Single species 5 year simulation analysis - species specific parameter input

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

Single species, 5m² (Achillea millefolium)

Standard procedures

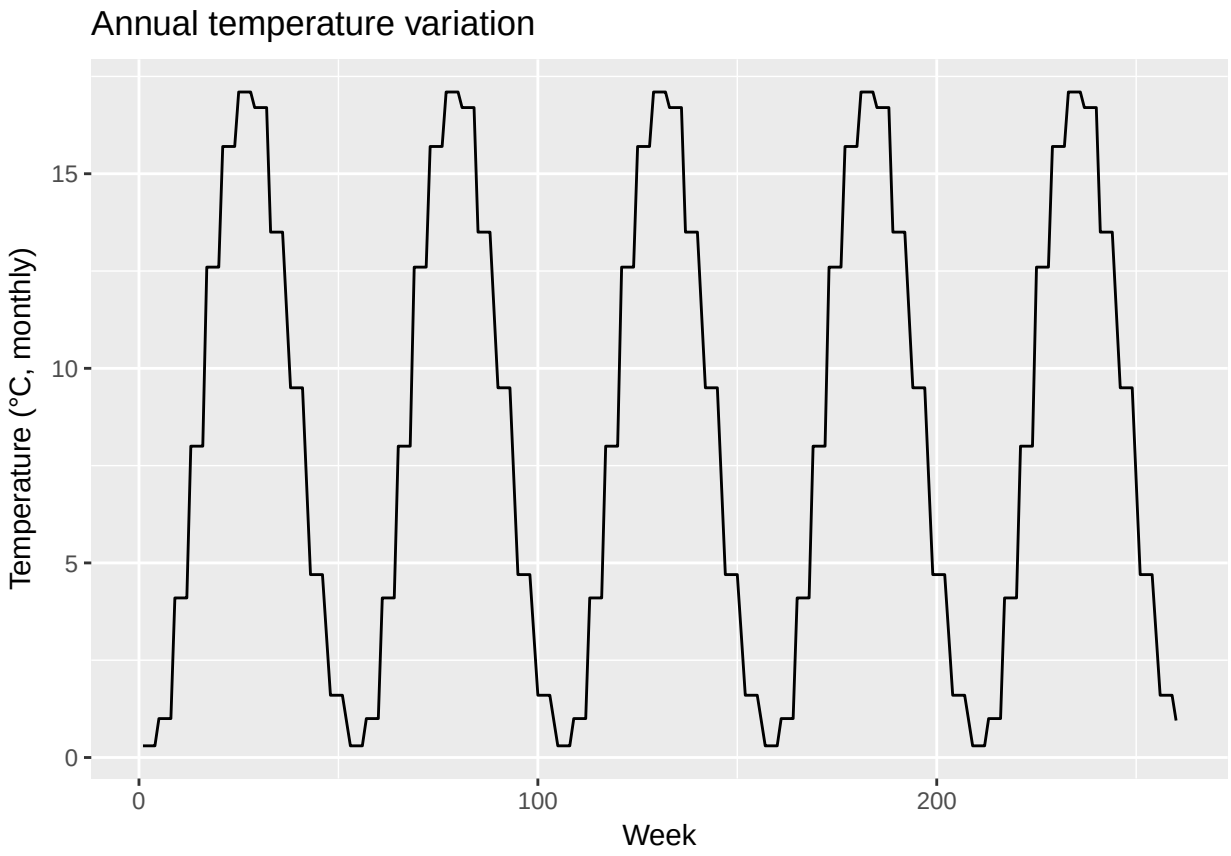
Set outputs folder, specific ID and get file

