

Robust Correlation toolbox Manual

The toolbox allows performing robust correlations analyses along with various assumption checks and data visualization.

When using the toolbox for article please cite:

Pernet, C.R., Wilcox, R. & Rousselet, G.A. (2012). Robust correlation analyses: old tools but new toolbox for psychology research. *Front. in Psychology*.

Since you are likely to use the skipped-correlation which depends on an estimation of the robust centre of the data, then also cite:

Rousseeuw, P.J. (1984), "Least Median of Squares Regression," Journal of the American Statistical Association, Vol. 79, pp. 871-881.

Rousseeuw, P.J. and Van Driessen, K. (1999), "A Fast Algorithm for the Minimum Covariance Determinant Estimator," *Technometrics*, 41, pp. 212-223.

Verboten, S., & Hubert, M. (2005). LIBRA: a MATLAB Library for Robust Analysis, *Chemometrics and Intelligent Laboratory Systems*(75), 127-136.

If the test of multivariate normality is reported cite:

Trujillo-Ortiz, A., R. Hernandez-Walls, K. Barba-Rojo and L. Cupul-Magana. (2007). HZmvntest:Henze-Zirkler's Multivariate Normality Test. A MATLAB file.

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1 - Before starting

If you are not familiar with Matlab, all you need to do to get the toolbox to work is to set the path. That means that you tell Matlab where the toolbox is located. The easiest way to do so is to click at the top of the Matlab window on *File* → *Set Path* , then click on Add with Subfolders and select the Corr_toolbox.

2 - Importing data in Matlab

For a Matlab novice it might seem complicated to import data. This is however as easy as with any other software. With the software functions, we also saved the Anscombe's quartet data.

Import excel file data: the easiest way is, from the Matlab 'Current Folder' window, double click on Anscombe.xls. The import wizard is now open and the data are already selected (figure 1). At the top left of the wizard, you have the choice about how to import, select 'Column vectors' and then click on 'Import'. You should now have in the 'Workspace' 8 variables called X1, X2, X3, X4, Y1, Y2, Y3, Y4.

