Visualizing Atlantis Tool (vat)
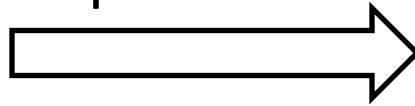
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Atlantis summit 2015

About vat

- Interactive R package used with the Atlantis ecosystem model.

- Created by Christopher Desjardins

- Available at https://github.com/mareframe/vat

The start page

Visualizing Atlantis Diagnostic Tool

The visualizing Atlantis diagnostic tool, `vadt` , is developed by Christopher David Desjardins at the Science Institute at the University of Iceland as a part of the EU MareFrame project. The `vat` package is released under the GPL v3 or later and source code is available at http://github.com/mareframe/vat.

At present, `vadt` is able to:

- Replicate the functionality of Olive
- Display animated GIFs showing changes in biomass over time for each functional group in the model created with the `animate_vadt` function.
- Plot structural, reserve, total numbers, length-at-age, and biomass disaggregated by age for each functional group
- Present diet information. For vertebrates, the units are number eaten per second and for invertebrates, the units are mg N/m3 eaten per second
- Present aggregated plots of vertebrates and invertebrates

To start the application, click a tab, e.g. **Spatial Plots**, etc. Then select the functional group you are interested. Some plots have tabs on the left side of the page which can be clicked (e.g. the Interactive Plots tab).

