1. The following questions are on the data and model described in Q3 of HW3:
    - Examine the tolerances and variance inflation factors from this model. Do you think any collinearity is present based on the tolerance and VIF? Why or why not?

Table 1.1: Tolerances & Variance Inflation Factors

Variable	Label	DF	Tolerance	Variance Inflation
Intercept	Intercept	1	.	0
height	Height (cm)	1	0.00218	458.04764
weight	Weight (kg)	1	0.00142	703.44629
bmi		1	0.00564	177.45037
area	Body Surface Area (M**2)	1	0.00073266	1364.89752
age	Age (years)	1	0.92307	1.08334
avtrel	Average Treadmill Elevation (deg)	1	0.00172	580.38969
avtrsp	Average Speed of Treadmill (mph)	1	0.01276	78.39302
int		1	0.00126	795.44895
temp	Air Temperature (deg C)	1	0.03447	29.01379
barm	Barometric Pressure (mmHg)	1	0.94420	1.05910
hum	Relative Humidity %	1	0.03429	29.16692

- There is a good amount of evidence to suggest collinearity in:
    - BMI and body surface area can be predicted/derived from height and weight.
    - Average treadmill elevation, average treadmill speed, and their interaction are collinear.
    - Temperature and relative humidity can be somewhat “predicted” once one of them is known.
- Age and barometric pressure do not appear to be collinear. This makes sense since age cannot guarantee height and weight among adults. Barometric pressure would probably tend to stay constant or within a narrow range of values while humidity can vary much more.

- Conduct an eigenanalysis of the scaled SSCP and correlation matrices, presenting a table formatted like Table 8.6.2 in Muller and Fetterman.
  (a) Does there appear to be any collinearity between the intercept and the covariates? Why or why not? If so, list the variables?

Table 1.2: Eigenvalues & Condition Index – Scaled SSCP Matrix

Number	Eigenvalue	CondIndex
1	11.9049480	1.00
2	0.0360383	18.18
3	0.0293709	20.13
4	0.0161788	27.13
5	0.0066991	42.16
6	0.0049049	49.27
7	0.0015550	87.50
8	0.0002515	217.55
9	0.0000375	563.68
10	0.0000097	1109.52
11	0.0000049	1563.90
12	0.0000015	2772.26

Table 1.3: Eigenvectors – Scaled SSCP Matrix

	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6
inter	0.289612	0.003847	-.041736	0.011264	-.428489	0.169349
height	0.289592	-.012406	-.076762	-.085857	-.320422	-.333604
weight	0.288434	-.239953	-.360268	-.362654	0.422414	-.270732
bmi	0.288728	-.206145	-.292000	-.169993	0.215099	0.744305
area	0.289363	-.111646	-.201362	-.220653	0.010005	-.386236
age	0.287541	-.065062	-.310877	0.876080	0.184729	-.112124
avtrel	0.288114	0.542971	0.114554	-.008826	0.189245	0.156326
avtrsp	0.289555	0.081696	-.006435	-.063918	-.344231	-.063169
int	0.287589	0.621228	0.147453	-.079888	0.268208	-.082800
temp	0.288619	-.262600	0.436206	0.056399	0.018763	0.043500
barm	0.289608	0.005253	-.047742	0.006020	-.425070	0.178686
hum	0.287332	-.355890	0.642383	0.046041	0.217990	-.043461

	Prin7	Prin8	Prin9	Prin10	Prin11	Prin12
inter	-.160576	0.078500	-.338231	-.161589	0.611844	-.393890
height	-.210883	0.038668	-.291386	0.338828	0.023636	0.665223
weight	-.018722	-.039185	0.238215	-.394929	0.334969	0.139220
bmi	0.123098	0.027757	-.194962	0.269726	-.143594	0.111429
area	-.132498	0.015069	-.118058	0.290762	-.440686	-.595672
age	0.045774	0.011125	0.001522	-.001560	-.002277	-.001034
avtrel	-.507446	0.047211	-.121532	-.414212	-.312294	0.071559
avtrsp	0.689454	-.012728	-.115575	-.438188	-.311166	0.071916
int	0.359344	-.055730	0.120806	0.416970	0.313806	-.072700
temp	-.078823	-.802916	0.031595	0.002606	-.009520	-.007541
barm	-.155432	0.124637	0.804979	0.091474	-.071280	0.006178
hum	0.047328	0.569193	-.016930	0.000288	0.007634	0.005636

Several of the scaled SSCP condition indices are greater than 30 and multiple eigenvalues are close to zero; thus, indicating collinarity with the intercept.

