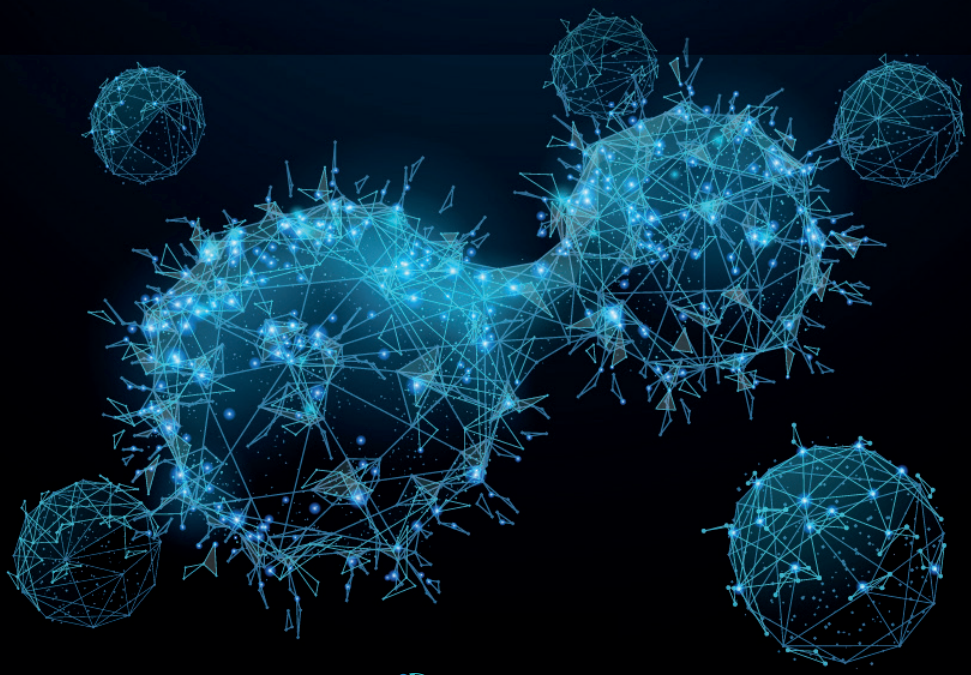
Inaugural Symposium

Intelligent Oncology

The Potential of AI to Cure Cancer

Freiburg, Germany | 30.09.2022
9:00 – 18:00 | Otto-Krayer-Haus

www.intelligent-oncology.org/events/



CRIION
COLLABORATIVE RESEARCH INSTITUTE
INTELLIGENT ONCOLOGY

MERTELSMANN
FOUNDATION

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KLINIKUM FREIBURG

PROGRAM

09:00 - 09:10	**Introduction** *Prof. Roland Mertelsmann and Prof. Joschka Bödecker, CRIION*
09:10 - 09:15	**Welcome remarks from Baden-Württemberg** *Nadyne Saint-Cast, Abgeordnete im Landtag Baden-Württemberg, Bündnis 90/Die Grünen*
09:15 - 09:20	**Welcome remarks from the city of Freiburg** *Thomas Stoffel, Leiter Abteilung Wirtschafts-förderung der Freiburg Touristik Wirtschaft und Messe GmbH & Co. KG*
09:20 - 09:35	**Welcome remarks from the University and University Hospital** *Chancellor Christina Leib-Keßler* *Chief medical director Prof. Frederik Wenz* *Dekan Prof. Roland Zengerle* *Medical director Prof. Justus Duyster*
	Coffee break
	Session I: AI-assisted Diagnosis and Treatment *chairs: Prof. Melanie Börries & Prof. Joschka Boedecker*
10:00 - 10:30	**AI in cancer genomics** *Dr. Quaid Morris, Memorial Sloan Kettering Cancer Center New York, USA*
10:30 - 11:00	**AI in hematology: computer vision and machine learning for improved diagnosis and risk stratification** *Dr. Jan Moritz Middeke, University Hospital Dresden, Germany*
11:00 - 11:30	**Towards clinical decision support in oncology: Data integration, outcome models, and intuitive software** *Dr. Nikolaus Schultz, Memorial Sloan Kettering Cancer Center, USA*
	Lunch break & poster presentations

Session II: Towards a Better Understanding of Cancer via AI

chairs: Prof. Robert Zeiser & Prof. Rolf Backofen

13:30 - 14:00	**Dissecting intra-tumor heterogeneity by single cell RNA-seq** *Dr. Itay Tirosh, Weizmann Institute, Israel*
14:00 - 14:30	**SIMON says: Deciphering the human immune responses using machine learning** *Dr. Adriana Tomic, University of Oxford, United Kingdom*
14:30 - 15:00	**Clinical intelligent systems in the wild?** *Prof. Lena Maier-Hein, German Cancer Research Center Germany (online)*
15:00 - 15:30	**The deep learning architecture of AlphaFold** *Prof. Olaf Ronneberger, Google DeepMind, United Kingdom (cancelled)*

Coffee break & poster presentations

Session III: On the Practical Use of AI in Oncology

chairs: Dr. Florian Scherer & Prof. Roland Zengerle

16:00 - 16:30	**Droplet microfluidics in antibody discovery and personalized cancer therapy** *Prof. Christoph Merten, EPFL, Switzerland*
16:30 - 17:00	**Predicting adaptive immunity using systems immunology and machine learning** *Dr. Victor Greiff, University of Oslo, Norway*
17:00 - 17:30	**Philosophy of AI for health** *Dr. Ignacio Mastroleo, University of Buenos Aires, Argentina*
17:30 - 17:50	**WrapUp: Learing to cure cancer & Poster award ceremony**
17:50 - 18:00	**Farewell**