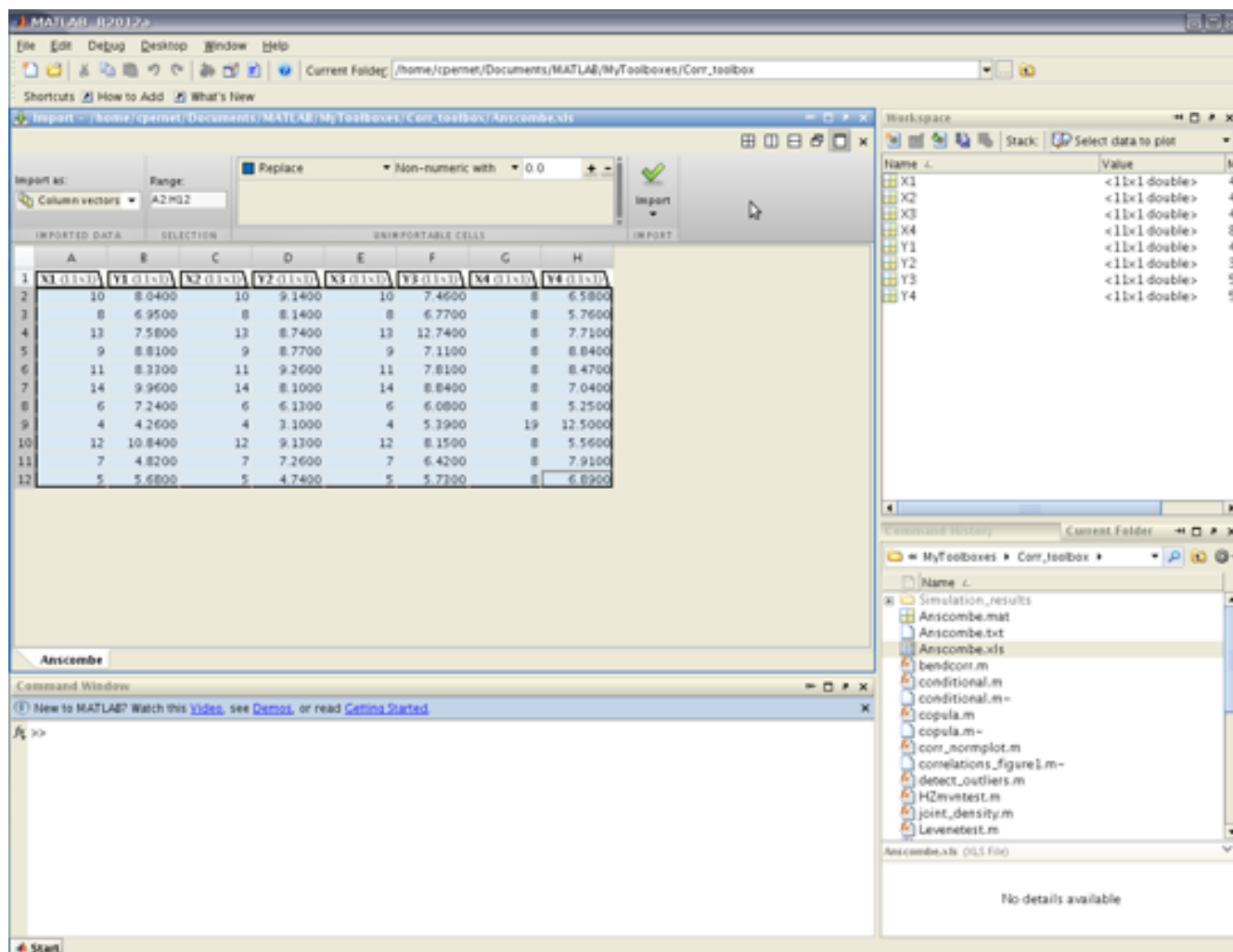


Figure 1. Matlab import wizard for the excel file 'Anscombe.xls'.

Import text file data: the easiest way is, from the Malab 'Current Folder' window, right click on Anscombe.txt, and select Import Data. The import wizard is now open (figure 2). Simply click next and finished. You should now have all the variables loaded in the 'Workspace' as a single matrix called Anscombe.

