

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

- Secretory signal peptides:
- are short (20-30 residues) N-terminal amino acid sequences,
 - direct a protein to the endomembrane system and next to the extracellular localization,
 - possess three distinct domains with variable length and characteristic amino acid composition (Hegde and Bernstein, 2006).
 - are universal enough to direct properly proteins in different secretory systems; artificially introduced bacterial signal peptides can guide proteins in mammals (Nagano and Masuda, 2014) and plants (Moeller et al., 2009),
 - tag among others hormones, immune system proteins, structural proteins, and metabolic enzymes.

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.

Organization of signal peptide

- n-region: mostly basic residues (Nielsen and Krogh, 1998),
- h-region: strongly hydrophobic residues (Nielsen and Krogh, 1998),
- c-region: a few polar, uncharged residues (Jain et al., 1994).

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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