

Dissolved CO₂ measurement and other physical parameters

```
# Housekeeping
sweave.dir <- getwd()
library(ggplot2)
library(plyr)
library(reshape)

## Attaching package: 'reshape'

## The following object(s) are masked from 'package:plyr':
##
## rename, round_any

library(devtools)

## Warning: package 'devtools' was built under R version 2.15.1

library(gridExtra)

## Warning: package 'gridExtra' was built under R version 2.15.1

## Loading required package: grid

setwd("~/Dropbox/co2_selection")
source_url("https://raw.githubusercontent.com/edielivon/Useful-R-functions/master/Growth%20curves/00_s")

## Error: http client error (404)

source_url("https://raw.githubusercontent.com/gist/2594954/6f664f27315cf4d2e202329975935afaf60b466d/ggplot2")

CO2 <- CO2[CO2$period == 1 | CO2$period == 6]

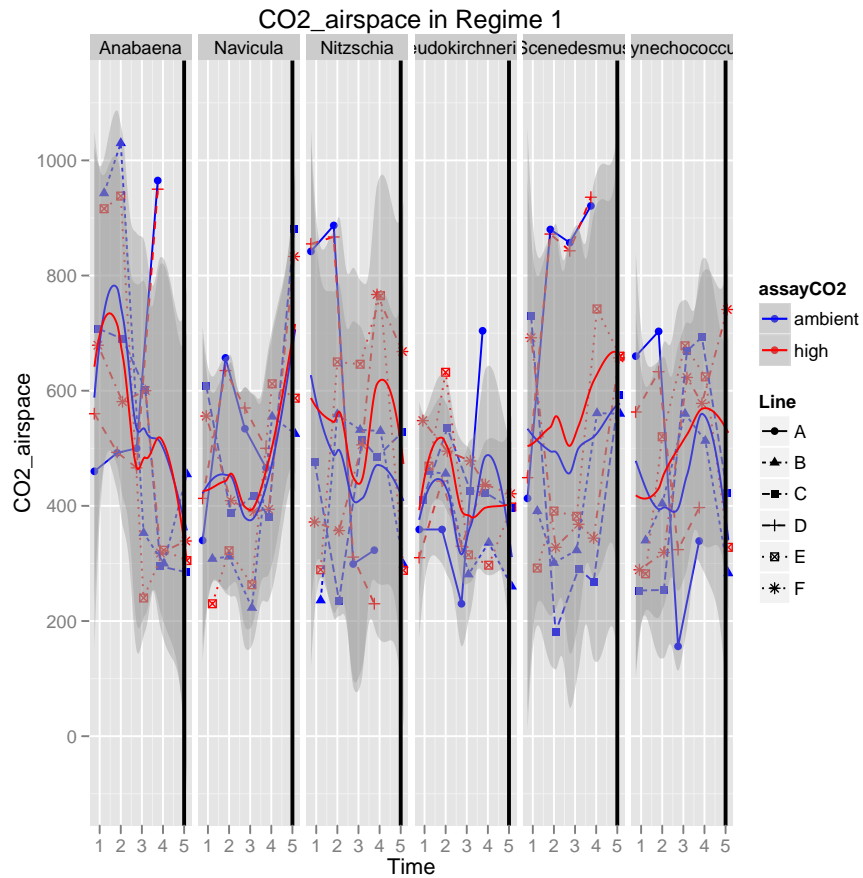
# Load data
load(file = "./Outputs/CO2media.RData")

setwd(sweave.dir)

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
```

```
## loess. Use 'method = x' to change the smoothing method.  
  
## geom_smooth: method="auto" and size of largest group is  
<1000, so using  
