Multiple Linear Regression

Example: Blood Viscosity and Packed Cell Volume

The following blood viscosity data studied earlier are a good example of where multiple regression could be used. Recall that the data blood viscosity in samples taken from 32 hospital patients. We wish to model viscosity (y) as a function three covariates

- Packed Cell Volume (PCV), x_1.
- Plasma Fibrinogen, x_2.
- Plasma Protein, x_3.

Unit	Viscosity y	PCV x_1	Plasma Fib. x_2	Plasma Pro. x_3
1	3.71	40.00	344	6.27
2	3.78	40.00	330	4.86
3	3.85	42.50	280	5.09
4	3.88	42.00	418	6.79
5	3.98	45.00	774	6.40
6	4.03	42.00	388	5.48
7	4.05	42.50	336	6.27
8	4.14	47.00	431	6.89
9	4.14	46.75	276	5.18
10	4.20	48.00	422	5.73
11	4.20	46.00	280	5.89
12	4.27	47.00	460	6.58
13	4.27	43.25	412	5.67
14	4.37	45.00	320	6.23
15	4.41	50.00	502	4.99
16	4.64	45.00	550	6.37
17	4.68	51.25	414	6.40
18	4.73	50.25	304	6.00
19	4.87	49.00	472	5.94
20	4.94	50.00	728	5.16
21	4.95	50.00	716	6.29
22	4.96	49.00	400	5.96
23	5.02	50.50	576	5.90
24	5.02	51.25	354	5.81
25	5.12	49.50	392	5.49
26	5.15	56.00	352	5.41
27	5.17	50.00	572	6.24
28	5.18	47.00	634	6.50
29	5.38	53.25	458	6.60
30	5.77	57.00	1070	4.82
31	5.90	54.00	488	5.70
32	5.90	54.00	488	5.70

We consider four analyses:

$$\begin{aligned}
\textbf{Multiple regression:} \quad y &= \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \epsilon \\
\textbf{Regression on } \boldsymbol{x_1}\textbf{:} \quad y &= \beta_0 + \beta_1 x_1 + \epsilon \\
\textbf{Regression on } \boldsymbol{x_2}\textbf{:} \quad y &= \beta_0 + \beta_2 x_2 + \epsilon \\
\textbf{Regression on } \boldsymbol{x_3}\textbf{:} \quad y &= \beta_0 + \beta_3 x_3 + \epsilon
\end{aligned}$$

Multiple Regression

Model Summary[b]

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	.885[a]	.784	.761	.30370

a. Predictors: (Constant), Plasma Protein (g/100ml), Plasma Fibrinogen (mg/100ml), Packed Cell Volume (%)

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	9.368	3	3.123	33.856	.000[a]
	Residual	2.582	28	.092		
	Total	11.950	31			

a. Predictors: (Constant), Plasma Protein (g/100ml), Plasma Fibrinogen (mg/100ml), Packed Cell Volume (%)

b. Dependent Variable: Blood Viscosity (cP)

Multiple Regression: Parameter Estimates

Tests are of the hypotheses
H0 : beta equal to 0
Ha : beta not equal to zero

Coefficients[a]

Model		Unstandardized Coefficients B	Unstandardized Coefficients Std. Error	Standardized Coefficients Beta	t	Sig.	95% Confidence Interval for B Lower Bound	95% Confidence Interval for B Upper Bound
1	(Constant)	-1.378	.897		-1.537	.136	-3.215	.458
	Packed Cell Volume (%)	.117	.014	.839	8.584	.000	.089	.145
	Plasma Fibrinogen (mg/100ml)	.000	.000	.111	1.147	.261	.000	.001
	Plasma Protein (g/100ml)	.040	.097	.037	.412	.683	-.159	.239

a. Dependent Variable: Blood Viscosity (cP)

Only the packed cell volume coefficient is significantly different from zero (p < 0.001)

The other covariates do not seem to be significantly different from zero.

Regression on Packed Cell Volume only

Model Summary

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	.879[a]	.772	.765	.30116

a. Predictors: (Constant), Packed Cell Volume (%)

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	9.230	1	9.230	101.764	.000[a]
	Residual	2.721	30	.091		
	Total	11.950	31			

a. Predictors: (Constant), Packed Cell Volume (%)

b. Dependent Variable: Blood Viscosity (cP)

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	95% Confidence Interval for B	
		B	Std. Error	Beta			Lower Bound	Upper Bound
1	(Constant)	-1.223	.584		-2.094	.045	-2.416	-.030
	Packed Cell Volume (%)	.122	.012	.879	10.088	.000	.098	.147

a. Dependent Variable: Blood Viscosity (cP)

PCV is a significant term in the model ($p < 0.001$)

Regression on Plasma Protein only

Model Summary

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	.457[a]	.209	.183	.56129

a. Predictors: (Constant), Plasma Fibrinogen (mg/100ml)

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	2.499	1	2.499	7.932	.009[a]
	Residual	9.451	30	.315		
	Total	11.950	31			

a. Predictors: (Constant), Plasma Fibrinogen (mg/100ml)

b. Dependent Variable: Blood Viscosity (cP)

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	95% Confidence Interval for B	
		B	Std. Error	Beta			Lower Bound	Upper Bound
1	(Constant)	3.871	.292		13.236	.000	3.274	4.468
	Plasma Fibrinogen (mg/100ml)	.002	.001	.457	2.816	.009	.000	.003

a. Dependent Variable: Blood Viscosity (cP)

Plasfib is a significant term in the model (p = 0.009)

Regression on Plasma Fibrinogen only

Model Summary

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	.101[a]	.010	-.023	.62791

a. Predictors: (Constant), Plasma Protein (g/100ml)

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	.122	1	.122	.310	.582[a]
	Residual	11.828	30	.394		
	Total	11.950	31			

a. Predictors: (Constant), Plasma Protein (g/100ml)

b. Dependent Variable: Blood Viscosity (cP)

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	95% Confidence Interval for B	
		B	Std. Error	Beta			Lower Bound	Upper Bound
1	(Constant)	5.296	1.174		4.510	.000	2.898	7.694
	Plasma Protein (g/100ml)	-.110	.198	-.101	-.556	.582	-.515	.295

a. Dependent Variable: Blood Viscosity (cP)

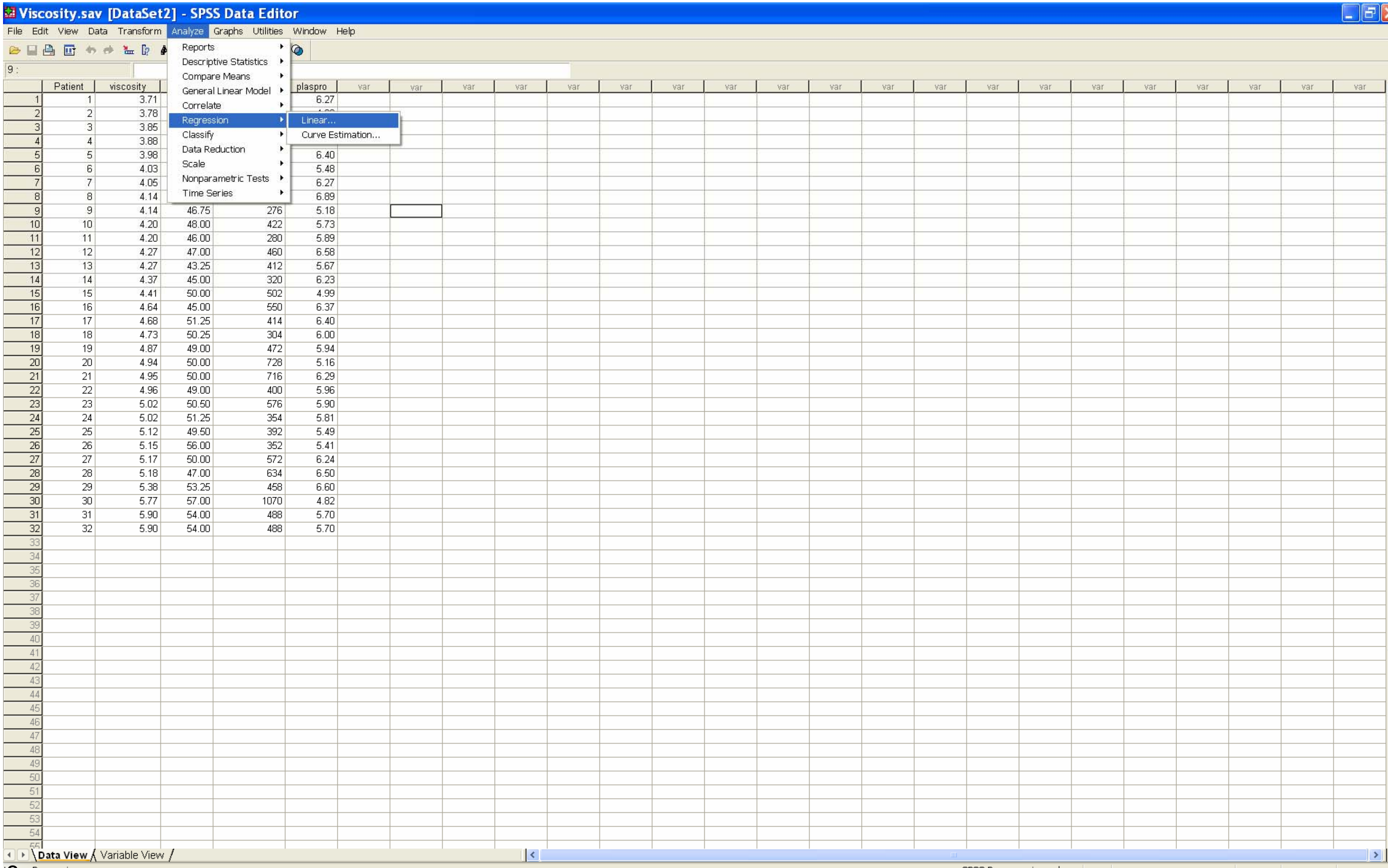
Plaspro is not a significant term in the model (p =0.582)

Blood Viscosity Data Set

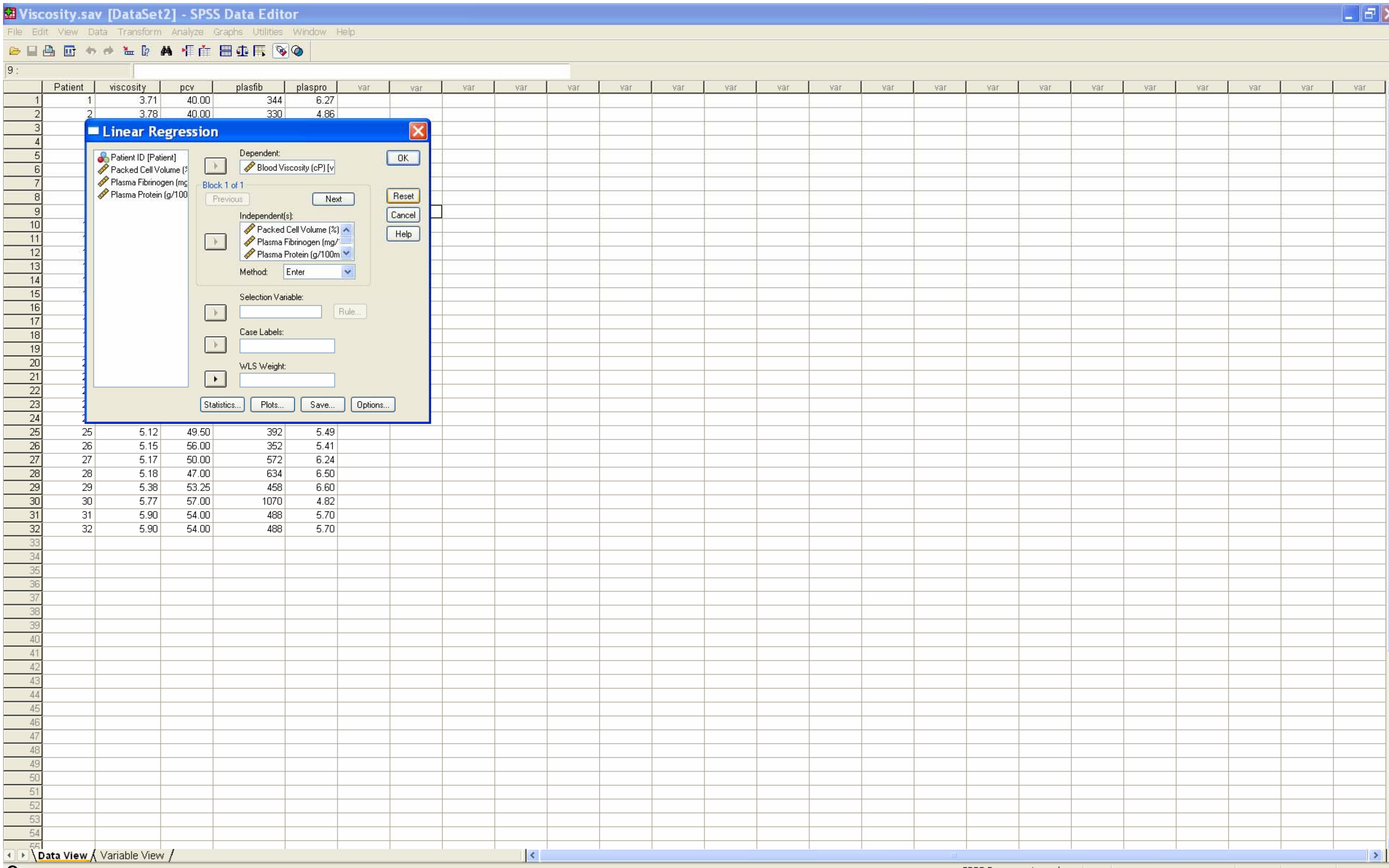
Viscosity.sav [DataSet2] - SPSS Data Editor

	Patient	viscosity	pcv	plasfib	plaspro
1	1	3.71	40.00	344	6.27
2	2	3.78	40.00	330	4.86
3	3	3.85	42.50	280	5.09
4	4	3.88	42.00	418	6.79
5	5	3.98	45.00	774	6.40
6	6	4.03	42.00	388	5.48
7	7	4.05	42.50	336	6.27
8	8	4.14	47.00	431	6.89
9	9	4.14	46.75	276	5.18
10	10	4.20	48.00	422	5.73
11	11	4.20	46.00	280	5.89
12	12	4.27	47.00	460	6.58
13	13	4.27	43.25	412	5.67
14	14	4.37	45.00	320	6.23
15	15	4.41	50.00	502	4.99
16	16	4.64	45.00	550	6.37
17	17	4.68	51.25	414	6.40
18	18	4.73	50.25	304	6.00
19	19	4.87	49.00	472	5.94
20	20	4.94	50.00	728	5.16
21	21	4.95	50.00	716	6.29
22	22	4.96	49.00	400	5.96
23	23	5.02	50.50	576	5.90
24	24	5.02	51.25	354	5.81
25	25	5.12	49.50	392	5.49
26	26	5.15	56.00	352	5.41
27	27	5.17	50.00	572	6.24
28	28	5.18	47.00	634	6.50
29	29	5.38	53.25	458	6.60
30	30	5.77	57.00	1070	4.82
31	31	5.90	54.00	488	5.70
32	32	5.90	54.00	488	5.70

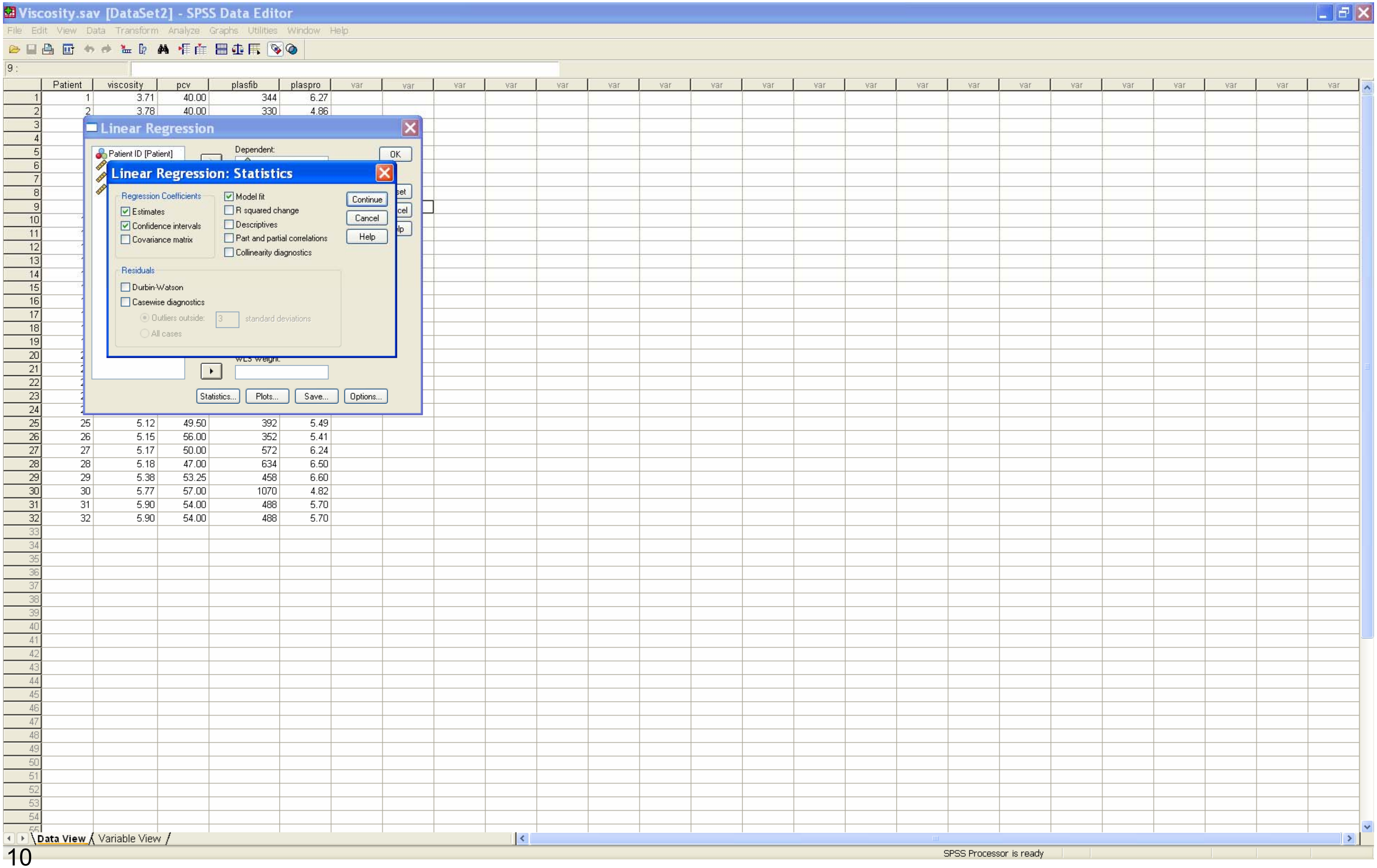
Use the *Analyze*, *Regression*, *Linear* pulldown selections



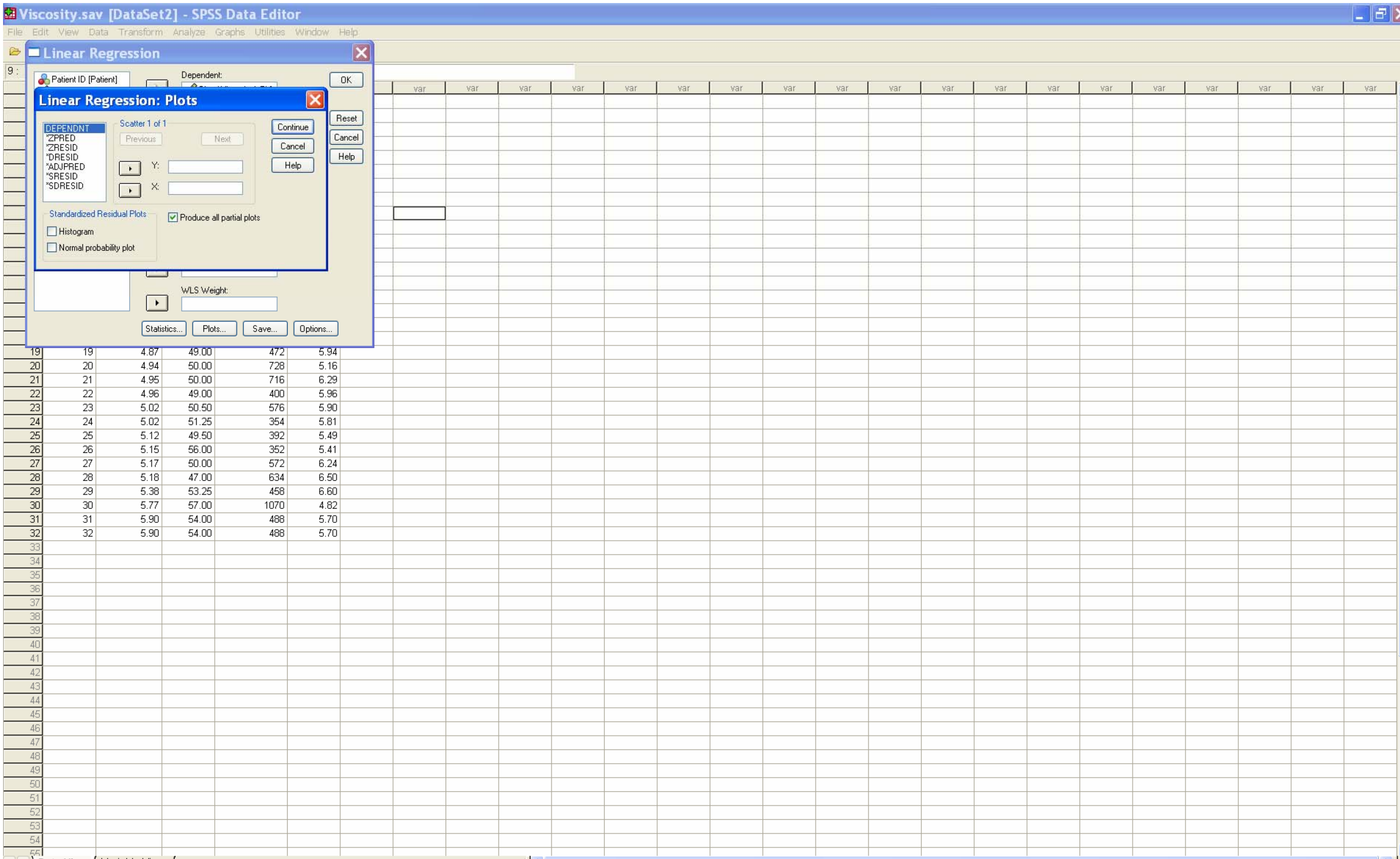
Select the Dependent variable (**viscosity**) and the three independent variables (**pcv**, **plasfib** and **plaspro**)



Click the *Statistics* button: on the *Statistics* dialog, select *Estimates*, *Confidence Intervals* and *Model fit.* Click *Continue*.

