R12 - Interactions

HCI/PSYCH 522 Iowa State University

April 26, 2022

Independent variables

- Functions (f(X))
- Dummy variables for categorical variables $(X_1 = I())$
- Higher order terms (X^2)
- Additional explanatory variables (X_1, X_2)
- Interactions (X_1X_2)
 - Continuous-continuous
 - Continuous-categorical
 - Categorical-categorical

Definition

Two independent variables are said to interact if the effect that one of them has on the mean of the dependent variable depends on the value of the other.

When to include interaction terms

Adapted from The Statistical Sleuth (3rd ed) page 250:

- when a research question pertains to an interaction
- when good reason exists to suspect an interaction or
- when statistical evidence exists to include the interaction.

R code for interaction

```
longnosedace <- read_csv("longnosedace.csv")</pre>
lm_dace <- lm(log(count) ~ do2 + no3 + do2:no3, data = longnosedace)</pre>
summary(lm_dace)$coef
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.9149442 2.25394656 -0.8495961 0.39876678
## do2 0.5111851 0.26781104 1.9087529 0.06085177
## no3 1.0972513 0.85554847 1.2825121 0.20436193
## do2:no3 -0.1023408 0.09821613 -1.0419953 0.30139605
lm_dace2 <- lm(log(count) ~ do2 * no3, data = longnosedace)</pre>
summarv(lm_dace2)$coef
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.9149442 2.25394656 -0.8495961 0.39876678
## do2 0.5111851 0.26781104 1.9087529 0.06085177
## no3 1.0972513 0.85554847 1.2825121 0.20436193
## do2:no3 -0.1023408 0.09821613 -1.0419953 0.30139605
```

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R code for interaction

```
glm_dace <- glm(count ~ do2 + no3 + do2:no3, data = longnosedace, family = poisson)</pre>
summary(glm_dace)$coef
##
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.2297477 0.41254423 -0.5569044 5.775927e-01
      0.3883040 0.04764847 8.1493475 3.658932e-16
## do2
## no3 1.2056535 0.13101995 9.2020603 3.511513e-20
## do2:no3 -0.1171250 0.01504934 -7.7827322 7.097476e-15
glm_dace2 <- glm(count ~ do2 * no3, data = longnosedace, family = poisson)</pre>
summary(glm_dace2)$coef
               Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -0.2297477 0.41254423 -0.5569044 5.775927e-01
## do2
      0.3883040 0.04764847 8.1493475 3.658932e-16
## no3 1.2056535 0.13101995 9.2020603 3.511513e-20
## do2:no3 -0.1171250 0.01504934 -7.7827322 7.097476e-15
```

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F-test or Chi-squared test to help assess the need for an interaction

```
lm_dace \leftarrow lm(log(count) \sim do2 * no3, data = longnosedace)
drop1(lm dace, test="F")
## Single term deletions
## Model:
## log(count) ~ do2 * no3
          Df Sum of Sq RSS ATC F value Pr(>F)
                       81.141 20.831
## <none>
## do2:no3 1 1.3984 82.540 19.975 1.0858 0.3014
glm_dace <- glm(count ~ do2 * no3, data = longnosedace, family = poisson)
drop1(glm dace, test="Chi")
## Single term deletions
## Model:
## count ~ do2 * no3
          Df Deviance
                         ATC
                                LRT Pr(>Chi)
## <none>
               2310.6 2646.6
## do2:no3 1 2375.8 2709.9 65.273 6.521e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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F-test or Chi-squared test to help assess the need for an interaction

```
glm_breaks <- glm(breaks ~ wool*tension, data = warpbreaks, family = poisson)
summary(glm breaks)$coef
                Estimate Std. Error z value
                                                   Pr(>|z|)
## (Intercept) 3.7967368 0.04993753 76.029734 0.000000e+00
## W001B
              -0.4566272 0.08019202 -5.694172 1.239721e-08
## tensionM
              -0.6186830 0.08440012 -7.330357 2.295399e-13
## tensionH
              -0.5957987 0.08377723 -7.111702 1.146202e-12
## woolB:tensionM 0.6381768 0.12215312 5.224400 1.747203e-07
## woolB:tensionH 0.1883632 0.12989529 1.450115 1.470263e-01
drop1(glm_breaks, test="Chi")
## Single term deletions
## Model:
## breaks ~ wool * tension
               Df Deviance
                             AIC
                                    LRT Pr(>Chi)
## <none>
          182.31 468.97
## wool:tension 2 210.39 493.06 28.087 7.962e-07 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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F-test or Chi-squared test to help assess the need for an interaction

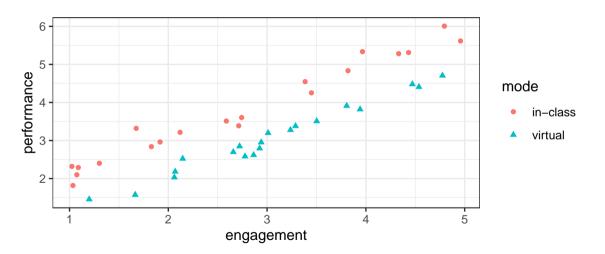
```
glm_breaks <- glm(breaks ~ wool*tension, data = warpbreaks, family = poisson)
summary(glm breaks)$coef
                Estimate Std. Error z value
                                                   Pr(>|z|)
## (Intercept) 3.7967368 0.04993753 76.029734 0.000000e+00
## W001B
              -0.4566272 0.08019202 -5.694172 1.239721e-08
## tensionM
              -0.6186830 0.08440012 -7.330357 2.295399e-13
## tensionH
              -0.5957987 0.08377723 -7.111702 1.146202e-12
## woolB:tensionM 0.6381768 0.12215312 5.224400 1.747203e-07
## woolB:tensionH 0.1883632 0.12989529 1.450115 1.470263e-01
drop1(glm_breaks, test="Chi")
## Single term deletions
## Model:
## breaks ~ wool * tension
               Df Deviance
                             AIC
                                    LRT Pr(>Chi)
## <none>
          182.31 468.97
## wool:tension 2 210.39 493.06 28.087 7.962e-07 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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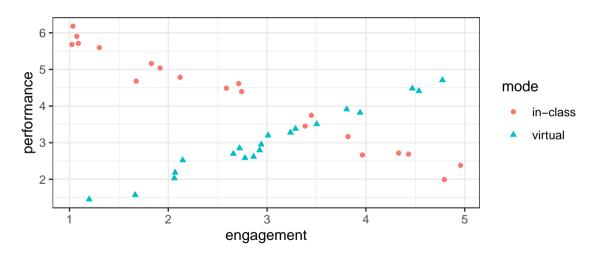
No Interaction = Parallel Lines

A model without an interaction is often referred to as a main effects model. Models without an interaction result in parallel lines.

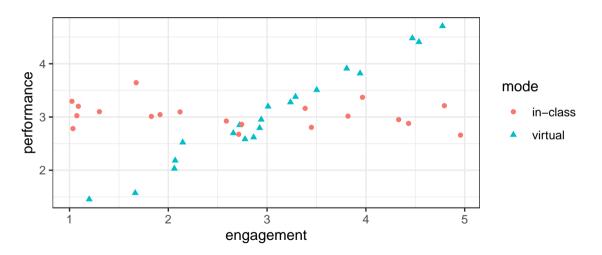
No interaction



With interaction (extreme)



With interaction (not so extreme)



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