

Physiology Regressions

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View the first few lines of the data

```
MasterDatset <- merge(ClearanceRate, RespirationRate)
```

```
kable(print(head(MasterDatset)))
```

```
##      Date  pH Fed_Unfed Run Replicate Number ClearanceRate_L_hour_mm
## 1 20210914 7.5      <NA>   1         A      1          0.006687805
## 2 20210914 7.5      <NA>   1         B      1          0.003926900
## 3 20210914 7.5      <NA>   1         C      1          0.005119827
## 4 20210914 7.5      <NA>   2         A      2          0.003182271
## 5 20210914 7.5      <NA>   2         B      2          0.010737757
## 6 20210914 7.5      <NA>   2         D      1          0.005400082
## Length.um. resp_ng_L_umLength_hr
## 1    1970.48              0.4870950
## 2    2097.18              1.0429664
## 3    2880.12              0.4885092
## 4    2212.22              1.2484436
## 5    2822.12              1.3554425
## 6    2726.53              0.4339081
```

| Date | pH | Fed_Unfed | Run | Replicate | Number | ClearanceRate_L_hour_mm | Length.um. | resp_ng_L_um |
|----------|-----|-----------|-----|-----------|--------|-------------------------|------------|--------------|
| 20210914 | 7.5 | NA | 1 | A | 1 | 0.0066878 | 1970.48 | |
| 20210914 | 7.5 | NA | 1 | B | 1 | 0.0039269 | 2097.18 | |
| 20210914 | 7.5 | NA | 1 | C | 1 | 0.0051198 | 2880.12 | |
| 20210914 | 7.5 | NA | 2 | A | 2 | 0.0031823 | 2212.22 | |
| 20210914 | 7.5 | NA | 2 | B | 2 | 0.0107378 | 2822.12 | |
| 20210914 | 7.5 | NA | 2 | D | 1 | 0.0054001 | 2726.53 | |

plots

```
colnames(MasterDatset)
```

```
## [1] "Date"          "pH"
## [3] "Fed_Unfed"     "Run"
```

```
## [5] "Replicate" "Number"
## [7] "ClearanceRate_L_hour_mm" "Length.um."
## [9] "resp_ng_L_umLength_hr"
```

Clearance rate vs. Length ::

20210914

```
Clearance_Length_20210914 <- MasterDataset %>%
  dplyr::filter(Date == '20210914') %>%
  ggplot(aes((Length.um./1000), ClearanceRate_L_hour_mm , group =pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05))+
  geom_smooth(method = "lm", alpha = .15, aes(group=pH,colour = factor(pH))) +
  scale_fill_manual(values=c("#D55E00", "#56B4E9")) +
  labs(title = "20210914 Phys Regression: Clearance rate v. shell length",
  y = expression(~Clearance~rate~(" ~L~{-1}~{.}% hr~{-1}~{.}% mm~{-1}~{.}"),
  x = "shell Length (mm)") +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
  theme_classic() +
  facet_wrap(~ pH)
```

