

Introduction

Introduction

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MATFORSK (Norwegian Food Research Institute) is collaborating with the Technical University of Denmark (DTU) and the Faculty of Life Science¹ (KU-LIFE) at University of Copenhagen within the area of statistical methodology and strategies for quality assurance of sensory data. One integral part of this collaboration is the development of the software PanelCHECK. PanelCHECK is a tool that uses various of plots to evaluate results from descriptive analyses. These plots help the user to identify easily the performance of individual assessors and allow for precise and rapid feedback for future training sessions.

Frequently MATFORSK, DTU and KU-LIFE offers courses where participants are taught how to use PanelCHECK, how to interpret analysis results from the various plots and how to utilise the gained information in the best possible way. For more information about the courses please contact us at: panelcheck@matforsk.no. Also you may find information on upcoming events at www.matforsk.no/panelcheck.

PanelCHECK is open source software, meaning that it can be downloaded, used and distributed for free. Download the latest version at www.matforsk.no/panelcheck
PanelCHECK is published and distributed under the open source GPL (General Public Licence)

MATFORSK: www.matforsk.no

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¹Formerly known as Royal Veterinary and Agricultural University of Denmark (KVL).

Getting started

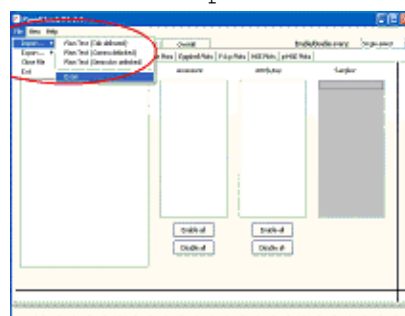
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Below you find a short guide for importing data and creating plots. For more information on plot types see *Chapter Analysis*.

First thing to do is to import sensory data acquired from a sensory panel. The data must be arranged such that assessors, samples, replicates and attributes are ordered column wise. In the following the example data set included in this installation will be used. More information on the structure of sensory data is found in *Sec. Importing data*.

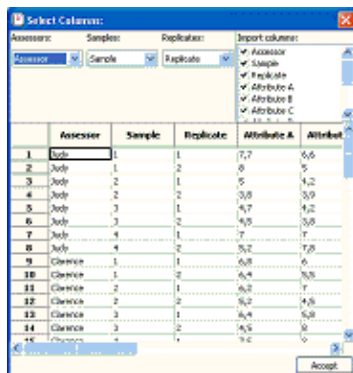
Guide to import data and making a MEAN & STD plot:

1. Select **File/Import.../Excel**
2. Find the example data set called `SampleData.xls`

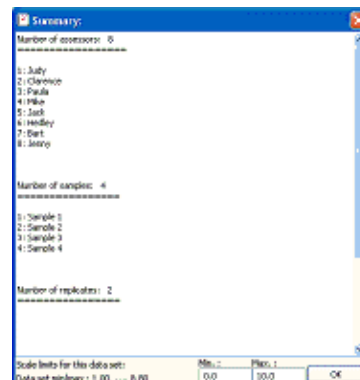


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3. In the present example the ordering of the columns are in correspondance with the default ordering, thus press **Accept** to continue the import.



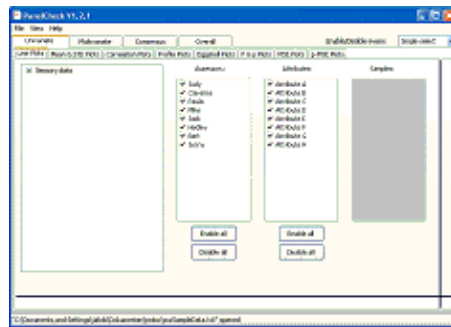
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4. Another popup will appear, giving you various information on the data. Press **OK** and the import will continue and finish.

Having imported the sensory data, the panelCHECK now looks like:

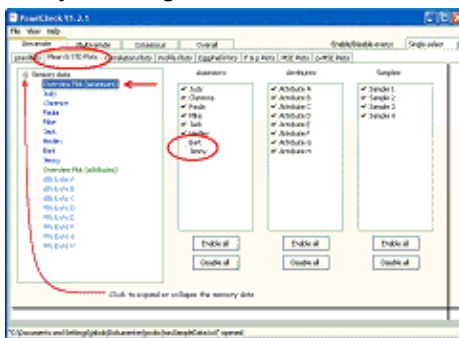


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5. Assume you want to plot the means and standard deviations of attributes and assessors for each assessor.

