

Special Issue

Analysis of Amplification Curve Data

Message from the Guest Editors

Since the advent of PCR, amplification curve data has become common not only in molecular laboratories, but also in diagnostics and forensics. Although the principles of nucleic acid quantification appear to be simple, the data analysis proves to be challenging. Despite almost thirty years of development of methods for nucleic acid quantification, there is still a need for more precise and reproducible solutions. Another issue is the variability of the implementations of quantification algorithms which are built using different assumptions depending on the software. This includes methods for the analysis of quantitative PCRs, digital PCRs, and melting curve analyses. To overcome obstacles from the process of data generation (preparing and processing the sample material, reporting the experimental conditions), the scientific community focused on developing data analysis methods and standards (such as MIQE and digital MIQE guidelines).

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