

Methods of Comparing Digital PCR Experiments

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Introduction

The outcome of digital PCR (dPCR) experiments are mean copies per partition (λ). Results are derived from the measured data, an ordered (in one or two dimensions) sequence of positive partitions. The usual analysis involves assumption the template molecules are Poisson distributed among partitions. On this premise, already proposed approaches, based on the confidence intervals ($?$, $?$) or uncertainty quantification ($?$, $?$), allow comparing experiments.

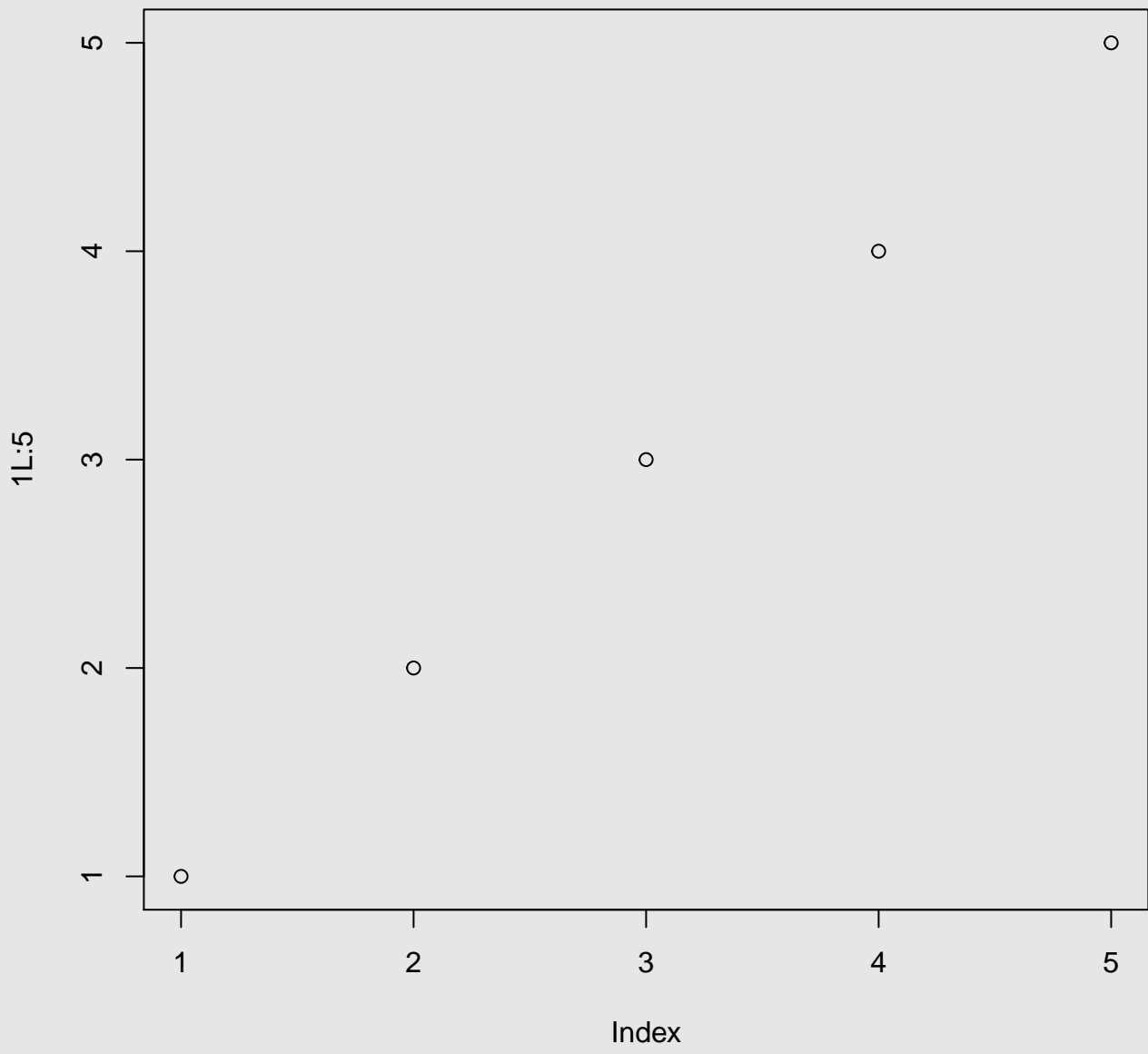
Evaluation

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

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

Bibliography