

respiratory treatment, di\_base ,random individual glimmix

#### The GLIMMIX Procedure

Model Information	
Data Set	WORK.RESPIEL
Response Variable	respstatus
Response Distribution	Multinomial (ordered)
Link Function	Cumulative Probit
Variance Function	Default
Variance Matrix Blocked By	ide
Estimation Technique	Residual PL
Degrees of Freedom Method	Containment

Class Level Information		
Class	Levels	Values
ide	111	1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055
treatment	2	A P
baseline	5	0 1 2 3 4

Number of Observations Read	444
Number of Observations Used	444

Response Profile		
Ordered Value	respstatus	Total Frequency
1	4	152
2	3	96
3	2	116
4	1	40
5	0	40
The GLIMMIX procedure is modeling the probabilities of levels of respstatus having lower Ordered Values in the Response Profile table.		

Dimensions	
G-side Cov. Parameters	1
Columns in X	7
Columns in Z per Subject	1
Subjects (Blocks in V)	111
Max Obs per Subject	4

Optimization Information	
Optimization Technique	Dual Quasi-Newton
Parameters in Optimization	1
Lower Boundaries	1
Upper Boundaries	0
Fixed Effects	Profiled
Starting From	Data

Iteration History					
Iteration	Restarts	Subiterations	Objective Function	Change	Max Gradient

Iteration History					
Iteration	Restarts	Subiterations	Objective Function	Change	Max Gradient
0	0	7	3067.8281291	0.57876935	1.069E-7
1	0	5	3907.8659143	0.45072499	0.000102
2	0	4	4689.2293045	0.25252662	0.000064
3	0	4	5281.8694096	0.11321525	0.000029
4	0	3	5586.5531436	0.04127545	0.000592
5	0	2	5698.9088062	0.01325565	0.00018
6	0	2	5733.9987499	0.00400253	0.000029
7	0	2	5744.4007817	0.00118503	1.594E-7
8	0	1	5747.4523187	0.00034896	8.049E-6
9	0	1	5748.3472902	0.00010231	6.915E-7
10	0	1	5748.6097401	0.00003007	5.859E-8
11	0	1	5748.6868092	0.00000884	3.242E-8
12	0	1	5748.7094566	0.00000260	1.939E-8
13	0	1	5748.7161136	0.00000239	0.000068
14	0	1	5748.720018	0.00000118	2E-7
15	0	0	5748.7192159	0.00000002	3.935E-6
16	0	0	5748.7190945	0.00000000	4.535E-6

Convergence criterion (PCONV=1.11022E-8) satisfied.

Fit Statistics	
-2 Res Log Pseudo-Likelihood	5748.72

Covariance Parameter Estimates			
Cov Parm	Subject	Estimate	Standard Error

Covariance Parameter Estimates			
Cov Parm	Subject	Estimate	Standard Error
Intercept	ide	1.3367	0.2525

Solutions for Fixed Effects							
Effect	respstatus	treatment	Estimate	Standard Error	DF	t Value	Pr >  t
Intercept	4		-1.9490	0.2239	108	-8.70	<.0001
Intercept	3		-0.9230	0.2145	108	-4.30	<.0001
Intercept	2		0.4340	0.2133	108	2.03	0.0443
Intercept	1		1.2440	0.2245	108	5.54	<.0001
treatment		A	0.9874	0.2490	330	3.97	<.0001
treatment		P	0	.	.	.	.
di_base			1.4983	0.2528	330	5.93	<.0001

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
treatment	1	330	15.72	<.0001
di_base	1	330	35.12	<.0001

```

proc glimmix data=respiel;
title respiratory treatment, di_base ,random individual glimmix;
class ide treatment baseline;
model respstatus(descending)=treatment di_base /dist=multinomial
link=cprobit solution ;
nloptions maxiter=100;
random intercept/subject=ide;
run;

data respiel ;
    set respira.kochcorel;
    dichot=(respstatus=3 or respstatus=4);
    di_base=baseline=3 or baseline=4;
    if age<23 then cage=1;
    if 22<age<31 then cage=2;
    if 30<age<43 then cage=3;
    if age>42 then cage=4;
    if cage=1 then ca1=1;
    else ca1=0;
    if cage=2 then ca2=1;
    else ca2=0;
    if cage=3 then ca3=1;
    else ca3=0;
    centreat=center*treat;
    if respstatus=0 then resp0=1;
    else resp0=0;
    if respstatus=1 then resp1=1;
    else resp1=0;
    if respstatus=2 then resp2=1;
    else resp2=0;
    if respstatus=3 then resp3=1;
    else resp3=0;
    if respstatus=4 then resp4=1;
    else resp4=0;
    ide=(1000*center)+id;
    if treatment="A" then treat=1;
    else treat=3;
    centreat=center*treat;
run;

```