Homework1

BIOS6643 Fall 2021

8/20/2021

Question 1 Acknowledgment

Please acknowledge that you read the **Homework expectations.pdf** document in the Homework module on Canvas, and agree to it (the easiest HW question you will get, but need to complete for credit).

Question 2 The simplest longitudinal analysis (2 time points)

Background: The data **cholesterol.txt** contains cholesterol levels (adapted from Rosner, 2006). The data are a sample of cholesterol levels taken from 24 hospital employees who were on a standard American diet and who agreed to adopt a vegetarian diet for one month. Serum cholesterol measurements (mcg/dl) were made before adopting the vegetarian diet and one month after. (For this exercise, "summarize results" means just give the highlights of the analysis - retype and/or cut and paste necessary info but do not include all SAS output.)

a. **Change-score model**: Let Y_{i1} and Y_{i2} denote the pre and post cholesterol level for subject i, $i = 1, \ ..., \ 24$, and let $d_i = Y_{i2} - Y_{i1}$. Perform the linear regression of d_i on the intercept alone (i.e., the model statement in PROC GLM would be "*model* $di = ;$"). Summarize results.

```
Dependent Variable: change

R-Square     Coeff Var      Root MSE    change Mean
0.000000     -85.99953      16.80574      -19.54167

Source                     DF     Type III SS     Mean Square    F Value    Pr > F
Intercept                   1     9165.041667     9165.041667      32.45    <.0001

Parameter          Estimate           SE      t Value    Pr > |t|
Intercept     -19.54166667      3.43045776       -5.70      <.0001
```

The R^2 is 0. You might think this means that the model is bad, but remember that the R^2 is a measure of model improvement over the model with the simple intercept. Since this model is in fact the simple intercept model, there cannot be any improvement over it. The estimate of -19.54 shows that the average drop in cholesterol was almost 20 mcg/dl, which was very significant. Since we only have an intercept in the model, note that cholesterol change levels are predicted to be the same for all subjects. However, this is not to say that a necessary assumption of the data is that cholesterol changes are the same. Remember that for a paired t-test, we assume that changes scores are normally distributed. Nevertheless, with this simple model we are not able to model change scores as a function of baseline score, which is important, as the following parts will demonstrate.

b. In the output, look at the test for the intercept. What simple test yields the same results?

Paired t-test

c. **Baseline-as-covariate model**: Now perform a linear regression for the post cholesterol value, using the baseline variable as a covariate. Summarize results.

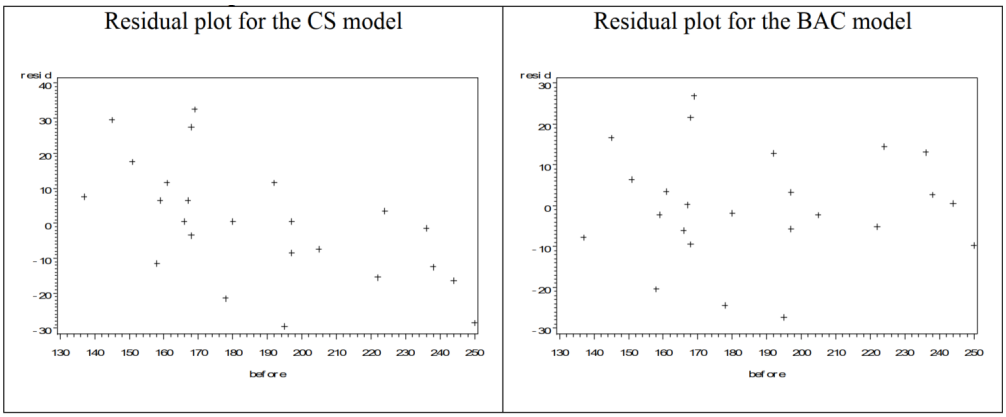
Dependent Variable: after

R-Square	Coeff Var	Root MSE	after Mean
0.746251	8.202918	13.80141	168.2500

Parameter	Estimate	SE	t Value	Pr > |t|
Intercept	37.15761196	16.53937361	2.25	0.0350
before	0.69807351	0.08678594	8.04	<.0001

We are performing a simple linear regression of 'after' score on 'before' score. Since the slope is different than 1, there is some evidence that the cholesterol scales 'before' and 'after' are not commensurate. However, the test above compares the slope with 0 and not 1 (we will get back to this issue momentarily). This fitted model demonstrates not only that subjects lowered their cholesterol with this diet (with the range of cholesterol tested), but that those with higher cholesterol dropped more. For example, a subject with a 'before' cholesterol of 200 has an expected 'after' cholesterol of $37.16 + 200(0.698) = 176.76 mcg/dl$, a drop of over 23 points, while a subject starting at 150 is expected to drop to 141.86 mcg/dl, less than 10 points. Now we have a way of predicting post-diet cholesterol that takes into account pre-diet starting points.

d. Compare the change-score (CS) and baseline-as-covariate (BAC) models. What are pro's and con's of each? Also construct residual plots (residual vs. before) to help answer.



