Joakim Lundeberg, *Prof, Dept of Gene Technology, KTH at SciLifeLab works on method development and accompanying tools to understand gene expression in tissue section.*

Transcriptional landscapes in health and disease interpreted by AI

The cell is a fundamental unit of life, yet we know surprisingly little about them. Specific types of cells exist in every organ, and serve specialized functions defined by the specific genes and proteins active in each cell type. Comprehensive maps of molecularly defined human cell types are underway through the Human Cell Atlas (https://www.humancellatlas.org) effort using primarily single cell RNA sequencing. The technologies to assemble spatial maps that will describe and define the cellular basis of health and disease is less well clear. We have developed and established the Spatial Transcriptomics technology (aka Visium from 10X Genomics), in which tissue imaging is merged with spatial RNA sequencing and resolved by machine learning strategies. Spatial Transcriptomics technology was the first method to provide unbiased whole transcriptome analysis with spatial information from tissue and has since the initial publication been used in multiple biological systems in health and disease.

Henrik Hult, *PhD, KTH, 2003. Postdoc at University of Copenhagen and Cornell University. Assistant Professor, Brown University. Professor of Mathematical Statistics, KTH. Currently director of the Brummer and Partners MathDataLab and programme leader at MedTechLabs.*

Interpolation in auto-encoders with bridge processes

Auto-encoding models provide an efficient framework for sample generation of complex data as well as for analysing feature learning. They are efficient in performing interpolations between data-points in semantically meaningful ways. In this talk, we introduce a method for generating random sequences from variational auto encoders and random interpolations. The distribution of interpolation paths is represented as the distribution of a bridge process constructed from an artificial random data generating process in the latent space, having the latent distribution as its invariant distribution.

Hedvig Kjellström, *Professor in the Division of Robotics, Perception and Learning at KTH in Stockholm, Sweden. She received an MSc in Engineering Physics and a PhD in Computer Science from KTH in 1997 and 2001, respectively. The topic of her doctoral thesis was 3D reconstruction of human motion in video. Between 2002 and 2006 she worked as a scientist at the Swedish Defence Research Agency, where she focused on Information Fusion and Sensor Fusion. In 2007 she returned to KTH, pursuing research in activity analysis in video. Her present research focuses on methods for enabling artificial agents to interpret the behavior of humans and other animals, and also to behave in ways interpretable to humans. These ideas are applied in performing arts, healthcare, veterinary science, and smart society. In 2010, she was awarded the Koenderink Prize for fundamental contributions in Computer Vision for her ECCV 2000 article on human motion reconstruction, written together with Michael Black and David Fleet. She has written around 100 papers in the fields of Computer Vision, Machine Learning, Robotics, Information Fusion, Cognitive Science, Speech, and Human-Computer Interaction. She is mostly active within Computer Vision, where she is an Associate Editor for IEEE TPAMI and regularly serves as Area Chair for the major conferences.*

AI and Social Robots - a New Way Forward in Dementia Diagnostics

In this talk I will describe EACare, our collaboration with the Memory Clinic at Karolinska University Hospital in developing AI and Social Robotics technology to improve the diagnostics and treatment of dementia, especially Alzheimer's disease. The main goal of this multidisciplinary project is to develop a robot head with communicative skills capable of interacting with elderly people in a human-like manner.

The robot will be able to analyze their mental and psychological status via powerful audiovisual sensing

and assessing their mental abilities to identify subjects in high risk or possibly at the first stages of depressive or dementing disorders. The framework can be employed in three different contexts: Firstly, as a pre-clinical testing tool to give advice about further medical evaluation; secondly, as a new kind of examination tool in the battery of tests used in diagnostic process at the Memory Clinic; and thirdly to provide tools for dementia preventive training.

Emma Lundberg, *Professor in Cell Biology Proteomics at KTH Royal Institute of Technology, Sweden, and Director of the Cell Atlas, part of the Human Protein Atlas program. She just returned to Sweden after a three-year sabbatical at Stanford University and the Chan-Zuckerberg Biohub. In the interface between bioimaging, proteomics and artificial intelligence her research aims to define the spatiotemporal organization of the human proteome at a subcellular level, with the goal to understand how variations and deviations in protein expression patterns can contribute to cellular function and disease. In addition to this, Dr. Lundberg has a keen interest in open science and citizen science.*

Spatiotemporal dissection of the human proteome - a crowdsourced and gamified approach
Resolving the spatial distribution of the human proteome at a subcellular level increases our understanding of human biology and disease. In the Human Protein Atlas project, we are systematically mapping the human proteome in a multitude of human cells and organs using microscopy. I will present how this set of millions of images constitute a resource for biology and various approaches for the computational interpretation of subcellular patterns in such images. In addition, I will present results from crowd-sourced efforts such as a Kaggle challenge and the citizen science effort “Project Discovery” integrated into a massively-multiplayer online game that has engaged more than 300,000 players world-wide. In summary, I will demonstrate the importance of spatial proteomics data for improved single cell biology and present how the freely available Human Protein Atlas database can be used as an image resource in life science.

