

dpcReport: POC tests analysis framework

Michał Burdukiewicz¹, Piotr Sobczyk², Paweł Mackiewicz¹ and Stefan Rödiger³

¹University of Wrocław, Department of Genomics, Poland

²Wrocław University of Technology, Department of Mathematics, Poland

³Faculty of Natural Sciences, Brandenburg University of Technology Cottbus–Senftenberg, Germany

Introduction

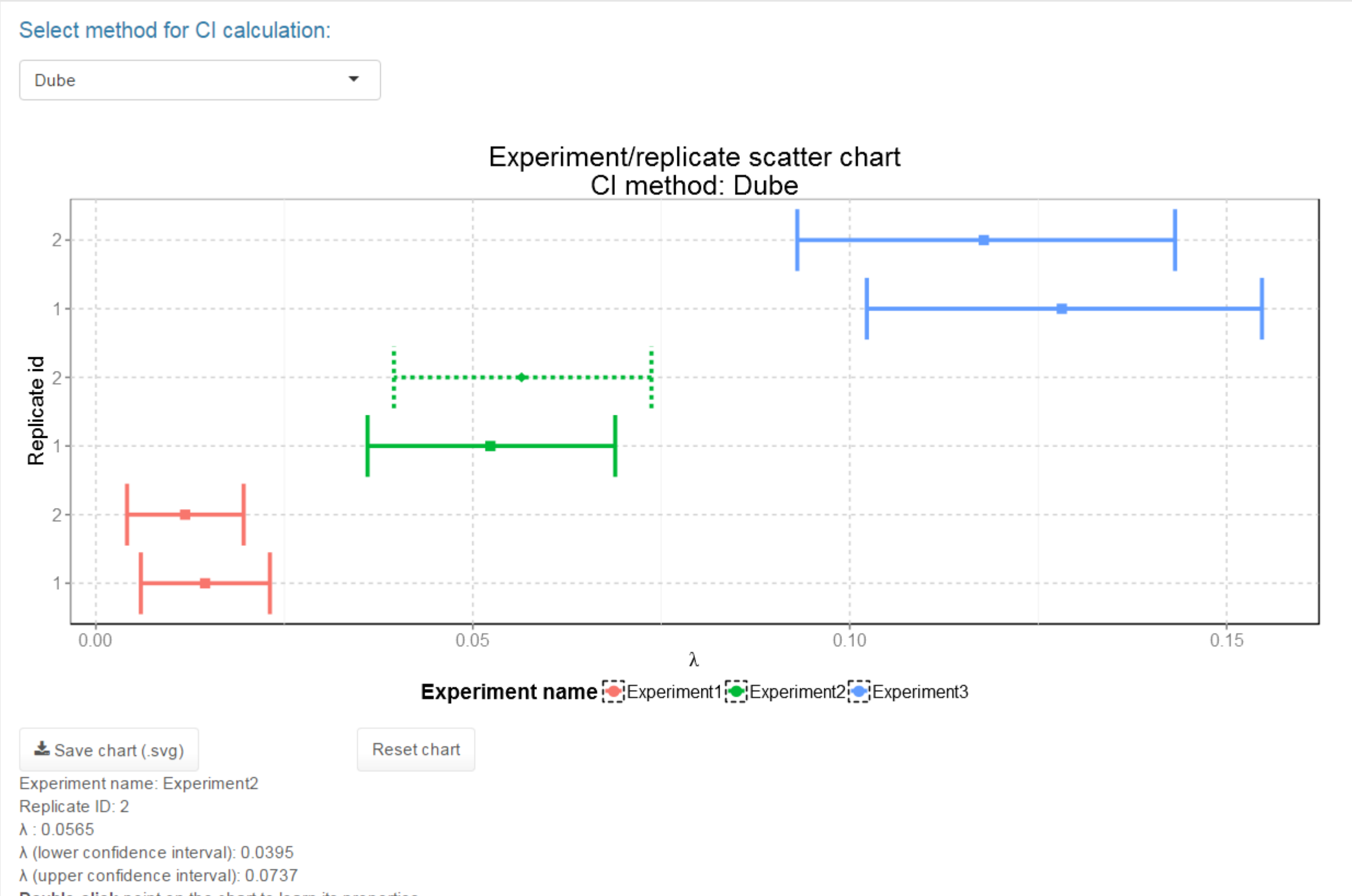
Point-of-Care tests brings the medical examination to the patient. The hardware necessary for such diagnosis should be completed with a suitably portable analysis framework. We introduce dpcReport, a versatile open source cross-platform software for analysis of digital PCR (dPCR) experiments. It might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

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).

