

transplant_growth_lengths_Sep_June23

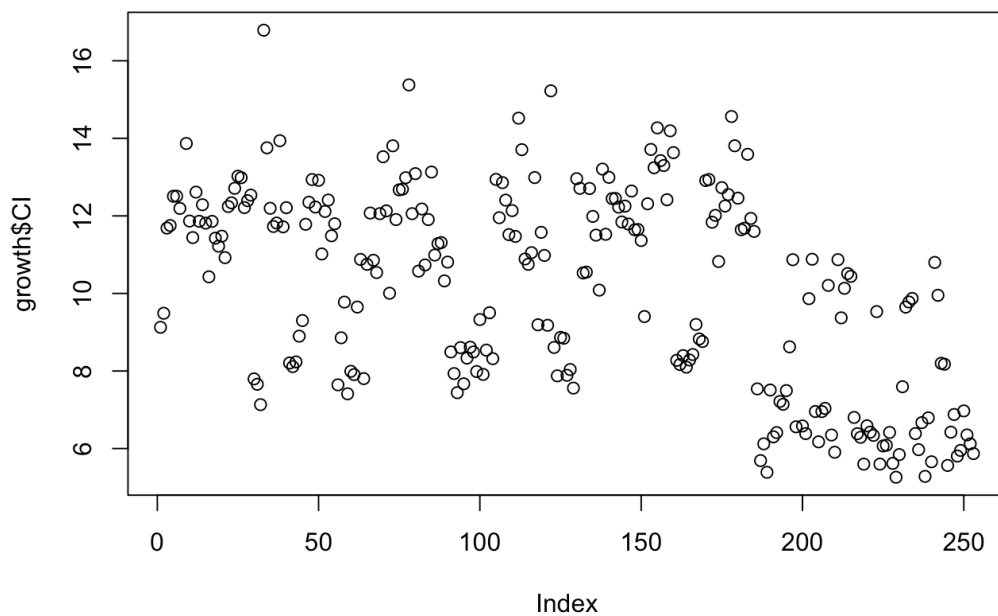
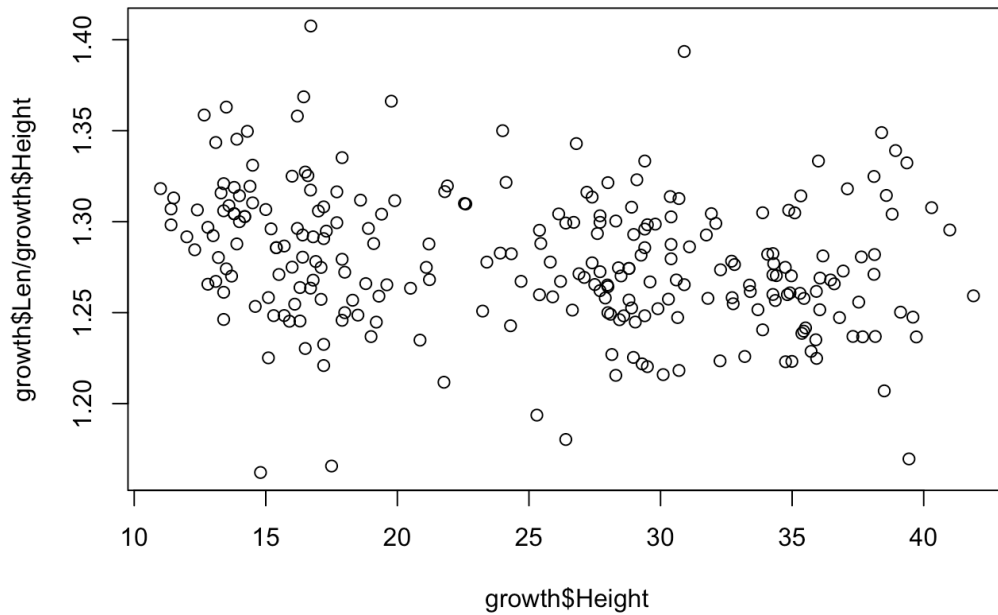
```
'data.frame':  555 obs. of  43 variables:
 $ Start_date
: chr  "9/27/2022" "9/27/2022" "9/27/2022" "9/27/2022" ...
 $ Site
: chr  "Ptown" "Ptown" "Ptown" "Ptown" ...
 $ Treatment
: chr  "N" "N" "N" "N" ...
 $ Buried_Dec
: chr  "N" "N" "N" "N" ...
 $ Location_code
: chr  "A2" "A2" "A2" "A2" ...
 $ color.1
: chr  "R" "Y" "B" "L" ...
 $ color.2
: chr  "" "" "" "" ...
 $ Start_len_mm
: num  13.8 12.8 11.8 11.2 10.3 ...
 $ Start_height_mm
: num  10.86 9.74 9.45 8.13 8.11 ...
 $ Start_thickness_mm
: num  5.92 5.31 5.25 4.55 4.61 4.13 4.46 4.16 3.91 5.68 ...
 $ Collection.month
: chr  "December" "December" "December" "December" ...
 $ Collection1_date
: chr  "12/4/2022" "12/4/2022" "12/4/2022" "12/4/2022" ...
 $ Elapsed_days
: int  68 68 68 68 68 68 68 68 68 202 ...
 $ depth_cm
: chr  "4+" "4+" "" "" ...
 $ color_collection
: chr  "R" "NO LABEL" "" "" ...
 $ L_mm_extra
: num  24.1 21.6 NA NA NA NA NA NA NA NA ...
 $ H_mm_extra
: num  19.3 17.1 NA NA NA NA NA NA NA NA ...
 $ T_mm
: num  11.2 10 NA NA NA NA NA NA NA NA ...
 $ Collection.notes
: chr  "" "" "" "" ...
 $ Dissection.ID.label
: chr  "P125" "P126" "" "" ...
```

```

$ Label.different.when.collected
: chr "" "no label" "" "" ...
$ Biodeposition.label
: chr "" "" "" "" ...
$ Dead_or_missing
: chr "N" "N" "Y" "Y" ...
$ Len
: num 23.9 21.5 NA NA NA NA NA NA NA 37.5 ...
$ Height
: num 19.2 17.1 NA NA NA NA NA NA NA 29.6 ...
$ Thickness
: num 11.2 10 NA NA NA NA NA NA NA ...
$ Est..growth.by.height
: num 8.44 7.36 NA NA NA NA NA NA NA ...
$ Est.start.height.from.linear.function
: num 10.5 9.6 9.3 8.2 8.2 7.8 8 7.7 7.4 10.3 ...
$ Start_height.from.marking
: num 11 9.7 NA NA NA ...
$ Growth.increment.from.mark_height
: num 10.9 9.3 NA NA NA NA NA NA NA 23.5 ...
$ Tin.only
: num 1.09 1.1 NA NA NA ...
$ Tin...gonad...somatic.tissue
: num 1.25 1.22 NA NA NA ...
$ Reweigh..if.necessary.
: num NA NA NA NA NA NA NA NA NA ...
$ Ash.weight..tin...gonad...somatic.tissue.
: num 1.18 1.15 NA NA NA ...
$ DW
: num 0.152 0.115 NA NA NA NA NA NA NA 0.727 ...
$ AFDW
: num 0.07 0.067 NA NA NA ...
$ Ratio.for.samples.with.DW.0.01g
: chr "46%" "58%" "" "" ...
$
Corrected.AFDW.using.an.average.of.82...Used.for..20.samples.wi
th...organic...7.which.was.identifed.to.caused.by.incomplete..
anoxic..muffle.furnace.issues.: num 0.1246 0.0943 NA NA NA ...
$ Notes
: chr "" "Most likely Y (2nd of color series) given start
height" "" "" ...
$ X..gonad
: chr "" "" "" "" ...
$ X..digestive
: chr "" "" "" "" ...

```

```
$ Shell.weight
: num  NA NA NA NA NA NA NA NA NA NA NA ...
$ Start.height.function.params
: num  0.839 1.389 NA NA NA ...
```



```

if(reporting_period == "summer"){
wd <- "~/GitHub/EAD-ASEB-Ssolidissima-0A/projects/Transplant_gro
growth_summer <- read.csv(file = paste(wd,"June2022_Sep2022_sur

growth<-growth_summer

growth <- growth[!is.na(growth$Collection.month),]
growth$Elapsed_days <- as.numeric(growth$Elapsed_days)
growth$Collection1_date <- as.Date(growth$Collection_date, form
growth$Site <- as.factor(growth$Site)
growth$Collection.month <- factor(growth$Collection.month)
levels(growth$Collection.month)[levels(growth$Collection.month)

growth$Site <- factor(growth$Site, levels = c("Ptown", "Eel_Pond
levels(growth$Site) <- c("Prov", "Eel Pond", "Dennis")
growth$Collection.month <- factor(growth$Collection.month, leve
levels(growth$Collection.month) <- c("Jul", "Aug", "Sep")

growth_summer <- growth

# For growth measurements, just use animals that were alive upon

growth <- growth[growth$AliveOrDead=="L",]
growth <- growth[!is.na(growth$Collection.month),]

plot(growth$Len/growth$Height, xlim = c(340,360))
mean(growth$Len/growth$Height, na.rm = TRUE) #1.285
growth[growth$Len/growth$Height>1.2,]
growth[growth$Len/growth$Height<1.1,]
plot(growth$Len/growth$Height~growth$Height)

growth$Treatment <- as.factor(growth$Treatment)
growth$CI <- growth$AFDW/(growth$Len^3)*1000000

plot(growth$CI)
growth[growth$CI>10,]

growth <- growth[growth$CI<10,]
plot(growth$CI)

growth$AFDW <- growth$AFDW_g
growth$DW <- as.numeric(growth$DW_g)

```

```
}
```

```
##-----
##          I still need to fill in any QC'ed data      --
##          with the ratio of length to height         --
## But first, I want to check the notebook / frozen clams --
##-----

#growth[!is.na(growth$Start_len_mm),]

#growth <- growth[!is.na(growth$L_mm),]
#growth <- growth[growth$AliveOrDead=="L",]

growth$len_tot <- growth$Len-growth$Start_len_mm #len_tot is gro
growth$len_per_day <- growth$len_tot/growth$Elapsed_days

growth$height_tot <- growth$Height-growth$Start_height_mm
growth$height_per_day <- growth$height_tot/growth$Elapsed_days
growth$ratio.LH <- growth$height_tot/growth$len_tot

growth <- growth[growth$ratio.LH < 1 & growth$ratio.LH > 0,]

mean(growth$len_tot, na.rm = TRUE)
```

```
[1] 21.09983
```

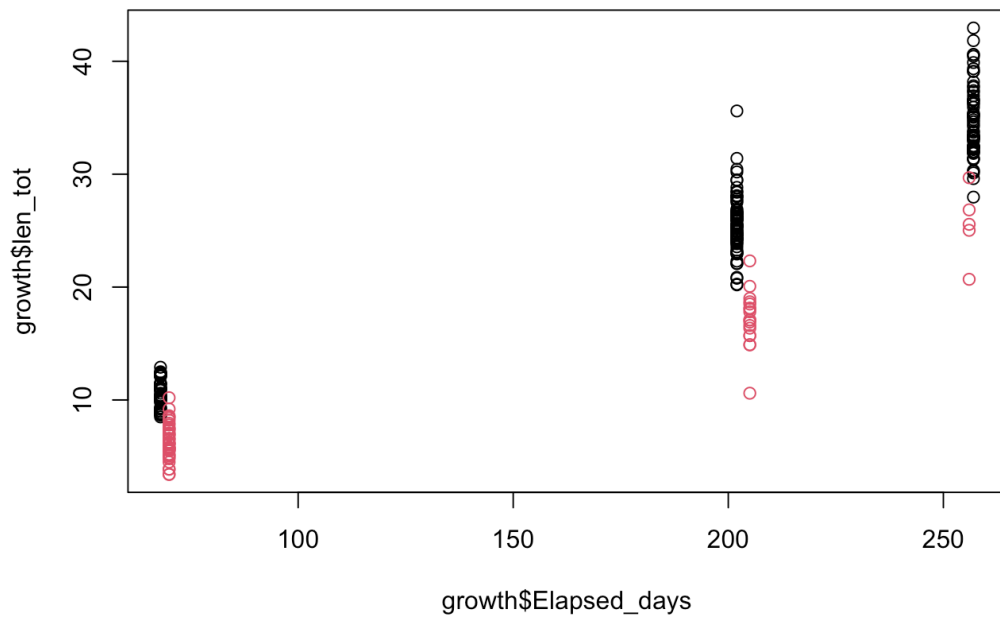
```
mean(growth$len_per_day, na.rm = TRUE)
```

```
[1] 0.1245683
```

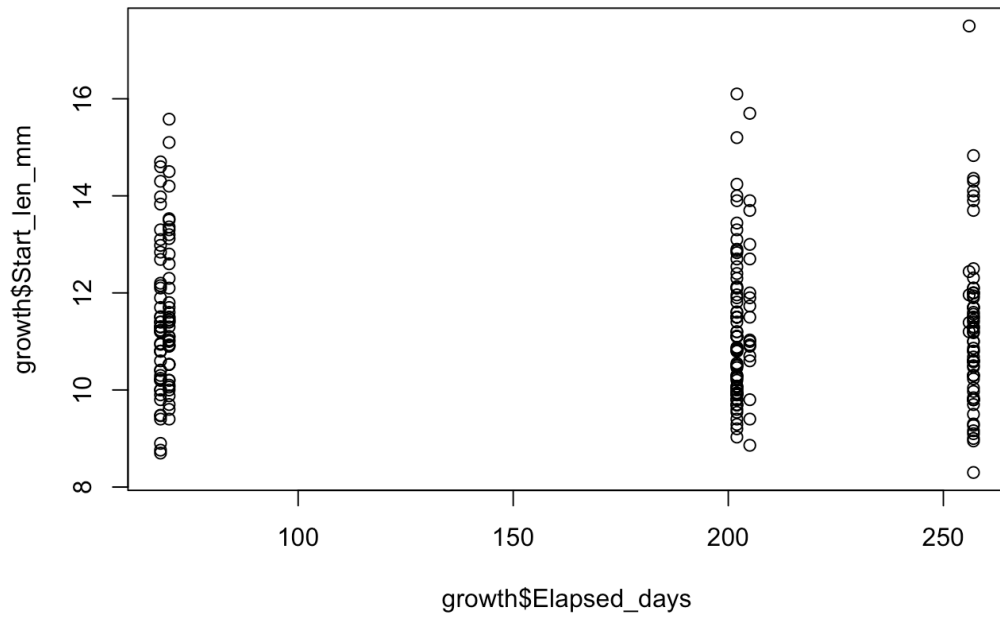
```
#growth[growth$len_tot<=0,"Len"]<- NA
```

Plot total change in length as a function of starting length

```
par(mfrow = c(1,1))
plot(growth$Elapsed_days, growth$len_tot, col = growth$Site)
```



```
plot(growth$Elapsed_days, growth$Start_len_mm)
```



Ptown treatment comparison

```
growth <- growth[!is.na(growth$len_tot),]  
mod_growth_full <- lme(len_tot/Elapsed_days*30~Treatment+Collection.month,  
  #*Collection.month,  
  #+Start_len_mm+Start_len_mm:Site,  
  random = ~1|Location_code,  
  data = growth)
```

```
library(svglite)  
library(ftExtra)
```

Registered S3 method overwritten by 'ftExtra':

```
method          from  
as_flextable.data.frame flextable
```

Attaching package: 'ftExtra'

The following object is masked from 'package:flextable':

```
separate_header
```

The following object is masked from 'package:huxtable':

```
as_flextable
```

```
#Commenting out b/c seems to be causing memory usage issues  
  
#https://ardata-fr.github.io/flextable-book/plotting-flextable.html  
ft <- as_flextable(mod_growth_full, fit = "fixed", just = "center")  
  add_header_lines("Growth (mm/day)")  
ft
```

Growth (mm/day)

group	Estimate	Standard Error	df	statistic
Fixed effects				
(Intercept)	4.550	0.101	215	44.977
TreatmentS	-0.110	0.082	215	-1.346

Collection.monthApr		-0.540	0.105	215	-5.136
Collection.monthJun		-0.429	0.121	215	-3.537
SiteEel Pond		-1.673	0.079	215	-21.109
Random effects					
Location_code	sd_(Intercept)	0.216			
Residual	sd_Observation	0.454			

Signif. codes: 0 <= '***' < 0.001 < '***' < 0.0

square root of the estimated residual variance: 0.5
data's log-likelihood under the model: -177.2
Akaike Information Criterion: 368.4
Bayesian Information Criterion: 392.9

```
gr <- gen_grob(ft)
plot(gr)
```

Growth (mm/day)						
group		Estimate	Standard Error	df	statistic	p-value
Fixed effects						
(Intercept)		4.550	0.101	215	44.977	0.0000 ***
TreatmentS		-0.110	0.082	215	-1.346	0.1798
Collection.monthApr		-0.540	0.105	215	-5.136	0.0000 ***
Collection.monthJun		-0.429	0.121	215	-3.537	0.0005 ***
SiteEel Pond		-1.673	0.079	215	-21.109	0.0000 ***
Random effects						
Location_code	sd_(Intercept)	0.216				
Residual	sd_Observation	0.454				

Signif. codes: 0 <= '***' < 0.001 < '***' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 0.5
data's log-likelihood under the model: -177.2
Akaike Information Criterion: 368.4
Bayesian Information Criterion: 392.9


```
library(patchwork)

ggarrange(gr,gr)
```

