Ben Goodwin

DS6371

HW12

Question 1)

Part A

SAS input for non-transformed data:

FILENAME REFFILE '/folders/myfolders/sasuser.v94/Crab17.csv';

PROC IMPORT DATAFILE=REFFILE

DBMS=CSV

OUT=crabby;

GETNAMES=YES;

RUN;

proc sgplot data=crabby;

styleattrs wallcolor=blanchedalmond;

scatter x=Height y=Force / group = Species

markerattrs = (symbol=CircleFilled size=7)

FILLEDOUTLINEDMARKERS;

run;

SAS output for non-transformed data:

Chart, scatter chart

Description automatically generated

SAS input for transformed data:

DATA logdata;

SET crabby;

LOGVAR=log10(Force);

RUN;

proc sgplot data=logdata;

styleattrs wallcolor=blanchedalmond;

scatter x=Height y=LOGVAR / group = Species

markerattrs = (symbol=CircleFilled size=7)

FILLEDOUTLINEDMARKERS;

run;

SAS output for transformed data:

Chart, scatter chart

Description automatically generated

Part B

Mu\_hat|height,species=beta\_0+beta\_1\*Height+beta\_2\*Species+beta\_3\*interaction(Height\*Species)

Part C

SAS Input:

proc glm data=crabby plots=all;

class Species(ref="Lophopanopeus bellus");

model Force = Height|Species /solution clparm;

run;

SAS Output:

Graphical user interface, text, application

Description automatically generated

Table

Description automatically generated

Graphical user interface, table

Description automatically generated

Part D

Residual Plot:

Chart, scatter chart

Description automatically generated

Appropriateness: The residuals seem to be spread out in a random manner, there is no obvious trend to the data.

Studentized Residual Plot:

Chart, scatter chart

Description automatically generated

Appropriateness: The studentized residuals indicate the data is very similar to one another, there is slight visual evidence for 1 outlier.

Histogram of Residuals:

Chart, histogram

Description automatically generated

Appropriateness: The residuals look very close to normally distributed

Quantile-Quantile Plot:

Chart, scatter chart

Description automatically generated

Appropriateness: The qq-plot looks about as ideal as one should look. The residuals match up very neatly with the normal quantiles and even match at the tails.

Part E

I have determined that the model is sufficient.

Interpretation of force coefficient:

Interpretation: With a height of 0 the Lophopanopeus bellus crab would exert -17.25 force units.

With a height of 0 the cancer productus would exert 8.24823 force units than the baseline Lophopanopeus bellus.

With a height of 0 the Hemigrapsus Nudus would exert 20.41259323 force units than the baseline Lophopanopeus bellus.

Interpretation of height coefficient:

For a one unit increase in height the Lophopanopeus bellus crab we can expect a 3.8486 increase in force units. The Cancer Productus, for a one unit increase in height in the Lophopanopeus Bellus will produce a -1.1687 increase in force units. And finally The Hemigrapsus will gain a -3.078 increase in force units.

Part F

Mu{force|Height for Hemigrapsus Nudus}: -17.25249079+3.84863387\*height

Mu{force|Height for Cancer Productus}: -9.00425074+2.67983032\*height

Mu{force|Height for Lophopanopeus Bellus }…3.1601025+0.14480222\*height