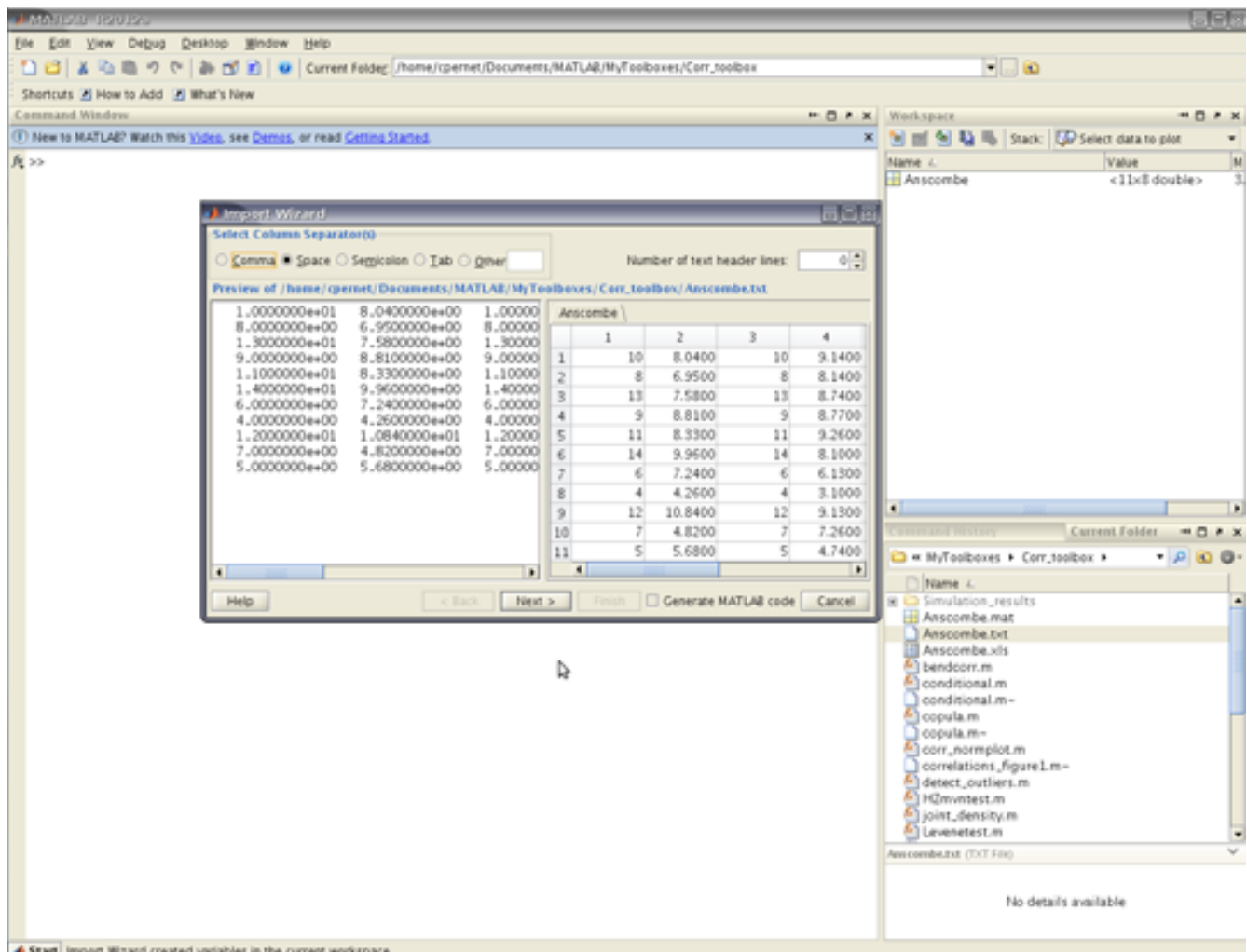


Figure 2. Matlab import wizard for the text file 'Anscombe.txt'.

Load data already in Matlab format: once the data have been imported, it is easier to save them in Matlab format (see help save) to be used later. Here the data can be accessed by double clicking on Anscombe.mat from the Malab 'Current Folder' window.

3 - One-step analysis between 2 variables

When only 2 variables are tested, the full range of tests and plots can be performed by simply calling the *robust_correlation.m* function. Load the data *Anscombe.mat* (section 2) and in the Matlab command window, type:

```
correlation_results = robust_correlation(Anscombe(:,1),Anscombe(:,2))
```

The function successively performs the following operations:

- (1) Plots the data with (i) a scatter plot, (ii) the marginal (normalized) histograms with the corresponding Gaussian curves and (iii) the bivariate histogram (*corr_normplot.m*)
- (2) Plots the joint density as a mesh and its isocontour (*joint_density.m*).
- (3) Tests bivariate normality (*Hzmvttest.m*)
- (4) Tests heteroscedasticity (*variance_honogeneity.m*)
- (5) Looks for outliers (*detect_outliers.m*)
- (6) Performs all types of correlations (*Pearson.m Spearman.m bendcorr.m skipped-correlation.m*)

As the different tests are performed, outputs appears in the Matlab command window and as well as graphics (figures 3 and 4). In addition, there is now a structure called *correlation_results* with all the results. For instance if you type *correlation_results.Pearson* it returns the r, t, p values, the bootstrapped confidence intervals and something telling you if it is significant or not (decision based on the bootstrapped confidence intervals).