Growth (mm/day)							Growth (mm/day)						
group		Estimate	Standard Error	df	statistic	p-value	group		Estimate	Standard Error	df	statistic	p-value
Fixed effects							Fixed effects						
	(Intercept)	4.550	0.101	215	44.977	0.0000 ***		(Intercept)	4.550	0.101	215	44.977	0.0000 ***
	TreatmentS	-0.110	0.082	215	-1.346	0.1798		TreatmentS	-0.110	0.082	215	-1.346	0.1798
	Collection.monthApr	-0.540	0.105	215	-5.136	0.0000 ***		Collection.monthApr	-0.540	0.105	215	-5.136	0.0000 ***
	Collection.monthJun	-0.429	0.121	215	-3.537	0.0005 ***		Collection.monthJun	-0.429	0.121	215	-3.537	0.0005 ***
	SiteEel Pond	-1.673	0.079	215	-21.109	0.0000 ***		SiteEel Pond	-1.673	0.079	215	-21.109	0.0000 ***
Random effects							Random effects						
Location_code	sd_(Intercept)	0.216					Location_code	sd_(Intercept)	0.216				
Residual	sd_Observation	0.454					Residual	sd_Observation	0.454				
Signif. codes: 0 <= '***' < 0.001 < '***' < 0.01 < '*' < 0.05							Signif. codes: 0 <= '***' < 0.001 < '***' < 0.01 < '*' < 0.05						
square root of the estimated residual variance: 0.5							square root of the estimated residual variance: 0.5						
data's log-likelihood under the model: -177.2							data's log-likelihood under the model: -177.2						
Akaike Information Criterion: 368.4							Akaike Information Criterion: 368.4						
Bayesian Information Criterion: 392.9							Bayesian Information Criterion: 392.9						

```
library(tables)
tab <- tabular(
  (Species + 1) ~ (n = 1) + Format(digits = 2) *
    (Sepal.Length + Sepal.Width) * (mean + sd),
  data = iris
)
as_flextable(tab)
```

		Sepal.Length		Sepal.Width	
Species	n	mean	sd	mean	sd
setosa	50	5.01	0.35	3.43	0.38
versicolor	50	5.94	0.52	2.77	0.31
virginica	50	6.59	0.64	2.97	0.32
All	150	5.84	0.83	3.06	0.44

```
#Length change
#https://stackoverflow.com/questions/77037940/how-to-convert-nl

summary(mod_growth_full)
```

Linear mixed-effects model fit by REML

Data: growth

AIC	BIC	logLik
368.4321	392.8835	-177.216

Random effects:

Formula: ~1 | Location_code
(Intercept) Residual

StdDev: 0.2161049 0.454428

Fixed effects: len_tot/Elapsed_days * 30 ~ Treatment +
Collection.month + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	4.549824	0.10115823	215	44.97730	0.0000
Treatments	-0.110329	0.08197825	215	-1.34583	0.1798
Collection.monthApr	-0.539846	0.10510634	215	-5.13619	0.0000
Collection.monthJun	-0.428697	0.12119840	215	-3.53715	0.0005
SiteEel Pond	-1.672723	0.07924195	215	-21.10906	0.0000

Correlation:

	(Intr)	TrtmnS	Cllc.A	Cllc.J
Treatments	-0.458			
Collection.monthApr	-0.627	-0.007		
Collection.monthJun	-0.658	0.039	0.573	
SiteEel Pond	-0.435	0.021	0.244	0.386

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-2.92913521	-0.60445434	-0.04832064	0.62530974	2.61565396

Number of Observations: 248

Number of Groups: 29

```
anova(mod_growth_full)
```

numDF	denDF	F-value	p-value
-------	-------	---------	---------

1	215	5.62e+03	0
1	215	1.39	0.24
2	215	17.5	9.32e-08
1	215	446	0

```
# summary(mod_growth_ful)$tTable %>%
# as_tibble(rownames="variable") %>%
# knitr::kable(digits=3)

fit <- linear_reg() %>%
  set_engine("lm") %>%
  fit(formula = mpg ~ cyl, data = mtcars)
fit %>% tidy()
```

term	estimate	std.error	statistic	p.value
(Intercept)	37.9	2.07	18.3	8.37e-18
cyl	-2.88	0.322	-8.92	6.11e-10

```
fit %>% glance()
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC
0.726	0.717	3.21	79.6	6.11e-10	1	-81.7	163.4

```
mod_growth_full <- lmer(len_tot/Elapsed_days*30~Treatment+Coll
```

```
#as_flextable(mod_growth_full, options(show.signif.stars = FALSE))

mod.out <- anova(mod_growth_full)
mod.out%>%
  kbl(caption = "Mixed model output")%>%
  kable_classic(full_width=F, html_font = "Cambria")%>%
  kable_styling(bootstrap_options = c("striped","hover","condens
```

Mixed model output

	npars	Sum Sq	Mean Sq	F value
Treatment	1	0.2861897	0.2861897	1.385874
Collection.month	2	7.2154542	3.6077271	17.470425
Site	1	92.0169408	92.0169408	445.592208

```
# mod.out <- coeff(mod_growth_full)
mod.out%>%
  kbl(caption = "Mixed model output")%>%
  kable_classic(full_width=F, html_font = "Cambria")%>%
  kable_styling(bootstrap_options = c("striped","hover","condens
```

Mixed model output

	npars	Sum Sq	Mean Sq	F value
Treatment	1	0.2861897	0.2861897	1.385874
Collection.month	2	7.2154542	3.6077271	17.470425
Site	1	92.0169408	92.0169408	445.592208

```
#write.csv(summary(mod_growth_full), "LMER output_growth.csv")
```

```
mod_growth_full.CI <- lme(CI~Treatment+Collection.month+Site,
```

```

      #+Start_len_mm+Start_len_mm:Site,
      random = ~1|Location_code,
      data = growth)
summary(mod_growth_full.CI)

```

Linear mixed-effects model fit by REML

Data: growth

	AIC	BIC	logLik
	750.6729	775.1244	-368.3365

Random effects:

Formula: ~1 | Location_code
(Intercept) Residual

StdDev: 0.2262083 1.036618

Fixed effects: CI ~ Treatment + Collection.month + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	8.845526	0.1821654	215	48.55766	0.0000
Treatments	-0.154781	0.1506118	215	-1.02768	0.3053
Collection.monthApr	3.808401	0.1859536	215	20.48038	0.0000
Collection.monthJun	2.726700	0.2098696	215	12.99235	0.0000
SiteEel Pond	-2.735380	0.1685048	215	-16.23325	0.0000

Correlation:

	(Intr)	TrtmnS	Cllc.A	Cllc.J
Treatments	-0.530			
Collection.monthApr	-0.655	0.090		
Collection.monthJun	-0.666	0.118	0.541	
SiteEel Pond	-0.484	0.057	0.268	0.366

Standardized Within-Group Residuals:

	Min	Q1	Med	Q3	Max
	-3.33642362	-0.52816591	-0.04810808	0.49213942	6.13877998

Number of Observations: 248

Number of Groups: 29

```

# M_int<-update(mod_growth_full, ~. - Start_len_mm:Site)
# M <- update(M_int, ~. - Treatment:Site)
# M2 <- update(M_int, ~. - Start_len_mm)
#
# summary(M_int)
# summary(M)
# summary(M2)
# AIC(mod_growth_full,M_int,M,M2)

```

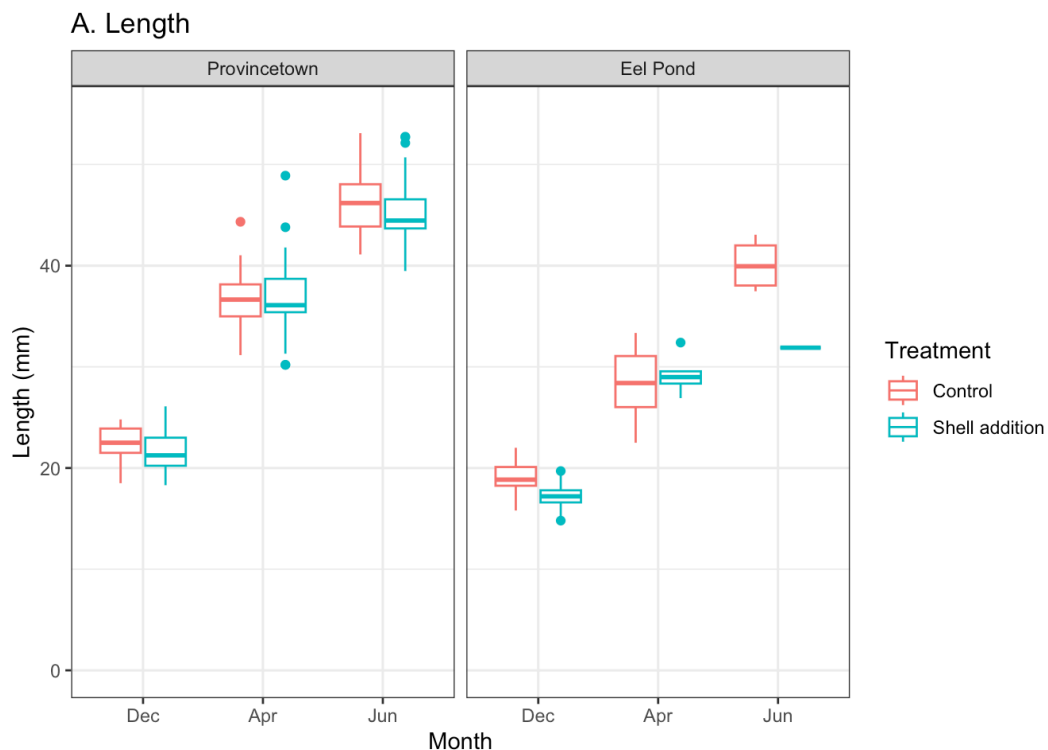
```
#banner(snug = TRUE, bandChar = "-") # <--- create a small banner

# Remove growth measurements that are <(-2)... There are none.
#growth_dec[growth_dec$growth_height<0,]
#growth_dec <- growth_dec[growth_dec$growth_height>(-2),]
```

```
growth$Site <- factor(growth$Site)

levels(growth$Treatment) <- c("Control","Shell addition")

gg0 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  ylim(0,55)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('A. Length')+
  facet_wrap(facets = "Site")
gg0
```

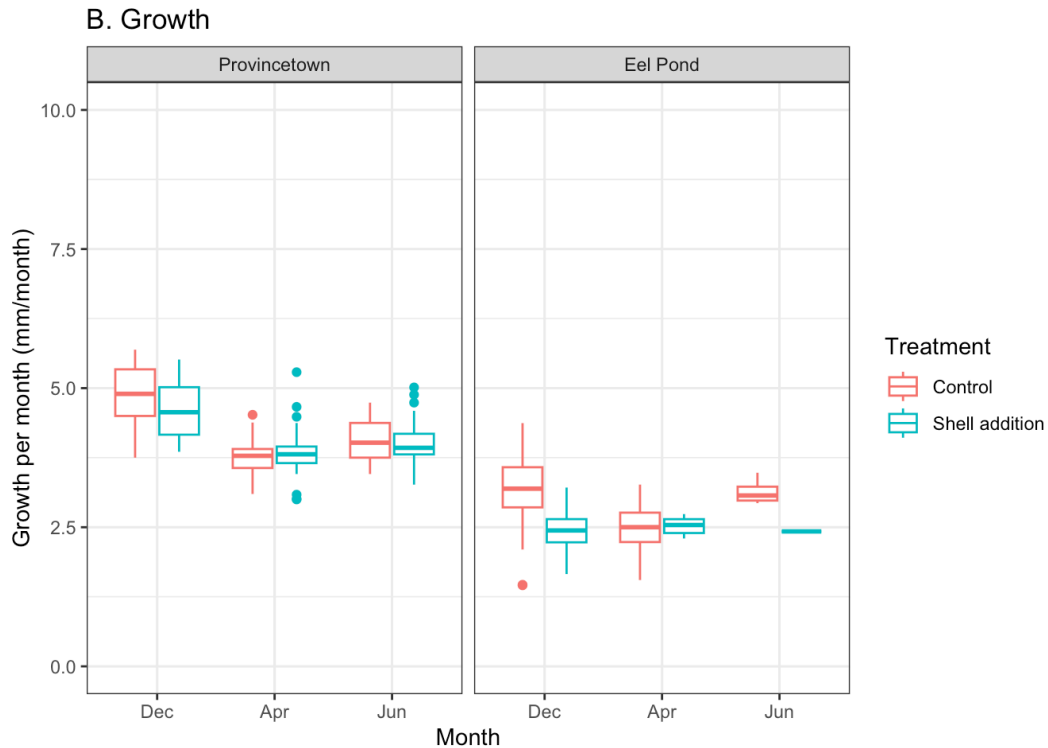


```
gg1 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
```

```

xlab("Month") +
ylab("Growth per month (mm/month)") +
ylim(0,10) +
scale_color_discrete(name="Treatment") +
ggtitle('B. Growth') +
facet_wrap(facets = "Site")
gg1

```



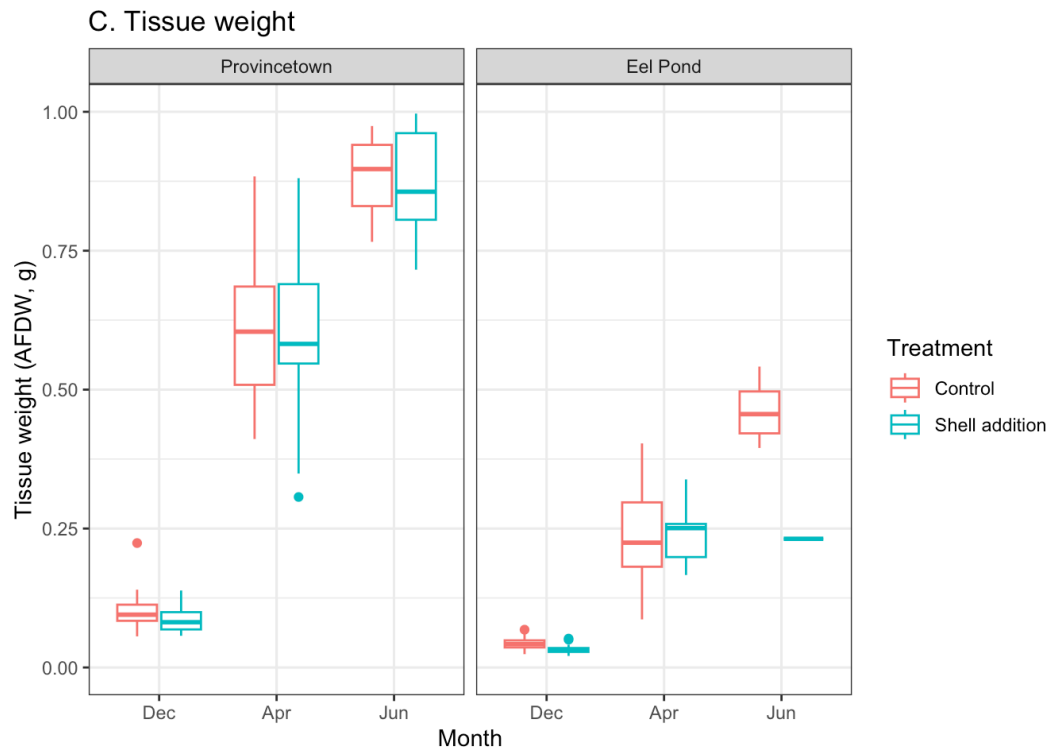
```

gg2 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot() +
  xlab("Month") +
  ylab("Tissue weight (AFDW, g)") +
  ylim(0,1) +
  scale_color_discrete(name="Treatment") +
  ggtitle('C. Tissue weight') +
  facet_wrap(facets = "Site")

```

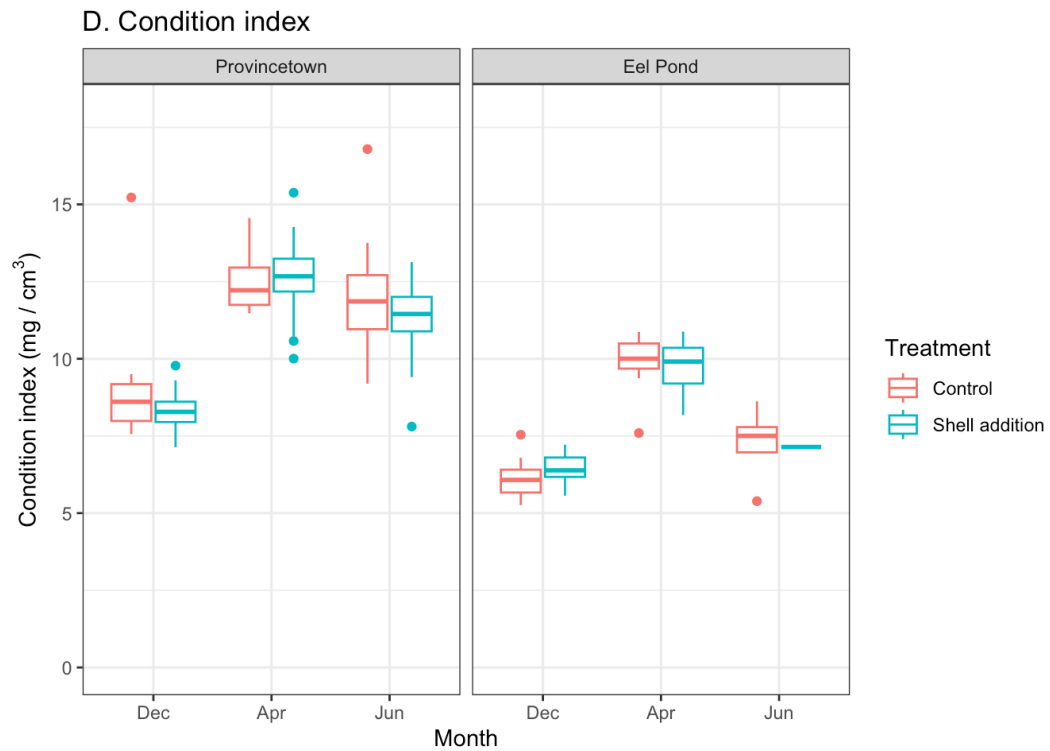
```
gg2
```

Warning: Removed 48 rows containing non-finite outside the scale range
(`stat_boxplot()`).



