

# model-calibration

*Alexander Keth*

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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, "VMPPA_setas.bgm")
```

# 1 Whole system plots!

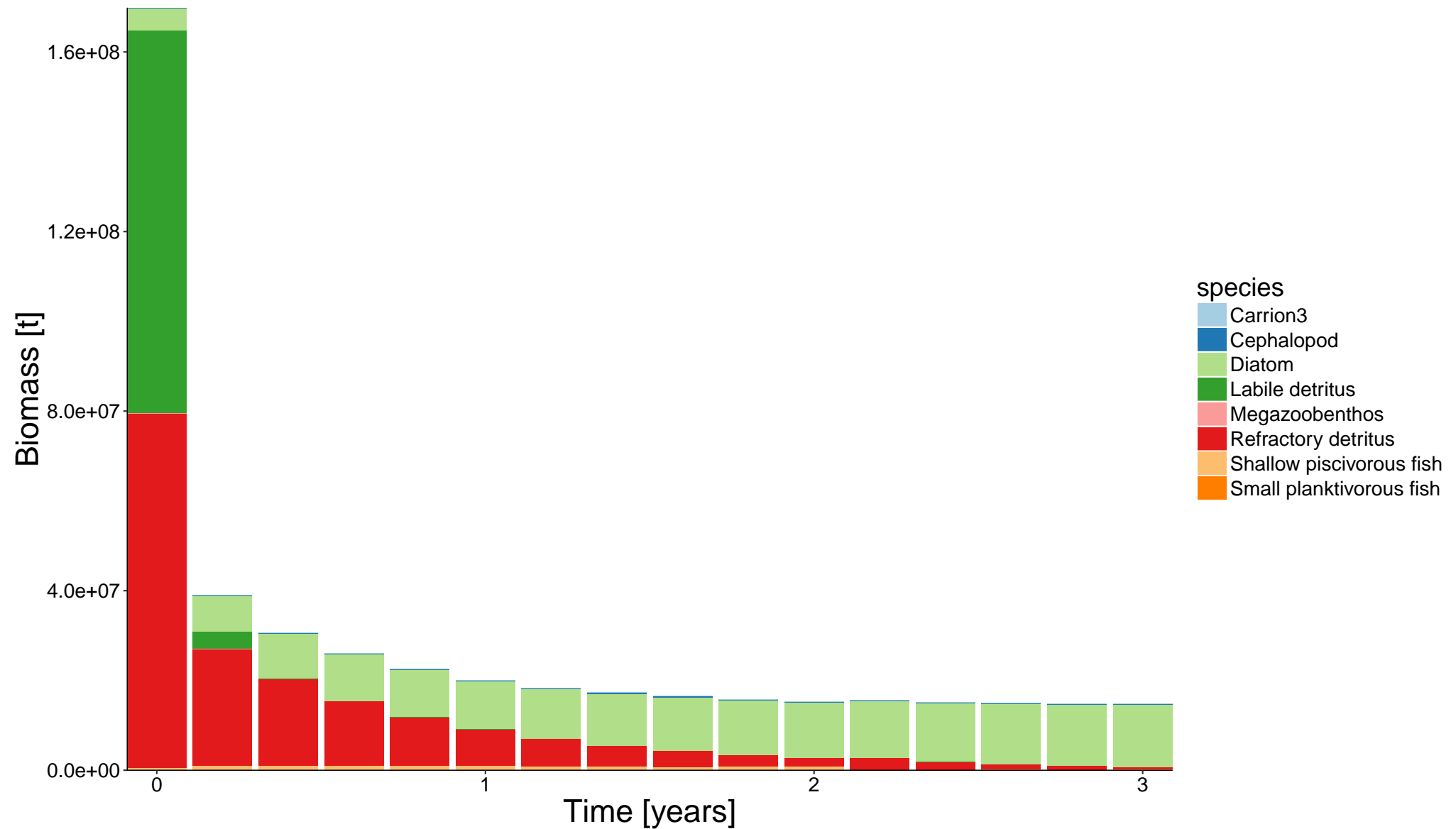
## 1.1 Overall biomass

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

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

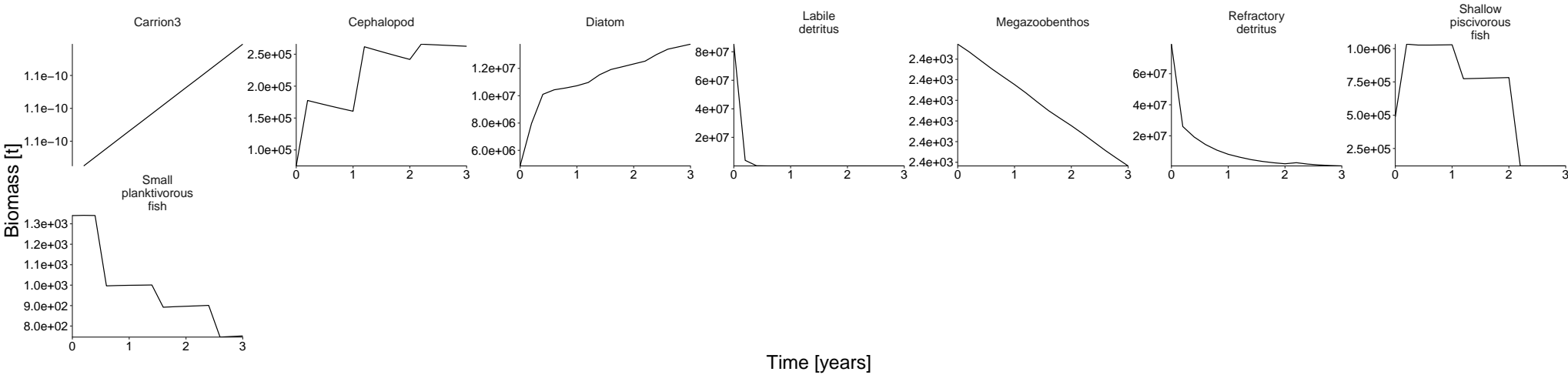
```
plot <- plot_bar(df_bio)
```

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



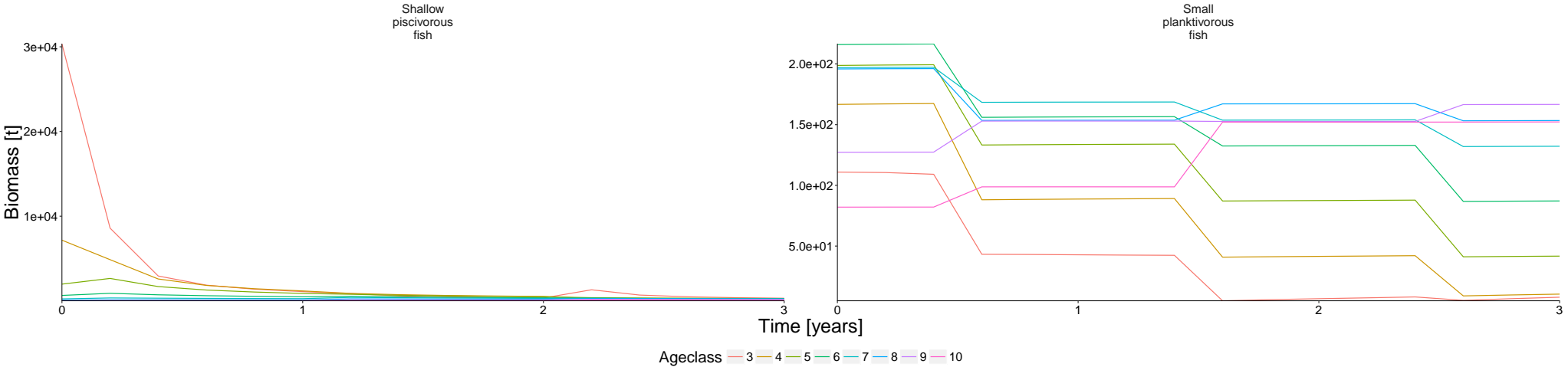
1.2 Biomass timeseries

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



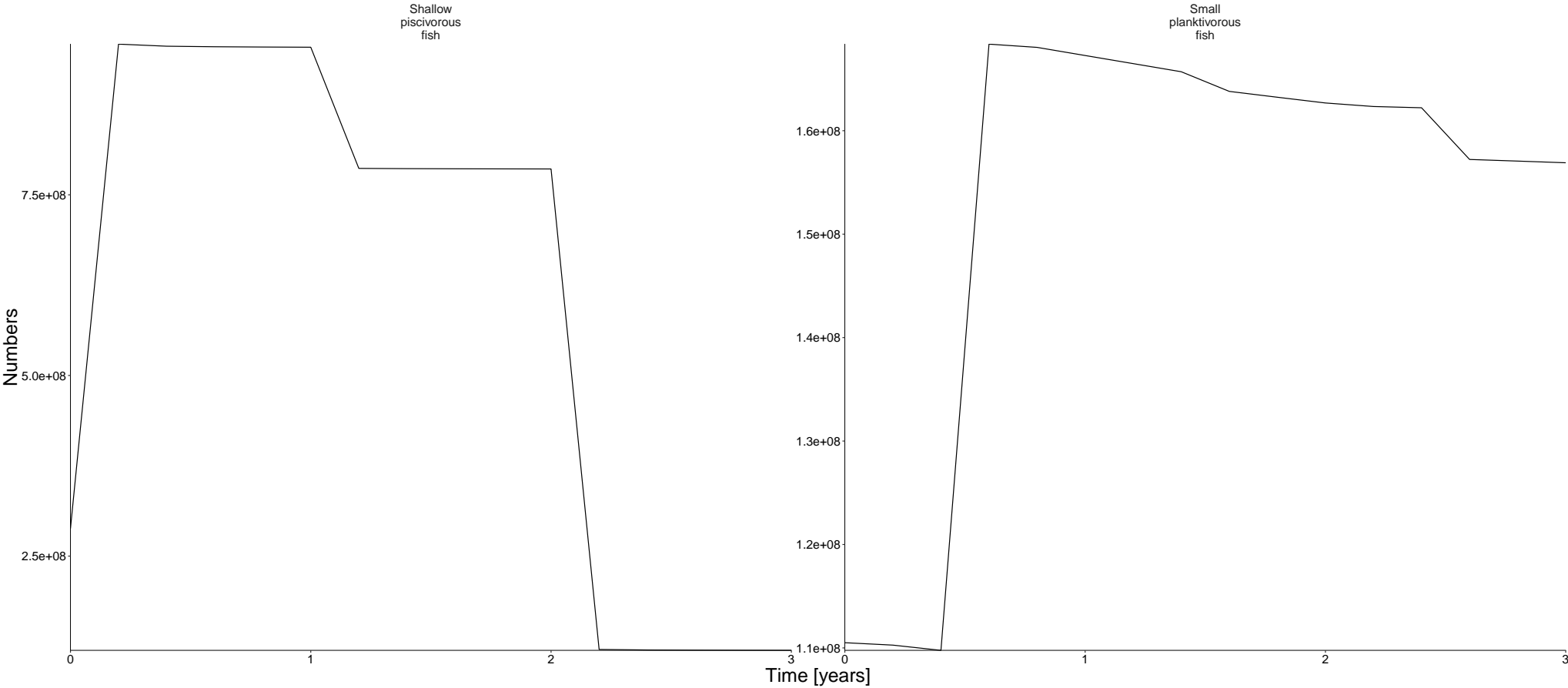
1.3 Biomass@age timeseries

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



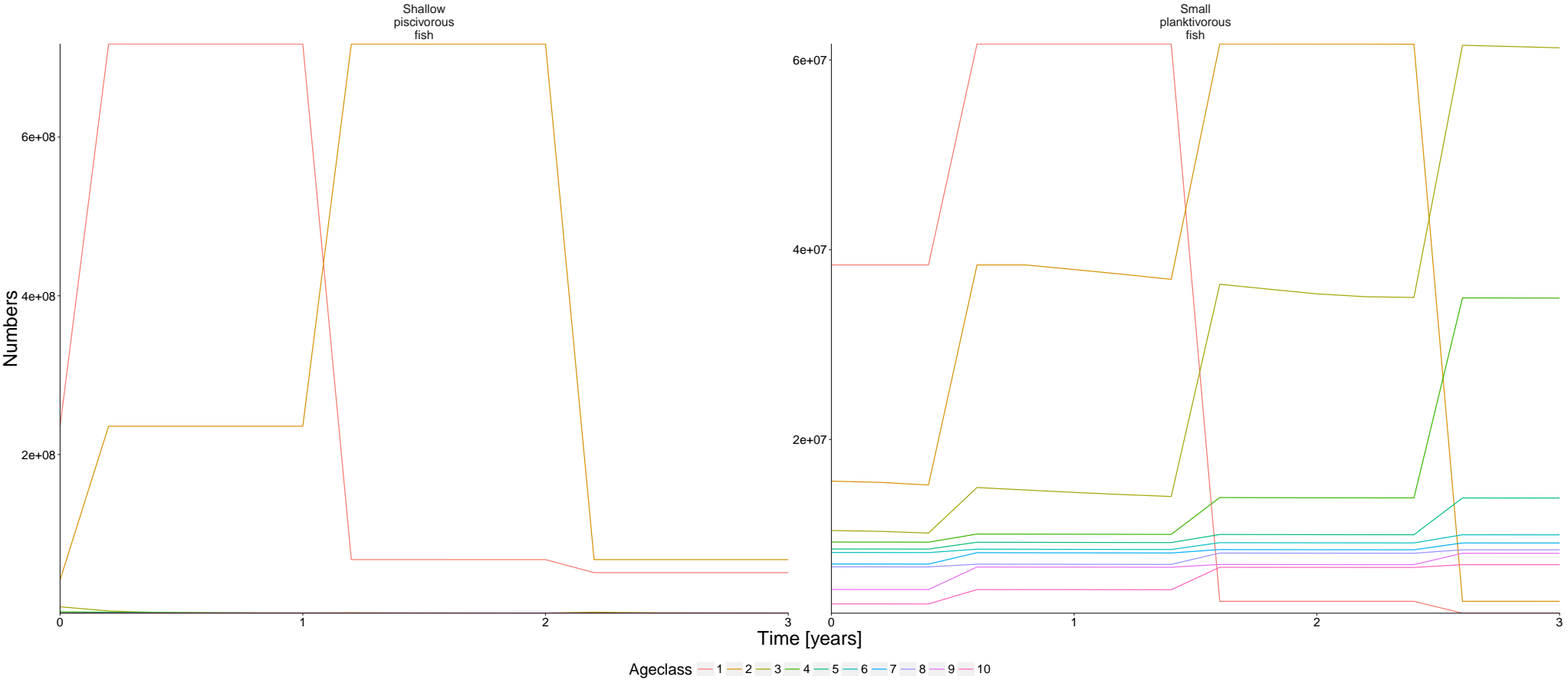
1.4 Number timeseries

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



1.5 Number@age timeseries

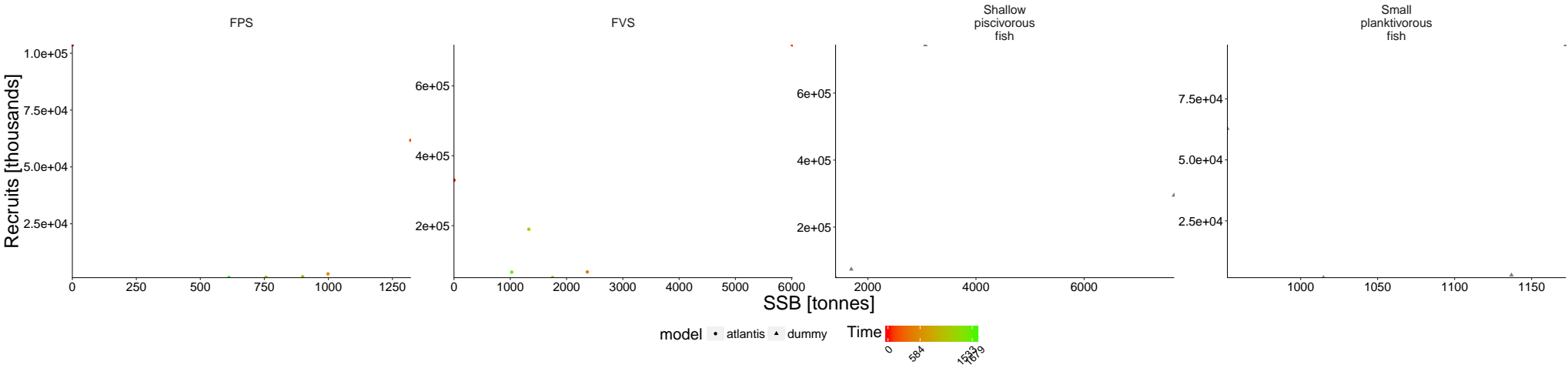
```
plot <- plot_line(result$num_age, col = "agecl")
update_labels(p = plot, labels = list(x = "Time [years]", y = "Numbers", colour = "Ageclass"))
```





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)
```

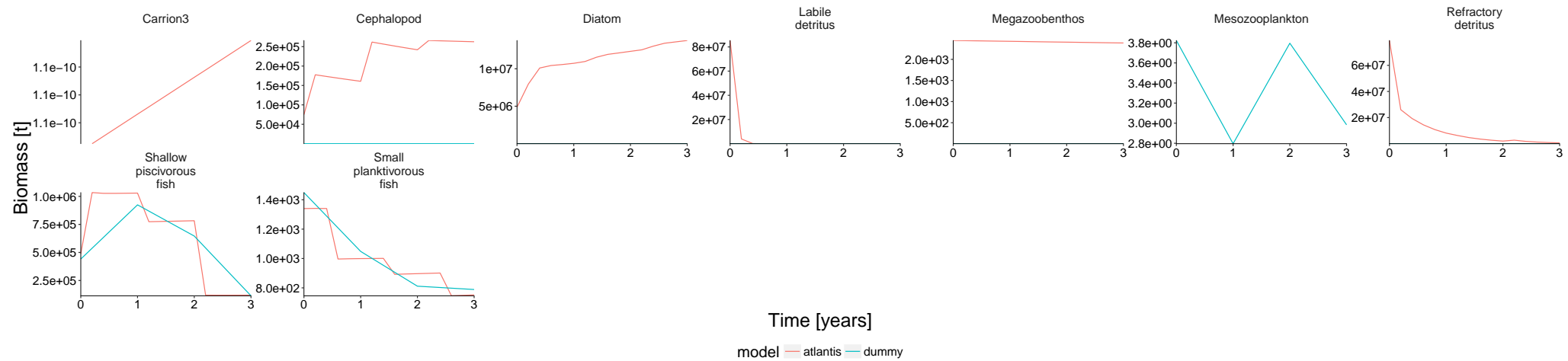
```
# Show atlantis as first factor!
```

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

```
# Create plot
```

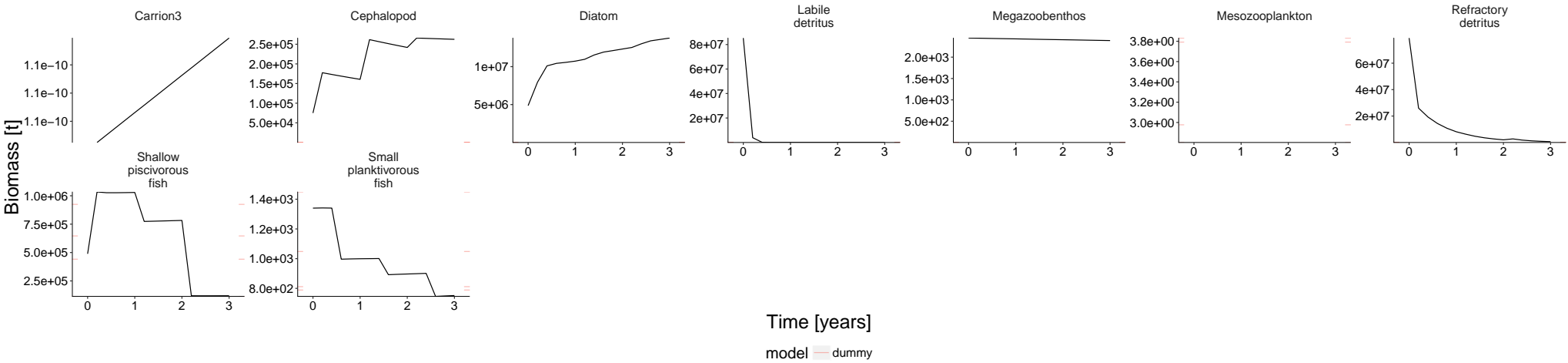
```
plot <- plot_line(comp, col = "model")
```