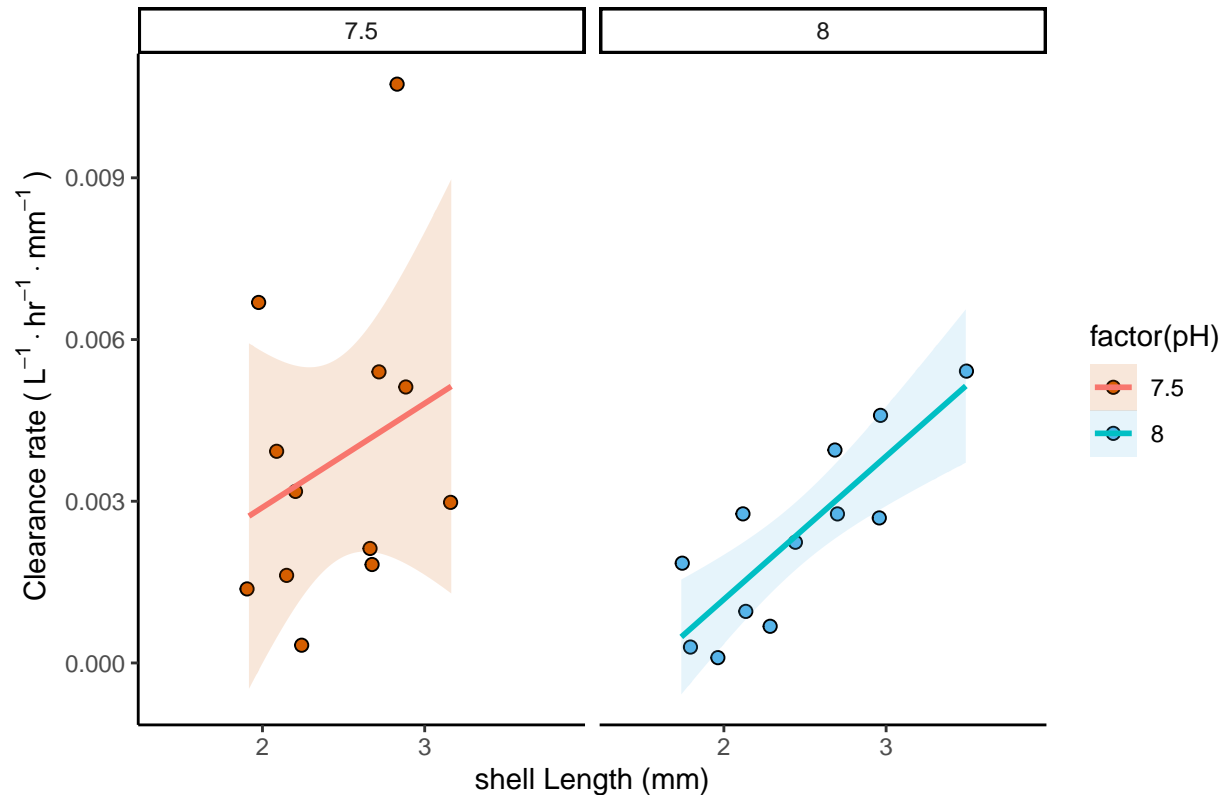
Clearance_Length_20210914

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: position_jitterdodge requires non-overlapping x intervals
```

```
## Warning: position_jitterdodge requires non-overlapping x intervals
```

202010914 Phys Regression: Clearance rate v. shell length



```
# 202109130
Clearance_Length_20210930 <- MasterDataset %>%
  dplyr::filter(Date == '20210930') %>%
  ggplot(aes((Length.um./1000), ClearanceRate_L_hour_mm , group =pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05))+
  geom_smooth(method = "lm", alpha = .15, aes(group=pH,colour = factor(pH))) +
  scale_fill_manual(values=c("#D55E00","#56B4E9")) +
  labs(title = "202010930 Phys Regression: Clearance rate v. shell length",
    y = expression(~Clearance~rate~"(" ~L~^{-1}~"~.% hr^{-1}~"~.% mm^{-1}~"~)"),
    x = "shell Length (mm)") +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
  theme_classic() +
  facet_wrap(~ Fed_Unfed*pH)

