STAT 8320 Spring 2015 Assignment 5

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▶ **1. Solution.** (a).

$$\begin{aligned} f(\lambda|y_i) &= \frac{f(y_i|\lambda)f(\lambda)}{f(y_i} \\ &= \frac{\frac{\lambda^{y_i+a-1}}{\Gamma(a)b^a y_i!}e^{-\lambda(1+1/b)}}{f(y_i)} \\ &\propto \frac{\lambda^{y_i+a-1}}{\Gamma(a)b^a y_i!}e^{-\lambda(1+1/b)} \\ &\propto \lambda^{y_i+a-1}e^{-\lambda(1+1/b)} \end{aligned}$$

So $\lambda|y_i \sim \text{GAM}(y_i + a - 1, \frac{1}{1+1/b})$, and

$$f(\lambda|y_i) = \frac{\lambda^{y_i+a-1}}{\Gamma(y_i+a)\left(\frac{b}{1+b}\right)^{y_i+a}}e^{-\lambda(1+1/b)}$$

Thus,

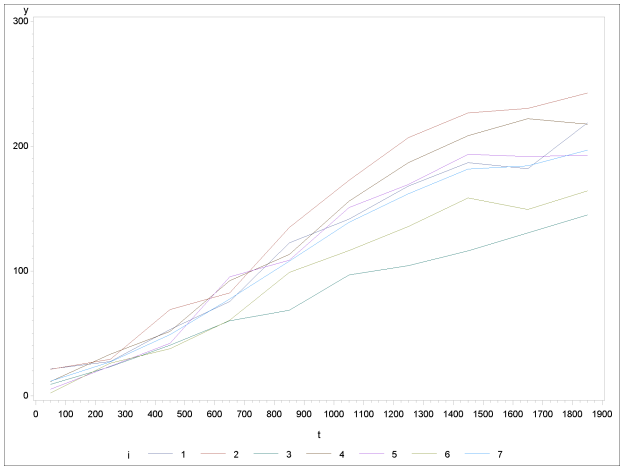
$$\begin{aligned} f(y_i) &= \int_0^\infty f(y_i|\lambda)f(\lambda)d\lambda = \frac{f(y_i|\lambda)f(\lambda)}{f(\lambda|y_i)} \\ &= \frac{\frac{\lambda^{y_i+a-1}}{\Gamma(a)b^a y_i!}e^{-\lambda(1+1/b)}}{\frac{\lambda^{y_i+a-1}}{\Gamma(y_i+a)\left(\frac{b}{1+b}\right)^{y_i+a}}e^{-\lambda(1+1/b)}} \\ &= \frac{\Gamma(y_i+a)}{\Gamma(a)y_i!}\left(\frac{1}{1+b}\right)^a\left(\frac{b}{1+b}\right)^{y_i} \\ &= \binom{a+y_i-1}{a-1}\left(\frac{b}{1+b}\right)^{y_i} \end{aligned}$$

We can conclude that $y_i \sim \text{NB}(\frac{1}{1+b}, a)$.

(b) From the theories in generalized linear model, we have already known that negative binomial distribution usually is used to fixed the over-dispersion problem of count data when Poisson distribution assumption or independence assumption are no longer valid. And we also know that in most time the over-dispersion may be caused by the dependence of data, like some repeated measurements in student attendance example. The GLMM essentially takes covariates between dependent data into model, so it also can model the over-dispersed count data. Or in other words, the derivation in part (a) just shows that negative binomial distribution can work well with over-dispersed count data.

▶ **2. Solution.** (a). Before we fit this nonlinear mixed model, we should firstly plot the profile of the data, trying to acquire some intuitive result from the plot. As the Figure 1 shows, different plants are label as 1 to 6, and number 7 represents the average profile. We can approximately know that the max value is between 150 and 250, and the inflection point should be between 500 and 1000. Without loss of generality, we set the initial value of (β_1, β_2) as (200, 850). Then we can solve the β_3 based on the data, and it is about 350. Next, by using PROC MEANS in SAS, we can get the standard deviations at different time points. Because $1 + e^{-(t_{ij}-\beta_2)/\beta_3}$ is relatively large, it is reasonable to assume that the variance of Y is mostly from σ^2. So we set the initial value of σ^2 as 40. As t_{ij} grows, the denominator becomes smaller and smaller, then the proportion of σ_u^2 in variance of Y becomes larger, and it seems that σ_u^2 should be between 400 to 1600, so we set the initial value of σ_u^2 as 900.