The residual plot for the CS model has an obvious pattern demonstrating lack of fit; the BAC model has no such pattern.

e. **Hybrid model**: Consider the model of change score (d_i) using baseline cholesterol as a covariate.

(i). Write the model {in terms of beta coefficients}. Then re-express the model in terms of Y_{i2}. Collect terms and determine the slope of the Y_{i1} term. What is the relationship between the Hybrid and BAC models? You can answer this based on both the equation you wrote, plus the models you fit with SAS or R.

$$
\begin{aligned}
d_i &= \beta_0 + \beta_1 Y_{i1} + \epsilon_i \\
Y_{i2} - Y_{i1} &= \beta_0 + \beta_1 Y_{i1} + \epsilon_i \\
Y_{i2} &= \beta_0 + (1+\beta_1) Y_{i1} + \epsilon_i \\
Y_{i2} &= \beta_0' + \beta_1' Y_{i1} + \epsilon_i
\end{aligned}
$$

We are essentially fitting the same model, where $1+\beta_1 = \beta_1'$ This same relationship will hold for the estimates. Thus, the estimate of the slope in the hybrid model should be 1 less than the estimate of the slope in the BAC model: $\widehat{\beta}_1 = \widehat{\beta}_1' - 1$ So it should be: $0.698 - 1 = -0.302$. Checking with SAS:

```
Dependent Variable: change
                 R-Square     Coeff Var      Root MSE    change Mean
                 0.354901     -70.62555      13.80141      -19.54167

Parameter          Estimate           SE        t Value    Pr > |t|
Intercept      37.15761196     16.53937361           2.25       0.0350
before         -0.30192649      0.08678594          -3.48       0.0021
```

(ii). Write the hypotheses for the test reported in the PROC GLM output {for the 'before' variable, near the end}, in terms of .

The slope in the hybrid model is β_1, but note that the test of H_0: $\beta_1 = 0$ is equivalent to H_0:$\beta_1' - 1 = 0$, i.e., $H_0 : \beta_1' = 1$ vs. $H_1 : \beta_1' \neq 1$. So really, the BAC and hybrid models are the same, but the output differs slightly due to the different parameterization. In particular, the test for the 'before' slope in the BAC model compares with 0, and in the hybrid model compares it to 1 (thinking in terms of the same BAC slope). The comparison with 1 is probably of more interest: This indicates that the before and after scales are not equivalent. (This test does not include location differences.)

f. Fit the data using a mixed model, with an UN structure for repeated measures. In this case, don't include baseline as covariate, since it is already an outcome. How do results compare with the Hybrid model? What are pro's and con's of each approach?

```
data chol; set chol; if time="pre" then realtime=0; else realtime=1;
proc sort data=chol; by id realtime; run;
proc mixed data=chol;
  class realtime;
  model chol=realtime / solution;
  repeated realtime / subject=id type=un r rcorr;
  estimate 'mean at time 0' intercept 1 realtime 1 0;
  estimate 'mean at time 1' intercept 1 realtime 0 1; run;
```

```
Solution for Fixed Effects
Effect      realtime       Estimate       SE      DF      t Value Pr > |t|
Intercept                  168.25         5.4697  23      30.76   <.0001
realtime    0              19.5417        3.4305  23      5.70    <.0001
realtime    1              0              .       .       .       .

Estimates
Label              Estimate       SE      DF      t Value         Pr > |t|
mean at time 0     187.79         6.7687  23      27.74           <.0001
mean at time 1     168.25         5.4697  23      30.76           <.0001
```

Notice that the change estimate is EXACTLY the same as that from the CS model. This helps reaffirm that if it is only mean change you are concerned about, we can use the simple difference approach. We know some advantages of the BAC and Hybrid models relative to the CS model, but we can also see some advantages of the longitudinal approach. First, we get estimates of actual cholesterol values at pre and post times, rather than just the change estimate. We also get an estimate of the correlation between pre and post times, as well as variance estimates at each time point. The longitudinal model would also allow us to add time-varying covariates, if they were of interest. Note that an alternative approach to modeling the data longitudinally would be to include a random intercept and slope for each subject, and allow a covariance between them (i.e., UN structure for $\boldsymbol{G}$). One disadvantage of the longitudinal model is that it is more difficult to characterize the relationship between change values with starting values.

