A framework for the read-in, analysis, intra/inter assay comparison and report of dPCR experiments

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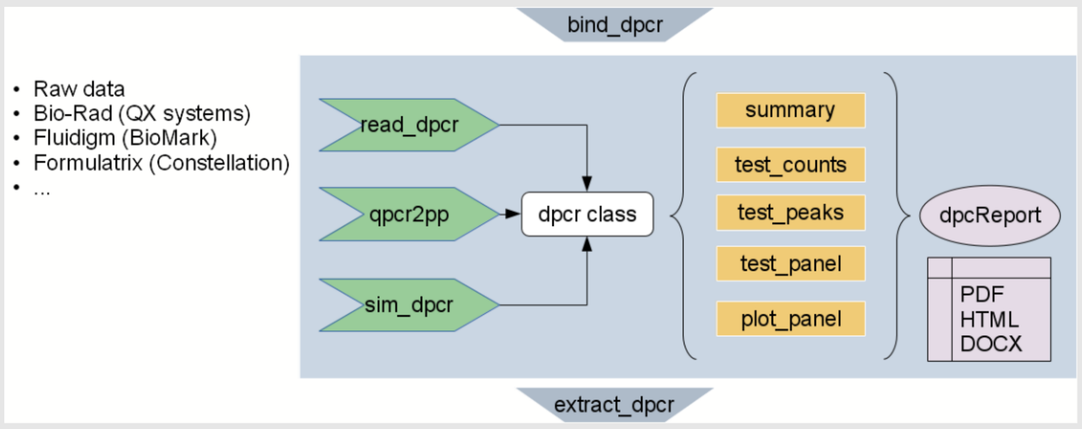
Introduction

dpcR is versatile open source cross-platform software, which provides functions to process and study dPCR data independent of the hardware. Our software can be used for data analysis and presentation, as a framework for novel technical developments and as reference for statistical methods in dPCR analysis.

We based our framework on the sophisticated statistical computing environment R, so the most fundamental interface is a command-line. To move the hurdle of learning new software from users to developers, we also designed a stand-alone graphical interface, accessible also as the interactive web application.

Workflow



The central concept of the workflow is dpcr object, an abstract representation of dPCR data regardless of its source. It allows integration results obtained from various systems in one framework.

Workflow

Vendor	System	Format	Type
Bio-Rad	QX100 & QX200	CSV	Summary export
Fluidigm	BioMark	CSV	Summary export
Formulatrix	Constellation Digital PCR	CSV	Summary export

The number of structured export data formats handled by *dpcR* is growing. Numerous data formats can be processed with the functionality provided by the **R** environment (see Rödiger et al. (2015)).

Graphical User Interface

Bla

Bibliography

Rödiger, S., Burdukiewicz, M., Blagodatskikh, K. A., and Schierack, P. (2015). R as an Environment for the Reproducible Analysis of DNA Amplification Experiments. *The R Journal*, 7(2):127–150.