Individual biomass growth: juvenile maturation

This analysis verifies how individual growth has been affected by increasing the MTE constant for juvenile growth `b0jg` from 6.7023e8 to 6.7023e10, as detailed in the report of issue `609`.

```r
library(tidyverse);
library(stringr);
```

Standard procedures

Set outputs folder, specific ID and get files

Check individual variation

```r
biomass <- outdata %>%
  select(week,id,stage,sp,veg,repr)

#Individual adult biomass variation
indweekmass.plot <- ggplot(filter(biomass, stage == "a"), aes(x=week, y= veg, color = factor(id)))
indweekmass.plot +
  geom_line() +
  labs(x = "Week", y = "Individual vegetative biomass (g)",
       title = "Adult weekly weight")+
  theme(legend.position = "none")
```

Adult weekly weight
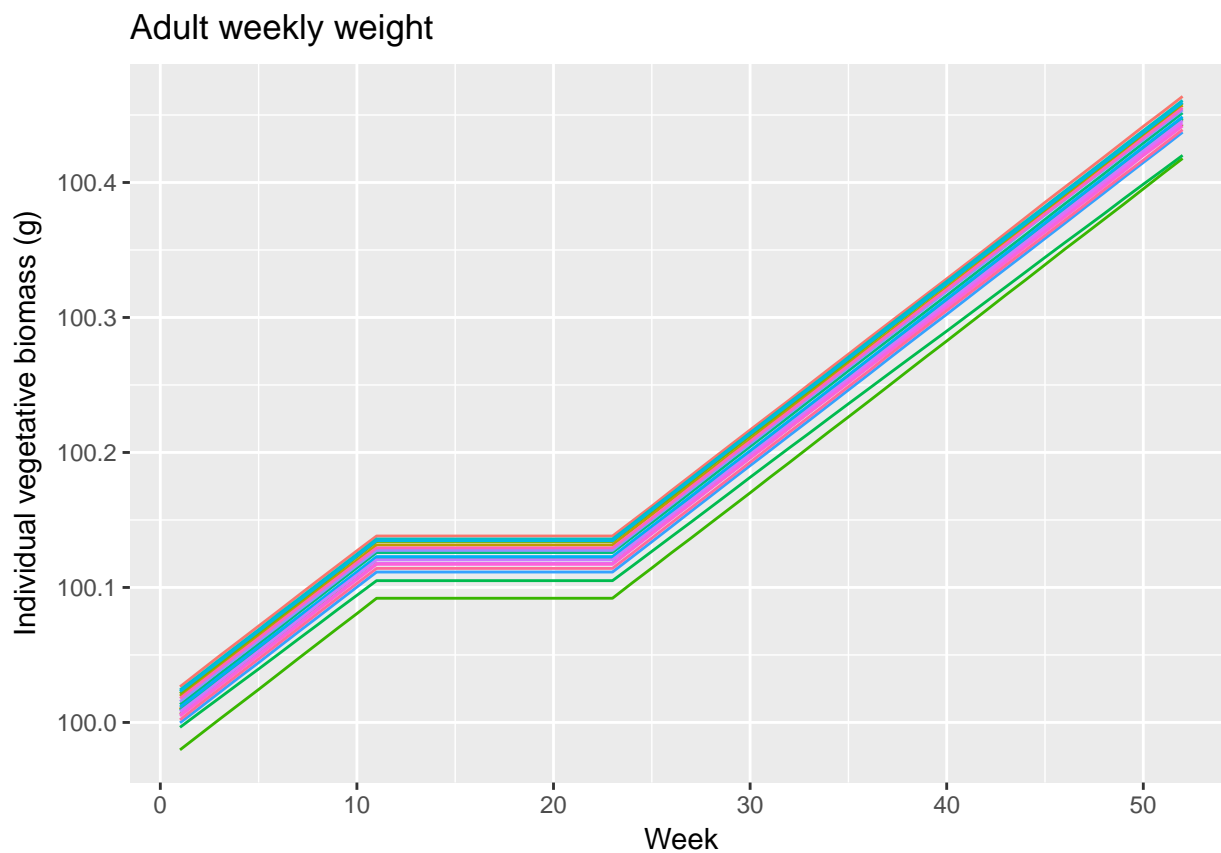

```
#Individual juvenile biomass variation
juvweekmass.plot <- ggplot(filter(biomass, stage == "j"), aes(x=week, y= veg, color = factor(id)))
juvweekmass.plot +
  geom_line() +
  labs(x = "Week", y = "Individual vegetative biomass (g)",
       title = "Juvenile weekly weight")+
  theme(legend.position = "none")
```

