

Biodeposition

Quarto

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Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
library(ggplot2)
library(ggpubr)
library(data.table)
```

Warning: package 'data.table' was built under R version 4.3.2

```
setwd("~/GitHub/EAD-ASEB-Ssolidissima-OA/data")

bd <- fread("Biodeposition_experiment_summary - Biodeposition_results.csv")
```

```
# bd <- bd[!is.na(bd$Month),]
# bd <- bd[!is.na(bd$Site),]
print(rownames(bd))
```

```
[1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12" "13" "14" "15"
[16] "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28" "29" "30"
[31] "31" "32" "33" "34" "35" "36" "37" "38" "39" "40" "41" "42" "43" "44" "45"
[46] "46" "47" "48" "49" "50" "51" "52" "53" "54" "55" "56" "57" "58" "59" "60"
[61] "61" "62" "63" "64" "65" "66" "67" "68" "69" "70" "71" "72" "73" "74" "75"
[76] "76" "77" "78" "79" "80" "81" "82" "83" "84" "85" "86" "87" "88"
```

```
#bd <- bd[complete.cases(bd), ]
bd<- bd[bd$Month == "September"|bd$Month == "April"|bd$Month == "June",]
bd$Site <- as.factor(bd$Site)
bd$Month <- as.factor(bd$Month)
bd$Month <- factor(bd$Month, levels=c("September", "April", "June"))
bd$Treatment <- as.factor(bd$Treatment)
bd$Treatment <- factor(bd$Treatment, levels=c("N", "S", "OUT"))

print(rownames(bd))
```

```
[1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12" "13" "14" "15"
[16] "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28" "29" "30"
[31] "31" "32" "33" "34" "35" "36" "37" "38" "39" "40" "41" "42" "43" "44" "45"
[46] "46" "47" "48" "49" "50" "51" "52" "53" "54" "55" "56" "57" "58" "59" "60"
[61] "61" "62" "63" "64" "65" "66" "67" "68" "69" "70" "71" "72" "73" "74" "75"
[76] "76" "77" "78" "79" "80" "81" "82" "83" "84" "85" "86" "87" "88"
```

```
#bd$Treatment[bd$Site=="Eel Pond"] <- "N"
bd <- bd[bd$TPM>=.9,]
bd$OER
```

```
[1] 0.6610 0.6330 0.7620 0.6880 0.6260 0.7190 0.6600 0.7920 0.6790 0.4160
[11] 0.4770 0.5150 0.5170 0.8040 0.8650 0.4860 0.4950 0.5060 0.5730 0.2850
[21] 0.3020 0.3010 0.2570 0.2520 0.3360 0.2160 0.0220 0.0200 1.4430 2.4430
[31] 1.1340 2.1460 1.0450 1.5230 1.3900 1.0990 1.8670 1.1550 1.0480 0.9185
[41] 0.6570 1.0155 0.5185 1.4725 0.5925 0.6650 0.5275 0.5625 0.6550 0.4660
[51] 1.2115 1.1005 0.5065 1.0010 0.9720 0.9530 0.3250 0.7330 1.1570 0.4130
[61] 0.7610 0.4320 0.5550 0.5120 0.6860 0.6800 0.5070 0.4390 0.5760 0.7930
```

```
str(bd)
```

Classes 'data.table' and 'data.frame': 70 obs. of 39 variables:

```
$ Month                      : Factor w/ 3 levels "September","April",...: 1 1 1 1 1 1 1
1 1 1 ...
$ Site                       : Factor w/ 2 levels "Eel Pond","Provincetown": 2 2 2 2 2 2
2 2 2 2 ...
$ Biodeposition chamber      : int   3 4 7 8 13 14 17 18 5 6 ...
$ Treatment                  : Factor w/ 3 levels "N","S","OUT": 1 1 1 1 1 1 1 2 2 ...
$ Mesocosm                   : chr   "A" "A" "C" "C" ...
$ Clam ID                    : chr   "Y" "GL" "Y" "BL" ...
$ Length                     : num   34 35.1 31.4 34.5 33.8 35.6 36.9 35.3 34.3 31.5 ...
$ Height                     : num   25.4 27.1 23.9 26.6 26.3 27.6 27.3 27 27.5 24.5 ...
$ Dry.weight                  : num   0.247 0.319 0.242 0.311 0.297 0.354 0.382 0.303 0.33
0.237 ...
$ AFDW                       : num   0.181 0.236 0.174 0.225 0.226 0.283 0.276 0.242
0.245 0.177 ...
$ Duration of collection period : num   2 2 2 0.866 2 2 2 2 2 2 ...
$ TPM                        : num   3.76 2.91 3.25 1.09 2.57 ...
$ PIM                        : num   2.439 1.644 1.732 0.492 1.315 ...
$ POM                        : num   1.322 1.266 1.523 0.596 1.253 ...
$ Perc_organic                : num   35.1 43.5 46.8 54.8 48.8 ...
$ ER                          : num   1.88 1.46 1.63 1.26 1.28 ...
$ OER                         : num   0.661 0.633 0.762 0.688 0.626 0.719 0.66 0.792 0.679
0.416 ...
$ IER                         : num   1.22 0.822 0.866 0.568 0.658 0.951 0.968 1.24 0.774
0.404 ...
$ Pseudofaeces TPM           : num   NA NA NA NA NA NA NA NA NA NA ...
$ Species standardization coefficient: num   0.76 0.76 0.76 0.76 0.76 0.76 0.76 0.76 0.76 0.76
...
```

```

$ IER_scaled      : num  3.53 1.96 2.55 1.38 1.65 2.09 2.01 3.07 1.8 1.21 ...
$ OER_scaled      : num  1.91 1.51 2.24 1.67 1.58 1.58 1.37 1.96 1.58 1.24
...
$ IRR             : num  0 0.49 0 0 0 0 0 0 0 ...
$ ORR             : num  0 0.4 0 0 0 0 0 0 0 ...
$ RR              : num  0 0.89 0 0 0 0 0 0 0 ...
$ p               : num  NA 0.45 NA NA NA NA NA NA NA ...
$ f               : num  0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75
...
$ SE              : num  NA 0.4 NA NA NA NA NA NA NA ...
$ IFR             : num  3.53 2.45 2.55 1.38 1.65 2.09 2.01 3.07 1.8 1.21 ...
$ CR              : num  4.7 3.26 3.39 1.84 2.2 2.79 2.68 4.09 2.74 1.84 ...
$ FR              : num  13.22 9.17 9.53 5.17 6.19 ...
$ Perc RR         : num  0 9.69 0 0 0 0 0 0 0 ...
$ TIR             : num  13.22 8.28 9.53 5.17 6.19 ...
$ OFR             : num  9.69 6.72 6.99 3.79 4.54 5.75 5.52 8.43 5.19 3.49
...
$ OIR             : num  9.69 6.33 6.99 3.79 4.54 5.75 5.52 8.43 5.19 3.49
...
$ i               : num  0.73 0.76 0.73 0.73 0.73 0.73 0.73 0.73 0.74 0.74
...
$ AR              : num  7.77 4.82 4.75 2.12 2.96 4.16 4.15 6.47 3.62 2.24
...
$ AE              : num  0.8 0.76 0.68 0.56 0.65 0.72 0.75 0.77 0.7 0.64 ...
$ Notes           : chr  "" "" "" "" ...
- attr(*, ".internal.selfref")=<externalptr>

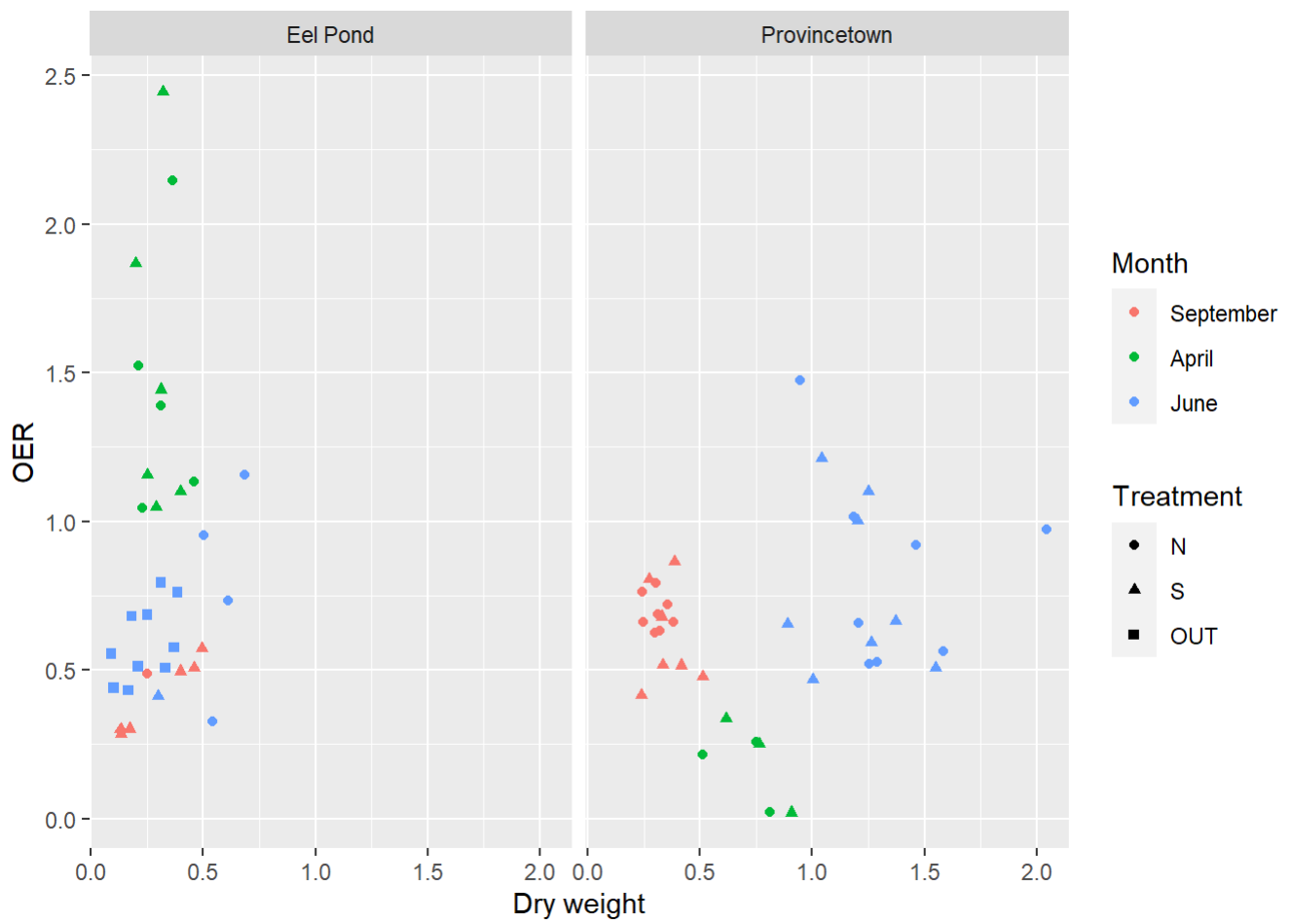
```

OER

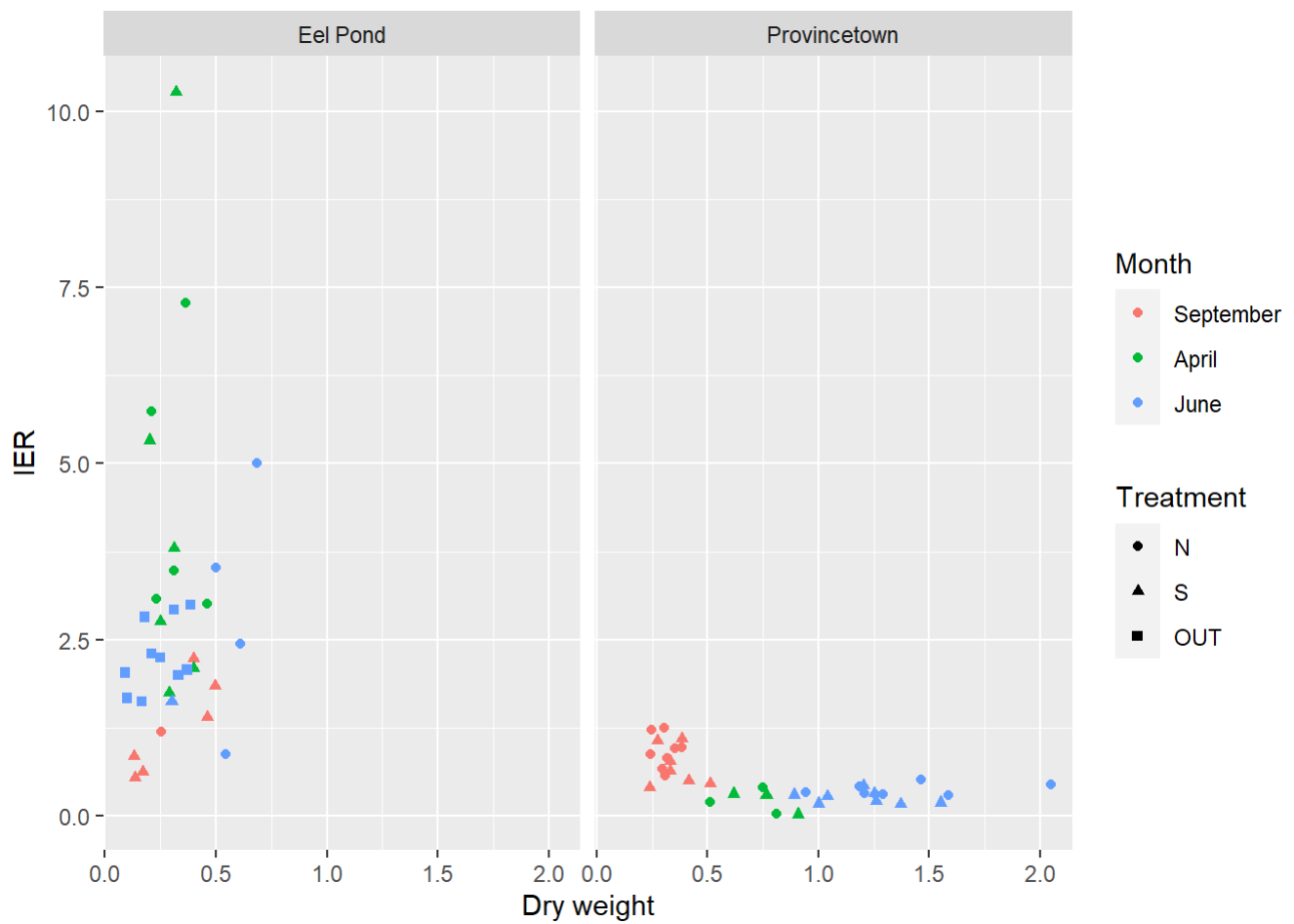
```

