

# Package: shellfishrisks (via r-universe)

November 26, 2024

**Title** Package for running agent based model exploring genetic risks of aquaculture production

**Version** 0.1.1

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**Description** This package runs an agent based model in Python, exploring the genetic risks of aquaculture production on wild populations.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**URL** <https://nwfsc-cb.github.io/shellfish-genetic-risks/>,<https://github.com/nwfsc-cb/shellfish-genetic-risks>

**BugReports** <https://github.com/nwfsc-cb/shellfish-genetic-risks/issues>

**RoxygenNote** 7.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**Roxygen** list(markdown = TRUE)

**Imports** purrr, dplyr, ggplot2, reticulate, magrittr, stringr, tidyr, readr (>= 2.0.0), here, foreach, doParallel

**Config/pak/sysreqs** libicu-dev libpng-dev python3 libx11-dev

**Repository** <https://nmfs-opensci.r-universe.dev>

**RemoteUrl** <https://github.com/nwfsc-cb/shellfish-genetic-risks>

**RemoteRef** HEAD

**RemoteSha** ce5064d9277559ee1d005ce47384b67d4a9b0447

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|--------------------|--|
| generate_ctrl_file | <i>Generate a control file from the default template</i> |
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## Description

Generate a control file from the default template

## Usage

```
generate_ctrl_file(ctrl_file_name = "ctrl", destdir = ".")
```

## Arguments

ctrl\_file\_name the desired name of the control file  
 destdir the directory to store the control file in

## Value

the file path of the control file

## Examples

```
## Not run:
generate_ctrl_file()
## End(Not run)
```

---

|                |   |
|----------------|---|
| install_pypkgs | <i>Install Required Python Packages</i> |
|----------------|---|

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**Description**

Install Required Python Packages

**Usage**

```
install_pypkgs(method = "auto", conda = "auto")
```

**Arguments**

|        |                              |
|--------|------------------------------|
| method | python install method        |
| conda  | path to the conda executable |

**Examples**

```
## Not run:  
install_pylibs()  
  
## End(Not run)
```

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|                |                             |
|----------------|-----------------------------|
| load_shellfish | <i>load shellfish model</i> |
|----------------|-----------------------------|

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**Description**

load shellfish model

**Usage**

```
load_shellfish(condaenv = "r-reticulate")
```

**Arguments**

|          |                            |
|----------|----------------------------|
| condaenv | the Conda environment used |
|----------|----------------------------|

**Examples**

```
## Not run:  
load_shellfish()  
  
## End(Not run)
```

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|                |                       |
|----------------|-----------------------|
| plot_shellfish | <i>Plot Shellfish</i> |
|----------------|-----------------------|

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**Description**

plot\_shellfish returns a ggplot2 object with the desired plot specified by the type argument.

**Usage**

```
plot_shellfish(results, type = "rvars")
```

**Arguments**

|         |   |
|---------|---|
| results | a list of results generated by shellfishrisks::serve_shellfish  |
| type    | The type of plot to generate, one of <ul style="list-style-type: none"><li>• "rvars": plot values from the pop_rvars objects</li><li>• "fst": plot fst outcomes</li><li>• "popsize": plot the subpopulation sizes</li></ul> |

**Value**

a ggplot2 object

**Examples**

```
## Not run:  
  
results <- serve_shellfish(batches = c("spam", "eggs"))  
  
plot_shellfish(results, type = "rpart")  
  
## End(Not run)
```

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|                 |  |
|-----------------|--|
| run_ctrl_folder | <i>Run all control files in a folder</i> |
|-----------------|--|

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**Description**

Run all control files in a folder

**Usage**

```
run_ctrl_folder(ctrl_folder, reps = 1, cores = 1)
```

**Arguments**

|             |   |
|-------------|---|
| ctrl_folder | the location of the folder containing the control files       |
| reps        | the number of reps per control file                           |
| cores       | the number of cores. Set to greater than 1 to run in parallel |

**Examples**

```
## Not run:  
  
run_ctrl_folder("my_control_files", cores = 6)  
  
## End(Not run)
```

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run\_shellfishrisk\_ctrlfile

*Run shellfishrisk from control file*

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**Description**

Run shellfishrisk from control file

**Usage**

```
run_shellfishrisk_ctrlfile(  
  batch = "demo",  
  reps = 1,  
  coreid = 1,  
  ctrl_file_path  
)
```

**Arguments**

|                |  |
|----------------|--|
| batch          | the name of the batch                        |
| reps           | the number of reps to run                    |
| coreid         | no id  |
| ctrl_file_path | the file path to the control file to be used |

**Value**

nothing

serve\_shellfish      *Load and Serve Shellfish Genetics Results*

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**Description**

Load and Serve Shellfish Genetics Results

**Usage**

```
serve_shellfish(batches, results_dir = NA)
```

**Arguments**

results\_dir      the name of the directory where results are stored  
batch            the name of the batch of results

**Value**

a list containing each of the results objects

**Examples**

```
## Not run:  
  
results <- serve_shellfish(batch = "dev")  
  
## End(Not run)
```

---

theme\_shellfish      *ggplot2 theme for shellfishrisks*

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**Description**

ggplot2 theme for shellfishrisks

**Usage**

```
theme_shellfish(...)
```

**Arguments**

...

**Examples**

```
ggplot(mtcars, aes(mpg)) + geom_histogram() + shellfishrisks::theme_shellfish()
```

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