## loess. Use 'method = x' to change the smoothing method.  
  
## geom_smooth: method="auto" and size of largest group is  
<1000, so using  
## loess. Use 'method = x' to change the smoothing method.  
  
## geom_smooth: method="auto" and size of largest group is  
<1000, so using  
## loess. Use 'method = x' to change the smoothing method.
```



```
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

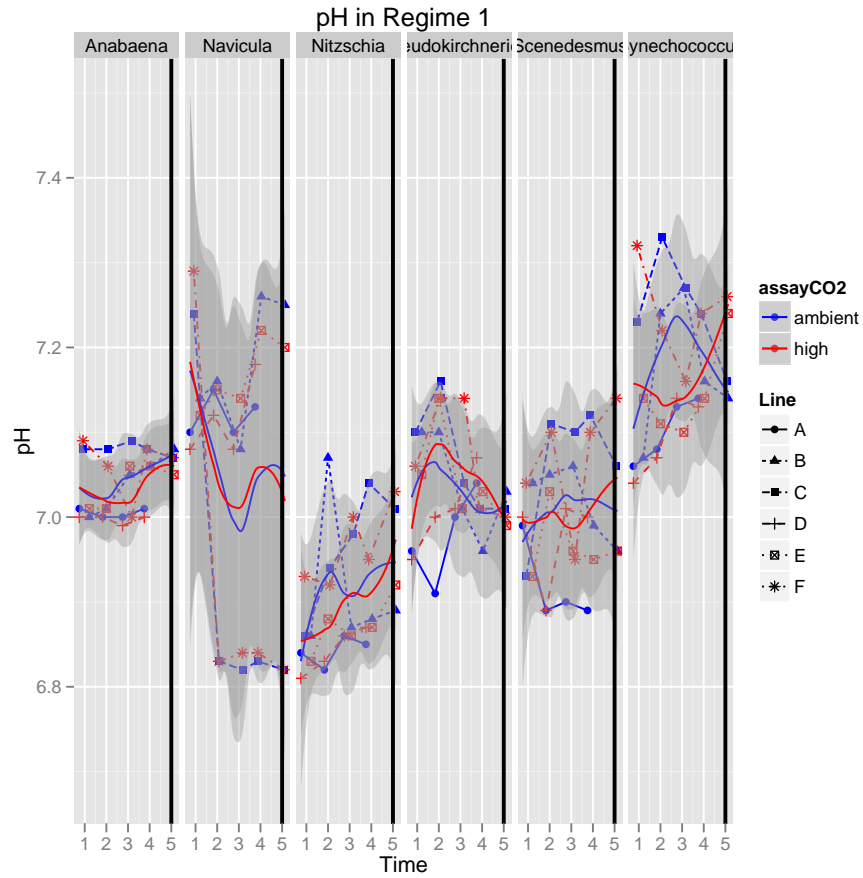
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
```

```
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.
```



```
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

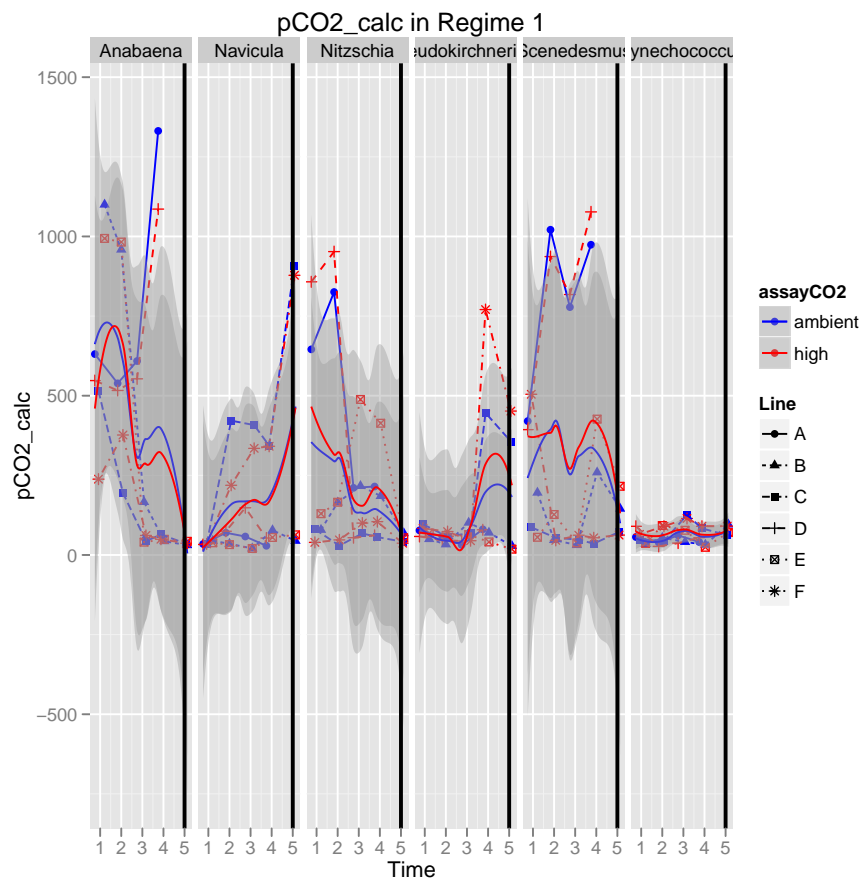
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

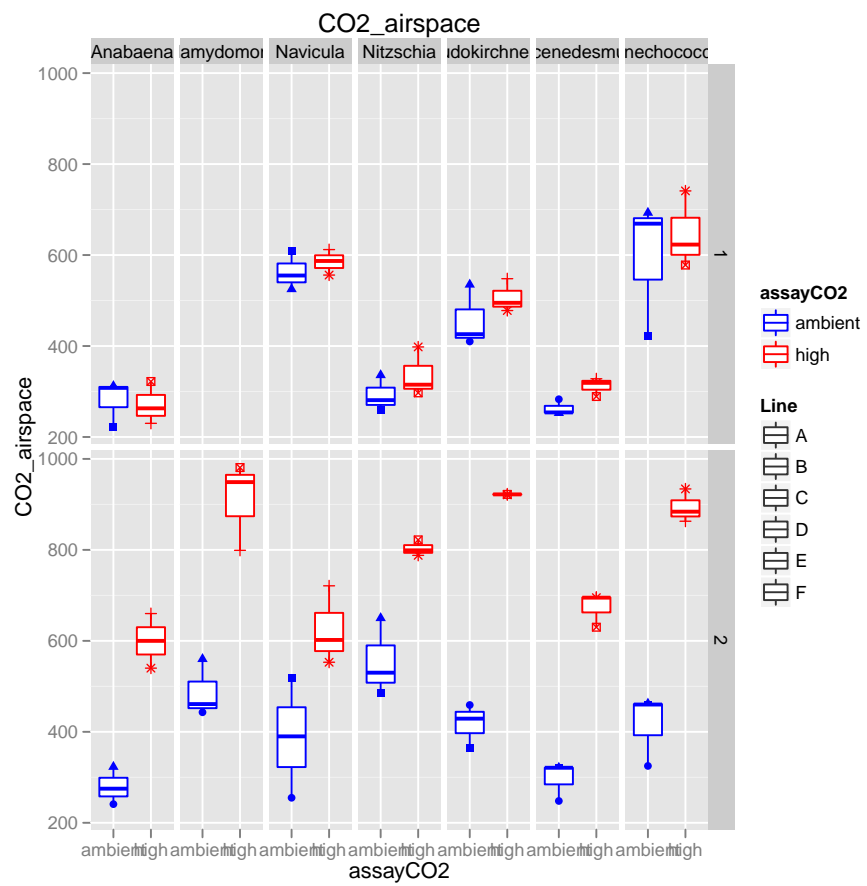
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.
```

```
## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.

## geom_smooth: method="auto" and size of largest group is
<1000, so using
## loess. Use 'method = x' to change the smoothing method.
```