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).

Test panel

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.

This functionality is enhanced with a tool for analysis of manually selected regions of the array.

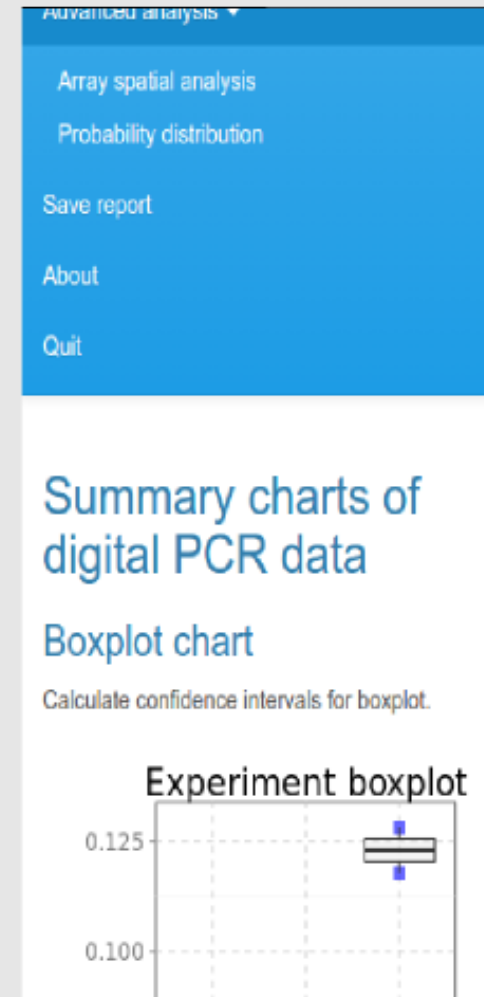
Comparison of dPCR experiments

dpcReport uses two methods of comparing dPCR experiments, able to simultaneously compare λ values (mean number of template molecules per partition) of multiple runs. One of them is based on Generalized Linear Models, where we employ a simplistic model reflecting relationships between variables in dPCR results and next pairwise compared using multiple t-tests as described elsewhere Bretz et al. (2010).

