Single species 1 year simulation analysis: id_counter implementation

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

Single species, 5m² (Achillea millefolium)

The only objective of this analysis is verifying that the implementation of `id_counter` did not affect the functioning of the code. Moreover, the results (similar to previous ones) show that the previous individual tagging system was working properly. Longer simulations might reveal the vulnerabilities of that system, but this analysis is not aimed at that. The new system will be implemented from here on, since the code is running properly with it.

Standard procedures

Set outputs folder, specific ID and get file

Clean raw data

Verify input

Temperature variation #TODO use landscape configuration output

```
temperature <- as_tibble(read.csv(file.path(indir,"envtimeseries_19995y.csv"), header =TRUE))

ggplot(temperature, aes(x=week, y =meantemp_ts))+
  geom_line()+
  labs(x = "Week", y = "Temperature (°C, monthly)",
       title = "Annual temperature variation")
```

Annual temperature variation
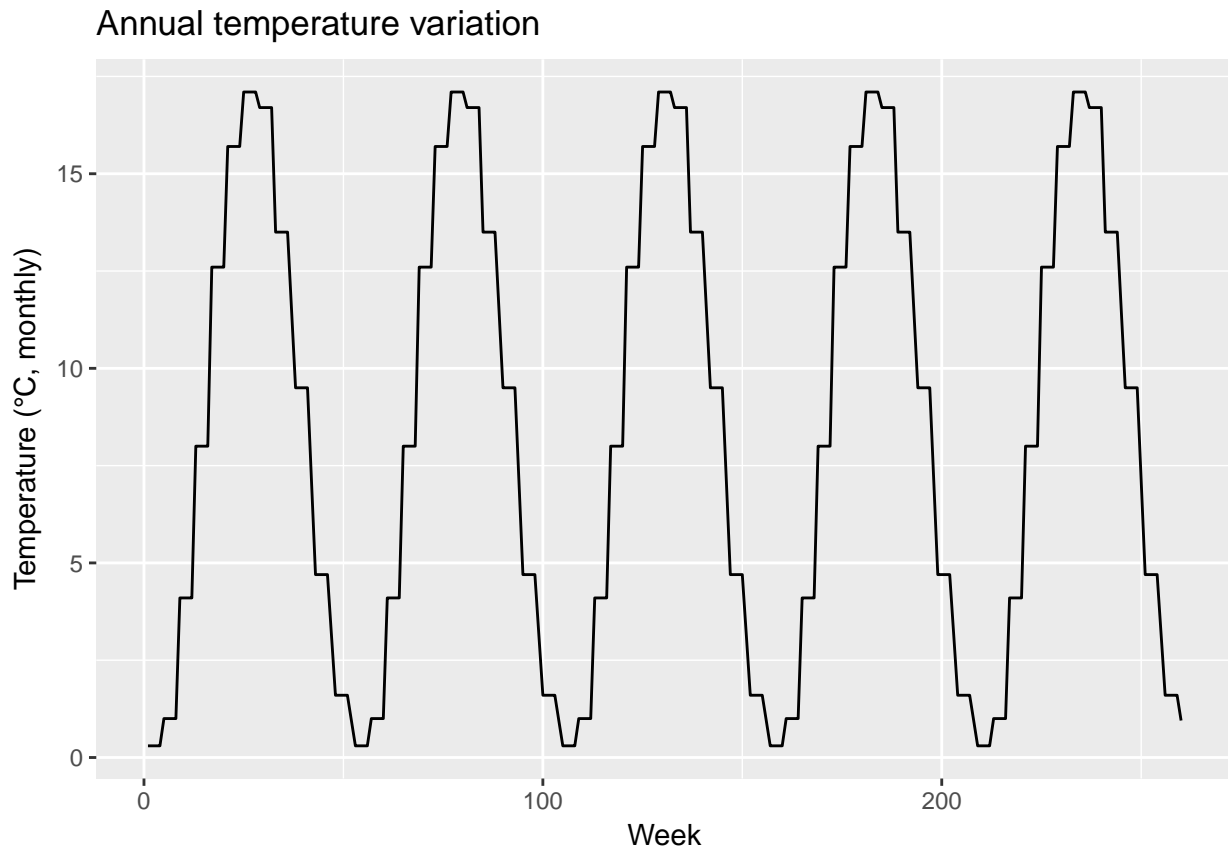
**Ladscape configuration**