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



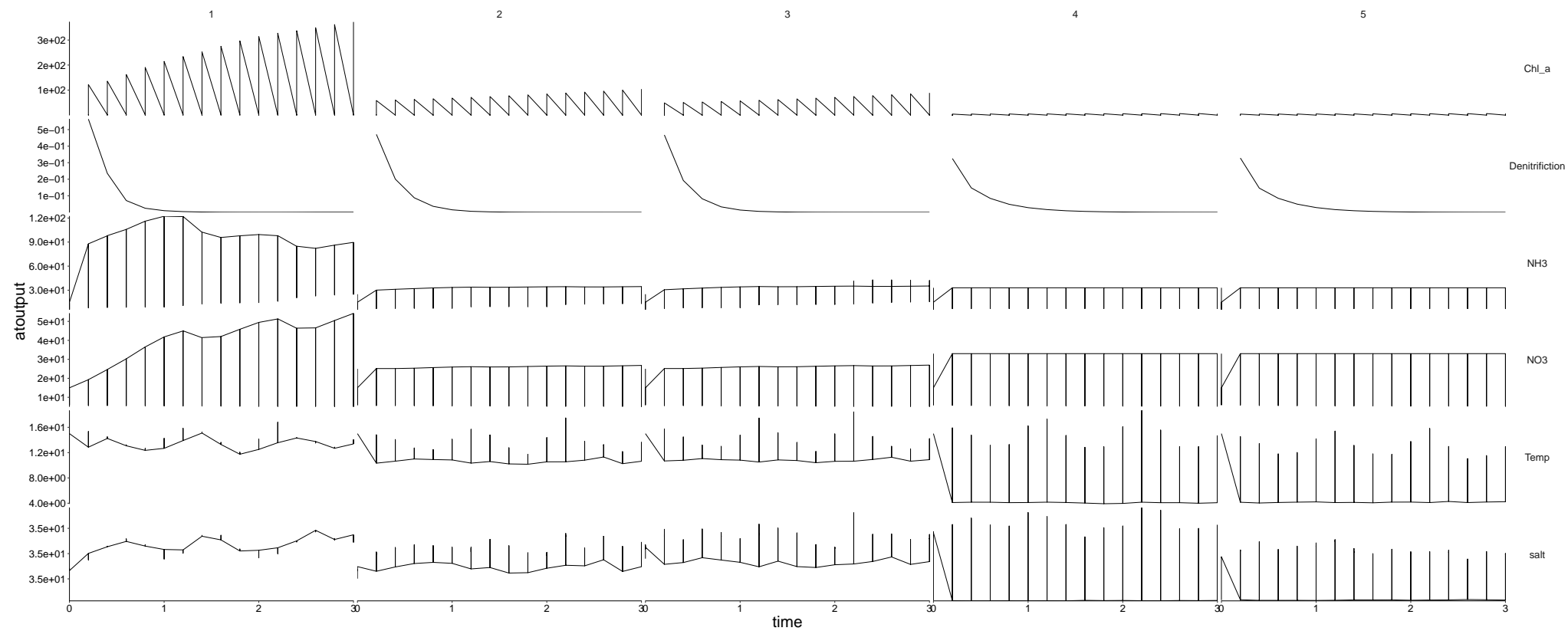
1.8 Biomass benchmark 2

```
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")
```



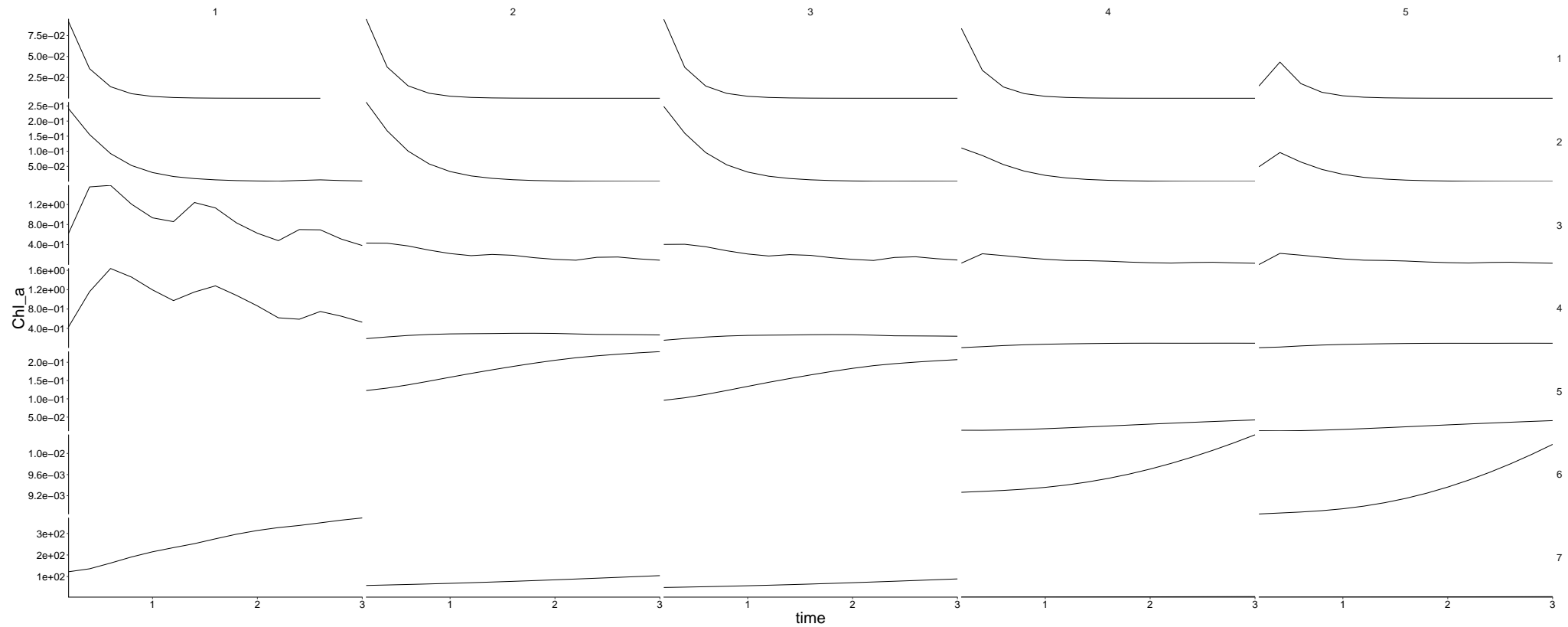
## 2 Physics

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

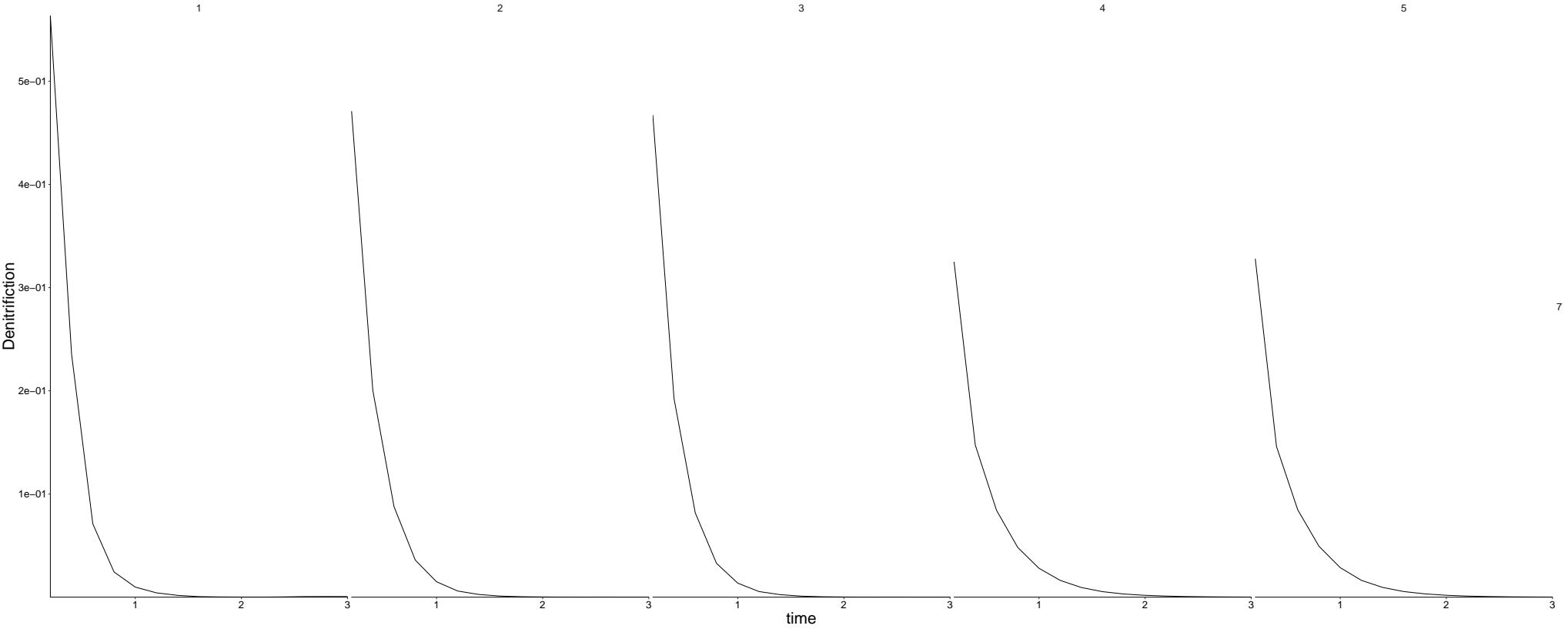
plots <- lapply(physics, plot_line, wrap = NULL) %>%
  lapply(., custom_grid, grid_x = "polygon", grid_y = "layer")

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")
}
```

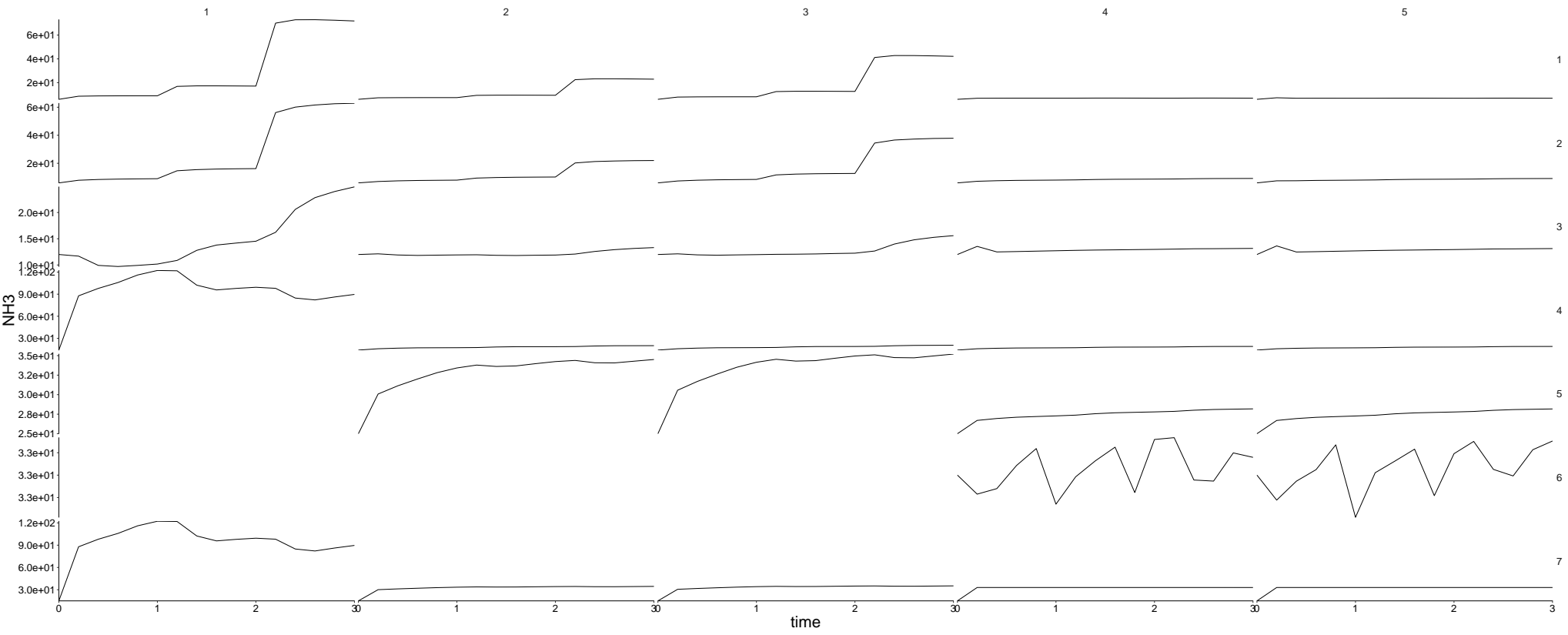
### 2.1 Chl\_a



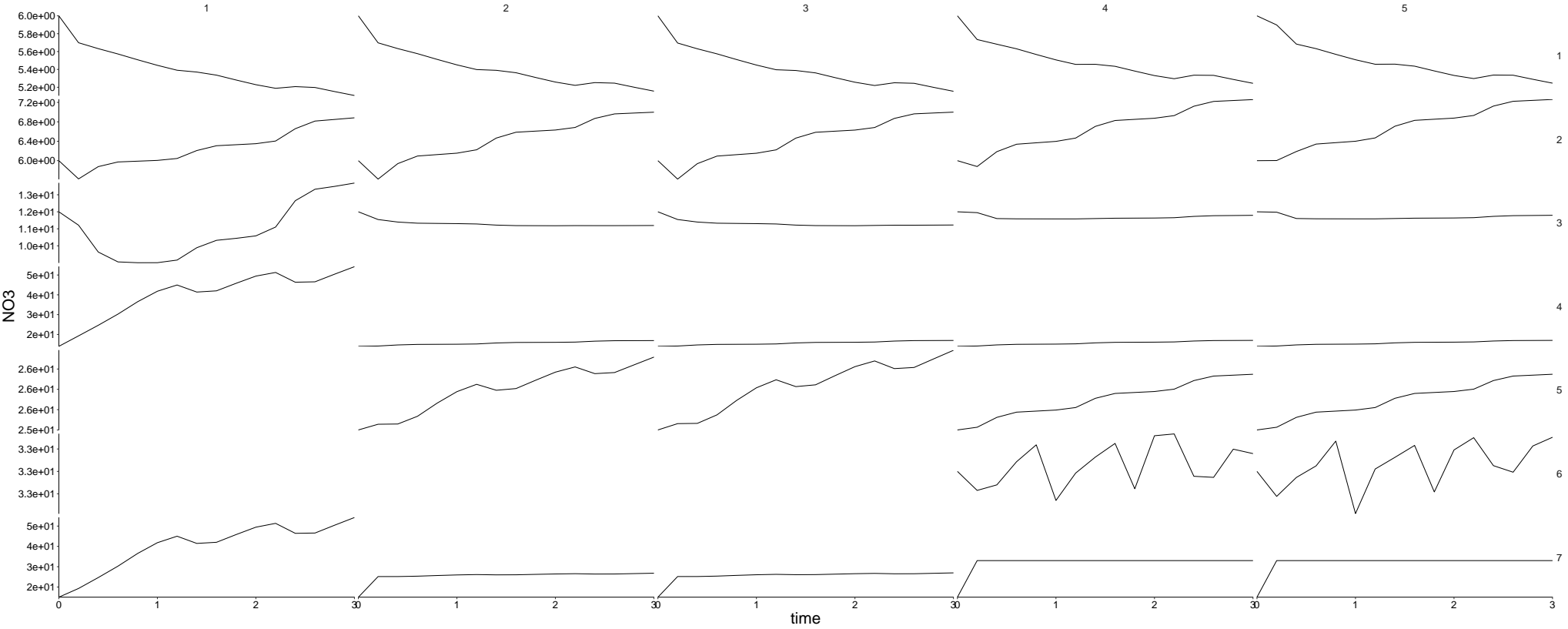
2.2 Denitrification



2.3 NH3

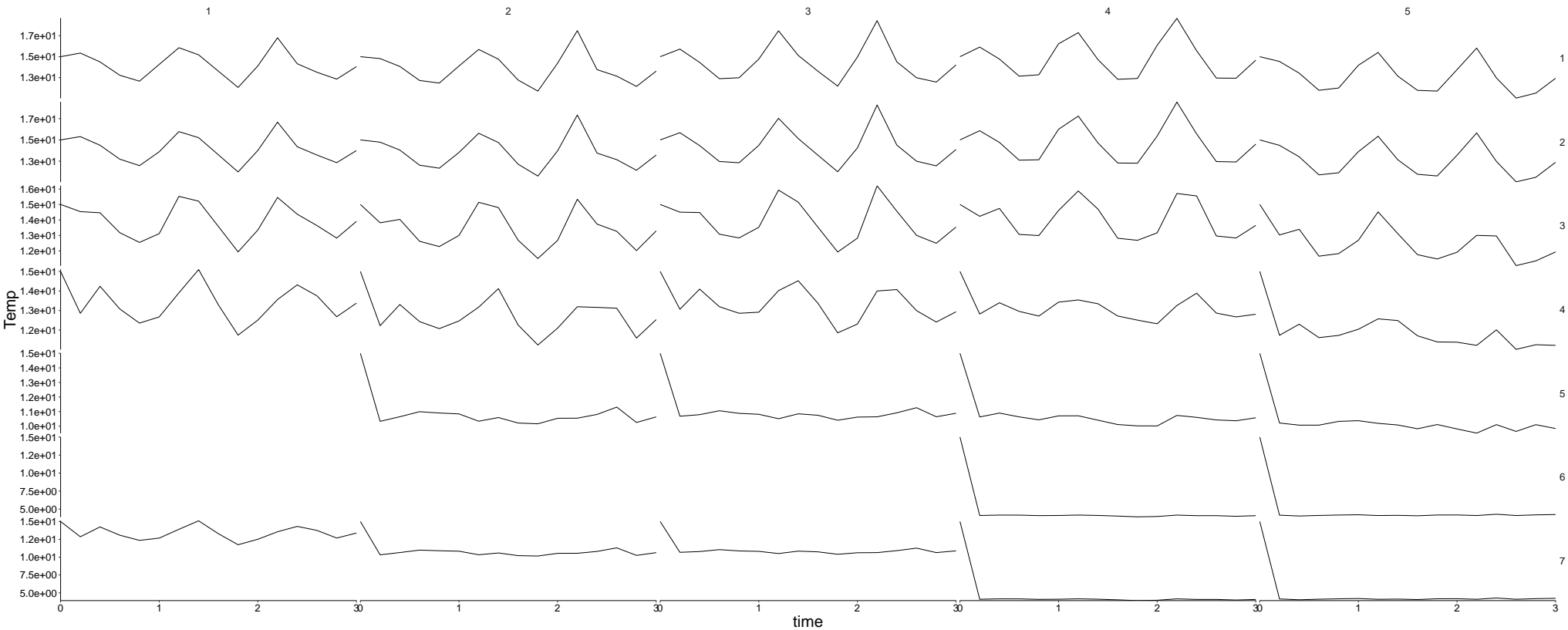


2.4 NO3

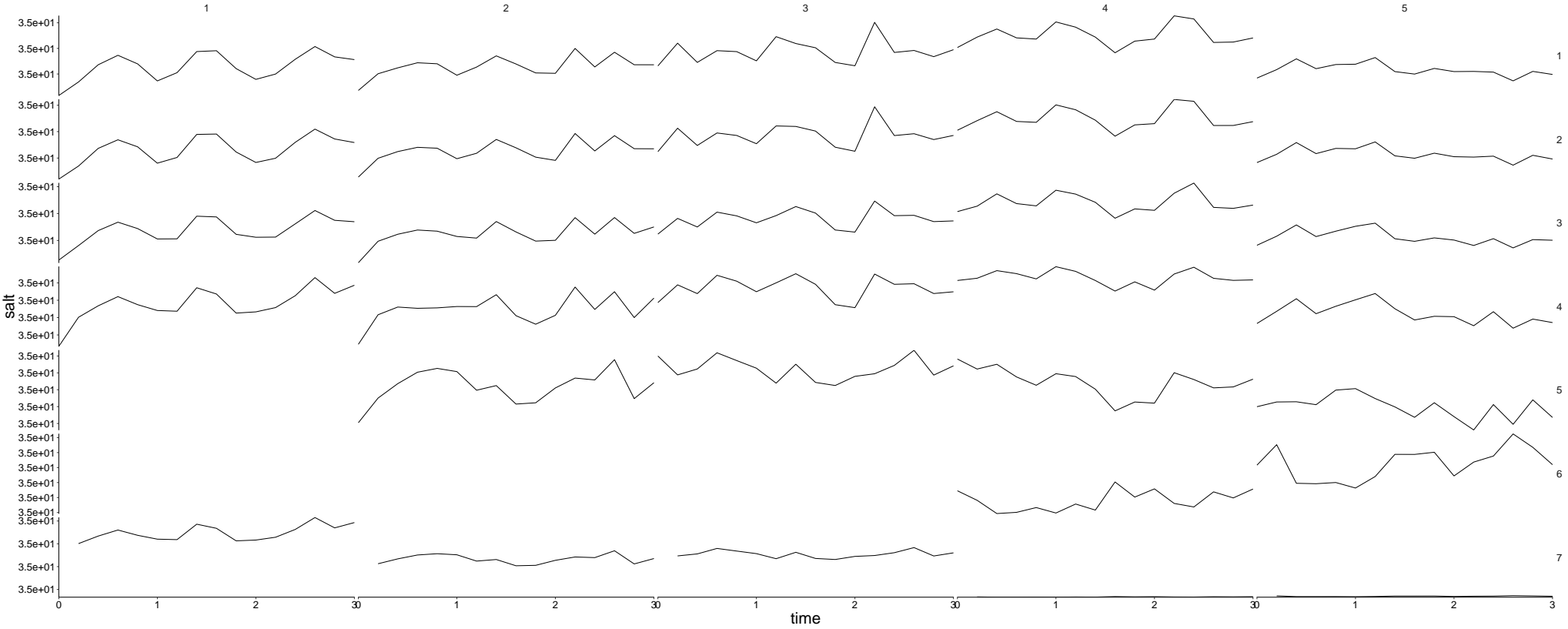




2.5 Temp

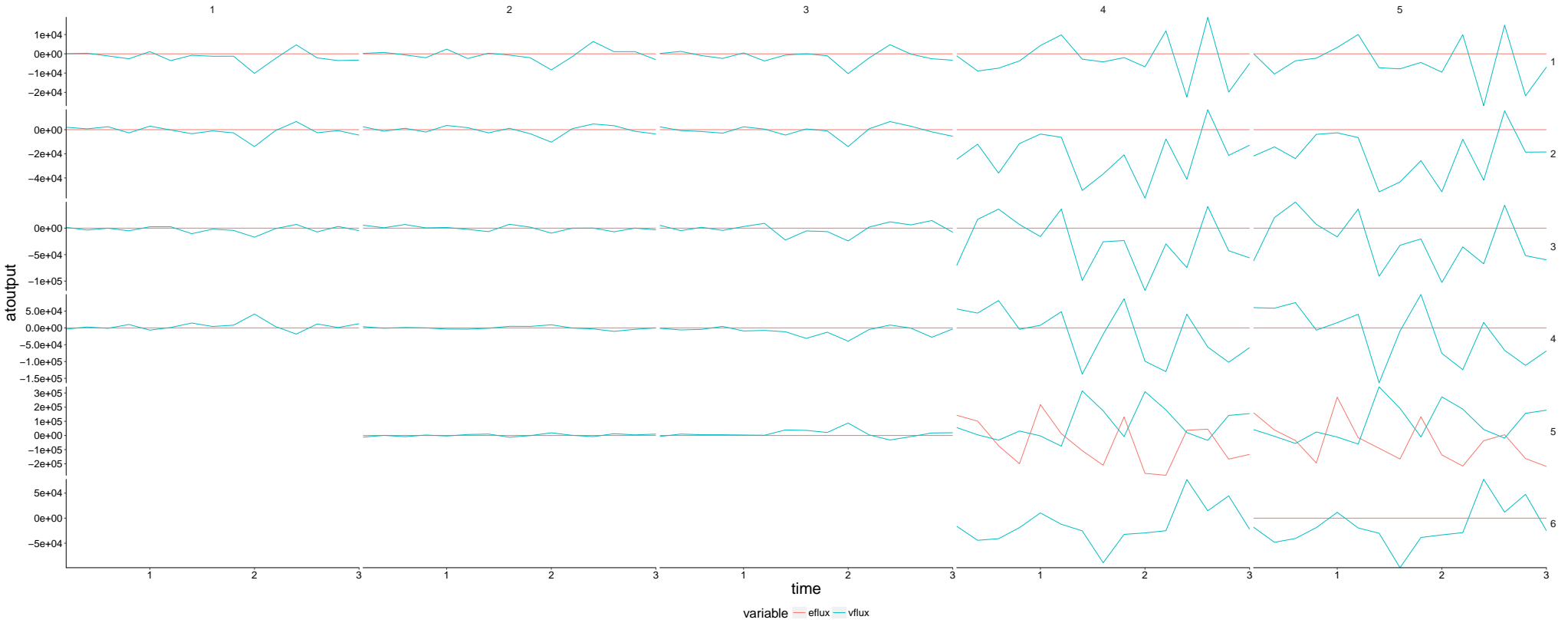


2.6 salt



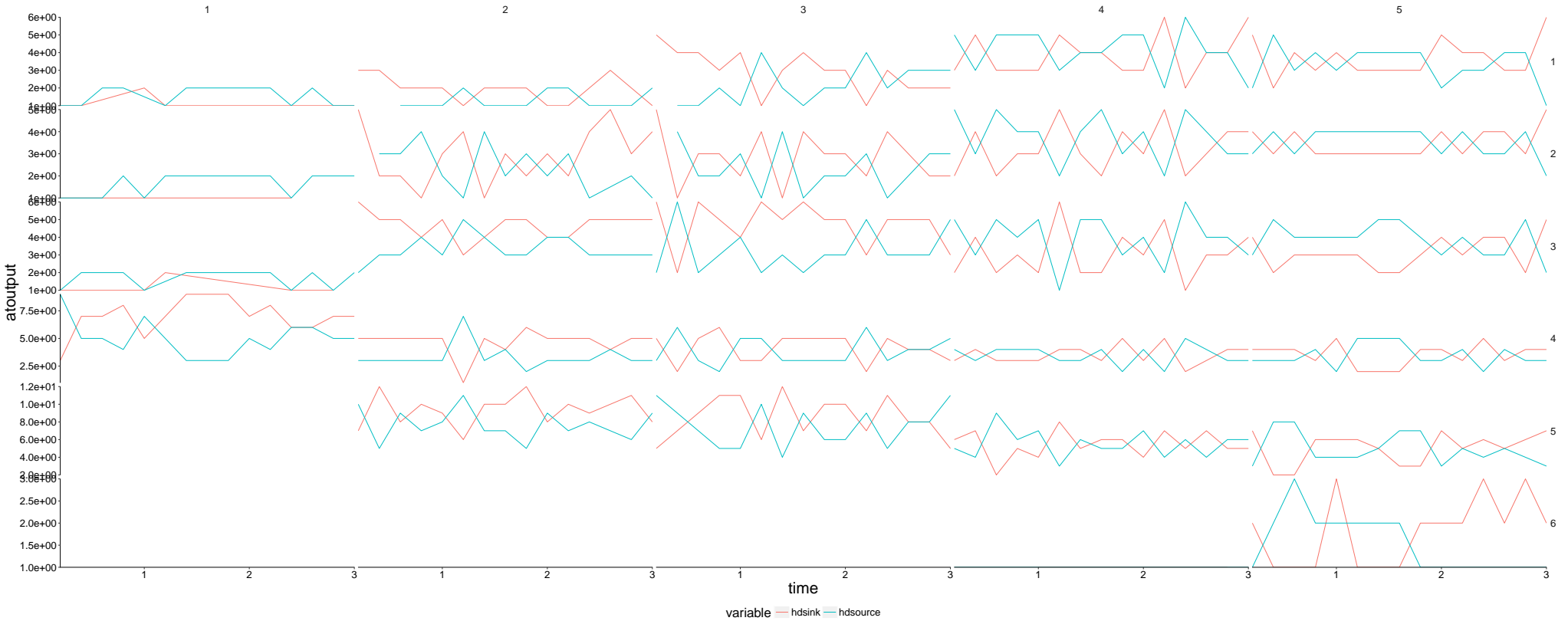
2.7 Fluxes 1

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



2.8 Fluxes 2

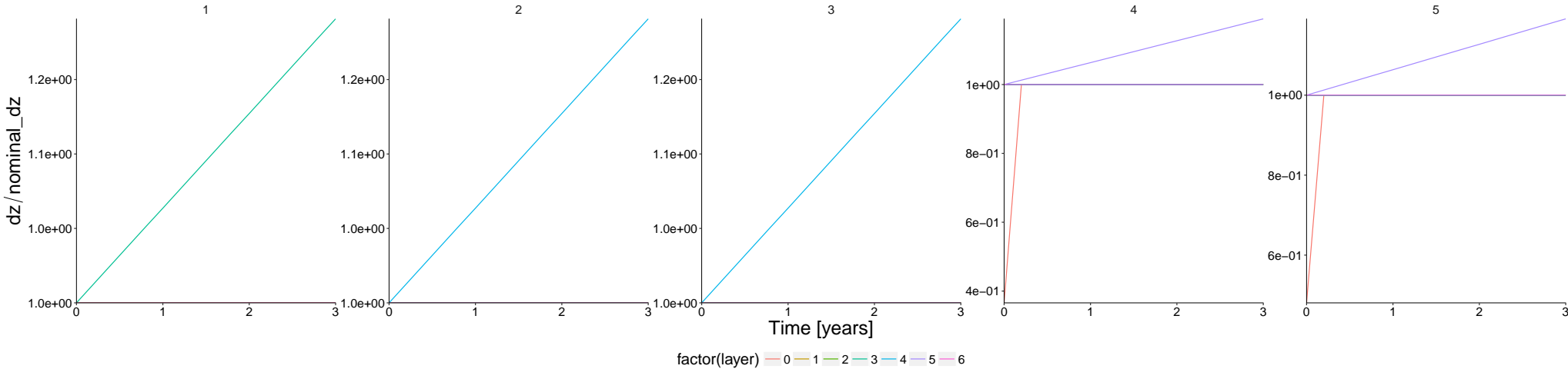
```
plot <- flip_layers(result$sink) %>%  
  plot_line(wrap = NULL, col = "variable")  
custom_grid(plot, grid_x = "polygon", grid_y = "layer")
```



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
```

