Statistics/Data analysis

```
      name:  <unnamed>
       log:  C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli
> cation files\Anoll Kam Marcellin Bovitz Analyses.smcl
  log type:  smcl
 opened on:  10 Jan 2025, 13:39:49

1 .
2 . /*Cleaning the data*/
3 . clear

4 . cd "C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP replication
> files\"
C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP replication files

5 .
6 . use "Anoll Kam Marcellin Bovitz June 2022 Survey.dta"

7 .
8 . gen newdate = dofc(StartDate)

9 . gen double newtime = hh(StartDate)

10.
11. //Dropping test data
12. drop if newdate<22816
  (2 observations deleted)

13. drop if newdate==22816 & newtime==10
  (1 observation deleted)

14.
15. //Removing those who have not consented
16. drop if agree~=1
  (20 observations deleted)

17.
18. //Removing those under 18
19. gen ageyears = age
  (7 missing values generated)

20. destring ageyears, force replace
  ageyears: contains nonnumeric characters; replaced as int
  (9 missing values generated)

21. drop if ageyears<18 | ageyears>105
  (15 observations deleted)

22. sum ageyears

    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
    ageyears |      3,617    46.44954    15.57761        18         99

23.
24. //Keeping those who pass the attention check
25. keep if check_closeread_4==1 & check_closeread_5==1
  (637 observations deleted)

26.
```

```
27. //Take the first respondent of those with duplicate IP addresses
28. duplicates tag IPAddress, gen(dupIP)

  Duplicates in terms of IPAddress

29. egen IPdups = group(IPAddress) if dupIP>0
  (2,863 missing values generated)

30. egen rank = rank(StartDate), track

31. bysort IPdups: egen firstrank = min(rank)

32. drop if firstrank~=rank & dupIP>0
  (61 observations deleted)

33.
34. //Sample characteristics
35. //We ordered 900 White Dems, 900 White Reps, 900 Blacks
36. //Race
37. gen White = .
  (2,919 missing values generated)

38. replace White = 1 if race_5==1
  (1,941 real changes made)

39. replace White = 0 if race_1==1 | race_2==1|race_3==1|race_4==1|race_6==1
  (1,044 real changes made)

40. tab White
```

White	Freq.	Percent	Cum.
0	**1,044**	**36.17**	**36.17**
1	**1,842**	**63.83**	**100.00**
Total	**2,886**	**100.00**	

```
41.
42. gen Black = .
  (2,919 missing values generated)

43. replace Black = 1 if race_3==1
  (968 real changes made)

44. replace Black = 0 if race_1==1 | race_2==1|race_4==1|race_5==1|race_6==1
  (1,992 real changes made)

45.
46. gen race = 0

47. replace race = 1 if White==1
  (1,842 real changes made)

48. replace race = 2 if Black==1
  (894 real changes made)

49. lab def race 0"Other" 1"White" 2"Black"

50. lab val race race
```

```
51.
52. //Party
53. gen REP = 0

54. replace REP = 1 if strong_rep==1|strong_rep==2|lean==1
  (996 real changes made)

55. gen DEM = 0

56. replace DEM = 1 if strong_dem==1|strong_dem==2|lean==2
  (1,632 real changes made)

57. tab1 REP DEM
```

-> tabulation of REP

REP	Freq.	Percent	Cum.
0	**1,923**	**65.88**	**65.88**
1	**996**	**34.12**	**100.00**
Total	**2,919**	**100.00**	

-> tabulation of DEM

DEM	Freq.	Percent	Cum.
0	**1,287**	**44.09**	**44.09**
1	**1,632**	**55.91**	**100.00**
Total	**2,919**	**100.00**	

```
58.
59. gen pid3cat = .
  (2,919 missing values generated)

60. replace pid3cat = 0 if REP==1
  (996 real changes made)

61. replace pid3cat = 1 if DEM==1
  (1,632 real changes made)

62. replace pid3cat = .5 if lean==3
  (249 real changes made)

63. tab pid3cat
```

pid3cat	Freq.	Percent	Cum.
0	**996**	**34.62**	**34.62**
.5	**249**	**8.65**	**43.27**
1	**1,632**	**56.73**	**100.00**
Total	**2,877**	**100.00**	

```
64. lab def pid3cat 0 "REP" 1 "DEM"

65. lab val pid3cat pid3cat

66. tab pid3cat race
```

pid3cat	race: Other	White	Black	Total
REP	**44**	**883**	**69**	**996**
.5	**25**	**66**	**158**	**249**
DEM	**81**	**888**	**663**	**1,632**
Total	**150**	**1,837**	**890**	**2,877**

```
67.
68. //Finalizing sample
69. keep if (White==1 & REP==1)|(White==1 & DEM==1)|(Black==1)
  (254 observations deleted)

70. gen samplegroups = .
  (2,665 missing values generated)

71. replace samplegroups = 1 if White==1 & REP==1
  (883 real changes made)

72. replace samplegroups = 2 if White==1 & DEM==1
  (888 real changes made)

73. replace samplegroups = 3 if Black==1
  (894 real changes made)

74. lab def samplegroups 1"White REP" 2"White DEM" 3"Black"

75. lab val samplegroups samplegroups

76. tab samplegroups
```

samplegroups	Freq.	Percent	Cum.
White REP	**883**	**33.13**	**33.13**
White DEM	**888**	**33.32**	**66.45**
Black	**894**	**33.55**	**100.00**
Total	**2,665**	**100.00**	

```
77.
78. /*Treatment*/
79. gen expcond = .
  (2,665 missing values generated)

80. replace expcond = 1 if treatment =="gene"
  (879 real changes made)

81. replace expcond = 2 if treatment =="neutral"
  (894 real changes made)

82. replace expcond = 3 if treatment =="ses"
  (892 real changes made)

83. lab def expcond 1 "Genetic Frame" 2"Neutral" 3"SES Frame"

84. lab val expcond expcond

85.
86. recode expcond (1=1)(2 3=0)(else=.), gen(genecond)
  (1,786 differences between expcond and genecond)

87. recode expcond (3=1)(1 2=0)(else=.), gen(sescond)
  (2,665 differences between expcond and sescond)

88. lab var genecond "Genetic Framing"

89. lab var sescond "SES Framing"
```

```
90.
91.
92. //MANIPULATION CHECK//
93. //open-ends (check_article)
94. //any appearance of gene/genetic/genetics
95. //vs. any appearance of socioeconomic/SES/socio/econ
96. gen comment_lower = lower(check_article)
  (12 missing values generated)

97. *replace period and commas with space
98. replace comment_lower = subinstr(comment_lower, ".", " ",.)
  (1,341 real changes made)

99. replace comment_lower = subinstr(comment_lower, ",", " ",.)
  (276 real changes made)

100 set more off

101 foreach word in gene genes heredity inherit genetic genetics genetically counseling
  > biology  {
    2. gen `word'=1 if strpos(comment_lower," `word' ")>0
    3. }
  (2,654 missing values generated)
  (2,645 missing values generated)
  (2,665 missing values generated)
  (2,663 missing values generated)
  (2,406 missing values generated)
  (2,538 missing values generated)
  (2,614 missing values generated)
  (2,632 missing values generated)
  (2,664 missing values generated)

102 egen anygeneopen=anymatch(gene-biology), val(1)

103 tab anygeneopen expcond, col chi2
```

Key
frequency *column percentage*

see notes	expcond Genetic F	Neutral	SES Frame	Total
0	**482** **54.84**	**864** **96.64**	**870** **97.53**	**2,216** **83.15**
1	**397** **45.16**	**30** **3.36**	**22** **2.47**	**449** **16.85**
Total	**879** **100.00**	**894** **100.00**	**892** **100.00**	**2,665** **100.00**

Pearson chi2(**2**) = **750.9674** Pr = **0.000**

```
104 foreach word in socio social socioeconomic status economy economic disadvantage disa
  > dvantages therapy SES {
    2. gen `word'=1 if strpos(comment_lower," `word' ")>0
    3. }
  (2,654 missing values generated)
  (2,603 missing values generated)
  (2,422 missing values generated)
  (2,648 missing values generated)
  (2,665 missing values generated)
  (2,607 missing values generated)
  (2,644 missing values generated)
  (2,616 missing values generated)
  (2,652 missing values generated)
  (2,665 missing values generated)
```

```
105 egen anySESopen  =anymatch(socio-SES), val(1)

106 tab anySESopen expcond, col chi2
```

Key
frequency *column percentage*

see notes	expcond Genetic F	Neutral	SES Frame	Total
0	**863** **98.18**	**878** **98.21**	**554** **62.11**	**2,295** **86.12**
1	**16** **1.82**	**16** **1.79**	**338** **37.89**	**370** **13.88**
Total	**879** **100.00**	**894** **100.00**	**892** **100.00**	**2,665** **100.00**