[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT

```

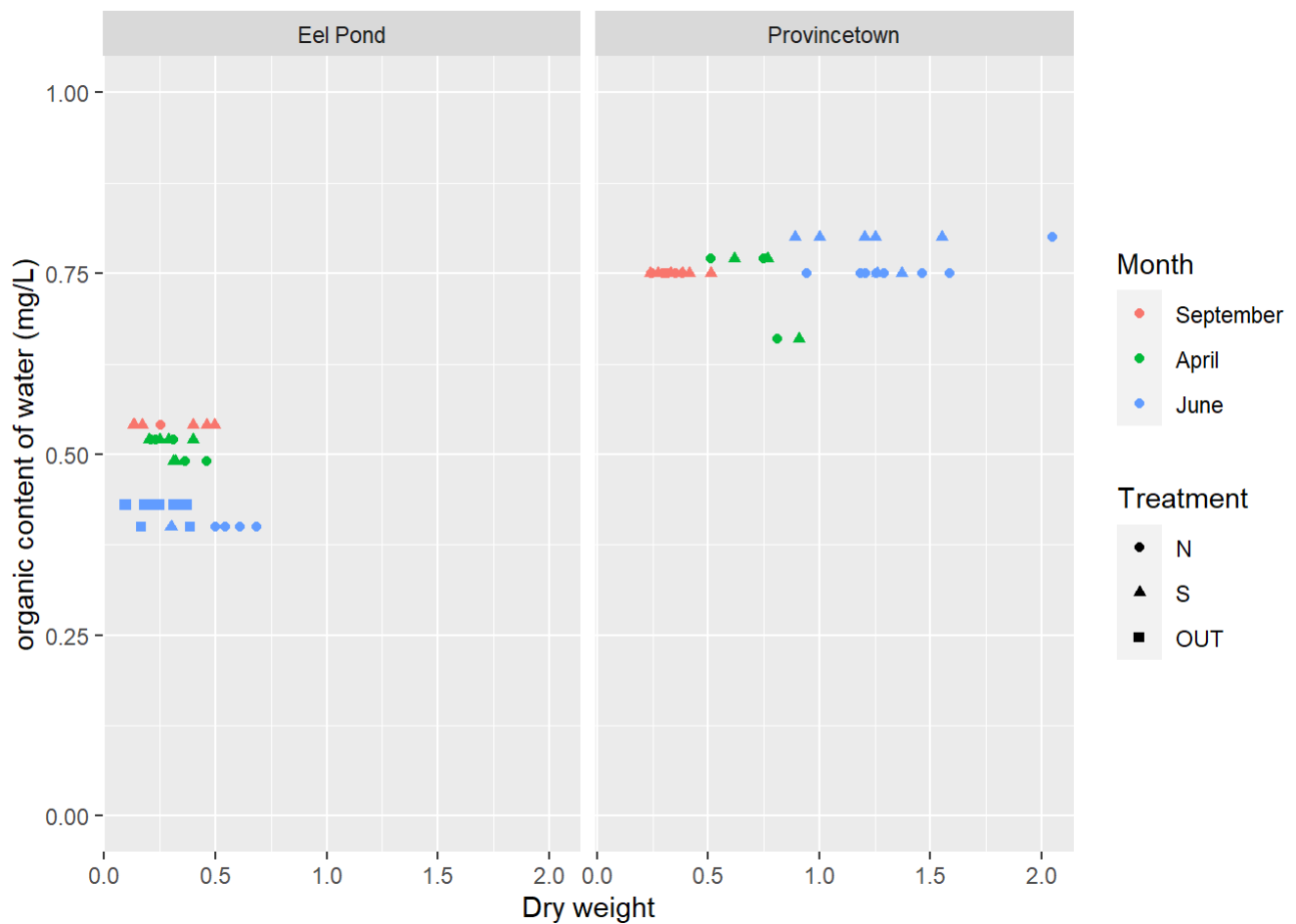


```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```



```
[1] 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75
[16] 0.54 0.54 0.54 0.54 0.54 0.54 0.54 0.77 0.77 0.77 0.77 0.66 0.66 0.49 0.49
[31] 0.49 0.49 0.52 0.52 0.52 0.52 0.52 0.52 0.52 0.75 0.75 0.75 0.75 0.75 0.75
[46] 0.75 0.75 0.75 0.80 0.80 NA 0.80 0.80 0.80 0.80 0.40 0.40 0.40 0.40 0.40
[61] 0.40 0.40 0.43 0.43 0.43 0.43 0.43 0.43 0.43 0.43
```

Warning: Removed 1 rows containing missing values (`geom_point()`).



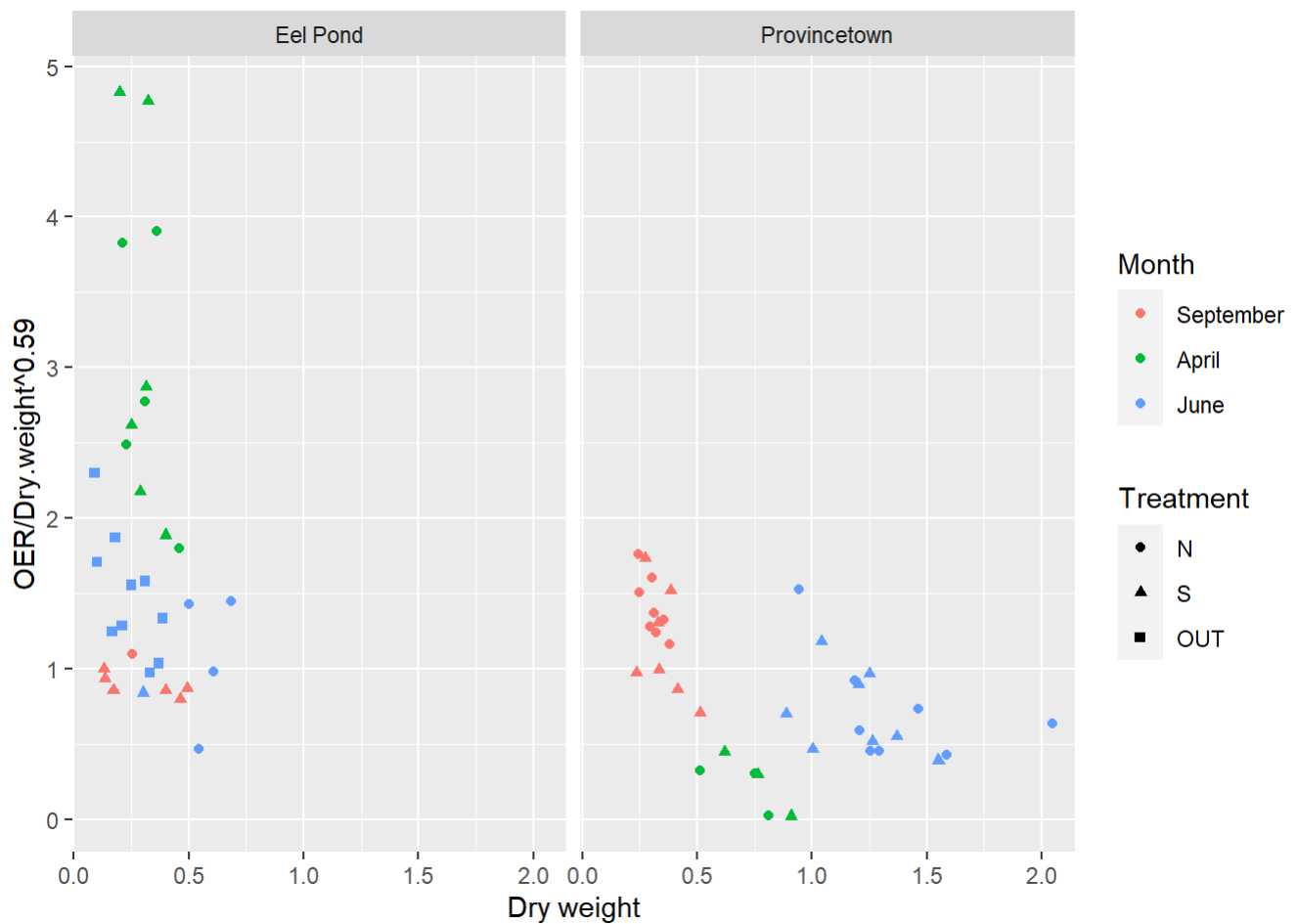
Check out new scaling from QC and subsetting Emilien's data

```
bd$Treatment
```

```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```

```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=OER/Dry.weight^.59, color = Month))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  #ylab("OER new scaling")+
  #ylim(0,9)+
  #scale_color_discrete(name="Site")+
  #ggtitle ('OER as a function of DW')+
  facet_wrap(~ Site)
```

```
gg1
```

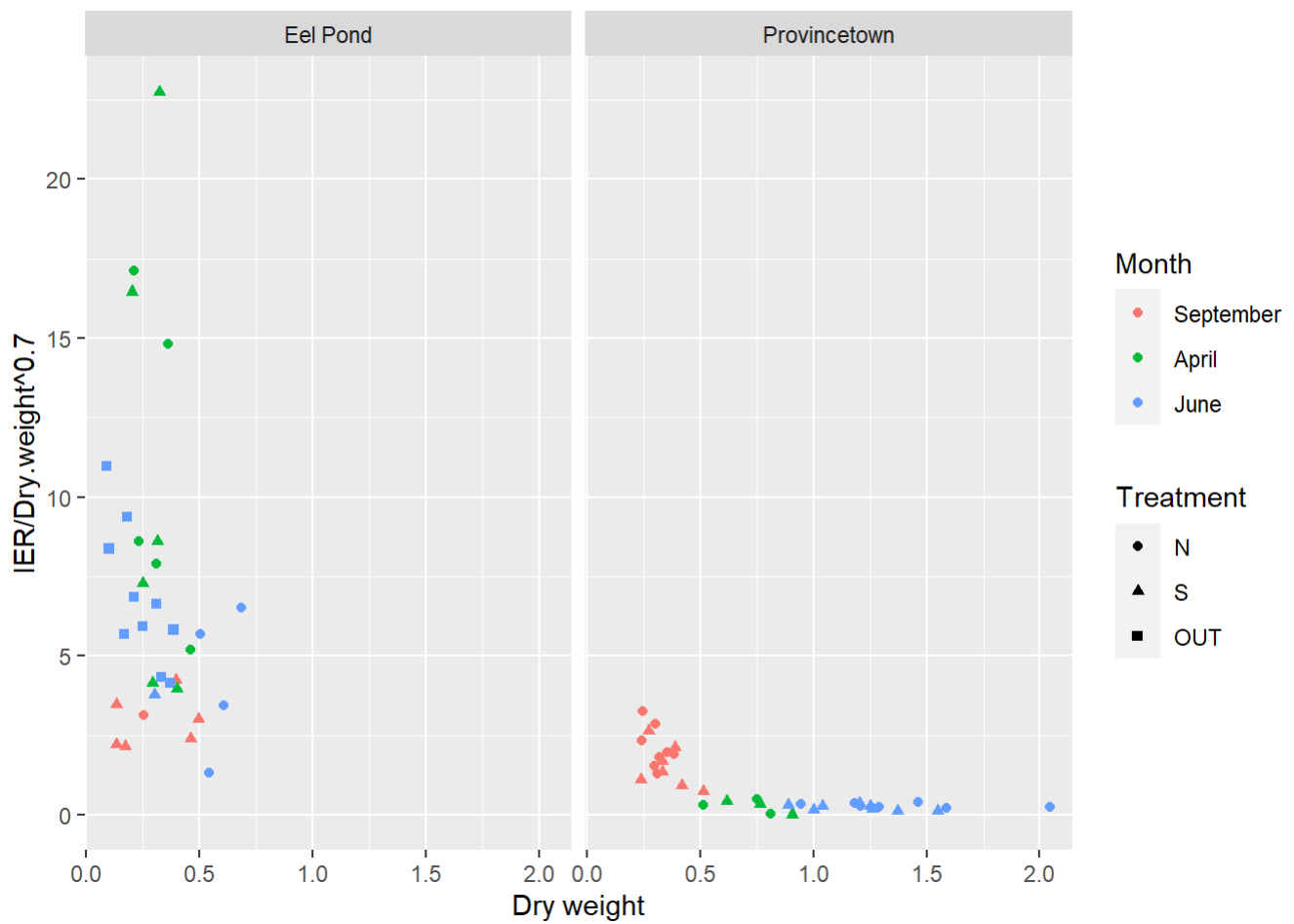


```
bd$Treatment
```

```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```

```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=IER/Dry.weight^.70, color = Month))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  # ylab("IER")+
  #ylim(0,9)+
  #scale_color_discrete(name="Site")+
  #ggtitle ('OER as a function of DW')+
  facet_wrap(~ Site)
```

