

## R CODE

```
##### LOGISTIC FINAL #####
```

```
##### 1. SERIOLA #####
```

```
# i. Ca. Ichthyocystis
```

```
# TEMPERATURE
```

```
mylogit <- glm( presence ~ temp , data = logisticData, family = "binomial")
```

```
summary(mylogit)
```

```
confint(mylogit)
```

```
plot(mylogit)
```

```
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
```

```
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
```

```
head(predicted.classes)
```

```
logit = log(probabilities/(1-probabilities))
```

```
# WEIGHT
```

```
mylogit <- glm( presence ~ weight , data = logisticData, family = "binomial")
```

```
summary(mylogit)
```

```
confint(mylogit)
```

```
plot(mylogit)
```

```
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
```

```
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
```

```
head(predicted.classes)
```

```
logit = log(probabilities/(1-probabilities))
```

```
# LENGTH
```

```
mylogit <- glm( presence ~ length , data = logisticData, family = "binomial")
```

```
summary(mylogit)
```

```
confint(mylogit)
```

```
plot(mylogit)
```

```
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
```

```
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
```

```
head(predicted.classes)
```

```
logit = log(probabilities/(1-probabilities))
```

```
# MULTI-VARIABLE
```

```
mylogit <- glm( presence ~ temp + length + weight , data = logisticData, family =  
"binomial")
```

```
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
#####
# ii. Chlamydia
```

```
# TEMPERATURE
mylogit <- glm( presenceChlam ~ temp , data = logisticData, family = "binomial")
```

```
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# WEIGHT
mylogit <- glm( presenceChlam ~ weight , data = logisticData, family = "binomial")
```

```
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# LENGTH
mylogit <- glm( presenceChlam ~ length , data = logisticData, family = "binomial")
```

```
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```

probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))

```

## # MULTI-VARIABLE

```

mylogit <- glm( presenceChlam ~ temp + length + weight, data = logisticData, family =
"binomial")

```

```

summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))

```

```

probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))

```

## ##### 2. SEABREAM #####

### # i. Ca. Ichthyocystis

#### # Temperature

```

mylogit <- glm( presence ~ temp , data = logisticDataSeabream, family = "binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))

```

```

probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))

```

#### # Weight

```

mylogit <- glm( presence ~ weight , data = logisticDataSeabream, family = "binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))

```

```

probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))

```

```
# Length
mylogit <- glm( presence ~ length , data = logisticDataSeabream, family = "binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# Multi-variable
mylogit <- glm( presence ~ temp + weight , data = logisticDataSeabream, family =
"binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
#####
# ii. Chlamydia
```

```
# Temperature
mylogit <- glm( presenceChlam ~ temp , data = logisticDataSeabream, family = "binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# Weight
mylogit <- glm( presenceChlam ~ weight , data = logisticDataSeabream, family =
"binomial")
summary(mylogit)
```

```
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# Length
mylogit <- glm( presenceChlam ~ length , data = logisticDataSeabream, family =
"binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```

```
# Multi-variable
mylogit <- glm( presenceChlam ~ temp + weight , data = logisticDataSeabream, family =
"binomial")
summary(mylogit)
confint(mylogit)
plot(mylogit)
exp(coef(mylogit))
```

```
probabilities <- predict(mylogit, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
logit = log(probabilities/(1-probabilities))
```