

| <i>Option</i> |
|---|
| % QCs missing per feature <= |
| ↓ Every Batch |
| ↓ Any Batch |
| ↓ Complete |
| <input checked="" type="checkbox"/> QC < LOQ* = missing |
| LOQ* = <input type="checkbox"/> x max(Blank) |

| Action | |
|--|--|
| Feature is kept if there are less than (or equal to) the specified % of missing QC samples. | |
| % missing QC calculated per batch and peak kept if every batch has <= specified % missing QC | |
| % missing QC calculated per batch and peak kept if any batch has <= specified % missing QCs | |
| % missing QC calculated across all batches | |
| consider any QC sample with signal < the LOQ* to be missing | |
| estimated Limit Of Quantification = \square x maximum Blank value | |

| <i>Label</i> |
|---------------------------------|
| Log Transformed Correction |
| Remove Zeros |
| QC Outlier Detection Method |
| QC Outlier Detection %CI |
| QC Outlier Replacement Strategy |
| Within-Batch Correction Mode |
| Between-Batch Correction Mode |
| QCRSC Cross Validation Method |

QCRSC Monte Carlo repetitions

Blank Ratio Method

| <i>Options</i> |
|--|
| "true"/"false" |
| "true"/"false" |
| "None", "Percentile", "Linear", "Quadratic", "Cubic" |
| value between between 0.9 and 0.99 |
| "Ignore", "Median", "NaN" |
| "Mean", "Linear", "Spline", "Sample" |
| "QC", "Reference", "Sample" |
| "3-Fold", "5-Fold", "7-Fold", "Leaveout" |

integer

"QC","Median","Percentile"

| Explanation |
|---|
| Perform Log_{10} transformation on data before correction (to ensure normal distribution) |
| There is no such thing as zero. Samples is either detected (value) or not detected (missing). Zeros mess up statistics. |
| The 'linear'/quadratic/cubic' options fit a simple polynomial function to the QC data using robust least squares regression. Points outside the population confidence interval are deemed outliers. The 'percentile' option implements the standard non-parametric $< Q1 - 1.5 \text{ IQR}$ or $> Q3 + 1.5 \text{ IQR}$ outlier detection method on the QC samples. |
| Set the Confidence interval for the polynomial methods above. 90%-99% |
| For the corrected data. Either ignore outliers or replace with the QC median value or remove (replace with "not a number" NaN). |
| Three correction modes. "Spline" is the default QCRSC algorithm that requires optimisation of the smoothing parameter for every feature. "Linear" is a simple Robust (bisquare) linear regression based on the QC values & requires no smoothing optimisation. "Mean" equalises the QC mean across batches & ignores within batch systematic change. "Sample" ignores the QCs and corrects using linear regression based on the samples labelled 'Sample'. N.B. If the number of QC samples in a batch is 5 or less then the Spline algorithm switches to a linear correction ($N \leq 5$ is too few for effectively fitting a non-linear curve with cross-validation). N.B. The 'Sample' option is not recommended and is primarily included to illustrate how poor this approach is to within-batch correction (or as a last resort for data with no QCs). |
| QC' = both the intra- and inter-batch based on the QC samples; 'Reference' = intra-batch correction based on the QCs but the inter-batch correction uses the samples labelled as 'Reference'. 'Sample' = both the intra-batch & inter-batch correction uses the samples labelled as 'Sample'. N.B. The 'Sample' option is not recommended and is primarily included to illustrate how poor this approach is to between-batch correction (or as a last resort for data with no QCs). |
| Type of cross-validation used for optimising the smoothing parameter value. |

The number of Monte Carlo (random) resamples of the k-fold cross validation. The resulting cvMSE the mean of the generated set of cvMSEs.

$\text{BlankRatio} = 100 * \max(\text{BlankValue}) / \text{SampleReferenceValue}$. 'QC' sets the SampleReferenceValue as the median QC value; 'Median' sets the SampleReferenceValue as the median Sample value; 'Percentile' sets $\text{BlankRatio} = \% \text{ of Samples} < \max(\text{BlankValue}) * \text{RelativeLOD}$ (RelativeLOD is a user defined constant - default 1.5). In this instance missing values are considered Blank values

| <i>Label</i> |
|---|
| <i>Missing Samples Filter:</i> |
| Every-Batch/Any-Batch/Complete |
| % missing per feature <= |
| Before/After |
| <i>Filter Bank:</i> |
| ON/OFF |
| Mode |
| QC-RSD |
| <i>PCA preprocessing:</i> |
| log10 Transform |
| Autoscale / Mean Center |
| <i>PCA Missing value imputation:</i> |
| KNN column |
| KNN row |
| k = |
| blank/20%min |
| <i>PCA projection:</i> |
| Project in QC samples |
| Project in Blank samples |
| Project in Reference samples |

| Explanation |
|--|
| Remove features where there are low number of total samples. |
| Should the filter bank calculate its feature-wise statistics across all batches (complete) or calculate for each batch individually and if 'Every Batch' then every batch must pass the % missing threshold for a given feature to be retained, else if 'Any Batch' then only one batch as to pass the threshold for the peak to be kept. |
| % allowed missing Samples. e.g. if 20% then a given feature is removed if number of missing samples labeled 'Sample' > 20%. |
| Compare the performance statistics/visualisations before or after correction. Use this to convince yourself of the utility of the correction algorithm. |
| |
| Apply the dial setting to the feature selection filter. |
| Leave on 'Complete' unless performing large scale studies over many batches. For a given peak: 'Max qcRSD' defers to the using the stats from the worst batch (batch with highest qcRSD) for all filter settings. 'minQC' defers to the best batch (batch with lowest qcRSD) for all filter settings. 'Median qcRSD' defers to the most representative batch for all filter settings. 'Complete' calculates the stats across all batches. |
| QC Relative Standard Deviation filter setting. Typically set to 20-30% (i.e. features |
| |
| Apply a log10 transformation to all data. |
| Perform autoscaling (mean center then divide by standard deviation) or just mean center to each individual feature. Scaling is always performed after the transformation. |
| |
| KNN missing value imputation replacing with the nearest feature |
| KNN missing value imputation replacing with the nearest sample |
| Replaces missing values with a weighted mean of the k nearest-neighbor columns/rows. KNN imputation always performed after transformation & scaling. |
| Replaces missing values with the maximum blank value for that feature or if no blanks detected 20% of the lowest value. blank/20%min is always performed before transformation or scaling. |
| |
| PCA model is generated using only the Sample data. This removes any possible bias from the QC, Blank, or Reference samples. The QC, Blank, or Reference sample data can be applied to the PCA model (projected through) and plotted with the Sample data. |