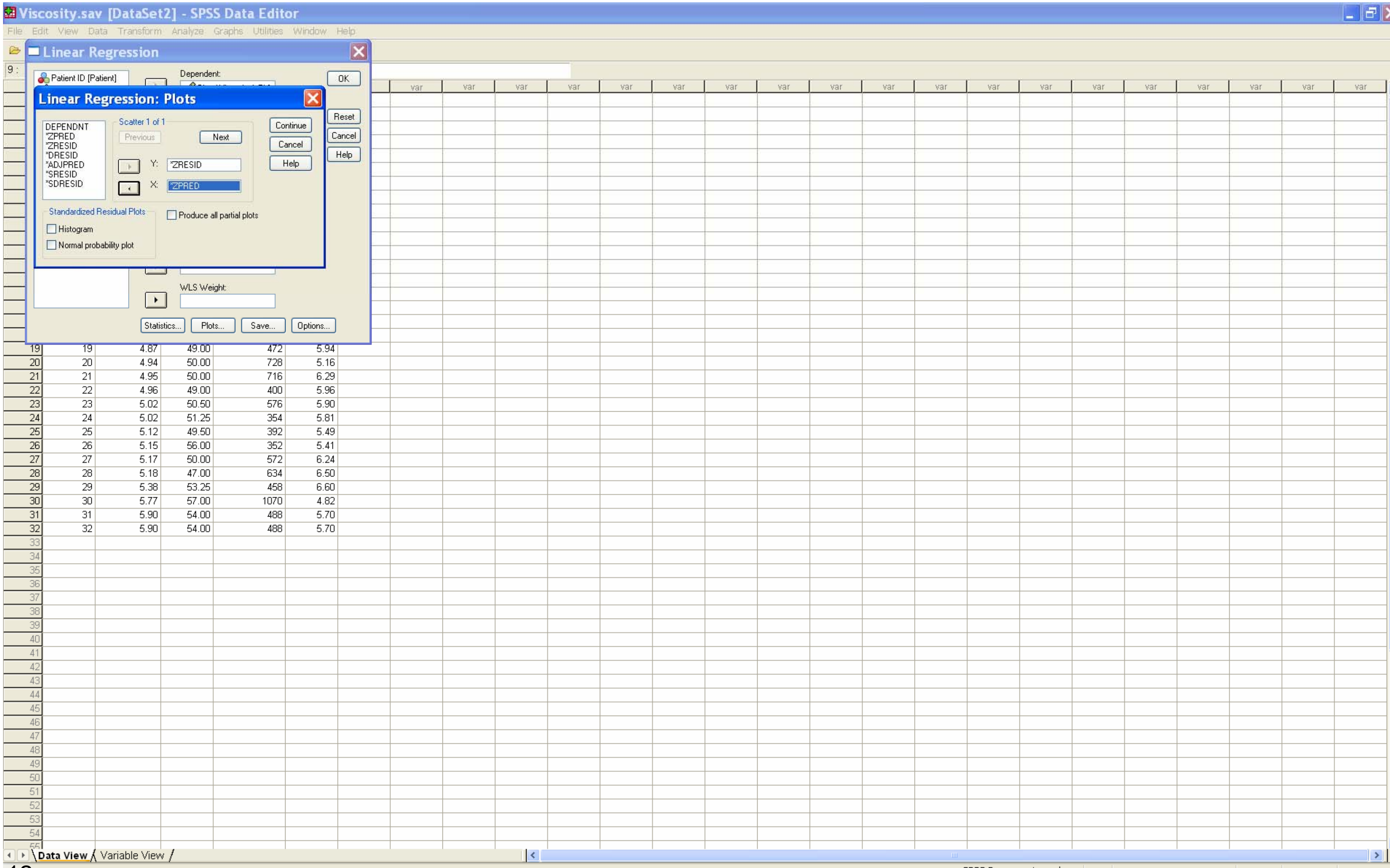


Click the *Plots* button



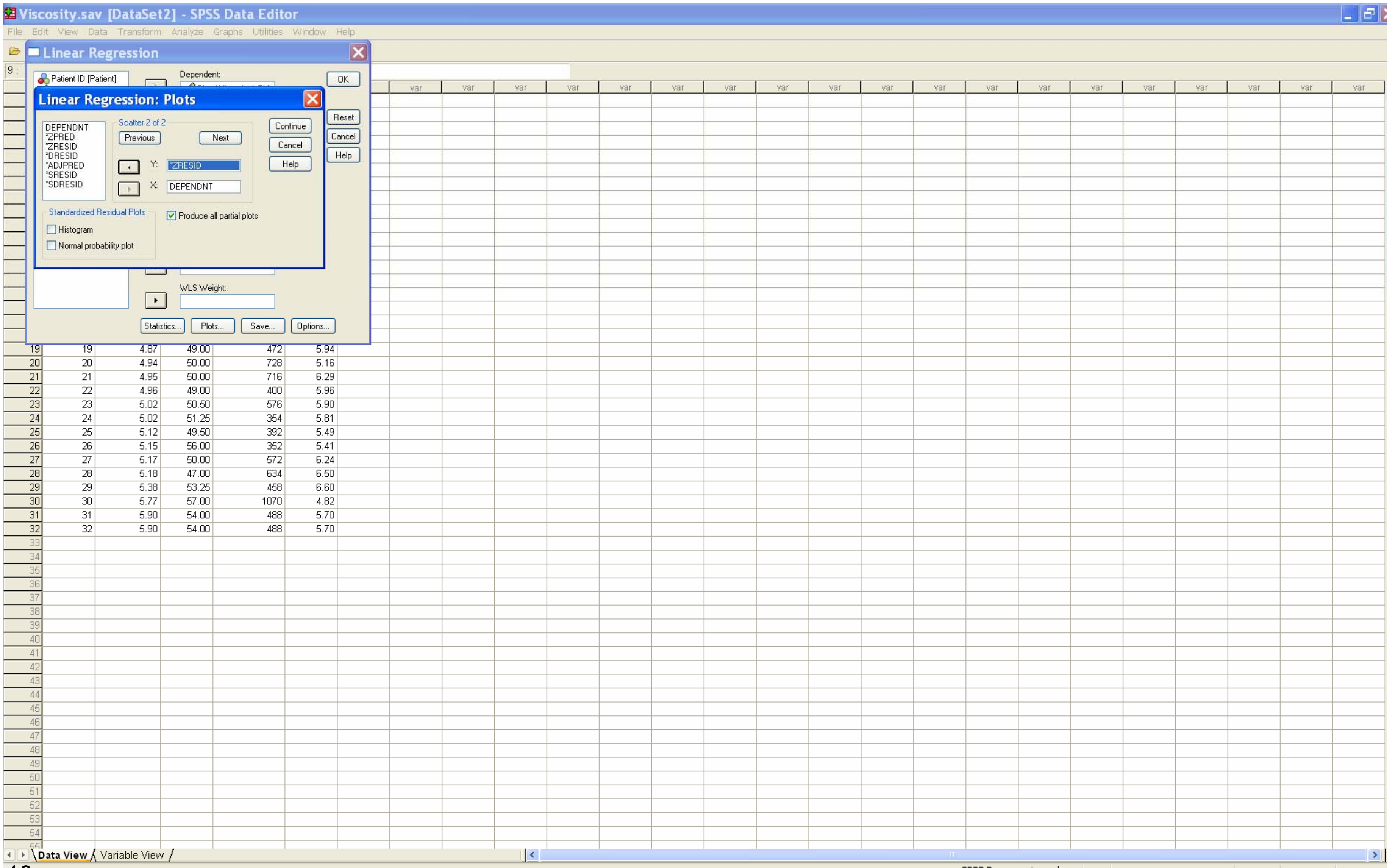
Select ***ZRESID** for the *Y* variable and ***ZPRED** for the *X* variable.

Then click *Next.*

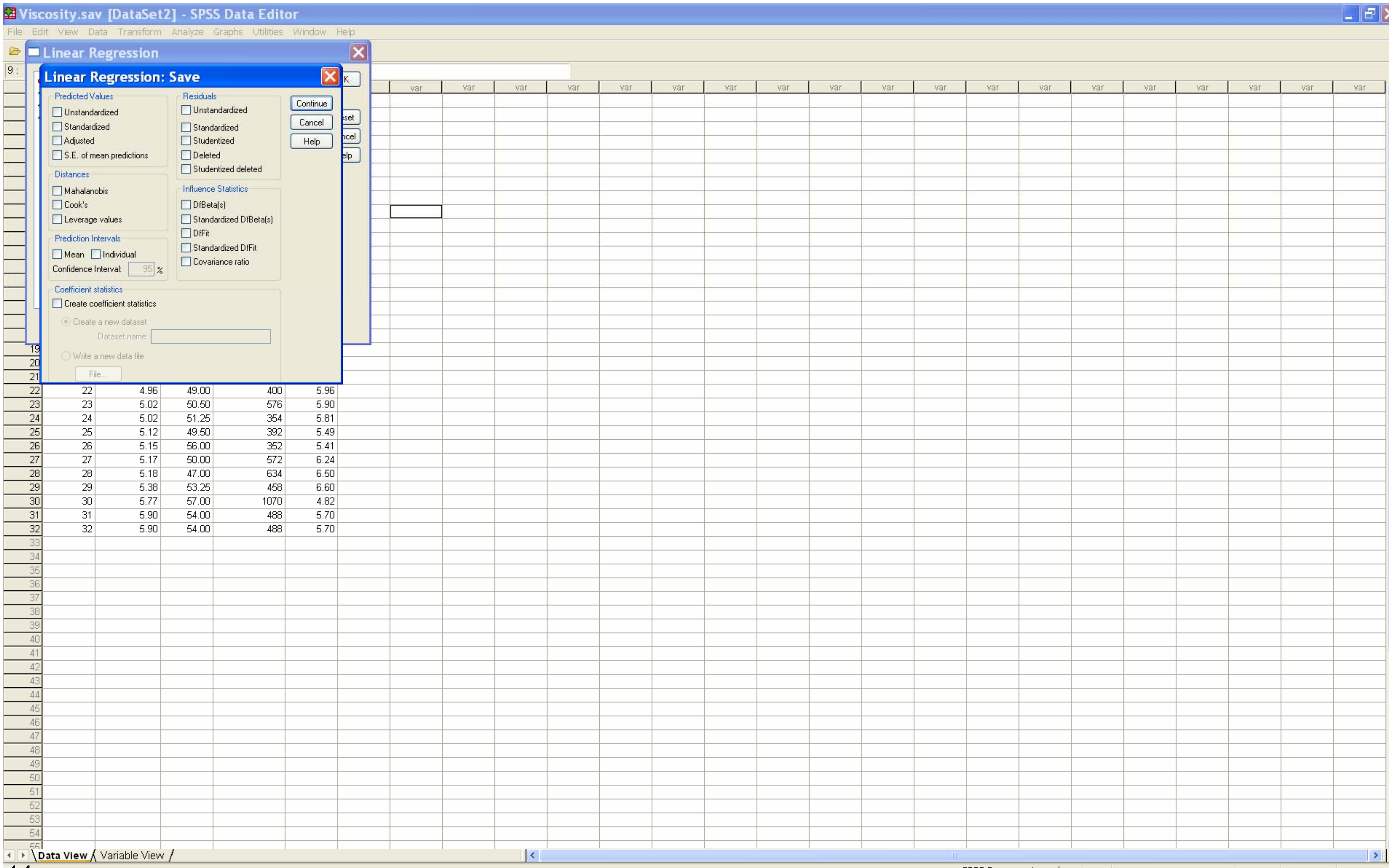


Select ***ZRESID** for the *Y* variable and ***ZPRED** for the *X* variable.

Then click *Produce all partial Plots.* Then *Continue.*

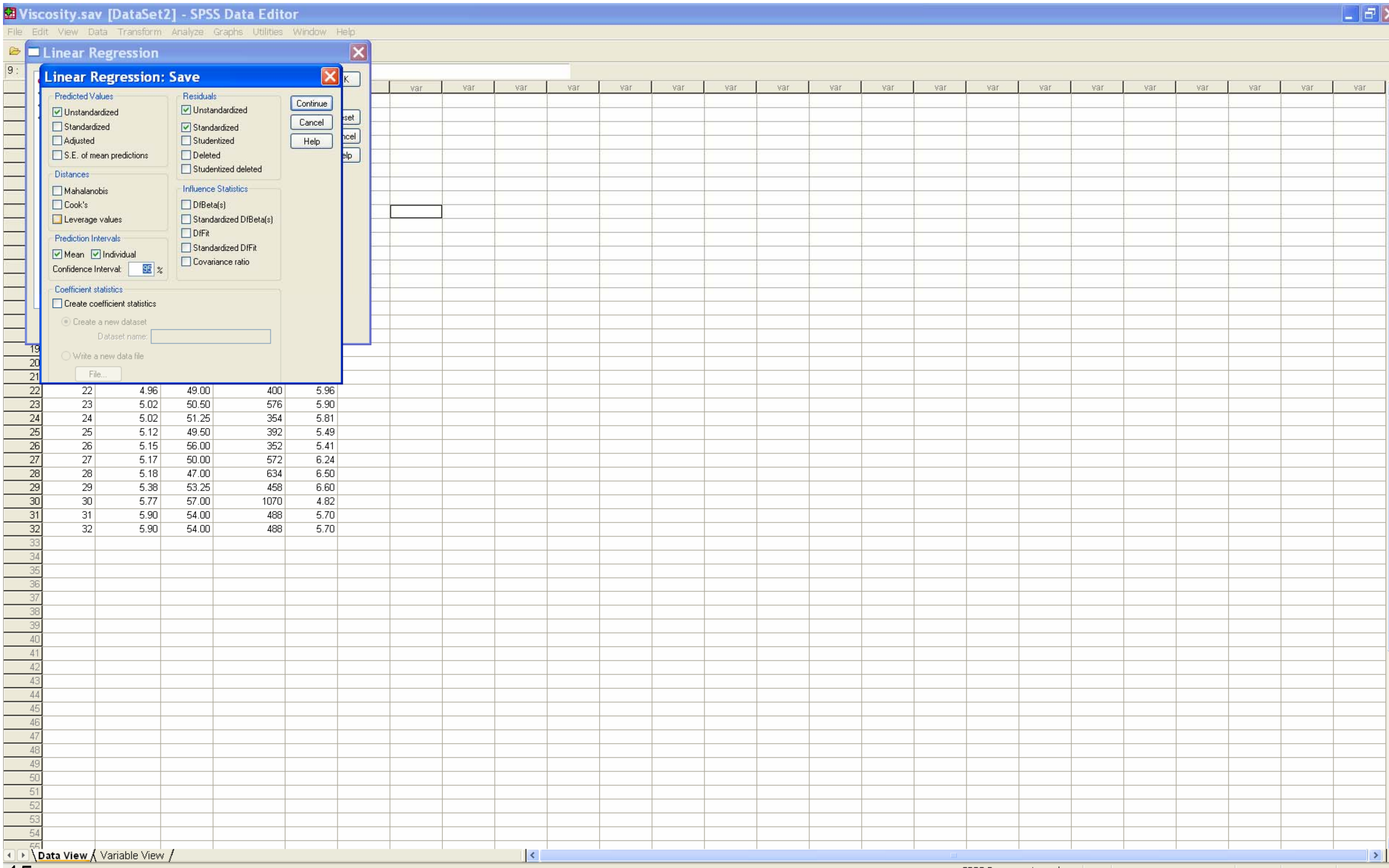


Click the *Save* button, to compute and store the residuals etc.

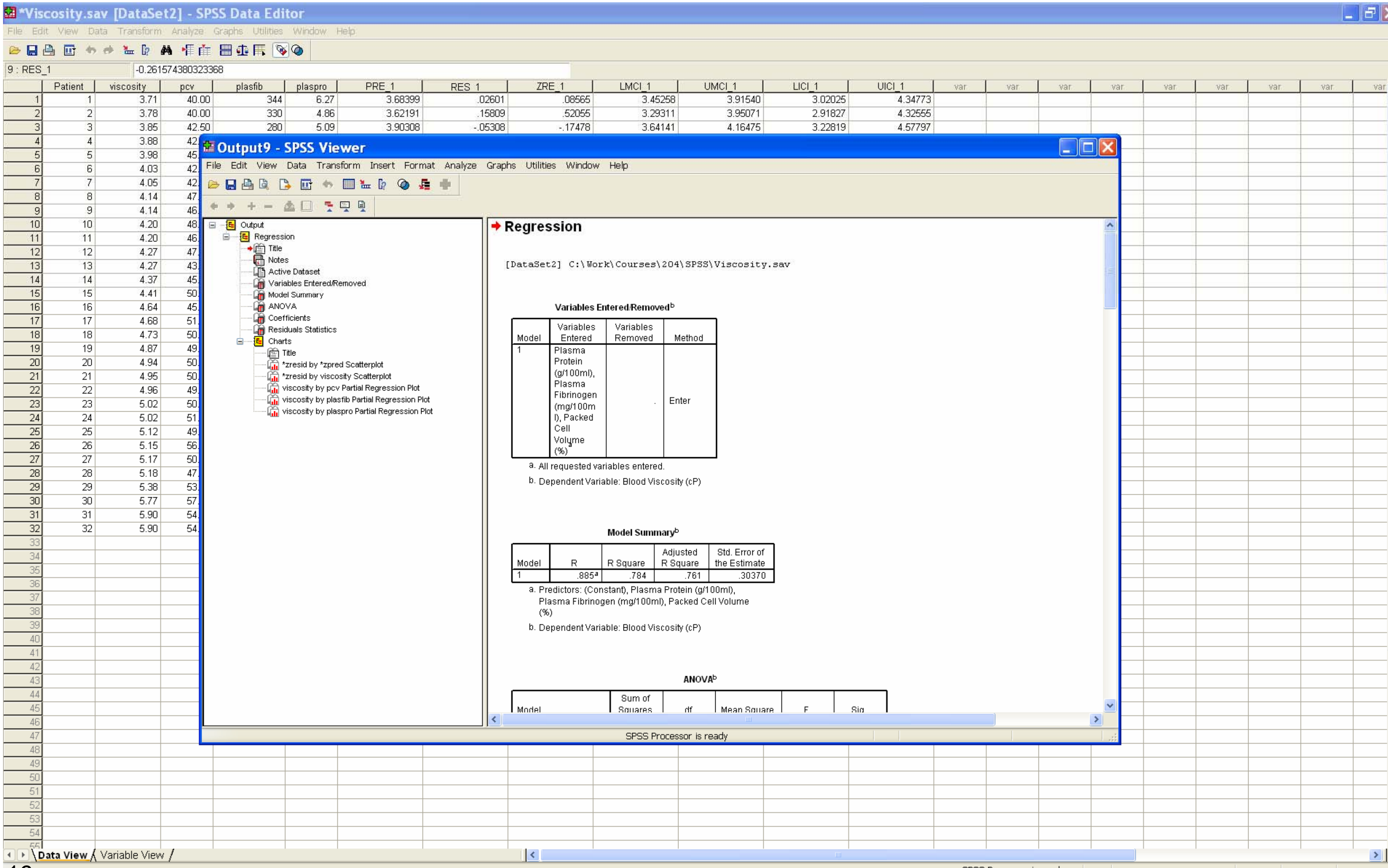


Select the quantities to store as new variables in the data set.

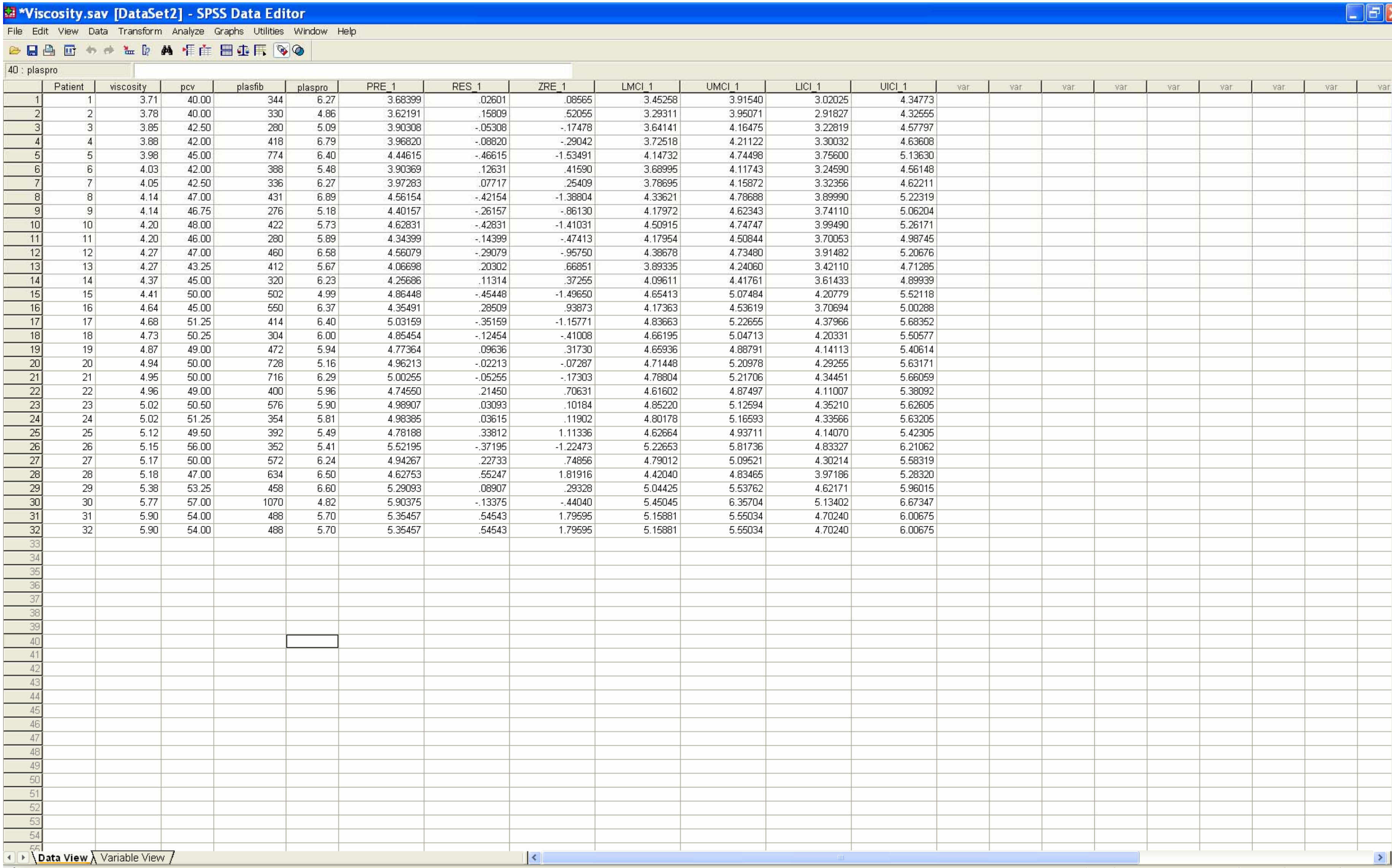
Click *Continue*.



Click OK and the output is generated.



New variables have been computed.



	Patient	viscosity	pcv	plasfib	plaspro	PRE_1	RES_1	ZRE_1	LMCI_1	UMCI_1	LICI_1	UICI_1
1	1	3.71	40.00	344	6.27	3.68399	.02601	.08565	3.45258	3.91540	3.02025	4.34773
2	2	3.78	40.00	330	4.86	3.62191	.15809	.52055	3.29311	3.95071	2.91827	4.32555
3	3	3.85	42.50	280	5.09	3.90308	-.05308	-.17478	3.64141	4.16475	3.22819	4.57797
4	4	3.88	42.00	418	6.79	3.96820	-.08820	-.29042	3.72518	4.21122	3.30032	4.63608
5	5	3.98	45.00	774	6.40	4.44615	-.46615	-1.53491	4.14732	4.74498	3.75600	5.13630
6	6	4.03	42.00	388	5.48	3.90369	.12631	.41590	3.68995	4.11743	3.24590	4.56148
7	7	4.05	42.50	336	6.27	3.97283	.07717	.25409	3.78695	4.15872	3.32356	4.62211
8	8	4.14	47.00	431	6.89	4.56154	-.42154	-1.38804	4.33621	4.78688	3.89990	5.22319
9	9	4.14	46.75	276	5.18	4.40157	-.26157	-.86130	4.17972	4.62343	3.74110	5.06204
10	10	4.20	48.00	422	5.73	4.62831	-.42831	-1.41031	4.50915	4.74747	3.99490	5.26171
11	11	4.20	46.00	280	5.89	4.34399	-.14399	-.47413	4.17954	4.50844	3.70053	4.98745
12	12	4.27	47.00	460	6.58	4.56079	-.29079	-.95750	4.38678	4.73480	3.91482	5.20676
13	13	4.27	43.25	412	5.67	4.06698	.20302	.66851	3.89335	4.24060	3.42110	4.71285
14	14	4.37	45.00	320	6.23	4.25686	.11314	.37255	4.09611	4.41761	3.61433	4.89939
15	15	4.41	50.00	502	4.99	4.86448	-.45448	-1.49650	4.65413	5.07484	4.20779	5.52118
16	16	4.64	45.00	550	6.37	4.35491	.28509	.93873	4.17363	4.53619	3.70694	5.00288
17	17	4.68	51.25	414	6.40	5.03159	-.35159	-1.15771	4.83663	5.22655	4.37966	5.68352
18	18	4.73	50.25	304	6.00	4.85454	-.12454	-.41008	4.66195	5.04713	4.20331	5.50577
19	19	4.87	49.00	472	5.94	4.77364	.09636	.31730	4.65936	4.88791	4.14113	5.40614
20	20	4.94	50.00	728	5.16	4.96213	-.02213	-.07287	4.71448	5.20978	4.29255	5.63171
21	21	4.95	50.00	716	6.29	5.00255	-.05255	-.17303	4.78804	5.21706	4.34451	5.66059
22	22	4.96	49.00	400	5.96	4.74550	.21450	.70631	4.61602	4.87497	4.11007	5.38092
23	23	5.02	50.50	576	5.90	4.98907	.03093	.10184	4.85220	5.12594	4.35210	5.62605
24	24	5.02	51.25	354	5.81	4.98385	.03615	.11902	4.80178	5.16593	4.33566	5.63205
25	25	5.12	49.50	392	5.49	4.78188	.33812	1.11336	4.62664	4.93711	4.14070	5.42305
26	26	5.15	56.00	352	5.41	5.52195	-.37195	-1.22473	5.22653	5.81736	4.83327	6.21062
27	27	5.17	50.00	572	6.24	4.94267	.22733	.74856	4.79012	5.09521	4.30214	5.58319
28	28	5.18	47.00	634	6.50	4.62753	.55247	1.81916	4.42040	4.83465	3.97186	5.28320
29	29	5.38	53.25	458	6.60	5.29093	.08907	.29328	5.04425	5.53762	4.62171	5.96015
30	30	5.77	57.00	1070	4.82	5.90375	-.13375	-.44040	5.45045	6.35704	5.13402	6.67347
31	31	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675
32	32	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675

Full information on the new variables is available.

*Viscosity.sav [DataSet2] - SPSS Data Editor

File Edit View Data Transform Analyze Graphs Utilities Window Help

	Name	Type	Width	Decimals	Label	Values	Missing	Columns	Align	Measure
1	Patient	Numeric	4	0	Patient ID	None	None	8	Right	Nominal
2	viscosity	Numeric	10	2	Blood Viscosity (cP)	None	None	10	Right	Scale
3	pcv	Numeric	10	2	Packed Cell Volume (%)	None	None	8	Right	Scale
4	plasfib	Numeric	10	0	Plasma Fibrinogen (mg/100ml)	None	None	11	Right	Scale
5	plaspro	Numeric	10	2	Plasma Protein (g/100ml)	None	None	8	Right	Scale
6	PRE_1	Numeric	11	5	Unstandardized Predicted Value	None	None	13	Right	Scale
7	RES_1	Numeric	11	5	Unstandardized Residual	None	None	13	Right	Scale
8	ZRE_1	Numeric	11	5	Standardized Residual	None	None	13	Right	Scale
9	LMCI_1	Numeric	11	5	95% L CI for viscosity mean	None	None	13	Right	Scale
10	UMCI_1	Numeric	11	5	95% U CI for viscosity mean	None	None	13	Right	Scale
11	LICI_1	Numeric	11	5	95% L CI for viscosity individual	None	None	13	Right	Scale
12	UICI_1	Numeric	11	5	95% U CI for viscosity individual	None	None	13	Right	Scale

Data View | **Variable View**

SPSS Processor is ready

Results: Model Summary

R squared and Adjusted R squared are quite high, so the fit is moderately good.

