SciLifeLab Science Summit 2019

Artificial Intelligence for Life Sciences

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#SciLifeLabSummit

Speaker abstracts

SciLifeLab

Keynote speakers

Hiroaki Kitano

The Systems Biology Institute/Sony Computer Science Laboratories, Inc.

Nobel Turing Challenge for Creating the Engine of Scientific Discovery: Moonshot of AI, Robotics and Systems Biology

Nobel Turing Challenge would be the ultimate challenge the scientific community can tackle. It aims at (1) developing AI system including substantial robotics components that can make major scientific discoveries some of which worth Nobel Prize (called as "Scientific Discovery Challenge"), and (2) actually win the prize without the selection committee noticed that it is actually an AI system, not a human researcher (Cybernetic Personality Challenge). Primary focus on this challenge will be biomedical science area for Physiology and Medicine Award (Kitano, H., AI Magazine, 37(1) 2016).

This grand challenge project shall take a form of globally distributed "Virtual Big Science" project (Kitano, H., et al., Nature Chemical Biology, 7, 323-326, 2011). A part of the project shall resemble RoboCup (Kitano, H., et al., AI Magazine, 18(1) 73-85, 1997), but it will have substantially different aspects reflecting the difference of domains and objectives.

In the mid 90s, I advocated "Systems Biology" with the aim of promoting systems-oriented view in biology and to introduce more systematic measurements, proper applications of engineering, mathematical, and information science principles into life science (Kitano, H., Science, 295, 1662-1664, 2002; Kitano, H., Nature, 420, 206-210, 2002). This endeavor has been successful and systems biology is one of normal approach in biomedical and pharmaceutical sciences. The progress in systems biology revealed new limitations in life science that stems from our cognitive limitations to understand complex, non-linear, high dimensional, and dynamical systems, with overwhelming data and publications each of which unveils only a fragment of systems. I am increasingly convinced that systems biology is the research approach suitable for AI rather than for human researchers.

With recent breakthroughs in AI, exponentially increasing data production capabilities, and massive computing power, disruptive innovations in biomedical sciences are on the horizon. Time is ripe to embark on a new aggressive challenge. The fundamental breakthrough will come at the stage AI to generate hypotheses and quickly verify them using their knowledge bases, simulation, and robotics experimental systems. It means that AI systems can keep discovering new knowledge with minimal or zero human interventions. Even a mid-term achievement of Scientific Discovery Challenge alone will be a game changer. Cybernetic Personality Challenge force us to consider what are origin of curiosity, how do we distinguish human and machines in professional domains? Series of discoveries along the challenges will trigger fundamental transformations of industry and more largely on the shape of our civilization.

Ross D. King

Professor of Machine Intelligence, University of Manchester

Automating Science using Robot Scientists

A Robot Scientist is a physically implemented robotic system that applies techniques from artificial intelligence to execute cycles of automated scientific experimentation. A Robot Scientist can automatically execute cycles of hypothesis formation, selection of efficient experiments to discriminate between hypotheses, execution of experiments using laboratory automation equipment, and analysis of results. The motivation for developing Robot Scientists is to both to better understand the scientific method, and to make scientific research more efficient. The Robot Scientist 'Adam' was the first machine to autonomously discover scientific knowledge: it formed and experimentally confirmed novel hypotheses. Adam worked in the domain of yeast functional genomics. The Robot Scientist 'Eve' was originally developed to automate early-stage drug development, with specific application to neglected tropical disease such as malaria, African sleeping sickness, etc. More recently my colleagues and I have adapted Eve to work on yeast systems biology, and cancer. We argue that it is likely that advances in AI and lab automation will drive the development of ever-smarter Robot Scientists. The Physics Nobel Frank Wilczek is on record as saying that in 100 years' time the best physicist will be a machine. If this comes to pass it will transform our understanding of science and the Universe.

Eran Segal

Department of Computer Science And Applied Math, Weizmann Institute of Science

Personalized Medicine based on Gut Microbiome and Clinical Data

Accumulating evidence supports a causal role for the human gut microbiome in obesity, diabetes, metabolic disorders, cardiovascular disease, and numerous other conditions. I will present our research on the role of the human microbiome in health and disease, ultimately aimed at developing machine learning algorithms for personalized medicine that combine human genetics, microbiome, and nutrition.

In one project, we tackled the subject of personalization of human nutrition, using a cohort of over 1,000 people in which we measured blood glucose response to >50,000 meals, lifestyle, medical and food frequency questionnaires, blood tests, genetics, and gut microbiome. We showed that blood glucose responses to meals greatly vary between people even when consuming identical foods; devised the first machine learning algorithm for accurately predicting personalized glucose responses to food based on clinical and microbiome data; and showed that personalized diets based on our algorithm successfully balanced blood glucose levels in prediabetic individuals. I will also present an algorithm that we devised for identifying variability in microbial sub-genomic regions and associated algorithms that we developed for predicting based on disease phenotypes based on this new layer of metagenomic information that we extract from microbiome samples.

