

Ch8 - Ex2: Depression as Function of Genes and Amount of Stress

CORR depress genes stress /STAT.

	Mean	Std. Deviation	N
depress	50.48	11.310	48
genes	.50	.505	48
stress	20.19	5.009	48

	depress	genes
genes	.076	
	.606	
stress	.571	-.256
	.000	.079

TTEST /VARI = depress /GROUP = genes(0,1) .

	genes	N	Mean	Std. Deviation	Std. Error Mean
depress	0	24	49.63	9.568	1.953
	1	24	51.33	12.974	2.648

	t	df	Sig. (2-tailed)	Mean Difference	Std. Error Difference
depress	-.519	46	.606	-1.708	3.291

GLM depress BY genes /PRINT = DESCR.

Dependent Variable: depress

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
genes	35.021	1	35.021	.270	.606
Error	5976.958	46	129.934		
Corrected Total	6011.979	47			

REGRESS /DEP = depress /ENTER genes /SAVE PRED(prdd.g) RESI(resd.g) .

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	35.021	1	35.021	.270	.606
	Residual	5976.958	46	129.934		
	Total	6011.979	47			

Model		Unstandardized Coefficients			Sig.
		B	Std. Error	t	
1	(Constant)	49.625	2.327	21.328	.000
	genes	1.708	3.291	.519	.606

TTEST /VARI = stress /GROUPS = genes(0,1) .

genes		N	Mean	Std. Deviation	Std. Error Mean
stress	0	24	21.46	4.746	.969
	1	24	18.92	5.038	1.028

t-test for Equality of Means					
	t	df	Sig. (2-tailed)	Mean Difference	Std. Error Difference
stress	1.799	46	.079	2.542	1.413

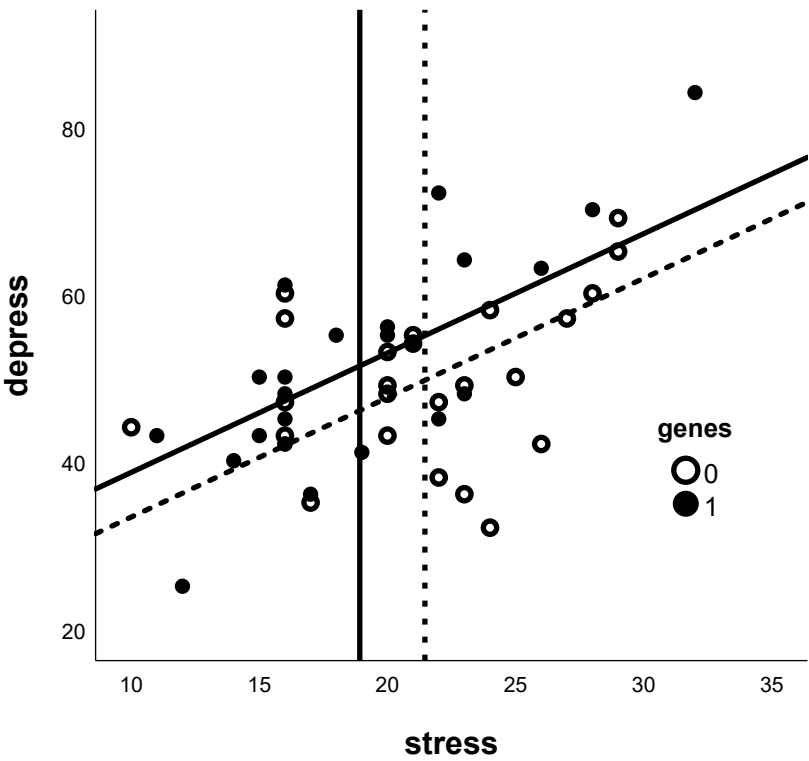
REGRESS /DEP = depress /ENTER genes /ENTER stress /SAVE PRED(prdd.gn) .

Model	R	R Square
1	.076	.006
2	.616	.379

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	35.021	1	35.021	.270	.606
	Residual	5976.958	46	129.934		
	Total	6011.979	47			
2	Regression	2280.158	2	1140.079	13.748	.000
	Residual	3731.821	45	82.929		
	Total	6011.979	47			

Model	Unstandardized Coefficients		t	Sig.	
	B	Std. Error			
1	(Constant)	49.625	2.327	21.328	.000
	genes	1.708	3.291	.519	.606
2	(Constant)	18.994	6.174	3.077	.004
	genes	5.337	2.720	1.962	.056
	stress	1.427	.274	5.203	.000

GRAPH /SCATTERPLOT(BIVAR)=stress WITH depress BY genes.



COMPUTE gxs = genes*stress.

REGRESS /DEP = depress /ENTER genes stress /ENTER gxs /SAVE PRED(prdd.gnx).