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")
```



Ladscape configuration

Temperature

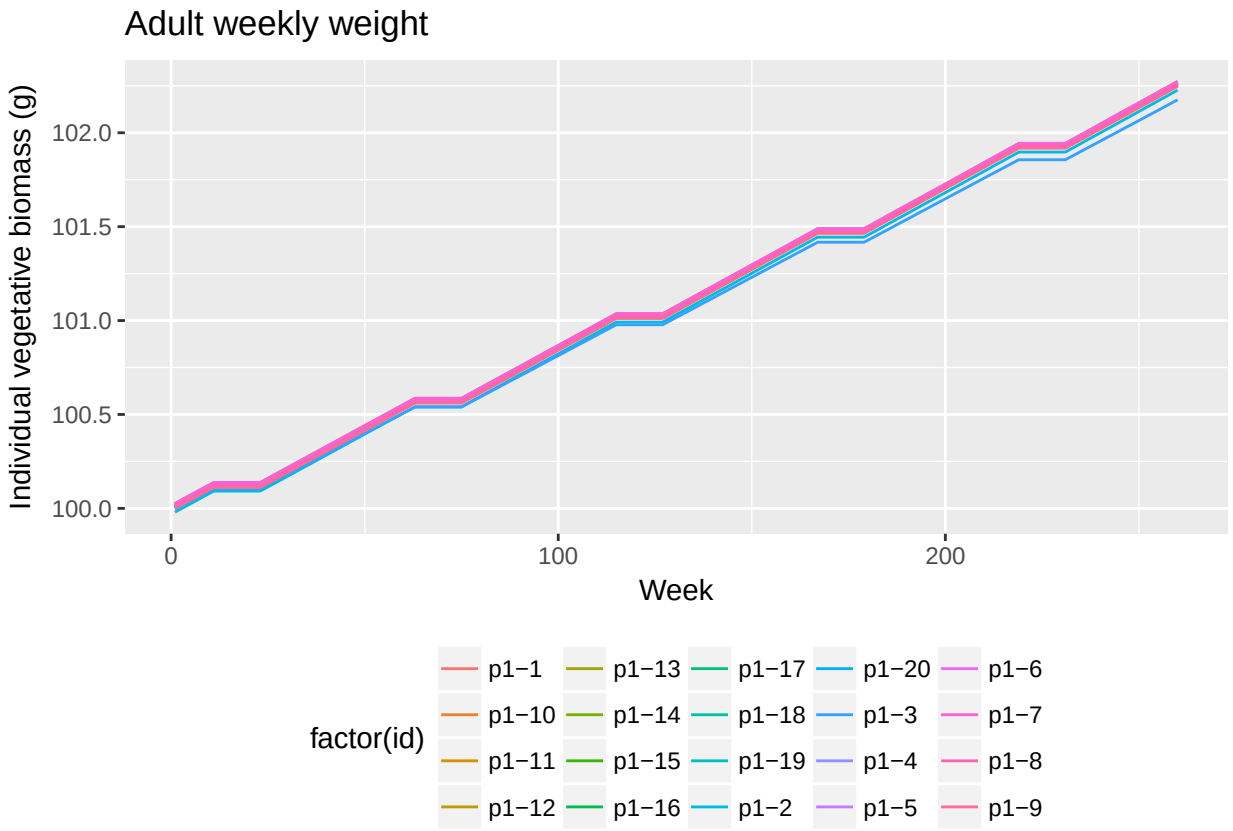
Output results

Growth

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

Check individual variation

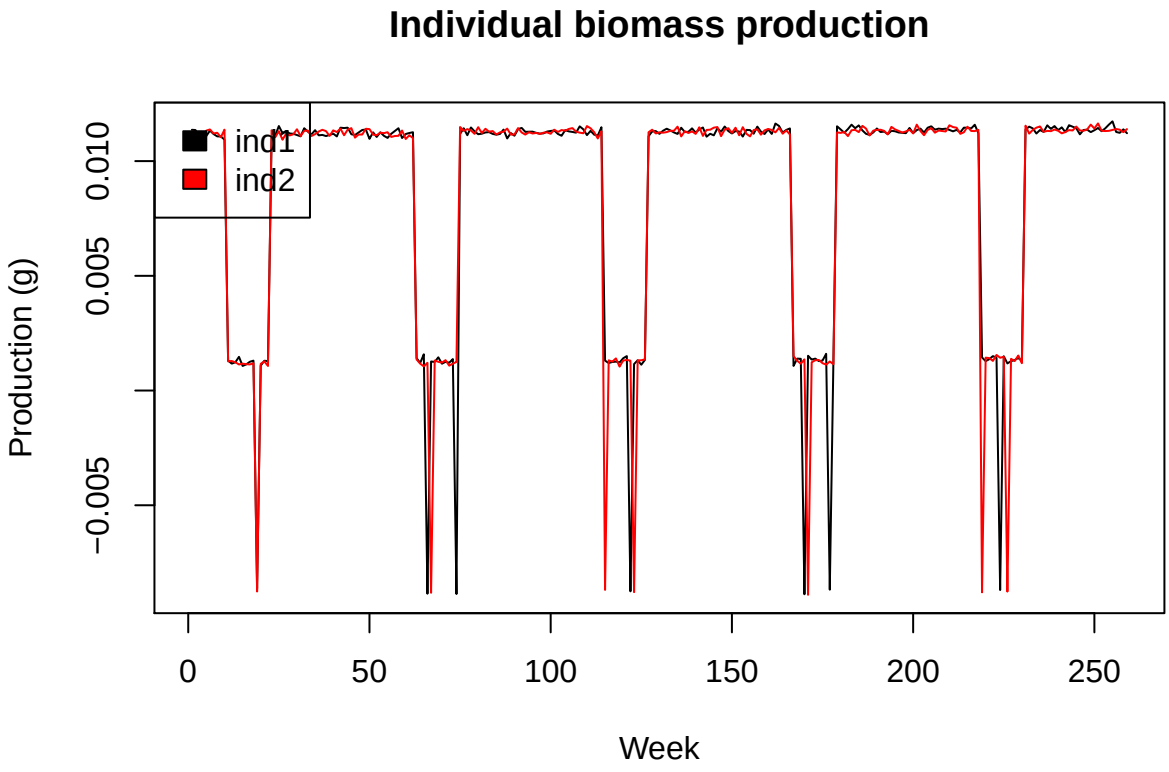
```
biomass <- outdata %>%
  select(week,id,stage,sp,veg,repr)

