Centre for Ecology & Hydrology
NATURAL ENVIRONMENT RESEARCH COUNCIL

SeabORD User Guide (v1.2)

User Guide for SeabORD version 1.2

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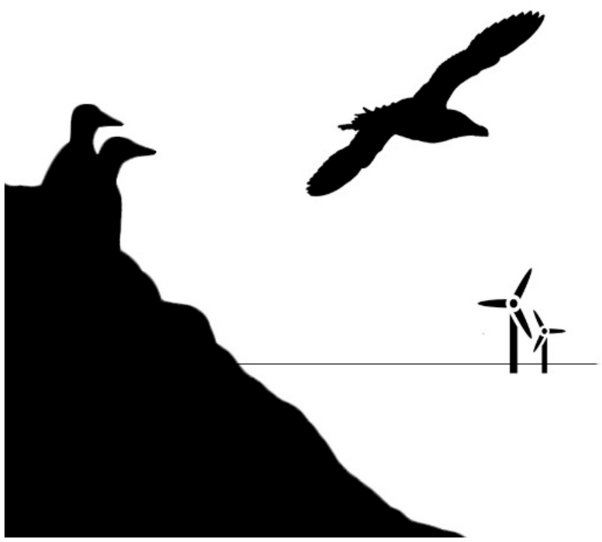

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1 Introduction

The prototype tool described here (SeabORD) quantifies the fate of displaced and barrier-affected seabirds encountering offshore renewable energy developments (ORDs), significantly improving existing methods for estimating the impact of marine developments on breeding seabirds.

The tool estimates the survival and reproductive success for individuals from breeding colonies affected by offshore renewable energy developments using an individual-based stochastic simulation model describing the foraging, energetics and reproductive success of seabirds during the breeding season. The model is fully described in the associated report (Searle, et al. 2018). Four species are modelled: Common guillemot, black-legged kittiwake, razorbill and Atlantic puffin. The prototype tool outputs estimates for both individual and population level impacts of ORDs on the breeding success and survival of adult birds. In addition, the methodology underpinning the tool allows for a quantitative linkage to be made between observations derived from snapshot surveys through to the average demographic consequences for those observed individuals.

This document describes how to install and run the prototype tool to estimate individual and population level impacts of ORDs (wind farms and tidal arrays) on breeding seabirds.

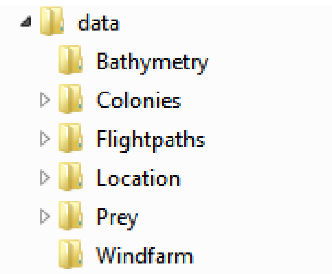
1.1 Installing the model application

SeabORD is distributed with two components

1. **The model application installer.** Two SeabORD installer files are supplied; SeabORDinstaller.exe and SeabORDInstaller_mcr.exe. The larger of the two files (SeabORDInstaller_mcr.exe) includes MATLAB Runtime while the smaller file will

download MATLAB Runtime from the web. When SeabORD is installed for the first time, MATLAB Runtime will be installed if required (see Section 1.2).

2. **A folder containing a default set of data files.** This data folder (and everything inside it) should be copied to a suitable location on a local or network drive, for example C:\Users*yourname*\SeabORD - all input and output files will be read from or written to here. (This is not the same as the location of the model installation shown in Figure 1-1) The files within the data folder are described in detail in the sections below.



SeabORD v1.2 is only available for Windows (64 bit) and has been tested on Windows 7 and Windows 10. It requires Microsoft Office to create the Excel output files.

- Double-click on the chosen installer file - **SeabORDinstaller.exe** (does not include MATLAB Runtime) or **SeabORDInstaller_mcr.exe** (much larger file includes MATLAB Runtime).
- Click NEXT and select the installation folder (the default is usually best). Remember to tick the box to add a shortcut on the desktop.

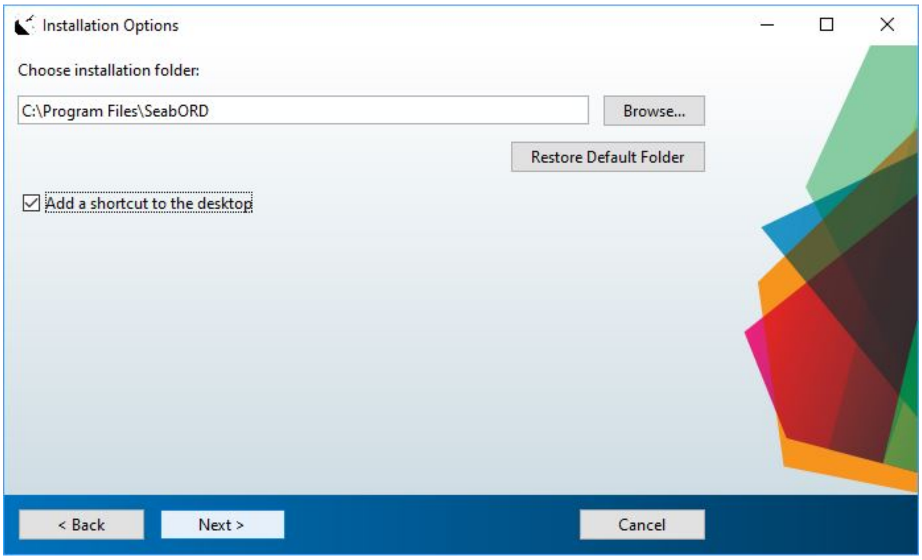


Figure 1-1 Installing SeabORD. Remember to tick the box if you wish to add a shortcut to your desktop.

- The installer will then check to see if you have already have MATLAB Runtime and then either proceed to the next step, download Runtime or install it directly. Full download and installation may take an hour or more depending on connection speed.

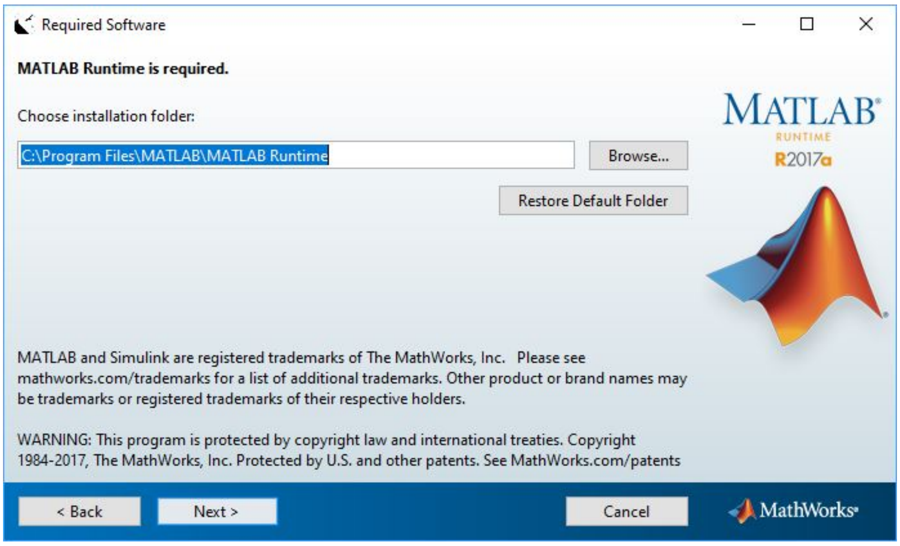


Figure 1-2 SeabORD requires MATLAB Runtime

- Accept the terms and conditions and, for the last stage, the SeabORD Installer will install the model tool.

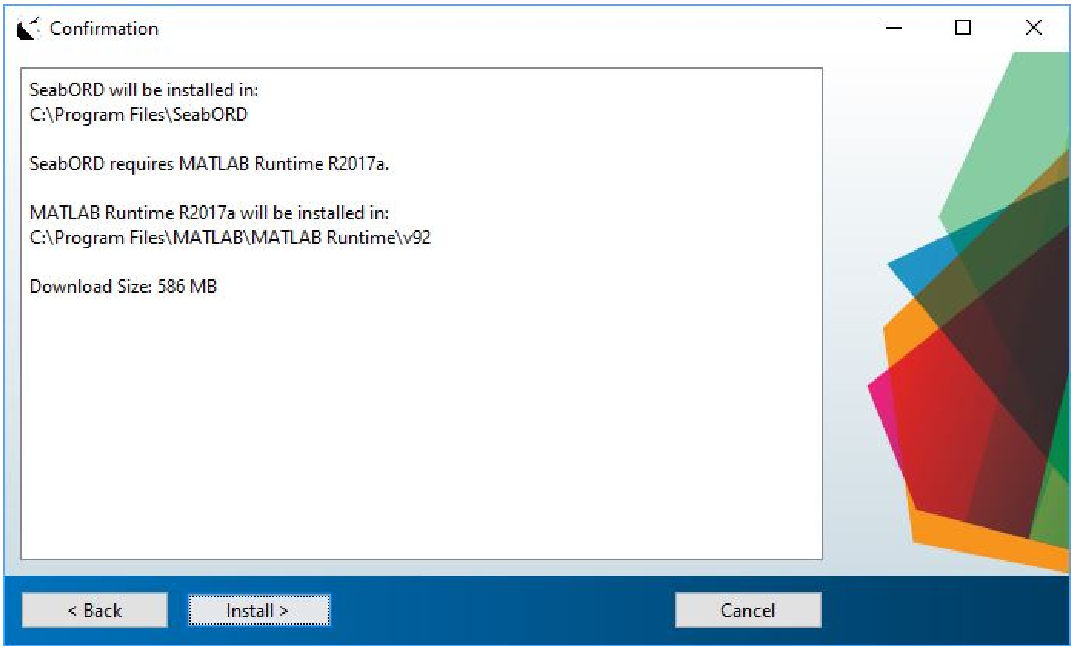


Figure 1-3 Final confirmation before SeabORD will finish installing.

1.2 MATLAB Runtime

The MATLAB Runtime enables the execution of MATLAB files on computers without an installed version of MATLAB. End users can download the MATLAB Runtime installer (free) from `http://www.mathworks.com/products/compiler/mcr`.

SeabORD v1.2 was created using MATLAB R2017a. You must install the appropriate version of MATLAB Runtime, which is 9.2.

The MATLAB Runtime file is very large and takes a long time (an hour or more) to install the first time it is used. When SeabORD is installed, the installation will check if MATLAB Runtime is already available; if MATLAB Runtime has not been installed SeabORD will automatically install it.

1.3 Model Outline

There are five phases in each simulation run for SeabORD v1.2 as illustrated in Figure 1-4.

1. The user sets parameters in the graphical interface to define the details for the simulation that will be executed.
2. SeabORD carries out a 'check-in' process. This involves taking the parameters set by the user and checking the input data files that will be needed to successfully run the simulation. The check-in process will indicate an error if parameters have not been specified by the user or if certain mandatory files are missing and cannot be generated within the model run. A warning, or advisory note, is shown if some input files are missing but the model has sufficient information to generate them during the simulation. This warning serves to indicate to the user that the simulation will take slightly longer

to run in comparison to the case where all input files have already been created (e.g., by previous model runs).

3. After check-in is complete with no errors, the user can run the model. The first stage (*Boarding*) involves loading or generating the required input data. There is a graphical output screen shown here so the user can monitor progress (see Section 3.2).

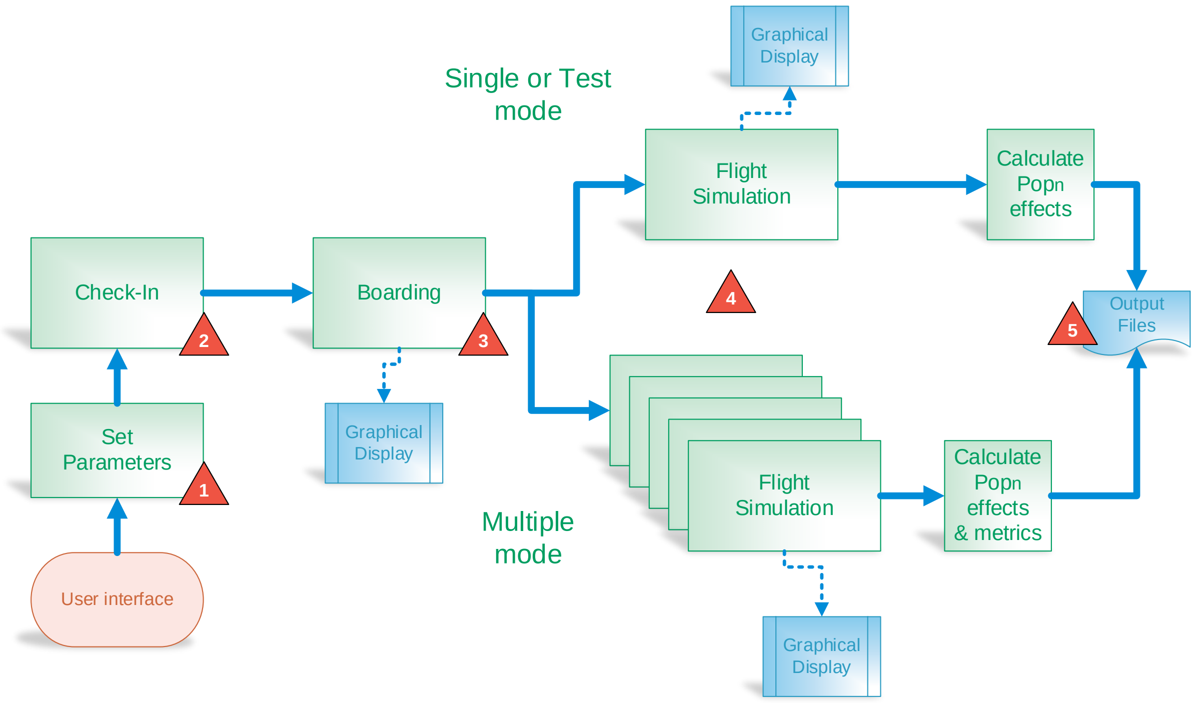


Figure 1-4 Diagram outlining the phases followed in a full simulation run for SeabORD version 1.0

4. Once all the input datasets are loaded, the flight simulations can start. SeabORD v1.2 has two modes.
    a. In single mode the model simulates one breeding season and the user can manually create 'matched pairs' of runs (with and without ORDs). This mode is intended for testing purposes only and the output metrics should not be considered to be robust estimates of ORD effects. It is only after **multiple** paired simulations have been run that stochastic variation between runs can be properly accounted for and appropriate assessments of output uncertainty provided. Therefore, output from single mode is restricted to showing changes in adult mass and chick survival with and without ORDs present. Final metrics (i1-i6) are not presented.
    b. In 'multiple mode' the model simulates a number of matched pairs of runs (with and without ORDs) to allow for assessments of uncertainty in model outputs for ORD effects (provided by 95% prediction intervals for each metric). Each paired run uses a different random number seed resulting in variation in bird locations, stochastic decisions and energetic consequences across paired model runs. Output from all paired runs is then used to provide a single estimate for the

impact of ORDs with uncertainty. Based on testing of the prototype tool for each species in the Forth-Tay region we strongly recommend running between 10 and 50 paired runs to properly assess uncertainty in impact assessments.

