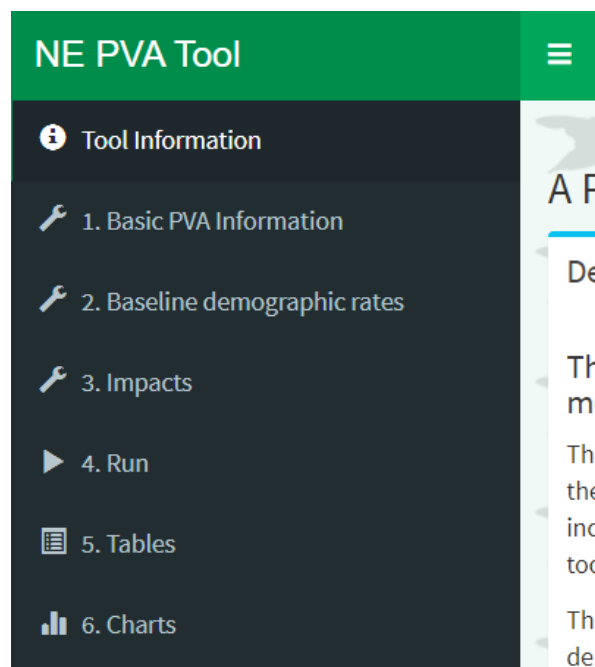


In addition to the information front page the main menu has links to six further 'tabs', or pages, in the tool: Input parameters and options for the PVA are presented in the first three pages (tabs numbered 1-3), the Run tab controls execution of the analysis (tab 4) and the outputs are displayed in tabular (tab 5) and chart form (tab 6). Each page contains a number of boxes that group together related parameters.

Most parameter boxes can be collapsed or expanded using the +/- in the top right corner of the header. Some boxes also offer additional guidance information accessed by clicking on the blue "i" icon in the lower left corner (note that the functionality of these icons is limited in some browsers due to browser capability – for full functionality users should use Chrome).

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[2] http://publications.naturalengland.org.uk/publication/4926995073073152

# 1.3 Overview of tool layout

1. **Basic PVA Information:** start by defining general information about the required model run including

   a. A reference name for the run to facilitate data management

   b. A run type (Simulation, Validation or Sensitivity) option that will control visibility of options on subsequent tabs

   c. Model options for the types of stochasticity to include (environmental and demographic)

   d. A switch to specify if density dependence should be included in the model

   e. The number of simulations to run per model

   f. A random seed used for matching simulations

   g. Number of years to use for burn-in

2. **Baseline demographic rates** define the baseline demographic rates to be used in the model including

   a. Insert pre-set species-specific values if required

   b. Specify or review basic demographic rates for age at first breeding and productivity parameters used to formulate demographic stochasticity

   c. Set the number of subpopulations to be used in the model

   d. Select the units for setting initial population size

   e. Specify if immature baseline demographic rates are to be used

   f. Enter the initial population size, year in which initial population size applies, productivity rates, survival rates for adults (and immatures if required), and effect of density dependence (if required).

3. **Impacts:** Define the impacts to be applied within a PVA run including

   a. The number of impact scenarios (1-10)

   b. Define how impacts affect different components of the population

   c. Define if impacts affect a relative change in demographic rates or operate as fixed harvesting of individuals

   d. Define the period over which impacts take effect

   e. Define how demographic rates are affected by impacts

4. **Run:** after the input parameters and options are set, execute the specified PVA from this tab

a. Define the period over which outputs are required

b. Define any conservation-related parameters for impact metrics (e.g., a target population size or a quasi-extinction threshold)

c. Specify the units for outputs

5. **Tables:** output data and summary metrics from a PVA are displayed on this tab and can be downloaded

6. **Charts:** following a PVA run, key output is presented as charts on the final tab

# 1.4 Using the tool

The PVA tool is used in a browser. The recommended browser is Chrome; it will work in any browser but some features may not display as intended (for example, each numeric box has a 'spinner' to enable the value to be increased or decreased, but this feature does not function as intended in Internet Explorer).

The layout of the tool is fully responsive meaning that it will work on most size screens including tablets and 'phones. Use the browser zoom options to resize the interface for optimum viewing or personal preference.

Depending on the number of subpopulations and impact scenarios selected, the interface has to carry out numerous operations and the model run may be extensive. If any operation takes more than 500ms a 'Please wait' graphic will be shown.

# 1.5 Basic PVA information tab

## 1.5.1 Run type

The tool has three main modes of running; select the appropriate mode from the options in the 'PVA run details' box and supply a short reference name. The reference name is repeated on the other pages and used in naming any downloaded files.

Depending on which of these three run types are selected, the rest of the tool tabs will update to guide users to specify only the necessary inputs for the selected type. Boxes that do not require an entry will be greyed out.

There is also an option in this box to reset all the parameters on all tabs back to the default values. This can also be achieved by refreshing the browser by reloading the page.

### 1.5.2 Simulation

Use this option to generate PVAs that simulate future population trajectories based upon specified demographic rates, initial population size(s), and scenarios of impact. Note that this mode may be used without any impacts specified to generate a baseline population forecast.

### 1.5.3 Validation

Select the Validation option to produce 'historical' population forecasts using a specified PVA model, for the purpose of validation against observed population data. This model can be used for baseline projections only, with no impact scenarios, and for only one population (selection of this option disables the impacts tab contents).

### 1.5.4 Sensitivity

Use this option to run a local sensitivity analysis associated with a specified PVA. This model can only be used for one population, one impact scenario, and without density dependent effects on demographic rates. The sensitivity analysis examines the sensitivity of the PVA outputs (projected population sizes and impact metrics) to the values of five key input parameters: initial population size, baseline adult survival, baseline productivity, impact of scenario on adult survival, and impact of scenario on productivity.

## 1.6 Basic information about the Population Viability Analysis

The tool implements a PVA model by constructing a Leslie matrix based on the structure and parameters provided by the user. In all cases, the tool assumes a post-breeding census and an equal sex-ratio. Users must define age at first breeding, and specify whether demographic rates are available for adults only, or for both adults and younger age classes. Users must also specify if demographic and environmental stochasticity are

to be included in the model. Based upon these decisions, the tool then constructs a Leslie Matrix, and implements life events assuming a post-breeding census, as illustrated below (Figure 1).

Use the options in this box to specify if the PVA model is to include environmental stochasticity, demographic stochasticity, and density dependence in demographic rates. Density dependence may only be included using a log-linear model for the effect of population density on untransformed demographic rates (note other options are available within the underlying R package, but are not available via the Tool interface).
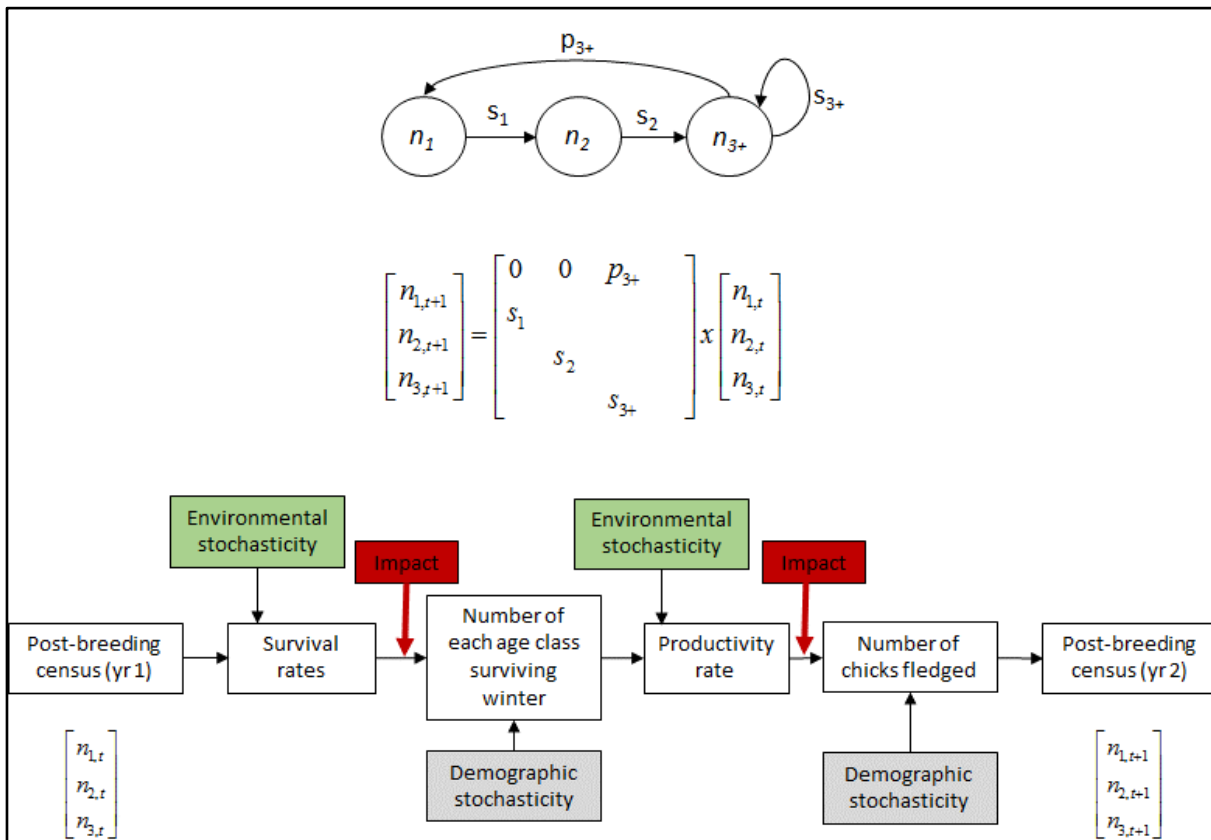