Pearson chi2(**2**) = **646.3993** Pr = **0.000**

```
107
108
109 //BALANCE CHECK
110 recode gender (1=0)(2=1)(else=.), gen(female)
  (2,665 differences between gender and female)

111 recode educ (3 5=0)(6=.25)(7=.5)(8=.75)(9 10=1)(else=.), gen(ed5cat)
  (2,664 differences between education and ed5cat)

112 recode income (1=0)(4=.2)(5=.4)(6=.6)(8=.8)(10 12=1)(else=.), gen(faminc6)
  (2,665 differences between income and faminc6)

113 lab var ed5cat "Education"

114 lab var female "Female"

115 lab var ageyears "Age"

116 lab var pid3cat "Party ID"

117 lab var faminc6 "Income"

118 lab var expcond "Experimental Condition"

119 hotelling ageyear female ed5cat faminc6 pid3cat Black if sescond~=1, by(genecond)
```

-> genecond = 0

Variable	Obs	Mean	Std. dev.	Min	Max
ageyears	**882**	**46.95125**	**15.26419**	**18**	**84**
female	**882**	**.5079365**	**.5002207**	**0**	**1**
ed5cat	**882**	**.4328231**	**.3463893**	**0**	**1**
faminc6	**882**	**.4557823**	**.3650689**	**0**	**1**
pid3cat	**882**	**.6071429**	**.47482**	**0**	**1**
Black	**882**	**.3253968**	**.4687888**	**0**	**1**

-> genecond = 1

Variable	Obs	Mean	Std. dev.	Min	Max
ageyears	871	47.15385	15.56283	18	99
female	871	.5086108	.5002131	0	1
ed5cat	871	.4259472	.3325685	0	1
faminc6	871	.4516648	.3640688	0	1
pid3cat	871	.6211251	.468516	0	1
Black	871	.3409874	.4743135	0	1

2-group Hotelling's T-squared = **1.0134339**
F test statistic: **((1753-6-1)/(1753-2)(6)) x 1.0134339 = .16842333**

H0: Vectors of means are equal for the two groups
F(**6,1746**) = **0.1684**
Prob > F(**6,1746**) = **0.9852**

```
120 hotelling ageyear female ed5cat faminc6 pid3cat Black if genecond~=1, by(sescond)
```

-> sescond = 0

Variable	Obs	Mean	Std. dev.	Min	Max
ageyears	882	46.95125	15.26419	18	84
female	882	.5079365	.5002207	0	1
ed5cat	882	.4328231	.3463893	0	1
faminc6	882	.4557823	.3650689	0	1
pid3cat	882	.6071429	.47482	0	1
Black	882	.3253968	.4687888	0	1

-> sescond = 1

Variable	Obs	Mean	Std. dev.	Min	Max
ageyears	879	46.22981	15.44428	18	86
female	879	.5119454	.5001419	0	1
ed5cat	879	.4032992	.3352071	0	1
faminc6	879	.4323095	.3533801	0	1
pid3cat	879	.6001138	.4751094	0	1
Black	879	.337884	.4732581	0	1

2-group Hotelling's T-squared = **4.6501505**
F test statistic: **((1761-6-1)/(1761-2)(6)) x 4.6501505 = .77282206**

H0: Vectors of means are equal for the two groups
F(**6,1754**) = **0.7728**
Prob > F(**6,1754**) = **0.5913**

```
121
122 table (var) (expcond), statistic(mean ageyear female ed5cat faminc6 pid3cat Black) s
  > tatistic(sd ageyear female ed5cat faminc6 pid3cat Black) statistic(count expcond) nf
  > ormat(%9.2f mean sd) nototals
```

	Experimental Condition		
	Genetic Frame	Neutral	SES Frame
Age			
Mean	**47.09**	**46.71**	**45.99**
Standard deviation	**15.58**	**15.38**	**15.54**
Female			
Mean	**0.51**	**0.51**	**0.51**
Standard deviation	**0.50**	**0.50**	**0.50**
Education			
Mean	**0.43**	**0.43**	**0.40**
Standard deviation	**0.33**	**0.35**	**0.34**

Income			
Mean	**0.45**	**0.45**	**0.43**
Standard deviation	**0.36**	**0.37**	**0.35**
Party ID			
Mean	**0.62**	**0.61**	**0.60**
Standard deviation	**0.47**	**0.47**	**0.47**
Black			
Mean	**0.34**	**0.33**	**0.34**
Standard deviation	**0.47**	**0.47**	**0.47**
Experimental Condition			
Number of nonmissing values	**879**	**894**	**892**

```
123 collect levelsof result

  Collection: Table
   Dimension: result
      Levels: count mean sd

124 collect style header result, level(hide)

125 collect title "Means, SD, N per Experimental Condition"

126 collect preview
```

Means, SD, N per Experimental Condition

	Experimental Condition		
	Genetic Frame	Neutral	SES Frame
Age	**47.09**	**46.71**	**45.99**
	15.58	**15.38**	**15.54**
Female	**0.51**	**0.51**	**0.51**
	0.50	**0.50**	**0.50**
Education	**0.43**	**0.43**	**0.40**
	0.33	**0.35**	**0.34**
Income	**0.45**	**0.45**	**0.43**
	0.36	**0.37**	**0.35**
Party ID	**0.62**	**0.61**	**0.60**
	0.47	**0.47**	**0.47**
Black	**0.34**	**0.33**	**0.34**
	0.47	**0.47**	**0.47**
Experimental Condition	**879**	**894**	**892**

```
127
128
129 /*DVs*/
130 recode bat1_health (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen
  > (genes_health)
  (2,665 differences between bat1_health and genes_health)

131 recode bat2_health (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen
  > (ses_health)
  (2,665 differences between bat2_health and ses_health)

132
133 recode bat1_edu (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen(ge
  > nes_edu)
  (2,665 differences between bat1_edu and genes_edu)
```

```
134 recode bat2_edu (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen(se
  > s_edu)
  (2,665 differences between bat2_edu and ses_edu)

135
136 recode bat1_crime (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen(
  > genes_crime)
  (2,665 differences between bat1_crime and genes_crime)

137 recode bat2_crime (1=0 "not at all")(2=.33)(3=.67)(4=1 "A great deal")(else=.), gen(
  > ses_crime)
  (2,665 differences between bat2_crime and ses_crime)

138
139 gen genes_index = (genes_health+genes_edu+genes_crime)/3
  (2 missing values generated)

140 gen ses_index = (ses_health+ses_edu+ses_crime)/3
  (3 missing values generated)

141 alpha genes_health genes_edu genes_crime

  Test scale = mean(unstandardized items)

  Average interitem covariance:     .0616805
  Number of items in the scale:            3
  Scale reliability coefficient:      0.7733

142 alpha ses_health ses_edu ses_crime

  Test scale = mean(unstandardized items)

  Average interitem covariance:     .0840417
  Number of items in the scale:            3
  Scale reliability coefficient:      0.8851

143 corr genes_index ses_index
  (obs=2,660)

             | genes_~x ses_in~x
-------------+------------------
 genes_index |   1.0000
   ses_index |   0.1159   1.0000


144
145 **********TABLE 1**********
146 foreach v of varlist genes_index genes_health genes_edu genes_crime ses_index ses_he
  > alth ses_edu ses_crime {
    2. reg `v' genecond sescond
    3. est store `v'
    4. }

      Source |       SS           df       MS      Number of obs   =     2,663
-------------+----------------------------------   F(2, 2660)      =      8.09
       Model |  1.28385755         2  .641928773   Prob > F        =    0.0003
    Residual |  211.039725     2,660  .079338242   R-squared       =    0.0060
-------------+----------------------------------   Adj R-squared   =    0.0053
       Total |  212.323582     2,662  .079760925   Root MSE        =    .28167

------------------------------------------------------------------------------
 genes_index | Coefficient  Std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
    genecond |   .0489863   .0133868     3.66   0.000     .0227367     .075236
     sescond |   .0049631   .0133337     0.37   0.710    -.0211824    .0311087
       _cons |   .3604442   .0094257    38.24   0.000     .3419617    .3789267
------------------------------------------------------------------------------
```

Source	SS	df	MS	Number of obs	=	2,664
				F(2, 2661)	=	26.07
Model	4.92894024	2	2.46447012	Prob > F	=	0.0000
Residual	251.529136	2,661	.09452429	R-squared	=	0.0192
				Adj R-squared	=	0.0185
Total	256.458076	2,663	.096304197	Root MSE	=	.30745

genes_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0677174	.0146078	4.64	0.000	.0390737	.0963611
sescond	-.0362922	.014554	-2.49	0.013	-.0648305	-.0077538
_cons	.537402	.0102884	52.23	0.000	.517228	.557576

