

dpcR a Swiss-army knife for the analysis of digital PCR experiments

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ABSTRACT

The digital Polymerase Chain Reaction (dPCR) is emerging in all research areas, such as life-sciences and diagnostics since it enables an absolute quantification of nucleic acids. Different approaches for statistical analysis were proposed. However, most analysis is done in closed source software as provided by the vendors. This makes it harder to compare results, such as the confidence interval estimates. A unified open software framework for reproducible research is not available.

To perform dPCR analysis we implemented peer-review statistical methods and plots into the dpcR framework, based on the sophisticated statistical computing environment R. dpcR is versatile open source cross-platform software framework, which provides functions to process dPCR data independent of the hardware. Our software can be used for data analysis and presentation, as framework for novel technical developments and as reference for statistical methods in dPCR analysis. Features such as functions to estimate the underlying Poisson process, calculation of confidence intervals based on single samples as well as on replicates, a novel Generalized Linear Model-based procedure to compare digital PCR experiments and a spatial randomness test for assessing plate effects have been integrated. We use a plug-in like architecture and abstraction layers to make the framework usable for droplets and (real-time) chamber based technologies.

dpcR was implemented with interfaces to the command-line, graphical user interfaces and interactive web application. dpcR can be used by novices in a graphical user interface or by experts via a command-line interface. The dpcR framework can be used to build a custom-made analyser according to the wishes of the user. The dpcR

framework is an open environment, which can be adopted to the growing knowledge in dPCR.

INTRODUCTION

Real-time quantitative PCR (qPCR) is the standard approach to quantify nucleic acids (12). The quantification of the amplification is not done by determining a C_q-value derived from an amplification curve. qPCR is a well established and robust technology, which allows precise quantification of DNA material in high throughput fashion. However, the quantification by qPCR is challenging at very low and very high concentrations. At low DNA concentration Monte Carlo effect play a role and at high concentration inhibition processes start to dominate the qPCR. Thus, the qPCR is only usable in the working range of the calibrator. In addition, pre-processing and data analysis is affected by numerous adverse effects (18, 20).

The digital PCR (dPCR) is an alternative method to quantify nucleic acids. The chemical basis of the dPCR is similar to the qPCR, which includes master-mix preparation and thermal cycling of the sample. In contrast to qPCR the amplification reaction does not take place in a single reaction chamber. Rather its a process of clonal amplification in small separate "partitions" (e.g., nl volume droplets of water oil emulsions, chambers on micro structured chips). The number of positive partition in relation to the number of total partitions. By applying Poisson statistics it is possible to determine the number of the starting material in given volume. Therefore, the dPCR does not require an external calibration (15, 19). Since approximately ten years the digital PCR (dPCR) is gaining momentum in the mainstream user-base. dPCR will likely have the same impact as qPCR in the nucleic acid methodology (8, 10, 15). There is an intensive research on dPCR platforms with the overall aim to make to technology broadly usable, cheap, robust and to enable high sample throughput.

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A first proposal for digital PCR like approach and the use of the Poisson distribution to quantify the number of molecules on a “sample” was shown by Ruano et al. 1990 (PNAS) with the single molecule dilution (SMD) PCR (17). In 1999 Vogelstein et al. (PNAS) described the first true digital PCR (21). Application of the dPCR cover all applications of conventional qPCR, including investigation of alleles, gene expression analysis and absolute quantification of PCR products. For absolute quantification the qPCR relied on an external calibrator (calibration curve) which was derived serial decadic dilution (e.g., 1:10 → 1:100 → 1:1000) of a known target input quantity. The real-time monitoring of the PCR product formation enabled to determine quantification points (C_q). The C_q are strictly related to the input quantity. A simple arithmetic operation (after logarithmic transformation of the concentration) is sufficient to determine any nucleic acid quantity (7).

qPCR dPCR Number of copies/DNA per volume (e.g., ng/l, copies/l) total number of compartments * ln (...)