Model Summary[b]

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	.885[a]	.784	.761	.30370

a. Predictors: (Constant), Plasma Protein (g/100ml), Plasma Fibrinogen (mg/100ml), Packed Cell Volume (%)

b. Dependent Variable: Blood Viscosity (cP)

Results: ANOVA

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	9.368	3	3.123	33.856	.000[a]
	Residual	2.582	28	.092		
	Total	11.950	31			

a. Predictors: (Constant), Plasma Protein (g/100ml), Plasma Fibrinogen (mg/100ml), Packed Cell Volume (%)

b. Dependent Variable: Blood Viscosity (cP)

The ANOVA for the multiple regression has a highly significant F value, with a p-value < 0.001. Here

H0 : E[Y] = beta.0
H1 : E[Y] = beta.0 + beta.*1 x1* + beta.*2 x2* + beta.*3 x3*

This result implies that the multiple regression (Ha) fits significantly better than the model with no dependence on any of the predictors (H0).

Results: Parameter Estimates

Coefficients[a]

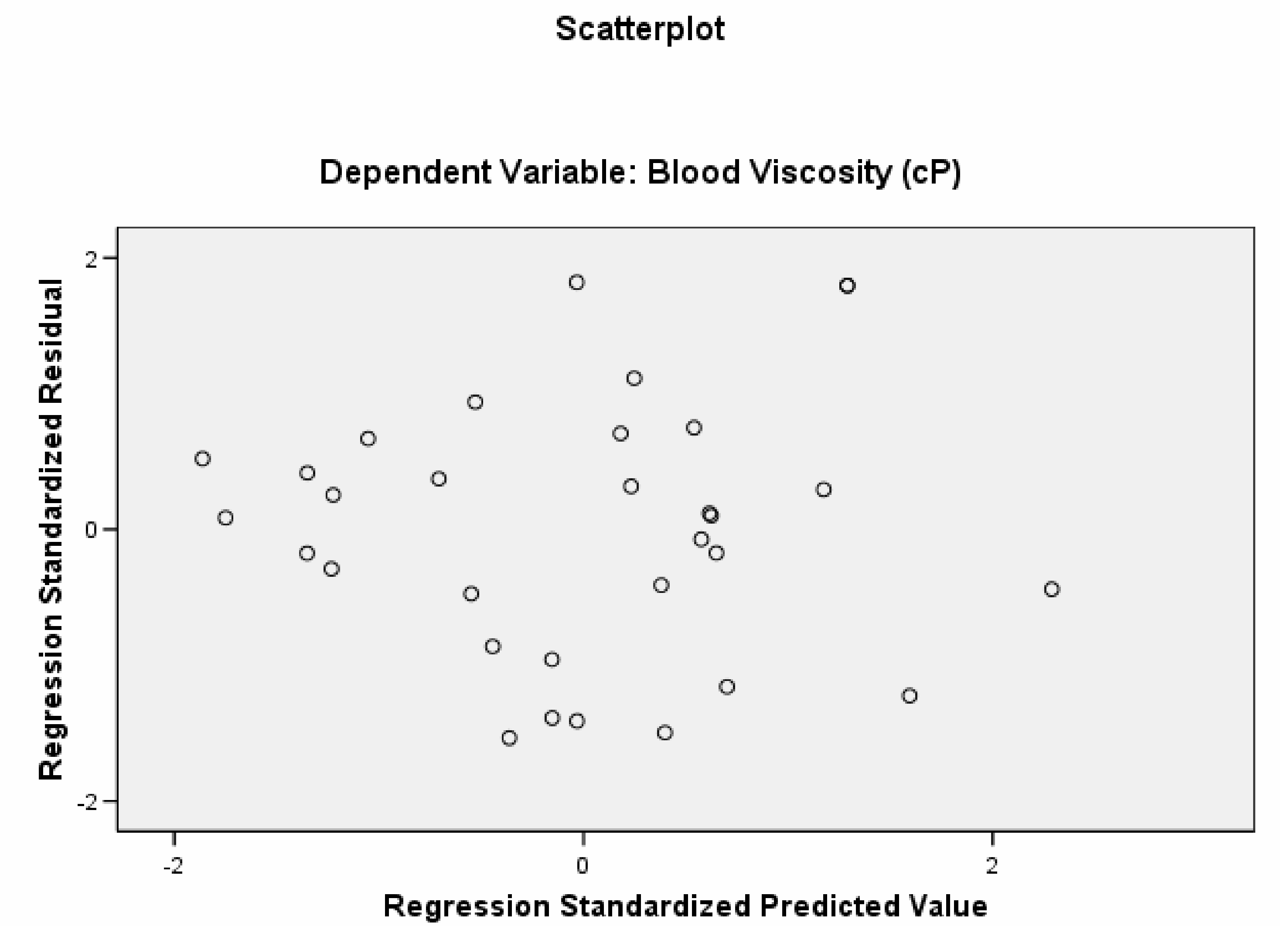
Model		Unstandardized Coefficients B	Unstandardized Coefficients Std. Error	Standardized Coefficients Beta	t	Sig.	95% Confidence Interval for B Lower Bound	95% Confidence Interval for B Upper Bound
1	(Constant)	-1.378	.897		-1.537	.136	-3.215	.458
	Packed Cell Volume (%)	.117	.014	.839	8.584	.000	.089	.145
	Plasma Fibrinogen (mg/100ml)	.000	.000	.111	1.147	.261	.000	.001
	Plasma Protein (g/100ml)	.040	.097	.037	.412	.683	-.159	.239

a. Dependent Variable: Blood Viscosity (cP)

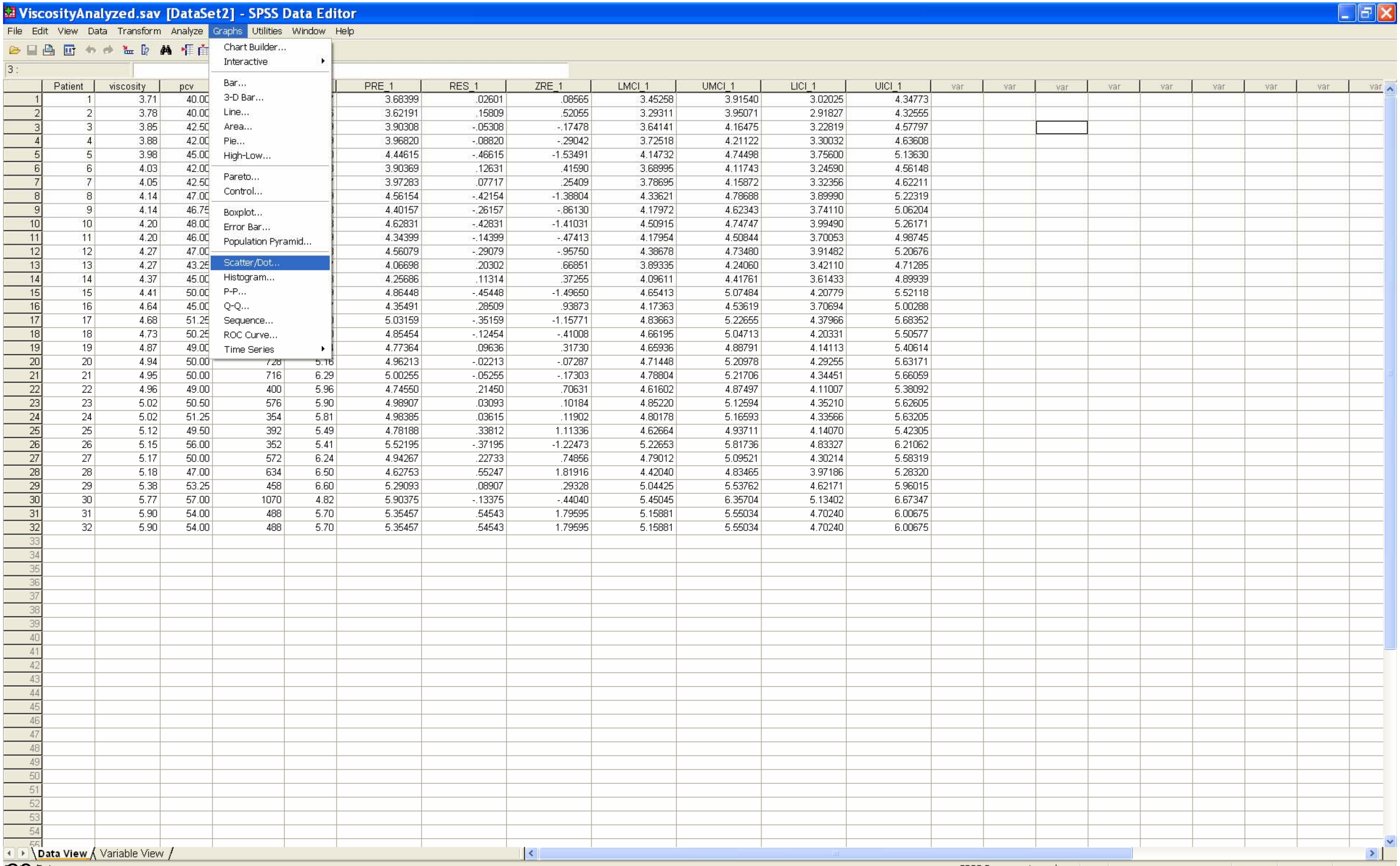
The coefficient and standard error for Plasma Fibrinogen are not exactly zero, but are zero to three decimal places.

Only the Packed Cell Volume coefficient is significantly different from zero ($p < 0.001$). The intercept (Constant), Plasma Fibrinogen, and Plasma Protein coefficients are not significantly different from zero (p=0.136, 0.261, 0.683 respectively)

Results: Scatterplot of Standardized Residual vs Predicted Value

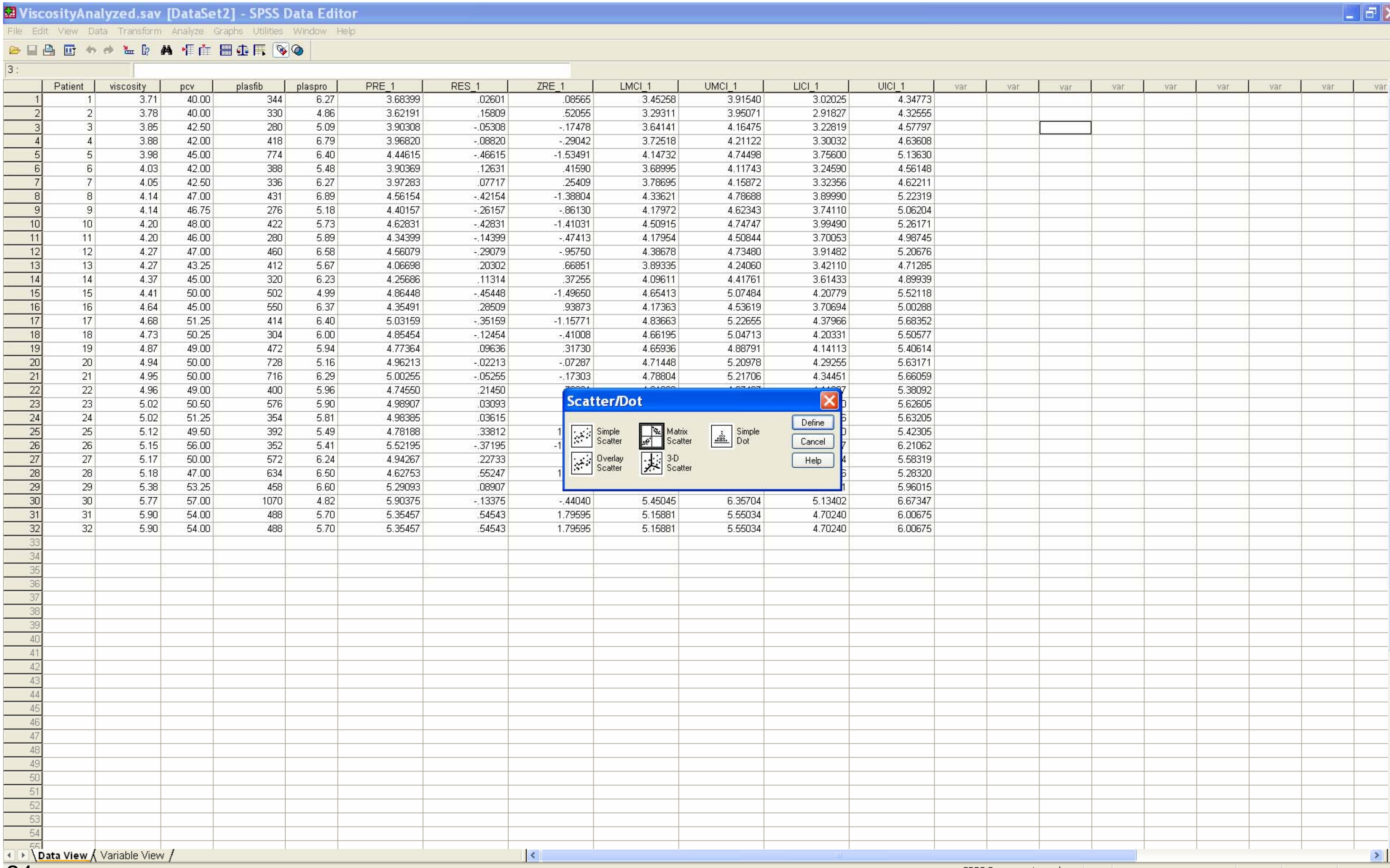


Obtaining: Plots of Residuals vs Covariates



	Patient	viscosity	pcv			PRE_1	RES_1	ZRE_1	LMCI_1	UMCI_1	LICI_1	UICI_1
1	1	3.71	40.00			3.68399	.02601	.08565	3.45258	3.91540	3.02025	4.34773
2	2	3.78	40.00			3.62191	.15809	.52055	3.29311	3.95071	2.91827	4.32555
3	3	3.85	42.50			3.90308	-.05308	-.17478	3.64141	4.16475	3.22819	4.57797
4	4	3.88	42.00			3.96820	-.08820	-.29042	3.72518	4.21122	3.30032	4.63608
5	5	3.98	45.00			4.44615	-.46615	-1.53491	4.14732	4.74498	3.75600	5.13630
6	6	4.03	42.00			3.90369	.12631	.41590	3.68995	4.11743	3.24590	4.56148
7	7	4.05	42.50			3.97283	.07717	.25409	3.78695	4.15872	3.32356	4.62211
8	8	4.14	47.00			4.56154	-.42154	-1.38804	4.33621	4.78688	3.89990	5.22319
9	9	4.14	46.75			4.40157	-.26157	-.86130	4.17972	4.62343	3.74110	5.06204
10	10	4.20	48.00			4.62831	-.42831	-1.41031	4.50915	4.74747	3.99490	5.26171
11	11	4.20	46.00			4.34399	-.14399	-.47413	4.17954	4.50844	3.70053	4.98745
12	12	4.27	47.00			4.56079	-.29079	-.95750	4.38678	4.73480	3.91482	5.20676
13	13	4.27	43.25			4.06698	.20302	.66851	3.89335	4.24060	3.42110	4.71285
14	14	4.37	45.00			4.25686	.11314	.37255	4.09611	4.41761	3.61433	4.89939
15	15	4.41	50.00			4.86448	-.45448	-1.49650	4.65413	5.07484	4.20779	5.52118
16	16	4.64	45.00			4.35491	.28509	.93873	4.17363	4.53619	3.70694	5.00288
17	17	4.68	51.25			5.03159	-.35159	-1.15771	4.83663	5.22655	4.37966	5.68352
18	18	4.73	50.25			4.85454	-.12454	-.41008	4.66195	5.04713	4.20331	5.50577
19	19	4.87	49.00			4.77364	.09636	.31730	4.65936	4.88791	4.14113	5.40614
20	20	4.94	50.00	728	5.16	4.96213	-.02213	-.07287	4.71448	5.20978	4.29255	5.63171
21	21	4.95	50.00	716	6.29	5.00255	-.05255	-.17303	4.78804	5.21706	4.34451	5.66059
22	22	4.96	49.00	400	5.96	4.74550	.21450	.70631	4.61602	4.87497	4.11007	5.38092
23	23	5.02	50.50	576	5.90	4.98907	.03093	.10184	4.85220	5.12594	4.35210	5.62605
24	24	5.02	51.25	354	5.81	4.98385	.03615	.11902	4.80178	5.16593	4.33566	5.63205
25	25	5.12	49.50	392	5.49	4.78188	.33812	1.11336	4.62664	4.93711	4.14070	5.42305
26	26	5.15	56.00	352	5.41	5.52195	-.37195	-1.22473	5.22653	5.81736	4.83327	6.21062
27	27	5.17	50.00	572	6.24	4.94267	.22733	.74856	4.79012	5.09521	4.30214	5.58319
28	28	5.18	47.00	634	6.50	4.62753	.55247	1.81916	4.42040	4.83465	3.97186	5.28320
29	29	5.38	53.25	458	6.60	5.29093	.08907	.29328	5.04425	5.53762	4.62171	5.96015
30	30	5.77	57.00	1070	4.82	5.90375	-.13375	-.44040	5.45045	6.35704	5.13402	6.67347
31	31	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675
32	32	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675

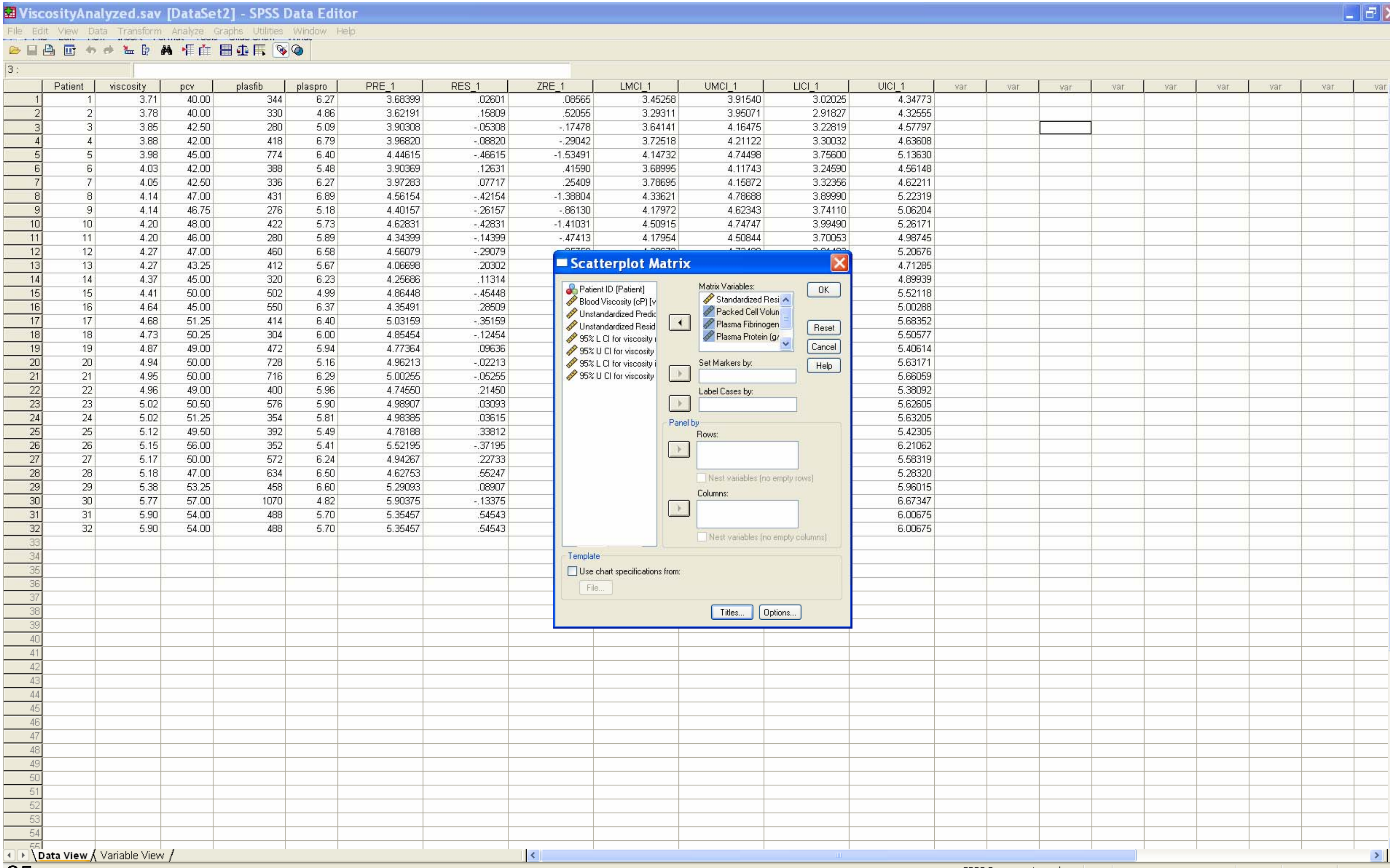
Use the *Matrix Scatter* option, and click *Define*



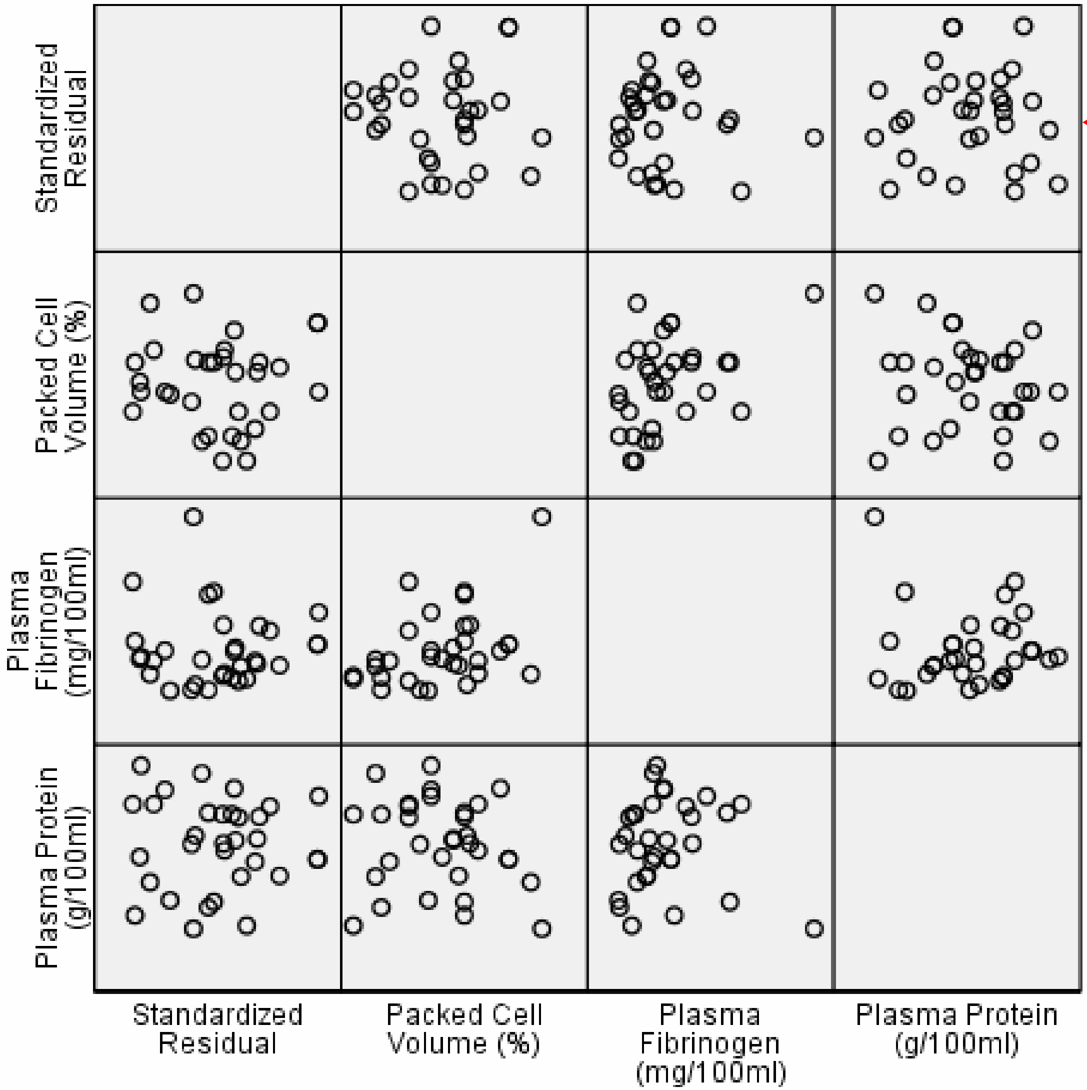
	Patient	viscosity	pcv	plasfib	plaspro	PRE_1	RES_1	ZRE_1	LMCI_1	UMCI_1	LICI_1	UICI_1
1	1	3.71	40.00	344	6.27	3.68399	.02601	.08565	3.45258	3.91540	3.02025	4.34773
2	2	3.78	40.00	330	4.86	3.62191	.15809	.52055	3.29311	3.95071	2.91827	4.32555
3	3	3.85	42.50	280	5.09	3.90308	-.05308	-.17478	3.64141	4.16475	3.22819	4.57797
4	4	3.88	42.00	418	6.79	3.96820	-.08820	-.29042	3.72518	4.21122	3.30032	4.63608
5	5	3.98	45.00	774	6.40	4.44615	-.46615	-1.53491	4.14732	4.74498	3.75600	5.13630
6	6	4.03	42.00	388	5.48	3.90369	.12631	.41590	3.68995	4.11743	3.24590	4.56148
7	7	4.05	42.50	336	6.27	3.97283	.07717	.25409	3.78695	4.15872	3.32356	4.62211
8	8	4.14	47.00	431	6.89	4.56154	-.42154	-1.38804	4.33621	4.78688	3.89990	5.22319
9	9	4.14	46.75	276	5.18	4.40157	-.26157	-.86130	4.17972	4.62343	3.74110	5.06204
10	10	4.20	48.00	422	5.73	4.62831	-.42831	-1.41031	4.50915	4.74747	3.99490	5.26171
11	11	4.20	46.00	280	5.89	4.34399	-.14399	-.47413	4.17954	4.50844	3.70053	4.98745
12	12	4.27	47.00	460	6.58	4.56079	-.29079	-.95750	4.38678	4.73480	3.91482	5.20676
13	13	4.27	43.25	412	5.67	4.06698	.20302	.66851	3.89335	4.24060	3.42110	4.71285
14	14	4.37	45.00	320	6.23	4.25686	.11314	.37255	4.09611	4.41761	3.61433	4.89939
15	15	4.41	50.00	502	4.99	4.86448	-.45448	-1.49650	4.65413	5.07484	4.20779	5.52118
16	16	4.64	45.00	550	6.37	4.35491	.28509	.93873	4.17363	4.53619	3.70694	5.00288
17	17	4.68	51.25	414	6.40	5.03159	-.35159	-1.15771	4.83663	5.22655	4.37966	5.68352
18	18	4.73	50.25	304	6.00	4.85454	-.12454	-.41008	4.66195	5.04713	4.20331	5.50577
19	19	4.87	49.00	472	5.94	4.77364	.09636	.31730	4.65936	4.88791	4.14113	5.40614
20	20	4.94	50.00	728	5.16	4.96213	-.02213	-.07287	4.71448	5.20978	4.29255	5.63171
21	21	4.95	50.00	716	6.29	5.00255	-.05255	-.17303	4.78804	5.21706	4.34451	5.66059
22	22	4.96	49.00	400	5.96	4.74550	.21450					5.38092
23	23	5.02	50.50	576	5.90	4.98907	.03093					5.62605
24	24	5.02	51.25	354	5.81	4.98385	.03615					5.63205
25	25	5.12	49.50	392	5.49	4.78188	.33812					5.42305
26	26	5.15	56.00	352	5.41	5.52195	-.37195					6.21062
27	27	5.17	50.00	572	6.24	4.94267	.22733					5.58319
28	28	5.18	47.00	634	6.50	4.62753	.55247					5.28320
29	29	5.38	53.25	458	6.60	5.29093	.08907					5.96015
30	30	5.77	57.00	1070	4.82	5.90375	-.13375	-.44040	5.45045	6.35704	5.13402	6.67347
31	31	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675
32	32	5.90	54.00	488	5.70	5.35457	.54543	1.79595	5.15881	5.55034	4.70240	6.00675

