

# model-calibration

*Alexander Keth*

*2017-08-16*

## Contents

0.1	User Input . . . . .	3
<b>1</b>	<b>Whole system plots!</b>	<b>4</b>
1.1	Overall biomass . . . . .	4
1.2	Biomass timeseries . . . . .	5
1.3	Biomass@age timeseries . . . . .	6
1.4	Number timeseries . . . . .	7
1.5	Number@age timeseries . . . . .	8
1.6	SSB & Recruitment . . . . .	9
1.7	Biomass benchmark . . . . .	10
1.8	Biomass benchmark 2 . . . . .	11
1.9	Physics . . . . .	12
<b>2</b>	<b>Physics</b>	<b>13</b>
2.1	Chl_a . . . . .	13
2.2	Denitrification . . . . .	14
2.3	NH3 . . . . .	15
2.4	NO3 . . . . .	16
2.5	Temp . . . . .	17
2.6	salt . . . . .	18
2.7	Fluxes 1 . . . . .	19
2.8	Fluxes 2 . . . . .	20
2.9	Relative change of water column height compared to nominal_dz . . . . .	21
<b>3</b>	<b>Calibration plots</b>	<b>22</b>
3.1	Structural nitrogen . . . . .	22
3.2	Reserve nitrogen . . . . .	23
3.3	Biomass per ageclass . . . . .	24
3.4	Eat per ageclass . . . . .	25
3.5	Growth per ageclass . . . . .	26
3.6	Growth in relation to initial conditions . . . . .	27
3.7	Numbers . . . . .	28
3.8	Biomass . . . . .	29
<b>4</b>	<b>Distribution plots</b>	<b>30</b>
4.1	Numbers @ age . . . . .	30
4.2	Biomass @ age . . . . .	31
<b>5</b>	<b>Diet Plots</b>	<b>32</b>
5.1	Diet plot 1: Cephalopod . . . . .	33

5.2	Diet plot 2: Diatom	34
5.3	Diet plot 3: Labile detritus	35
5.4	Diet plot 4: Megazoobenthos	36
5.5	Diet plot 5: Refractory detritus	37
5.6	Diet plot 6: Shallow piscivorous fish	38
5.7	Diet plot 7: Small planktivorous fish	39
<b>6</b>	<b>Spatial Plots 1</b>	<b>40</b>
6.1	Spatial Plot 1: Carrion3 1	40
6.2	Spatial Plot 2: Cephalopod 1	41
6.3	Spatial Plot 3: Diatom 1	42
6.4	Spatial Plot 4: Labile detritus 1	43
6.5	Spatial Plot 5: Megazoobenthos 1	44
6.6	Spatial Plot 6: Refractory detritus 1	45
6.7	Spatial Plot 7: Shallow piscivorous fish 1	46
6.8	Spatial Plot 8: Shallow piscivorous fish 2	47
6.9	Spatial Plot 9: Small planktivorous fish 1	48
6.10	Spatial Plot 10: Small planktivorous fish 2	49
<b>7</b>	<b>Spatial Plots 2</b>	<b>50</b>
7.1	Spatial Plot 1: Carrion3	51
7.2	Spatial Plot 2: Cephalopod	52
7.3	Spatial Plot 3: Diatom	53
7.4	Spatial Plot 4: Labile detritus	54
7.5	Spatial Plot 5: Megazoobenthos	55
7.6	Spatial Plot 6: Refractory detritus	56
7.7	Spatial Plot 7: Shallow piscivorous fish	57
7.8	Spatial Plot 8: Small planktivorous fish	58

NOTE: This vignette 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.R` 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 `model-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")
```

## 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")
```

# 1 Whole system plots!

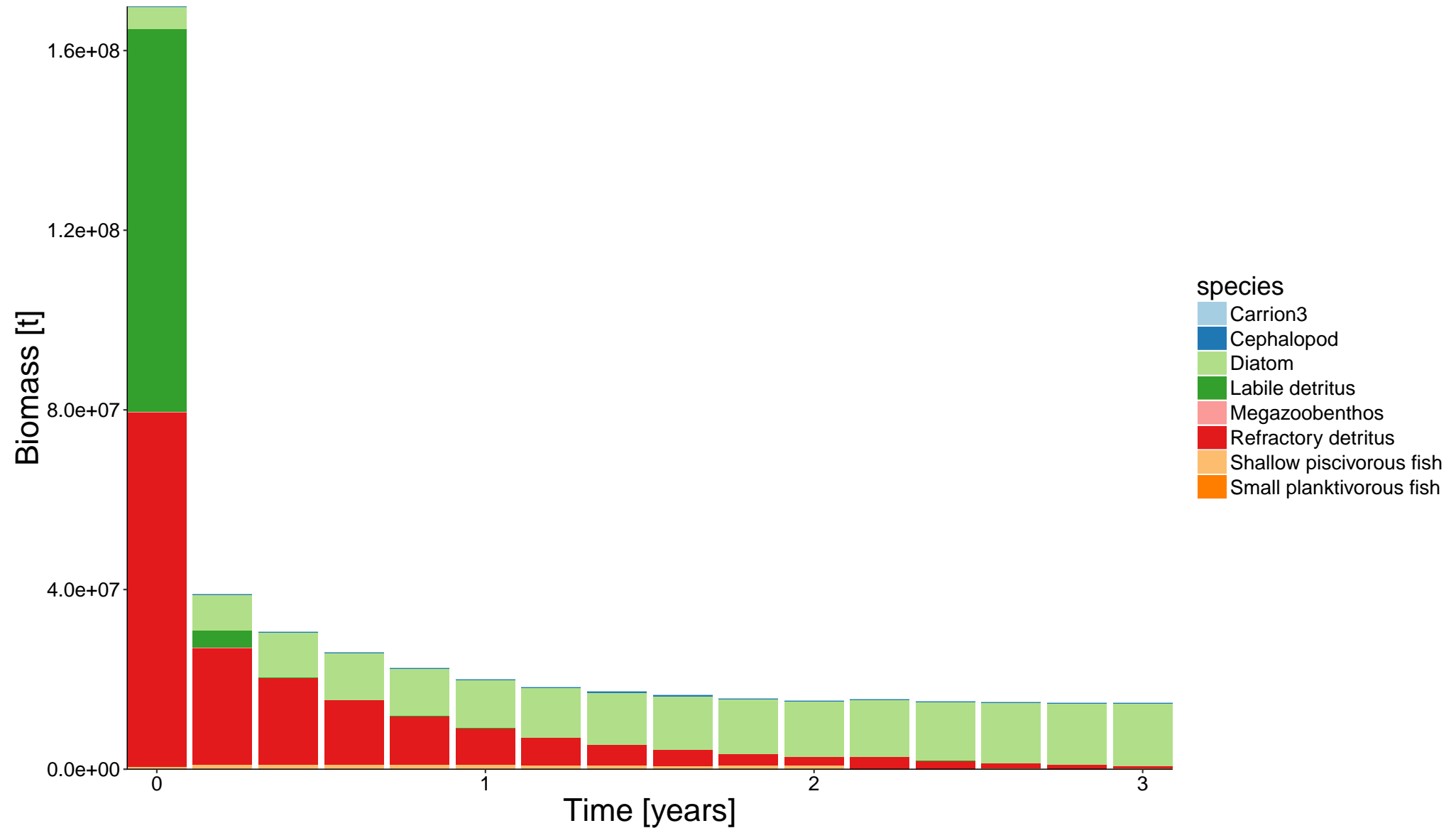
## 1.1 Overall biomass

```
df_bio <- combine_groups(result$biomass, group_col = "species", combine_thresh = 10)
```

```
## Joining, by = "species"
```

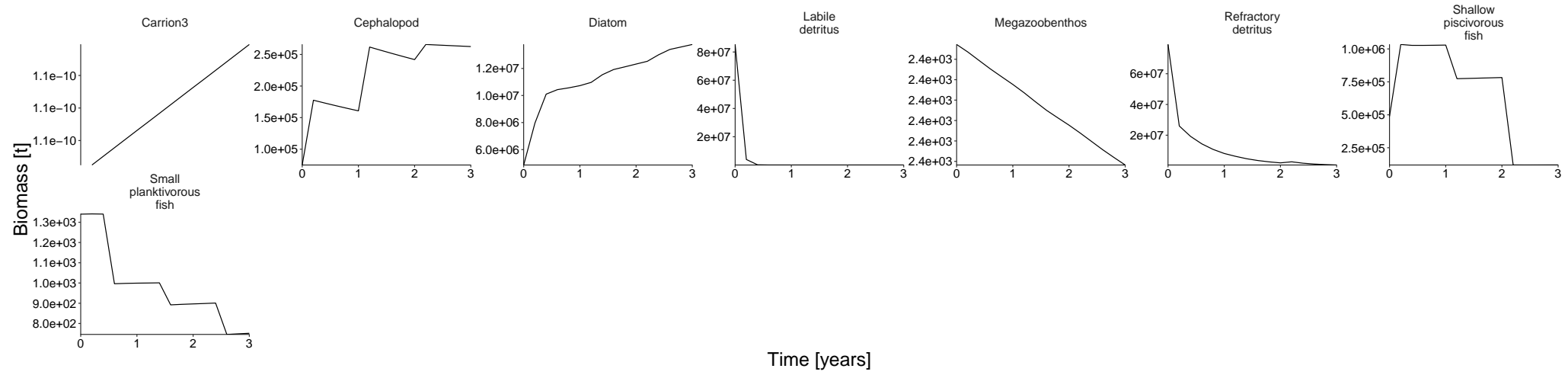
```
plot <- plot_bar(df_bio)
```

```
update_labels(plot, labels = gen_labels)
```



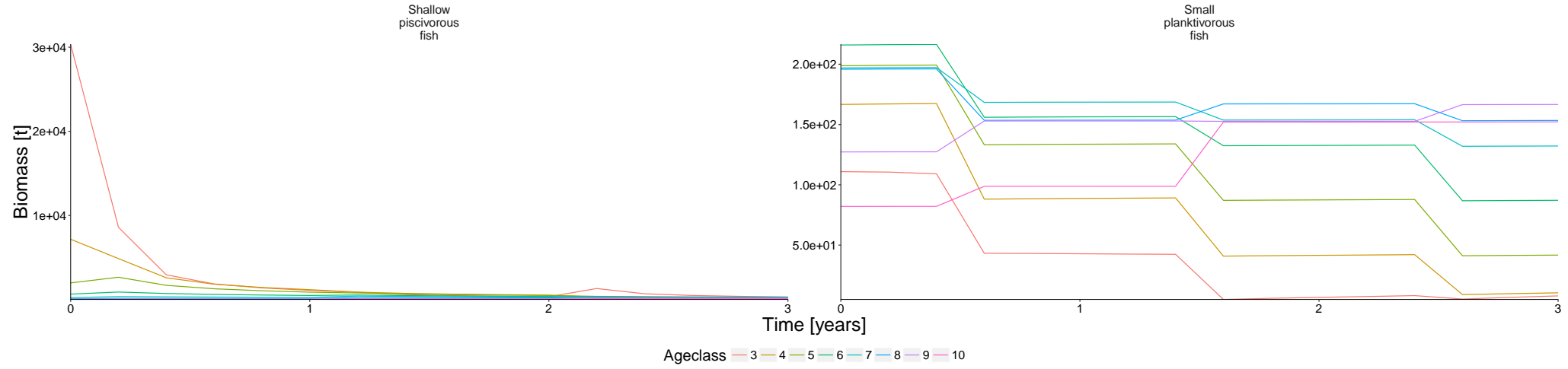
## 1.2 Biomass timeseries

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



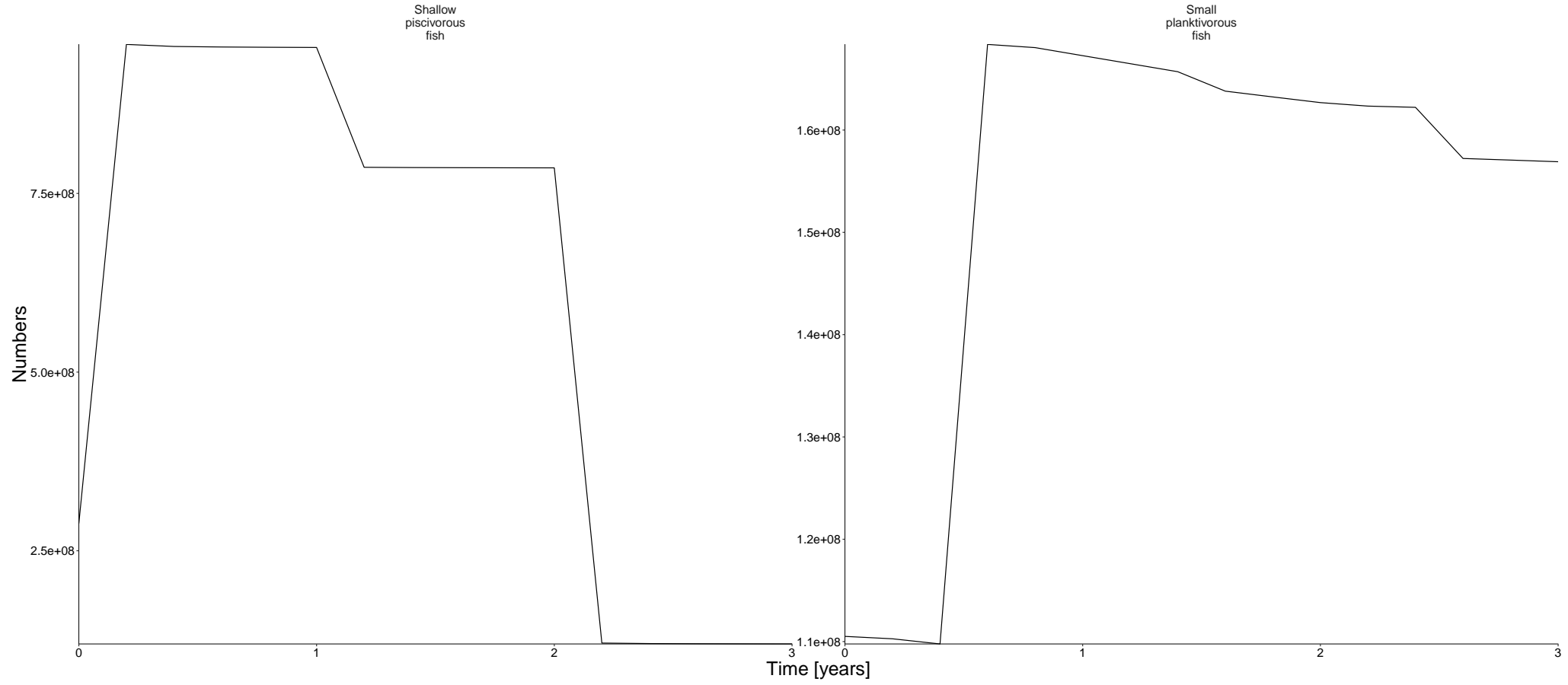
### 1.3 Biomass@age timeseries

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



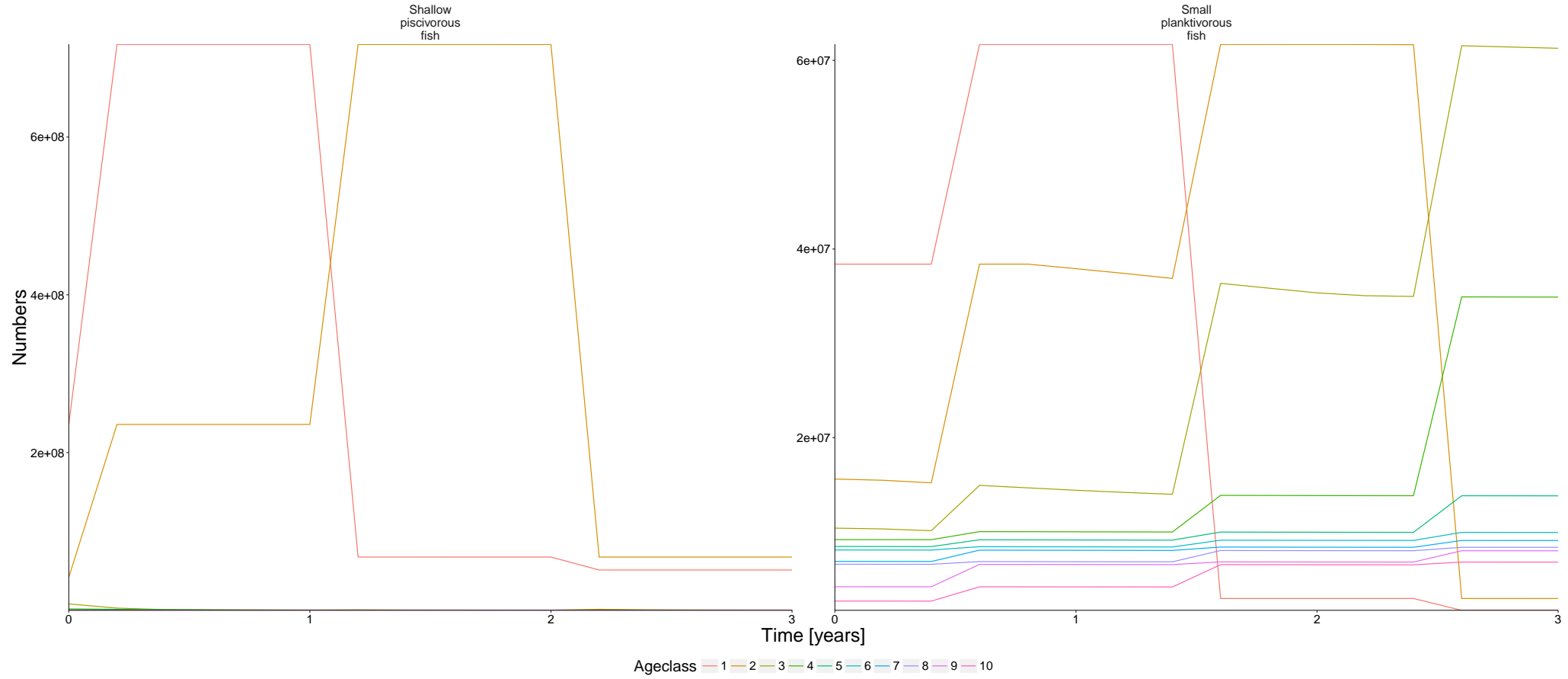
## 1.4 Number timeseries

```
plot <- plot_line(result$numns)
update_labels(p = plot, labels = list(x = "Time [years]", y = "Numbers"))
```



## 1.5 Number@age timeseries

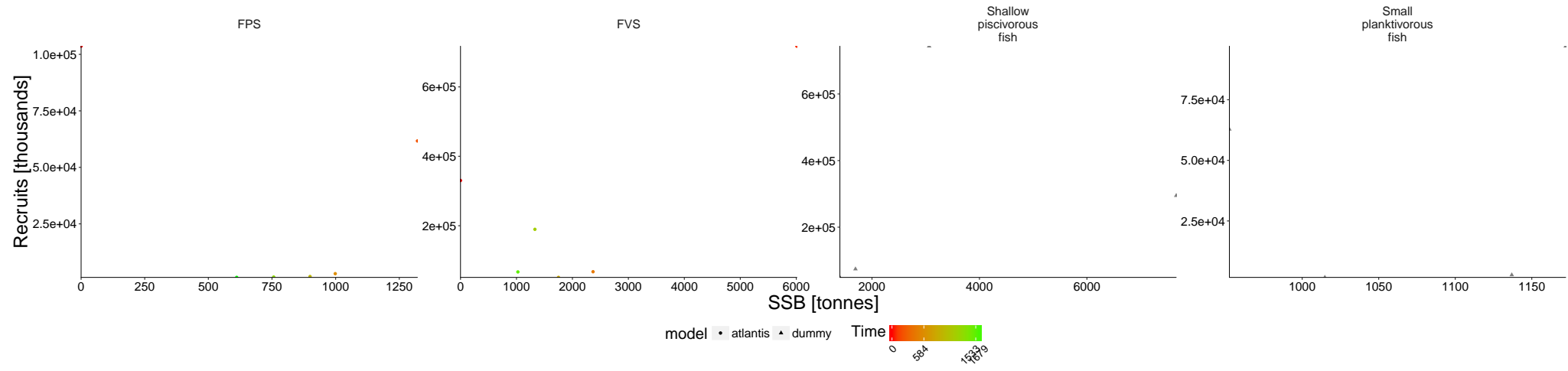
```
plot <- plot_line(result$num_age, col = "agec1")  
update_labels(p = plot, labels = list(x = "Time [years]", y = "Numbers", colour = "Ageclass"))
```





## 1.6 SSB & Recruitment

```
plot_rec(result$ssb_rec, ex_data = ex_rec_ssb)
```



## 1.7 Biomass benchmark

```
names(ex_bio)[names(ex_bio) == "biomass"] <- "atoutput"
```

```
data <- result$biomass
```

```
data$model <- "atlantis"
```

```
comp <- rbind(ex_bio, data, stringsAsFactors = FALSE)
```