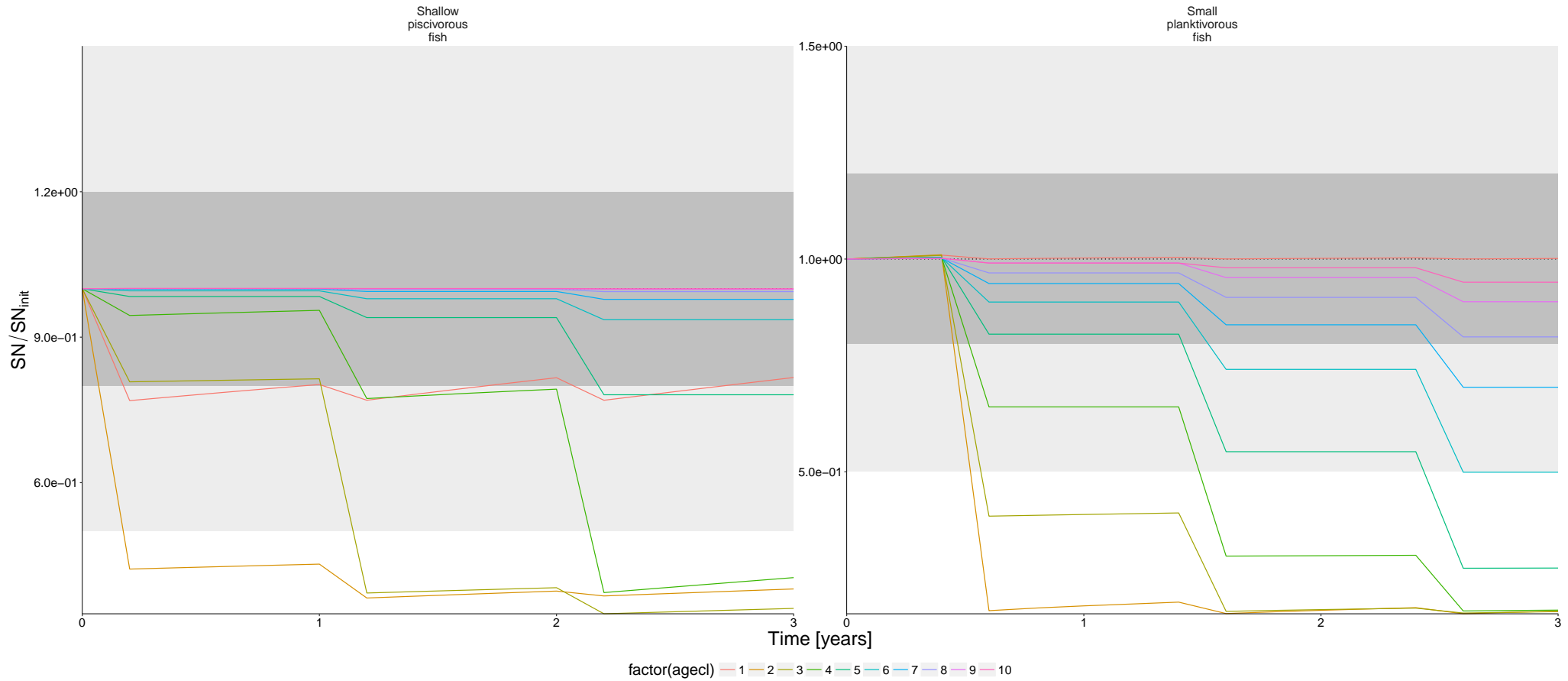
```
plot <- plot_line(check_dz, x = "time", y = "check_dz", wrap = "polygon", col = "layer")
update_labels(plot, list(x = "Time [years]", y = expression(dz/nominal_dz)))
```



### 3 Calibration plots

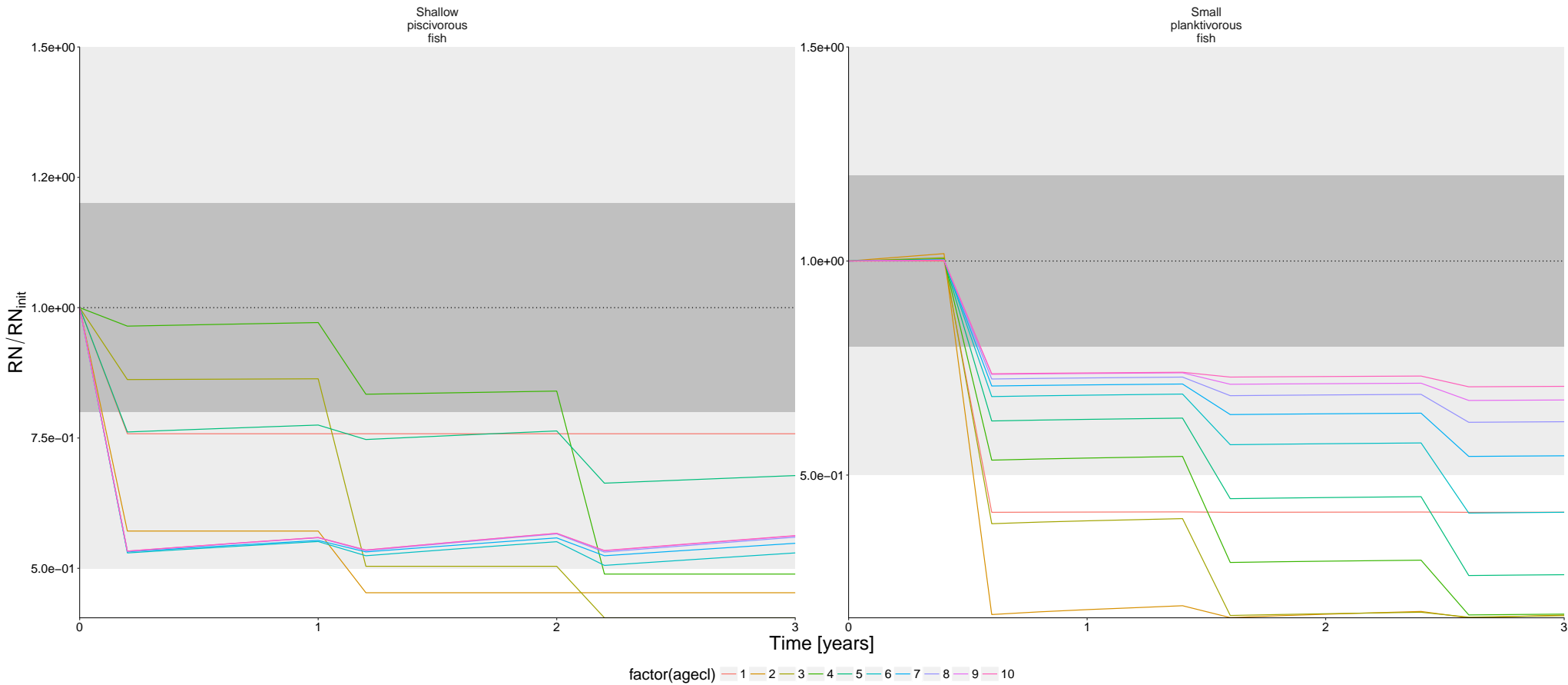
#### 3.1 Structural nitrogen

```
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)
```