```
CI_label <- expression(paste("Condition index (mg / ", "cm"^3, "
gg3 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab(CI_label)+
  ylim(0,18)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('D. Condition index')+
  facet_wrap(facets = "Site")
```

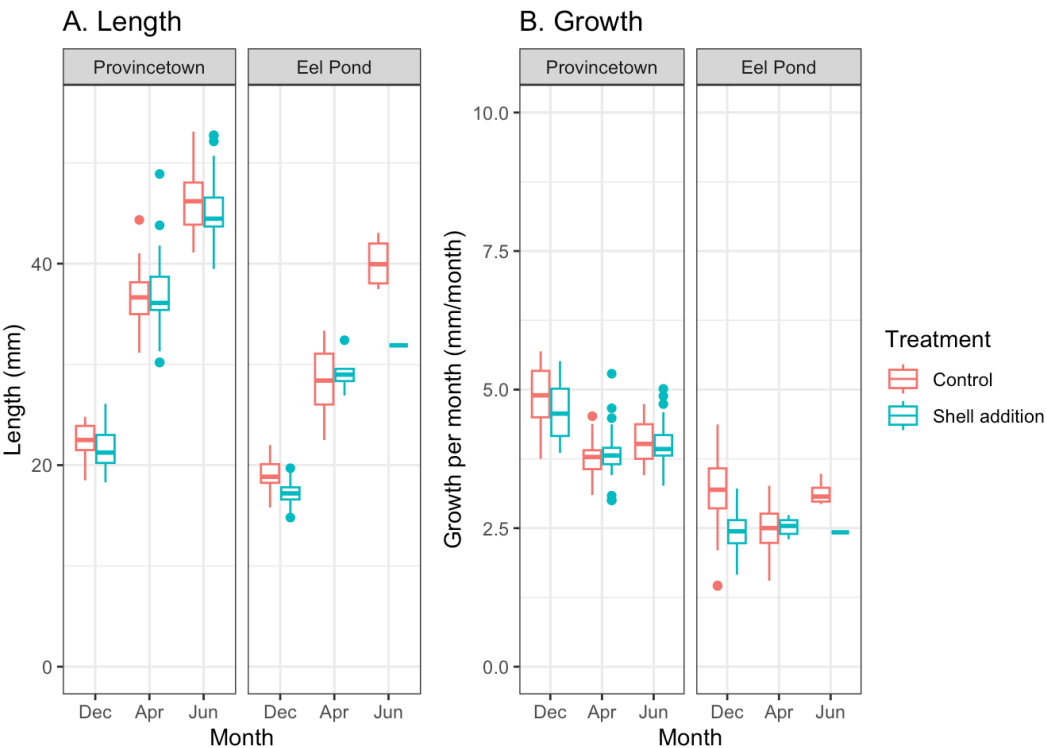
```
gg3
```

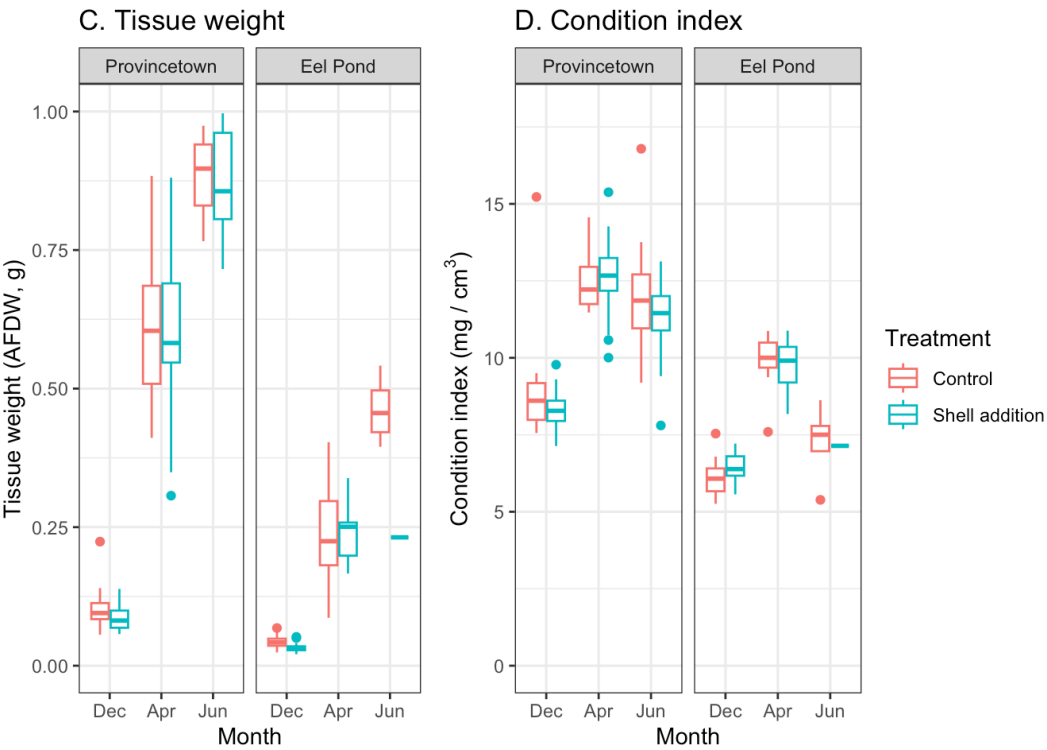
```
ggarrange(gg0,gg1,gg2,gg3, ncol=2, common.legend = TRUE, legend
```

Warning: Removed 48 rows containing non-finite outside the scale range (``stat_boxplot()``).

\$`1`



\$`2`

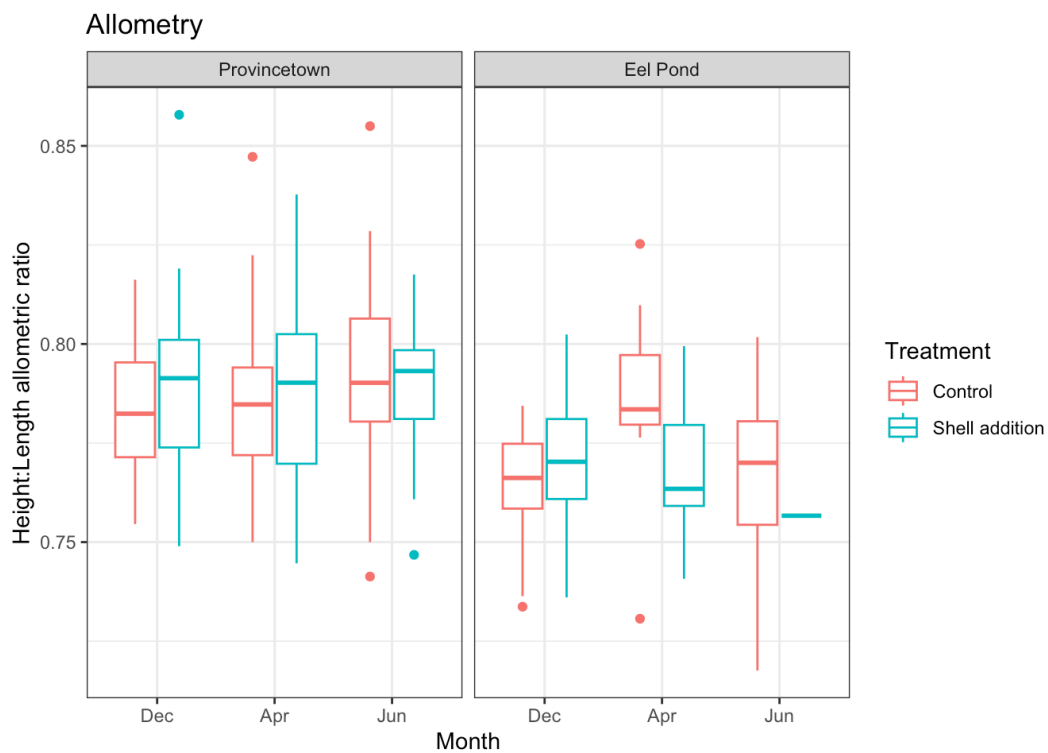


attr(,"class")

```
[1] "list"      "ggarrange"
```

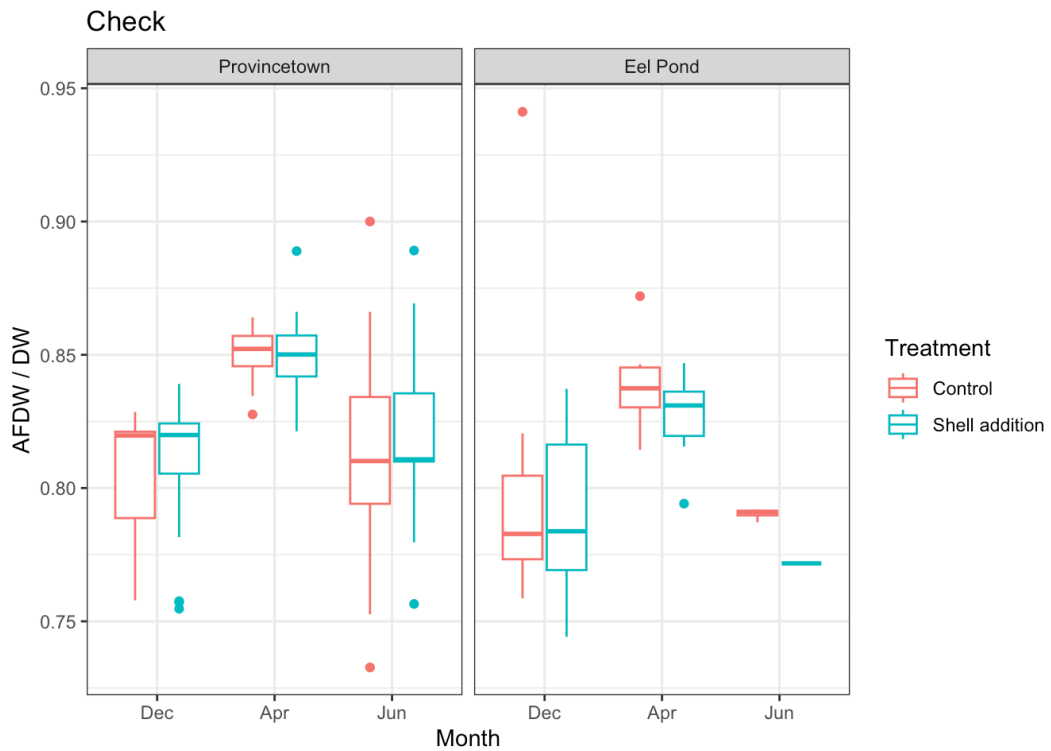
```
gg4 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Height:Length allometric ratio")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Allometry')+
  facet_wrap(facets = "Site"))
```

```
gg4
```

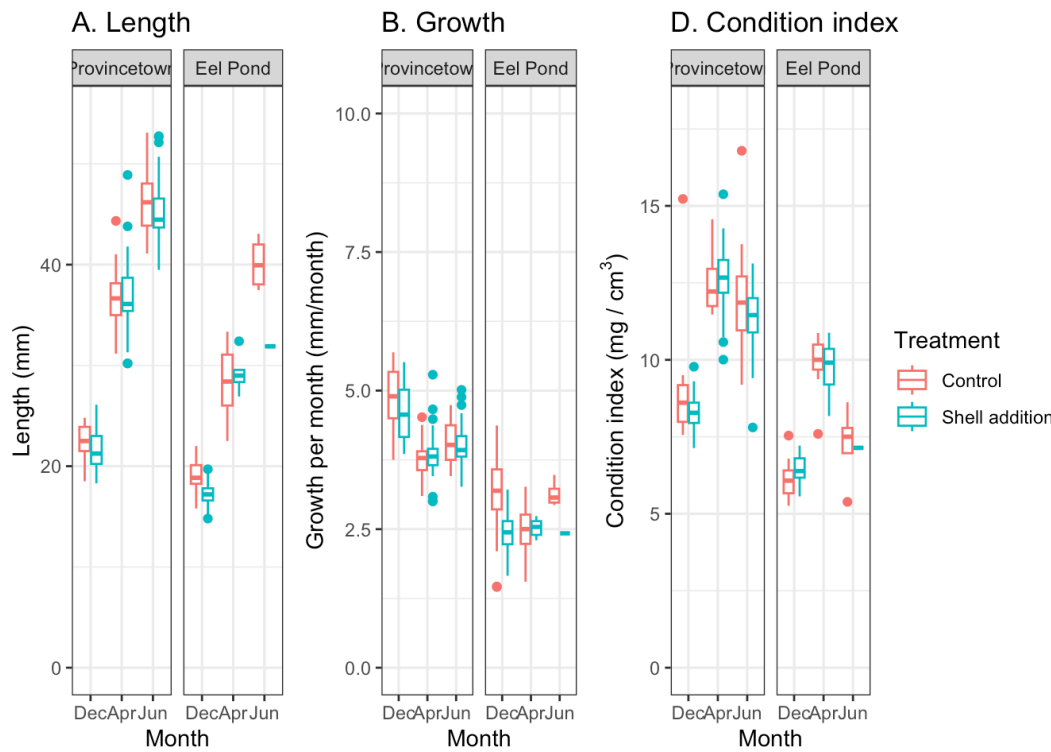


```
gg5 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("AFDW / DW")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Check')+
  facet_wrap(facets = "Site"))
```

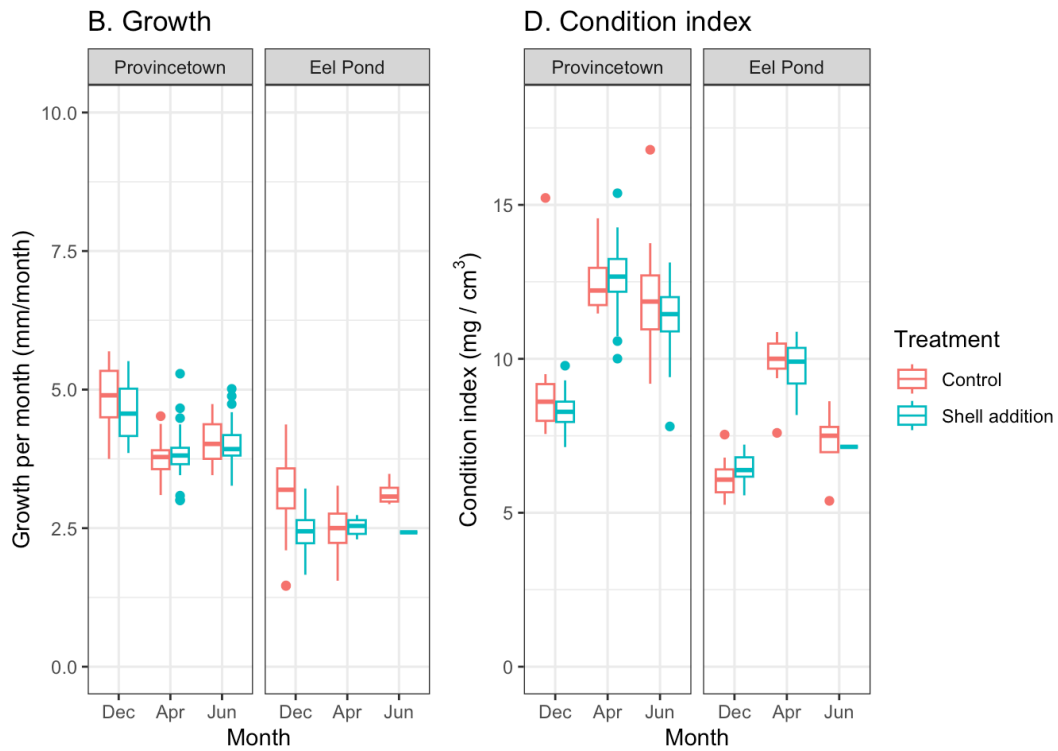
```
gg5
```



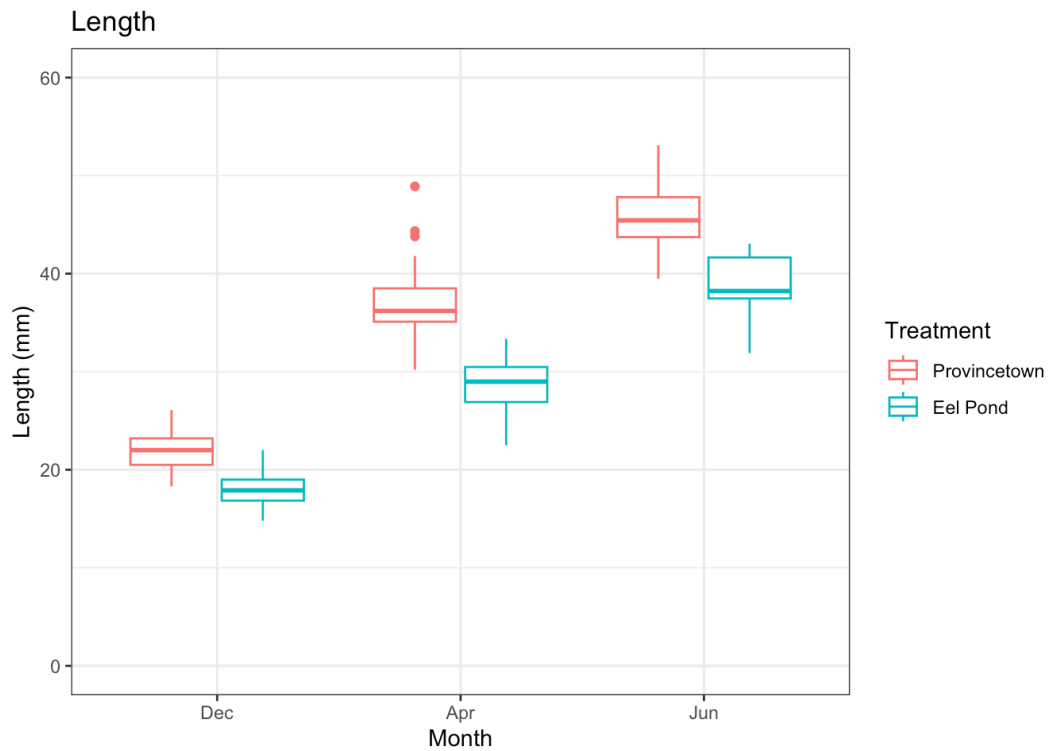
```
ggarrange(gg0,gg1,gg3, ncol=3, common.legend = TRUE, legend = "right")
```



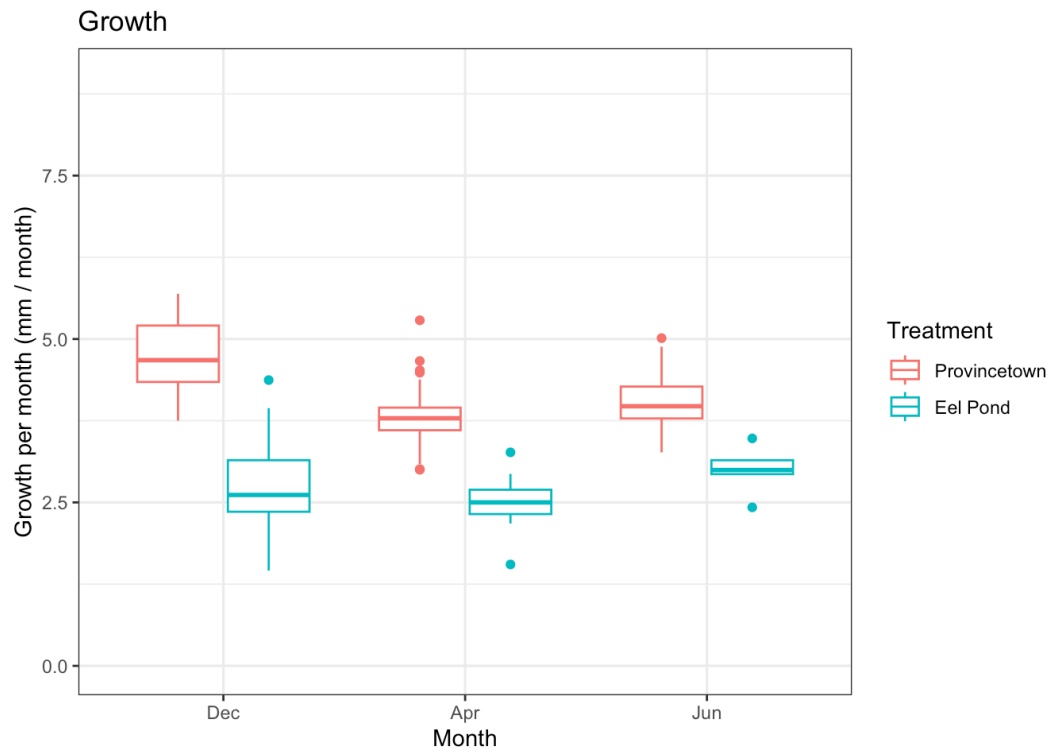
```
ggarrange(gg1,gg3, ncol=2, common.legend = TRUE, legend = "right")
```