By looking at the elements of the 12th Prinicipal Component, the elements corresponding to the intercept, height, weight, bmi, and area have values father from zero relative to the other variables.

This would suggest that height, weight, bmi, and area span the intercept.

(b) Does there appear to be any collinearity among the covariates? Why or why not? If so, list the variables?

Table 1.4: Eigenvalues & Condition Index - Correlation

Number	Eigenvalue	CondIndex
1	3.00984215	1.0000
2	2.44782689	1.1089
3	2.02476481	1.2192
4	1.11320127	1.6443
5	1.01325013	1.7235
6	0.80927943	1.9285
7	0.56109511	2.3161
8	0.01770758	13.0374
9	0.00187374	40.0791
10	0.00070517	65.3317
11	0.00045372	81.4475

Table 1.5: Eigenvectors – Correlation

	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6
height	0.392316	0.296786	0.032498	-.431698	0.052791	0.294700
weight	0.558767	0.051052	-.092125	0.096942	0.000376	-.170215
bmi	0.367229	-.183577	-.143312	0.493420	-.041432	-.472648
area	0.549273	0.157720	-.048934	-.111776	0.019229	-.000896
age	0.092890	-.065940	-.101323	0.368850	0.755491	0.497666
avtrel	-.199140	0.514774	-.034223	0.298870	0.116311	-.185008
avtrsp	0.074811	0.479606	0.086722	-.079394	-.115421	0.054060
int	-.148534	0.589598	-.004523	0.228684	0.068080	-.138848
temp	0.091766	-.044660	0.676385	0.168590	-.008712	0.038468
barm	0.065437	0.035488	-.176120	0.457649	-.626029	0.594893
hum	0.093072	-.022211	0.678255	0.162613	-.029775	0.036111