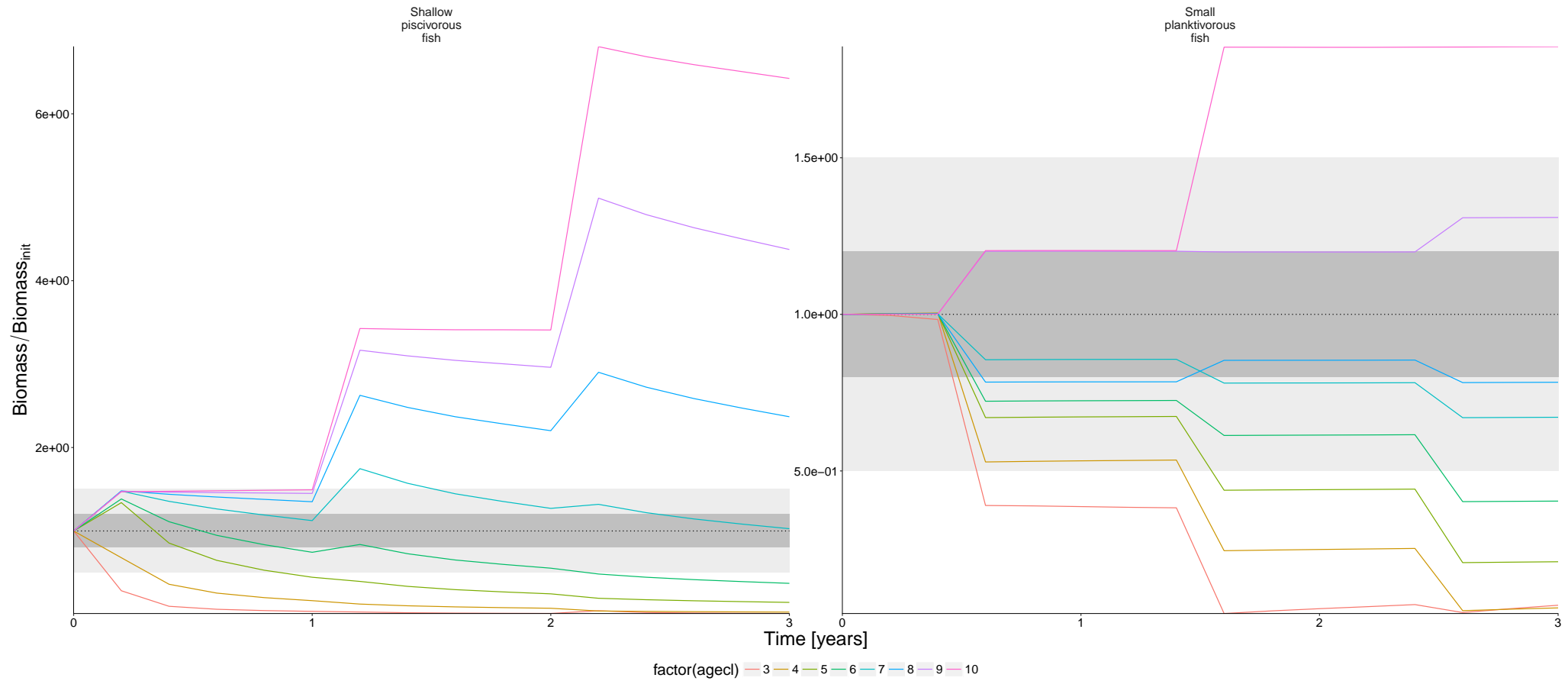
### 3.2 Reserve nitrogen

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



### 3.3 Biomass per ageclass

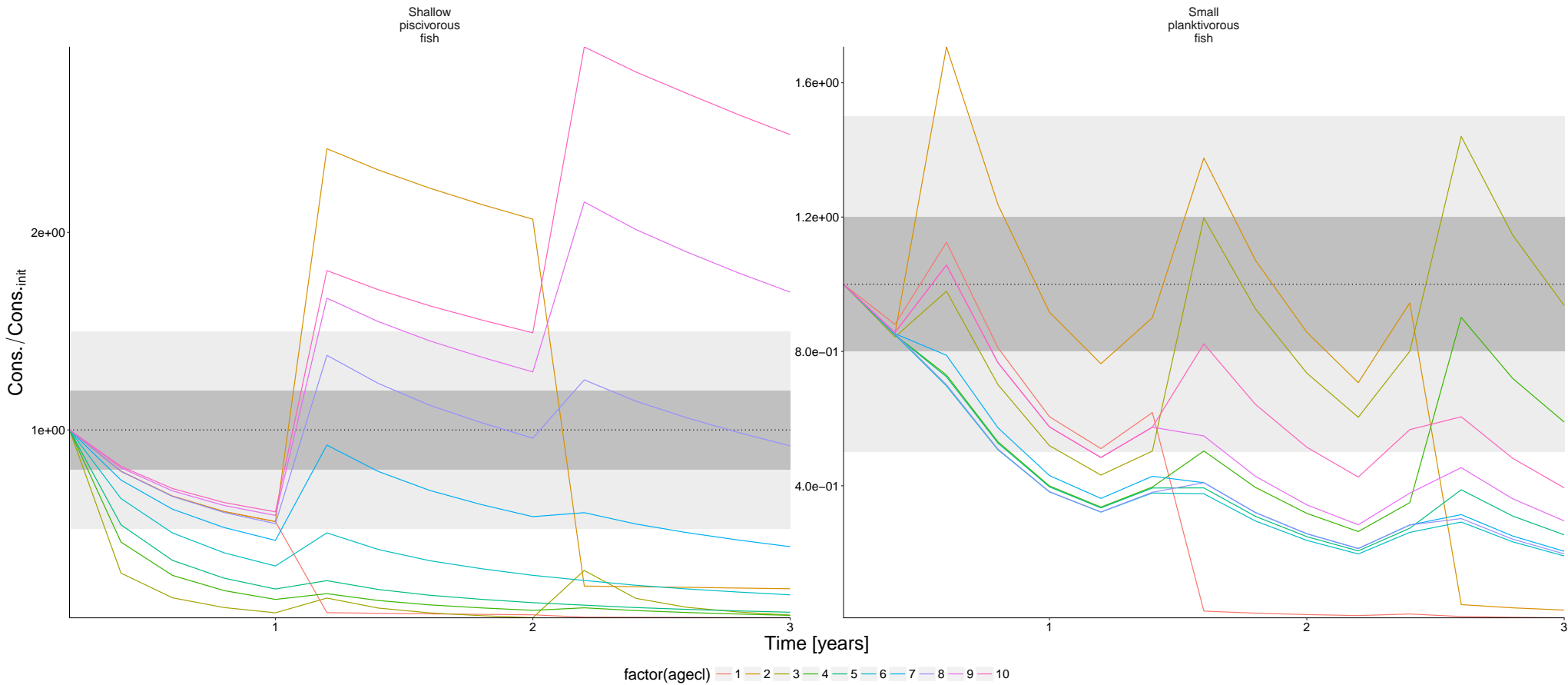
```
df_rel <- convert_relative_initial(result$biomass_age)
plot <- plot_line(df_rel, col = "agecl")
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)
```





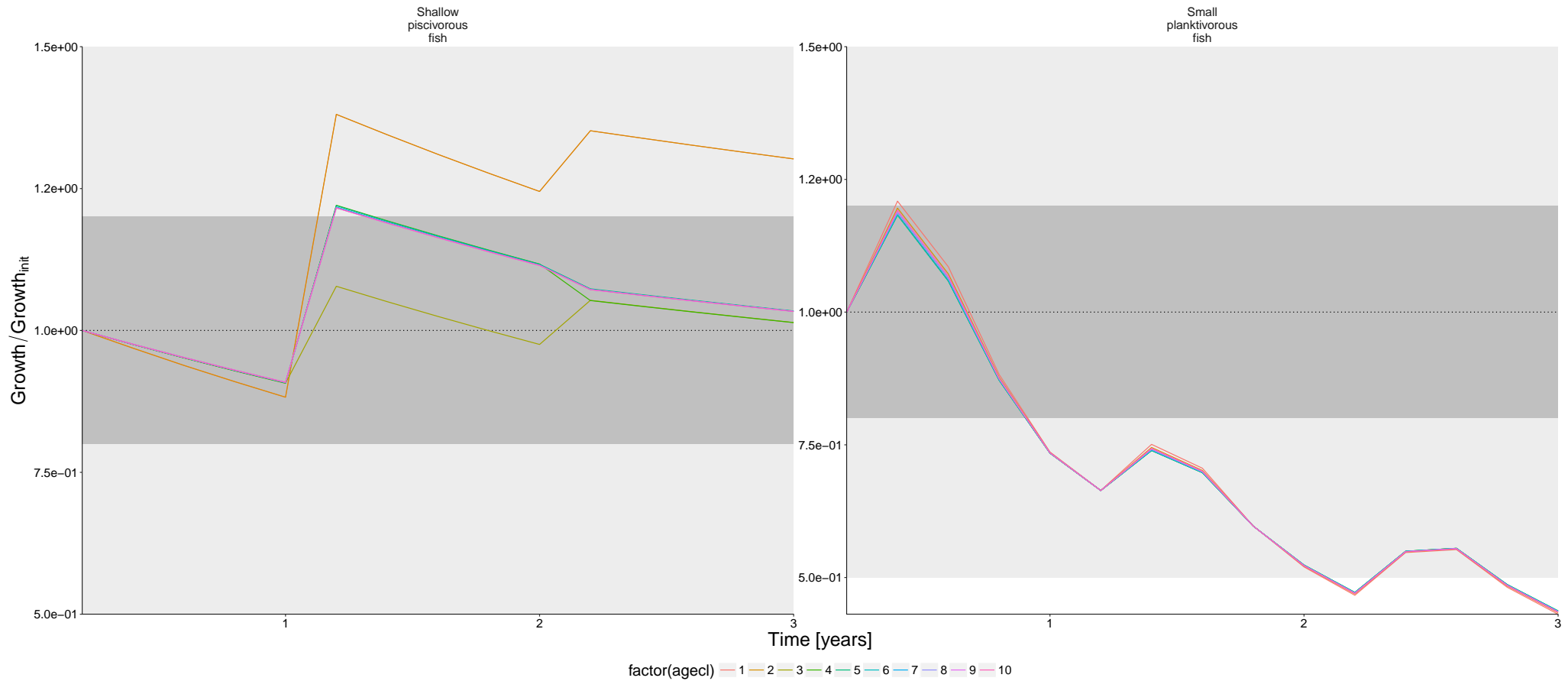
3.4 Eat per ageclass

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



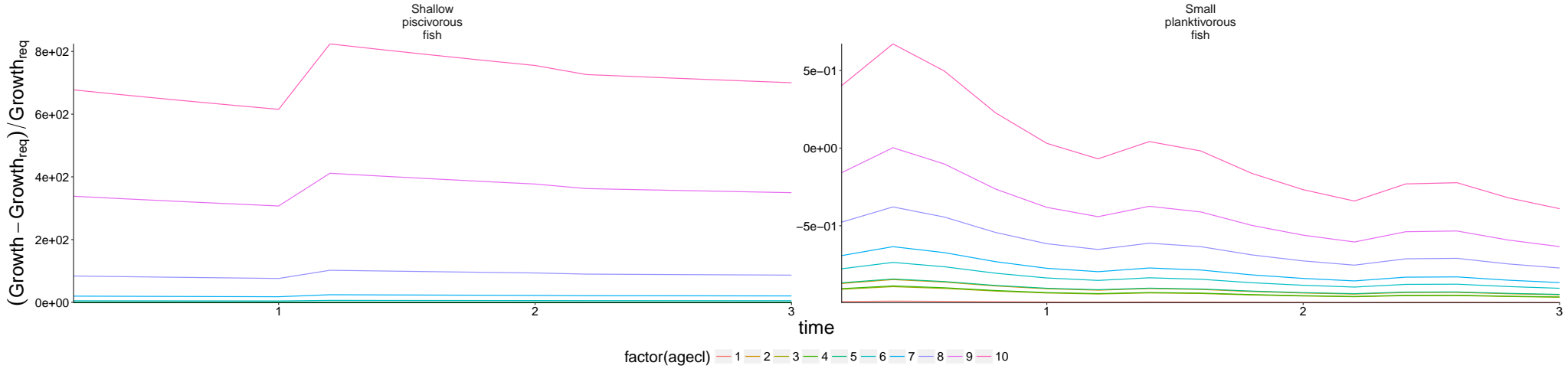
### 3.5 Growth per ageclass

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



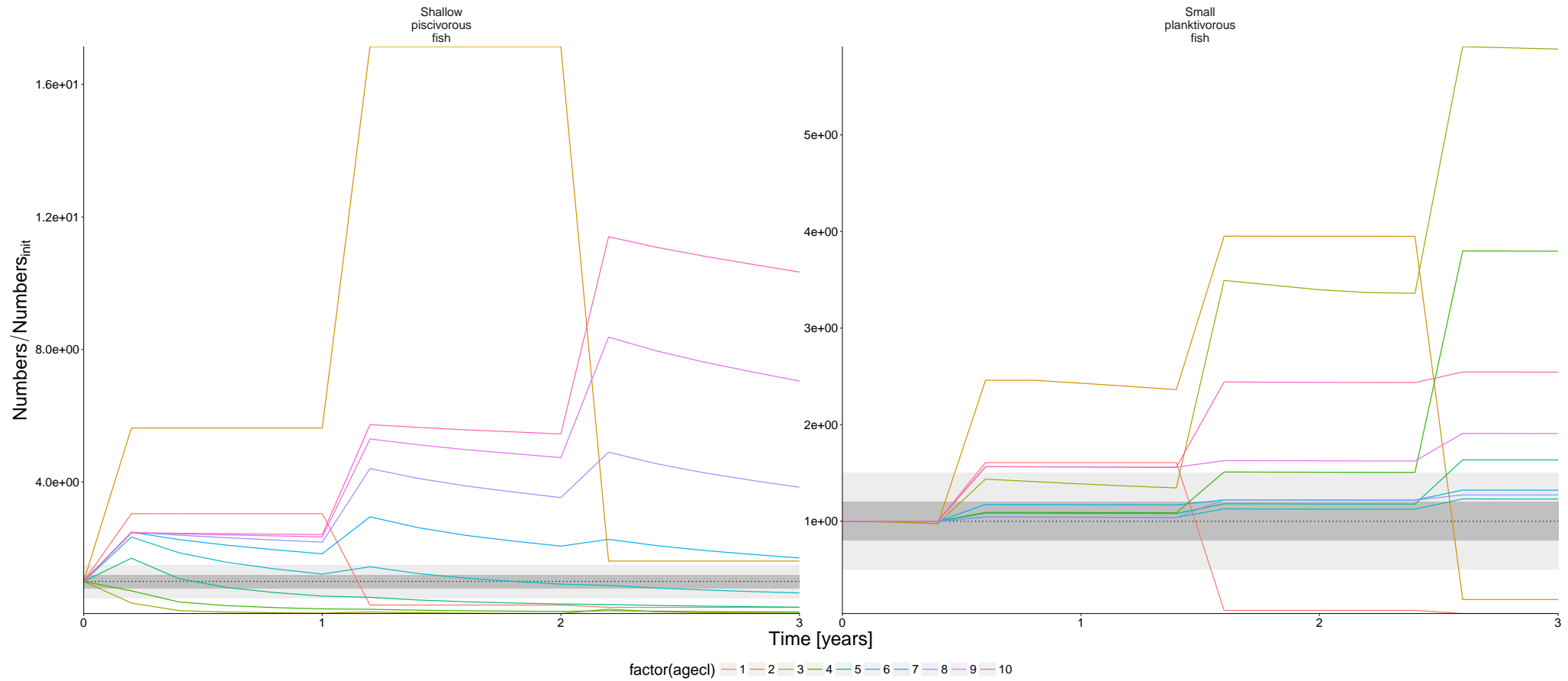
3.6 Growth in relation to initial conditions

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



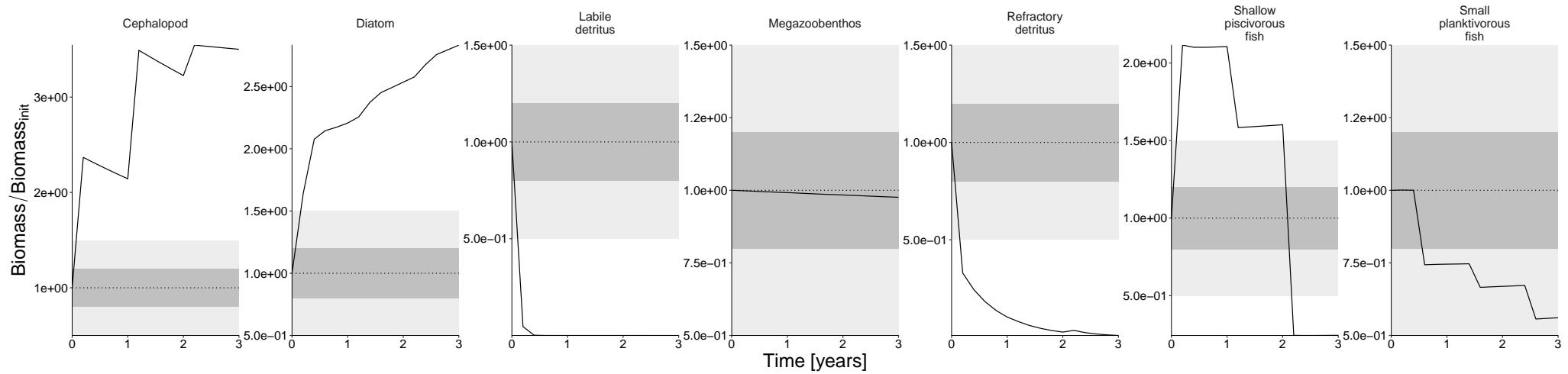
### 3.7 Numbers

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



### 3.8 Biomass

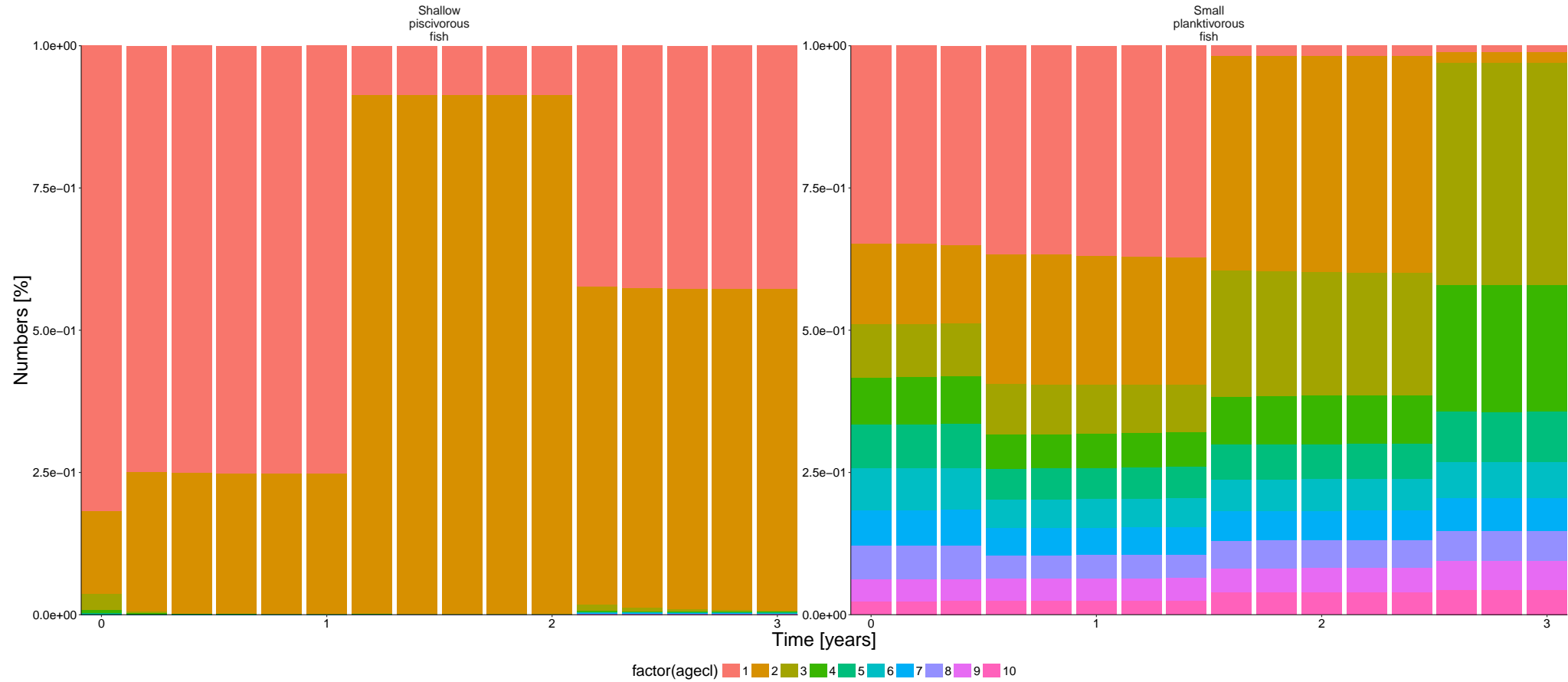
```
df_rel <- convert_relative_initial(result$biomass)
plot <- plot_line(df_rel)
plot <- update_labels(plot, list(x = "Time [years]", y = expression(Biomass/Biomass[init])))
plot_add_box(plot)
```



## 4 Distribution plots

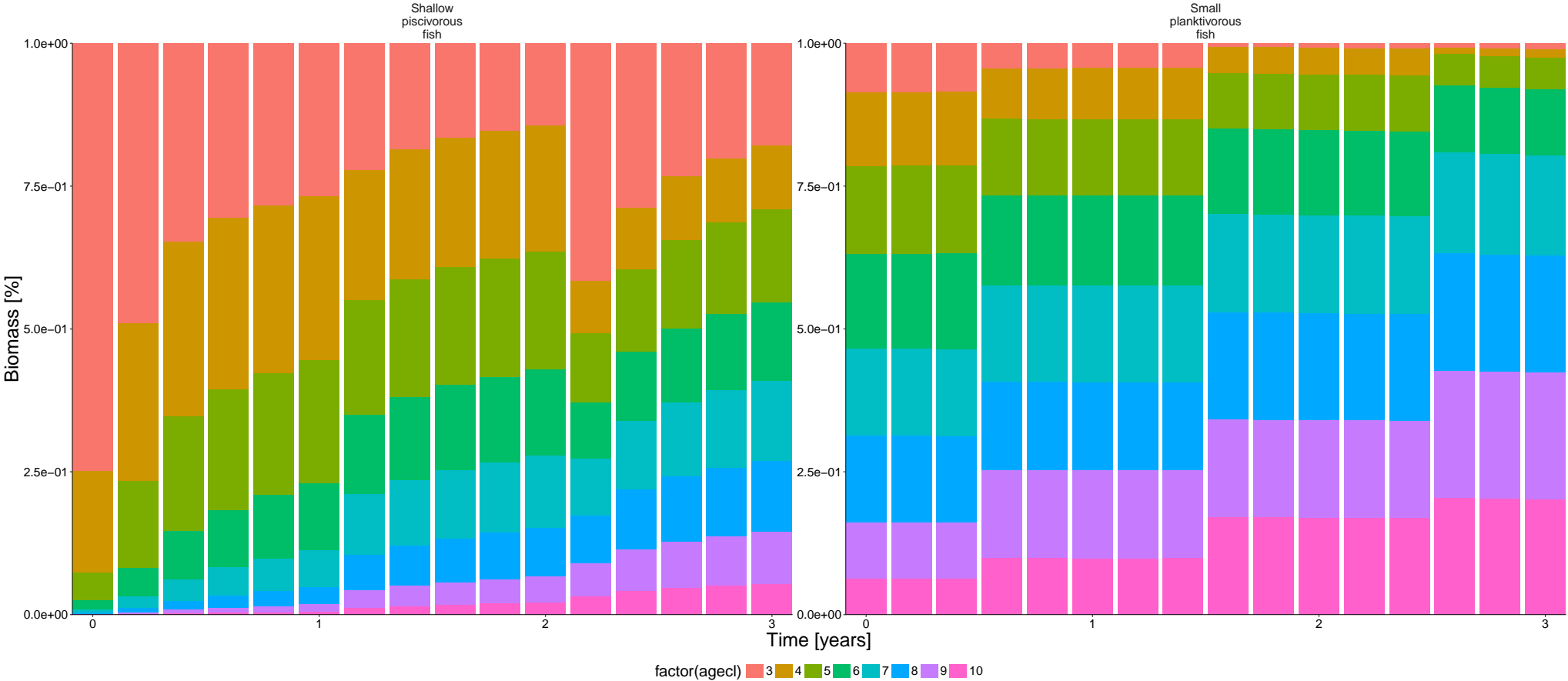
### 4.1 Numbers @ age

```
df <- agg_perc(result$nums_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 [%]"))
```

