

# Pondo\_\_Allom\_\_Params

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## Introduction:

### Install the BAAD Package:

Install the package from github:

```
#install.packages("devtools")
#devtools::install_github("richfitz/datastorr")
#devtools::install_github("traitecoevo/baad.data")
```

### Review the data:

```
baad <- baad.data::baad_data()
d_baad <- baad$data
head(d_baad)
```

```
##      studyName      location latitude longitude vegetation map mat grouping
## 1 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
## 2 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
## 3 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
## 4 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
## 5 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
## 6 Abe1981 Japan-Oumu-46      45      143      BorF  NA  NA      <NA>
##      lai      species      speciesMatched      family pft
## 1 NA Abies sachalinensis Abies sachalinensis Pinaceae EA
## 2 NA Abies sachalinensis Abies sachalinensis Pinaceae EG
## 3 NA Abies sachalinensis Abies sachalinensis Pinaceae EG
## 4 NA Abies sachalinensis Abies sachalinensis Pinaceae EG
## 5 NA Abies sachalinensis Abies sachalinensis Pinaceae EG
## 6 NA Abies sachalinensis Abies sachalinensis Pinaceae EG
##      growingCondition status light age a.lf a.ssba a.ssbh a.ssbh a.ssbh a.shba
## 1 PM NA <NA> NA NA NA NA NA NA NA
## 2 PM NA <NA> NA NA NA NA NA NA NA
## 3 PM NA <NA> NA NA NA NA NA NA NA
## 4 PM NA <NA> NA NA NA NA NA NA NA
## 5 PM NA <NA> NA NA NA NA NA NA NA
## 6 PM NA <NA> NA NA NA NA NA NA NA
##      a.shbh a.shbh a.ssbh a.ssbh a.ssbh a.stba a.stbh a.stbh a.stbh
## 1 NA NA NA NA NA 0.18973040 0.13074052 0.066508302
## 2 NA NA NA NA NA 0.14286569 0.09731397 0.056410438
## 3 NA NA NA NA NA 0.19658523 0.07068583 0.035298935
## 4 NA NA NA NA NA 0.07068583 0.04523893 0.020611989
## 5 NA NA NA NA NA 0.02198274 0.01583677 0.008992024
## 6 NA NA NA NA NA 0.18957602 0.12692348 0.059828490
##      a.cp a.cs h.t h.c d.ba d.bh h.bh d.cr c.d m.lf m.ss m.sh m.sb
## 1 NA NA 21.96 8.90 0.4915 0.408 1.3 NA 13.06 49.2 NA NA NA
## 2 NA NA 19.70 8.02 0.4265 0.352 1.3 NA 11.68 28.0 NA NA NA
```

```
## 3  NA  NA 20.10  9.50 0.5003 0.300  1.3  NA 10.60 19.9  NA  NA  NA
## 4  NA  NA 19.23 11.60 0.3000 0.240  1.3  NA  7.63 11.1  NA  NA  NA
## 5  NA  NA 16.14  9.35 0.1673 0.142  1.3  NA  6.79  3.8  NA  NA  NA
## 6  NA  NA 22.26 11.02 0.4913 0.402  1.3  NA 11.24 33.4  NA  NA  NA
##   m.st m.so m.br m.rf m.rc m.rt m.to a.ilf ma.ilf r.st r.ss r.sb r.sh
## 1 516.8 566.0 113.8  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
## 2 427.7 455.7  84.9  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
## 3 255.0 274.9  30.2  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
## 4 172.9 184.0  14.4  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
## 5  58.6  62.4   4.6  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
## 6 561.9 595.3  61.3  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
##   n.lf n.ss n.sb n.sh n.rf n.rc
## 1  NA  NA  NA  NA  NA  NA
## 2  NA  NA  NA  NA  NA  NA
## 3  NA  NA  NA  NA  NA  NA
## 4  NA  NA  NA  NA  NA  NA
## 5  NA  NA  NA  NA  NA  NA
## 6  NA  NA  NA  NA  NA  NA
```

Refine (subset) the data for Pinus Ponderosa:

```
pipo <- d_baad[ which(d_baad$species == 'Pinus ponderosa'), ]
#head(pipo)
```