#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")
```



Linear growth outside the reproductive season.

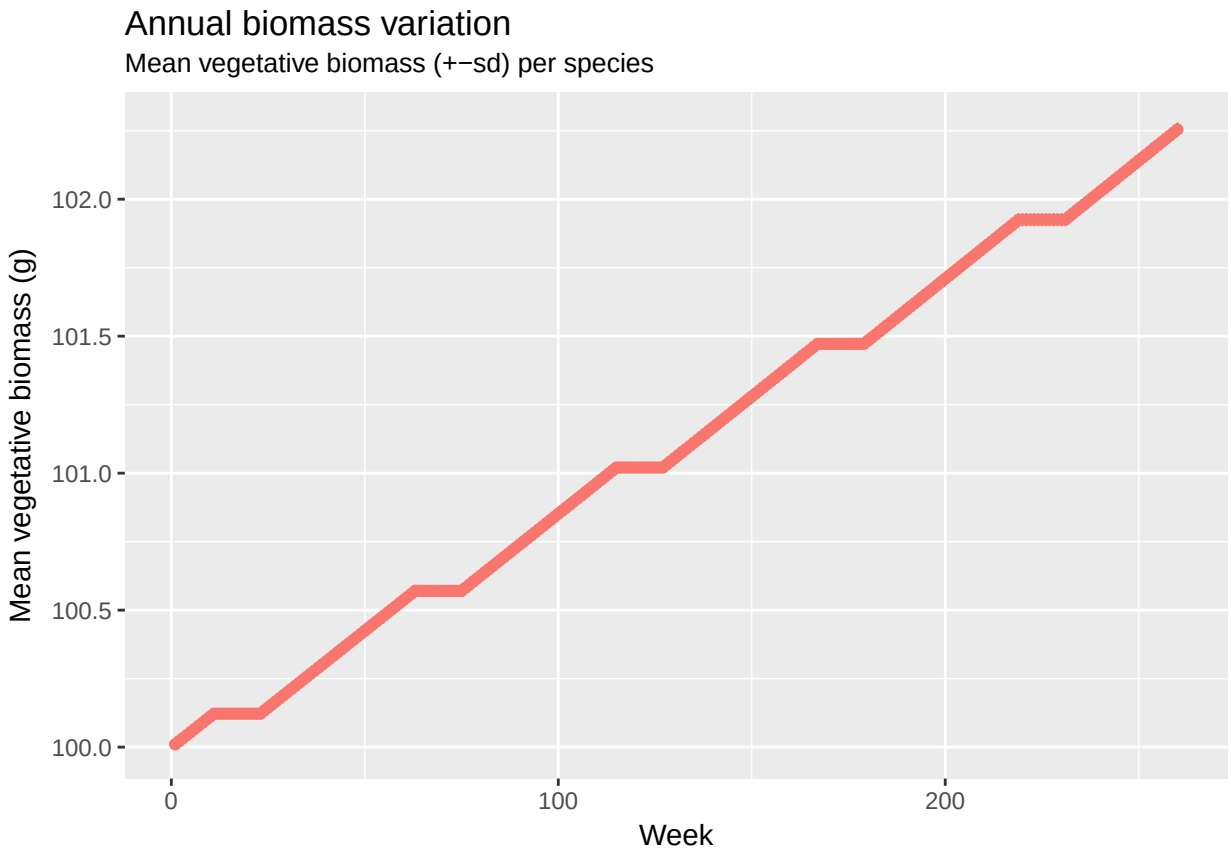
Check if production is the same at all time steps:

