# model-calibration

## Alexander Keth 2017-05-18

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NOTE: This vigentte is optimised for longer simulation runs. Therefore the output is not as pleasant due to the fact that the dummy setas file have a running time of 5 years.

In order to use this vignette make sure to render model-preprocess.Rmd first. Either save the resulting list of dataframes as shown in data-raw/data-vignette-model-preprocess.Rmd or render both vignettes model-preprocess.Rmd and model-calibration.Rmd in the same R-instance. Of course, you can also use a personalised version of mode-preprocess.Rmd. Please make sure to add all resulting dataframes to the list of dataframes at the end of the preprocess vignette and change model-calibration.Rmd accordingly.

```
library("atlantistools")
library("ggplot2")
library("gridExtra")

fig_height2 <- 11
gen_labels <- list(x = "Time [years]", y = "Biomass [t]")

# You should be able to build the vignette either by clicking on "Knit PDF" in RStudio or with
# rmarkdown::render("model-calibration.Rmd")</pre>
```

#### 0.1 User Input

This section is used to read in the SETAS dummy files. Please change this accordingly.

```
result <- preprocess

d <- system.file("extdata", "setas-model-new-trunk", package = "atlantistools")

# External recruitment data
ex_rec_ssb <- read.csv(file.path(d, "setas-ssb-rec.csv"), stringsAsFactors = FALSE)

# External biomass data
ex_bio <- read.csv(file.path(d, "setas-bench.csv"), stringsAsFactors = FALSE)

# bgm file
bgm <- file.path(d, "VMPA_setas.bgm")</pre>
```

#### 1 Whole system plots!

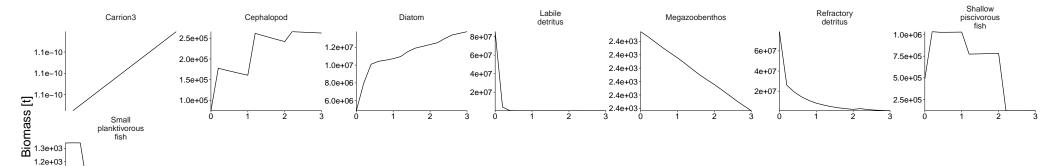
#### 1.1 Overall biomass

```
df_bio <- combine_groups(result$biomass, group_col = "species", combine_thresh = 10)</pre>
## Joining, by = "species"
plot <- plot_bar(df_bio)</pre>
update_labels(plot, labels = gen_labels)
    1.6e+08-
    1.2e+08-
                                                                                                                            species
Biomass [t]
                                                                                                                               Carrion3
                                                                                                                               Cephalopod
                                                                                                                               Diatom
                                                                                                                               Labile detritus
                                                                                                                               Megazoobenthos
                                                                                                                               Refractory detritus
                                                                                                                               Shallow piscivorous fish
                                                                                                                               Small planktivorous fish
    4.0e+07-
    0.0e+00
                                                                                                                     3
                                                         Time [years]
```

#### 1.2 Biomass timeseries

1.1e+03 1.0e+03 9.0e+02 8.0e+02

```
plot <- plot_line(result$biomass)
update_labels(plot, labels = gen_labels)</pre>
```



Time [years]

#### 1.3 Biomass@age timeseries

```
plot <- plot_line(result$biomass_age, col = "agecl")
update_labels(p = plot, labels = c(gen_labels, list(colour = "Ageclass")))

Shallow pischorous fish

2.0e+02

1.5e+02

1.5e+02

Time [years]
```

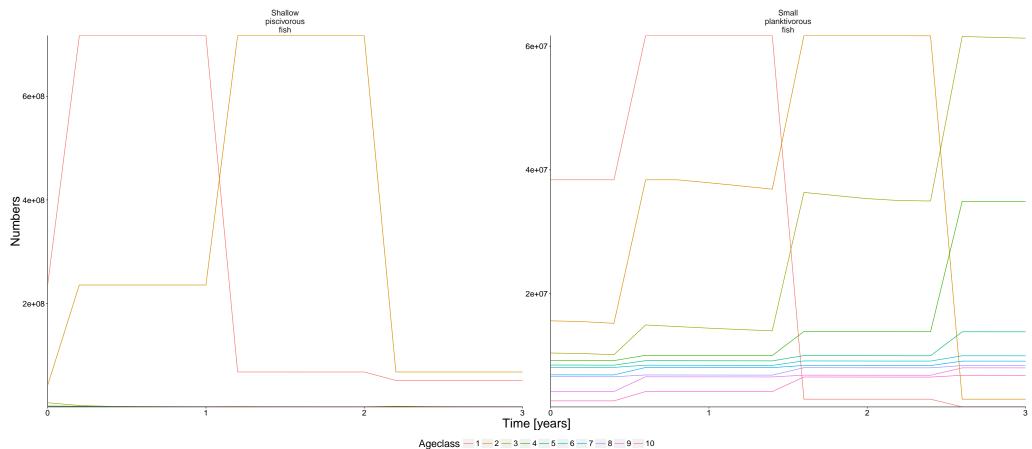
Ageclass - 3 - 4 - 5 - 6 - 7 - 8 - 9 - 10

#### 1.4 Number timeseries

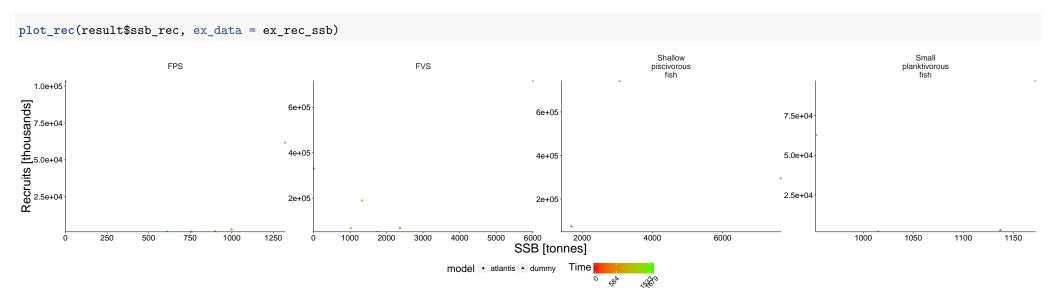
```
plot <- plot_line(result$nums)</pre>
update_labels(p = plot, labels = list(x = "Time [years]", y = "Numbers"))
                                                      Shallow
piscivorous
fish
                                                                                                                                                              Small
planktivorous
fish
                                                                                                           1.6e+08
   7.5e+08
                                                                                                           1.5e+08
Numbers
2.0e+08-
                                                                                                           1.4e+08
                                                                                                           1.3e+08
                                                                                                           1.2e+08
   2.5e+08-
                                                                                                       Time [years]
```

#### 1.5 Number@age timeseries

```
plot <- plot_line(result$nums_age, col = "agecl")
update_labels(p = plot, labels = list(x = "Time [years]", y = "Numbers", colour = "Ageclass"))</pre>
```



#### 1.6 SSB & Recruitment



#### Biomass benchmark

7.5e+05

5.0e+05

2.5e+05

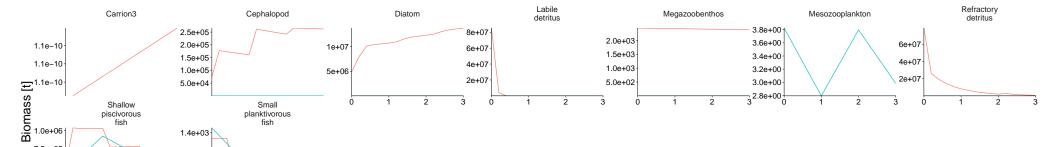
1.4e+03-

1.2e+03-

1.0e+03-

8.0e+02-

```
names(ex_bio)[names(ex_bio) == "biomass"] <- "atoutput"</pre>
data <- result$biomass</pre>
data$model <- "atlantis"</pre>
comp <- rbind(ex_bio, data, stringsAsFactors = FALSE)</pre>
# Show atlantis as first factor!
comp$model <- factor(comp$model, levels = c("atlantis", sort(unique(comp$model))[sort(unique(comp$model)) != "atlantis"]))</pre>
# Create plot
plot <- plot_line(comp, col = "model")</pre>
update_labels(plot, gen_labels)
```

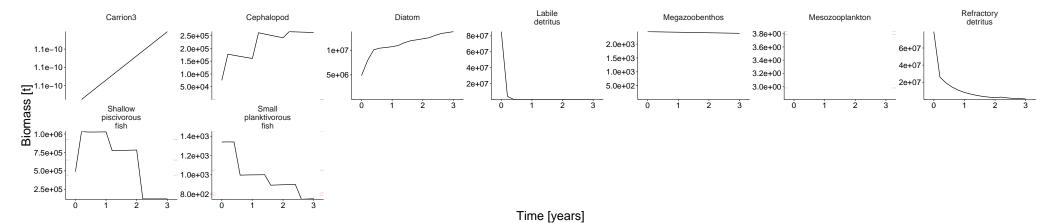


Time [years]

model - atlantis - dummy

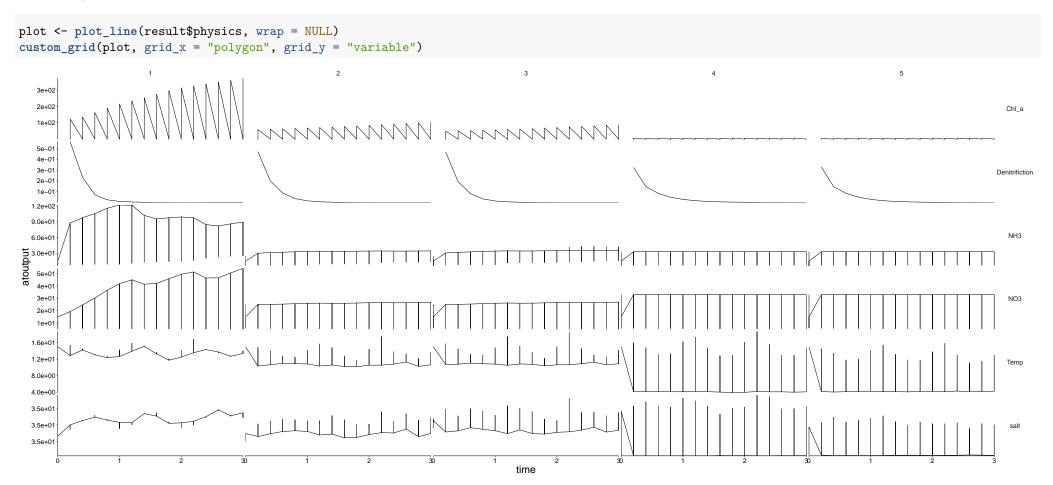
#### 1.8 Biomass benchmark 2

```
plot <- plot_line(result$biomass) %>% update_labels(labels = gen_labels)
plot_add_range(plot, ex_bio)
```



