AI for Life Science @ KTH

9.00 – 9.05	**Welcome and Introduction** Tobias Oechtering and Peter Savolainen, KTH	
9.05 – 9.55	**Plenary Talk: ITU/WHO Focus Group on Artificial Intelligence for Health.** Thomas Wiegand, HHI Fraunhofer Institute & TU Berlin	
9.55 – 10.10	**Digital image data and healthcare - a case for machine learning.** Örjan Smedby, KTH	
10.10 – 10.25	**AI and Social Robots - a New Way Forward in Dementia Diagnostics.** Hedvig Kjellström, KTH	
10.25 – 10.45	Break	
10.45 – 11.35	**Plenary Talk: Combining AI and population-wide disease trajectories in N=1 precision medicine** Søren Brunak, NNF Center for Protein Research	
11.35 – 11.50	**Interpolation in auto-encoders with bridge processes** Henrik Hult, KTH	
11.50 – 12.05	**Models and algorithms for somatic evolution in cancer** Jens Lagergren, KTH	
12.05 –13.00	Break	
13.00 – 13.50	**Plenary Talk: Spatiotemporal dissection of the human proteome - a crowdsourced and gamified approach** Emma Lundberg, KTH & Stanford	
13.50 – 14.05	**Transcriptional landscapes in health and disease interpreted by AI** Joakim Lundeberg, KTH	
14.05 – 14.25	Break	
14.25 –15.55	Parallel breakout sessions 1. AI challenges and opportunities with Stockholm Health Data Center 2. Future of advanced AI supported imaging for life science research 3. AI and data science challenges and models in life science research 4. AI and data science for diagnostics and health decision support 5. AI and modelling for epidemiology research	
16.00 – 17.00	**Panel Session "The future of AI and Life Science in Sweden" with** - Maja Fjaestad, State Secretary, Ministry for Health and Social Affairs - Clara Hellner, Research and Innovation Director for Region Stockholm - Jenni Nordborg, National Coordinator for Life Science - Dan Hill, Director of Strategic Design, Vinnova - Louise Callenberg, Head of Digital Collaboration & Renewal, SKR, - Peder Blomgren, VP and Head of Data Office, R&D, Astra Zeneca, Moderated by Paulina Modlitba Söderlund	

Event organized by KTH Research Platforms on Digitalization and Life Science Technology

ITU/WHO FOCUS GROUP ON ARTIFICIAL INTELLIGENCE FOR HEALTH

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

Abstract: 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.

DIGITAL IMAGE DATA AND HEALTHCARE - A CASE FOR MACHINE LEARNING

Örjan Smedby, Professor in Division of Biomedical Engineering and Health Systems, KTH

Abstract: 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.

AI AND SOCIAL ROBOTS - A NEW WAY FORWARD IN DEMENTIA DIAGNOSTICS

Hedvig Kjellström, Professor in Division of Robotics, Perception and Learning, KTH

Abstract: 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.

COMBINING AI AND POPULATION-WIDE DISEASE TRAJECTORIES IN N=1 PRECISION MEDICINE

Søren Brunak, Professor in Bioinformatics at Technical Univ. of Copenhagen, Professor of Disease System Biology at Univ. of Copenhagen, Research Director, NNF Center for Protein Research

Abstract: 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.

INTERPOLATION IN AUTO-ENCODERS WITH BRIDGE PROCESSES

Henrik Hult, Professor in Mathematical Statistics, KTH

Abstract: 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.

MODELS AND ALGORITHMS FOR SOMATIC EVOLUTION IN CANCER.

Jens Lagergren, Professor in Division of Computational Science and Technology, KTH

In 1976, Peter Nowell summarised the evidence that cancer arises due to somatic evolution. Today, there is a wealth of data, particularly single-cell and spatial data, that allows us to understand this process on a molecular level. Interestingly, several types of classical evolutionary analysis translate into clinically relevant variants concerning somatic evolution. These analyses typically require cutting edge machine learning methodologies.

SPATIOTEMPORAL DISSECTION OF THE HUMAN PROTEOME – A CROWDSOURCED AND GAMIFIED APPROACH

Emma Lundberg, Visiting Assoc. Professor at Stanford University, Professor in Celluar and Clinical Proteomic, KTH, Director of Cell Atlas of the Human Protein Atlas, SciLifeLab

Abstract: 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.

TRANSCRIPTIONAL LANDSCAPES IN HEALTH AND DISEASE INTERPRETED BY AI
Joakim Lundeberg, Professor in Gene Technology, KTH, SciLifeLab

Abstract: 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 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, 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.

Breakout Session 1
AI CHALLENGES AND OPPORTUNITIES WITH STOCKHOLM HEALTH DATA CENTER
In this breakout session we will learn more about the Region Stockholm center for health data, the possibilities and limitations of the as well as briefly about the I-AID project (integrated AI diagnostics) presented by center representatives Peter Andersson and Sven-Åke Lööv. In the second part, Cecilia Magnusson Sjöberg from Stockholm University will reflect on legal issues working with health data and raise awareness about seldom asked questions. In two following group work sessions, the participants will get the opportunity to discuss those issues but also pitch their own related solution approach or problem.