Select the standardized residuals, and the three covariates for the

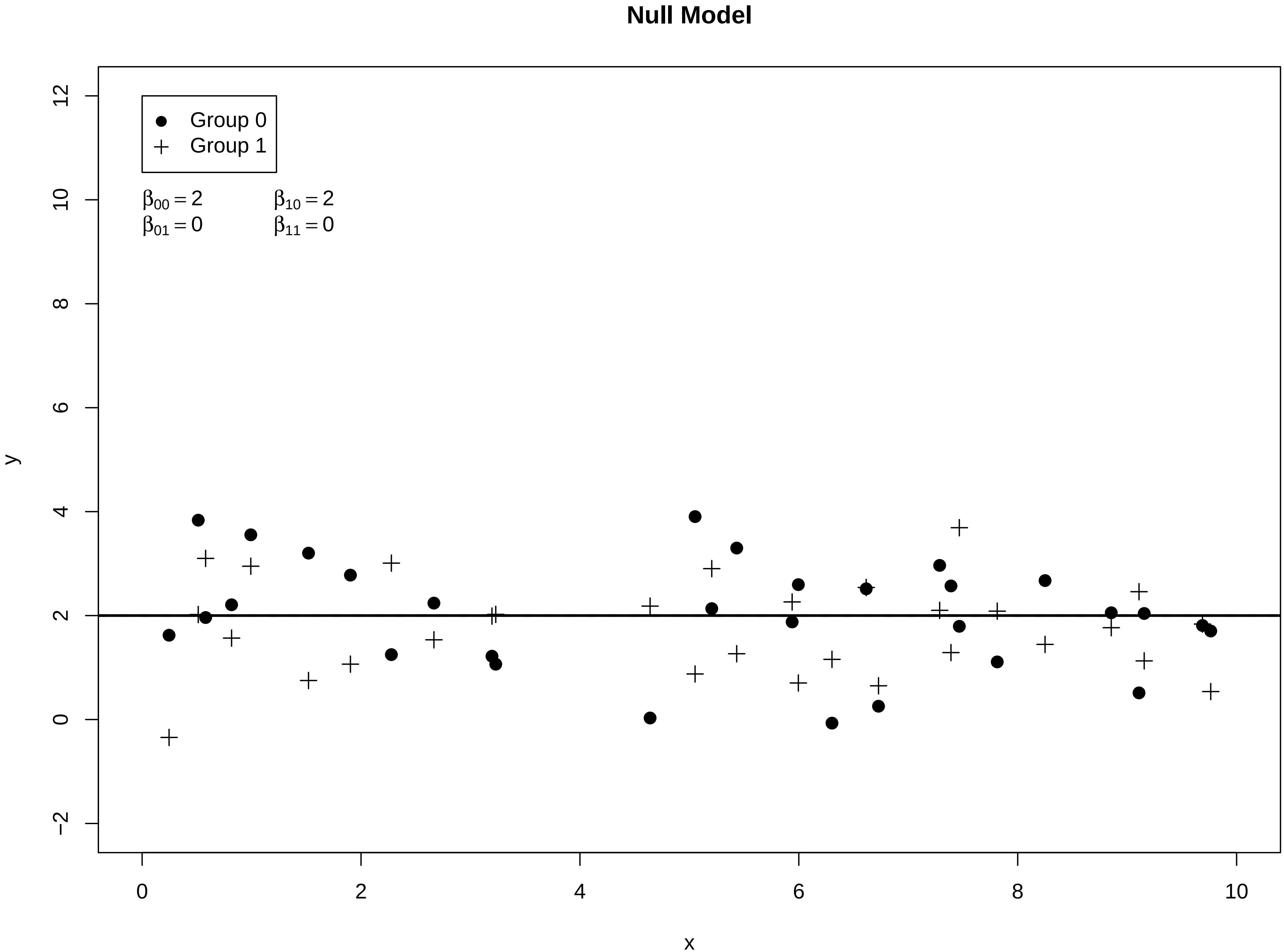
Matrix Variables. Click *OK.*

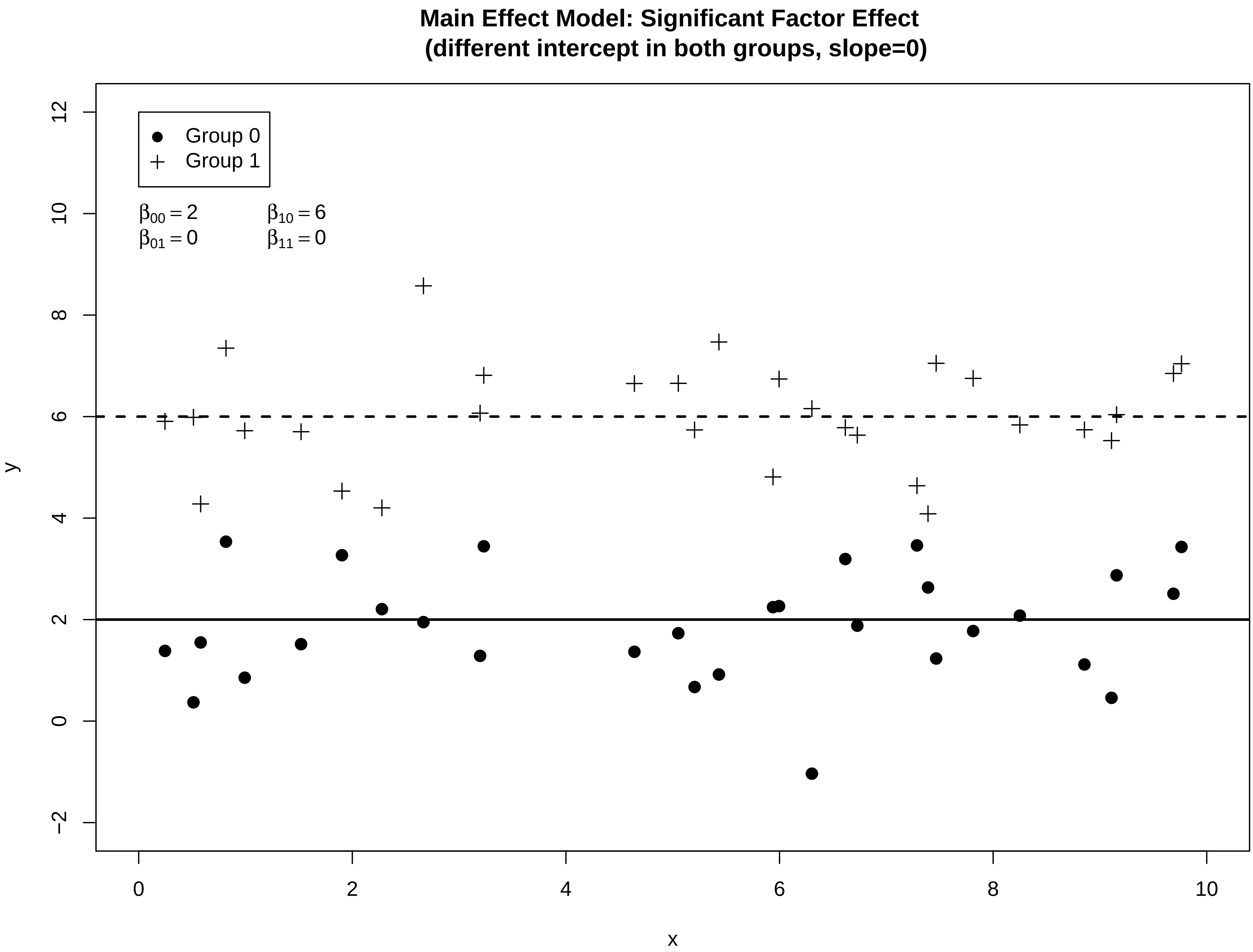


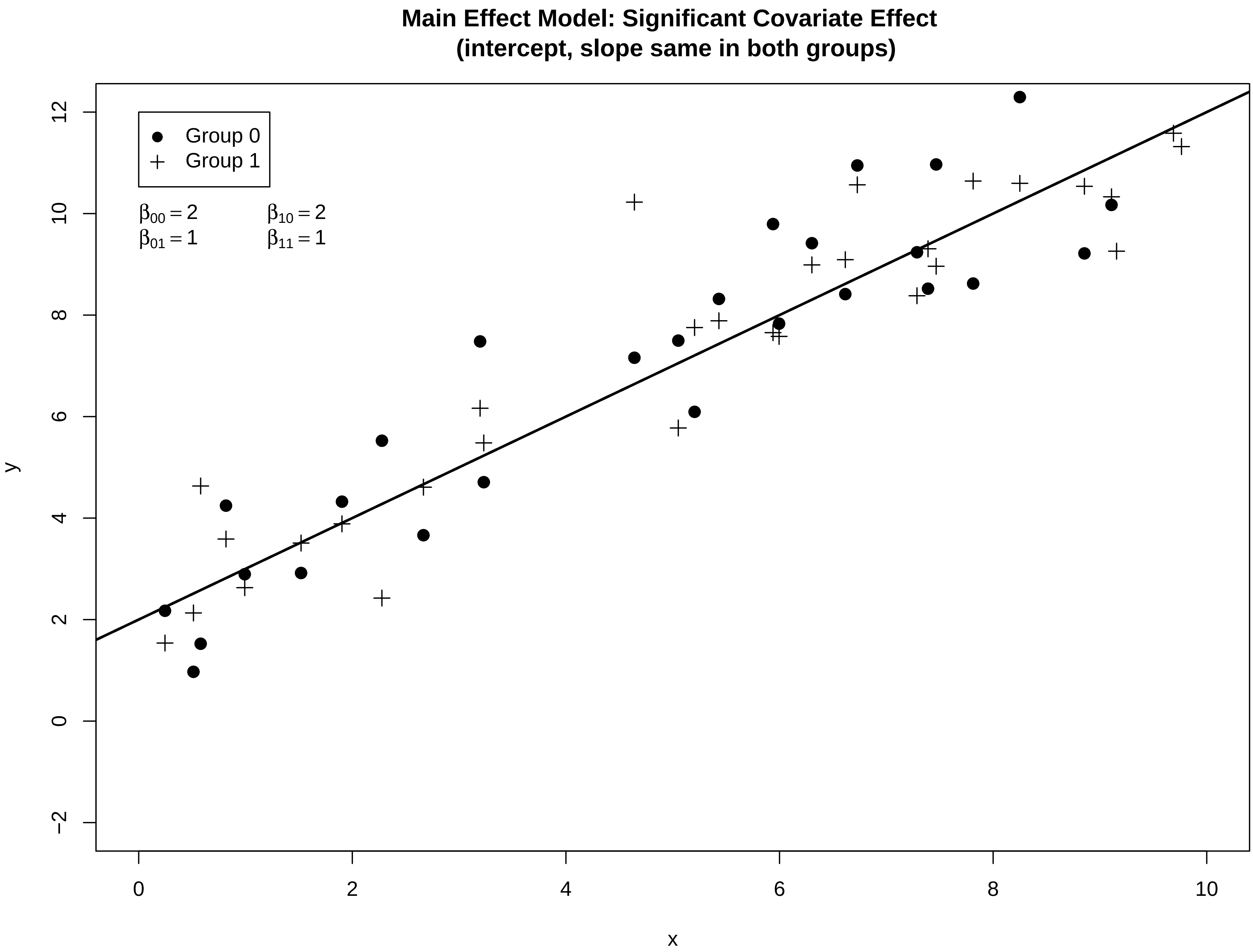
Results: Scatterplot Matrix

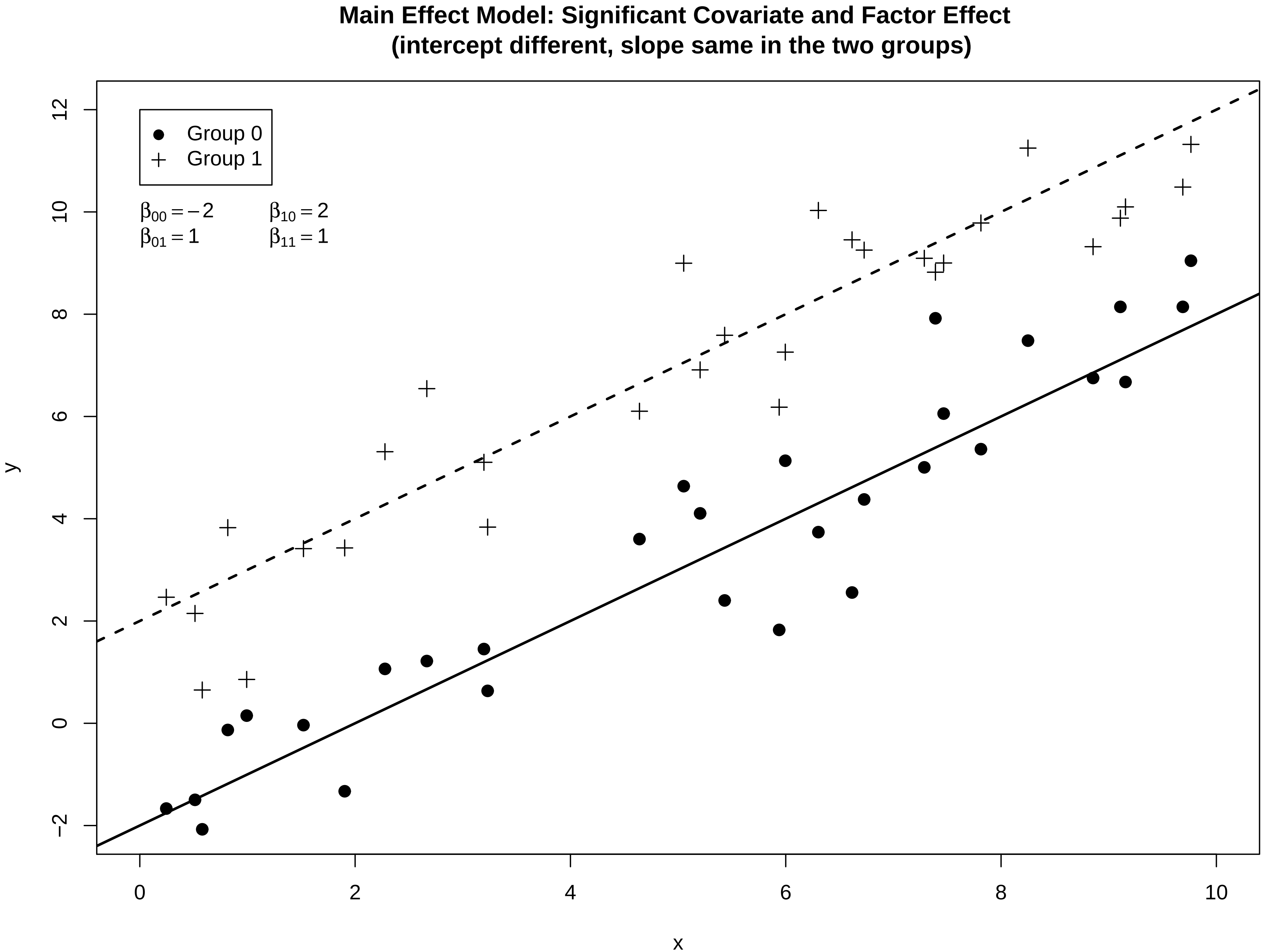


No real pattern in the plot of standardized residuals against the three predictors.

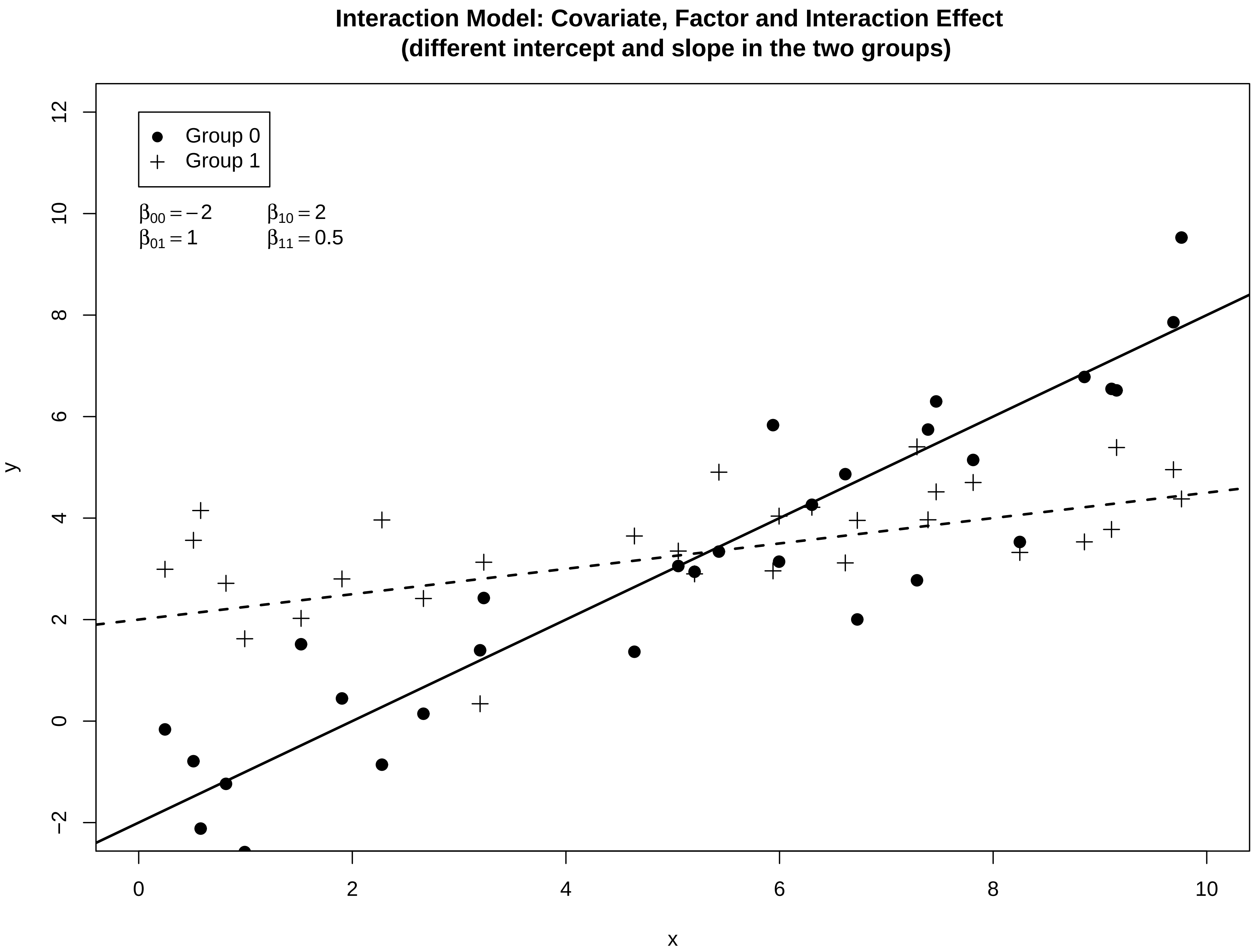

Null Model
Group 0
Group 1
$\beta_{00} = 2$
$\beta_{10} = 2$
$\beta_{01} = 0$
$\beta_{11} = 0$
y
x
12
10
8
6
4
2
0
−2
0
2
4
6
8
10

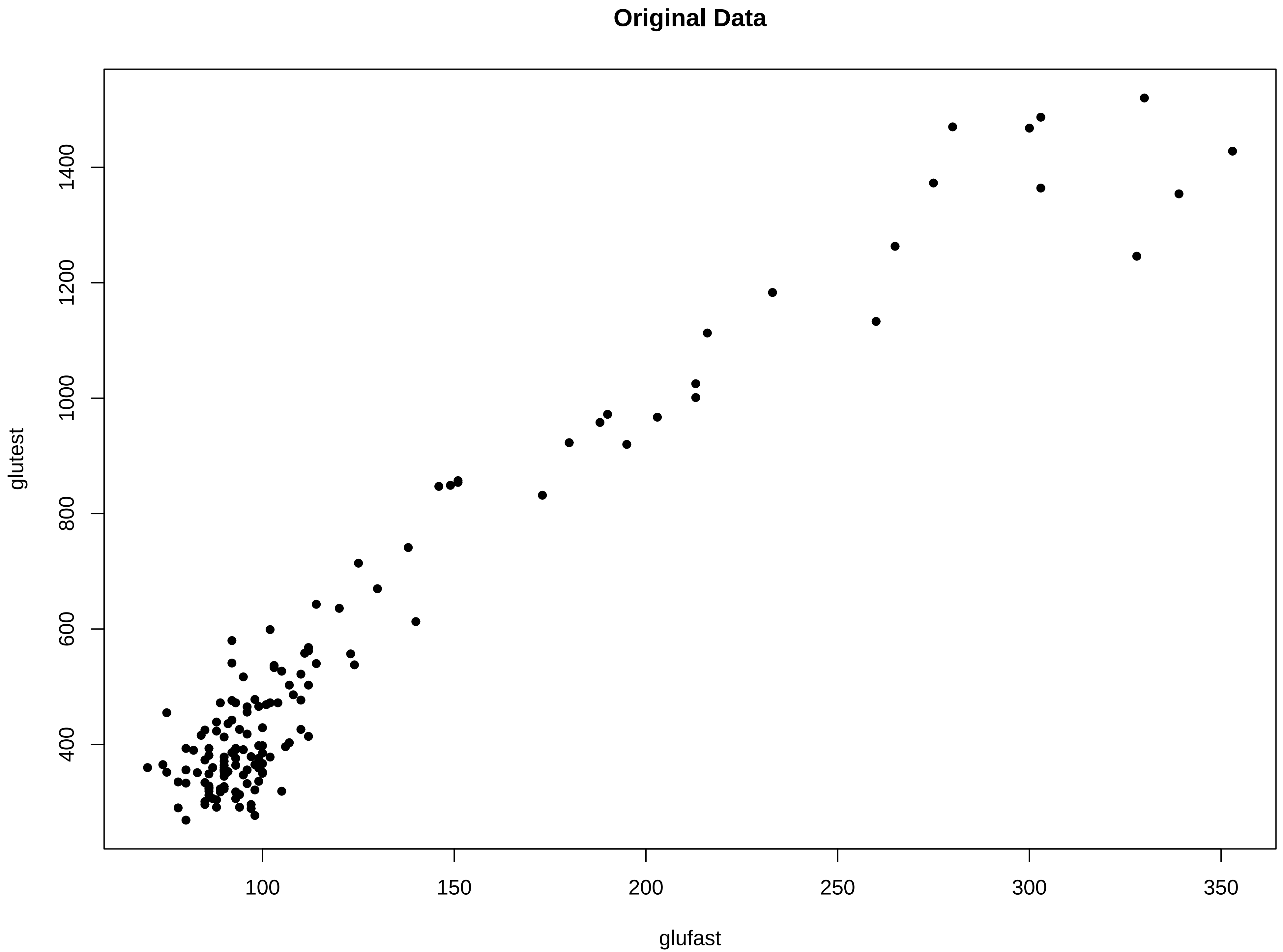

Main Effect Model: Significant Factor Effect
(different intercept in both groups, slope=0)
Group 0
Group 1
$\beta_{00} = 2$
$\beta_{10} = 6$
$\beta_{01} = 0$
$\beta_{11} = 0$
y
x
−2
0
2
4
6
8
10
12
0
2
4
6
8
10