Juvenile weekly weight
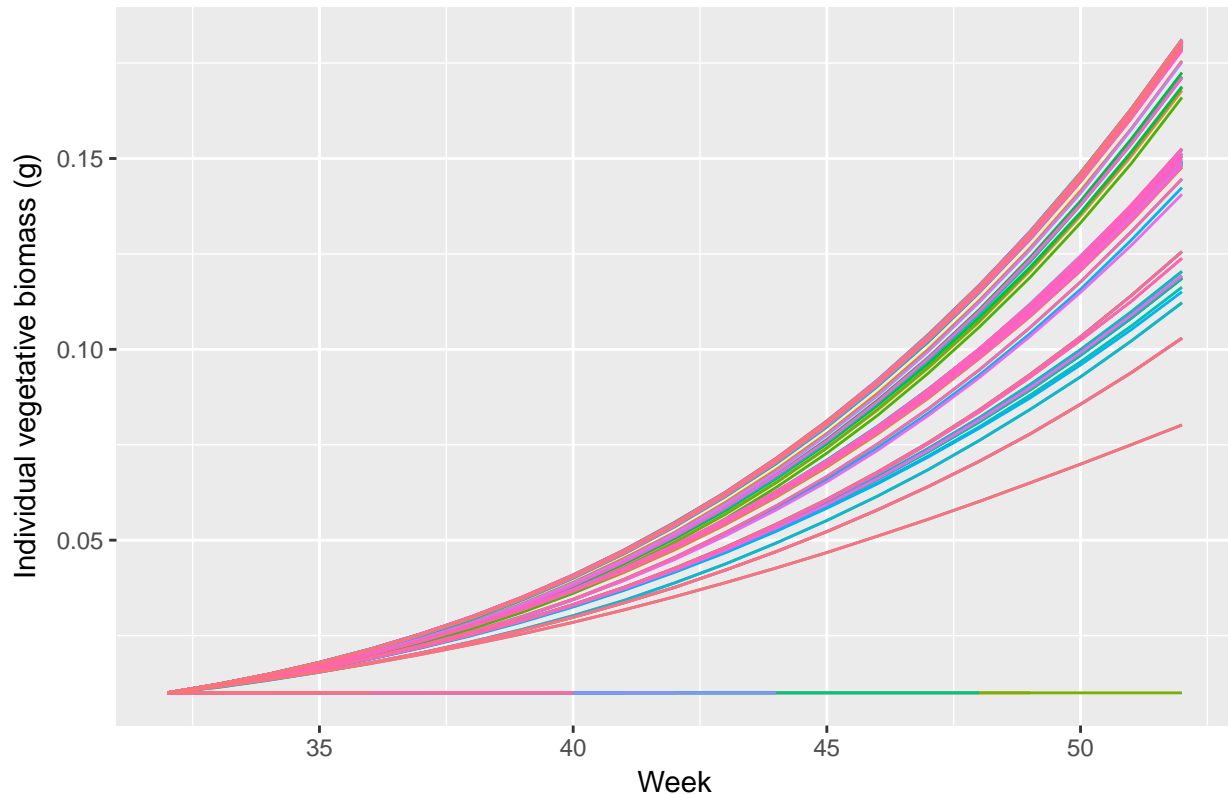
This growth rate is higher that previously, when `b0jg = 6.7023e8`. The juveniles accumulated 0.3 g after 60 years, whereas here, they accumulate 0.15g in less than one year. Next step is check for any inconsistencies on unit conversion in the model.