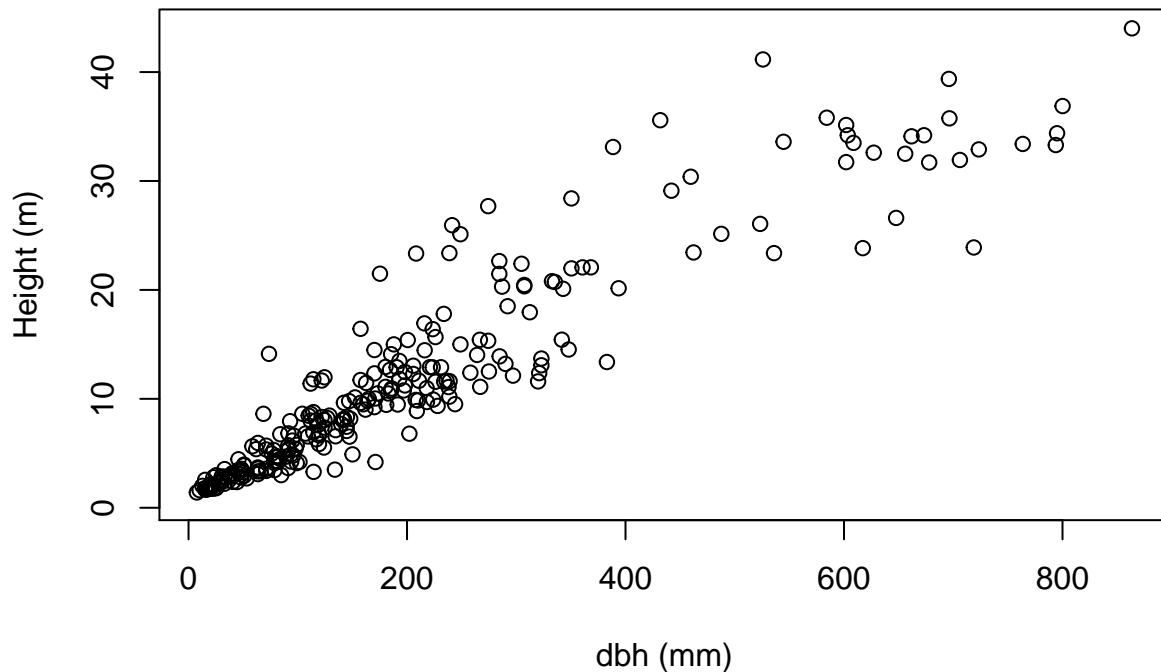
Plot raw data, dbh to height.

```
# Set variables from the data.

# Diameter at breast height (dbh) will be used for most allometric calculations
dbh <- (pipo$d.bh)*1000
# Height
h <- (pipo$h.t)

plot(h~dbh,
     main="Diameter at breast height (dbh) to Height",
     xlab = "dbh (mm)",
     ylab = "Height (m)")
```

## Diameter at breast height (dbh) to Height



FATES uses the dbh to height relationship from O'Brien et al., 1995. The  $\log_{10}(\text{Height } (m))$  is regressed on  $\log_{10}(\text{DBH } (mm))$ . Where slope is p1 or `fates_allom_d2h1` and intercept is p2 or `fates_allom_d2h2` in the parameter file.

$$\log_{10} \text{Height} = \log_{10} \text{DBH} * \text{slope} + \text{intercept}$$

So modeled height would be. I want to solve for the best fit p1 and p2 given height and dbh data from BAAD.

$$\text{Height} = 10^{(\log_{10}(\min(d, \text{dbhmax})) * p1 + p2)}$$

*# But first I will test out just a linear model*

```
d2hmod <- lm(h~dbh)
coef(d2hmod)
```

```
## (Intercept)      dbh
##  1.88991834  0.04858541
```

*# Then a linear model with log10(h) regressed on log10(dbh)*

```
d2hmodlog <- lm(log10(h)~log10(dbh))
coef(d2hmodlog)
```

```
## (Intercept) log10(dbh)
## -0.8150832  0.8181127
```

