

6. Exporting data • narwind

 offshore-wind.github.io/narwind/articles/model_export.html

Exporting data

There are two ways to save the results of an analysis conducted in **narwind**.

The first is to save the R objects returned by the model as an **.rda** (or 'R data') file using the `save()` command. **This is essential** as running the agent-based model can be time-consuming and repeat analyses should therefore be avoided. To do this, execute the following line of code, making sure to replace the path and file name with appropriate values:

```
save(model_base, file = "path/to/a/folder/of/choice/filename.rda")
```

During package testing, a typical **.rda** file containing outputs from a run of the agent-based model with **nsim = 1000** was between 500 Mb and 1 Gb in size.

In addition to the above, the `export()` function can be used to save model outputs as a Microsoft Excel spreadsheet (.xlsx), stored in the user's current working directory. `export()` can be used with both outputs from the agent-based model and the population model. In the former case, a separate file will be produced for each cohort in **cohort**, so we recommend using this option only for short simulation runs (**nsim = 100**), or using the **cohort** and **whale** arguments to extract data for specific individuals/cohorts.

Note that if the simulation run was given a label when using `narw()`, then this label is appended to the output file name.

In the below example, the first line of code exports data from the agent-based model for the first 10 females in the lactating cohort (ID = 5). The second line of code exports population projection data.

```
export(model_base, whale = 1:10, cohort = 5)
export(proj_base, prefix = "NARW_abundance")
```

All arguments to `export()` are listed below.

Object class	Argument	Default value	Description
narwsim	obj	-	Input model object, as returned by <code>narw()</code> .
	prefix	"narwsim"	Character string. Prefix appended to the output file name.

Object class	Argument	Default value	Description
	<code>whale</code>	<code>1:nsim</code>	Positive integer indicating the individual(s) for which data should be extracted. By default, all individuals are included.
	<code>cohort</code>	<code>1:6</code>	Positive integer or vector of positive integers indicating which cohort(s) should be considered. Defaults to all cohorts.
<code>narwproj</code>	<code>obj</code>	<code>-</code>	Input projection object, as returned by <code>predict(.)</code> .
	<code>prefix</code>	<code>"narwproj"</code>	Character string. Prefix appended to the output file name.
	<code>...</code>		Additional arguments passed to <code>write.xlsx</code>

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