model — dummy

#### 1.9 Physics



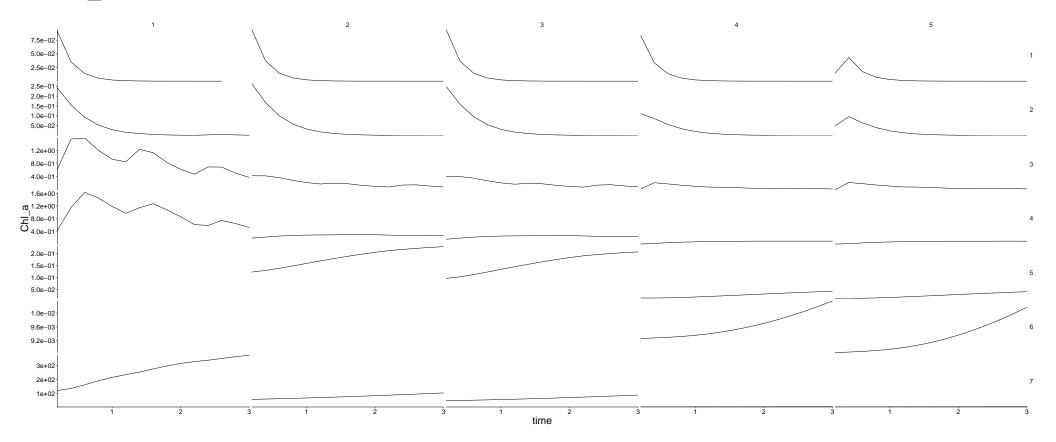
#### 2 Physics

```
physics <- result$physics %>%
  flip_layers() %>%
  split(., .$variable)

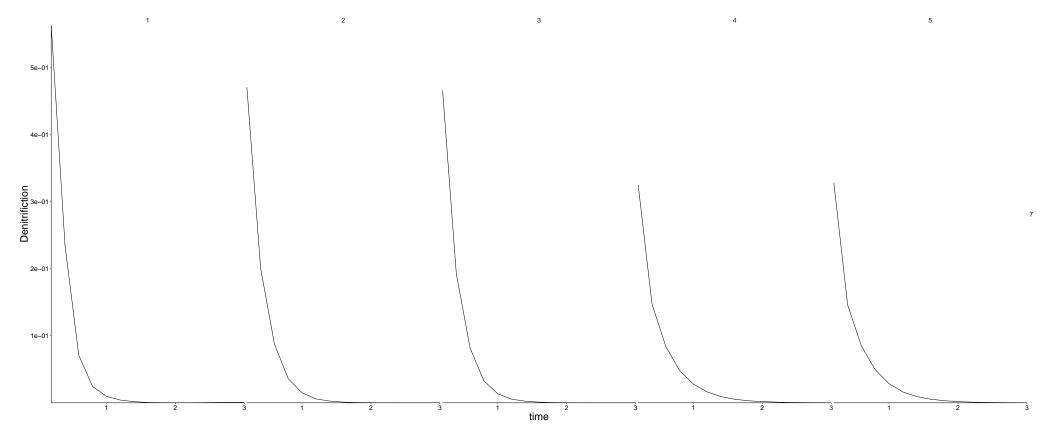
plots <- lapply(physics, plot_line, wrap = NULL) %>%
  lapply(., custom_grid, grid_x = "polygon", grid_y = "layer")

for (i in seq_along(plots)) {
  cat(paste0("## ", names(plots)[i]), sep = "\n")
  plot <- update_labels(plots[[i]], labels = list(y = names(plots)[i]))
  print(plot)
  cat("\n\n")
}</pre>
```

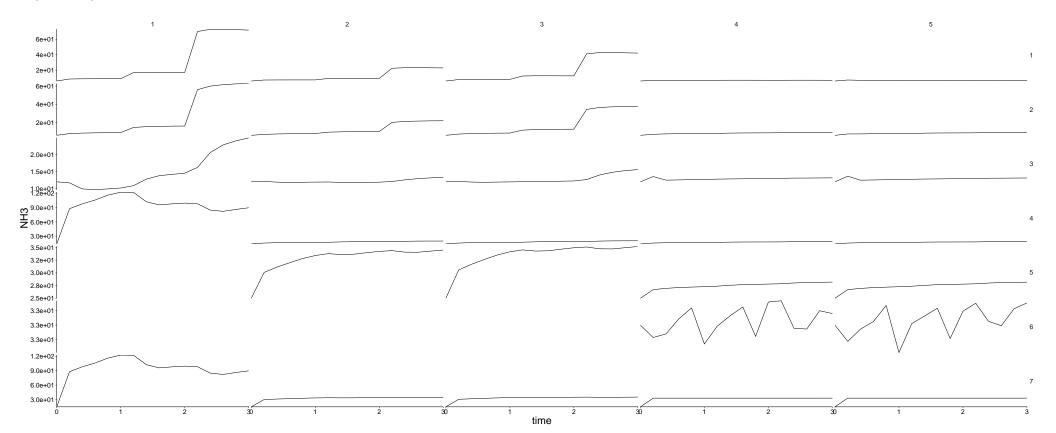
#### 2.1 Chl\_a



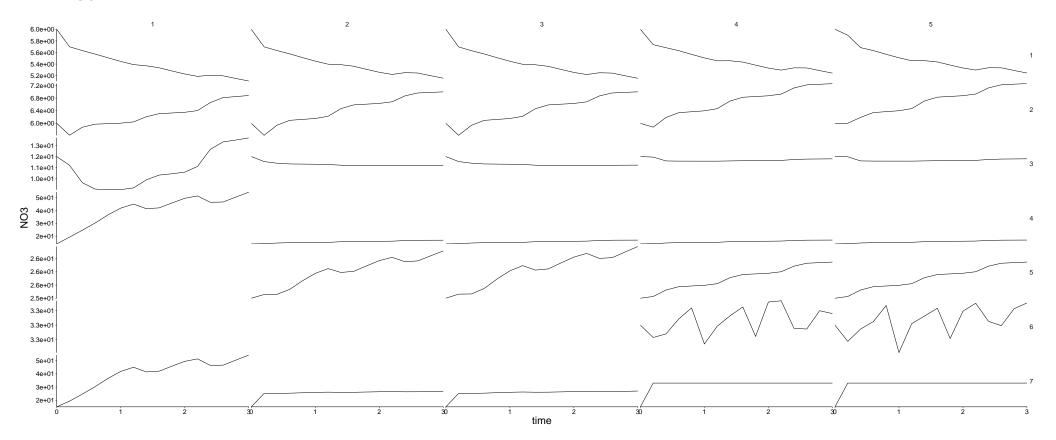
### 2.2 Denitrifiction



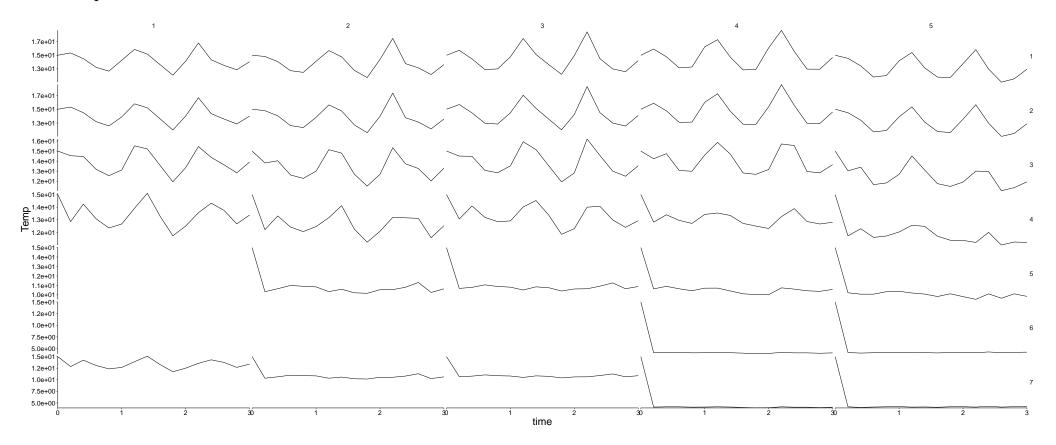
### 2.3 NH3



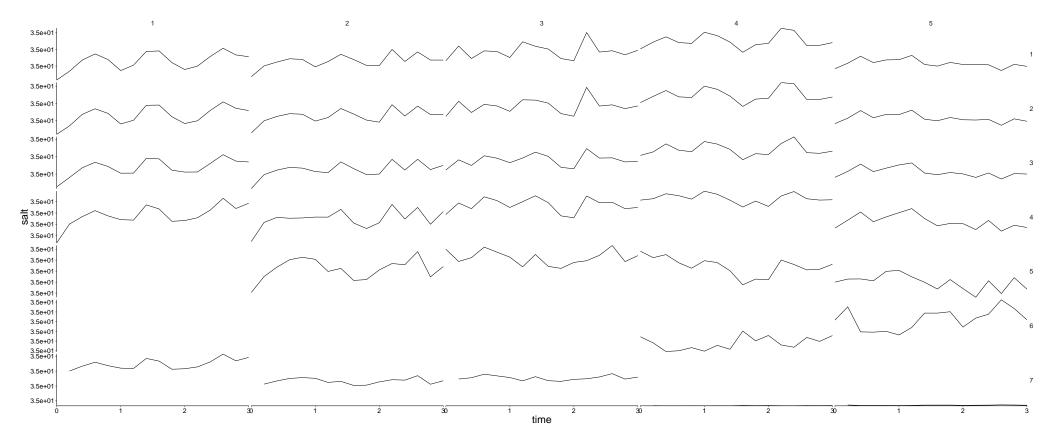
### 2.4 NO3



## 2.5 Temp



#### **2.6** salt



#### 2.7 Fluxes 1

```
plot <- flip_layers(result$flux) %>%
  plot_line(wrap = NULL, col = "variable")
custom_grid(plot, grid_x = "polygon", grid_y = "layer")
    1e+04
    0e+00
   -1e+04
   -2e+04
    0e+00
   -2e+04
   -4e+04
    0e+00
    -5e+04
-1e+05
5.0e+04
    -1e+05
   0.0e+00
  -5.0e+04
  -1.0e+05
  -1.5e+05
    3e+05
    2e+05
    1e+05
    0e+00
   -1e+05
   -2e+05
    5e+04
    0e+00
   -5e+04
```