Temperature

Output results

Growth

1. Plot individual vegetative biomass, weekly
2. Get species-specific biomass mean and variation weekly

Check individual variation

```
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 = "bottom")
```

Adult weekly weight
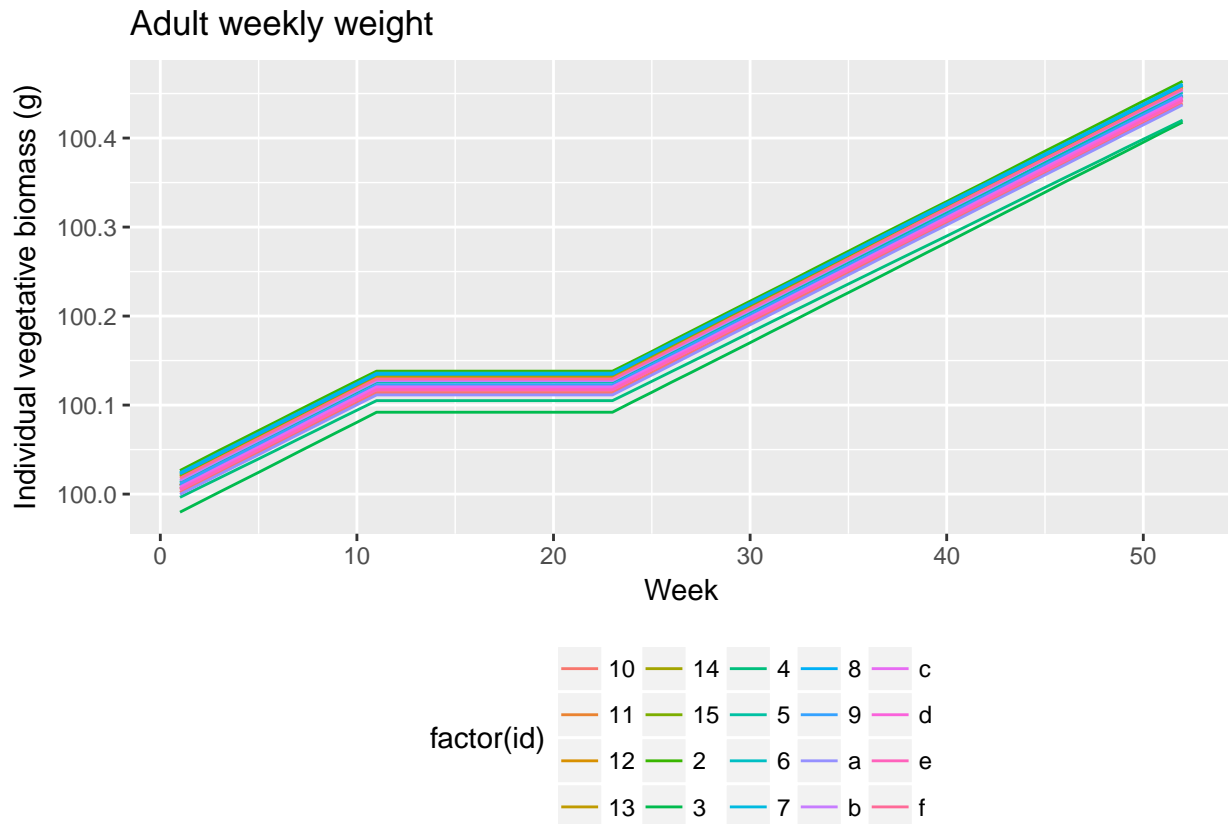
Linear growth outside the reproductive season.