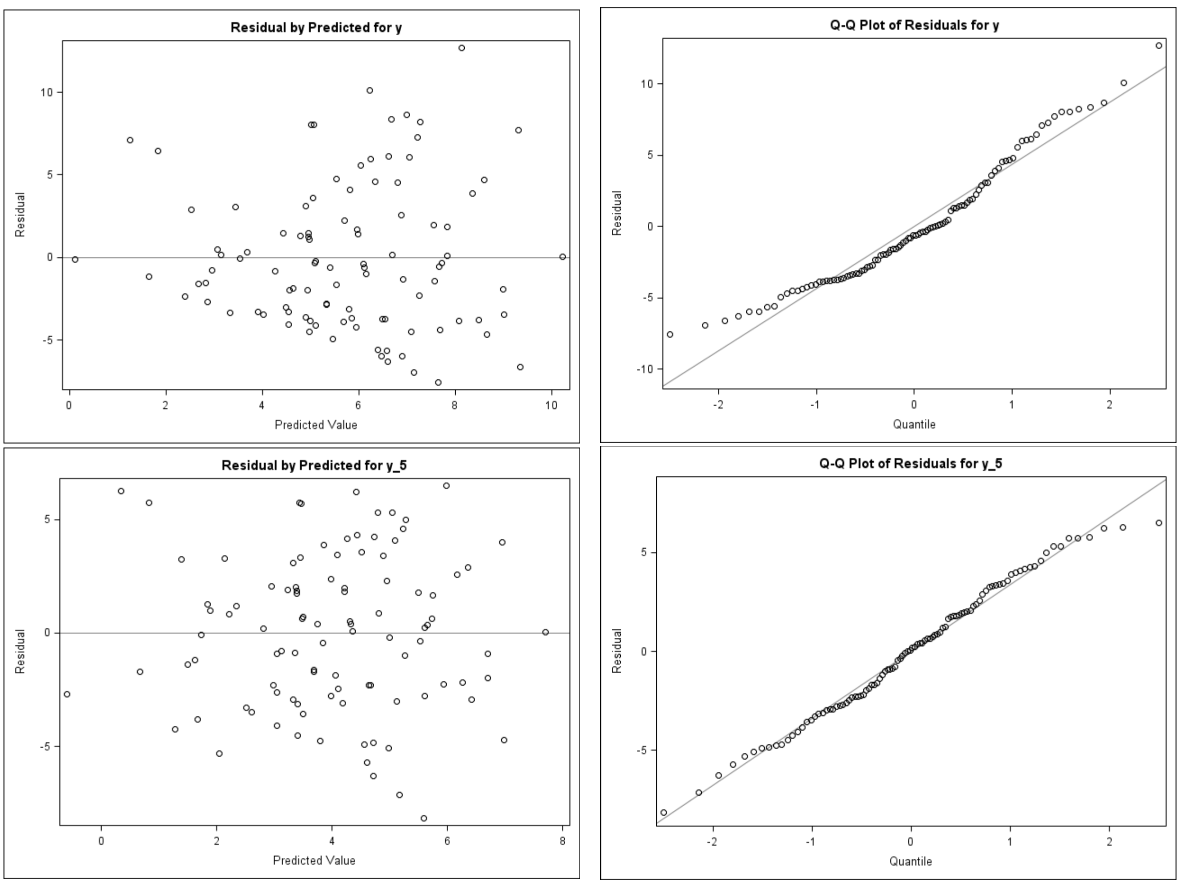
	Prin7	Prin8	Prin9	Prin10	Prin11
height	-.259751	0.018476	0.520184	-.036531	0.375786
weight	-.058566	0.003991	-.634360	-.174066	0.449619
bmi	0.168277	0.006166	0.554743	0.038138	0.069126
area	-.143725	-.017816	-.095960	0.175724	-.772725
age	0.148534	-.013550	-.001968	0.003505	-.002419
avtrel	-.397123	-.000850	-.061237	0.611781	0.146172
avtrsp	0.825059	0.015953	-.032894	0.221914	0.054851
int	-.081491	0.009784	0.071012	-.715838	-.172852
temp	-.055085	0.706224	-.008134	0.004308	-.015415
barm	-.090203	0.006020	0.003518	-.000885	-.001557
hum	-.042697	-.707081	0.009525	-.007438	0.015737

From the eigenanalysis of the correlation matrix, there appears to be other collinearity within the variables besides the intercept.

By looking at the elements of the 11th Principal Component, the elements corresponding to the height, weight, bmi, area, average treatmill elevation, average treadmill speed, the interaction, temperature, and humidity have values father from zero relative to age and barometric pressure.

2. Find the Box-Cox transformation of the simulated data (BoxCox.dat) and compare the residual plots of the raw and transformed data.

Box-Cox Transformation Information for y				
Lambda		R-Square	Log Like	
0.00		0.19	-147.31	
0.25		0.19	-124.38	*
0.50	+	0.18	-122.59	<
0.75		0.17	-131.76	
1.00		0.16	-147.64	
< - Best Lambda * - 95% Confidence Interval + - Convenient Lambda				



The residual plot for the non-transformed y-values shows a slight pattern with the residuals being clustered closer together for smaller predicted values of y with the dispersion increasing as the predicted values of y increase. This indicates that the assumptions of homogeneity of variance and linearity might be violated. Due to curvature, the Q-Q plot for the non-transformed y-values also indicates that the assumption of Gaussian errors might be violated.

After transforming the y-values using a Box-Cox transformation with lambda=0.50, the residual plot is scattered equally regardless of the predicted value of y_5 and the Q-Q plot no longer contains a curve in the middle. This suggests the Box-Cox transformation of y does not violate the assumptions of homogeneity, linearity, nor Gaussian errors.