&∀Αριαλ>Υνδερ τηε Υνιωαριατε φαν σελεχτ τηε φαν ναμεδ MEAN & ΣΤΔ Πλοτσ.

- Also assume that you are not interested in the assessors named Bart and Jenny, and therefore uncheck them in the list of assessors.
- Expand the Sensory Data by clicking on the +.
- Double-click on **Overview Plot (assessors)**.
- A plot with the 6 assessors appears.
- By clicking on one of the small histograms a full size plot of that histogram appears.



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From this kind of plot, it is possible to compare the assessors agreement on attributes and to some extent how equal the samples are. Further interpretation is left to the reader and *Chapter Analysis*.

Operating PanelCHECK

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The following sections gives a few explanations on how to use PanelCHECK.

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- [Exporting](#)

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- [Plots](#)

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- [Overview Plots](#)

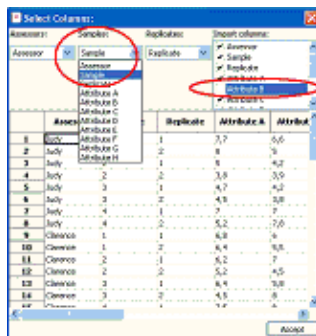
Importing data

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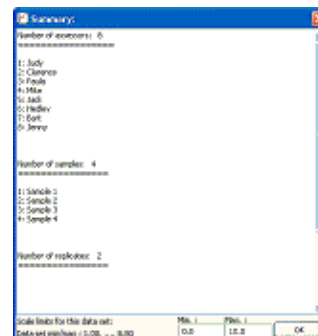
Import of data has been considerably improved. Besides TAB delimited tables, both COMMA and SEMICOLON delimited tables may be imported.

Also the order of the Assessor, Sample and Replicate, need no longer to be in that specific order. During the process of data import you will be asked (see the figure below) to specify the columns where the Assessors, Samples and Replicates are placed. However, by default above order is assumed, which is also the order required by older versions of PanelCHECK.

Furthermore, you may exclude import of some Attributes, that you might not be of you interest at that time.



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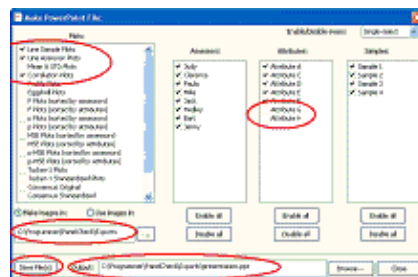
Exporting

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Exporting (in the File menu) is a features that enables systematic generation of figures and Powerpoint presentations.

When exporting a popup will appear. Check boxes for each plot type defines the plots to be exported. In the Assessor, Attributes and Sample list specific assessors, attributes and samples may be disabled, just like on the main screen, when single plots are created.

When the plot types of interest have been selected, the presentation is created by pressing **Save File(s)**. By default the presentation is saved in a sub folder of the PanelCHECK installation path (usually C:\Programs\PanelCheck\ for an English version of Windows XP) called Exports and with file name presentation.ppt.



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Note: Exporting to Powerpoint requires Powerpoint to be installed on the computer.

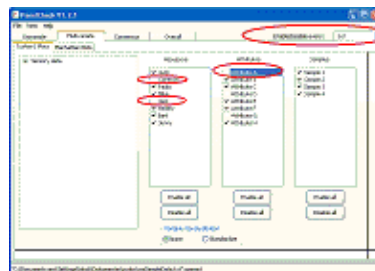
Enable and disable

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Assessor, Samples and Attributes may be exclude from the analysis, by unchecking them in the corresponding lists.

Systematic exclusion of for instance every 3rd attribute is possible by setting the value of "enable/disable every" to "3rd".

In the figure below the assessors called Clarence and Jack has been disabled from the analysis. Furthermore, every third attribute, beginning from "Attribute A", has been excluded by clicking on "Attribute A" text (not the check box).



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Plots and figures

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There are two types of plots you can invoke by double-clicking on the tree control on the left side of the interface.

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Plots

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By double-clicking on an item in the control tree a line plot will appear, including all scores for the item and its contents. E.g. double-click on an assessor will include all the replicates for this assessor since replicates is a lower level to assessors.

