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(71) Applicant (for all designated States except US): **LIFE TECHNOLOGIES CORPORATION** [US/US]; 5791 Van Allen Way, Carlsbad, CA 92008 (US).

(72) Inventor; and

(75) Inventor/Applicant (for US only): **GEORGE, Wallace R.** [US/US]; 151 Frisbie Street, Oakland, CA 94611 (US).

(74) Agent: **WONG, Denise, H.**; 5791 Van Allen Way, Carlsbad, CA 92008 (US).

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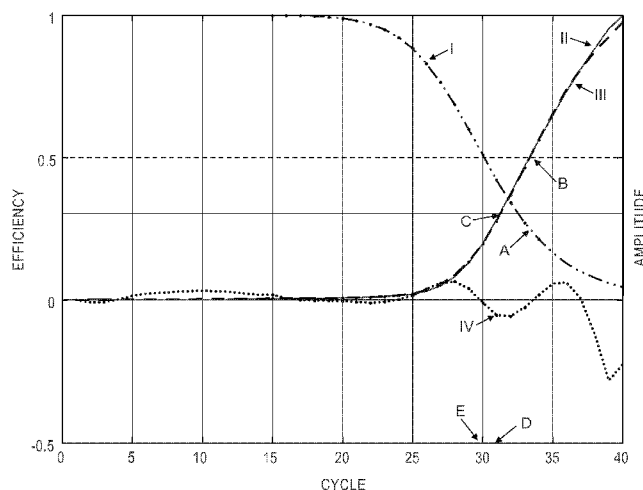


FIG. 4

(57) Abstract: A method for determining a cycle threshold for a PCR amplification curve is provided. The method includes receiving a data set for a plurality of biological samples for a PCR amplification reaction. The data set includes a plurality of amplification curves, each amplification curve associated with a biological sample of the plurality of biological samples. The method further includes performing a nonlinear optimization comprising a fit of each amplification curve to a complementary modeled amplification curve to determine a best-fit set of parameters for a modeled efficiency curve and associated amplification curve. The modeled amplification curve is based on a modeled efficiency curve. The method includes determining a cycle threshold value for each biological sample based on a complementary relationship of the modeled efficiency curve to the modeled amplification curve. In an embodiment, the nonlinear optimization is a constrained nonlinear optimization.