*Figure 1 Illustrative diagram for how the tool constructs a Leslie Matrix based on user-specified information. In this example, age at first breeding has been set at 3 years, and there are separate survival rates for all age classes. All adults (at age at first breeding or older) are assumed to have the same survival and productivity rates. All models assume a post-breeding census, with life events progressing through over-winter survival and then breeding in the following spring. If environmental stochasticity is included, it affects the survival and productivity rates within the Leslie Matrix in each year of simulation. Impacts are applied to the realised rates (after environmental stochasticity), and may either affect the survival and productivity rates, or 'cull' individuals from a specified section of the population as a fixed harvest. If selected, demographic stochasticity is then implemented to derive the realised number of individuals surviving the over-winter period, and the realised number of chicks successfully fledged. This results in the new number of individuals in each age class in the following year. Note that the model assumes no senescence in older age classes.*

To run an entirely deterministic model, set 'model to use for environmental stochasticity' to 'Deterministic' and the 'include demographic stochasticity in model?' switch to 'No'. To add environmental stochasticity select the 'Beta/Gamma' option. This will set the model to assume that survival rates have a beta distribution; and that the productivity rate has a beta distribution if an upper constraint on productivity (brood size per pair) is selected (see
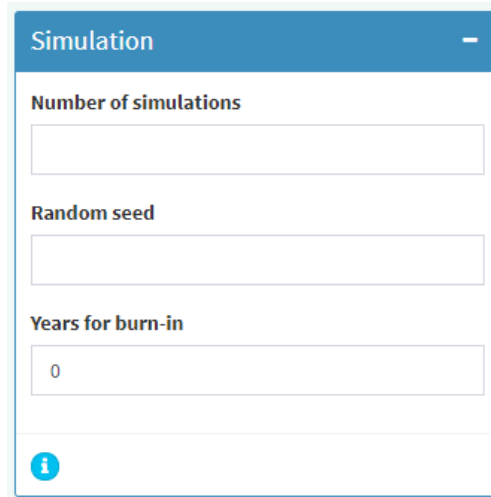
Section 1.8.2), and a gamma distribution if no upper constraint on productivity has been set.

When demographic stochasticity is not included, the survival and productivity rates are translated into actual numbers of birds surviving and chicks fledged each year by simply multiplying the rates by the relevant population sizes, and then rounding to the nearest whole number. If demographic stochasticity is included in the model, then the number of birds surviving (of each age) is simulated from a binomial distribution, and the number of chicks fledged is simulated either from a binomial distribution (if an upper constraint on productivity has been set) or a Poisson distribution (if no upper constraint on productivity has been set).



## 1.7 Simulation

Select the number of matched paired simulations to run, set a random seed, and specify if a set number of years are to be run initially for a 'burn-in' period. By using the same random seed and identical model specification, simulations may be repeated exactly. Note that if the random seed is left blank, the tool will automatically set a random seed, and record it in this seed field (and the model log file) after the run has finished. The burn-in period is used to ensure that the age structure is stable when starting to run the main PVA calculations – the burn-in period is used to estimate the equilibrium age structure.

If running an entirely deterministic PVA (i.e. without demographic stochasticity or environmental stochasticity, and with no standard error on the impacts) the number of simulations will be irrelevant, but a number still needs to be supplied; in this case, our recommendation would be to use a single simulation (i.e. number of simulations = 1), in order to keep the computational time as low as possible.
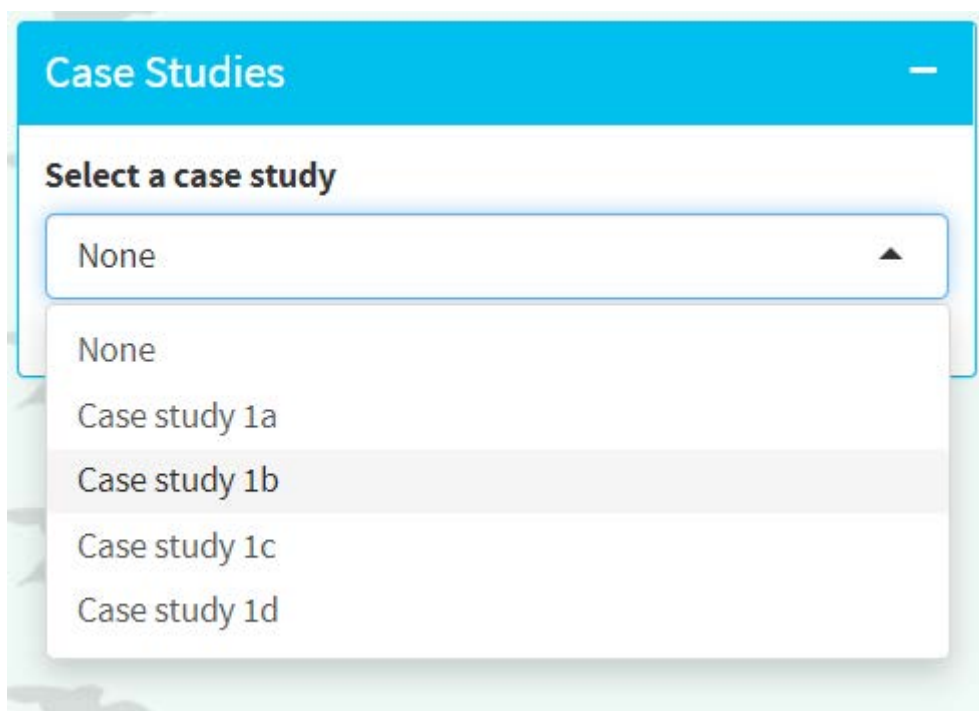
## 1.7.1 Using exemplar case studies

The tool has some in-built case studies that users may select to demonstrate use of the tool in 'Simulation' mode for a range of PVA models with alternative structures. The difference between each case study and the first (1a) are **bold and underlined**.



Selecting one of these case studies will pre-populate all required fields in the tool, allowing users to run the example and inspect model output, without having to enter any additional inputs to the tool. Users should note that some of the case studies have a large number of simulations, and so may take several minutes to run.

**Case study 1a:**

- Run type: Simulation

- Environmental stochasticity set to (beta/gamma) with an upper constraint on productivity set (see below). This means the model assumes both survival and productivity rates have a beta distribution, defined by the mean and SD entered in the baseline demographic rates

- Demographic stochasticity is included, with an upper constraint on productivity set (see below). This means the model assumes the number of birds surviving (of each age) and the number of chicks fledged are both simulated from a binomial distribution, defined by the mean and SD entered in the baseline demographic rates

- No density dependence is included

- Age at first breeding = 2; and maximum clutch size = 2

- Units for initial population sizes are set to breeding pairs

- 5000 matched paired simulations are to be run

- Output is requested for all years between 2017-2045

- The target population size is set to 83,700 breeding adults

- The quasi-extinction threshold is set to 20 breeding adults

- Units for outputs are set to be breeding adults

- There are two subpopulations with different demographic rates

- Rates not specified separately for immatures (meaning that adult survival rates are also used for immatures)

- Five impact scenarios are included, with impacts occurring over 2020-2045, impact specified as a relative harvest (a change to the demographic rates), the same impact applied to each of the two subpopulations, and there are no standard errors for impact sizes.


**Case study 1b:**

- Run type: Simulation

- Environmental stochasticity set to (beta/gamma) with an upper constraint on productivity set (see below). This means the model assumes both survival and productivity rates have a beta distribution, defined by the mean and SD entered in the baseline demographic rates

- Demographic stochasticity is included, with an upper constraint on productivity set (see below). This means the model assumes the number of birds surviving (of each age) and the number of chicks fledged are both simulated from a binomial distribution, defined by the mean and SD entered in the baseline demographic rates

- No density dependence is included

- Age at first breeding = 4; and maximum clutch size = 2

- Units for initial population sizes are set to breeding pairs

- 5000 matched paired simulations are to be run

- Output is requested for all years between 2017-2045

- The target population size is set to 83,700 breeding adults

- The quasi-extinction threshold is set to 20 breeding adults

- Units for outputs are set to be breeding adults

- There are two subpopulations with different demographic rates

- **Rates are specified separately for immatures** (meaning that adult survival rates and immature survival rates differ)

- Five impact scenarios are included, with impacts occurring over 2020-2045, impact specified as a relative harvest (a change to the demographic rates), impacts do not differ between adults and immatures, the same impact applied to each of the two subpopulations, and impacts are specified without standard errors.


