**Summary of models to test the independence of CIT Success, Family History of Depression and Family History of Bipolar disorder.**

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| --- | --- | --- | --- | --- | --- |
| **Family Hx Bipolar** | **Family Hx Depression** | **CIT Success** | | **Count of CIT Success** | |
| **0** | **0** | 0 | | 517 | |
| **0** | **0** | 1 | | 305 | |
| **0** | **1** | 0 | | 532 | |
| **0** | **1** | 1 | | 384 | |
| **1** | **0** | 0 | | 29 | |
| **1** | **0** | 1 | | 12 | |
| **1** | **1** | 0 | | 76 | |
| **1** | **1** | 1 | | 55 | |
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| |  |  |  | | --- | --- | --- | | **Model** | **Residual Deviance** | **Df** | | Complete Indep | 43.272 | 4 | | Joint Indep BD | 6.4193 | 3 | | Joint Indep BC | 43.241 | 3 | | Joint Indep DC | 37.918 | 3 | | Homogenous | 0.82322 | 4 | | NoBD | 37.887 | 4 | | NoBC | 1.0656 | 4 | | NoDC | 6.3881 | 2 | | | |  | |  | |
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**Interpretation**: We wanted to examine if family history of Bipolar disorder and Family History of depression are associated with CIT Success. Upon comparison of the residual deviances of all the models, the residiual deviance is the least for Full homogeneous model of 0.82322. If we remove Bipolar depression and CIT success from the homogeneous mdel, we find that the increase in G square is 0.242 for 2 additional dgrees of freedom which seems to fit the data . This means that smallest loss in residual deviance is associated with removing the association between Bipolar depression and CIT success.

**Conclusion:** We can conclude that Bipolar depression and CIT success are independent of each other holding other things constant. while Family history of depression is associated with CIT Success and also Family history of Bipolar disorder. Since CIT is measured after family history we can conclude that Family History of depression affects CIT success and not vice versa.

Analysis with Rcode:

>CImodel = glm(CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression + CIT.Success), data=CIT, family=poisson)

>summary(CImodel)

Call:

glm(formula = CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success), family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

1.9248 -0.3314 -1.8418 0.3545 -2.8213 -3.8638 2.3980 2.7017

Coefficients:

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

(Intercept) 6.16218 0.03942 156.340 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.31300 0.07993 -28.937 < 2e-16 \*\*\*

Family.Hx.Depression 0.19327 0.04598 4.204 2.63e-05 \*\*\*

CIT.Success -0.42295 0.04679 -9.039 < 2e-16 \*\*\*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.235 on 7 degrees of freedom

Residual deviance: 43.272 on 4 degrees of freedom

AIC: 104.39

Number of Fisher Scoring iterations: 4

>JImodelBD = glm(CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression + CIT.Success + Family.Hx.Bipolar \* Family.Hx.Depression), data=CIT, family=poisson)

>summary(JImodelBD)

Call:

glm(formula = CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Bipolar \* Family.Hx.Depression),

family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

0.9073 -1.1407 -0.9172 1.1150 0.8269 -1.1010 -0.3563 0.4330

Coefficients:

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

(Intercept) 6.20787 0.03949 157.197 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.99817 0.16002 -18.736 < 2e-16 \*\*\*

Family.Hx.Depression 0.10828 0.04804 2.254 0.0242 \*

CIT.Success -0.42295 0.04679 -9.039 < 2e-16 \*\*\*

Family.Hx.Bipolar:Family.Hx.Depression 1.05335 0.18529 5.685 1.31e-08 \*\*\*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.2348 on 7 degrees of freedom

Residual deviance: 6.4193 on 3 degrees of freedom

AIC: 69.535

Number of Fisher Scoring iterations: 4

>JImodelBC = glm(CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression + CIT.Success + Family.Hx.Bipolar \* CIT.Success), data=CIT, family=poisson)

>summary(JImodelBC)

Call:

glm(formula = CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Bipolar \* CIT.Success), family = poisson,

data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

1.9476 -0.3590 -1.8174 0.3239 -2.8872 -3.7865 2.3159 2.8061

Coefficients:

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

(Intercept) 6.16115 0.03986 154.586 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.30163 0.10236 -22.486 < 2e-16 \*\*\*

Family.Hx.Depression 0.19327 0.04598 4.204 2.63e-05 \*\*\*

CIT.Success -0.42035 0.04904 -8.572 < 2e-16 \*\*\*

Family.Hx.Bipolar:CIT.Success -0.02892 0.16387 -0.176 0.86

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.235 on 7 degrees of freedom

Residual deviance: 43.241 on 3 degrees of freedom

AIC: 106.36

Number of Fisher Scoring iterations: 5

>JImodelDC = glm(CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression + CIT.Success + Family.Hx.Depression \* CIT.Success), data=CIT, family=poisson)

>summary(JImodelDC)

Call:

glm(formula = CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Depression \* CIT.Success), family = poisson,

data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

0.8988 0.9652 -0.9092 -0.7789 -3.1170 -3.5063 2.7107 2.3211

Coefficients:

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

(Intercept) 6.20825 0.04340 143.057 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.31300 0.07993 -28.937 < 2e-16 \*\*\*

Family.Hx.Depression 0.10756 0.05896 1.824 0.0681 .