Check if production is the same at all time steps:

```r
production <- biomass %>%
  mutate(total = veg+repr) %>%
  group_by(week,id)
# Look at 2 individuals just for detail
ind1 = diff(production$total[which(production$id == "2")],lag = 1)
ind2 = diff(production$total[which(production$id == "3")],lag = 1)
plot(ind1, type = "l", ylab = "Production (g)", xlab = "Week", main ="Individual biomass production")
lines(ind2, type = "l", col ="red")
legend("topleft", c("ind1","ind2"), fill =c("black","red"))
```

Individual biomass production
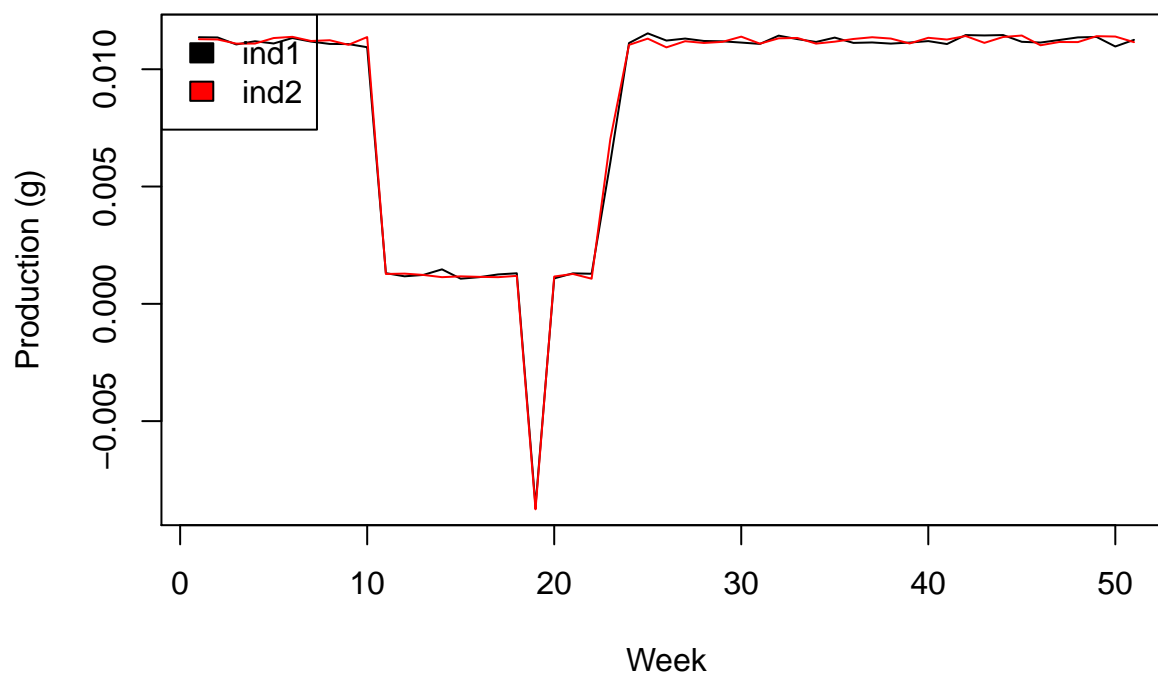

Check variation at species-level

```
# Species-specific biomass
spmass <- biomass%>%
  group_by(week, sp, stage) %>%
  summarise(veg.mean = mean(veg), veg.sd = sd(veg), repr.mean = mean(repr), repr.sd = sd(repr))

spmass.plot <- ggplot(spmass, aes(x=week, y= veg.mean, color = factor(sp))) #only one sp, not necessary
pd <- position_dodge(0.1) # move them .05 to the left and right

ggplot(filter(spmass, stage =="a"), aes(x=week, y= veg.mean, color = factor(stage))) +
  geom_line() +
  geom_errorbar(aes(ymin=veg.mean-veg.sd, ymax=veg.mean+veg.sd), colour = "black", width=.1, position=p
  geom_line(position=pd) +
  geom_point(position=pd)+
  labs(x = "Week", y = "Mean vegetative biomass (g)",
       title = "Annual biomass variation",
       subtitle = "Mean vegetative biomass (+-sd) per species")+
  theme(legend.position = "none")
```