**Case study 1c:**
- Run type: Simulation
- Environmental stochasticity set to (beta/gamma) with an upper constraint on productivity set (see below). This means the model assumes both survival and productivity rates have a beta distribution, defined by the mean and SD entered in the baseline demographic rates
- Demographic stochasticity is included, with an upper constraint on productivity set (see below). This means the model assumes the number of birds surviving (of each age) and the number of chicks fledged are both simulated from a binomial distribution, defined by the mean and SD entered in the baseline demographic rates
- No density dependence is included
- Age at first breeding = 2; and maximum clutch size = 2
- Units for initial population sizes are set to breeding pairs

- 5000 matched paired simulations are to be run

- Output is requested for all years between 2017-2045

- The target population size is set to 83,700 breeding adults

- The quasi-extinction threshold is set to 20 breeding adults

- Units for outputs are set to be breeding adults

- There are two subpopulations with different demographic rates

- Rates not specified separately for immatures (meaning that adult survival rates are also used for immatures)

- Five impact scenarios are included, with impacts occurring over 2020-2045, impact specified as an **absolute harvest** (a fixed cull of individuals in each year of the impact period), the same impact applied to each of the two subpopulations, and standard errors of impacts are not included.


**Case study 1d:**
- Run type: Simulation

- Environmental stochasticity set to (beta/gamma) with an upper constraint on productivity set (see below). This means the model assumes both survival and productivity rates have a beta distribution, defined by the mean and SD entered in the baseline demographic rates

- Demographic stochasticity is included, with an upper constraint on productivity set (see below). This means the model assumes the number of birds surviving (of each age) and the number of chicks fledged are both simulated from a binomial distribution, defined by the mean and SD entered in the baseline demographic rates

- **Density dependence is included**

- Age at first breeding = 2; and maximum clutch size = 2

- Units for initial population sizes are set to breeding pairs

- 5000 matched paired simulations are to be run

- Output is requested for all years between 2017-2045

- The target population size is set to 83,700 breeding adults

- The quasi-extinction threshold is set to 20 breeding adults

- Units for outputs are set to be breeding adults

- There are two subpopulations with different demographic rates

- Rates not specified separately for immatures (meaning that adult survival rates are also used for immatures)

- Five impact scenarios are included, with impacts occurring over 2020-2045, impact specified as a relative harvest (a change to the demographic rates), the same impact applied to each of the two subpopulations, and there are no standard errors for impact sizes.

# 1.8 Baseline demographic rates tab

## 1.8.1 Species-specific values

Here the user may choose to select a species to pre-populate parameters for a PVA using previously reported national or colony specific demographic rates (JNCC Seabird Monitoring Programme for breeding success data, or Horswill & Robinson 2015 for survival data). The tool will input the mean (rounded) age at first breeding reported in Horswill & Robinson (2015). These inserted values may subsequently be edited. The species option can be left unselected (set to 'None') if users wish to enter bespoke parameter values, they are provided here only as a guide.

To use the species-specific values, first select a 'Species' (Atlantic puffin in the example below), then select from a set of eight geographical regions to source and pool estimates of breeding success ('Region type to use for breeding success data'; ICES in the example below). This selection dictates the specific list of regional sectors over which breeding success may be pooled (listed under 'Sector to use within breeding success region'); in the example below, one of the ICES sectors has been selected, 'IVa').



The inter-annual standard deviation of productivity is determined as in Horswill & Robinson (2015) to be the maximum of [i] the mean of colony-specific inter-annual standard deviation and [ii] the standard deviation of colony-specific means. Year-by-colony combinations with very small sample sizes (less than five nests) are excluded from the calculations. Default values of productivity are only produced for regions if they contain

at least five years of productivity data (from any colonies: i.e., five years of data for a single colony within the region, or one year of data for each of five colonies within the region, would both be sufficient).

Eight regional classification are considered: "Site" involves solely using data for the site of interest, "global" involves using available data for all Seabird 2000 colonies within the British Isles (England, Northern Ireland, Scotland, Wales, Channel Islands and Isle of Man) and the remaining classifications are based upon pooling within regions – regional definitions that are considered are ICES Regions, JNCC Regional Seas, MSFD regions, Countries (England, Wales, Scotland, Northern Ireland, Channel Islands, Isle of Man), and the overall "abundance" and "breeding success" regional classifications from Cook & Robinson 2010 (which we denote "CRA" and "CRB" respectively).

*Table 1. Summary of the eight regional classifications used within the tool to set pre-defined demographic rates for available species.*

| Region Name | Description | Reference |
|---|---|---|
| **Country** | Country level data for: England, Northern Ireland, Scotland, Wales, Channel Islands, Isle of Man | JNCC Seabird 2000: http://jncc.defra.gov.uk/seabird2000 |
| **CRA** | Cook & Robinson 2010 BTO report: Abundance clusters | Cook & Robinson 2010: https://www.bto.org/sites/default/files/shared_documents/publications/research-reports/2010/rr573.pdf |
| **CRB** | Cook & Robinson 2010 BTO report: Breeding success clusters | Cook & Robinson 2010: https://www.bto.org/sites/default/files/shared_documents/publications/research-reports/2010/rr573.pdf |
| **Global** | All Seabird 2000 subsites | JNCC Seabird 2000: http://jncc.defra.gov.uk/seabird2000 |
| **ICES** | International Council for Exploration of the Sea | https://www.ices.dk/marine-data/maps/Pages/default.aspx |
| **MSFD** | Marine Strategy Framework Directive | https://www.eea.europa.eu/data-and-maps/data/europe-seas |
| **JNCC Regional Seas** | JNCC Regional Seas | http://jncc.defra.gov.uk/page-1612 |
| **Site** | Individual Seabird 2000 subsites | JNCC Seabird 2000: http://jncc.defra.gov.uk/seabird2000 |

Note that for some species, regions and sector combinations, breeding success cannot be calculated due to a lack of empirical data; this means the productivity value will remain blank in the interface and a value must be supplied manually by the user before the model will run.

Finally, the user then has the option to choose the dataset they wish to use for providing survival rates ('Available colony-specific survival rates'). For most species, this is simply the 'National' estimate provided in Horswill & Robinson (2015), but for several species more site-specific data sources are provided as options. In the example above the user has selected to use survival rates from the Isle of May estimated between 1984 and 2008.

Default survival rates (age-specific means and standard deviations) are based upon the overall, national values given in Horswill & Robinson (2015); however, rates are recalculated from the source data, rather than using the published values, in order to adjust for some issues in the calculations of the standard deviations reported in Horswill & Robinson (2015). The selection of studies is identical to that in Horswill & Robinson (2015), and we also follow the decision of that report to calculate the mean as a weighted mean. Means are weighted by length of time series for some species and ages (adults for: great cormorant, black-legged kittiwake, herring gull, lesser black-backed gull and common tern), whilst a simple (unweighted) mean is used for all other combinations of species and age. Standard deviations are, similarly, either a weighted or an unweighted mean of the standard deviations associated with individual studies. In some cases, the individual studies used by Horswill & Robinson (2015) report standard errors, rather than standard deviations. Where this occurred, we converted these into standard deviations by multiplying the standard error by the square root of the length of the time series (because, at least in simple situations, the standard error of the mean is equal to the standard deviation divided by the square root of the sample size).

There is a reset button provided that will reset only the boxes on the Baseline demographic rates tab back to the initial values.
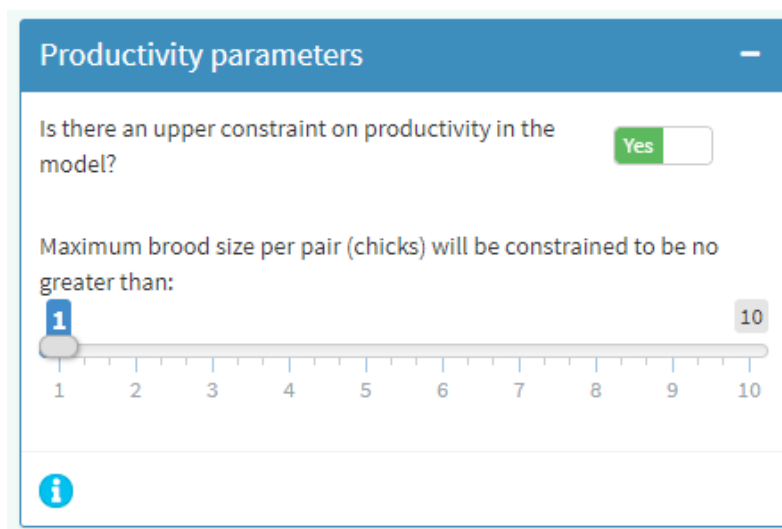
## 1.8.2 Age at first breeding

An age at first breeding is required to structure the Leslie Matrix underlying the population model. Age at first breeding is used to create age-classes for 'immatures' (all birds below age at first breeding), and to specify the age above which all individuals are considered to be breeding adults. In the example below, the slider has been used to set the age at first breeding to five, meaning that immatures are all birds aged one to four (with age classes: 0-1 [chicks], 1-2, 2-3, 3-4 [immatures]), and breeding adults are all birds aged five or older. An appropriate number of age class fields will be created in the tool based on this setting.

