

Programmer's Guide for R Utility for Correcting for Plate/Batch/Lot and Nonspecific Binding Artifacts

Lines 48-53: Function for calculating finite-population variance based on specimen volume, fold dilution, and pipette volume.

Lines 59-87: Remove rows of missing data, logarithm transform, and plot data that contain artifacts (Figure 1).

Lines 88-120: Fit linear mixed model separately to each SP MFI (and NC MFI) values for removal of plate artifacts using estimated population marginal means.

Lines 121-131: Plot data with plate artifacts removed (Figure 2).

Lines 132-146: Estimation of technical variance for use in error-in-variables regression.

Lines 147-179: Error-in-variables regression of each SP MFI regressed on NC MFI. Lines 158-168 perform parallel processing of repeat cross-validation. Line 160 performs bootstrap resampling for these repeats.

Lines 180-191: Plot each SP MFI vs. NC MFI (Figure 3).

Lines 192-202: Plot dpMFI data that are corrected for plate and nonspecific binding artifacts (Figure 4).