```
production <- biomass %>%
  mutate(total = veg+repr) %>%
  group_by(week,id)
# Look at 2 individuals just for detail
ind1 = diff(production$total[which(production$id == "p1-1")],lag = 1)
ind2 = diff(production$total[which(production$id == "p1-2")],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"))
```



Check variation at species-level

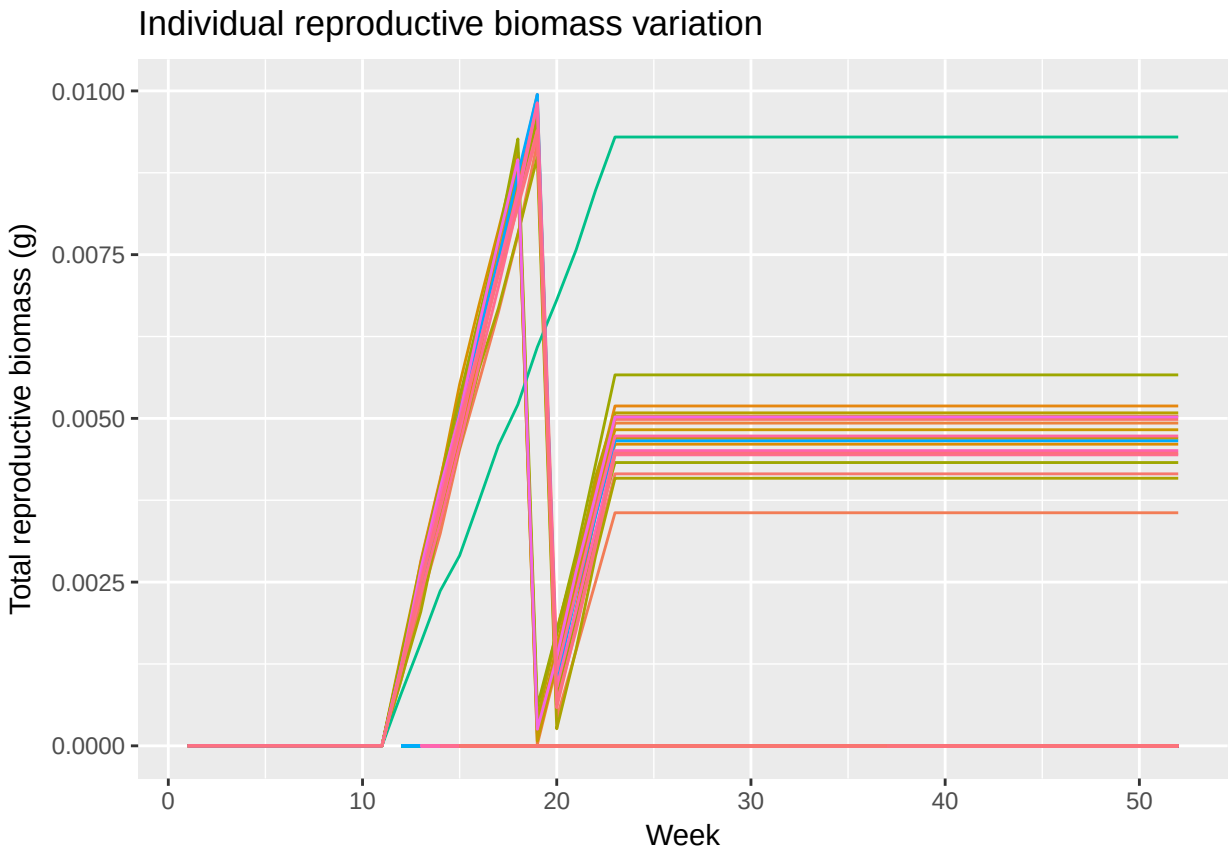
```
# Species-specific biomass
spmass <- biomass%>%
  group_by(week, sp, stage) %>%
  summarise(veg.mean = mean(veg), veg.sd = sd(veg), repr.mean = mean(repr), repr.sd = sd(repr))