Source	SS	df	MS	Number of obs	=	2,664
				F(2, 2661)	=	2.73
Model	.623197954	2	.311598977	Prob > F	=	0.0652
Residual	303.32784	2,661	.113990169	R-squared	=	0.0021
				Adj R-squared	=	0.0013
Total	303.951038	2,663	.11413858	Root MSE	=	.33762

genes_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0372517	.0160417	2.32	0.020	.0057963	.0687071
sescond	.0222431	.015978	1.39	0.164	-.0090875	.0535737
_cons	.2504362	.0112918	22.18	0.000	.2282946	.2725779

Source	SS	df	MS	Number of obs	=	2,665
				F(2, 2662)	=	2.78
Model	.761709996	2	.380854998	Prob > F	=	0.0625
Residual	365.186574	2,662	.137185039	R-squared	=	0.0021
				Adj R-squared	=	0.0013
Total	365.948284	2,664	.137367974	Root MSE	=	.37038

genes_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0404047	.0175932	2.30	0.022	.005907	.0749024
sescond	.0280479	.0175284	1.60	0.110	-.0063228	.0624187
_cons	.2943848	.0123875	23.76	0.000	.2700946	.3186749

Source	SS	df	MS	Number of obs	=	2,662
				F(2, 2659)	=	0.30
Model	.057118836	2	.028559418	Prob > F	=	0.7404
Residual	252.57115	2,659	.09498727	R-squared	=	0.0002
				Adj R-squared	=	-0.0005
Total	252.628269	2,661	.094937343	Root MSE	=	.3082

ses_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0112363	.0146476	-0.77	0.443	-.0399581	.0174854
sescond	-.0041408	.0145978	-0.28	0.777	-.032765	.0244833
_cons	.6671749	.0103193	64.65	0.000	.6469402	.6874096

Source	SS	df	MS	Number of obs	=	2,664
				F(2, 2661)	=	0.92
Model	.205672692	2	.102836346	Prob > F	=	0.3993
Residual	297.969319	2,661	.111976445	R-squared	=	0.0007
				Adj R-squared	=	-0.0001
Total	298.174992	2,663	.11196958	Root MSE	=	.33463

ses_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0140929	.0158992	-0.89	0.375	-.0452689	.0170832
sescond	.0070934	.0158407	0.45	0.654	-.0239679	.0381547
_cons	.6573124	.0111979	58.70	0.000	.6353549	.67927

Source	SS	df	MS		
Model	.06869301	2	.034346505	Number of obs	= 2,665
Residual	321.174066	2,662	.120651415	F(2, 2662)	= 0.28
				Prob > F	= 0.7523
Total	321.242759	2,664	.120586621	R-squared	= 0.0002
				Adj R-squared	= -0.0005
				Root MSE	= .34735

ses_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0100036	.016499	-0.61	0.544	-.0423557	.0223485
sescond	-.0113637	.0164383	-0.69	0.489	-.0435967	.0208693
_cons	.6617897	.0116171	56.97	0.000	.6390103	.6845692

Source	SS	df	MS		
Model	.034508403	2	.017254201	Number of obs	= 2,663
Residual	313.324196	2,660	.117791051	F(2, 2660)	= 0.15
				Prob > F	= 0.8637
Total	313.358704	2,662	.117715516	R-squared	= 0.0001
				Adj R-squared	= -0.0006
				Root MSE	= .34321

ses_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0085002	.0163068	-0.52	0.602	-.0404754	.023475
sescond	-.0062709	.0162513	-0.39	0.700	-.0381374	.0255956
_cons	.6813102	.011485	59.32	0.000	.6587898	.7038306

```
147 est table genes_index genes_health genes_edu genes_crime ses_index ses_health ses_ed
  > u ses_crime,  b(%9.2f) se stats(N) style(col) eq(1)
```

Variable	genes_index	genes_health	genes_edu	genes_crime	ses_index	ses_health
ses_edu	ses_crime					
genecond	0.05	0.07	0.04	0.04	-0.01	-0.01
-0.01	-0.01					
	0.01	0.01	0.02	0.02	0.01	0.02
0.02	0.02					
sescond	0.00	-0.04	0.02	0.03	-0.00	0.01
-0.01	-0.01					
	0.01	0.01	0.02	0.02	0.01	0.02
0.02	0.02					
_cons	0.36	0.54	0.25	0.29	0.67	0.66
0.66	0.68					
	0.01	0.01	0.01	0.01	0.01	0.01
0.01	0.01					
N	2663	2664	2664	2665	2662	2664
2665	2663					

Legend: b/se

```
148 est table genes_index genes_health genes_edu genes_crime ses_index ses_health ses_ed
  > u ses_crime,  b(%9.2f) star(.05 .01 .001) stats(N) style(col) eq(1)
```

| Variable | genes_index | genes_health | genes_edu | genes_crime | ses_inde
> x | ses_health | ses_edu | ses_crime | | | |
|---|---|---|---|---|---|
| genecond | 0.05*** | 0.07*** | 0.04* | 0.04* | -0.01
> | -0.01 | -0.01 | -0.01 | | | |
| sescond | 0.00 | -0.04* | 0.02 | 0.03 | -0.00
> | 0.01 | -0.01 | -0.01 | | | |
| _cons | 0.36*** | 0.54*** | 0.25*** | 0.29*** | 0.67
> *** | 0.66*** | 0.66*** | 0.68*** | | | |
| N | 2663 | 2664 | 2664 | 2665 | 2662
> | 2664 | 2665 | 2663 | | | |

```
  >              Legend: * p<.05; ** p<.01; *** p<.001

149
150 /*Testing equivalence across conditions*/
151 suest genes_health genes_edu

  Simultaneous results for genes_health, genes_edu

                                                      Number of obs = 2,665
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
genes_health_mean						
genecond	.0677174	.0141624	4.78	0.000	.0399596	.0954753
sescond	-.0362922	.0148271	-2.45	0.014	-.0653527	-.0072316
_cons	.537402	.0100765	53.33	0.000	.5176525	.5571516
genes_health_lnvar						
_cons	-2.358898	.0211703	-111.43	0.000	-2.400391	-2.317405
genes_edu_mean						
genecond	.0372517	.0158664	2.35	0.019	.0061542	.0683492
sescond	.0222431	.0159154	1.40	0.162	-.0089505	.0534368
_cons	.2504362	.0109596	22.85	0.000	.2289558	.2719167
genes_edu_lnvar						
_cons	-2.171643	.0235114	-92.37	0.000	-2.217725	-2.125562

```
152 test [genes_health_mean]genecond=[genes_edu_mean]genecond

  ( 1)  [genes_health_mean]genecond - [genes_edu_mean]genecond = 0

            chi2(  1) =    3.51
          Prob > chi2 =    0.0611
```

```
153 //reporting one-tailed p-values which require halving the two-tailed p-value reporte
  > d
154 disp .0611/2
  .03055

155
156 suest genes_health genes_crime

  Simultaneous results for genes_health, genes_crime

                                                      Number of obs = 2,665
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
genes_health_mean						
genecond	.0677174	.0141624	4.78	0.000	.0399596	.0954753
sescond	-.0362922	.0148271	-2.45	0.014	-.0653527	-.0072316
_cons	.537402	.0100765	53.33	0.000	.5176525	.5571516
genes_health_lnvar						
_cons	-2.358898	.0211703	-111.43	0.000	-2.400391	-2.317405
genes_crime_mean						
genecond	.0404047	.0174683	2.31	0.021	.0061675	.074642
sescond	.0280479	.0173908	1.61	0.107	-.0060373	.0621332
_cons	.2943848	.0120181	24.50	0.000	.2708298	.3179398
genes_crime_lnvar						
_cons	-1.986425	.0198758	-99.94	0.000	-2.02538	-1.947469

```
157 test [genes_health_mean]genecond=[genes_crime_mean]genecond

   ( 1)  [genes_health_mean]genecond - [genes_crime_mean]genecond = 0

           chi2(  1) =    2.45
         Prob > chi2 =    0.1178

158 //reporting one-tailed p-values which require halving the two-tailed p-value reporte
  > d
159 disp .1178/2
  .0589

160
161 //calculating effect size
162 //difference of means/sd
163 ttest genes_index if sescond==0, by(genecond)

  Two-sample t test with equal variances
```

