Software Requirements Specification document for qPCR analysis
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Summary:
This package will take Ct values from your qPCR and perform various forms of analyses on your data. Analyses will include primer efficiency calculations, delta-delta Ct analysis, the pfaffl method, and polysome profiling analysis. All inputs must include triplicate Cts and be .csv files.

Input format:

1. **Primer efficiency**
A csv file with the following headers:
    a. Gene [string]
    b. Dilution [#]
    c. Ct1 [float]
    d. Ct2 [float]
    e. Ct 3 [float]

2. **Pfaffl methods**

A csv file with the following headers:
    a. Gene [string]
    b. Condition [string]
    c. Replicate [#]
    d. Ct1 [float]
    e. Ct2 [float]
    f. Ct 3 [float]

3. **Polysome profiling**
A csv file with the following headers:
    a. Gene [string]
    b. Condition [string]
    c. Replicate [#]
    d. Fraction [#]
    e. Ct1 [float]
    f. Ct2 [float]
    g. Ct 3 [float]

Other Requirements:
Python v3.8>
Numpy
Pandas

Matplotlib