Question 3 First-order autoregressive process

Consider a first-order autoregressive process, $\epsilon_t = \phi\epsilon_{t-1} + Z_t$, where $Z_t \sim \mathcal{N}(0,\ \sigma^2)$, where t is an integer for discrete units of time (e.g., days), and $|\phi| < 1$. In order to derive the quantities below, say that this is an 'infinite process' (i.e., t extends backwards in time to infinity). First, by iteration we can show that $\epsilon_t = Z_t + \phi Z_{t-1} + ... + \phi^k Z_{t-k} + \phi^{k+1}\epsilon_{t-k-1}$. If we keep going, we get the expression $\epsilon_t = \sum_{j=0}^{\infty} \phi^j Z_{t-j}$.

[We can show that this equality holds since $\sum_{j=0}^{k} \phi^j Z_{t-j}$ is mean-square convergent as $k \to \infty : E[X_t - \sum_{j=0}^{k} \phi^j Z_{t-j}]^2 = \phi^{2k+2} E[X_{t-k-1}^2] \overset{k \to \infty}{\longrightarrow} 0$ since $E[X_t^2]$ is constant over t.]

a. Determine $E[\epsilon_t]$

$E[\epsilon_t] = E[\sum_{j=0}^{\infty} \phi^j Z_{t-j} = \sum_{j=0}^{\infty} \phi^j E[Z_{t-j}] = 0$

b. Determine $Cov[\epsilon_t, \epsilon_{t+h}]$

First consider h to be a nonnegative integer:

$$
\begin{aligned}
Cov[\epsilon_t,\ \epsilon_{t+h}] &= E[\epsilon_t \epsilon_{t+h}] - \mu_{\epsilon_t}\mu_{\epsilon_{t+h}} = E[\epsilon_t \epsilon_{t+h}] \\
&= E[(\sum_{j=0}^{\infty} \phi^j Z_{t-j})(\sum_{k=0}^{\infty} \phi^k Z_{t+h-k})] = \sum_{j=0}^{\infty}\sum_{k=0}^{\infty} \phi^j \phi^k E[Z_{t-j} Z_{t+h-k}] \\
&= \sum_{t-j=t+h-k} \phi^{j+k} E[Z_{t-j} Z_{t+h-k}] + \sum_{t-j \neq t+h-k} \phi^{j+k} E[Z_{t-j} Z_{t+h-k}] \\
&= \sum_{j=0}^{\infty} \phi^{h+2j} E[Z_{t-j}^2] + \sum_{t-j \neq t+h-k} \phi^{j+k} E[Z_{t-j}] E[Z_{t+h-k}] \\
&= \sum_{j=0}^{\infty} \phi^{h+2j} E[Z_{t-j}^2] + \sum_{t-j \neq t+h-k} \phi^{j+k} \times 0 \times 0 \\
&= \sum_{j=0}^{\infty} \phi^{h+2j} \sigma^2 + 0 = \sigma^2 \phi^h \sum_{j=0}^{\infty} \phi^{2j} = \sigma^2 \frac{\phi^h}{1-\phi^2}
\end{aligned}
$$

Z terms have the same index when $t-j = t+h-k$, i.e., when $k = j+h$. So in line 6, replace k with $j+h$ for terms in the summation and reduce the summation to $k = 0$ to $k = \infty$.

c. Determine $Corr[\epsilon_t, \epsilon_{t+h}]$

$$
Corr[\epsilon)_t,\ \epsilon_{t+h}] = \frac{Cov[\epsilon_t,\ \epsilon_{t+h}]}{\sqrt{Var[\epsilon_t] Var[\epsilon_{t+h}]}} \frac{\frac{\sigma^2 \phi^h}{1-\phi^2}}{\sqrt{\frac{\sigma^2}{(1-\phi^2)}}\sqrt{\frac{\sigma^2}{(1-\phi^2)}}} = \phi^h
$$

for nonnegative h. Considering any integer h, the correlation is $\phi^{|h|}$

d. Is $\{\epsilon_t\}$ a stationary process?

Yes, the mean is constant for all t, $Cov(\epsilon_t,\ \epsilon_{t+h})$ does not depend on t, for any integer h, and variance is finite.