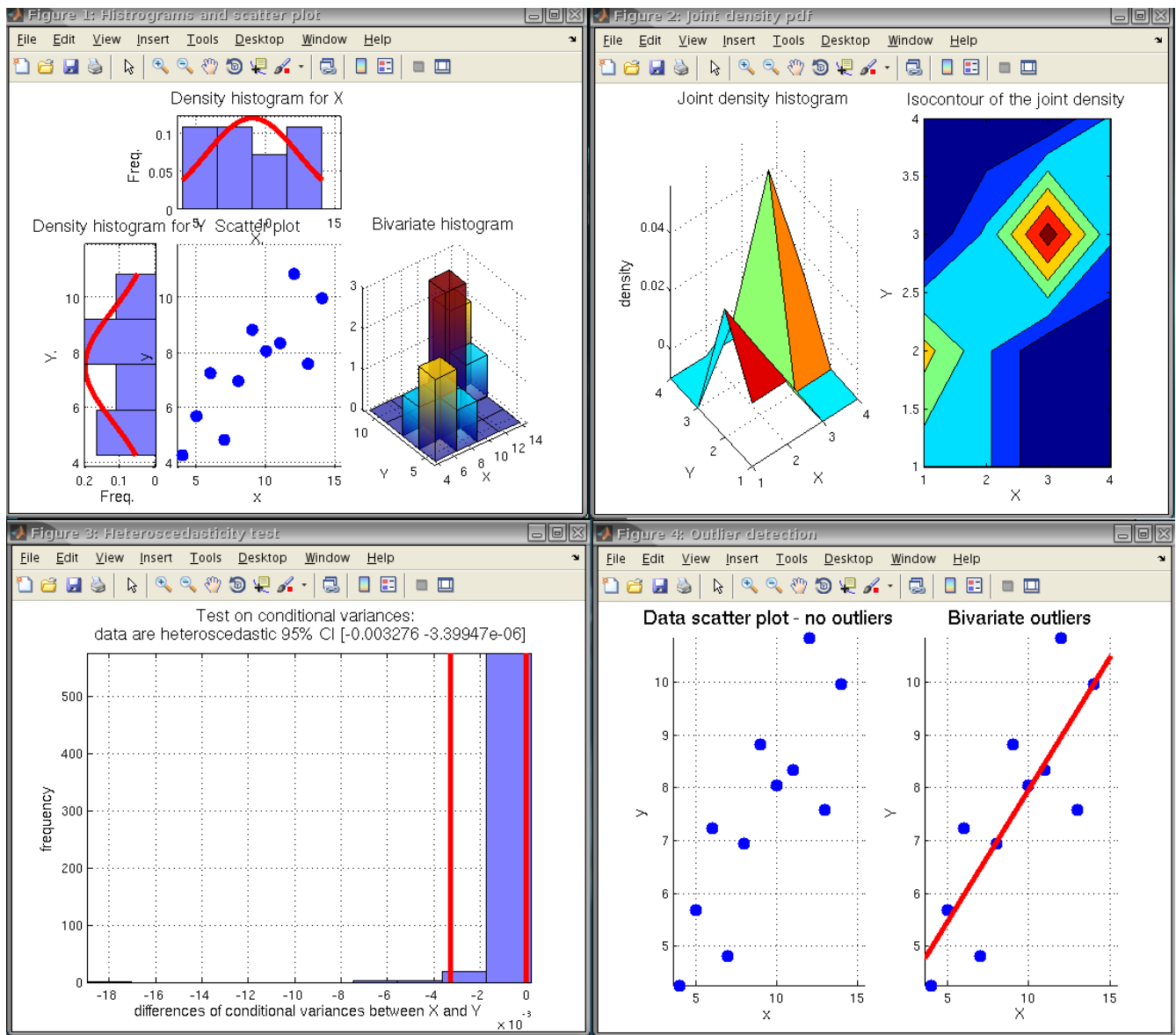


Figure 3. Graphical outputs returned by the correlation toolbox for the 1st Anscombe's quartet: Top left (Figure 1) = scatter plots and histograms – top right (Figure 2) = mesh and isocontours of the joint density – Bottom left (Figure 3) = histogram of the differences in the conditional variances of bootstrapped data – Bottom right (Figure 4) = univariate and bivariate outliers –