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
0	893	.3604442	.0090176	.2694745	.342746	.3781424
1	878	.4094305	.0094519	.2800689	.3908796	.4279815
Combined	1,771	.3847299	.0065535	.2757905	.3718766	.3975832
diff		-.0489863	.0130592		-.0745995	-.0233732

```
    diff = mean(0) - mean(1)                                      t =  -3.7511
H0: diff = 0                                     Degrees of freedom =     1769

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0001         Pr(|T| > |t|) = 0.0002          Pr(T > t) = 0.9999
```

```
164 disp -.0489863/.2757905
  -.17762142

165
166 ttest genes_health if sescond==0, by(genecond)

  Two-sample t test with equal variances
```

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
0	893	.537402	.0100802	.3012287	.5176183	.5571858
1	879	.6051195	.0099556	.2951633	.5855799	.624659
Combined	1,772	.5709932	.0071283	.3000686	.5570124	.5849741
diff		-.0677174	.01417		-.0955092	-.0399257

```
    diff = mean(0) - mean(1)                                      t =  -4.7789
H0: diff = 0                                     Degrees of freedom =     1770

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000

167 disp -.0677174/.3000686
  -.22567306

168
169
170 *****HETEROGENEITY*****
171 **********START FIGURE 5**********
172 *****PLACE FULL RESULTS IN APPENDIX*****
173 forval j=1/3 {
    2. foreach v of varlist genes_index genes_health genes_edu genes_crime ses_index ses
  > _health ses_edu ses_crime {
    3. reg `v' genecond sescond if samplegroups==`j'
    4. est store `v'_`j'
    5. }
    6. }
```

Source	SS	df	MS		
				Number of obs	= 883
				F(2, 880)	= 2.09
Model	.284083546	2	.142041773	Prob > F	= 0.1245
Residual	59.8496404	880	.068010955	R-squared	= 0.0047
				Adj R-squared	= 0.0025
Total	60.1337239	882	.068178825	Root MSE	= .26079

genes_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0280362	.0215588	1.30	0.194	-.0142764	.0703487
sescond	-.0157477	.0212944	-0.74	0.460	-.0575414	.0260461
_cons	.3777118	.0149819	25.21	0.000	.3483073	.4071163

Source	SS	df	MS		
				Number of obs	= 883
				F(2, 880)	= 9.18
Model	1.51402462	2	.757012309	Prob > F	= 0.0001
Residual	72.5572571	880	.082451428	R-squared	= 0.0204
				Adj R-squared	= 0.0182
Total	74.0712817	882	.083981045	Root MSE	= .28714

genes_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.020058	.0237374	0.84	0.398	-.0265306	.0666465
sescond	-.076236	.0234463	-3.25	0.001	-.1222532	-.0302187
_cons	.5813201	.016496	35.24	0.000	.5489441	.6136962

Source	SS	df	MS	Number of obs	=	883
				F(2, 880)	=	1.17
Model	.250529457	2	.125264728	Prob > F	=	0.3124
Residual	94.6073427	880	.107508344	R-squared	=	0.0026
				Adj R-squared	=	0.0004
Total	94.8578722	882	.107548608	Root MSE	=	.32788

genes_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0412355	.0271054	1.52	0.129	-.0119633	.0944342
sescond	.022865	.026773	0.85	0.393	-.0296814	.0754114
_cons	.2484819	.0188365	13.19	0.000	.2115122	.2854515

Source	SS	df	MS	Number of obs	=	883
				F(2, 880)	=	0.34
Model	.080882124	2	.040441062	Prob > F	=	0.7121
Residual	104.792151	880	.11908199	R-squared	=	0.0008
				Adj R-squared	=	-0.0015
Total	104.873033	882	.118903666	Root MSE	=	.34508

genes_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0228151	.0285271	0.80	0.424	-.033174	.0788041
sescond	.0061279	.0281773	0.22	0.828	-.0491746	.0614305
_cons	.3033333	.0198245	15.30	0.000	.2644246	.3422421

Source	SS	df	MS	Number of obs	=	882
				F(2, 879)	=	2.59
Model	.459484149	2	.229742074	Prob > F	=	0.0756
Residual	77.9551709	879	.088686201	R-squared	=	0.0059
				Adj R-squared	=	0.0036
Total	78.414655	881	.089006419	Root MSE	=	.2978

ses_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0371966	.0246382	-1.51	0.131	-.0855532	.01116
sescond	-.0541384	.0243366	-2.22	0.026	-.101903	-.0063738
_cons	.5201766	.0171366	30.35	0.000	.4865432	.55381

Source	SS	df	MS	Number of obs	=	882
				F(2, 879)	=	1.25
Model	.252002135	2	.126001067	Prob > F	=	0.2864
Residual	88.4521516	879	.100628159	R-squared	=	0.0028
				Adj R-squared	=	0.0006
Total	88.7041537	881	.100685759	Root MSE	=	.31722

ses_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0345221	.0262447	-1.32	0.189	-.0860317	.0169874
sescond	-.0365849	.0259234	-1.41	0.159	-.0874639	.014294
_cons	.5068543	.0182539	27.77	0.000	.4710279	.5426807

Source	SS	df	MS	Number of obs	=	883
				F(2, 880)	=	3.36
Model	.78060013	2	.390300065	Prob > F	=	0.0351
Residual	102.168378	880	.116100429	R-squared	=	0.0076
				Adj R-squared	=	0.0053
Total	102.948978	882	.116722197	Root MSE	=	.34074

ses_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0296086	.0281677	-1.05	0.293	-.0848923	.0256751
sescond	-.0718275	.0278223	-2.58	0.010	-.1264333	-.0172217
_cons	.519538	.0195747	26.54	0.000	.4811194	.5579566

Source	SS	df	MS		
Model	.539310997	2	.269655498	Number of obs	= 883
Residual	102.584446	880	.116573234	F(2, 880)	= 2.31
				Prob > F	= 0.0995
Total	103.123757	882	.116920359	R-squared	= 0.0052
				Adj R-squared	= 0.0030
				Root MSE	= .34143

ses_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0484041	.028225	-1.71	0.087	-.1038002	.0069921
sescond	-.0549478	.0278789	-1.97	0.049	-.1096647	-.0002309
_cons	.5350825	.0196145	27.28	0.000	.4965858	.5735793

Source	SS	df	MS		
Model	.870587695	2	.435293848	Number of obs	= 887
Residual	58.2891439	884	.065937946	F(2, 884)	= 6.60
				Prob > F	= 0.0014
Total	59.1597316	886	.066771706	R-squared	= 0.0147
				Adj R-squared	= 0.0125
				Root MSE	= .25678

genes_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0532021	.02109	2.52	0.012	.0118098	.0945943
sescond	-.0214341	.021108	-1.02	0.310	-.0628617	.0199935
_cons	.3004251	.0148751	20.20	0.000	.2712305	.3296197

Source	SS	df	MS		
Model	2.38146813	2	1.19073407	Number of obs	= 887
Residual	79.8544133	884	.090333047	F(2, 884)	= 13.18
				Prob > F	= 0.0000
Total	82.2358814	886	.092817022	R-squared	= 0.0290
				Adj R-squared	= 0.0268
				Root MSE	= .30055

genes_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0775942	.0246849	3.14	0.002	.0291464	.1260421
sescond	-.048434	.024706	-1.96	0.050	-.0969233	.0000552
_cons	.4901007	.0174107	28.15	0.000	.4559296	.5242717

Source	SS	df	MS		
Model	.409462137	2	.204731068	Number of obs	= 888
Residual	78.042783	885	.088183936	F(2, 885)	= 2.32
				Prob > F	= 0.0987
Total	78.4522451	887	.088446725	R-squared	= 0.0052
				Adj R-squared	= 0.0030
				Root MSE	= .29696

genes_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0362555	.0243692	1.49	0.137	-.0115726	.0840837
sescond	-.0150026	.0243901	-0.62	0.539	-.0628717	.0328665
_cons	.1938462	.0171735	11.29	0.000	.1601406	.2275517

Source	SS	df	MS	Number of obs	=	888
				F(2, 885)	=	1.84
Model	.394540758	2	.197270379	Prob > F	=	0.1590
Residual	94.7606596	885	.107074192	R-squared	=	0.0041
				Adj R-squared	=	0.0019
Total	95.1552003	887	.107277565	Root MSE	=	.32722

genes_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.04265	.0268528	1.59	0.113	-.0100526	.0953525
sescond	-.0039722	.0268757	-0.15	0.883	-.0567198	.0487754
_cons	.2204348	.0189237	11.65	0.000	.1832942	.2575754