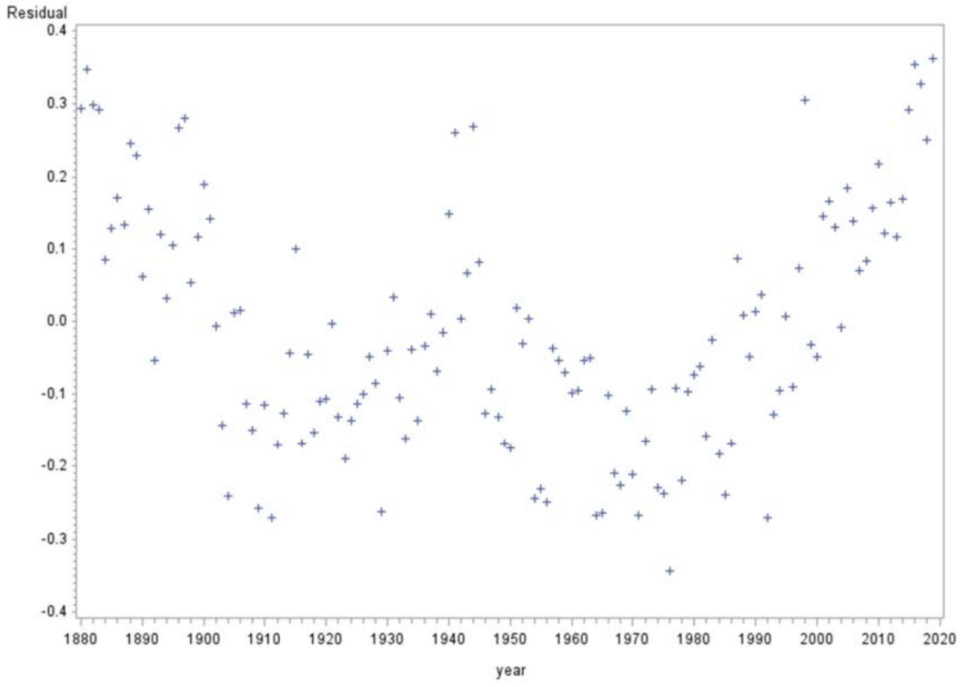
Question 4 Global temperature

Background: Here, we have time series data. The primary point of the exercise is to better understand the two main parts of a predictive model, the mean and error. Use PROC MIXED in SAS to fit the linear time trend with AR(1) error model with the global average temperature data. Temperatures are for 1880-2019, mean-corrected (or 'anomalies') based on 20th Century average, reported in $^{\circ}C$, and for land and ocean combined. These are newer data than those in the lecture notes. Below is SAS code that you can use to fit the model. The **'subject=intercept'** option tells SAS there is one process.

```
proc mixed data=teaching.global_temp_anomalies method=ml;
    model temp=year / solution outp=tempout;
    repeated / type=AR(1) subject=intercept; run;
```

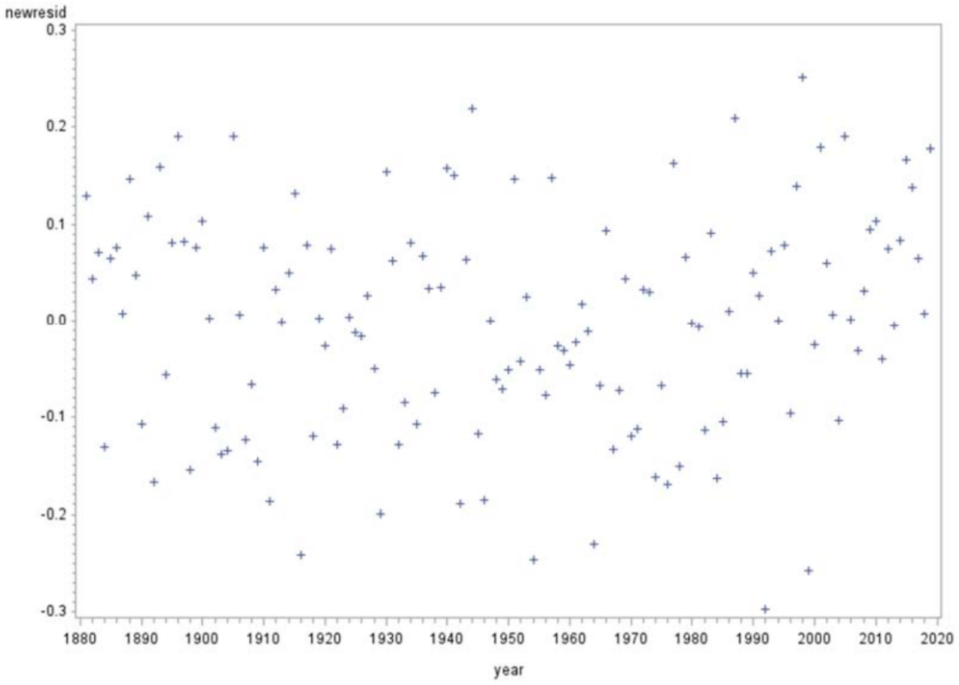
a. Create a Residual plot (residuals versus year) based on the fitted data from the model ($\hat{y}_t = \hat{\beta}_0 + \hat{\beta}_1 t$ are predicted values; $y_t - \hat{y}_t$ are residuals). What patterns do you notice? What do you think the plot is telling you?