MareFrame

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 613571

Distribution by boxes
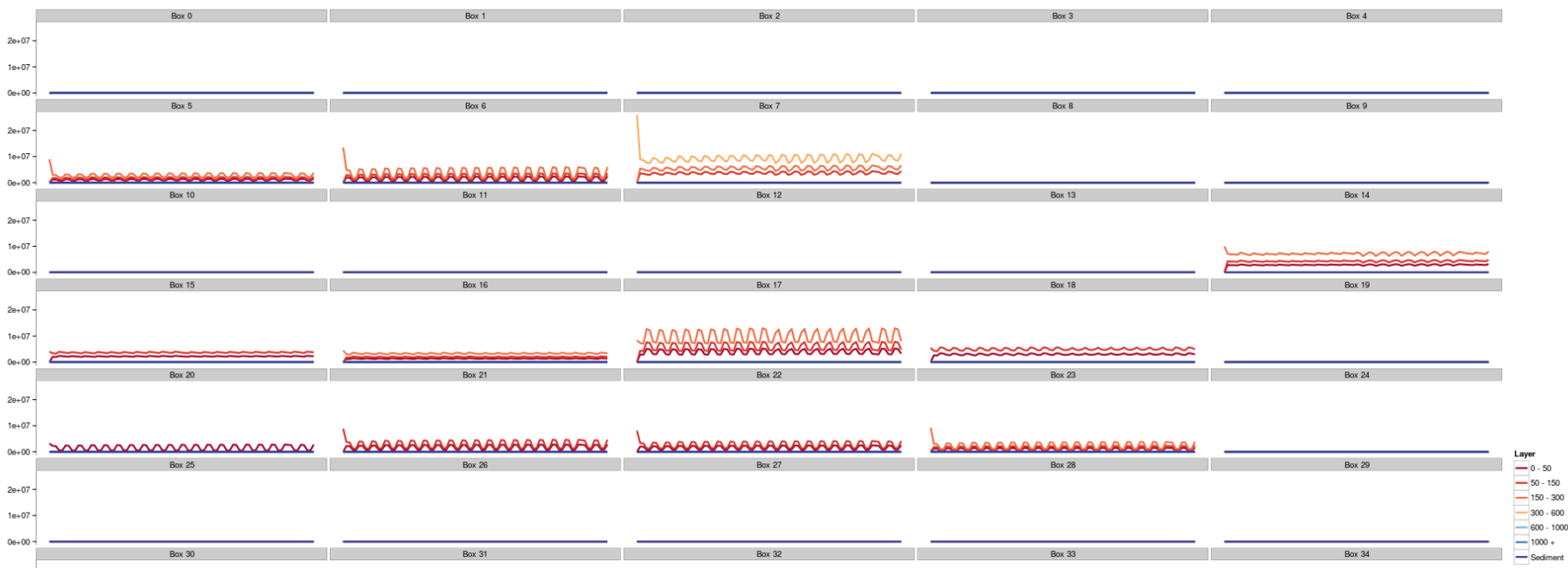
Growth
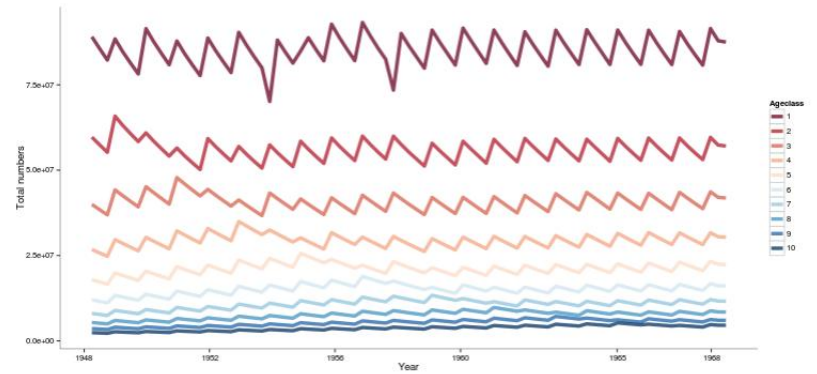