

Progenesis[®] QI

THE NEXT GENERATION IN LC-MS DATA ANALYSIS

Visualize and analyze your complex LC-MS data to support your omics research by quantifying your analytes. Find differences between samples rapidly, objectively, and reliably using multivariate statistics.

www.nonlinear.com/missing-values

THE PROBLEM: MISSING VALUES IN YOUR DATA

Missing values are holes in your data set that can mislead you in your conclusions. They are surprisingly common and can have significant impact on your research.

What are missing values and why are they so important?

FALSE NEGATIVES



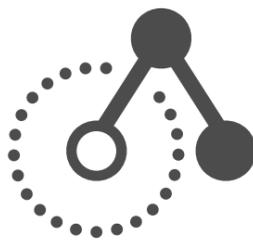
FALSE POSITIVES



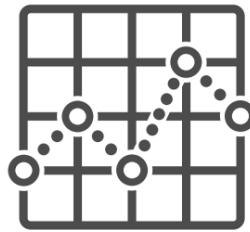
Missing values can be introduced in significant numbers by ineffective data analysis software. *This can be avoided if an efficient analysis method is used.*

MISSING VALUES ARE IMPORTANT BECAUSE...

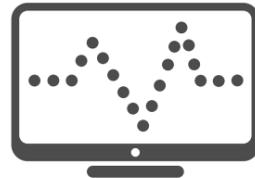
For a true understanding of your scientific data you need **consistent measurements** of all analytes across all samples.



You may miss expression changes that are present in your data.



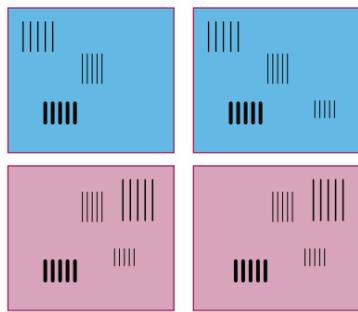
Missing values leads to ineffective or misleading statistics.



Inconsistent measurements lead to inconsistent results.

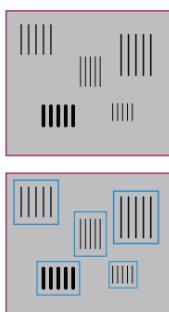
DON'T SETTLE FOR MISSING VALUES

With unique alignment and co-detection algorithms, Progenesis QI Software offers **100% matching** with **no missing values** for reliable multivariate statistics.



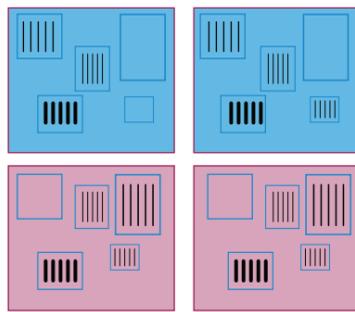
1

Retention time alignment of all individual runs.



2

Single aggregate run created with all ions from every sample detected on the aggregate run.



3

Isotope profiles detected on the aggregate run are applied to all individually aligned runs.

RESULTS?

Complete data set, i.e. no missing values, and any analyte identified on one run is applied to all runs.

PROGENESIS QI BRINGS IT ALL TOGETHER

Only with **100% matching** and **no missing values** can you then be confident in your results. With reliable statistics to lead you to your biological discoveries.