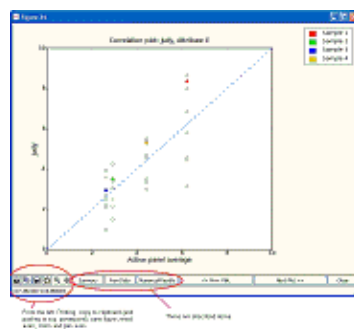
The toolbar at the bottom of plots gives the possibility to print, save, zoom and pan/rotate axes the figure. Also summary, raw data and numerical results can be accessed.

Summary is a list of Assessors, Samples, Replicates and Attributes on which the analysis is performed. If anything unchecked, it will not be included in the summary and the analysis.

Raw data covers like the summary only the Assessor, Samples, Replicates and Attributes that are enabled for analysis. Furthermore, the attribute values are included and arranged as a spreadsheet.

Numerical Results presents the results of the analysis and is dependent on the plot type. For instance for the [Line Plots](#) the average, minimum, maximum and std. deviation for each attribute are displayed.

Example: Correlation Plot



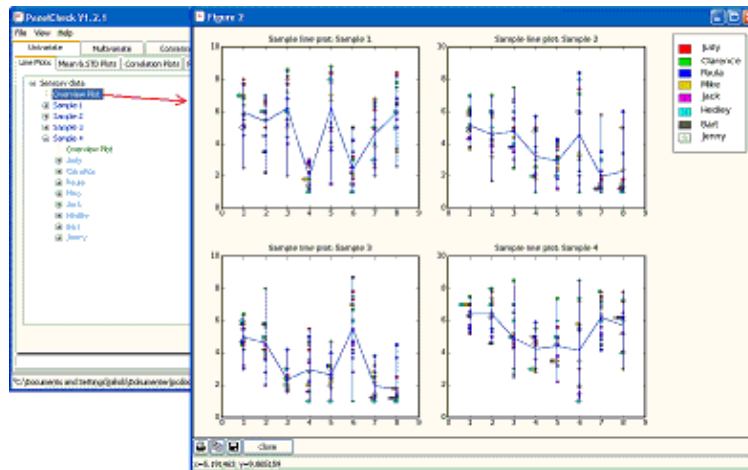
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Note: In Tucker-1 and consensus plots there are additional buttons on the figure, which controls the number of principal components (PC), and their association with x- and y-axes.

Overview Plots

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For all plots types (except F & p plots) overview plots are possible. The overview will make one plot for each Assessor or Sample on the same window. A plot for a specific Assessor or Sample may be achieved from the overview plots by clicking on the corresponding graph.



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Note: Since the overviews are quite compressed the labels on the x-axis are replaced by numbers. Also the toolbar on the bottom of the window is limited to printing and saving.

Analysis

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In the following sections the various analyses and plots are shortly described.

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- [Correlation Plots](#)

&∀τεμπ0015.ητμλ∇>Profile Plots

- [Eggshell Plots](#)

&∀τεμπ0017.ητμλ∇>F & p Plots

- [MSE Plots](#)

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- [Tucker-1 Plots](#)

&∀τεμπ0022.ητμλ∇>Manhattan Plots

- Consensus
- PCA [Original](#)

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- [Mixed Model ANOVA](#)

Univariate

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A statistical analysis method is univariate if the models depend on only one variable.

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← Correlation Plots

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← Eggshell Plots

- [F & p Plots](#)

← MSE Plots

- [p-MSE Plots](#)

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262–270

Line Plots

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A line plot shows the attributes along the x-axis and score of the assessor along the y-axis, together with the average over samples and replicates.

By double-clicking on an item in the control tree a line plot will appear, including all scores for the item and its contents. E.g. double-click on an assessor will include all the replicates for this assessor since replicates is a lower level to assessors.

Note: Specific assessors and attributes may be excluded from the analysis, by disabling them.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262&"left" >

Mean & STD Plots

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In a Mean & STD plot, the data is grouped either by Assessors (assessors along the x-axis) or Attributes (attributes along the x-axis) and averages is calculated over Samples and Replicates is plotted in a histogram with STD values indicated by stems.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262<"left" >

Correlation Plots

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The correlation plot shows data for one attribute at a time. The sample score of each assessor is plotted against the panel average score for the same sample. One assessor is highlighted (red filled spots) while the remaining assessors are shown with unfilled spots. If an assessor agrees completely with the panel average, the sample will fall on the blue dashed line.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262&"left" >

Profile Plots

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A profile plot show the samples along the x-axis and scores for each assessor on the y-axis, together with the average over assessors. The most left sample is ranked lowest (low attribute intensity) be the consensus and vice versa.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262&"left" >

Eggshell Plots

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An eggshell plot shows how each assessor ranks all tested samples in relation to the consensus. The bold purple line represents the consensus line (consensus sample ranking) while each of the remaining lines represents the sample ranking of one specific assessor. The closer the line of a one assessor is to the consensus line, the more this assessor agrees ranking-wise with the consensus. The most left sample is ranked lowest (low attribute intensity) by the consensus and vice versa.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262&"left" >

F & p Plots

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This function generates F plots, plotting F-values from a one-way ANOVA for each assessor. Each vertical line is the F-value of one specific assessor for a specific attribute.

