ReferenceRangeR

Quick Start Guide

1. Copy your data
Paste raw lab data directly from your LIS or spreadsheet. Age and sex data are optional. Up to 200,000 results are allowed. Use built-in demo data to explore features without uploading your own. Invalid results are automatically marked in red. If the sex data labels can be assigned manually if necessary.

2. Check sex differences (optional)
Boxplots & violin plots for male, female, non-binary groups are created. Differences between the groups are calculated and compared to the permissible uncertainty (pU). Wilcoxon or Kruskal-Wallis tests are performed to check for significance.

3. Check age drift (optional)
Drift detection algorithm identifies age trends. The tool suggests optimal age groupings based on data distribution and the pU.

4. Advanced mode (optional)
The advanced mode offers additional features, e.g. an additional trimester column, a setting for the number of age groups, bootstrap iterations and a modified Box-Cox transformation in refineR.

5. Select limits for comparison (optional)
When verifying an existing reference interval, e.g. from the assay manufacturer, the data can be added by activating the checkbox in the 'reference interval' tab. This will provide a graphical comparison in the resulting plot.

6. Select method (optional)
The method best suited for your data can be selected in the 'reference interval' tab. The results might vary for different sample size, pathological fraction or skewness. At this time no general recommendation exists, the choice of method is strongly dependent on the particular data set.

 Pathological fraction >20%: refineR, kosmic or TMC
 High fraction of values below the quantification limit: TMC
 Heavily skewed distribution: TMC or refineR

7. <u>Calculate</u>