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=pd
  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")
```



Same for reproductive biomass Individual variation

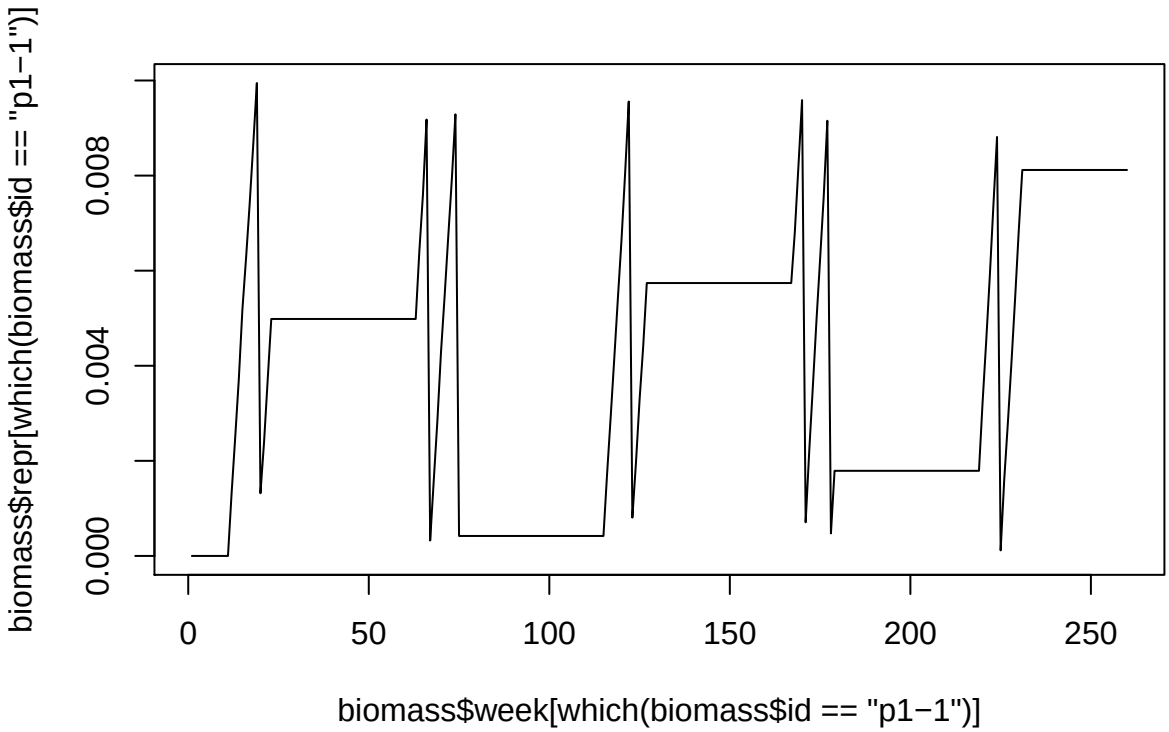
```
indrepmass.plot <- ggplot(biomass, aes(x=week, y= repr, color = factor(id)))
indrepmass.plot +
  geom_line() +
  xlim(1,52) +
  labs(x = "Week", y = "Total reproductive biomass (g)",
       title = "Individual reproductive biomass variation") +
  theme(legend.position = "none")
```