The dPCR has some principle assumptions and fundamental properties. First of all the chemical reaction should be not affected by inhibitors. The distribution of the single molecule target regions follows a Poisson distribution. The Poisson distribution appears like a normal distribution but without negative values and being zero the lowest. First a large number (n) of amplifications reactions as required to have a high statistical power. Therefore in practical terms a massive number of PCR reactions is needed. For Poisson distributions an n of XY (get reference from table/text book form statistics/biostatistics?) is considered large. Second that the molecules required for the amplification amplifications reactions are randomly distributed in the compartments. Visual analysis, Ripley’s K functions or ??? can be used to test for randomness of the reaction and thus to exclude the clustering of positive reactions. A clustering of positive wells might be due to sample loading or analysis process (systematical error). The outcome of an amplification can be no amplification at all (less than 1 copy per volume), an unsaturated reaction with a binary/“multinary” amplification (usable to calculate the “concentration”) or a saturated reaction where virtually all compartments are positive.

Calculation of the “Concentration” Reference to “Supplement”

Calculation of the uncertainty To determine the uncertainty of the calculations two approach have been proposed in the peer-review literature (2, 5). The uncertainty is dependent on the number of PCR reactions (reference to *dpcR* functions). Reference to “Supplement” and *dpcR* functions.

Interactive use and graphical representation with *shiny* (4).

Import and export of results figures and data.

There are currently two technical approaches to dPCR. dPCRs may use (microfluidic)chambers or emulsion based chambers (QX200TM(Bio-Rad), RainDropTMSystem (RainDance)). Chamber based dPCR systems have fixed geometries, including the volume of the reaction chambers. Despite the fact that dPCRs is an endpoint analysis the chamber based technologies allow generally the real-time monitoring of the amplification reaction and subsequent confirmation of the amplification reaction be melting curve analysis. Thus, such technologies enable easier trouble

shooting and quality management of the data. However, the downside of these technologies is the fixed limited number of compartments and the price. The emulsion based dPCRs are easier to perform since the compartments are generated by microfluidic technologies and have practically no limitation regarding the number of compartments. This results in a higher statistical power to quantify small differences in sample quantities. The emulsion chambers are made of water-in-oil emulsions with similar sizes.

Two-sided exact tests and matching confidence intervals for discrete data (6)

Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing (1)

Interval Estimation for a Binomial Proportion (3)

We have chosen **R** because it is the *lingua franca* in biostatistics and broadly used in other disciplines (15). There are many packages in existence which enable the fast development of new methods and plotting facilities. As most **R** packages depend on one or more other packages (11) depends *dpcR* on other packages, resulting in a complex network of recursive dependencies. Core packages *qpcR* (13), *shiny* (4), *MBmca* (14), *chipPCR* (16) and further packages as shown in the dependency graph (Supplement XYZ).

R has a rich set of tool to arrange data (reshape?) in order to prepare them for the analysis. This is important when it comes to the question how experiments should be treated. It is possible to analyze the PCR reaction the panels independently (effect on CI and uncertainty) or to pool/aggregate all reactions (effect on CI and uncertainty) to achieve higher sensitivity/certainty.

MATERIALS AND METHODS

Materials subsection one

The source code is open source (GPL-3 or later) and hosted at *github.com*. The stable package is freely available from Bioconductor.

One basic design decision was to structure specific properties of digital PCR systems (droplet vs. chamber) in auxiliary functions and to perform central calculation specific to Poisson statistics in independent main functions. Chamber digital PCR systems fundamentally rely on the proper preprocessing of qPCR data. We have chosen to implement the core functionality by a dependency to the *qpcR* **R** package (13). The main functions (e.g., for analysis, simulations, plotting), several auxiliary helper functions (e.g., data import) and data set of different dPCR systems are listed in Table XY. Further dependencies to 3rd party packages include *pracma*, ... (see Figure 3). See the vignette for details.

The workflow is shown Figure 1.

The GUI employs advanced plots based on *ggplot2* (9).