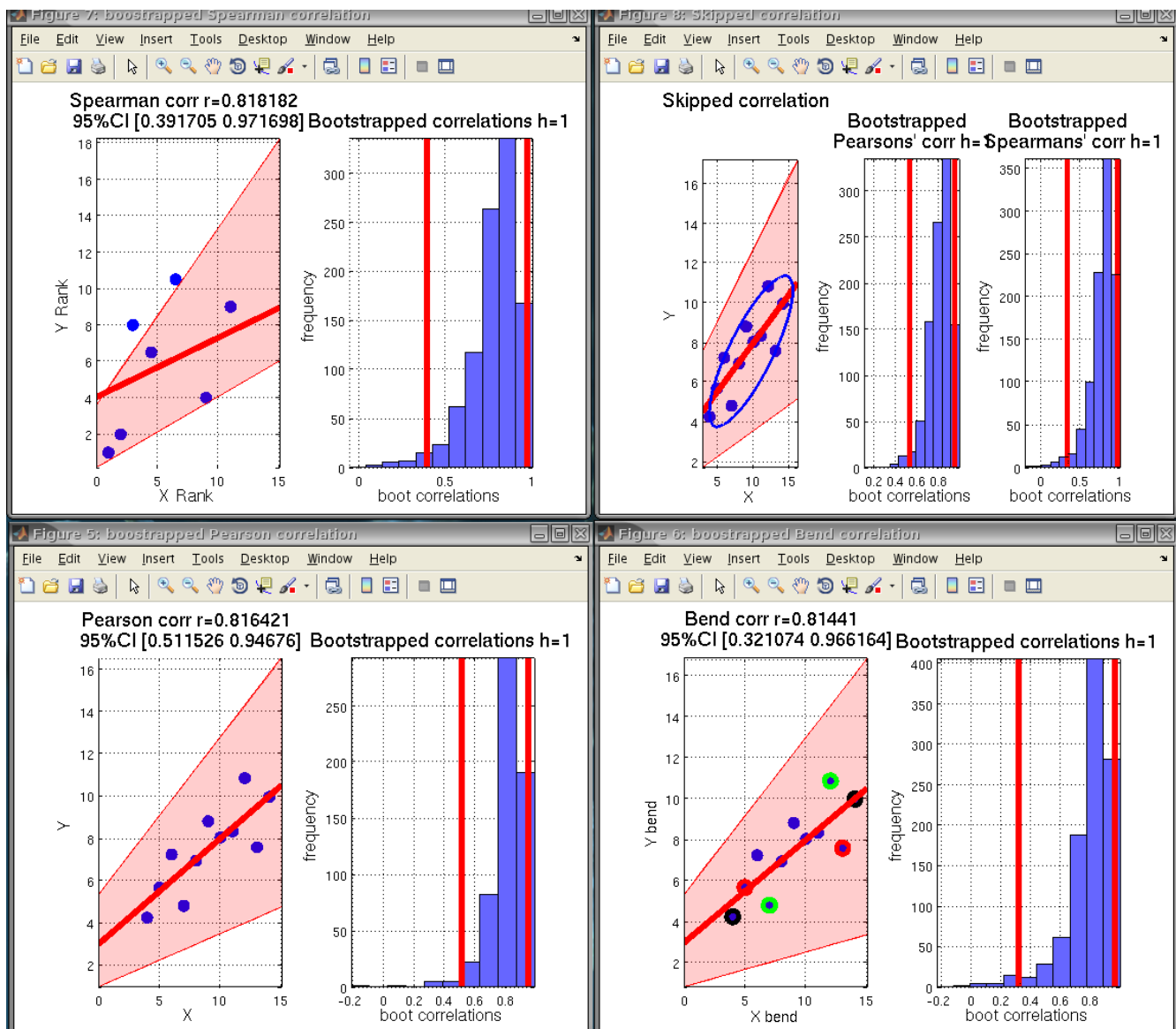


Figure 4. Graphical outputs returned by the correlation toolbox for the 1st Anscombe's quartet: Top-left (Figure 7) = Spearman correlation with 95% CI and the histogram of correlations for bootstrapped data - Top right (Figure 8) = Skipped Pearson correlation with 95% CI and the histograms of Pearson's and Spearman's correlations for bootstrapped data. Bottom left (Figure 5) = Pearson correlation with 95% CI and the histogram of correlations for bootstrapped data - Bottom right (Figure 6) = 20% bend correlation with 95% CI and the histogram of correlations for bootstrapped data.

