

Supplement S2 (Scripts for R and analysis) to: Añino Y. et al. 2024: Estimating the body size of orchid bees (Hymenoptera: Apidae: Euglossini) using the distance between their tegulae. — *Eur. J. Entomol.* **121**: 37–39.

# Estimation of Body Size Using Intertegular Span in Orchid bee.

Año et al. 2023  
2023-09-13

## Complete database

All individuals are included

```
library(readxl)
library(MASS)
library(ggplot2)
library(rstatix)
library(dplyr)
library(ggrepel)
library(viridis)
library(tidyverse)

data = read_excel("/Users/yoss/Desktop/ITD_Euglossini.xlsx", sheet = "BASE")
```

## Complete database

All individuals are included

```
num_ind <- 23
Color <- viridis(num_ind)

df_ITD <- data %>%
  group_by(Specie) %>%
  summarise_at(vars(ITD), list(mean=mean, sd=sd)) %>%
  as.data.frame()

colnames(df_ITD) <- c("SPECIE", "ITD_MEAN", "STD_ITD")

df_MG <- data %>%
  group_by(Specie) %>%
  summarise_at(vars(dryweight), list(mean=mean, sd=sd)) %>%
  as.data.frame()

colnames(df_MG) <- c("SPECIE", "MG_MEAN", "STD_MG")

data_cross <- inner_join(df_ITD, df_MG, by="SPECIE")
Genus <- c(rep("Eufriesea",4), rep("Euglossa",15), rep("Eulaema",3), rep("Exaraete",1))
data_cross <- data_frame(Genus, data_cross$SPECIE, data_cross$ITD_MEAN, data_cross$STD_ITD,
  data_cross$MG_MEAN, data_cross$STD_MG)
colnames(data_cross) <- c("Genus", "SPECIE", "ITD_MEAN", "STD_ITD", "MG_MEAN", "STD_MG")

library(kableExtra)
DataA <- kable(data_cross, format = "markdown", col.names = c("Genus", "Specie", "ITD_Mean", "ITD_SD", "DryWeight_Mean", "DryWeight_SD"))
DataA
```

Genus	Specie	ITD_Mean	ITD_SD	DryWeight_Mean	DryWeight_SD
Eufriesea	Eufriesea anisochlora	4.866000	0.2023648	0.0926000	0.0109909
Eufriesea	Eufriesea machroglossa	6.015200	0.0281549	0.1312000	0.0214639
Eufriesea	Eufriesea pulchra	6.187400	0.0623602	0.1534000	0.0432296
Eufriesea	Eufriesea surinamensis	5.729200	0.0534154	0.1614000	0.0244499
Euglossa	Euglossa asarophora	4.195200	0.1207506	0.0570000	0.0106536
Euglossa	Euglossa cognota	3.980200	0.1699109	0.0442000	0.0106864
Euglossa	Euglossa cybella	4.075200	0.0492768	0.0482000	0.0059749
Euglossa	Euglossa dadsoni	3.557800	0.0493477	0.0336000	0.0049392
Euglossa	Euglossa despecta	3.460400	0.3272939	0.0256000	0.0055946
Euglossa	Euglossa imperialis	4.145400	0.0696118	0.0676000	0.0094499
Euglossa	Euglossa maculilabris	3.692000	0.1514034	0.0363333	0.0056882
Euglossa	Euglossa mixta	3.731200	0.1403627	0.0346000	0.0051769
Euglossa	Euglossa purpurea	3.542000	0.0420000	0.0233333	0.0083865
Euglossa	Euglossa sapphirina	3.043800	0.0360375	0.0234000	0.0060663
Euglossa	Euglossa tridentata	3.804600	0.1427806	0.0410000	0.0067454
Euglossa	Euglossa turbinifex	3.300667	0.0773649	0.0280000	0.0095394
Euglossa	Euglossa variabilis	3.142333	0.1014413	0.0280000	0.0072111
Euglossa	Euglossa villosa	3.390200	0.2044228	0.0328000	0.0074967
Euglossa	Euglossa villosiventris	3.552333	0.0490748	0.0436667	0.0056882
Eulaema	Eulaema cirigliata	6.468000	0.0628259	0.2124000	0.0439010
Eulaema	Eulaema meriana	7.733000	0.1623946	0.4058000	0.0306953
Eulaema	Eulaema nigrita	5.043800	0.0592427	0.1552000	0.0145671
Exaraete	Exaraete smragdina	4.848000	0.0959557	0.1552000	0.0188600