Session outline:

14:25 - 14:30	Welcome, Tobias Oechtering, KTH, Information Science and Engineering
14:30 - 14:55	Presentation (on challenges and opportunities) Centre for Health Data – Peter Andersson, Sven-Åke Lööv, Region Stockholm
14:55 - 15:10	Q&A followed by group work on challenges and opportunities (incl networking, people are asked to pitch/introduce themselves)
15:10 - 15:15	Brief reports from group work
15:15 - 15:20	Break
15:20 - 15:30	Seldom asked questions - legal issues to reflect on when working with health data - Cecilia Magnusson Sjöberg, SU, The Swedish Law and Informatics Institutes
15:30 - 15:45	Q&A followed by group work reflecting on questions (incl networking, people are asked to pitch/introduce themselves)
15:45 - 15:50	Brief reports from group work
15:50 - 15:55	Wrap up

Breakout Session 2
FUTURE OF ADVANCED AI SUPPORTED IMAGING FOR LIFE SCIENCE RESEARCH
In this breakout session, we will have "reversed pitches" followed by mingling, with the hope that "users" and "developers" of AI imaging tools can meet. We will try to revive the mingling of the "real-life" conferences of the old days. Therefore, instead of Zoom we use Remo as a webinar tool. This tool allows us to mingle freely among virtual tables, so that people can have a discussion and others can listen in and comment, just as a real-life conference coffee break. We start with short pitches, to let the participants know about each other's projects/expertise/problems, so that you may contact each other during the mingling. Thus, each presenter gives a quick overview of their research and presents a "reversed pitch", presenting a problem/task/challenge they need help with, or a solution/method they think can help others.

Session outline:

14:30 – 14:40	Introduction, Peter Savolainen
14:40 – 15.10	Reverse pitches
15:10 – 15:50	Mingling
15:50 – 15:55	Wrap up, Peter Savolainen

Breakout Session 3
AI AND DATA SCIENCE CHALLENGES AND MODELS IN LIFE SCIENCE RESEARCH

14.25 – 14.35	Short introduction, Anna Herland
14.35 – 15.25	Short Reverse Pitches, 6-7 min talks Each presenter gives a quick overview of their research and present a "reverse pitch" a problem / task / challenge related to their research related to AI/Data Science or Life Science data access/generation. • Erik Lindahl KTH https://www.scilifelab.se/researchers/erik-lindahl/ • Petter Brodin KI https://brodinlab.com/ • Erik Wernersson KI https://ki.se/en/mbb/magda-bienko-group • Joakim Jalden KTH https://www.kth.se/profile/jalden • Simon Elässer KI https://elsaesserlab.wordpress.com/ • Lars Arvestad SU https://www.scilifelab.se/researchers/lars-arvestad/ • Claudia Kutter KI https://ki.se/en/mtc/claudia-kutter-group
15.30-15.55	Discussion and Q and A session with the presenters in 3 separate zoom rooms (links will be provided for all registered to the workshop)

Room 1	Room 2	Room 3
Erik Lindahl KTH Petter Brodin KI Moderator: Anna Herland and Saumey Jain	Erik Wernersson KI Joakim Jalden KTH Moderator: Dimitris Voulgaris and Sharulatha Ravisankar	Simon Elässer KI Lars Arvestad KTH Moderator: Polyxeni Nikolakopoulou and Noora Isoaho

15.55	Return to the main workshop.

Breakout Session 4

In this breakout session, we will cover issues, methods and applications to support decision making in clinical settings, focusing on both clinicians and patients as user groups. Talks will cover early diagnostics and warning systems aimed at prevention and mitigation, natural language processing and cognitive support in intensive and critical care.

Session outline:

14.25 – 14.35	Introduction and Session Structure, Jayanth Raghothama
14.35 – 15.20	Short Pitches • Ashish Kumar, KI, Cross-trait analysis in respiratory and metabolic phenotypes – opportunities and challenges in correlating health outcomes and OMICs' public repositories • Annaclaudia Montanino, Getinge, Using machine learning to optimally adjust patient model parameters • Saikat Chatterjee, KTH, AI for Real-Time Early Warning Systems • Jawad Elomari, RISE, Early Warning Systems in Healthcare • Petra Szeszula, Andningmed, Smart intuitive inhaler for respiratory diseases • Martin Jacobsson, KTH, Using machine learning to predict and prevent perioperative hypotension and its complications • Johan Lundin, KI, Point-of-Care Diagnostics of Cancer and Infectious Diseases with AI-Supported Mobile Microscopy
15.20 – 15.25	Break, split into breakout rooms
15.20 – 15.55	Discussions in breakout rooms
15.55	Return to main workshop

Breakout Session 5

In this breakout session, we will cover methods and models for epidemiology, focusing in particular on the Covid-19 pandemic.

Session outline:

14.30 – 14.35	Introduction Lukas Käll
14.35 – 15.00	Digital Infectious Disease Epidemiology Michael Höhle, SU
15.00 – 15.25	Bayesian modelling of Covid 19 disease progress Arne Elofsson, SU
15.25 – 15.50	Global analysis of more than 50,000 SARS-Cov-2 genomes reveals epistasis between 8 viral genes Erik Aurel, KTH
15.50 – 15.55	Wrap Up, Lukas Käll

Event organizers

KTH RESEARCH **P**LATFORM ON **D**IGITALIZATION

- Tobias Oechtering, platform director, KTH Information Science and Engineering
- Jayanth Raghothama, platform vice-director, KTH Health Informatics and Logistics

KTH RESEARCH **P**LATFORM ON **L**IFE **S**CIENCE **T**ECHNOLOGY

- Peter Savolainen, platform director, KTH Gene Technology, SciLifeLab
- Lukas Käll, platform vice-director, KTH Gene Technology, SciLifeLab
- Anna Herland, platform vice-directors, KTH Micro- and Nanosystems

supported by

- Susanna Berglund, administrative platform support, KTH Research Office
- Daniel Vare, technical support, KTH Project Manager