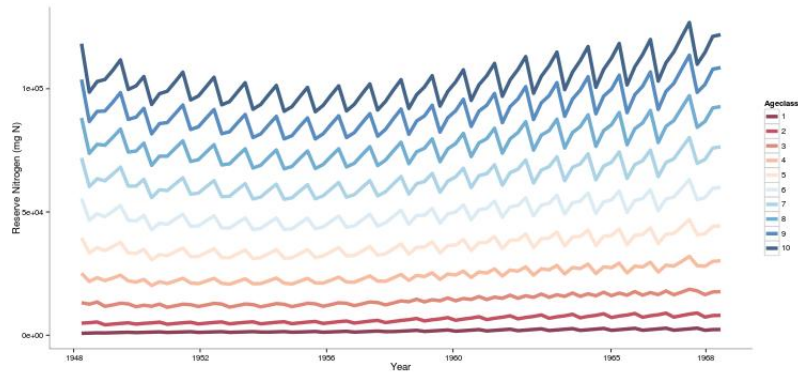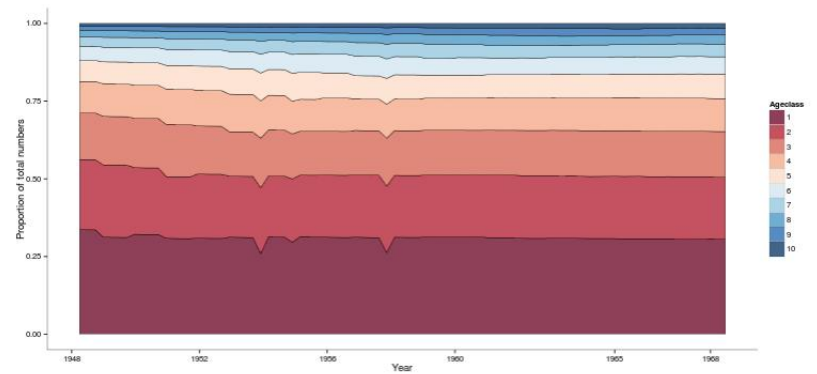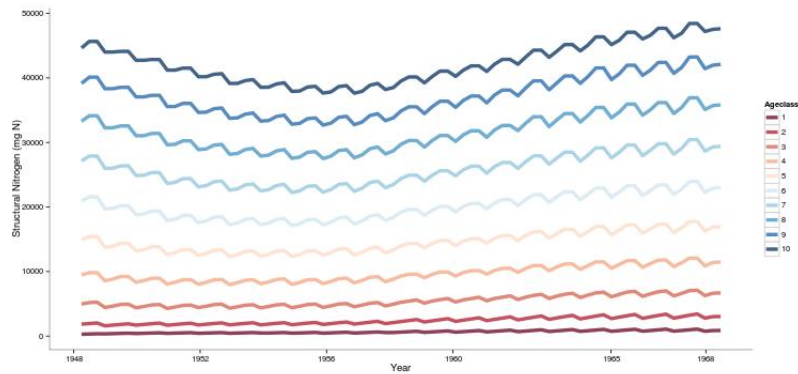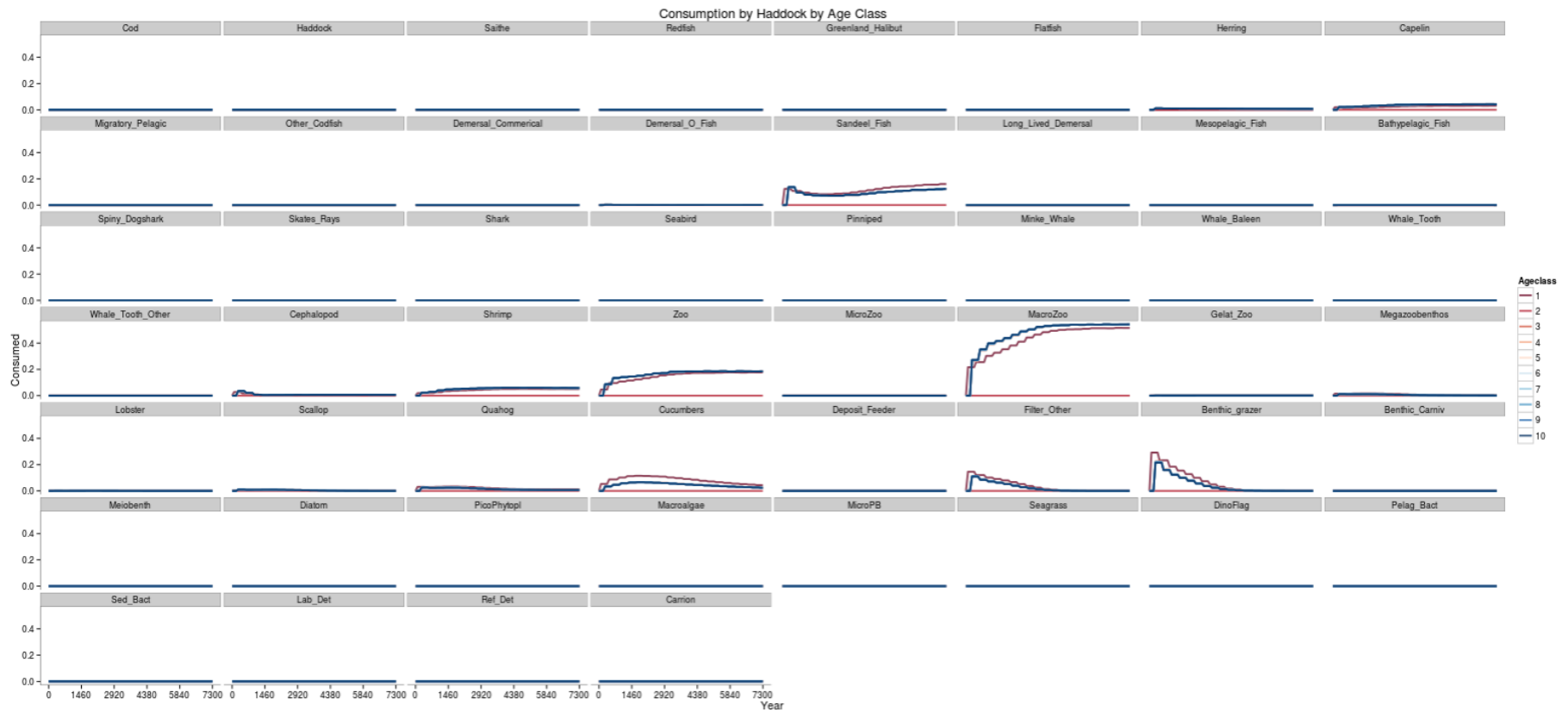
Diet