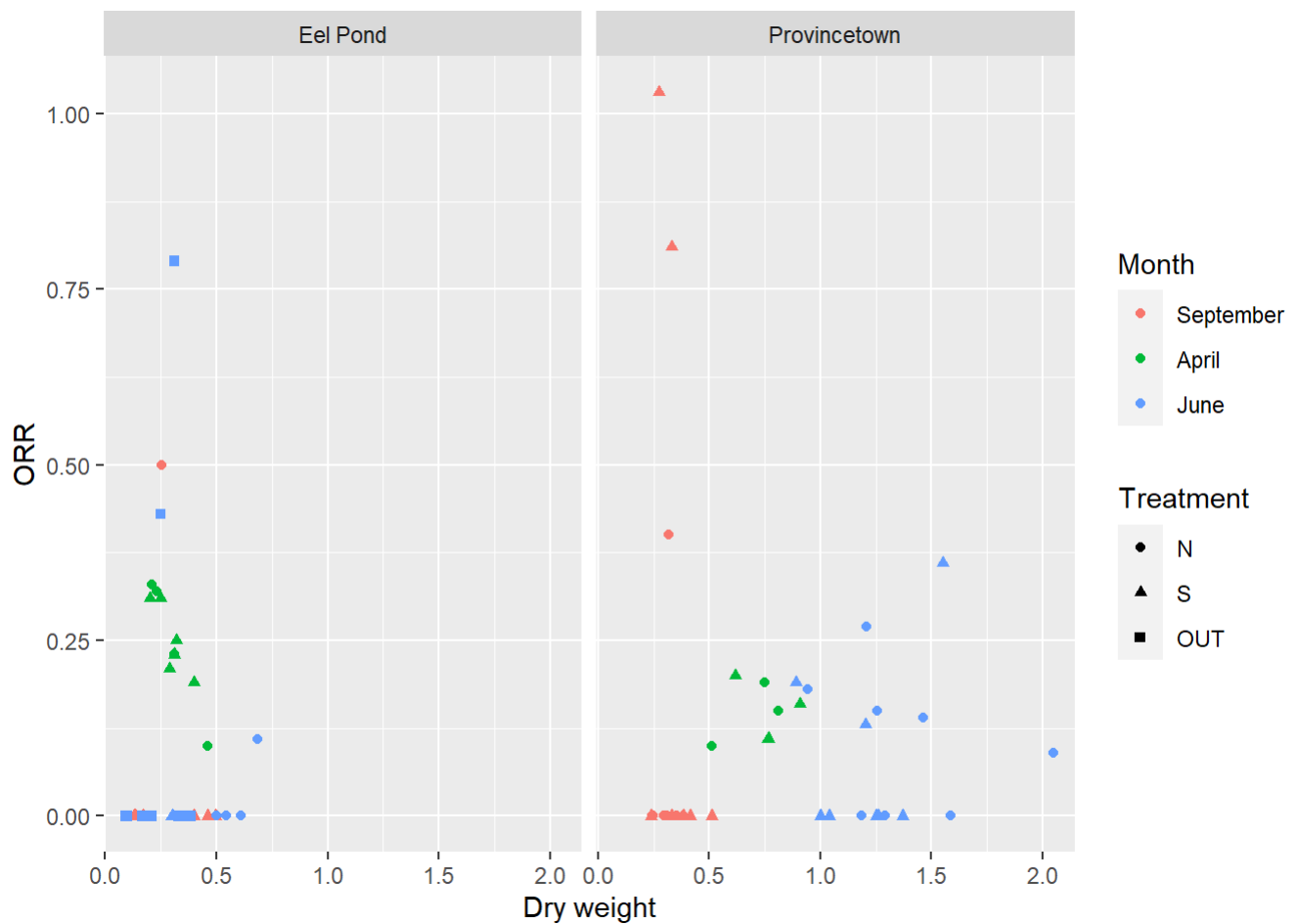
```
gg1
```



```
bd$Treatment
```

```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```

```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=ORR, color = Month))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  #ylab("ORR")+
  #ylim(0,9)+
  #scale_color_discrete(name="Site")+
  #ggtitle ('OER as a function of DW')+
  facet_wrap(~ Site)
gg1
```

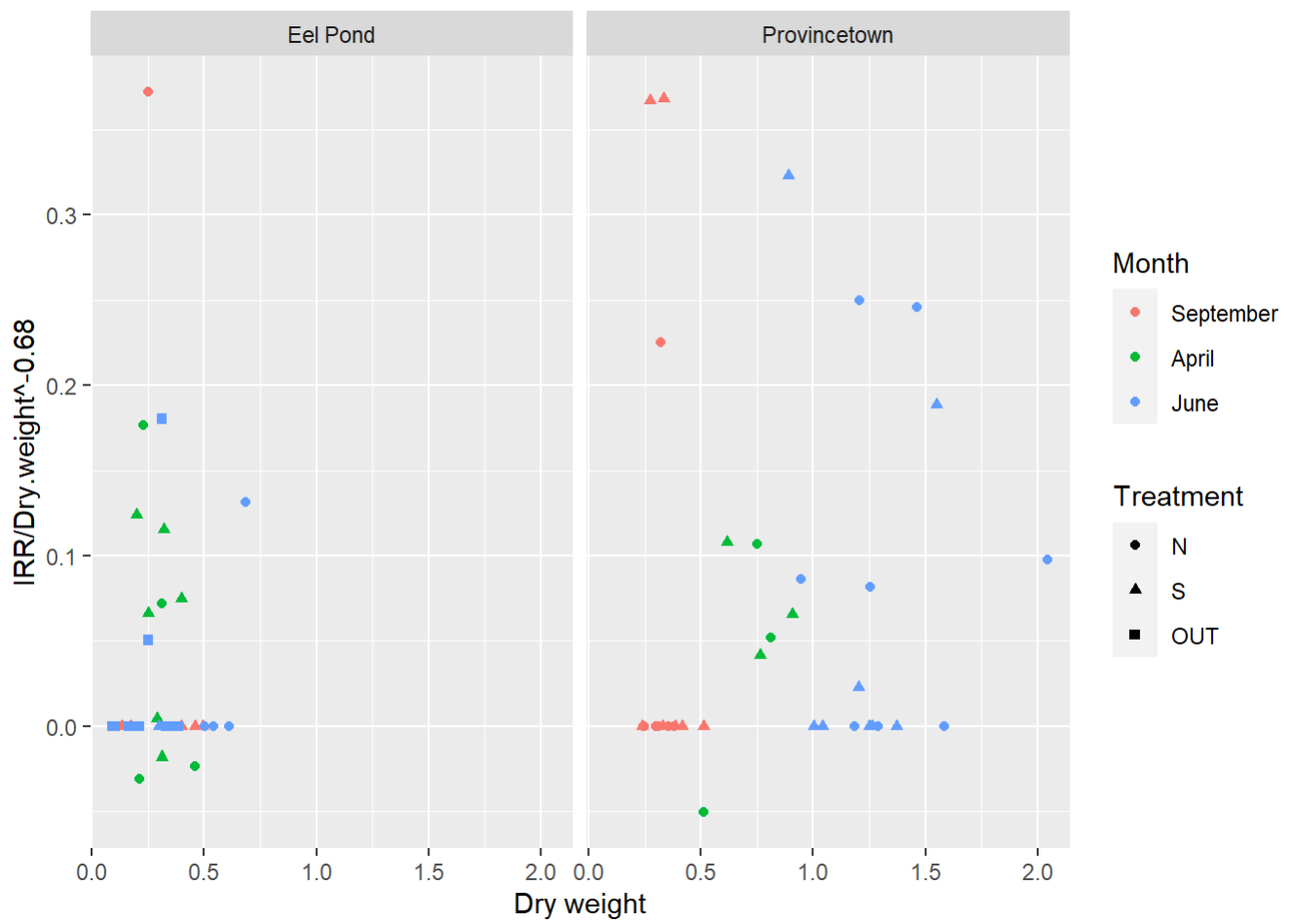



```
bd$Treatment
```

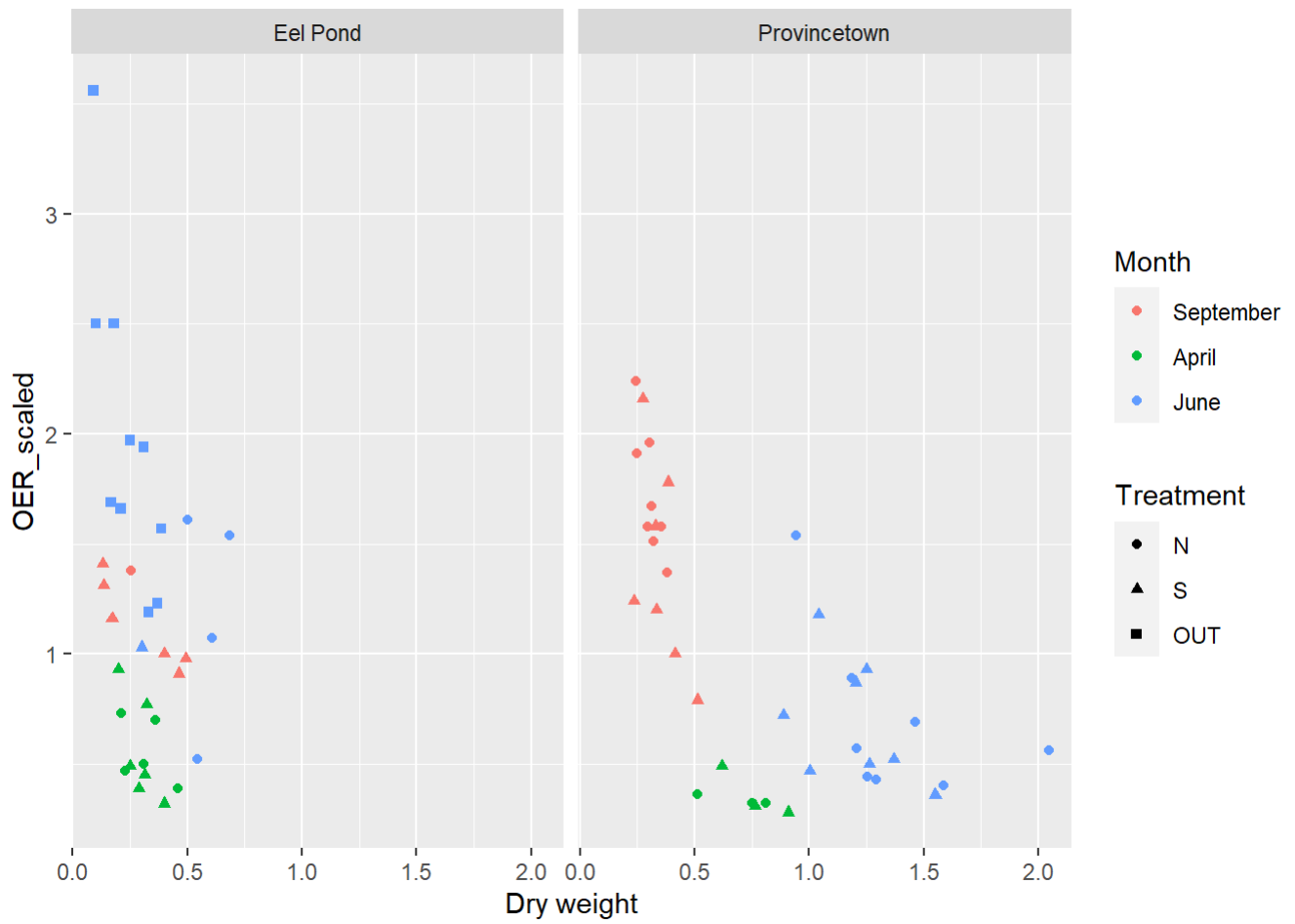
```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```

```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=IRR/Dry.weight^-.68, color = Month))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  # ylab("IRR")+
  #ylim(0,9)+
  #scale_color_discrete(name="Site")+
  #ggtitle ('OER as a function of DW')+
  facet_wrap(~ Site)
```

```
gg1
```



