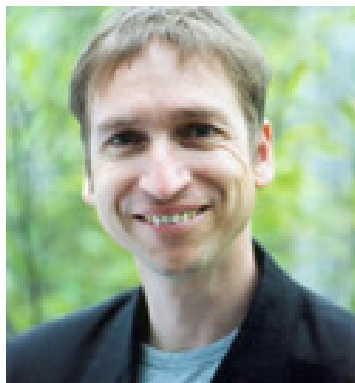


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SCIENTIFIC VITA:

- 1992-1995 Ph.D. study at University of Heidelberg (Ruprecht-Karl-Universität Heidelberg);
- 1995-1996 Postdoctoral student at the Institute of Scientific Computing (IWR), University of Heidelberg
- 1996 Guest researcher at the *Institut Albert Bonniot*, Université Grenoble
- 1996-1999 Head of the biocomputing group „Structure and function in cell biology“, IWR, University of Heidelberg, Germany
- 2000 Head of the bioinformatics group „Intelligent bioinformatics systems“ at the German Cancer Research Center (dkfz)
- since 2002 Head of division „Theoretical Bioinformatics“ at the German Cancer Research Center (DKFZ), Heidelberg, presently with 25 researchers
- since 2002 Director of department “Bioinformatics and Functional Genomics” and full professor (C4) at University of Heidelberg
- since 2002 Chair: National Platform (SMP Bioinformatics; National Genome Research Network (NGFN))

AWARDS:

BioFuture prize from the German Ministry for Education and Research (1999); Nominated for full professor positions (C4) at University of Giessen, University of Bonn and University of Heidelberg (2002/2003); Microsoft Research award “Computational tools for advancing science” (2005); Award for new innovative research by Helmholtz Society: “Systems Biology of Complex Diseases” (2005)

FIELDS OF INTEREST:

The bioinformatics group Theoretical Bioinformatics works on the development of bioinformatics systems for the analysis and mathematical modelling of complex processes in molecular and cell biology. In the recent years an increasing number of high-throughput screening systems have been developed in molecular biology. While in the past decade most such techniques were devoted to sequencing the genome of humans and other organisms, more recently such techniques emerged to relating genomic structure to function. One example is the DNA chip technology, which allows the screening of the expression level of all genes in a given organism under different conditions in one experiment. With this technology the study of the genetic effects of certain drugs has become possible thus paving the way for optimised design of new drugs and therapies. High throughput screening techniques generate a huge amount of data, which is difficult or even impossible to analyse without computer assistance. The development of fully automated computerized systems for the analysis of complex data in molecular biology is at the core of our group. Further, we work

on mathematical models and simulation of biochemical pathways with a particular focus on their spatio-temporal behaviour.

SELECTED PUBLICATIONS (since 2000)

Bacher CP, Guggiari M, Brors B, Augui S, Clerc P, Avner P, Eils R*, Heard E* (2006). Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. **Nat Cell Biol** 8, 293-299 [*equal contribution]

Schardt JA, Meyer M, Hartmann CH, Schubert F, Schmidt-Kittler O, Fuhrmann C, Polzer B, Petronio M, Eils R, Klein CA (2005). Genomic analysis of single cytokeratin-positive cells from bone marrow reveals early mutational events in breast cancer. **Cancer Cell** 8, 227-239

Bulashevskaya S, Eils R (2005). Inferring regulatory logic from gene expression data. **Bioinformatics** 21, 2706-2713

Lenart P, Bacher CP, Daigle N, Hand A, Eils R, Terasaki M, Ellenberg J (2005). A contractile nuclear actin network drives chromosome congression in oocytes. **Nature** 436, 812-818

König R, Eils R (2004). Gene expression analysis on biochemical networks using the potts spin model. **Bioinformatics** 20, 1500-1505

Bentele M, Lavrik I, Ulrich M, Stosser S, Heermann DW, Kalthoff H, Krammer PH, Eils R (2004). Mathematical modeling reveals threshold mechanism in CD95-induced apoptosis. **J Cell Biol** 166, 839-851

Wiemer J, Schubert F, Granzow M, Ragg T, Fieres J, Mattes J, Eils R (2003). Informatics United: exemplary studies combining medical informatics, neuroinformatics and bioinformatics. **Methods Inf Med** 42, 126-133

Gerlich D, Kalbfuss B, Beaudouin J, Daigle N, Eils R*, Ellenberg J (2003). Inheritance of chromosome topology throughout mitosis. **Cell** 112, 751-764 [*corresponding author]

Beaudouin J, Gerlich D, Daigle N, Eils R, Ellenberg J (2002). Nuclear envelope breakdown proceeds by microtubule-induced tearing of the lamina. **Cell** 108, 83-96

Gerlich D, Beaudouin J, Gebhard M, Ellenberg J, Eils R (2001). 4-D Imaging and Quantitative Reconstruction to Analyse Complex Spatiotemporal Processes in Live Cells. **Nat Cell Biol** 3, 852-855