

dpcR: web server and R package for analysis of digital PCR experiments

Michał Burdukiewicz^{1*}, Piotr Sobczyk², Paweł Mackiewicz¹, Stefan Rödiger³
*michalburdukiewicz@gmail.com

¹University of Wrocław, Department of Genomics

²Wrocław University of Technology, Faculty of Pure and Applied Mathematics

³Brandenburg University of Technology Cottbus-Senftenberg, Institute of Biotechnology

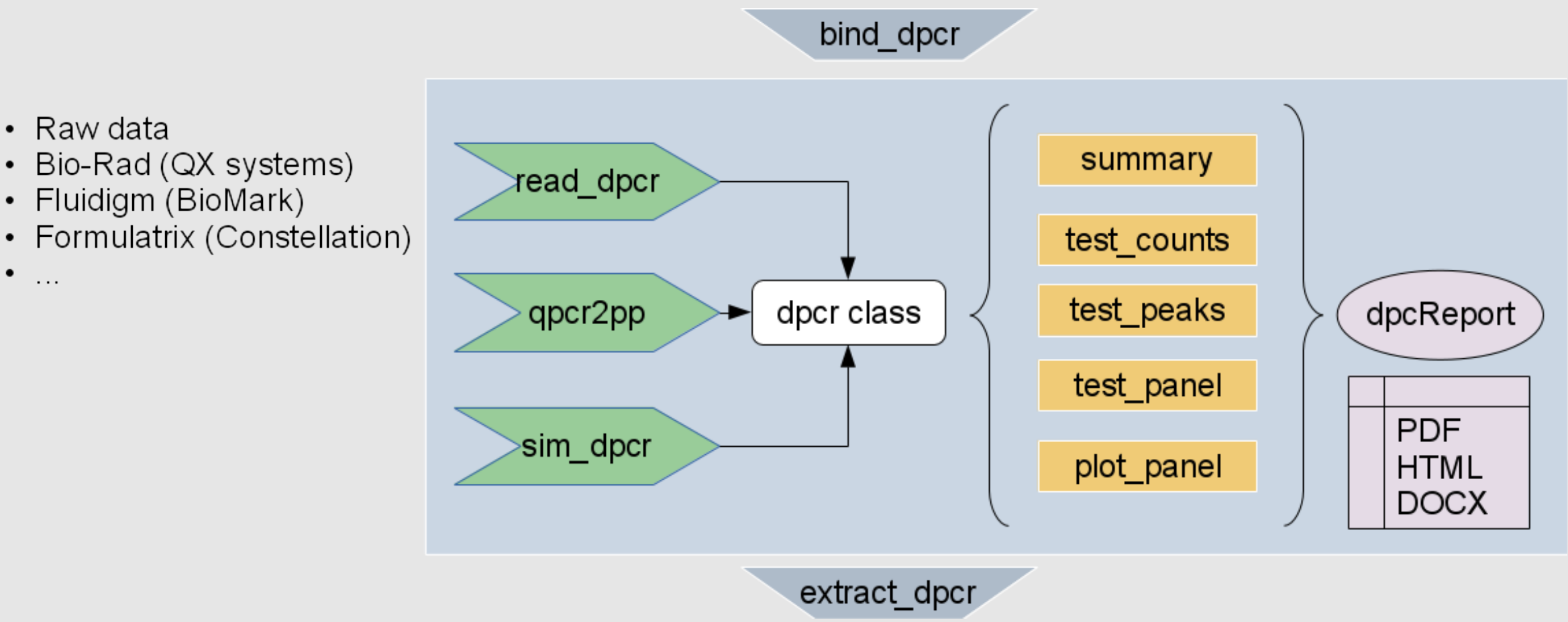
Introduction

dPCR reaction consists of multiple amplifications occurring in numerous small partitions. The result of dPCR is a binary vector describing states of partitions (positive in case of detected amplification, negative otherwise). This data is further used to estimate the main parameter, λ , which may be interpreted as the mean number of template molecules per partition. We created dpcR, an open source tool for reproducible analysis of dPCR data, fully compatible with dMIQE requirements.

Conclusions

Hidden semi-Markov models can be used to accurately predict the presence of secretory signal peptides effectively extracting information from very data sets. Prediction of cleavage site position still requires refinement.

dpcR workflow



dpcR workflow. The diagram shows main functions available at each step of a dPCR data analysis.

Availability and funding

signal.hsmm web server:
www.smorfland.uni.wroc.pl/signalhsmm
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Hidden semi-Markov model (HSMM) of a signal peptide

- Assumptions of the model:
- the observable distribution of amino acids arises due to being in a certain region (state),
 - a duration of the state (the length of given region) is modeled by a probability distribution (other than geometric distribution as in typical hidden Markov models).

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