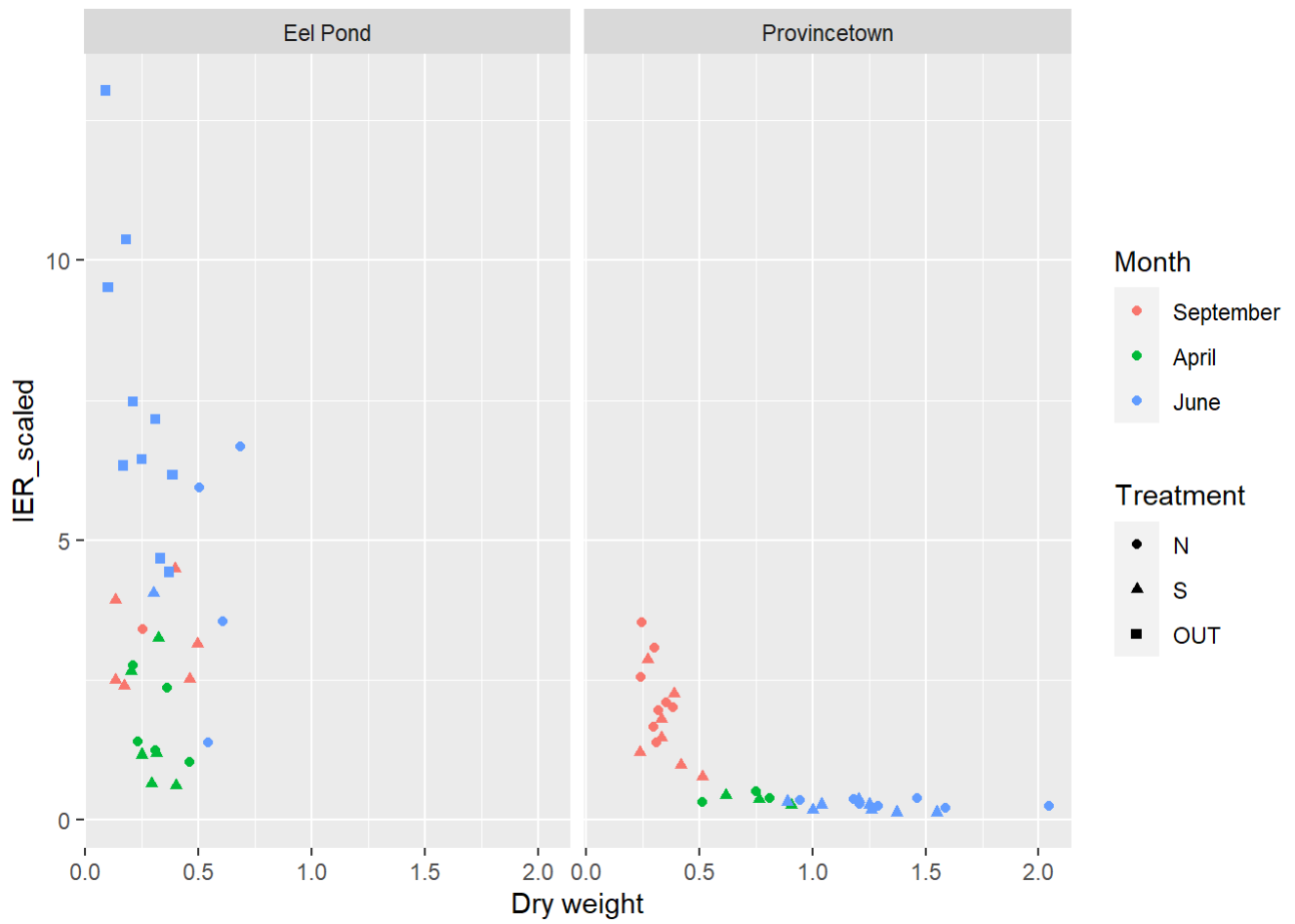
```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```



```

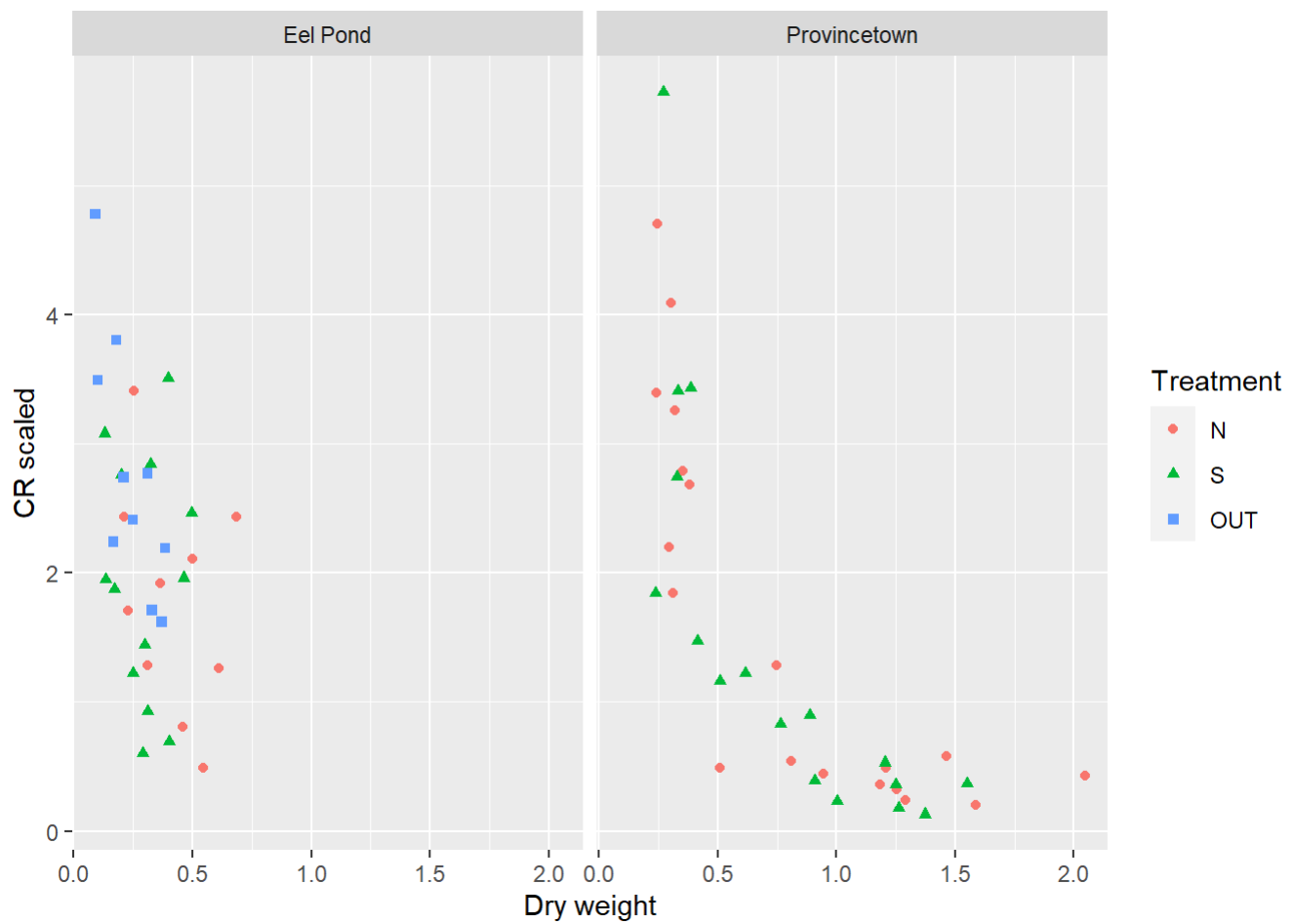
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT

```



```
[1] N  N  N  N  N  N  N  N  S  S  S  S  S  S  S  N  S  S  S
[20] S  S  S  N  S  S  N  N  S  S  S  N  N  N  N  N  S  S  S
[39] S  N  N  N  N  N  S  S  N  N  S  S  S  S  S  S  N  N  N
[58] N  N  S  OUT OUT OUT OUT OUT OUT OUT OUT OUT OUT
Levels: N S OUT
```

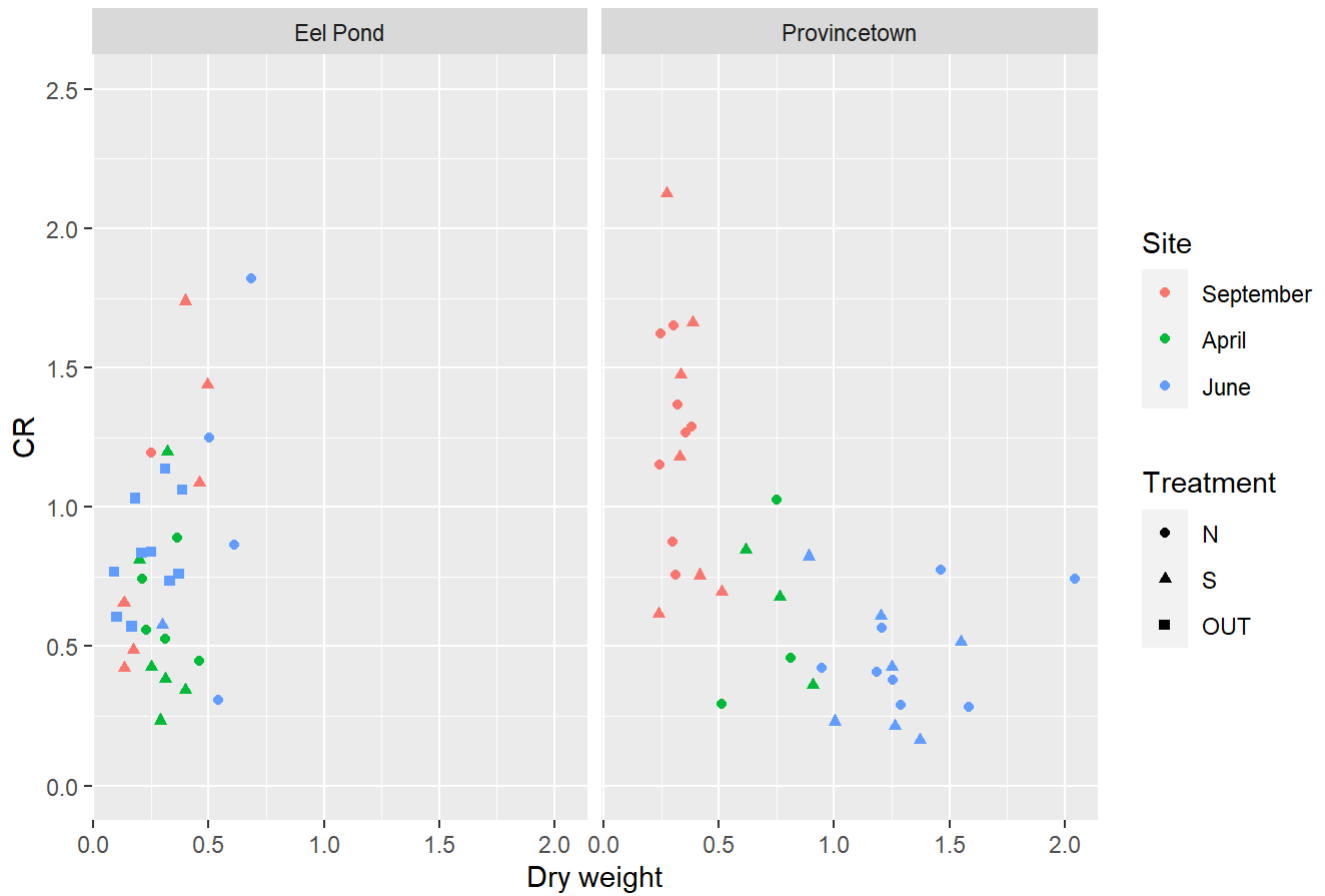
Warning: Removed 1 rows containing missing values (`geom_point()`).