## 1.8.3 Productivity parameters

The Productivity parameters box contains a switch and a slider; the slider will be hidden if the switch is set to 'No'. If an upper constraint on productivity is required, set the switch to 'yes' and set an upper limit on the number of chicks per pair with the slider. Selecting this option affects how environmental and demographic stochasticity are formulated within the model.
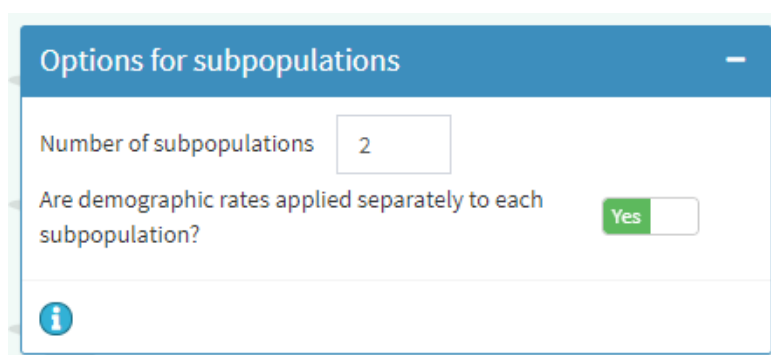


## 1.8.4 Options for subpopulations

A PVA can be generated for up to ten subpopulations using either the same or different demographic rates per subpopulation. Predicted population sizes are summed to provide projected population size and output metrics for the entire population (not separately for individual subpopulations).
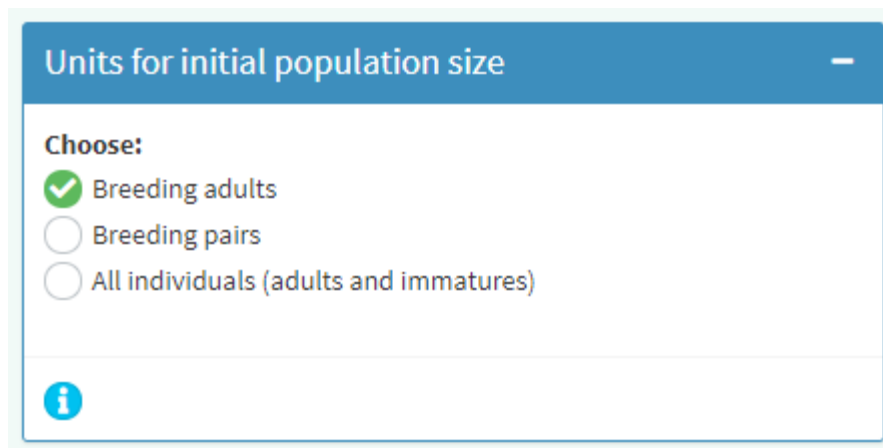
This flexibility is included to enable PVAs to be run at SPA or regional scales, where multiple colonies are included, and where impacts may affect individual colonies (subpopulations) in the same way, or in different ways.

Setting the number of subpopulations defines the model structure and the number of fields set up throughout the tool interface. If 'No' is selected for the switch, the same set of baseline demographic rates is used for all subpopulations (only subpopulation 1 will have active fields for data input and the model assumes the same values apply to all subpopulations.)
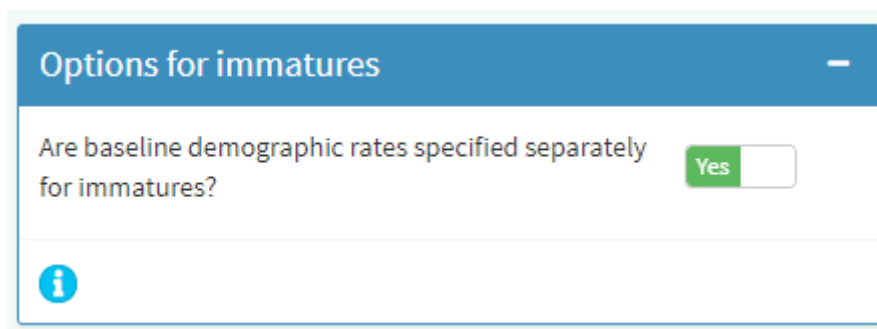
### 1.8.5 Units for initial population size

Initial population size(s) can be entered as counts of breeding adults (individuals), breeding pairs, or as all individuals (summed immatures and adults). Note that users entering information for some species, such as common guillemots and razorbills, will need to make the appropriate adjustments to ensure the appropriate units are used when entering initial population sizes in the tool. Select the required option here to ensure the input data are correctly interpreted in the model. Immatures are defined as any individuals below age at first breeding (not including chicks) as defined earlier in the model settings.



### 1.8.6 Options for immatures

If different demographic rates (survival) for adults versus immatures are available they can be included in the model separately. If 'yes' is selected, the appropriate number of fields will be set up in the interface. If 'No' is selected, the same set of demographic rates (survival) are used for both adults and immatures.



### 1.8.7 Populating rates for each subpopulation

As illustrated below, a parameter box is created for each subpopulation with a table of input fields for initial population size, the year in which this estimate was made (note that this year may precede the year for which outputs are specified to start), productivity rate per pair, adult survival rate and immatures survival rates per age class. Based on the options selected above, some fields may be 'greyed out' (inactive).

**Baseline demographic rates: 1** −

Specify productivity and survival rates for subpopulation 1

| Initial population size | Productivity rate per pair | Adult survival rate |
|---|---|---|
| **Year** | **Mean** | **Mean** |
| 2012 | 0.3 | 0.89 |
| **Initial population size** | **Standard deviation** | **Standard deviation** |
| 791 | 0.11 | 0.02 |
| | **Effect of density dependence** | **Effect of density dependence** |

Immature survival rates

| **Mean for age class 0-1** | **Standard dev. for age class 0-1** | **Effect of DD for age class 0-1** |
|---|---|---|
| | | |
| **Mean for age class 1-2** | **Standard dev. for age class 1-2** | **Effect of DD for age class 1-2** |
| | | |

For example, if two subpopulations have been specified with demographic rates applied separately to each subpopulation, two tables for entering demographic rates for 'Subpopulation 1' and 'Subpopulation 2' will be created in the tool interface

If density dependence has been selected, users will also enter the effect of density dependence on each demographic rate.

## 1.8.8 Including density dependence

Within the tool, there is one method for including density dependence effects of population size (breeding adults) on demographic rates. The method assumes that the effects of density dependence on the untransformed demographic rates (productivity and/or survival) are a linear function of $\log_{10}$(population size), where population size is the number of breeding adults. When the density dependence option is selected in the Basic Information tab, the effect of density dependence on the mean rate for productivity and survival must be entered (see example boxes below). A zero must be entered in either of these boxes, rather than leaving them blank, to signify no effect of density on that demographic rate. The effect of density on each of the rates should be entered as a percentage point change in the mean demographic rate. For instance, entering a value of -0.003 would result in a 0.3% reduction in the mean rate, so a mean value of 0.9 (90% survival rate) would be changed to a value of 0.897 (89.7% survival rate). The implication

of this density dependent effect, is that for every 10-fold change in population size, there is a corresponding 0.3% reduction in the mean rate.

Negative (compensatory) or positive (depensatory) density dependent effects can be included in the model by entering the effect of density dependence as a negative change (compensatory) or as a positive change (depensatory).

It is important to note that the density dependent model implies that the basline demographic rates for productivity and survival (mean and SD) provided represent the mean demographic rates for a population in the absence of ddcensity dependence. In reality, any empirical measurements for productivity and survival rates are likely to have been based on populations that do experience density dependent effects. Therefore, this facility within the tool should only be used for exploratory analyses for how density dependent effects may affect population trajectories and impact sizes.

The underlying R package contains four methods for implementing density dependent effects, based on the types of outputs that are typically produced when density dependent models are fitted to real data sets. This should be used instead of running a PVA via the tool interface for more sophisticated analyses aimed at quantifying the effects of density dependence on PVA assessments.
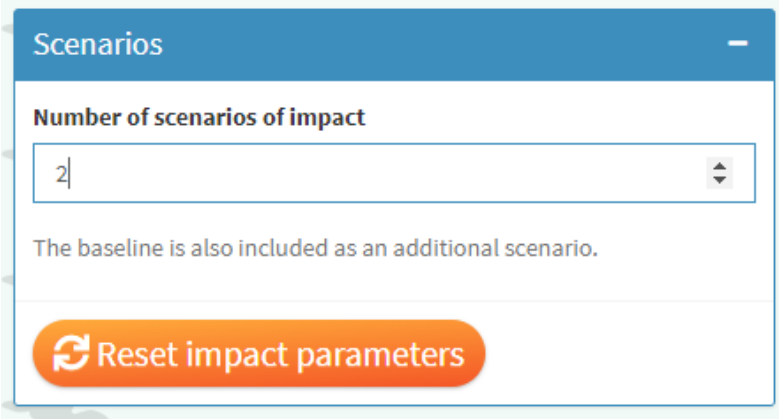
# 1.9 Impacts tab

## 1.9.1 Scenarios

Enter the number of distinct impact scenarios to be run (maximum ten). This defines the number of scenarios for the PVA and controls the input tables within the interface. The 'baseline' run, with no impact, is always included as an additional scenario. To run a population projection with no impact (i.e., to run the baseline scenario only), input zero here.