```
## Warning: Removed 42643 rows containing missing values (geom_path).
```



Individual reproductive biomass allocation:

```
plot(biomass$week[which(biomass$id == "p1-1")],biomass$repr[which(biomass$id == "p1-1")], type = "l")
```



It seems like the shedd!() function is not working. Reproductive biomass seems to be varying only as a function

of seed production. Check population variation: Moreover, it seems like the reproductive biomass allocation is very small:

```
max(biomass$repr[which(biomass$id == "p1-1")])
```

```
## [1] 0.009947166
```

```
which.max(biomass$repr[which(biomass$id == "p1-1")][1:52])
```

```
## [1] 19
```

Maximum value of 0.0099 g at week 19 (on the first year). ###Reproduction

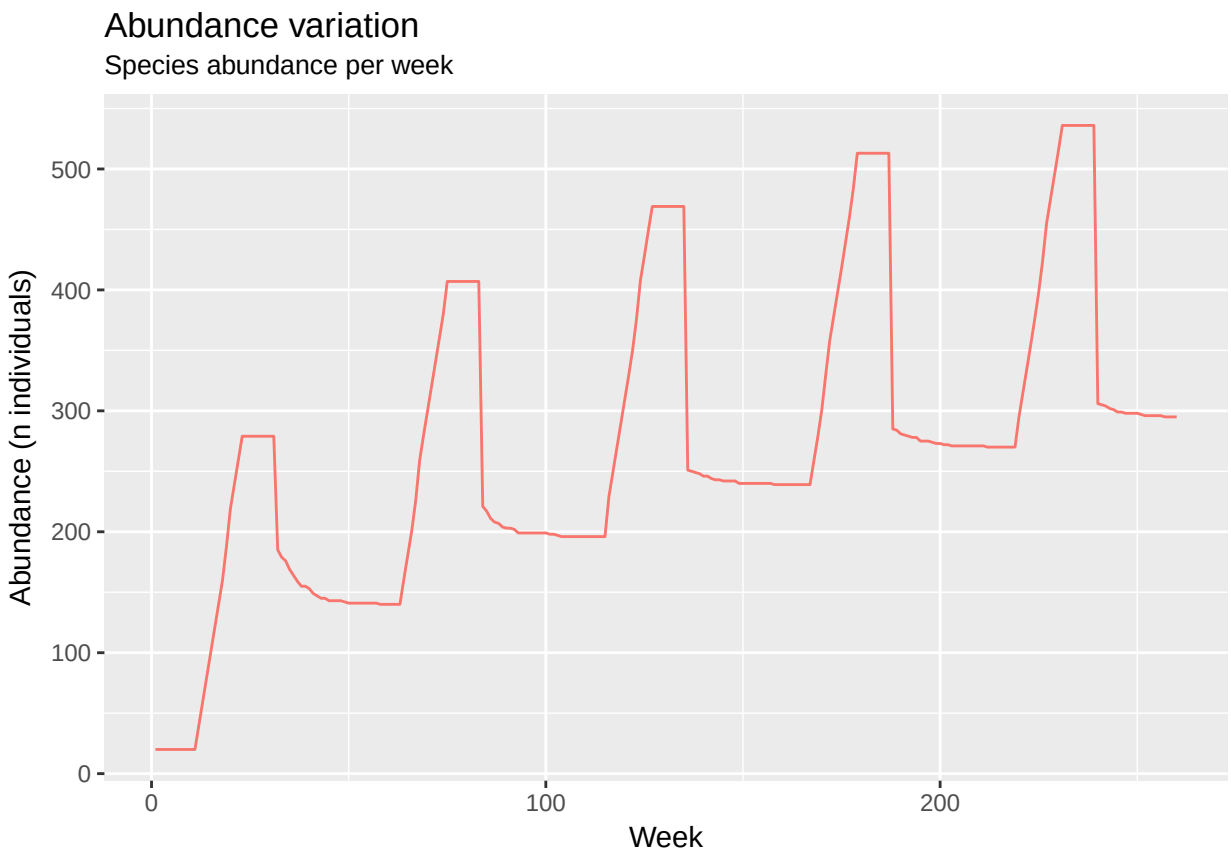
1. Check if reproduction is happening