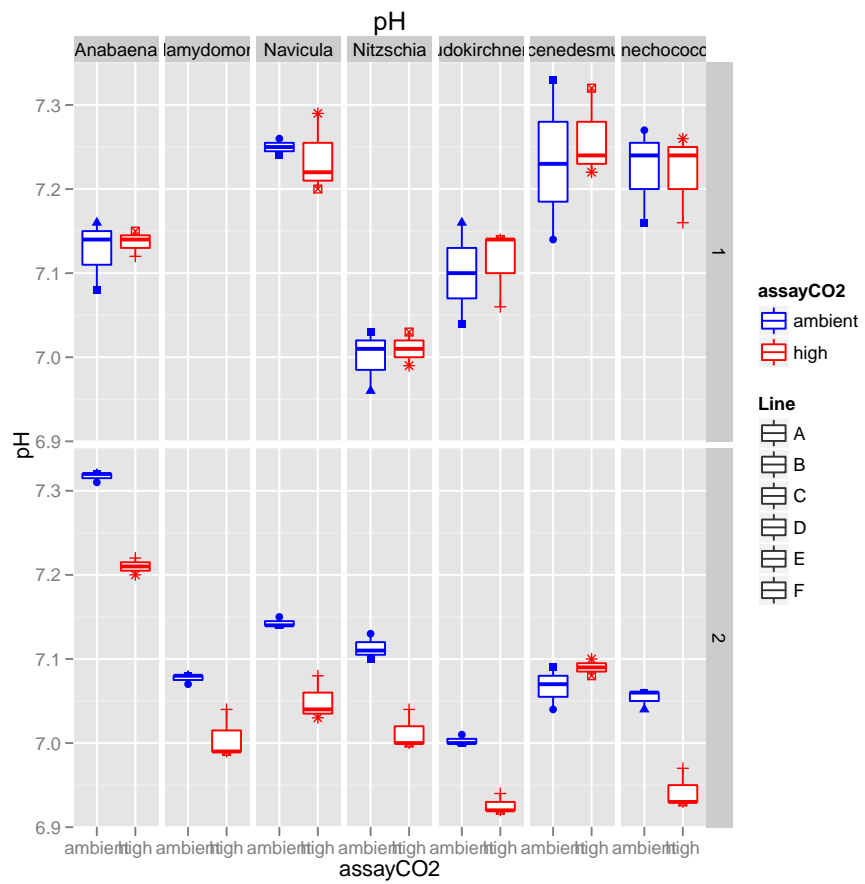
| | Species | assayCO2 | CO2_airspace_1 | CO2_airspace_2 |
|----|---------------------|----------|----------------|----------------|
| 1 | Anabaena | ambient | 326.7 | 296.7 |
| 2 | Anabaena | high | 591.7 | 673.7 |
| 3 | Chlamydomonas | ambient | NaN | 415.7 |
| 4 | Chlamydomonas | high | NaN | 893.7 |
| 5 | Navicula | ambient | 290.7 | 279.7 |
| 6 | Navicula | high | 544.7 | 600.0 |
| 7 | Nitzschia | ambient | 291.0 | 488.0 |
| 8 | Nitzschia | high | 594.3 | 909.7 |
| 9 | Pseudokirchneriella | ambient | 302.7 | 555.3 |
| 10 | Pseudokirchneriella | high | 553.3 | 803.0 |
| 11 | Scenedesmus | ambient | 300.3 | 387.7 |
| 12 | Scenedesmus | high | 584.3 | 625.3 |
| 13 | Synechococcus | ambient | 245.7 | 417.7 |
| 14 | Synechococcus | high | 485.7 | 922.0 |

