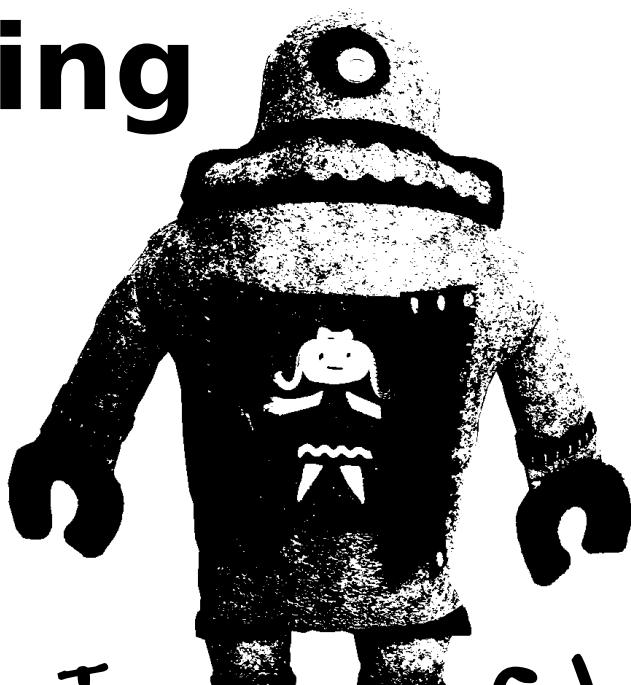


Machine Learning



In Structural Bioinformatics

**One day conference@The Biocenter
University of Copenhagen, Denmark
Wednesday April 23rd, 2008**

Speakers

Kanti V. Mardia, The University of Leeds, UK
Hans-Andrea Loeliger, ETH, Zürich, CH
Airlie McCoy, University of Cambridge, UK
Michael Habeck, Max Planck Institute for Biological Cybernetics, DE
Steen L. Hansen, University of Copenhagen, DK
Douglas Theobald, Brandeis University, US
Wouter Boomsma, University of Copenhagen, DK
Scott C. Schmidler, Duke University, Durham, US
Alexei Podtelezhnikov, Michigan Technological University, US

Organized by Thomas Hamelryck
Bioinformatics center, University of Copenhagen.
Registration is obligatory but free, and includes coffee+lunch.
Conference website: <http://wiki.binf.ku.dk/MLSB08>

Machine learning in Structural Bioinformatics

**One day conference@The Biocenter
University of Copenhagen, Denmark
Wednesday April 23rd, 2008**

Program 9h00-9h10

Welcome – Thomas Hamelryck, Thomas Schou (www.biosys.dk)

9h10-9h55

Can shape analysis and directional statistics revolutionize
structural protein bioinformatics?

Kanti V. Mardia, The University of Leeds, UK

9h55-10h40

An introduction to Factor Graphs

Hans-Andrea Loeliger, ETH, Zürich, CH

10h40-11h25

Maximum likelihood methods in protein crystallography

Arlie McCoy, University of Cambridge, UK

Coffee break (11h25-11h45)

11h45-12h30

Bayesian methods for protein structure determination

Michael Habeck, Max Planck Institute for Biological Cybernetics, DE

12h30-13h15

Determination of macromolecular structure using
small-angle scattering and Bayesian methods

Steen L. Hansen, University of Copenhagen, DK

Lunch (13h15-14h15)

14h15-15h00

Procrustes meets Theseus:

Bayesian superpositioning and analysis of macromolecules

Douglas Theobald, Brandeis University, US

15h00-15h45

A generative, probabilistic model of protein structure

Wouter Boomsma, University of Copenhagen, DK

Coffee break (15h45-16h05)

16h05-16h50

Statistical prediction and molecular simulation

Scott C. Schmidler, Duke University, Durham, US

16h50-17h35

Learning about protein energetics by minimizing contrastive divergence

Alexei Podtelezhnikov, Michigan Technological University, US