time
variable — eflux — vflux

#### 2.8 Fluxes 2

1.0e+00

```
plot <- flip_layers(result$sink) %>%
  plot_line(wrap = NULL, col = "variable")
custom_grid(plot, grid_x = "polygon", grid_y = "layer")
                                                                  2
   6e+00
   5e+00
   4e+00
   3e+00-
   2e+00
   $€‡00
   4e+00
   3e+00-
   2e+00
   68±88
   5e+00
    4e+00
    3e+00
2e+00
1e+00
7.5e+00
   5.0e+00
  2.5e+00
   1.2e+01
   1.0e+01
   8.0e+00
  6.0e+00
  4.0e+00
   3:00+00
  2.5e+00
  2.0e+00
   1.5e+00
```

time
variable — hdsink — hdsource

#### 2.9 Relative change of water column height compared to nominal\_dz

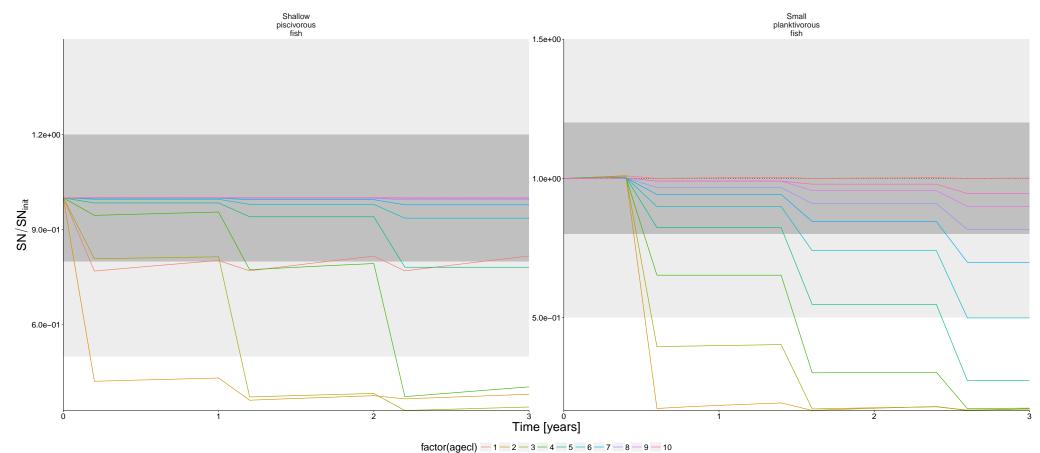
```
check_dz <- result$dz %>%
  dplyr::left_join(result$nominal_dz, by = c("polygon", "layer")) %>%
  dplyr::mutate(check_dz = atoutput.x / atoutput.y) %>%
  dplyr::filter(!is.na(check_dz)) # remove sediment layer
plot <- plot_line(check_dz, x = "time", y = "check_dz", wrap = "polygon", col = "layer")</pre>
update_labels(plot, list(x = "Time [years]", y = expression(dz/nominal_dz)))
                                                                                          3
                                                                                                                           4
                                                                                                                                                            5
   1.2e+00
                                     1.2e+00
                                                                       1.2e+00
                                                                                                         1e+00
                                                                                                                                          1e+00
dz/nominal_dz
                                     1.1e+00
                                                                       1.1e+00
                                                                                                         8e-01
                                                                                                                                          8e-01
                                                                                                         6e-01
   1.0e+00
                                     1.0e+00
                                                                       1.0e+00
                                                                                                                                          6e-01
                                                                                                         4e-01
  1.0e+00 ⊬
0
                                    _31.0e+00
                                                                      ____1.0e+00
                                                                                   Time [years]
```

factor(layer) - 0 - 1 - 2 - 3 - 4 - 5 - 6

## 3 Calibration plots

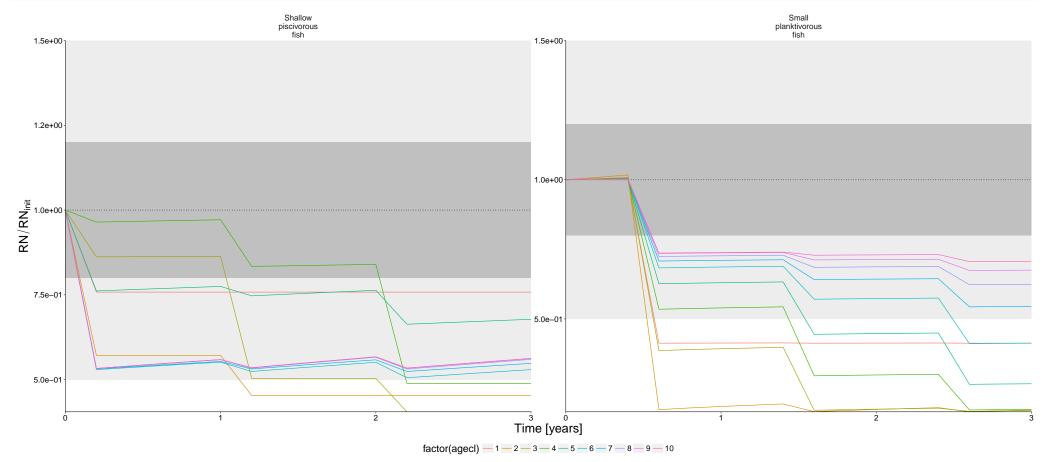
#### 3.1 Structural nitrogen

```
df_rel <- convert_relative_initial(result$structn_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(SN/SN[init])))
plot_add_box(plot)</pre>
```



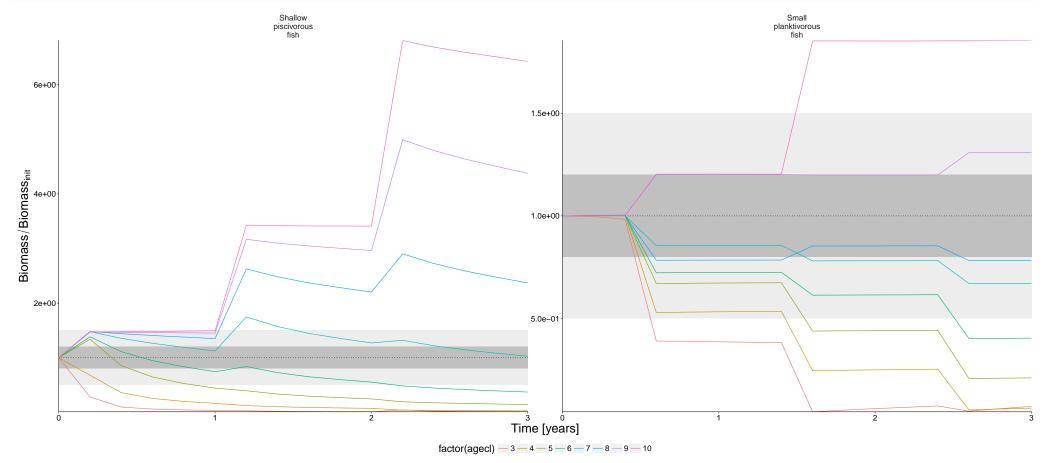
#### 3.2 Reserve nitrogen

```
df_rel <- convert_relative_initial(result$resn_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(RN/RN[init])))
plot_add_box(plot)</pre>
```



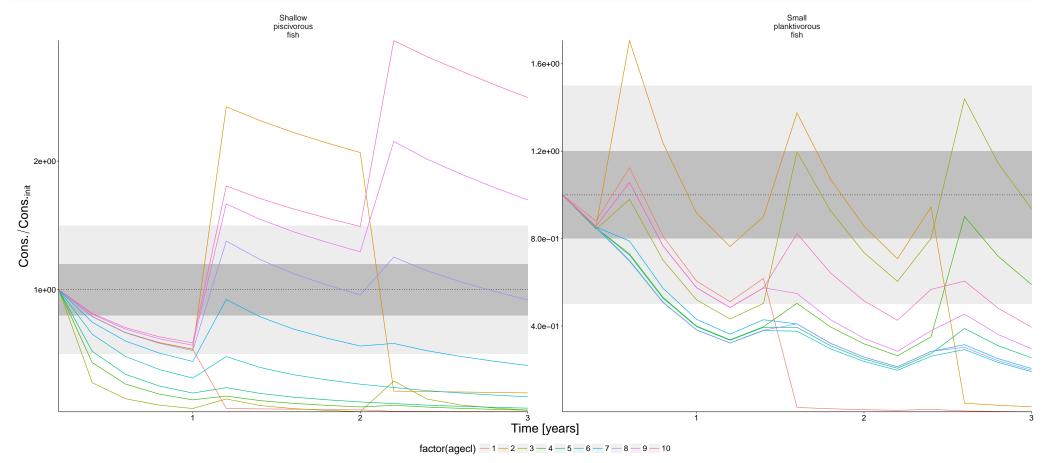
#### 3.3 Biomass per ageclass

```
df_rel <- convert_relative_initial(result$biomass_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)</pre>
```