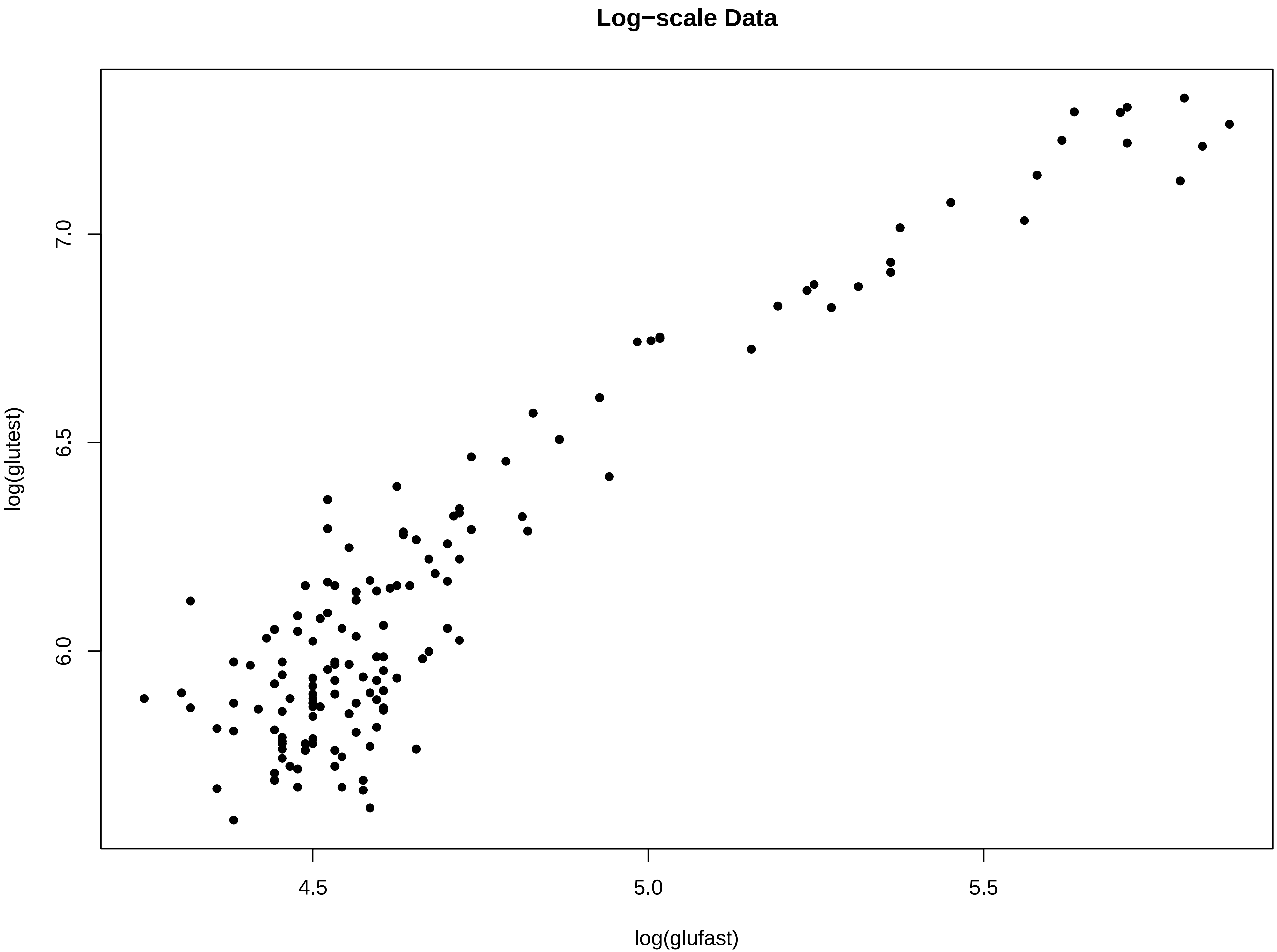

Main Effect Model: Significant Covariate Effect
(intercept, slope same in both groups)
Group 0
Group 1
$\beta_{00} = 2$
$\beta_{10} = 2$
$\beta_{01} = 1$
$\beta_{11} = 1$
y
x
−2
0
2
4
6
8
10
12
0
2
4
6
8
10



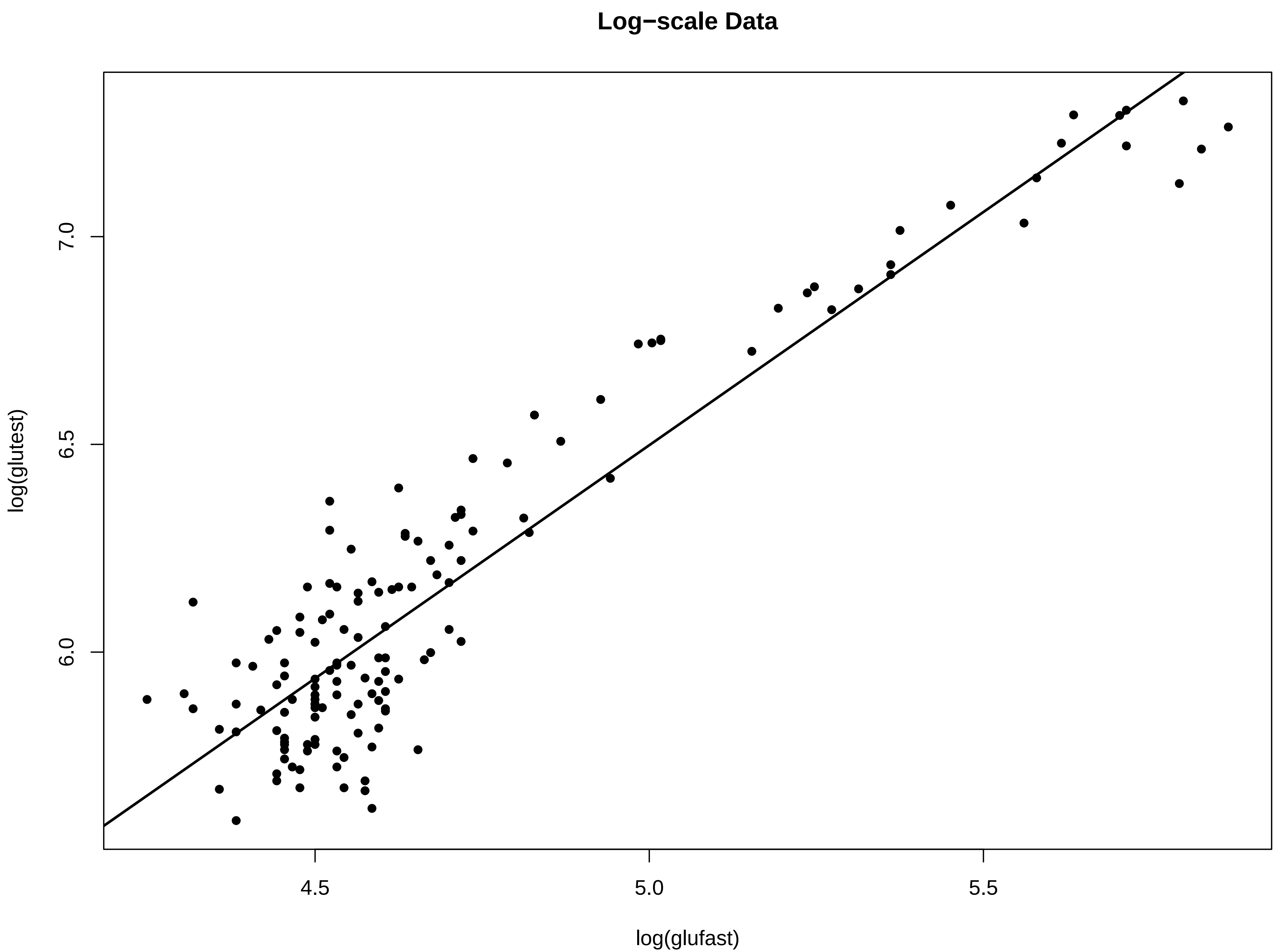
Main Effect Model: Significant Covariate and Factor Effect
(intercept different, slope same in the two groups)
Group 0
Group 1
β00 = −2
β10 = 2
β01 = 1
β11 = 1
−2
0
2
4
6
8
10
12
y
x

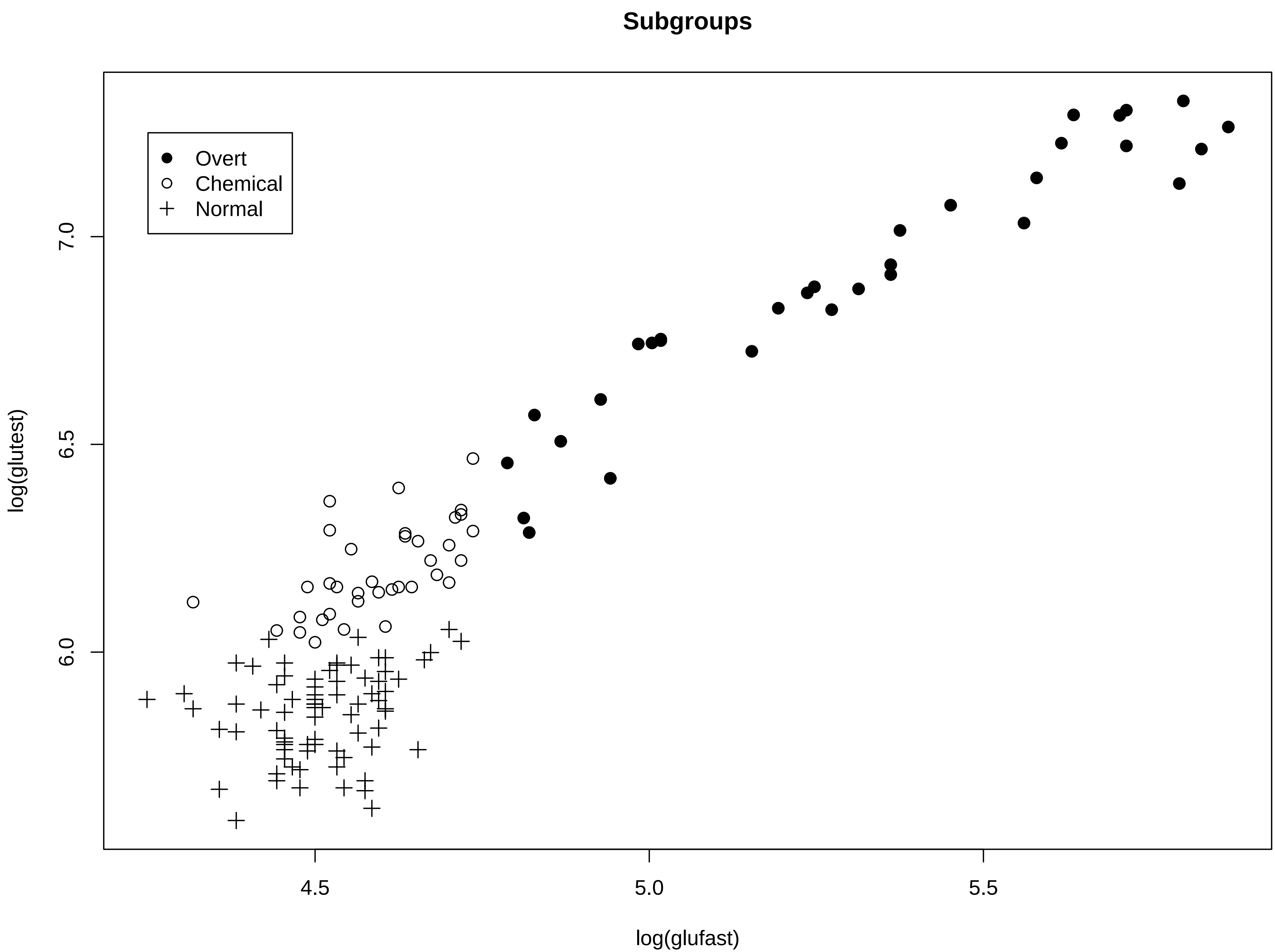

Interaction Model: Covariate, Factor and Interaction Effect
(different intercept and slope in the two groups)
Group 0
Group 1
$\beta_{00} = -2$
$\beta_{10} = 2$
$\beta_{01} = 1$
$\beta_{11} = 0.5$
y
x
0
2
4
6
8
10
−2
12


Original Data
glutest
glufast
400
600
800
1000
1200
1400
100
150
200
250
300
350



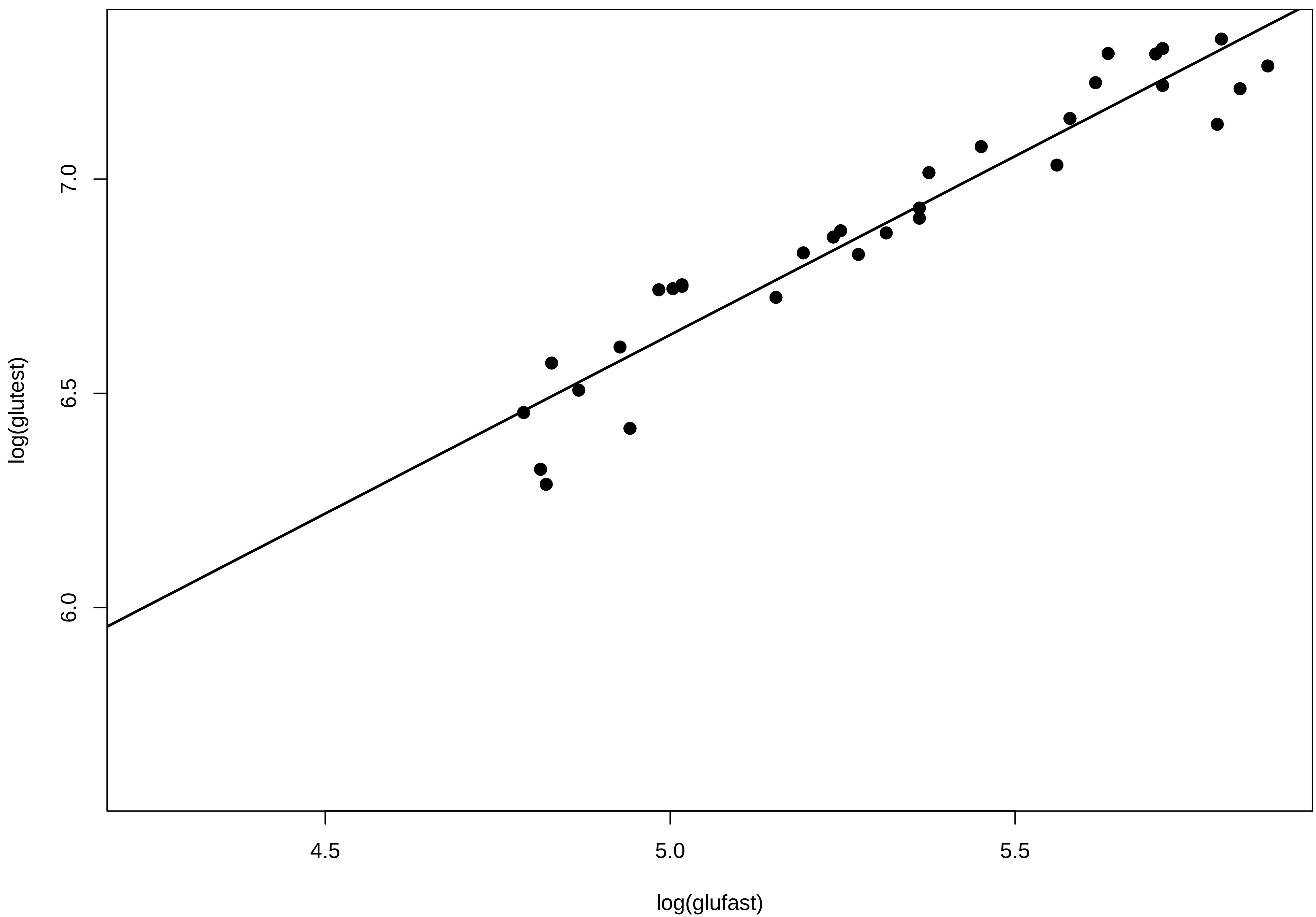
Log−scale Data
log(glutest)
7.0
6.5
6.0
4.5
5.0
5.5
log(glufast)

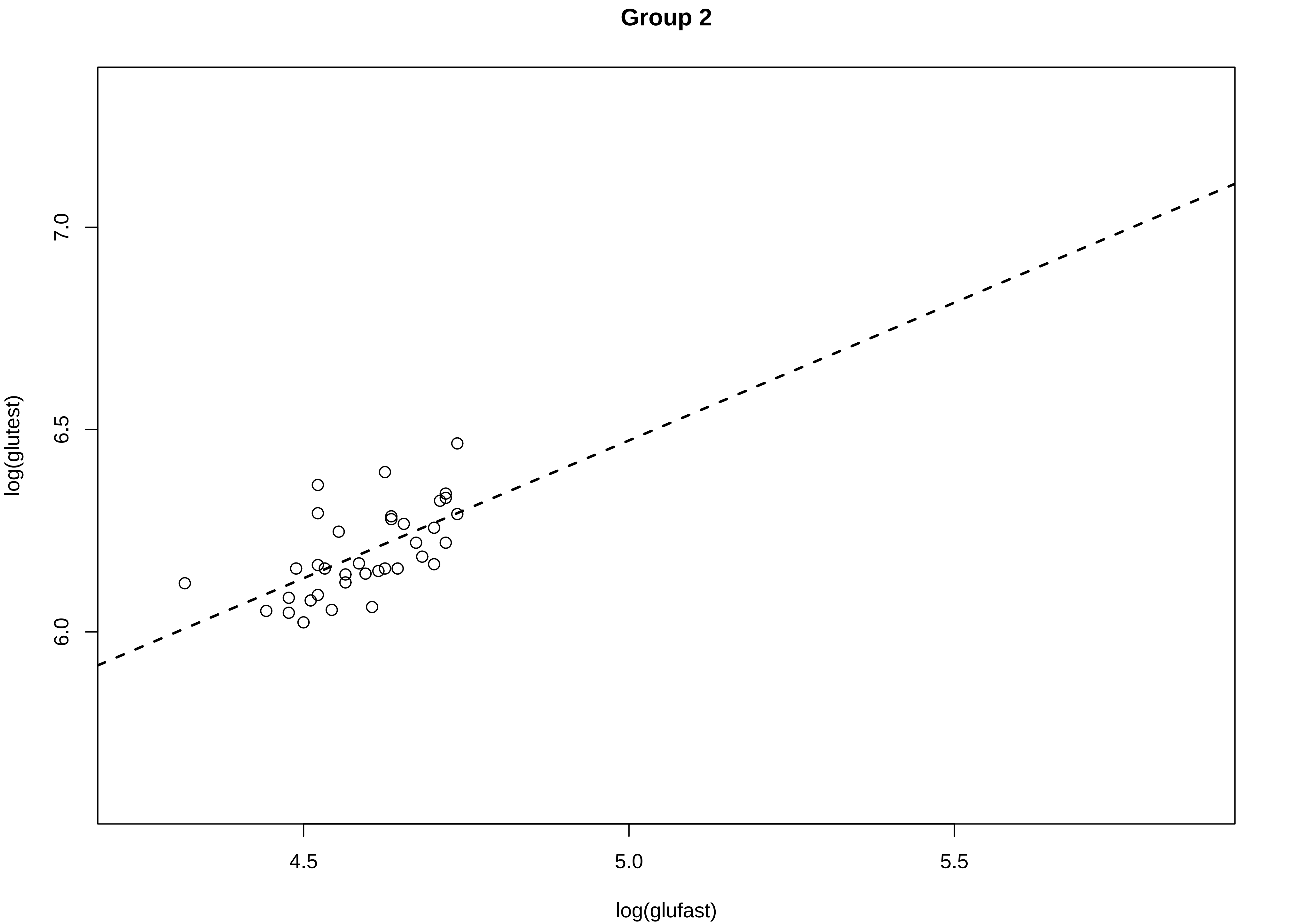

Log−scale Data
7.0
6.5
6.0
log(glutest)
4.5
5.0
5.5
log(glufast)



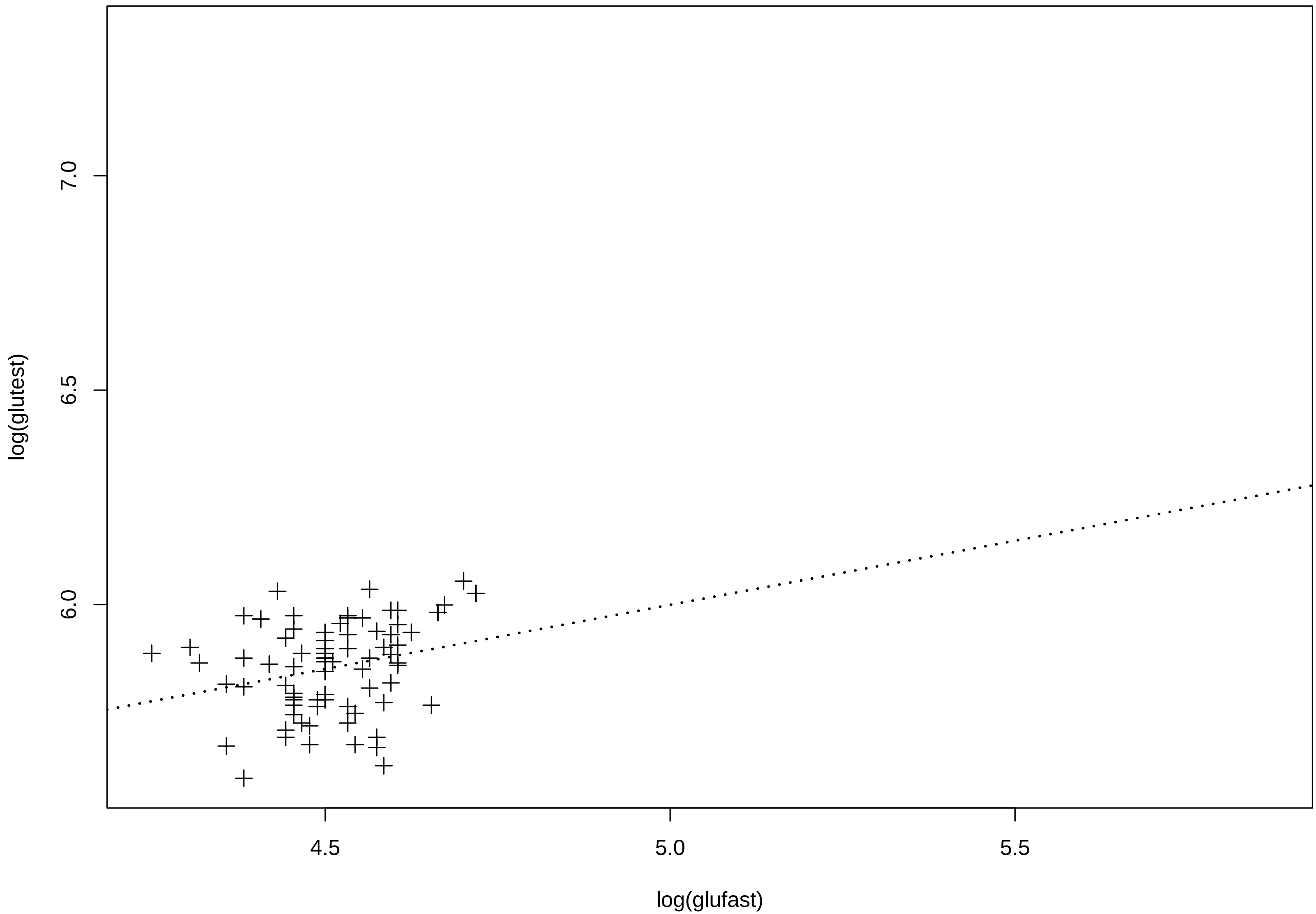
Subgroups
Overt
Chemical
Normal
log(glutest)
6.0
6.5
7.0
log(glufast)
4.5
5.0
5.5

