BIOS 663 HW 5

Yue Jiang

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Exercise 1.

(a). To test whether all cell means are equal, we perform a one-way ANOVA and an F-test on the group means. Our null hypothesis is H_0: all βs are equal, and our alternative hypothesis is H_A: at least one of the β_is is not equal to the others. Given our data, we have an F-statistic of 116.2 on 3 numerator and 690 denominator degrees of freedom, which corresponds to a p-value less than 0.0001. Thus, at the $\alpha = 0.05$ level, we reject the null hypothesis in favor of the alternative. There is sufficient evidence to suggest that at least one of the tasks has a different log cotinine level than the others. That is, there is sufficient evidence to suggest that not all cell means are equal.

(b). Our overall test of the task effect was significant, so we perform step-down analysis of all pairwise comparisons using the Scheffe correction. A summary of the findings can be found below:

Comparison	Est. Mean Δ	df	F-statistic	F/(G-1)	p-value
Task1 - Task2	0.9208	3, 690	19.5760	6.5253	0.0002
Task1 - Task3	1.6739	3, 690	131.8710	43.9572	<0.0001
Task1 - Task4	2.6993	3, 690	332.6840	110.895	<0.0001
Task2 - Task3	0.7531	3, 690	12.9897	4.3299	0.0049
Task2 - Task4	1.7785	3, 690	71.3780	23.7927	<0.0001
Task3 - Task4	1.0254	3, 690	47.2588	15.7529	<0.0001

(c). For cell mean coding, the parameter estimates are the cell means for each group. That is, β_i the sample mean of log cotinine for task *i*. In this type of coding, since we have a cell mean estimate for each group, there is no intercept term. The essence, contrast, and θ_0 matrices to test that average cotinine for workers involved in priming are greater than the levels for all other task groups are given below:

$$\text{Es}(\mathbf{X}) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}; \quad \mathbf{C} = \begin{bmatrix} 1 & -1/3 & -1/3 & -1/3 \end{bmatrix}; \quad \boldsymbol{\theta_0} = \begin{bmatrix} 0 \end{bmatrix}$$

(d). For reference cell coding with task 4 as the reference group, the parameter estimates are the difference between levels in each group and the reference, which serves as our intercept. That is, β_i is the difference between mean log cotinine levels of task *i* and task 4, for i = 1, 2, 3, and β_4 is the

mean log cotinine level among task 4. The essence, contrast, and θ_0 matrices to test that average cotinine for workers involved in priming are greater than the levels for all other task groups are given below:

$$\text{Es}(\mathbf{X}) = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 \end{bmatrix}; \quad \mathbf{C} = \begin{bmatrix} 0 & 1 & -1/3 & -1/3 \end{bmatrix}; \quad \boldsymbol{\theta_0} = \begin{bmatrix} 0 \end{bmatrix}$$

Exercise 2.

(a). For the full model in every cell, we include each main effect, as well as all two-way interactions, noting that task is a categorical predictor with four levels, wet is a categorical predictor with two levels, and lnnsmoke is a continuous predictor.

Variable	Estimate	Interpretation
Intercept	0.83429	Predicted log cotinine given task 4, dry conditions, and 0 lnnsmoke
Task1	3.07755	Pred. diff. in predicted log cotinine given dry conditions and 0 lnnsmoke between task 1 and task 4
Task2	2.16704	Pred. diff. in predicted log cotinine given dry conditions and 0 lnnsmoke between task 2 and task 4
Task3	0.93629	Pred. diff. in predicted log cotinine given dry conditions and 0 lnnsmoke between task 3 and task 4
Wet	0.28201	Pred. diff. in log cotinine given 0 lnnsmoke and task 4
lnnsmoke	1.84393	Expected change in log cotinine for each additional unit of lnnsmoke, given dry conditions and task 4
Task1*Wet	0.29159	Pred. diff. in predicted log cotinine given 0 lnnsmoke between task 1 wet and task 4 dry
Task2*Wet	0.04327	Pred. diff. in predicted log cotinine given 0 lnnsmoke between task 2 wet and task 4 dry
Task3*Wet	0.03414	Pred. diff. in predicted log cotinine given 0 lnnsmoke between task 3 wet and task 4 dry
Task1*lnnsmoke	-1.37148	Pred. diff. in the effect of lnnsmoke on log cotinine between task 1 and task 4 for any given wet/dry condition
Task2*lnnsmoke	-1.05515	Pred. diff. in the effect of lnnsmoke on log cotinine between task 2 and task 4 for any given wet/dry condition
Task3*lnnsmoke	-0.43972	Pred. diff. in the effect of lnnsmoke on log cotinine between task 3 and task 4 for any given wet/dry condition
Wet*lnnsmoke	-0.22634	Pred. diff. in the effect of lnnsmoke on log cotinine between wet and dry conditions for any given task

(b). Note that when we compare the two models, the ANCOVA model is nested within the full model in every cell. Thus, we will test whether the full model contributes additional information beyond the ANCOVA model regarding the relationship between the predictors and the response.