Next, I will create a function to represent the O'Brien calculation used for dbh to height relationships.

```
obrien <- function(dbh, p1, p2){
  height <- 10^((log10(dbh))* p1 + p2)
  return(height)
}
```

```

dbins <- c(100,200,300,400,500,600,700,800,900) # Remember in O'Brien dbh is in mm.

# Use default parameters from O'Brien et al 1995
default <- obrien(dbins, 0.7, -0.2)
# Use the parameters from the log10 linear model d2hmodlog
lmfit <- obrien(dbins, 0.82, -0.82)

coef(lm(default~dbins))

## (Intercept)      dbins
## 11.67774249  0.07124032

coef(lm(lmfit~dbins))

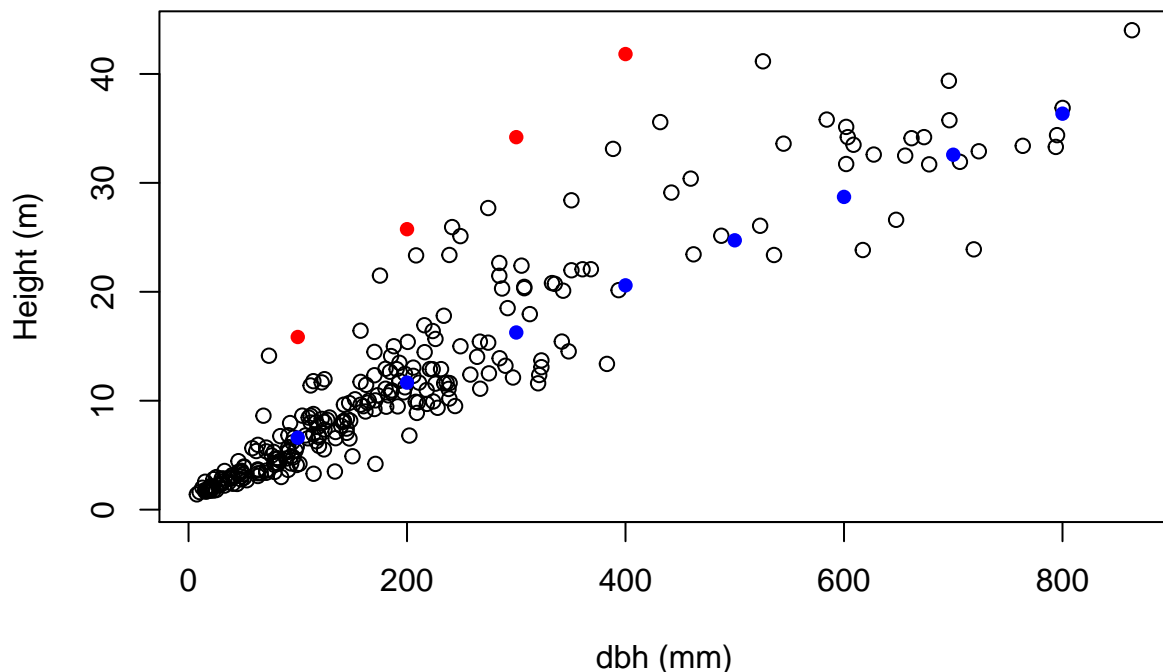
## (Intercept)      dbins
##  3.45859976  0.04142493

plot(h~dbh,
     main="Diameter at breast height (dbh) to Height",
     xlab = "dbh (mm)",
     ylab = "Height (m)")

points(default~dbins, col="red", pch=16) # default O'Brien slope (0.7) and intercept (-0.2)
points(lmfit~dbins, col="blue", pch=16) # BAAD data slope (0.82) and intercept (-0.82)

```

### Diameter at breast height (dbh) to Height



```

#curve(1.89+0.05*x, add=T, col="blue", lwd=1) # linear model coefficients
#curve(-0.82 + (0.82*x), add=T, col="green", lwd=2) # log regression coefficients from d2hmodlog
#curve(10^(-0.2)+(10^0.7*x), add=T, col="red", lwd=4) # linear model using default coefficients from O'
#curve(11.7 + 0.07*x, add=T, col="red", lty=2, lwd=2) # linear model using default coefficients from O'
#curve(3.46 + 0.04*x, add=T, col="blue", lty=2, lwd=2) # linear fit of slope and intercept to points mo

```