

I. Estimated standard errors for cell means

- A. Using the pooled estimate of the variance of the source population to estimate the standard error of the mean for cell means

i. One-way between groups ANOVA

For a one-way between groups ANOVA, we normally assume homogeneity of variance in the groups (e.g., $\sigma^2_1 = \sigma^2_2$), and so we can estimate the common population variance using MS_{error} from the ANOVA:

$$\hat{\sigma}_M = \sqrt{\frac{MS_{S/A}}{n}}$$

ii. Two-way between groups ANOVA

For a two-way between groups ANOVA, we also normally assume homogeneity of variance in the groups, so we can once again estimate the common population variance using the MS_{error} from the ANOVA. To find an estimate of the standard error to use when graphing cell means, we can use the $MS_{S/AB}$ and the cell n .

$$\hat{\sigma}_M = \sqrt{\frac{MS_{S/AB}}{n}}$$

- B. Use the cell standard deviations to estimate the cell standard errors.

If you want to make graphs with standard error bars that are descriptive (rather than inferential), then use the cell standard deviations divided by the square root of the cell n , rather than the MS_{error} from the overall ANOVA. Done in this way, these bars will differ slightly across the cells of the design.

II. Standard errors for main effect means

- A. Use square root of the pooled error term from overall ANOVA and divide by the square root of the number of observations in each main effect mean. For example, for factor A:

$$\hat{\sigma}_{M_A} = \sqrt{\frac{MS_{S/AB}}{bn}}$$

- B. Use a “partially pooled” error term from just the cells involved in that particular main effect mean, and then divide by the number of observations. One way to get this partially pooled error term is to run anovas that are like simple main effect tests, and use the pooled error terms from those to estimate the main effect mean standard errors. The other way to do it is to calculate a pooled estimate of variance by hand from the cell variances. If the cell n’s are equal, you can just average the relevant s^2 values. If the cell n’s are not equal, you can weight each cell s^2 by n-1, and divide by the sum of the weights.
- C. A wrong way to calculate main effect mean standard errors! Don’t do this except to see why it is wrong.

This method ignores one of the two factors in a two-way design and estimates the population variance from all the scores in a given level of the other factor. This is incorrect because the estimate of the population variance will include variance due to the factor that was ignored. See the numerical example below. It illustrates how this can inflate the estimated standard errors of the main effect means.

III. Example using data in Handout #15

A. Estimates of cell standard errors

(i) Pooled error from one-way ANOVA: $MS_{S/A} = 7.38$, $\hat{\sigma}_M = \sqrt{\frac{7.38}{8}} = 0.96$

or, pooled error from two-way ANOVA: $MS_{S/AB} = 7.38$, $\hat{\sigma}_M = \sqrt{\frac{7.38}{8}} = 0.96$

(ii) Separately for each group: $\hat{\sigma}_{Y_{A1}} = 1.01$, $\hat{\sigma}_{Y_{A2}} = 1.05$, $\hat{\sigma}_{Y_{A3}} = 1.10$, $\hat{\sigma}_{Y_{A4}} = 0.59$

Cell $s^2 = 8.21, 8.84, 9.70$, and 2.79 for A_1 to A_4 , respectively.

B. Estimates of main effect standard errors:

- (i) Using pooled error from ANOVA, let factor A be “Drug 1” and factor B be “Drug 2.”

$$\hat{\sigma}_{M_A} = \sqrt{\frac{7.38}{16}} = 0.6792 \quad \text{AND} \quad \hat{\sigma}_{M_B} = 0.6792$$

Notice that estimated main effect standard errors are smaller than estimated cell standard errors from the pooled method (see A.i. above). This makes sense because each main effect mean has twice the observations of a cell mean in a 2 x 2 design.

(ii) “Partially pooled” estimate of variance

For the standard error of main effect mean of “Drug 1 Absent” we average the s^2 values for cells A_1 and A_3 : $(8.21 + 9.70) = 8.96$. Then dividing by 16, and taking square root, the estimated SE = .75. Similarly for “Drug 1 Present” we use cells A_2 and A_4 , so that estimated SE = .60. For main effect mean of “Drug 2 Absent” the estimated SE = .73, and for “Drug 2 Present” the estimated SE = .62.

Notice that some of these estimated se’s are larger and some are smaller than the estimates that came from the completely pooled error term method (see B.i. above).

- (iii) The wrong way. Find s^2 for all scores in “Drug 1 Absent,” ignoring Drug 2: $s^2 = 9.30$. Using this, the estimated SE = .76 for “Drug 1 Present,” $s^2 = 8.46$, and estimated SE = .73. For “Drug 2 Absent,” $s^2 = 11.46$, and estimated SE = .85. Finally, for “Drug 2 Present,” $s^2 = 12.83$, and the estimated SE = .90.

Notice that the standard errors estimated in this way are pretty “bloated” compared to (i) or (ii) because variance due to the ignored factor is included in the s^2 .