| | assayCO2 | CO2_airspace_1 | CO2_airspace_2 |
|---|----------|----------------|----------------|
| 1 | ambient | 292.8 | 405.8 |
| 2 | high | 559.0 | 775.3 |

CO2airspace

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|-------------------------------------------------------|----|--------|----------|----------|-----------|--------|
| <i>temp</i> [, "assayCO2"] | 1 | 637602 | 637602.2 | 109.9446 | 1.932e-10 | 1 |
| <i>temp</i> [, "Species"] | 5 | 32149 | 6429.7 | 1.1087 | 3.819e-01 | 1 |
| <i>temp</i> [, "assayCO2"]: <i>temp</i> [, "Species"] | 5 | 4161 | 832.1 | 0.1435 | 9.801e-01 | 1 |
| <i>Residuals</i> | 24 | 139183 | 5799.3 | NA | NA | 1 |

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|-------------------------------------------------------|----|---------|---------|---------|-----------|--------|
| <i>temp</i> [, "assayCO2"] | 1 | 1433752 | 1433752 | 313.710 | 9.567e-17 | 2 |
| <i>temp</i> [, "Species"] | 6 | 425163 | 70861 | 15.505 | 9.287e-08 | 2 |
| <i>temp</i> [, "assayCO2"]: <i>temp</i> [, "Species"] | 6 | 101056 | 16843 | 3.685 | 7.986e-03 | 2 |
| <i>Residuals</i> | 28 | 127969 | 4570 | NA | NA | 2 |



| | Species | assayCO2 | pH_1 | pH_2 |
|----|---------------------|----------|-------|-------|
| 1 | Anabaena | ambient | 7.117 | 7.067 |
| 2 | Anabaena | high | 7.230 | 7.090 |
| 3 | Chlamydomonas | ambient | NaN | 7.053 |
| 4 | Chlamydomonas | high | NaN | 6.943 |
| 5 | Navicula | ambient | 7.097 | 7.317 |
| 6 | Navicula | high | 7.210 | 7.210 |
| 7 | Nitzschia | ambient | 7.123 | 7.077 |
| 8 | Nitzschia | high | 7.147 | 7.007 |
| 9 | Pseudokirchneriella | ambient | 7.167 | 7.113 |
| 10 | Pseudokirchneriella | high | 7.193 | 7.013 |
| 11 | Scenedesmus | ambient | 7.117 | 7.143 |
| 12 | Scenedesmus | high | 7.217 | 7.050 |
| 13 | Synechococcus | ambient | 7.147 | 7.003 |
| 14 | Synechococcus | high | 7.147 | 6.927 |

