

EG VCBM 2023

Eurographics Workshop on Visual Computing for Biology and Medicine

– Full and Short Paper Proceedings –

Norrköping, Sweden
September 20 – 22, 2023

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Postfach 2926, 38629 Goslar, Germany

Published by the Eurographics Association
–Postfach 2926, 38629 Goslar, Germany–
in cooperation with
Institute of Computer Graphics & Knowledge Visualization at Graz University of Technology
and
Fraunhofer IGD (Fraunhofer Institute for Computer Graphics Research), Darmstadt

ISBN 978-3-03868-216-5

ISSN 2070-5786 (online)

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Keynote

Peering into the Molecular Mechanisms of Life with Data, Computers & Visualization

Erik Lindahl

Stockholm University, Sweden

Biographical Note

Erik is a professor in Computational biophysics at KTH Royal Institute of Technology and Stockholm University. His research focus on that, with help from genetic information and experimental structures, model properties and dynamics in biological macro molecules such as proteins and cell membranes. His work has resulted in one of the worlds most spread programs for biomoleculare modeling (Gromacs), which is used for distributed calculations in the Folding@Home-project. His research group has made important discoveries concerning how proteins are placed i cell membranes, how ion channels are opened and closed, and how virus infects cells by fusion with cell membranes. The development of computation methods for biomolecules has as a link between theory and experiment led to breakthrough in applications, for example within the pharmaceutical industry.

Capstone

Deep Learning-Based Automatic Diagnosis and Prognostication in Radiology and Nuclear Medicine Imaging

Ida Häggström

Chalmers University of Technology, Sweden

Biographical Note

Ida is an Associate Professor in the Computer Vision group at the department of Electrical Engineering at Chalmers University of Technology, working with machine and deep learning techniques for medical image analysis. She completed two Master's degrees in Engineering Physics followed by Medical Physics, and proceeded with a PhD in Medical Physics at Umeå University, graduating in 2015. She then moved to Memorial Sloan Kettering Cancer Center in New York, USA for a postdoctoral fellowship, followed by working as a Research Associate and Senior Research Scientist, and returned to Sweden and Chalmers University of Technology in late 2021.