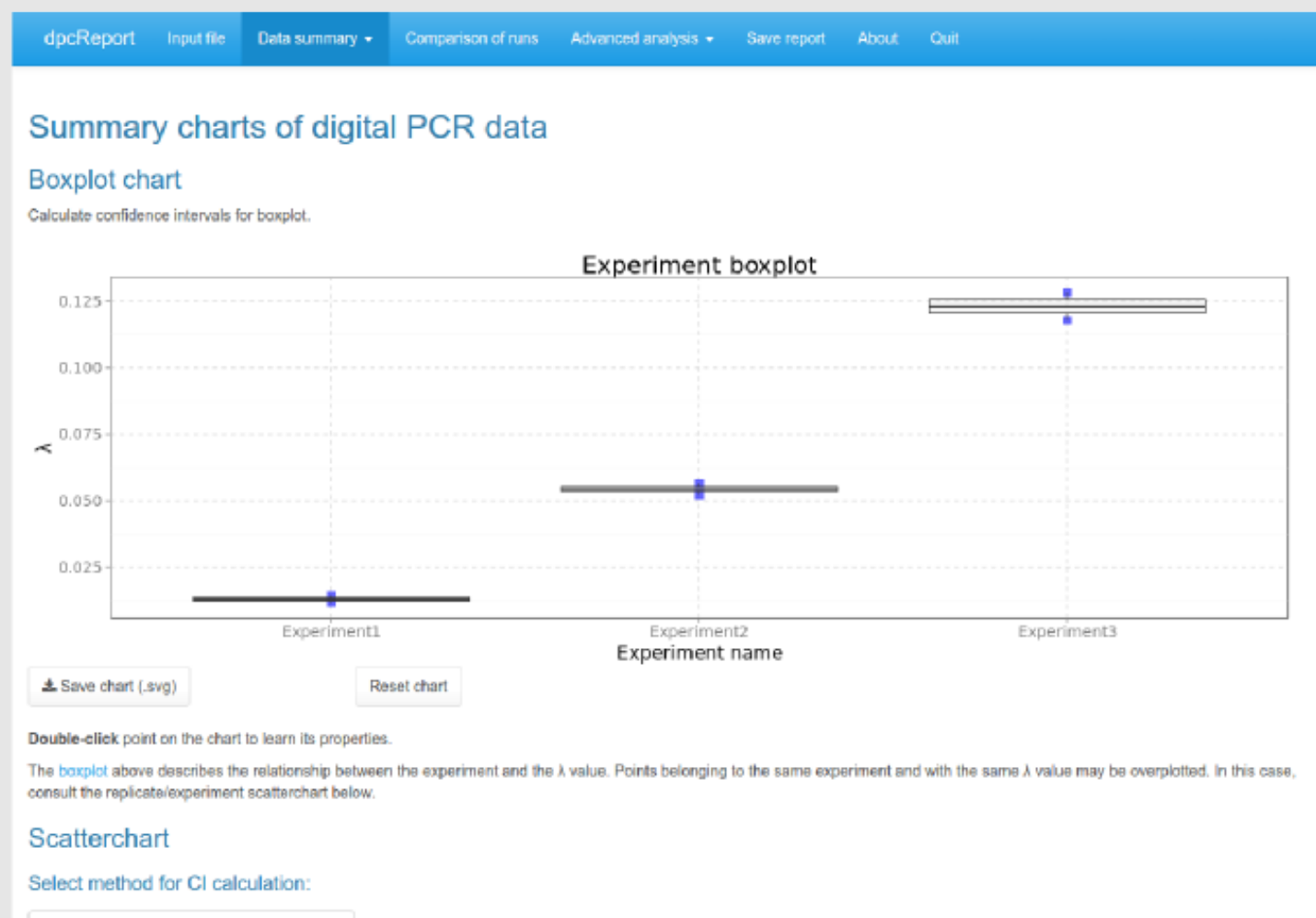
The second method pairwise compares the $\hat{\lambda}$ from two or more dPCR experiments using the uniformly most powerful (UMP) ratio test (Fay, 2010). We use Benjamini-Hochberg correction for p-values (Benjamini and Hochberg, 1995) to control the family-wise error rate. Additionally, this method computes simultaneous confidence intervals for estimated λ values.

