**Analysis at the "population level" (nests were considered sampling units)**

Goal: To Investigate the influence of the number of chicks in the nests on the response variables: average growth (Average growth model with/without covariables), coefficient variance of average growth (Growth variation model – with/ without co-variables), and chicks survivorship (Survival Model – with / without co-variables).

List of models and their respective predictions and effect size files are provided below.

# Average growth model - without co-variables

**Model**: glm (day\_14\_weight~rear\_Cs\_at\_start\_of\_rearing, data=pop\_data)

**Model predictions:** “predictions\_mean\_growth\_without\_covariables.1.csv”

**Effect size:** “effect\_size\_mean\_growth\_without\_covariables.1.txt”

# Average growth model - with co-variables

**Model:** glm (day\_14\_weight~rear\_Cs\_at\_start\_of\_rearing + rear\_area + rear\_nest\_LD + Treatment, data=pop\_data)

**Model predictions:** “predictions\_mean\_growth\_cov.2.csv”

**Effect size:** “effect\_size\_mean\_growth\_cov.2.txt”

# Growth variation model - without co-variables

**Model:** glm (day\_14\_weight\_CV~rear\_Cs\_at\_start\_of\_rearing, data=pop\_data)

**Model predictions:** “predictions\_CV\_growth\_without\_cov.3.csv”

**Effect size:** “effect\_size\_CV\_growth\_without\_cov.3.txt”

# Growth variation model - with co-variables

**Model:** glm (day\_14\_weight\_CV~rear\_Cs\_at\_start\_of\_rearing+ rear\_area + rear\_nest\_LD + Treatment, data = pop\_data)

**Model predictions: “**predictions\_CV\_growth\_cov.4.csv”

**Effect size:** "effect\_size\_CV\_growth\_cov.4.txt"

#Survival Model - Without co-variables

**Model:** glm (cbind(number\_chicks\_fledged\_from\_rear\_nest, rear\_Cs\_at\_start\_of\_rearing) ~ rear\_Cs\_at\_start\_of\_rearing, data=pop\_data, family="binomial")

**Model predictions:** “predictions\_mean\_surv\_without\_cov.5.csv”

**Effect size:** “effect\_mean\_surv\_without\_cov.5.txt”

#Survival Model - With co-variables

**Model:** glm (cbind (number\_chicks\_fledged\_from\_rear\_nest, rear\_Cs\_at\_start\_of\_rearing) ~ rear\_Cs\_at\_start\_of\_rearing + rear\_area + rear\_nest\_LD + Treatment, data=pop\_data, family="binomial")

**Model predictions: “**predictions\_mean\_surv\_cov.6.csv”

**Effect size:**  "effect\_mean\_Surv\_cov.6.txt"

**Analysis at the "individual level" (chicks were considered sampling units)**

Goal: To explore the effect of net rearing manipulation and clutch size from which the chick hatched on chicks weight (Id Growth model – with/without co-variables) and survival (Survival model – with/ without co-variables)

# Id Growth model - without co-variables

**Model:** lmer (day\_14\_weight ~ hatch\_nest\_CS + net\_rearing\_manipulation + (1|rear\_Box), data=ind\_data, REML=FALSE)

**Model predictions:** "predictions\_id\_growth\_without\_cov.7.csv"

**Effect size:** “effect\_size\_id\_growth\_without\_cov.7.txt”

# Id Growth model - with co-variables

**Model: “**model\_id\_growth\_cov”

**Model predictions:** "predictions\_id\_growth\_cov.8.csv"

**Effect size:** "effect\_size\_id\_growth\_cov.8.txt"

#Survival model - without co-variables

**Model:** glmer (chick\_survival\_to\_first\_breed\_season ~ hatch\_nest\_CS + net\_rearing\_manipulation + (1|rear\_Box), data=ind\_data, family="binomial")

**Model predictions:** "predictions\_id\_surv\_without\_cov.9.csv"

**Effect size:** " effect\_size\_id\_surv\_without\_cov.9.txt "

#Survival model - with co-variables

**Model:** glmer (chick\_survival\_to\_first\_breed\_season~hatch\_nest\_CS + net\_rearing\_manipulation + rear\_area+rear\_nest\_LD+home\_or\_away + (1|rear\_Box), data=ind\_data, family="binomial",nAGQ=20, glmerControl (optimizer = "bobyqa"))

**Model predictions: “**predictions\_id\_surv\_cov.10.csv”

**Effect size:** "effect\_size\_id\_surv\_cov.10.txt"