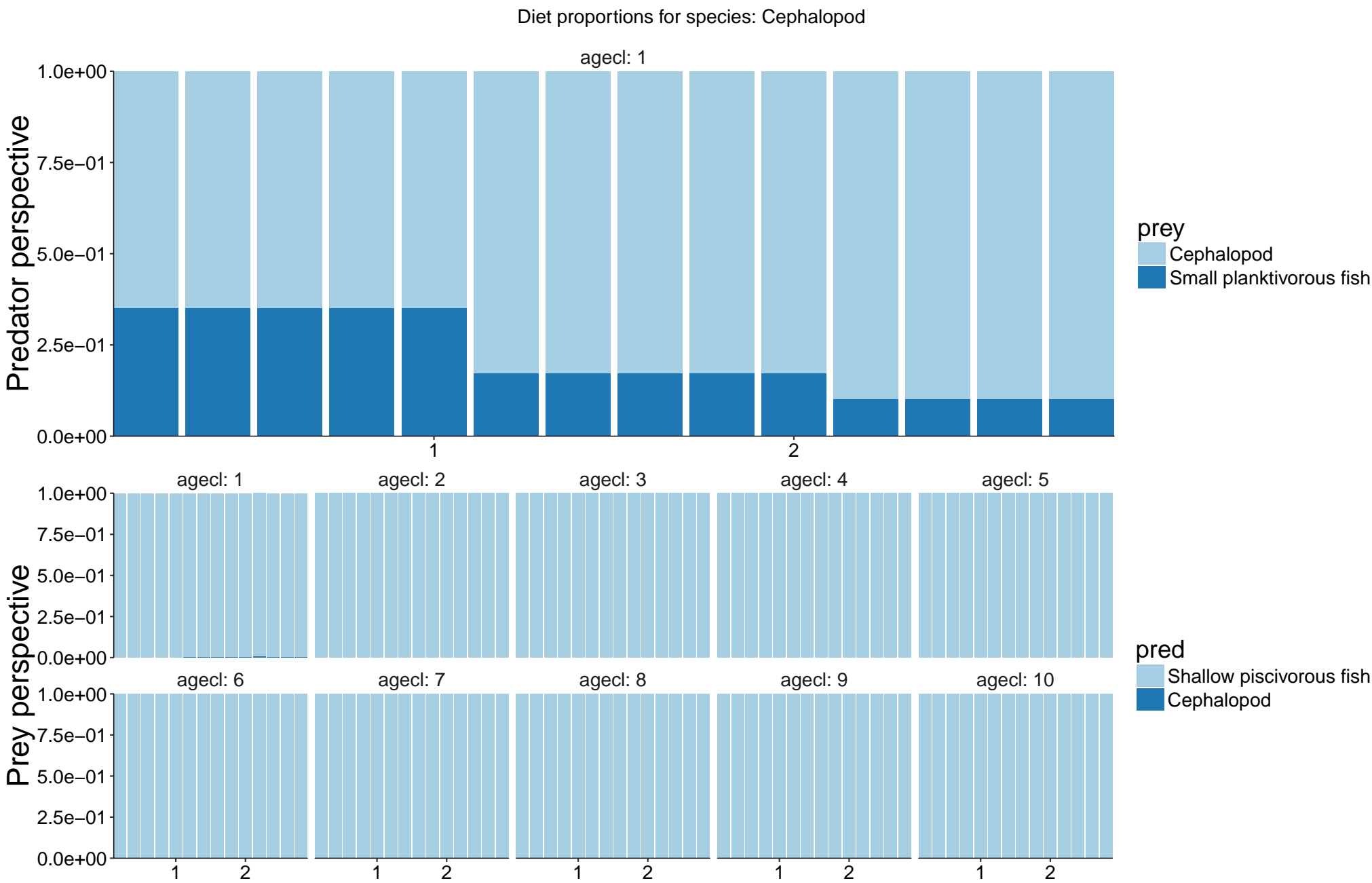


## 5 Diet Plots

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

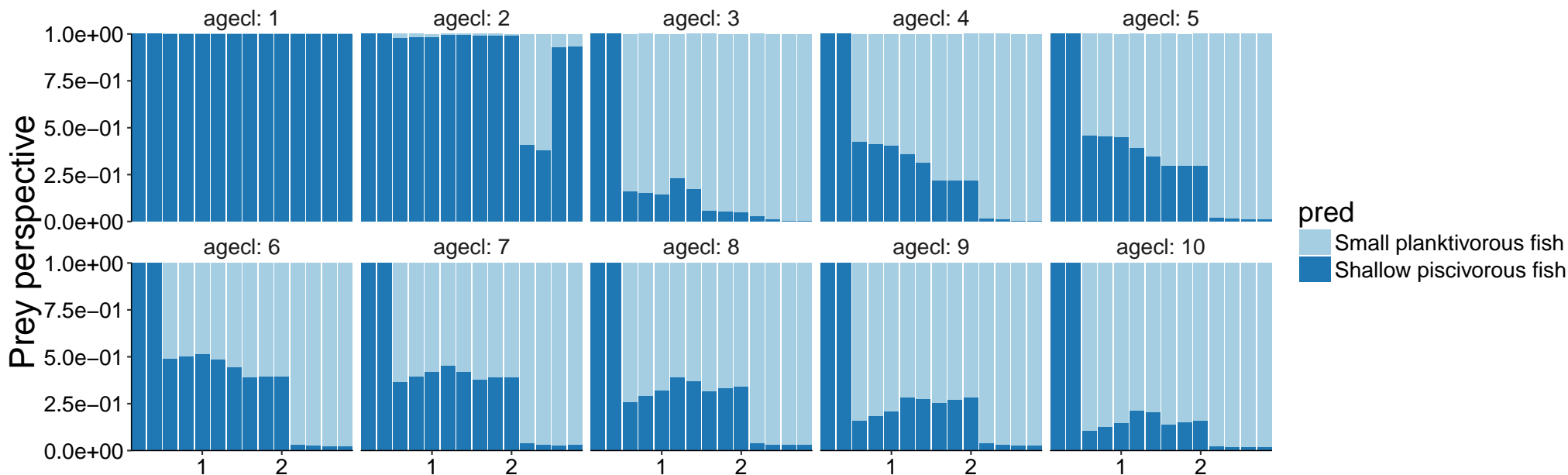


5.1 Diet plot 1: Cephalopod

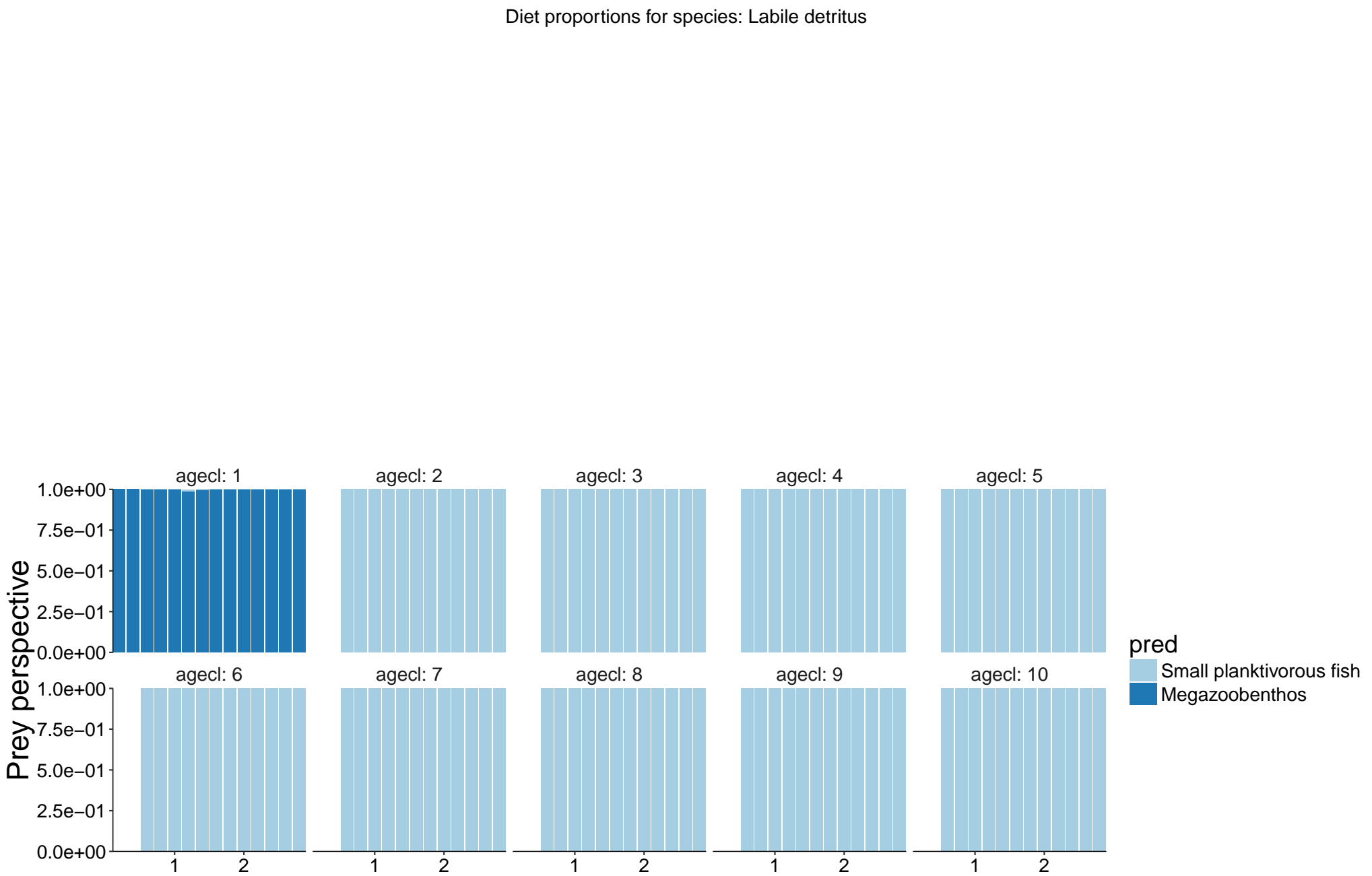


5.2 Diet plot 2: Diatom

Diet proportions for species: Diatom



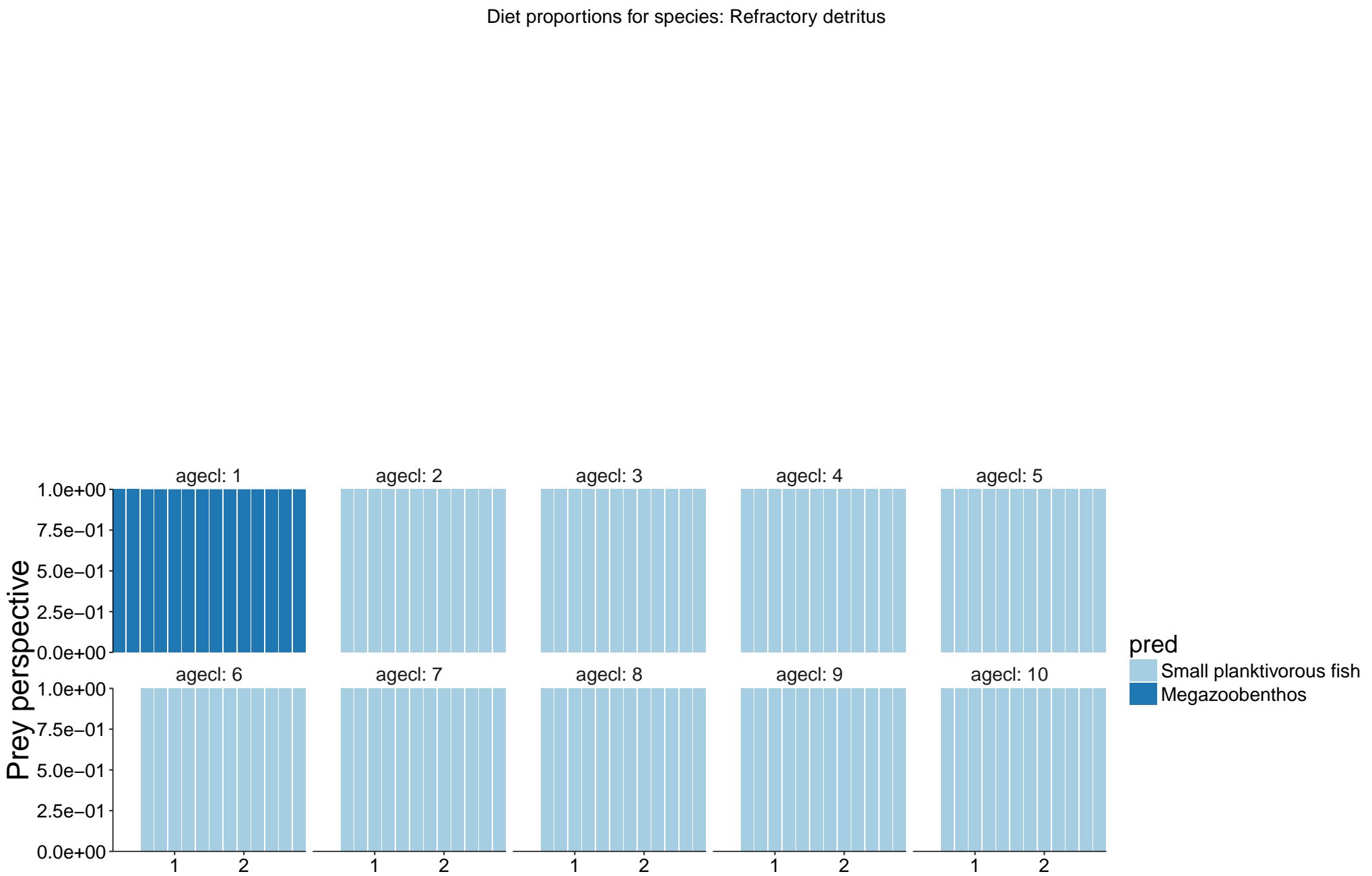
5.3 Diet plot 3: Labile detritus



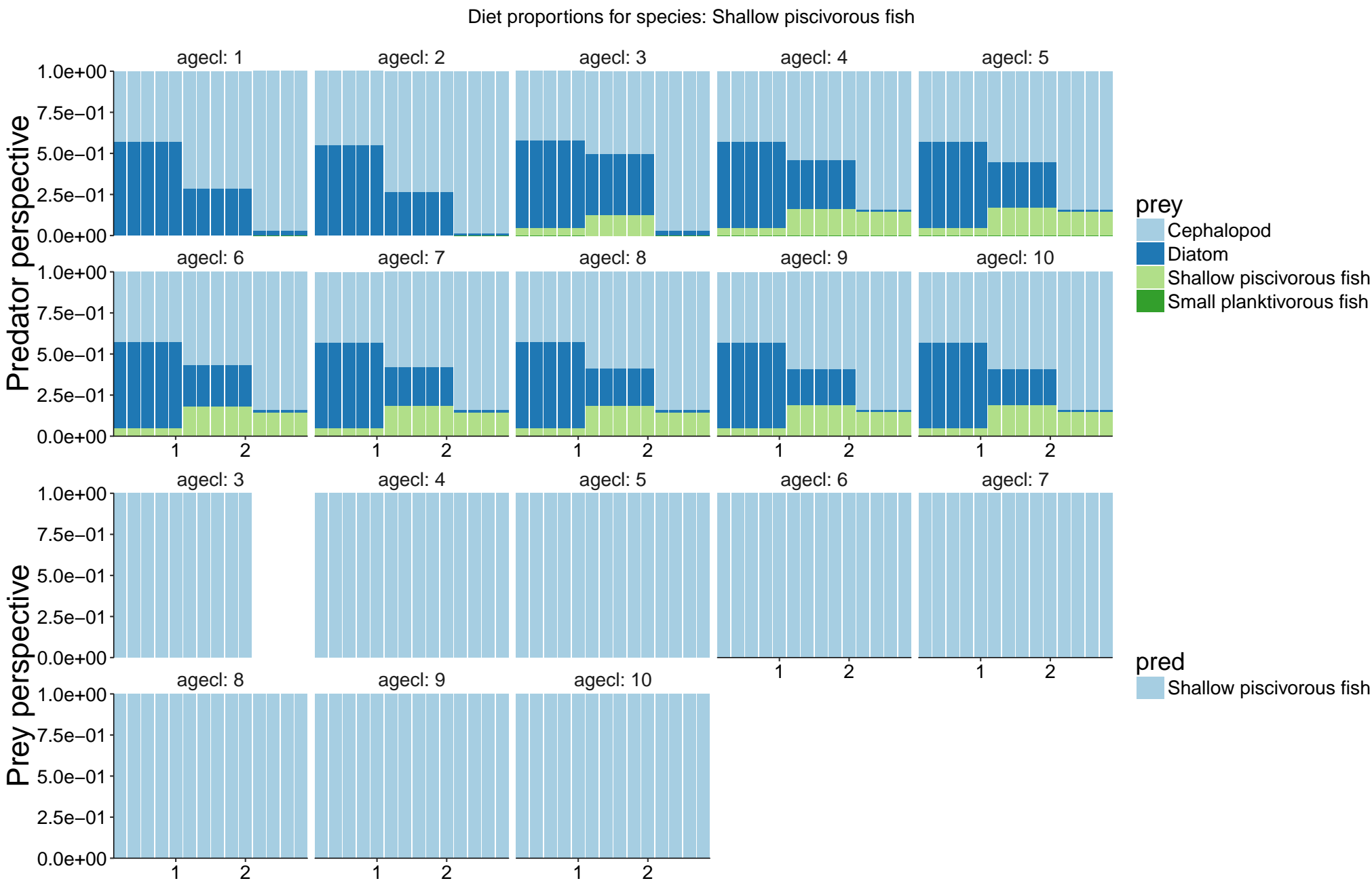