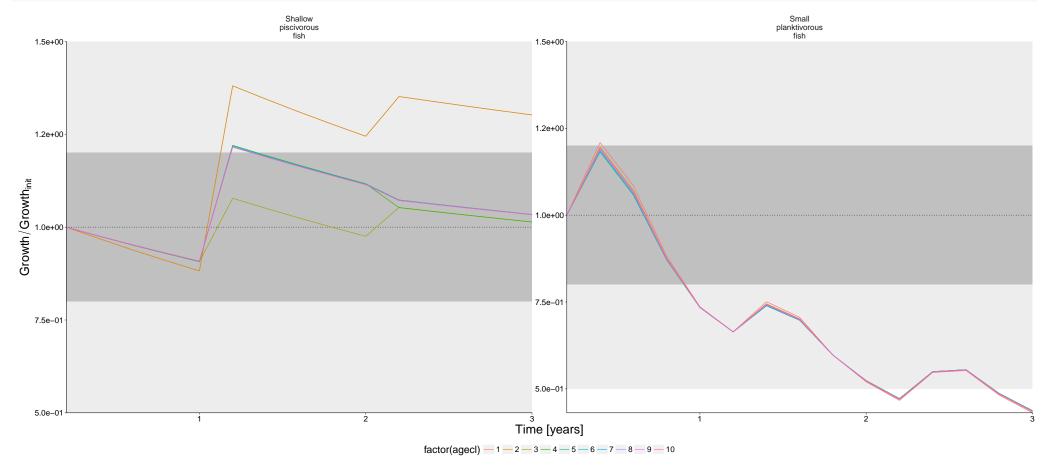
#### 3.4 Eat per ageclass

```
df_rel <- convert_relative_initial(result$eat_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Cons./Cons.[init])))
plot_add_box(plot)</pre>
```



#### 3.5 Growth per ageclass

```
df_rel <- convert_relative_initial(result$growth_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Growth/Growth[init])))
plot_add_box(plot)</pre>
```



#### 3.6 Growth in relation to initial conditions

```
plot <- plot_line(result$growth_rel_init, y = "gr_rel", col = "agecl")
update_labels(plot, list(y = expression((Growth - Growth[req])/Growth[req])))

Small
planktworous
fish

5e-01

0e+00

-5e-01

2

3

1

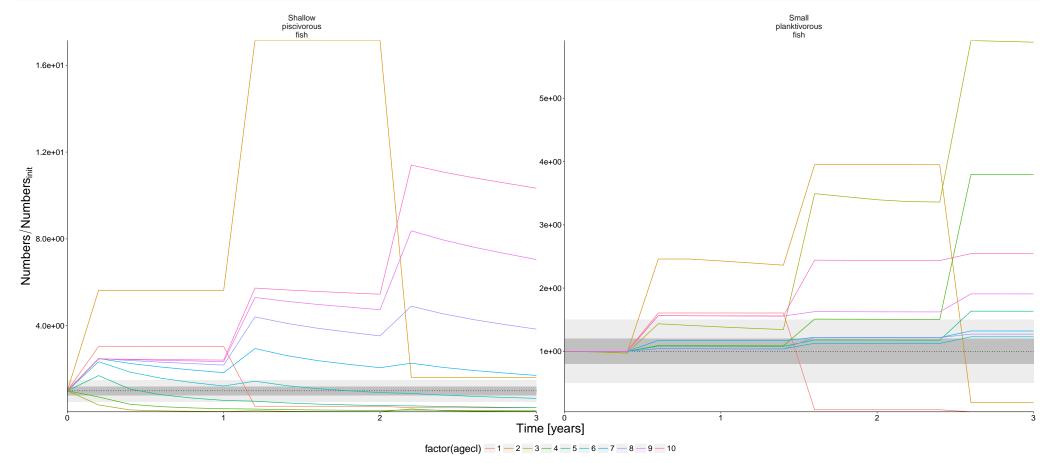
2

3
```

time factor(agecl) — 1 — 2 — 3 — 4 — 5 — 6 — 7 — 8 — 9 — 10

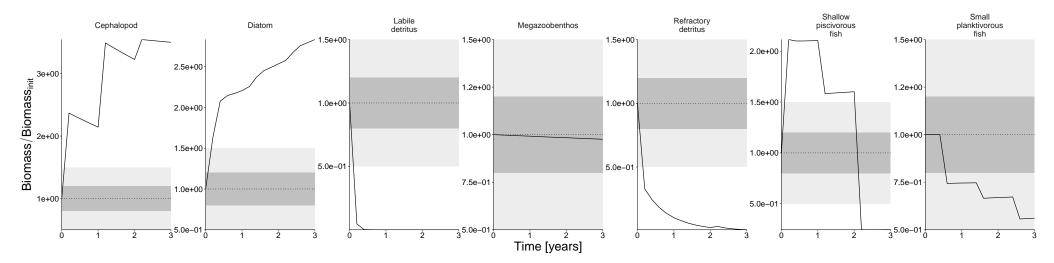
#### 3.7 Numbers

```
df_rel <- convert_relative_initial(result$nums_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Numbers/Numbers[init])))
plot_add_box(plot)</pre>
```



#### 3.8 Biomass

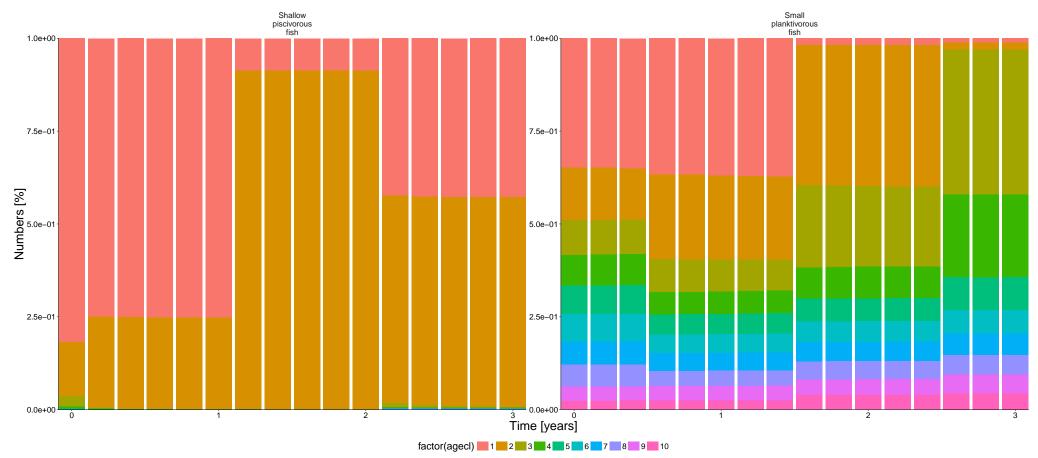
```
df_rel <- convert_relative_initial(result$biomass)
plot <- plot_line(df_rel)
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)</pre>
```



### 4 Distribution plots

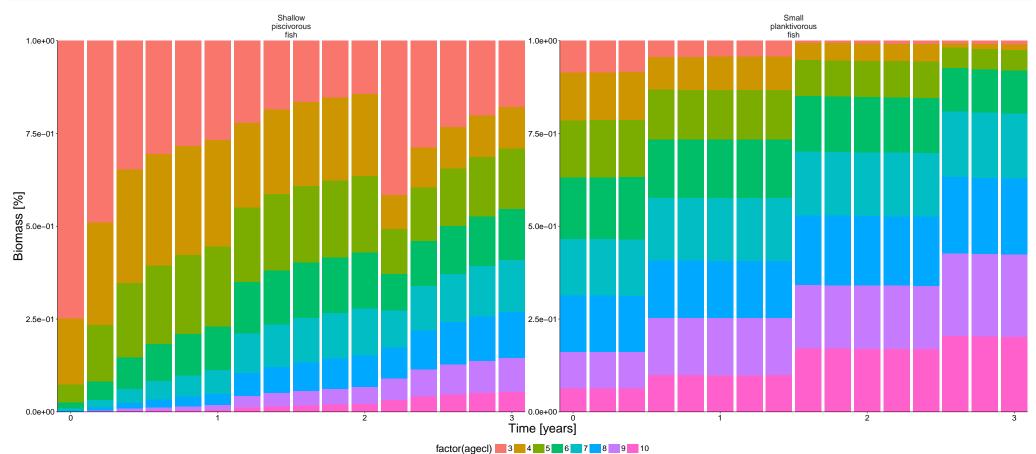
#### 4.1 Numbers @ age

```
df <- agg_perc(result$nums_age, groups = c("time", "species"))
plot <- plot_bar(df, fill = "agecl", wrap = "species")
update_labels(plot, labels = list(x = "Time [years]", y = "Numbers [%]"))</pre>
```



#### 4.2 Biomass @ age

```
df <- agg_perc(result$biomass_age, groups = c("time", "species"))
plot <- plot_bar(df, fill = "agecl", wrap = "species")
update_labels(plot, labels = list(x = "Time [years]", y = "Biomass [%]"))</pre>
```



## 5 Diet Plots

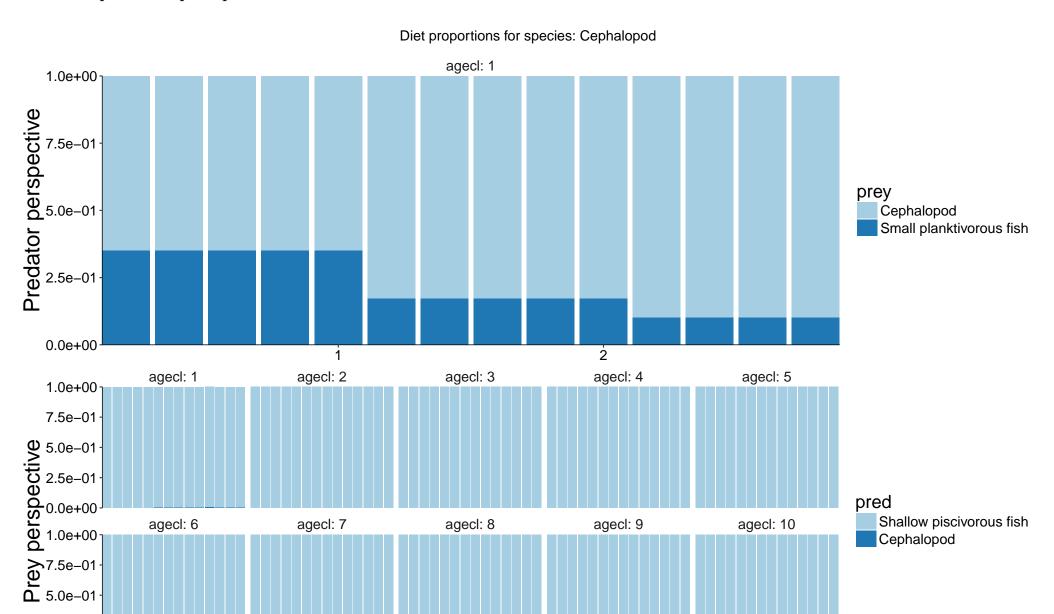
```
## Joining, by = c("time", "pred", "agecl", "prey")
## Joining, by = c("time", "pred", "agecl", "prey")
```

