

Outline for all DAWG ANOVA Modules

Step 1. Start SAS program (begin SAS session).

Step 2. Decide if you have a Specialized Feature.

Download an example file for first run through your DAWG module.

Step 3. Access your data: copy and paste it into the SAS Editor Window.

Step 4. Create program statements to read in the data:

- Click your Specialized Feature in the gray box and copy the statements that pop up into SAS, before the data values in the Editor Window.
- If using your own data, modify the INPUT statement to indicate your variable names.
- Delete any header text that you may have pasted (such as a row of variable names).
- Put a semicolon on the line following the data.
- Add the PROC PRINT; RUN; statements below the data.

Step 5. Run SAS program to read data: With cursor in Editor Window, hit the Submit () icon on the toolbar.

- In Results Viewer window, verify that the correct number of observations is present, and that variable values match your original data.

Step 6. Download and save the macro file (right-click, Save Target As or Save Link Target As) to your computer in an easy-to-remember directory. Skip this step if you previously saved danda.sas, but keep an eye out for new versions.

Step 7. Perform analysis.

- Based on your specialized features, click in gray table to obtain the two %MMAOV statements that you will copy into the SAS Editor Window.
- In the Editor Window, change the %INCLUDE statement to identify where you saved the macro.
- If you are running your own data, modify the code words as explained in the bottom gray table popups.
- Do the transformation step, if you found on a prior run that this was necessary.
- Run the program (click the Submit icon)

Step 8. Check Log Window. If errors occurred, go to the Editor Window, make corrections and re-run.

Step 9. Interpret results

- From the gray table, pick an output with your specialized feature, and animal or plant choice. This file will appear in a separate popup window as a pdf file with clickable comments.
- Click on the red arrows to read about output that is used in scientific reporting. These include the ANOVA table, treatment means, and differences among the means.
- Go to your SAS Results Viewer window and verify that you can find the tables discussed in the pdf.
- If you returned to this step after transforming your data, you will need to interpret transformed means.

Step 10. However, for your interpreted results in Step 9 to be accurate and meaningful, you must check the diagnostic output. These are indicated by yellow arrows in the pdf output you opened in Step 9.

- Go through the ANOVA diagnostics Module and the pdf to check normality, equal variance, outliers, etc. If problems are found data corrections and/or transformation are needed, and you will go back to Step 7 to rerun the analysis.
- You may need to repeat the Step 7-10 analysis loop several times before all diagnostic issues are resolved.

SAS Editor Window

The screenshot shows the SAS Editor window titled "Editor - Untitled1". The window contains a SAS program with the following code:

```
DATA one;  
  INPUT Treatment $ Exper_Unit Weight;  
  DATALINES;  
  TRT-A 1 12.7  
  TRT-A 2 16.6  
  TRT-A 3 15.7  
  TRT-A 4 16.9  
  TRT-A 5 14.2  
  TRT-B 6 23.2  
  TRT-B 7 20.9  
  TRT-B 8 25.0  
  TRT-B 9 24.6  
  TRT-B 10 25.7  
  TRT-C 11 20.1  
  TRT-C 12 19.9  
  TRT-C 13 20.8  
  TRT-C 14 20.6  
  TRT-C 15 23.0  
  TRT-D 16 21.7  
  TRT-D 17 19.8  
  TRT-D 18 18.4  
  TRT-D 19 19.3  
  TRT-D 20 21.9  
;  
PROC PRINT;  
RUN;  
%INCLUDE 'c:\DANG\MMAOV.SAS';  
%MMAOV(One, Weight, CLASS=Treatment, FIXED=Treatment );
```

Annotations in the image indicate the following steps:

- Step 4** program statements to read in the data (pointing to the `DATA one;` and `DATALINES;` statements)
- Step 3** copy data (pointing to the data rows)
- Step 4** add semicolon (pointing to the semicolon at the end of the data block)
- Step 6** check that data were read correctly (pointing to the `PROC PRINT;` and `RUN;` statements)
- Step 7** Get and modify statements from pop-ups, to perform analysis (pointing to the `%INCLUDE` and `%MMAOV` macro statements)