

# dpcReport: web server and software suite for unified analysis of digital PCRs and digital assays

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dPCR software

Aim

Reproducibility

## dPCR software

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Words, words

# Aim

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Create framework for dPCR data analysis:

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- tailored for the most common tasks,

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Create framework for dPCR data analysis:

- tailored for the most common tasks,
- unified,
- reproducible.

# Reproducibility

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Scientific software supports reproducibility, otherwise it is not scientific.

A report must contain enough information to allow the full reproduction of the conducted analysis.

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## dpcReport

Report generated on 2017-03-27 07:12:26 using [dpcR](#) R package.

Detected input file: 20130918\_Dilution\_log10.csv.

md5 checksum of the input file: 6bf3306199dd7af439d1c8acd08e23c1

**The input was modified manually in dpcReport application.**

File format: QX100.

## Data summary table

Run	Experiment name	Replicate ID	Assay	Method	$\lambda$	$\lambda$ (lower CI)	$\lambda$ (upper CI)	Concentration	Concentration (lower CI)	Concentration (upper CI)	k	n
ABS1.A09.gDNA + P 10 <sup>4</sup>	ABS1	A09.gDNA + P 10 <sup>4</sup>	ileS	dube	0.07	0.07	0.08	970.44	0.08	0.09	936	13346
ABS1.A09.gDNA + P 10 <sup>4</sup>	ABS1	A09.gDNA + P 10 <sup>4</sup>	ileS	bhat	0.07	0.07	0.08	970.44	0.08	0.09	936	13346
ABS1.B09.gDNA	ABS1	B09.gDNA	ileS	bhat	0.07	0.07	0.08	1171.87	0.08	0.09	1140	11688

# Date and time

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# Input file name

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# Input file checksum

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Changes in case of the manual alteration of the input file.

# Manual alterations inside dpcReport

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## R Session

```
## R version 3.3.3 (2017-03-06)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 14.04.5 LTS
##
## locale:
## [1] LC_CTYPE=pl_PL.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=pl_PL.UTF-8      LC_COLLATE=pl_PL.UTF-8
## [5] LC_MONETARY=pl_PL.UTF-8  LC_MESSAGES=pl_PL.UTF-8
## [7] LC_PAPER=pl_PL.UTF-8     LC_NAME=C
## [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=pl_PL.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] xtable_1.8-2      knitr_1.15.1      digest_0.6.12
## [4] dplyr_0.5.0       DT_0.2            ggplot2_2.2.1
## [7] rhandsontable_0.3.4 shinythemes_1.1.1 shiny_1.0.0
## [10] dpcR_0.4
##
## loaded via a namespace (and not attached):
## [1] jsonlite_1.2      binom_1.1-1      splines_3.3.3
## [4] assertthat_0.1    highr_0.6        Rfit_0.23.0
## [7] chipPCR_0.0.8-11  yaml_2.1.14      outliers_0.14
## [10] robustbase_0.92-7 lattice_0.20-34  quantreg_5.29
## [13] quadprog_1.5-5    polyclip_1.5-6   colorspace_1.3-1
## [16] sandwich_2.3-4    htmltools_0.3.5  httpuv_1.3.3
## [19] Matrix_1.2-8      plyr_1.8.4       SparseM_1.74
## [22] mvtnorm_1.0-5     ptw_1.9-11      scales_0.4.1
## [25] tensor_1.5        pracma_1.9.5     MatrixModels_0.4-1
## [28] tibble_1.2        mgcv_1.8-16      TH.data_1.0-7
## [31] dgof_1.2          lazyeval_0.2.0   survival_2.40-1
## [34] magrittr_1.5      readxl_0.1.1     mime_0.5
## [37] deldir_0.1-12     evaluate_0.10    nlme_3.1-131
```

## Reproducibility of the workflow

An analysis conducted in a GUI-based software, as *dpcReport*, is more challenging to reproduce.

*dpcReport* exports all steps of the analysis, including parameters adjusted manually by the user, in form of the **R** code that recreates the whole workflow.

# Reproducibility of the workflow

## R code

The R code below may be used to recreate reported results.

```
# Load packages
library(dpcR)
# if you do not have dpcR package, install it from GitHub:
# devtools::install_github("michbur/dpcR")
library(ggplot2) # ggplot2 library for nice plots
# Define theme for plots
cool_theme <- theme(plot.background=element_rect(fill = "transparent", colour = "transparent"),
panel.grid.major = element_line(colour="lightgrey", linetype = "dashed"), panel.background =
element_rect(fill = "white", colour = "black"), legend.background = element_rect(fill="NA"),
legend.position = "bottom", axis.text = element_text(size = 14), axis.title.x = element_text(size=17,
vjust = -0.1), axis.title.y = element_text(size = 17, vjust = 1), strip.text = element_text(size = 17,
face = "bold"), strip.background = element_rect(fill = "#9ecae1", colour = "black"), legend.text =
element_text(size=14), legend.title = element_text(size = 17), plot.title = element_text(size = 22),
legend.key = element_rect(fill = "white", colour = "black", linetype = "dashed", size = 0.5))
# Read and adjust data
# The input file is assumed to be in the current R working directory
input_data <- read_dpcr("20130918_Dilution_log10.csv", format = "QX100")

#####
# Print only table from summary.dpcr function
summary(input_data, print = FALSE)[["summary"]]

#####
# Prepare data for plots
plot_data <- summary(input_data, print = FALSE)[["summary"]]
plot_data <- plot_data[plot_data[["method"]] == "dube", ]
ggplot(plot_data, aes(x = experiment, y = lambda, ymax = lambda.up, ymin = lambda.low)) + geom_point(size
= 4, alpha = 0.6, shape = 2, colour = "blue") + cool_theme + geom_boxplot(outlier.colour = NA, fill =
adjustcolor("lightgrey", alpha.f = 0.25), shape = 15) + ggtitle(paste0("Experiment boxplot\nCI method: ",
```

*dpcReport* is the integrated environment for the analysis of dPCR data.

Web server: `www.smorfland.uni.wroc.pl/shiny/dpcReport`

R package (including your local instance of dpcReport):

`www.github.com/michbur/dpcR`

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- Stefan Rödiger,
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(<https://cran.r-project.org/package=biogram>):
  - Piotr Sobczyk,
  - Chris Lauber,
- **AmyLoad** database ([comprec-lin.iiar.pwr.edu.pl/amyload](http://comprec-lin.iiar.pwr.edu.pl/amyload)):
  - Paweł Woźniak,