```
gg0 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  ylim(0,60)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Length')#+
  #facet_wrap(facets = "Site")
gg0
```

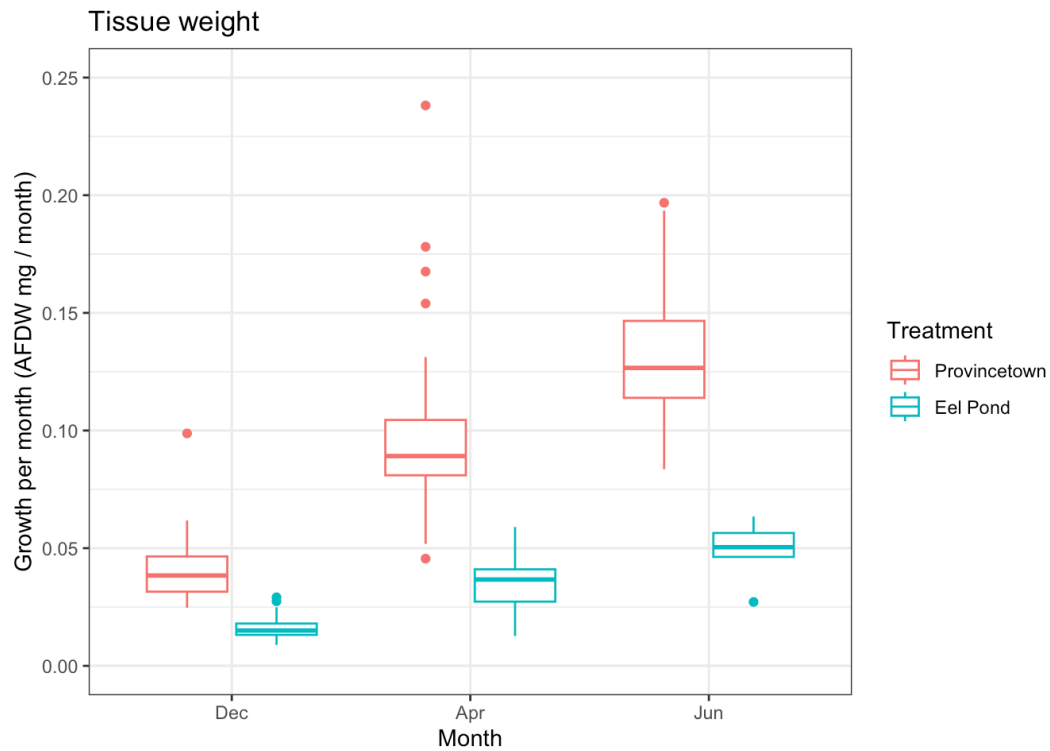


```
gg1 <- ggplot(data = growth, aes(x=as.factor(Collection.month),  
  geom_boxplot()+  
  xlab("Month") +  
  ylab("Growth per month (mm / month)")+  
  ylim(0,9)+  
  scale_color_discrete(name="Treatment")+  
  ggtitle ('Growth')#+  
  #facet_wrap(facets = "Site")  
gg1
```



```
gg2 <- ggplot(data = growth, aes(x=as.factor(Collection.month),  
  geom_boxplot()+  
  xlab("Month") +  
  ylab("Growth per month (AFDW mg / month)")+  
  ylim(0,.25)+  
  scale_color_discrete(name="Treatment")+  
  ggtitle ('Tissue weight')#+  
  #facet_wrap(facets = "Site")
```

```
gg2
```



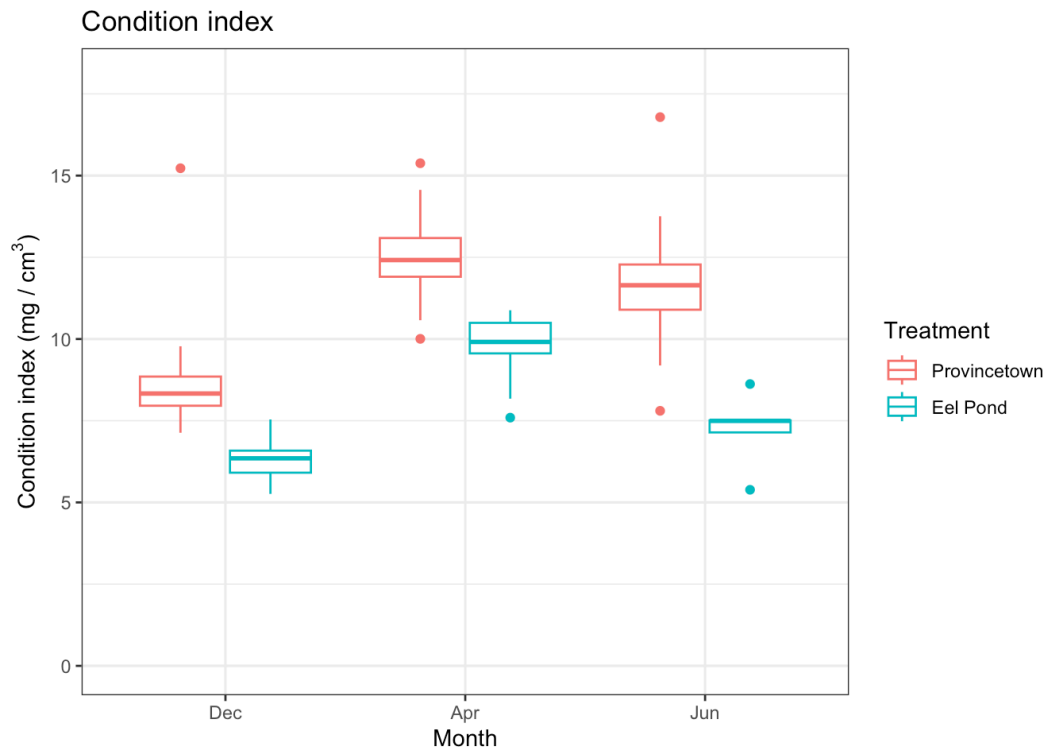
```

CI_label <- expression(paste("Condition index( g ", "mm"^-3, 10^-3, "cm"^-3, "mg / cm^3)"))
CI_label <- expression(paste("Condition index (mg / ", "cm"^-3, "cm^3, "mg / cm^3)"))

gg3 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  #ylab("Condition index (mg / cm^3)"))+
  ylab(CI_label)+
  ylim(0,18)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Condition index')#+
  #facet_wrap(facets = "Site")

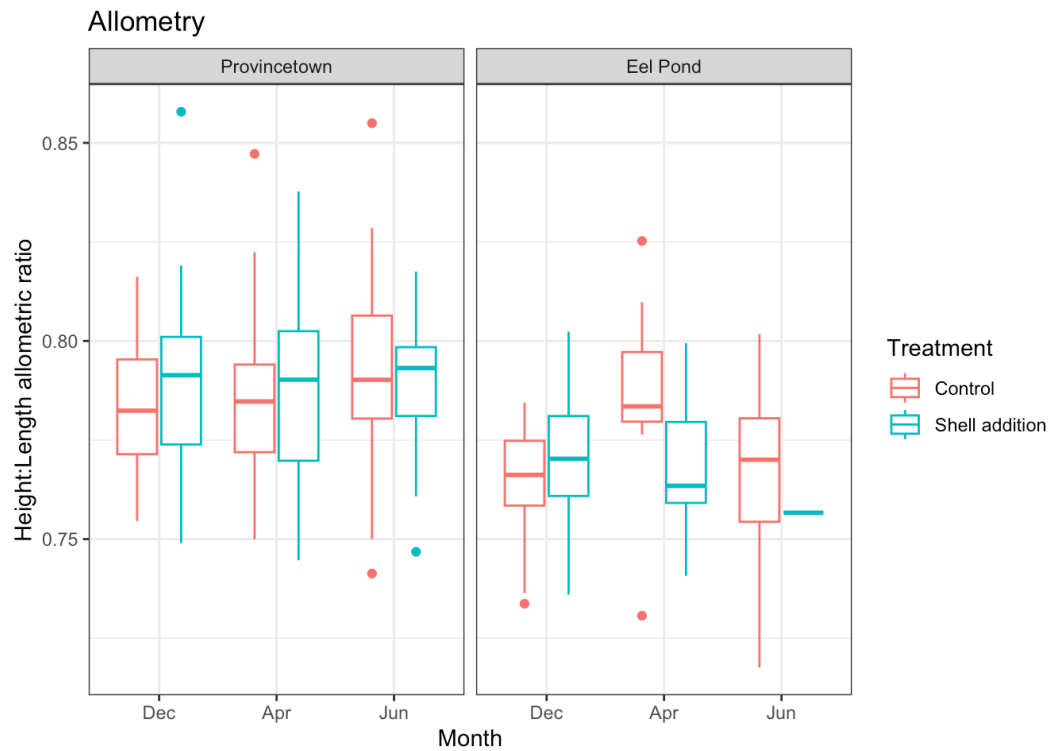
gg3

```

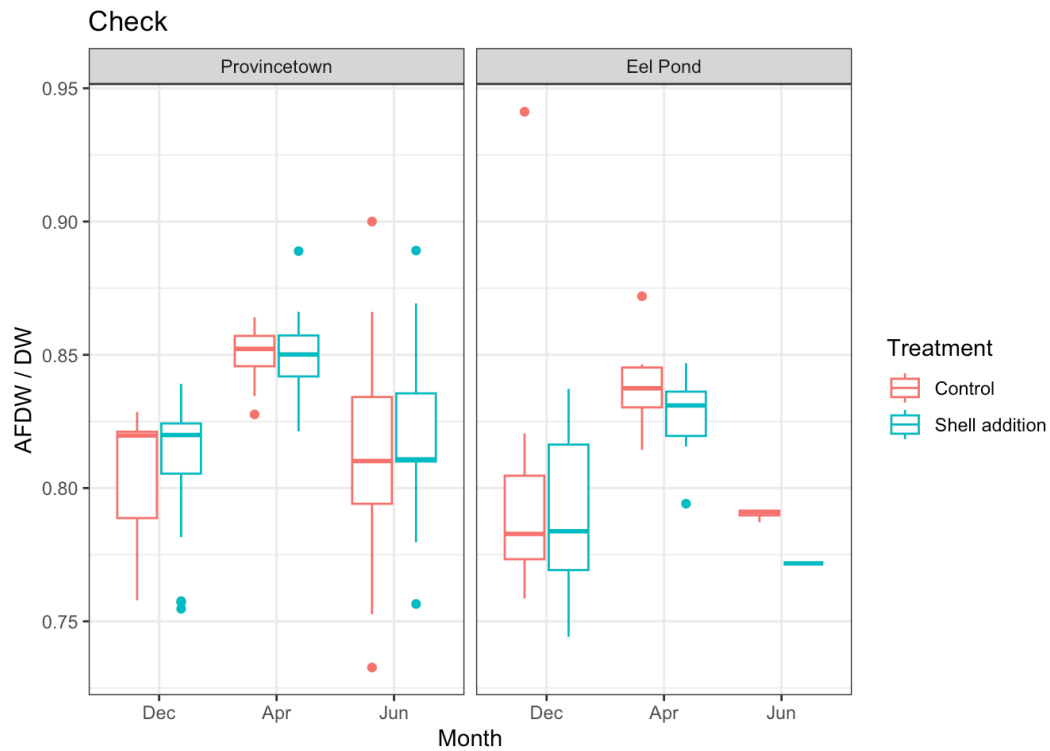
```
gg4 <- ggplot(data = growth, aes(x=as.factor(Collection.month),  
  geom_boxplot()+  
  xlab("Month") +  
  ylab("Height:Length allometric ratio")+  
  #ylim(0,9)+  
  scale_color_discrete(name="Treatment")+  
  ggtitle ('Allometry')+  
  facet_wrap(facets = "Site"))
```

gg4

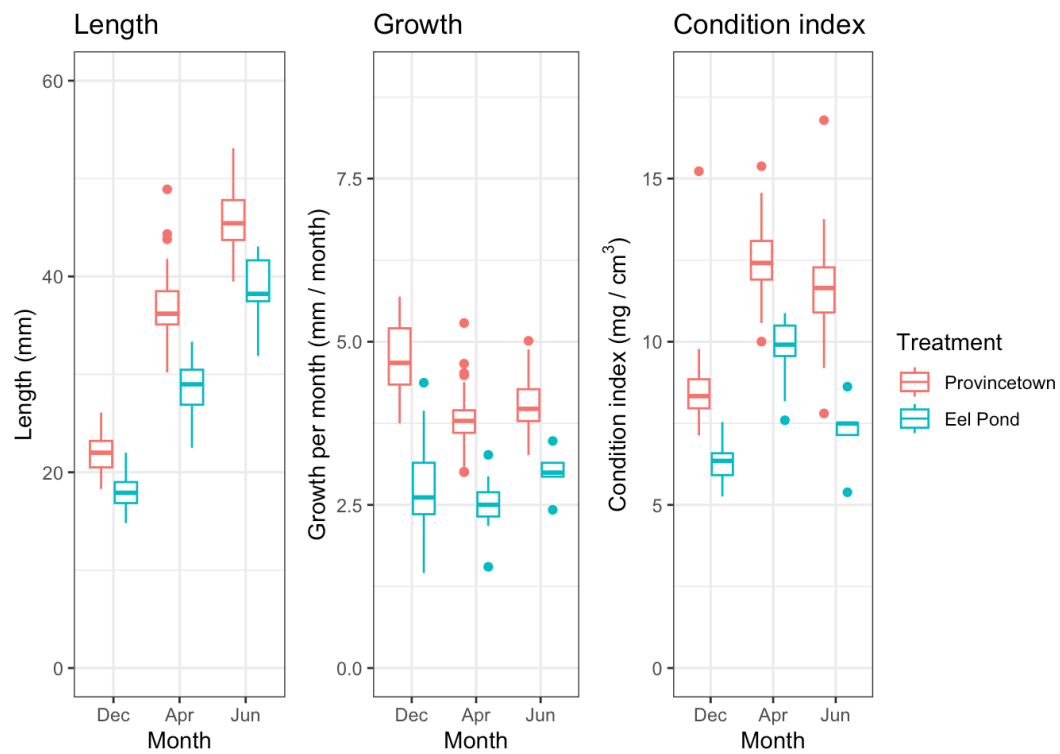


```
gg5 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("AFDW / DW")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Check')+
  facet_wrap(facets = "Site")
```

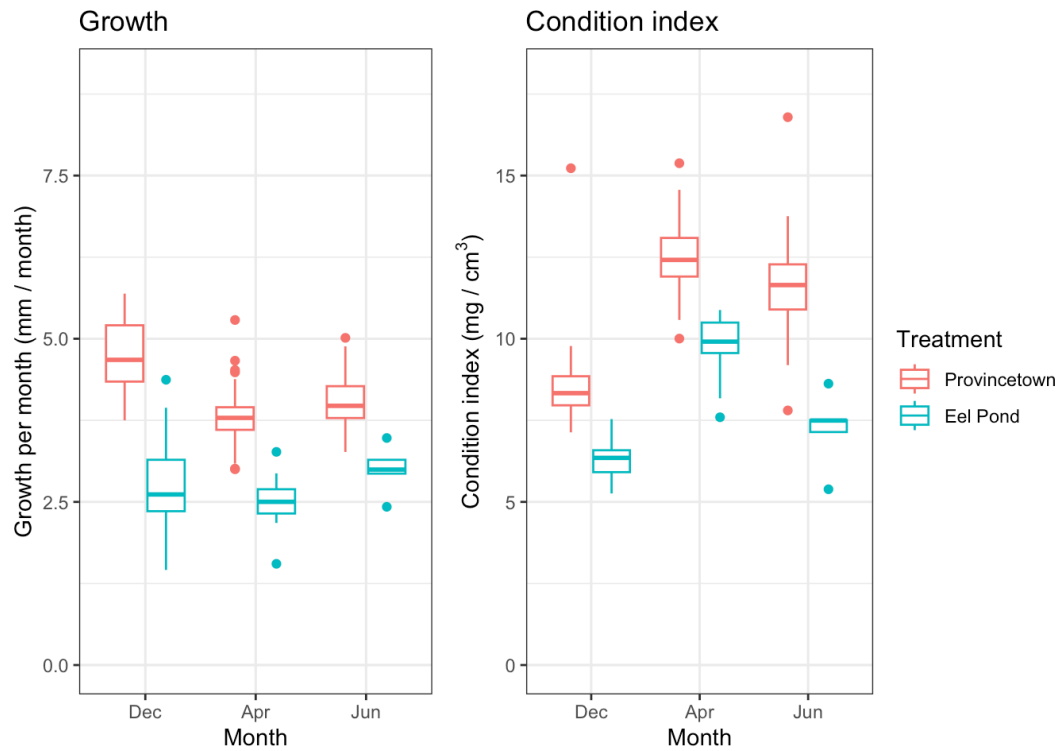
```
gg5
```