5.4 Diet plot 4: Megazoobenthos



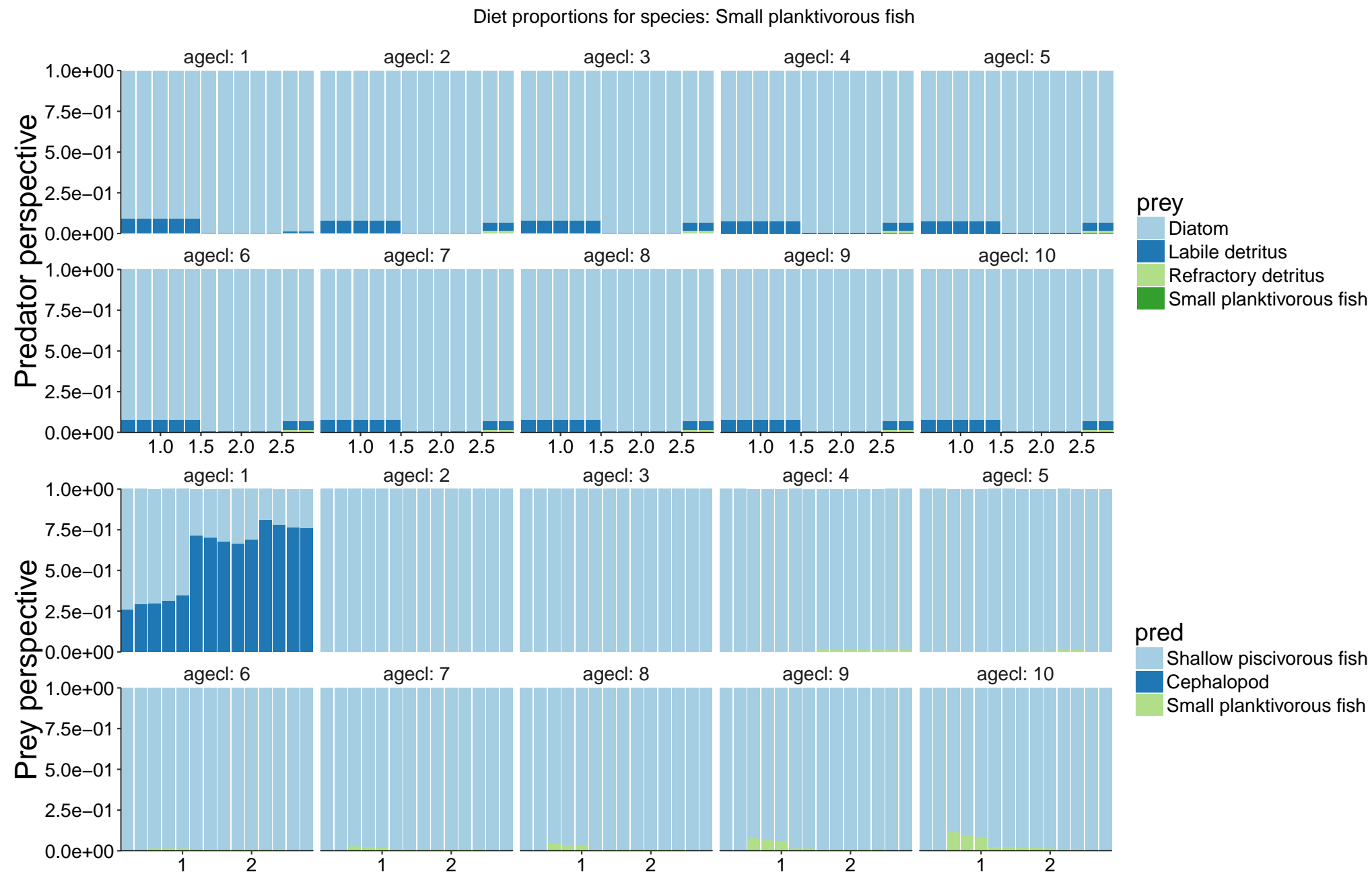
5.5 Diet plot 5: Refractory detritus



5.6 Diet plot 6: Shallow piscivorous fish



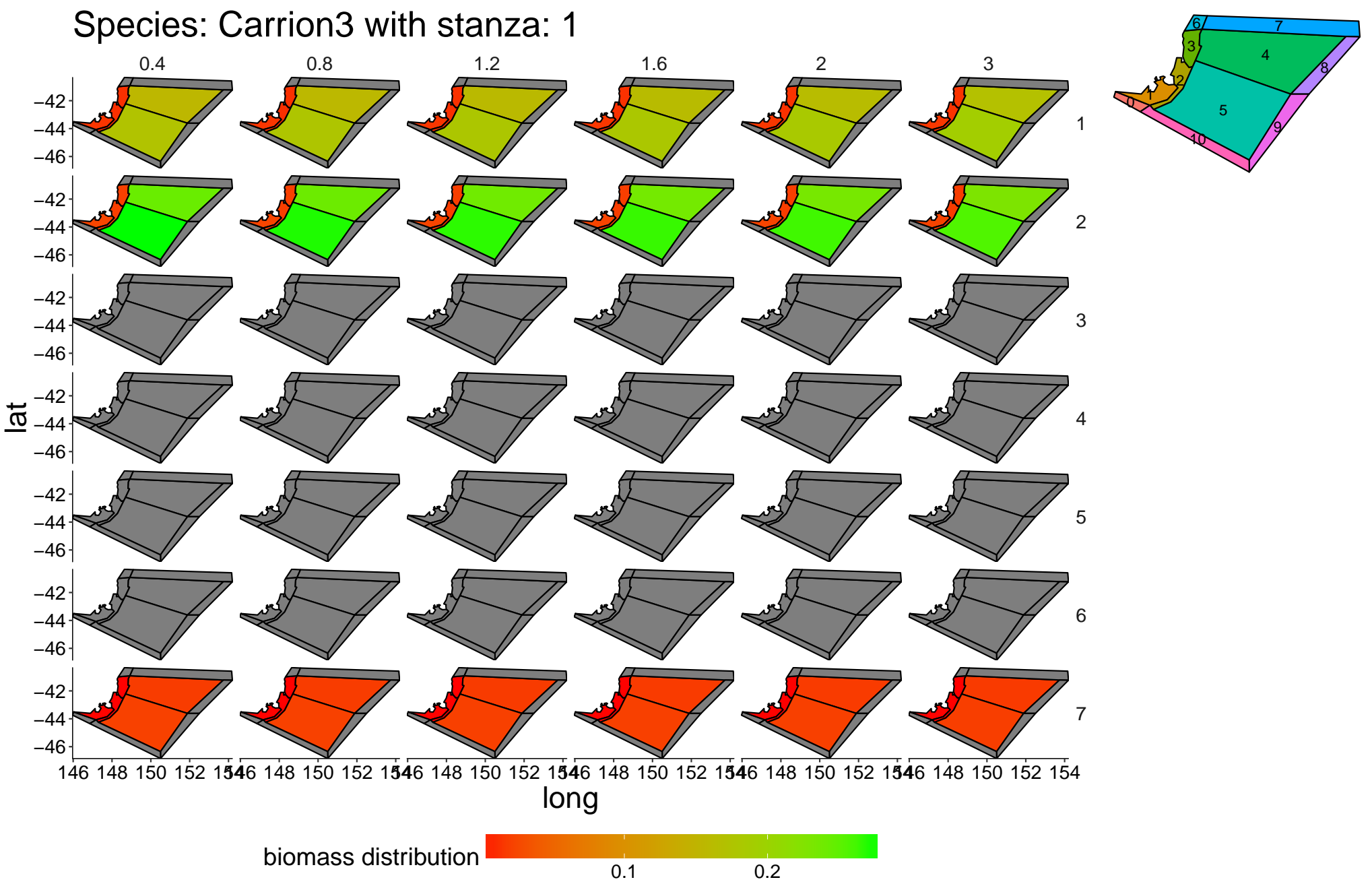
### 5.7 Diet plot 7: Small planktivorous fish



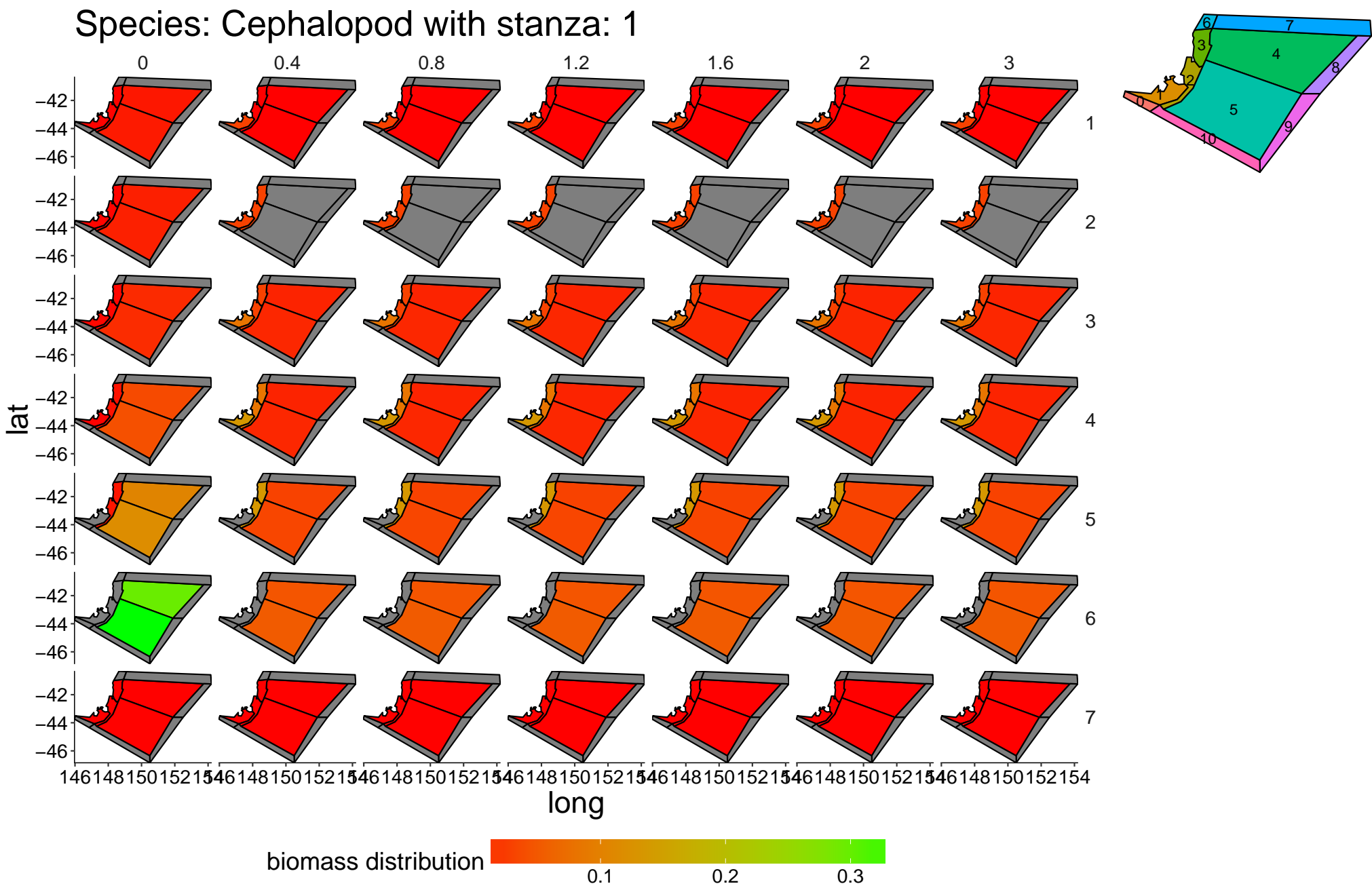
6 Spatial Plots 1

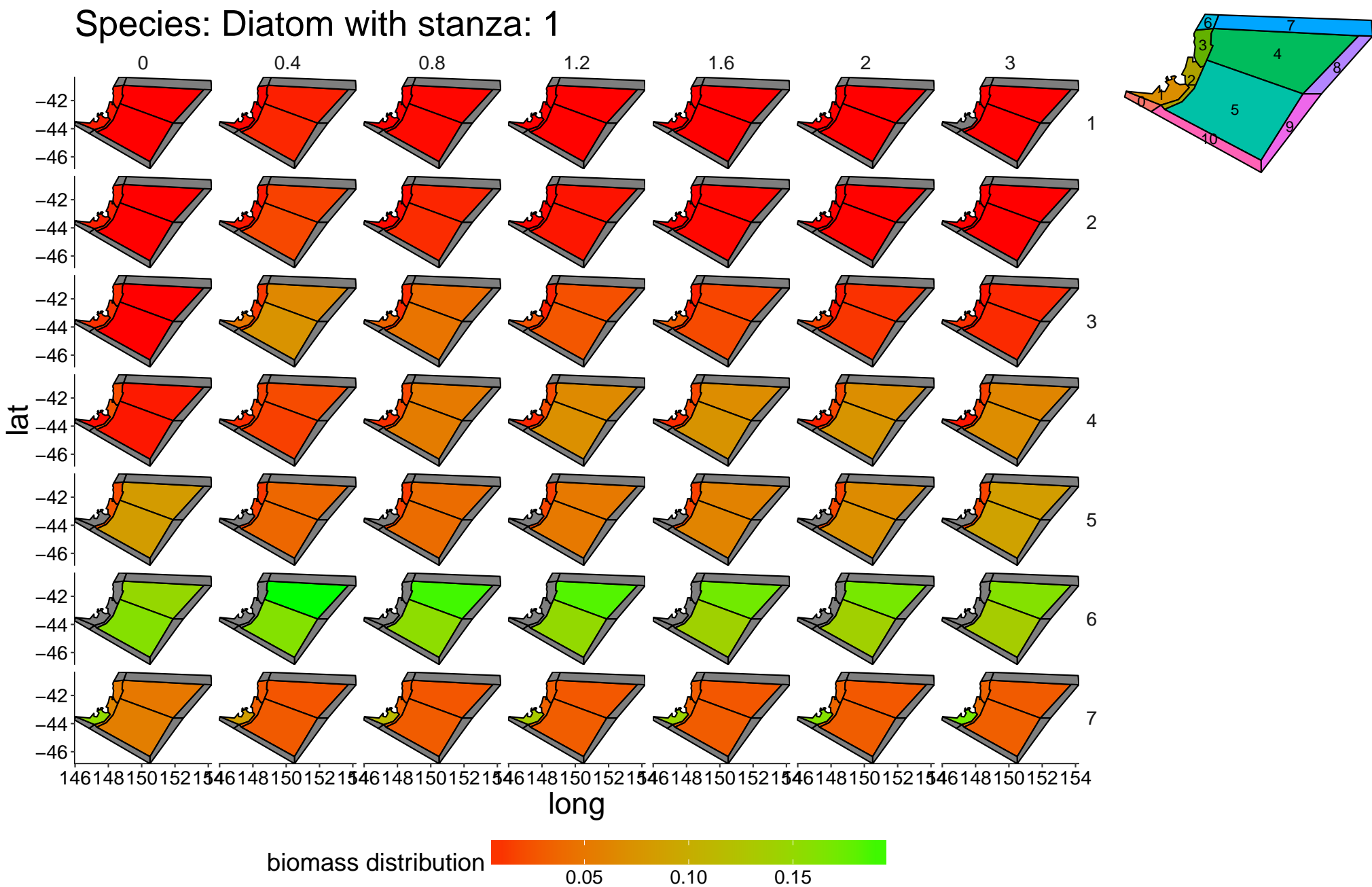
## Joining, by = "polygon"