## Power regression between dry body mass and ITD (mm). AVERAGE

```
model_power_cross <- nls(ITD_MEAN ~ a * MG_MEAN^b, data = data_cross, start = list(a = 1, b = 1))
model1 <- lm(log(ITD_MEAN) ~ log(MG_MEAN), data = data_cross)
```

## Coefficients

```
summary(model_power_cross)

##
## Formula: ITD_MEAN ~ a * MG_MEAN^b
## Parameters:
## Estimate Std. Error t value Pr(>|t|)
## a 10.18147 0.43194 23.57 <2e-16 ***
## b 0.31425 0.01711 18.36 2.05e-14 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.3227 on 21 degrees of freedom
## Number of iterations to convergence: 8
## Achieved convergence tolerance: 4.979e-06
```

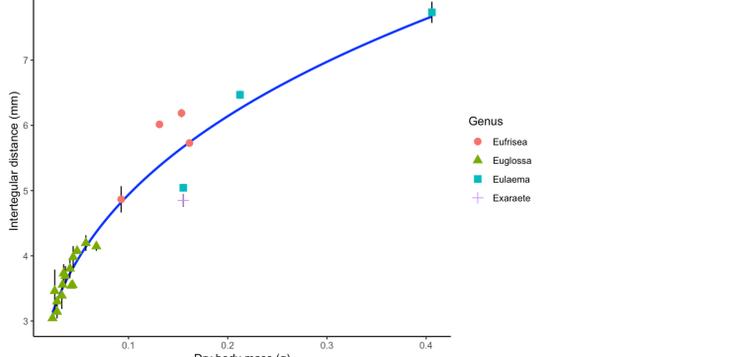
## Adjusted R-squared and p-value

```
summary(model1)

##
## Call:
## lm(formula = log(ITD_MEAN) ~ log(MG_MEAN), data = data_cross)
##
## Residuals:
## Min 1Q Median 3Q Max
## -0.15215 -0.03977 0.01427 0.03821 0.11582
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.31006 0.04938 46.78 <2e-16 ***
## log(MG_MEAN) 0.31097 0.01719 18.09 2.77e-14 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.06482 on 21 degrees of freedom
## Multiple R-squared: 0.9397, Adjusted R-squared: 0.9368
## F-statistic: 327.2 on 1 and 21 DF, p-value: 2.768e-14
```

## Graphic

```
library(ggplot2)
ggplot(data_cross, aes(x = MG_MEAN, y = ITD_MEAN)) +
  geom_smooth(method = "nls", formula = y ~ a * x^b, se = FALSE, color = "blue", method.args = list(start = list(a = 1, b = 1))) +
  labs(x = "Dry body mass (g)", y = "Intertegular distance (mm)") +
  geom_errorbar(aes(ymin = ITD_MEAN - STD_ITD, ymax = ITD_MEAN + STD_ITD)) +
  theme_classic() + geom_point(aes(shape=Genus, color=Genus), size=3)
```



## Power regression between dry body mass and ITD (mm) ALL INDIVIDUALS

```
model_potencial <- nls(ITD ~ a * dryweight^b, data = data, start = list(a = 1, b = 1))
model2 <- lm(log(ITD) ~ log(dryweight), data = data)
```

## Coefficients

```
summary(model_potencial)

##
## Formula: ITD ~ a * dryweight^b
## Parameters:
## Estimate Std. Error t value Pr(>|t|)
## a 9.952767 0.227917 43.67 <2e-16 ***
## b 0.303193 0.009388 32.30 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.3864 on 103 degrees of freedom
## Number of iterations to convergence: 8
## Achieved convergence tolerance: 3.641e-07
```