2.5e-01

0.0e+00

ż

ż

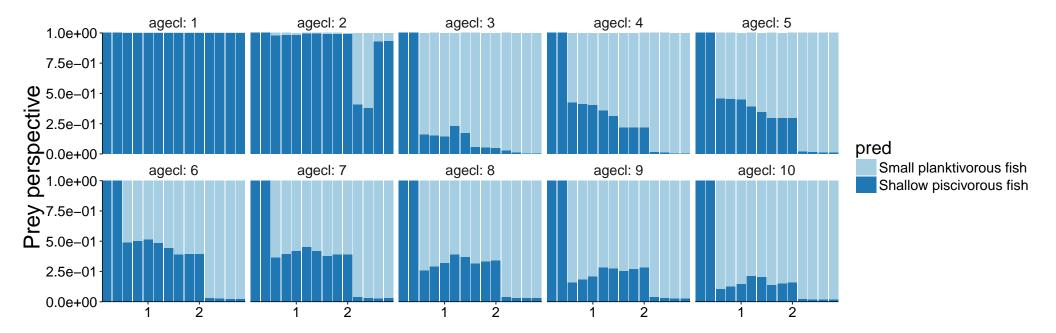


ż

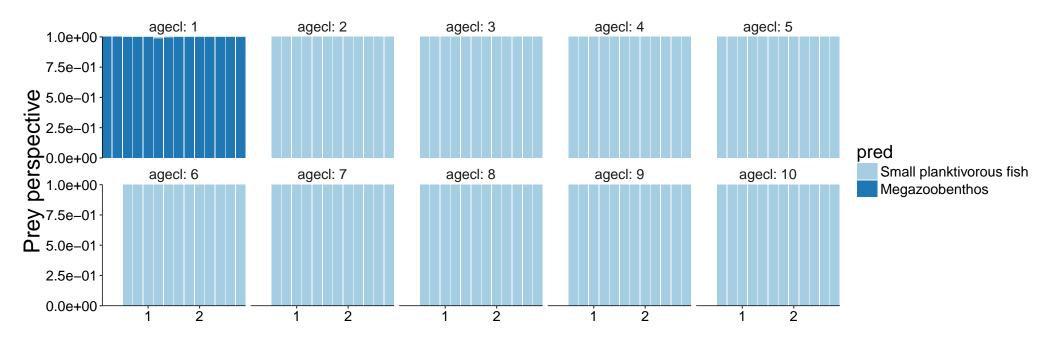
2

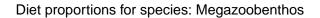
ż

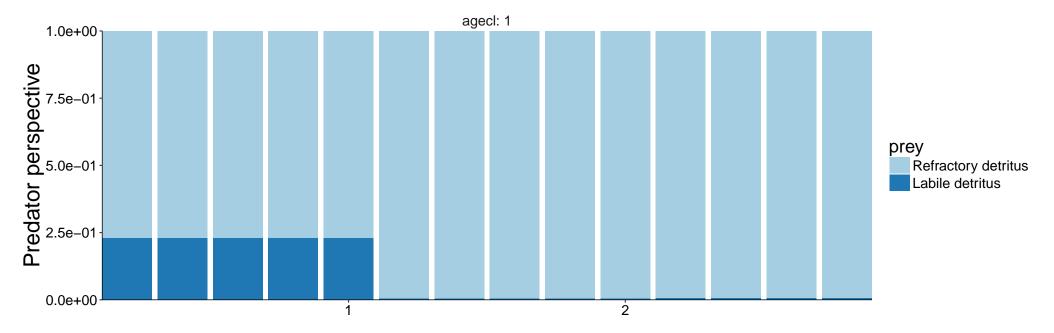
Diet proportions for species: Diatom



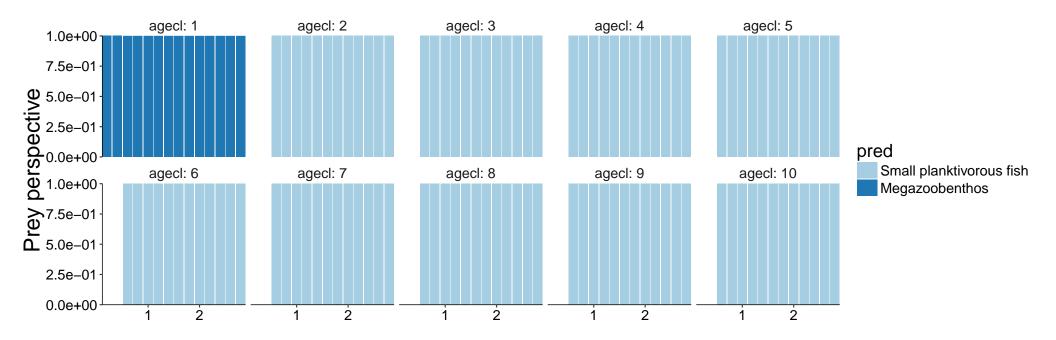
Diet proportions for species: Labile detritus