The F-value is a measure of the ability of an assessor to discriminate between samples. The higher the F-value, the better.

The radio buttons under sorted by, decides whether the F-values are sorted by assessors or attributes.

The &"left" >The red and black horizontal lines indicate the significance level at 1% and 5%, respectively.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262–269.

MSE Plots

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This function generates MSE plots, plotting MSE-values from a one-way ANOVA for each assessor. Each vertical line is the MSE-value of one specific assessor for a specific attribute. An MSE-value can be used as a measure of ability to deliver good replicates. The lower the MSE-value, the better.

The radio buttons under sorted by, decides whether to sort by assessors or attributes.

The &"left" >

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262–269.

p-MSE Plots

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This function generates p-MSE plots, plotting p- and MSE-values from a one-way ANOVA for each assessor. MSE values are plotted along the x-axis and the p-values are along the y- axis. Each point in the plot represents one assessor for a specific attribute.

p-values and MSE-values are measures of discrimination and repeatability, respectively. The closer a point is to the origo (low values for both, p and MSE), the better the assessor has performed.

Further reading:

Oliver Tomic, Asgeir Nilsen, Magni Martens, Tormod Næs, *Visualization of sensory profiling data for performance monitoring*, LWT **40** (2007) 262&"left" >

Multivariate

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Statistical methods where the models attempt to include several (more than one) independent variables.

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∀Tucker-1 Plots

- [Manhattan Plots](#)

Tucker-1 Plots

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Two types of plots are generated for the Tucker-1 method. The common scores plot, the first type, displays how the samples relate to each other based on the assessors

The more noise an attribute of an assessor contains, the closer the point will appear in the middle. The more structured information an attribute contains, the closer it will appear to the outer circle (100 % explained variance for that attribute).

In both plots the first two principal components (PC) are shown. The buttons with arrows are used to change the PC on the x- and y-axes. At most 4 PCs are possible.

It is possible to highlight either one specific assessor or one specific attribute in the plot.

In the tree control all assessors and attributes are listed, together with “Common Scores” (on the top of the control tree). By selecting a specific assessor, all correlation loadings for this assessor are plotted. Similarly, for a specific attribute.

By default no Variable standardization of the data takes place. Alternatively, data may be standardized by checking the respective radio button.

Variable standardization

For the Tucker-1 analysis, data may be standardized the following way:

$$x_{\text{new}} = (x_{\text{new}} - x_{\text{new}}) / \text{STD}(x)$$

This is also known as autoscaling. By default the value is None.

Manhattan Plots

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Not yet implemented.

Consensus

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In consensus the attention is put on the samples instead of the panel. Hence, consensus concerns the product while the panel is assumed static and well-trained.

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Original

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Consensus on the original data, i.e. no standardization is performed, is a plain PCA analysis comprising scores, loadings, correlation and explained variances for the first two principal components (PC).

The PC number to be used may be changed by clicking the buttons with arrows on the figures. The maximum number of PCs calculated depends on how many samples or attributes the data set contains. The lowest number of any of the two will be the number of PCs calculated.

Further reading:

Risvik E. & Naes T., *Multivariate Analysis of Data in Sensory Science*, 1996 (Elsevier Science).

Standardized

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In the standardized consensus analysis, the data is standardized prior to the PCA analysis. Otherwise the analysis is similar, see Section [Original](#).

Standardization of data is important, if it is suspected that some assessors avoids to use the full scale or is disagreed with the other assessors on the span of one or more attributes. Typically, results are improved by applying standardization, but not necessarily more correct.

STATIS

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STATIS is a very intuitive and visually powerful analysis method. Like PCA it decomposes the variation in a dataset into principal components and monitor the assessors in the principal component space according to their evaluations of the samples together with the average scores of the samples (or attributes).