For the full model in every cell, assigning β_9 through β_{12} to be the coefficients for the additional terms (the interactions between task and lnnsmoke and wet and lnnsmoke), our H_0 is $\beta_i = 0$ (for i = 9, 10, 11, 12), which we are testing against H_A: at least one is not zero. The test statistic is F distributed and equal to = 32.91, with 4 and 689 degrees of freedom.

The p-value associated with this statistic is <0.0001, which is significant at the $\alpha = 0.05$ level. Thus, we reject the null hypothesis. There is sufficient evidence to conclude that at least one of the additional betas is not equal to zero. That is, we choose the full model - at least one of the additional terms contributes information about our response, log cotinine. This is corroborated by examining the coefficients of the interaction terms involving both categorical and continuous predictors, which are significant (in the full model in every cell).

(c). Note that the model in part (c) is against nested, this time in the ANCOVA model. Performing a nested F-test like in part (b), we are testing the hypothesis that H_0: the βs corresponding to wet (including the interaction with task) are zero; that is, wet conditions are not related to cotinine levels. The alternative hypothesis is that wet conditions are related to cotinine levels - at least one of the βs is not zero. We find that the F statistic is 2.95 on 4 and 689 degrees of freedom, corresponding to a p-value of 0.0196, which is significant at $\alpha = 0.05$. Thus, we reject the null hypothesis. There is sufficient evidence to conclude that at least one of the additional betas is not equal to zero. That is, wet conditions appear to be related to cotinine levels.

Thus, we will perform step-down analysis to determine where the differences lie. With our full ANCOVA model, we have the following table of slopes, with mean slopes in each cell not weighted for population size.

Note that we are comparing within each task to see whether there is a significant difference between wet and dry conditions, and we will perform an F-test on 1 and 685 degrees of freedom for each group, as we can think of this test for each task as a nested F-test (our full model includes lnnsmoke, the individual task, and wet, and our reduced model does not contain wet). Our null hypothesis is H_0: within each task, cotinine levels are the same across wet and dry conditions, and our alternative is that they are not the same within each task (we are performing four tests).

	Task 1	Task 2	Task 3	Task 4
Wet	4.08665	3.05279	2.19640	1.37497
Dry	3.50140	2.84614	2.02499	1.27248
$F_{1,685}$	10.35	0.45	0.73	0.26
p-value	0.0014	0.5025	0.3932	0.6106

We find that at the $\alpha = 0.0125$ level (adjusted with the Bonferroni correction for multiple comparisons), the only group of task that has a significant difference between wet and dry is task 1.

Exercise 3.

(a). The predicted probabilities can be found in the table below. In all cases, the predicted probabilities were equal (barring very slight differences) to the sample proportions.

	Task 1	Task 2	Task 3	Task 4
Wet	0.5695462	0.2400145	0.1677162	0.1000022
Dry	0.4090969	0.2500023	0.1428644	0.1351349

(b). We are testing the null hypothesis H_0: all of the probabilities in each category combination are correct, against the alternative H_A: at least one of the probabilities is incorrect. We find that the Pearson Goodness-of-Fit statistic is χ^2_3 distributed, with a value of 3.2866, corresponding to a p-value of 0.3495, which is not significant at the $\alpha = 0.05$ level. Hence, we fail to reject the null. There is insufficient evidence to suggest that the expected probabilities are not correct. In particular, there is sufficient evidence to suggest that the reduced model is adequate in predicting the probability of having high cotinine.

(c). A table of the parameter estimates and interpretations is found below:

Variable	Estimate	Interpretation
Intercept	-2.0134	Predicted log-odds of high cotinine given dry conditions and task 4
Task1	1.8955	Predicted log-odds of high cotinine given dry conditions and task 1
Task2	0.7858	Predicted log-odds of high cotinine given dry conditions and task 2
Task3	0.1427	Predicted log-odds of high cotinine given dry conditions and task 3
Wet	0.2891	Predicted log-odds of high cotinine given wet conditions and task 4

(d). After adding BMI to our reduced model, we find that $\beta_{BMI} = 0.03898$. Thurs, each additional unit increase in BMI increases the odds of having high cotinine by a multiplicative factor of $e^{0.03898} = 1.03975$; each 3 unit increase in BMI increases the odds of having high cotinine by a multiplicative factor of $e^{3\times 0.03898} = 1.12405$.