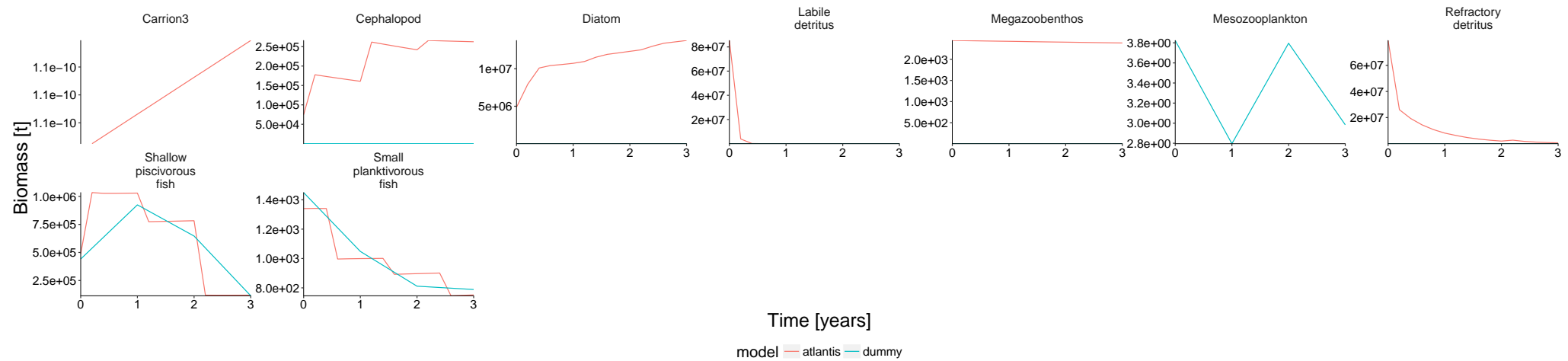
```
# Show atlantis as first factor!
```

```
comp$model <- factor(comp$model, levels = c("atlantis", sort(unique(comp$model))[sort(unique(comp$model)) != "atlantis"]))
```

```
# Create plot
```

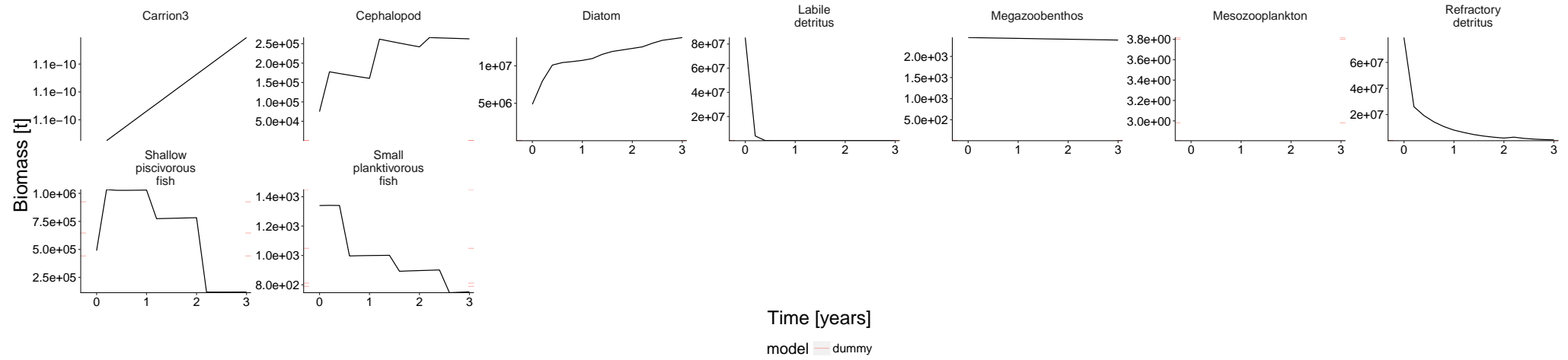
```
plot <- plot_line(comp, col = "model")
```

```
update_labels(plot, gen_labels)
```



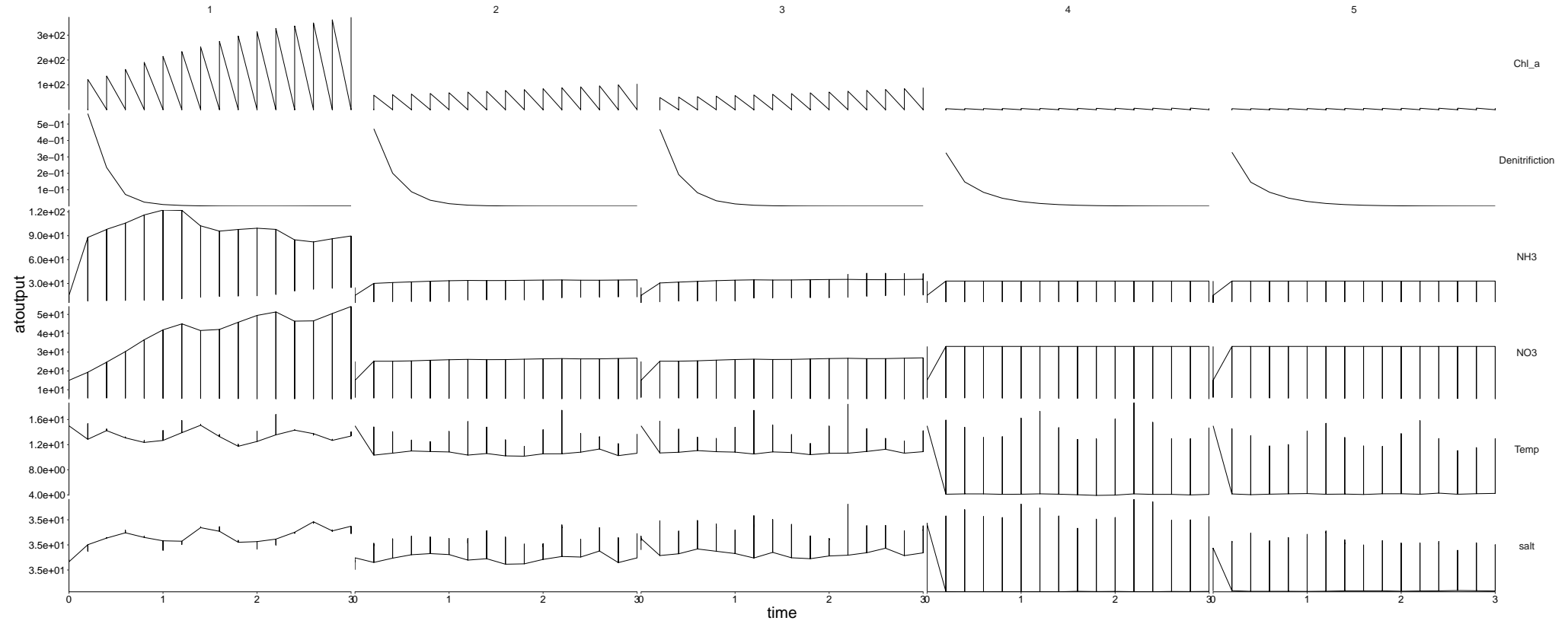
## 1.8 Biomass benchmark 2

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



## 1.9 Physics

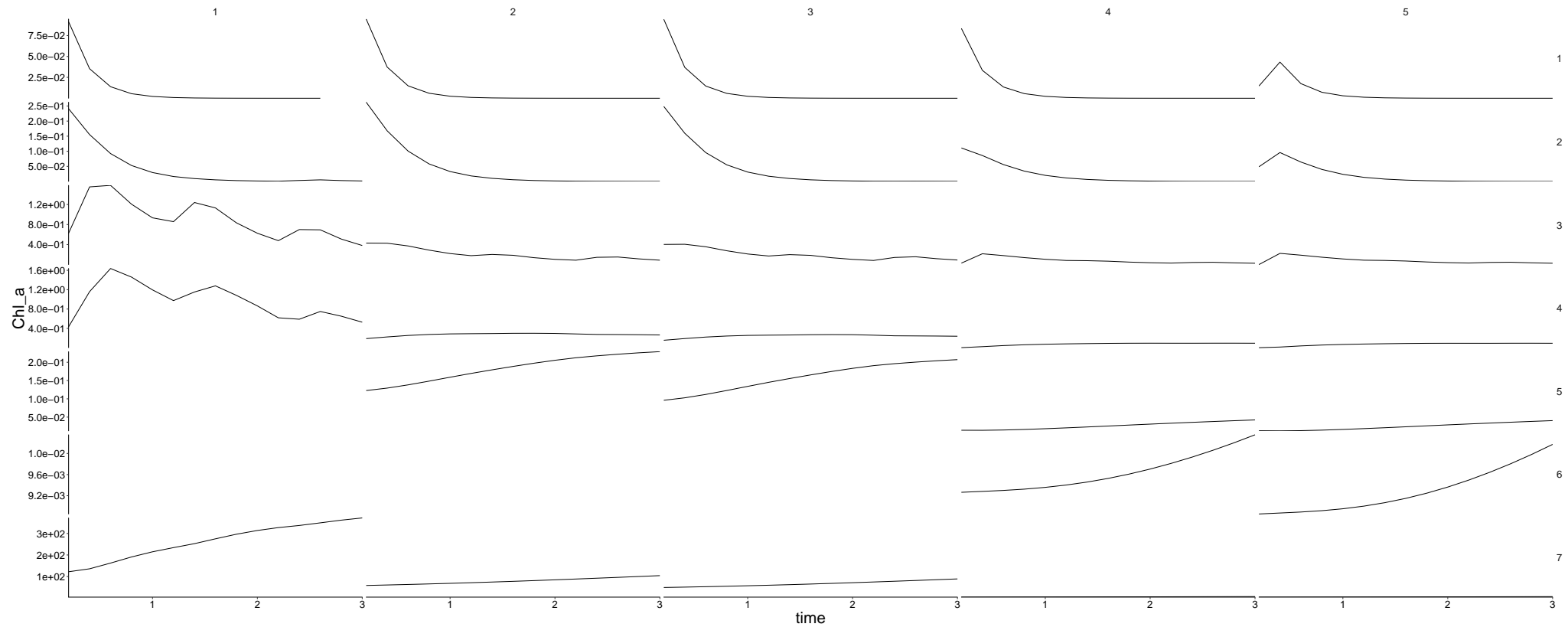
```
plot <- plot_line(result$physics, wrap = NULL)  
custom_grid(plot, grid_x = "polygon", grid_y = "variable")
```



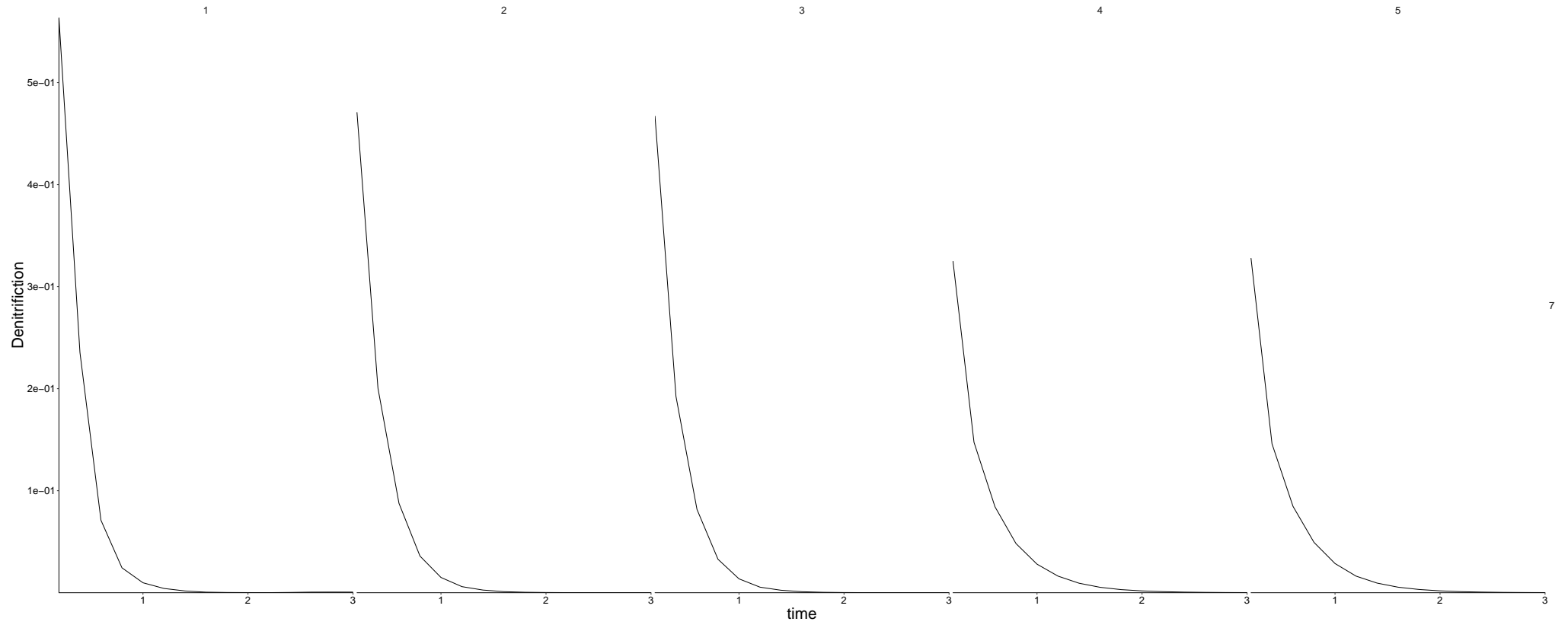
## 2 Physics

```
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")  
}
```