Figure 1: Profile of Plant Growth



Then we use the PROC NLIN and PROC NLMIXED to fit the nonlinear model and the nonlinear mixed model respectively. The results about parameters are listed as Figure 2 and Figure 3.

Figure 2: Parameters of Nonlinear Models

Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits		Skewness
beta1	199.7	10.3827	178.9	220.4	0.5330
beta2	797.8	55.1103	687.4	908.1	0.3725
beta3	300.7	42.8631	214.8	386.5	0.4782

Figure 3: Parameters of Nonlinear Mixed Models

Parameter Estimates

Parameter	Estimate	Standard Error	DF	t Value	Pr > |t|	Alpha
beta1	199.41	15.2372	5	13.09	<.0001	0.05
beta2	797.42	14.6250	5	54.52	<.0001	0.05
beta3	298.48	11.4146	5	26.15	<.0001	0.05
resvar	49.8315	9.5902	5	5.20	0.0035	0.05
varu	1346.95	784.96	5	1.72	0.1468	0.05

Parameter Estimates

Parameter	Lower	Upper	Gradient
beta1	160.24	238.58	4.83E-7
beta2	759.82	835.01	-3.07E-6
beta3	269.14	327.82	2.884E-6
resvar	25.1791	74.4838	2.602E-6
varu	-670.87	3364.76	-1.06E-8

From these output, we can answer the questions like,

1. To test
$$H_0 : \beta_3 = 350 \qquad \text{v.s.} \qquad H_A : \beta_3 \neq 350$$
we can easily reject the null hypothesis because the Wald-type confidence intervals of both models do not contain 350, which is equivalent to a Wald test. We also can use the ESTIMATE statement in PROC NLMIXED to estimate $\beta_3 - 350$, as Figure 4

Figure 4: Additional Estimates

Additional Estimates

Label	Estimate	Standard Error	DF	t Value	Pr > |t|	Alpha
Beta_3=350?	-51.5207	11.4146	5	-4.51	0.0063	0.05

Additional Estimates

Label	Lower	Upper
Beta_3=350?	-80.8627	-22.1786

It is obviously that we should reject the null hypothesis, which is the same result as above. So β_3 does not equal 350.

2. To test whether the random effect is necessary. Because the method of parameter estimate of mixed model is not based on likelihood, we cannot use likelihood ratio test. So we still use the Wald-type confidence interval. Because the interval contains zero, we cannot reject the null hypothesis, that is, the random effect is not significant. Furthermore, we can see that the estimate of parameters of fixed effect does not change too much, so this also indicates that it is not necessary to introduce random effect into model.

   But, we should be cautious about the result, because from the parameter estimates of parameter of nonlinear model, skewness of all parameters is much greater than 0.25, which means all parameters have vary apparent skewness. This makes the inferences unreliable.

▶ 3. Solution.

Firstly, we fit the generalize linear model using PROC GENMOD,

▶ **4. Solution.** (a)

$$\boldsymbol{Y} = \begin{pmatrix} X_1 \\ X_3 \end{pmatrix} \sim \mathrm{N}\left(\begin{pmatrix} -3 \\ 2 \end{pmatrix}, \begin{pmatrix} 4 & 0 \\ 0 & 3 \end{pmatrix} \right)$$

(b)

$$\begin{aligned} \boldsymbol{Y}|X_2 &\sim \mathrm{N}\left(\begin{pmatrix} -3 \\ 2 \end{pmatrix} + \begin{pmatrix} \frac{x_2}{2} - \frac{1}{2} \\ \frac{x_2}{2} - \frac{1}{2} \end{pmatrix}, \begin{pmatrix} 3.5 & -0.5 \\ -0.5 & 2.5 \end{pmatrix} \right) \\ &= \mathrm{N}\left(\begin{pmatrix} \frac{x_2}{2} - \frac{7}{2} \\ \frac{x_2}{2} + \frac{3}{2} \end{pmatrix}, \begin{pmatrix} 3.5 & -0.5 \\ -0.5 & 2.5 \end{pmatrix} \right) \end{aligned}$$