5. The final stage (*Landing*) of the model run involves calculating the metrics assessing ORD impacts and writing output files.

1.4 Versions

The first released version of SeabORD was v1.0.

Changes between v1.1 and v1.2 –

- Changes to the median regional prey level input and matched pair runs. In v1.1 the user entered one value for the median prey and every season in the run (single or multiple mode) used the same value. In v1.2 the user supplies and upper and lower bound value for the median prey. Each simulated season uses a random value chosen from between these two bounds. See accompanying Final Report for a full explanation for this change.
- Execution speed will be faster when setting up a new region. Generating the shortest flight path from colony to foraging area and back can be a time-consuming process. In v1.1 the flight paths for all possible forage sites (within the specified region) were generated at the beginning of a model run. The flightpaths were saved in a data file for use in subsequent simulations meaning they only had to be generated once. In v1.2, to make execution time more efficient, the flightpaths are generated only when first needed. For larger regions this greatly reduces the number of flight path calculations during simulations but, as the paths are saved in the same way, they are still available for later simulations. Thus the more the model is used, the faster the execution time will be during the flightpath generation stage. With this change, the 'zone with ORDs' images can be difficult to interpret as some paths will not have been calculated leaving gaps in the map.
- Improvements to the way user-supplied input data files are handled (prey distribution and bird distribution files)

Changes between v1.0 and v1.1 –

- Improvements to the output spreadsheet layout
- Graphical interface changed to remove the prey level selection dial. Corresponding code changes to provide output metrics for poor, moderate and good conditions.

2 Setting up a simulation run

2.1 Launching the model

During installation the SeabORD installer will have added an icon to the desktop (if this option was ticked). Double-click this to launch the interface. Note that there can be a short delay before the interface pops up on the screen, particularly the first time it is opened.

Before the flight simulation can be carried out, a 'check-in' process is needed to specify the parameters for the run. Launching the model opens the check-in window (see Figure 2-1).

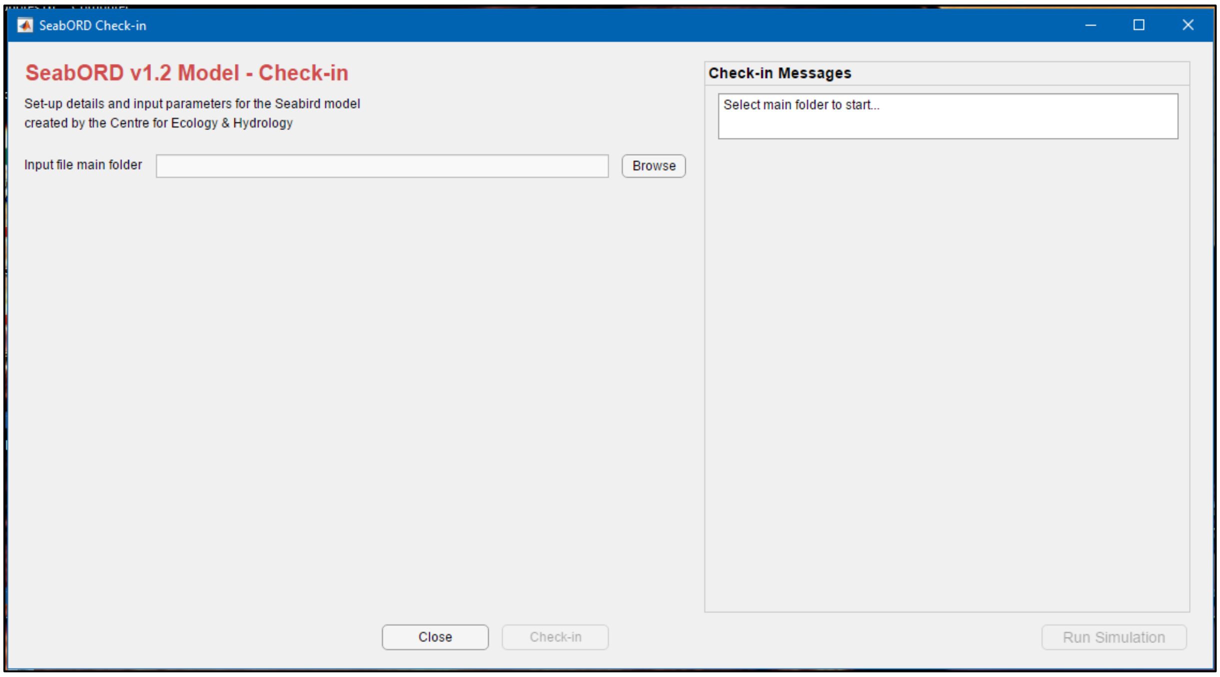


Figure 2-1 The main check-in window for SeabORD

Use the Close button to remove the check-in window. It will not close while a flight simulation is running but can be minimised in the usual way.

2.2 Main folder

The first task is to identify the folder within which SeabORD can locate input files and write output files. This can be any folder; it can contain other files and folders but a copy of the supplied data folder must be placed within it. Use the Browse button to navigate to and select the chosen folder. (Note: do not select the data folder itself, but the one above it!). In this guide, the main folder will be referred to as *<$mainfolder>* in the text to indicate the exact text is user-defined.

*(Note: Using **Windows 10,** the file browser pop-up window does not always appear on screen and other buttons cannot be clicked. If this happens, look for the SeabORD icon in the task bar at the foot of the desktop and click it – this will activate the file browser window which will have opened normally but is hidden.)*

After the main folder is selected, the check-in window will show six tabs; Colony, Species, ORDs, Prey, Additional Information and Simulation (see Figure 2-2). Each tab must be completed with the appropriate information to execute a flight simulation run.

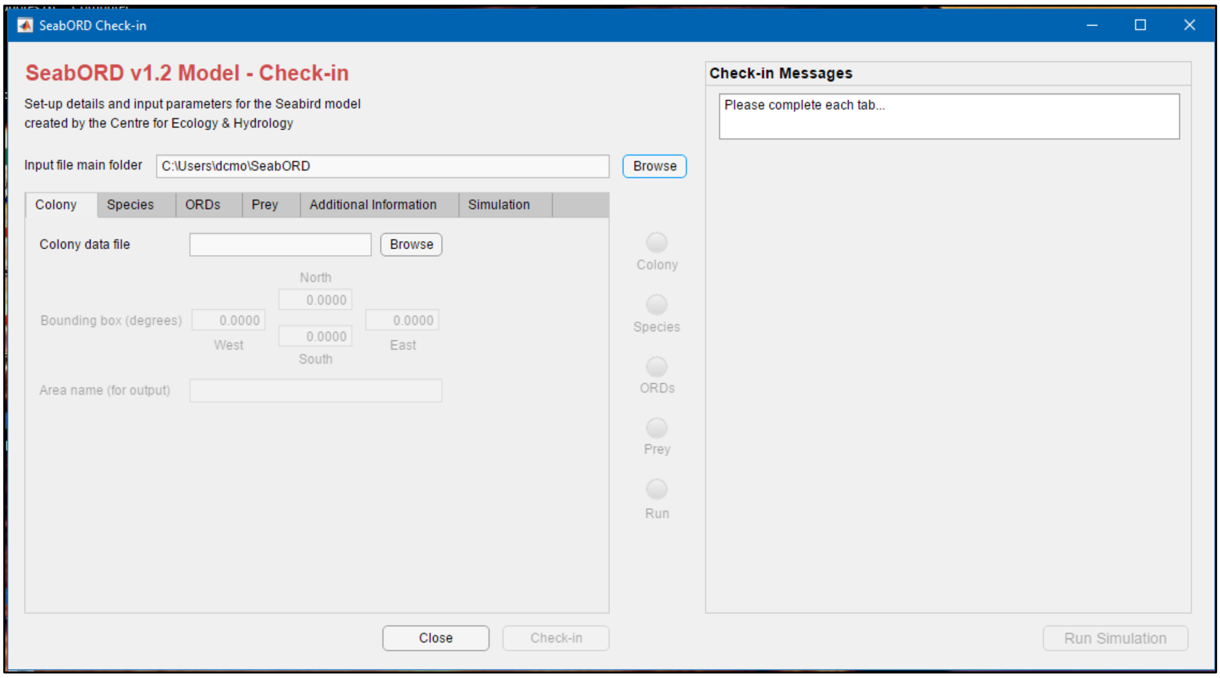


Figure 2-2 The Check-in window guides the user through setting up the model in preparation for the flight simulation.

2.3 Colony Tab

Use the Browse button to locate and open a spreadsheet with your chosen colony location information. The location file should be placed in <$mainfolder>\data\Colonies. The supplied data file, 'Forth and Tay.xlsx', can be used as a template for new regions.

Colonies are represented by a single point. For linear colonies that extend along a coastline users should choose a suitable central point.

The format to be followed is illustrated in Figure 2-3:

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Region name:	Forth and Tay											
2	North limit (degrees)	58.9634											
3	South limit (degrees)	54.5704											
4	East limit (degrees)	1.0387											
5	West limit (degrees)	-4.113											
6													
7	**Colony**	**SPA**	**Other**	**code**	**Geometry**	**Easting**	**Northing**	**long**	**lat**	**GuObsNpairs**	**RzObsNpairs**	**KwObsNpairs**	**PuObsNpairs**
8	Boddam to Collieston	Buchan Ness to Collieston Coast	Boddam	bod	Point	412006.8356	838103.4918	-1.8000	57.4333	17753	0	12542	0
9	Fowlsheugh	Fowlsheugh	Fowlsheugh	fow	Point	387956.7362	780859.5398	-2.1978	56.9191	37277	4883	9388	0
10	Isle of May	Forth Islands	IsleOfMay	iom	Point	365447.9042	699094.6061	-2.5567	56.1833	19891	3467	3766	52291
11	St Abb's Head	St Abbs to Fast Castle	StAbbsHead	sta	Point	391020.8046	669392.9523	-2.1437	55.9251	29079	1262	4314	0
12													
13													

Figure 2-3 Screenshot showing an example of a colony file

Column B, rows 1 to 5 give the location reference name (which is used to create folders to store data files – alpha-numeric characters only) and the north, south, east and west bounding box degrees in decimal format.

Row 7 is interpreted as variable names and should be in the following order:

- **Colony** full name – for reference only
- **SPA** – for reference only, can be left blank
- **Other** – this is the name of the colony that is used in any user-supplied data files. Data acquired from different sources, such as bird density data, may use alternative names for colonies. Text in this column will be used to read data from user-defined files. This could be the same as the three letter identifier ('code') used throughout SeabORD.
- **code** – a three letter identifier for the colony which has to be unique because it will be used throughout the model code to identify birds with their respective colonies.
- **Geometry** – for colonies this must be a point location given as latitude and longitude (WGS84) in the next columns
- **long** – the longitude in decimal format identifying the colony central point
- **lat** – the latitude in decimal format identifying the colony central point
- **GuObsNpairs** – the observed number of pairs of guillemots at this colony
- **RzObsNpairs** - the observed number of pairs of razorbills at this colony
- **KwObsNpairs** - the observed number of pairs of kittiwakes at this colony
- **PuObsNpairs** - the observed number of pairs of puffins at this colony

Rows 8 to 13 contain the data for each colony, one colony per row. The observed number of pairs should be entered as 0 if unknown or if the species is not present (i.e., it cannot be left blank).

Note that this file and the stated observed number of pairs is a record for the region as a starting point for the tool (in this example, Forth and Tay) and does not need to be changed unless new information is available. The actual species used and the number of pairs (fraction of the population) simulated is selected in the interface before each individual run of the model.

