eppendorf

Your Normalization – Effortless!

Normalization in a single command

The enhanced feature set 2 implements one of the most requested features from epMotion® users: An improved normalization feature in epBlue. Instead of using csv-import, normalization will become a single command. And the best part, it is not only as precise as manual or csv-based normalization, but it is also even faster than both other options!

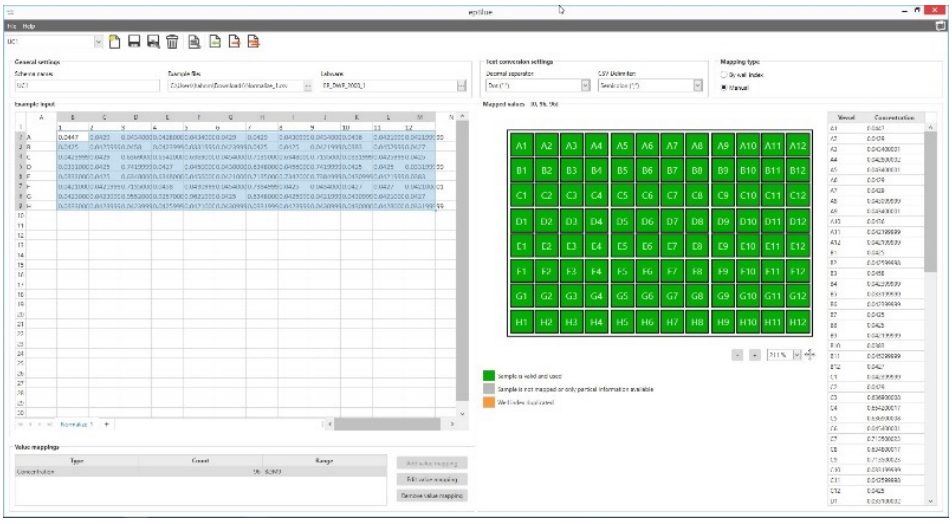
> No third-party program needed
> Drag and drop normalize commands in your method
> Automatic normalization calculation, no spreadsheets needed
> Adjust parameters before the run without changing the method
> Results can be exported for effortless documentation

www.eppendorf.com/epBlue

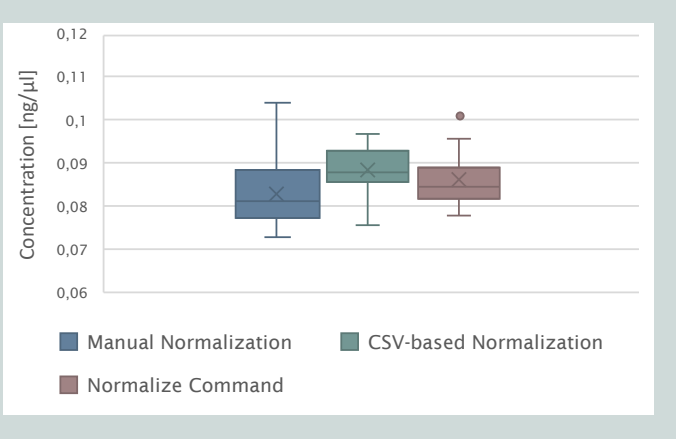
Your Normalization Now Faster and Easier

Drag and drop the new normalize command in your existing methods or use it as a stand-alone method.

The new data layout editor is easy to use and allows handling data sets directly coming from your plate reader.

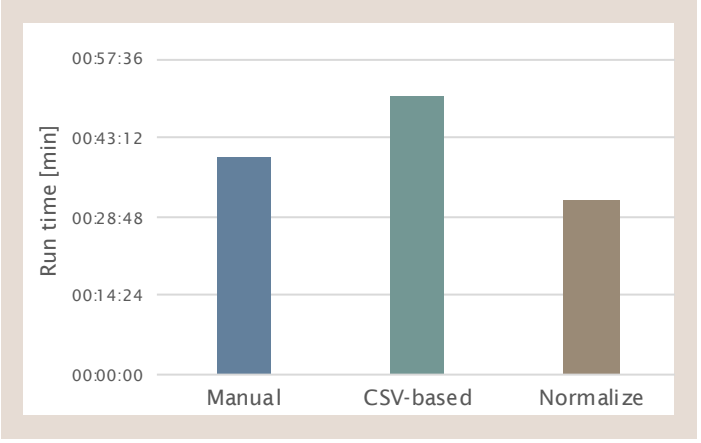


Same Performance...



Normalization of human gDNA present in a 96-well plate at 8 concentrations in triplicates (24 wells) to a target value of 0,1 ng/µl. Measurement of the gDNA concentrations in the destination plate by fluorometric quantification. Fluorometric method results in ~10% lower concentration measurements systematically.

Shorter Runtimes!



Processing time comparison for the normalization of 96 samples using water. Transfer from source 96 well plate to target 96 well plate. Diluent is presented in a reservoir.

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