Model	R	R Square
1	.616	.379
2	.679	.461

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	2280.158	2	1140.079	13.748	.000
	Residual	3731.821	45	82.929		
	Total	6011.979	47			
2	Regression	2774.251	3	924.750	12.567	.000
	Residual	3237.728	44	73.585		
	Total	6011.979	47			

Model		Unstandardized Coefficients			Sig.
		B	Std. Error	t	
2	(Constant)	34.250	8.275	4.139	.000
	genes	-21.851	10.800	-2.023	.049
	stress	.717	.377	1.901	.064
	gxs	1.342	.518	2.591	.013

SPLIT FILE BY genes.

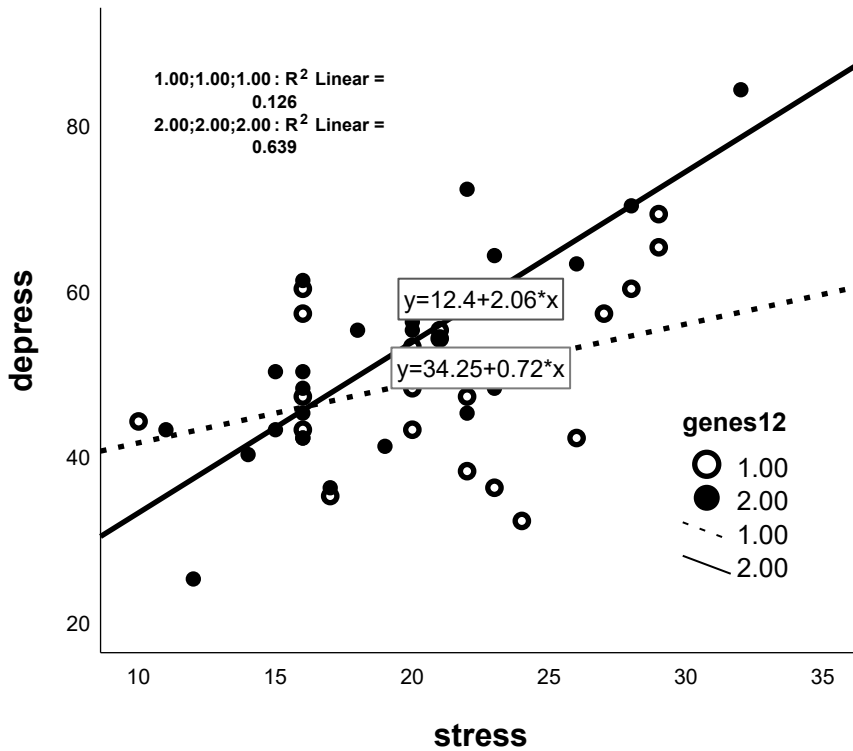
REGRESS /DEP = depress /ENTER stress.

genes	Model	R	R Square
0	1	.355	.126
1	1	.799	.639

genes	Model		Sum of Squares	df	Mean Square	F	Sig.
0	1	Regression	265.917	1	265.917	3.180	.088
		Residual	1839.708	22	83.623		
		Total	2105.625	23			
1	1	Regression	2473.313	1	2473.313	38.921	.000
		Residual	1398.020	22	63.546		
		Total	3871.333	23			

genes	Model	Unstandardized Coefficients				
		B	Std. Error	t	Sig.	
0	1	(Constant)	34.250	8.822	3.882	.001
		stress	.717	.402	1.783	.088
1	1	(Constant)	12.398	6.450	1.922	.068
		stress	2.058	.330	6.239	.000

```
RECODE genes (0=1) (1=2) INTO genes12.
GRAPH /SCATTERPLOT(BIVAR)=stress WITH depress BY genes12.
```

