**Linear regressions scripts**

**###Hoplitaspis\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Hoplitaspis)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Hoplitaspis", ylab="Prosoma length", xlab="Prosoma width", Hoplitaspis)

abline(linearmodel, col="red")

summary(linearmodel)

**###Eurypterus\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Eurypterus)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Eurypterus", ylab="Prosoma length", xlab="Prosoma width", Eurypterus)

abline(linearmodel, col="red")

summary(linearmodel)

**###Limulus\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Limulus)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Limulus polyphemus", ylab="Prosoma length", xlab="Prosoma width", Limulus)

abline(linearmodel, col="red")

summary(linearmodel)

**###Euproops\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Euproops)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Euproops danae", ylab="Prosoma length", xlab="Prosoma width", Euproops)

abline(linearmodel, col="red")

summary(linearmodel)

**###Prolimulus\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Prolimulus)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Prolimulus woodwardi", ylab="Prosoma length", xlab="Prosoma width", Prolimulus)

abline(linearmodel, col="red")

summary(linearmodel)

**###Paleolimulus\_Prosoma\_length~Prosoma\_width**

linearmodel=lm(log1p(Prosoma\_length)~log1p(Prosoma\_width), data = Paleolimulus\_kunguricus)

plot(log1p(Prosoma\_length)~log1p(Prosoma\_width), pch=19, cex=1, xlim = c(0, 5), ylim = c(0, 5), main="Paleolimulus kunguricus", ylab="Prosoma\_length", xlab="Prosoma width", Paleolimulus\_kunguricus2)

abline(linearmodel, col="red")

summary(linearmodel)