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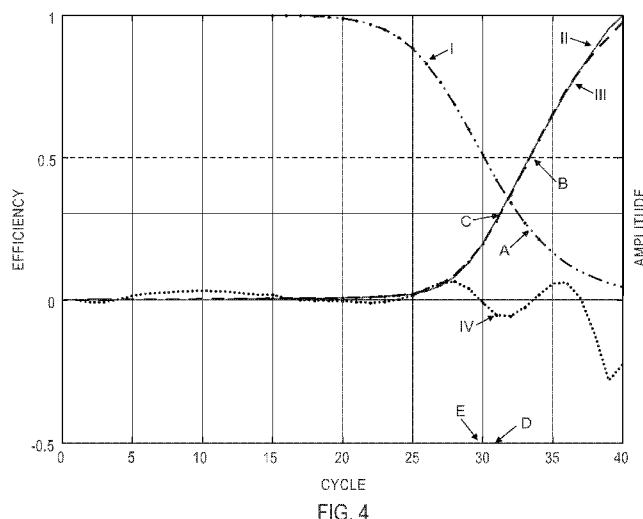
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(57) Abstract: A method for determining a cycle threshold for a PCR amplification curve is provided. The method includes receiving a data set for a plurality of biological samples for a PCR amplification reaction. The data set includes a plurality 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.