3. Investigators are interested in the effect of dermal nicotine exposure in a population of Latino tobacco workers in North Carolina. (Nicotine can be absorbed from tobacco leaves through the skin and can cause nicotine poisoning, which is characterized by nausea, vomiting, headache, and dizziness.) Data were collected on tobacco work tasks and risk factors for exposure to nicotine during a summer tobacco work season. Nicotine exposure was measured by levels of cotinine, a nicotine metabolite, contained in saliva. Other covariates of interest include age, body mass index, education, work conditions (working in wet conditions is believed to increase nicotine absorption), type of tobacco work ("priming" refers to picking or harvesting the tobacco and is expected to result in highest nicotine exposures, "barning" refers to putting the harvested tobacco into a barn for curing, "topping" refers to breaking the flower off the top of the plant, and "other" refers to farm work that does not involve tobacco contact, such as driving a truck), and smoking (smokers would also have nicotine exposure through cigarettes, and it is not known whether exposure to tobacco leaves would increase cotinine levels to a similar extent in both smokers and non-smokers).

   The variables are available in the file tobacco.dat and listed in the following order.
   - COTININE: salivary cotinine concentration (in ng/mL)
   - AGE: age (in years)
   - BMI: body mass index (in kg/m2)
   - EDUC: years of education
   - WET: takes value 1 if work conditions on day of measurement were wet and takes value 0 otherwise
   - TASK: takes value 1 for priming, 2 for barning, 3 for topping, and 4 for other work not involving tobacco contact
   - LNNSMOKE: natural logarithm of (1 + number of cigarettes smoked per day)

   To report a test, provide H_0, the test statistic, the degrees of freedom, the p-value, the decision (accept/reject H_0), and an interpretation of the result in terms of the subject matter.

- One-Way ANOVA: For these questions, use the log of salivary cotinine as the response and task as the only predictor.
  - Report a test of whether all cell means are equal.

    H_0: All cell-means equal ($\mu_{Priming} = \mu_{Barning} = \mu_{Topping} = \mu_{Other}$)
    H_1: At least one cell-mean differs from another cell-mean.

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
Usual Overall Test	3	790.4453988	263.4817996	116.20	<.0001

F (3, 690) = 116.20 with p < 0.0001.
Reject H_0.
There is evidence to suggest that at least two of the cell-means differ.

  - If your overall test of the task effect was significant, examine all pairwise comparisons using the Scheffe correction. Summarize your findings in a table including columns for the estimated mean difference, degrees of freedom, *F* statistic, *p*-value, and a Scheffe confidence interval for the mean difference. Explain your findings in language the investigator can understand.

Table 3.1: Pairwise Comparisons

	Estimated Mean Difference	Degrees of Freedom	F	p-value	Scheffe 95% Confidence Interval
Priming v. Barning	0.9208	1, 690	19.58	0.0002	[0.3376, 1.5040]
Priming v. Topping	1.6738	1, 690	131.87	<0.0001	[1.2654, 2.0823]
Priming v. Other	2.6993	1, 690	332.68	<0.0001	[2.2845, 3.1140]
Barning v. Topping	0.7531	1, 690	12.99	0.0049	[0.1675, 1.3386]
Barning v. Other	1.7785	1, 690	71.38	<0.0001	[1.1885, 2.3684]
Topping v. Other	1.0254	1, 690	47.26	<0.0001	[0.6074, 1.4434]

The average values for the log of salivary cotinine concentration (in mg/mL) found in Latino tobacco workers in North Carolina differs significantly depending on the task workers preformed.

- Provide a table of parameter estimates and standard errors using (a) cell mean coding and (b) reference cell coding, and give the interpretations of parameters in both coding schemes. In addition, provide the $\boldsymbol{C}$ and $\boldsymbol{\theta_0}$ matrices used to test the hypothesis that average cotinine levels for workers involved in priming are greater than the average continine levels for all other workers.

