agr1<-with(estagr[estagr$bointun!=0,],glm(fe\_est~mal\_agr+I(fe\_estug^2),family="poisson",na.action="na.exclude"))

Call:

glm(formula = fe\_est ~ mal\_agr + I(fe\_estug^2), family = "poisson",

na.action = "na.exclude")

Deviance Residuals:

Min 1Q Median 3Q Max

-44.778 -5.613 0.345 6.712 13.055

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 6.827e+00 4.648e-03 1468.66 <2e-16 \*\*\*

mal\_agr -1.426e-02 1.363e-03 -10.46 <2e-16 \*\*\*

I(fe\_estug^2) 1.365e-05 7.585e-08 179.98 <2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Null deviance: 38312 on 157 degrees of freedom

Residual deviance: 13295 on 155 degrees of freedom

(12 observations deleted due to missingness)

AIC: Inf

Number of Fisher Scoring iterations: 4

glm(formula = fe\_est ~ mal\_agr + I(fe\_estug^2), family = "quasipoisson",

na.action = "na.exclude")

Deviance Residuals:

Min 1Q Median 3Q Max

-44.778 -5.613 0.345 6.712 13.055

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 6.827e+00 4.080e-02 167.321 <2e-16 \*\*\*

mal\_agr -1.426e-02 1.197e-02 -1.191 0.235

I(fe\_estug^2) 1.365e-05 6.658e-07 20.505 <2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 77.04434)

Null deviance: 38312 on 157 degrees of freedom

Residual deviance: 13295 on 155 degrees of freedom

(12 observations deleted due to missingness)

agr1<-with(estagr[estagr$bointun!=0,],glm(mal\_agr~fe\_estug+I(fe\_estug^2),family="poisson",na.action="na.exclude"))

Call:

glm(formula = mal\_agr ~ fe\_estug + I(fe\_estug^2), family = "poisson",

na.action = "na.exclude")

Deviance Residuals:

Min 1Q Median 3Q Max

-2.3493 -1.0959 -0.2754 0.6213 2.7060

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 1.065e+00 2.321e-01 4.590 4.44e-06 \*\*\*

fe\_estug 7.103e-05 3.600e-03 0.020 0.984

I(fe\_estug^2) -1.136e-05 1.272e-05 -0.893 0.372

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 222.87 on 157 degrees of freedom

Residual deviance: 212.27 on 155 degrees of freedom

(12 observations deleted due to missingness)

AIC: 609.46

Number of Fisher Scoring iterations: 5

Call:

glm(formula = mal\_agr ~ fe\_estug + I(fe\_estug^2), family = "quasipoisson",

na.action = "na.exclude")

Deviance Residuals:

Min 1Q Median 3Q Max

-2.3493 -1.0959 -0.2754 0.6213 2.7060

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1.065e+00 2.651e-01 4.018 9.12e-05 \*\*\*

fe\_estug 7.103e-05 4.112e-03 0.017 0.986

I(fe\_estug^2) -1.136e-05 1.453e-05 -0.782 0.436

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 1.304508)

Null deviance: 222.87 on 157 degrees of freedom

Residual deviance: 212.27 on 155 degrees of freedom

(12 observations deleted due to missingness)

AIC: NA

Number of Fisher Scoring iterations: 5

Call:

glm(formula = fe\_est ~ mal\_agr)

Deviance Residuals:

Min 1Q Median 3Q Max

-1099.01 -344.73 -98.14 279.06 2665.49

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1317.34 53.54 24.604 < 2e-16 \*\*\*

mal\_agr -59.73 19.59 -3.049 0.00261 \*\*

\_\_

Call:

glm(formula = mal\_agr ~ fe\_estug, family = "poisson", na.action = "na.exclude")

Deviance Residuals:

Min 1Q Median 3Q Max

-2.2988 -1.5881 -0.2330 0.7566 3.2647

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 1.1622 0.1247 9.318 < 2e-16 \*\*\*

fe\_estug -0.4279 0.1048 -4.083 4.45e-05 \*\*\*

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 401.82 on 202 degrees of freedom

Residual deviance: 383.79 on 201 degrees of freedom

(14 observations deleted due to missingness)

AIC: 791.23

**Code to test models from Jeffery**

agr2a <- with(estagr,glm(mal\_agr~fe\_estug,family="poisson",na.action ="na.exclude"))

to a model that includes a polynomial term (the square of estradiol):

agr3a <- with(estagr,glm(mal\_agr ~ fe\_estug + I(fe\_estug^2),

family="poisson",

na.action ="na.exclude"))

And then compare these two models to see if the more complex model (agr3a) provides a significantly better fit:

anova(agr3a, agr2a, test = "Chisq")

Analysis of Deviance Table

Model 1: mal\_agr ~ fe\_estug + I(fe\_estug^2)

Model 2: mal\_agr ~ fe\_estug

Resid. Df Resid. Dev Df Deviance Pr(>Chi)

1 200 383.74

2 201 383.79 -1 -0.051959 0.8197 stick with the simpler model

if the p-value of the output is less than 0.05, the more complex model is sufficiently better than the simpler model. If the p-value is above 0.05, the complex model is not sufficiently better, and you would stick with the simpler model, agr2a.

for specific female

agr\_fb <- with(estagr[estagr$id == "bm", ],

glm(mal\_agr ~ fe\_estug,

family = "poisson",

na.action = "na.exclude"))

Or, if you want to include the squared value of estradiol in the model:

agr\_fb <- with(estagr[estagr$id == "b", ],

glm(mal\_agr ~ fe\_estug + I(fe\_estug^2),

family = "poisson",

na.action = "na.exclude"))