As soon as the file is selected, the data will be imported by SeabORD and listed on the Colony tab. Each colony has a switch allowing the user to choose to run the model with one or more colonies. Switching off colonies where a breeding colony for the relevant species exists should only be used for test runs – this is because turning off a colony alters the competition effects for foraging individuals from other colonies by changing the bird density in the area meaning estimates of ORD impacts may be reduced, and results cannot be compared to runs in which all colonies are simulated.

Note that the point location for the colony must not be inland, but on the coast. The model includes coastline data (see Appendix 1.) and if the colony point is positioned on land (inside the coastline polygon) the flightpath-finding routines will give unpredictable results because some routines count the number of times a bird crosses the coastline on a particular route option. If this happens, move the colony point a few metres further out to sea. Users can check colony positioning in relation to the coastline within the model by using GIS software to map the SeabORD coastline data and colony point locations outwith the tool.

In the current version of the model interface, a maximum of six colonies can be included per run. This is a limitation of the graphical user interface not the underlying model; in the current version (SeabORD v1.2) information added below row 13 will be ignored.

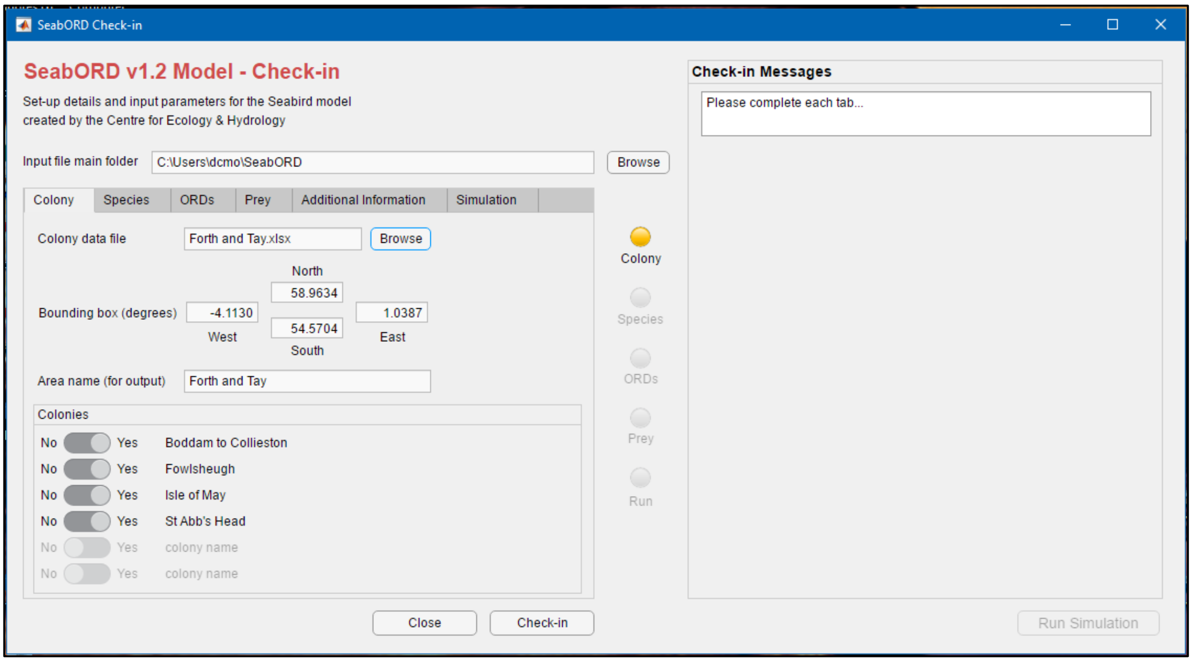


Figure 2-4 After the Colony data file is selected, the file is imported and the details listed on the Colony tab.

The Colony ‘lamp’ will turn amber to indicate some variables have been set.

2.4 The Seabirds

The Species tab is used to specify the species, the fraction of the population that is susceptible to displacement and barrier effects, the foraging distribution (forage site selection) and the type of flightpath-finding method to use.

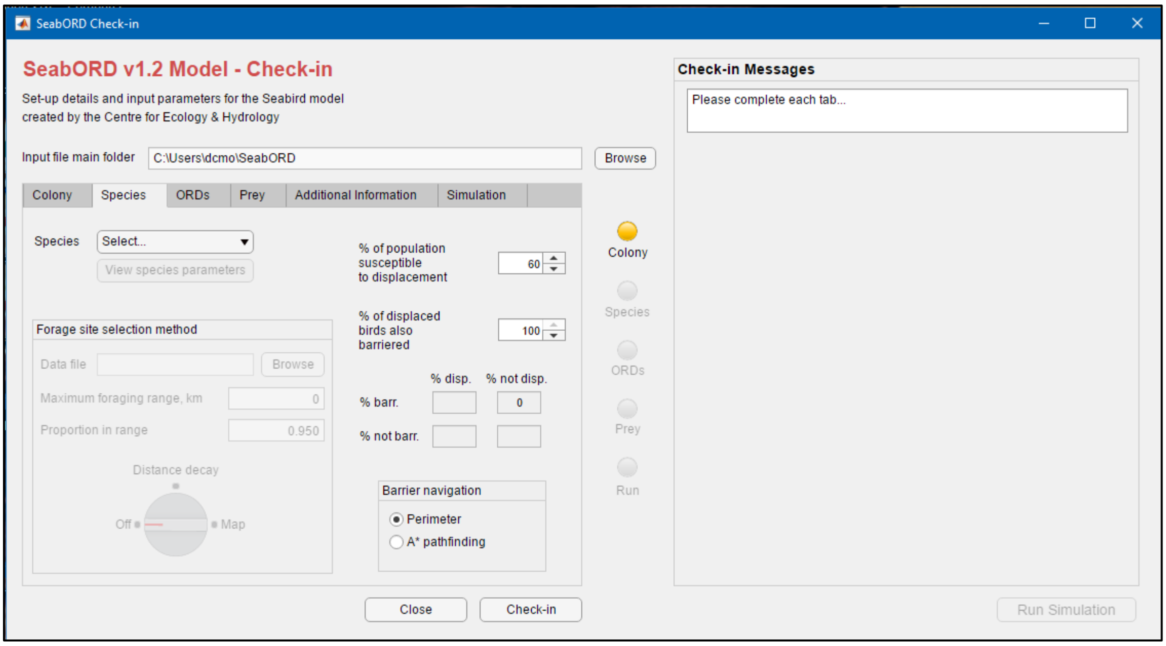
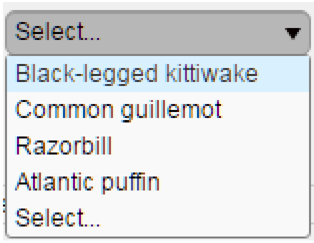


Figure 2-5 The Species tab enables the user to set parameters affecting the bird species used, the behaviour of the birds when selecting foraging locations and how they respond to encountering an offshore renewable development in their intended flight path.

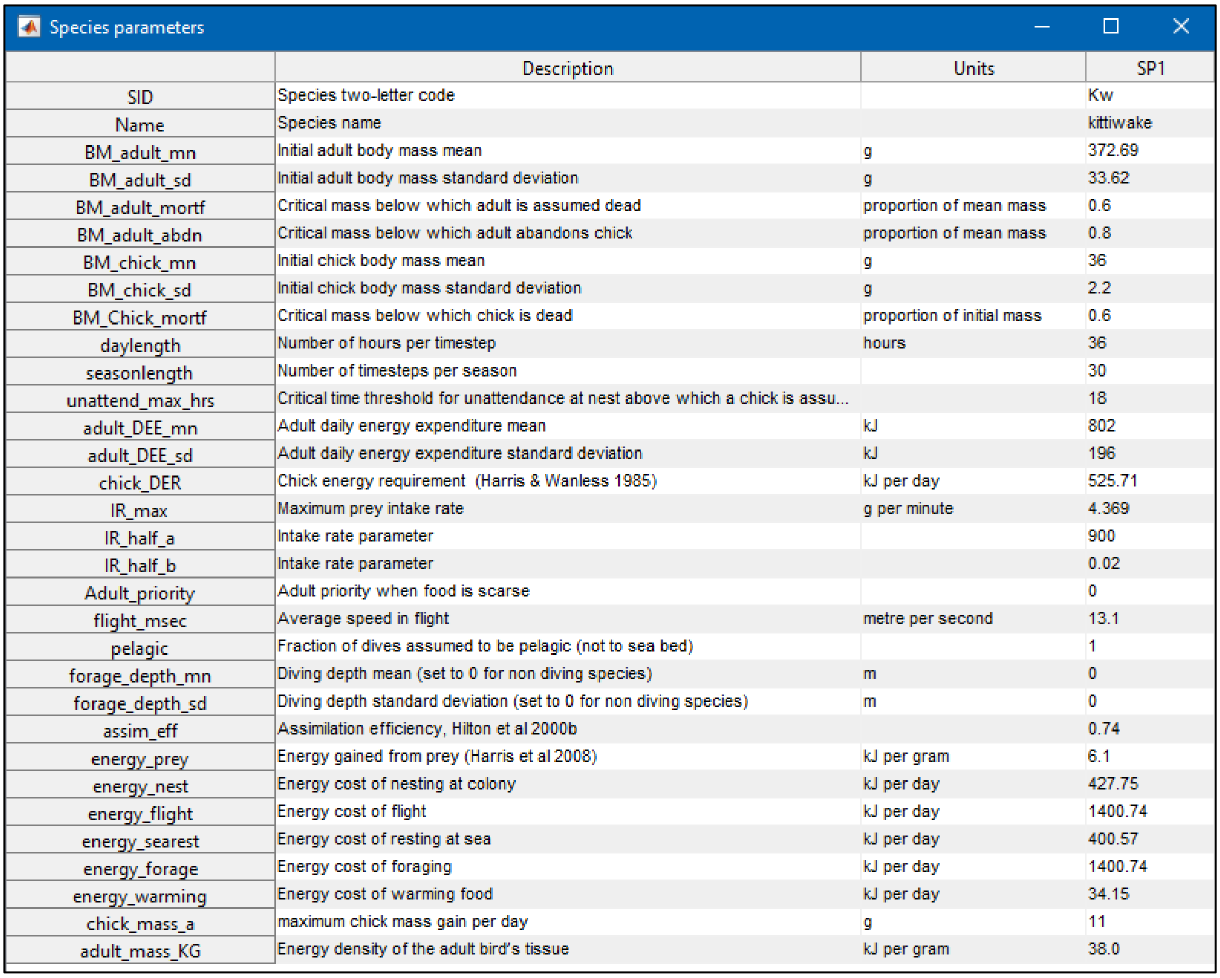
The Species ‘lamp’ will turn amber to indicate some variables have been set.

2.5 Species

The Species ‘drop-down’ offers the user a choice between four species; Black-legged kittiwake, Common guillemot, Razorbill and Atlantic puffin.



Making a selection activates other controls including the Forage site selection panel and a ‘View species parameters’ button. The latter opens a pop-up window that can be resized as required to view the fixed parameters for the chosen species (see Figure 2-6). See associated report (Searle, et al. 2017) for a discussion of the sources for these parameters and their use in model processes.



Species parameters

	Description	Units	SP1
SID	Species two-letter code		Kw
Name	Species name		kittiwake
BM_adult_mn	Initial adult body mass mean	g	372.69
BM_adult_sd	Initial adult body mass standard deviation	g	33.62
BM_adult_mortf	Critical mass below which adult is assumed dead	proportion of mean mass	0.6
BM_adult_abdn	Critical mass below which adult abandons chick	proportion of mean mass	0.8
BM_chick_mn	Initial chick body mass mean	g	36
BM_chick_sd	Initial chick body mass standard deviation	g	2.2
BM_Chick_mortf	Critical mass below which chick is dead	proportion of initial mass	0.6
daylength	Number of hours per timestep	hours	36
seasonlength	Number of timesteps per season		30
unattend_max_hrs	Critical time threshold for unattendance at nest above which a chick is assu...		18
adult_DEE_mn	Adult daily energy expenditure mean	kJ	802
adult_DEE_sd	Adult daily energy expenditure standard deviation	kJ	196
chick_DER	Chick energy requirement (Harris & Wanless 1985)	kJ per day	525.71
IR_max	Maximum prey intake rate	g per minute	4.369
IR_half_a	Intake rate parameter		900
IR_half_b	Intake rate parameter		0.02
Adult_priority	Adult priority when food is scarse		0
flight_msec	Average speed in flight	metre per second	13.1
pelagic	Fraction of dives assumed to be pelagic (not to sea bed)		1
forage_depth_mn	Diving depth mean (set to 0 for non diving species)	m	0
forage_depth_sd	Diving depth standard deviation (set to 0 for non diving species)	m	0
assim_eff	Assimilation efficiency, Hilton et al 2000b		0.74
energy_prey	Energy gained from prey (Harris et al 2008)	kJ per gram	6.1
energy_nest	Energy cost of nesting at colony	kJ per day	427.75
energy_flight	Energy cost of flight	kJ per day	1400.74
energy_searest	Energy cost of resting at sea	kJ per day	400.57
energy_forage	Energy cost of foraging	kJ per day	1400.74
energy_warming	Energy cost of warming food	kJ per day	34.15
chick_mass_a	maximum chick mass gain per day	g	11
adult_mass_KG	Energy density of the adult bird’s tissue	kJ per gram	38.0

Figure 2-6 The fixed species parameters can be viewed using the ‘View species parameters’ button. Columns can be resized as needed.

