

dpcReport: POC tests analysis framework

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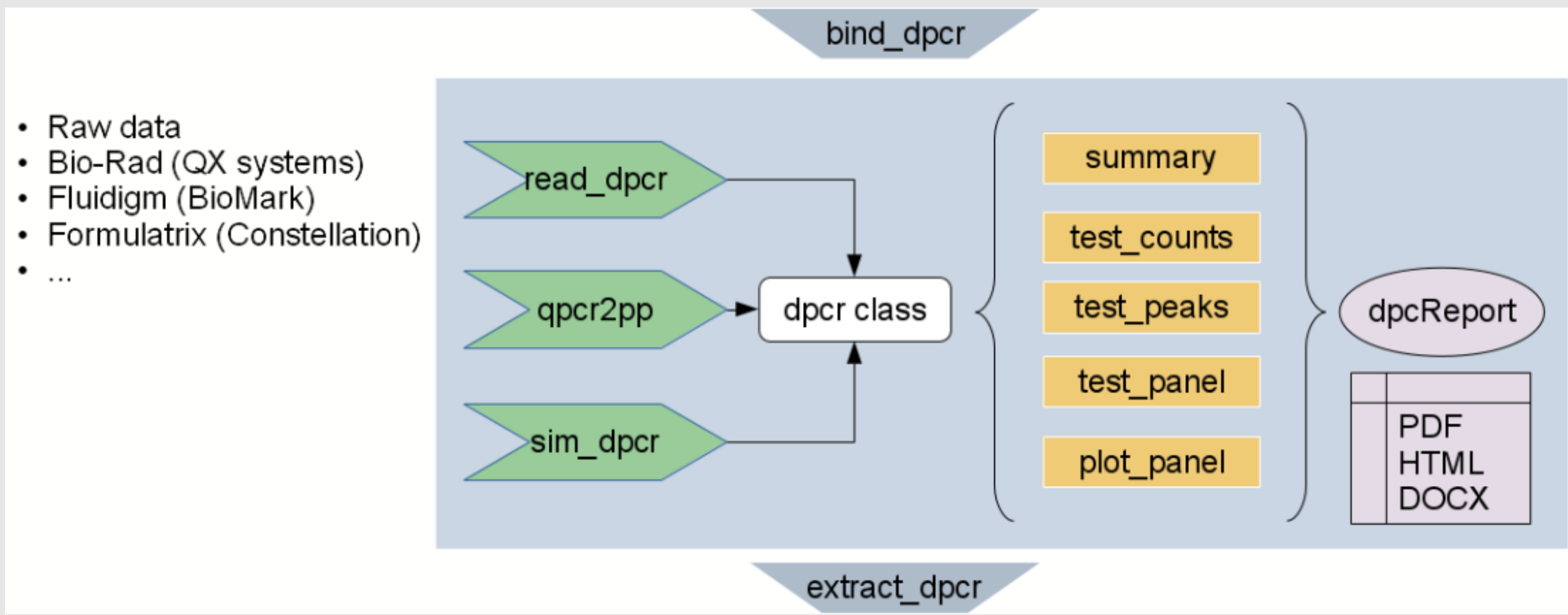
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Introduction

Point-of-Care tests brings the medical examination to the patient. The hardware necessary for such diagnosis should be completed with a suitably portable analysis framework. We introduce *dpcReport*, a versatile open source cross-platform software for analysis of digital PCR (dPCR) experiments. It might be accessed as a web server from any modern personal computer or even a smartphone, greatly enhancing its portability.