In the first simulation after implementing `id_counter`, at each time step, individuals appear $2^{(t)}$ times in the output. This happened with all embryos/juveniles: it is a remaining issue from using id_counter: it was not being updated in main.jl.

```
# find if there are repeated id numbers:
peaks <- biomass %>%
  select(week,id)
peaks$id[which(duplicated(peaks))]
```

```
## factor(0)
## 279 Levels: 1 10 100 101 102 103 104 105 106 107 108 109 10a 10b ... ff
```

```
# verify if the repetitions are for the smae individual
peaks2 <- biomass %>%
  select(week,id, stage)
peaks2$id[which(duplicated(peaks2))]
```

```
## factor(0)
## 279 Levels: 1 10 100 101 102 103 104 105 106 107 108 109 10a 10b ... ff
```
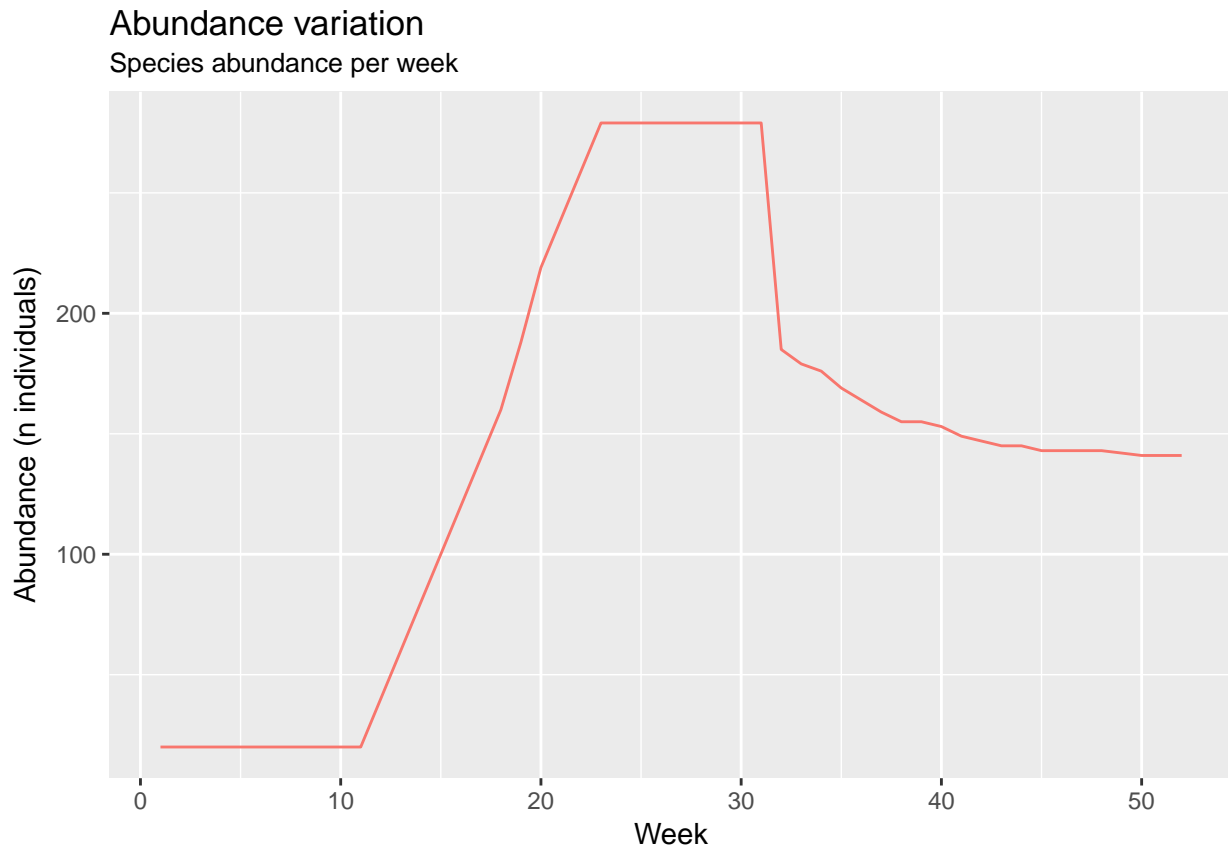
Plot populations, weekly

```
weekabund <- outdata %>% group_by(week, sp) %>% summarize(abundance = n())
```

```
weekabund.plot <- ggplot(weekabund, aes(x = week, y = abundance, color = factor(sp)))

weekabund.plot +
  geom_line() + #TODO differentiate species with colorgeom_line(color = "forestgreen")
  labs(x = "Week", y = "Abundance (n individuals)",
       title = "Abundance variation",
       subtitle = "Species abundance per week")+
  theme(legend.position = "none")
```