Table 3.2: Parameter Estimates

Cell Mean Coding			
	Estimates	Standard Errors	
Priming	4.5086	0.1022	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 4.5086 mg/mL.
Barning	3.5878	0.1813	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 3.5878 mg/mL.
Topping	2.8347	0.1039	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 2.8347 mg/mL.
Other	1.8093	0.1070	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 1.8093 mg/mL.
Reference Cell Coding – Solution 1			
	Estimates	Standard Errors	
Intercept	1.8093	0.1070	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 1.8093 mg/mL.
Priming	2.6993	0.1480	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 2.6993 mg/mL higher than those whose task is not priming, barning, or topping.
Barning	1.7785	0.2105	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 1.7785 mg/mL higher than those whose task is not priming, barning, or topping.
Topping	1.0254	0.1492	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 1.0254 mg/mL higher than those whose task is not priming, barning, or topping.
Reference Cell Coding – Solution 2			
	Estimates	Standard Errors	
Intercept	4.5086	0.1022	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 4.5086 mg/mL.
Barning	-0.9208	0.2081	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 0.9208 mg/mL lower than those whose task is priming.
Topping	-1.6738	0.1458	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 1.6738 mg/mL lower than those whose task is priming.
Other	-2.6993	0.1480	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 2.6993 mg/mL lower than those whose task is priming.

H_0: $\mu_{priming} = (\mu_{barning} + \mu_{topping} + \mu_{other})/3$

Cell Mean Coding: $H_0: \ \beta_{priming} - \frac{\beta_{barning}+\beta_{topping}+\beta_{other}}{3} = 0$

C = [1 -1/3 -1/3 -1/3] θ_0 = 0

Reference Cell Coding – Solution 1:

$$H_0: \ \beta_0 + \beta_{priming} = \frac{(\beta_0)+(\beta_0+\beta_{barning})+(\beta_0+\beta_{topping})}{3} \equiv$$

$$H_0: \ \beta_0 + \beta_{priming} = \beta_0 + \frac{1}{3}\left(\beta_{barning} + \beta_{topping}\right) \quad \equiv \quad H_0: \ \beta_1 - \frac{1}{3}(\beta_2 + \beta_3) = 0$$

C = [0 1 -1/3 -1/3] θ_0 = 0

Reference Cell Coding – Solution 2:

$$H_0: \ \beta_0 = \frac{(\beta_0+\beta_{other})+(\beta_0+\beta_{barning})+(\beta_0+\beta_{topping})}{3} \equiv$$

$$H_0: \ \beta_0 = \beta_0 + \frac{1}{3}\left(\beta_{barning} + \beta_{topping} + \beta_{other}\right) \quad \equiv \quad H_0: \frac{1}{3}(\beta_1 + \beta_2 + \beta_3) = 0$$

C = [0 1/3 1/3 1/3] θ_0 = 0

Note all these solutions assume equal sample sizes in the groups. You could factor the group sample sizes into these calculations.

- Two-Way ANOVA: For these questions, use the log of salivary cotinine as the response and task and wet as predictors.
  - Fit the two-way ANOVA model with full interaction, and interpret all parameter estimates in your model, clearly stating which coding scheme you used. Discuss the validity of the HILE Gauss assumptions for this model.

Table of task by wet

task	wet: No	wet: Yes	Total
Priming	66	151	217
Barning	44	25	69
Topping	49	161	210
Other	148	50	198
Total	307	387	694