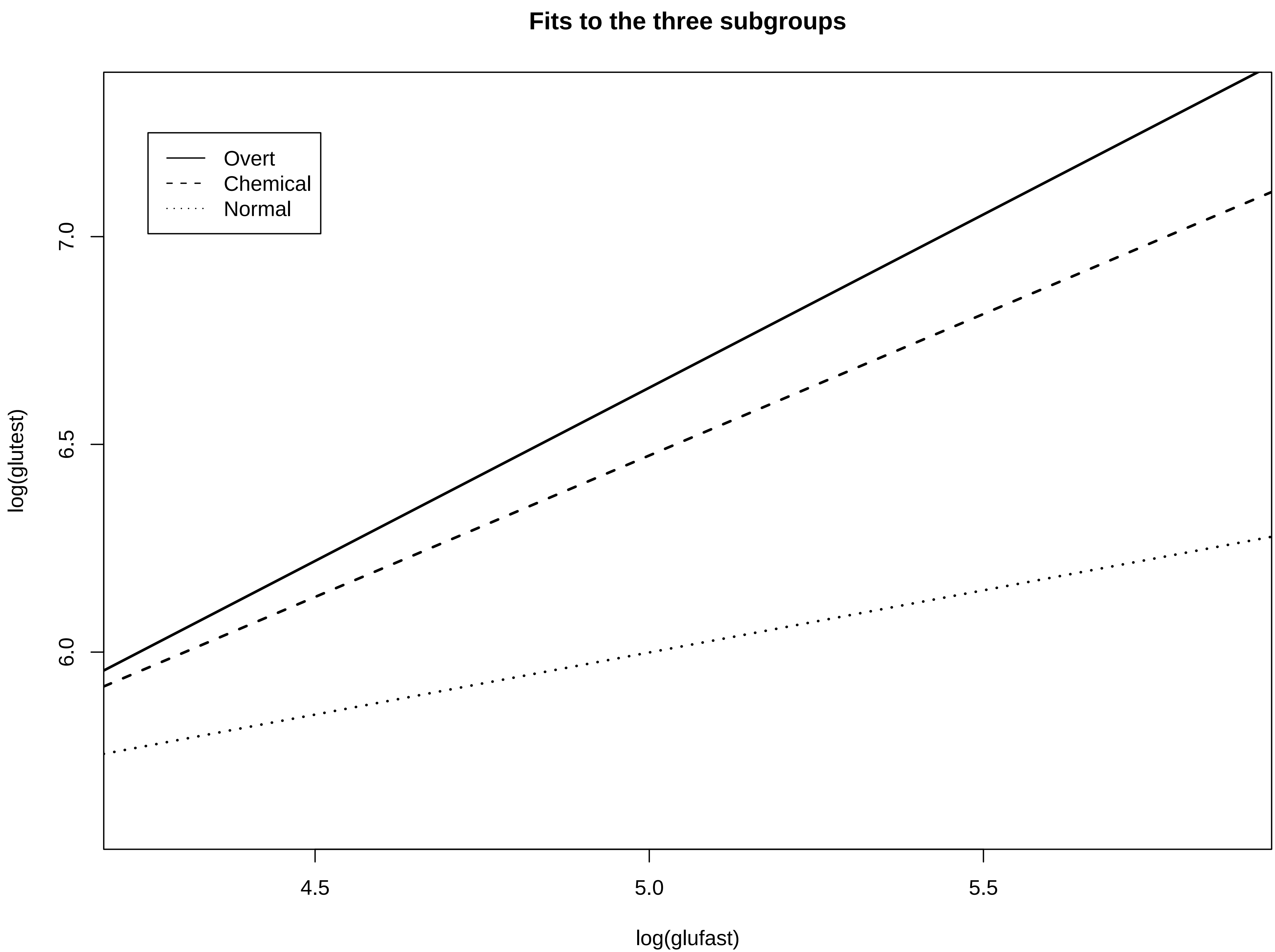
Group 1



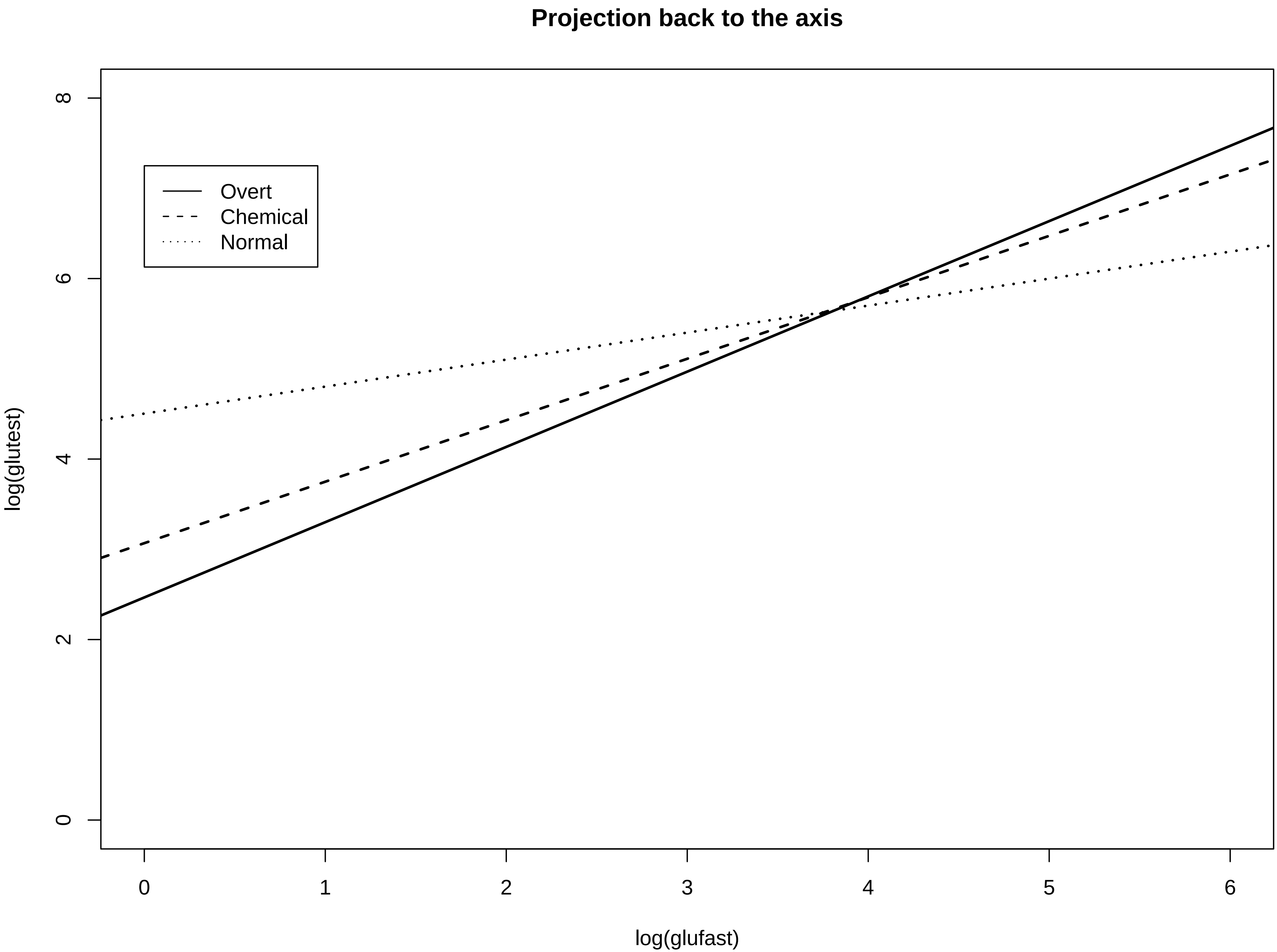

Group 2
log(glutest)
7.0
6.5
6.0
4.5
5.0
5.5
log(glufast)

Group 3





Fits to the three subgroups
Overt
Chemical
Normal
7.0
6.5
6.0
log(glutest)
4.5
5.0
5.5
log(glufast)


Projection back to the axis
Overt
Chemical
Normal
log(glutest)
log(glufast)
0
2
4
6
8
0
1
2
3
4
5
6

Factor Predictor Regression

We need to take some care when combining factor predictors and covariates in the regression model. Suppose that we have only two predictors

- A **covariate**, x_1
- A **factor predictor**, x_2, now taking L levels, with the levels being indexed by $l = 1, 2, \ldots, L$.

We want to build a model that takes into account both x_1 and x_2.

Example : Binary Factor $L = 2$

Suppose that factor predictor x_2 takes two levels, labelled 0 and 1, that identify two data subgroups. Five models can be considered, that correspond to different straight-line models

- **MODEL 0 : Same intercept**, **slope zero**, in the two subgroups
- **MODEL 1 : Different intercept**, **slope zero**, in the two subgroups
- **MODEL 2 : Same intercept**, **same non-zero slope**, in the two subgroups
- **MODEL 3 : Different intercept**, **same non-zero slope**, in the two subgroups
- **MODEL 4 : Different intercept**, **different non-zero slopes**, in the two subgroups

We can write out the models in terms of the usual slope and intercept parameters. The general model can be written

$$y = \begin{cases} \beta_{00} + \beta_{01} x_1 + \epsilon & \text{GROUP 0} \quad (l = 0) \\ \\ \beta_{10} + \beta_{11} x_1 + \epsilon & \text{GROUP 1} \quad (l = 1) \end{cases}$$

- **MODEL 0 :** $\beta_{00} = \beta_{10} = \beta_0, \; \beta_{01} = \beta_{11} = 0$
- **MODEL 1 :** $\beta_{00} \neq \beta_{10}, \; \beta_{01} = \beta_{11} = 0$
- **MODEL 2 :** $\beta_{00} = \beta_{10} = \beta_0, \; \beta_{01} = \beta_{11} = \beta_1 \neq 0$
- **MODEL 3 :** $\beta_{00} \neq \beta_{10}, \; \beta_{01} = \beta_{11} = \beta_1 \neq 0$
- **MODEL 4 :** $\beta_{00} \neq \beta_{10}, \; \beta_{01} \neq \beta_{11}$

The numbers of parameters, p, in each model are as follows:

$$\begin{array}{lcll}
\text{MODEL 0} & : & p = 1 & \beta_0 \\
\text{MODEL 1} & : & p = 2 & \beta_{00}, \beta_{10} \\
\text{MODEL 2} & : & p = 2 & \beta_0, \beta_1 \\
\text{MODEL 3} & : & p = 3 & \beta_{00}, \beta_{10}, \beta_1 \\
\text{MODEL 4} & : & p = 4 & \beta_{00}, \beta_{10}, \beta_{10}, \beta_{11}
\end{array}$$

SPSS Parameterization: The default parameterization used by SPSS is different from the one described above. SPSS takes a baseline group, and looks for **differences** in the parameters compared to the baseline group. The baseline group is taken to be the last listed subgroup for the factor predictor; in the binary example above, the baseline group would be Group 1.

The interaction model is therefore written

$$y = [\beta_0 + (1 - x_2)\delta_{00}] + [(\beta_1 + (1 - x_2)\delta_{01})x_1] + \epsilon$$

- δ_{00} is the **change in intercept** from Group 1 to Group 0
- δ_{01} is the **change in slope** from Group 1 to Group 0

Example: Diabetes Data Set

The data in the data set **DIABETES.SAV** contain information on 68 diabetes patients falling into two clinically different categories (overt and chemical diabetics) and 76 normal controls. Measurements of plasma glucose in blood samples when fasting and in a dietary test are recorded.

The objective is to predict the the test glucose levels from the fasting glucose levels in the three subgroups, and to find out if there is any significant difference between the subgroups.

In this analysis, there is a single response variable, one covariate and one factor predictor:

- y : **glutest**, the test glucose level
- x_1 : covariate **glufast**, the fasting glucose level
- x_2 : factor predictor **group**, the diabetes group
  - GROUP 1: Overt Diabetic
  - GROUP 2: Chemical Diabetic
  - GROUP 3: Normal Patients

Tests of Between-Subjects Effects

Dependent Variable: Log(GluTest)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
~~Corrected Model~~	~~27.187[a]~~	~~5~~	~~5.437~~	~~569.463~~	~~.000~~
~~Intercept~~	~~.973~~	~~1~~	~~.973~~	~~101.906~~	~~.000~~
group	.104	2	.052	5.447	.005
loggluf	.675	1	.675	70.702	.000
group * loggluf	.155	2	.077	8.099	.000
Error	1.318	138	.010		
~~Total~~	~~5509.040~~	~~144~~			
Corrected Total	28.504	143			

a. R Squared = .954 (Adjusted R Squared = .952)

Parameter Estimates

Dependent Variable: Log(GluTest)

Parameter	B	Std. Error	t	Sig.	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
Intercept	$\boxed{4.504}$	.559	8.060	.000	3.399	5.608
[group=1]	$\boxed{-2.037}$	.619	-3.289	.001	-3.262	-.813
[group=2]	-1.436	.958	-1.499	.136	-3.330	.458
[group=3]	0[a]	.	.	.	.	.
loggluf	$\boxed{.299}$	.124	2.414	.017	.054	.544
[group=1] * loggluf	$\boxed{.535}$	.134	4.001	.000	.270	.799
[group=2] * loggluf	.382	.210	1.820	.071	-.033	.797
[group=3] * loggluf	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

The first ANOVA table demonstrates that there **is** a significant interaction between the covariate and the factor predictor ($F = 8.099$, p-value < 0.001). This means that there is a **significantly different slope** in **at least two of the three** subgroups.

The second table gives the slope and intercept parameters in the three groups. The SPSS parameterization is not directly in terms of the slopes and intercepts, but looks at **differences** from baseline subgroup, Group 3. For example, the Group 1 intercept and slope are, respectively,

$$\text{INTERCEPT} : 4.504+(-2.037) = 2.467 \qquad \text{SLOPE} : 0.299+0.535 = 0.834.$$

Diabetes Data Set

Diabetes.sav [DataSet1] - SPSS Data Editor

File Edit View Data Transform Analyze Graphs Utilities Window Help

33 :

	id	relwt	glufast	glutest	instest	sspg	group
1	1	.81	80	356	124	55	Normal
2	2	.95	97	289	117	76	Normal
3	3	.94	105	319	143	105	Normal
4	4	1.04	90	356	199	108	Normal
5	5	1.00	90	323	240	143	Normal
6	6	.76	86	381	157	165	Normal
7	7	.91	100	350	221	119	Normal
8	8	1.10	85	301	186	105	Normal
9	9	.99	97	379	142	98	Normal
10	10	.78	97	296	131	94	Normal
11	11	.90	91	353	221	53	Normal
12	12	.73	87	306	178	66	Normal
13	13	.96	78	290	136	142	Normal
14	14	.84	90	371	200	93	Normal
15	15	.74	86	312	208	68	Normal
16	16	.98	80	393	202	102	Normal
17	17	1.10	90	364	152	76	Normal
18	18	.85	99	359	185	37	Normal
19	19	.83	85	296	116	60	Normal
20	20	.93	90	345	123	50	Normal
21	21	.95	90	378	136	47	Normal
22	22	.74	88	304	134	50	Normal
23	23	.95	95	347	184	91	Normal
24	24	.97	90	327	192	124	Normal
25	25	.72	92	386	279	74	Normal
26	26	1.11	74	365	228	235	Normal
27	27	1.20	98	365	145	158	Normal
28	28	1.13	100	352	172	140	Normal
29	29	1.00	86	325	179	145	Normal
30	30	.78	98	321	222	99	Normal
31	31	1.00	70	360	134	90	Normal
32	32	1.00	99	336	143	105	Normal
33	33	.71	75	352	169	32	Normal
34	34	.76	90	353	263	165	Normal
35	35	.89	85	373	174	78	Normal
36	36	.88	99	376	134	80	Normal
37	37	1.17	100	367	182	54	Normal
38	38	.85	78	335	241	175	Normal
39	39	.97	106	396	128	80	Normal
40	40	1.00	98	277	222	186	Normal
41	41	1.00	102	378	165	117	Normal
42	42	.89	90	360	282	160	Normal
43	43	.98	94	291	94	71	Normal
44	44	.78	80	269	121	29	Normal
45	45	.74	93	318	73	42	Normal
46	46	.91	86	328	106	56	Normal
47	47	.95	85	334	118	122	Normal
48	48	.95	96	356	112	73	Normal
49	49	1.03	88	291	157	122	Normal
50	50	.87	87	360	292	128	Normal
51	51	.87	94	313	200	233	Normal
52	52	1.17	93	306	220	132	Normal
53	53	.83	86	319	144	138	Normal
54	54	.82	86	349	109	83	Normal
55	55	.86	96	332	151	109	Normal

Data View / Variable View

SPSS Processor is ready

Create two new variables **loggluf** and **logglut** for the logged variables

*Diabetes.sav [DataSet1] - SPSS Data Editor

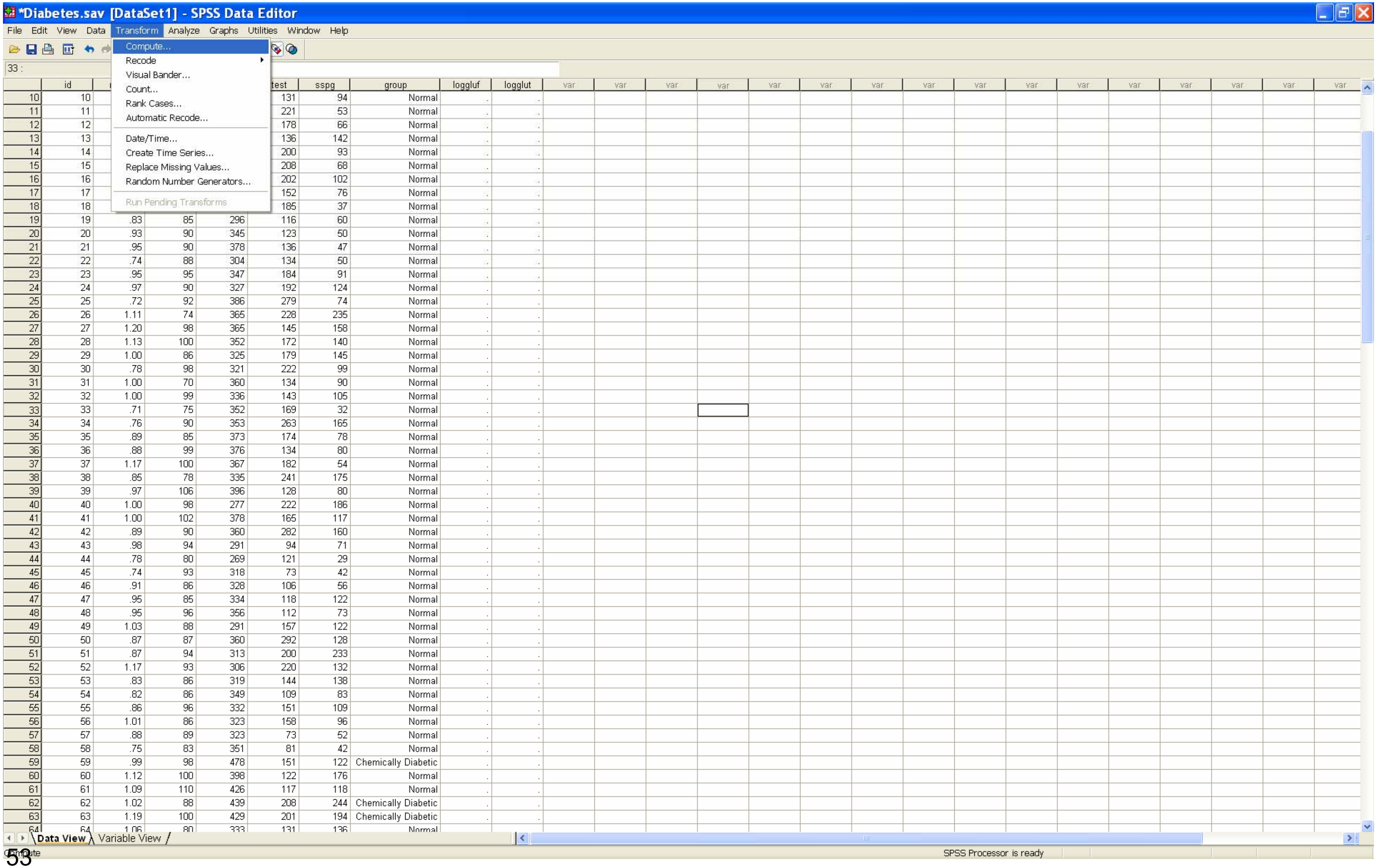
File Edit View Data Transform Analyze Graphs Utilities Window Help

	Name	Type	Width	Decimals	Label	Values	Missing	Columns	Align	Measure
1	id	Numeric	11	0	Patient ID	None	None	8	Right	Scale
2	relwt	Numeric	11	2	Relative Weight	None	None	8	Right	Scale
3	glufast	Numeric	11	0	Fasting Plasma Glucose	None	None	8	Right	Scale
4	glutest	Numeric	11	0	Test Plasma Glucose	None	None	8	Right	Scale
5	instest	Numeric	11	0	Plasma Insulin during Test	None	None	8	Right	Scale
6	sspg	Numeric	11	0	Steady State Plasma Glucose	None	None	8	Right	Scale
7	group	Numeric	11	0	Clinical Group	{1, Overt Diabe	None	14	Right	Ordinal
8	loggluf	Numeric	8	2	Log(GluFast)	None	None	8	Right	Scale
9	logglut	Numeric	8	2	Log(GluTest)	None	None	8	Right	Scale

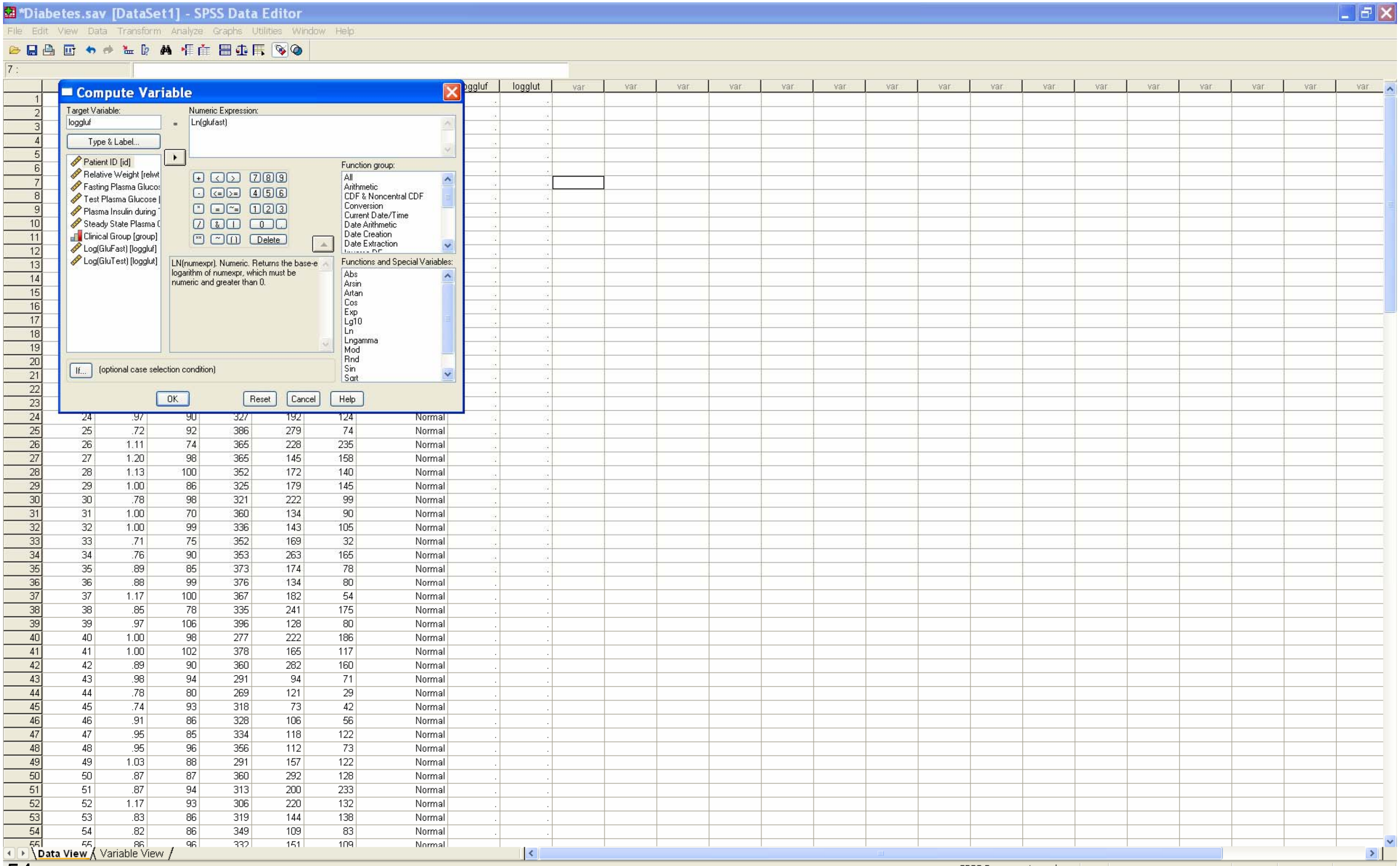
Data View **Variable View**

SPSS Processor is ready

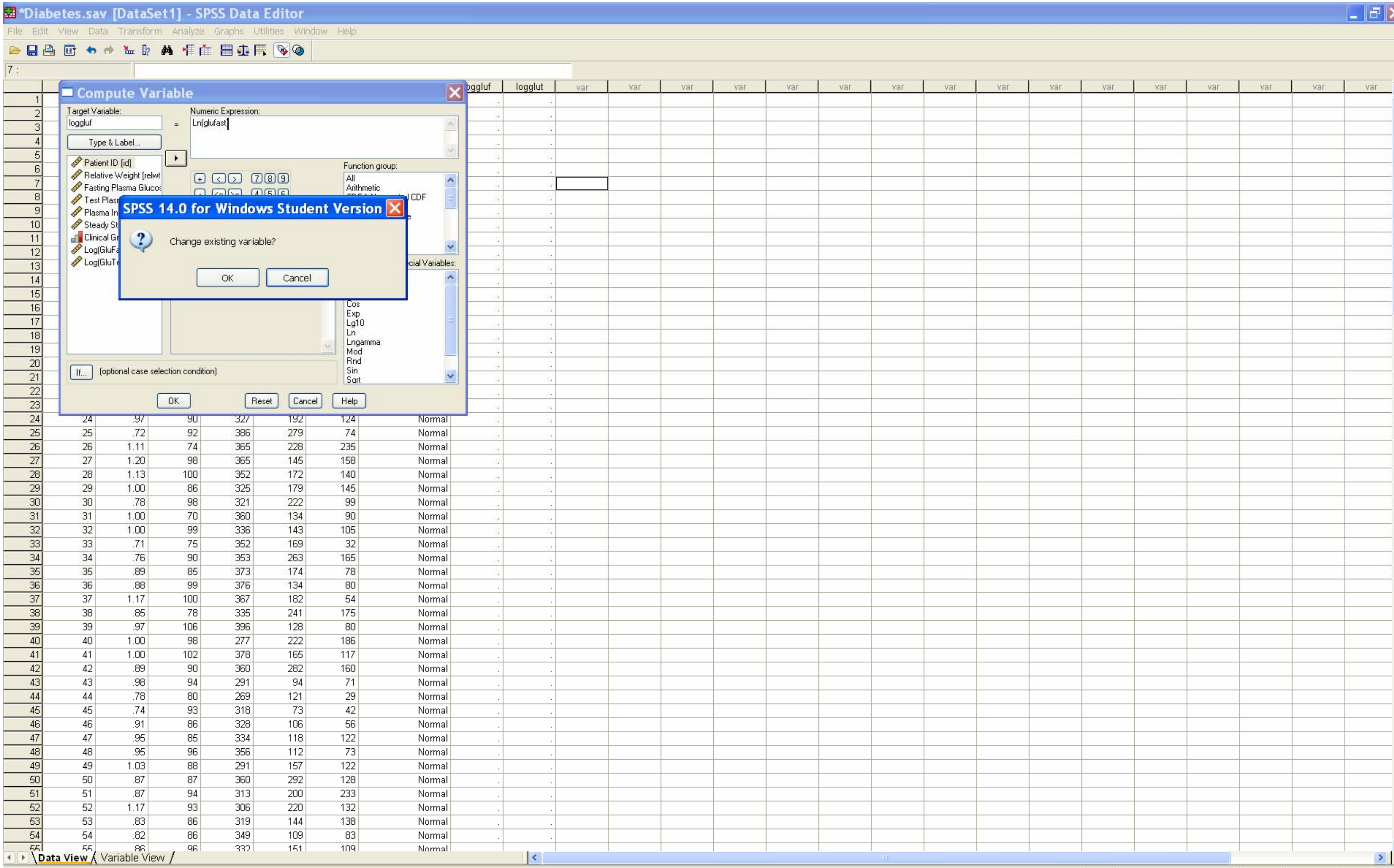
Use the *Compute* pulldown menu to compute the log transform