```
ggarrange(gg0,gg1,gg3, ncol=3, common.legend = TRUE, legend = "right")
```

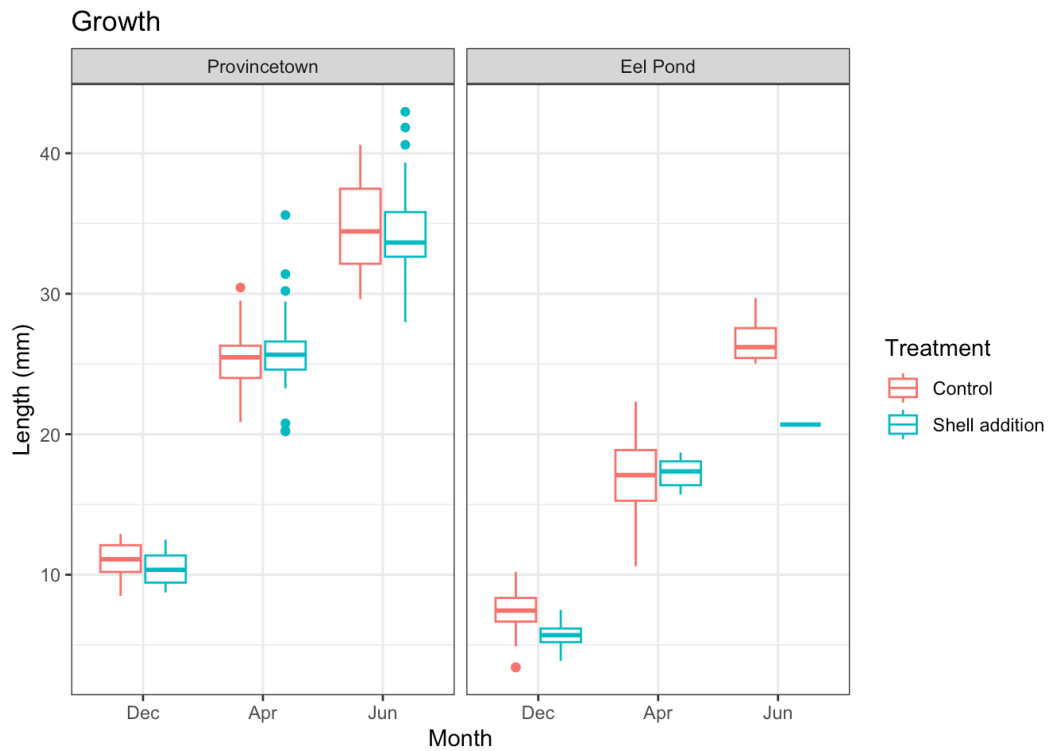


```
ggarrange(gg1,gg3, ncol=2, common.legend = TRUE, legend = "right")
```

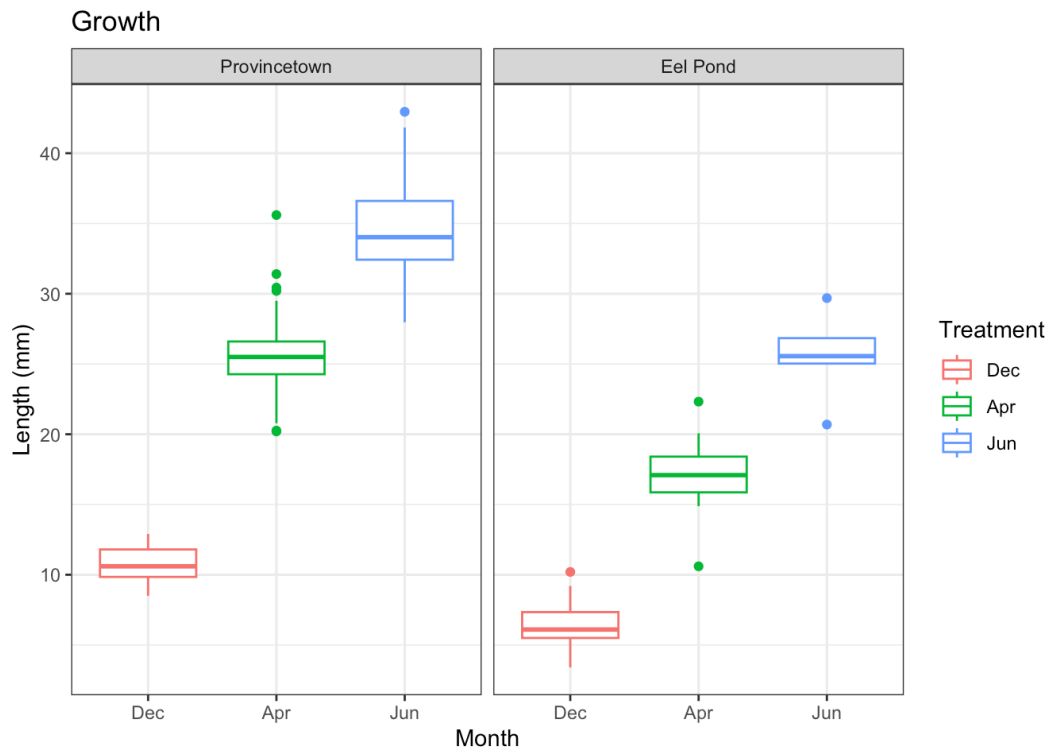


Initial and final lengths and weights for DEB model

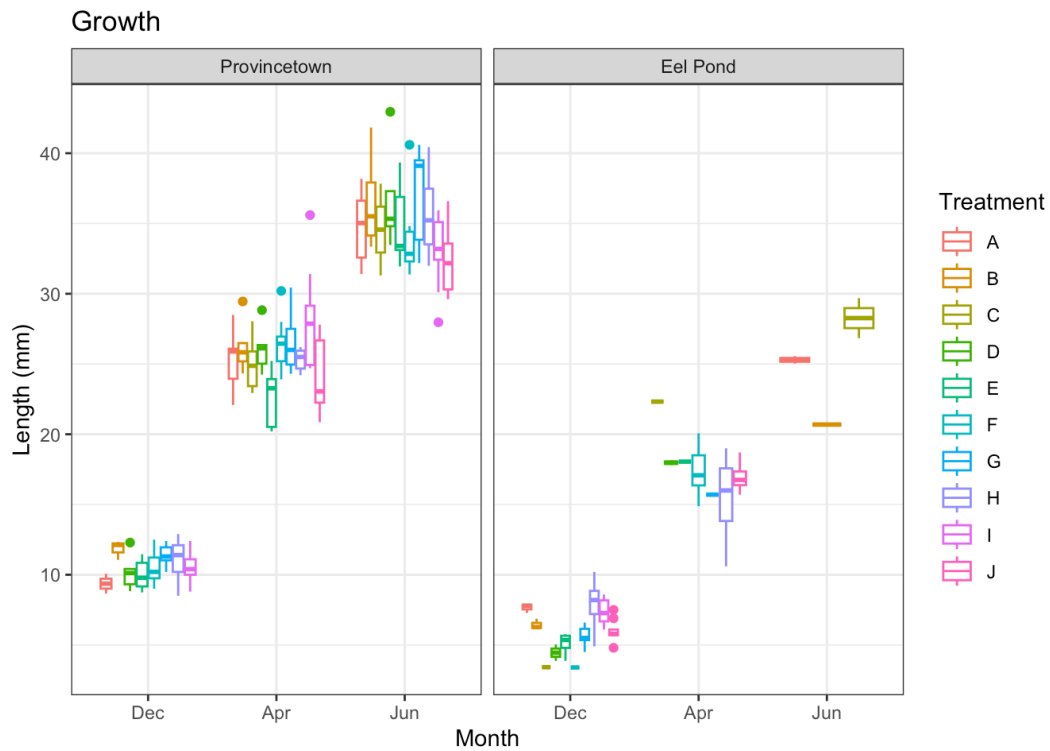
```
gg1 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(facets = "Site")
gg1
```



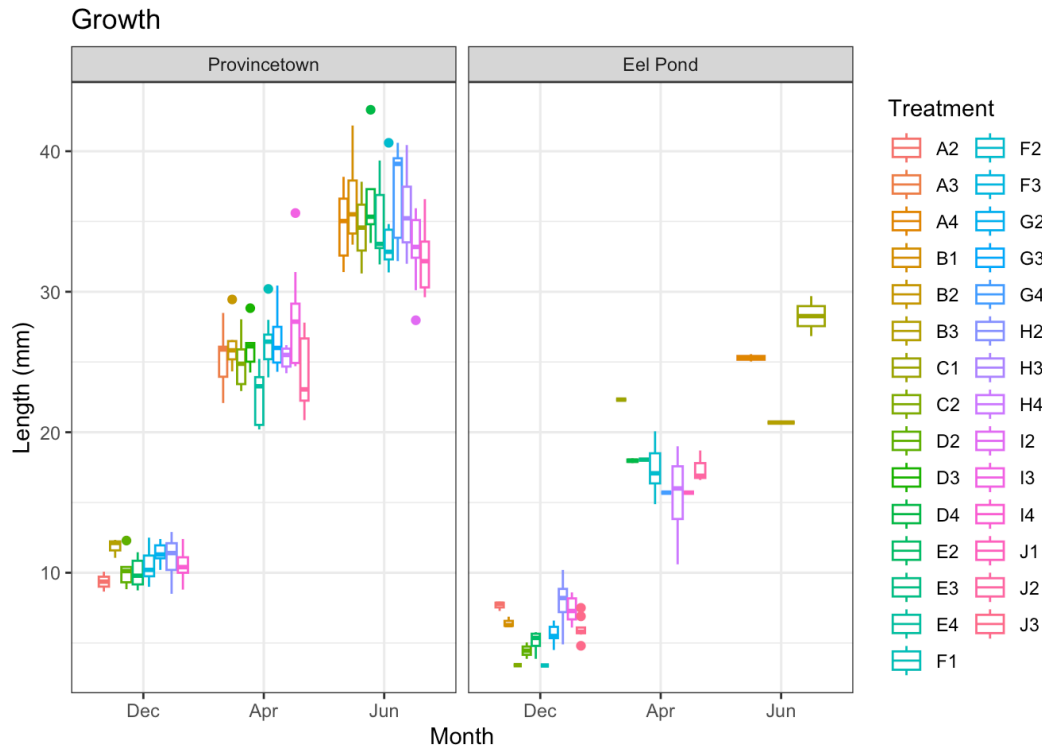
```
gg2 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(facets = "Site")
gg2
```



```
growth$row <- as.factor(substr(growth$Location_code,1,1))
gg3 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(facets = "Site")
gg3
```



```
gg4 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (mm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(facets = "Site")
gg4
```



```
growth$Start_len_mm
```

```
[1] 13.83000 12.84000 13.44000 12.54000 11.81000 11.11000
10.46000  9.92000
 [9]  9.81000 14.36000 11.44000 11.94000 10.58000  9.84000
10.04000  8.95000
[17] 14.10000 10.30000 10.68000  9.27000 14.24000 12.83000
12.10000 10.08000
[25] 10.07000 10.24000  9.69000  9.69000 13.98000 10.24000
 8.76000 14.83000
[33] 11.56000 11.96000 11.61000 10.86000  9.94000 10.27000
 9.54000 12.98000
[41] 12.69000 11.51000  9.48000  9.47000 12.87000 10.83000
10.55000  9.92000
[49] 10.05000  9.29000 10.23000 11.18000  9.80000  8.30000
12.15000 10.41000
[57] 11.23000 10.94000 10.96000 12.31000 11.26000 10.86000
10.47000  9.16000
[65]  9.97000  9.30000 12.13000 10.83000 10.52000  9.94000
10.88000 10.00000
[73]  9.03000 15.20000 16.10000 11.60000  9.40000 10.50000
10.80000  9.20000
[81]  9.70000 14.30000 12.10000 11.70000 11.30000  9.80000
 9.70000 14.30000
```



```

[89] 12.10000 12.20000 11.30000 11.70000 10.40000 10.00000
8.90000 13.30000
[97] 11.90000 11.40000 11.20000 10.80000 9.80000 13.90000
14.00000 11.10000
[105] 11.50000 10.00000 11.50000 10.80000 9.90000 9.80000
13.90000 14.00000
[113] 11.20000 11.00000 10.60000 10.30000 9.80000 14.60000
13.10000 11.30000
[121] 11.40000 11.50000 10.00000 9.90000 10.20000 8.70000
12.10000 12.00000
[129] 12.00000 10.60000 10.80000 10.30000 9.10000 9.50000
12.70000 12.30000
[137] 11.50000 10.50000 11.10000 11.20000 12.50000 12.00000
11.70000 11.40000
[145] 11.50000 10.80000 11.00000 11.30000 9.00000 13.30000
11.50000 12.40000
[153] 10.30000 10.20000 11.10000 9.60000 9.80000 14.70000
11.30000 11.20000
[161] 10.80000 10.80000 10.60000 10.20000 10.30000 9.40000
13.70000 11.90000
[169] 11.50000 11.70000 11.60000 10.60000 10.50000 9.80000
12.90000 13.10000
[177] 12.10000 11.90000 11.40000 10.30000 9.90000 11.20000
13.12000 10.91000
[185] 10.06000 17.50000 12.44000 10.52714 10.52714 10.52714
11.20000 11.96000
[193] 11.39000 11.03000 15.58000 13.36000 10.93000 11.73000
10.93000 13.53000
[201] 12.80000 11.03000 9.88000 8.86000 15.10000 15.70000
12.70000 11.50000
[209] 9.40000 10.60000 14.20000 13.30000 11.70000 12.30000
9.70000 11.10000
[217] 10.00000 13.90000 12.60000 13.20000 10.90000 11.60000
10.20000 11.80000
[225] 11.10000 11.90000 9.80000 10.90000 11.00000 14.50000
11.40000 9.60000
[233] 11.40000 11.44444 11.44444 13.00000 13.70000 12.00000
10.70000 13.50000
[241] 12.10000 11.50000 11.30000 10.20000 9.40000 10.10000
11.00000 11.50000

```

```

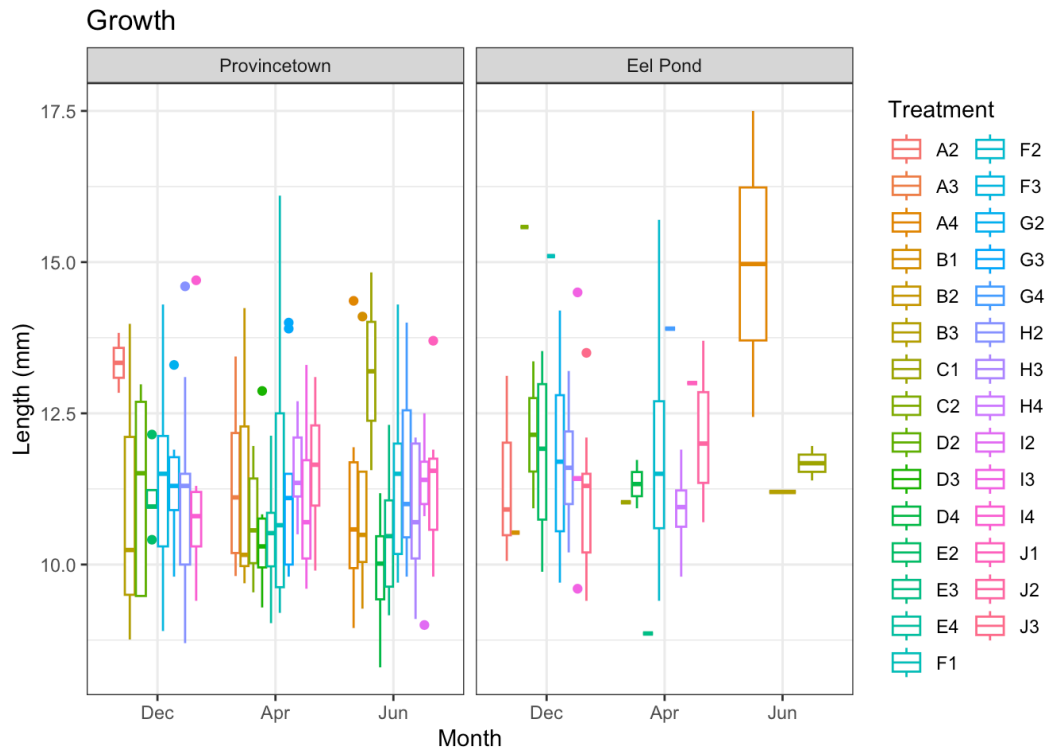
gg5 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +

```

```

ylab("Length (mm)")+
#ylim(0,9)+
scale_color_discrete(name="Treatment")+
ggtitle ('Growth')+
facet_wrap(facets = "Site")
gg5