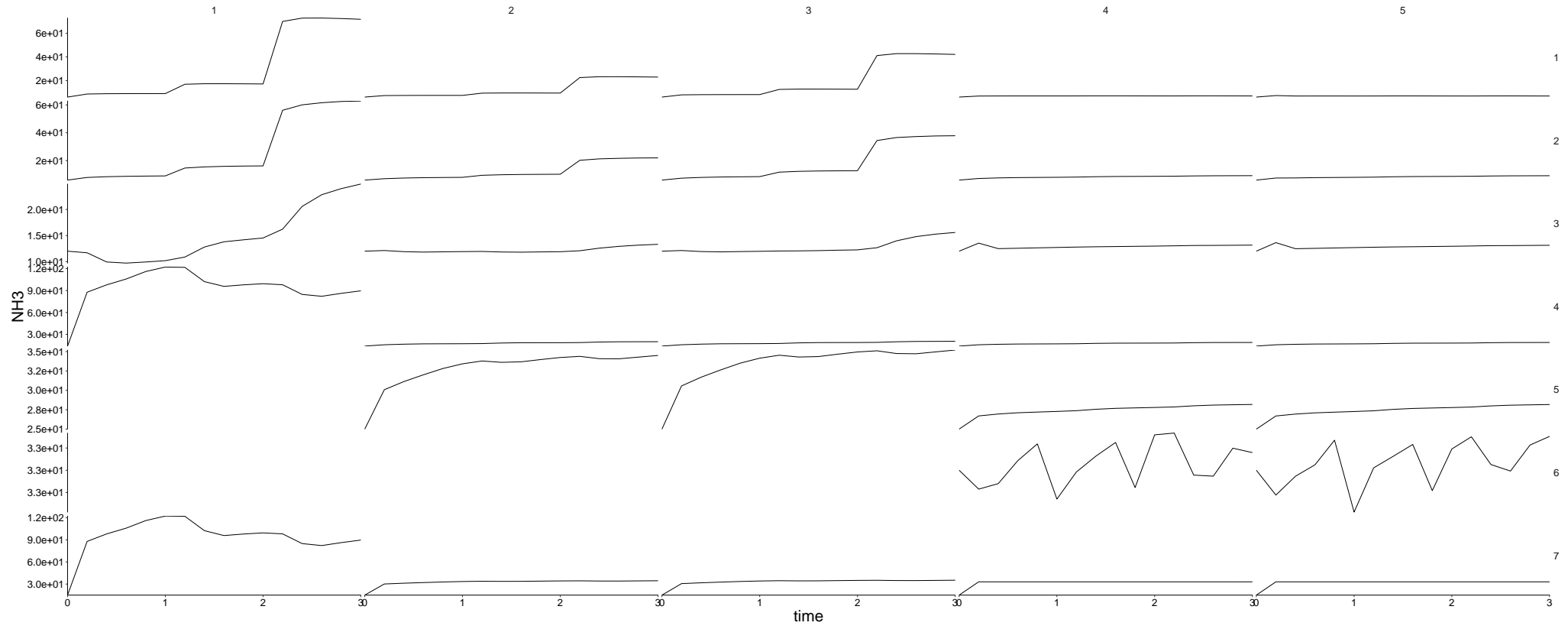
### 2.1 Chl\_a



## 2.2 Denitrification



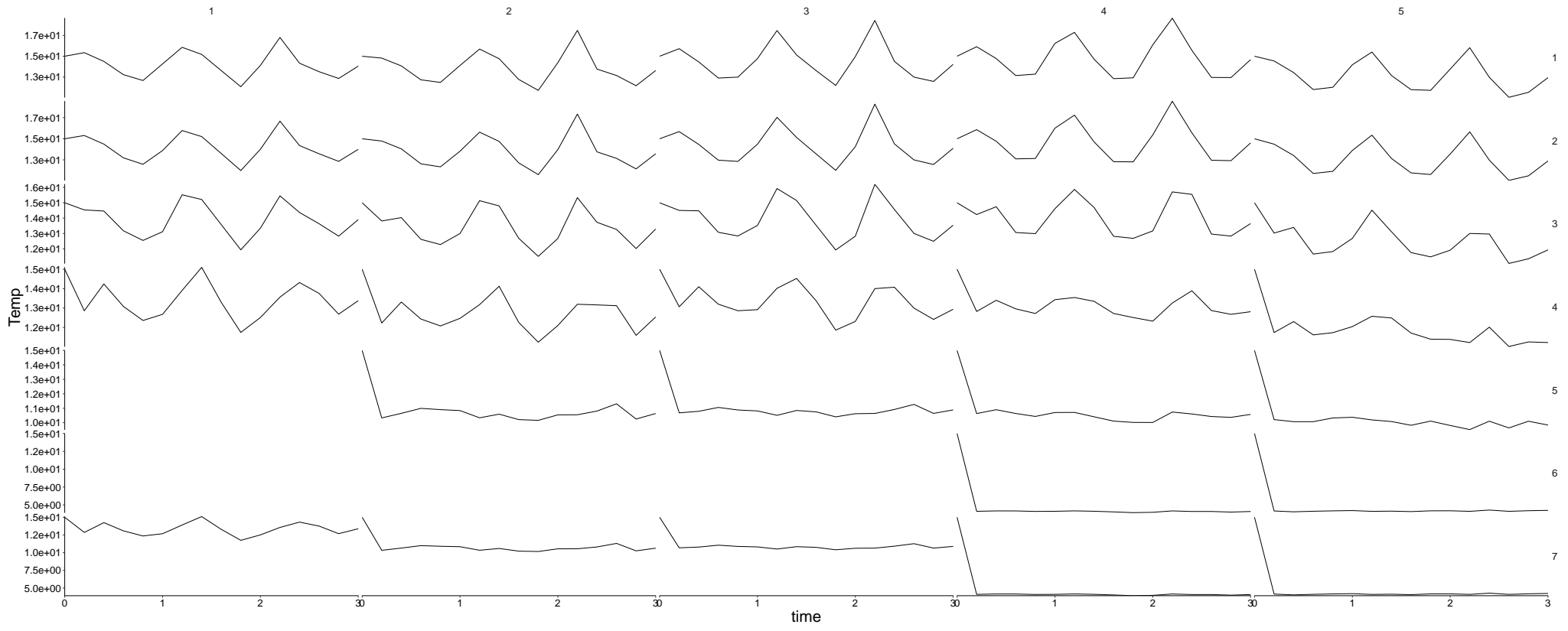
## 2.3 NH3



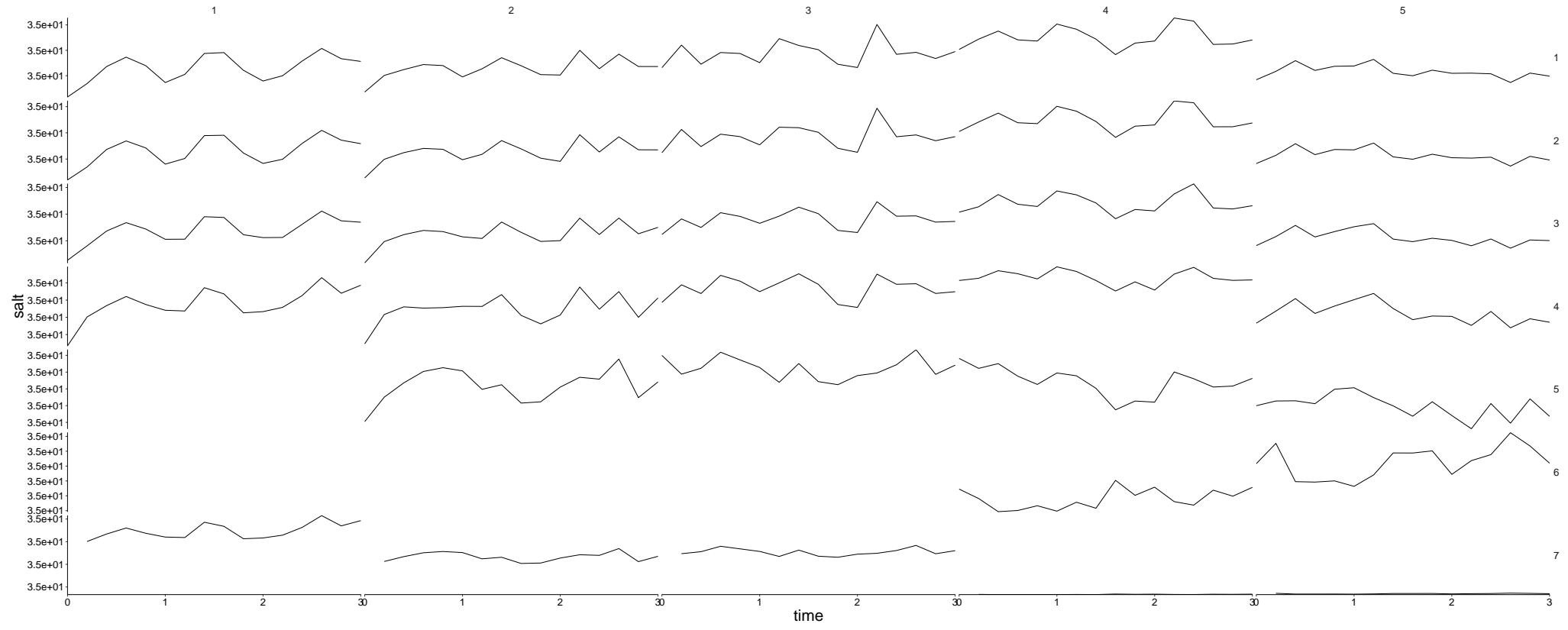




# 2.5 Temp

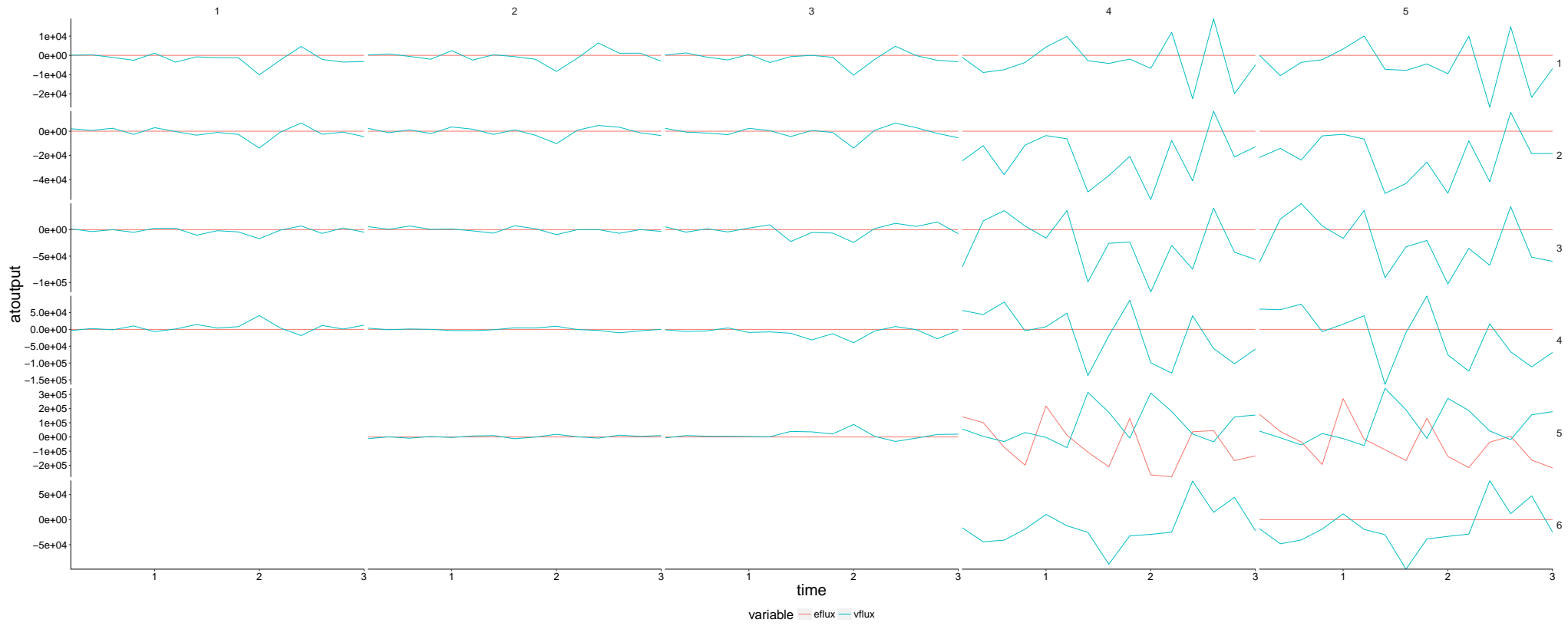


## 2.6 salt



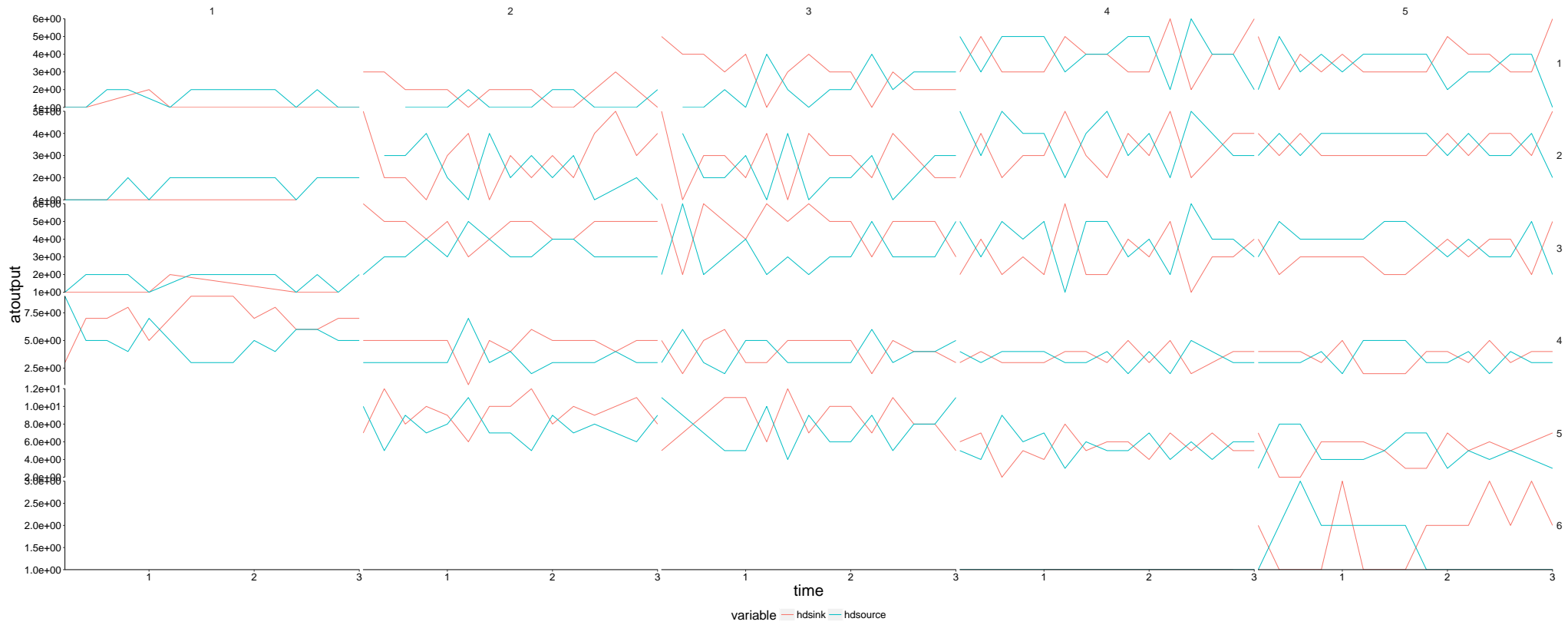
## 2.7 Fluxes 1

```
plot <- flip_layers(result$flux) %>%  
  plot_line(wrap = NULL, col = "variable")  
custom_grid(plot, grid_x = "polygon", grid_y = "layer")
```



## 2.8 Fluxes 2

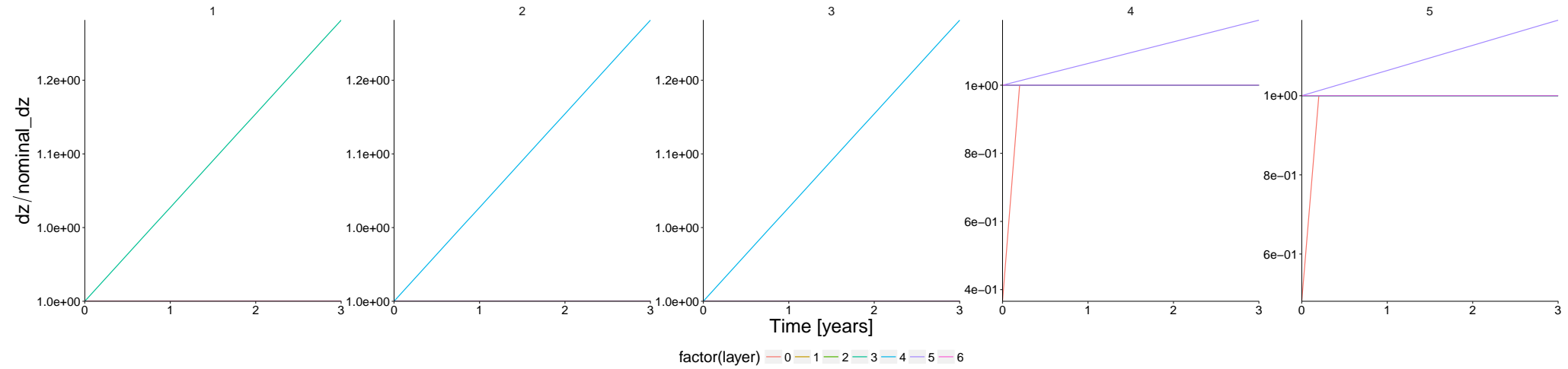
```
plot <- flip_layers(result$sink) %>%  
  plot_line(wrap = NULL, col = "variable")  
  custom_grid(plot, grid_x = "polygon", grid_y = "layer")
```



## 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
```

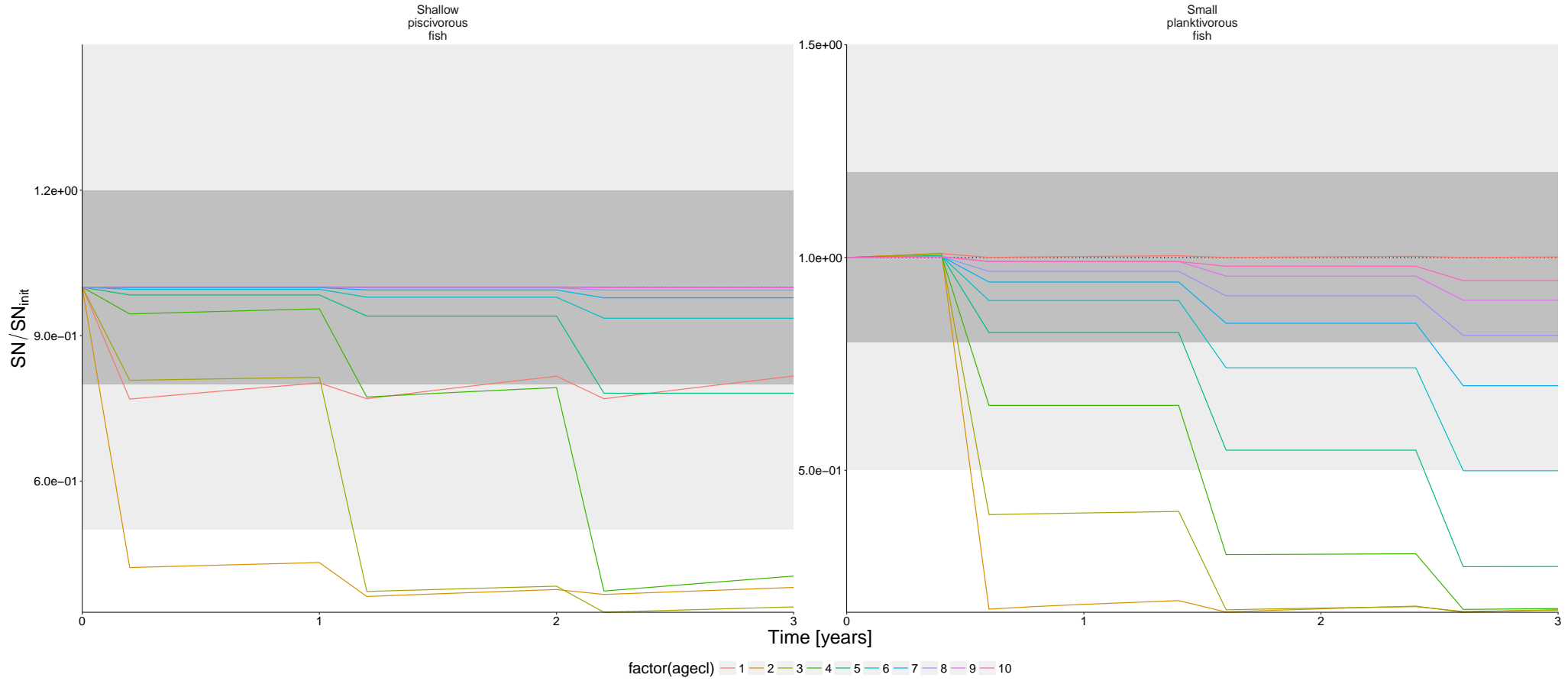
```
plot <- plot_line(check_dz, x = "time", y = "check_dz", wrap = "polygon", col = "layer")  
update_labels(plot, list(x = "Time [years]", y = expression(dz/nominal_dz)))
```



### 3 Calibration plots

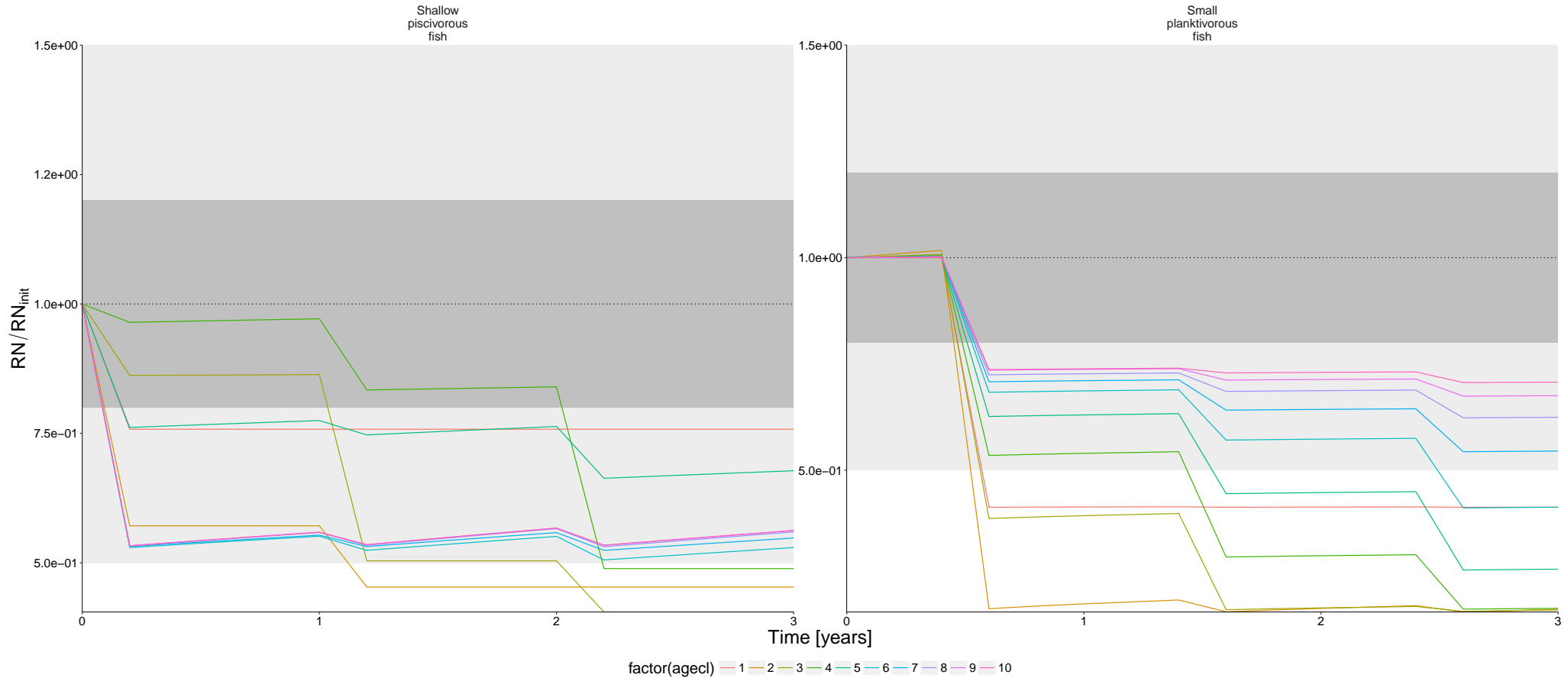
#### 3.1 Structural nitrogen

```
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)
```



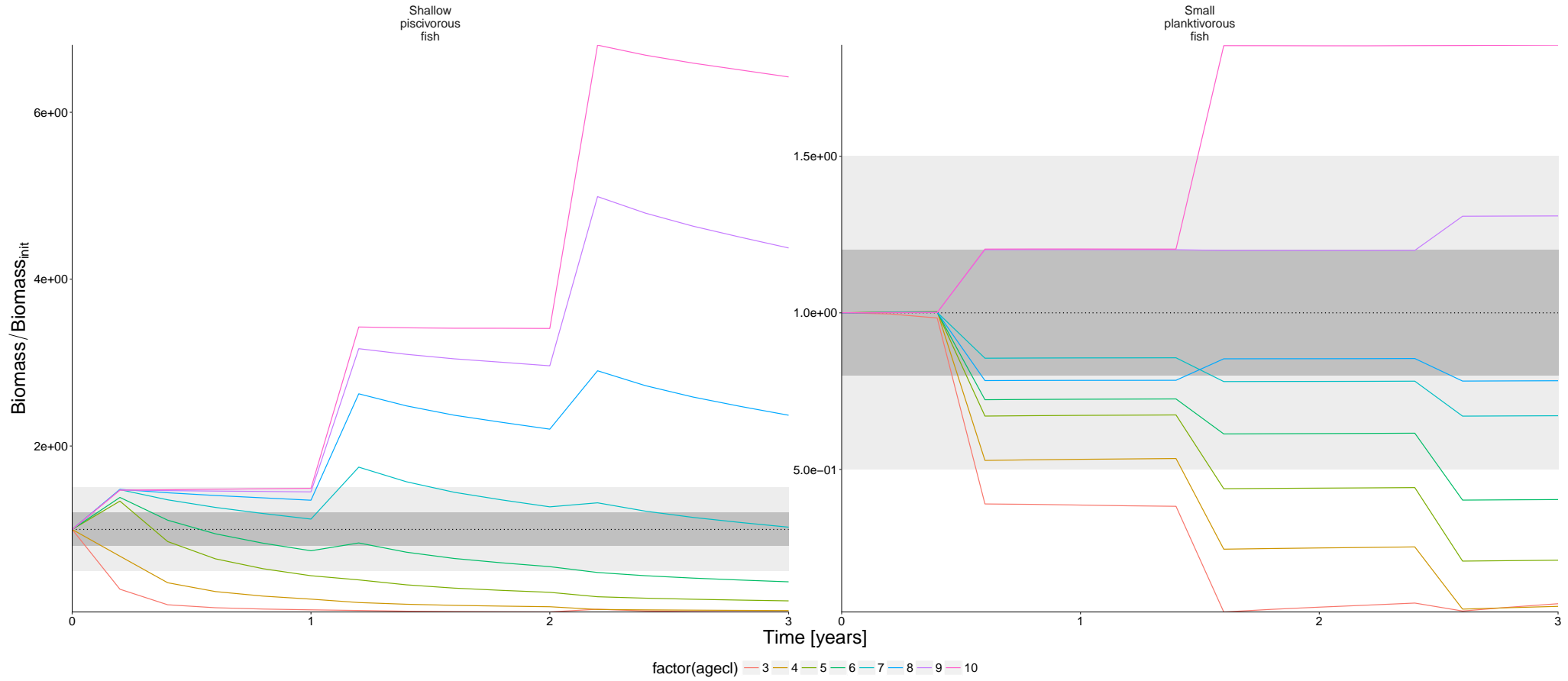
### 3.2 Reserve nitrogen