Clearance_Length_20210930
```

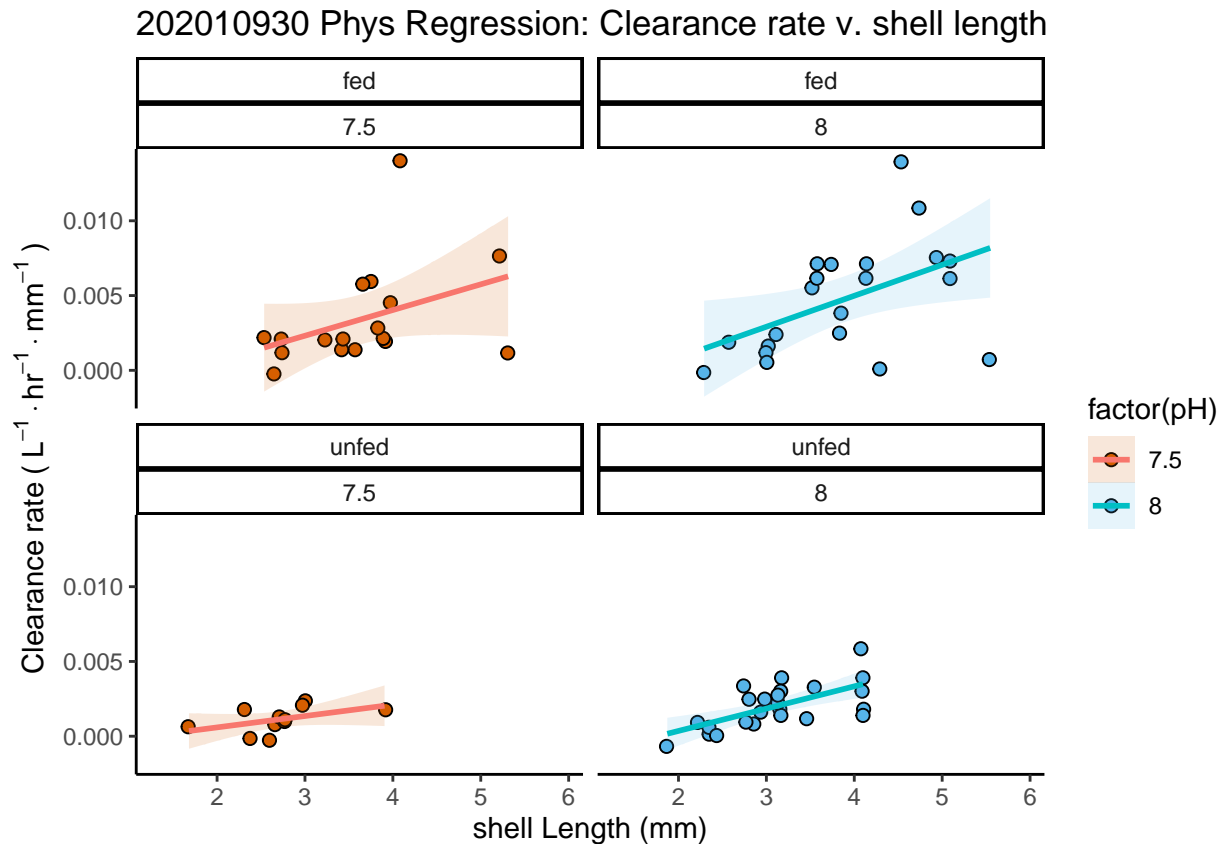
```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: position_jitterdodge requires non-overlapping x intervals
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```



Respiration rate vs. Length ::