Each scenario can be given a short reference name that will be used in the output tables and charts (scenario names will appear on output charts). If left blank, the tool will insert a letter corresponding to the box label (*i.e.* A, B, …, J)

The reset button will set all the parameters and boxes on the impacts tab back to null values.

## 1.9.2 Options

A number of switches can be set to Yes or No to configure model options



Specify if impacts are applied separately to each subpopulation (e.g., impacts are different and known for each individual subpopulation).

Specify if impacts are to be specified separately for immatures and adults (e.g., immatures are known to have a different level of impact than adults).

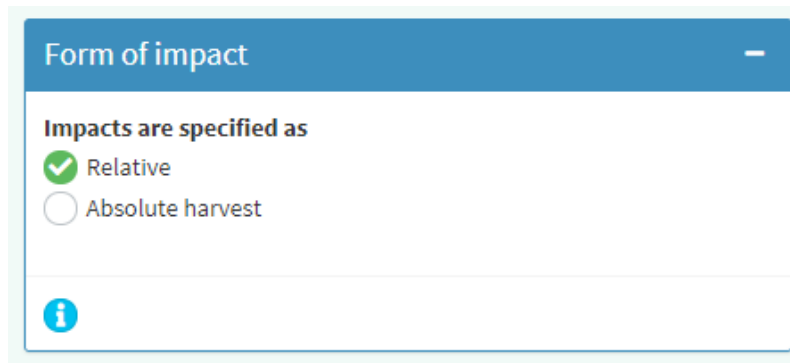Select if standard errors are available for impact rates.

Select if random seeds should be matched for different impact scenarios. This question is only relevant if standard errors are available for the impacts. If standard errors are available for impacts, specify here if random seeds should be matched across the alternative impact scenarios. Selecting 'yes' means you are making the assumption that the uncertainties for each impact scenario are in some way related to one another.

Setting these options will change the number of fields appropriately, or disable some boxes (greyed out).

## 1.9.3 Form of impact

Impacts can be expressed as a relative harvest (i.e., a fixed change in demographic rates for survival and/or productivity), or as an absolute harvest (i.e., a fixed number of added mortalities arising from the impact for each year, regardless of population size). Set this to the required value to ensure the model interprets input values correctly.

Note that the "absolute harvest" option should only be used in situations where the number of additional mortalities associated with the scenario is independent of the population size – e.g., if the scenario is for a cull of 100 individuals per year, regardless of population size. In situations where the number of individuals killed is a proportion of the population size (as will usually be the case when quantifying the impact of offshore wind farms), the "relative" option should be used (in this way the number of additional mortalities is assumed to be proportional to the population size).
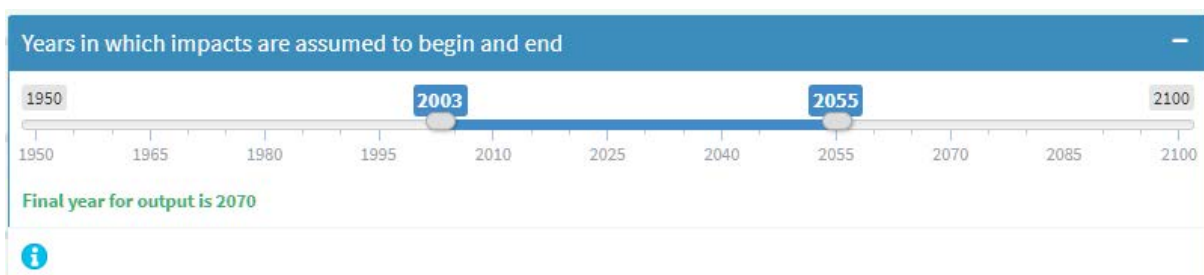
## 1.9.4 Years in which impacts are assumed to begin and end

Use the slider to set the start and end year of the period of impact. Note that the first year of impact must be later than the most recent year associated with an initial population size (i.e., if we are considering three subpopulations, with initial population sizes in year 2013, 2014 and 2016, then the year in which the impacts begin cannot be earlier than 2017). This is because the tool will only estimate population sizes from the first year with an initial population size. Therefore, a subpopulation with an initial count in 2016 will not have a population size estimate for years preceding 2017, meaning that the summation of population sizes over all subpopulations in years preceding 2017 is not possible.

Note that starting the impacts in the year following the initial year implies that the impact is first felt in the overwinter survival from the initial year to the following year. This is because the model assumes a post-breeding census. For example, if the initial year for the model run is 2010, setting the first impact year to be 2011 implies that the impact is first felt in the overwinter survival from year 2010 to 2011, and in the breeding of the spring of 2011 (Fig. 1).

The final year of impacts may be specified to be later than the final year for which output will be produced, in which case the impact is effectively assumed to continue on indefinitely after the first year of impact.

The start and end years can be set independently by dragging the end points, or the impact period can be moved as a whole by dragging the blue bar between the end points. A note is provided as a reminder of the output settings on tab 4.



A parameter box is created for each impact scenario with a table of input fields. Based on the options selected, some fields may be 'greyed out' (inactive).

## 1.9.5 Specifying the magnitude of impacts

In the example below, impacts for relative harvests are entered into the tool as, for example, 'survival rate in the baseline minus survival rate in the scenario'. Therefore, for an impact scenario with a 0.05% percentage point reduction in the mean survival rate, the impact on the mean survival rate is entered in the tool as 0.0005. For example, 100 additional mortalities on a population of 5000 would be a 2% percentage point reduction in the mean survival rate and users should enter 0.02 in the impact box. To enter a positive impact, for instance an increase in adult survival of 0.05% percentage points, a minus sign needs to be used (e.g., -0.0005) to represent a reduction in the mortality rate caused by the impact.
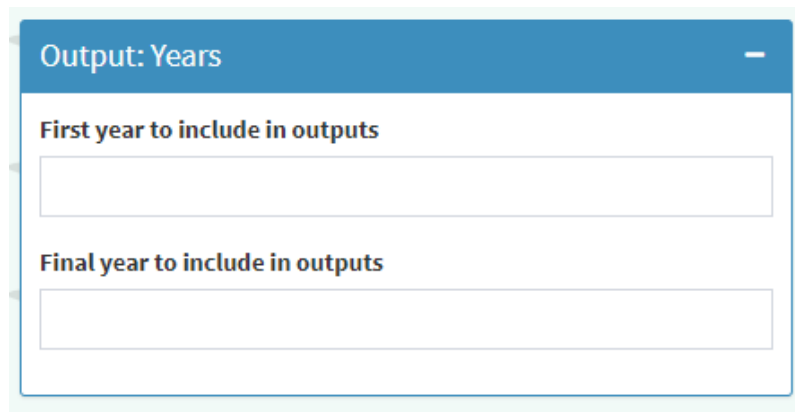
If an "absolute harvest" were to be specified, the number of additional birds killed must be specified, rather than the increase in mortality rate. For instance, by specifying that 100 adults are killed in every year of impact. Absolute harvest impacts may be entered as the number of mortalities for chicks, immatures, or adults (or any combination of the three). If no mortalities are required for one of these stages, users must enter a zero rather than leave the field empty.

# 1.10 Run tab

## 1.10.1 Output: years

The tool will produce outputs for each year during the specified period; depending on the run type, the start year may be disabled (in 'Validation' model the tool automatically outputs data from the year specified for initial population size; in 'Sensitivity' mode, the tool only outputs the final year – the last year the user has specified for the simulation). Note that the final year to include in outputs must be later than the first year in which impacts are assumed to start, when at least one impact has been specified. A warning will appear if the final year for outputs is earlier than the impact start.

**Output: Years**        −

First year to include in outputs

Final year to include in outputs

## 1.10.2 Output: target population size
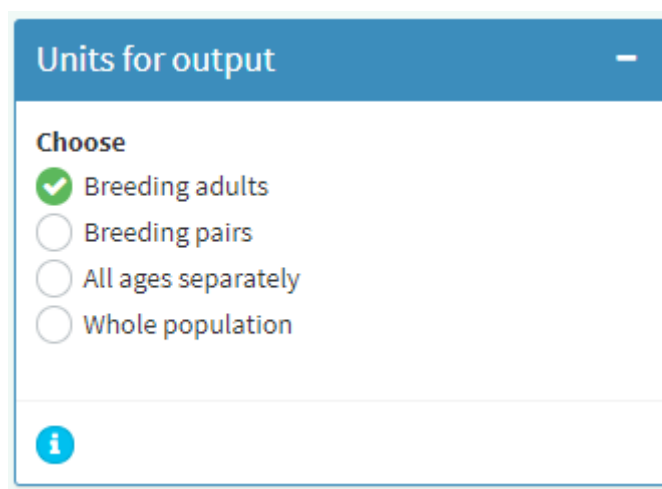
If required, the user can set a target population size for assessing effects of impacts, and a quasi-extinction threshold. The tool will output the percentage of simulations in which the impacted final population size exceeds the user-specified target population size (pc_ImpSims_above_TPS), or falls below the quasi-extinction threshold (Quasi_Extinction). Note that this applies to the summed population size over all subpopulations, if two or more subpopulations are specified. Population sizes must be entered in the same units as set for outputs (see below). These values can be left blank.