```
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)
```



### 3.3 Biomass per ageclass

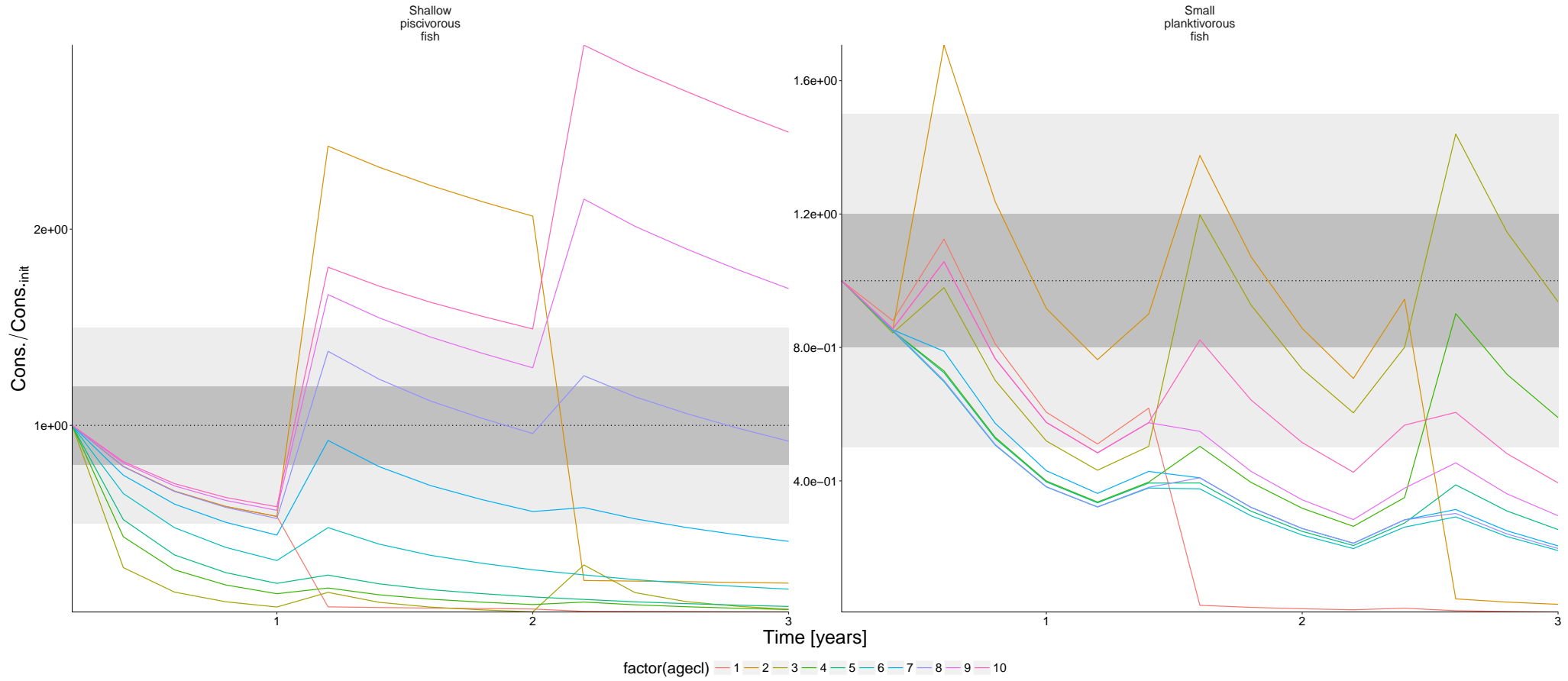
```
df_rel <- convert_relative_initial(result$biomass_age)
plot <- plot_line(df_rel, col = "agec1")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)
```





### 3.4 Eat per ageclass

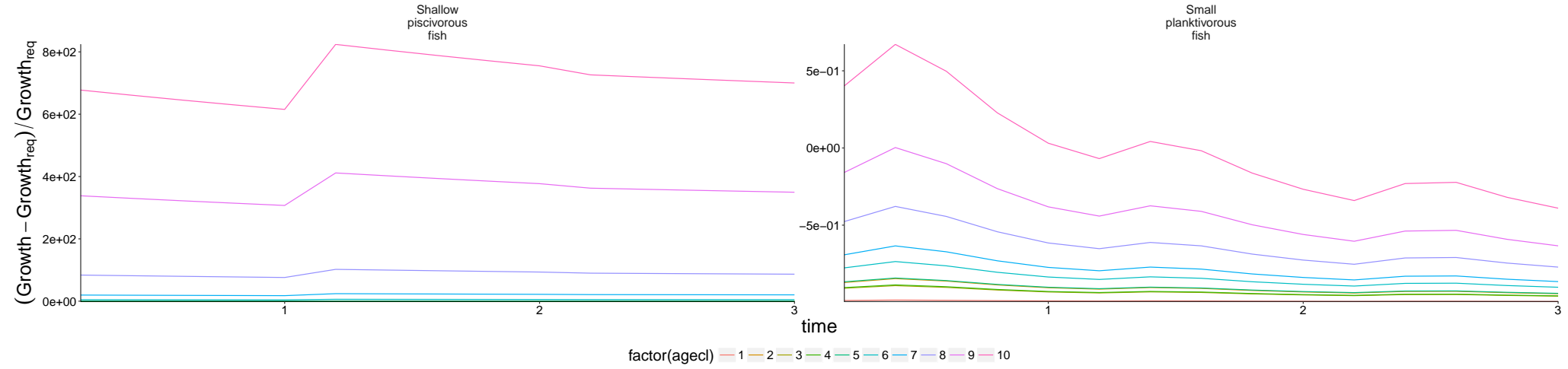
```
df_rel <- convert_relative_initial(result$eat_age)  
plot <- plot_line(df_rel, col = "agecl")  
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Cons./Cons.[init])))  
plot_add_box(plot)
```





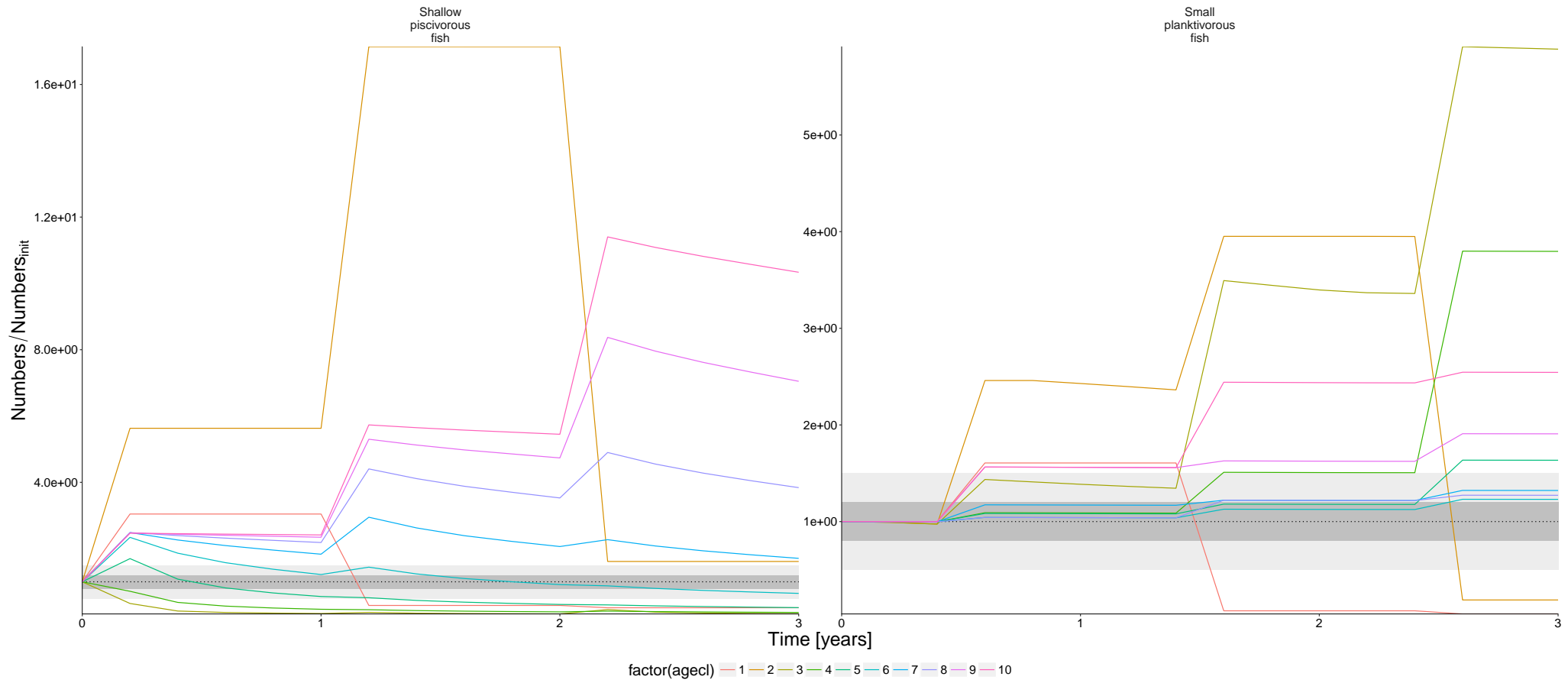
### 3.6 Growth in relation to initial conditions

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



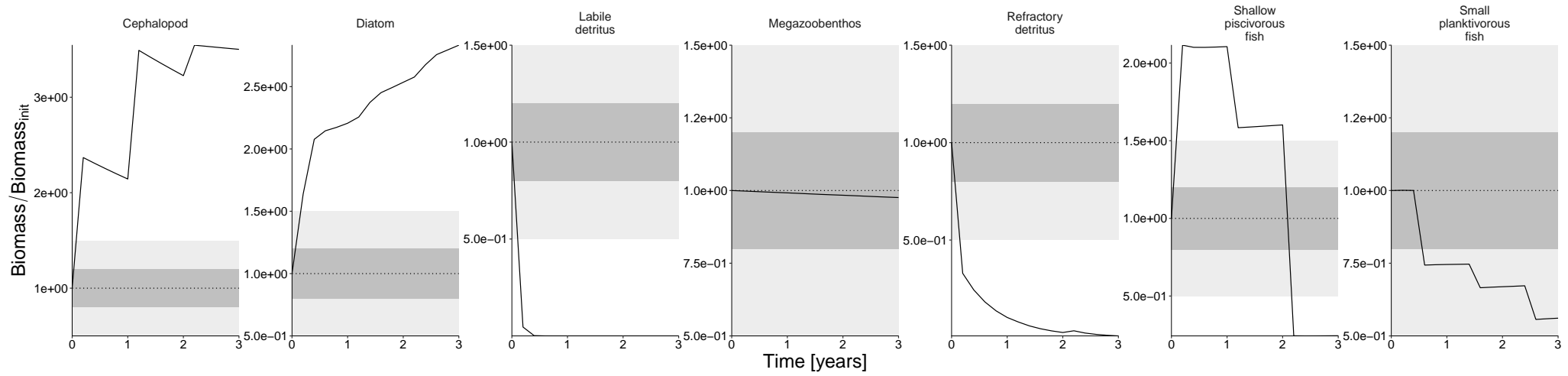
### 3.7 Numbers

```
df_rel <- convert_relative_initial(result$num_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)
```



### 3.8 Biomass

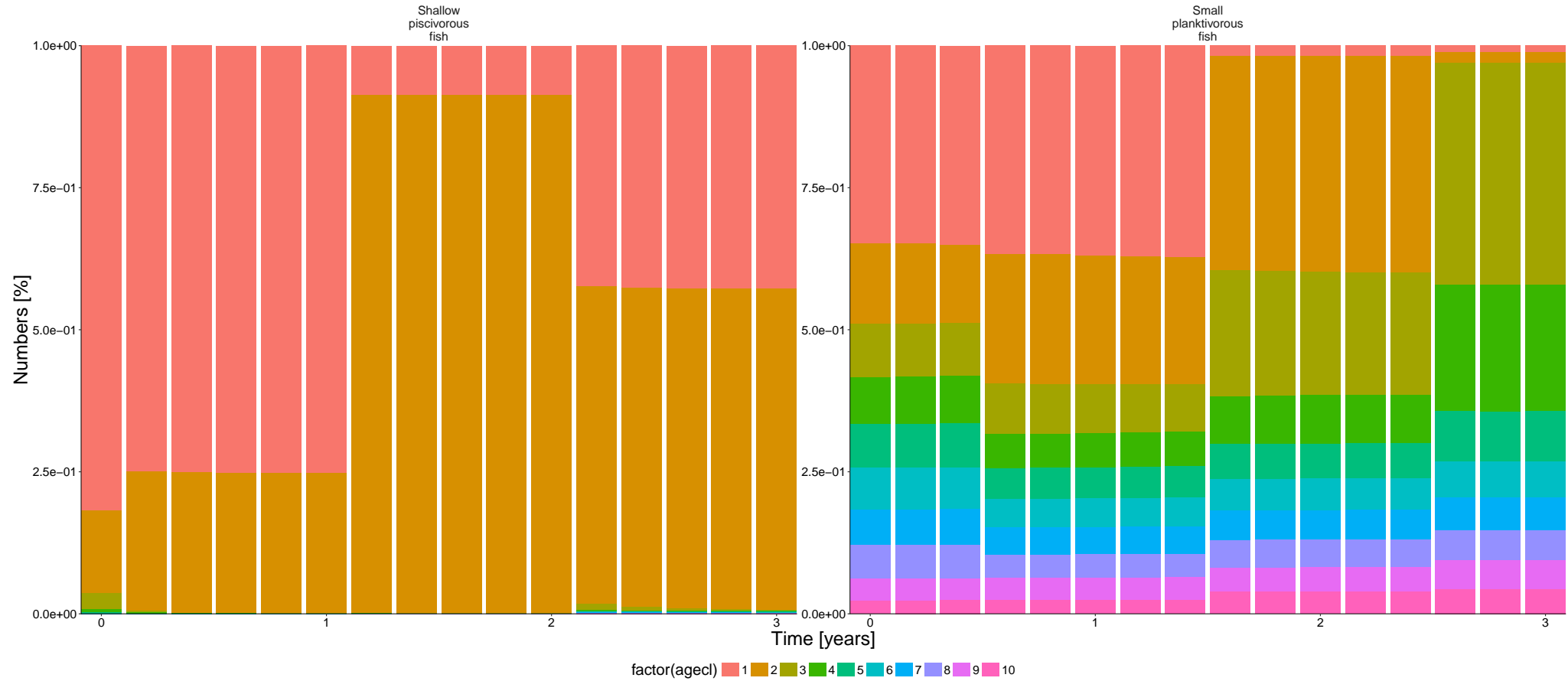
```
df_rel <- convert_relative_initial(result$biomass)
plot <- plot_line(df_rel)
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)
```



## 4 Distribution plots

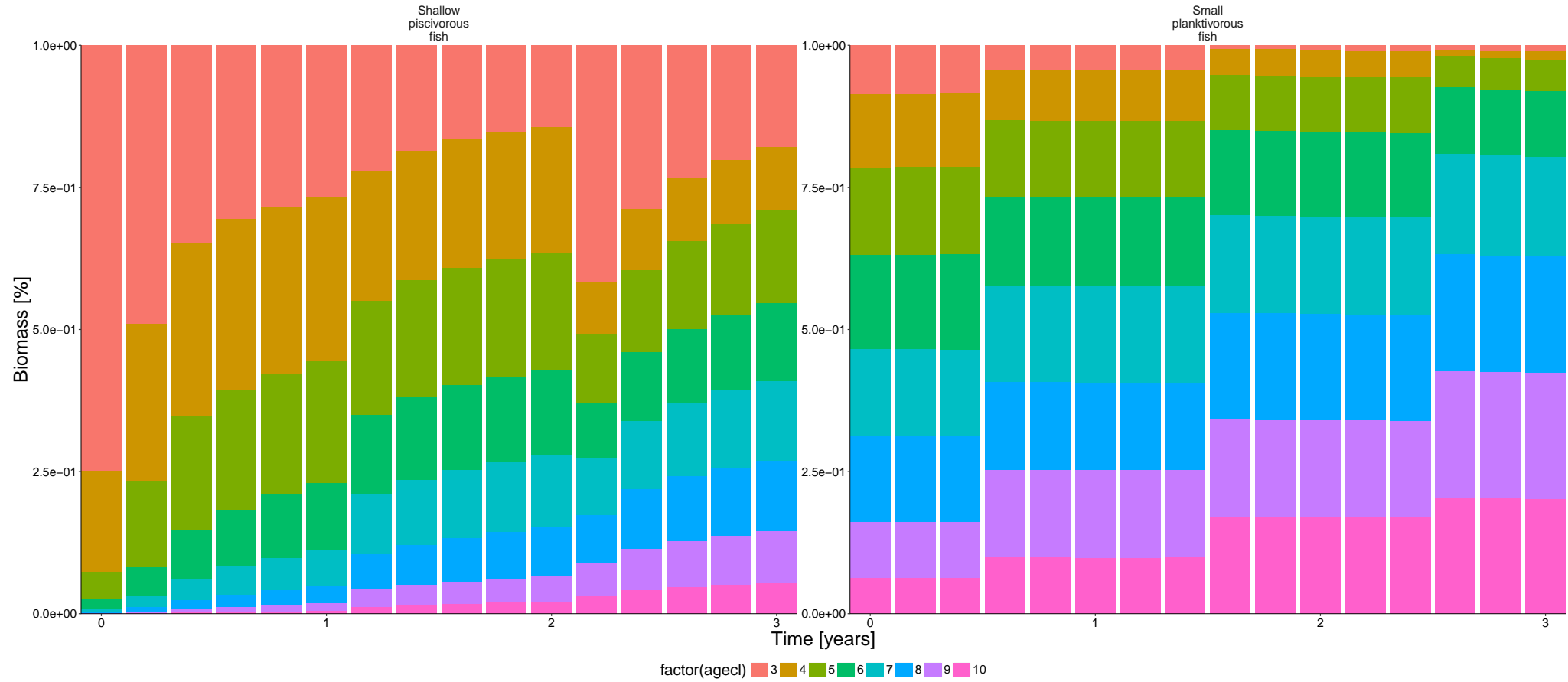
### 4.1 Numbers @ age

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



## 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 [%]"))
```