Source	SS	df	MS	Number of obs	=	887
				F(2, 884)	=	2.90
Model	.436093063	2	.218046532	Prob > F	=	0.0553
Residual	66.3530473	884	.075060008	R-squared	=	0.0065
				Adj R-squared	=	0.0043
Total	66.7891403	886	.075382777	Root MSE	=	.27397

ses_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0063231	.0224828	-0.28	0.779	-.0504491	.0378028
sescond	.0436815	.0225214	1.94	0.053	-.0005202	.0878832
_cons	.7503345	.0158441	47.36	0.000	.7192379	.781431

Source	SS	df	MS	Number of obs	=	888
				F(2, 885)	=	4.26
Model	.804951316	2	.402475658	Prob > F	=	0.0145
Residual	83.6687943	885	.094541011	R-squared	=	0.0095
				Adj R-squared	=	0.0073
Total	84.4737456	887	.095235339	Root MSE	=	.30748

ses_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0092601	.0252323	-0.37	0.714	-.0587822	.040262
sescond	.0588702	.0252539	2.33	0.020	.0093057	.1084346
_cons	.7295652	.0177818	41.03	0.000	.6946659	.7644645

Source	SS	df	MS	Number of obs	=	888
				F(2, 885)	=	1.67
Model	.314966108	2	.157483054	Prob > F	=	0.1894
Residual	83.6178638	885	.094483462	R-squared	=	0.0038
				Adj R-squared	=	0.0015
Total	83.9328299	887	.094625513	Root MSE	=	.30738

ses_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0110761	.0252246	-0.44	0.661	-.0605832	.0384309
sescond	.0333441	.0252462	1.32	0.187	-.0162053	.0828935
_cons	.7606355	.0177763	42.79	0.000	.7257468	.7955242

Source	SS	df	MS	Number of obs	=	887
				F(2, 884)	=	1.66
Model	.307608186	2	.153804093	Prob > F	=	0.1905
Residual	81.8381889	884	.092577137	R-squared	=	0.0037
				Adj R-squared	=	0.0015
Total	82.1457971	886	.092715347	Root MSE	=	.30426

ses_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0013668	.0249688	0.05	0.956	-.0476383	.050372
sescond	.0402553	.0250117	1.61	0.108	-.0088339	.0893446
_cons	.7608027	.0175961	43.24	0.000	.7262677	.7953377

Source	SS	df	MS		
Model	.66375717	2	.331878585	Number of obs	= 893
Residual	84.7253449	890	.095197017	F(2, 890)	= 3.49
				Prob > F	= 0.0310
Total	85.389102	892	.095727693	R-squared	= 0.0078
				Adj R-squared	= 0.0055
				Root MSE	= .30854

genes_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0639992	.0253642	2.52	0.012	.0142187	.1137798
sescond	.049433	.0253434	1.95	0.051	-.0003068	.0991727
_cons	.4037785	.0180559	22.36	0.000	.3683414	.4392157

Source	SS	df	MS		
Model	1.93295099	2	.966475494	Number of obs	= 894
Residual	95.0348978	891	.10666094	F(2, 891)	= 9.06
				Prob > F	= 0.0001
Total	96.9678488	893	.108586617	R-squared	= 0.0199
				Adj R-squared	= 0.0177
				Root MSE	= .32659

genes_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.1052129	.026826	3.92	0.000	.0525634	.1578623
sescond	.0151464	.026826	0.56	0.572	-.037503	.0677959
_cons	.5401027	.0191122	28.26	0.000	.5025925	.577613

Source	SS	df	MS		
Model	.455333848	2	.227666924	Number of obs	= 893
Residual	121.600423	890	.136629689	F(2, 890)	= 1.67
				Prob > F	= 0.1895
Total	122.055757	892	.136833809	R-squared	= 0.0037
				Adj R-squared	= 0.0015
				Root MSE	= .36963

genes_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.031989	.0303865	1.05	0.293	-.0276486	.0916267
sescond	.0552369	.0303616	1.82	0.069	-.0043519	.1148256
_cons	.310411	.0216312	14.35	0.000	.2679568	.3528651

Source	SS	df	MS		
Model	.932601102	2	.466300551	Number of obs	= 894
Residual	151.874462	891	.170453942	F(2, 891)	= 2.74
				Prob > F	= 0.0654
Total	152.807063	893	.171116532	R-squared	= 0.0061
				Adj R-squared	= 0.0039
				Root MSE	= .41286

genes_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0523675	.0339122	1.54	0.123	-.0141897	.1189246
sescond	.0779156	.0339122	2.30	0.022	.0113585	.1444728
_cons	.3608219	.0241608	14.93	0.000	.3134031	.4082407

Source	SS	df	MS	Number of obs	=	893
				F(2, 890)	=	0.02
Model	.002835184	2	.001417592	Prob > F	=	0.9816
Residual	67.9536814	890	.076352451	R-squared	=	0.0000
				Adj R-squared	=	-0.0022
Total	67.9565166	892	.076184436	Root MSE	=	.27632

ses_index	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0020471	.0227166	-0.09	0.928	-.0466314	.0425372
sescond	-.0043727	.0227166	-0.19	0.847	-.0489569	.0402116
_cons	.7342841	.0161981	45.33	0.000	.7024931	.7660751

Source	SS	df	MS	Number of obs	=	894
				F(2, 891)	=	0.09
Model	.016968435	2	.008484217	Prob > F	=	0.9160
Residual	86.0986534	891	.096631485	R-squared	=	0.0002
				Adj R-squared	=	-0.0020
Total	86.1156218	893	.096434067	Root MSE	=	.31086

ses_health	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0105995	.0255336	-0.42	0.678	-.0607125	.0395135
sescond	-.0041211	.0255336	-0.16	0.872	-.0542341	.0459919
_cons	.7389384	.0181915	40.62	0.000	.7032352	.7746415

Source	SS	df	MS	Number of obs	=	894
				F(2, 891)	=	0.00
Model	.000856368	2	.000428184	Prob > F	=	0.9960
Residual	95.1765781	891	.106819953	R-squared	=	0.0000
				Adj R-squared	=	-0.0022
Total	95.1774345	893	.106581674	Root MSE	=	.32683

ses_edu	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	-.0000454	.026846	-0.00	0.999	-.0527341	.0526433
sescond	.0020476	.026846	0.08	0.939	-.0506411	.0547363
_cons	.7081849	.0191265	37.03	0.000	.6706468	.7457231

Source	SS	df	MS	Number of obs	=	893
				F(2, 890)	=	0.19
Model	.036446112	2	.018223056	Prob > F	=	0.8304
Residual	87.2276373	890	.098008581	R-squared	=	0.0004
				Adj R-squared	=	-0.0018
Total	87.2640834	892	.09782969	Root MSE	=	.31306

ses_crime	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
genecond	.0083425	.0257373	0.32	0.746	-.0421704	.0588554
sescond	-.0072056	.0257373	-0.28	0.780	-.0577185	.0433072
_cons	.75189	.0183521	40.97	0.000	.7158716	.7879085

```
174 forval j=1/3 {
    2. est table genes_index_`j' genes_health_`j' genes_edu_`j' genes_crime_`j' ses_inde
  > x_`j' ses_health_`j' ses_edu_`j' ses_crime_`j', b(%9.2f) se stats(N) style(col) eq(1
  > )
    3. est table genes_index_`j' genes_health_`j' genes_edu_`j' genes_crime_`j' ses_inde
  > x_`j' ses_health_`j' ses_edu_`j' ses_crime_`j', b(%9.2f) star(.05 .01 .001) stats(N)
  >  style(col) eq(1)
    4. }
```

Variable	genes_i~1	genes_h~1	genes_e~1	genes_c~1	ses_ind~1	ses_hea~1
ses_edu_1	ses_cri~1					
genecond	0.03	0.02	0.04	0.02	-0.04	-0.03
	-0.03	-0.05				
	0.02	0.02	0.03	0.03	0.02	0.03
	0.03	0.03				
sescond	-0.02	-0.08	0.02	0.01	-0.05	-0.04
	-0.07	-0.05				
	0.02	0.02	0.03	0.03	0.02	0.03
	0.03	0.03				
_cons	0.38	0.58	0.25	0.30	0.52	0.51
	0.52	0.54				
	0.01	0.02	0.02	0.02	0.02	0.02
	0.02	0.02				
N	883	883	883	883	882	882
	883	883				

```
>               Legend: b/se
```

Variable	genes_inde~1	genes_heal~1	genes_edu_1	genes_crim~1	ses_index
_1	ses_health_1	ses_edu_1	ses_crime_1		
genecond	0.03	0.02	0.04	0.02	-0.04
	-0.03	-0.03	-0.05		
sescond	-0.02	-0.08**	0.02	0.01	-0.05
*	-0.04	-0.07**	-0.05*		
_cons	0.38***	0.58***	0.25***	0.30***	0.52
***	0.51***	0.52***	0.54***		
N	883	883	883	883	882
	882	883	883		

```
>               Legend: * p<.05; ** p<.01; *** p<.001
```