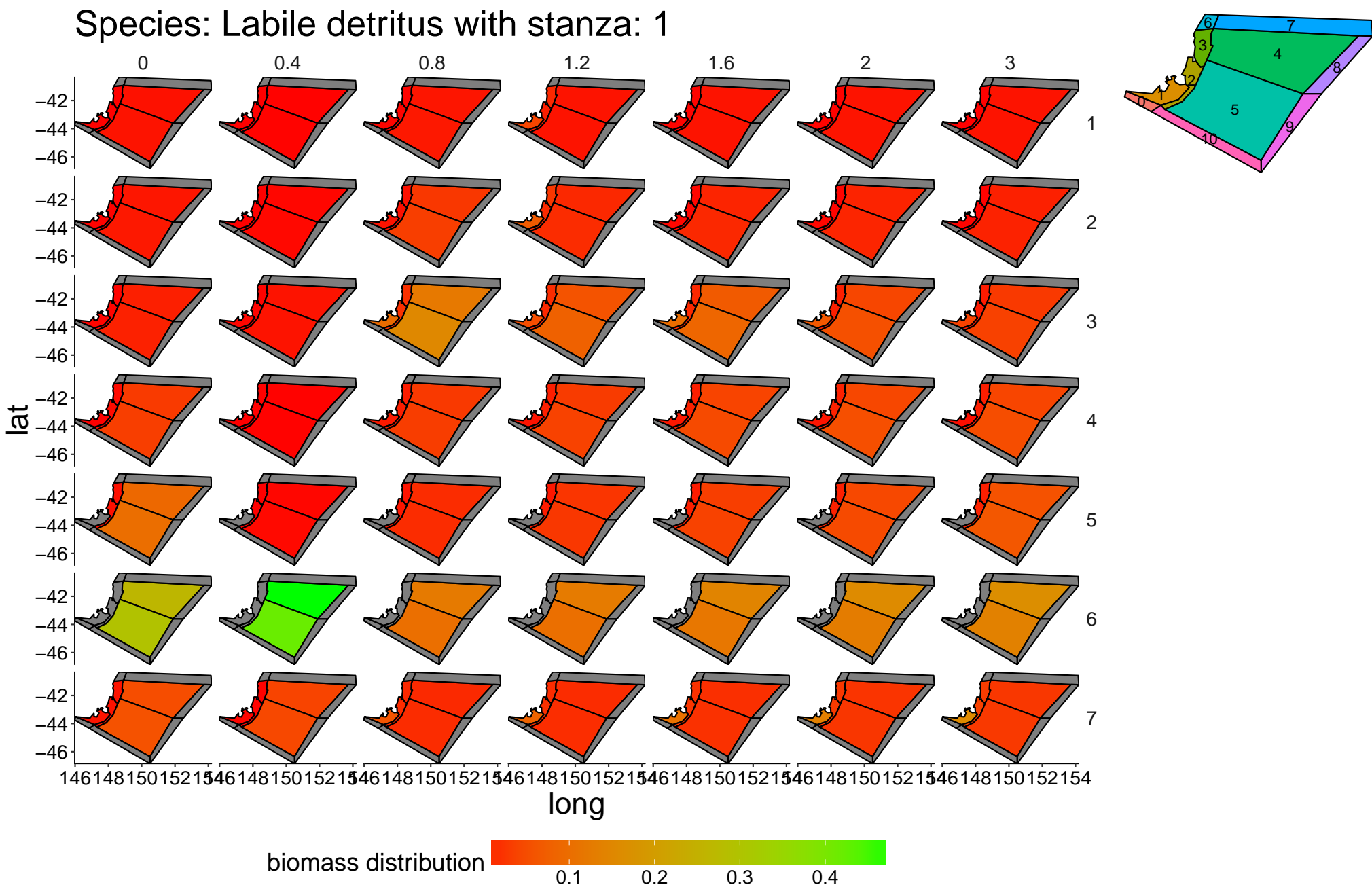
6.1 Spatial Plot 1: Carrion3 1

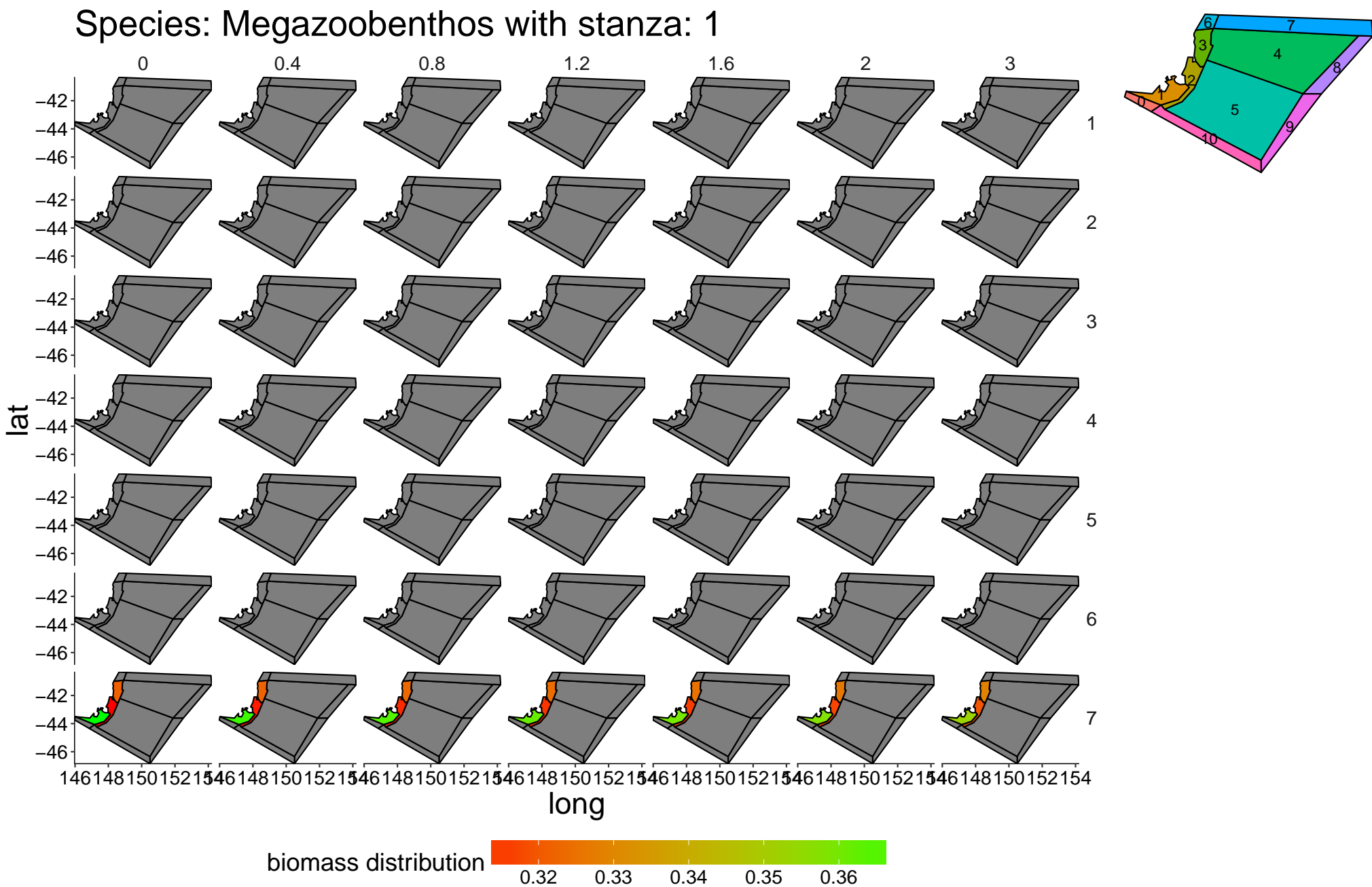


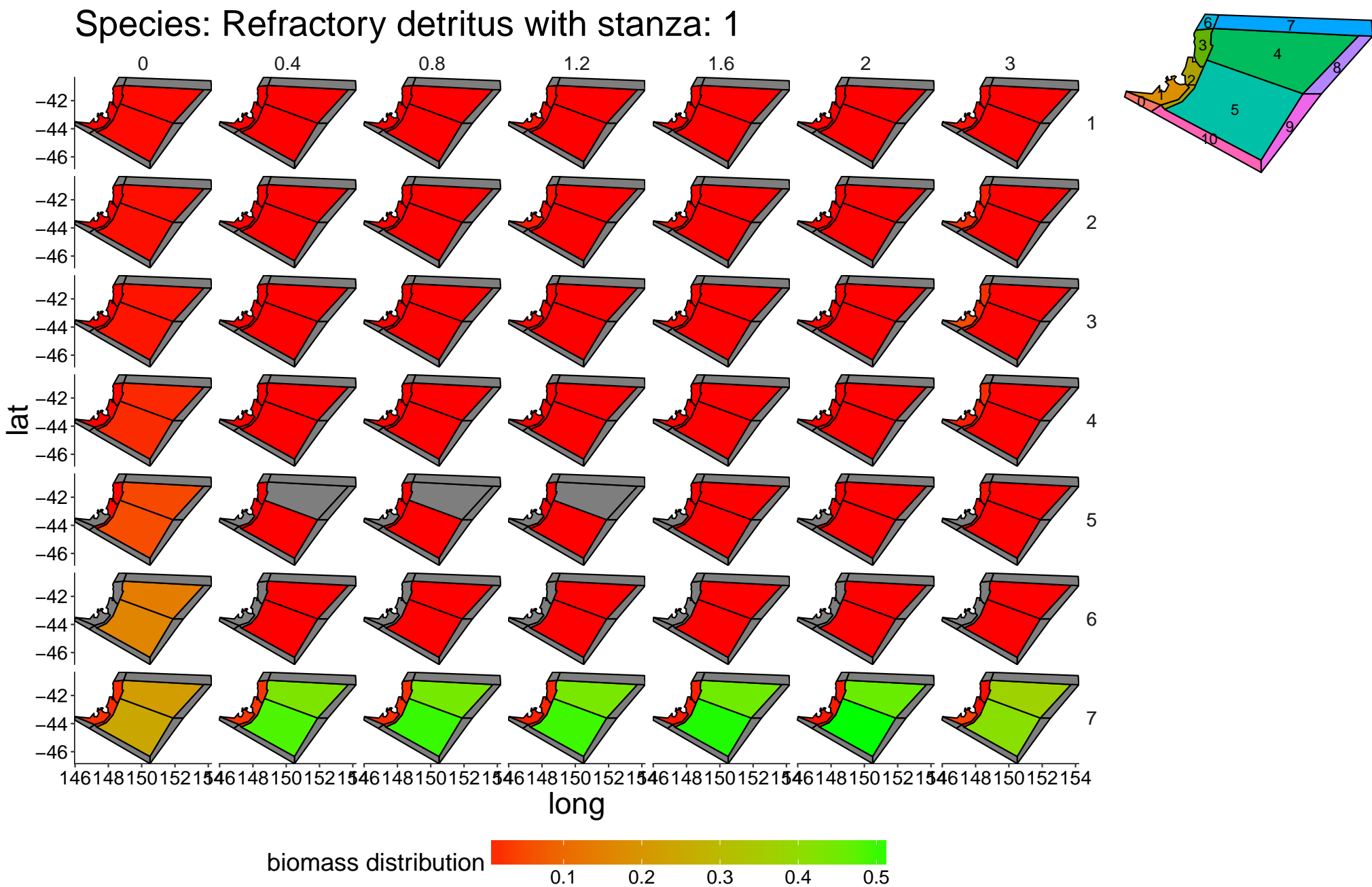


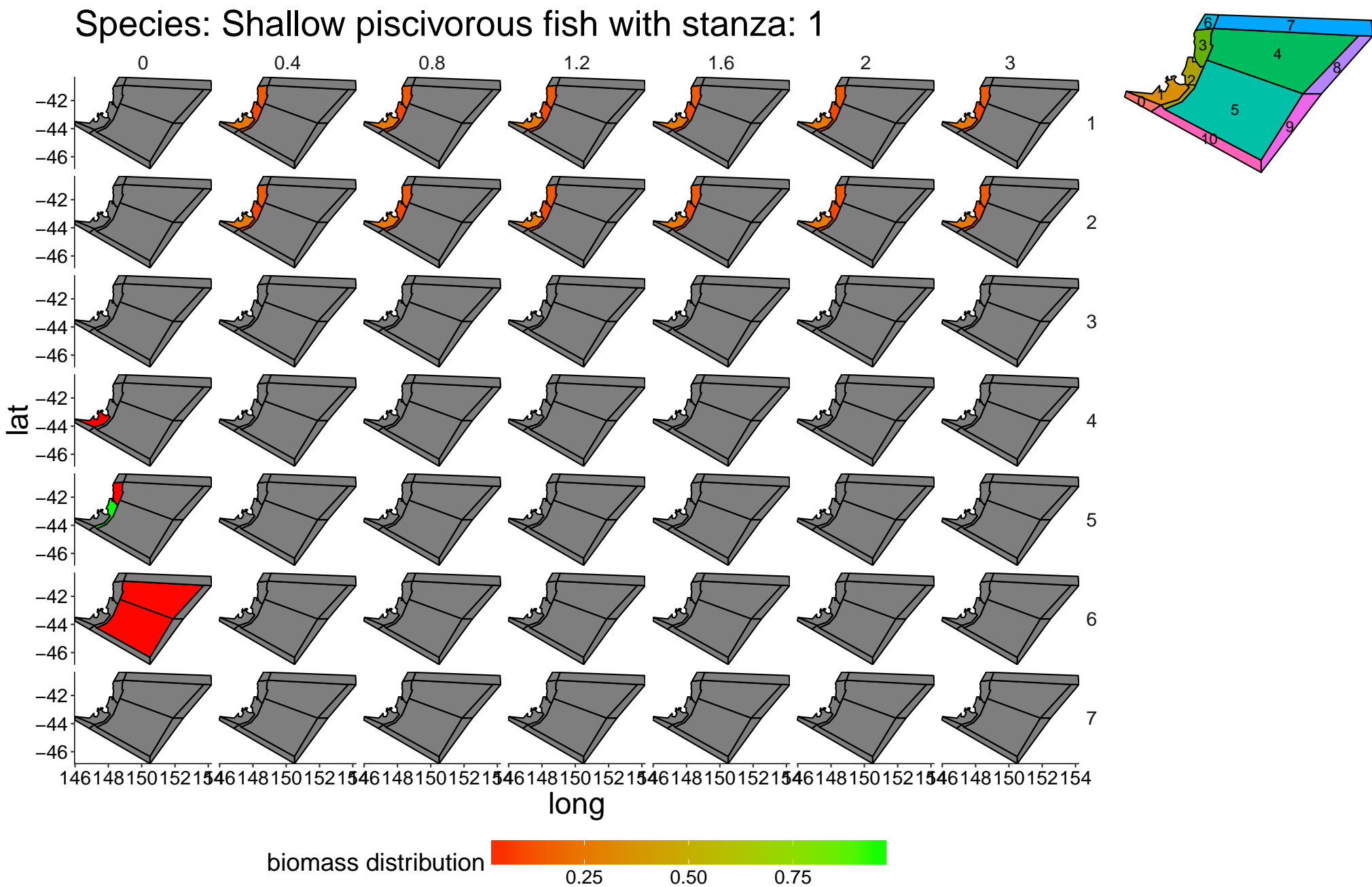


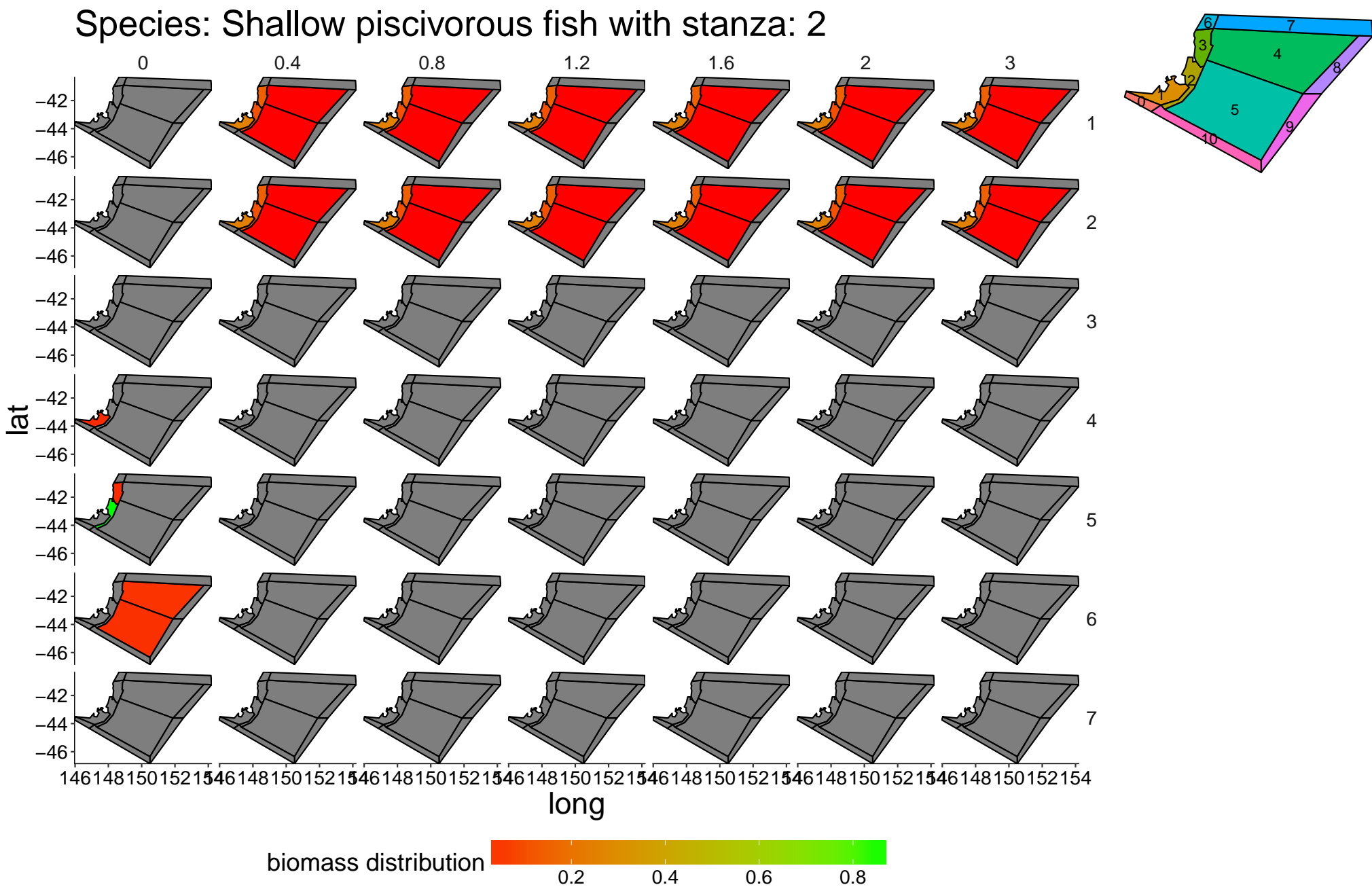




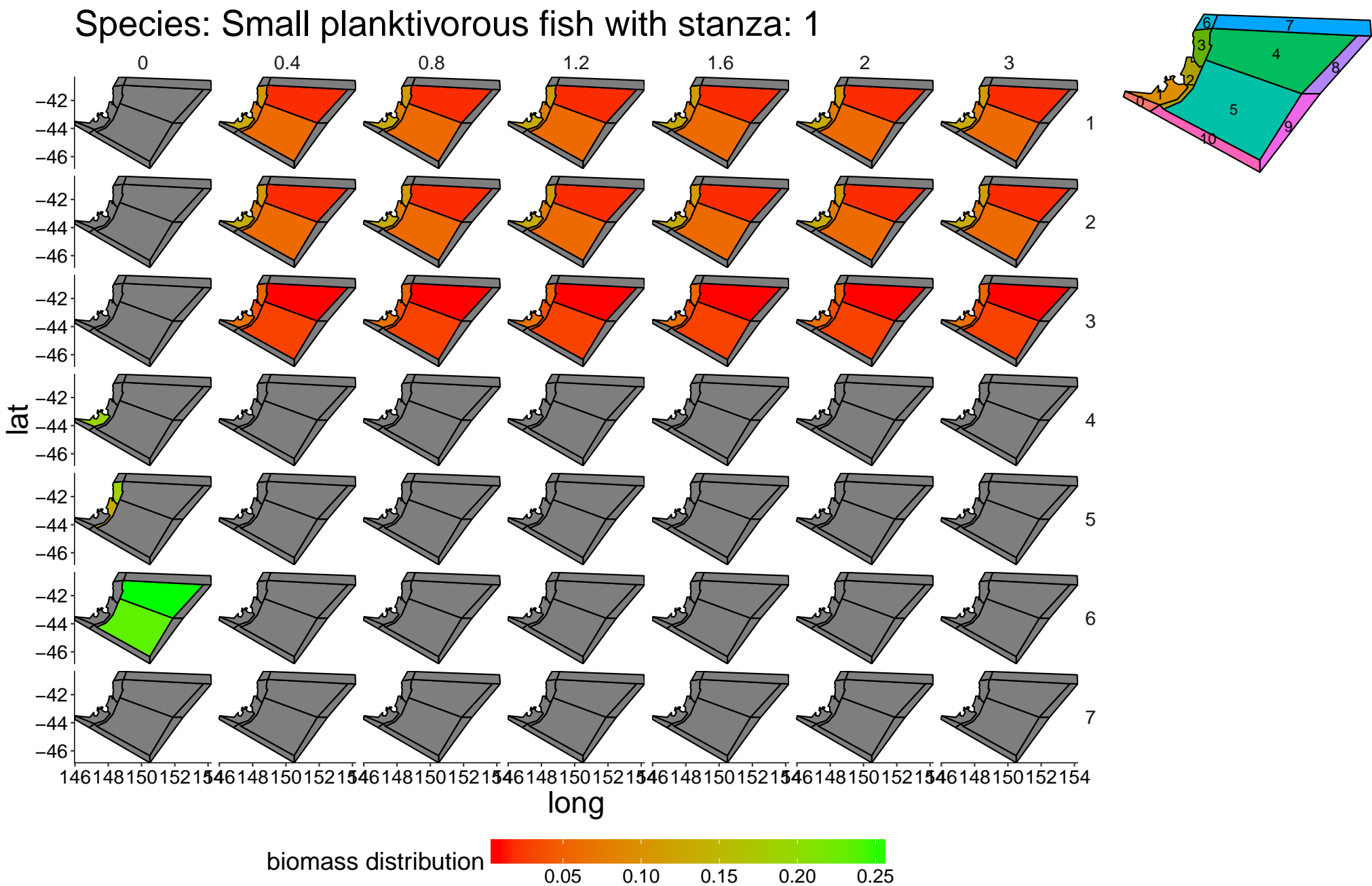




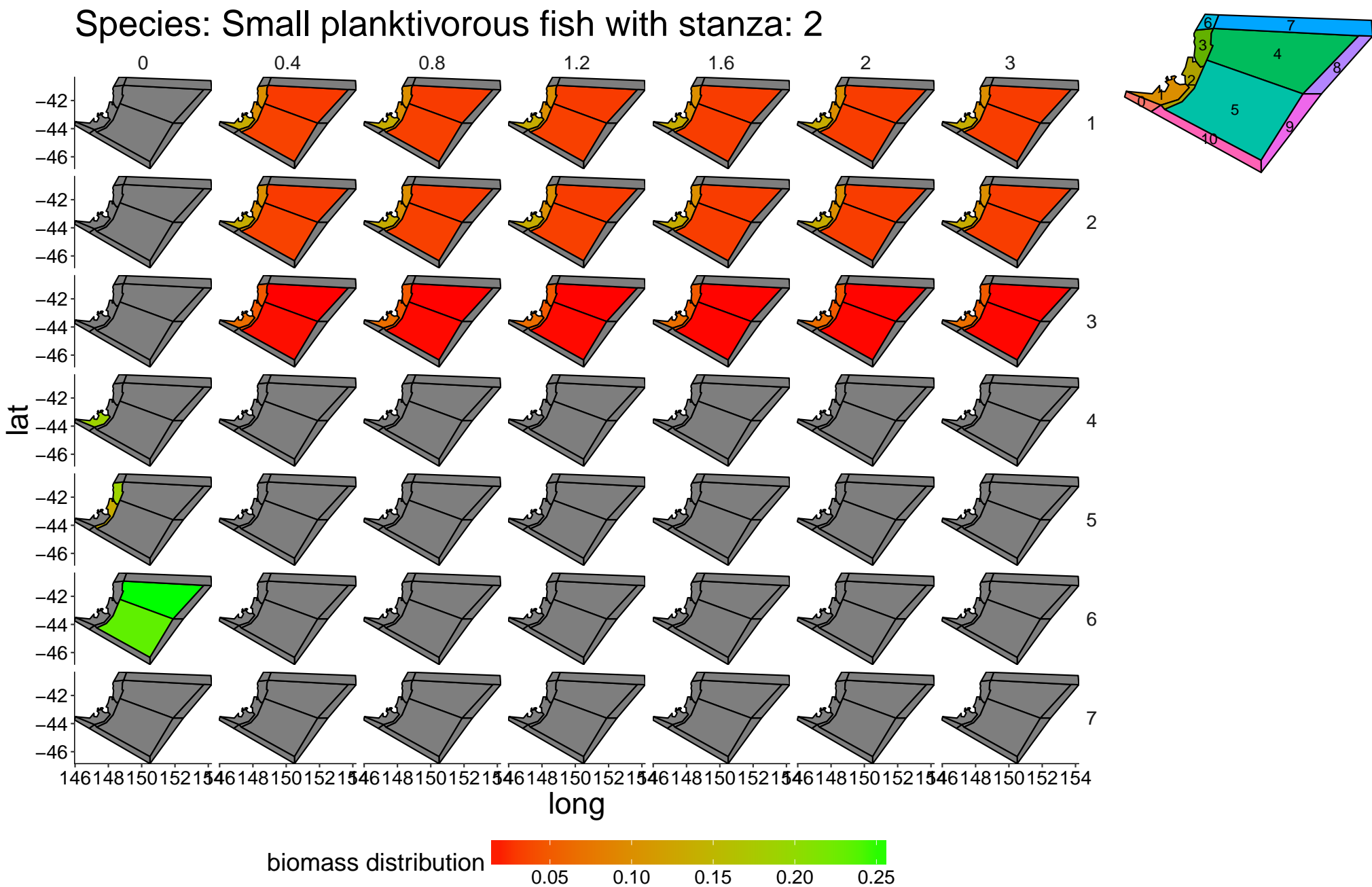










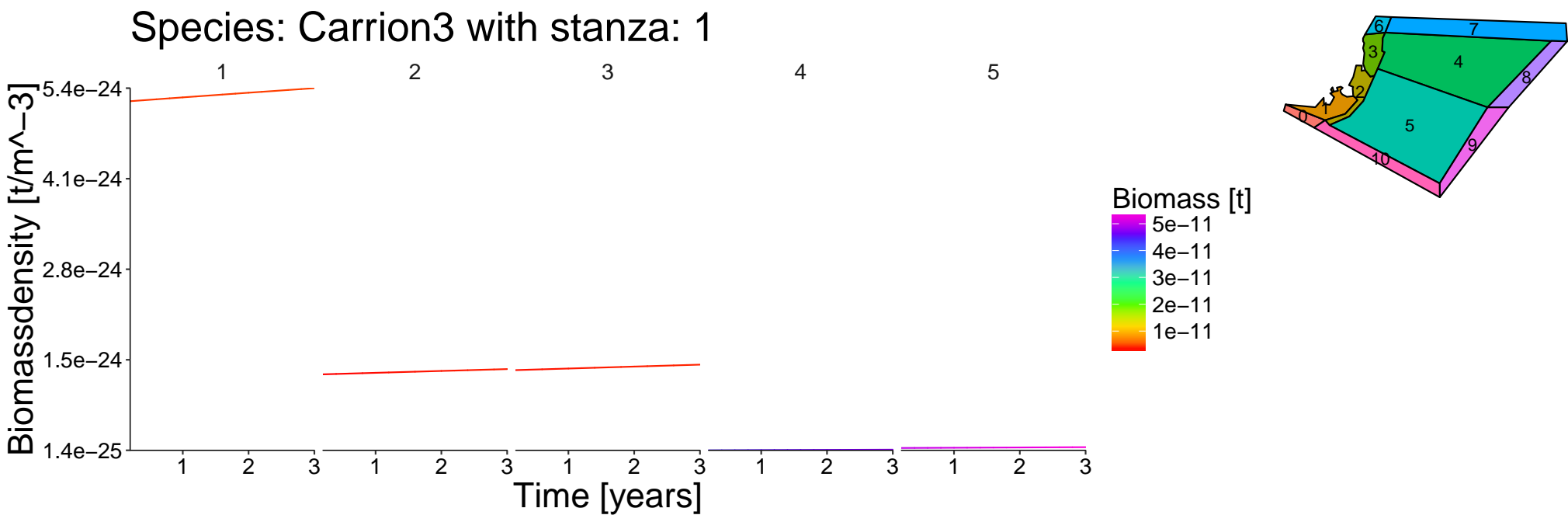


## 7 Spatial Plots 2

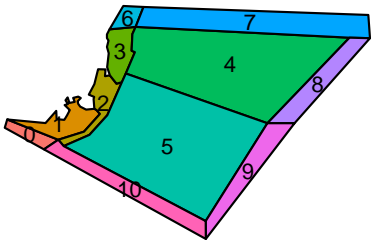
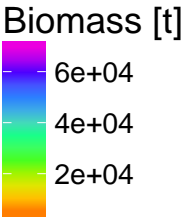
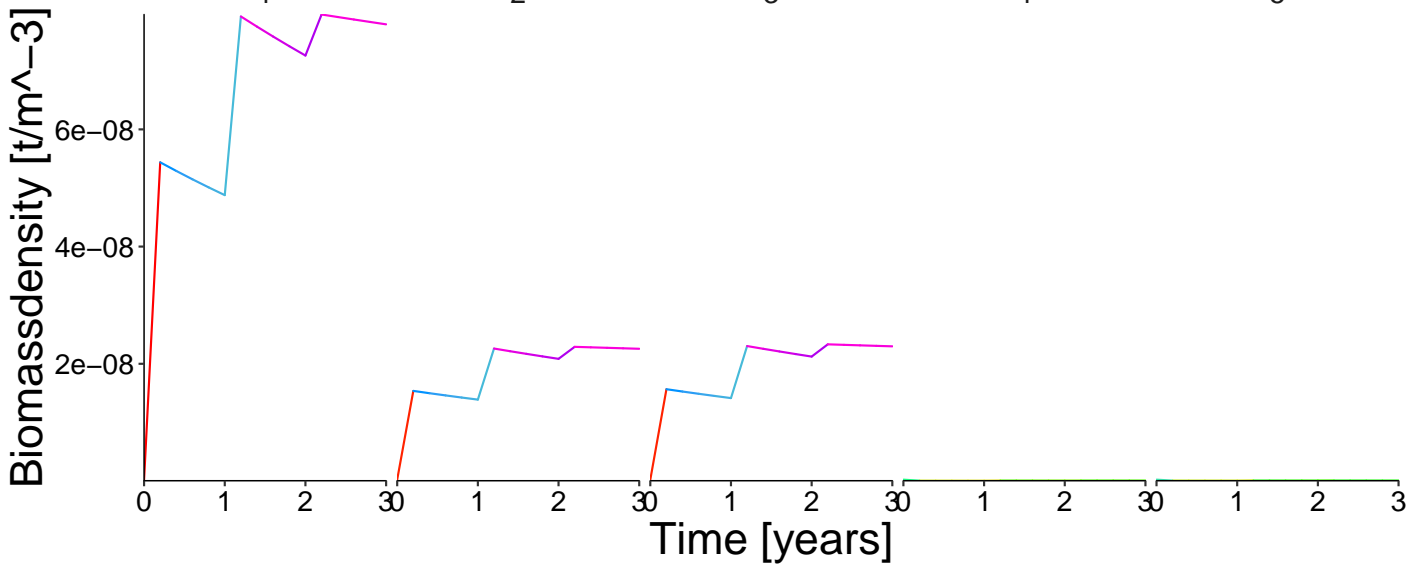
```
## Joining, by = c("time", "polygon")

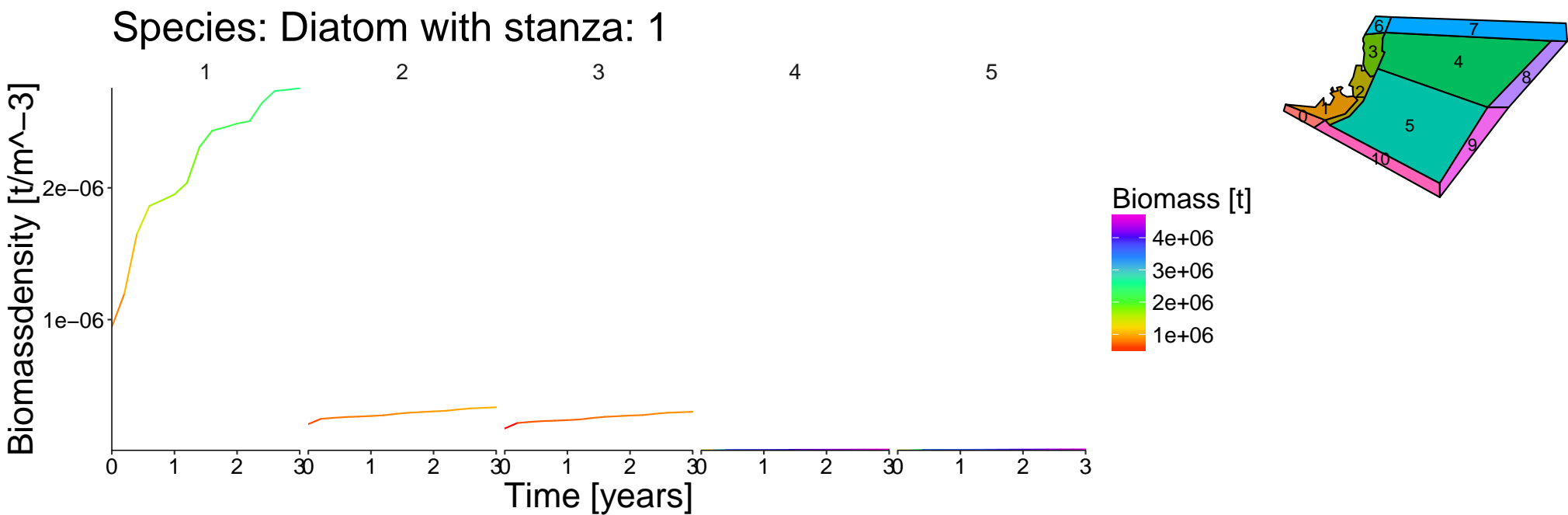