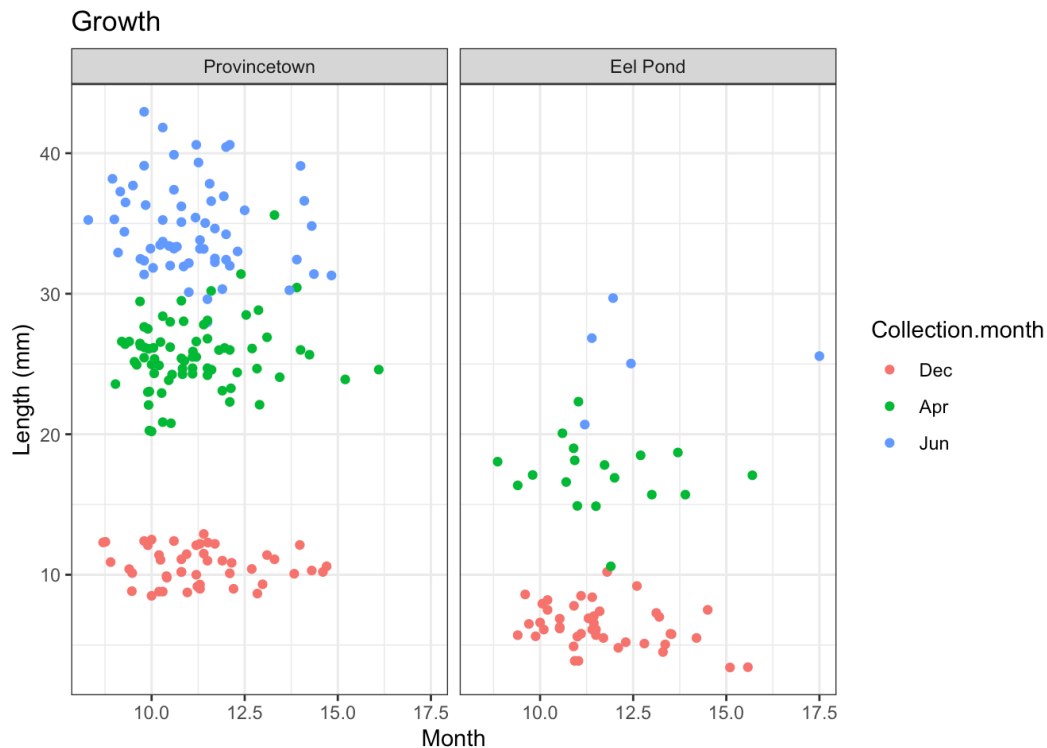
```



```

gg5 <- ggplot(data = growth, aes(x=Start_len_mm, y=len_tot, color=Treatment)) +
  geom_point() +
  xlab("Month") +
  ylab("Length (mm)") +
  #ylim(0,9)+
  scale_color_discrete(name="Collection.month") +
  ggtitle ('Growth') +
  facet_wrap(facets = "Site")
gg5

```



```
#So for each cage we want Site, month collected, start date, end date, and
str(growth)
```

```
'data.frame':  248 obs. of  51 variables:
 $ Start_date
: chr  "9/27/2022" "9/27/2022" "9/27/2022" "9/27/2022" ...
 $ Site
: Factor w/ 2 levels "Provincetown",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ Treatment
: Factor w/ 2 levels "Control","Shell addition": 1 1 1 1 1 1 1
1 1 1 ...
 $ Buried_Dec
: chr  "N" "N" "" "" ...
 $ Location_code
: chr  "A2" "A2" "A3" "A3" ...
 $ color.1
: chr  "R" "Y" "R" "Y" ...
 $ color.2
: chr  "" "" "" "" ...
 $ Start_len_mm
: num  13.8 12.8 13.4 12.5 11.8 ...
 $ Start_height_mm
: num  10.86 9.74 10.63 9.29 9.32 ...
```

```

$ Start_thickness_mm
: num  5.92 5.31 5.68 5.01 5.02 4.62 4.44 4.13 4.33 5.86 ...
$ Collection.month
: Factor w/ 3 levels "Dec","Apr","Jun": 1 1 2 2 2 2 2 2 2 3 ...
$ Collection1_date
: Date, format: "2022-12-04" "2022-12-04" ...
$ Elapsed_days
: num  68 68 202 202 202 202 202 202 202 257 ...
$ depth_cm
: chr  "4+" "4+" "S" "Deep" ...
$ color_collection
: chr  "R" "NO LABEL" "" "" ...
$ L_mm_extra
: num  24.1 21.6 NA NA NA ...
$ H_mm_extra
: num  19.3 17.1 NA NA NA ...
$ T_mm
: num  11.2 10 NA NA NA ...
$ Collection.notes
: chr  "" "" "" "" ...
$ Dissection.ID.label
: chr  "P125" "P126" "P51" "P.1" ...
$ Label.different.when.collected
: chr  "" "no label" "" "" ...
$ Biodeposition.label
: chr  "" "" "3" "" ...
$ Dead_or_missing
: chr  "N" "N" "N" "N" ...
$ Len
: num  23.9 21.5 37.5 41 37.8 ...
$ Height
: num  19.2 17.1 29.6 31.7 29.4 ...
$ Thickness
: num  11.2 10 NA 18.5 16.2 ...
$ Est..growth.by.height
: num  8.44 7.36 NA NA NA NA NA NA NA ...
$ Est.start.height.from.linear.function
: num  10.5 9.6 10.3 9.2 9.2 8.6 8.2 7.7 7.7 10.6 ...
$ Start_height.from.marking
: num  11 9.7 10.85 9.77 9.3 ...
$ Growth.increment.from.mark_height
: num  10.9 9.3 23.5 27.2 24.3 ...
$ Tin.only
: num  1.095 1.104 1.083 0.989 1.001 ...
$ Tin...gonad...somatic.tissue

```

```

: num  1.25 1.22 1.81 1.96 1.78 ...
$ Reweigh..if.necessary.
: num  NA NA NA NA NA NA NA NA NA NA ...
$ Ash.weight..tin...gonad...somatic.tissue.
: num  1.18 1.15 1.19 1.15 1.11 ...
$ DW
: num  0.152 0.115 0.727 0.973 0.783 ...
$ AFDW
: num  0.1246 0.0943 0.6162 0.8117 0.6755 ...
$ Ratio.for.samples.with.DW.0.01g
: chr  "46%" "58%" "85%" "83%" ...
$
Corrected.AFDW.using.an.average.of.82...Used.for..20.samples.wi
th...organic...7.which.was.identified.to.caused.by.incomplete..
anoxic..muffle.furnace.issues.: num  0.1246 0.0943 0.6162
0.8117 0.6755 ...
$ Notes
: chr  "" "Most likely Y (2nd of color series) given start
height" "" "" ...
$ X..gonad
: chr  "" "" "" "" ...
$ X..digestive
: chr  "" "" "" "" ...
$ Shell.weight
: num  NA NA NA NA NA ...
$ Start.height.function.params
: num  0.839 1.389 NA NA NA ...
$ AliveOrDead
: chr  "Alive" "Alive" "Alive" "Alive" ...
$ CI
: num  9.13 9.49 11.68 11.75 12.51 ...
$ len_tot
: num  10.07 8.66 24.06 28.49 25.99 ...
$ len_per_day
: num  0.148 0.127 0.119 0.141 0.129 ...
$ height_tot
: num  8.34 7.36 18.97 22.45 20.08 ...
$ height_per_day
: num  0.1226 0.1082 0.0939 0.1111 0.0994 ...
$ ratio.LH
: num  0.828 0.85 0.788 0.788 0.773 ...
$ row
: Factor w/ 10 levels "A","B","C","D",...: 1 1 1 1 1 1 1 1 1 1
...

```

```

growth$Start_date <- as.Date(strptime(growth$Start_date, format

df_summary <- growth %>%
  group_by(Collection.month,as.factor(Location_code),Site) %>%
  filter(AliveOrDead=="Alive") %>%
  filter(Start_len_mm<=13&Start_len_mm>=10) %>%
  summarise(
    Li = round(mean(Start_len_mm, na.rm = TRUE),1),

    Lf = round(mean(Len, na.rm = TRUE),1),

    Elapsed_days = round(mean(Elapsed_days, na.rm = TRUE),1),

    Start_date = unique(Start_date, na.rm = TRUE),

    End_date = unique(Collection1_date, na.rm = TRUE),

    Ave_growth = round(mean(Len-Start_len_mm, na.rm = TRUE),1)

  )

```

`summarise()` has grouped output by 'Collection.month', 'as.factor(Location_code)'. You can override using the `.groups` argument.

```

# Perc_SE = round(sd(X..organic*100, na.rm = TRUE) ,
#                  sqrt(sum(!is.na(X..organic))),0),

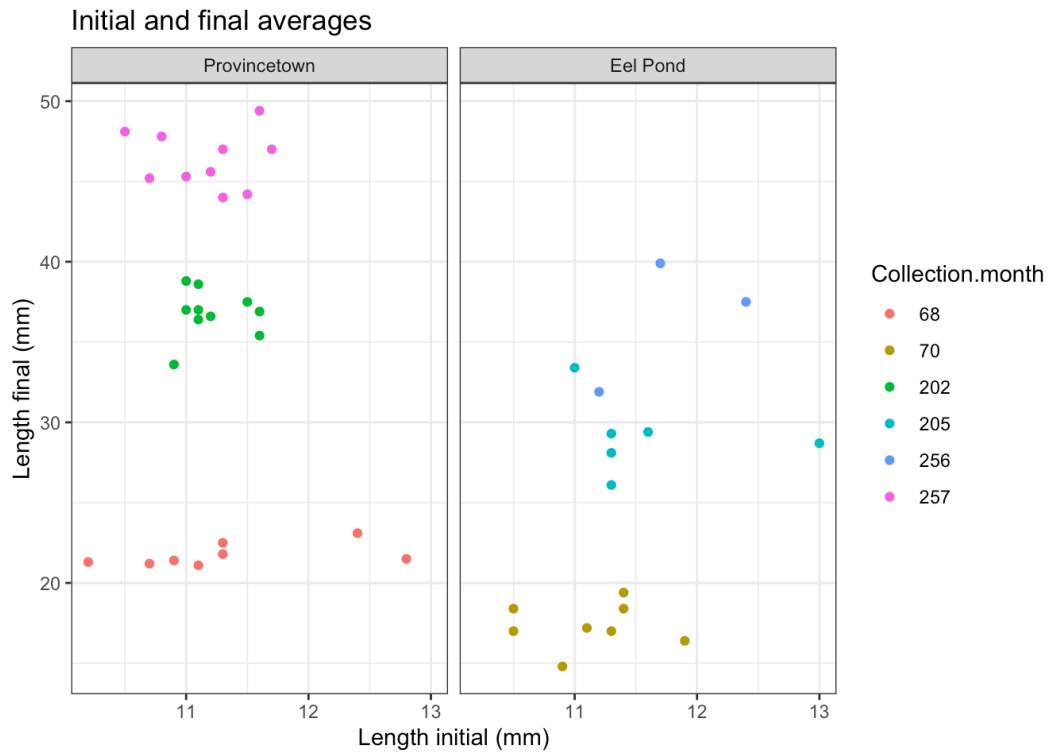
# Remove negative growths by adjusting initial lengths to match
# df_summary$Li[(df_summary$Lf-df_summary$Li)<0]<- df_summary$Lf

#OK a little less weird... final lengths are just set to the same
df_summary$Lf[(df_summary$Lf-df_summary$Li)<0]<- df_summary$Li

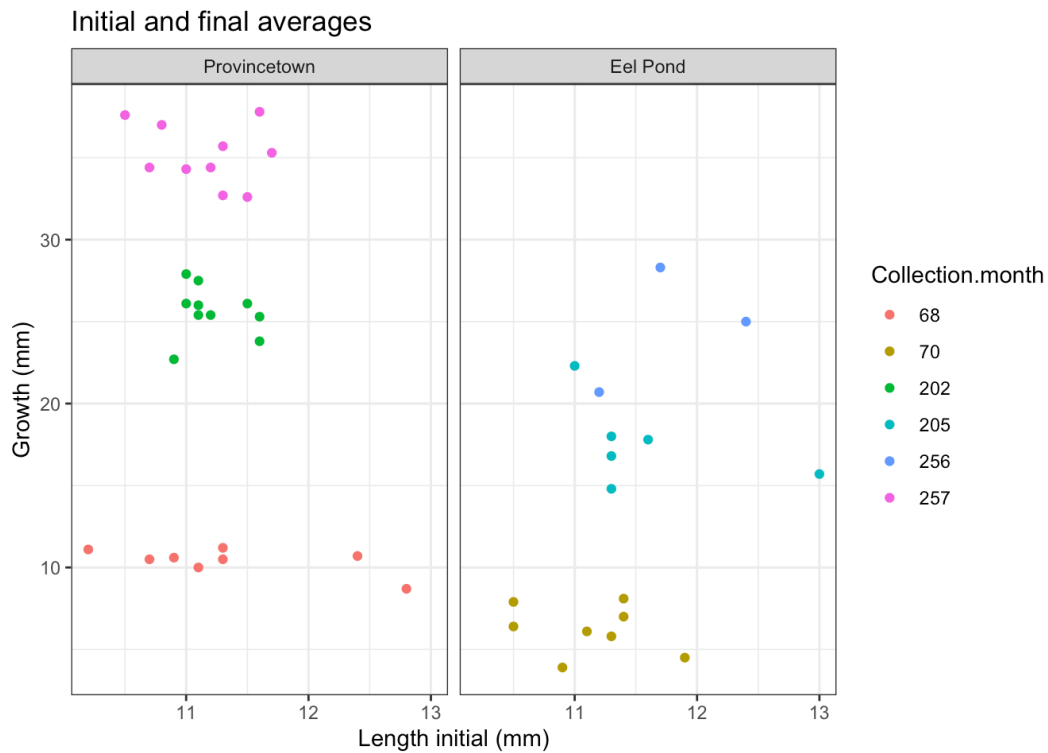
gg5 <- ggplot(data = df_summary, aes(x=Li, y=Lf, color = as.factor(Collection.month))) +
  geom_point() +
  xlab("Length initial (mm)") +
  ylab("Length final (mm)") +
  ylim(0,9) +
  scale_color_discrete(name="Collection.month") +

```

```
ggtitle ('Initial and final averages')+
facet_wrap(facets = "Site")
gg5
```

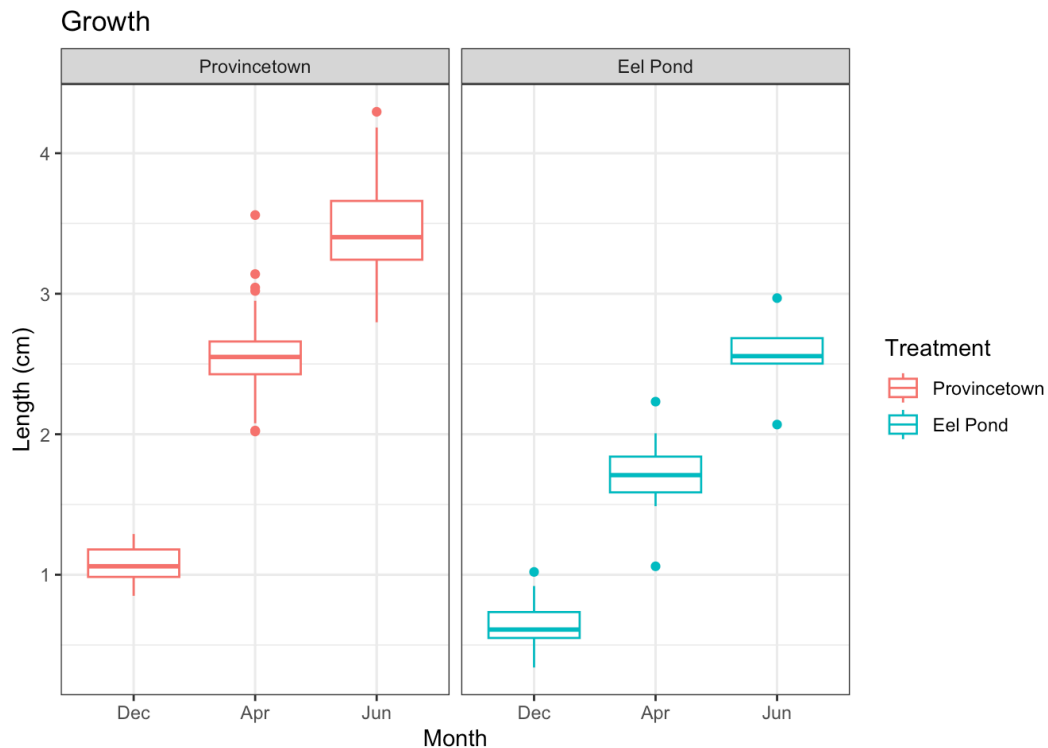


```
gg5 <- ggplot(data = df_summary, aes(x=Li, y=Ave_growth, color =
  geom_point()+
  xlab("Length initial (mm)") +
  ylab("Growth (mm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Collection.month")+
  ggtitle ('Initial and final averages')+
  facet_wrap(facets = "Site")
gg5
```



```
# write.csv(df_summary, file="~/GitHub/EAD-ASEB-Ssolidissima-0A/
```

```
gg2 <- ggplot(data = growth, aes(x=as.factor(Collection.month),
  geom_boxplot()+
  xlab("Month") +
  ylab("Length (cm)")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(~Site)
gg2
```

```
growth$Collection1_date
```

```
[1] "2022-12-04" "2022-12-04" "2023-04-17" "2023-04-17"
"2023-04-17"
[6] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-06-11"
[11] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[16] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[21] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[26] "2023-04-17" "2023-04-17" "2023-04-17" "2022-12-04"
"2022-12-04"
[31] "2022-12-04" "2023-06-11" "2023-06-11" "2023-04-17"
"2023-04-17"
[36] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2022-12-04"
[41] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2023-04-17"
[46] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[51] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2022-12-04"
```

[56] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2023-06-11"
[61] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[66] "2023-06-11" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[71] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[76] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[81] "2023-04-17" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[86] "2023-06-11" "2023-06-11" "2022-12-04" "2022-12-04"
"2022-12-04"
[91] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2022-12-04"
[96] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2022-12-04"
[101] "2022-12-04" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[106] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[111] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[116] "2023-06-11" "2023-06-11" "2022-12-04" "2022-12-04"
"2022-12-04"
[121] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2022-12-04"
[126] "2022-12-04" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[131] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-04-17"
[136] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[141] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-06-11"
[146] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-04-17"
[151] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[156] "2023-04-17" "2023-04-17" "2022-12-04" "2022-12-04"
"2022-12-04"
[161] "2022-12-04" "2022-12-04" "2022-12-04" "2022-12-04"
"2022-12-04"
[166] "2022-12-04" "2023-06-11" "2023-06-11" "2023-06-11"

