Something about Computer Science

Karsken Bælg

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Department of Computer Science
Aarhus University
Denmark

Something about Computer Science

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by
Karsken Bælg
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Abstract

A short summary of the contributions in the thesis …

Acknowledgements

Thanks to . . .

Karsken Bælg,
Århus, May 15, 2009.

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Part I

Overview

Chapter 1

Introduction

We'll start the war from right here
— Theodore Roosevelt, Jr., Utah Beach, June 6, 1944.

Blah blah blah …

The section and page number is in the header … and theorems etc. are numbered according to the chapter as in Theorem 1.1.

Theorem 1.1 *The statement* $2 + 2 = 4$ *is seems to be true, unless* $\mathbf{P} = \mathbf{NP}$*, in which case we are not sure …*

Chapter 2

Comparison of Sequences

This was their finest hour
— Winston S. Churchill, House of Commons, June 18, 1940.

Blah blah blah . . .

This is written using the "todo" macro

Chapter 3

Regularities in Sequences

Never was so much owed by so many to so few
— Winston S. Churchill, House of Commons, August 20, 1940.

Blah blah blah . . . [This is written using the "remark" macro]

Part II

Papers

Chapter 4

Measures on Hidden Markov Models

The paper *Measures on hidden Markov models* presented in this chapter has been published in part as a technical report [1] and a conference paper [2].

[1] R. B. Lyngsø, C. N. S. Pedersen, and H. Nielsen. Measures on hidden Markov models. Technical Report RS-99-6, BRICS, April 1999.

[2] R. B. Lyngsø, C. N. S. Pedersen, and H. Nielsen. Metrics and similarity measures for hidden Markov models. In *Proceedings of the 7th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, pages 178–186, 1999.

The technical report extends the conference paper by adding a section about generalising the measures to other types of hidden Markov models than left-right models. Except for minor typographical changes the content of this chapter is equal to the technical report [1]. An implementation of the method for comparison of left-right hidden Markov models presented in this chapter is available at `www.daimi.au.dk/∼cstorm/hmmcomp`.

Measures on hidden Markov models

Rune B. Lyngsø[*] Christian N. S. Pedersen[†] Henrik Nielsen[‡]

Abstract

Hidden Markov models were introduced in the beginning of the 1970's as a tool in speech recognition. During the last decade they have been found useful in addressing problems in computational biology such as characterizing sequence families, gene finding, structure prediction and phylogenetic analysis. In this paper we propose several measures between hidden Markov models. We give an efficient algorithm that computes the measures for left-right models, e.g. profile hidden Markov models, and discuss how to extend the algorithm to other types of models. We present an experiment using the measures to compare hidden Markov models for three classes of signal peptides.

4.1 Introduction

A hidden Markov model describes a probability distribution over a potentially infinite set of sequences ...

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[*] Department of Computer Science, University of Aarhus, Ny Munkegade, 8000 Århus C, Denmark. E-mail: `rlyngsoe@daimi.au.dk`.

[†] Basic Research In Computer Science (BRICS), Center of the Danish National Research Foundation, Department of Computer Science, University of Aarhus, Ny Munkegade, 8000 Århus C, Denmark. E-mail: `cstorm@brics.dk`.

[‡] Center for Biological Sequence Analysis, Center of the Danish National Research Foundation, Technical University of Denmark, Denmark. E-mail: `hnielsen@cbs.dtu.dk`.

Bibliography

[1] R. B. Lyngsø, C. N. S. Pedersen, and H. Nielsen. Measures on hidden Markov models. Technical Report RS-99-6, BRICS, April 1999.

[2] R. B. Lyngsø, C. N. S. Pedersen, and H. Nielsen. Metrics and similarity measures for hidden Markov models. In *Proceedings of the 7th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, pages 178–186, 1999.