4 - Calling specific function

Data visualization

To get the scatter plot with histograms type:

```
corr_normplot(Anscombe(:,1), Anscombe(:,2));
```

To get the joint density type:

```
density = joint_density(Anscombe(:,1), Anscombe(:,2));
```

It will not only plots the joint density, but also returns it as output variable (here density) such as density =

```
0.0221    0.0221         0         0
0.0442    0.0221         0         0
0         0.0221    0.0663    0.0221
0         0         0         0.0221
```

It is also possible to only plot the isocontours by typing

```
density = joint_density(Anscombe(:,1), Anscombe(:,2),0);
```

Assumption checking

To test for multivariate normality, type:

```
HZmvntest([Anscombe(:,1), Anscombe(:,2)]);
```

Note the square brackets [] as the functions needs a single matrix as input

Variance homogeneity can be tested simply by typing:

```
[h,CI] = variance_homogeneity(Anscombe(:,1),Anscombe(:,2));
```

If h=1 data have different variances, if h = 0 data have the same variances.

CI is the percentile bootstrap 95% confidence interval of the difference between variances.

By default the function normalizes the data and uses conditional variances (see conditional.m). It is however possible to force the function to use the original variances by typing

```
[h,CI] = variance_homogeneity(Anscombe(:,1),Anscombe(:,2),0);
```

To detect outliers using robust estimators (i.e. the normalized Median Absolute Deviation and Mid Covariance Determinant) type:

```
outliers = detect_outliers(Anscombe(:,1),Anscombe(:,2));
```

the output (outliers) is a structure with outliers.univariate.X returning indices of univariate outliers in X, outliers.univariate.Y returning indices of univariate outliers in Y and outliers.bivariate returning bivariate outliers (in each cases 0 means it a good data point and 1 means this is an outlier)

Correlations

Pearson

```
[r,t,p] = Pearson(Anscombe(:,1),Anscombe(:,2))
```

returns the correlation (r) value along with the t and p-values and make a plot of the data with a line representing the best linear fit

```
[r,t,p] = Pearson(Anscombe(:,1),Anscombe(:,2),0)
```

allows to compute without making a figure

```
[r,t,p,hboot,CI] = Pearson(Anscombe(:,1),Anscombe(:,2),1,10/100)
```

allows to obtain a decision about significance (hboot) based upon the bootstrapped confidence intervals (CI) at the desired type 1 level (here 10% - default is 5%). Note the difference in graphical outputs, because bootstrap was used, CI and the histogram of bootstrapped correlations are also plotted.

Spearman

```
[r,t,p] = Spearman(Anscombe(:,1),Anscombe(:,2))
```

returns the correlation (r) value along with the t and p-values and make a plot of the data with a line representing the best linear fit. Note the difference with Pearson - the scatter plot is for the ranked data.

```
[r,t,p] = Spearman(Anscombe(:,1),Anscombe(:,2),0)
```

allows to compute without making a figure

```
[r,t,p,hboot,CI] = Spearman(Anscombe(:,1),Anscombe(:,2),1,10/100)
```

allows to obtain a decision about significance (hboot) based upon the bootstrapped confidence intervals (CI) at the desired type 1 level (here 10% - default is 5%). Note the difference in graphical outputs, because bootstrap was used, CI and the histogram of bootstrapped correlations are also plotted.

Percentage bend correlation

```
[r,t,p] = bendcorr(Anscombe(:,1),Anscombe(:,2))
```

returns the correlation (r) value along with the t and p-values and make a plot of the data with a line representing the best linear fit. In the graphical output different colors are used to indicate which data points were weighted down (red for data in X, green for data in Y and black if in both X and Y). The percentage bend correlation is not an estimate of Pearson's correlation - it is however a measure of the linear relationship between X and Y.

```
[r,t,p,hboot,CI] = bendcorr(Anscombe(:,1),Anscombe(:,2),0,40)
```

allows to obtain a decision about significance (hboot) based upon the bootstrapped 95% confidence intervals (CI) - additional arguments indicate not to plot the data (0) and use 40% bending rather than the default 20%.

