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1974/08/24, Langen (Hessen)

SCIENTIFIC VITA

1995 – 2001	Diploma studies in Business and Computer Science, University of Cologne
2001 – 2006	Ph. D. studies in Computer Science (Bioinformatics) at the University of Cologne, Center for Applied Computer Science and Cologne University Bioinformatics Center
2001	Guest Scientist at Los Alamos National Laboratory, Bioscience Division
2006 – 2007	Postdoctoral Researcher at the German Cancer Research Center (dkfz), Division Theoretical Bioinformatics
since 2007	Head of Viroquant Junior Research Group Modeling, Bioquant, University of Heidelberg

FIELDS OF INTEREST

- Systems Biology and Bioinformatics
- Method development for the analysis of molecular and cellular experimental high-throughput data
- Mathematical modeling and analysis of complex processes in molecular and cell biology, with a particular focus on Virus-Host interactions
- Machine learning tools and statistical learning algorithms in Bioinformatics and Systems Biology

PUBLICATIONS (10 selected)

L. Kaderali, N. Radde (2007). *Inferring Gene Regulatory Networks from Gene Expression Data*. In: A. Kelemen, A. Abraham, Y. Chen (Editors), *Computational Intelligence in Bioinformatics*. Studies in Computational Intelligence, Springer-Verlag, Heidelberg, in press.

N. Radde, **L. Kaderali** (2007). *Inference of an Oscillating Model for the Yeast Cell Cycle*. *Discrete Applied Mathematics*, to appear.

M. Zapatka, **L. Kaderali** (2007). *Statistische Analyse von Daten klinischer Studien*. *GynSpectrum* 3, 18-19.

L. Kaderali (2007). *Individualized Predictions of Survival Time Distributions from Gene Expression Data using a Bayesian MCMC Approach*. S. Hochreiter and R. Wagner (Eds.): *BIRD 2007, LNBI Lecture Notes in Bioinformatics* 4414, 77-89.

N. Radde, **L. Kaderali** (2007). *Bayesian Inference of Gene Regulatory Networks using Gene Expression Time Series Data*. S. Hochreiter and R. Wagner (Eds.): *BIRD 2007, LNBI Lecture Notes in Bioinformatics*, 4414, 1-15.

A. Schramm, J. Vandesompele, J. H. Schulte, S. Dreesmann, **L. Kaderali**, B. Brors, R. Eils, F. Speleman, A. Eggert (2007). *Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome*. *Clinical Cancer Research* 13(5), 1459-1465.

L. Kaderali, T. Zander, U. Faigle, J. Wolf, J. L. Schultze, R. Schrader (2006). *CASPAR: A Hierarchical Bayesian Approach to predict Survival Times in Cancer from Gene Expression Data*. *Bioinformatics* 22, 1495-1502.

M. Leber, **L. Kaderali**, A. Schönhuth, R. Schrader (2005). *A fractional programming approach to efficient DNA melting temperature calculation*. *Bioinformatics* 21, 2375-2382.

L. Kaderali, A. Deshpande, J. P. Nolan, P. S. White (2003). *Primer-design for multiplexed genotyping*. *Nucleic Acids Research* 31, 1796-1802.

L. Kaderali, A. Schliep (2001). *Selecting signature oligonucleotides to identify organisms using DNA arrays*. *Bioinformatics* 18, 1340-1349.

CURRENT RESEARCH PROJECTS:

Statistical Analysis of RNAi Screens

Genome-wide RNAi knockouts permit the functional characterization of individual genes by studying their effect on a particular phenotypic trait under consideration. Within [VIROQUANT](#), RNAi screens are used to study the effect of host genes on virus entry, replication and exit.

Knock-outs are carried out on a high-throughput experimental platform, read-outs are gathered automatically by HT microscopy. These microscope images are then fed into

a bioinformatics pipeline, involving image recognition, quality control and statistical data analysis.

In close collaboration with our experimental and image recognition partners, we develop tools for the statistical analysis of these data, providing quantitative assessments of the effect a particular gene knockout has.

Modeling Virus-Cell Interactions

Viruses depend on their host cells for their replication and spread, understanding virus-host interactions is therefore an important component of a model-driven development of new anti-viral therapies.

Based on the RNAi screening and imaging data acquired within [VIROQUANT](#), we develop quantitative models describing virus-cell interactions. By combining RNAi data from our experimental partners with other publicly available and proprietary information, and by mapping this data onto models of virus-cell interaction, our ultimate aim is to understand how viruses hijack cellular mechanisms and could be targeted by new therapeutic approaches.

Inference of Biochemical Networks from High-Throughput Data

Given experimental measurements of concentrations of cellular components, one can ask for the underlying biochemical network determining the system under consideration. The focus may be, for example, on gene regulatory networks, signal transduction networks, or metabolic networks, depending on the biological question at hand.

In this project, we develop computational tools for the inference of the underlying network from experimental measurements. By integrating mechanistic models such as Boolean networks or ordinary differential equations into a fully Bayesian framework, we can compute distributions over network topologies and model parameters, and can easily integrate prior biological knowledge into the modeling framework. This framework allows it to answer many important questions, for example by scoring alternative models against one another, in evaluating model predictions quantitatively, and in experiment design.

Survival Analysis

Gene expression data have been shown to correlate with therapy response and patient survival in many cancers. Such data can assist a clinician in evaluating treatment options, and genes found to correlate with survival may hint at novel targets for drug design.

However, due to the high dimensional nature of the experimental data, computational tools are needed for data analysis. In this project, we are using the Cox regression model in combination with a sparse prior distribution on model parameters to predict survival times in years and months for the individual patient from microarray measurements. Using a Bayesian approach, we can compute survival probabilities and distributions over survival time for each patient, providing valuable information for the treating physician. In collaboration with clinical partners, we have demonstrated the feasibility of the approach on various cancer types.