Variable	genes_i~2	genes_h~2	genes_e~2	genes_c~2	ses_ind~2	ses_hea~2
ses_edu_2	ses_cri~2					
genecond	0.05	0.08	0.04	0.04	-0.01	-0.01
	-0.01	0.00				
	0.02	0.02	0.02	0.03	0.02	0.03
	0.03	0.02				
sescond	-0.02	-0.05	-0.02	-0.00	0.04	0.06
	0.03	0.04				
	0.02	0.02	0.02	0.03	0.02	0.03
	0.03	0.03				
_cons	0.30	0.49	0.19	0.22	0.75	0.73

	0.76	0.76					
		0.01	0.02	0.02	0.02	0.02	0.02
	0.02	0.02					
N	887	887	888	888	887	888	888
	888	887					

Legend: b/se

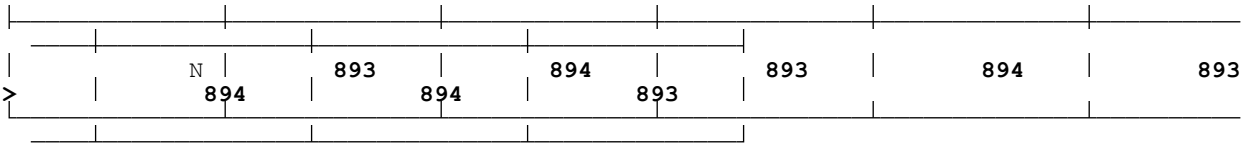
Variable	genes_inde~2	genes_heal~2	genes_edu_2	genes_crim~2	ses_index
_2 ses_health_2	ses_edu_2	ses_crime_2			
genecond	0.05*	0.08**	0.04	0.04	-0.01
	-0.01	-0.01	0.00		
sescond	-0.02	-0.05	-0.02	-0.00	0.04
	0.06*	0.03	0.04		
_cons	0.30***	0.49***	0.19***	0.22***	0.75
***	0.73***	0.76***	0.76***		
N	887	887	888	888	887
	888	888	887		

Legend: * p<.05; ** p<.01; *** p<.001

Variable	genes_i~3	genes_h~3	genes_e~3	genes_c~3	ses_ind~3	ses_hea~3
ses_edu_3	ses_cri~3					
genecond	0.06	0.11	0.03	0.05	-0.00	-0.01
	-0.00	0.01				
		0.03	0.03	0.03	0.03	0.02	0.03
	0.03	0.03				
sescond	0.05	0.02	0.06	0.08	-0.00	-0.00
	0.00	-0.01				
		0.03	0.03	0.03	0.03	0.02	0.03
	0.03	0.03				
_cons	0.40	0.54	0.31	0.36	0.73	0.74
	0.71	0.75				
		0.02	0.02	0.02	0.02	0.02	0.02
	0.02	0.02				
N	893	894	893	894	893	894
	894	893					

Legend: b/se

Variable	genes_inde~3	genes_heal~3	genes_edu_3	genes_crim~3	ses_index
_3 ses_health_3	ses_edu_3	ses_crime_3			
genecond	0.06*	0.11***	0.03	0.05	-0.00
	-0.01	-0.00	0.01		
sescond	0.05	0.02	0.06	0.08*	-0.00
	-0.00	0.00	-0.01		
_cons	0.40***	0.54***	0.31***	0.36***	0.73
***	0.74***	0.71***	0.75***		



> Legend: * p<.05; ** p<.01; *** p<.001

```
175
176 coefplot (genes_index, mcolor(black) mfcolor(white) lcolor(gray)) (genes_index_2, mc
  > olor(blue) lcolor(blue)) (genes_index_3, mcolor(black) lcolor(black)) (genes_index_1
  > , mcolor(red)) , legend(label(2 "All") label(4 "White DEM") label(6 "Black") label(8
  >  "White GOP") row(4) position(3)) xline(0) title("DV: Genes Index") name(genes_index
  > , replace) keep(genecond sescond)

177
178 coefplot (ses_index, mcolor(black) mfcolor(white) lcolor(gray)) (ses_index_2, mcolor
  > (blue) lcolor(blue)) (ses_index_3, mcolor(black) lcolor(black)) (ses_index_1, mcolor
  > (red)) , legend(label(2 "All") label(4 "White DEM") label(6 "Black") label(8 "White
  > GOP") row(4) position(3)) xline(0) title("DV: SES Index") name(ses_index, replace) k
  > eep(genecond sescond)

179
180 graph combine genes_index ses_index, ycommon xcommon ysize(6) xsize(12)

181 graph export Figure5.pdf, replace
  file Figure5.pdf saved as PDF format

182 **********END FIGURE 5**********
183
184 *test for difference in effect size
185 suest genes_index_1 genes_index_2

  Simultaneous results for genes_index_1, genes_index_2

                                                  Number of obs = 1,770
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
genes_index_1_mean						
genecond	.0280362	.021629	1.30	0.195	-.014356	.0704283
sescond	-.0157477	.0208964	-0.75	0.451	-.0567038	.0252084
_cons	.3777118	.0145084	26.03	0.000	.3492758	.4061478
genes_index_1_lnvar						
_cons	-2.688086	.0438059	-61.36	0.000	-2.773944	-2.602229
genes_index_2_mean						
genecond	.0532021	.0208529	2.55	0.011	.0123311	.094073
sescond	-.0214341	.020806	-1.03	0.303	-.0622132	.0193449
_cons	.3004251	.0141447	21.24	0.000	.2727021	.3281481
genes_index_2_lnvar						
_cons	-2.719041	.0479084	-56.76	0.000	-2.81294	-2.625143

```
186 test [genes_index_1_mean]genecond=[genes_index_2_mean]genecond

  ( 1)  [genes_index_1_mean]genecond - [genes_index_2_mean]genecond = 0

           chi2(  1) =    0.70
         Prob > chi2 =    0.4022
```

```
187 suest genes_index_1 genes_index_3
```

Simultaneous results for genes_index_1, genes_index_3

Number of obs = **1,776**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
genes_index_1_mean						
genecond	**.0280362**	**.021629**	**1.30**	**0.195**	**-.0143559**	**.0704283**
sescond	**-.0157477**	**.0208963**	**-0.75**	**0.451**	**-.0567038**	**.0252084**
_cons	**.3777118**	**.0145084**	**26.03**	**0.000**	**.3492758**	**.4061478**
genes_index_1_lnvar						
_cons	**-2.688086**	**.0438058**	**-61.36**	**0.000**	**-2.773944**	**-2.602229**
genes_index_3_mean						
genecond	**.0639992**	**.0243343**	**2.63**	**0.009**	**.0163048**	**.1116936**
sescond	**.049433**	**.025853**	**1.91**	**0.056**	**-.001238**	**.100104**
_cons	**.4037785**	**.017464**	**23.12**	**0.000**	**.3695497**	**.4380074**
genes_index_3_lnvar						
_cons	**-2.351807**	**.0314744**	**-74.72**	**0.000**	**-2.413495**	**-2.290118**

```
188 test [genes_index_1_mean]genecond=[genes_index_3_mean]genecond
```

(1) **[genes_index_1_mean]genecond - [genes_index_3_mean]genecond = 0**

chi2(1) = **1.22**
Prob > chi2 = **0.2693**

```
189
190
191 **********FOOTNOTE & APPENDIX
192 //timing
193 sum treat_timer_First_Click treat_timer_Last_Click treat_timer_Page_Submit
```

Variable	Obs	Mean	Std. dev.	Min	Max
tr~rst_Click	**2,665**	**31.49364**	**73.6226**	**0**	**2208.32**
tr~ast_Click	**2,665**	**46.35247**	**96.65928**	**0**	**2208.32**
treat_time~t	**2,665**	**50.14526**	**97.27279**	**1.195**	**2210.284**

```
194 table expcond samplegroups, stat(mean treat_timer_Page_Submit) nformat(%9.2f)
```

	samplegroups			
	White REP	White DEM	Black	Total
Experimental Condition				
Genetic Frame	**52.72**	**49.60**	**70.81**	**57.87**
Neutral	**36.03**	**27.66**	**53.58**	**38.96**
SES Frame	**52.02**	**46.31**	**62.70**	**53.74**
Total	**46.76**	**41.12**	**62.45**	**50.15**

```
195
```

```
196 //word length of surprise recall
197 gen wordcount = wordcount(comment_lower)