2.5.1 Displacement & barrier behaviour

There are two parameters that can be set to define the ORD-related behaviour of simulated birds. The first sets the percentage of the population that are susceptible to displacement: all individuals that are displacement-susceptible will be displaced to an alternative nearby foraging location if their preferred foraging location is within an ORD.

The second parameter sets the percentage of displacement-susceptible birds that are also susceptible to barrier effects. All barrier-susceptible birds will navigate around an ORD if their foraging location lies beyond it (see associated report for more details).

If a tidal array is to be simulated the user must ensure barrier percentages are set to zero since birds in flight are not expected to navigate around a tidal array, unlike a wind farm.

Figure 2-7 Displacement- and barrier-susceptibility settings

The values can be changed using the 'spinner' arrows to the right of the box or by manually editing the numbers.

To clarify how these parameters work, the interface displays the population break-down into the three possible groups (it is not feasible for a bird to be barrier-susceptible but not displacement-susceptible because it is not considered plausible that a bird will be willing to forage in a wind farm, but not fly through it; as such, barrier-susceptible birds must always be displaced from foraging in an ORD footprint). If these display boxes are empty, change the parameters to force a recalculation (see Figure 2-7).

2.5.2 Forage site selection method

The dial on the Species tab is used to specify the method for forage site selection as follows.

2.5.2.1 Off

The default option is 'off' indicating the site selection method has not been chosen. The model will not run with the dial in this position. If the bird species is changed, the dial returns to the 'off' position to ensure the filename and other settings are reset correctly.

2.5.2.2 Distance decay

If "distance decay" is selected, two parameters are required: a foraging range (in km), and a proportion (0-1) of the population whose foraging locations are assumed to fall within this range.

If it is known from existing data, for example, that birds spend 50% of their time foraging within 20km of the colony, then we can specify the foraging range parameter to be 20km and the proportion to be 0.5. These input parameters are used to determine the rate at which the density of foraging birds declines in relation to distance from colony.

Note that we only recommend using the distance decay option it situations where "Map" inputs (derived from GPS data) are unavailable: if it is possible to use the "Map" option then we would always recommend doing this in preference to using the "Distance decay" option.

It is up to the user to select a suitable value for these parameters such that the resulting bird density map matches expectations for how density of foraging birds decreases with distance from the focal colony. For kittiwakes in the Forth-Tay region we estimate this parameter to be 0.995, based on a visual comparison with the foraging densities estimated from limited GPS tracking data for this species on the Forth Islands. These estimates may be applied in other locations, but we caution that users should visually inspect the resulting bird density maps in new locations and assess the extent to which they agree with an understanding of bird usage in the area.

2.5.2.3 Map

If 'Map' is selected, the data file field become active. Choose an appropriate data file using the browse button. This will be a comma separated values (csv) file containing the bird density for each grid cell that will be used for foraging. Note that no error checking is carried out – SeabORD v1.2 assumes that the chosen data file contains only data for the correct species and location, but the file can contain data for many colonies. The format is described below.

Example files are located in <$mainfolder>\data\Colonies\<region> where region is 'Forth and Tay' (see section 2.3 to set the Region). These example files are named <species>_birddensity.csv (but user-supplied files can have any name).

When the 'map' option is selected the user must supply a simple comma separated values (csv) file with the following rows and columns:

- The first line is a single row header with names 'Site, Longitude, Latitude, Var1'
- A row for each valid grid cell with four comma separated values giving the colony name, the coordinates of the grid and a variable specifying the relative density. All colonies should be given in a single file for a given region.

```
Site,Longitude,Latitude,Var1
IsleOfMay,-1.153717906,56.12087207,-1.683700732
IsleOfMay,-1.145381794,56.12087207,-1.70121837
IsleOfMay,-1.137045682,56.12087207,-1.718287124
IsleOfMay,-1.12870957,56.12087207,-1.734860235
IsleOfMay,-1.120373458,56.12087207,-1.750887523
--
```

The model assumes that the 'Var1' column contains an estimate, on a natural log scale (ln), for the relative density of birds from the colony of interest at each location in space. The relative density values do not necessarily need to have been scaled to sum to one, although if they have been (prior to log transformation) this is fine. There is no restriction regarding the methodology that was used to calculate the relative density values, or the nature of the raw data that they may have been estimated from - in particular, they may either have been estimated using local data from the colony of interest, or using a predictive map of densities for birds originating from the colony of interest (such as those developed by (Wakefield, et al., in review)). The assumption is that the values contained in 'Var1' can be converted into UD (utilisation distribution) values through the calculation:

Density = exp(Var1)

Normalised Density = Density/sum(Density)

The value of the Normalised Density at a particular location can also be regarded as the probability that a randomly selected bird will be at that location.

We have provided 'map' files for species with local GPS data (Forth-Tay: guillemot, kittiwake, razorbill, puffin).

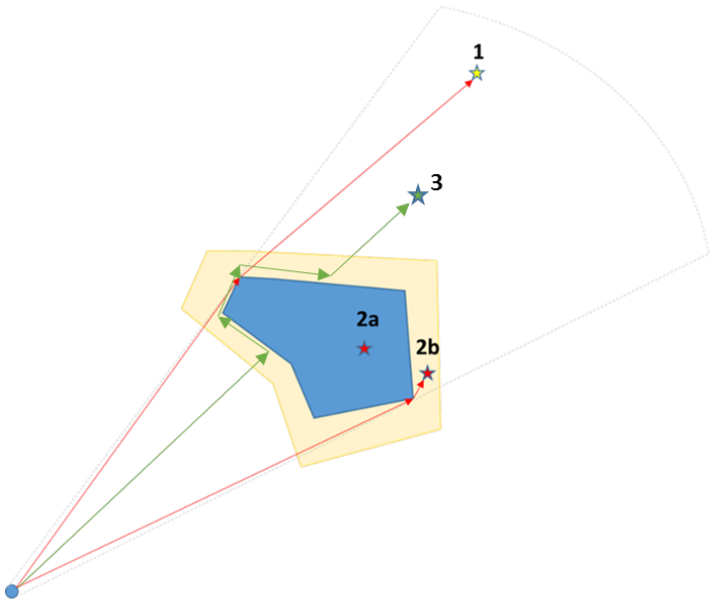
The supplied latitude and longitude values do not have to match exactly with the grid specified within SeabORD (see Appendix 3.), the data points will be encoded onto the regular grid.

At the start of a model run SeabORD selects all the forage locations for the season for each bird, using the random number specified (see Figure 2-13). Note that for 100,000 birds this can take up to one hour the first time it is required. For a given seed the selected sites will be saved in a file for future use but will be recalculated for each new random number seed.

2.5.3 Barrier navigation method

During the flight simulation, if a bird encounters an ORD and is barrier-susceptible it will navigate around the obstruction. SeabORD v1.2 includes two alternative options for this; perimeter and A* pathfinding (see Appendix 2.).

When 'Perimeter' barrier navigation is selected a bird flying from the colony (lower left, Figure 2-8) will follow the green path (e.g. to 3) only diverting from a direct straight line path when it encounters the windfarm. If 'A* pathfinding' barrier navigation is selected it will follow the red route (e.g. to 1), which is the shortest possible path. These two options represent extremes for paths followed by birds in flight encountering a barrier.



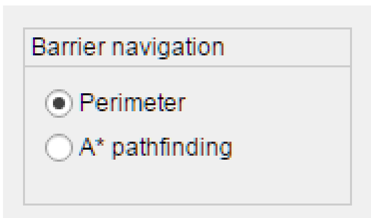


Figure 2-8 If a bird (starting from the colony lower left) selects location 1 or 3 and is barrier-susceptible it has to navigate around the windfarm.

The pathfinding routines can be computationally intensive and take some time to execute. However, as the path only has to be calculated once for a given region and colony (all species are assumed to follow the same path), SeabORD v1.2 will save any calculated path to use in later simulation runs. Thus when a simulation is carried out at a new location or for a new ORD it will be slow for the first attempt but then get considerably faster on each subsequent run.

Both flight path options use the basic ORD footprint (specified in the shapefile, see Section 2.6.1) plus a border to control where the birds will fly. The birds always fly around the border thus if this is increased the birds avoid the ORD leaving a wider exclusion zone.

Flightpaths from every colony to every grid square selected in a given season are first calculated assuming no ORD obstructions but with birds navigating around the coast. This always uses the A* method. Precalculated paths are supplied for 'Forth and Tay'. The files are named consistently, for example, the file for the Isle of May colony ('iom') will be

<$mainfolder>\data\Flightpaths\Forth and Tay\Waypoints_iom_526_617.mat

(where 526_617 identifies the size of the gridded area in this region).

When the ORDs are added into the simulation a second set of flight paths must be calculated depending on the barrier type, the border size and the location of the ORDs. The files for these are stored as, for example

<$mainfolder>\data\Flightpaths\Forth and Tay\WFPerimeter_iom_526_617_WFA_WFC_500.mat

<$mainfolder>\data\Flightpaths\Forth and Tay\WFwaypoints_iom_526_617_WFA_500.mat

where '500' indicates a 500m border. Note that SeabORD v1.2 will always use the paths in these files if it finds one with the expected name. Thus if an ORD is changed (but the name stays the same) the user will need to manually delete or move the old files to force a new set of paths to be generated. These files will increase in size every time a simulation run is carried out until the path to every possible forage location has been found.

2.6 Offshore renewable developments

The location and shape of each offshore renewable development is specified in a similar way to the bird colonies. There is a simple spreadsheet located in the <$mainfolder>\data\Windfarm folder. When this file is selected in the graphical interface, it is loaded immediately and the contents used to populate the ORDs tab.

The ORDs 'lamp' will turn amber to indicate some variables have been set.

2.6.1 Selecting existing ORDs

The ORD specification file has four columns. The first row gives the column names which are Windfarm, Region, code and Shapefile (see Figure 2-9).

- Windfarm – a reference name
- Region – a note of the appropriate region (which must match the name given in the colony file, see Figure 2-3)
- code – a three-letter name for the ORD (used in data files)

- ShapeFile – the name of the shapefile that contains the footprint polygon coordinates (without the file extension).

	A	B	C	D	E
1	**Windfarm**	**Region**	**code**	**ShapeFile**	
2	WFA	Forth and Tay	WFA	WFA_WGS84	
3	WFB	Forth and Tay	WFB	WFB_WGS84	
4	WFC	Forth and Tay	WFC	WFC_WGS84	
5					
6					
7					

Figure 2-9 Screenshot showing the layout of the ORD specification file.

The shapefiles are located in the <$mainfolder>\data\Windfarm folder. SeabORD v1.2 expects there to be one closed polygon per shapefile, using the WGS84 coordinate system. If more than one polygon is found, only the first is used.

This version of SeabORD does not have an option to flag directly if an individual ORD is a windfarm, tidal array or other type of ORD. The difference must be enacted by setting the displacement and barrier effects appropriately (see Section 2.5.1). For example, for a tidal array, the barrier effects must be set to zero. This applies to all ORDs identified in a given run. Therefore, only multiple wind farms (with barrier effects) or multiple tidal arrays (with no barrier effects) may be simulated. It is not currently possible to simulate combinations of wind farms and tidal arrays.

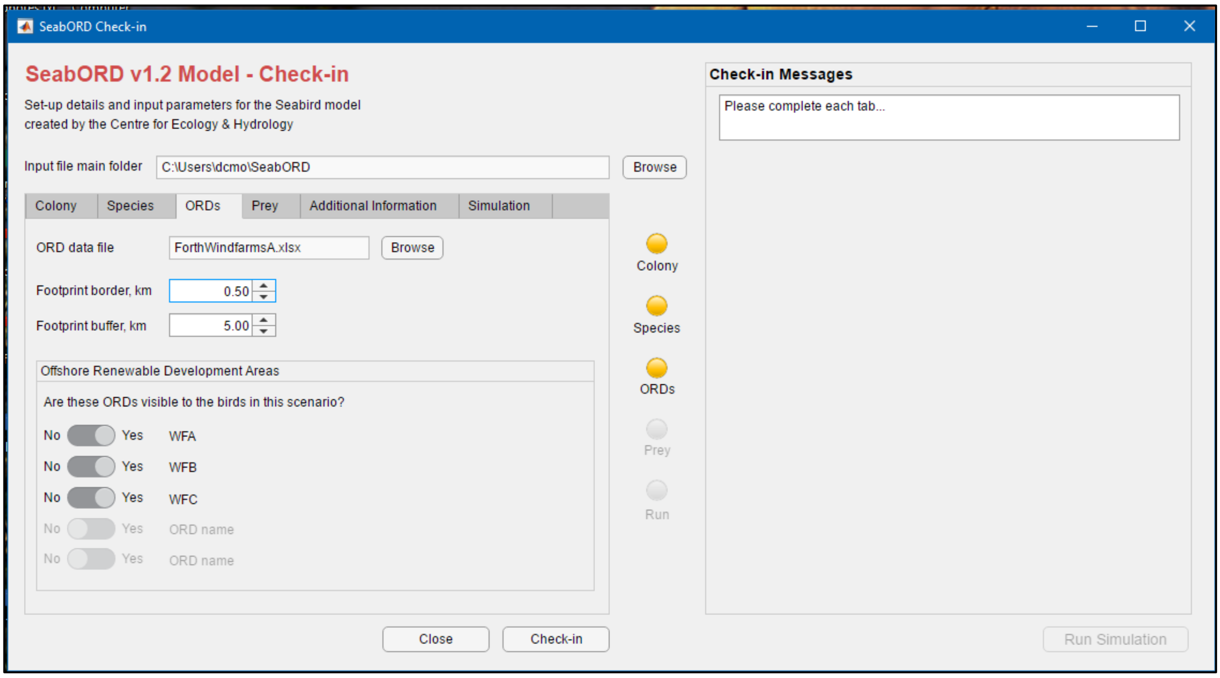


Figure 2-10 The ORDs tab displays the information about the offshore renewable developments in this region.