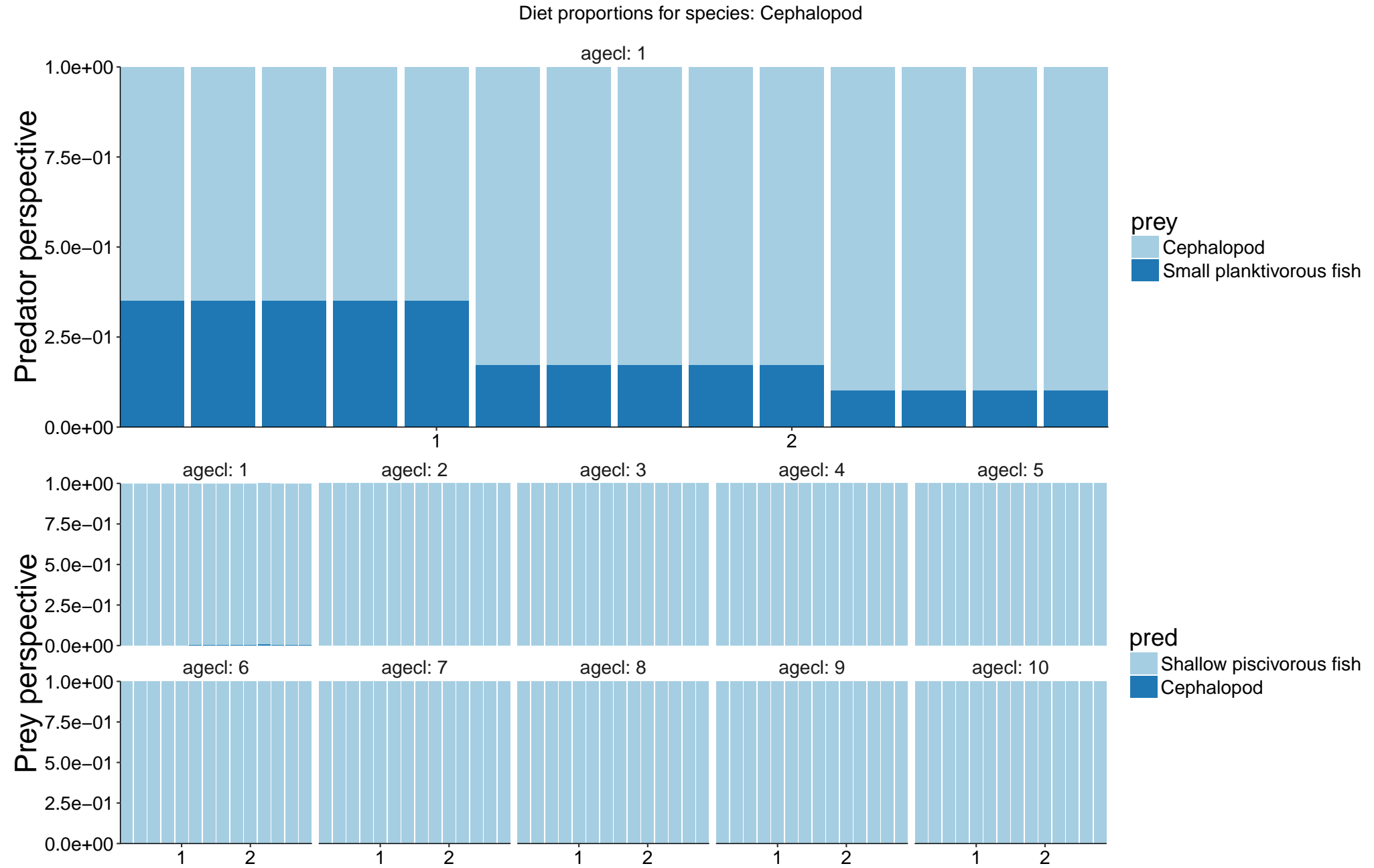


## 5 Diet Plots

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

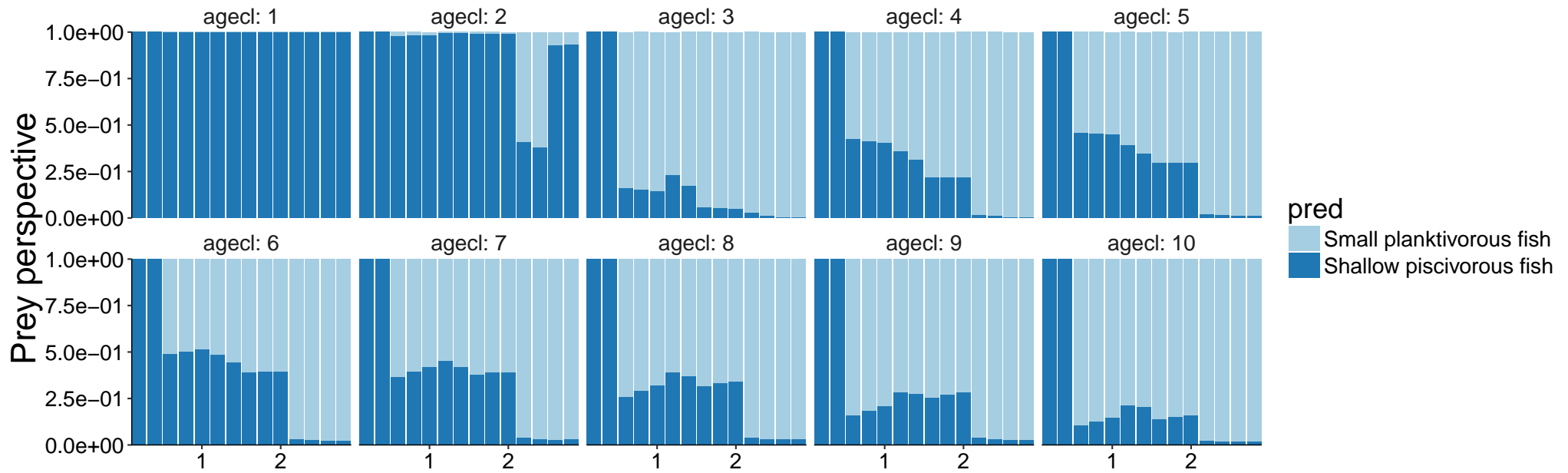


## 5.1 Diet plot 1: Cephalopod



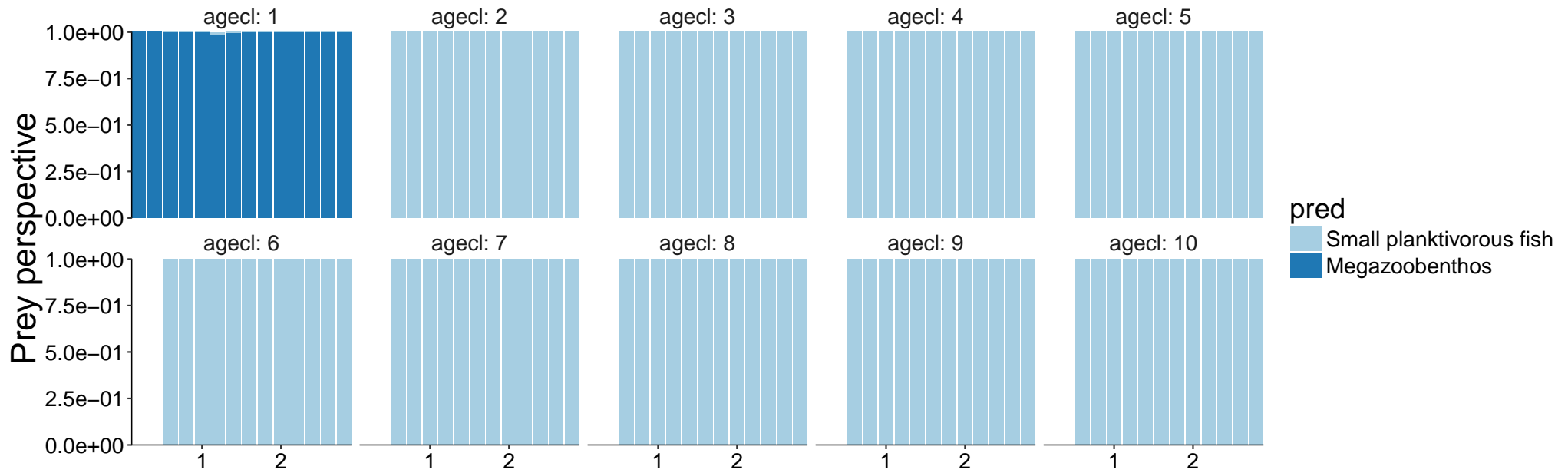
## 5.2 Diet plot 2: Diatom

Diet proportions for species: Diatom

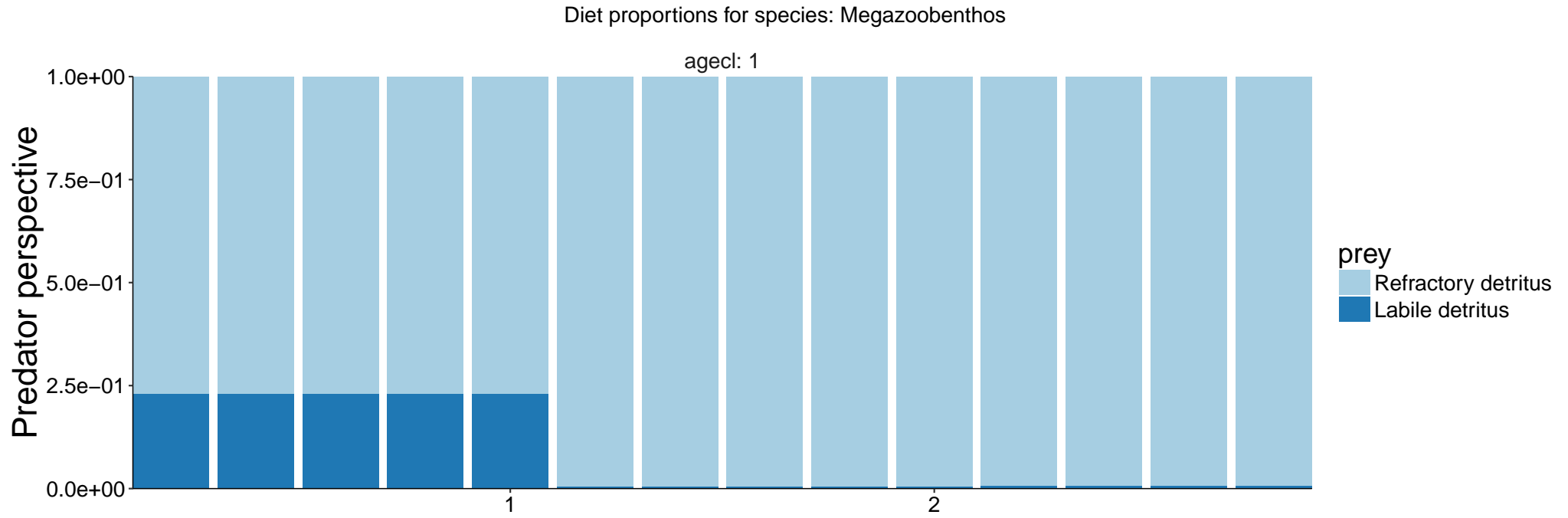


### 5.3 Diet plot 3: Labile detritus

Diet proportions for species: Labile detritus

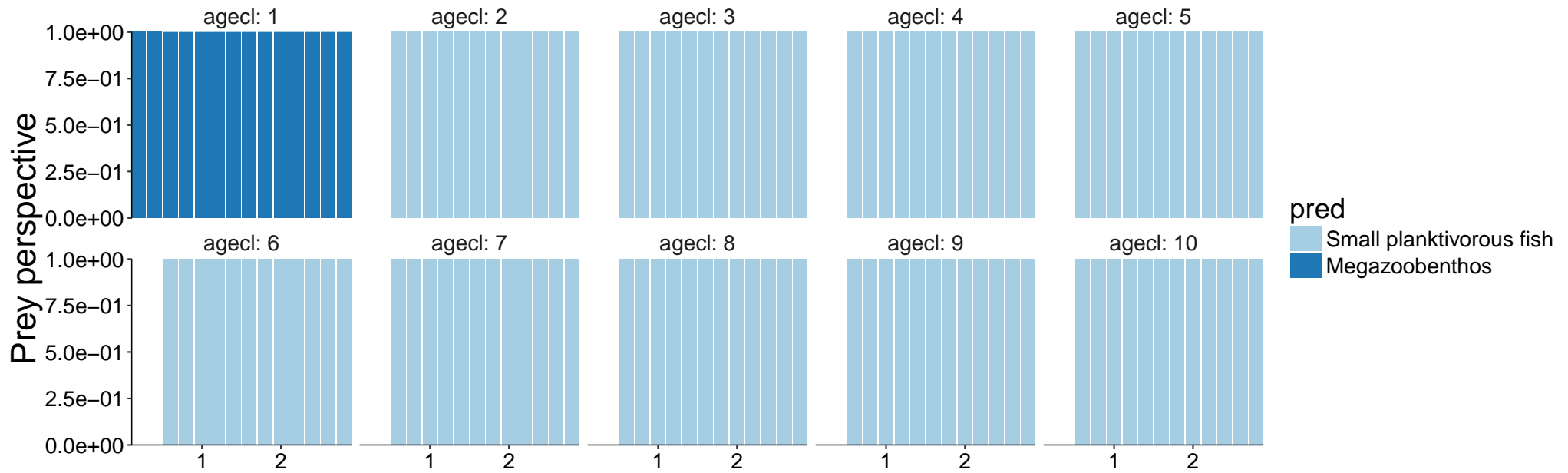


## 5.4 Diet plot 4: Megazoobenthos

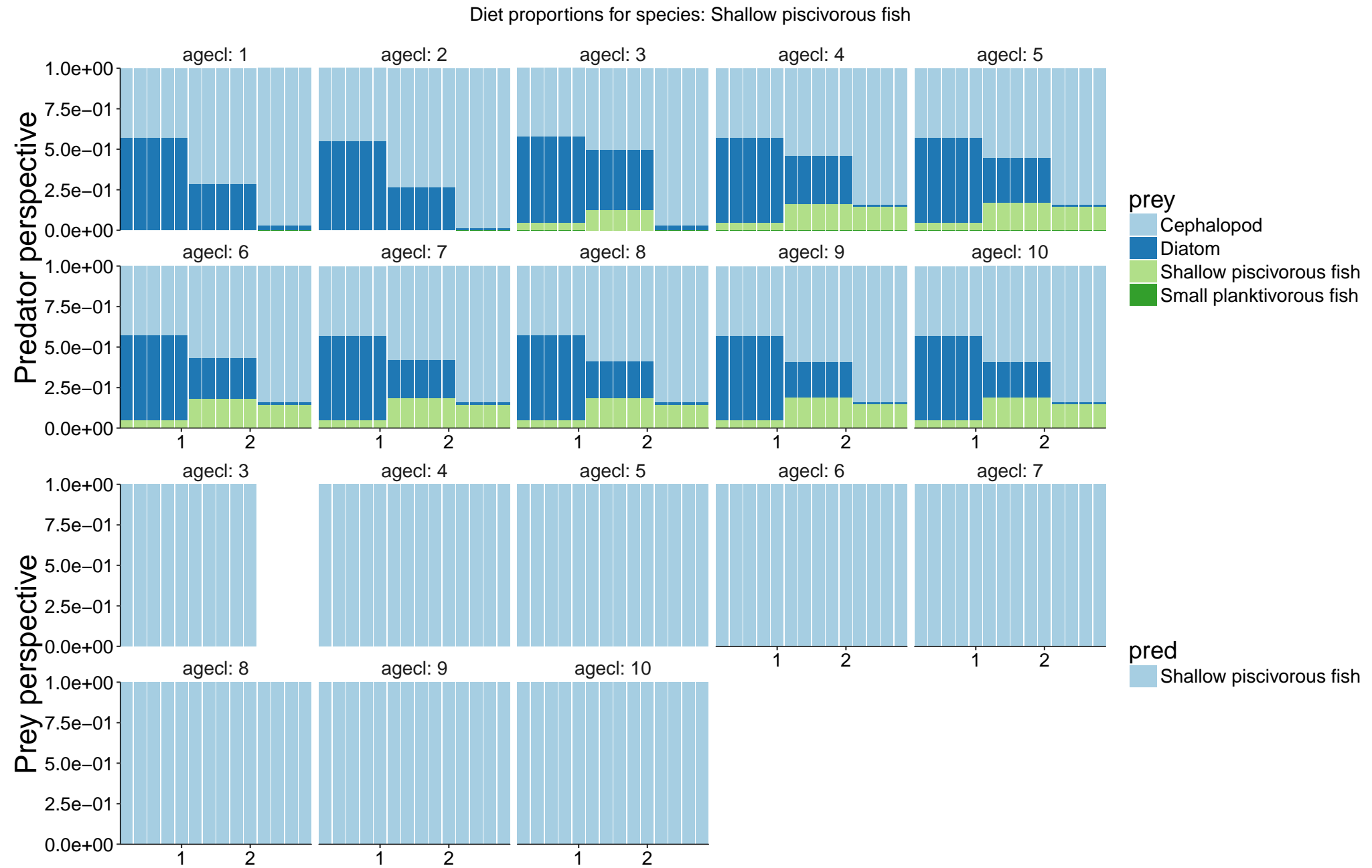


## 5.5 Diet plot 5: Refractory detritus

Diet proportions for species: Refractory detritus

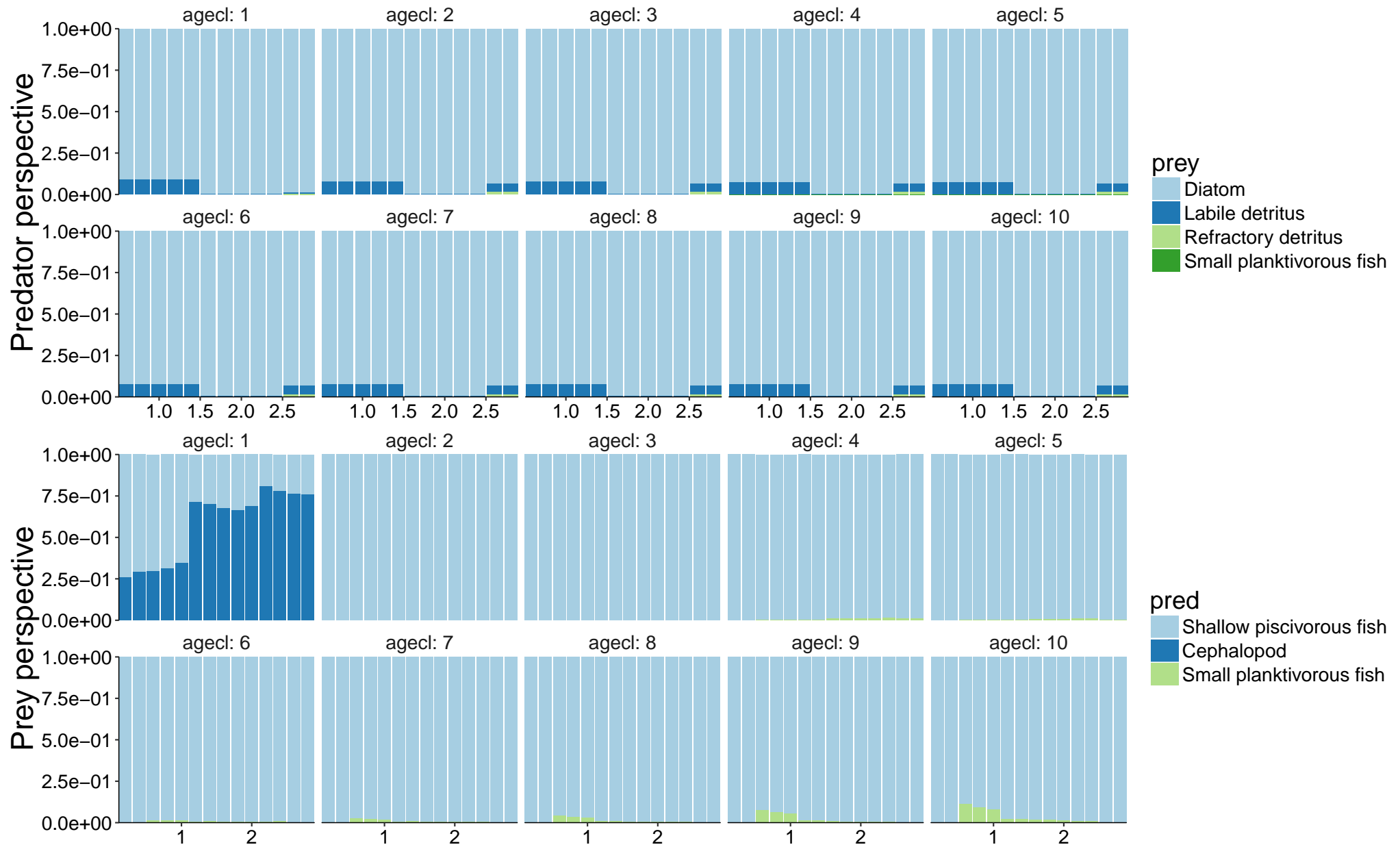


## 5.6 Diet plot 6: Shallow piscivorous fish



## 5.7 Diet plot 7: Small planktivorous fish

Diet proportions for species: Small planktivorous fish

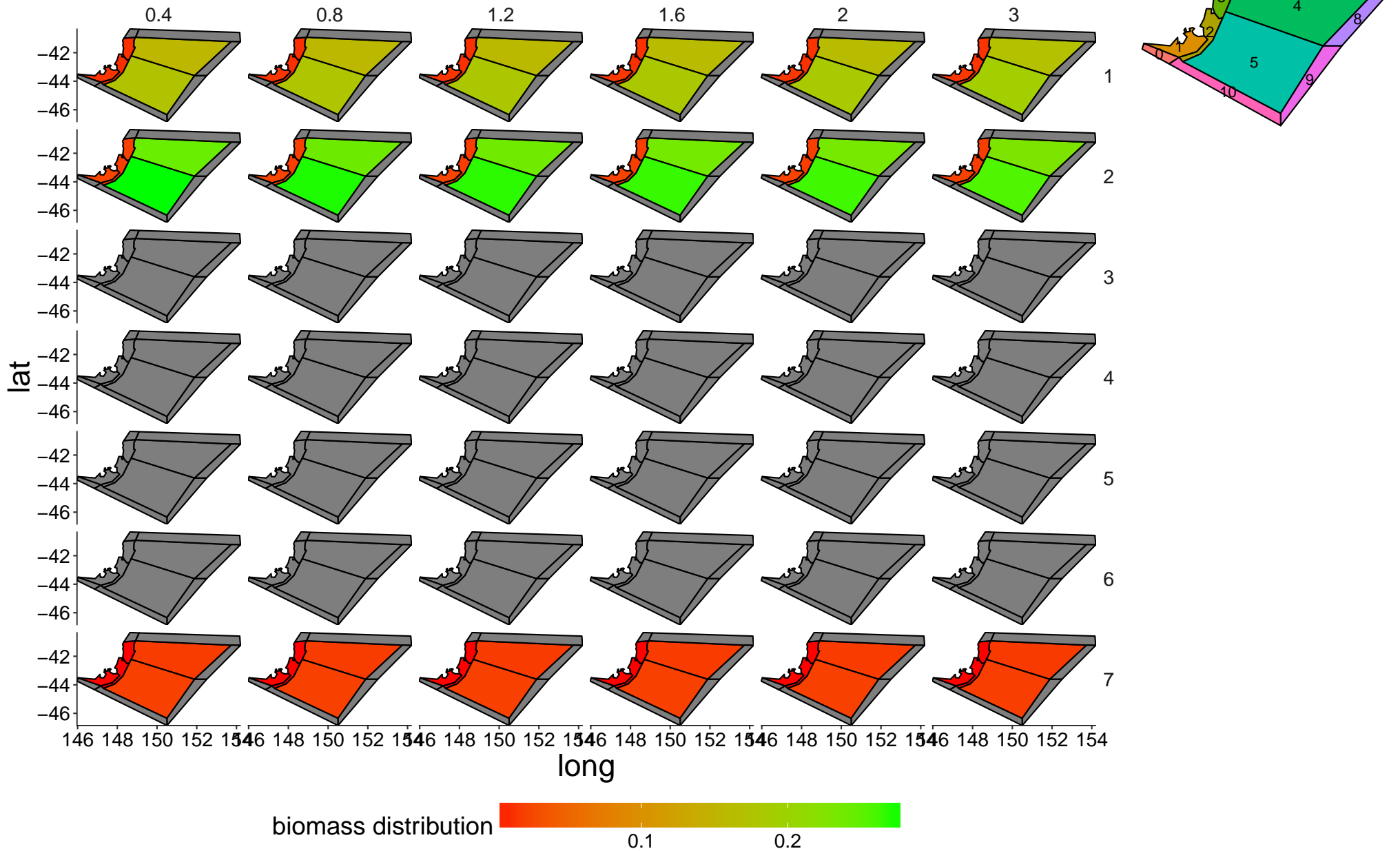


