

Med and Max SVL comparsion

1. Min-Max Snout-Vent-Length comparison:

Pgls regression (max SVL):

```
mod_max <- pgls(log10(DF) ~log10(SVL),c_data_max,"ML")
summary(mod_max)

##
## Call:
## pgls(formula = log10(DF) ~ log10(SVL), data = c_data_max, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.039787 -0.012576  0.004247  0.012590  0.032447
##
## Branch length transformations:
##
## kappa  [Fix]   : 1.000
## lambda [ ML]   : 0.614
## lower bound : 0.000, p = 0.19339
## upper bound : 1.000, p = 0.33543
## 95.0% CI    : (NA, NA)
## delta  [Fix]   : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.86945     0.45538 10.6931 2.148e-11 ***
## log10(SVL)  -0.91398     0.29259 -3.1238 0.004126 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01998 on 28 degrees of freedom
## Multiple R-squared: 0.2584, Adjusted R-squared: 0.232
## F-statistic: 9.758 on 1 and 28 DF, p-value: 0.004126
```

Pgls regression (med SVL):

```
mod_med <- pgls(log10(DF) ~log10(SVL),c_data_med,"ML")
summary(mod_med)

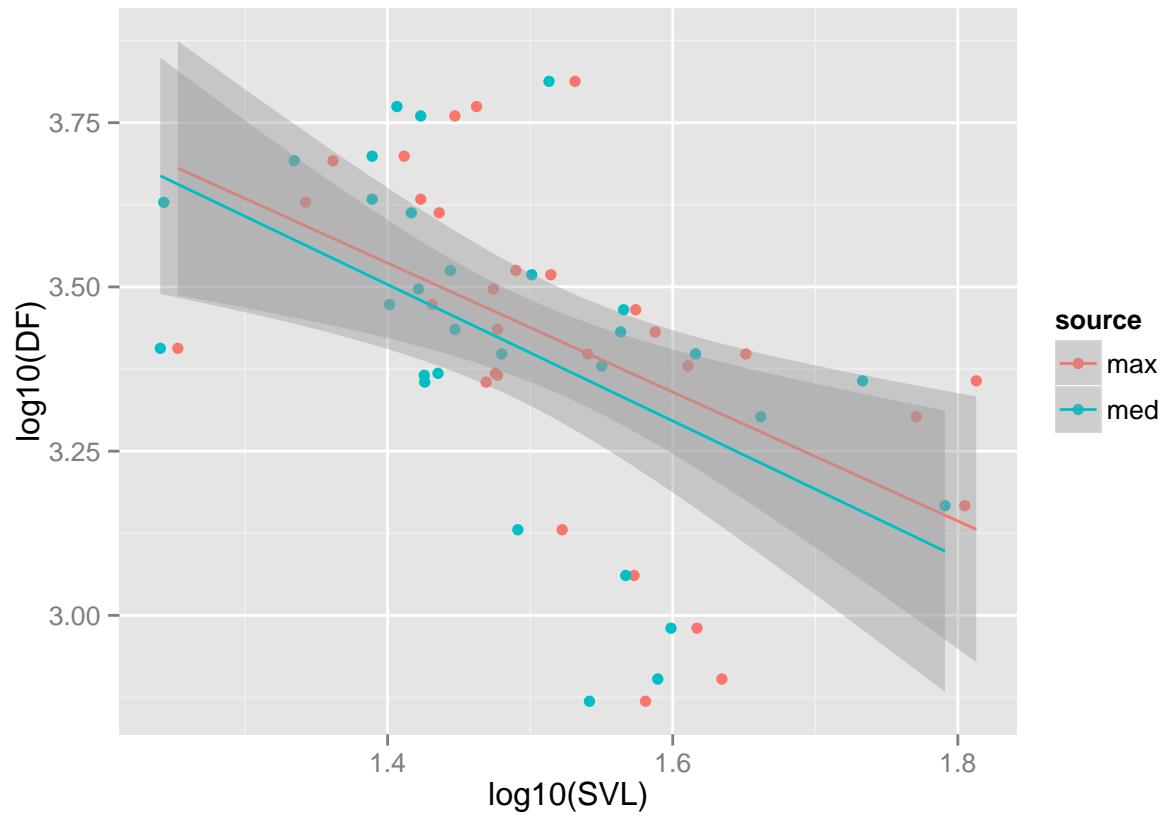
##
## Call:
## pgls(formula = log10(DF) ~ log10(SVL), data = c_data_med, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -0.042195 -0.013183 -0.002727 0.008226 0.031049
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.742
## lower bound : 0.000, p = 0.1081
## upper bound : 1.000, p = 0.50584
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 4.96739 0.44610 11.1351 8.516e-12 ***
## log10(SVL) -0.99844 0.29169 -3.4229 0.001925 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02038 on 28 degrees of freedom
## Multiple R-squared: 0.295, Adjusted R-squared: 0.2698
## F-statistic: 11.72 on 1 and 28 DF, p-value: 0.001925
```

Os coeficientes são ligeiramente diferentes entre os dois modelos. No modelo com tamanho corpóreo médio o β é menor, ou seja, a frequência dominante decai mais rapidamente. O R^2 do modelo com SVL_med é maior do que o com o max.

Regression Graphs:

```
g1 <- ggplot(mat,aes(y=log10(DF),x=log10(SVL),colour=source))+
  geom_point()+
  geom_smooth(method="lm",se=T);g1
```



7. Links summary:

1. [raw data](#)
2. [source code](#)
2. [species list](#)
3. [Study phylogeny](#)
4. Sensitive analysis code