(c)

$$\begin{aligned} X_2|\boldsymbol{Y} &\sim \mathrm{N}\left(2 + \begin{pmatrix} 1 & 1 \end{pmatrix} \begin{pmatrix} \frac{1}{4} & 0 \\ 0 & \frac{1}{3} \end{pmatrix} \begin{pmatrix} x_1 + 3 \\ x_3 - 2 \end{pmatrix}, 2 - \begin{pmatrix} 1 & 1 \end{pmatrix} \begin{pmatrix} \frac{1}{4} & 0 \\ 0 & \frac{1}{3} \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \right) \\ &= \mathrm{N}\left(\frac{1}{4}x_1 + \frac{1}{3}x_3 + \frac{13}{12}, \frac{17}{12} \right). \end{aligned}$$

(d)

$$Z \sim \mathrm{N}(-3 + 3 \cdot 1, 4 + 3^3 \cdot 2 + 2 \cdot 3 \cdot 1) = \mathrm{N}(0, 28)$$

▶ **5. Solution.** (a). The hypotheses are

$$H_0 : \mu_{11} = \mu_{12} = \mu_{13} \qquad \text{v.s.} \qquad H_a : \text{ at least two means are not equal}$$

or we can write null hypothesis as

$$H_0 : \boldsymbol{C}_1 \boldsymbol{\mu}_1 = \boldsymbol{0}$$

where

$$\boldsymbol{C}_1 = \begin{pmatrix} 1 & -1 & 0 \\ 0 & 1 & -1 \end{pmatrix}$$

The statistics are

$$\begin{aligned} T^2 &= n_1 (\boldsymbol{C}\bar{\boldsymbol{y}})' (\boldsymbol{C}\boldsymbol{S}\boldsymbol{C}')^{-1} (\boldsymbol{C}\bar{\boldsymbol{y}}) = 111.4286 \\ F &= \frac{n_1 - c}{(n_1 - 1)c} T^2 = 53.3929 \sim f_{c, n_1 - c} \end{aligned}$$

where $c = 2$ and $n_1 = 25$. The critical value of F statistic is $f_{0.95,2,23} = 3.422$, so $F > f_{0.95,2,23}$ and P-value is 2.28E^{-09}. We will reject the null hypothesis, that is, the mean concentrations are significantly different at three time points.

(b).

i The common covariance is

$$\boldsymbol{S}_{pool} = \frac{(n_1-1)\boldsymbol{S} + (n_2-1)\boldsymbol{W}}{(n1-1)+(n_2-1)} = \begin{pmatrix} 28.4 & 10.8 & 12.4 \\ 10.8 & 15.8 & 5.6 \\ 12.4 & 5.6 & 39.4 \end{pmatrix}$$

where $n_2 = 17$. The degree of freedom is 25+17-2=40.

ii The hypotheses are

$$H_0 : \boldsymbol{\Sigma}_A = \boldsymbol{\Sigma}_B \qquad \text{v.s.} \qquad H_A : \boldsymbol{\Sigma}_A \neq \boldsymbol{\Sigma}_B$$

The statistic is

$$M = (n_1+n_2-2)\log|\boldsymbol{S}_{pool}| - (n_1-1)\log|\boldsymbol{S}| - (n_2-1)\log|\boldsymbol{W}| = 1.1948$$
$$C^{-1} = 1 - \frac{2\times 3^2 + 3\times 3 - 1}{6\times(3+1)\times(2-1)}\left\{\frac{1}{n_1-1} + \frac{1}{n_2-1} - \frac{1}{n_1+n_2-2}\right\} = 0.9142$$
$$MC^{-1} = 1.1948 \times 0.9142 = 1.0923 \sim \chi^2_6$$

Because $MC^{-1} = 0.9142 < \chi^2_{0.95,6} = 12.592$ and P-value is 0.9819, we cannot reject the null hypothesis, which means that the assumption of same population covariance are reliable.

iii The squared Mahalanobis distance between $\boldsymbol{y} - \boldsymbol{z}$ is

$$T^2 = (\boldsymbol{y}-\boldsymbol{z})'\left[\boldsymbol{S}_{pool}\left(\frac{1}{n_1}+\frac{1}{n_2}\right)\right]^{-1}(\boldsymbol{y}-\boldsymbol{z}) = 18.03155$$

iv The hypotheses are

$$H_0 : \boldsymbol{y} - \boldsymbol{z} = \boldsymbol{0} \qquad \text{v.s.} \qquad H_A : \boldsymbol{y} - \boldsymbol{z} = \boldsymbol{0}$$

The statistic can be computed from the Mahalanobis distance from part (iii)

$$F = \frac{n_1+n_2-3-1}{(n_1+n_2-2)\times 3}T^2 = 5.70999 \sim f_{3,38}$$

Because $F = 5.70999 > f_{0.95,3,38} = 2.851$ with P-value=0.0025. We will reject the null hypothesis, so drug A and drug B do not have equal means.