```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=CR*Dry.weight^.76, color = Month ))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  ylab("CR")+
  ylim(0,2.5)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled CR as a function of DW')+
  facet_wrap(~ Site)
gg1
```

Warning: Removed 1 rows containing missing values (`geom_point()`).

Unscaled CR as a function of DW

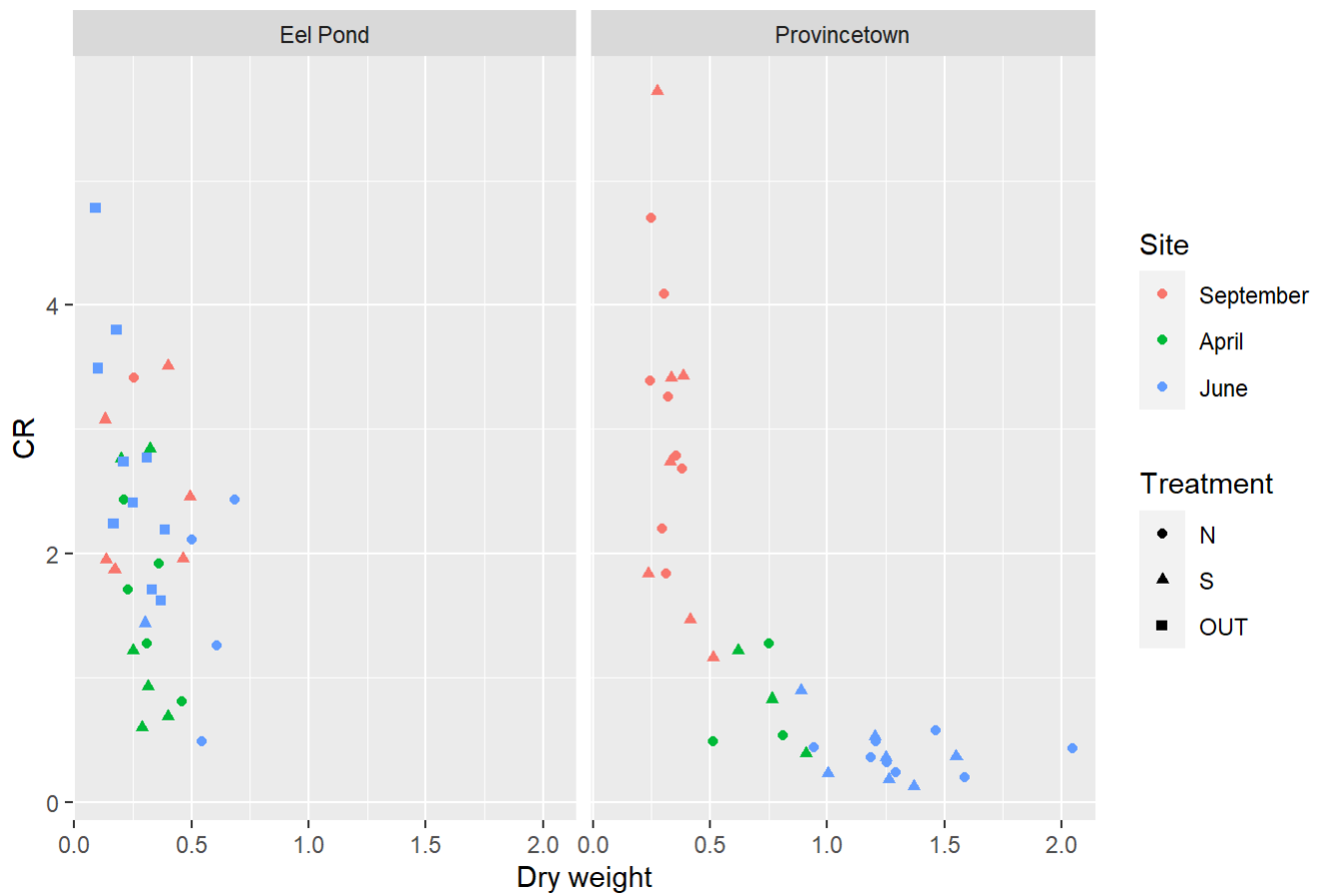


```
gg2 <- ggplot(data = bd, aes(x=Dry.weight, y=CR, color = Month ))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  ylab("CR")+
  #ylim(0,9)+
  scale_color_discrete(name="Site")+
  ggtitle ('Scaled CR as a function of DW')+
  facet_wrap(~ Site)
```

gg2

Warning: Removed 1 rows containing missing values (`geom_point()`).

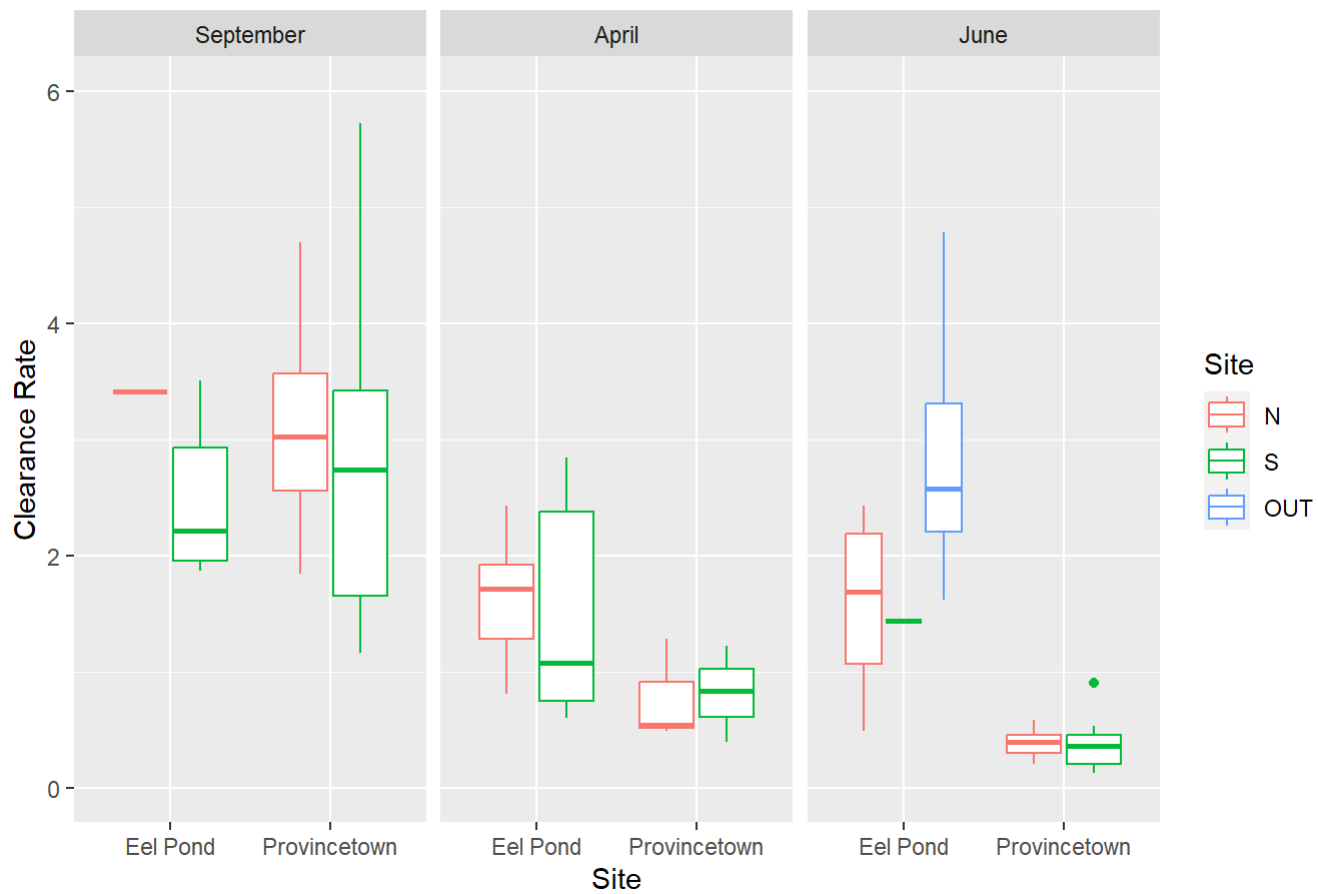
Scaled CR as a function of DW



```
gg3 <- ggplot(data = bd, aes(x=Site, y=CR, col = Treatment))+
  geom_boxplot()+
  #xlab("Dry weight") +
  ylab("Clearance Rate")+
  ylim(0,6)+
  scale_color_discrete(name="Site")+
  ggtitle ('Scaled CR')+
  facet_wrap(~ Month)
gg3
```

Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).

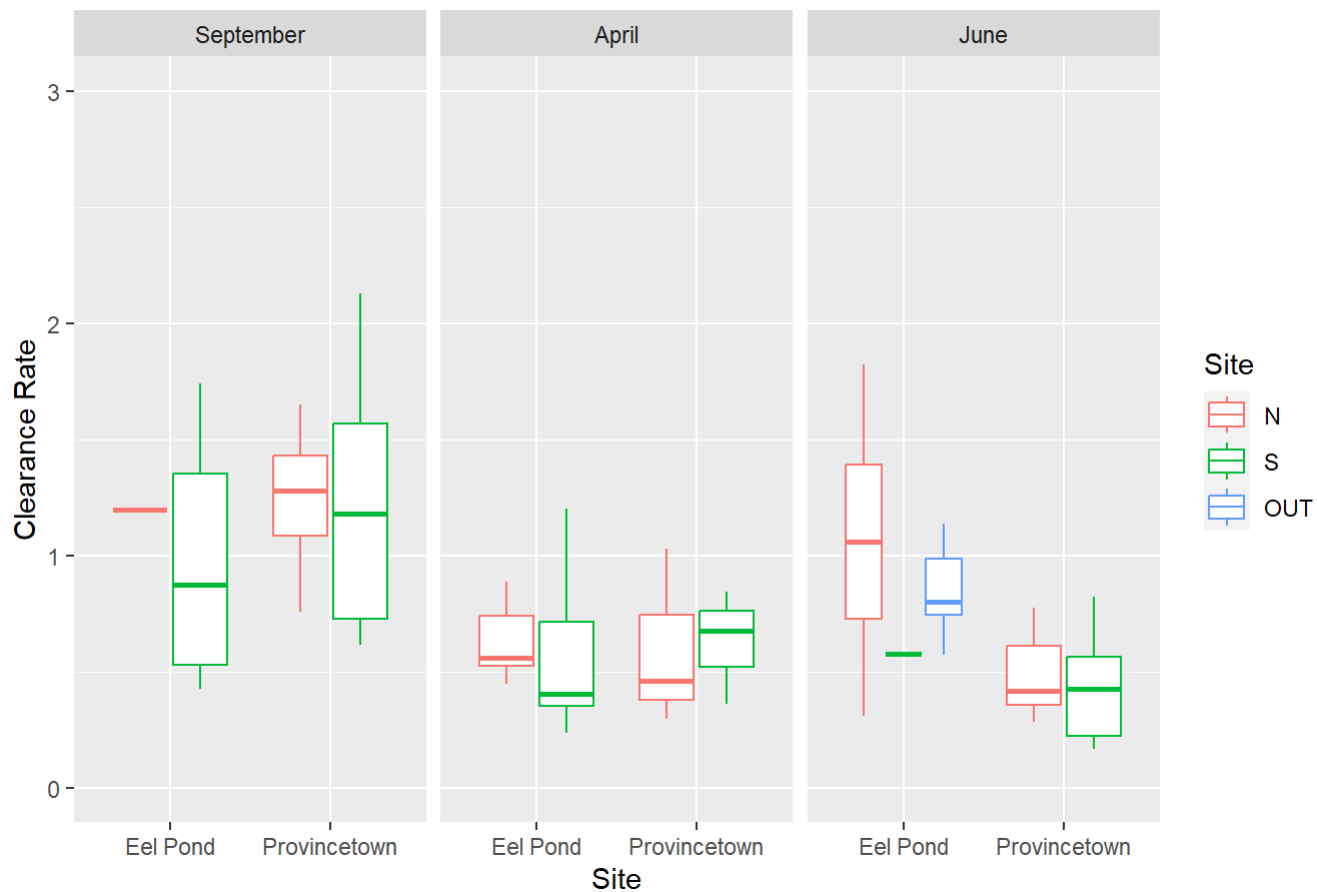
Scaled CR