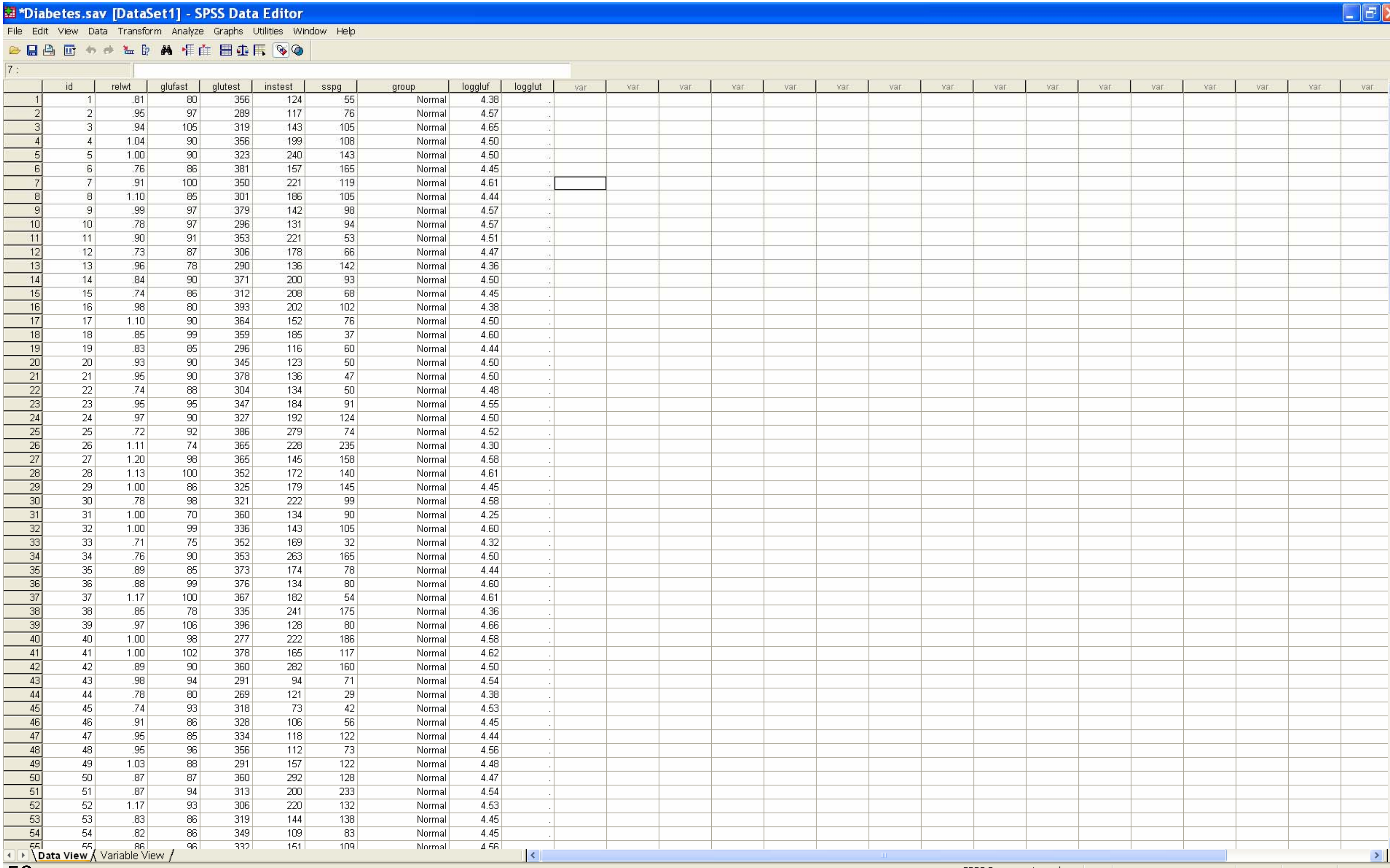
In *Target Variable* insert **loggluf**, and in *Numeric Expression* type **Ln(glufast),** and click OK



Click OK when the confirmation screen appears



The log transformed variable **loggluf** is computed.



*Diabetes.sav [DataSet1] - SPSS Data Editor

File Edit View Data Transform Analyze Graphs Utilities Window Help

7 :

	id	relwt	glufast	glutest	instest	sspg	group	loggluf	logglut
1	1	.81	80	356	124	55	Normal	4.38	.
2	2	.95	97	289	117	76	Normal	4.57	.
3	3	.94	105	319	143	105	Normal	4.65	.
4	4	1.04	90	356	199	108	Normal	4.50	.
5	5	1.00	90	323	240	143	Normal	4.50	.
6	6	.76	86	381	157	165	Normal	4.45	.
7	7	.91	100	350	221	119	Normal	4.61	.
8	8	1.10	85	301	186	105	Normal	4.44	.
9	9	.99	97	379	142	98	Normal	4.57	.
10	10	.78	97	296	131	94	Normal	4.57	.
11	11	.90	91	353	221	53	Normal	4.51	.
12	12	.73	87	306	178	66	Normal	4.47	.
13	13	.96	78	290	136	142	Normal	4.36	.
14	14	.84	90	371	200	93	Normal	4.50	.
15	15	.74	86	312	208	68	Normal	4.45	.
16	16	.98	80	393	202	102	Normal	4.38	.
17	17	1.10	90	364	152	76	Normal	4.50	.
18	18	.85	99	359	185	37	Normal	4.60	.
19	19	.83	85	296	116	60	Normal	4.44	.
20	20	.93	90	345	123	50	Normal	4.50	.
21	21	.95	90	378	136	47	Normal	4.50	.
22	22	.74	88	304	134	50	Normal	4.48	.
23	23	.95	95	347	184	91	Normal	4.55	.
24	24	.97	90	327	192	124	Normal	4.50	.
25	25	.72	92	386	279	74	Normal	4.52	.
26	26	1.11	74	365	228	235	Normal	4.30	.
27	27	1.20	98	365	145	158	Normal	4.58	.
28	28	1.13	100	352	172	140	Normal	4.61	.
29	29	1.00	86	325	179	145	Normal	4.45	.
30	30	.78	98	321	222	99	Normal	4.58	.
31	31	1.00	70	360	134	90	Normal	4.25	.
32	32	1.00	99	336	143	105	Normal	4.60	.
33	33	.71	75	352	169	32	Normal	4.32	.
34	34	.76	90	353	263	165	Normal	4.50	.
35	35	.89	85	373	174	78	Normal	4.44	.
36	36	.88	99	376	134	80	Normal	4.60	.
37	37	1.17	100	367	182	54	Normal	4.61	.
38	38	.85	78	335	241	175	Normal	4.36	.
39	39	.97	106	396	128	80	Normal	4.66	.
40	40	1.00	98	277	222	186	Normal	4.58	.
41	41	1.00	102	378	165	117	Normal	4.62	.
42	42	.89	90	360	282	160	Normal	4.50	.
43	43	.98	94	291	94	71	Normal	4.54	.
44	44	.78	80	269	121	29	Normal	4.38	.
45	45	.74	93	318	73	42	Normal	4.53	.
46	46	.91	86	328	106	56	Normal	4.45	.
47	47	.95	85	334	118	122	Normal	4.44	.
48	48	.95	96	356	112	73	Normal	4.56	.
49	49	1.03	88	291	157	122	Normal	4.48	.
50	50	.87	87	360	292	128	Normal	4.47	.
51	51	.87	94	313	200	233	Normal	4.54	.
52	52	1.17	93	306	220	132	Normal	4.53	.
53	53	.83	86	319	144	138	Normal	4.45	.
54	54	.82	86	349	109	83	Normal	4.45	.
55	55	.86	96	332	151	109	Normal	4.56	

Data View / Variable View

SPSS Processor is ready

The same procedure computes the log transformed variable **logglut**; we log transform the glutest variable using the *Compute* pulldown

*Diabetes.sav [DataSet1] - SPSS Data Editor

File Edit View Data Transform Analyze Graphs Utilities Window Help

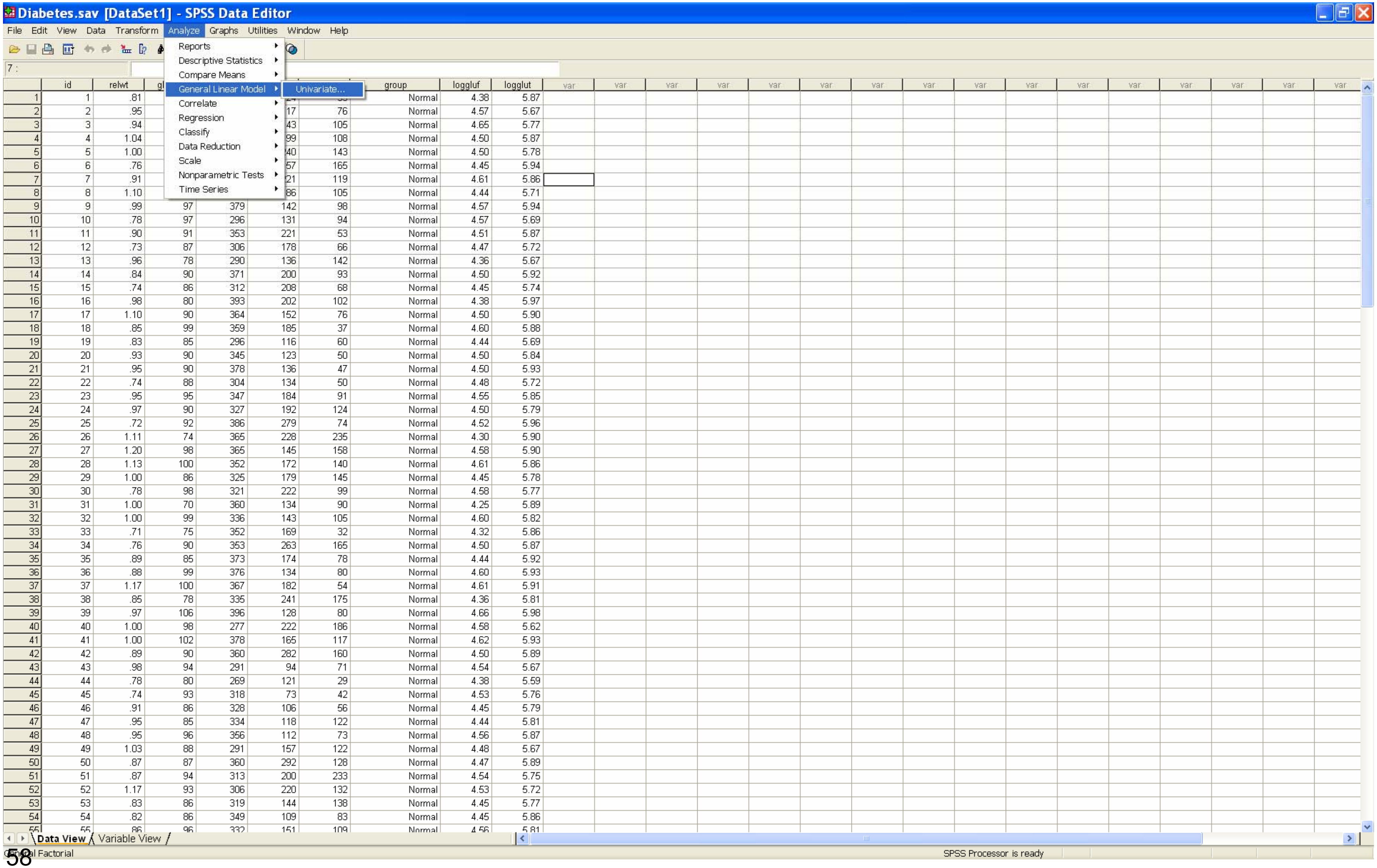
7 :

	id	relwt	glufast	glutest	instest	sspg	group	loggluf	logglut
1	1	.81	80	356	124	55	Normal	4.38	5.87
2	2	.95	97	289	117	76	Normal	4.57	5.67
3	3	.94	105	319	143	105	Normal	4.65	5.77
4	4	1.04	90	356	199	108	Normal	4.50	5.87
5	5	1.00	90	323	240	143	Normal	4.50	5.78
6	6	.76	86	381	157	165	Normal	4.45	5.94
7	7	.91	100	350	221	119	Normal	4.61	5.86
8	8	1.10	85	301	186	105	Normal	4.44	5.71
9	9	.99	97	379	142	98	Normal	4.57	5.94
10	10	.78	97	296	131	94	Normal	4.57	5.69
11	11	.90	91	353	221	53	Normal	4.51	5.87
12	12	.73	87	306	178	66	Normal	4.47	5.72
13	13	.96	78	290	136	142	Normal	4.36	5.67
14	14	.84	90	371	200	93	Normal	4.50	5.92
15	15	.74	86	312	208	68	Normal	4.45	5.74
16	16	.98	80	393	202	102	Normal	4.38	5.97
17	17	1.10	90	364	152	76	Normal	4.50	5.90
18	18	.85	99	359	185	37	Normal	4.60	5.88
19	19	.83	85	296	116	60	Normal	4.44	5.69
20	20	.93	90	345	123	50	Normal	4.50	5.84
21	21	.95	90	378	136	47	Normal	4.50	5.93
22	22	.74	88	304	134	50	Normal	4.48	5.72
23	23	.95	95	347	184	91	Normal	4.55	5.85
24	24	.97	90	327	192	124	Normal	4.50	5.79
25	25	.72	92	386	279	74	Normal	4.52	5.96
26	26	1.11	74	365	228	235	Normal	4.30	5.90
27	27	1.20	98	365	145	158	Normal	4.58	5.90
28	28	1.13	100	352	172	140	Normal	4.61	5.86
29	29	1.00	86	325	179	145	Normal	4.45	5.78
30	30	.78	98	321	222	99	Normal	4.58	5.77
31	31	1.00	70	360	134	90	Normal	4.25	5.89
32	32	1.00	99	336	143	105	Normal	4.60	5.82
33	33	.71	75	352	169	32	Normal	4.32	5.86
34	34	.76	90	353	263	165	Normal	4.50	5.87
35	35	.89	85	373	174	78	Normal	4.44	5.92
36	36	.88	99	376	134	80	Normal	4.60	5.93
37	37	1.17	100	367	182	54	Normal	4.61	5.91
38	38	.85	78	335	241	175	Normal	4.36	5.81
39	39	.97	106	396	128	80	Normal	4.66	5.98
40	40	1.00	98	277	222	186	Normal	4.58	5.62
41	41	1.00	102	378	165	117	Normal	4.62	5.93
42	42	.89	90	360	282	160	Normal	4.50	5.89
43	43	.98	94	291	94	71	Normal	4.54	5.67
44	44	.78	80	269	121	29	Normal	4.38	5.59
45	45	.74	93	318	73	42	Normal	4.53	5.76
46	46	.91	86	328	106	56	Normal	4.45	5.79
47	47	.95	85	334	118	122	Normal	4.44	5.81
48	48	.95	96	356	112	73	Normal	4.56	5.87
49	49	1.03	88	291	157	122	Normal	4.48	5.67
50	50	.87	87	360	292	128	Normal	4.47	5.89
51	51	.87	94	313	200	233	Normal	4.54	5.75
52	52	1.17	93	306	220	132	Normal	4.53	5.72
53	53	.83	86	319	144	138	Normal	4.45	5.77
54	54	.82	86	349	109	83	Normal	4.45	5.86
55	55	.86	96	332	151	109	Normal	4.56	5.81

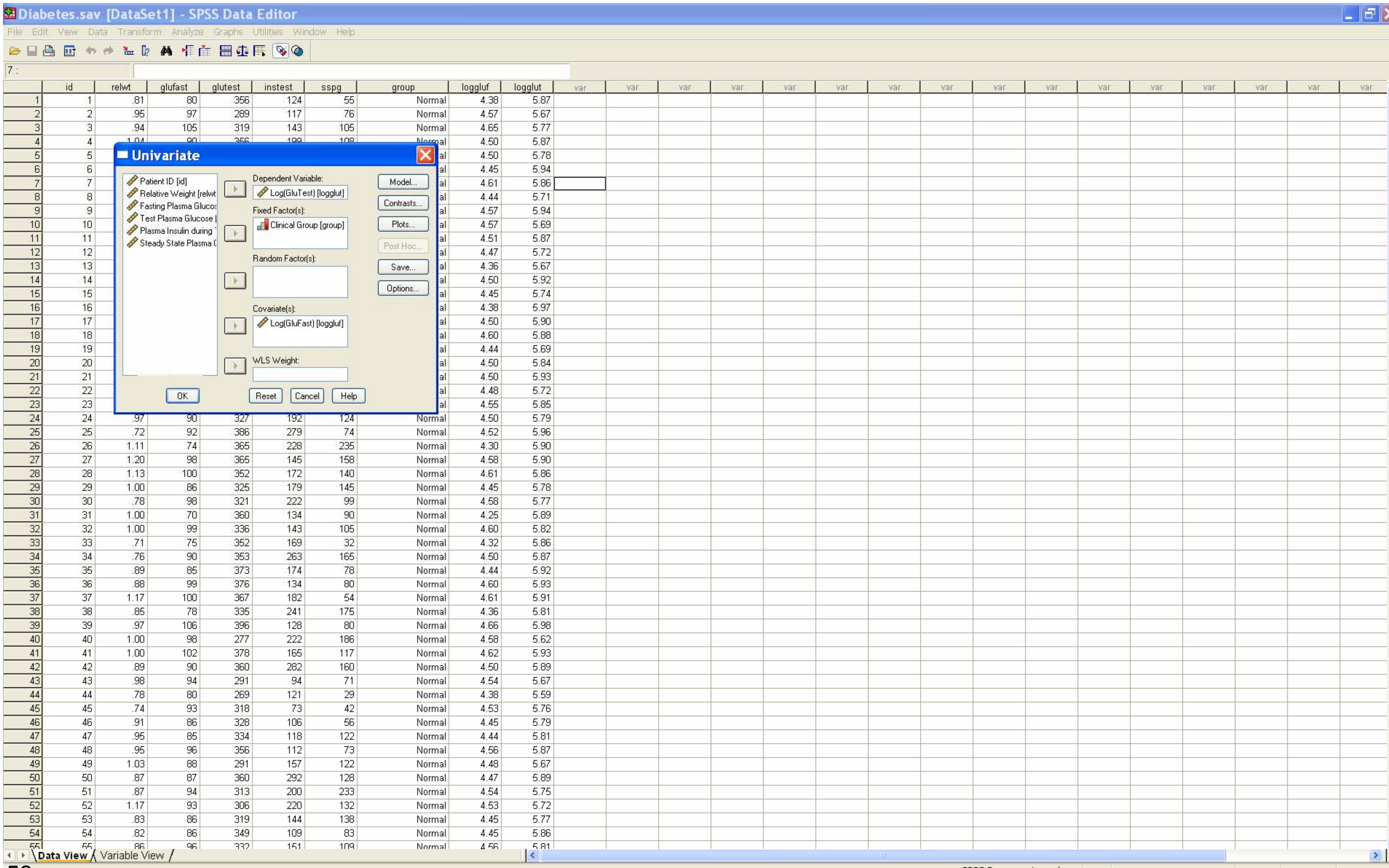
Data View / Variable View

SPSS Processor is ready

We now perform the linear regression using the *General Linear Model* pulldown. [8]

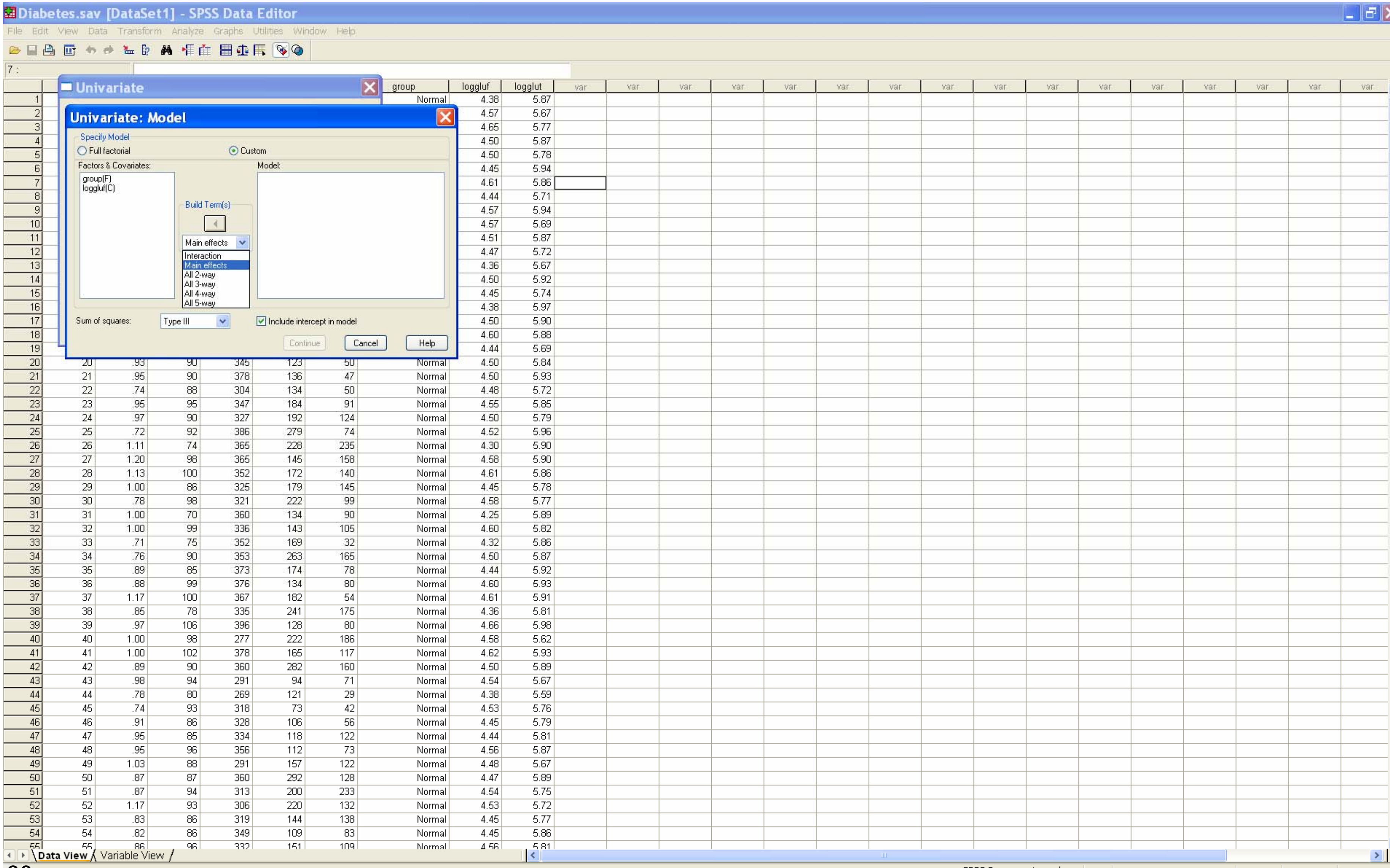


Select the *Dependent Variable* (**logglut**), the *Fixed Factor* (**grou**p) and the *Covariate* (**loggluf**).