Biomass
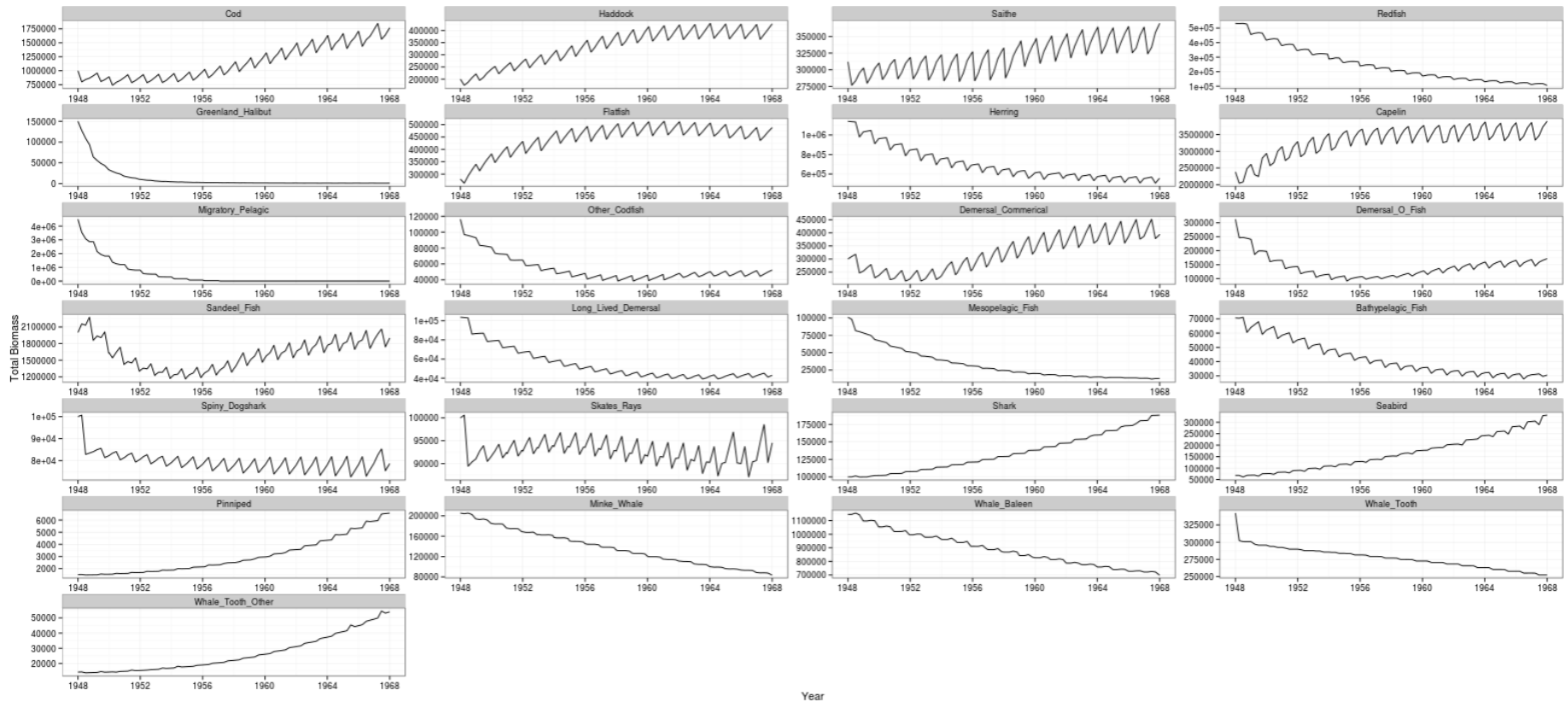
How it works

To Install:

```
library(devtools)
install_github(repo = "mareframe/vat")
```

To Run:

```
create_vadt()
```

This creates an object of class vadt containing all the data needed for vadt().

```
animate_vadt()
```

This function creates optional animated plots for vadt().

```
vadt()
```

This is the function that launches the actual Shiny application.

How it works

```
setwd('C:/Users/erlas/Dropbox/PostDoc/Atlantis/model')


obj <- create_vadt(outdir = "Bio4/", fgfile = "GroupsIceland.csv",
                   ncout = "Output4", startyear = 1948, toutinc = 30,
                   biolprm = "Biology4.prm", diet = TRUE)



vadt(obj, anim = NULL)
```