```

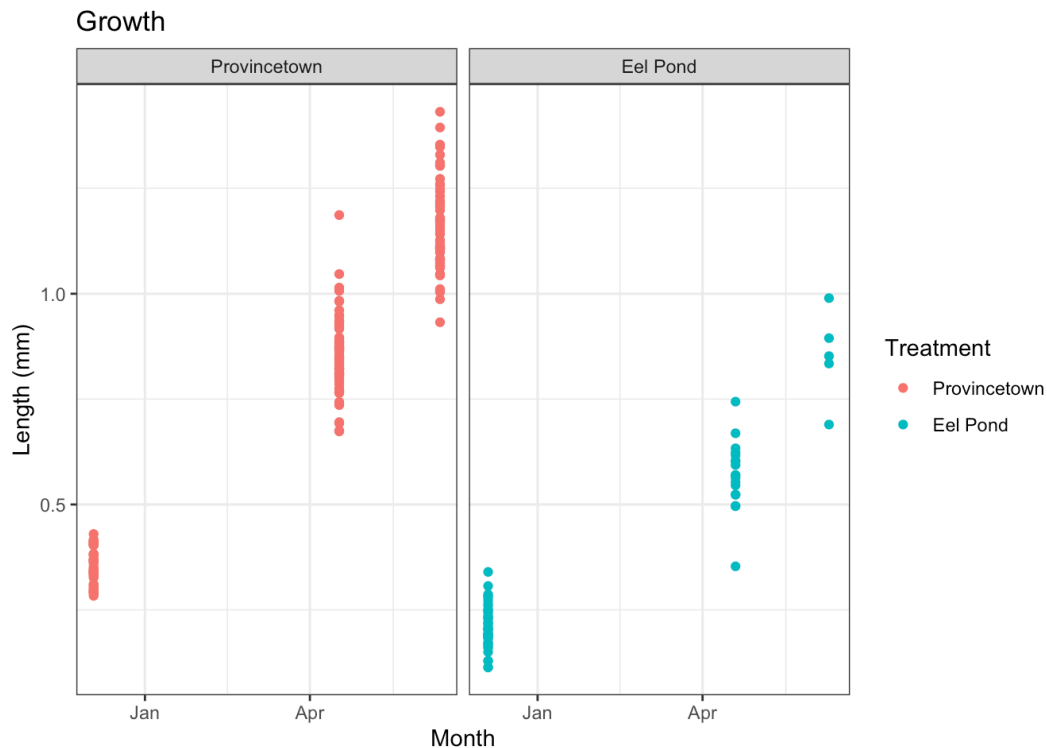
"2023-06-11"
[171] "2023-06-11" "2023-06-11" "2023-06-11" "2023-06-11"
"2023-04-17"
[176] "2023-04-17" "2023-04-17" "2023-04-17" "2023-04-17"
"2023-04-17"
[181] "2023-04-17" "2023-04-17" "2022-12-05" "2022-12-05"
"2022-12-05"
[186] "2023-06-09" "2023-06-09" "2022-12-05" "2022-12-05"
"2022-12-05"
[191] "2023-06-09" "2023-06-09" "2023-06-09" "2023-04-19"
"2022-12-05"
[196] "2022-12-05" "2022-12-05" "2023-04-19" "2023-04-19"
"2022-12-05"
[201] "2022-12-05" "2022-12-05" "2022-12-05" "2023-04-19"
"2022-12-05"
[206] "2023-04-19" "2023-04-19" "2023-04-19" "2023-04-19"
"2023-04-19"
[211] "2022-12-05" "2022-12-05" "2022-12-05" "2022-12-05"
"2022-12-05"
[216] "2022-12-05" "2022-12-05" "2023-04-19" "2022-12-05"
"2022-12-05"
[221] "2022-12-05" "2022-12-05" "2022-12-05" "2022-12-05"
"2022-12-05"
[226] "2023-04-19" "2023-04-19" "2023-04-19" "2023-04-19"
"2022-12-05"
[231] "2022-12-05" "2022-12-05" "2022-12-05" "2022-12-05"
"2022-12-05"
[236] "2023-04-19" "2023-04-19" "2023-04-19" "2023-04-19"
"2022-12-05"
[241] "2022-12-05" "2022-12-05" "2022-12-05" "2022-12-05"
"2022-12-05"
[246] "2022-12-05" "2022-12-05" "2022-12-05"

```

```

gg2 <- ggplot(data = growth, aes(x=Collection1_date, y=len_tot/
  geom_point()+
  xlab("Month") +
  ylab("Length (mm)") +
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(~Site)
gg2

```



Shape coefficient parameter

```
str(growth)
```

```
'data.frame':  248 obs. of  51 variables:
 $ Start_date
: Date, format: "2022-09-27" "2022-09-27" ...
 $ Site
: Factor w/ 2 levels "Provincetown",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ Treatment
: Factor w/ 2 levels "Control","Shell addition": 1 1 1 1 1 1 1
1 1 1 ...
 $ Buried_Dec
: chr  "N" "N" "" "" ...
 $ Location_code
: chr  "A2" "A2" "A3" "A3" ...
 $ color.1
: chr  "R" "Y" "R" "Y" ...
 $ color.2
: chr  "" "" "" "" ...
 $ Start_len_mm
: num  13.8 12.8 13.4 12.5 11.8 ...
```

```

$ Start_height_mm
: num  10.86 9.74 10.63 9.29 9.32 ...
$ Start_thickness_mm
: num  5.92 5.31 5.68 5.01 5.02 4.62 4.44 4.13 4.33 5.86 ...
$ Collection.month
: Factor w/ 3 levels "Dec","Apr","Jun": 1 1 2 2 2 2 2 2 2 3 ...
$ Collection1_date
: Date, format: "2022-12-04" "2022-12-04" ...
$ Elapsed_days
: num  68 68 202 202 202 202 202 202 202 257 ...
$ depth_cm
: chr  "4+" "4+" "S" "Deep" ...
$ color_collection
: chr  "R" "NO LABEL" "" "" ...
$ L_mm_extra
: num  24.1 21.6 NA NA NA ...
$ H_mm_extra
: num  19.3 17.1 NA NA NA ...
$ T_mm
: num  11.2 10 NA NA NA ...
$ Collection.notes
: chr  "" "" "" "" ...
$ Dissection.ID.label
: chr  "P125" "P126" "P51" "P.1" ...
$ Label.different.when.collected
: chr  "" "no label" "" "" ...
$ Biodeposition.label
: chr  "" "" "3" "" ...
$ Dead_or_missing
: chr  "N" "N" "N" "N" ...
$ Len
: num  23.9 21.5 37.5 41 37.8 ...
$ Height
: num  19.2 17.1 29.6 31.7 29.4 ...
$ Thickness
: num  11.2 10 NA 18.5 16.2 ...
$ Est..growth.by.height
: num  8.44 7.36 NA NA NA NA NA NA NA ...
$ Est.start.height.from.linear.function
: num  10.5 9.6 10.3 9.2 9.2 8.6 8.2 7.7 7.7 10.6 ...
$ Start_height.from.marking
: num  11 9.7 10.85 9.77 9.3 ...
$ Growth.increment.from.mark_height
: num  10.9 9.3 23.5 27.2 24.3 ...
$ Tin.only

```

```

: num  1.095 1.104 1.083 0.989 1.001 ...
$ Tin...gonad...somatic.tissue
: num  1.25 1.22 1.81 1.96 1.78 ...
$ Reweigh..if.necessary.
: num  NA NA NA NA NA NA NA NA NA ...
$ Ash.weight..tin...gonad...somatic.tissue.
: num  1.18 1.15 1.19 1.15 1.11 ...
$ DW
: num  0.152 0.115 0.727 0.973 0.783 ...
$ AFDW
: num  0.1246 0.0943 0.6162 0.8117 0.6755 ...
$ Ratio.for.samples.with.DW.0.01g
: chr  "46%" "58%" "85%" "83%" ...
$
Corrected.AFDW.using.an.average.of.82...Used.for..20.samples.wi
th...organic...7.which.was.identified.to.caused.by.incomplete..
anoxic..muffle.furnace.issues.: num  0.1246 0.0943 0.6162
0.8117 0.6755 ...
$ Notes
: chr  "" "Most likely Y (2nd of color series) given start
height" "" "" ...
$ X..gonad
: chr  "" "" "" "" ...
$ X..digestive
: chr  "" "" "" "" ...
$ Shell.weight
: num  NA NA NA NA NA ...
$ Start.height.function.params
: num  0.839 1.389 NA NA NA ...
$ AliveOrDead
: chr  "Alive" "Alive" "Alive" "Alive" ...
$ CI
: num  9.13 9.49 11.68 11.75 12.51 ...
$ len_tot
: num  10.07 8.66 24.06 28.49 25.99 ...
$ len_per_day
: num  0.148 0.127 0.119 0.141 0.129 ...
$ height_tot
: num  8.34 7.36 18.97 22.45 20.08 ...
$ height_per_day
: num  0.1226 0.1082 0.0939 0.1111 0.0994 ...
$ ratio.LH
: num  0.828 0.85 0.788 0.788 0.773 ...
$ row
: Factor w/ 10 levels "A","B","C","D",...: 1 1 1 1 1 1 1 1 1 1

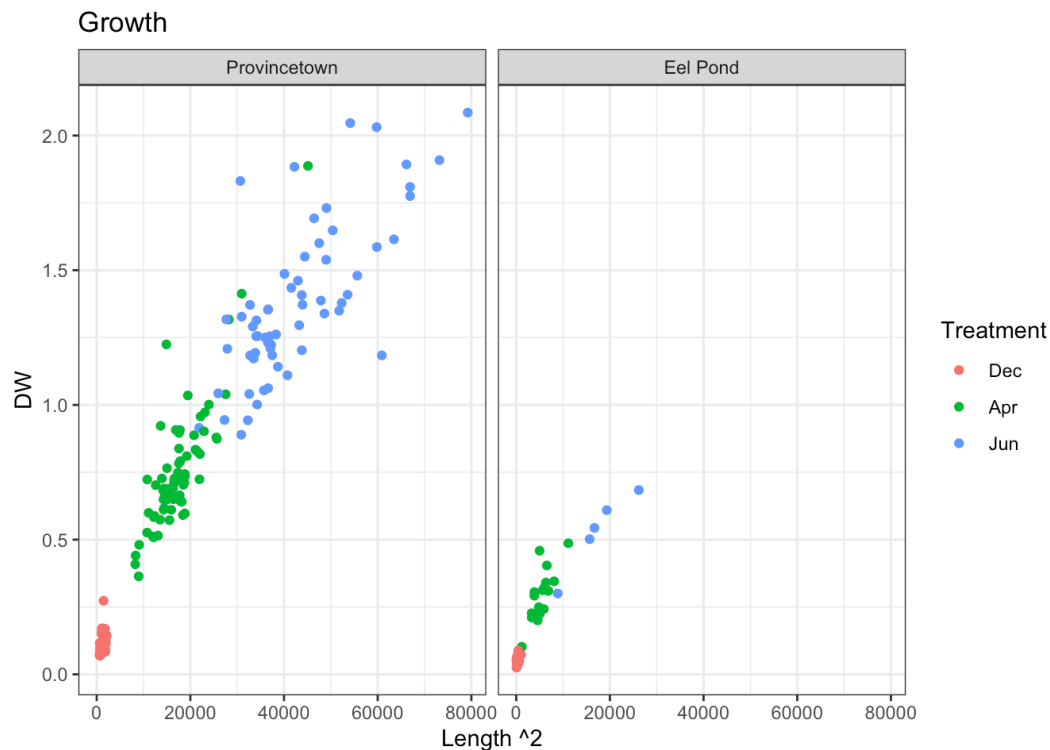
```

...

```

gg5 <- ggplot(data = growth, aes(x=len_tot^3, y=DW, color = Col
  geom_point()+
  xlab("Length ^2") +
  ylab("DW")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')+
  facet_wrap(facets = "Site")
gg5

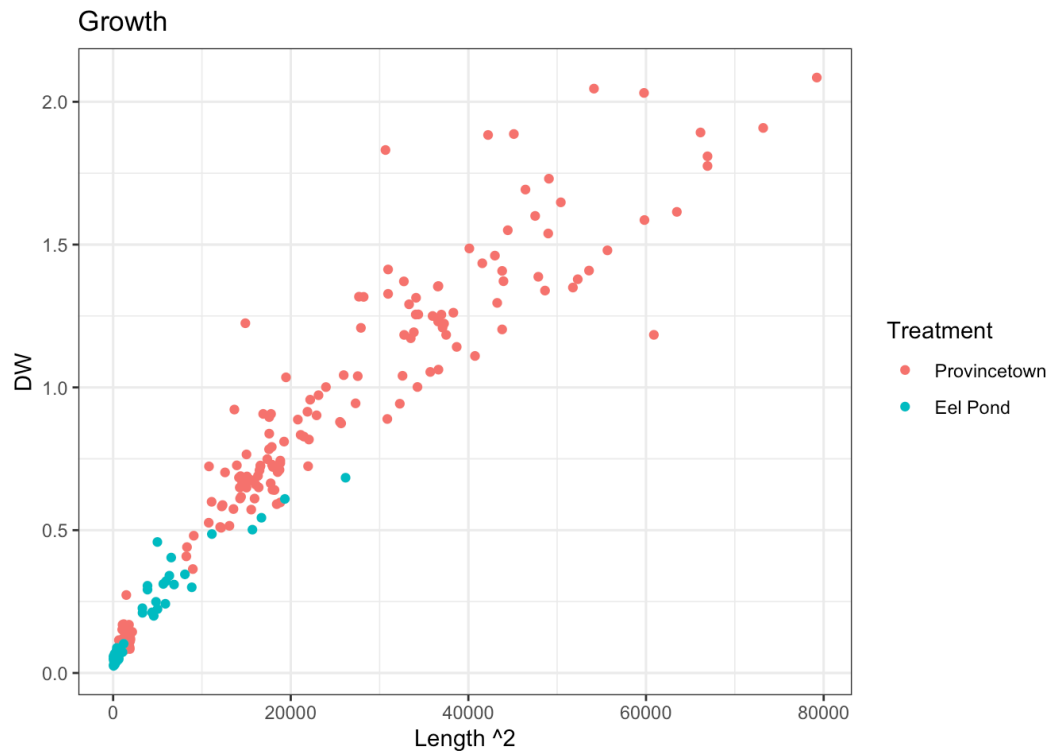
```



```

gg5 <- ggplot(data = growth, aes(x=len_tot^3, y=DW, color = Site
  geom_point()+
  xlab("Length ^2") +
  ylab("DW")+
  #ylim(0,9)+
  scale_color_discrete(name="Treatment")+
  ggtitle ('Growth')#+
  #facet_wrap(facets = "Site")
gg5

```



```
nls(data = growth, DW~(shape*len_tot/10)^3,
     start = list(shape = .5))
```

Nonlinear regression model

model: $DW \sim (\text{shape} * \text{len_tot}/10)^3$

data: growth

shape

0.3209

residual sum-of-squares: 8.765

Number of iterations to convergence: 4

Achieved convergence tolerance: 4.771e-06

```
# param <- NA
# param$shape <- 0.3209
```

Survival

```
#Summer
if(reporting_period == "summer"){
  growth_summer$Collection.month[growth_summer$Collection.month==
```



```

growth <- growth_summer

growth$Site <- factor(growth$Site, levels = c("Ptown", "Eel_Pond", "Dennis"))
levels(growth$Site) <- c("Prov", "Eel Pond", "Dennis")
growth$Collection.month <- factor(growth$Collection.month, levels = c("Jul", "Aug", "Sep"))
levels(growth$Collection.month) <- c("Jul", "Aug", "Sep")

library(dplyr)

live_count <- growth %>%
  group_by(Site, Collection.month, Treatment) %>%
  summarise(live = sum(AliveOrDead == 'L', na.rm = TRUE),
            dead = sum(AliveOrDead == 'D', na.rm = TRUE))

gg1 <- ggplot(data = live_count, aes(x = Collection.month, y = live)) +
  geom_line(aes(linetype = Treatment)) +
  geom_point(aes(shape=Treatment)) +
  ylim(0,1) +
  ylab("Proportion surviving (unitless)") +
  xlab("Collection month") +
  scale_color_brewer(palette="Set1")
gg1

str(growth)

df_summary <- growth %>%
  group_by(Collection.month, Location_code, Site, Treatment) %>%
  #filter(AliveOrDead=="Alive") %>%
  #filter(Start_len_mm<=13&Start_len_mm>=10) %>%
  summarise(live = sum(AliveOrDead == 'L', na.rm = TRUE), n = n())

df_summary$prop <- df_summary$live / df_summary$n

#Nope this is how I analyze growth
# m1 <- lme(data = df_summary, prop ~ Site + Treatment * Collection.month)
# summary(m1)
#
# m1 <- lmer(data = df_summary, prop ~ Site * Treatment * Collection.month)
# m2 <- lmer(data = df_summary, prop ~ Site + Treatment + Collection.month)
# AICc(m1, m2)

m1 <- lm(data = df_summary, prop ~ Site + Treatment * Collection.month)
summary(m1)

```

```

gg1 <- ggplot(data = df_summary, aes(x = Collection.month, y = 
  #geom_line(aes(linetype = Treatment))+
  #geom_point(aes(shape=Treatment))+
  geom_boxplot()+
  ylim(0,1)+
  ylab("Proportion surviving (unitless))+
  xlab("Collection month")+
  scale_color_brewer(palette="Set1")+
  scale_color_discrete(name="Treatment")+
  facet_wrap(~Site)
gg1
}

```

```

#Fall through spring
if(reporting_period == "fall_spring"){
  growth <- growth_fall_spring

#growth$Site <- factor(growth$Site, levels = c("Ptown", "Eel Pond"))
#levels(growth$Site) <- c("Prov", "Eel Pond")
levels(growth$Collection.month) <- c("Dec", "Apr", "Jun")

growth$AliveOrDead[growth$Dead_or_missing=="N"]<-"L"
growth$AliveOrDead[growth$Dead_or_missing=="Y"]<-"D"

live_count <- growth %>%
  group_by(Site, Collection.month, Treatment) %>%
  summarise(live = sum(AliveOrDead == 'L', na.rm = TRUE),
            dead = sum(AliveOrDead == 'D', na.rm = TRUE))
live_count <- live_count[live_count$Treatment!="Outside cage",]

gg2 <- ggplot(data = live_count, aes(x = Collection.month, y = 
  geom_line(aes(linetype = Treatment))+
  geom_point(aes(shape=Treatment))+
  ylim(0,1)+
  ylab("Proportion surviving (unitless))+
  xlab("Collection month")+
  scale_color_brewer(palette="Set1")
gg2

ggarrange(gg1,gg2,ncol=2, common.legend = TRUE, legend = "right"

```

```

df_summary <- growth %>%
  group_by(Collection.month, Location_code, Site, Treatment) %>%
  #filter(AliveOrDead=="Alive") %>%
  #filter(Start_len_mm<=13&Start_len_mm>=10) %>%
  summarise(live = sum(AliveOrDead == 'L', na.rm = TRUE), n = n())

df_summary$prop <- df_summary$live / df_summary$n
df_summary <- df_summary[df_summary$Treatment!="Outside cage",]