In the current version of the model interface, a maximum of five ORDs can be included per run. This is a limitation of the graphical user interface not the underlying model but in the current version (SeabORD v1.2) information added below row 6 of the data file will be ignored.

Individual ORDs can be switched on or off to indicate if they are 'visible' to the birds or not for the flight simulation. If all the ORDs are switched to 'off' then the birds are unaffected by them but their location is known so that an 'at-sea survey' can be carried out (see Section 2.9). All single 'baseline' runs should be simulated with ORDs switched off so that birds are unaffected by them. These baseline runs then form the first part of a paired run where population estimates for adult survival and breeding success are made in the absence of ORDs (e.g., pre-construction). Snapshot at-sea surveys should only be simulated when all ORDs are turned off as they are intended to represent pre-construction estimates of bird use within ORD footprints (see Section 2.8 and associated report for more explanation).

The footprint border and buffer, both in kilometres, can be changed using the 'spinner' arrows or by editing the value manually.

Note that changing the border will affect the flightpaths and will trigger a new set of input files to be generated – this can take a long time (e.g., several hours, particularly in areas with complicated coastlines and/or many islands).

The buffer zone describes the area around the ORD into which birds will be displaced to forage. Changing the buffer width will not affect the flightpaths for birds but will affect competition by changing the density of birds foraging within the buffer.

See associated report for more discussion on how the 'border' and 'buffer' are used within the model simulations.

Users should note that SeabORD v1.2 requires ORD files to be specified even in 'baseline' runs with no 'visible' ORDs. This is necessary to allow correct matching to an ORD run and to enable a potential snapshot at-sea surveys to be run during baseline 'pre-construction' scenarios (see Section 2.8).

2.6.2 Adding new ORDs

To add a new ORD, first create a shapefile using GIS software that can output shapefiles. SeabORD v1.2 expects there to be one closed polygon per shapefile, using the WGS84 coordinate system.

Next, add the name of the shapefile and a suitable, short unique name for the ORD into a spreadsheet as described in Section 2.6.1.

The shapefile should include only a polygon for the basic footprint. A border is automatically added around the footprint using the distance specified in the 'footprint border' box on the ORD tab.

2.7 Prey availability

The Prey tab has a dial to set the preferred forage availability for the simulation. The dial will initially be set to 'off' and the model will not run until another option is selected (Figure 2-11).

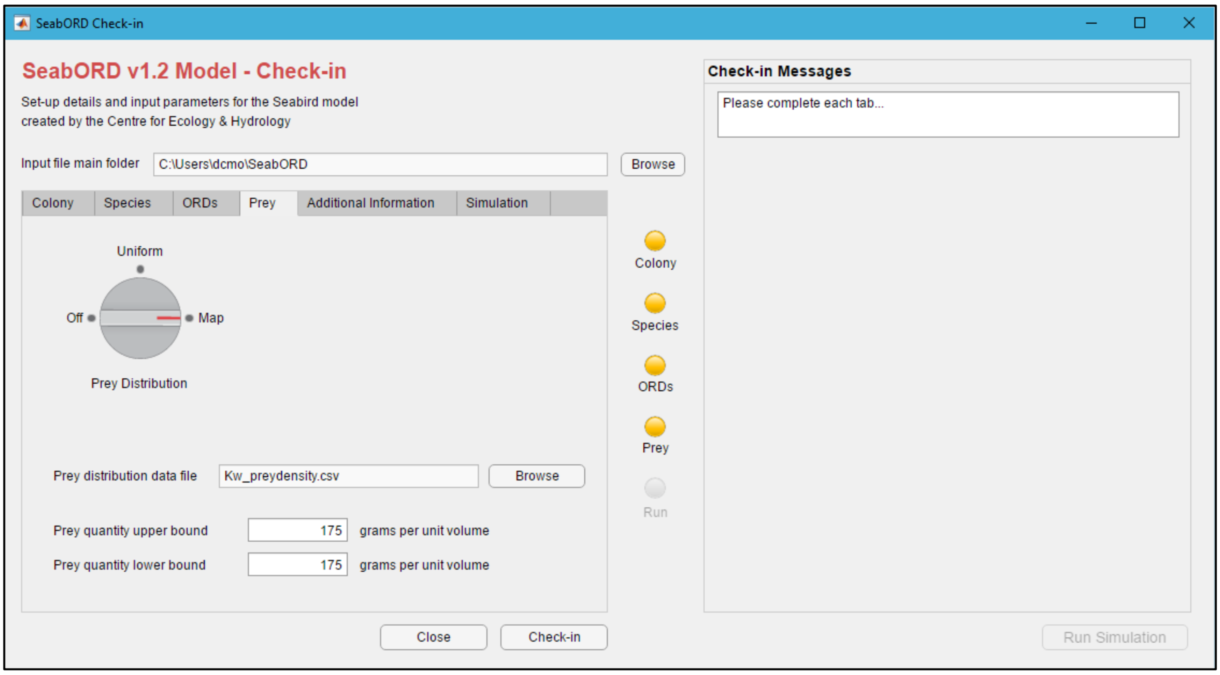


Figure 2-11 The Prey tab is used to set the prey availability

We recommend that when using a new region users first complete baseline runs with a range of values to assess how the specified median prey densities affect adult mass change and chick survival when no ORDs are present. It is important to note that depending on the prey level selected, a different baseline adult survival parameter will be used within the calculation of the final wind farm effect (additional mortality due to the ORD). Therefore, users must be very careful to ensure the prey amount selected in the tool represents the scenario they wish to run (poor, moderate or good prey conditions), or alternative values that can be justified from locally available data. This can be checked by examining the output from a baseline run for a given prey value where for each colony it will be indicated if the prey conditions represented a good, moderate or poor run.

We have provided mapped prey for the case study region (Forth-Tay). The parameter within SeabORD used to define the total prey availability (grams/per unit foraging volume) must be adjusted (see Project final report). We have made this adjustment for the maps included with SeabORD in the two case study regions, however it is likely that should a new prey map be used within the model, a new adjustment may need to be made.

When a new prey map is used in place of those provided, we recommend that users first complete a set of baseline runs with a range of prey values to assess how well model results match those in Table 2-1 below, or alternative values that can be justified from locally available data. If model results do not match well, users will need to adjust these values accordingly until suitable output from the baseline run is achieved.

Upper and lower boundaries for 'moderate' regional prey conditions are set by comparing model output in baseline runs (no ORDs present) for the change in adult mass (percent) and the nest or chick mortality (percent). Using empirical data (Harris (1979); Harris & Wanless (1988); Gaston & Hipfner (2006); Nelson (2013); Newell et al. (2016)) we identified percent adult mass loss over the course of the chick-rearing season and nest survival rates (for kittiwakes) or chick survival rates (for auks) that reflect those observed during 'moderate' environmental conditions (Table 2-1). Because adult mass loss (%) is the most reliable model output (less variable than chick survival) and of primary interest to population trends in long-lived species such as seabirds, because of its influence on over-wintering survival probability of adults (Oro & Furness 2002; Erikstad et al. 2009), we base the upper bound for moderate conditions solely using changes in adult mass loss. The lower bound is set using both adult mass loss and chick/nest survival (Table 2-1). If, however, chick or nest survival should fall below the 5th percentile observed in empirical data before the adult mass loss lower bound is reached, we consider that corresponding regional prey value to represent the lower bound of moderate conditions for that species. For instance, in black-legged kittiwakes, if at the end of a baseline run adult mass loss was 8% but nest survival was 10%, this would be classed as 'poor' conditions.

Table 2-1. Conditions used to set upper and lower boundaries for the median regional prey value corresponding to 'moderate' conditions for each species.

	Percent adult mass loss		**Chick/nest survival**
	Upper bound	**Lower bound**	**Lower bound**
Black-legged kittiwake	5	15	11
Common guillemot	3.5	10.5	49
Razorbill	3.5	10.5	50
Atlantic Puffin	3.5	10.5	50

2.7.1 Uniform

If the Prey Distribution dial is turned to 'Uniform', prey availability will be set at a constant initial value for all forage locations, specified in the Prey quantity boxes. If the upper and lower bounds are set to the same value, the value is used for every run in a 'multiple' paired run simulation. If the upper and lower bounds are set to different values (upper must be higher than lower) then a random value is chosen to be used for a given matched pair using stratified sampling (see Final Report for a full explanation of this method). In a 'multiple' run with 10 matched pairs, 10 values will be chosen using stratified random sampling between the upper and lower values.

2.7.2 Map

When 'Map' is selected prey availability data are imported from a comma separated values (csv) file. The file name box becomes active and the browse button enables the user to locate and select an appropriate file.

SeabORD v1.2 will search in the folder <$mainfolder>\data\Prey\<region>\ so any new data files should be placed there.

The file can have any name but the format of the content must be as follows

- The first line is a single row header with names 'Site, Longitude, Latitude, Var1'
- The subsequent rows contain four variables separated by commas giving the colony name, the coordinates of the grid and a variable specifying the relative prey availability.

All colonies should be given in a single file for a given region. If the file has holds a combined regional map, the first column should be any one of the colony names.

For example

```
Site,Longitude,Latitude,Var1
Fowlsheugh,-2.15405135,58.44661751,0.051665969
Fowlsheugh,-2.145715238,58.44661751,0.12845348
Fowlsheugh,-2.137379126,58.44661751,0.202554878
IsleOfMay,-1.312104035,54.82879128,-14.23060741
IsleOfMay,-1.303767923,54.82879128,-14.28225972
IsleOfMay,-1.320440147,54.83712728,-13.98762559
…
```

The value, Var1, is processed in two stages to create the input required for the model. The 'raw' data are imported and normalised for each colony (the resulting 'Var1' sums to one for all grid squares visited by the birds from a given colony). If there are any grid squares used by more than one colony, the mean value is used. The normalised values are then categorised into a number of 'bins' and the values adjusted so that the specified prey value is the median value. The relative distribution of prey is the same in each case, as given in the input file, but the actual value is adjusted to be consistent with the species parameters.

The supplied latitude and longitude values do not have to match exactly with the grid specified within SeabORD (see Appendix 3.), the data points will be encoded onto the regular grid.

2.8 Additional information

2.8.1 Population Size

The Additional Information tab (Figure 2-12) includes a box where the number of birds in the simulation can be adjusted during testing. The actual (maximum) number of pairs of birds in the full population is defined in an input file as described above (Section 2.3). The fraction of population specified here is applied as a simple multiplier of those numbers.

Model outputs are relatively insensitive to how large a fraction of the total population size is run. In 'test' mode it is useful to be able to run only a fraction of the population (e.g., to simulate around 1000 individuals) rather than the entire population to check initial output more rapidly. However, in 'multiple' or 'batch' model we recommend that as large a fraction of the population as computationally feasible is simulated because this ensures that uncertainty is quantified correctly.

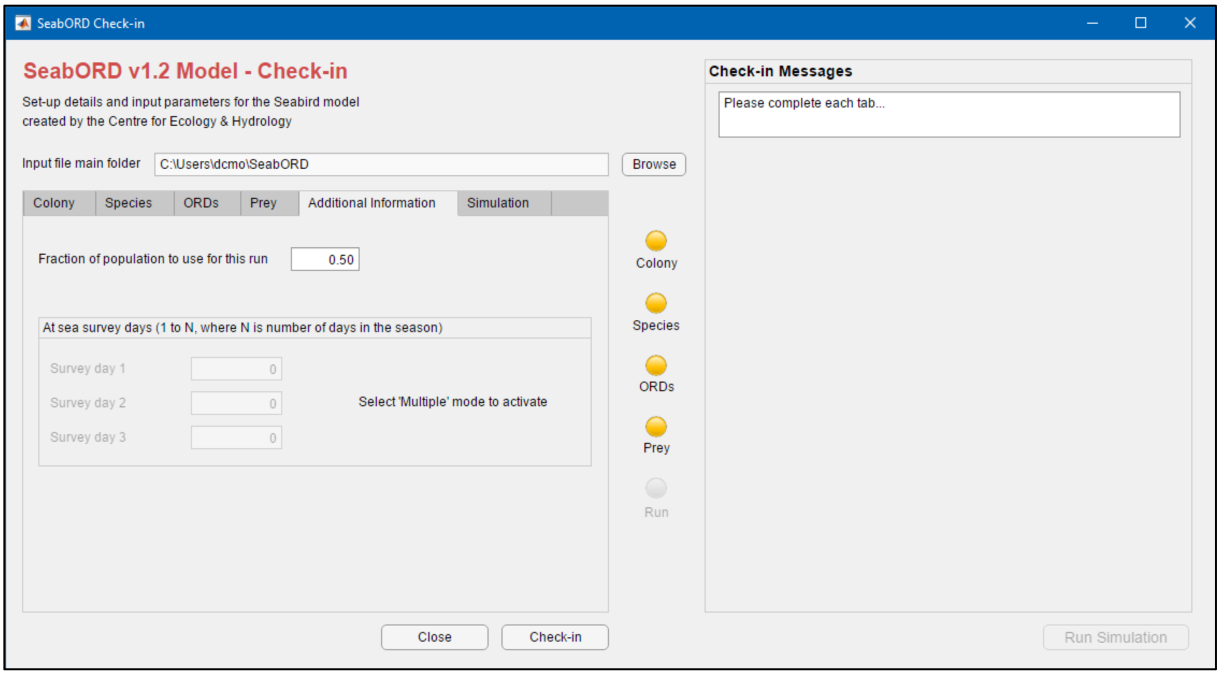


Figure 2-12 The Additional Information tab enable the user to control the number of birds simulated and the timing of any 'At-sea surveys'.