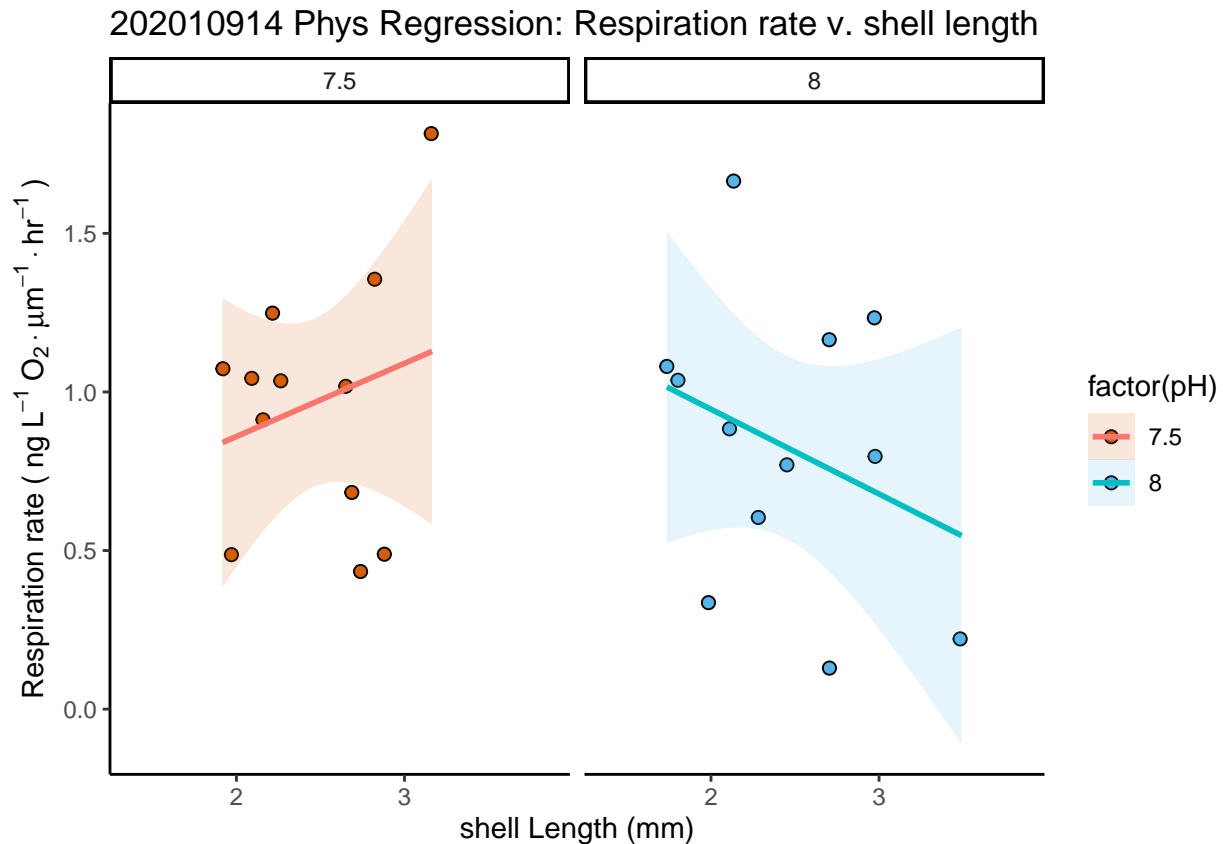
```
# 20210914
Resp_Length_20210914 <- MasterDataset %>%
  dplyr::filter(Date == '20210914') %>%
  ggplot(aes((Length.um./1000), resp_ng_L_umLength_hr , group =pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05))+
  geom_smooth(method = "lm", alpha = .15, aes(group=pH,colour = factor(pH))) +
  scale_fill_manual(values=c("#D55E00", "#56B4E9")) +
  labs(title = "20210914 Phys Regression: Respiration rate v. shell length",
  y = expression(Respiration~rate~"("~ng~L~{-1}~O[2]~{.}%mu*m~{-1}~{.}% hr~{-1}~)" ),
  x = "shell Length (mm)") +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
  theme_classic() +
  facet_wrap(~ pH)

Resp_Length_20210914
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
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# 202109130
Resp_Length_20210930 <- MasterDataset %>%
  dplyr::filter(Date == '20210930') %>%
  ggplot(aes((Length.um./1000), resp_ng_L_umLength_hr , group =pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05))+
  geom_smooth(method = "lm", alpha = .15, aes(group=pH,colour = factor(pH))) +
  scale_fill_manual(values=c("#D55E00","#56B4E9")) +
  labs(title = "202010930 Phys Regression: Respiration rate v. shell length",
    y = expression(Respiration~rate~("("~ng~L^{-1}~0[2]~%.~mu*m^{-1}~%.~hr^{-1}~%")),
    x = "shell Length (mm)") +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
  theme_classic() +
  facet_wrap(~ Fed_Unfed*pH)

Resp_Length_20210930
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## 'geom_smooth()' using formula 'y ~ x'
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```

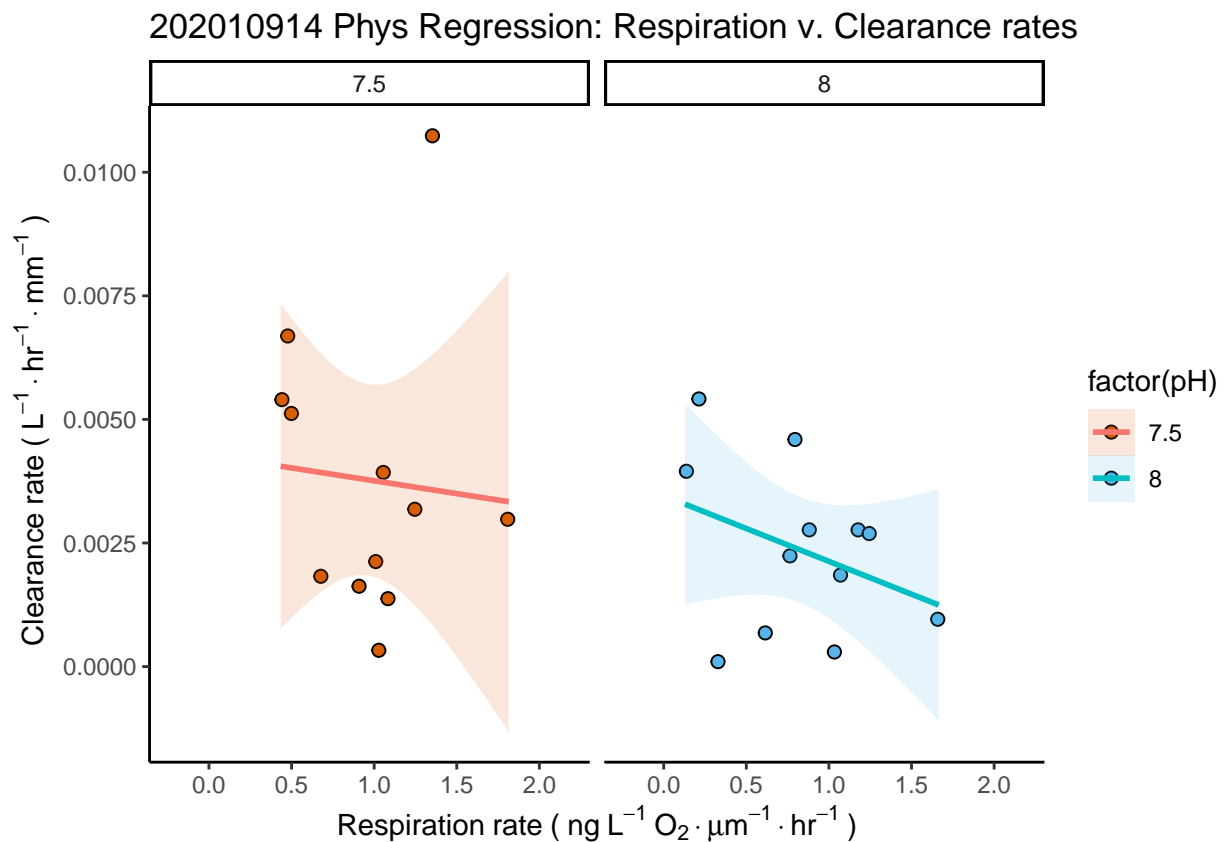