Graphical User Interface

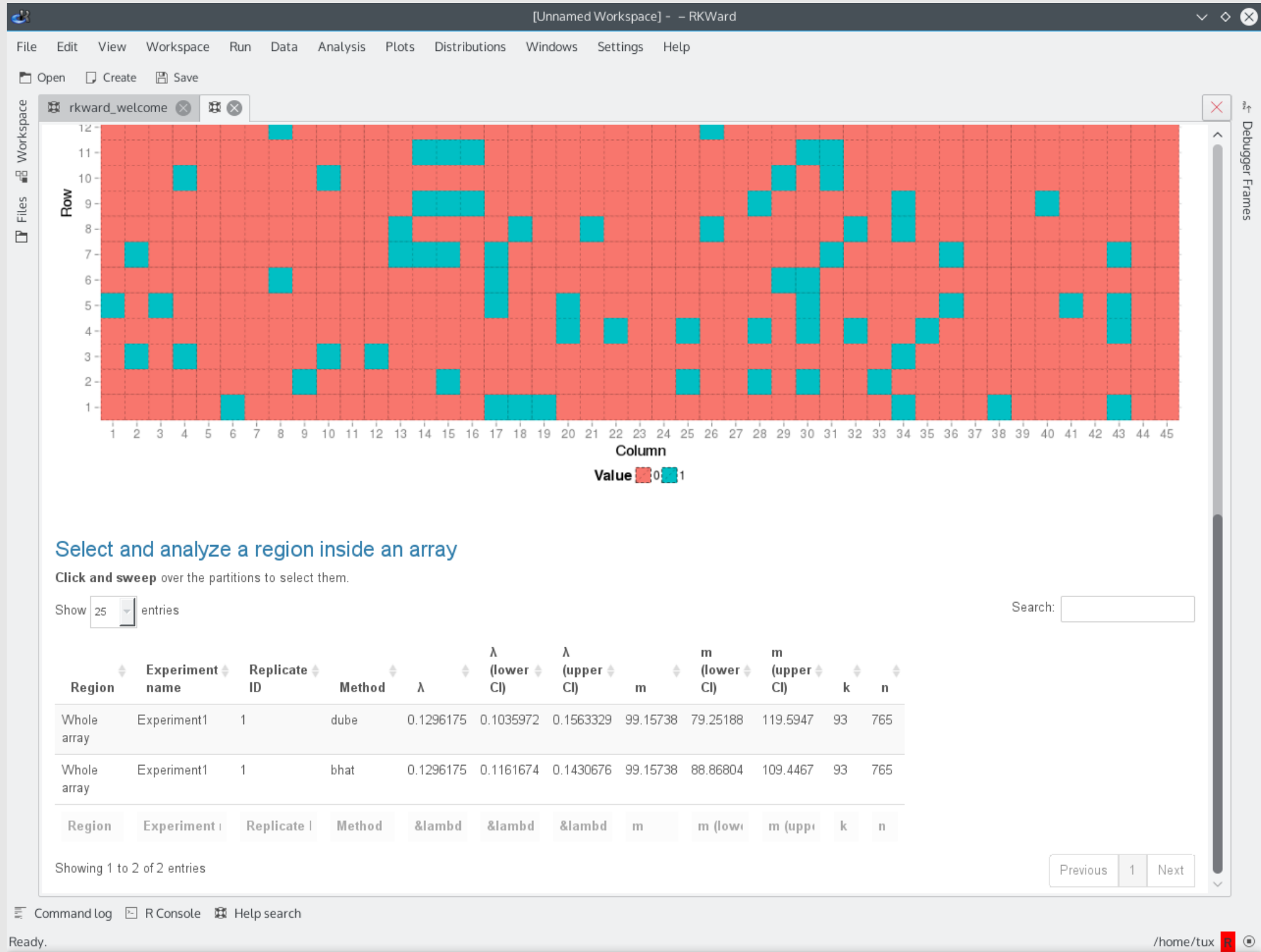
Mobile device



Desktop device



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



Additionally, dpcReport is accessible through **R** IDE/GUI such as **RKWARD** Rödiger et al. (2012) or **RStudio**. Moreover, it may be downloaded and installed as a standalone application.

Summary

The dpcReport is a freeware multi-platform software designed to assist researchers in the analysis of dPCR data.

Availability

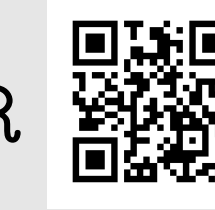
dpcReport (standalone version for Microsoft Windows[®]):

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

dpcReport (web server):

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

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



Bibliography

- Baddeley, A. and Turner, R. (2005). spatstat: An R package for analyzing spatial point patterns. *Journal of Statistical Software*, 12(6):1–42.
- Benjamini, Y. and Hochberg, Y. (1995). Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. *Journal of the Royal Statistical Society: Series B (Methodological)*, 57(1):289–300.
- Bretz, F., Hothorn, T., and Westfall, P. (2010). *Multiple Comparisons Using R*. Chapman & Hall/CRC Press, Boca Raton, Florida, USA.
- Fay, M. (2010). Two-sided exact tests and matching confidence intervals for discrete data. *Proceedings of the National Academy of Sciences of the United States of America*, 2(1):53–58.
- 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.
- Rödiger, S., Friedrichsmeier, T., Kapat, P., and Michalke, M. (2012). RKWard: A Comprehensive Graphical User Interface and Integrated Development Environment for Statistical Analysis with R. *Journal of Statistical Software*, 49(9):1–34.