**Output: Target population size**        −

Target population size to use in calculating impact metrics

Quasi-extinction threshold to use in calculating impact metrics

These values must be entered using the same units as specified for outputs

ℹ

### 1.10.3 Units for output

Outputs can be presented as the number of breeding adults only (i.e., breeding individuals), the number of breeding pairs only, the number of individuals of each age separately (all ages separately), or for the whole population. Note that "breeding adults" will output the *actual* projected number of breeding adults in the population – for some species (e.g. razorbill and common guillemot) this will not generally be equal to the number of individuals that are actually counted within colony census data due to differences in counting methods across species.

If 'All ages separately' is selected, the charts will show only data for adult birds. The table output contains data for all age classes.



### 1.10.4 Run

The final box on the Run tab contains a progress bar and a button to execute the model when ready.

Based on the selections made on the tabs, the tool calculates the total number of numeric parameters that must be filled in for the complete set of options required for the model run. The bar indicates how many of these numeric fields are empty and how many have values entered. This total is only a guide and does not include the switches or sliders (as these are by definition always set to some value which must be checked carefully by the user).

The Run button can be pressed to initiate a model run at any time, but if any mandatory fields are empty, an error message will be displayed.

Once a run has been started, a log file is generated (Microsoft Word format). The file name includes the user-supplied reference name plus a date stamp. Individual browser settings control whether the file is saved automatically to a pre-defined location (often the 'downloads' folder) or whether the user is prompted for a location to save the file (note that the log file download process may not work with Firefox, or with some firewall settings).
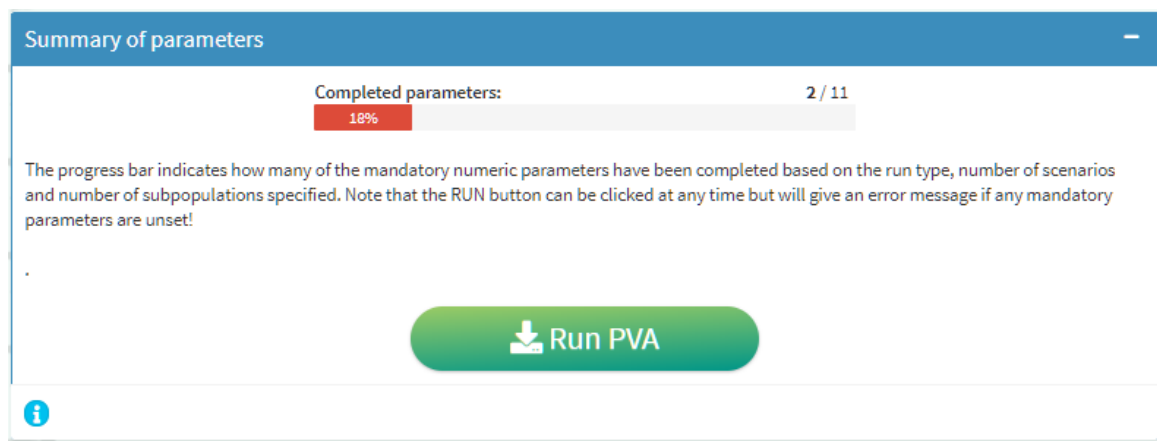
While the PVA is running a 'busy indicator' will show on screen
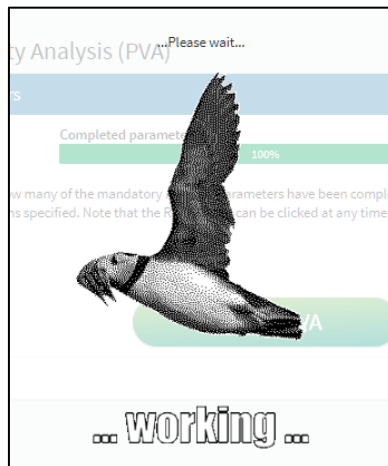


When a run has finished, an alert will be displayed: click anywhere to dismiss the alert.
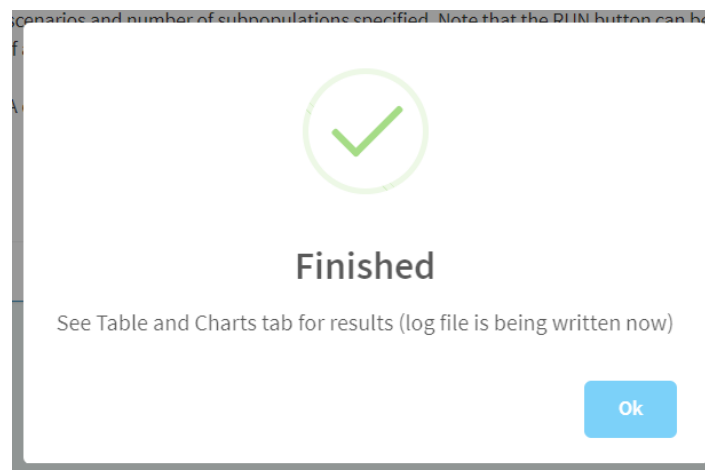
# 1.11 Validation mode

Validation mode is designed to run a PVA for a historical period, to compare the results against observed count data.

When validation mode is selected, an extra component is added to the tool interface, and other components are hidden or disabled (greyed out). Under validation, the number of subpopulations is fixed at one, so multiple populations may not be included in this mode. The number of impact scenarios is fixed at zero, because validation runs only use 'baseline' projections. The tool will generate a population forecast using the model specified, and the observed population sizes will be added to the output chart, for a visual comparison of model fit (Figure 2).On the 'Run' tab, a box is created with a table for data to be entered and used to validate the projected population size from the PVA model. Enter a year and an observed population size in the same units as selected for output.

Up to twenty validation data points may be entered.
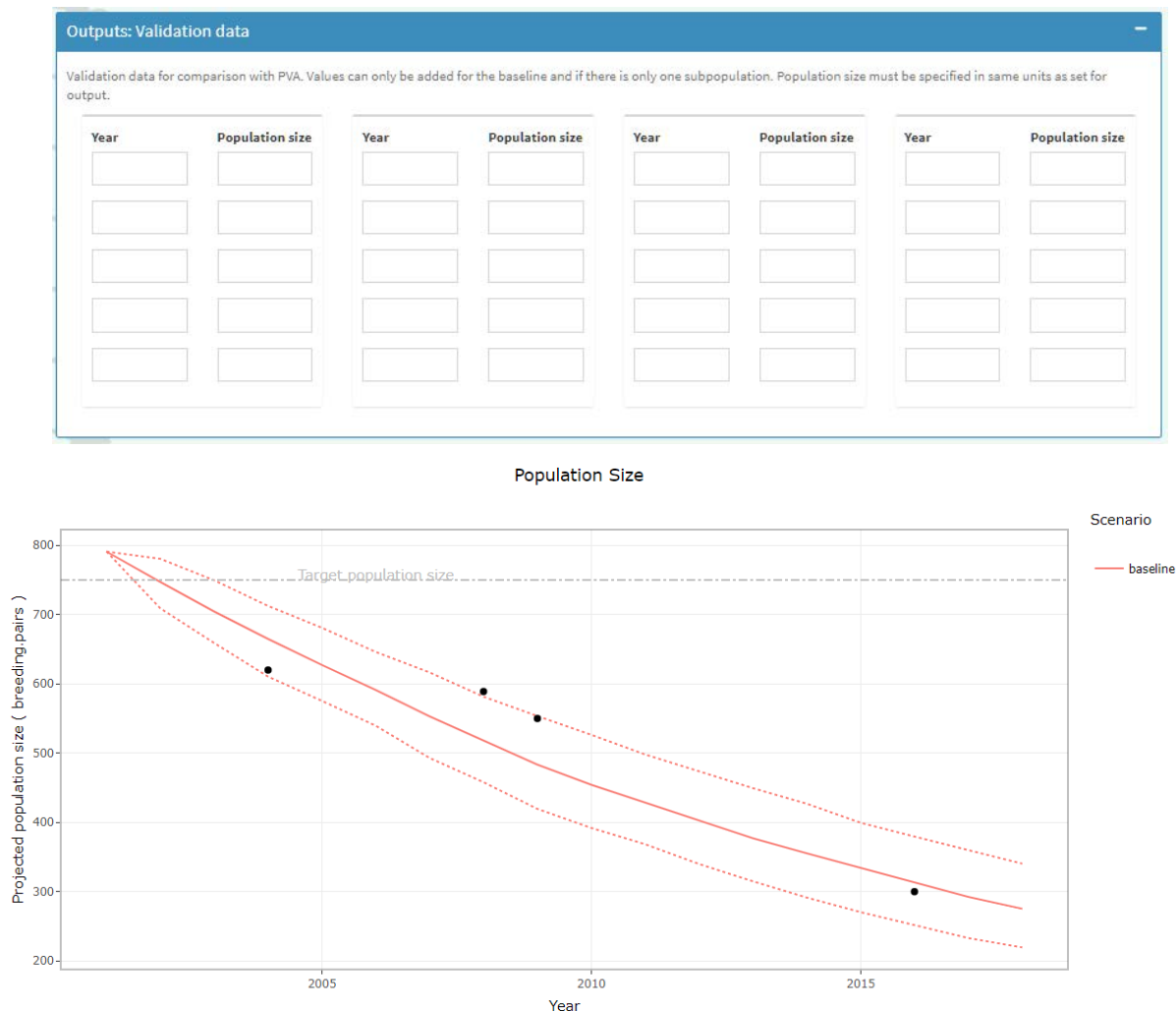




*Figure 2. Example chart output from a 'Validation' run. The tool generates a population forecast (solid red line: median population size; dotted red lines: 95% confidence intervals) and adds user-specified observed population sizes to the plot. This allows for a visual inspection of model fit. Note that Validation mode only allows for projection of a single baseline population (no impact scenarios).*

# 1.12 Sensitivity Mode

In this mode, the tool runs the specified PVA for multiple combinations of five key input parameters, performing a local sensitivity analysis

- initial population size

- baseline productivity rate

- baseline adult survival rate

- impact of scenario upon productivity rate (relative harvest)

- impact of scenario upon adult survival rate (relative harvest)

(note that the R package underlying the tool also contains an option for performing global sensitivity analysis, see R package documentation for full information[3]).