Skipped-correlation

```
[r,t,h] = skipped_correlation(Anscombe(:,1),Anscombe(:,2))
```

```
[r,t,h] = skipped_correlation(Anscombe(:,1),Anscombe(:,2),0)
```

returns the correlation (r) values along with the t values of Pearson and

Spearman tests performed on data after removing bivariate outliers. Note no p value is computed, but the T value is thresholded such as a decision h can be returned for a level $\alpha = 5\%$. This is performed with adjustments related to the sample size to maintain the type 1 error rate. By default, the function also makes a plot of the data with an ellipse containing non outlying data and a line representing the best linear fit to the remaining data points. It is essential to understand that outlier removal is based on normality, and Spearman is computed on the same data as Pearson.

```
[r,t,h,outid,hboot,CI] = skipped_correlation(Anscombe(:,1),Anscombe(:,2))
```

Also returns outlier data in outid (same as using outlier_detect) and add 95% bootrapped confidence intervals (CI) with the decision about significance (hboot).

5 - Multiple testing solutions

When performing multiple tests, we increase the chances to make a false positive error. This is only true for families, i.e when tests relate to each other. That if you do 2 tests on pairs of variables not related (at all) to each other, then it's fine. If on the other hand variables are related, errors cumulate. For instance for two tests each set at 5% of making an error, we have in fact 7.5% chances ($5\% + 5\%*5\%$) to make an error over the two tests. We illustrate here how to correct for this using the pairs 1, 2 and 3 of the Anscombe's quartet. For each pair X is the same, so we clearly have a family of tests.

Pearson and Spearman

```
[r,t,p,hboot,CI] = Pearson(Anscombe(:,1),Anscombe(:,[2 4 6]))  
[r,t,p,hboot,CI] = Pearson(Anscombe(:,[1 3 5]),Anscombe(:,[2 4 6]))  
[r,t,p,hboot,CI] = Spearman(Anscombe(:,1),Anscombe(:,[2 4 6]))  
[r,t,p,hboot,CI] = Spearman(Anscombe(:,[1 3 5]),Anscombe(:,[2 4 6]))
```

Here either one vector and a matrix or two matrices of data were input, and correlations are always computed column-wise (the function will simply repeats the vector `Anscombe(:,1)` for 1 vector and a matrix as inputs)

Multiple comparison correction is simply accounted for using Bonferroni correction. That is only p values below say 1.67% ($5\% / 3$ tests) should be considered and, accordingly, confidence intervals are adjusted to 98.33%.

Percentage bend correlation

```
[r,t,p,hboot,CI,H,pH] = bendcorr(Anscombe(:,1),Anscombe(:,[2 4 6]))  
[r,t,p,hboot,CI,H,pH] = bendcorr(Anscombe(:,[1 3 5]),Anscombe(:,[2 4 6]))
```

As for Pearson and Spearman, a vector and a matrix or 2 matrices can be input and correlations are computed column-wise. Also, hboot and CI are adjusted using a Bonferonni correction.

In output, H and pH can also be added to compute an omnibus test of independence between all pairs, i.e. testing that the matrix of correlation is equal to the identity matrix (0 everywhere except the diagonal being 1). H is the measure of association between all pairs (like r is the measure between two variables for 1 pair) and pH is the p value associated to this test.

Skipped-correlation

```
[r,t,h,outid,hboot,CI] = skipped_correlation(Anscombe(:,1),Anscombe(:,[2 4 6]))
```

A vector and a matrix are used as inputs, and h returns the significance with a adjustment for multiple comparisons given we have only Anscombe(:,1) against 3 other variables.

```
[r,t,h,outid,hboot,CI] = skipped_correlation(Anscombe(:,[1 3 5]),Anscombe(:,[2 4 6]))
```

Two matrices are used as inputs, and h returns the significance with a adjustment for multiple comparisons testing that all correlations are 0

In both cases, r and t are only computed for Spearman, because only Spearman provides a good type 1 error rate in the context of multiple comparisons - hboot and CI are adjusted using a Bonferroni correction.

6 - References

Henze, N. and Zirkler, B. (1990), A Class of Invariant Consistent Tests for Multivariate Normality. [Communication in Statistics - Theory and Methods, 19\(10\): 3595-3618.](#)

Pernet, C.R., Wilcox, R. & Rousselet, G.A. (2012). Robust correlation analyses: old tools but new toolbox for psychology research. *Front. in Psychology*.

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