## 6 Spatial Plots 1

## Joining, by = "polygon"

### 6.1 Spatial Plot 1: Carrion3 1

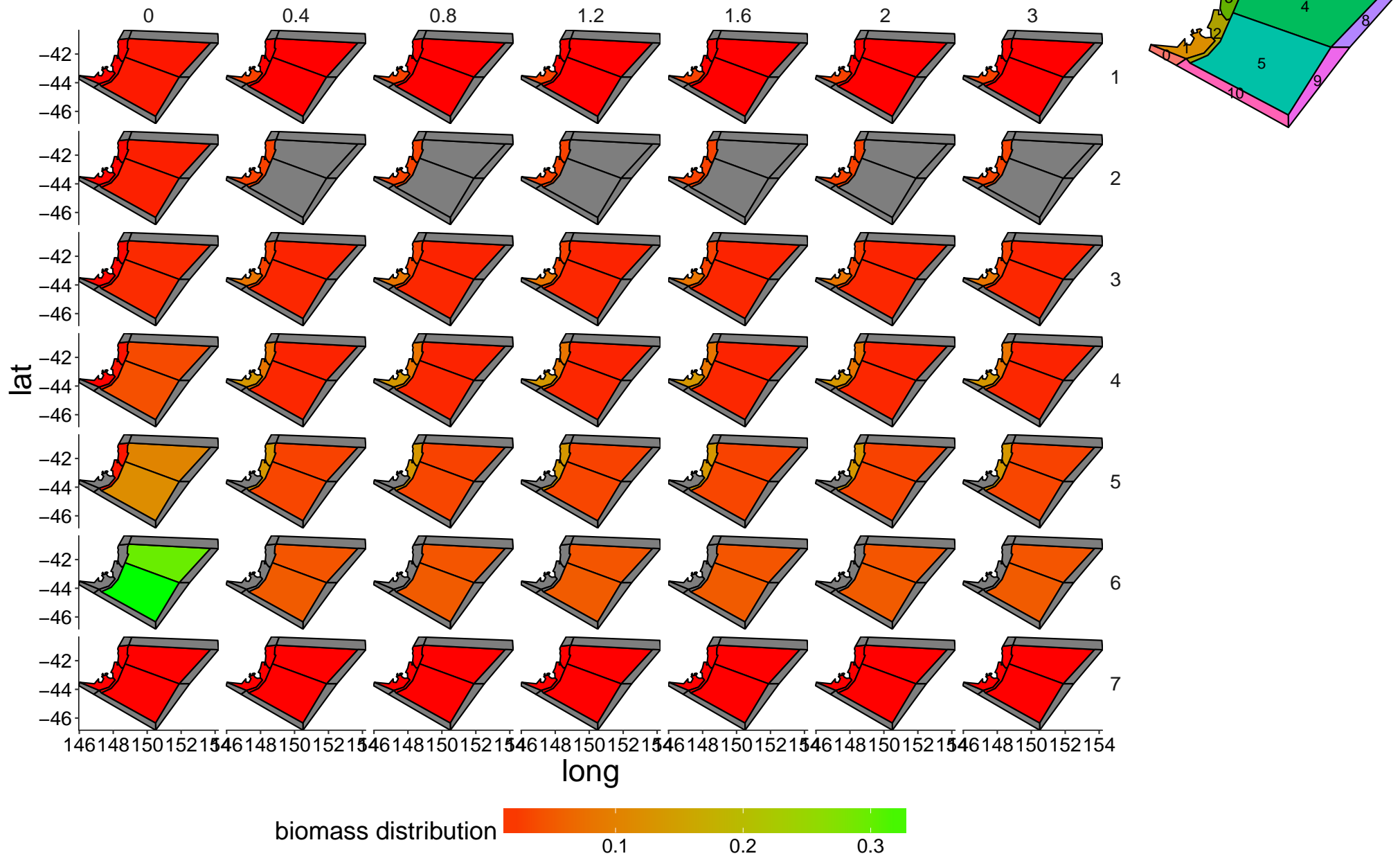
Species: Carrion3 with stanza: 1





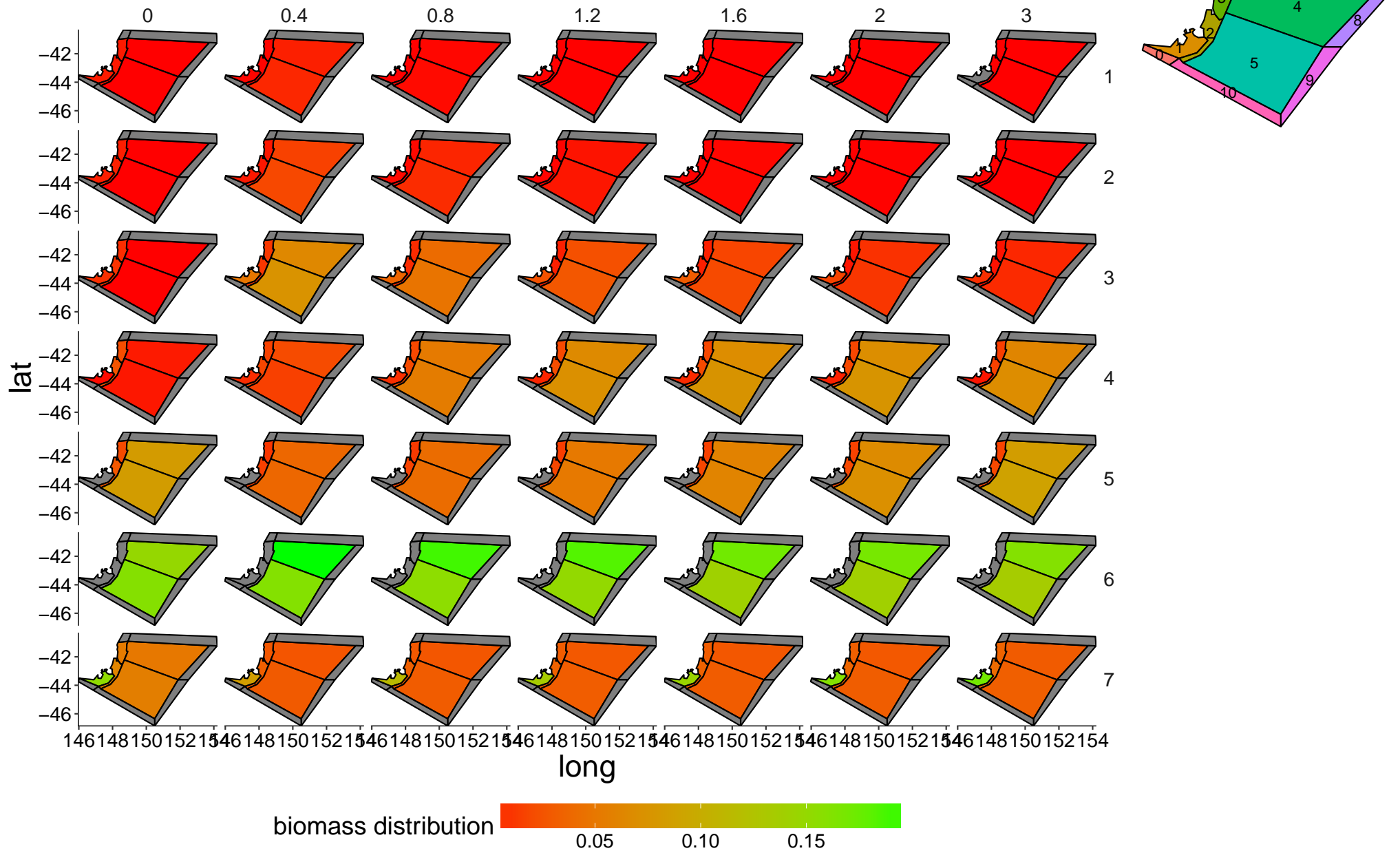
## 6.2 Spatial Plot 2: Cephalopod 1

Species: Cephalopod with stanza: 1



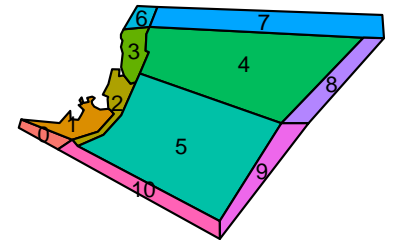
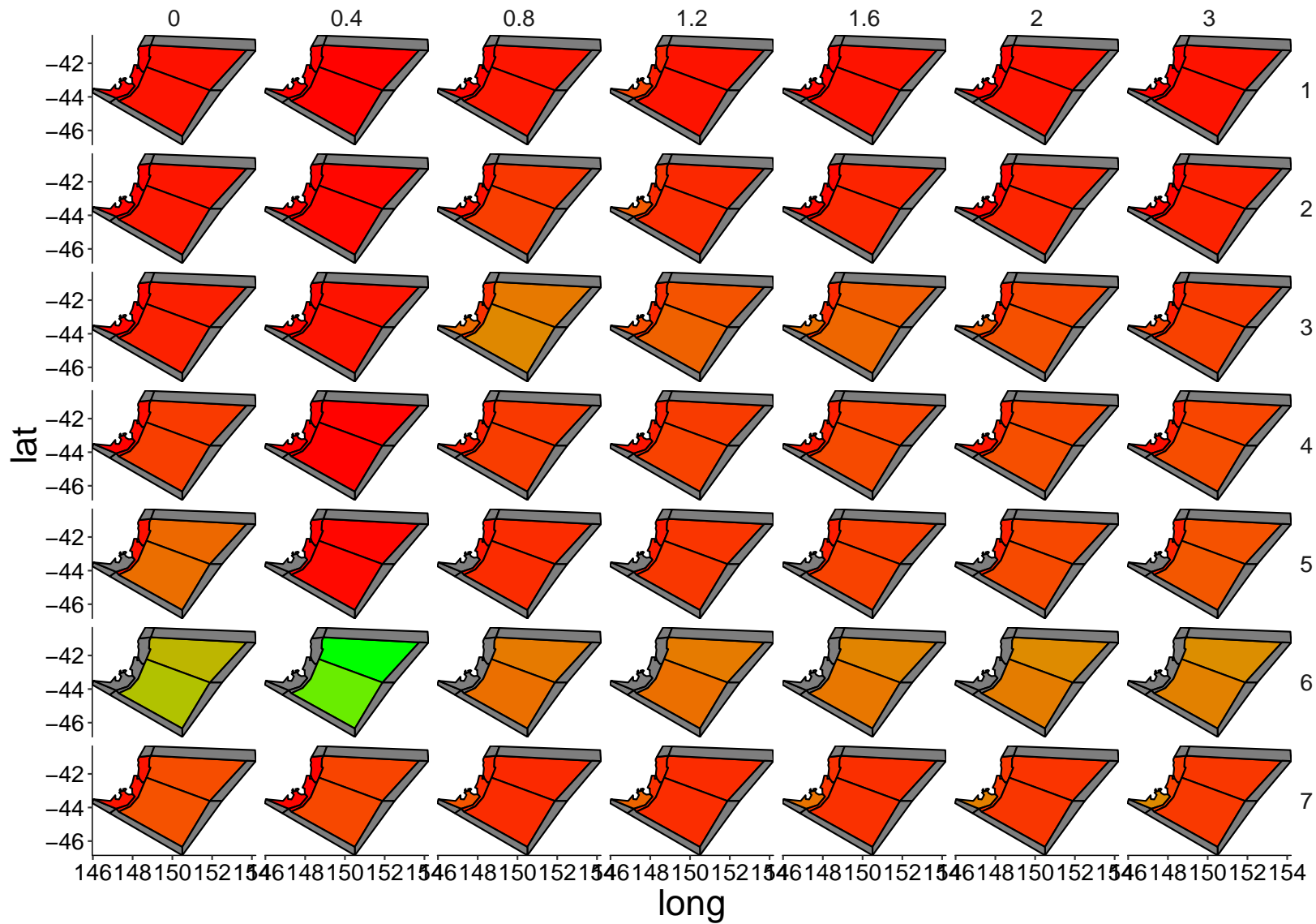
### 6.3 Spatial Plot 3: Diatom 1

Species: Diatom with stanza: 1



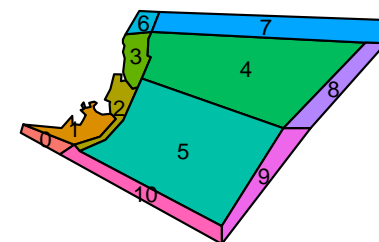
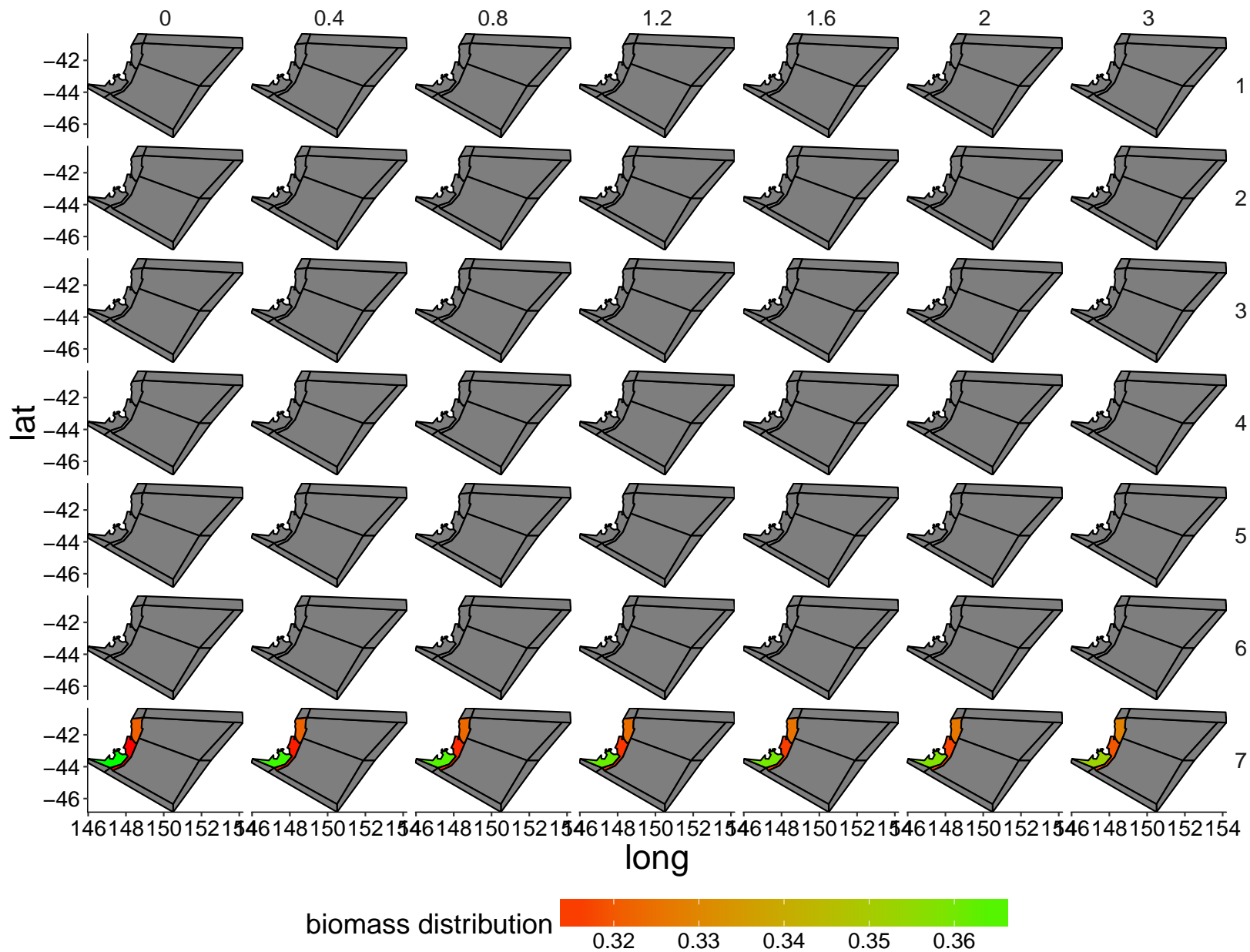
6.4 Spatial Plot 4: Labile detritus 1

Species: Labile detritus with stanza: 1



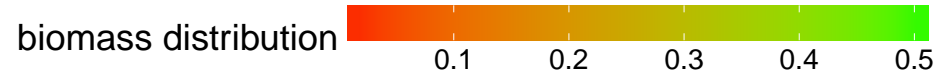
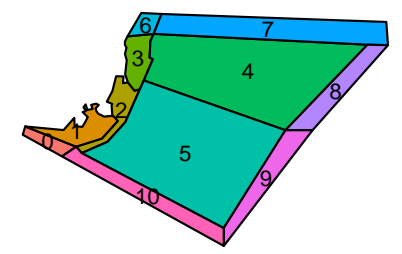
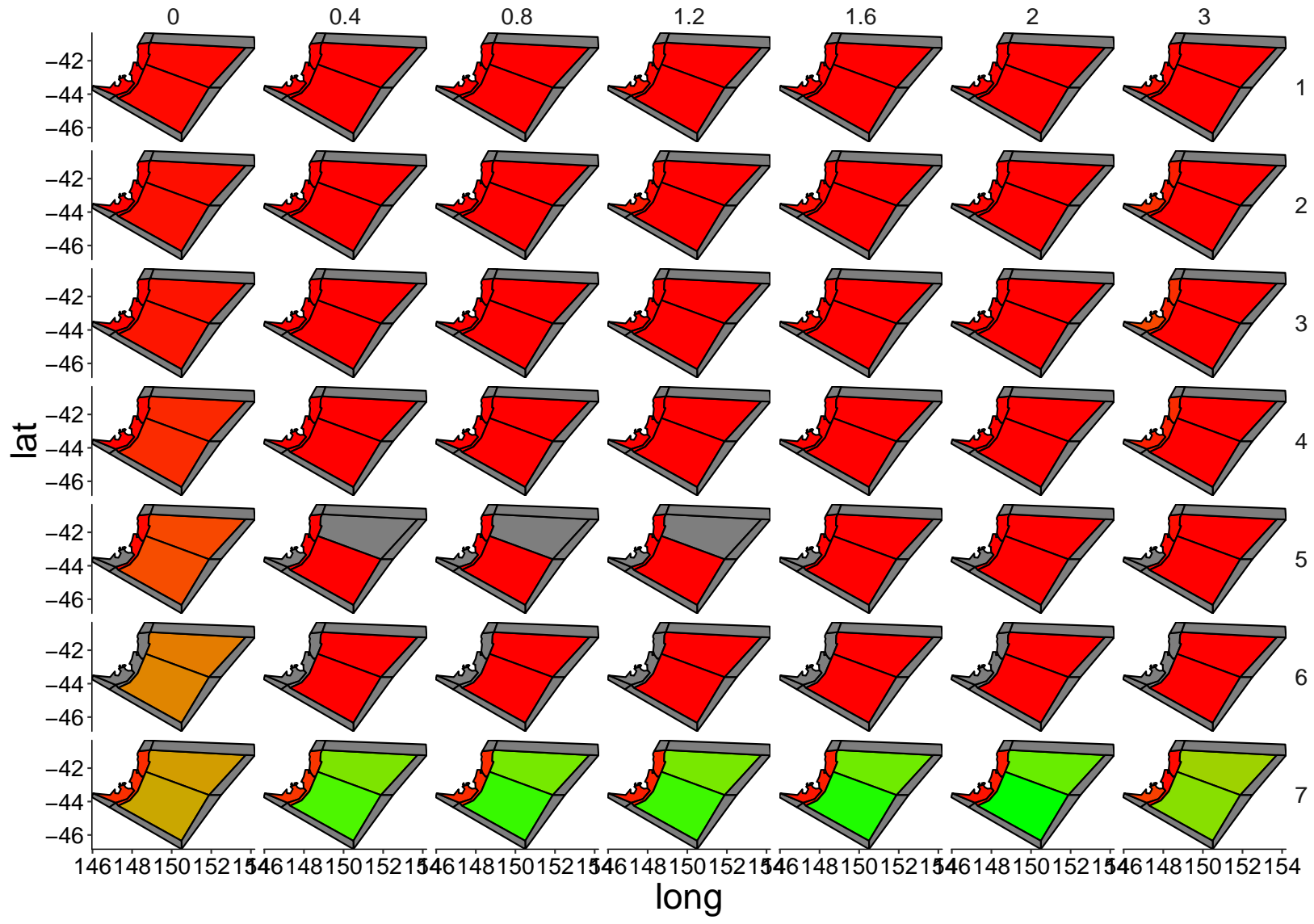
## 6.5 Spatial Plot 5: Megazoobenthos 1

Species: Megazoobenthos with stanza: 1



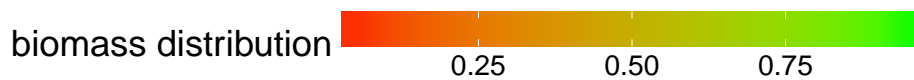
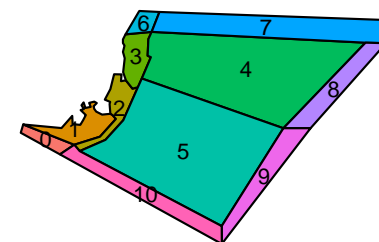
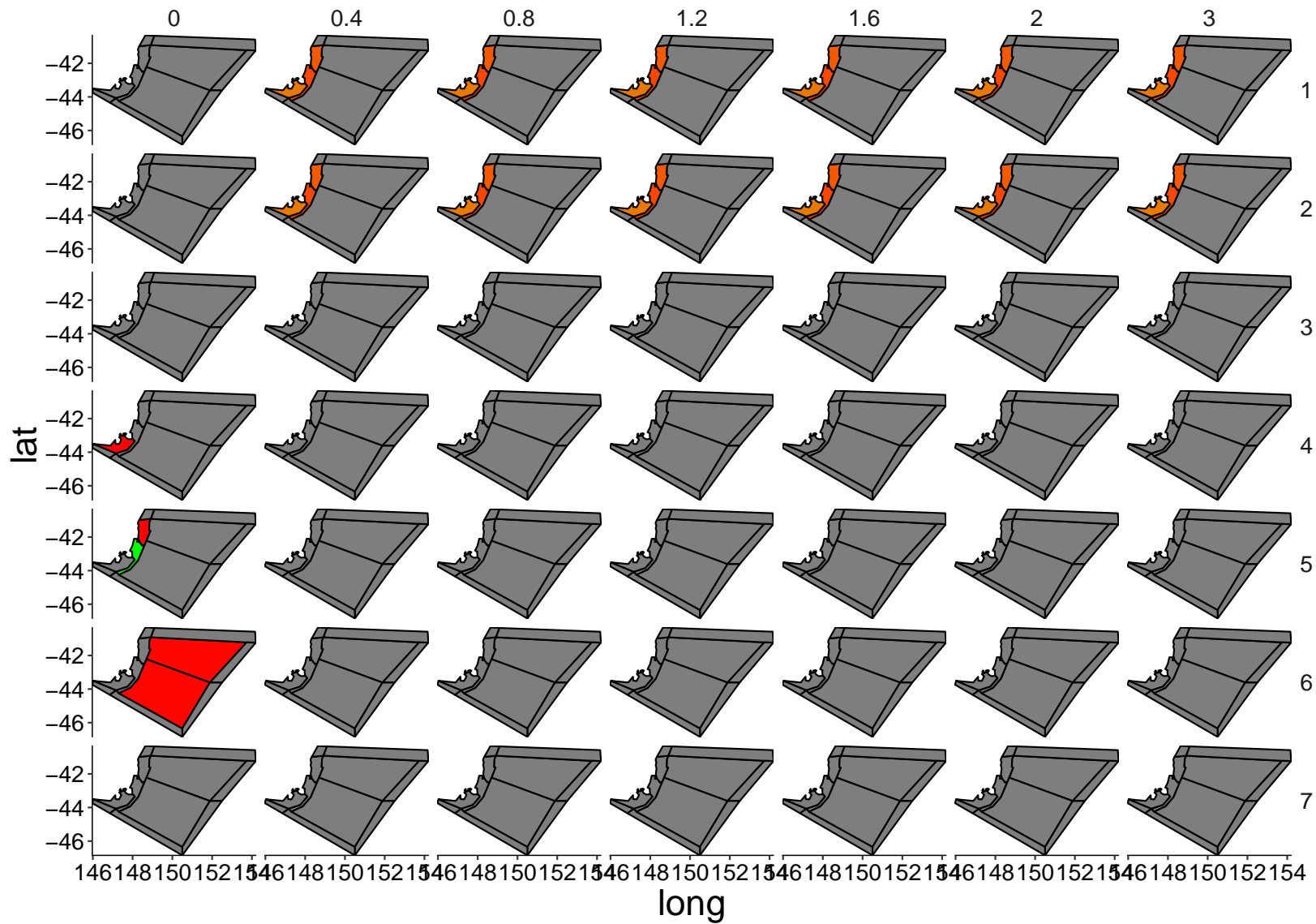
6.6 Spatial Plot 6: Refractory detritus 1