v To test the parallel profiles, the hypotheses are

$H_0 : \mu_{11}-\mu_{21} = \mu_{12}-\mu_{22} = \mu_{13}-\mu_{23}$ v.s. $H_A :$ at least two difference not equal

or we can rewrite the null hypothesis as

$$H_0 : \boldsymbol{C_2}(\boldsymbol{y} - \boldsymbol{z}) = 0$$

where $\boldsymbol{C_2} = \begin{pmatrix} 1 & -1 & 0 \\ 0 & 1 & -1 \end{pmatrix}$.

The statistics are

$$T^2 = \frac{n_1 n_2}{n_1 + n_2}(\boldsymbol{C}(\bar{\boldsymbol{y}} - \bar{\boldsymbol{z}}))'(\boldsymbol{CSC}')^{-1}(\boldsymbol{C}(\bar{\boldsymbol{y}} - \bar{\boldsymbol{z}})) = 14.2658$$
$$F = \frac{n_1 + n_2 - c - 1}{(n_1 + n_2 - 2)c}T^2 = 6.7849 \sim f_{c,n_1+n_2-c-1}$$

Because $F = 6.7849 > f_{0.95,2,39} = 3.238$ with P-value=0.0030. We will reject the null hypothesis, so there is a significant interaction between drug and time.