198 table expcond samplegroups, stat(mean wordcount) nformat(%9.2f)
```

	samplegroups			
	White REP	White DEM	Black	Total
Experimental Condition				
Genetic Frame	**15.11**	**17.19**	**14.97**	**15.76**
Neutral	**13.16**	**14.28**	**13.12**	**13.52**
SES Frame	**16.30**	**19.66**	**14.26**	**16.72**
Total	**14.84**	**17.03**	**14.13**	**15.33**

```
199 reg wordcount i.expcond i.samplegroups
```

Source	SS	df	MS		
				Number of obs	= **2,665**
				F(4, 2660)	= **21.25**
Model	**8917.80722**	**4**	**2229.45181**	Prob > F	= **0.0000**
Residual	**279071.95**	**2,660**	**104.914267**	R-squared	= **0.0310**
				Adj R-squared	= **0.0295**
Total	**287989.758**	**2,664**	**108.104263**	Root MSE	= **10.243**

wordcount	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
expcond						
Neutral	**-2.249207**	**.4865942**	**-4.62**	**0.000**	**-3.203348**	**-1.295066**
SES Frame	**.9679589**	**.4868212**	**1.99**	**0.047**	**.0133725**	**1.922545**
samplegroups						
White DEM	**2.173945**	**.486813**	**4.47**	**0.000**	**1.219374**	**3.128515**
Black	**-.7514431**	**.4860379**	**-1.55**	**0.122**	**-1.704494**	**.2016074**
_cons	**15.28882**	**.4484056**	**34.10**	**0.000**	**14.40956**	**16.16808**

```
200 reg wordcount i.expcond i.samplegroups ageyear female ed5cat faminc6 pid3cat
```

Source	SS	df	MS		
				Number of obs	= **2,632**
				F(9, 2622)	= **13.14**
Model	**12105.1378**	**9**	**1345.01531**	Prob > F	= **0.0000**
Residual	**268431.795**	**2,622**	**102.376733**	R-squared	= **0.0431**
				Adj R-squared	= **0.0399**
Total	**280536.933**	**2,631**	**106.627492**	Root MSE	= **10.118**

wordcount	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
expcond						
Neutral	**-2.383657**	**.4834677**	**-4.93**	**0.000**	**-3.331674**	**-1.43564**
SES Frame	**.8326202**	**.4842147**	**1.72**	**0.086**	**-.1168614**	**1.782102**
samplegroups						
White DEM	**1.027103**	**1.216668**	**0.84**	**0.399**	**-1.358623**	**3.412829**
Black	**-1.483488**	**1.060512**	**-1.40**	**0.162**	**-3.563014**	**.596038**
ageyears	**-.0351586**	**.0132076**	**-2.66**	**0.008**	**-.0610569**	**-.0092603**
female	**1.182426**	**.4000735**	**2.96**	**0.003**	**.3979342**	**1.966918**
ed5cat	**3.349871**	**.6670955**	**5.02**	**0.000**	**2.041784**	**4.657958**
faminc6	**-.9830517**	**.6303781**	**-1.56**	**0.119**	**-2.219141**	**.2530373**
pid3cat	**.5070013**	**1.11202**	**0.46**	**0.648**	**-1.673524**	**2.687526**
_cons	**15.71126**	**.8898381**	**17.66**	**0.000**	**13.9664**	**17.45612**

```
201
202
203 **********UNPACKING SES CONDITION**********
204 *****Footnote 25*****
205 //in each condition, top words
206 //what words are uniquely predictive of one condition versus the others
207 preserve

208 keep comment_lower expcond

209 save openends.dta, replace
  (file openends.dta not found)
  file openends.dta saved

210 restore

211
212 * txttool is the command, commenttext is the variable to be used, gen(cleaned) creat
  > es a new variable with all lower case text
213 * bagwords breaks out every word into its own variable
214
215 use openends.dta, clear

216 preserve

217 keep if expcond ==1
  (1,786 observations deleted)

218 save openends_Genetic.dta, replace
  (file openends_Genetic.dta not found)
  file openends_Genetic.dta saved

219 restore

220 preserve

221 keep if expcond ==2
  (1,771 observations deleted)

222 save openends_Neutral.dta, replace
  (file openends_Neutral.dta not found)
  file openends_Neutral.dta saved

223 restore

224 preserve

225 keep if expcond ==3
  (1,773 observations deleted)

226 save openends_SES.dta, replace
  (file openends_SES.dta not found)
  file openends_SES.dta saved

227 restore

228
229 foreach v in Genetic Neutral SES {
    2. use openends_`v'.dta, clear
    3. txttool comment_lower, gen(cleaned_open) bagwords stem stopwords(stopword.txt)
    4. save "cleaned_open_`v'", replace
    5. }
  No prefix chosen for bagged words; default prefix w_ used
  Note that errors will result if new prefix/word combinations match any existing variab
  > les
  Input:   1194 unique words, 13852 total words
  Output:  793 unique words, 6891 total words
  Total time: 1.805 seconds
  (file cleaned_open_Genetic.dta not found)
  file cleaned_open_Genetic.dta saved
  No prefix chosen for bagged words; default prefix w_ used
  Note that errors will result if new prefix/word combinations match any existing variab
```

```
  > les
  Input:   893 unique words, 12088 total words
  Output:  563 unique words, 6172 total words
  Total time: 1.361 seconds
  (file cleaned_open_Neutral.dta not found)
  file cleaned_open_Neutral.dta saved
  No prefix chosen for bagged words; default prefix w_ used
  Note that errors will result if new prefix/word combinations match any existing variab
  > les
  Input:   1259 unique words, 14890 total words
  Output:  811 unique words, 7610 total words
  Total time: 2.303 seconds
  (file cleaned_open_SES.dta not found)
  file cleaned_open_SES.dta saved

230
231 //looking at the new dataset of bag of words
232 foreach v in Genetic Neutral SES {
    2. use cleaned_open_`v', clear
    3. foreach j of varlist w_* {
    4. egen mean`j' = mean(`j')
    5. }
    6. keep mean*
    7.
233 save "means_open_`v'", replace
    8. }
  (file means_open_Genetic.dta not found)
  file means_open_Genetic.dta saved
  (file means_open_Neutral.dta not found)
  file means_open_Neutral.dta saved
  (file means_open_SES.dta not found)
  file means_open_SES.dta saved

234
235 use  "means_open_Genetic", clear

236 drop if _n>1
  (878 observations deleted)

237 order _all, sequential

238 drop meanw_2-meanw_1968

239 rename meanw_long renamew_llong

240 rename meanw_* *

241 xpose, clear varname format(%6.2f)

242 sum v1, det

                            v1
-------------------------------------------------------------
      Percentiles      Smallest
 1%     .0011429       .0011429
 5%     .0011429       .0011429
10%     .0011429       .0011429       Obs                 788
25%     .0011429       .0011429       Sum of wgt.         788

50%     .0011429                      Mean           .0099666
                        Largest       Std. dev.      .0539364
75%     .0034286       .5714286
90%     .0137143       .5942857       Variance       .0029091
95%     .0228571              .6      Skewness       11.17718
99%     .2045714       .8651429       Kurtosis       142.0885
```

```
243 egen top50=pctile(v1), p(50)

244 egen top25=pctile(v1), p(75)

245 keep if v1>top25
  (616 observations deleted)

246 sum
```

Variable	Obs	Mean	Std. dev.	Min	Max
v1	172	.0402924	.1104706	.0045714	.8651429
_varname	0				
top50	172	.0011429	0	.0011429	.0011429
top25	172	.0034286	0	.0034286	.0034286

```
247 sum v1, det
```

v1

Percentiles	Smallest		
1% .0045714	.0045714		
5% .0045714	.0045714		
10% .0045714	.0045714	Obs	172
25% .0068571	.0045714	Sum of wgt.	172
50% .0125714		Mean	.0402924
	Largest	Std. dev.	.1104706
75% .0205714	.5714286		
90% .0502857	.5942857	Variance	.0122038
95% .184	.6	Skewness	5.155612
99% .6	.8651429	Kurtosis	31.19177

```
248 graph hbar v1 if v1>.02, over(_varname, sort(1) label(labsize(vsmall))) title("Top W
  > ords" "Genetic Condition") ytitle(" ") name(Genetic, replace)

249
250 use  "means_open_Neutral", clear

251 drop if _n>1
  (893 observations deleted)

252 order _all, sequential

253 drop meanw_99-meanw_400

254 rename meanw_* *

255 xpose, clear varname format(%6.2f)