2.8.2 At Sea Survey Days

If the user wishes to calculate the metric P2, which quantifies the ratio of ORD-related mortality (of either adults or chicks) to the number of birds seen within an at-sea snapshot survey in the footprint of an ORD (Searle, et al. 2017), then the number and day of simulation for snapshot surveys need to be specified. The tool is currently set to allow up to three snapshot surveys per simulated breeding season, which must all occur on separate days during the breeding season. If there is more than one ORD simulated within a run, surveys are assumed to occur simultaneously at all ORD footprints simulated during the model run on each day selected.

Each at-sea snapshot survey counts the number of birds that are simulated by the model to be flying over, or foraging within, each ORD footprint at a specific, randomly selected, moment in time on the day of the breeding season on which the user has specified a survey to take place. The metric P2 then calculates the ratio between ORD-related mortality (i.e., mortality with ORD - minus in the baseline) and this snapshot count of birds within ORD footprints. Results are presented for good, moderate and poor seasons as described for the P1 metric.

We caution that the value of P2 can vary substantially between snapshot surveys, so it is advisable to run multiple surveys.

2.9 Simulation

SeabORD v1.2 can be run in 'Single' mode or 'Multiple' (batch) mode.

In both cases a reference name can be used to identify a given run; the text is included in the output folder name. For example, if the text is 'run1' the output folder will be

<$mainfolder>\SimulationFiles\<region>_<species>_<timestamp>_run1_<type>

where <type> is automatically added and will be either 'BASE', 'SCENARIO', or 'NNpairs' indicating a single baseline run (no ORDs), a single scenario run (with ORDs) or a batch of NN pairs from a multiple run.

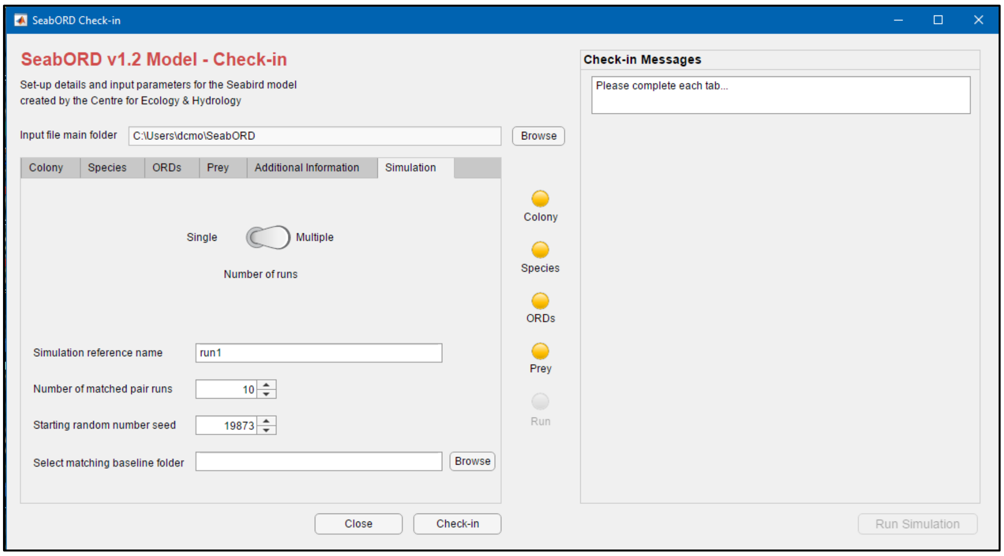


Figure 2-13 The final tab on the graphical interface allows the user to specify a single test run or a batch of matched pairs of runs.

2.9.1 Single or Test Mode

If the switch is set to 'Single' (see Figure 2.13) two additional parameter fields become active; 'Starting random number seed' and 'Select matching baseline folder'.

The first is the starting random number seed. This is used to initialize the pseudorandom number generator and setting this to a particular value controls the various stochastic elements in the model. Defining a given seed for a run allows the run to be repeatable. The seed entered in the tool can be any integer.

The second tells the model how to pair up a baseline with an ORD run. In single mode, the user manually defines a pair of simulations; baseline and scenario with ORDs. The runs are 'matched' by using the same seed (as well as other setting such as bird species and population number).

We recommend that a baseline run is carried out first, and a note made of the output folder name. Then 'switch on' the required ORDs (without changing any other settings) and add the name of the baseline folder to the box on the simulation tab. This tells SeabORD which data to load to calculate the ORD effect metrics.

Note that in single mode model output is restricted to showing the change in adult mass and chick survival over the breeding season, and final model metrics (i1-i6) are not provided. This is because we recommend that metrics are only interpreted when multiple paired runs have been made so that assessments of uncertainty are provided (95% prediction intervals based on the mean and standard deviation in model metrics across multiple paired runs).

2.9.2 Multiple or Batch Mode

If the switch is set to 'Multiple' (see Figure 2-13) two additional fields become active; a random seed and the number, N, of matched pairs required.

Based on testing of the prototype tool for each species in the Forth-Tay region we strongly recommend running as many paired runs as is computationally feasible to properly assess uncertainty in impact assessments, bearing in mind that a run with 30,000 birds and 10 pairs will take approximately 24 hours on a standard laptop, requiring around 2GB of RAM.

When this mode is selected the parameters set on the other five tabs are used for all runs, with only the random seed (and, optionally, the prey level) changing so that the stochastic elements of the model are varied. For example, if there are three ORDs and N = 50 the model will execute 100 seasons:

1. Seed 1 – no ORD baseline, prey level 1
2. Seed 1 – 3 ORDs + metrics comparing 1. and 2. , prey level 1
3. Seed 2 - no ORD baseline, prey level 2
4. Seed 2 – 3 ORDs + metrics comparing 3. and 4. , prey level 2
5. …
6. …

99. Seed 50 – no ORD baseline, prey level 50
100. Seed 50 – 3 ORDs + metrics comparing 99. and 100. , prey level 50

The final output will be a summary of the multiple paired runs.

In this mode, the model will give an error at Check-In if all ORDs are set to 'off' on the ORD tab because the baseline run is carried out by default.

In order to produce a single estimate for an effect size, we have developed a method that uses stratified random sampling to estimate effect sizes across the full range of 'moderate' conditions experienced by birds in the baseline (no ORDs present) and generate an average for each model metric (P1-P6). This method has the advantage that it incorporates uncertainty in model outputs deriving from uncertainty in prey levels, to produce both an overall mean estimate for each metric and a corresponding 95% prediction interval that includes prey uncertainty. The method involves the following steps, available within SeabORD, detailed in the accompanying 'Worked Example':

- Identify the median regional prey levels corresponding to the upper and lower boundaries of 'moderate' conditions based on adult mass change and chick/nest survival in baseline runs for each species and colony of interest (Table 2-1)
- Simulate *n* prey levels randomly from within this range (using stratified random sampling, with *n* strata of equal width and one prey value simulated per stratum) and run a set of *n* paired simulations (one paired simulation for each of the *n* prey levels) to produce *n* estimates for each metric with associated standard deviations and 95% prediction interval
- Combine the *n* estimates for each metric to produce a final, single mean estimate with associated 95% prediction intervals incorporating model uncertainty and uncertainty derived from prey levels

2.10 Check-In

When each tab has been completed, click Check-In and the model will run a short routine to confirm that all parameters have been set and all the required input files are available or can be generated.

If everything is in order, all the lamps will turn green and the **Run Simulation** button will become active.

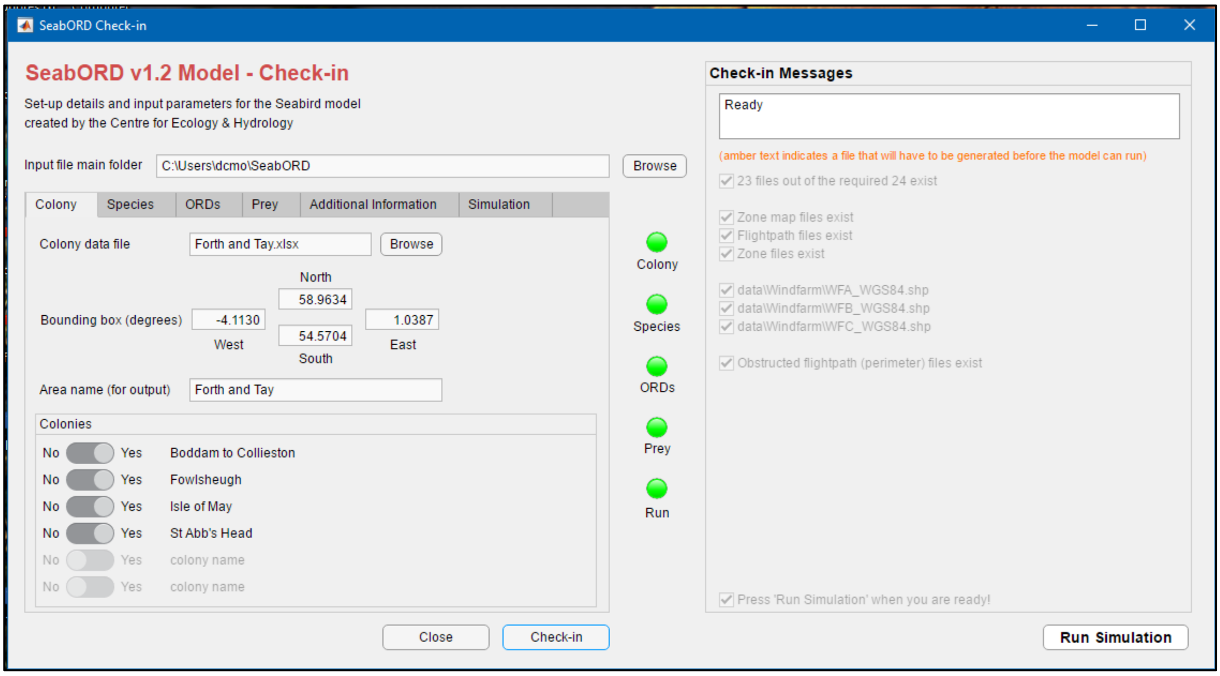


Figure 2-14 The Check-In procedure has found all the required files and the model can proceed to the flight simulation routines.

2.10.1 Check-in Errors

Errors that prevent the model from running will cause a 'red lamp' on the interface and an error message to be written in the messages box (see Figure 2-15). Correct the error and re-run the check-in routine.

Missing data files that cannot be created (these will have been supplied with SeabORD). Check if the wrong main folder has been selected (see Section 2.2)

- ERROR: File <$mainfolder>\data\Bathymetry\BathymetryMap_GEBCO.mat is missing
- ERROR: File <$mainfolder>\data\Bathymetry\Rg_GEBCO.mat is missing
- ERROR: File <$mainfolder>\data\Location\UKcoast.mat is missing
- ERROR: File <$mainfolder>\data\Windfarm\<shapefilename> is missing

Possible errors while setting up the tabs on the Check-In panels

- 'Please enable at least one colony!'
- 'Please select a bird species!'
- 'Please select a forage site selection method!'
- 'Please set maximum forage distance!'
- 'Please set the proportion of the population in range!'
- 'Please select a site selection data file!'

- 'Please select the ORD file (it is needed even if this scenario has no ORDs)'
- 'Please select the forage type!'

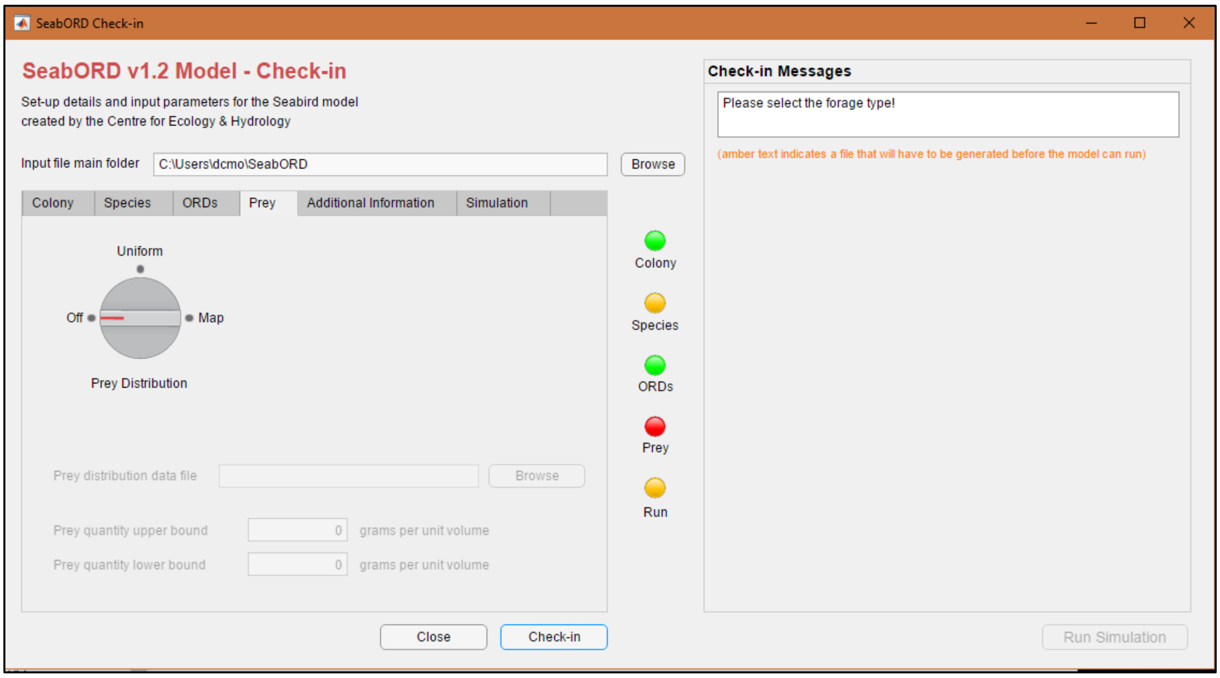


Figure 2-15 In this example the Prey tab has not been completed causing check-in to fail and set a red lamp

2.10.2 Check-in Warnings

At Check-in, warnings appear in amber. These indicate that the model will run but that some input files will have to be generated first, increasing the run time of the simulation. The warning is given so that the user can check if an error has been made in the input before opting to run the model thus avoiding recreating large input files unnecessarily.

