**Gamma GLM (continuous response with positive values and skew)**

**Check variables in dataset**

str(dataset)

class(dataset$IV1)

class(dataset$IV2)

class(dataset$DV)

To change categorical variables to factors:

dataset$IV1<-factor(dataset$IV1)

**Fit the full model**

Fit the full (most complex) model:

#Note the Gamma distribution does not have to have a log link.

**a. If you have one IV, and:**

> mod.1 <- glm(DV ~ IV, family = Gamma(log), data = dataset)

**b. If you have more than one IV**

> mod.1 <- glm(DV ~ IV.1 \* IV2, family = Gamma(log), data = dataset)

The default plot function which creates a QQ plot of the normal distribution isn’t very helpful for Gamma GLMs therefore we will validate our model by simulating residuals at the end.

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**Term selection**

Start with the most complex (‘full’) model, then drop IV terms one at a time. Compare the AIC

scores and select the model with the lowest score. For example,

> mod.1 <- glm(DV ~ IV.1 \* IV2, family = Gamma(log), data = dataset)

> mod.2 <- glm(DV ~ IV.1 + IV2, family = Gamma(log), data = dataset)

> mod.3 <- glm(DV ~ IV.1, family = Gamma(log), data = dataset)

> mod.4 <- glm(DV ~ IV2, family = Gamma(log), data = dataset)

Then, compare the models with the AIC:

> AIC(mod.1, mod.2, mod.3, mod.4) # select the best model (lowest AIC) …………………………………………………………………………………………………………………………………………….Go to validate

**Validate the fitted model**

Plot selected model residuals against fitted terms, and against all included and excluded

variables. Calculate the approx. R2 value.

> summary(model) # Shows summary model outputs

> plot(residuals(model)~ fitted(model)) #plots model residuals vs fitted

Check residuals plots for each IV:

> par(mfrow=c(1,1))

> plot(residuals(model)~ dataset$IV)

To perform post hoc analysis …………………………………………………………………………Go to post hoc analysis

**Post hoc analysis**

We can perform pairwise tests of the categorical IV(s) or interactions in our fitted model using the estimated marginal means.

library(emmeans) #package which extracts the estimated marginal means from a model for post hoc analysis of significant factors

1. **If we have one categorical IV:**

**#Note:** If you have multiple categorical IVs but no interaction, repeat these steps.

#extracts the estimated marginal means of the IV based upon the model

>emm.mod <- emmeans(model, ~ IV1)

#shows the estimated effect size of each level of the factor (note estimates are on the link scale)

>contrast(emm.mod)

#pairwise analysis between each factor level (note: negative estimate suggests that level1 < level2; positive estimate level1 > level2)

>pairs(emm.mod)

#plot the estimates marginal means (estimates on link scale)

>plot(emm.mod)

#Create a summary plot of the estimated marginal means of your IVs (particularly useful if you have an interaction).

#You can customize the plot using ggplot

>library(ggplot2) #package which allows you to create custom plots

#Here, we use Geom\_jitter to add the actual values from your dataset around the levels of each IV.

>emmip(model, ~ IV1, "response")+

> geom\_jitter(aes(x = IV1, y = DV, colour = IV1), data = dataset)

**b. If we have an interaction between two categorical IVs**

#test the effect of IV1 at each level of IV2.

>emm.mod <- emmeans(model, ~ IV1|IV2)

#**Note:** you can reverse the factor order to test the effect of IV2 at each level of IV1

>contrast(emm.mod)

>pairs(emm.mod)

>plot(emm.mod)

>library(ggplot2) #package which allows you to create custom plots

>emmip(model, ~ IV1|IV2, "response")+

> geom\_jitter(aes(x = IV1, y = DV, colour = IV1), data = dataset)

**c. If we have an interaction between a categorical IV (IV1) and a continuous IV (IV2)**

> emtrends(model, pairwise ~ IV1, var = "IV2")

> emmip(model, IV1 ~ IV2, cov.reduce = range)