Örjan Smedby, *graduated from Medical School at Uppsala University in 1983 and defended his doctoral thesis there in 1992. From 1999 to 2014 he was Professor of Medical Radiology at Linköping University. He was one of the founders of the Center for Medical Image Science and Visualization in Linköping. Since 2015 he is Professor in Medical Image processing and Visualization at KTH and director of the Jonasson Centre for Medical Imaging, a local research infrastructure.*

Digital image data and healthcare - a case for machine learning
Imaging plays a central role in modern healthcare for making diagnosis, for choosing and planning treatment, and for evaluating the results of treatment given. Various forms of imaging equipment - such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI) and positron Emission Tomography (PET) - produce accurate maps of the 3D anatomy of the patient's body. To extract the clinically most relevant features - often called quantitative imaging biomarkers - organs and pathological processes have to be delineated from the background, a process known as segmentation. Currently, the most promising approach for this process, as well as for direct classification of e.g. diseases, is machine learning. In machine learning, automated algorithms take care of both the selection of features to be included in the analysis and of the actual computation. Examples of diseases where such an approach is successful include tumours, cardiovascular diseases and neurodegenerative disorders.

Søren Brunak, *leading expert in bioinformatics, systems biology, and medical informatics through invention and introduction of new computational strategies for analysis and integration of biological and clinical data. His current group is named “Translational Disease Systems Biology” and aims at*

obtaining mechanistic understanding of disease as well as producing new patient stratification, risk prediction and treatment selection principles. The use of the patient trajectory concept is a major theme that exploits information on the patient-past in terms of prior diseases, comorbidities, prescriptions, lab values, omics data, wearable data, socio-economic data among other types of data. The impact of Brunak's research is a consequence of his ability to combine scientific disciplines in novel ways, including computer technology (supercomputer hardware, data protection techniques and software including machine learning techniques), biological, biomedical and biotechnological insights. His multi-disciplinary approaches, where concepts from different areas have been combined, have led to advances in the understanding of the function of biological systems, and thereby fundamentally improved the possibilities for control of disease via novel intervention strategies, and enhancement of health in general. Søren Brunak has been a member of the Royal Swedish Academy of Sciences since 2016, the Royal Danish Academy of Sciences and Letters since 2004 and the European Molecular Biology Organization since 2009.

Combining AI and population-wide disease trajectories in N=1 precision medicine

Multi-step disease trajectories are key to the understanding of human disease progression patterns and their underlying molecular level etiologies. We present approaches to the identification of frequent disease trajectories from population-wide healthcare data comprising millions of patients and corresponding strategies for linking disease co-occurrences to genomic individuality. We carry out temporal analysis of clinical data in a life-course oriented fashion. We use data covering 7-10 million patients from Denmark collected over a 20-40 year period and use them to "condense" millions of individual trajectories into a smaller set of recurrent ones. This set of trajectories can be interpreted as re-defined phenotypes representing a temporal diseaseome as opposed to a static one computed from non-directional comorbidities only. We discuss how to use single patient disease trajectories for machine learning based decision support in clinical settings.

Thomas Wiegand, *chair of ITU/WHO, Focus Group on Artificial Intelligence for Health (FG-AI4H), Professor at TU Berlin and Executive Director of Fraunhofer HHI*

ITU/WHO Focus Group on Artificial Intelligence for Health

Artificial intelligence (AI) for health has seen an enormous rise in interest. However, due to the complexity of AI models, it is difficult to distinguish good from bad AI-based solutions and to understand their strengths and weaknesses. This is crucial for clarifying responsibilities and for building trust among AI developers, AI regulators, and AI users. For this reason, the International Telecommunication Union (ITU) and the World Health Organization established the Focus Group on "Artificial Intelligence for Health" (FG-AI4H). FG-AI4H identifies issues on AI for health–relevant data, information, algorithms, and processes, which fosters opportunities for international standardization and the application of AI for health on a global scale. With members coming from research, healthcare, regulation, telecommunications, and health ministries, and complementary fields around the globe, FG-AI4H is able to draw on a wealth of expertise to produce (a) documentation that contains guidelines on how to evaluate AI for health from various perspectives (e.g., regulatory, ethical, and data or AI solution) and (b) an online platform (and complementary tools) for the benchmarking of AI for health.