```
gg4 <- ggplot(data = bd, aes(x=Site, y=CR*Dry.weight^.76, col = Treatment))+
  geom_boxplot()+
  #xlab("Dry weight") +
  ylab("Clearance Rate")+
  ylim(0,3)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled CR')+
  facet_wrap(~ Month)
gg4
```

Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).

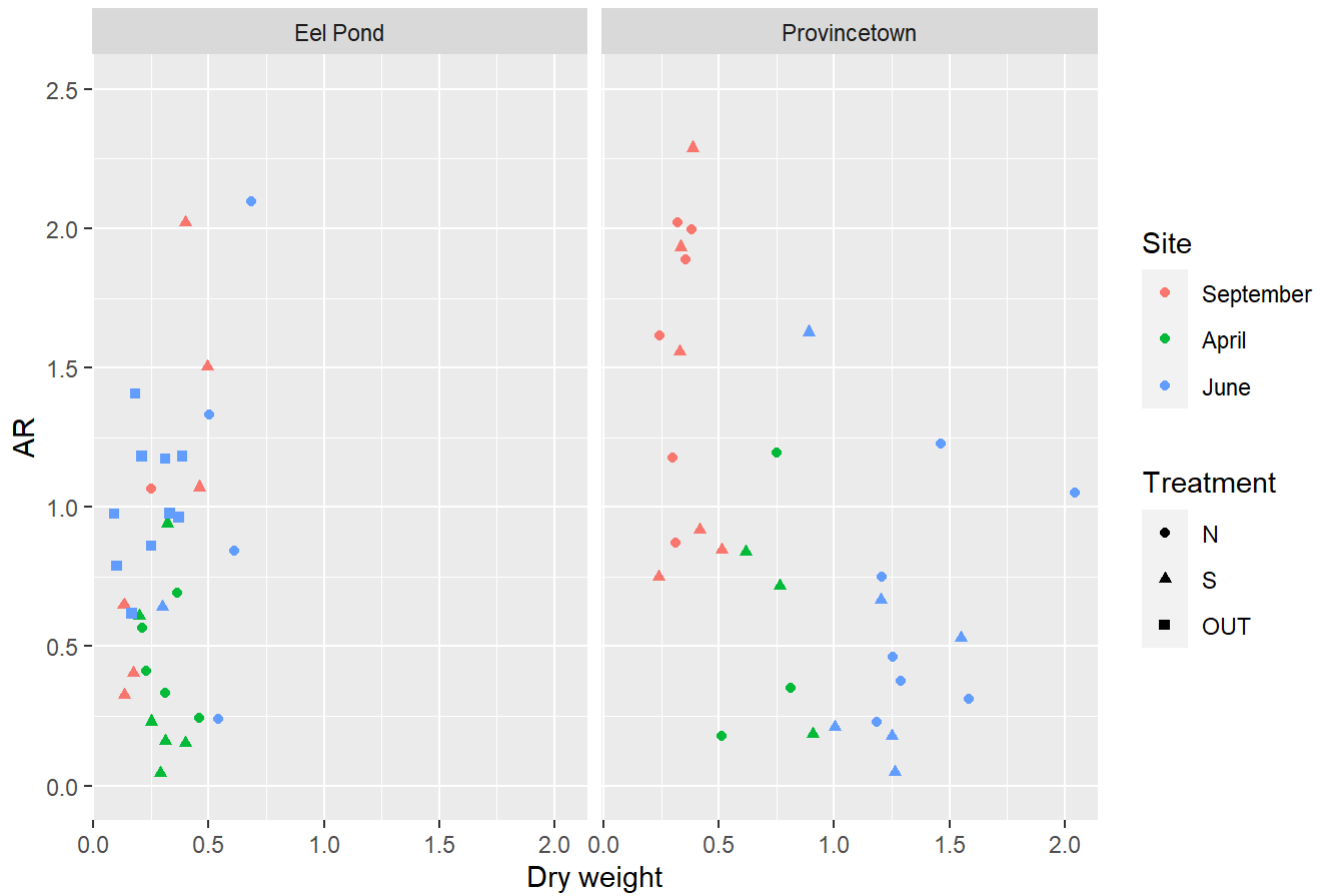
Unscaled CR



```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=AR*Dry.weight^.76, color = Month ))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  ylab("AR")+
  ylim(0,2.5)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled AR as a function of DW')+
  facet_wrap(~ Site)
gg1
```

Warning: Removed 6 rows containing missing values (`geom_point()`).

Unscaled AR as a function of DW

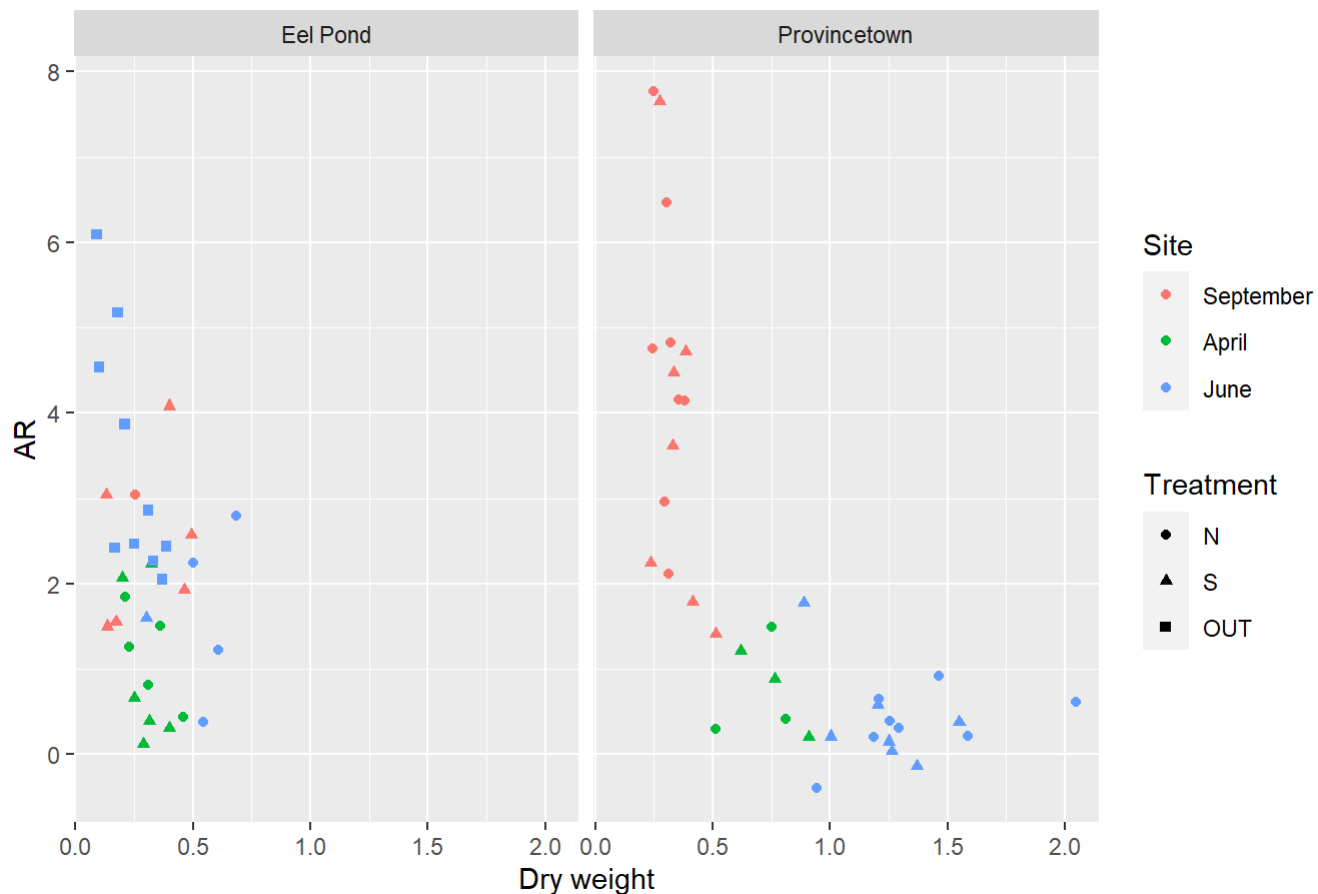


```
gg2 <- ggplot(data = bd, aes(x=Dry.weight, y=AR, color = Month ))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  ylab("AR")+
  #ylim(0,9)+
  scale_color_discrete(name="Site")+
  ggtitle ('Scaled AR as a function of DW')+
  facet_wrap(~ Site)
```

gg2

Warning: Removed 1 rows containing missing values (`geom_point()`).

Scaled AR as a function of DW

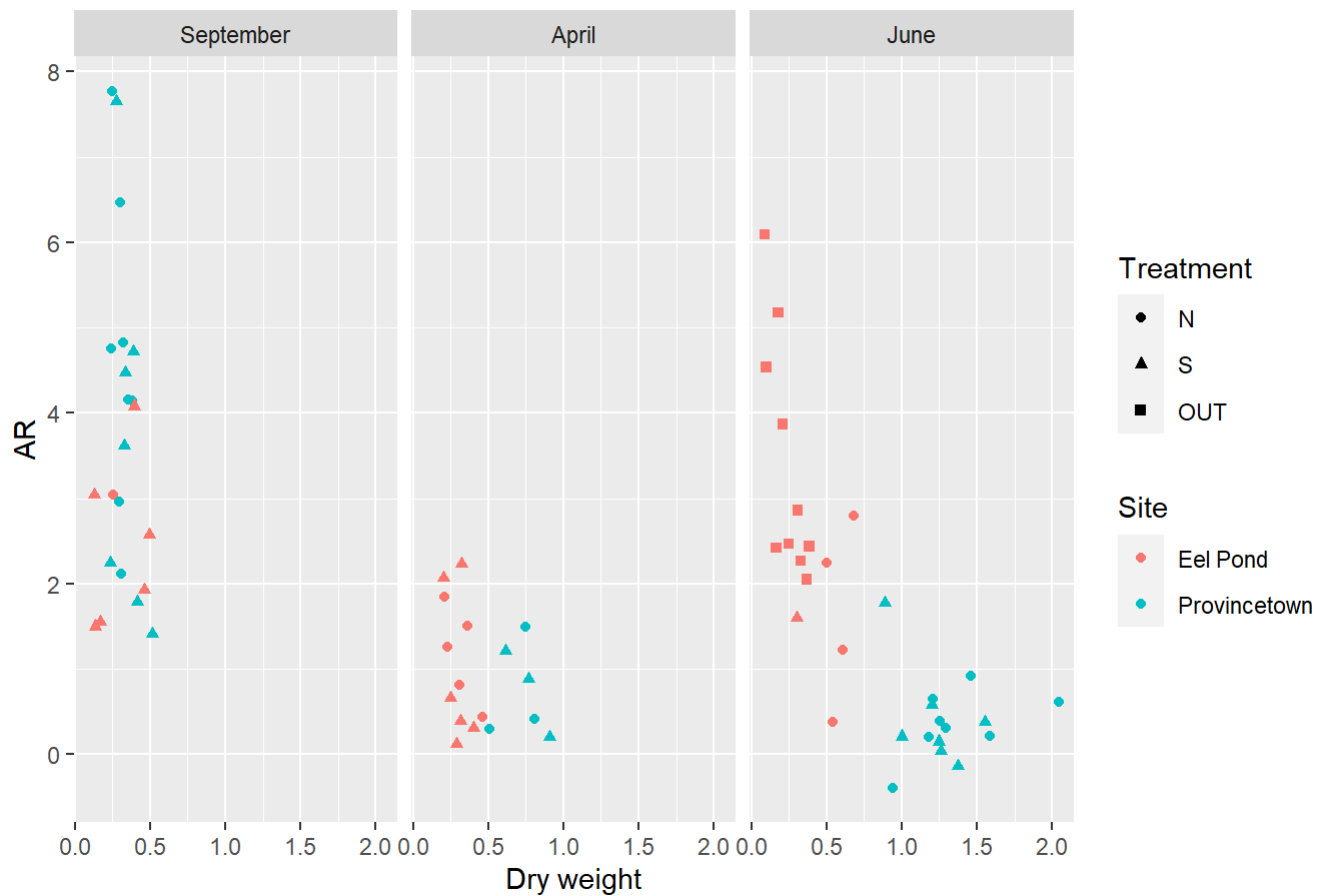