Further reading:

Abdi, H., & Valentin, D. (2007). STATIS. In N.J. Salkind (Ed.): Encyclopedia of Measurement and Statistics. Thousand Oaks (CA): Sage. pp. 955-962. (Get it [here](#)).

Overall

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Mixed Model ANOVA

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Replicate x Sample vs Error Plots / Replicate x Sample F-statistics

A Replicate*Sample vs Error plot depicts a bar for each attribute indicating whether there is inconsistency in sample differences from replicate to replicate. A colored bar (yellow, orange, red) means that there seems to be such and a grey bar that there is not.

The color of the bar indicates the corresponding P-value:

Yellow: P-value < 0.05

Orange: P-value < 0.01

Red: P-value < 0.001

The bar size equals the F-statistic for Replicate*Sample interaction

$$F = MS(\text{Rep*Sample}) / MS(\text{Error})$$

from a 3-way ANOVA with all main effects and 2-way interactions:

Attribute = Rep + Sample + Assessor + Rep*Sample + Assessor*Sample + Rep*Assessor

Note: This analysis and plot is only relevant IF the replications were carried out in different sessions, one session for each replication or a grouped collection of sessions for each replication. If the replications were merely carried out in a random order then the Replication effects (main and interactions) in this analysis are expected to be NS (apart from &"left" >

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

Sample x Assessor vs Error Plots / Sample x Assessor F-statistics

An Sample*Assessor vs Error plot depicts a bar for each attribute indicating whether there is inconsistency in sample differences from assessor to assessor. A colored bar (yellow, orange, red) means that there seems to be such and a grey bar that there is not.

The color of the bar indicates the corresponding P-value:

Yellow: P-value < 0.05

Orange: P-value < 0.01

Red: P-value < 0.001

The bar size equals the F-statistic for Sample*Assessor interaction

$$F = MS(\text{Sample*Assessor}) / MS(\text{Error})$$

from a 3-way ANOVA with all main effects and 2-way interactions:

Attribute = Rep + Sample + Assessor + Rep*Sample + Sample*Assessor + Rep*Assessor

Note: Formally this analysis is adequate IF the replications were carried out in different sessions, one session for each replication or a grouped collection of sessions for each replication. If the replications were merely carried out in a random order then the Replication effects (main and interactions) in this analysis are expected to be NS (apart from “chance significances”) and it will not generally influence the F-test for the Sample*Assessor interaction in any important way.

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

Sample vs Sample x Assessor Error Plots / Sample Fs Assessor Error

A Sample vs Sample*Assessor Error Plot depicts a bar for each attribute indicating whether there is sample differences using ONLY the Sample*Assessor interaction as the error term. A colored bar (yellow, orange, red) means that there seems to be such and a grey bar that there is not.

The color of the bar indicates the corresponding P-value:

Yellow: P-value < 0.05
 Orange: P-value < 0.01
 Red: P-value < 0.001

The bar size equals the F-statistic:

$$F = MS(\text{Sample}) / MS(\text{Sample} * \text{Assessor})$$

from a 2-way ANOVA:

$$\text{Attribute} = \text{Sample} + \text{Assessor} + \text{Sample} * \text{Assessor}$$

Note: This is the analysis of sample differences often used. However, this analysis is adequate ONLY IF the replications were carried out in a random order OR if the Replication*Sample interaction effect is negligible. If not, the results reported in the “Sample in 3-way Mixed Model Plot” should be used. If in doubt, also use the mixed model analysis, since it will correspond to the usual analysis whenever the assumptions for this are OK!

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

Sample in 3-way Mixed Model Plots / Sample Fs Replicate and Assessor Error

A Sample in 3-way Mixed Model Plot depicts a bar for each attribute indicating whether there is sample differences considering the random contributions from as well assessors as replications. A colored bar (yellow, orange, red) means that there seems to be such and a grey bar that there is not.

The color of the bar indicates the corresponding P-value:

Yellow: P-value < 0.05
 Orange: P-value < 0.01
 Red: P-value < 0.001

The bar size equals the F-statistic from the 3-way mixed ANOVA model:

$$\text{Attribute} = \text{Rep} + \text{Sample} + \text{Assessor} + \text{Rep*Sample} + \text{Sample*Assessor} + \text{Rep*Assessor}$$

where everything BUT the Sample main effect is considered random. This means that the F-statistic is given by

$$F = \text{MS}(\text{Sample}) / \text{MS}(\text{Denominator})$$

Where

$$\text{MS}(\text{Denominator}) = \text{MS}(\text{Sample*Assessor}) + \text{MS}(\text{Rep*Sample}) - \text{MS}(\text{Error})$$

And the denominator degrees of freedom are found by the Satterthwaite method.