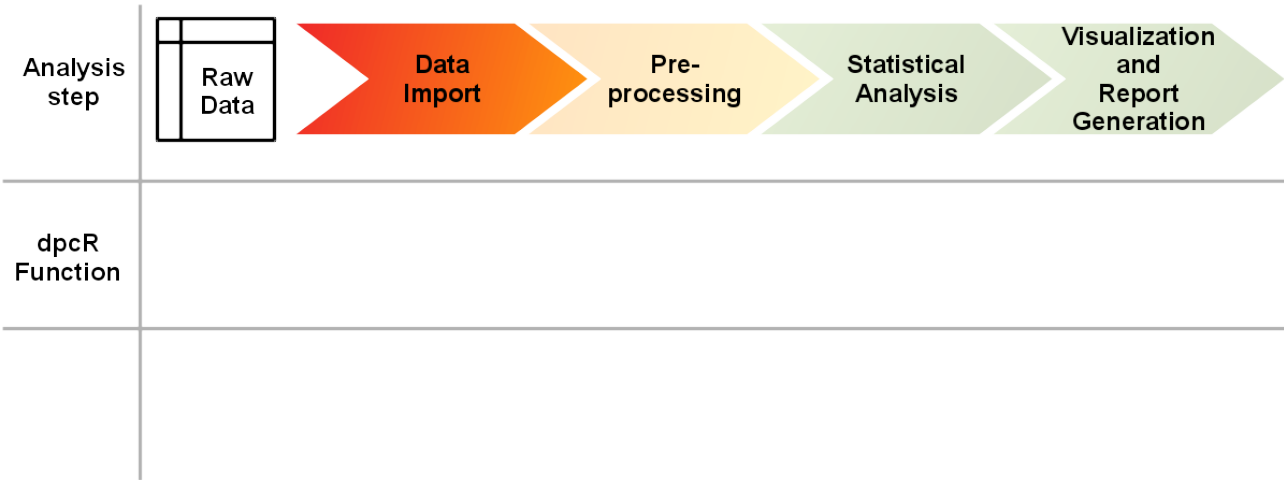


Figure 1. dpcR workflow. Show steps in dPCR data analysis.