```
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")
```



```r
which.max(weekabund$abundance[1:52]) #23
```

```
## [1] 23
```

```r
cbind(weekabund$abundance[1:52], biomass$repr[which(biomass$id == "p1-1")][1:52])
```

```
##       [,1]        [,2]
##  [1,]   20 0.000000000
##  [2,]   20 0.000000000
##  [3,]   20 0.000000000
##  [4,]   20 0.000000000
##  [5,]   20 0.000000000
##  [6,]   20 0.000000000
##  [7,]   20 0.000000000
##  [8,]   20 0.000000000
##  [9,]   20 0.000000000
## [10,]   20 0.000000000
## [11,]   20 0.000000000
## [12,]   40 0.001307212
## [13,]   60 0.002480390
## [14,]   80 0.003711844
## [15,]  100 0.005181214
## [16,]  120 0.006252796
## [17,]  140 0.007390671
## [18,]  160 0.008644332
## [19,]  188 0.009947166
## [20,]  219 0.001317532
## [21,]  239 0.002402520
## [22,]  259 0.003701659
## [23,]  279 0.004983967
## [24,]  279 0.004983967
## [25,]  279 0.004983967
## [26,]  279 0.004983967
## [27,]  279 0.004983967
## [28,]  279 0.004983967
## [29,]  279 0.004983967
## [30,]  279 0.004983967
## [31,]  279 0.004983967
## [32,]  185 0.004983967
## [33,]  179 0.004983967
## [34,]  176 0.004983967
## [35,]  169 0.004983967
## [36,]  164 0.004983967
## [37,]  159 0.004983967
## [38,]  155 0.004983967
## [39,]  155 0.004983967
## [40,]  153 0.004983967
## [41,]  149 0.004983967
## [42,]  147 0.004983967
## [43,]  145 0.004983967
## [44,]  145 0.004983967
## [45,]  143 0.004983967
## [46,]  143 0.004983967
## [47,]  143 0.004983967
```

```
## [48,]  143 0.004983967
## [49,]  142 0.004983967
## [50,]  141 0.004983967
## [51,]  141 0.004983967
## [52,]  141 0.004983967
```