Workflow



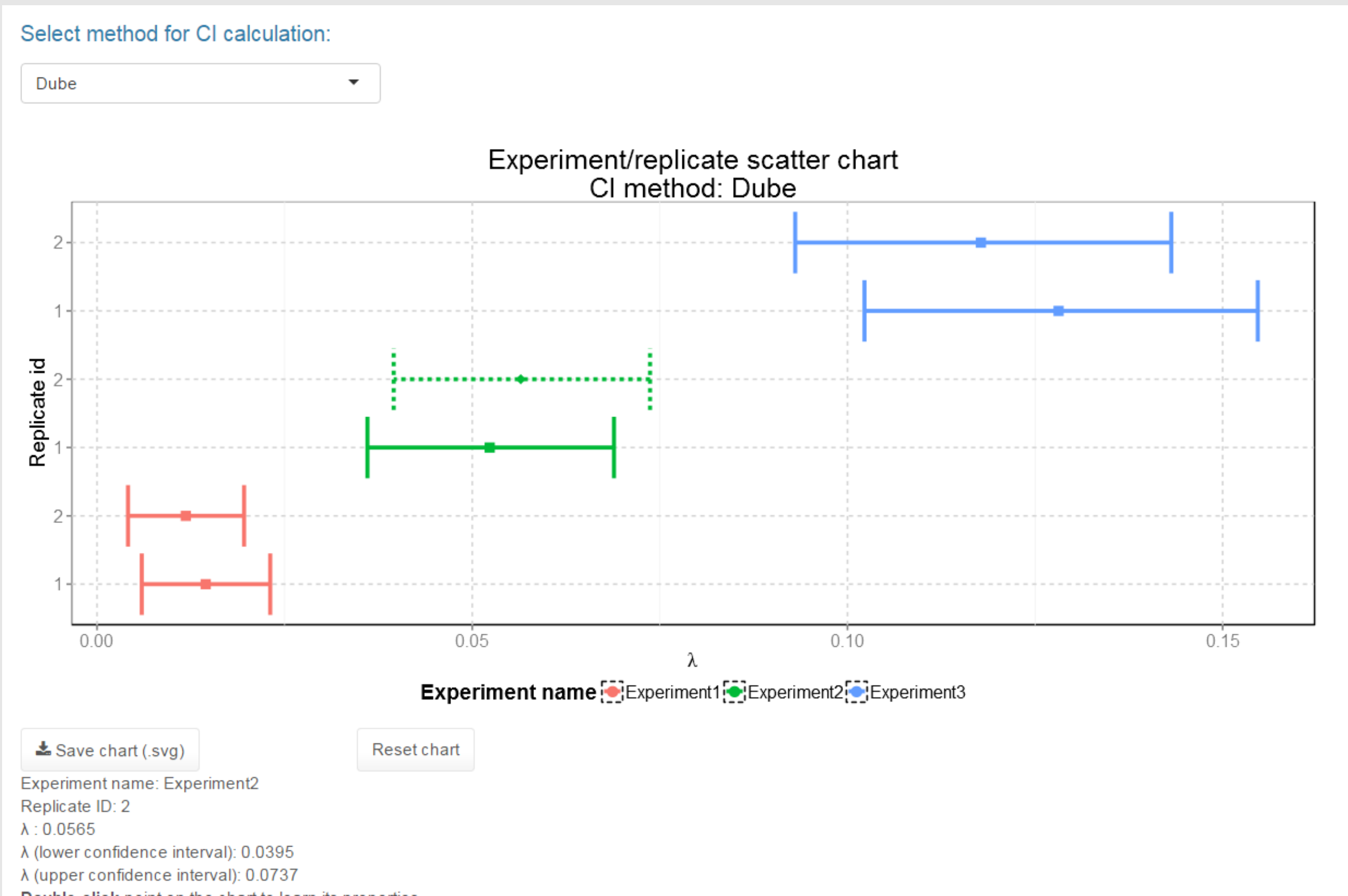
The aim of *dpcReport* is an exhaustive data analysis integrated into a single framework. Even the most basic data pre-processing (as renaming runs) does not require additional software, because it is already covered by *dpcReport*. Such approach is particularly suitable for POC framework, where access to the external software might be limited.