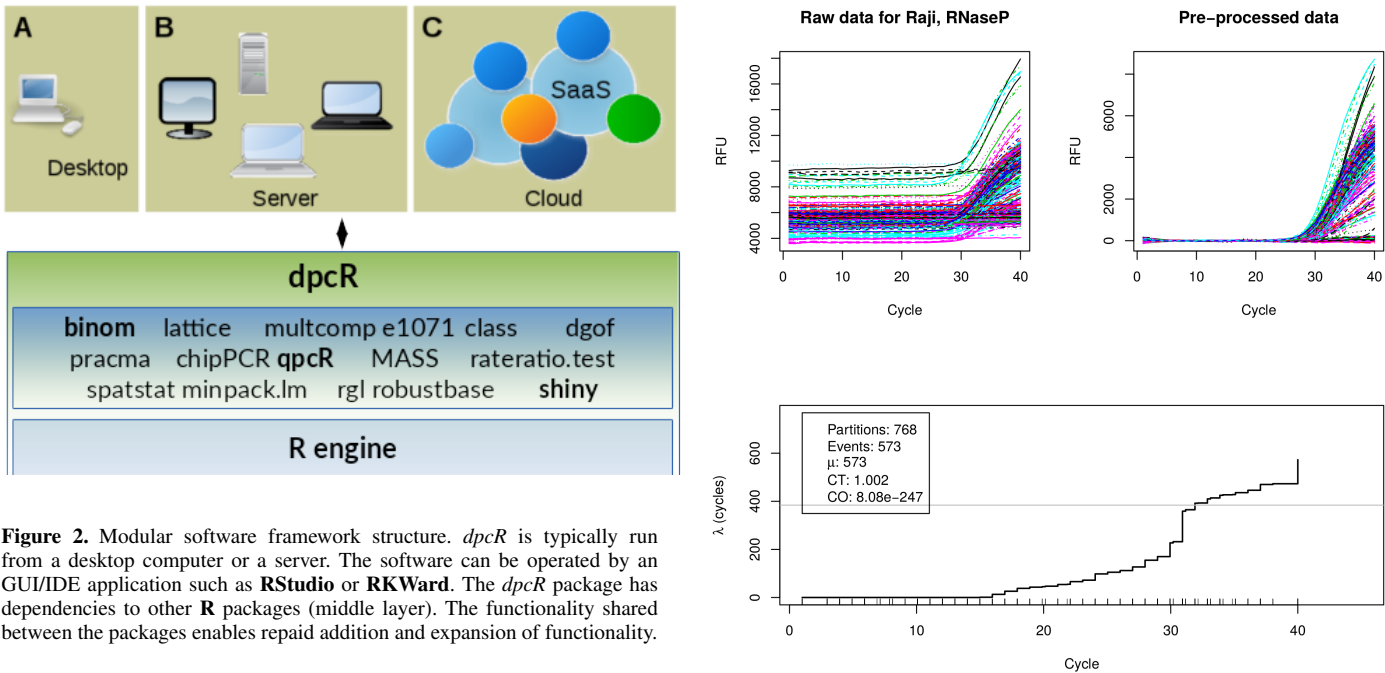


Figure 2. Modular software framework structure. dpcR is typically run from a desktop computer or a server. The software can be operated by an GUI/IDE application such as RStudio or RKWard. The dpcR package has dependencies to other R packages (middle layer). The functionality shared between the packages enables repaid addition and expansion of functionality.

Materials subsection one.

$$LD^r = \frac{LD}{A_{iso}} = 1.5S \left(3\cos^2\alpha_i - 1 \right)$$

(1)

Materials subsection two

(see Figure 4).
Text.

$$LD(t) = \sum_i a_i \exp\left(\frac{-t}{\tau_i}\right)$$

Text.

Figure 3. Uncover characteristics of dPCR data with the dpcR and chipPCR packages. Selected dPCR platforms are real-time platforms. The function qpcr2pp uses the real-time data and interprets them as dPCR (Poisson process). A) Raw data of The function were B) preprocessed (baselined, smoothed) with functions from the chipPCR package and C) finally analyzed (Cq calculation → binarize) with the qpcr2pp (qPCR to Poisson process) function from the dpcR package.

Materials subsection Statistical power - Monte Carlo simulations

The proposed framework was evaluated in three Monte Carlo experiments (2000 times repetitions each) with accordingly 1000, 5000 (results not shown) and 10k partitions. During each repetition of the Monte Carlo scheme, a set of partitions was randomly generated (5) with a determined number of