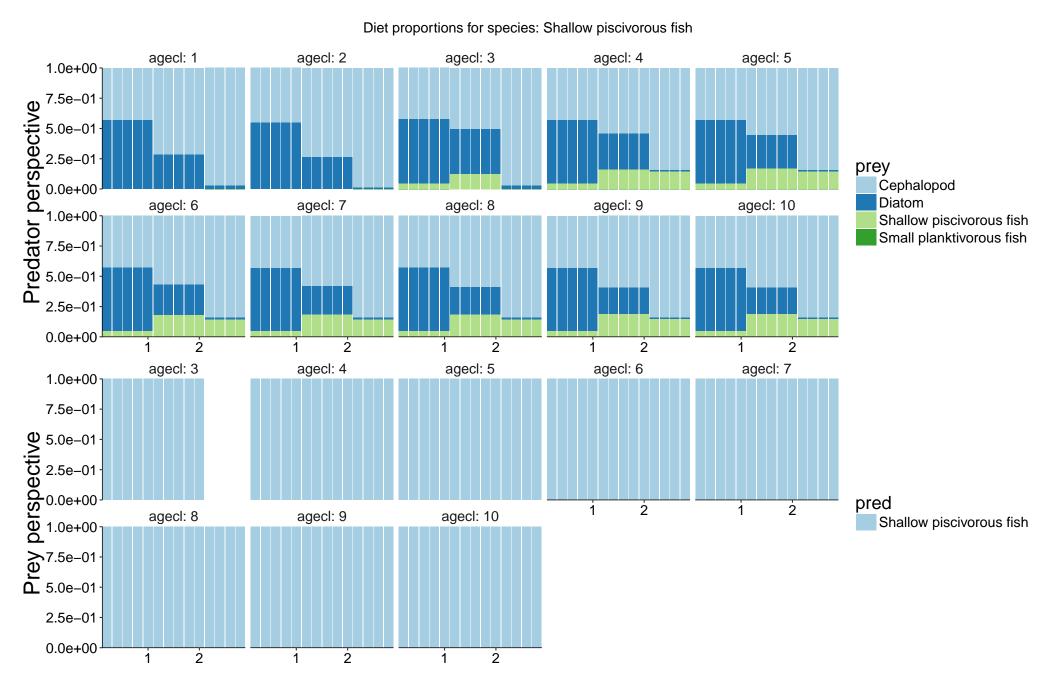


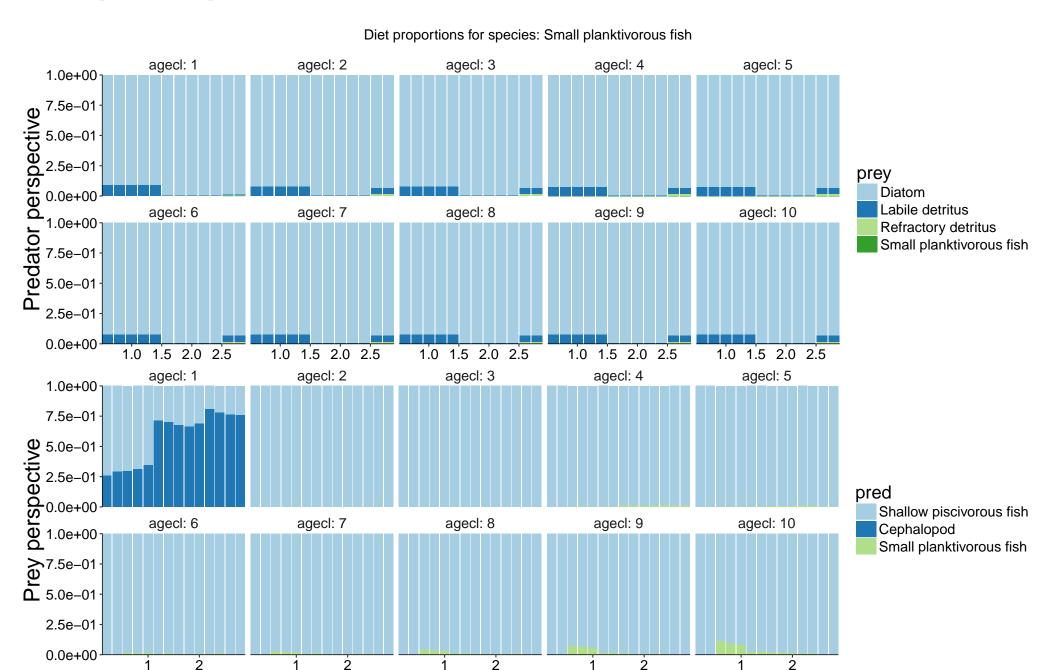




Diet proportions for species: Refractory detritus



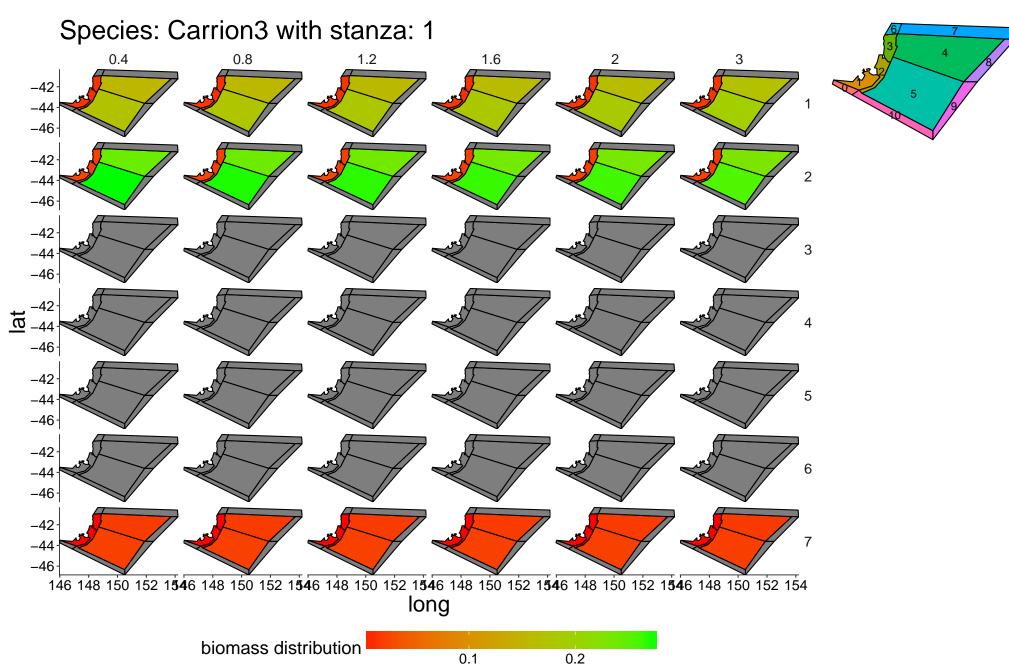


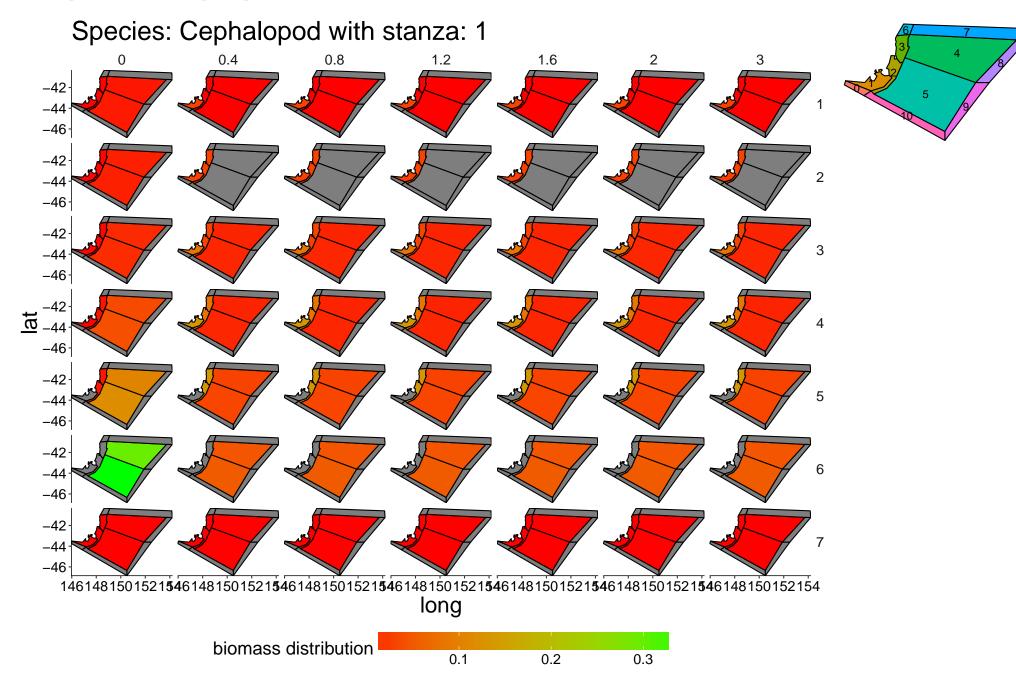


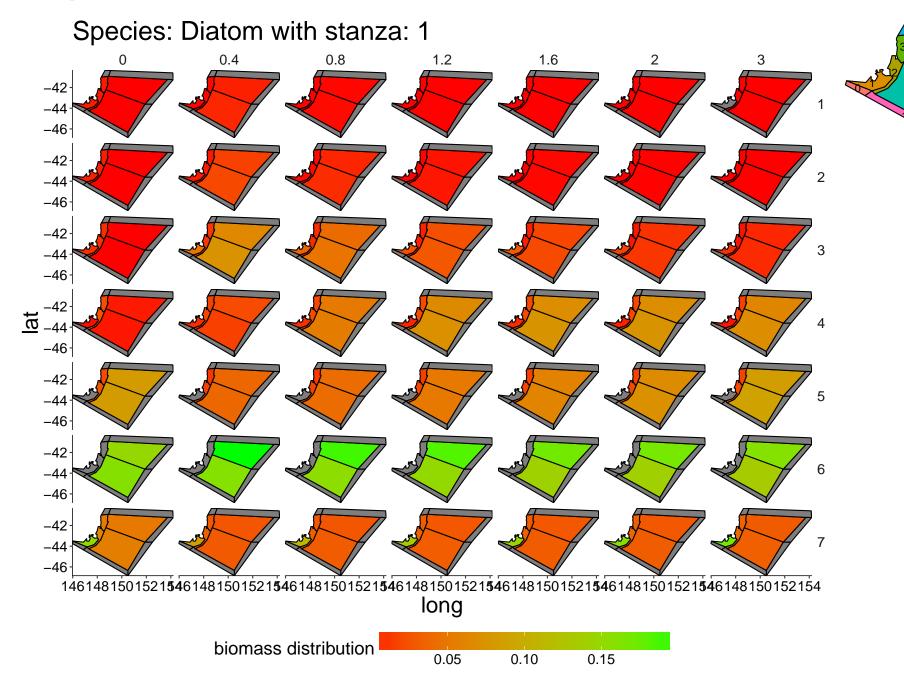
### 6 Spatial Plots 1

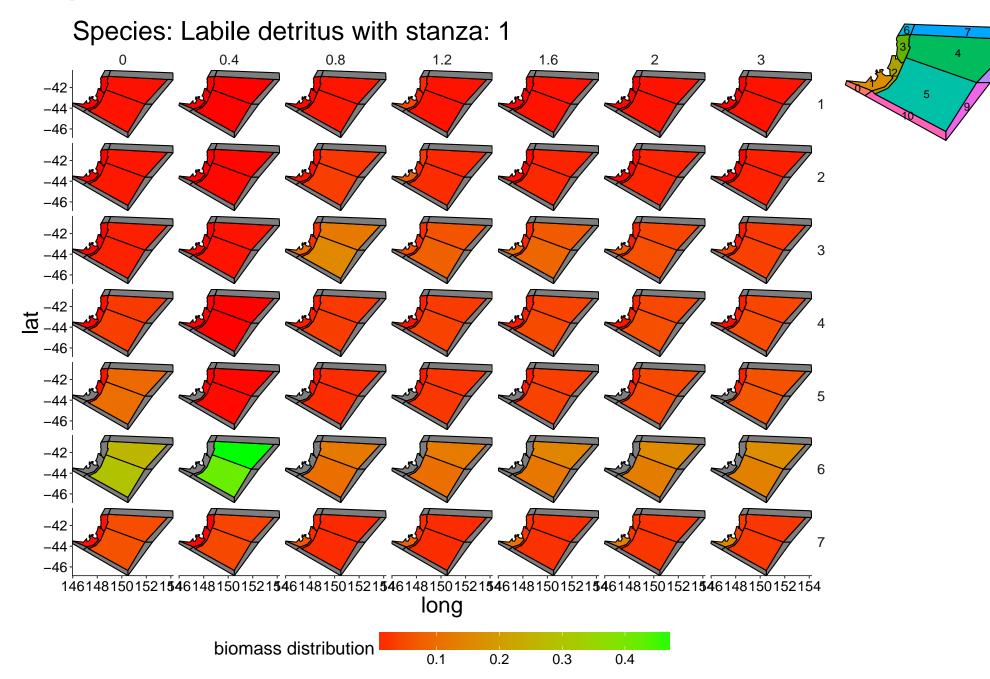
## Joining, by = "polygon"

