

# Methods of Comparing Digital PCR Experiments

Michał Burdukiewicz<sup>1</sup>, Piotr Sobczyk<sup>2</sup>, Paweł Mackiewicz<sup>1</sup>, Stefan Rödiger<sup>3</sup>

<sup>1</sup>University of Wrocław, Department of Genomics, Poland

<sup>2</sup>Wrocław University of Technology, Institute of Mathematics and Computer Science, Poland

<sup>3</sup>Faculty of Natural Sciences, Brandenburg University of Technology Cottbus–Senftenberg, Germany

## Introduction

quantification (Bretz et al., 2010), allow comparing experiments.

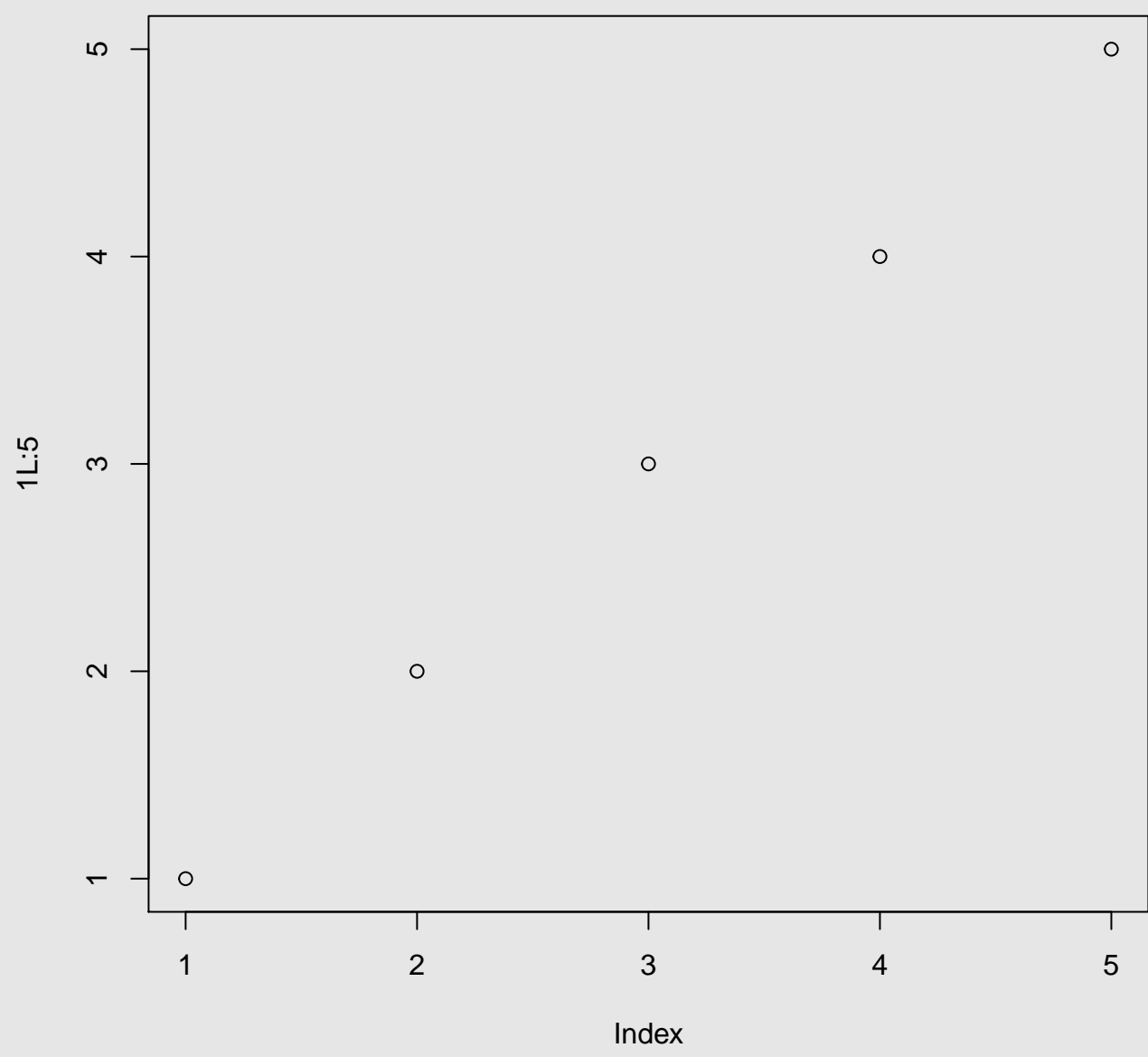
## Evaluation

stuff stuff stuff

## Summary

Hidden semi-Markov models can be used to accurately predict the presence of secretory signal peptides effectively extracting information from very small data sets.

## Classification of amino acids used by signal.hsmm



## Avaibility

dpcR web server:  
dpcR R package:  
<http://cran.r-project.org/web/packages/dpcR/>

## Bibliography

Bretz, F., Hothorn, T., & Westfall, P. (2010). *Multiple comparisons using R*. Boca Raton, Florida, USA: Chapman & Hall/CRC Press.