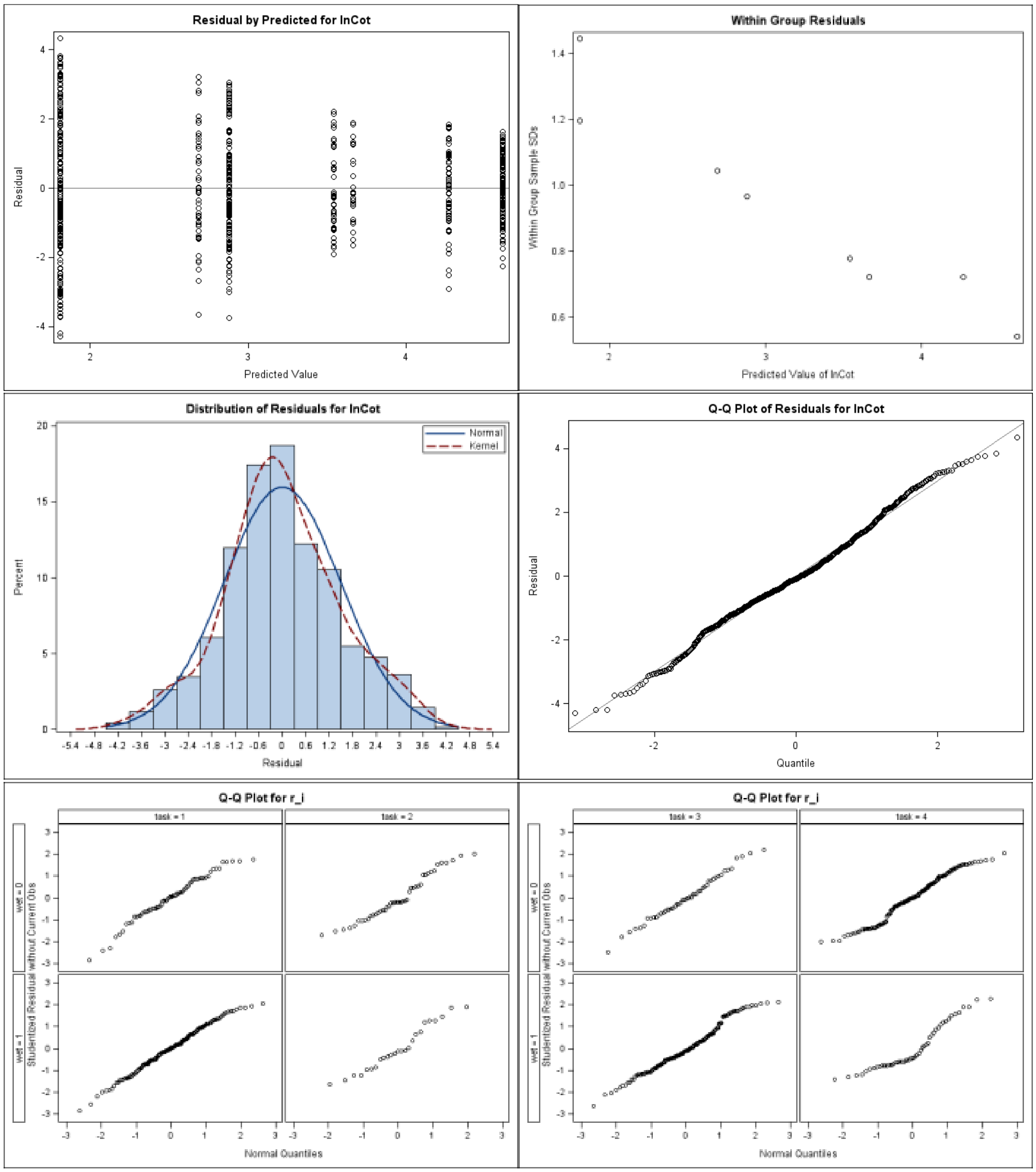
Complete & Not Balanced.

Cell Mean Coding -

$\ln(cotinine) = w0t1\,\hat{\beta}_1 + w1t1\,\hat{\beta}_2 + w0t2\,\hat{\beta}_3 + w1t2\,\hat{\beta}_4 + w0t3\,\hat{\beta}_5 + w1t3\,\hat{\beta}_6 + w0t4\hat{\beta}_7 + w1t4\,\hat{\beta}_8$

	Estimates	Standard Errors	
Priming & Not Wet	4.2693	0.1855	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 4.2693 mg/mL in non-wet working conditions.
Priming & Wet	4.6131	0.1226	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 4.6131 mg/mL in wet working conditions.
Barning & Not Wet	3.5427	0.2272	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 3.5427 mg/mL in non-wet working conditions.
Barning & Wet	3.6670	0.3014	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 3.6670 mg/mL in wet working conditions.
Topping & Not Wet	2.6882	0.2153	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 2.6882 mg/mL in non-wet working conditions.
Topping & Wet	2.8793	0.1188	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 2.8793 mg/mL in wet working conditions.
Other & Not Wet	1.8089	0.1239	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 1.8089 mg/mL in non-wet working conditions.
Other & Wet	1.8105	0.2131	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 1.8105 mg/mL in wet working conditions.

Assumptions:



Homogeneity – Within cells isn't as important as between cells. The scatter plot of the standard deviations of the residuals for each group reveals a potential pattern to the data. This assumption could be violated and since we have inequality of sample sizes between groups this could impact the testing accuracy.

Independence – given through the sample design.