In particular, if a new location, colony or ORD is added the zone files and flightpaths will have to be generated and this can take several hours.

3 Running the model

After the check-in process has been completed successfully (with no errors), the 'Run Simulation' button becomes active. Click it to start a run.

3.1 Boarding

For either 'single' or 'Multiple' mode the model first loads all the necessary data, loads any existing flight path files, selects the forage locations for all birds for the season and prepares for the flight simulation. This phase is called 'boarding'. During this process, a display window (as in Figure 3-1) shows various maps and text message to inform the user of progress.

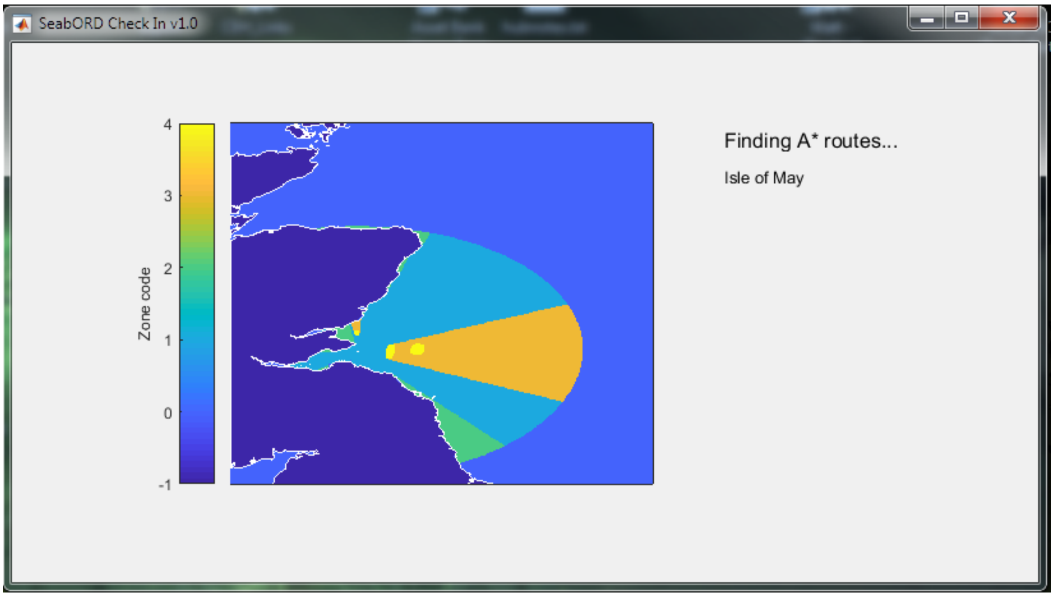


Figure 3-1 The boarding phase is carried out after check-in. Data files are loaded and maps displayed to allow the user to monitor progress

During the Boarding phase in 'Single' mode (see Section 2.9.1) key maps are saved as image files in the output folder. These can be used to check placement of ORDs etc. For example, the map in Figure 3-1 shows that the model is currently calculating the A* flightpath routes from the Isle of May to each required forage site,

- Sites in the pale blue zone (code 1) are accessible in a straight line from the colony
- Sites in the green zone (code 2) are accessible but the bird has to navigate around the coastline to avoid flying over land
- Sites in the orange zones (code 3) are obstructed by one or more windfarms; barrier-susceptible birds will fly around the footprint(s) to get there
- Sites in the yellow zones (code 4) are within the windfarm footprints (so displacement-susceptible birds will not forage there)

Beware! If the progress map window is manually closed using the red X, the model will stop running because it cannot find where to display updates!

When all the required input is loaded this window will close and a larger graphic display window will open.

3.2 Graphical Output

SeabORD v1.2 displays a number of graphs and a map during the flight simulation run (see Figure 3-2). These update at the end of every simulated timestep. The text area in the lower right corner updates throughout the timestep to alert the user to the current active calculations. The window can be resized (for example maximised to fill the screen) and the graphs will be rescaled to fill the window at the end of the next timestep. If the window is manually closed using the red X, the model will stop running because it cannot find where to display updates.

The main map (upper left) shows the chosen region and an accumulated sum of the number of birds foraging in the grid cells.

Below the map there are two charts showing three histograms; the current adult bird and chick body mass distribution, in grams, and the distribution of the number of flights (separate foraging trips) carried out by the birds for the latest completed timestep.

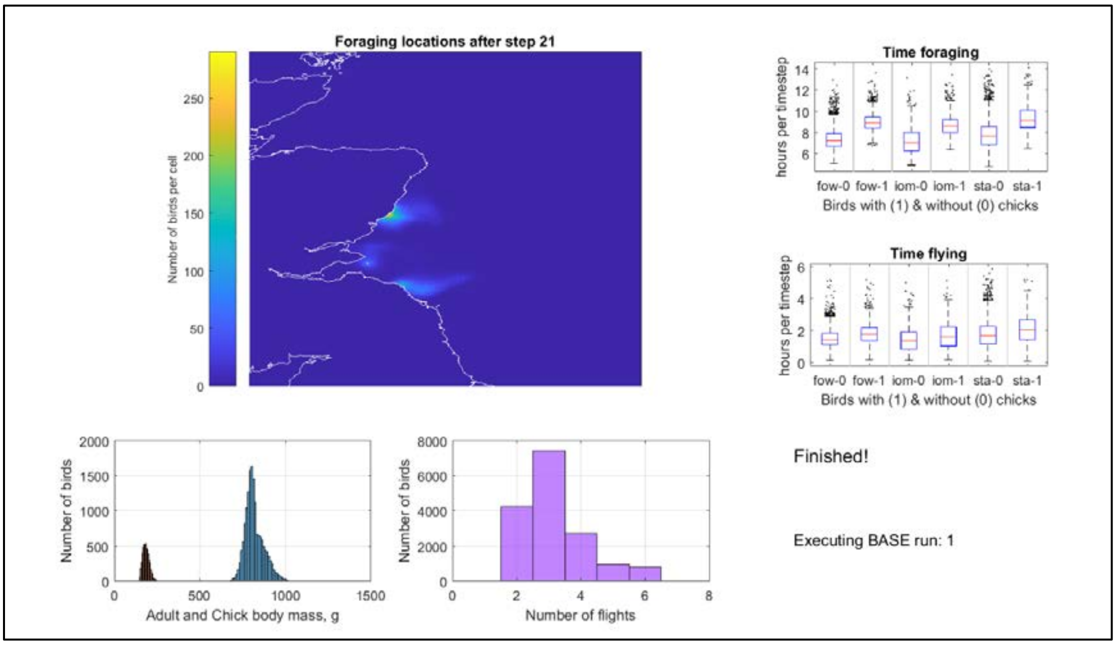


Figure 3-2 During execution of the flight simulation phase, there are four charts and a map displayed. These are updated at the end of every timestep.

The two box plots to the right of the map provide a visual representation of the time spent foraging and the time spent flying per timestep for every bird, divided by colony and groups with and without a chick. On each box, the central mark indicates the median, and the bottom and top edges of the box indicate the 25th and 75th percentiles, respectively. The whiskers extend to the most extreme data points not considered outliers, and the outliers are plotted individually using the '.' symbol.

At the end of the run, a snapshot of this window is saved in the output folder as an image file called finalgraphics.png.

4 Recommended Procedure

1. Carry out a set of 'baseline' runs (without ORDs) exploring a range of initial prey values, with a small number of birds (to minimise processing time)
    - Record the output adult body mass changes, chick survival and the indicated conditions for each colony of interest
    - Identify where results (adult body mass) switch over from moderate into poor and good conditions. This exercise will define the upper and lower bounds for prey values over which moderate conditions (adult mass loss) occur for each colony of interest and can then be used in the next phase to assess ORD impacts (Section 2.7)
2. Carry out one matched pair run with the chosen ORDs to initialise the required flightpath files and check execution time with the desired final population size.
3. Complete a multiple run with as many pairs of matched runs (baseline + scenario) as computationally feasible to produce a single estimate for each metric with associated 95% prediction intervals.

Each of these steps is described in detail in a separate document (Mobbs, et al. 2017) using a worked example with kittiwake in the Forth and Tay region and three sample ORDs.

5 Interpreting the results

5.1 Output files

The model produces a range of metrics for quantifying the ORD-related mortality of both adults and chicks. These metrics are defined, and described in more detail, in (Searle, et al.2017). Each of the metrics can be calculated, separately, in relation to both chick mortality and adult mortality.

All metrics are exported to an excel spreadsheet for each simulation run. The spreadsheet will be named ‘FinalSummary_<region>_<species>_<time>_<shortname>.xlsx’ and is written to the <$mainfolder>\SimulationFiles folder within a subfolder also named to indicate the region, species and time of execution plus the short name provided by the user (for example ‘ForthAndTay_Kw_Oct_05_2026_set3’). The output folder will automatically open using Windows Explorer when the model completes a simulation run.

In ‘single’ run (‘test’) mode the final spreadsheet displays output on initial population size, adult bird mass at the start and the end of the breeding season, adult survival *during the chick-rearing season*, breeding success, the percent loss of body mass for the adults over the chick-rearing season and an indication of whether this indicates a ‘poor’, ‘moderate’ or ‘good’ scenario for the birds at each colony. The output from a single baseline run (without an ORD) is shown in Table 5-1. For a single scenario run (with an ORD) the output will show two tables, one for the scenario run and one for the matching baseline (which will have been run previously and specified at the start for comparison).

Table 5-1: An example of the simple output provided from a ‘single mode’ baseline run

Colony	N	Adult survival %	Adult initial mass, g	Adult final mass, g	Breeding success	Type	% loss
bod	1254	100	375.27	356.10	91.20	Moderate	5.11
fow	938	100	371.02	336.41	39.36	Moderate	9.33
iom	376	100	374.39	342.76	60.53	Moderate	8.45
sta	432	100	372.47	336.47	2.33	Moderate	9.67

In multiple paired simulations, ‘batch’ mode, outputs are more extensive and results are averaged across multiple simulations, presented in a single output file with a mean and standard deviance for each metric.

Metric P1 (‘Additional Mortality’ or ‘Add.Mort’ in the output file) calculates the population-level impact of the ORD: it is equal to (mortality with ORD present - mortality in baseline) / (population size), and represents the overall impact of the ORD.

Metrics I1 - I6 use the same calculation as P1, but apply this to subsets of the population: to birds that are never directly impacted by the ORD (I1), to those that are directly impacted at least once (I2), to those that experience displacement but not barrier effects (I3), to those that experience barrier but not displacement effects (I4), and to those that experience both barrier and displacement effects at least once (I5). The final of this set of metrics, I6, focuses on birds that experience specific patterns of barrier and displacement effects – e.g. that were displaced on 5 days and experience barrier effects on 4 days - and so provides the most detailed breakdown of the effects into population sub-groups.

Metric P2 relates the population-level impacts of the ORD to the number of birds seen within an at-sea "snapshot" survey of the ORD, and is primarily designed to assist in quantifying the population-level consequences of an ORD based upon actual survey data from ORD footprints (e.g., boat-based or aerial transect data). The value of P2 within each run represents the mean value of P2 across the set of snapshots taken within that run.

The final output summary file contains 9 worksheets –

1. Summary: This sheet shows a summary of the parameters used to define the simulation run for reference, plus a set of figures indicating the ‘season type’ for each colony (‘poor’, ‘moderate’ or ‘good’) based on the adult mass loss over the season.
2. Add.Mort i0: This sheet shows detailed results for all birds in the simulation grouped by colony and a summary of the results assuming each possible season type. We know this was a moderate year so the moderate calculation apply here.
3. Add.Mort i1: As described for i0 but for birds that are never directly affected by the ORD.
4. Add.Mort i2: As described for i0 but for birds that are directly impacted at least once.
5. Add.Mort i3: As described for i0 but for birds that are displaced at least once, never barriered.
6. Add.Mort i4: As described for i0 but for birds barriered at least once, never displaced.
7. Add.Mort i5: As described for i0 but for birds barriered and displaced at least once.
8. Add.Mort i6: As described for i0 but shows all possible impact combinations grouped separately.
9. Survey: If an at-sea survey has been selected, results are exported to this sheet.