Input data

Vendor	System
Bio-Rad	QX100 & QX200
Fluidigm	BioMark
Formulatrix	Constellation Digital PCR

Results from systems described in the table above may be directly used as the input in the *dpcReport* workflow. Moreover, additional data formats can be processed with the functionality provided by the **R** environment Rödiger et al. (2015). Broad importing functionalities allow an integration of information from many dPCR systems.

Data summary



The summaries of input data are available as interactive tables (allowing filtering and selecting specified runs) and interactive charts (as presented on the figure above, where replicate 2 of experiment 2 is selected).

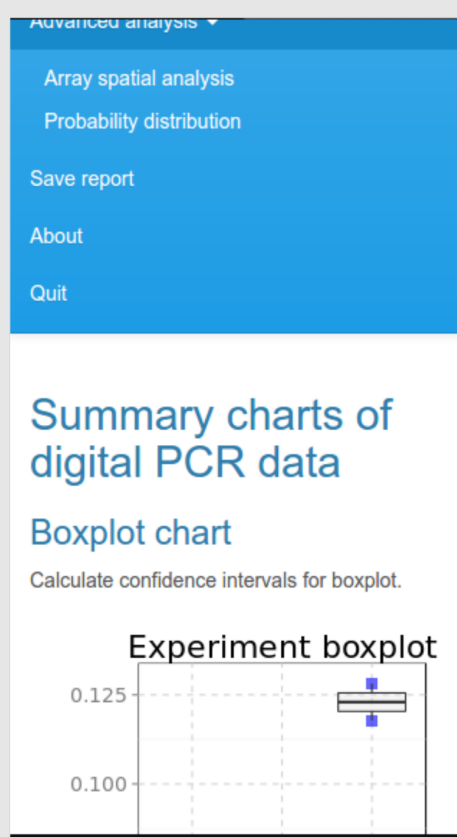
Statistical analysis

Array based dPCR experiments provide information about spatial distribution of partitions. Procedures belonging to spatial statistics verify if the status (positive, negative) of partition depends on its location. To address such questions, we implemented a Complete Spatial Randomness test (Baddeley and Turner, 2005) for dPCR arrays.