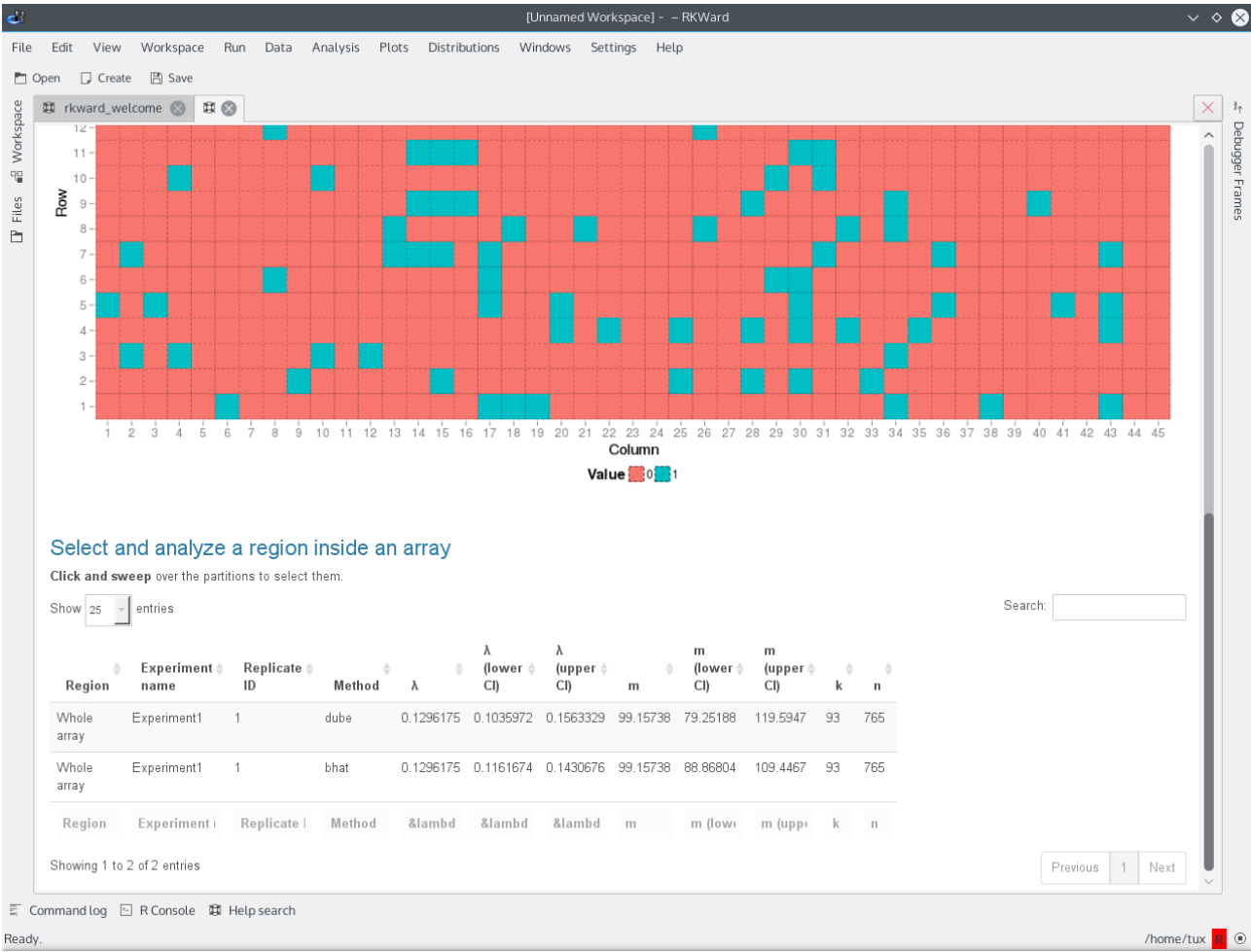


Figure 4. *dpcrReport()* function running in the graphical user interface and integrated development environment RKward.

molecules (‘Base number of molecules’ on X-axis). The set was copied and a number of molecules (‘Added number of molecules’ on Y-axis) was added to randomly chosen partitions. Two obtained arrays were compared using the proposed method. The mean p-values alongside with their standard deviation are presented in the chart below.

RESULTS

Results subsection one

Results subsection two

(see Table 1).
(see Figure ??a).

Table 1. This is a table caption

Col. head 1	Col. head 2 (%)	Col. head 3 (s ⁻¹)	Col. head 4 (%)	Col. head 5 (s ⁻¹)
Row 1	Row 1	Row 1	–	–
Row 2	Row 2	Row 2	Row 2	Row 2

This is a table footnote

Text.

Availability

<http://cran.r-project.org/web/packages/dpcR>
newline Source code: <https://github.com/michbur/dpcR>

DISCUSSION

We developed the *dpcR* package, which is a software framework for analysis of dPCR based on the open source statistical software **R**. *dpcR* provides the scientific community a broadly applicable tool for teaching purposes, data analysis and theoretical research based on simulations.

To accelerate the development of new approaches to dPCR. We implemented all existing statistical methods for dPCR and suggest the introduction of a standardized nomenclature for qPCR. The package enables the simulations and predictions of Poisson distribution for dPCR scenarios, the analysis of previously run dPCRs. Functions included may be used to simulate dPCRs, perform statistical data analysis, plotting of the results and simple report generation.