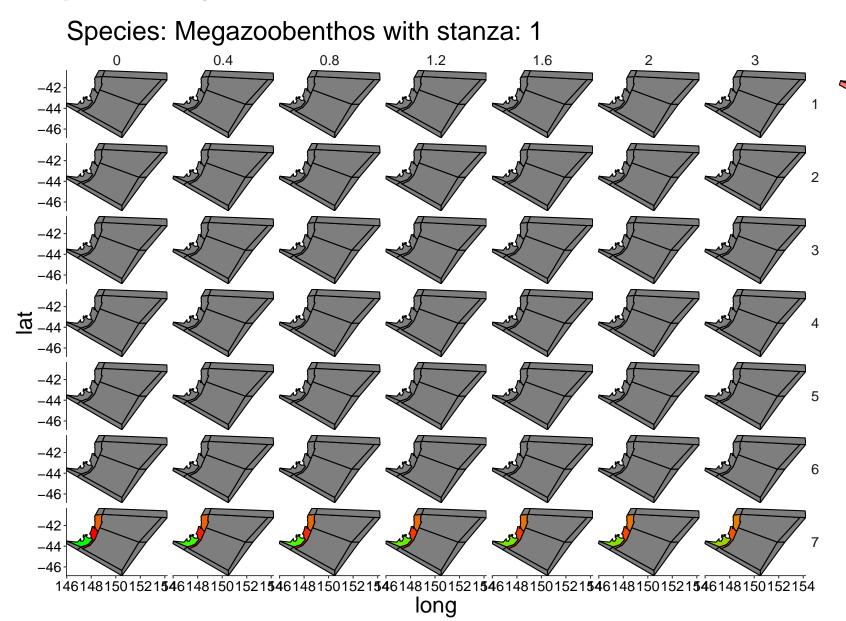
#### 6.1 Spatial Plot 1: Carrion3 1



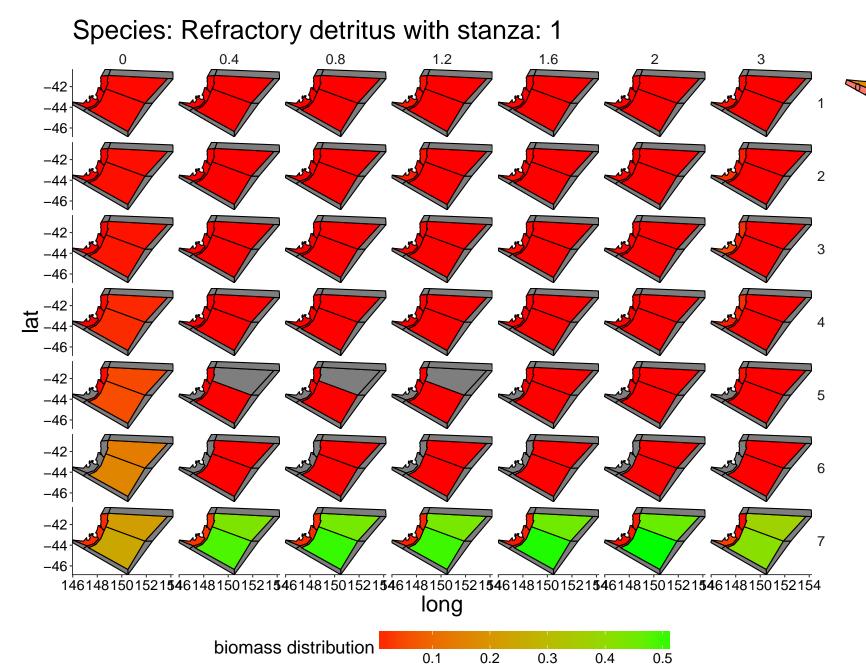


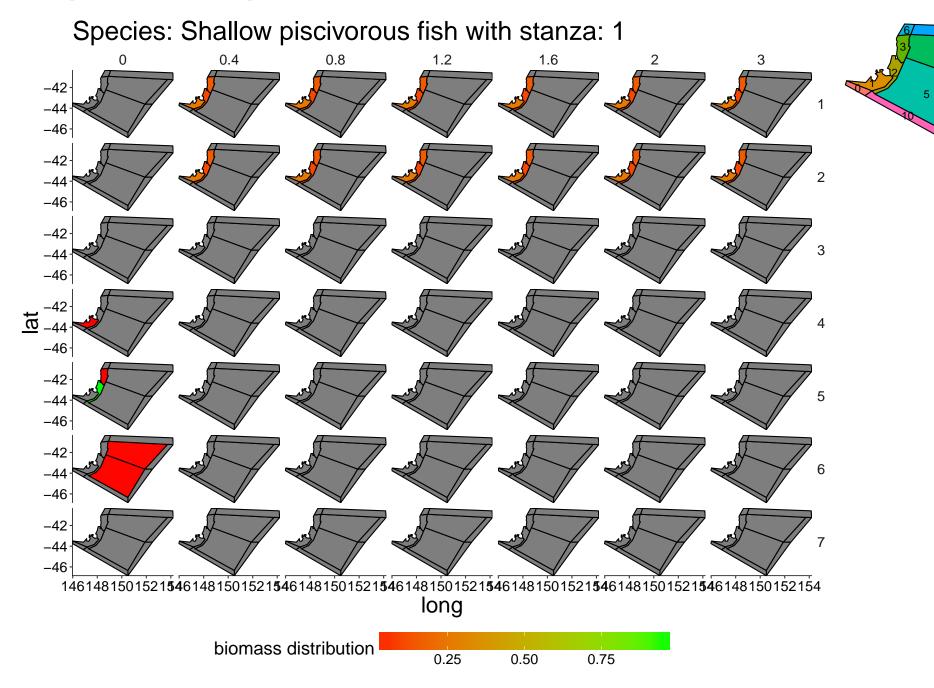


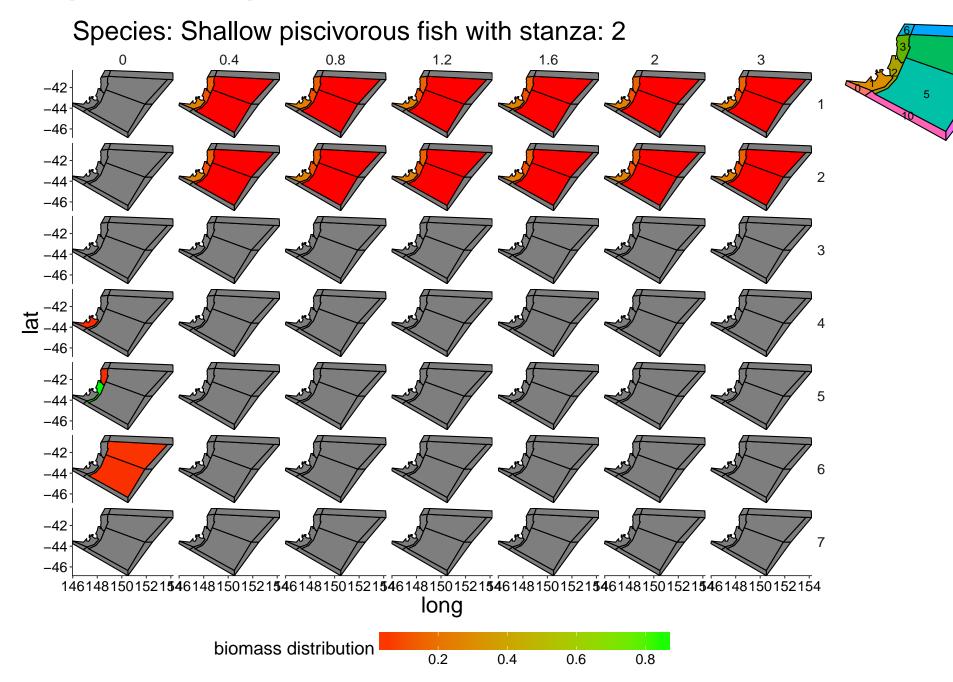


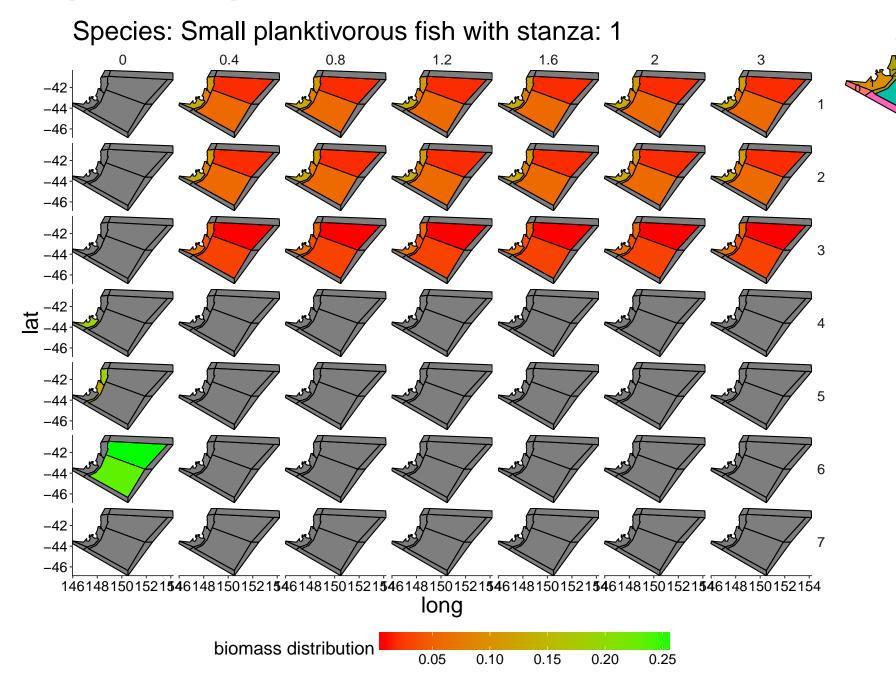


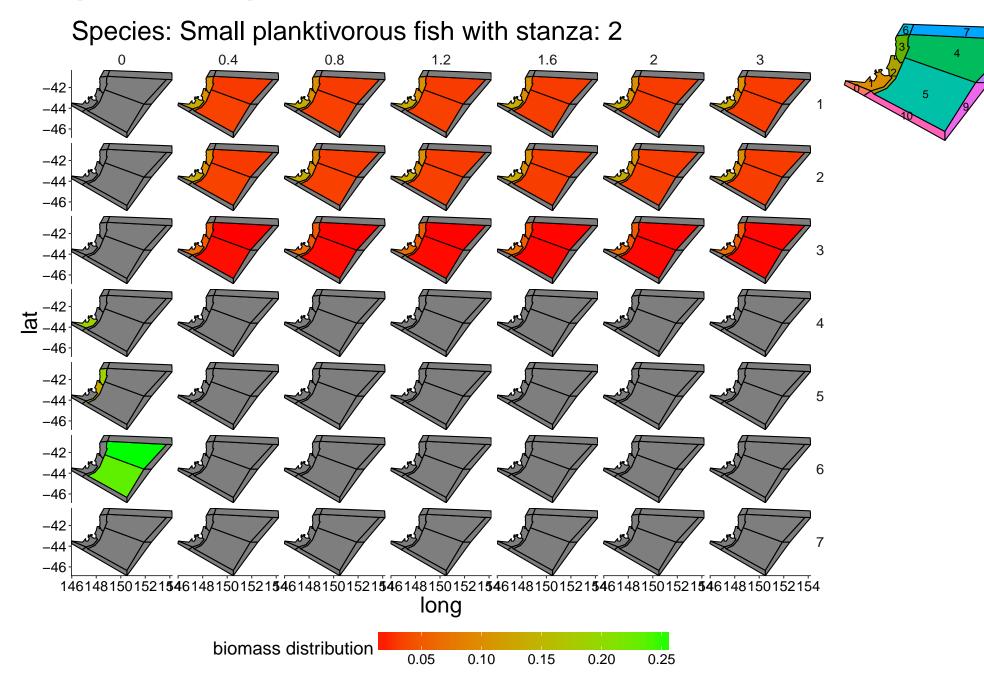
biomass distribution 0.32 0.33 0.34 0.35 0.36