Annual biomass variation
Mean vegetative biomass (+−sd) per species
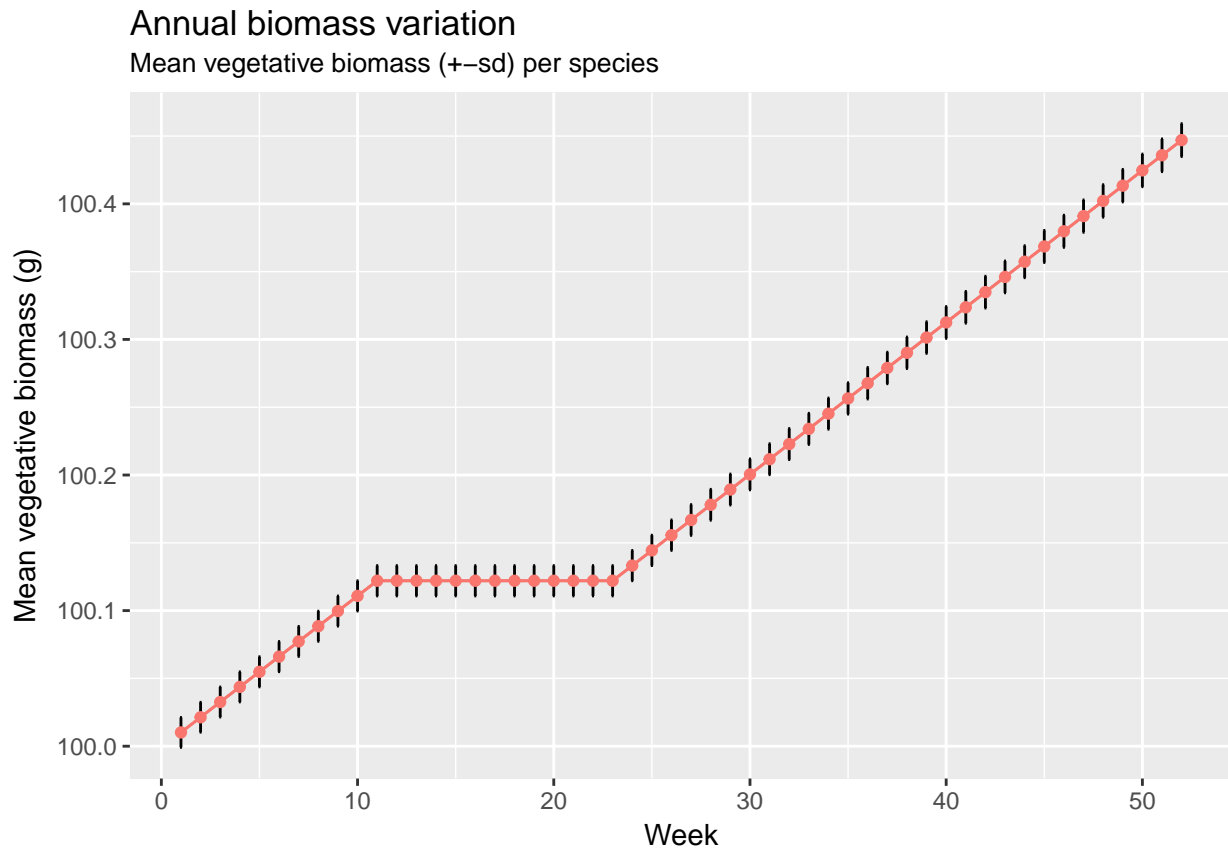
Same for reproductive biomass Individual variation

```r
indrepmass.plot <- ggplot(biomass, aes(x=week, y= repr, color = factor(id)))
indrepmass.plot +
  geom_line() +
  xlim(1,52) +
  labs(x = "Week", y = "Total reproductive biomass (g)",
       title = "Individual reproductive biomass variation") +
  theme(legend.position = "bottom")
```