## geom_path: Each group consists of only one observation. Do you need to
## adjust the group aesthetic?

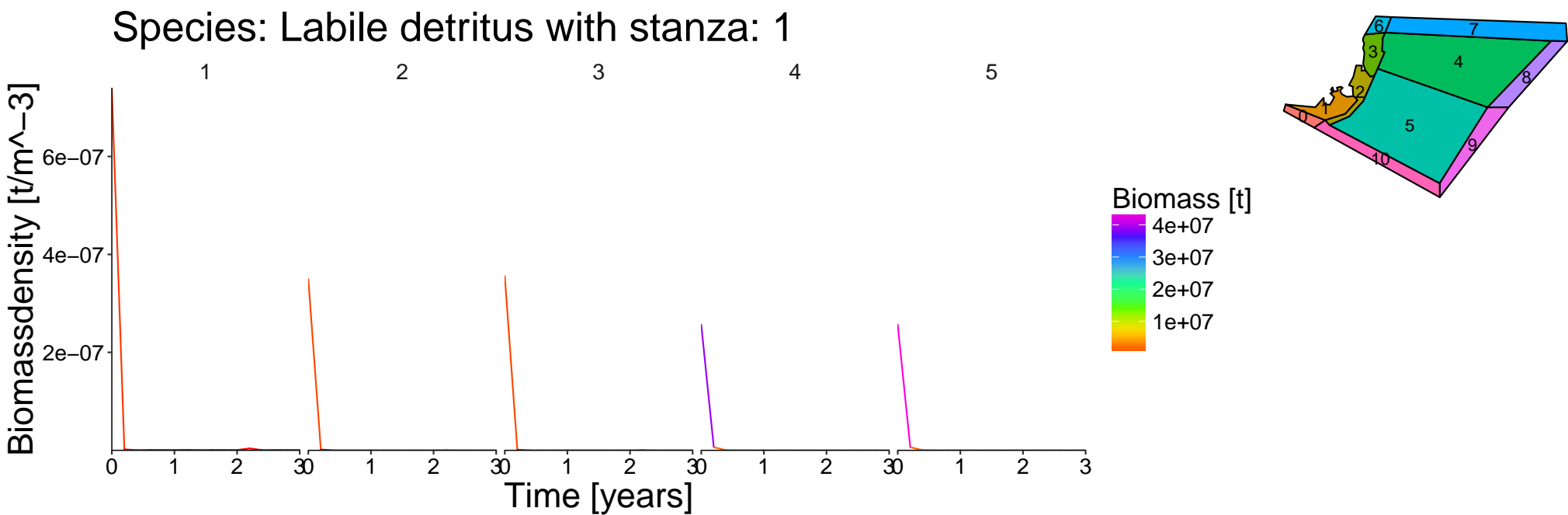
## geom_path: Each group consists of only one observation. Do you need to
## adjust the group aesthetic?
```



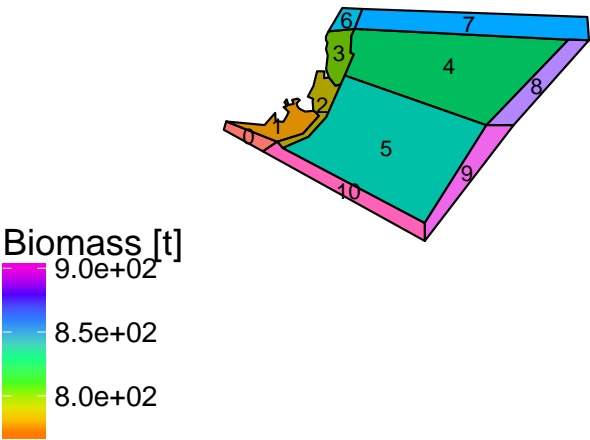
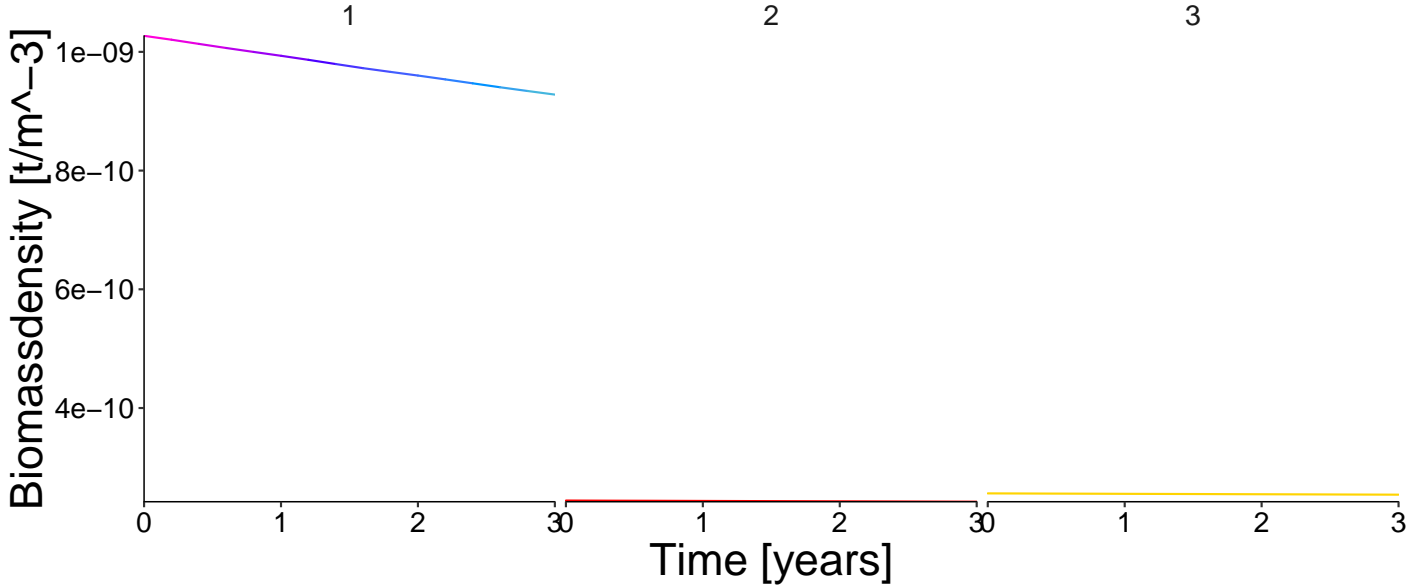
Species: Cephalopod with stanza: 1

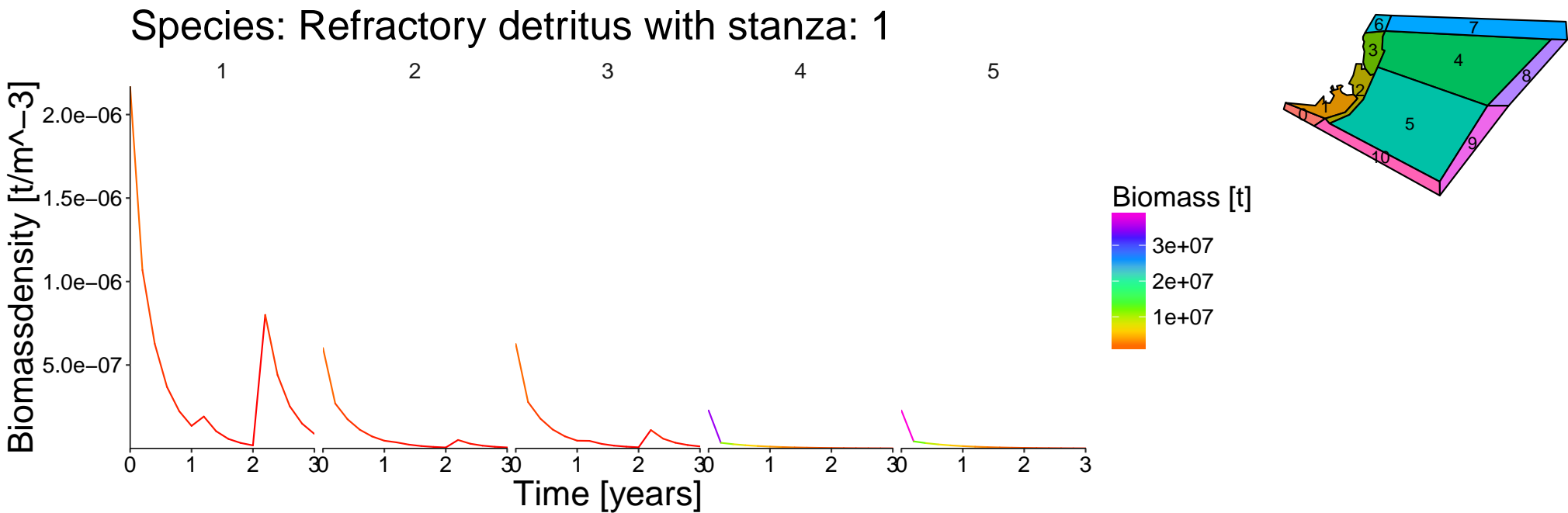






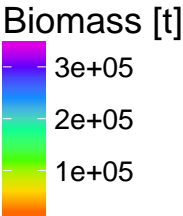
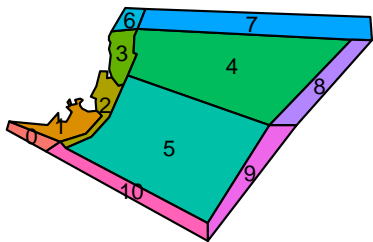
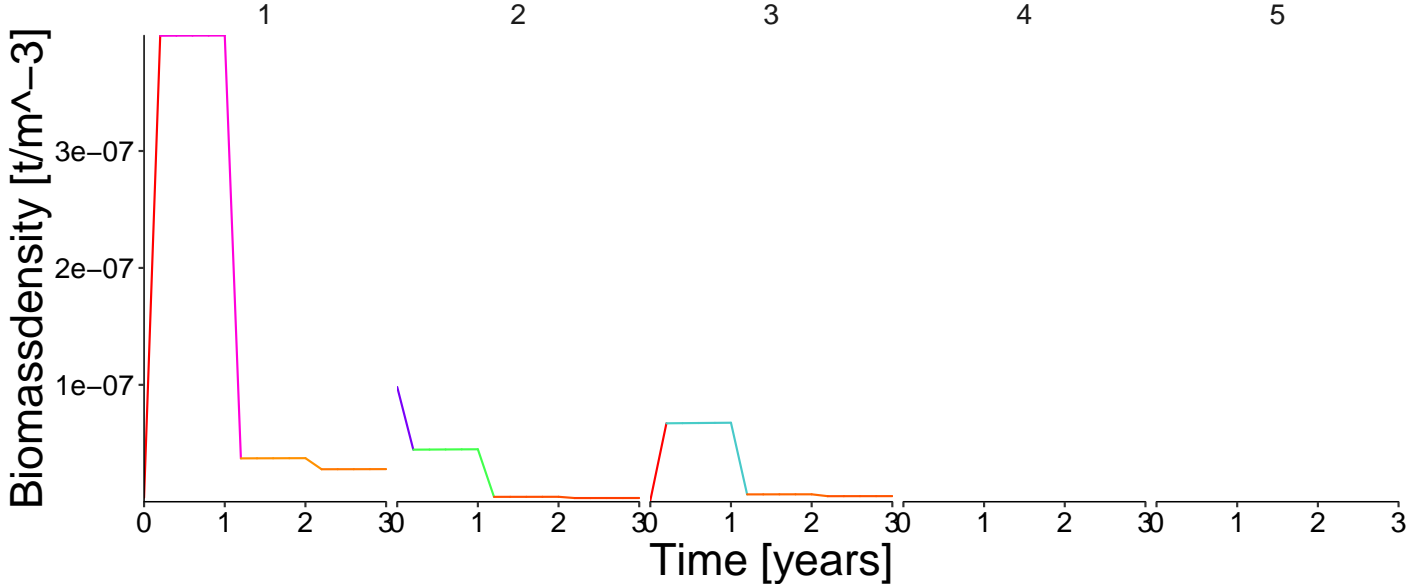
Species: Megazoobenthos with stanza: 1







Species: Shallow piscivorous fish with stanza: 1



Species: Shallow piscivorous fish with stanza: 2