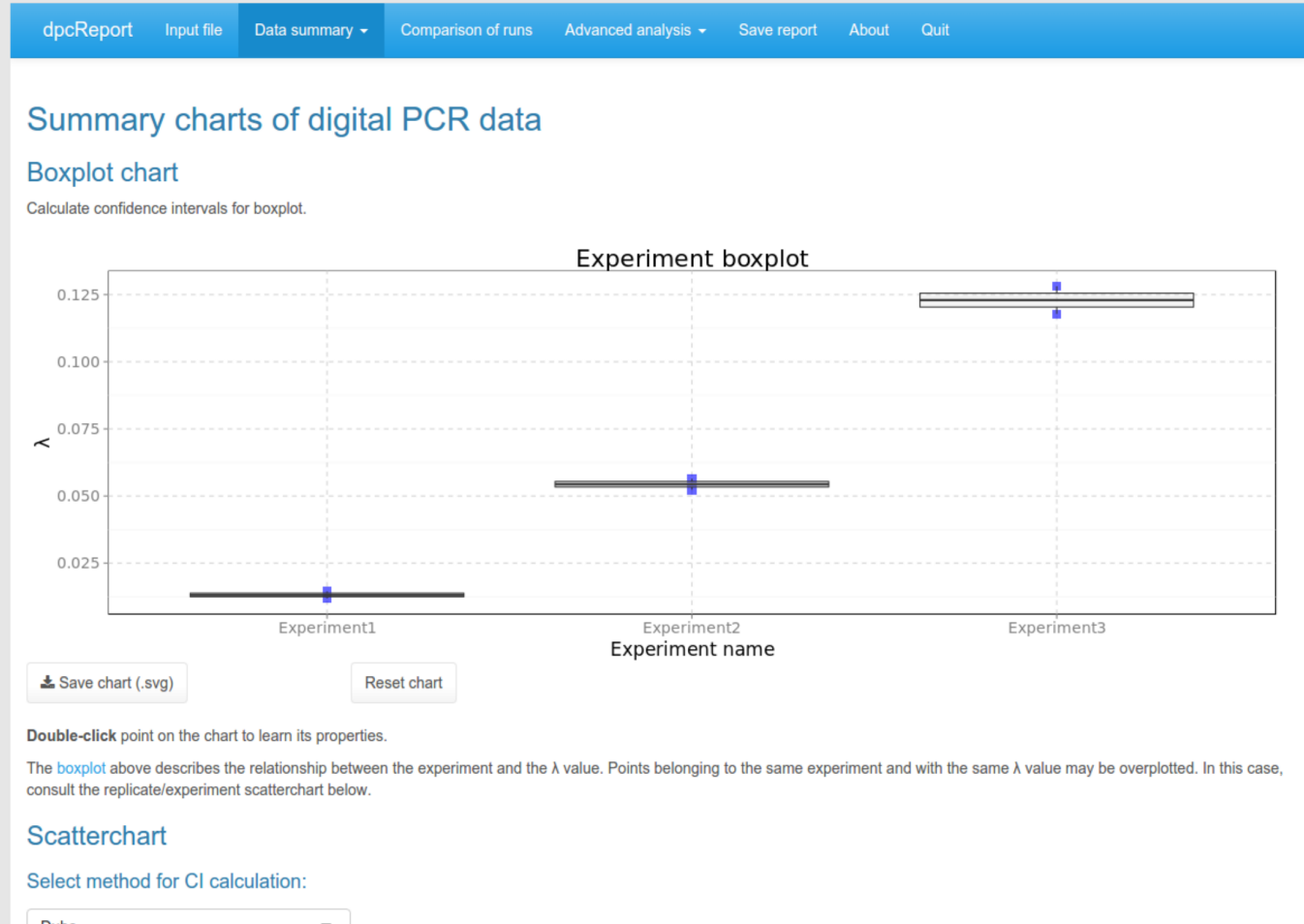
dpcReport uses two methods of comparing dPCR experiments, able to simultaneously compare λ values (mean number of template molecules per partition) of multiple runs. They are based respectively on Generalized Linear Models (Bretz et al., 2010) and on the uniformly most powerful (UMP) ratio test (Fay, 2010).