```
Resp_CR_20210914 <- MasterDataset %>%
  dplyr::filter(Date == '20210914') %>%
  ggplot(aes(Resp_ng_L_umLength_hr, ClearanceRate_L_hour_mm, group = pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05)) +
  geom_smooth(method = "lm", alpha = .15, aes(group = pH, colour = factor(pH))) +
  scale_fill_manual(values = c("#D55E00", "#56B4E9")) +
  labs(title = "20210914 Phys Regression: Respiration v. Clearance rates",
    y = expression(~Clearance~rate~"(" ~L~^{-1}~"~.% hr~^{-1}~"~.% mm~^{-1}~"~")"),
    x = expression(Respiration~rate~"(" ~ng~L~^{-1}~"~0[2]~"~.%\mu~m~^{-1}~"~.% hr~^{-1}~"~")")) +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
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```
# 202109130
Resp_CR_20210930 <- MasterDataset %>%
  dplyr::filter(Date == '20210930') %>%
  ggplot(aes(resp_ng_L_umLength_hr, ClearanceRate_L_hour_mm, group = pH, fill = factor(pH))) +
  geom_point(shape = 21, size = 2, position = position_jitterdodge(jitter.width = 0.05)) +
  geom_smooth(method = "lm", alpha = .15, aes(group=pH, colour = factor(pH))) +
  scale_fill_manual(values=c("#D55E00", "#56B4E9")) +
  labs(title = "202010914 Phys Regression: Respiration v. Clearance rates",
    y = expression(~Clearance~rate~"(" ~ L^{-1} %.% hr^{-1} %.% mm^{-1} ~")"),
    x = expression(Respiration~rate~"(" ~ ng~L^{-1} ~O_2 ~\mu m^{-1} ~hr^{-1} ~")") +
  # annotate("text", x=0.3, y=0.2, label = "Low Salinity") +
  # annotate("rect", xmin = 0, xmax = 0.62, ymin = 0, ymax = 0.25, alpha = .1) +
  theme_classic() +
  facet_wrap(~ pH*Fed_Unfed)

