

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. The sex data labels can be assigned manually, if necessary.

A screenshot of the 'Data Input' window in the ReferenceRangeR application. It features a table with columns for 'result', 'age', and 'sex'. The table has 11 rows, with the first row containing data and the others being empty. To the right of the table is a sidebar titled 'Assign sex variables:' with three dropdown menus labeled 'female:', 'male:', and 'diverse:'.

2. Check sex differences (optional)

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

3. Check age drift (optional)

A drift detection algorithm identifies age trends. The tool suggests age groups based on median similarity.

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. The discrepancy between estimated RIs and comparison limits is assessed quantitatively using the equivalence limits and are displayed graphically.

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. Calculate