```
gg2 <- ggplot(data = bd, aes(x=Dry.weight, y=AR, color = Site ))+
  geom_point(aes(shape=Treatment))+
  xlab("Dry weight") +
  ylab("AR")+
  #ylim(0,9)+
  scale_color_discrete(name="Site")+
  ggtitle ('Scaled AR as a function of DW')+
  facet_wrap(~ Month)
```

gg2

Warning: Removed 1 rows containing missing values (`geom_point()`).

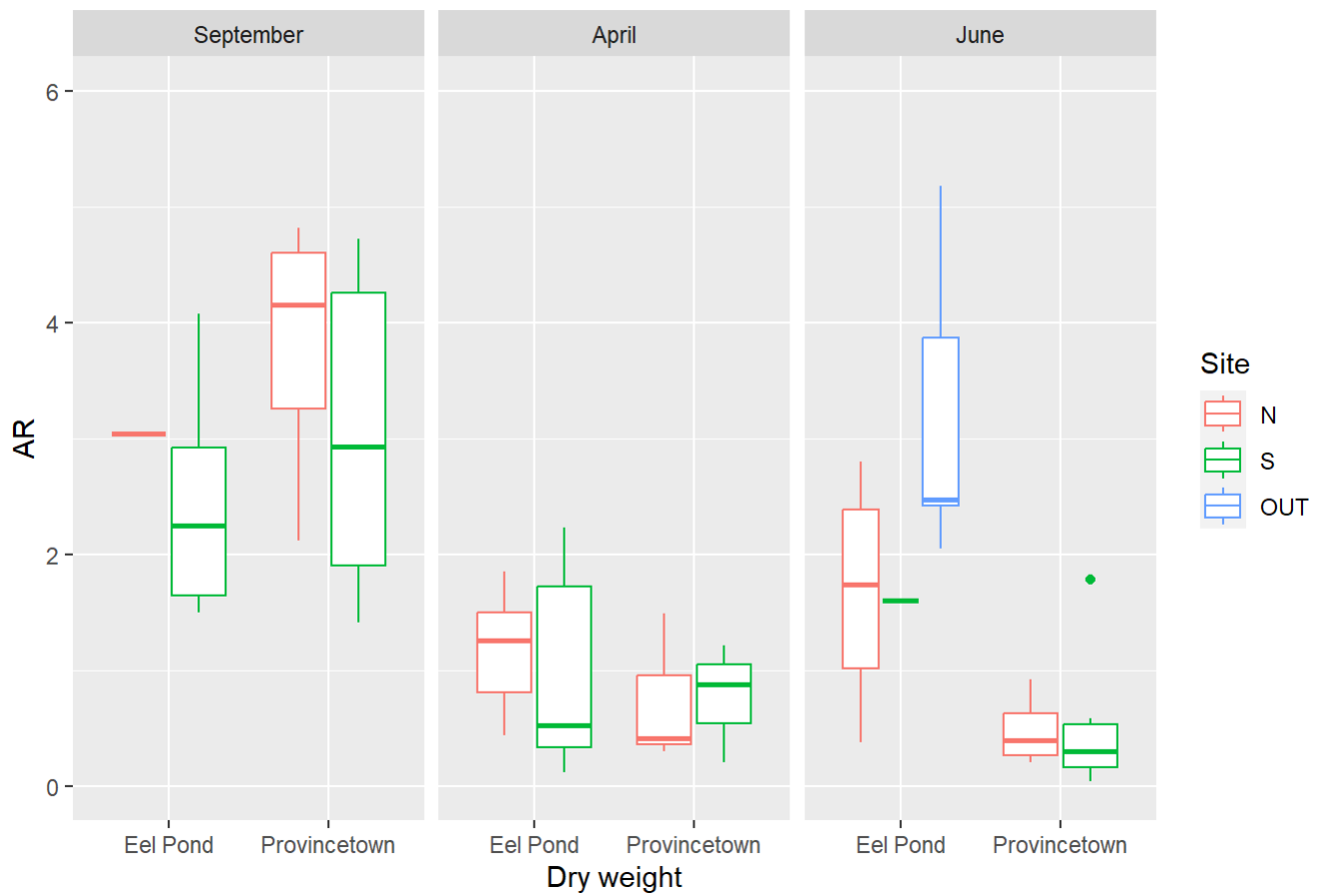
Scaled AR as a function of DW



```
gg3 <- ggplot(data = bd, aes(x=Site, y=AR, col = Treatment))+
  geom_boxplot()+
  xlab("Dry weight") +
  ylab("AR")+
  ylim(0,6)+
  scale_color_discrete(name="Site")+
  ggtitle ('Scaled AR')+
  facet_wrap(~ Month)
gg3
```

Warning: Removed 7 rows containing non-finite values (`stat_boxplot()`).

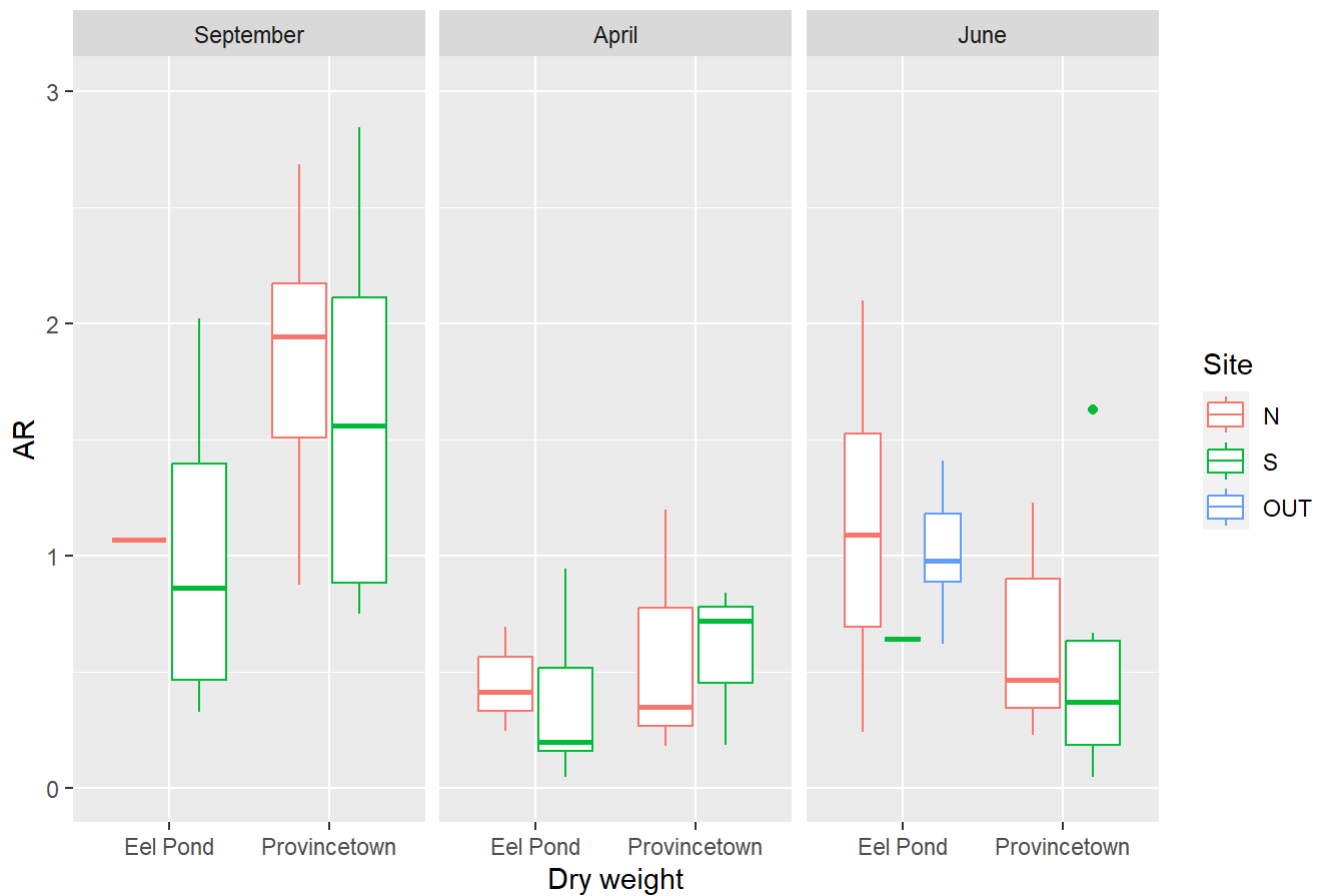
Scaled AR



```
gg4 <- ggplot(data = bd, aes(x=Site, y=AR*Dry.weight.76, col = Treatment))+
  geom_boxplot()+
  xlab("Dry weight") +
  ylab("AR")+
  ylim(0,3)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled AR')+
  facet_wrap(~ Month)
gg4
```

Warning: Removed 3 rows containing non-finite values (`stat_boxplot()`).

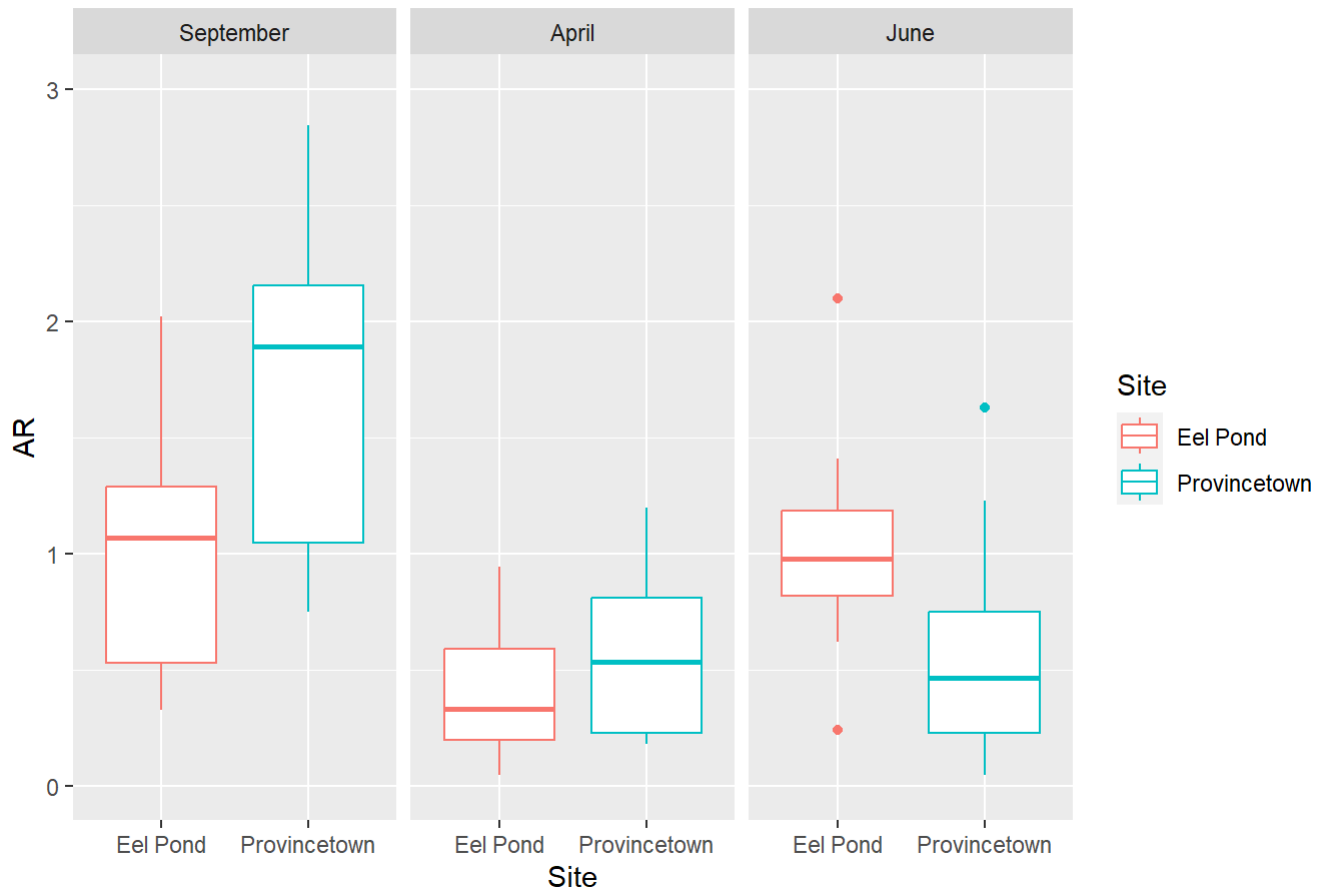
Unscaled AR



```
gg4 <- ggplot(data = bd, aes(x=Site, y=AR*Dry.weight.76, col = Site))+
  geom_boxplot()+
  #xlab("Dry weight") +
  ylab("AR")+
  ylim(0,3)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled AR')+
  facet_wrap(~ Month)
gg4
```

Warning: Removed 3 rows containing non-finite values (`stat_boxplot()`).

Unscaled AR



```
gm1 <- lm(AR*Dry.weight^0.76 ~ Site*Dry.weight*Month+Treatment,
          data = bd)
gm2 <- lm(AR*Dry.weight^0.76 ~ Site+Dry.weight,
          data = bd)
gm3 <- lm(AR ~ Treatment,
          data = bd[bd$Site=="Provincetown",]) #Separate analysis on Provincetown to confirm
summary(gm1)
```

Call:

```
lm(formula = AR * Dry.weight^0.76 ~ Site * Dry.weight * Month +
    Treatment, data = bd)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.18407	-0.26698	-0.07919	0.26462	1.32257

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.17523	0.45048	0.389	0.69879
SiteProvincetown	2.47106	0.78259	3.158	0.00258 **
Dry.weight	3.09740	1.33860	2.314	0.02444 *
MonthApril	0.51011	0.76689	0.665	0.50872

