



University of Central Florida

Technology Available for Licensing

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qPCR Analysis Software

UCF researchers developed a simple mathematical model that accurately describes the entire PCR reaction profile using only two reaction variables that depict the maximum capacity of the reaction and feedback inhibition. This model allows quantification that is more accurate than existing methods and takes advantage of the brighter fluorescence signals from later cycles. Because the model describes the entire reaction, the influences of baseline adjustment errors, reaction efficiencies, template abundance, and signal loss per cycle could be formalized. We determined that the common cycle-threshold method of data analysis introduces unnecessary variance because of inappropriate baseline adjustments, dynamic reaction efficiency, and also a reliance on data with a low signal-to-noise ratio. An additional benefit of the global fitting method described here is that researchers can evaluate the quality of their raw reaction data against a idealized model to better address experimental artifacts.

Background

Quantitative polymerase chain reactions (qPCR) are used to monitor relative changes in very small amounts of DNA. One drawback to qPCR is reproducibility: measuring the same sample multiple times can yield data that is so noisy that important differences can be dismissed. Numerous analytical methods have been employed that can extract the relative template abundance between samples. However, each method is sensitive to baseline assignment and to the unique shape profiles of individual reactions, which gives rise to increased variance stemming from the analytical procedure itself.

Looking for Partners

Looking for beta testers

Stage of Development

Beta testing of the web-based automated data analyzer and development of metrics to determine raw data quality.

Publication

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0037640;sessionid=75841E29A6FCD9951024375384ED3004>

Carr AC, Moore SD (2012) Robust Quantification of Polymerase Chain Reactions Using Global Fitting. PLoS ONE 7(5): e37640

$$yield = prev \left(1 + \left(\frac{max - prev}{max} \right) - \left(\frac{prev}{(Kd + prev)} \right) \right)$$

Benefits

- Takes advantage of later cycles
- Formalized baseline adjustments
- Works even with high signal-to-noise ratio's

Keywords

qPCR, DNA

Tech Category

Software

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