Individual reproductive biomass variation

Total reproductive biomass

0.0100
0.0075
0.0050
0.0025
0.0000

0   10   20   30   40   50

Week

factor(id)
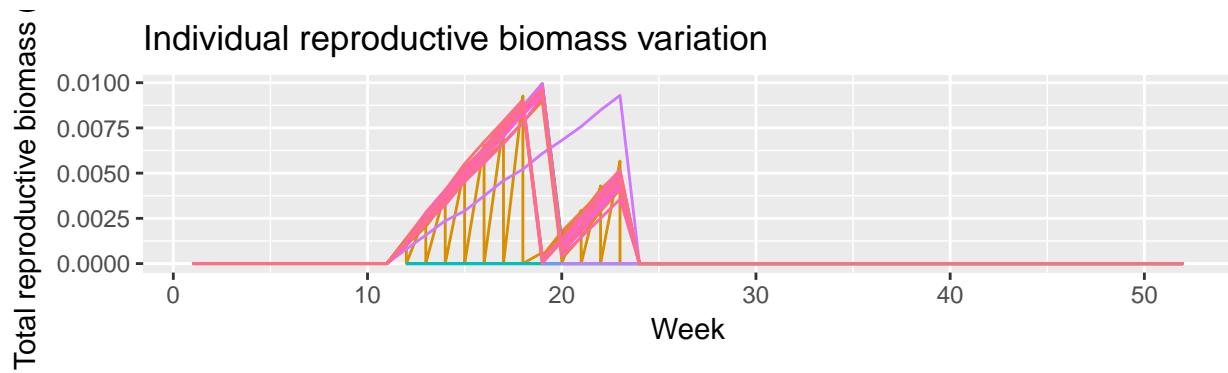
10	1a	23	2d	6
11	1b	24	2e	7
12	1c	25	2f	8
13	1d	26	3	9
14	1e	27	30	a
15	1f	28	31	b
16	2	29	32	c
17	20	2a	33	d
18	21	2b	4	e
19	22	2c	5	f

1. Check if reproduction is happening

```
levels(outdata$mated)
```

```
## [1] "false" "true"
```
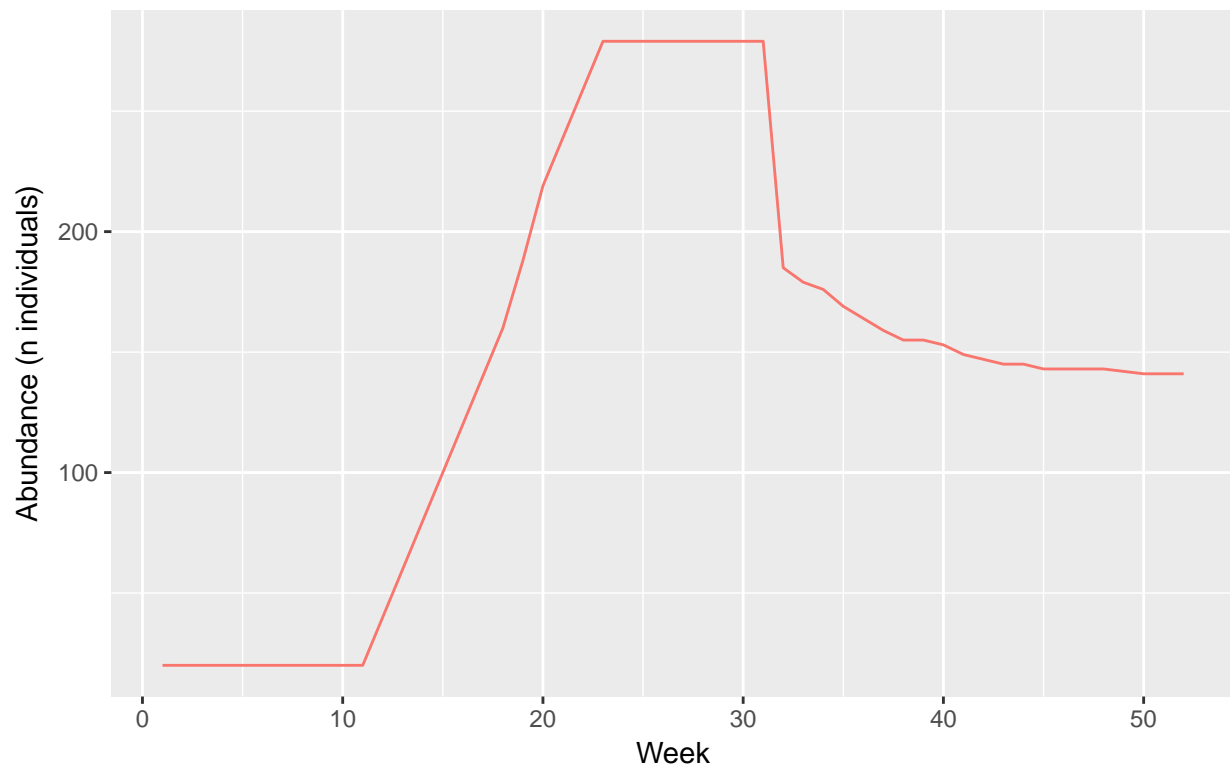
2. Plot populations, weekly

```
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


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

Population structure