Graphical User Interface

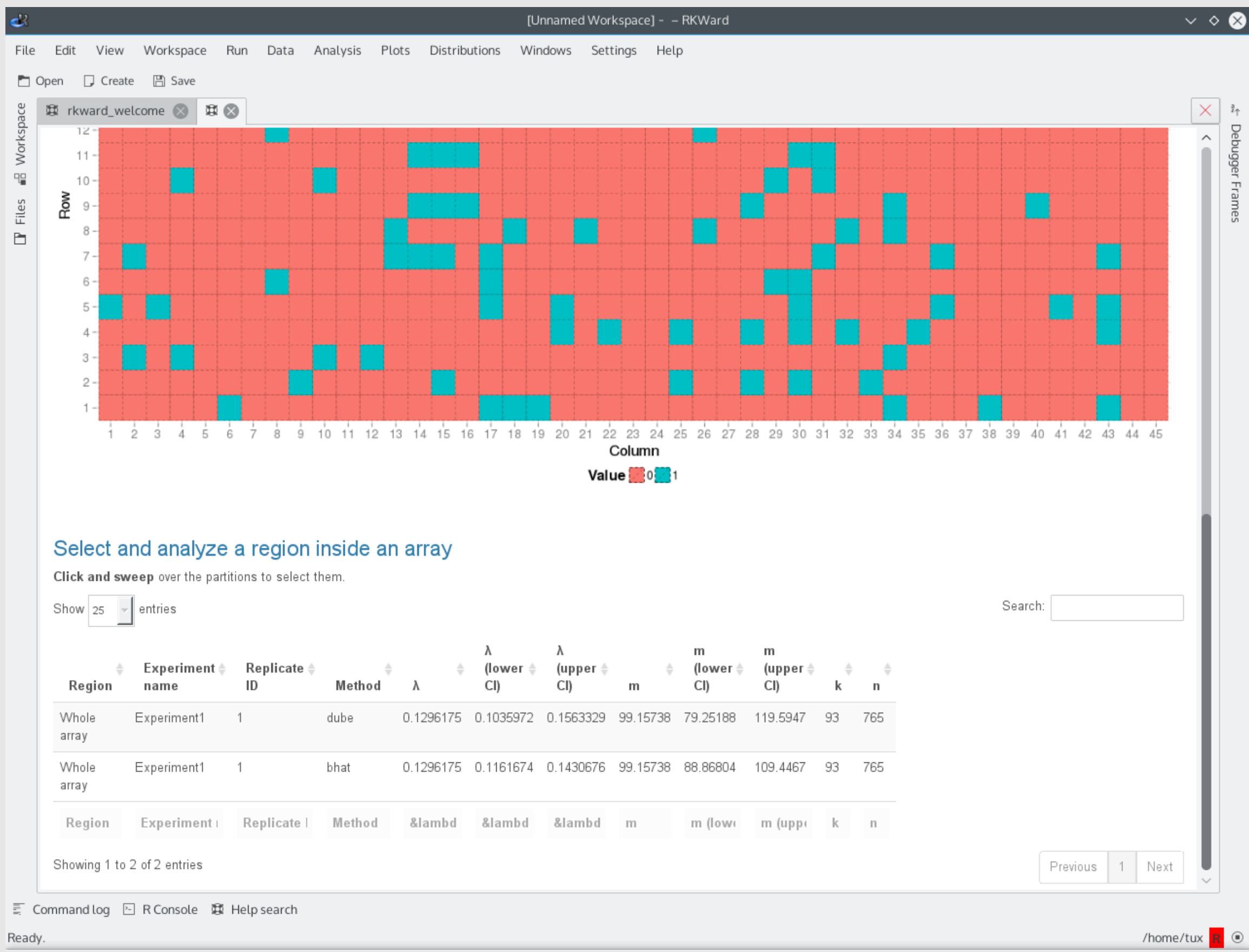
Mobile device



Desktop device



The *dpcReport* may be used as a web application accessible from every modern web browser, including web browsers for portable devices.



Additionally, *dpcReport* may be downloaded and installed *dpcReport* as a standalone application. For users with more experiences with **R**, *dpcReport* is accessible through **R** IDE/GUI such as **RKWord** (Rödiger et al., 2012) or **RStudio**.

dpcReport output

The structure of the output is fully modular. A final report created through the framework contains only parts of the analysis chosen by the investigator. It is also possible to save only selected charts or tables instead of creating the report.

The framework is based on the sophisticated statistical computing environment **R**. An important option of *dpcReport* is an export of the **R** source code used for the report generation is provided to the user. This code can be used for recreating the analysis in the **R** environment or prototyping more complicated workflows.

Summary

The philosophy of point-of-care testing require frameworks that can be used directly at the site of patient care. The portable and self-contained *dpcReport* fulfills such requirements and might be easily integrate into POCT routines involving dPCR assays.

Availability

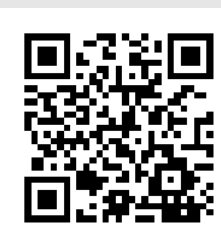
dpcReport (standalone version for Microsoft Windows[®]):

<http://sourceforge.net/projects/dpcreport/>



dpcReport (web server):

<http://www.smorfland.uni.wroc.pl/dpcReport>



dpcR package:

<https://github.com/michbur/dpcR>



Bibliography

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- Rödiger, S., Burdukiewicz, M., Blagodatskih, 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.
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