Linearity – This is okay given the design.

Existence – finite sample satisfies this.

Gaussian Errors – The overall histogram of residuals and overall and individual QQ plots appear to support this assumption.

- *Based on this model*, create a table of the estimated mean log cotinine levels, associated standard errors, and how each estimated mean is obtained from the model parameters (e.g., $\hat{\beta}_0 + \hat{\beta}_1$) for each task-wet combination.

Cell Mean Coding			
	Estimates	Standard Errors	$w0t1\,\hat{\beta}_1 + w1t1\,\hat{\beta}_2 + w0t2\,\hat{\beta}_3 + w1t2\,\hat{\beta}_4 + w0t3\,\hat{\beta}_5 + w1t3\,\hat{\beta}_6 + w0t4\hat{\beta}_7 + w1t4\,\hat{\beta}_8$
Grand Mean	3.1599	0.0699	$(\hat{\beta}_1 + \hat{\beta}_2 + \hat{\beta}_3 + \hat{\beta}_4 + \hat{\beta}_5 + \hat{\beta}_6 + \hat{\beta}_7 + \hat{\beta}_8)/8$
Priming	4.4412	0.1112	$(\hat{\beta}_1 + \hat{\beta}_2)/2$
Barning	3.6049	0.1887	$(\hat{\beta}_3 + \hat{\beta}_4)/2$
Topping	2.7837	0.1229	$(\hat{\beta}_5 + \hat{\beta}_6)/2$
Other	1.8097	0.1232	$(\hat{\beta}_7 + \hat{\beta}_8)/2$
Wet	3.2425	0.1017	$(\hat{\beta}_2 + \hat{\beta}_4 + \hat{\beta}_6 + \hat{\beta}_8)/4$
Not Wet	3.0773	0.0961	$(\hat{\beta}_1 + \hat{\beta}_3 + \hat{\beta}_5 + \hat{\beta}_7)/4$

Cell Mean Coding			
	Estimates	Standard Errors	
Priming & Not Wet	4.2693	0.1855	$\hat{\beta}_1$
Priming & Wet	4.6131	0.1226	$\hat{\beta}_2$
Barning & Not Wet	3.5427	0.2272	$\hat{\beta}_3$
Barning & Wet	3.6670	0.3014	$\hat{\beta}_4$
Topping & Not Wet	2.6882	0.2153	$\hat{\beta}_5$
Topping & Wet	2.8793	0.1188	$\hat{\beta}_6$
Other & Not Wet	1.8089	0.1239	$\hat{\beta}_7$
Other & Wet	1.8105	0.2131	$\hat{\beta}_8$

- The Full Model in Every Cell: For these questions, use the log of salivary cotinine as the response and task, and lnnsmoke as predictors.
  - Fit the full model in every cell. Provide and interpret estimates of all parameters for this model.

Cell Mean Coding - $\ln(cotinine) = \hat{\beta}_{0t1}t1 + \hat{\beta}_{0t2}t2 + \hat{\beta}_{0t3}t3 + \hat{\beta}_{0t4}t4 + \hat{\beta}_{1t1}(t1lnnsmoke) + \hat{\beta}_{1t2}(t2lnnsmoke) + \hat{\beta}_{1t3}(t3lnnsmoke) + \hat{\beta}_{1t4}(t4lnnsmoke)$			
	Estimates	Standard Errors	
Priming	4.3344	0.0932	Latino tobacco workers in NC whose task is priming have an average log of salivary cotinine concentration of 4.3344 mg/mL.
Barning	3.1134	0.1666	Latino tobacco workers in NC whose task is barning have an average log of salivary cotinine concentration of 3.1134 mg/mL.
Topping	2.0123	0.0985	Latino tobacco workers in NC whose task is topping have an average log of salivary cotinine concentration of 2.0123 mg/mL.
Other	0.9137	0.0957	Latino tobacco workers in NC whose task is not priming, barning, or topping have an average log of salivary cotinine concentration of 0.9137 mg/mL.
Priming & LNNSMOKE	0.2946	0.0887	Latino tobacco workers in NC whose task is priming average log of salivary cotinine concentration increases by 0.2946 mg/mL for every 1 unit increase in lnnsmoke.
Barning & LNNSMOKE	0.7221	0.1450	Latino tobacco workers in NC whose task is barning average log of salivary cotinine concentration increases by 0.7221 mg/mL for every 1 unit increase in lnnsmoke.
Topping & LNNSMOKE	1.2305	0.0894	Latino tobacco workers in NC whose task is topping average log of salivary cotinine concentration increases by 1.2305 mg/mL for every 1 unit increase in lnnsmoke.
Other & LNNSMOKE	1.7789	0.1022	Latino tobacco workers in NC whose task is not priming, barning, or topping average log of salivary cotinine concentration increases by 1.7789 mg/mL for every 1 unit increase in lnnsmoke.