In addition to the results presented in a spreadsheet the model output folder will include

- Parameter.m – a text file listing all user-defined parameters used in the simulation run for reference
- Finalgraphics.png – a screenshot of the final figure (see Figure 3-2)
- A set of images <species>_birddensity_<colony>.png showing the map of the chosen region and the input bird density. These maps are useful for checking any new density data have been imported as expected.
- An image <species>_preyavailability.png, showing the chosen prey distribution across the whole region. This is useful for checking the input prey density data have been imported or set as expected.
- A set of images BaseZonemap_<colony>.png (see Figure 5-1) used for checking the forage ranges and colony locations
- A set of images <sp>_ORDzonemap_<colony>.png (see Figure 5-2) used for checking the barrier-affected areas. Note that the individual areas are only identified when they are selected for use within a model run for the first time so the image will be patchy at first and become complete over time and frequent use of the model.

Figure 5-1 The model will save an image showing the forage locations for each colony (in this example, Isle of May) indicating areas the bird can reach directly (green) or by navigating around the coast (yellow)

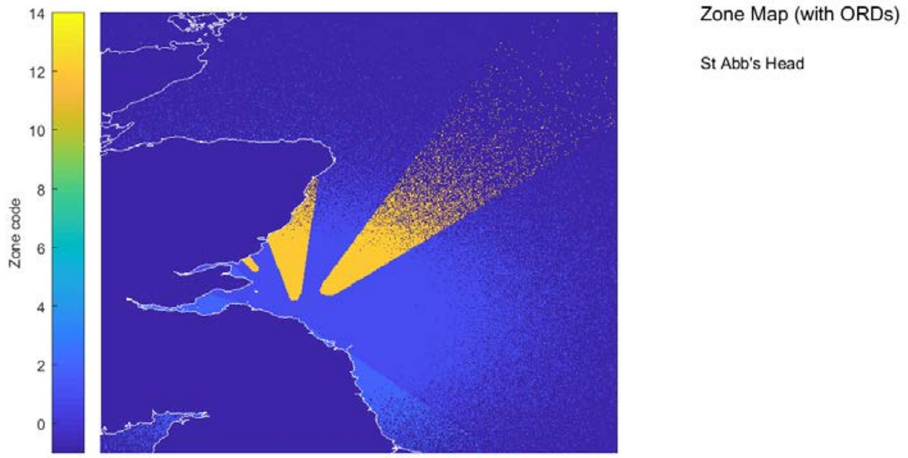


Figure 5-2 The model will save an image showing how the forage sites are affected by ORDs, for example this map indicates in orange the sites where birds from St Abb's Head will be barrier-affected. The individual areas are only identified when they are selected for use within a model run for the first time so the image will be patchy at first and become complete over time and frequent use of the model.

6 Troubleshooting

6.1 The Run simulation button is inactive

The ‘Run simulation’ button is only active if all required parameters have been set in the tool interface. If a parameter is missing there should be an appropriate message in the text box at the top right of the interface. Check each tab and then run the check-in again.

If the ‘Run Simulation’ button is still inactive even though all parameters have been set, check the location of the ‘data’ folder (see Sections 1.1 and 2.2). SeabORD may be unable to write directly to the chosen location (e.g. C:\Program Files). Try moving the ‘data’ folder to a more accessible location.

6.2 The model ran, but there is no output spreadsheet

Microsoft Excel may not be able to create the output file because the name is not valid. This can be for a variety of reasons (usually a strange character such as <, >, ?, etc) or because the full pathname for the file has exceeded the maximum 218 characters for Windows PCs. Try moving the working folder to a different location so that the full path is shorter.

6.3 I changed the colony location but the model still uses the old location

When the model runs it generates a ‘zone’ file that identifies if a given grid square is accessible to the birds from a colony in a straight line, by navigating around the coast. This is a time-consuming process but is fixed for each location (thus only needs to be calculated once). To speed up model execution, the zone file is saved in the data\Location folder. The file name is

ZoneMap_<colony>_<gridsize>

If you change the location of a colony without changing the colony name, SeabORD will use the old file. If you delete the appropriate zone file it will be re-generated the next time it is needed (or the user may change the name of the colony which will force a new file to be generated).

6.4 The model run stopped

SeabORD v1.2 creates a text file called seabordlog.txt. If the model stops unexpectedly an error message will be written to this log file explaining what happened. Possible reasons for a sudden stop -

- SeabORD continually updates the graphics windows during a run. If these windows are manually closed (using the X in the top corner of the window) the model will stop as it will be unable to find where to display results. The windows can be safely minimised (but will restore to full size on the next update).

- Memory exceeded. A run with about 30,000 birds used approximately 2.5GB RAM and a run with 300,000 birds uses approximately 15GB RAM.
- The prey value was set too low and all adult birds have expired at one or more colonies
- An input file was found by name, allowing the model to run, but was corrupted or unreadable.
- When using A* pathfinding, it is possible for the routine to become ‘stuck’ in a loop, (perhaps with an unusual ORD footprint) or simply take a very long time to complete (if a particular forage location is unreachable without crossing land causing the routine to examine every possible map cell path before giving up). Messages on the graphics windows should identify when this happens. In this version the only way to cancel execution is to use Windows task manager to stop the seabord.exe process.

7 Appendices

Appendix 1. Coastline data

The SeabORD model uses information about the coastline to determine if a given grid square is 'land' or 'sea'. The centre point of each grid square is used to define the type for the square. The model also displays maps of input and output data for the chosen region; these maps are enhanced by displaying the coastline.

The data for the coast were obtain from the National Oceanic and Atmospheric Administration (NOAA) website, National Centers for Environmental Information section (Wessel, 1996).

http://www.ngdc.noaa.gov/mgg/shorelines/data/gshhg/latest/

The coastline data for the UK was extracted from file *gshhg-shp-2.3.5/gshhs_f.b* and trimmed to extract a section bounded by 48˚N and 61˚N, 12˚W and 8˚E. The data were then saved in a MATLAB data file, *UKcoast.mat*. This file is imported for each simulation run by SeabORD and the appropriate coastline drawn on the maps.

If the model is used for an area outside these bounds, an error will halt the model as it will be unable to determine if each grid square is sea or land.

Licence:

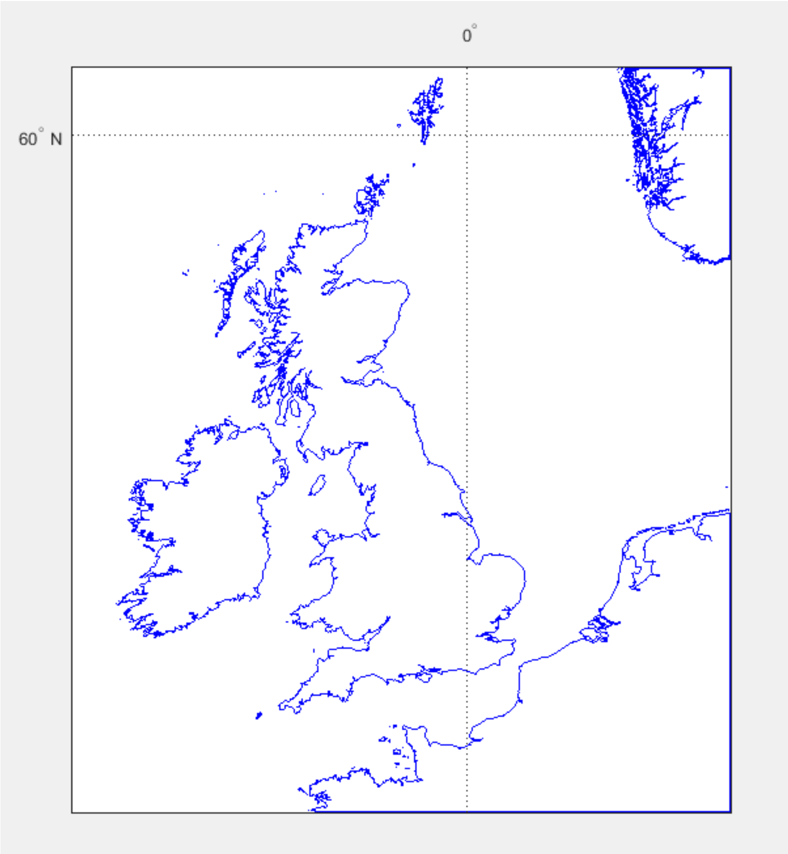


Figure 7-1 The coastline data included with SeabORD v1.2

Appendix 2. A* pathfinding

A* (pronounced as "A star") is a computer algorithm that is widely used in pathfinding routines, for example in simple computer games or mobile robot movements (Rabin, 2003). It is used for plotting an efficient path between multiple points, called nodes. In the case of SeabORD the nodes are the centre points of the regular grid across the region.

SeabORD uses an algorithm obtained from the File Exchange on the MATLAB community pages (Ueland, 2016). The following licence applies.

Appendix 3. Bathymetry data

SeabORD uses the GEBCO_2014 Grid, version 20150318, www.gebco.net. This is a continuous terrain model for ocean and land with a spatial resolution of 30 arc seconds (GEBCO, 2015). Details can be found on the GEBCO website and in Weatherall (2015).

Data for a region around the UK were downloaded from the website as a geotiff,

GEBCO2014_-15.0_46.0_6.0_63.0_30Sec_Geotiff.tif

and converted into MATLAB mat format for ease of use in the model. The extent of the available data is illustrated in Figure 7-2.

At the start of a model run, these data are imported and trimmed to fit the bounding box set by the user (see Section 2.3). This determines the number of grid 'squares' in the model and the coordinates of the centre point of each grid cell. The cell extent is 1/120 degrees which in the Forth and Tay area equates to a 'height' (N-S) of 0.926 km and 'width' (E-W) of about 0.478 km.

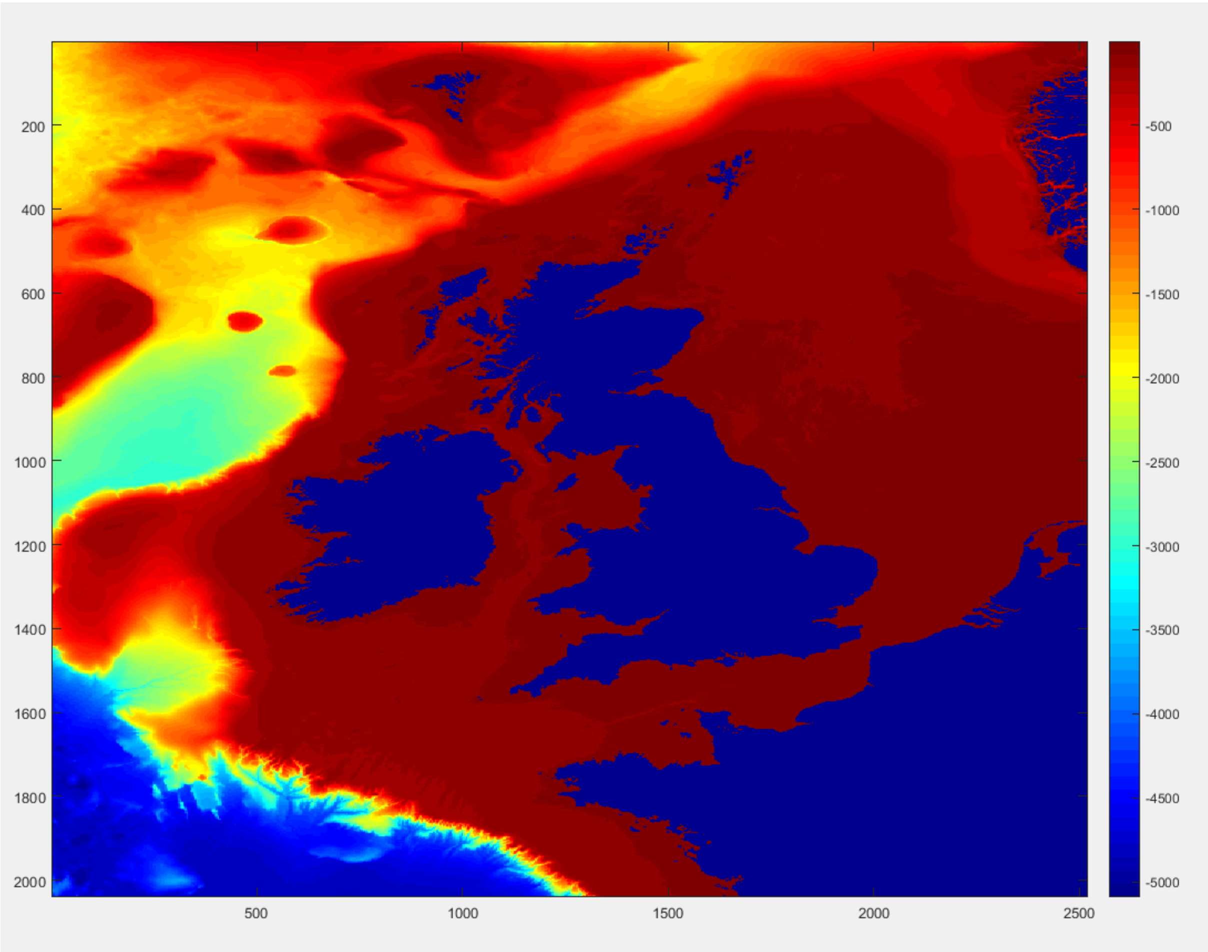


Figure 7-2 This illustrates the range of the GEBCO data that is included with SeabORD v1.2

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