Fabian Theis

Institute of Computational Biology, Helmholtz Center Munich

Modeling differentiation and stimulation response in single-cell genomics

Accurately modeling single cell state changes e.g. during differentiation or in response to perturbations is a central goal of computational biology. Single-cell technologies now give us easy and large-scale access to state observations on the transcriptomic and more recently also epigenomic level. In particular they allow resolving potential heterogeneities due to asynchronicity of differentiating or responding cells, and profiles across multiple conditions such as time points and replicates are being generated. In this talk I will quickly review how to estimate lineage formation using graph abstraction as extension of pseudotemporal ordering, and how to take additional information such as RNA velocity into account. I then ask how to generalize predictions to phenomena absent from training data i.e. out-of-sample. For this, I will present scGen, a model combining variational autoencoders and latent space vector arithmetics for high-dimensional single-cell gene expression data. In benchmarks across a broad range of examples, we show that scGen accurately models dose and infection response of cells across cell types, studies and species. In particular, we demonstrate that scGen learns cell type and species specific response implying that it captures features that distinguish responding from non-responding genes and cells.

National speakers

Fredrik Barrenäs

Department of Cell and Molecular Biology, Computational Biology and Bioinformatics, Uppsala University

One step closer to an HIV vaccine — What machine learning tells us about vaccine protection and immunity

The rhesus cytomegalovirus (RhCMV) strain 68-1 vaccine against simian immunodeficiency virus (SIV) induces a T cell response that protects over 50% of vaccinated rhesus macaques (RM) to clear infection against multiple SIV challenge including distinct challenge routes. To define the molecular features of the host response to vaccination and the underlying gene signature of vaccine protection we performed transcriptomic profiling of protected and non-protected RMs following vaccination prior to challenge. Two groups of 15 RMs were administered 68-1 RhCMV/SIV vaccine via oral or subcutaneous delivery. Following vaccination, RMs were subjected to repeated limiting dose intrarectal SIVmac239 challenge until infected as detected as plasma virus or the de novo development of SIV Vif-specific T cell response. Blood samples collected at time points near vaccine prime and boost, and before challenge, underwent mRNA-sequencing.

To discover host mechanisms involved in immune protection, we used a machine learning approach that identifies combinations of gene expression features able to predict vaccine protection. This approach, rule-based modeling (RBM) uses rough set theory to identify minimal sets of gene features able to distinguish protected and unprotected animals. RBM creates explicit IF-THEN rules that can be interpreted by an immunologist without computational training (e.g. IF gene A is upregulated after prime AND gene B does not change after boost THEN the animal is protected).

In the subcutaneous and orally-vaccinated groups, 53% and 60% of RMs cleared SIV infection after virus challenge, respectively. We first used Monte Carlo Feature Selection (MCFS), which used decision trees to rank gene features (consisting of a given gene, and its change over a given time window) by their contribution to classification, in combination with other gene features.

Using top 200 gene features obtained from MCFS, we applied R.ROSETTA to create a rule-based classifier that predicted protection with 90% accuracy. This classifier also correctly predicted outcomes in a separate set of 3 protected and 3 unprotected RhCMV/SIV vaccinated RMs. While linear modeling was only able to identify correlates of protection at day 3 post prime, BRM was able to use information from the first to last time point to predict vaccination outcomes.

The classifier suggested key roles for 3 immune regulators in predicting vaccine protection: (1) PPP3CA, a member of the T cell receptor pathway which phosphorylates NFATc. (2) SGPL1, which controls T cell trafficking from lymphoid tissues. (3) SGMS2, involved in macrophage LPS immune responses through TLR4. When clustering animals based on the number of rules they share, the classifier showed a very strong transcriptomic signature of protection in 9 of the 17 protected animals. By contrast, 3 of the animals activated only a small fraction of the protective signature.

This was done in collaboration with University of Washington (Connor Driscoll, Rich Green, Monica Rojas-Peña, Jean Chang, Elise Smith, Lynn Law, Michael Gale, Jr.) and the Oregon Health and Science University (Scott Hansen, Louis Picker) and other collaborators at Uppsala University (Jan Komorowski).

Helena Lindgren

Associate Professor, Department of Computing Science at Umeå University

Socially Intelligent Systems and Robots – when we need to Collaborate with the AI

There is an increasing awareness that intelligent systems such as service robots in healthcare need to manifest also social intelligence, in order to increase relevance, trust and acceptance among care takers, their relatives and care givers who interact with the system. The social aspects of activity include for example, situation awareness and relevant knowledge to select appropriate behaviour, to adapt to the situation and to the individual it should assist, motivate, guide in a transparent way and cooperate with the individual in pursuing goals, such as emotional wellbeing. Striving for such behaviour of the intelligent and social digital companion or robot, poses particular challenges on how the AI and the interaction with the AI are designed. In this talk I will exemplify how we may agree, disagree and resolve conflicts that we may have with the intelligent health service providing AI in the future.

Andreas Theodorou

Scientist, Department of Computing Science, Umeå University

AI Governance: Building Transparent and Trustworthy Systems

Artificial Intelligence (AI) applications are being used to predict and assess behaviour in multiple domains. However, if AI is to improve people's lives, then people must be able to trust AI, which means being able to understand – or at least be able to audit – what the system is doing and why.

Fortunately, technological problems of maintaining control are amenable to engineering. The real problem is establishing the social and political will for assigning and maintaining accountability for when artefacts are generated or used. In this talk, I will discuss how we can effectively govern intelligent systems through both technological and legal means.