CIT.Success -0.54372 0.07061 -7.700 1.36e-14 \*\*\*

Family.Hx.Depression:CIT.Success 0.21804 0.09439 2.310 0.0209 \*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.235 on 7 degrees of freedom

Residual deviance: 37.918 on 3 degrees of freedom

AIC: 101.03

Number of Fisher Scoring iterations: 4

>hommodel = glm(CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression + CIT.Success)^2, data=CIT, family=poisson)

>summary(hommodel)

Call:

glm(formula = CITCount ~ (Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success)^2, family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

-0.1023 0.1337 0.1012 -0.1187 0.4448 -0.6334 -0.2646 0.3187

Coefficients:

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

(Intercept) 6.25254 0.04360 143.419 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.96899 0.17021 -17.443 < 2e-16 \*\*\*

Family.Hx.Depression 0.01972 0.06096 0.323 0.7464

CIT.Success -0.53990 0.07103 -7.601 2.95e-14 \*\*\*

Family.Hx.Bipolar:Family.Hx.Depression 1.05766 0.18551 5.701 1.19e-08 \*\*\*

Family.Hx.Bipolar:CIT.Success -0.08131 0.16554 -0.491 0.6233

Family.Hx.Depression:CIT.Success 0.22433 0.09525 2.355 0.0185 \*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.23484 on 7 degrees of freedom

Residual deviance: 0.82322 on 1 degrees of freedom

AIC: 67.939

Number of Fisher Scoring iterations: 4

>NoBD = update(hommodel,.~.-(Family.Hx.Bipolar:Family.Hx.Depression))

>summary(NoBD)

Call:

glm(formula = CITCount ~ Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Bipolar:CIT.Success + Family.Hx.Depression:CIT.Success,

family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

0.9219 0.9383 -0.8852 -0.8101 -3.1840 -3.4311 2.6296 2.4274

Coefficients:

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

(Intercept) 6.20722 0.04380 141.725 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.30163 0.10236 -22.486 < 2e-16 \*\*\*

Family.Hx.Depression 0.10756 0.05896 1.824 0.0681 .

CIT.Success -0.54112 0.07212 -7.503 6.24e-14 \*\*\*

Family.Hx.Bipolar:CIT.Success -0.02892 0.16387 -0.176 0.8599

Family.Hx.Depression:CIT.Success 0.21804 0.09439 2.310 0.0209 \*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.235 on 7 degrees of freedom

Residual deviance: 37.887 on 2 degrees of freedom

AIC: 103

Number of Fisher Scoring iterations: 4

>NoBC = update(hommodel,.~.-(Family.Hx.Bipolar:CIT.Success))

>summary(NoBC)

Call:

glm(formula = CITCount ~ Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Bipolar:Family.Hx.Depression + Family.Hx.Depression:CIT.Success,

family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

-0.13433 0.17582 0.00315 -0.00370 0.58959 -0.81783 -0.00832 0.00979

Coefficients:

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

(Intercept) 6.25394 0.04347 143.881 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.99817 0.16002 -18.736 < 2e-16 \*\*\*

Family.Hx.Depression 0.02256 0.06059 0.372 0.7096

CIT.Success -0.54372 0.07061 -7.700 1.36e-14 \*\*\*

Family.Hx.Bipolar:Family.Hx.Depression 1.05335 0.18529 5.685 1.31e-08 \*\*\*

Family.Hx.Depression:CIT.Success 0.21804 0.09439 2.310 0.0209 \*

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.2348 on 7 degrees of freedom

Residual deviance: 1.0656 on 2 degrees of freedom

AIC: 66.181

Number of Fisher Scoring iterations: 4

>NoDC = update(hommodel,.~.-(Family.Hx.Depression:CIT.Success))

>summary(NoDC)

Call:

glm(formula = CITCount ~ Family.Hx.Bipolar + Family.Hx.Depression +

CIT.Success + Family.Hx.Bipolar:Family.Hx.Depression + Family.Hx.Bipolar:CIT.Success,

family = poisson, data = CIT)

Deviance Residuals:

1 2 3 4 5 6 7 8

0.9304 -1.1687 -0.8932 1.0848 0.7740 -1.0398 -0.4478 0.5489

Coefficients:

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

(Intercept) 6.20684 0.03993 155.440 < 2e-16 \*\*\*

Family.Hx.Bipolar -2.98680 0.17232 -17.333 < 2e-16 \*\*\*

Family.Hx.Depression 0.10828 0.04804 2.254 0.0242 \*

CIT.Success -0.42035 0.04904 -8.572 < 2e-16 \*\*\*

Family.Hx.Bipolar:Family.Hx.Depression 1.05335 0.18529 5.685 1.31e-08 \*\*\*

Family.Hx.Bipolar:CIT.Success -0.02892 0.16387 -0.176 0.8599

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1636.2348 on 7 degrees of freedom

Residual deviance: 6.3881 on 2 degrees of freedom

AIC: 71.503

Number of Fisher Scoring iterations: 4