  - Report an appropriate test of whether task is related to cotinine levels. If this test is significant, report step-down tests to determine exactly where differences lie. For all tests reported, be sure to state H_0 clearly and give explicit justification for which tests were used and why.

Use a test of coincidence; the hypothesis indicates that the slopes and intercepts are all equal regardless of task.

H_0: $\beta_{0t1} = \beta_{0t2} = \beta_{0t3} = \beta_{0t4}$ and $\beta_{1t1} = \beta_{1t2} = \beta_{1t3} = \beta_{1t4}$

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
TEST OF COINCIDENCE	6	922.1700624	153.6950104	119.29	<.0001

$F(6, 687) = 119.29$ p-value < 0.001 Reject H_0
Task is related either by slope or intercept to cotinine levels at the 0.01 level.

Step down to determine if the differences are in the slopes or intercepts.

H_0: $\beta_{1t1} = \beta_{1t2} = \beta_{1t3} = \beta_{1t4}$

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
STEPDOWN: EQUAL SLOPES	3	169.6441128	56.5480376	43.89	<.0001

$F(3,690) = 43.89$ p-value < 0.0001 Reject H_0

The slopes are significantly different from each other at the 0.01 level.

H_0: $\beta_{0t1} = \beta_{0t2} = \beta_{0t3} = \beta_{0t4}$

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
STEPDOWN: EQUAL INTERCEPTS	3	902.0132306	300.6710769	233.36	<.0001

$F(3,690) = 233.36$ p-value < 0.0001 Reject H_0

The intercepts are significantly different from each other at the 0.01 level.

Use pair-wise tests to determine exactly which intercepts/slopes are different.

$\alpha = 0.05 / 6 = 0.0083$ $\sim F(1, 692)$

H_0: $\beta_{0ti} = \beta_{0tj}$

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
PAIRWISE INTERCEPTS T1 V T2	1	52.7322641	52.7322641	40.93	<.0001
PAIRWISE INTERCEPTS T1 V T3	1	377.7620263	377.7620263	293.20	<.0001
PAIRWISE INTERCEPTS T1 V T4	1	845.0460533	845.0460533	655.87	<.0001
PAIRWISE INTERCEPTS T2 V T3	1	41.7145812	41.7145812	32.38	<.0001
PAIRWISE INTERCEPTS T2 V T4	1	168.9622476	168.9622476	131.14	<.0001
PAIRWISE INTERCEPTS T3 V T4	1	82.4489524	82.4489524	63.99	<.0001

Reject H_0 for all ij pairs

All intercepts are significantly different from each other at the 0.01 level.

H_0: $\beta_{1ti} = \beta_{1tj}$

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
PAIRWISE SLOPES T1 V T2	1	8.1529052	8.1529052	6.33	0.0121
PAIRWISE SLOPES T1 V T3	1	71.1683903	71.1683903	55.24	<.0001
PAIRWISE SLOPES T1 V T4	1	155.0229026	155.0229026	120.32	<.0001
PAIRWISE SLOPES T2 V T3	1	11.4843308	11.4843308	8.91	0.0029
PAIRWISE SLOPES T2 V T4	1	45.7480465	45.7480465	35.51	<.0001
PAIRWISE SLOPES T3 V T4	1	21.0166241	21.0166241	16.31	<.0001

Reject H_0 for all ij pairs except i=1 and j=2

Except for task 1 and 2, the slopes are significantly different from each other at the 0.01 level.