Abundance variation
Species abundance per week

1. Population structure

```
weekstruct <- outdata %>% group_by(week, sp, stage) %>% summarize(abundance = n())
weekstruct.plot <- ggplot(weekstruct, aes(x = week, y = abundance, color = factor(stage))) +
  geom_line()

weekstruct.plot+
  labs(x = "Abundance",
       y = "Week",
       title = "Population structure")+
  scale_color_discrete("Stages:", labels = c("Adults", "Seeds", "Juveniles"))+
  theme_minimal()
```

Population structure
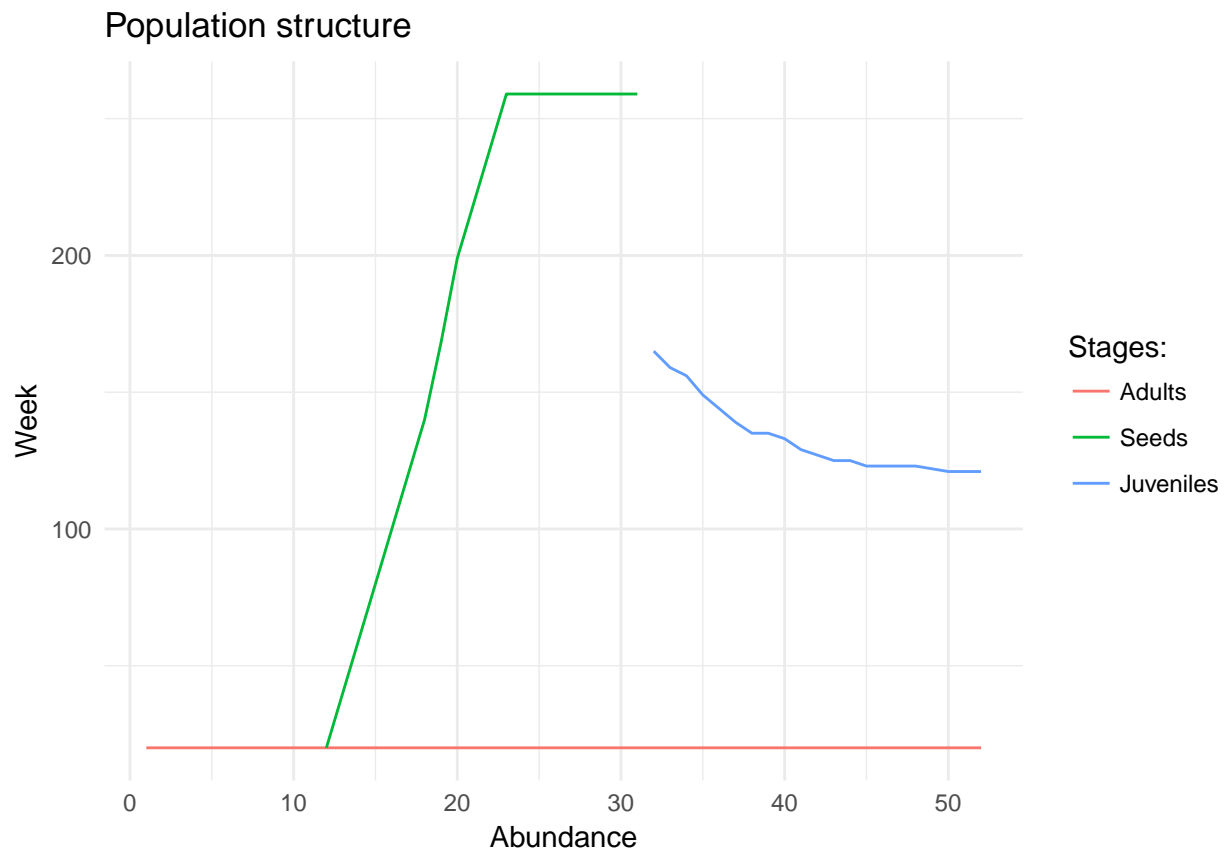
Individual growth is better, but not enough for juveniles to become adults during the groth season. Check weight conversions in code, because they might also be an issue.