The tool outputs how changes in the value of each of these five input parameters affects the value of the PVA outputs (impact metrics).

Density dependence may not be used in sensitivity mode, and this functionality can only be run for a single population, a single impact scenario, and with initial population size specified as number of breeding adults.

When this mode is selected, an additional box appears on the Basic Demographic Rates tab. To carry out the run in sensitivity mode, the model requires

- The number of different values to consider for each parameter, both above and below the set parameter value. The default value is 1, which means that for each of the five parameters a value of x% above and x% below the value of the parameter will be simulated, where x is set for each of the five parameters in the boxes below. A value of 3 means that three equally spaced values above and below the value of each parameter, up to the percentage specified by x, will be simulated (for instance, if x is set at 10%, the tool will simulate values for the parameter of -10%, -6.6%, -3.3%, +3.3%, +6.6%, +10%). Values of between 1 and 5 may be used.

- The range over which each parameter is to be changed as a percentage of the "standard" value of each parameter ('x' in the text above – for example specify '10' to change the parameter by plus or minus 10% of its set value). The tool will output a chart for how the values of each of the five parameters affect the model's estimate for all metrics except TPS_YR (Figure 3).

---

[3] https://github.com/naturalengland/Seabird_PVA_Tool

## Options: Sensitivity

Number of different values to use per parameter for the sensitivity analysis. The default value is 1, which means that for each of the five parameters a value of x% above and x% below the value of the parameter will be simulated, where x is set in the boxes below. A value of 3 means that three equally spaced values above and below the value of each parameter, up to the percentage specified by x, will be simulated (e.g., -10%, -6.6%, -3.3%, +3.3%, +6.6%, +10%). Please see user guidance for more information. Values of between 1 and 5 may be used.

> 1

Set ranges for each of the five PVA parameters: specify the range over which each parameter is to be changed as a percentage of the "standard" value of each parameter (e.g., specify '10' to change the parameter by 10% of its value)

| 1 = initial population size (% change in value of parameter) | 2 = baseline productivity (% change in value of parameter) | 3 = baseline adult survival (% change in value of parameter) |
| --- | --- | --- |
| | | |

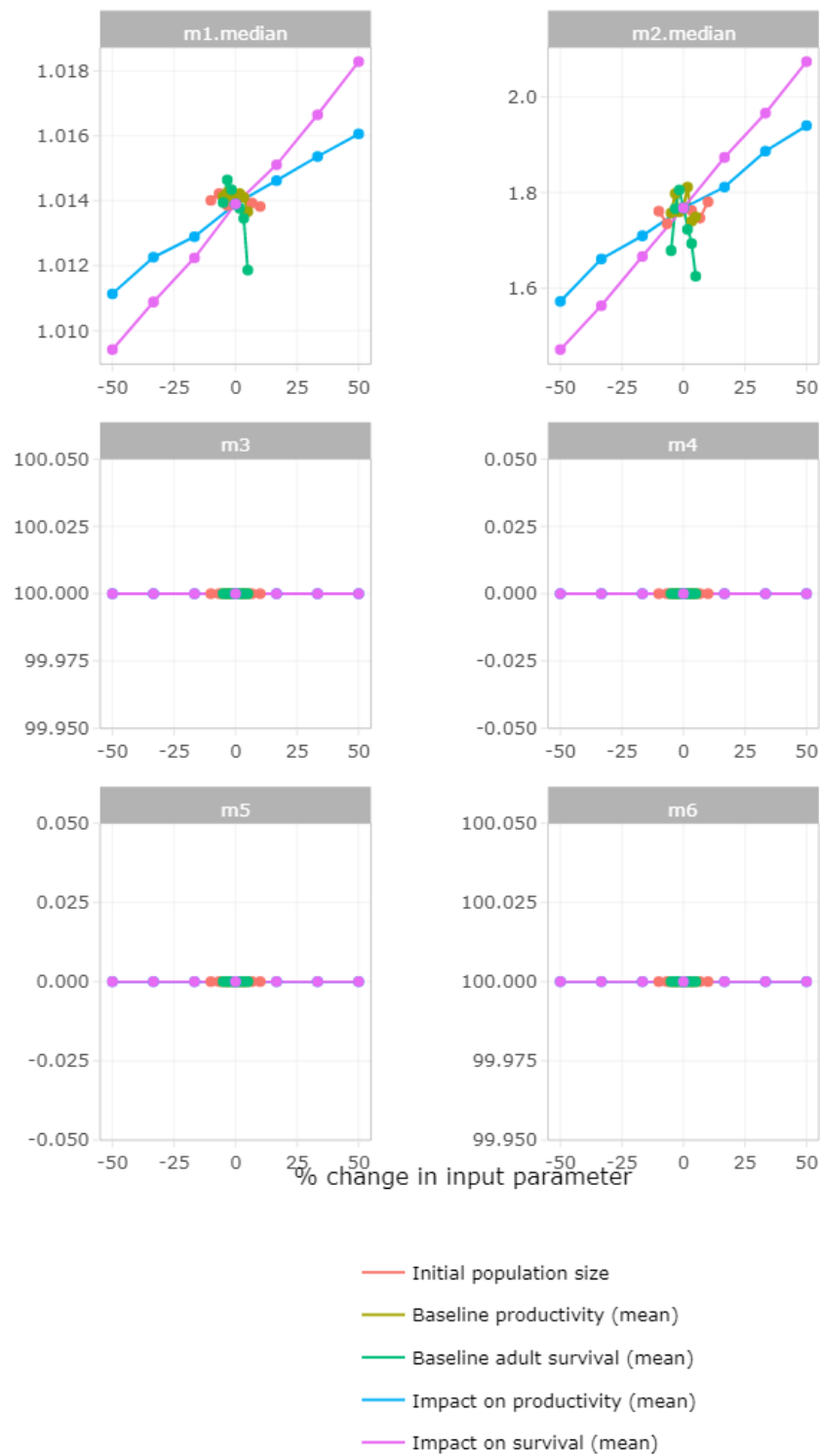| 4 = impact of scenario on productivity rate (% change in value of parameter) | 5 = impact of scenario on adult survival rate (% change in value of parameter) |
| --- | --- |
| | |

*Figure 3 Example charts created in Sensitivity mode, showing how the value of metrics M1-M6 change in relation to a percentage change in the value of one of five input parameters. Initial population size; Baseline productivity (mean); Baseline adult survival (mean) ; Impact on productivity rate (mean)  and Impact on survival (mean).*

# 1.13 Output

## 1.13.1 Tables

All of the model output is included in a single table on the 'Tables' tab of the interface. The tool also provides summary tables for some of the key output metrics (in Simulation mode only):

The data in the tables can be copied (Copy button) for pasting into a document, or downloaded as a Microsoft Excel (Excel button) or csv file (csv button). Columns can be hidden or revealed for more compact viewing using the visibility button.

In simulation mode, the tool produces five tables:

1. All metrics except TPS_YR for the each of the baseline and impact scenarios

2. Threshold-related metrics ('Quasi_Extinction' and 'pc_ImpSims_above_TPS') only

3. TPS_YR for the each of the baseline and impact scenarios (note that the calculation of this metric is dependent upon metric 'pc_ImpSims_above_TPS'; if pc_ImpSims_above_TPS is always <50%, metric TPS_YR cannot be calculated)

4. Population growth rate ('Annual_GR_ …') and Population percent change ('pc_Pop_Change_ …') for the each of the baseline and impact scenarios ('Population growth rate & population % change')

5. Full table of all outputs

The tool outputs seven main metrics in Simulation mode, all relating to how the impact scenarios affect various aspects of the population projection (Table 2):

- CGR: counterfactual of population growth rate: The ratio of annual growth rate under scenario to growth rate under the baseline for the same period
- CPS: counterfactual of final population size: The ratio of final population size in scenario to final population size in baseline
- QuantileUNIMP50pcIMP: quantile for the UNIMPACTED population that matches the 50% quantile for the IMPACTED population
- QuantileIMP50pcUNIMP: quantile for the IMPACTED population that matches the 50% quantile for the UNIMPACTED population
- Quasi_Extinction: Quasi-extinction risk – percentage of simulations in which final impacted population size is lower than the threshold for quasi-extinction
- pc_ImpSims_above_TPS: Percent of simulations in which the final impacted population size is more than target population size
- TPS_YR: the first year in which the impacted population reaches the specified target population size (note that if the impacted population does not reach the target population size within the time period of the run, this metric will be blank; users would need to extend the period of the run to find the value for TPS_YR).