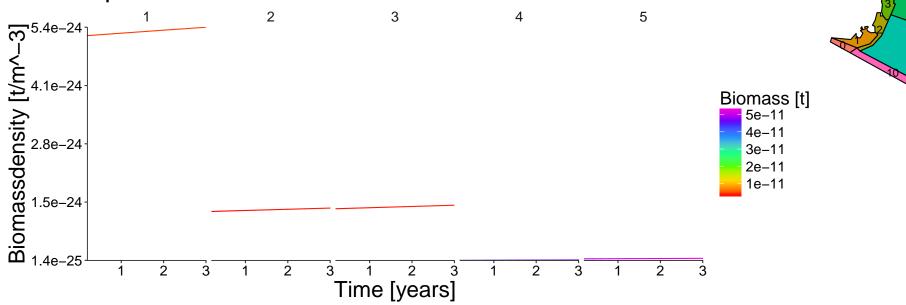
### 7 Spatial Plots 2

```
## Joining, by = c("time", "polygon")

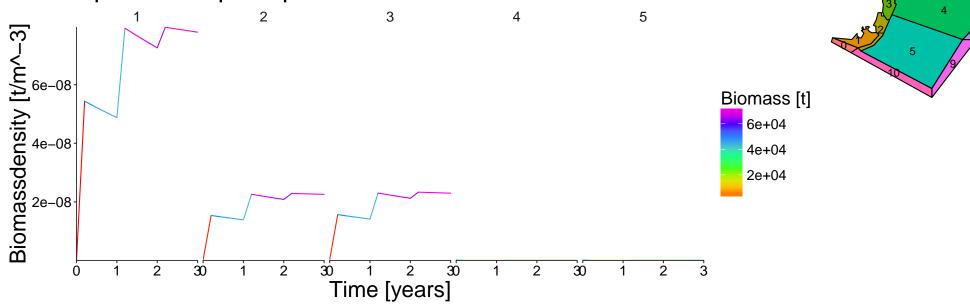
## geom_path: Each group consists of only one observation. Do you need to
## adjust the group aesthetic?

## geom_path: Each group consists of only one observation. Do you need to
## adjust the group aesthetic?
```

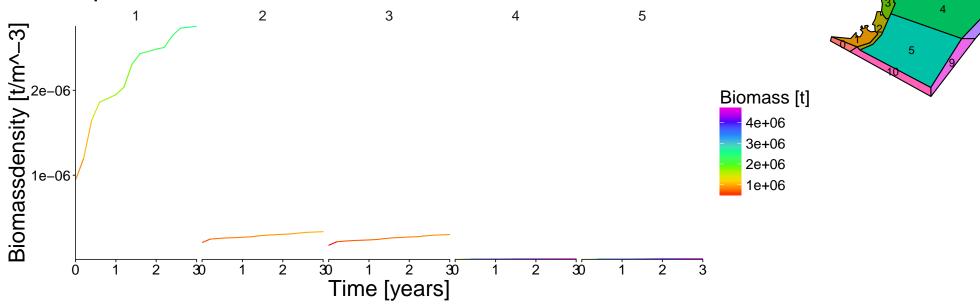
Species: Carrion3 with stanza: 1



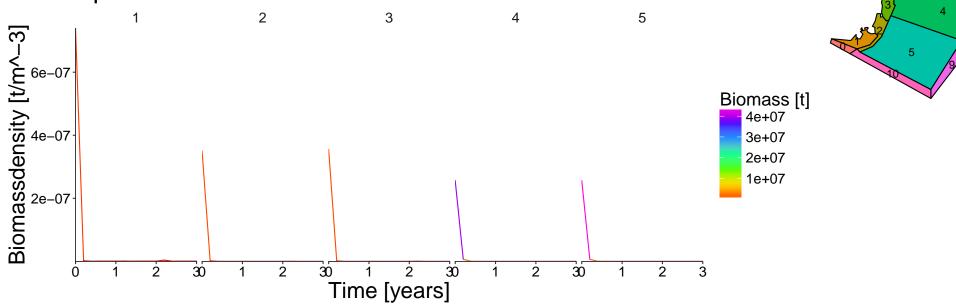
Species: Cephalopod with stanza: 1



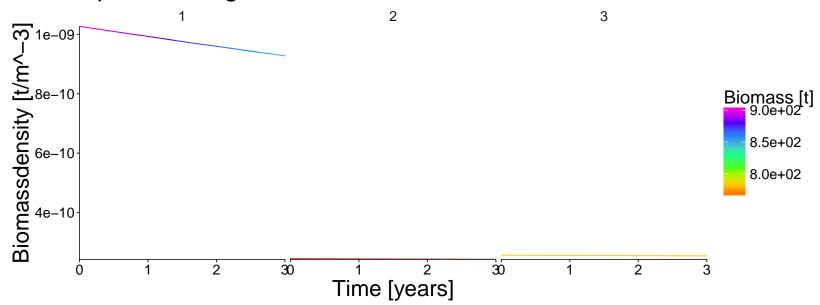


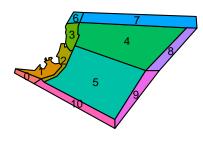




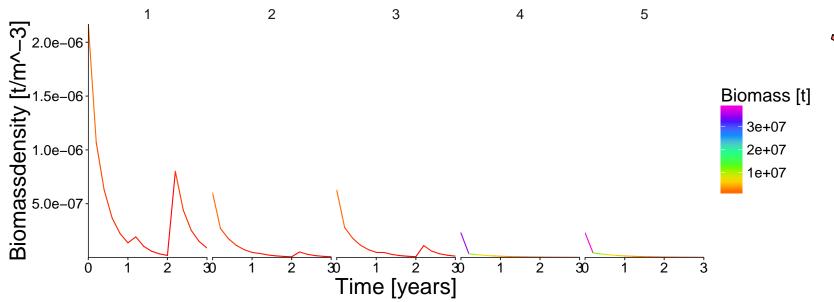


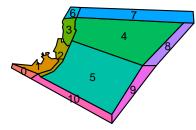
# Species: Megazoobenthos with stanza: 1





## Species: Refractory detritus with stanza: 1

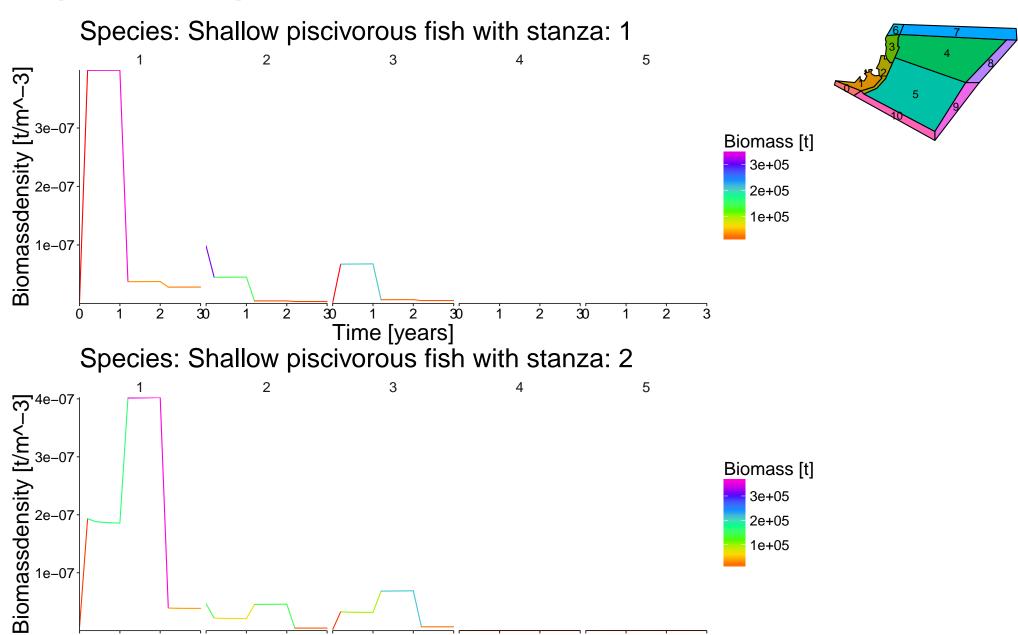




2

30

ż



30

Time [years]

30

2

ż

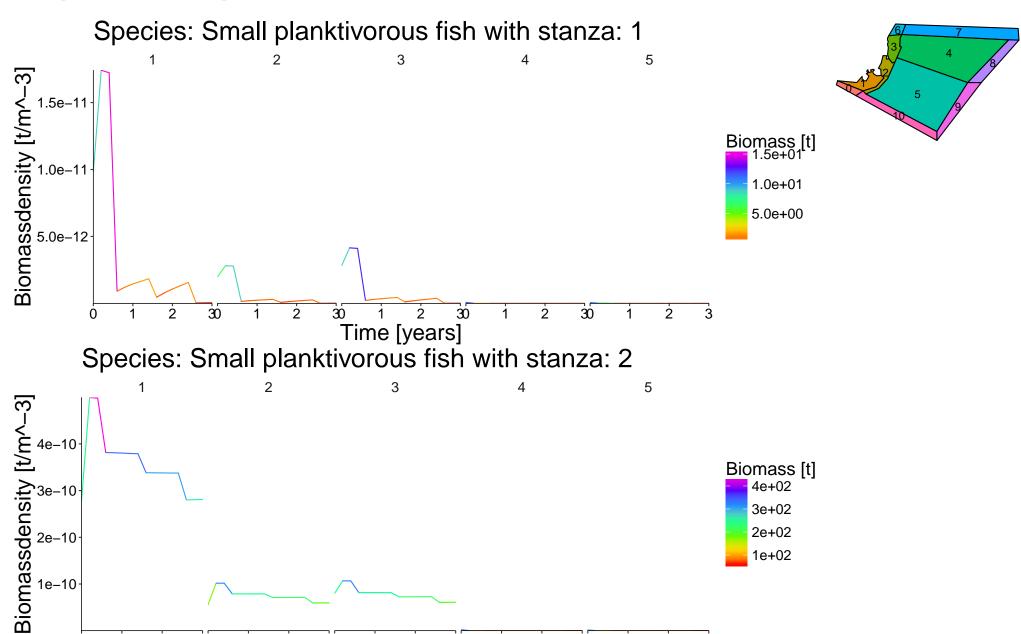
Ó

2

30

ż

30



30

Time [years]

30

2

ż