| | assayCO2 | pH_1 | pH_2 |
|---|----------|-------|-------|
| 1 | ambient | 7.128 | 7.110 |
| 2 | high | 7.191 | 7.034 |

pH

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|-------------------------------------------------------|----|----------|----------|---------|---------|--------|
| <i>temp</i> [, "assayCO2"] | 1 | 0.035469 | 0.035469 | 3.1243 | 0.08985 | 1 |
| <i>temp</i> [, "Species"] | 5 | 0.008792 | 0.001758 | 0.1549 | 0.97648 | 1 |
| <i>temp</i> [, "assayCO2"]: <i>temp</i> [, "Species"] | 5 | 0.019947 | 0.003989 | 0.3514 | 0.87625 | 1 |
| <i>Residuals</i> | 24 | 0.272467 | 0.011353 | NA | NA | 1 |

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|-------------------------------------------------------|----|----------|-----------|---------|-----------|--------|
| <i>temp</i> [, "assayCO2"] | 1 | 0.060952 | 0.0609524 | 209.84 | 1.556e-14 | 2 |
| <i>temp</i> [, "Species"] | 6 | 0.330762 | 0.0551270 | 189.78 | 2.412e-21 | 2 |
| <i>temp</i> [, "assayCO2"]: <i>temp</i> [, "Species"] | 6 | 0.019314 | 0.0032190 | 11.08 | 2.529e-06 | 2 |
| <i>Residuals</i> | 28 | 0.008133 | 0.0002905 | NA | NA | 2 |

| | Species | assayCO2 | pCO2_calc_1 | pCO2_calc_2 |
|----|---------------------|----------|-------------|-------------|
| 1 | Anabaena | ambient | 42.93 | 91.20 |
| 2 | Anabaena | high | 56.71 | 38.51 |
| 3 | Chlamydomonas | ambient | NaN | 72.29 |
| 4 | Chlamydomonas | high | NaN | 900.52 |
| 5 | Navicula | ambient | 80.49 | 148.62 |
| 6 | Navicula | high | 99.86 | 435.74 |
| 7 | Nitzschia | ambient | 57.57 | 119.57 |
| 8 | Nitzschia | high | 84.44 | 1048.47 |
| 9 | Pseudokirchneriella | ambient | 46.06 | 98.63 |
| 10 | Pseudokirchneriella | high | 75.60 | 635.03 |
| 11 | Scenedesmus | ambient | 51.14 | 70.93 |
| 12 | Scenedesmus | high | 61.85 | 362.10 |
| 13 | Synechococcus | ambient | 30.91 | 317.51 |
| 14 | Synechococcus | high | 55.19 | 962.00 |

| | assayCO2 | pCO2_calc_1 | pCO2_calc_2 |
|---|----------|-------------|-------------|
| 1 | ambient | 51.52 | 131.3 |
| 2 | high | 72.27 | 626.1 |

pCO2_calc

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|---------------------------------------------|----|---------|---------|---------|---------|--------|
| <i>temp[, "assayCO2"]</i> | 1 | 3877.5 | 3877.51 | 6.7019 | 0.01611 | 1 |
| <i>temp[, "Species"]</i> | 5 | 8484.1 | 1696.82 | 2.9328 | 0.03325 | 1 |
| <i>temp[, "assayCO2"]:temp[, "Species"]</i> | 5 | 417.9 | 83.58 | 0.1445 | 0.97982 | 1 |
| <i>Residuals</i> | 24 | 13885.7 | 578.57 | NA | NA | 1 |

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) | regime |
|---------------------------------------------|----|---------|---------|---------|-----------|--------|
| <i>temp[, "assayCO2"]</i> | 1 | 2570697 | 2570697 | 771.37 | 6.359e-22 | 2 |
| <i>temp[, "Species"]</i> | 6 | 1526029 | 254338 | 76.32 | 4.782e-16 | 2 |
| <i>temp[, "assayCO2"]:temp[, "Species"]</i> | 6 | 1062164 | 177027 | 53.12 | 5.148e-14 | 2 |
| <i>Residuals</i> | 28 | 93313 | 3333 | NA | NA | 2 |