*Table 2 Mathematical definition of the impact metrics reported by the tool, , in terms of the projected population sizes n_iy^((l)) for each simulation i=1,…,S and scenario l=1,…,L (where l=0 denotes the "baseline" scenario). Metrics are defined in relation to each output year (F), year associated with baseline population size (B, the population size in the year before the impact starts), and user-specified thresholds for quasi-extinction risk (u_"QE" ) and target population size (u_"TPS" ). Note that the 'output year', F, relates to each year within the simulation over the whole simulation period for which output is produced, regardless of whether the impact is currently in effect.*

| Metric | Name | Calculation of metric for a single simulation run | How are simulations combined to derive an overall metric? |
|---|---|---|---|
| **CGR** | Ratio of annual growth rate under scenario over the period $[B, F]$ to be equivalent growth rate under the baseline for this period | $\left(\dfrac{n_{iF}^{(l)}}{n_{iB}^{(l)}}\right)^{\frac{1}{F-B}} \Big/ \left(\dfrac{n_{iF}^{(0)}}{n_{iB}^{(0)}}\right)^{\frac{1}{F-B}}$ | Three possible summaries across simulations are reported: median, mean and SD |
| **CPS** | Ratio of final population size in scenario to final population size in baseline | $\left(\dfrac{n_{iF}^{(l)}}{n_{iF}^{(0)}}\right)$ | Three possible summaries across simulations are reported: median, mean and SD |
| **QuantileUNIMP 50pcIMP** | Percentage of simulations in which final baseline population size is lower than the median impacted final population size | $I\left(n_{iF}^{(0)} < \mathrm{median}_i\left(n_{iF}^{(l)}\right)\right)$ | Mean, multiplied by 100: this gives the percentage of simulations |
| **QuantileIMP 50pcUNIMP** | Percentage of simulations in which final impacted population size is lower than the median final population size under the baseline | $I\left(n_{iF}^{(l)} < \mathrm{median}_i\left(n_{iF}^{(0)}\right)\right)$ | Mean, multiplied by 100: this gives the percentage of simulations |
| **Quasi_ Extinction** | Quasi-extinction risk: percentage of simulations in which impacted final population size is lower than the threshold for quasi-extinction, $u_{\mathrm{QE}}$ | $I\left(n_{iF}^{(l)} < u_{\mathrm{QE}}\right)$ | Mean, multiplied by 100: this gives the percentage of simulations |
| **pc_ImpSims_ above_TPS** | Percentage of simulations in which impacted final population size exceeds the user-specified target population size $u_{\mathrm{TPS}}$) | $I\left(n_{iF}^{(l)} > u_{\mathrm{TPS}}\right)$ | Mean, multiplied by 100: this gives the percentage of simulations |

The tool also produces a summary table for the 'population growth rate' and the 'population percent change'. These are calculated as:

- *Population growth rate*: this is the annualised growth rate, calculated as the growth rate for each trajectory (baseline and all impact scenarios) from the year preceding the first year of impact to the final output year(final population size/starting population size)^1/number of years). In "baseline-only" runs (i.e. where no scenarios are used, and so no impacts are considered) the comparison is against the year associated within the initial count (or, if there are multiple subpopulations, the year associated with the initial count for the subpopulation with the most recent count). This output is listed in the table as 'Annual_GR_Median' (median annual growth rate), 'Annual_GR_LCI' (lower 95% confidence interval), and 'Annual_GR_UCI' (upper 95% confidence interval). Note that the 'final year' always relates to that specified by the user as the final year for which outputs are produced (which may or may not be after the end of impacts, depending upon the impact end year specified by the user).

- *Population percent change*: this is calculated as the percentage population increase or decrease, calculated over the same time period as "population growth rate". For instance, a population starting the impact period at 5,000 individuals and ending up with 10,000 individuals in the final year of outputwould result in a +100 % population percent change over this period.. Similarly, a population going from 5,000 to 2,500 would result in a -50% population percent change. This output is listed in the table as 'pc_Pop_Change_Median' (median percent population change), 'pc_Pop_Change_LCI' (lower 95% confidence interval), and 'pc_Pop_Change_UCI' (upper 95% confidence interval). Note that the 'final year' generally relates to that specified by the user as the final year for which outputs are produced (which may or may not be after the end of impacts, depending upon the impact end year specified by the user).

The full table of output includes all of the model output produced by the tool except metric TPS_YR (Table 3).

*Table 3 Model Output*

| Output name | Description | Units |
|---|---|---|
| Year | Year of model output | Years |
| Age_class | Units for output | Breeding individuals, breeding pairs, or all ages separately (user-specified) |
| Scenario | Name of scenario (baseline, and user-specified names for each impact scenario) | |
| Base_year | The year before the impact starts (this is the first year for which metrics are calculated) | True/false |
| Currently_Impacted | Indicator for whether current year of output is an impact year | True/false |
| YRS_From_First_IMP | The number of years since the start of the impact (the first of impact is 0) | numeric |
| Popsize_mean, popsize_SD, popsize_Median | The mean, standard deviation, and median of the simulated population sizes for each year of output | Breeding individuals, breeding pairs, or all ages separately (user-specified) |
| Popsize_1%_quantile, …, popsize_99%_quantile | The i$^{th}$ quantile for the projected population size | Breeding individuals, breeding pairs, or all ages separately (user-specified) |
| Annual_GR_Median, Annual_GR_Mean, Annual_GR_SD, Annual_GR_LCI, Annual_GR_UCI | The median, mean, standard deviation, lower 95% confidence interval and upper 95% confidence interval of the projected annual population growth rates | Population growth rate per year |
| pc_Pop_Change_Median, pc_Pop_Change_Mean, pc_Pop_Change_SD, pc_Pop_Change_LCI, pc_Pop_Change_UCI | The median, mean, standard deviation, lower 95% confidence interval and upper 95% confidence interval of the projected population percent change | Population percent change between year before impact starts and final year of output |
| CGR_Median, CGR_Mean, CGR_SD, CGR_LCI, CGR_UCI | The median, mean, standard deviation, lower 95% confidence interval and upper 95% confidence interval for CGR metrics | ratio |
| CPS_Median, CPS_Mean, CPS_SD, CPS_LCI, CPS_UCI | The median, mean, standard deviation, lower 95% confidence interval and upper 95% confidence interval for the "CPS" metric | ratio |
| QuantileUNIMP50pcIMP | Value of the metric "QuantileUNIMP50pcIMP" | % |
| QuantileIMP50pcUNIMP | Value of the metric "QuantileIMP50pcUNIMP" | % |
| Quasi_Extinction | Value of the metric "Quasi_Extinction" | % |
| pc_ImpSims_above_TPS | Value of the metric "pc_ImpSims_above_TPS" | % |

When run in Sensitivity mode, the tool adds ten additional columns to the start of the full table of outputs. Sensitivity mode only produces output for the final year of output as defined by the output options (the user specified year for the final year of output). These columns list the percent change in each of the five parameters involved in sensitivity:

- pcchange.inipop.vals: % change in initial population size

- pcchange.demobase.prod.mean: % change in productivity rate

- pcchange.demobase.survadult.mean: % change in adult survival rate

- pcchange.impact.prod.mean: % change in impact upon productivity rate

- pcchange.impact.survadult.mean: % change in impact upon adult survival rate

and the values of each of the five parameters involved in sensitivity:

- inipop.vals: initial population size

- demobase.prod.mean: productivity rate

- demobase.survadult.mean: adult survival rate

- impact.prod.mean: impact upon productivity rate

- impact.survadult.mean: impact upon adult survival rate

Various sensitivity and elasticity metrics can be calculated from the output in this table (we do not calculate any specific sensitivity/elasticity metrics within the tool to avoid excessively large amounts of output, and to allow users maximum flexibility in the calculation of sensitivity metrics).

## 1.13.2 Charts

A range of charts are produced, depending on the mode for a specific run. Note that charts are not always produced, depending on the type of run that has been completed. For instance, where there are multiple subpopulations with different impacts in 'Simulation' mode, the tool does not produce charts due to the complexity of the variables used in the model runs. Users will need to download the tabular output and create their own charts as required.

**Simulation mode:** the tool will produce charts for

- projected population size under the baseline and any scenarios
- projected counterfactual of population growth rate for each scenario of impact
- projected counterfactual of population size for each scenario of impact

**Validation mode**: the tool will produce one chart for the projected population size, with the observed 'validation' values overlaid as points.

**Sensitivity mode**: the tool will produce six charts for how the metrics (other than TPS_YR) are affected by the percent change in each of the five model parameters.

Charts may be manipulated using a menu that appears in the top right hand corner of the chart, when hovered over with the cursor. Options include

- Download the chart as a .png file (svg with Internet Explorer) using the 'camera' icon

- Zoom in and out and pan across the chart

- Display values for individual lines or all lines when hovering with the cursor

- Single-click on a line in the legend to hide/unhide that line or

- Double-click on a line in the legend to hide all other lines

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