#Nope this is how I analyze growth
# m1 <- lme(data = df_summary, prop ~ Site + Treatment * Collection.month)
# summary(m1)
#
# m1 <- lmer(data = df_summary, prop ~ Site * Treatment * Collection.month)
# m2 <- lmer(data = df_summary, prop ~ Site + Treatment + Collection.month)
# AICc(m1, m2)

m1 <- lm(data = df_summary, prop ~ Site + Treatment * Collection.month)
summary(m1)

gg2 <- ggplot(data = df_summary, aes(x = Collection.month, y = prop))
  #geom_line(aes(linetype = Treatment))+
  #geom_point(aes(shape=Treatment))+
  geom_boxplot()+
  ylim(0,1)+
  ylab("Proportion surviving (unitless)")+
  xlab("Collection month")+
  scale_color_brewer(palette="Set1")+
  scale_color_discrete(name="Treatment")+
  facet_wrap(~Site)
gg2

# I need to include missing clams as dead clams or else if we don't
}

```

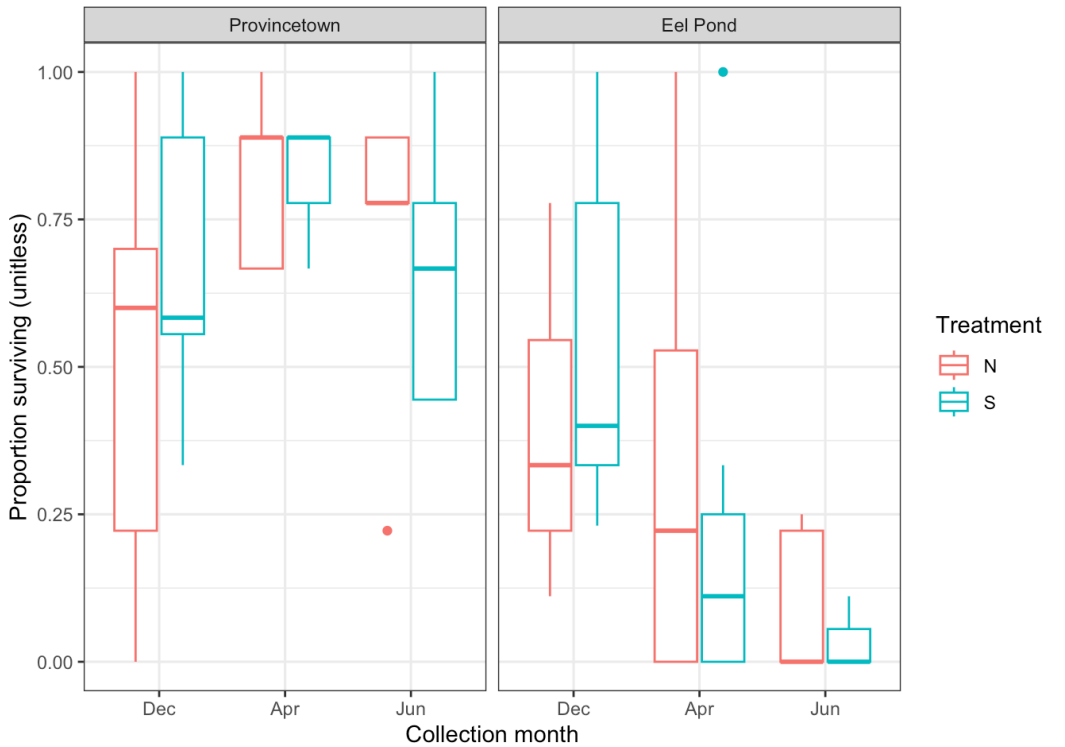
`summarise()` has grouped output by 'Site', 'Collection.month'.

You can

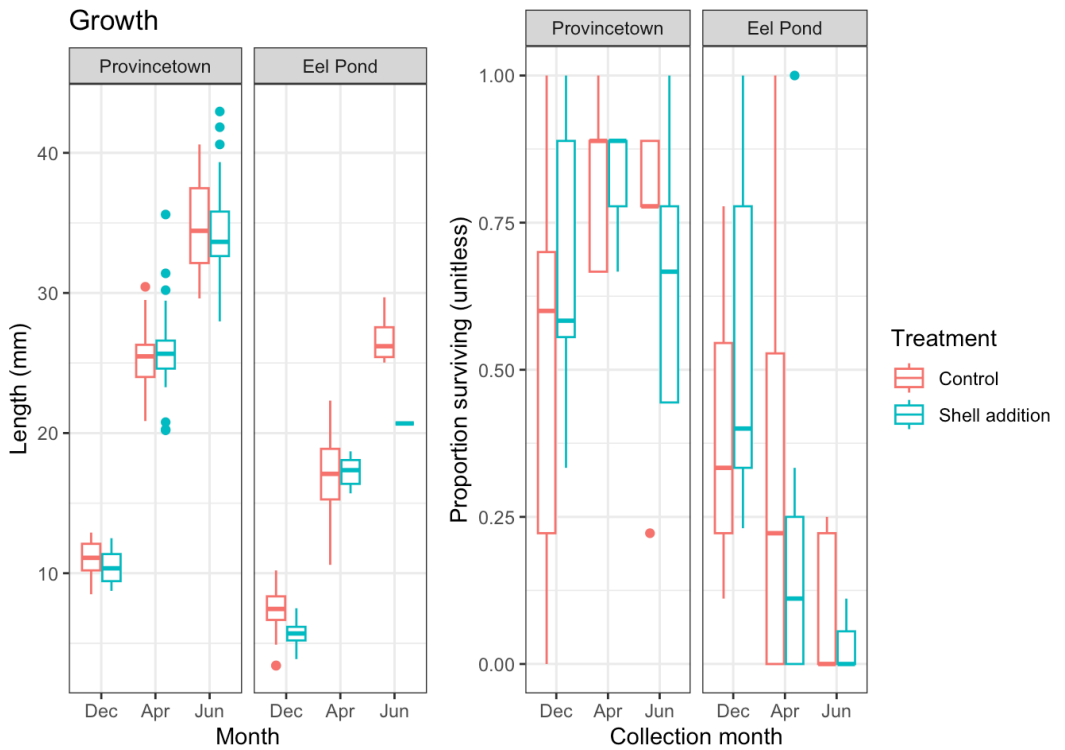
override using the `.groups` argument.

Scale for colour is already present. Adding another scale for colour, which

will replace the existing scale.



```
ggarrange(gg1,gg2, ncol=2, common.legend = TRUE, legend = "right")
```



#----- Plot for proposal

```

### Pool treatments
# # gg1 <- ggplot(data = growth_dec, aes(x=Site, y=len_tot/Elap:
# #   geom_boxplot()+
# #   xlab("Site") +
# #   ylab("Growth (mm/day)")+
# #   ylim(0,9/30)+
# #   #scale_color_discrete(name="Shell hash addition")+
# #   ggtitle ('Change in length Sep - Dec')
# # gg1
# # str(growth_dec)
# mod_growth_full <- lme(height_tot~Site+Start_len_mm+Start_len:
#                               random = ~1|Location_code, data = grow:
# summary(mod_growth_full)
# M_int<-update(mod_growth_full, ~. - Start_len_mm:Site)
# M2 <- update(M_int, ~. - Start_len_mm)
# summary(M2)
#
# (P <- mean(growth$len_per_day[growth$Site=="Ptown"]))
# (E <- mean(growth$len_per_day[growth$Site=="Eel Pond"]))
# E/P
# (P-E)/E #Overall Provincetown clam growth rate was 50% higher
# P/E
#
# (P <- mean(growth$CI[growth$Site=="Ptown"]))
# (E <- mean(growth$CI[growth$Site=="Eel Pond"]))
# E/P
# (P-E)/E #Overall Provincetown clam growth rate was 50% higher
# P/E
#
# (P.dec <- mean(growth$CI[growth$Site=="Ptown"&growth$Collectio
# (P.apr <- mean(growth$CI[growth$Site=="Ptown"&growth$Collectio
# (P.jun <- mean(growth$CI[growth$Site=="Ptown"&growth$Collectio
#
# P.apr / P.dec
#
# (E.dec <- mean(growth$CI[growth$Site=="Eel Pond"&growth$Collec
# (E.apr <- mean(growth$CI[growth$Site=="Eel Pond"&growth$Collec
# E.apr /E.dec
#
#
# summary <- growth_dec %>%
#   group_by(Site) %>%
#   summarize(mean_len = mean(len_tot, na.rm = TRUE),
#             sd_len = sd(len_tot, na.rm = TRUE))
#

```

```
#
#
# gg2 <- ggplot(data = summary, aes(x=Site, y=mean_len))+
#   geom_bar()
#
#
# barplot(growth_dec$len_per_day~site)
#
# +
#   xlab("Site") +
#   #scale_color_discrete(name="Shell hash addition")+
# gg2
```

```
head(growth)
```

Start_date	Site	Treatment	Buried_Dec	Location_code
9/27/2022	Provincetown	N	N	A2
9/27/2022	Provincetown	N	N	A2
9/27/2022	Provincetown	N	N	A2
9/27/2022	Provincetown	N	N	A2
9/27/2022	Provincetown	N	N	A2
9/27/2022	Provincetown	N	N	A2

```
growth <- growth_aliveANDdead
Alive_count <- growth %>% count(Treatment, Collection.month, Location_code)
```

```
head(Alive_count)
```

Treatment	Collection.month	Location_code	Site	Alive
N	Dec	A2	Provincetown	Alive
N	Dec	A2	Provincetown	Deac
N	Dec	A2	Eel Pond	Alive
N	Dec	A2	Eel Pond	Deac
N	Dec	C2	Eel Pond	Alive
N	Dec	C2	Eel Pond	Deac

```
Alive_count_inside_cage <- Alive_count[Alive_count$Treatment=="N",]  
mod_growth_full <- lme(n~Treatment*Collection.month,  
                      random = ~1|Location_code, data = Alive_count,  
                      summary(mod_growth_full) # Not really answering my question but
```

Linear mixed-effects model fit by REML
Data: Alive_count_inside_cage
AIC BIC logLik
524.0307 544.7105 -254.0154

Random effects:
Formula: ~1 | Location_code
(Intercept) Residual
StdDev: 0.0001693316 2.962654

Fixed effects: n ~ Treatment * Collection.month
Value Std.Error DF t-value
p-value
(Intercept) 5.705882 0.7185492 69 7.940838
0.0000
Treatments -0.261438 1.0019689 69 -0.260924
0.7949
Collection.monthApr -0.352941 1.0161820 69 -0.347321
0.7294

```

Collection.monthJun      -0.470588  1.0161820  69 -0.463094
0.6448
TreatmentS:Collection.monthApr -0.136958  1.3853605  69 -0.098861
0.9215
TreatmentS:Collection.monthJun  0.256913  1.4816994  69  0.173391
0.8629

```

Correlation:

(Intr) TrtmnS Cllc.A Cllc.J

TS:C.A

```

TreatmentS      -0.717
Collection.monthApr -0.707  0.507
Collection.monthJun -0.707  0.507  0.500
TreatmentS:Collection.monthApr  0.519 -0.723 -0.734 -0.367
TreatmentS:Collection.monthJun  0.485 -0.676 -0.343 -0.686
0.489

```

Standardized Within-Group Residuals:

	Min	Q1	Med	Q3	Max
	-1.5884009	-0.9343136	0.1433973	0.9034030	2.1244862

Number of Observations: 104

Number of Groups: 30

```

(gm1 <- glmer(as.factor(AliveOrDead) ~ Treatment * Collection.m
              data = growth, family = binomial))

```

fixed-effect model matrix is rank deficient so dropping 2
columns / coefficients

Warning in checkConv(attr(opt, "derivs"), opt\$par, ctrl =
control\$checkConv, : Model is nearly unidentifiable: large
eigenvalue ratio
- Rescale variables?

Generalized linear mixed model fit by maximum likelihood
(Laplace

Approximation) [glmerMod]

Family: binomial (logit)

Formula: as.factor(AliveOrDead) ~ Treatment * Collection.month
+ Site +

(1 | Location_code)

Data: growth

AIC	BIC	logLik	deviance	df.resid
624.5863	663.4571	-303.2932	606.5863	546

Random effects:

Groups	Name	Std.Dev.
Location_code	(Intercept)	1.173

Number of obs: 555, groups: Location_code, 30

Fixed Effects:

	(Intercept)	TreatmentOutside cage
	0.4275	-19.8327
TreatmentS	-3.0316	-1.6992
Collection.monthJun	-0.9085	2.2312
TreatmentS:Collection.monthApr	3.7885	2.8526

fit warnings:

fixed-effect model matrix is rank deficient so dropping 2
columns / coefficients

optimizer (Nelder_Mead) convergence code: 0 (OK) ; 0 optimizer
warnings; 1 lme4 warnings

```
summary(gm1) #Here there is an effect of treatment but it's sti
```

Generalized linear mixed model fit by maximum likelihood

(Laplace

Approximation) [glmerMod]

Family: binomial (logit)

Formula: as.factor(AliveOrDead) ~ Treatment * Collection.month
+ Site +

(1 | Location_code)

Data: growth

AIC	BIC	logLik	deviance	df.resid
624.6	663.5	-303.3	606.6	546

Scaled residuals:

Min	1Q	Median	3Q	Max
-6.5914	-0.6383	0.2396	0.5466	3.7377

Random effects:

Groups	Name	Variance	Std.Dev.
Location_code	(Intercept)	1.376	1.173

Number of obs: 555, groups: Location_code, 30

Fixed effects:

Estimate	Std. Error	z value
----------	------------	---------

```
Pr(>|z|)
(Intercept)          0.4275      0.4555    0.938
0.347999
TreatmentOutside cage -19.8327    512.0014  -0.039
0.969101
TreatmentS           -3.0316      0.6078  -4.988
6.11e-07 ***
Collection.monthApr  -1.6992      0.5842  -2.909
0.003629 **
Collection.monthJun   -0.9085      0.6253  -1.453
0.146276
SiteEel Pond         2.2312      0.2368   9.422  <
2e-16 ***
TreatmentS:Collection.monthApr  3.7885      0.8241   4.597
4.29e-06 ***
TreatmentS:Collection.monthJun  2.8526      0.8224   3.469
0.000523 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correlation of Fixed Effects:

```
(Intr) TrtmOc TrtmnS Clc.A Clc.J StElPn TS:C.A
Trtmnt0tsdc  0.001
TreatmentS   -0.595 -0.002
Clcctn.mntA -0.653 -0.001  0.488
Clcctn.mntJ -0.663 -0.002  0.489  0.496
SiteEelPond -0.129  0.000 -0.252 -0.098 -0.001
TrtmntS:C.A  0.477  0.002 -0.782 -0.692 -0.361  0.178
TrtmntS:C.J  0.447  0.002 -0.720 -0.299 -0.724  0.218  0.537
```

fit warnings:

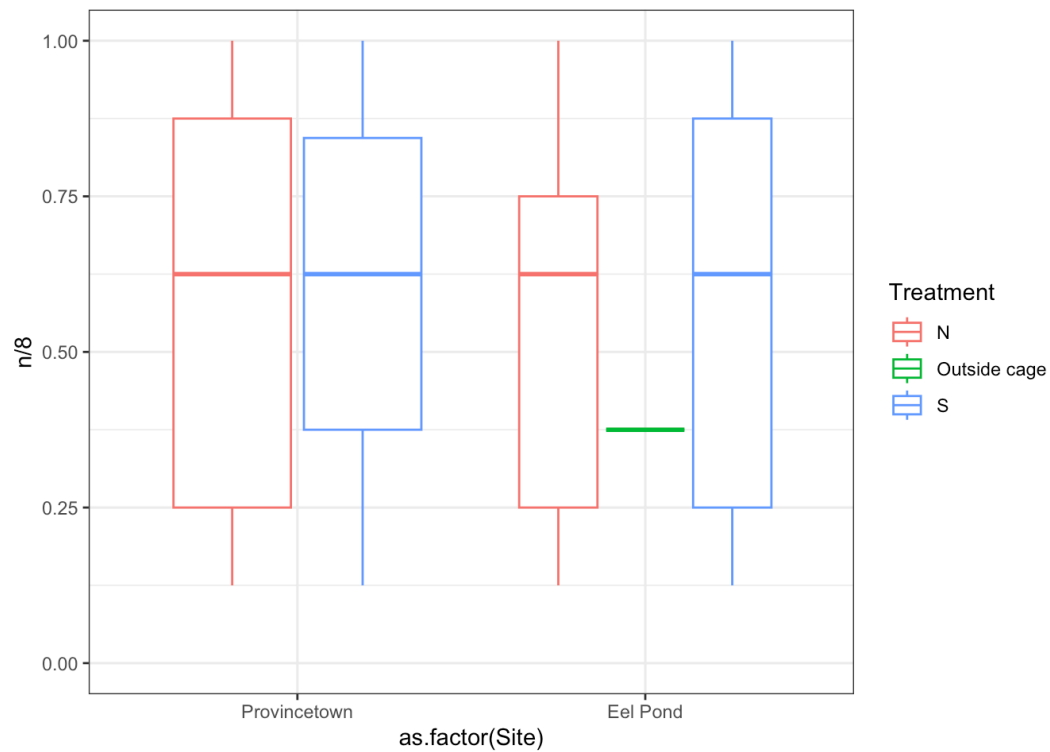
```
fixed-effect model matrix is rank deficient so dropping 2
columns / coefficients
optimizer (Nelder_Mead) convergence code: 0 (OK)
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
```

```
p <- ggplot(Alive_count, aes(x = as.factor(Site), y = n/8,
                             color = Treatment))+
  ylim(0,1)+
  geom_boxplot()

p
```

Warning: Removed 17 rows containing non-finite outside the

scale range
(`stat_boxplot()`).



```
# Generally high survival
# p + geom_boxplot() + facet_grid(Site ~ .)
#
# p <- ggplot(growth_dec, aes(x = Start_len_mm, y = AliveOrDead,
#                             color = Treatment))
#
# p + geom_boxplot() + facet_grid(Site ~ .)
```

```
Alive <- as.data.frame(Alive_count[Alive_count$AliveOrDead=="Al:
Alive$perc_alive <- Alive$n/9*100
#Alive
```