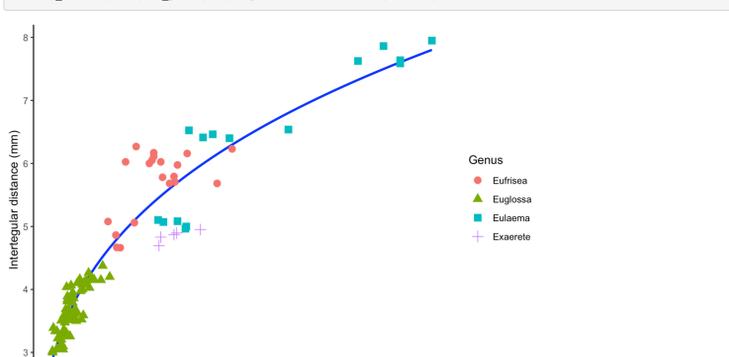
## Adjusted R-squared and p-value

```
summary(model2)

##
## Call:
## lm(formula = log(ITD) ~ log(dryweight), data = data)
##
## Residuals:
## Min 1Q Median 3Q Max
## -0.179061 -0.053562 0.007899 0.050463 0.206432
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.280855 0.026771 85.20 <2e-16 ***
## log(dryweight) 0.297740 0.009425 31.59 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.07903 on 103 degrees of freedom
## Multiple R-squared: 0.9065, Adjusted R-squared: 0.9055
## F-statistic: 998 on 1 and 103 DF, p-value: < 2.2e-16
```

## Graphic

```
ggplot(data, aes(x = dryweight, y = ITD)) +
  geom_smooth(method = "nls", formula = y ~ a * x^b, se = FALSE, color = "blue", method.args = list(start = list(a = 1, b = 1))) +
  labs(x = "Dry body mass (g)", y = "Intertegular distance (mm)") +
  theme_classic() + geom_point(aes(shape=Genus, color=Genus), size=3)
```



## Power regression between dry body mass and ITD (mm). EUGLOSSA INDIVIDUALS ONLY

```
library(readxl)
dataE = read_excel("/Users/yoss/Desktop/ITD_Euglossini.xlsx", sheet = "Euglossa")
model_potencialE <- nls(ITD ~ a * dryweight^b, data = dataE, start = list(a = 1, b = 1))
modelE <- lm(log(ITD) ~ log(dryweight), data = dataE)
```

## Coefficients

```
summary(model_potencialE)

##
## Formula: ITD ~ a * dryweight^b
## Parameters:
## Estimate Std. Error t value Pr(>|t|)
## a 8.04247 0.54069 14.88 <2e-16 ***
## b 0.23955 0.02069 11.58 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.2124 on 63 degrees of freedom
## Number of iterations to convergence: 10
## Achieved convergence tolerance: 3.775e-08
```

## Adjusted R-squared and p-value

```
summary(modelE)

##
## Call:
## lm(formula = log(ITD) ~ log(dryweight), data = dataE)
##
## Residuals:
## Min 1Q Median 3Q Max
## -0.119818 -0.044036 0.008616 0.037251 0.130009
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.08703 0.06922 30.15 <2e-16 ***
## log(dryweight) 0.24076 0.02093 11.50 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.059 on 63 degrees of freedom
## Multiple R-squared: 0.6774, Adjusted R-squared: 0.6723
## F-statistic: 132.3 on 1 and 63 DF, p-value: < 2.2e-16
```

## Graphic

```
ggplot(dataE, aes(x = dryweight, y = ITD)) +
  geom_smooth(method = "nls", formula = y ~ a * x^b, se = FALSE, color = "blue", method.args = list(start = list(a = 1, b = 1))) +
  labs(x = "Dry body mass (g)", y = "Intertegular distance (mm)") +
  theme_classic() + geom_point(aes(shape=Genus, color=Genus), size=3)
```