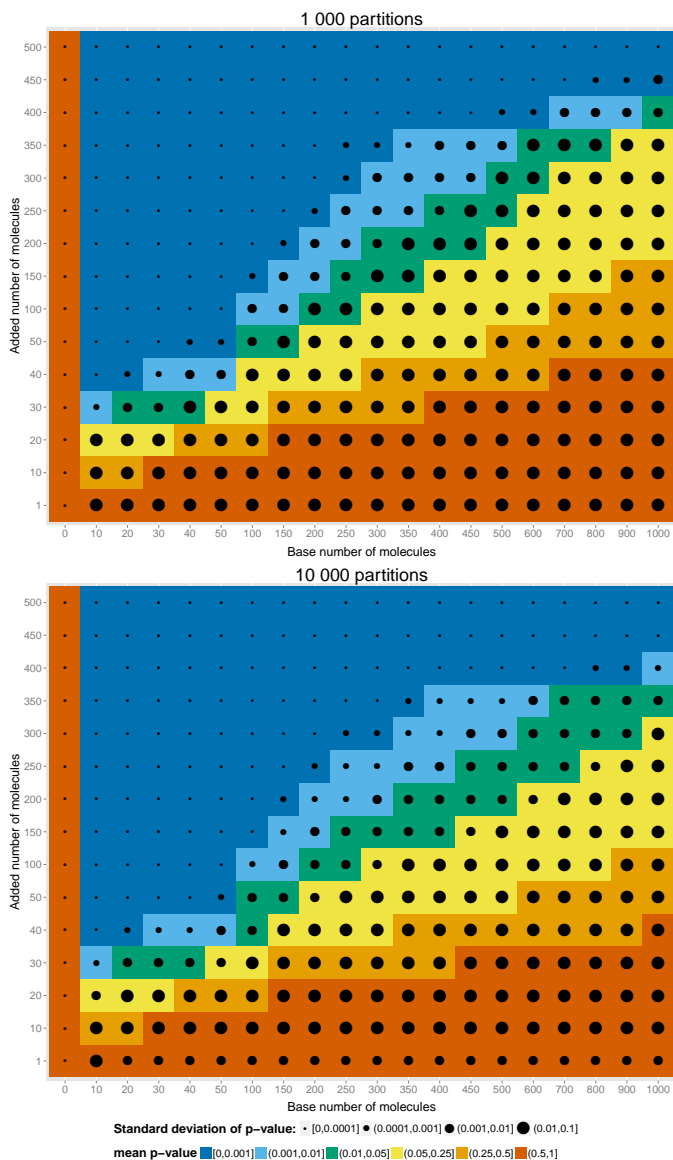


Figure 5. Our method, based on GLM, predicts estimated means copies per partitions using Poisson or binomial regression. Afterwards, estimates are compared against themselves using t-test. Obtained p-values and confidence intervals do not require further correction, because the familywise error is controlled through the whole analysis.

There are currently different software solutions for dPCR analysis such as the OpenArray software (Life Technologies) or XYZ (Bio-Rad). Most of the are black boxes which prevent deep insight into the data processing step. In addition most of the software solutions are aimed to be used in very specific scenarios and a mutual exclusive to alternative platforms (e.g., droplet vs. chamber-based). We have chosen **R** because it is the *lingua franca* in biostatistics and broadly used in other disciplines (15).

Discussion subsection one

Text.

Discussion subsection two

Text.

Discussion subsection three

CONCLUSION

In conclusion, *dpcR* provides means to understand how digital PCR works, to design, simulate and analyze experiments, and to verify their results (e.g., confidence interval estimation), which should ultimately improve reproducibility. We have built what we believe to be the first unified, cross-platform, dMIQE compliant, open source (GPL-3 or later) software framework for analyzing digital PCR experiments. Our framework, designated *dpcR*, is targeted at a broad user base including end users in clinics, academics, developers, and educators. We implemented existing statistical methods for dPCR and suggest the introduction of a standardized nomenclature for qPCR. Our framework is suitable for teaching and includes references for an elaborated set of methods for dPCR statistics. Our software can be used for (I) data analysis and visualization in research, (II) as software framework for novel technical developments, (III) as platform for teaching this new technology and (IV) as reference for statistical methods with a standardized nomenclature for dPCR experiments. The framework enables the simulations and predictions of Poisson distribution for dPCR scenarios, the analysis of previously run dPCRs. Due to the plug-in structure of the software it is possible to build custom-made analyzers.

The *dpcR* includes to invitation to the scientific community to join and support the development of *dpcR* (github?).

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Conflict of interest statement. None declared.

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