MonthJune	0.13123	0.79744	0.165	0.86989
Treatments	-0.08378	0.14717	-0.569	0.57149
TreatmentOUT	0.37085	0.45098	0.822	0.41444
SiteProvincetown:Dry.weight	-5.74908	2.32024	-2.478	0.01632 *
SiteProvincetown:MonthApril	-2.50614	1.55666	-1.610	0.11314
SiteProvincetown:MonthJune	-2.65692	1.21551	-2.186	0.03310 *
Dry.weight:MonthApril	-3.88836	2.42129	-1.606	0.11402
Dry.weight:MonthJune	-1.69307	1.80279	-0.939	0.35177
SiteProvincetown:Dry.weight:MonthApril	6.49811	3.46105	1.877	0.06576 .
SiteProvincetown:Dry.weight:MonthJune	4.64709	2.64008	1.760	0.08393 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5139 on 55 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.573, Adjusted R-squared: 0.4721

F-statistic: 5.678 on 13 and 55 DF, p-value: 1.958e-06

`summary(gm2)`

Call:

`lm(formula = AR * Dry.weight^0.76 ~ Site + Dry.weight, data = bd)`

Residuals:

Min	1Q	Median	3Q	Max
-1.26383	-0.45350	-0.07471	0.38898	1.60996

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.0858	0.1281	8.473	3.78e-12 ***
SiteProvincetown	0.6307	0.1827	3.452	0.000975 ***
Dry.weight	-0.8748	0.2089	-4.187	8.54e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6312 on 66 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.227, Adjusted R-squared: 0.2036

F-statistic: 9.692 on 2 and 66 DF, p-value: 0.000204

`summary(gm3)`

Call:

`lm(formula = AR ~ Treatment, data = bd[bd$Site == "Provincetown",
])`

Residuals:

Min	1Q	Median	3Q	Max
-2.6168	-1.7122	-0.8458	1.8198	5.8153

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.2268	0.5265	4.229	0.000167 ***
TreatmentS	-0.3921	0.7662	-0.512	0.612107

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.295 on 34 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.007645, Adjusted R-squared: -0.02154

F-statistic: 0.2619 on 1 and 34 DF, p-value: 0.6121

```
gm2 <- lm(AR*Dry.weight^0.76 ~ Site*Dry.weight,
          data = bd)
summary(gm2)
```

Call:

lm(formula = AR * Dry.weight^0.76 ~ Site * Dry.weight, data = bd)

Residuals:

Min	1Q	Median	3Q	Max
-1.24011	-0.47053	0.01922	0.37110	1.32959

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.4496	0.2502	1.797	0.07705 .
SiteProvincetown	1.3986	0.3158	4.429	3.71e-05 ***
Dry.weight	1.1409	0.7210	1.583	0.11838
SiteProvincetown:Dry.weight	-2.1803	0.7498	-2.908	0.00497 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5983 on 65 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.316, Adjusted R-squared: 0.2844

F-statistic: 10.01 on 3 and 65 DF, p-value: 1.644e-05

```
gm2 <- lm(AR*Dry.weight^0.76 ~ Site+Dry.weight,
          data = bd)
summary(gm2)
```

Call:

lm(formula = AR * Dry.weight^0.76 ~ Site + Dry.weight, data = bd)

Residuals:

	Min	1Q	Median	3Q	Max
	-1.26383	-0.45350	-0.07471	0.38898	1.60996

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.0858	0.1281	8.473	3.78e-12 ***
SiteProvincetown	0.6307	0.1827	3.452	0.000975 ***
Dry.weight	-0.8748	0.2089	-4.187	8.54e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6312 on 66 degrees of freedom

(1 observation deleted due to missingness)

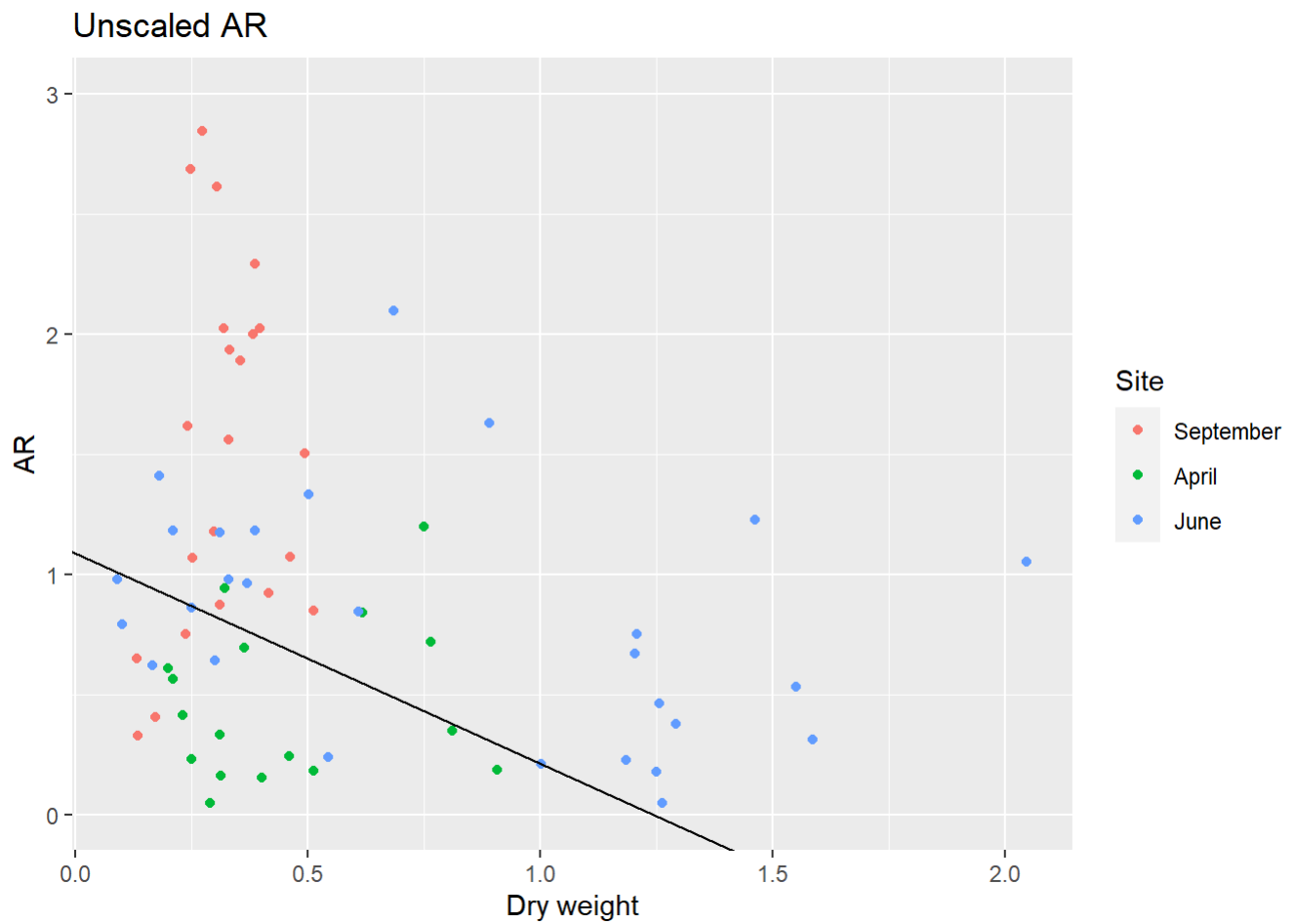
Multiple R-squared: 0.227, Adjusted R-squared: 0.2036

F-statistic: 9.692 on 2 and 66 DF, p-value: 0.000204

```
#effects(gm2)

gg4 <- ggplot(data = bd, aes(x=Dry.weight, y=AR*Dry.weight^.76, col = Month))+
  geom_point()+
  geom_abline(slope = coef(gm2)[["Dry.weight"]],
             intercept = coef(gm2)[["(Intercept)"]])+
  xlab("Dry weight") +
  ylab("AR")+
  ylim(0,3)+
  scale_color_discrete(name="Site")+
  ggtitle ('Unscaled AR')
#+
  #facet_wrap(~ Site)
gg4
```

Warning: Removed 3 rows containing missing values (`geom_point()`).

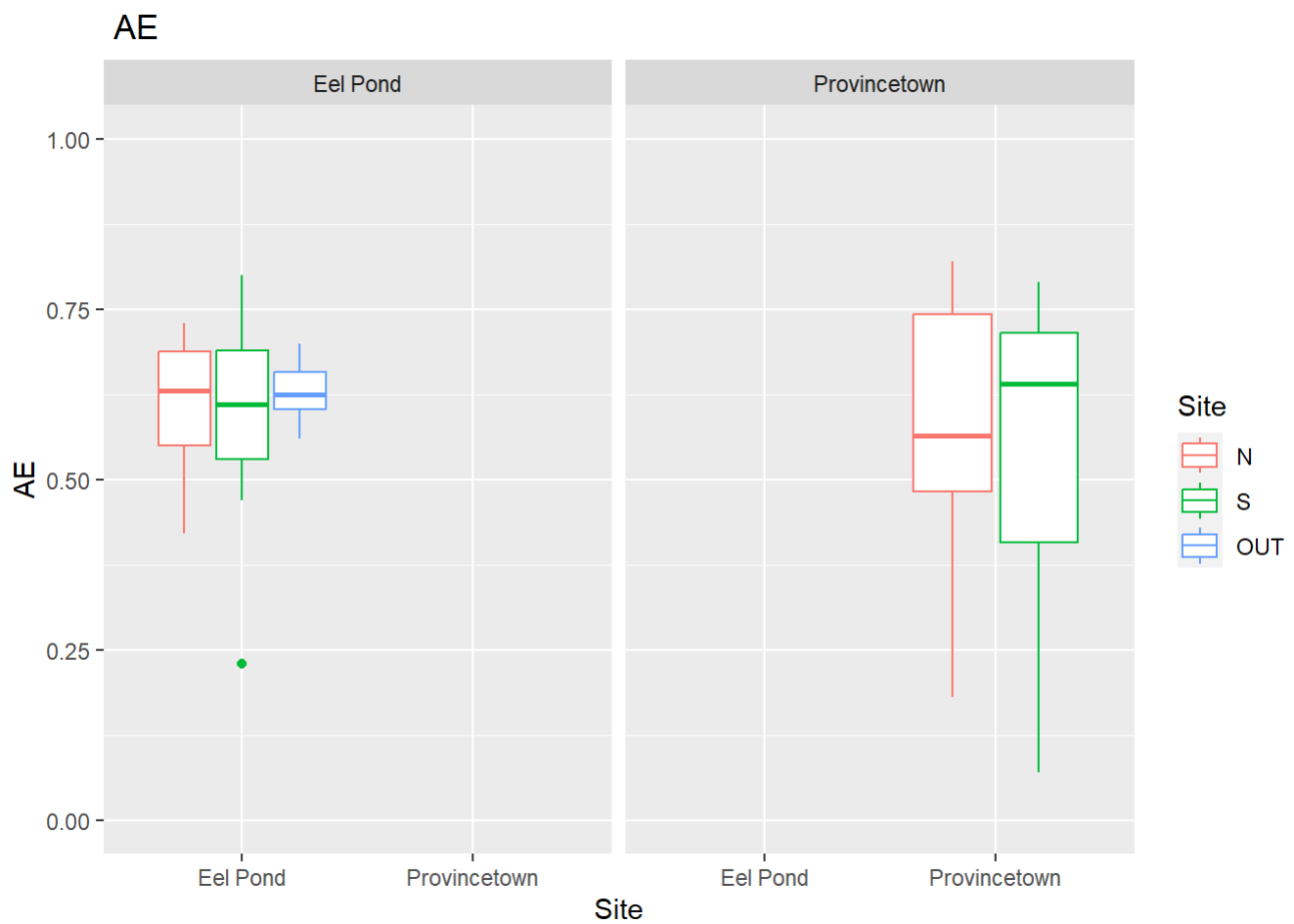


```
bd$Absorption.Efficiency....
```

NULL

```
gg1 <- ggplot(data = bd, aes(x=Site, y=AE, col = Treatment))+
  geom_boxplot()+
  xlab("Site") +
  ylab("AE")+
  ylim(0,1)+
  scale_color_discrete(name="Site")+
  ggtitle (' AE')+
  facet_wrap(~ Site)
gg1
```

Warning: Removed 3 rows containing non-finite values (`stat_boxplot()`).



```
gg1 <- ggplot(data = bd, aes(x=Dry.weight, y=AE, col = Treatment))+
  geom_point()+
  xlab("Site") +
  ylab("AE")+
  ylim(0,1)+
  scale_color_discrete(name="Site")+
  ggtitle (' AE')+
  facet_wrap(~ Site)
gg1
```

Warning: Removed 3 rows containing missing values (`geom_point()`).

AE