Species: Refractory detritus with stanza: 1



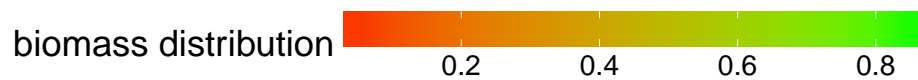
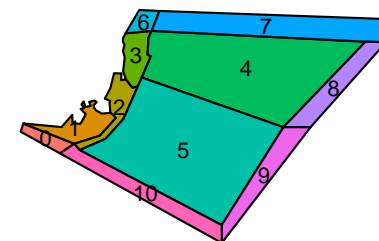
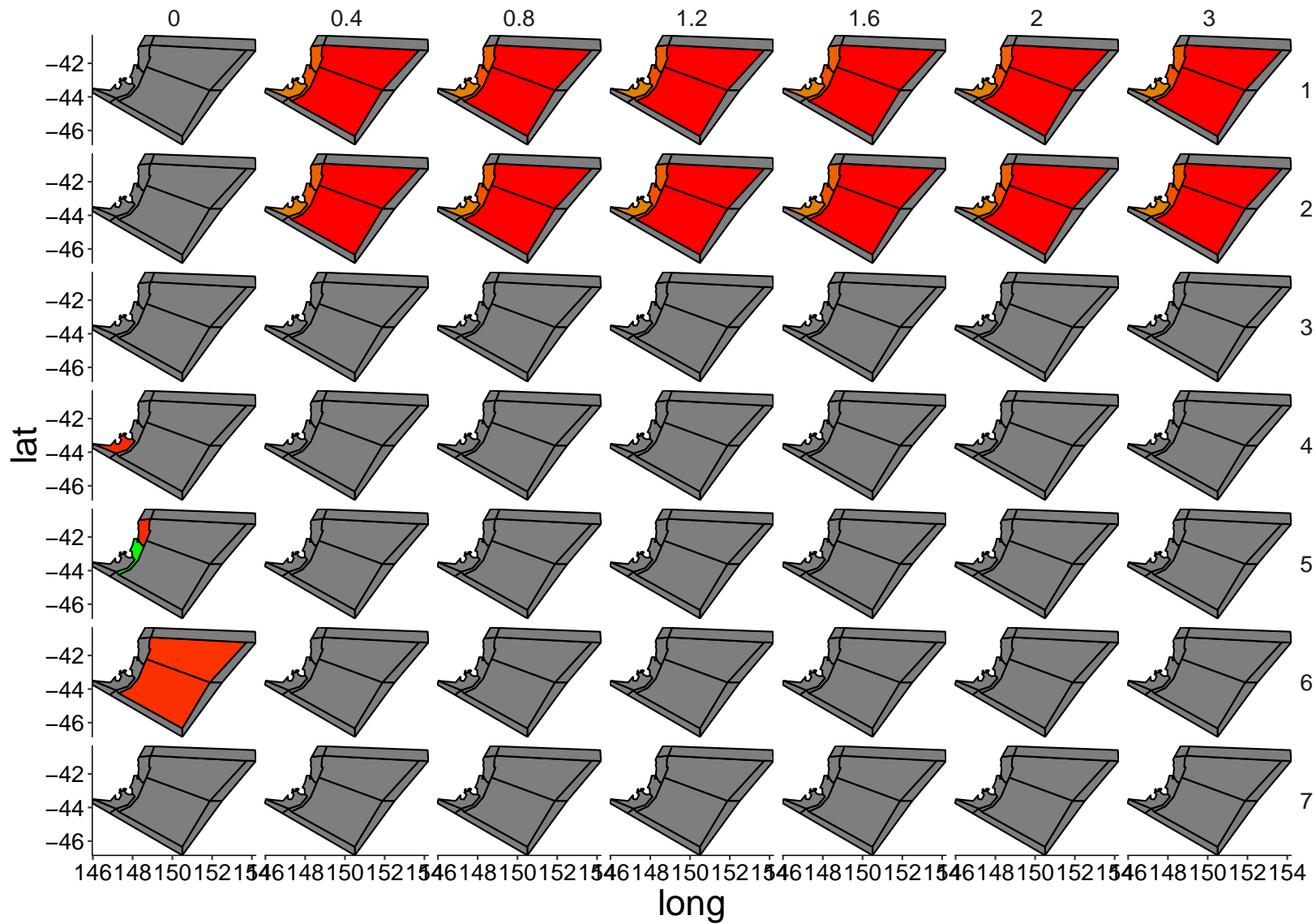
6.7 Spatial Plot 7: Shallow piscivorous fish 1

Species: Shallow piscivorous fish with stanza: 1



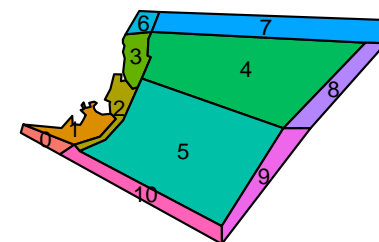
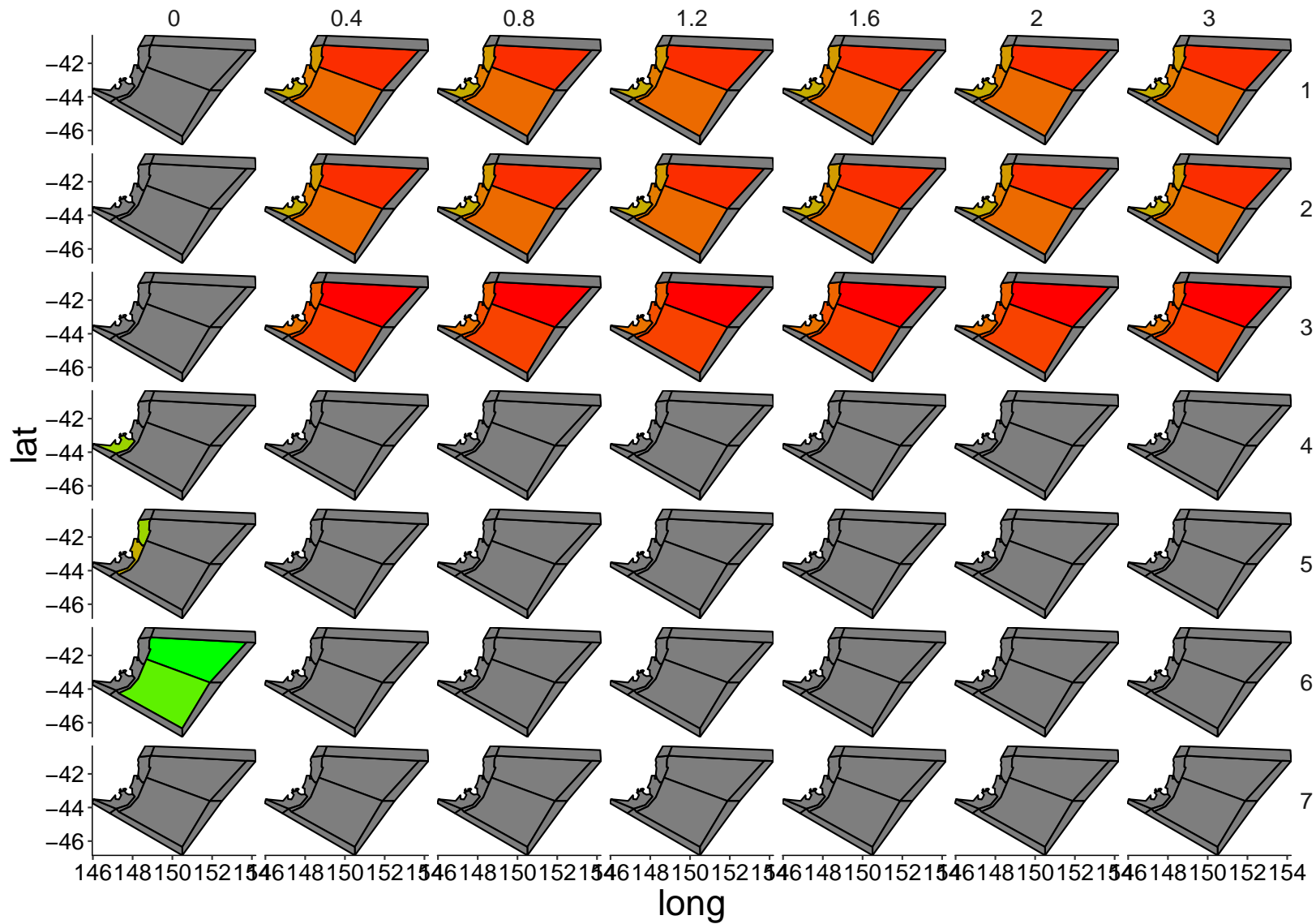
6.8 Spatial Plot 8: Shallow piscivorous fish 2

Species: Shallow piscivorous fish with stanza: 2



6.9 Spatial Plot 9: Small planktivorous fish 1

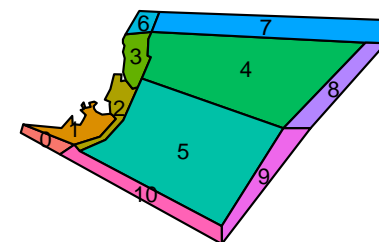
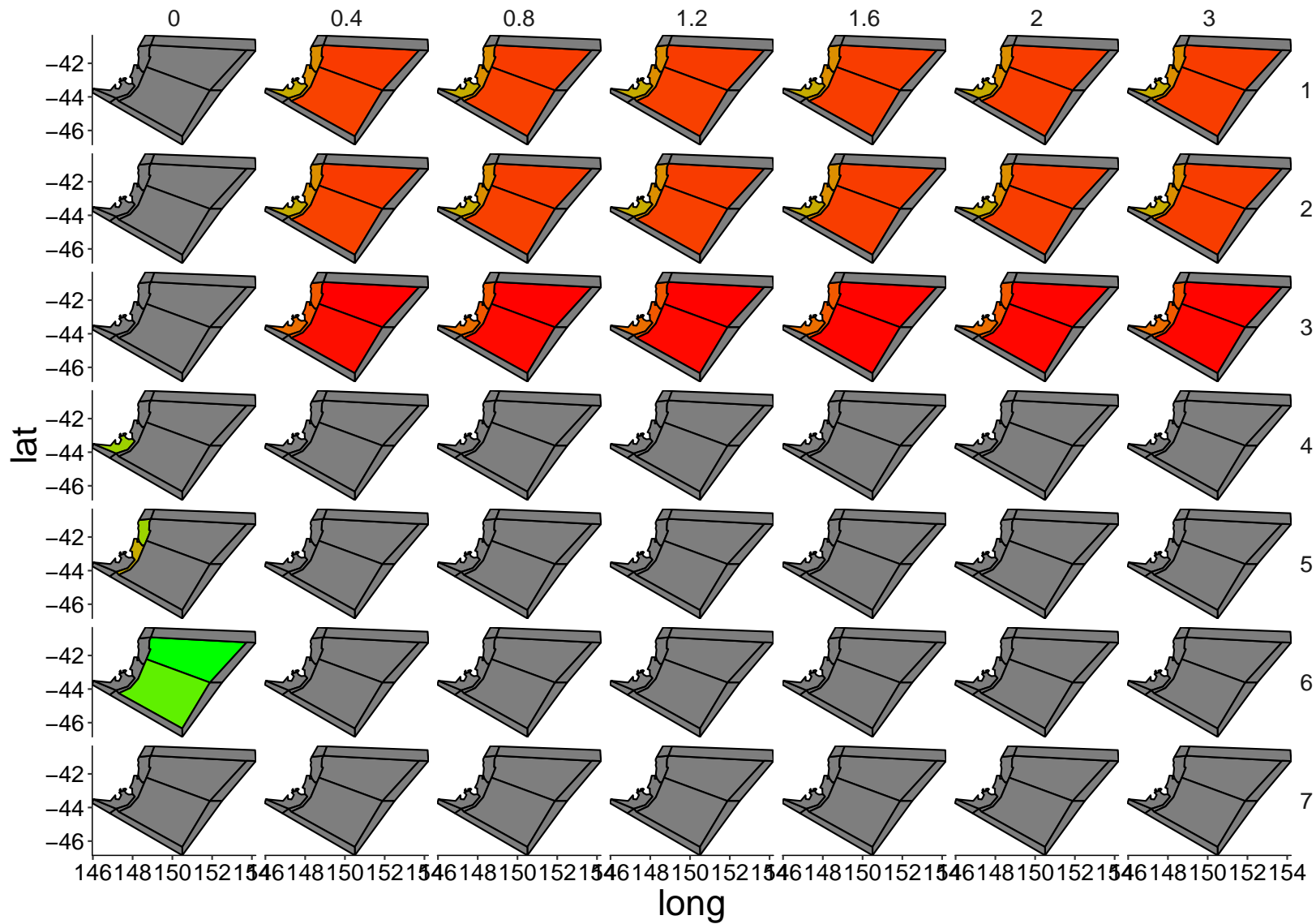
Species: Small planktivorous fish with stanza: 1





6.10 Spatial Plot 10: Small planktivorous fish 2

Species: Small planktivorous fish with stanza: 2



## 7 Spatial Plots 2

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

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

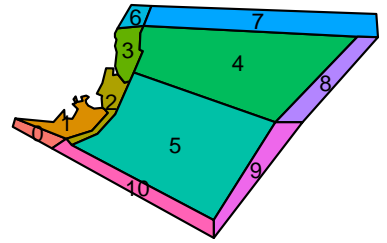
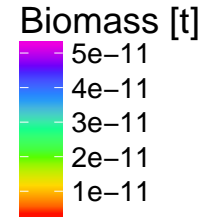
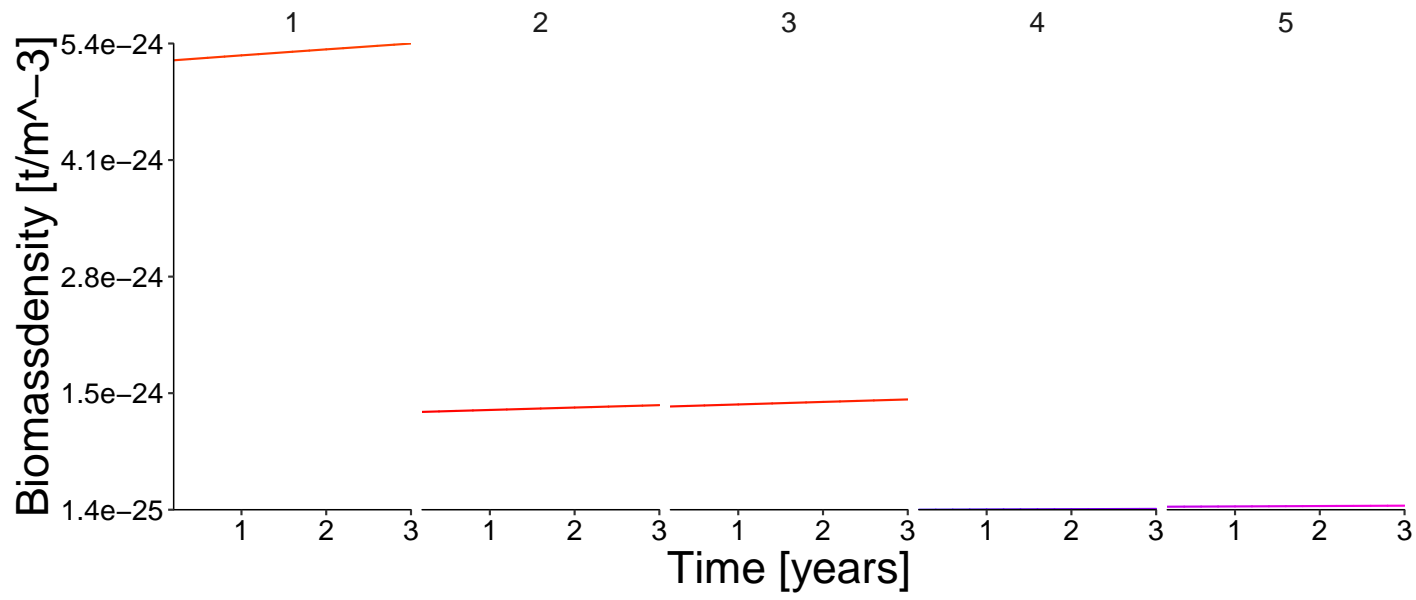
```
## adjust the group aesthetic?
```

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

```
## adjust the group aesthetic?
```

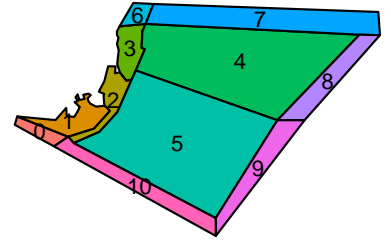
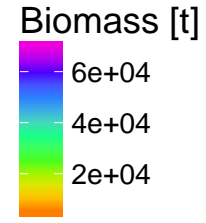
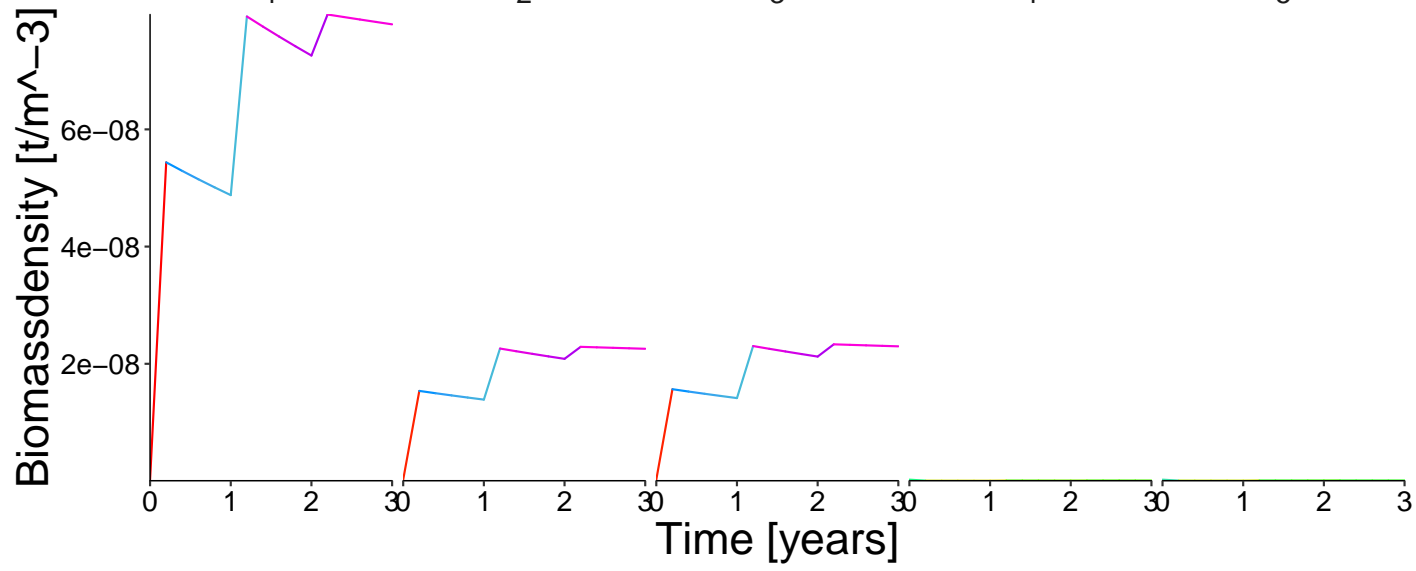
## 7.1 Spatial Plot 1: Carrion3