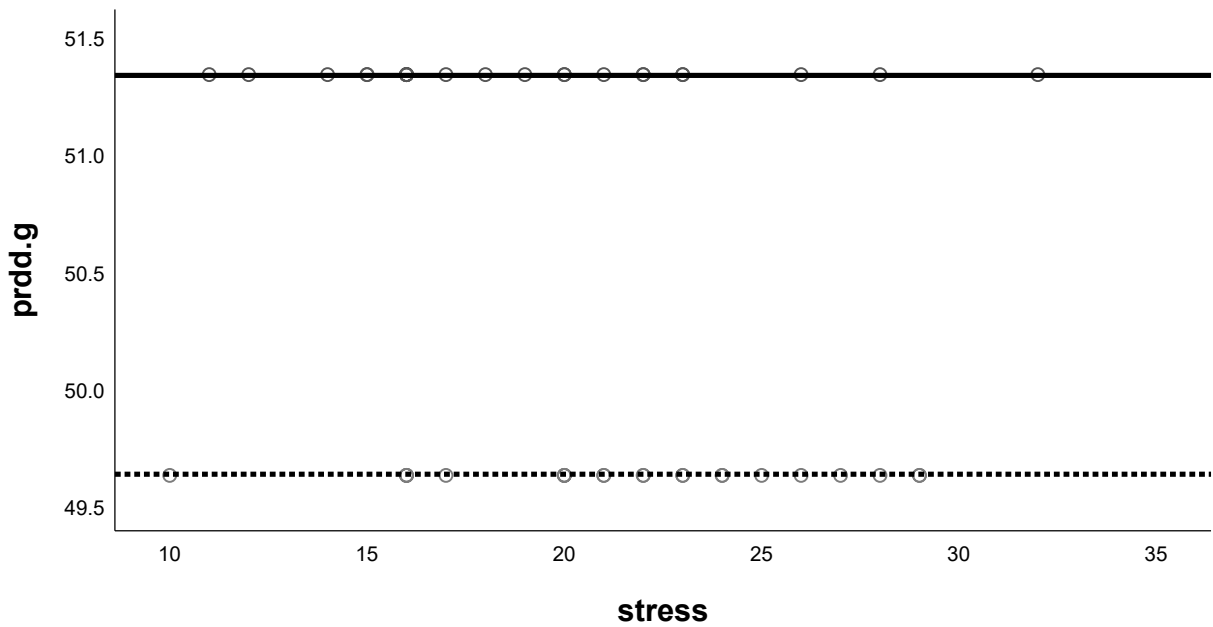


```
list.
o genes stress depress prdd.g resd.g prdd.gn gxs prdd.gnx
1 0 20 43 49.625 -6.625 47.543 .00 48.580
2 0 29 65 49.625 15.375 60.391 .00 55.029
3 0 23 49 49.625 -.625 51.826 .00 50.730
...
25 1 16 50 51.333 -1.333 47.170 16.00 45.330
26 1 32 84 51.333 32.667 70.010 32.00 78.262
27 1 22 72 51.333 20.667 55.735 22.00 57.680
...
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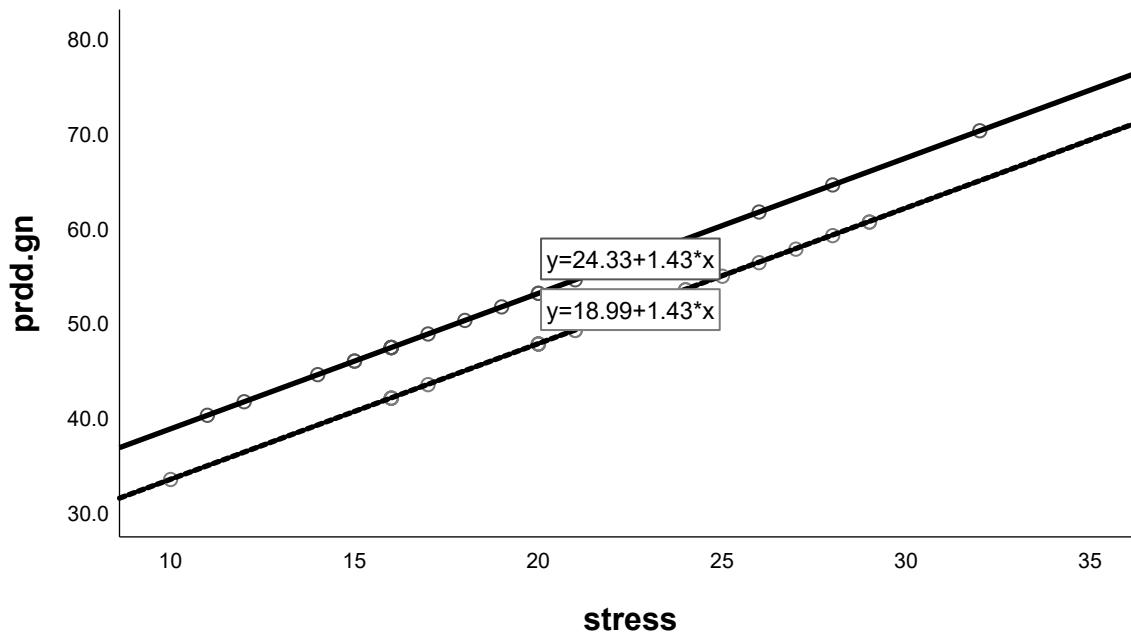
CORR depress genes stress gxs.

	depress	genes	stress
genes	.076		
	.606		
stress	.571	-.256	
	.000	.079	
gxs	.294	.938	.003
	.043	.000	.985

```
RECODE genes (0=1) (1=2) INTO genes12.  
VARI LABEL prdd.g ' ' prdd.gn ' ' prdd.gnx ' '.  
GRAPH /SCATTERPLOT(BIVAR)=stress WITH prdd.g BY genes12.
```



GRAPH /SCATTERPLOT(BIVAR)=stress WITH prdd.gn BY genes12.



GRAPH /SCATTERPLOT(BIVAR)=stress WITH prdd.gnx BY genes12.