Appendices

A SAS Code for Problem 3

```
libname da2 'C:\Users\psy6b\Desktop\8320 datasets';
ods graphics on;
options ls=70 ps=35;

/*To reading the data*/
data da2.h5q31;
   infile 'C:\Users\psy6b\Desktop\8320 datasets\ssttornado532001.dat';
   retain ss1-ss49;
   array ss{49} ss1-ss49;
   if _N_=1 then do;
      input ss1-ss49;
   end;
```

```
   loc+1;
   drop ss1-ss49;
   do t=1 to 49;
      sst=ss{t};
      input torn @;
      output;
   end;
run;
data da2.h5q32;
   infile 'C:\Users\psy6b\Desktop\8320 datasets\MOtornlatlon.dat';
   loc+1;
   input lat lon;
   run;
proc sql;
   create table da2.h5q3
   as select * from da2.h5q31 as a, da2.h5q32 as b
   where a.loc=b.loc;
   run;
quit;

/*Fitting different models*/
proc genmod data=da2.h5q3;
   class loc;
   model torn = sst sst*loc / dist=poisson link=log;
   output out=h5q3out1 resraw=Residual pred=Predicted lower=Lower
      upper=Upper;
run;
proc glimmix data=da2.h5q3 noitprint;
   class loc;
   model torn = sst sst*loc / dist=poisson link=log ddfm=betwithin
      solution;
   random intercept / subject=loc type=sp(exp)(lon lat);
   nloptions tech=newrap;
   covtest 'Random Int.' indep;
   output out=h5q3out2 pred(ilink)=predicted lcl(ilink)=lower
      ucl(ilink)=upper residual(ilink)=Residual;
run;
proc glimmix data=da2.h5q3 noitprint;
```

```
   class loc;
   model torn = sst sst*loc / dist=poisson link=log ddfm=betwithin
      solution;
   random sst / subject=loc type=sp(exp)(lon lat);
   nloptions tech=newrap;
   covtest 'Random Coef.' indep;
   output out=h5q3out3 pred(ilink)=predicted lcl(ilink)=lower
      ucl(ilink)=upper residual(ilink)=Residual;
run;
proc glimmix data=da2.h5q3 noitprint;
   class loc;
   model torn = sst sst*loc / dist=poisson link=log ddfm=betwithin
      solution;
   random intercept sst / subject=loc type=sp(exp)(lon lat);
   nloptions tech=newrap;
   covtest 'Random Int. & Coef.' indep;
   output out=h5q3out4 pred(ilink)=predicted lcl(ilink)=lower
      ucl(ilink)=upper residual(ilink)=Residual;
run;


/*Processing output*/
proc sort data=h5q3out1;
   by loc;
run;
data h5q3eval1;
   set h5q3out1;
   by loc;
   keep loc torn predicted residual lat lon;
   retain sumtorn sumpred sumres;
   if first.loc then do;
      sumtorn=0;
      sumpred=0;
      sumres=0;
   end;
   sumtorn+torn;
   sumpred+predicted;
   sumres+residual;
```

```
   if last.loc then do;
      torn=sumtorn;
      predicted=sumpred;
      residual=sumres;
      output;
   end;
run;
proc sort data=h5q3out2;
   by loc;
run;
data h5q3eval2;
   set h5q3out2;
   by loc;
   keep loc torn predicted residual lat lon;
   retain sumtorn sumpred sumres;
   if first.loc then do;
      sumtorn=0;
      sumpred=0;
      sumres=0;
   end;
   sumtorn+torn;
   sumpred+predicted;
   sumres+residual;
   if last.loc then do;
      torn=sumtorn;
      predicted=sumpred;
      residual=sumres;
      output;
   end;
run;
proc sort data=h5q3out3;
   by loc;
run;
data h5q3eval3;
   set h5q3out3;
   by loc;
   keep loc torn predicted residual lat lon;
   retain sumtorn sumpred sumres;
```

```
   if first.loc then do;
      sumtorn=0;
      sumpred=0;
      sumres=0;
   end;
   sumtorn+torn;
   sumpred+predicted;
   sumres+residual;
   if last.loc then do;
      torn=sumtorn;
      predicted=sumpred;
      residual=sumres;
      output;
   end;
run;
proc sort data=h5q3out4;
   by loc;
run;
data h5q3eval4;
   set h5q3out4;
   by loc;
   keep loc torn predicted residual lat lon;
   retain sumtorn sumpred sumres;
   if first.loc then do;
      sumtorn=0;
      sumpred=0;
      sumres=0;
   end;
   sumtorn+torn;
   sumpred+predicted;
   sumres+residual;
   if last.loc then do;
      torn=sumtorn;
      predicted=sumpred;
      residual=sumres;
      output;
   end;
run;
```

```
data h5q3eval;
   set h5q3eval1(in=a) h5q3eval2(in=b) h5q3eval3(in=c)
      h5q3eval4(in=d);
   length model $23;
   if a then do;
      model='Independent';
   end;
   if b then do;
      model='Random Int.';
   end;
   if c then do;
      model='Random Coef.';
   end;
   if d then do;
      model='Random Int. & Coef.';
   end;
   label torn='Actual Measurements';
run;



/*Evaluating models*/
proc sort data=h5q3eval;
   by torn;
run;
proc sgpanel data=h5q3eval noautolegend;
   panelby model/columns=2 rows=2 spacing=5;
   scatter x=torn y=predicted/ datalabel=loc;
   series x=torn y=torn;
   keyword "Observations" "Reference Line";
run;
proc sql;
   title 'Model Comparation';
   select model,sum(residual*residual) label='Model Type' as SSR
      label='Sum of Squared Residual'
   from h5q3eval
   group by model;
quit;
```

```
/*Plotting the profile*/
data panelplot2;
   set h5q3out2;
   length type $20;
   keep loc t type resp;
   t=t+1952;
   type='measurement';
   resp=torn;
   output;
   type='cluster-specific';
   resp=predicted;
   output;
   type='lower bound';
   resp=lower;
   output;
   type='upper bound';
   resp=upper;
   output;
   run;
proc sgpanel data=panelplot2;
   where loc le 4 and loc ge 1;
   panelby loc/rows=2 columns=2 spacing=5;
   vline t/response=resp group=type;
   colaxis fitpolicy=thin alternate;
   rowaxis alternate;
run;
proc sgpanel data=panelplot2;
   where loc le 8 and loc ge 5;
   panelby loc/rows=2 columns=2 spacing=5;
   vline t/response=resp group=type;
   colaxis fitpolicy=thin alternate;
   rowaxis alternate;
run;
proc sgpanel data=panelplot2;
   where loc le 12 and loc ge 9;
   panelby loc/rows=2 columns=2 spacing=5;
   vline t/response=resp group=type;
```

```
   colaxis fitpolicy=thin alternate;
   rowaxis alternate;
run;
proc sgpanel data=panelplot2;
   where loc le 16 and loc ge 13;
   panelby loc/rows=2 columns=2 spacing=5;
   vline t/response=resp group=type;
   colaxis fitpolicy=thin alternate;
   rowaxis alternate;
run;
proc sgpanel data=panelplot2;
   where loc le 20 and loc ge 17;
   panelby loc/rows=2 columns=2 spacing=5;
   vline t/response=resp group=type;
   colaxis fitpolicy=thin alternate;
   rowaxis alternate;
run;
```

B Some Outputs for Promblem 3