Note: If the Rep*Sample variation is “too small”, that is, $\text{MS}(\text{Rep*Sample}) < \text{MS}(\text{Error})$ then this effect is assumed to be negligible and the “usual” $F = \text{MS}(\text{Sample}) / \text{MS}(\text{Sample*Assessor})$ is used instead. So for these attributes, the bars equal the bars in the “Sample vs Sample*Assessor Error Plot”.

Note: Formally this analysis is adequate IF the replications were carried out in different sessions, one session for each replication or a grouped collection of sessions for each replication. If the replications were merely carried out in a random order then the Replication effects (main and interactions) in this analysis are expected to be NS (apart from “chance significances”) and it will not generally influence the F-test for the Sample main effect in any important way. Hence, this analysis can be seen as the safer approach, IF in doubt about the situation: It will take the replication variation into account when necessary and in cases where it is not, it will provide roughly the same answers as the “usual” analysis.

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

Sample x Assessor 95% LSD values Plots

A Sample x Assessor 95% LSD values Plot simply depicts the sample average values including an LSD bar for each attribute. The LSD bar should be used as a dynamic measuring stick for each attribute: Two samples differing more than this bar are significantly different. The placement of samples on each side of the bar within each attribute is only to enhance readability, it says nothing about the samples. The LSD bar is based on the analysis using ONLY the Sample*Assessor interaction as the error term corresponding to the “Sample vs Sample*Assessor Error Plot”. Note that NO corrections for multiple comparisons are used here!

Note: This analysis is adequate ONLY IF the replications were carried out in a random order OR if the Replication*Sample interaction effect is negligible. If not, the results reported in the “3-way Mixed Model 95% LSD values Plot” should be used. If in doubt, also use the mixed model analysis, since it will correspond to the usual analysis whenever the assumptions for this are OK!

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

Sample x Assessor 95% Bonferroni LSD values Plots

A Sample x Assessor 95% Bonferroni LSD values Plot simply depicts the sample average values including an LSD bar for each attribute. The LSD bar should be used as a dynamic measuring stick for each attribute: Two samples differing more than this bar are significantly different. The placement of samples on each side of the bar within each attribute is only to enhance readability, it says nothing about the samples. The LSD bar is based on the analysis using ONLY the Sample*Assessor interaction as the error term corresponding to the "Sample vs Sample*Assessor Error Plot". The Bonferroni correction for multiple comparisons is used. For non pre-planned sample comparisons this is a more correct approach compared to the un-corrected approach. The corrected approach will always provide a wider LSD bar.

Note: This analysis is adequate ONLY IF the replications were carried out in a random order OR if the Replication*Sample interaction effect is negligible. If not, the results reported in the "3-way Mixed Model 95% LSD values Plot" should be used. If in doubt, also use the mixed model analysis, since it will correspond to the usual analysis whenever the assumptions for this are OK!

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

3-way Mixed Model 95% LSD values Plots

A 3-way Mixed Model 95% LSD values Plot simply depicts the sample average values including an LSD bar for each attribute. The LSD bar should be used as a dynamic measuring stick for each attribute: Two samples differing more than this bar are significantly different. The placement of samples on each side of the bar within each attribute is only to enhance readability, it says nothing about the samples. The LSD bar is based on the analysis using the 3-way mixed ANOVA model corresponding to the "Sample in 3-way Mixed Model Plot". Note that NO correction for multiple comparisons are used here!

Note: Formally this analysis is adequate IF the replications were carried out in different sessions, one session for each replication or a grouped collection of sessions for each replication. If the replications were merely carried out in a random order then the Replication effects (main and interactions) in this analysis are expected to be NS (apart from "chance significances") and it will not generally influence the F-test for the Sample main effect in any important way. Hence, this analysis can be seen as the safer approach, IF in doubt about the situation: It will take the replication variation into account when necessary and in cases where it is not, it will provide roughly the same answers as the "usual" analysis.

Note: Specific attributes, assessors and samples may be excluded from the analysis, by disabling them in the checkboxes.

3-way Mixed Model 95% Bonferroni LSD values Plots

A 3-way Mixed Model 95% Bonferroni LSD values Plot simply depicts the sample average values including an LSD bar for each attribute. The LSD bar should be used as a dynamic measuring stick for each attribute: Two samples differing more than this b