256 sum v1, det
```

v1

Percentiles	Smallest		
1% .0011223	.0011223		
5% .0011223	.0011223		
10% .0011223	.0011223	Obs	561
25% .0011223	.0011223	Sum of wgt.	561
50% .0011223		Mean	.0123177
	Largest	Std. dev.	.066568
75% .003367	.6083053		
90% .0123457	.6251403	Variance	.0044313
95% .026936	.7598204	Skewness	9.661116
99% .3580247	.8619528	Kurtosis	103.91

```
257 egen top50=pctile(v1), p(50)

258 egen top25=pctile(v1), p(75)

259 keep if v1>top25
  (422 observations deleted)

260 sum
```

Variable	Obs	Mean	Std. dev.	Min	Max
v1	139	.0450306	.1286372	.0044893	.8619528
_varname	0				
top50	139	.0011223	0	.0011223	.0011223
top25	139	.003367	0	.003367	.003367

```
261 sum v1, det
```

v1

Percentiles	Smallest		
1% .0044893	.0044893		
5% .0044893	.0044893		
10% .0044893	.0044893	Obs	139
25% .0056117	.0044893	Sum of wgt.	139
50% .0089787		Mean	.0450306
	Largest	Std. dev.	.1286372
75% .0224467	.6083053		
90% .0650954	.6251403	Variance	.0165475
95% .2289562	.7598204	Skewness	4.667233
99% .7598204	.8619528	Kurtosis	25.24346

```
262 graph hbar v1 if v1>.02, over(_varname, sort(1) label(labsize(vsmall))) title("Top W
  > ords" "Neutral Condition") ytitle(" ") name(Neutral, replace)

263
264 use  "means_open_SES", clear

265 drop if _n>1
  (891 observations deleted)

266 order _all, sequential

267 drop meanw_9-meanw_99

268 rename meanw_long renamew_llong

269 rename meanw_* *

270 xpose, clear varname format(%6.2f)

271 sum v1, det
```

v1

Percentiles	Smallest		
1% .0011274	.0011274		
5% .0011274	.0011274		
10% .0011274	.0011274	Obs	809
25% .0011274	.0011274	Sum of wgt.	809
50% .0011274		Mean	.0105814
	Largest	Std. dev.	.0543389
75% .0045096	.5772266		
90% .0135287	.6020293	Variance	.0029527
95% .0259301	.6110485	Skewness	11.34533
99% .1668546	.9188275	Kurtosis	151.9435

```
272 egen top50=pctile(v1), p(50)

273 egen top25=pctile(v1), p(75)

274 keep if v1>top25
  (638 observations deleted)

275 sum
```

Variable	Obs	Mean	Std. dev.	Min	Max
v1	**171**	**.0438168**	**.1123462**	**.005637**	**.9188275**
_varname	**0**				
top50	**171**	**.0011274**	**0**	**.0011274**	**.0011274**
top25	**171**	**.0045096**	**0**	**.0045096**	**.0045096**

```
276 sum v1, det
```

v1

Percentiles		Smallest		
1%	**.005637**	**.005637**		
5%	**.005637**	**.005637**		
10%	**.005637**	**.005637**	Obs	**171**
25%	**.0078918**	**.005637**	Sum of wgt.	**171**
50%	**.0124014**		Mean	**.0438168**
		Largest	Std. dev.	**.1123462**
75%	**.0248027**	**.5772266**		
90%	**.0777903**	**.6020293**	Variance	**.0126217**
95%	**.1668546**	**.6110485**	Skewness	**5.201364**
99%	**.6110485**	**.9188275**	Kurtosis	**32.99769**

```
277 graph hbar v1 if v1>.02, over(_varname, sort(1) label(labsize(vsmall))) title("Top W
  > ords" "SES Condition") ytitle(" ") name(SES, replace)

278
279 graph combine Genetic Neutral SES, ycommon col(3) imargin(tiny)

280
281 //next, identify distinctive words
282 //pr(mention a given word|condition)
283 //what are the words where "condition" is most significant?
284 //DV: prevalence of the word
285 //IV: condition (dataset)
286 //stack dataset so that each line represents a different condition
287
288 use  "means_open_Genetic", clear

289 drop if _n>1
  (878 observations deleted)

290 order _all, sequential

291 drop meanw_2-meanw_1968

292 rename meanw_long renamew_llong

293 rename meanw_* *
```

```
294 xpose, clear varname format(%6.2f)

295 keep if v1>.02
  (744 observations deleted)

296 rename v1 Genetic

297 rename _varname word

298 save "top_words_Genetic", replace
  (file top_words_Genetic.dta not found)
  file top_words_Genetic.dta saved

299
300 use  "means_open_Neutral", clear

301 drop if _n>1
  (893 observations deleted)

302 order _all, sequential

303 drop meanw_99-meanw_400

304 rename meanw_* *

305 xpose, clear varname format(%6.2f)

306 keep if v1>.02
  (519 observations deleted)

307 rename v1 Neutral

308 rename _varname word

309 save "top_words_Neutral", replace
  (file top_words_Neutral.dta not found)
  file top_words_Neutral.dta saved

310
311 use  "means_open_SES", clear

312 drop if _n>1
  (891 observations deleted)

313 order _all, sequential

314 drop meanw_9-meanw_99

315 rename meanw_long renamew_llong

316 rename meanw_* *

317 xpose, clear varname format(%6.2f)

318 keep if v1>.02
  (750 observations deleted)

319 rename v1 SES

320 rename _varname word
```

```
321 save "top_words_SES", replace
  (file top_words_SES.dta not found)
  file top_words_SES.dta saved

322
323 use top_words_Genetic, clear

324 merge 1:1 word using top_words_Neutral
```

Result	Number of obs	
Not matched	**28**	
from master	**15**	(_merge==1)
from using	**13**	(_merge==2)
Matched	**29**	(_merge==3)

```
325 merge 1:1 word using top_words_SES, gen(_merge2)
```

Result	Number of obs	
Not matched	**38**	
from master	**18**	(_merge2==1)
from using	**20**	(_merge2==2)
Matched	**39**	(_merge2==3)

```
326
327 gen Gen_Only = .
  (77 missing values generated)

328 replace Gen_Only =1 if Genetic>0 & Genetic<1 & Neutral==.& SES==.
  (7 real changes made)

329 gen Neutral_Only =.
  (77 missing values generated)

330 replace Neutral_Only =1 if Neutral>0 & Neutral<1 & Genetic==. & SES==.
  (9 real changes made)

331 gen SES_Only =.
  (77 missing values generated)

332 replace SES_Only =1 if SES>0 & SES<1 & Genetic==. & Neutral==.
  (20 real changes made)

333 egen numberconditions = rownonmiss(Genetic Neutral SES)

334
335 //words that are unique to each condition
336 tab word if Gen_Only==1
```

word	Freq.	Percent	Cum.
base	**1**	**14.29**	**14.29**
common	**1**	**14.29**	**28.57**
counsel	**1**	**14.29**	**42.86**
famili	**1**	**14.29**	**57.14**
gene	**1**	**14.29**	**71.43**
preval	**1**	**14.29**	**85.71**
test	**1**	**14.29**	**100.00**
Total	**7**	**100.00**	

```
337 tab word if Neutral_Only==1
```

word	Freq.	Percent	Cum.
debat	1	11.11	11.11
expert	1	11.11	22.22
know	1	11.11	33.33
profession	1	11.11	44.44
puzzl	1	11.11	55.56
racial	1	11.11	66.67
read	1	11.11	77.78
scientist	1	11.11	88.89
sure	1	11.11	100.00
Total	9	100.00	

```
338 tab word if SES_Only==1
```

word	Freq.	Percent	Cum.
account	1	5.00	5.00
come	1	5.00	10.00
condit	1	5.00	15.00
disadvantag	1	5.00	20.00
econom	1	5.00	25.00
experi	1	5.00	30.00
face	1	5.00	35.00
ill	1	5.00	40.00
individu	1	5.00	45.00
patient	1	5.00	50.00
person	1	5.00	55.00
relat	1	5.00	60.00
situat	1	5.00	65.00
social	1	5.00	70.00
socioeconom	1	5.00	75.00
statu	1	5.00	80.00
tend	1	5.00	85.00
think	1	5.00	90.00
treat	1	5.00	95.00
trigger	1	5.00	100.00
Total	20	100.00	

```
339
340 *****cleaning up directory*****
341 foreach v in SES Genetic Neutral {
    2.         erase openends_`v'.dta
    3.         erase cleaned_open_`v'.dta
    4.         erase means_open_`v'.dta
    5.         erase top_words_`v'.dta
    6. }

342 erase openends.dta

343
344 log close
       name:  <unnamed>
        log:  C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli
> cation files\Anoll Kam Marcellin Bovitz Analyses.smcl
   log type:  smcl
  closed on:  10 Jan 2025, 13:40:08
```