Resp_CR_20210930
```

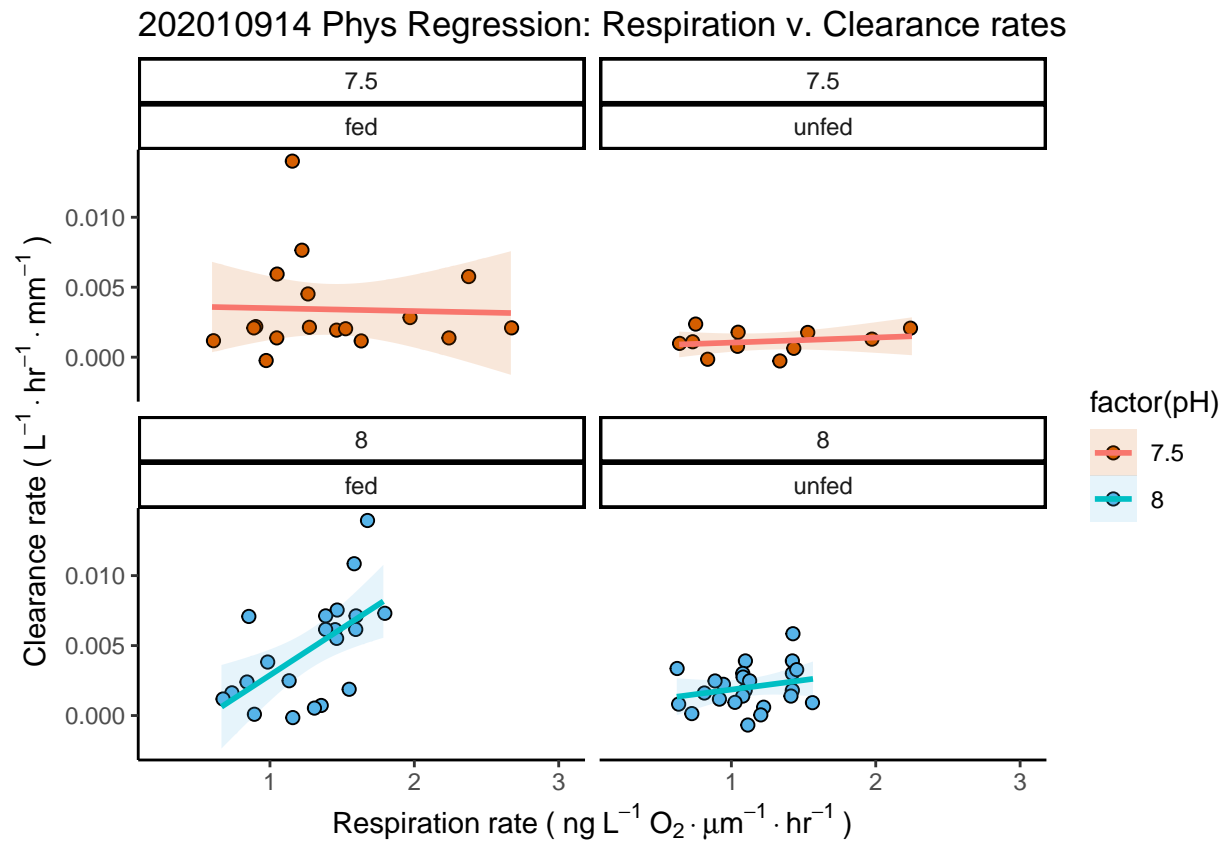
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## 'geom_smooth()' using formula 'y ~ x'
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```



```
# Save plots ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
```

```
pdf(paste0("C:/Users/samjg/Documents/Github_repositories/Airradians_OA/RAnalysis/Output/other/PhysRegression/"),
ggarrange(Clearance_Length_20210914, Clearance_Length_20210930,
  labels = c("A", "B"),
  ncol = 1, nrow = 2)
```

```
## 'geom_smooth()' using formula 'y ~ x'
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```

```
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```

```
dev.off()
```

```
## pdf
```

```
## 2
```

```
pdf(paste0("C:/Users/samjg/Documents/Github_repositories/Airradians_OA/RAnalysis/Output/other/PhysRegre  
ggarrange(Resp_Length_20210914, Resp_Length_20210930,  
  labels = c("A", "B"),  
  ncol = 1, nrow = 2)
```

```
## 'geom_smooth()' using formula 'y ~ x'
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```

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pdf(paste0("C:/Users/samjg/Documents/Github_repositories/Airradians_OA/RAnalysis/Output/other/PhysRegre  
ggarrange(Resp_CR_20210914, Resp_CR_20210930,  
  labels = c("A", "B"),  
  ncol = 1, nrow = 2)
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```

```
## pdf
```

```
## 2
```