## **Homework 4**

**Trevor Caughlin** 

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**Question 1.** Gamma distribution Explore the properties of the gamma distribution using the gamma probability density function in R:

```
args(dgamma)
## function (x, shape, rate = 1, scale = 1/rate, log = FALSE)
## NULL
```

Apply the curve function to explore how the shape and rate parameters alter the likelihood function. As output, include (1) a brief written explanation of how the shape and rate parameters determine the behavior of the function and (2) several different curves showing different parameter values for dgamma (For an example of similar code, see the beta distribution section of lecture 9).

**Question 2.** Find a published paper in your research area that uses either gamma or beta regression. Briefly (in one paragraph) answer the following questions:

What were the response and predictor variables? How were the results presented? Do you agree with the interpretation of the results?

If you have trouble finding a paper that uses one of these analyses, here are several choices:

```
http://onlinelibrary.wiley.com/doi/10.1111/mec.12059/full http://onlinelibrary.wiley.com/doi/10.1111/1365-2664.12531/full http://onlinelibrary.wiley.com/doi/10.1002/rse2.33/full
```

**Question 3:** Apply beta or gamma regression to your own data (or a dataset from data dryad). Note that the notation for gamma and beta regression is slightly different than the other models we have covered, and beta regression requires the "betareg" package:

```
#beta regression:
library("betareg")
#beta_model=betareg(response~predictor)

#gamma regression:
#gamma_model=glm(response~predictor,family=Gamma(link="log"))
```

As output, include (1) a plot with model predictions overlaid on raw data, (2) a verbal description of effect size, and (3) estimates of significance using confint

**Question 4:** Use rgamma to simulate a gamma-distributed random variable that is related to a predictor variable. Describe how you reparameterized R's default gamma parameters to represent a mean value. Include a plot of your response vs. predictor variable, and a description of a biological process your data could represent.

Hint:

```
#y <- rgamma(n, rate = shape / y_mean, shape = shape)</pre>
```