**EPID 5314: HW 5**

1. According to the output below, at the 95% level of confidence, the interaction term (female\*getpar) is NOT significant (p=**0.2857** > 0.05). This implies that there is NOT significant effect modification by gender on the effect of perceived availability of alcohol on heavy alcohol use in the 8th grade on a MULTIPLICATIVE scale.

Table

Description automatically generated

However, the **exposure estimate** DOES vary over the strata by gender (as shown below), so we must still test for effect modification by gender on an ADDITIVE scale.

**Female = 0 (‘Males’)**



Table

Description automatically generated

**Female = 1 (‘Females’)**

Table

Description automatically generated

According to the output below, at the 95% level of confidence, the interaction term (female\*getpar) is NOT significant (p=**0.0979** > 0.05). This implies that there is NOT significant effect modification by gender on the effect of perceived availability of alcohol on heavy alcohol use in the 8th grade on an ADDITIVE scale.

Table

Description automatically generated

Although the interaction detected is not statistically significant, it may still be biologically significant since the exposure estimate differs over strata formed by the gender variable. Since the interaction term on an additive scale is close to being significant (but is NOT close on a multiplicative scale), we will treat this as additive interaction in the following question since we are still interested in the potential biological interaction between gender and perceived availability of alcohol.

It should also be noted that statistical significance of interaction is model-specific, meaning that the specified model parameters and distribution will affect the outcome of the test. For example, when the distribution is set to normal rather than binomial, the interaction term is statistically significant on the additive scale (p = **0.0309** < 0.05). Thus, I have decided to treat this interaction as additive and meaningful, although the original model did not find it statistically significant.

Table

Description automatically generated



Since we are treating the potential biological interaction as additive rather than multiplicative (please see justification above), the correct effect measure to report is RD:

|  |  |  |
| --- | --- | --- |
| **Strata** | **Gender Specific Effect Estimate (RD)** | **95% Confidence Interval for RD** |
| Male, perceived alcohol availability = “in-between” (compared to “easy”) | -0.0234 | [-0.1054, 0.0586] |
| Male, perceived alcohol availability = “hard” (compared to “easy”) | -0.1381 | [-0.2041, -0.0722] |
| Female, perceived alcohol availability = “in-between” (compared to “easy”) | 0.0043 | [-0.0688, 0.0773] |
| Female, perceived alcohol availability = “hard” (compared to “easy”) | -0.0600 | [-0.1224, 0.0025] |

**SAS Code**

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\* Course: Data Analysis - EPID 5314 \*

\* Assignment: Homework 5 \*

\* Due Date: 9/30/2021 \*

\* Programmer(s): Jessie Ausman \*

\* Program Name: HW5 \*

\* Save Program/Log/Output: C:\Users\jessa\Desktop\EPID 5314\Homework5\*

\* Save Data Files: C:\Users\jessa\Desktop\EPID 5314\PNC Data File\PNC\*

\* Datasets \*

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/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* PART 0 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

\*read in data and create temp dataset;

libname bios "C:\Users\jessa\Desktop\EPID 5314\PNC Data File\PNC Datasets";

**data** pnc05;

set bios.pnc05;

**run**;

\*make hvyuse4 dichotomous Y/N - use N as ref;

**data** HW5;

set pnc05;

if hvyuse4 = **1** then hvyuse = **0**; \*0 = 'no';

else if hvyuse4 in (**2**,**3**,**4**,**5**,**6**) then hvyuse = **1**; \*1 = 'yes';

else if missing(hvyuse4) then hvyuse = **.**;

else;

**run**;

\*check coding;

**proc** **freq** data=HW5;

tables hvyuse4 hvyuse4\*hvyuse;

**run**;

\*recode getpar4 (0,1,2) - use 'easy' as ref;

**data** HW5\_1;

set HW5;

if getpar4 = **1** then getpar = **0**; \*0 = easy;

else if getpar4 = **2** then getpar = **1**; \*1 = in-between;

else if getpar4 = **3** then getpar = **2**; \*2 = hard;

else if missing(getpar4) then getpar = **.**;

else;

**run**;

**proc** **freq** data=HW5\_1;

tables getpar4 getpar4\*getpar;

**run**;

\*recode gender (0 1) - make 'male' ref;

**data** HW5\_2;

set HW5\_1;

if gender4 = **1** then female = **0**; \*if female = 0, then male;

else if gender4 = **2** then female = **1**; \*if female = 1, then female;

else if missing(gender4) then female = **.**;

else;

**run**;

**proc** **freq** data=HW5\_2;

tables gender4 gender4\*female;

**run**;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* PART 1 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

\*Assess EM of 'female' on association between 'getpar' (exposure) and 'hvyuse' (outcome)

on an MULTIPLICATIVE scale;

**proc** **genmod** data=HW5\_2 desc;

class female (param=ref ref='0') getpar (param=ref ref='0');

model hvyuse = getpar female getpar\*female / dist=binomial link=logit type3;

**run**;

\*p-value is nonsignificant on multiplicative scale;

**proc** **sort** data=HW5\_2;

by female;

**run**;

**proc** **genmod** data=HW5\_2 desc;

by female;

class getpar (param=ref ref='0');

model hvyuse = getpar/ dist=binomial link=logit type3;

**run**;

\*BUT exposure estimates vary across strata of gender - thus we must test for additive interaction;

\*Assess EM of 'female' on association between 'getpar' (exposure) and 'hvyuse' (outcome)

on an ADDITIVE scale;

**proc** **genmod** data=HW5\_2 desc;

class female (param=ref ref='0') getpar (param=ref ref='0');

model hvyuse = getpar female getpar\*female / dist=binomial link=identity type3; /\*identity link for linear probability model\*/

**run**;

\*check interaction using normal dist - model specific results;

**proc** **genmod** data=HW5\_2 desc;

class female (param=ref ref='0') getpar (param=ref ref='0');

model hvyuse = getpar female getpar\*female / dist=normal link=identity type3; /\*identity link for linear probability model\*/

**run**;

/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* PART 2 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/

\*estimate RD across strata of gender (IF EM IS ADDITIVE);

**proc** **genmod** data=HW5\_2 desc;

class female (param=ref ref='0') getpar (param=ref ref='0');

model hvyuse = getpar female getpar\*female / dist=binomial link=identity type3; /\*identity link for linear probability model\*/

estimate "RD for male in-between" getpar **1** **0** getpar\*female **0** **0**;

estimate "RD for male hard" getpar **0** **1** getpar\*female **0** **0**;

estimate "RD for female in-between" getpar **1** **0** getpar\*female **1** **0**;

estimate "RD for female hard" getpar **0** **1** getpar\*female **0** **1**;

**run**;

\*^ THIS IS THE CODE USED TO MAKE THE TABLE ABOVE;