The plot suggests lack of fit in the mean part of the model; a clear "W" shape.



b. In order to get a better idea whether the AR(1) process with linear time trend appears to fit the global temperature data, create a new residual plot using residuals that take into account both the mean and error parts of the model. Specifically, the new residual is $y_t - \tilde{y}_t$ where $\tilde{y}_t = \hat{y}_t + \hat{\phi}\nu_{t-1}$ and $\nu_t = y_t - \hat{y}_t$. [Note: PROC AUTOREG computes these type of residuals directly, but we'll stick with PROC MIXED since that's what we'll be using later in the course.] You can create these new residuals in a data step. Use the estimated correlation parameter from the SAS output. Based on this plot, what is your opinion about how the model fits the data? [Notes: in creating the new

residuals, you can obtain the correlation parameter estimate from the PROC MIXED output; to align 't' and '$t-1$' data, you can use the lag function in SAS.]



Considering mean and error together, the model looks pretty reasonable.

c. Based on your fitted model, what is the average increase in temperature per decade?

The average increase per decade is $10(0.007276) = 0.07\ ^oC$.

d. Try refitting the data using a polynomial trend for time (decide on the degree of the model by looking at the plot). How does the model fit compare with the one that using a simple linear trend for time? What happens to the correlation parameter estimate in this new model? What do you think about this fit compared with the simple linear model? (In answering this, don't worry about the '0' SE for higher-order terms; just focus on the fit itself.)

With either **quadratic** or **cubic** model, we get a better fit, although there is still a lack of fit in the mean part of the model (when considering the process that does not take the correlated errors into account). The residual plot for the mean shows lack of fit particularly around 1940 to 1945. The correlation parameter estimate decreases from 0.7395 (linear) to **0.4744 (quadratic)** to **0.4655 (cubic)**. What this suggests is that by increasing the complexity of the mean, less is required in the error part of the model. Still, it is not a great model and I'd be tempted to keep the simple linear with AR(1) for general interpretation. If we want the fit the mean process more accurately, we need to try harder, which leads us to the next part.

e. Perform a nonparametric regression fit of the data using PROC LOESS. Construct a residual plot and histogram. Do you think this a better/worse/different fit compared with the parametric fits with AR(1) errors? Explain.

```
proc loess data=teaching.global_temp_anomalies;
        ods output scoreresults=scoreout
            outputstatistics=statout;
        model temp = year / smooth= 0.3 residual clm degree=1;
score data=tempout / clm;
run;
symbol1 i=none; symbol2 i=join; symbol3 i=join line=2;
proc gplot data=tempout;
plot depvar*year=1 pred*year=2 lowercl*year=3 uppercl*year=3/ overlay;
run;
```

I would say that the fit here is decent. It is not a "better" fit than the parameter model overall, just different. But it is better (more nuanced) in terms of describing the mean process. Here, we increase the complexity of the mean part of the model, and so require less on the error part. If you fit a mixed model on the residuals of this LOESS fit, you will find the correlation parameter is around 0.28. But if you drop the smoothing parameter value in the LOESS fit to the 'best' AICC value, which is around 0.1, the correlation parameter decreases below 0.1. Collectively, what these different model fits show is that for a model that has the basic form Outcome=mean+error, if we have a simple 'mean', then to get an accurate model, we need a more complex 'error' (e.g., simple linear trend plus AR(1) errors). On the other hand, if we have a more complex mean, then the error structure can be simpler (LOESS fit nearly eliminated the need for an AR(1) structure, especially when using a lower smoothing parameter value).