Species: Carrion3 with stanza: 1



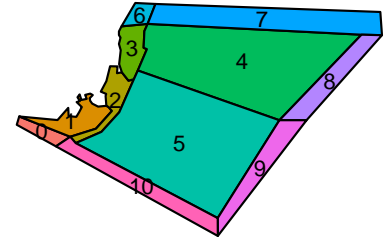
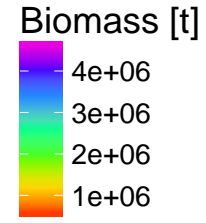
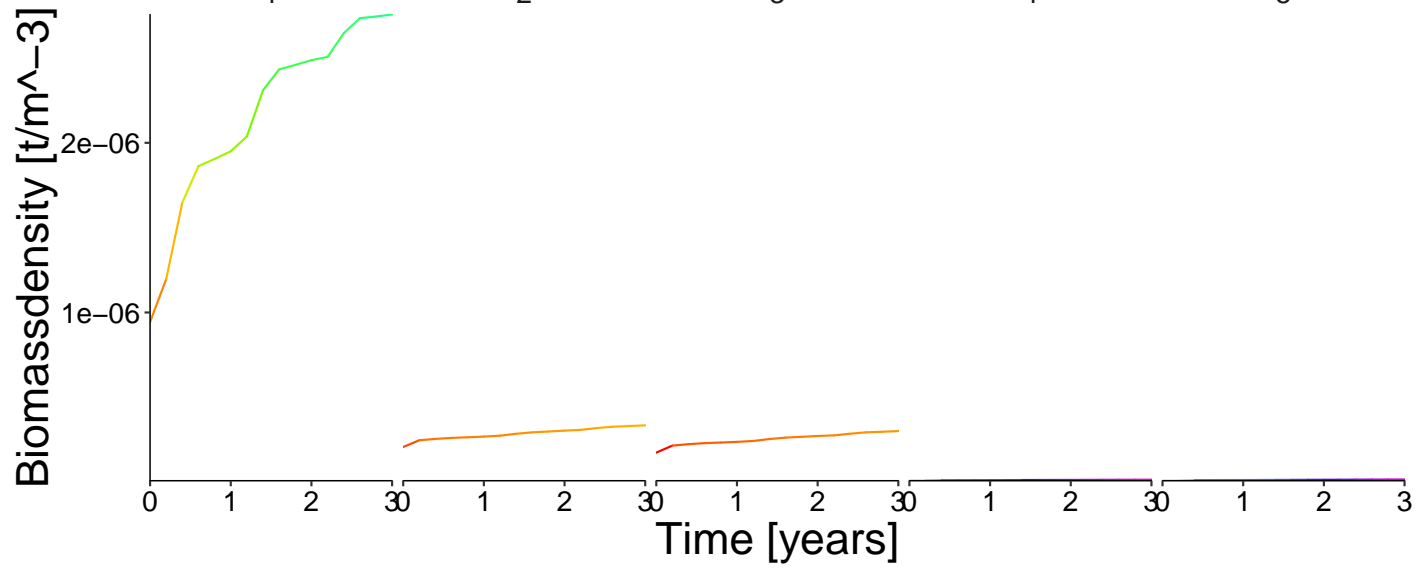
## 7.2 Spatial Plot 2: Cephalopod

Species: Cephalopod with stanza: 1



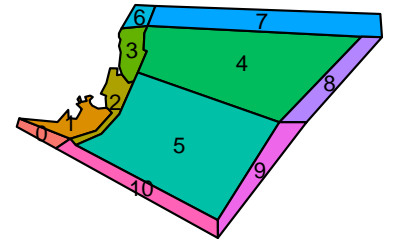
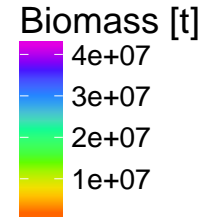
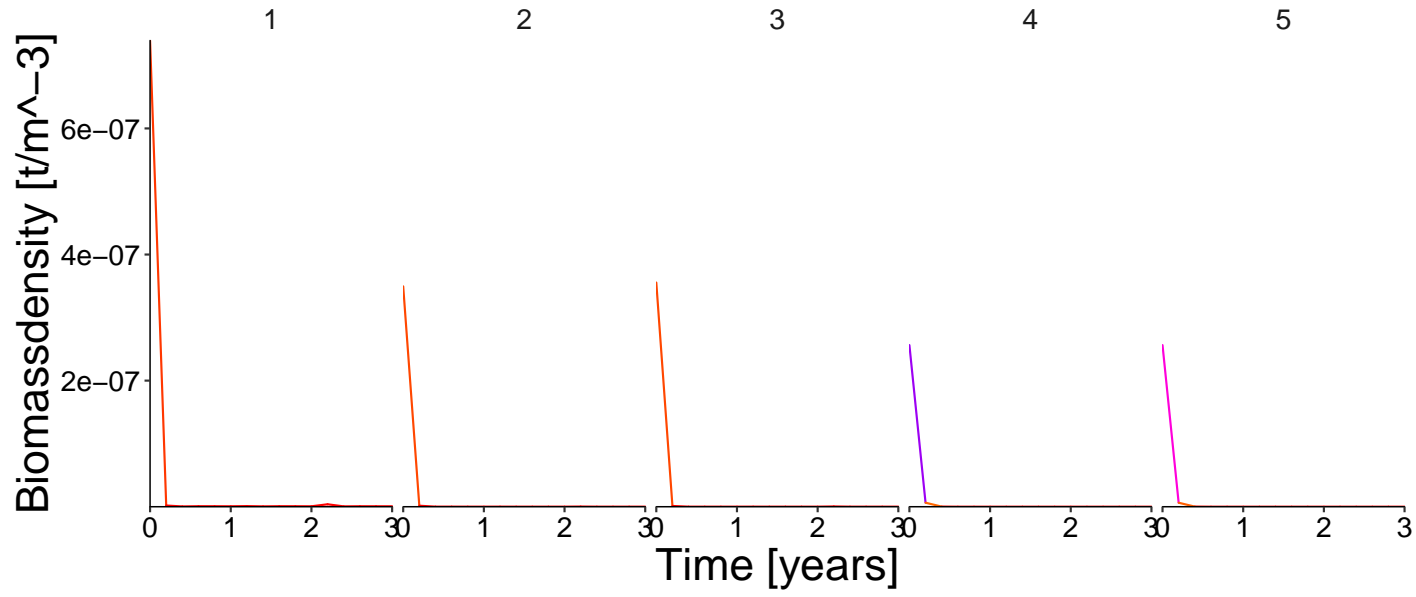
### 7.3 Spatial Plot 3: Diatom

Species: Diatom with stanza: 1



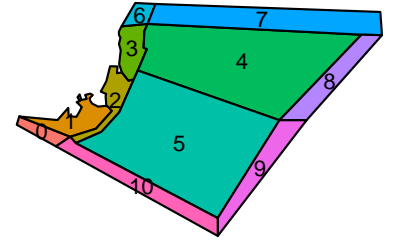
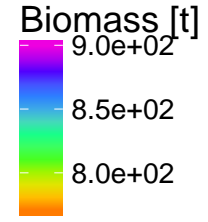
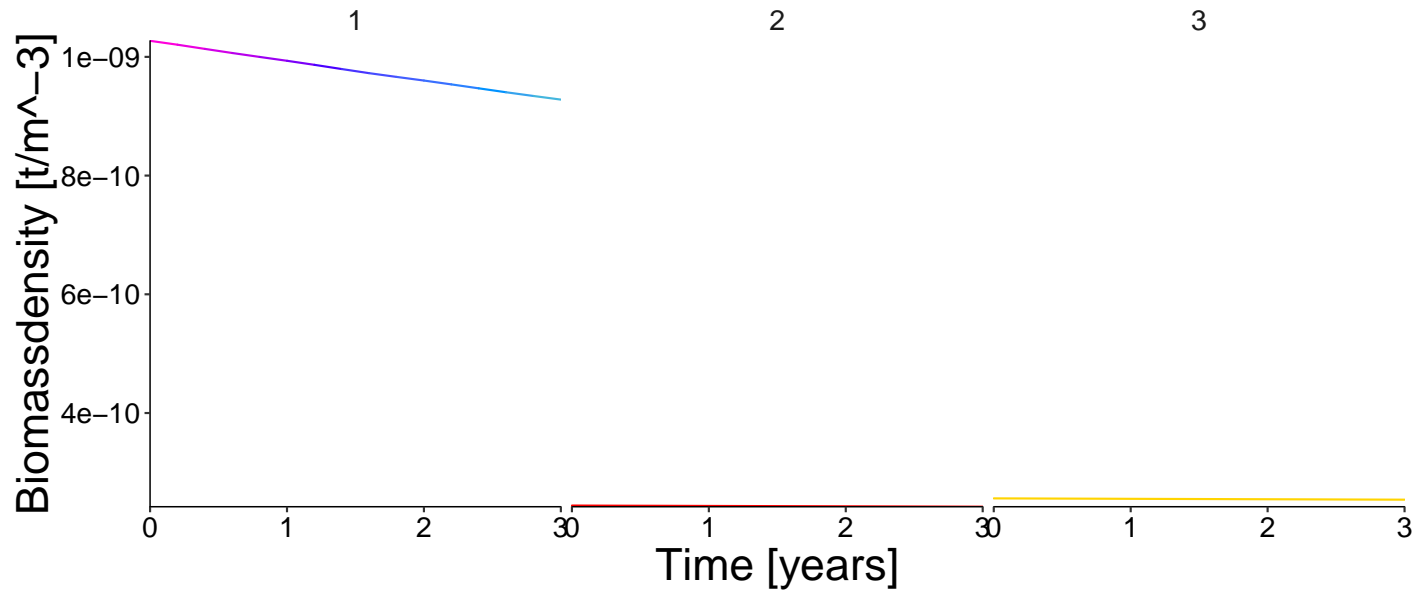
7.4 Spatial Plot 4: Labile detritus

Species: Labile detritus with stanza: 1



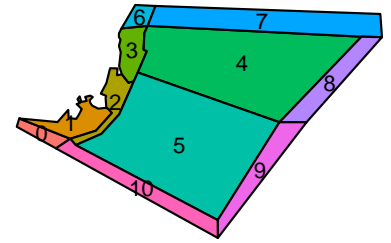
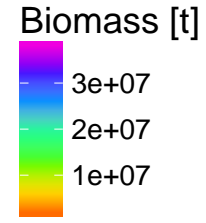
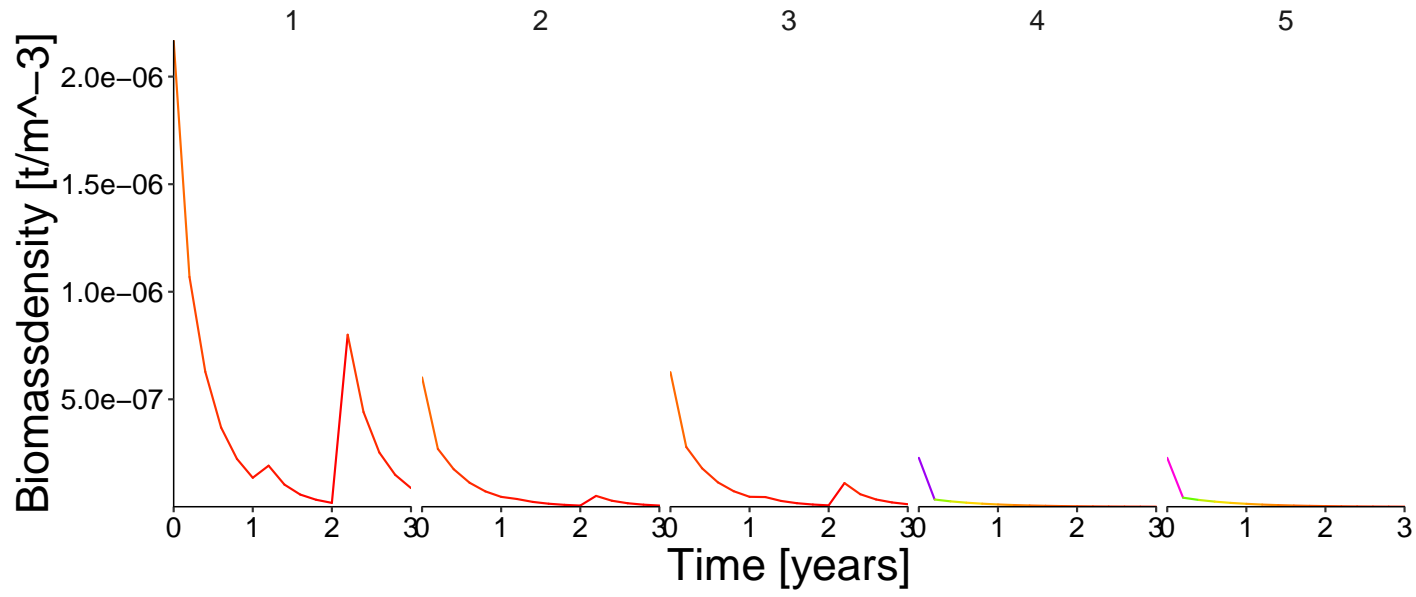
7.5 Spatial Plot 5: Megazoobenthos

Species: Megazoobenthos with stanza: 1



7.6 Spatial Plot 6: Refractory detritus

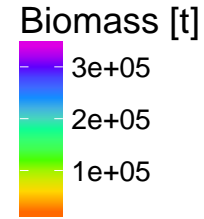
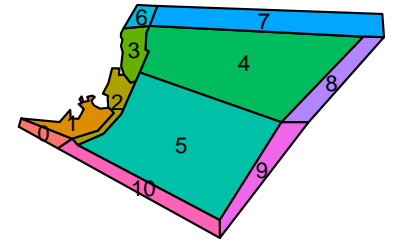
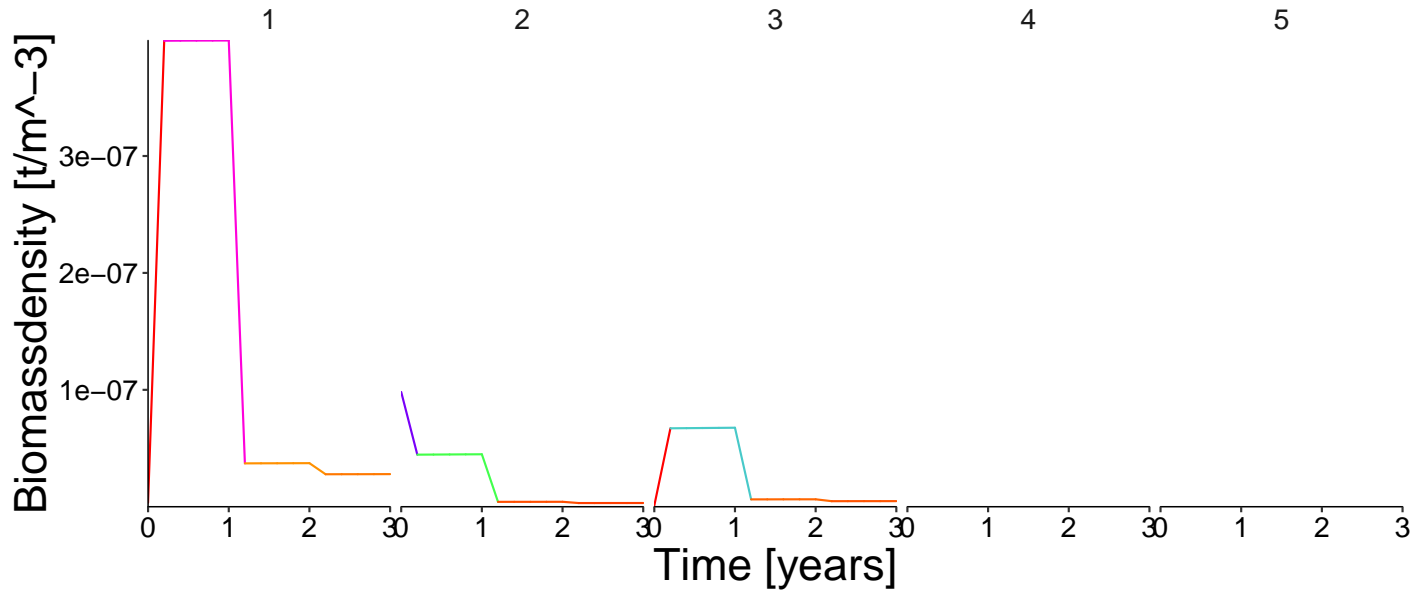
Species: Refractory detritus with stanza: 1



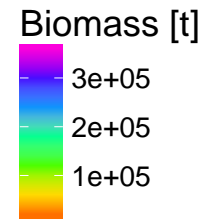
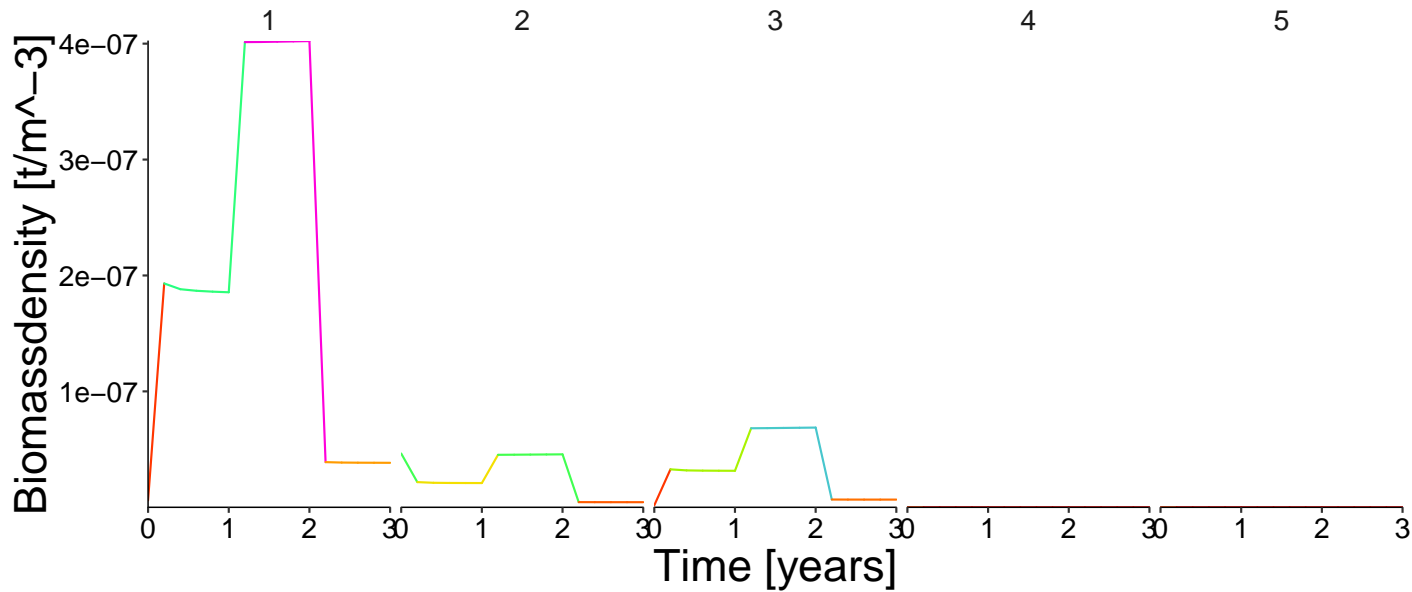


7.7 Spatial Plot 7: Shallow piscivorous fish

Species: Shallow piscivorous fish with stanza: 1

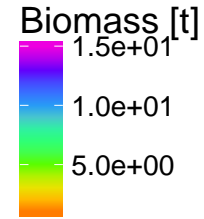
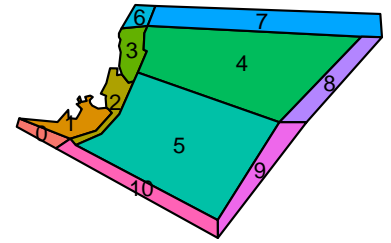
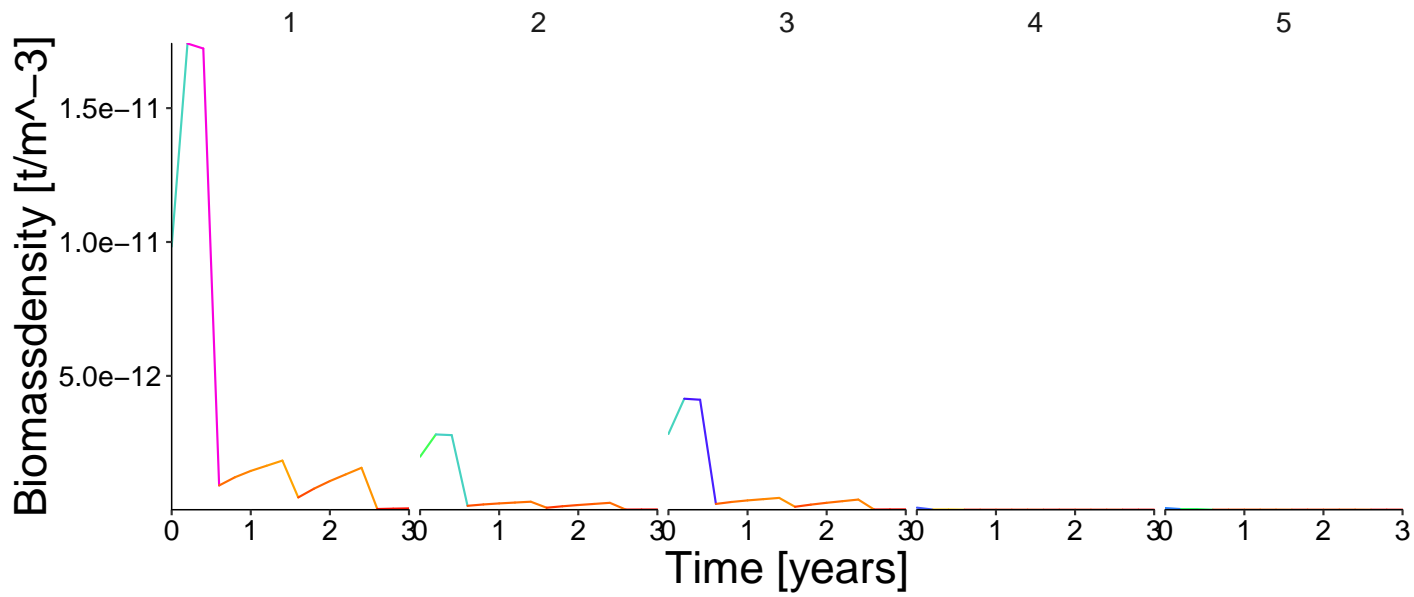


Species: Shallow piscivorous fish with stanza: 2



7.8 Spatial Plot 8: Small planktivorous fish

Species: Small planktivorous fish with stanza: 1



Species: Small planktivorous fish with stanza: 2