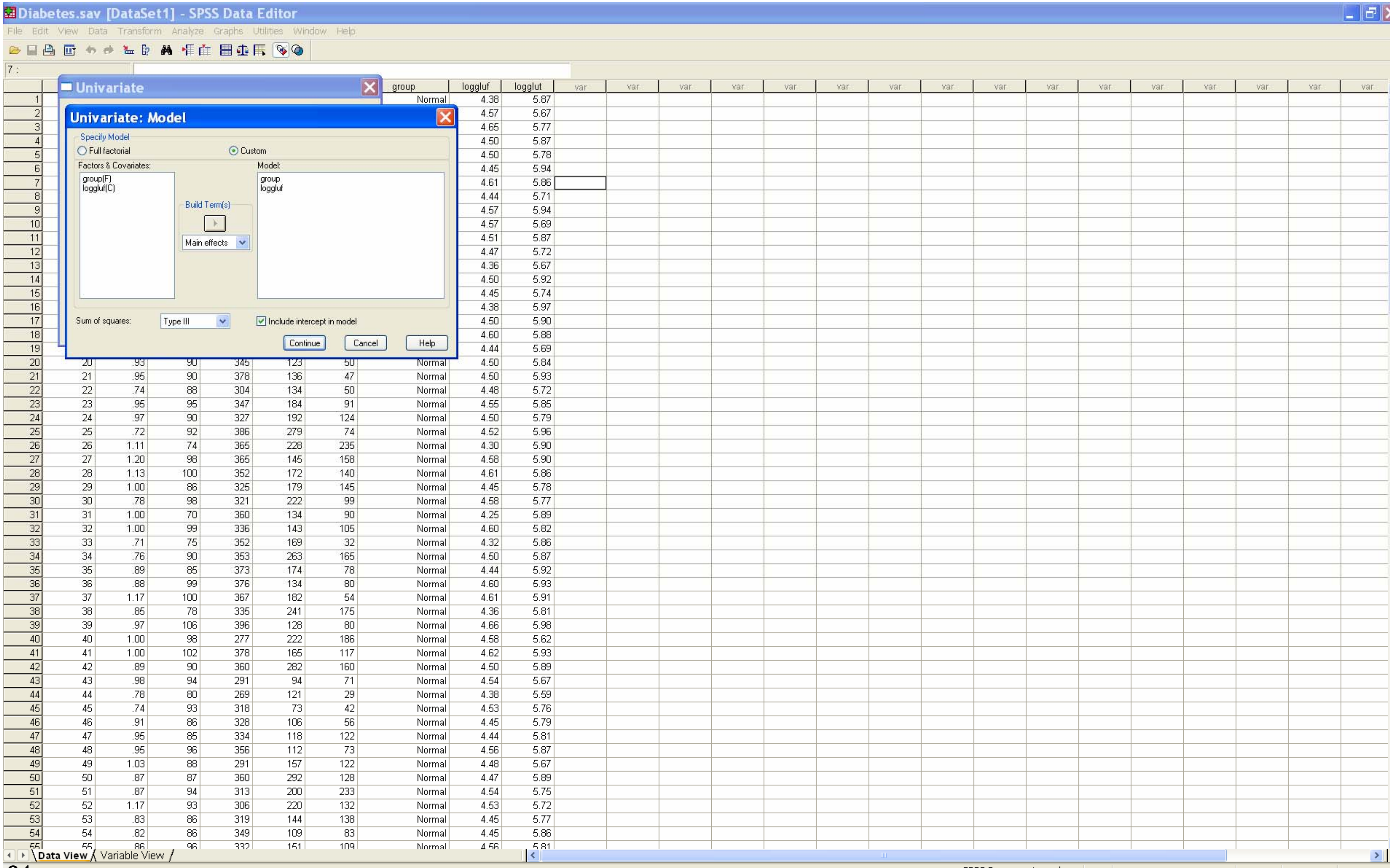


To specify the model, click the *Model* button to get the *Model Dialog*.

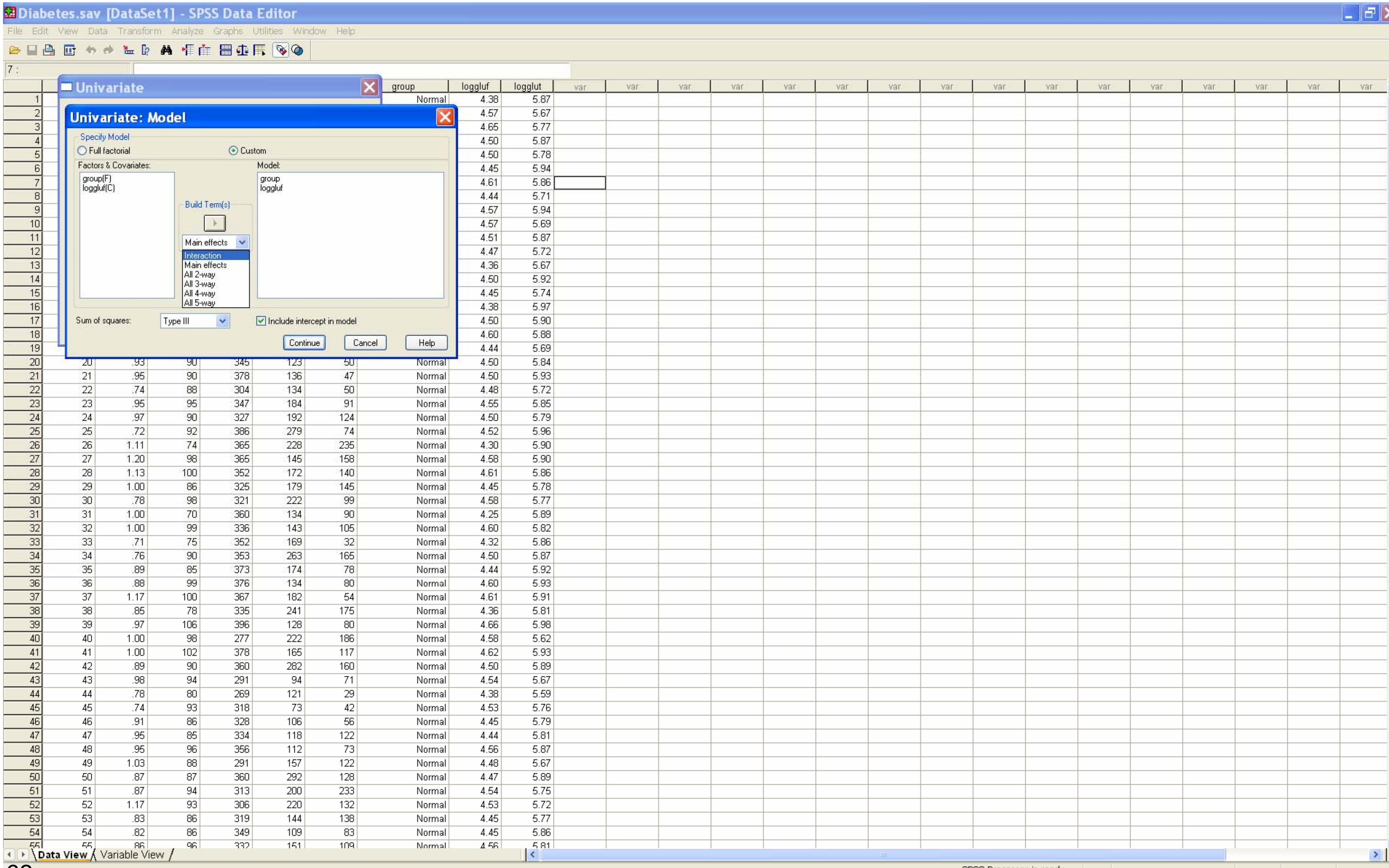
We wish to specify a *Custom* main effects plus interaction model.



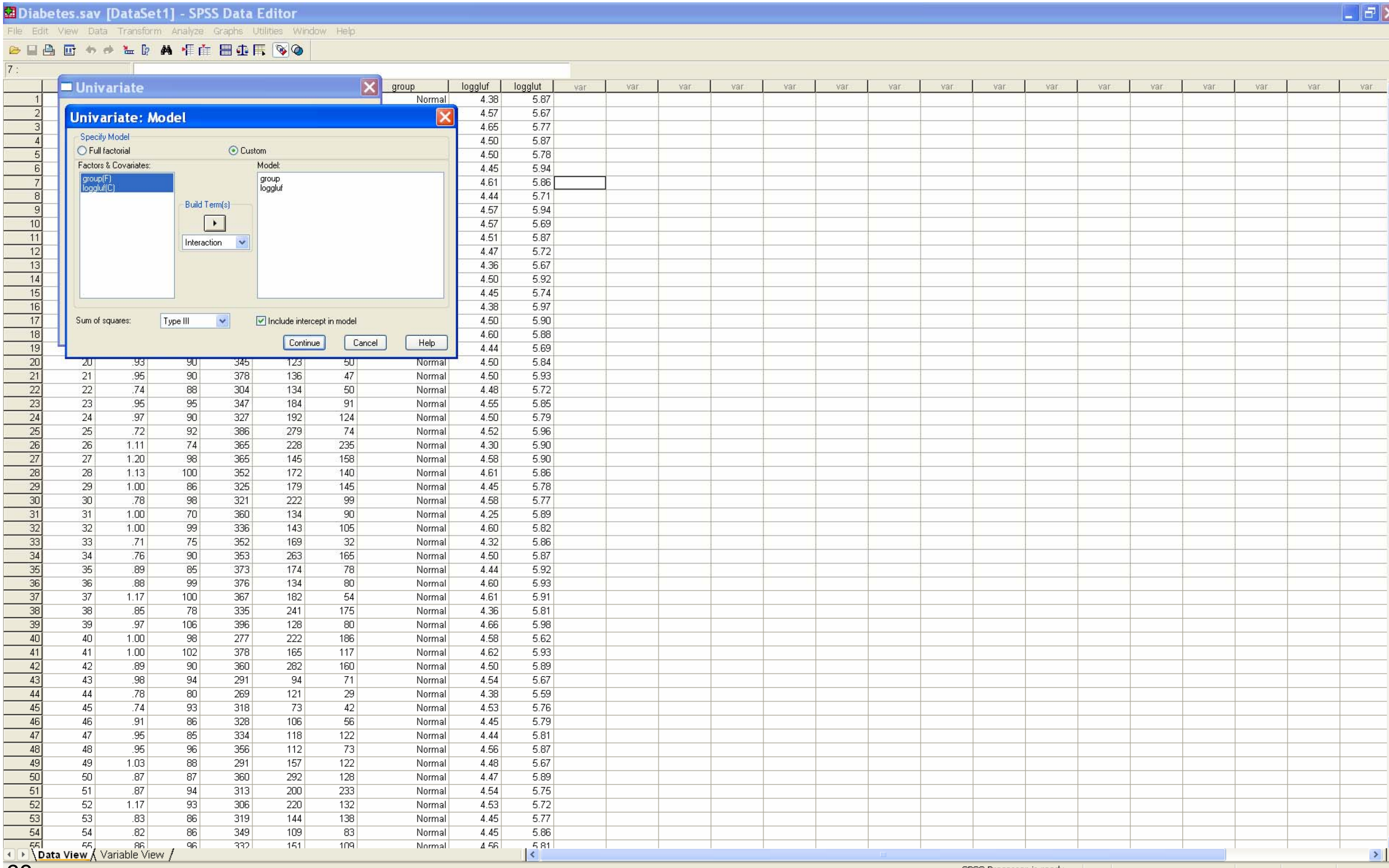
We select the factor and covariate as main effects.



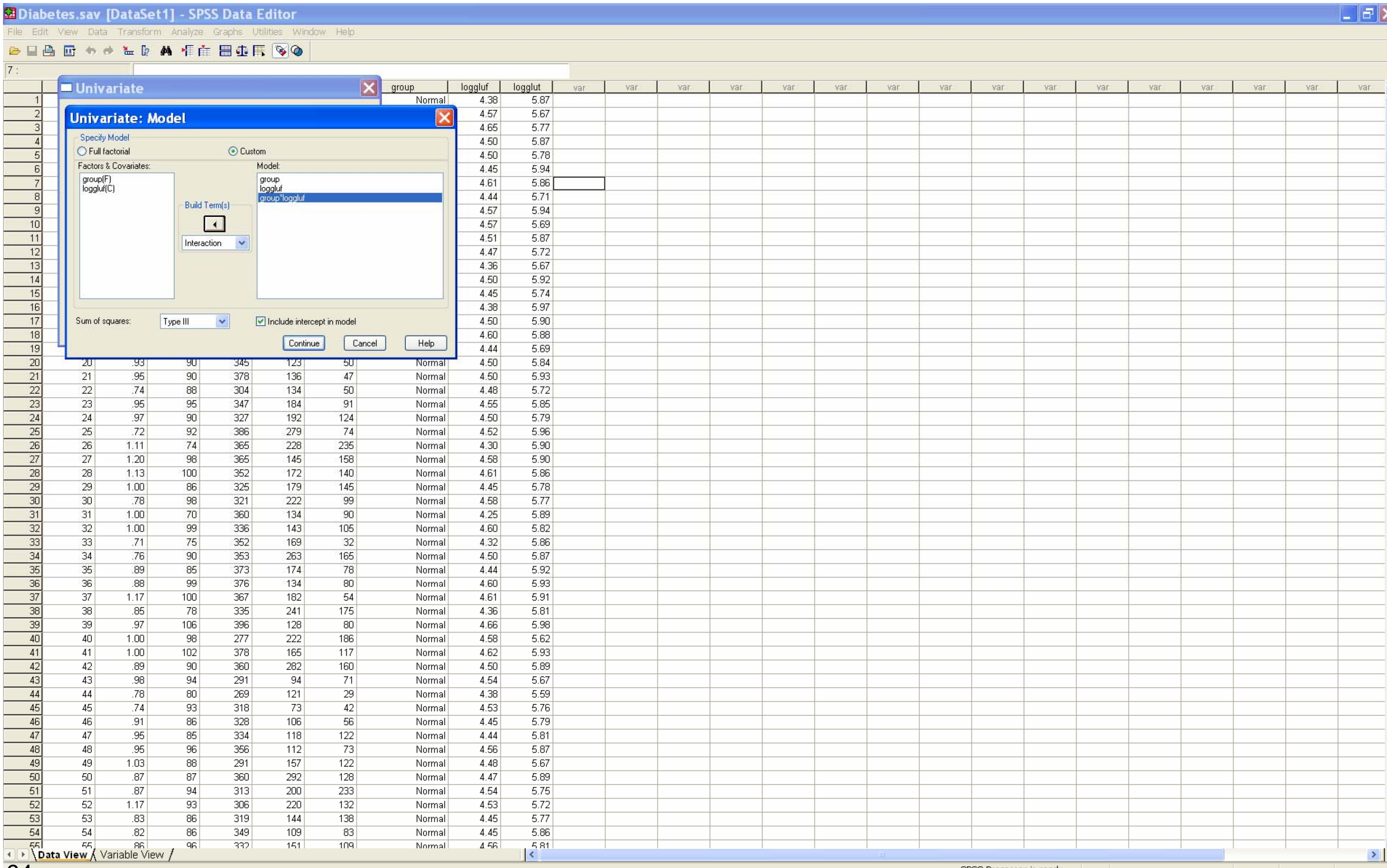
Select *Interaction* from the *Build Terms* pulldown.



Highlight the two variables, and click the *Build Terms* arrow.

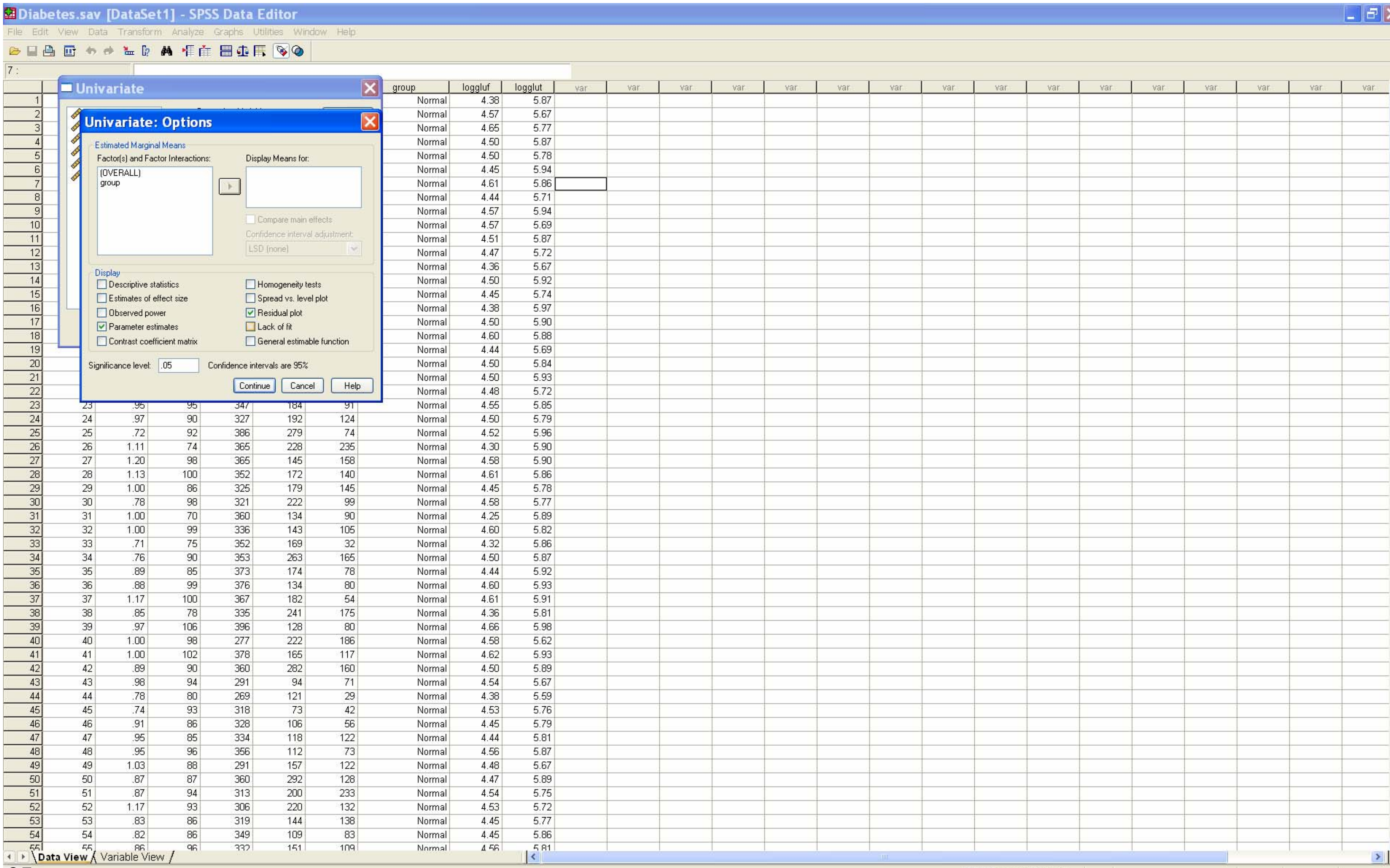


The *Custom* model has been built. Click *Continue*.

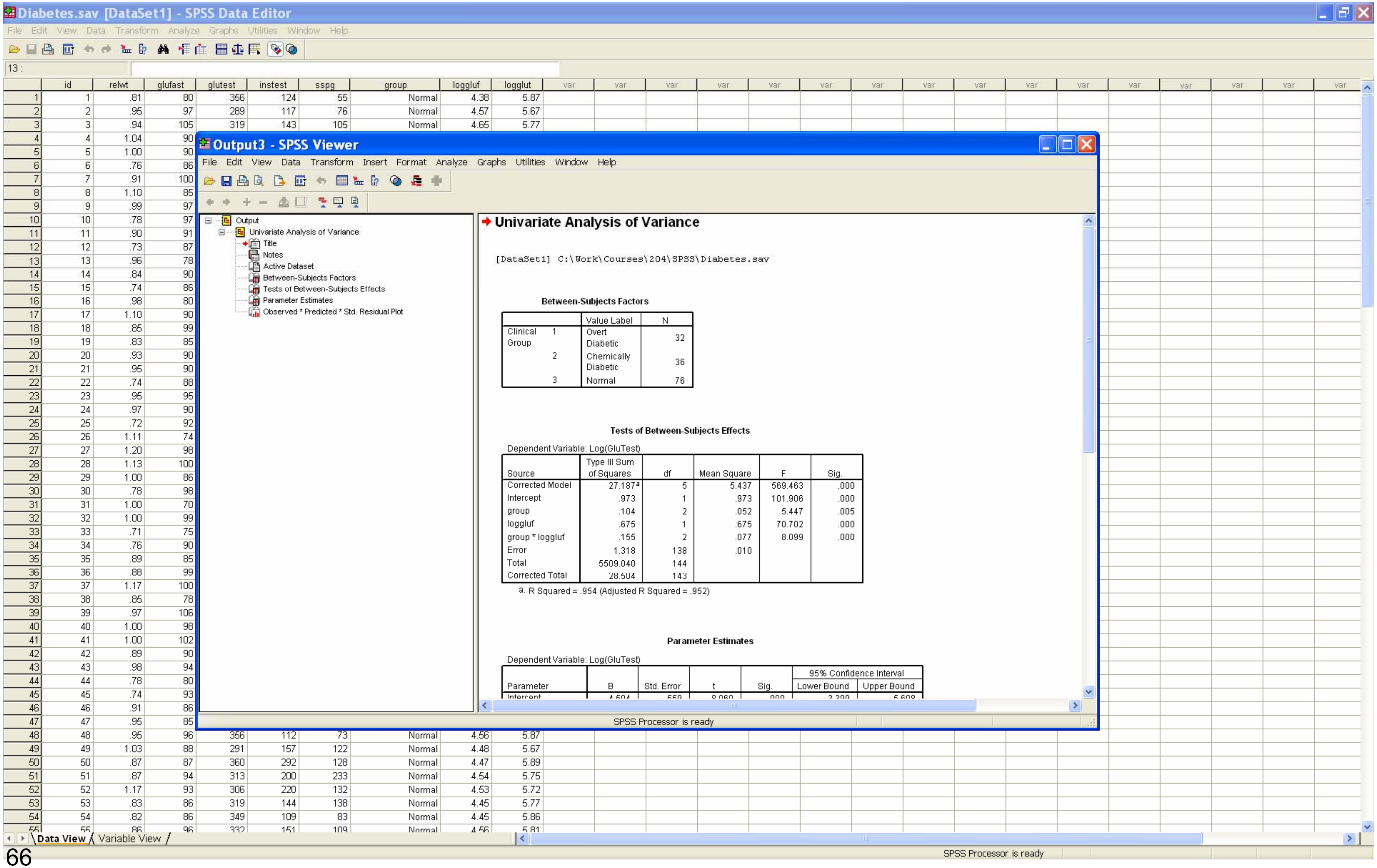


The model is now built. On the *General Linear Model* dialog, click *Options.*

Select *Parameter Estimates* and *Residual plot*



The output is generated.



The ANOVA table describes the results. It can be read in the same way as an ordinary ANOVA table. We note significant main effects and interaction.

Tests of Between-Subjects Effects

Dependent Variable: Log(GluTest)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
~~Corrected Model~~	~~27.187~~[a]	~~5~~	~~5.437~~	~~569.463~~	~~.000~~
~~Intercept~~	~~.973~~	~~1~~	~~.973~~	~~101.906~~	~~.000~~
group	.104	2	.052	5.447	.005
loggluf	.675	1	.675	70.702	.000
group * loggluf	.155	2	.077	8.099	.000
Error	1.318	138	.010		
~~Total~~	~~5509.040~~	~~144~~			
Corrected Total	28.504	143			

a. R Squared = .954 (Adjusted R Squared = .952)

The high R squared value means that the model fit is quite good overall.

The parameter estimates/standard errors are also computed.

The SPSS parameterization of the model is used.

Parameter Estimates

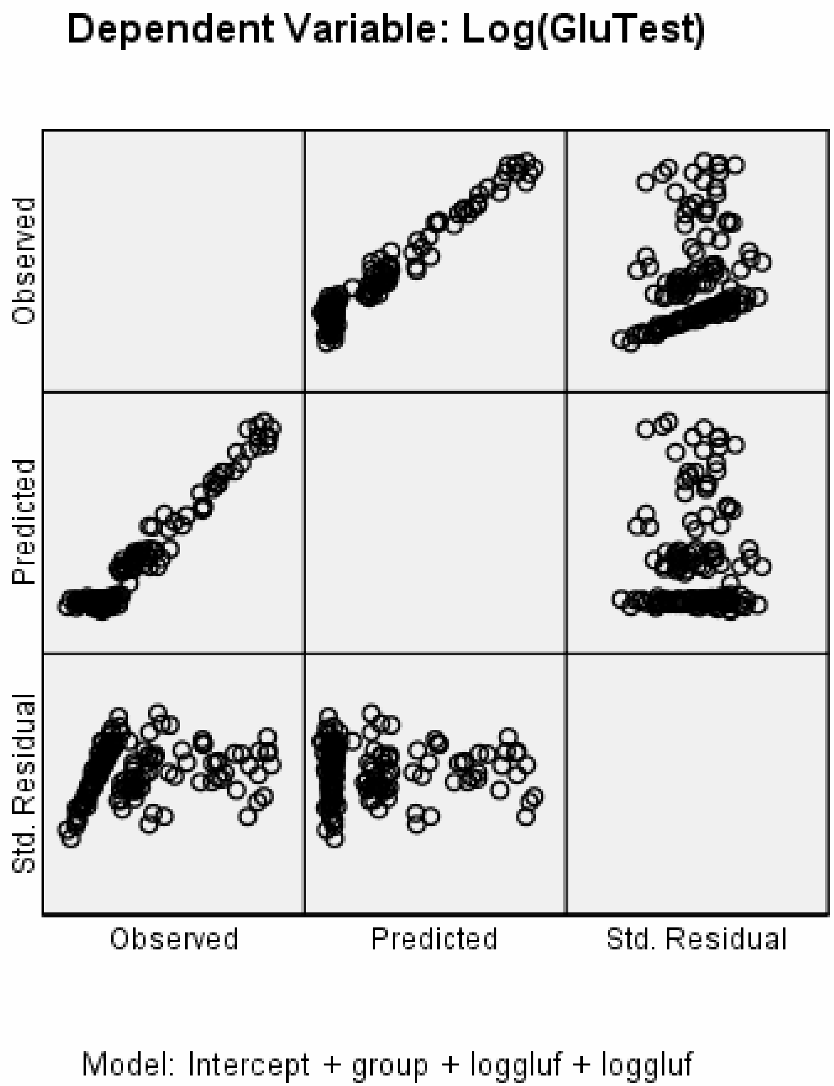
Dependent Variable: Log(GluTest)

Parameter	B	Std. Error	t	Sig.	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
Intercept	4.504	.559	8.060	.000	3.399	5.608
[group=1]	-2.037	.619	-3.289	.001	-3.262	-.813
[group=2]	-1.436	.958	-1.499	.136	-3.330	.458
[group=3]	0[a]	.	.	.	.	.
loggluf	.299	.124	2.414	.017	.054	.544
[group=1] * loggluf	.535	.134	4.001	.000	.270	.799
[group=2] * loggluf	.382	.210	1.820	.071	-.033	.797
[group=3] * loggluf	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

In the main effects plus interaction model, there are six parameters; we are fitting three separate straight lines to the three subgroups, and there are two parameters in each straight line.

The residual plots demonstrate no significant pattern.



No real pattern in the residuals indicates a reasonable fit.

However, there is mild evidence that the residual variance is not constant.