Networking Apéro

Dr. Victor Greiff
University of Oslo
Norway

Victor Greiff is an Associate Professor for Computational and Systems Immunology at the University of Oslo. His group develops machine learning, computational and experimental tools for analyzing antibody and T-cell repertoires to develop immune-repertoire-based immunodiagnostics and immunotherapeutics. Dr. Greiff received his PhD in Systems Immunology from Humboldt University (Germany) and performed his postdoctoral training at ETH Zürich (Switzerland).

Prof. Lena Maier-Hein
German Cancer Research Center
Germany

Lena Maier-Hein is a full professor at Heidelberg University (Germany) and managing director of the National Center for Tumor Diseases (NCT) Heidelberg. At the German Cancer Research Center (DKFZ) she is head of the division Intelligent Medical Systems (IMSY) and managing director of the „Data Science and Digital Oncology“ cross-topic program. Her research concentrates on machine learning-based biomedical image analysis with a specific focus on surgical data science, computational biophotonics and validation of machine learning algorithms.

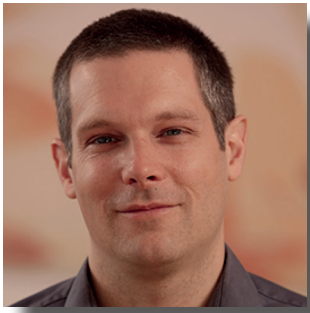
She is a fellow of the Medical Image Computing and Computer Assisted Intervention (MICCAI) society and of the European Laboratory for Learning and Intelligent Systems (ELLIS), president of the MICCAI special interest group on challenges and chair of the international surgical data science initiative.

Lena Maier-Hein serves on the editorial board of the journals Nature Scientific Data, IEEE Transactions on Pattern Analysis and Machine Intelligence and Medical Image Analysis. During her academic career, she has been distinguished with several science awards including the 2013 Heinz Maier Leibnitz Award of the German Research Foundation (DFG) and the 2017/18 Berlin-Brandenburg Academy Prize. She has received a European Research Council (ERC) starting grant (2015-2020) and consolidator grant (2021-2026).

Dr. Ignacio Mastroleo
University of Buenos Aires
Argentina

Dr. Mastroleo has a broad background in philosophy, with specific training and expertise in research ethics, and more recently on the ethics of medical innovation and the use of unproven interventions outside clinical trials during public health emergencies. He undertook his PhD, Postdoc, and early research career under the supervision of Dr. Florencia Luna, a world-leading bioethicist. His dissertation topic was on the ethics of post-trial access to beneficial medical interventions of human health research conducted in developing countries. He is now a tenured researcher at the National Research Council of Argentina (CONICET). He won The Manuel Velasco Suarez Award for Excellence in Bioethics (2014), one of the six Awards for Excellence in Inter-American Public Health awarded by the Pan American Health Organization (PAHO-WHO).

Since 2014, he has been an invited lecturer in ethics of human health research in the Bioethics Module of the IMBS Binational Master/PhD Program in Biomedical Sciences (CUAA-DAHZ) of the University of Freiburg, Germany and UBA, Argentina. Since 2018, he is the codirector of the Bioethics Module of the IMBS Master. (http://www.biomedmaster.org/people/faculty/argentina/). Since September 2019, he is a board member of the International Association of Bioethics (IAB). Since March 2020, Dr. Mastroleo has served as an ad-honorem expert in the World Health Organization (WHO) Ethics and COVID-19 Workgroup and, currently, WHO COVID-19 Ethics & Governance Workgroup. He was the leading writer of the recently published WHO ethics guidelines on the emergency use of unproven interventions outside research. He has also been a close collaborator with PAHO, WHO Regional Office for the Americas, in several consultancy activities for the Latin American region. Currently, Dr. Mastroleo is leading the Philosophy Research Program of AI for Health at the Collaborative Research Institute Intelligent Oncology (CRIION) in Freiburg, Germany.



Prof. Christoph Merten
EPFL
Switzerland

Christoph A. Merten (www.epfl.ch/labs/lbmm/) studied biochemistry at the University of Frankfurt and obtained his PhD on directed evolution of retroviral vectors for gene therapy applications at the Paul Ehrlich Institute in Langen, Germany. Subsequently he did a postdoc at the MRC Laboratory of Molecular Biology in Cambridge (UK), focussing on in vitro compartmentalization techniques. In 2005 he moved to the Institut de Science et d'Ingénierie Supramoléculaires (ISIS) in Strasbourg, France, where he became a junior group leader in 2007. Christoph then joined the European Molecular

Biology Laboratory in Heidelberg, Germany, as a Principal Investigator in 2010, where his group focused on microfluidic approaches in drug discovery, personalized medicine and genetics. Since 2020 he is a Professor in the School of Engineering at the Swiss Federal Institute of Technology in Lausanne (EPFL) and also holds an adjunct scientist position at the Ludwig Institute for Cancer Research (LICR).

Christoph´s group pioneered the use of droplet-microfluidics for large-scale cell-based assays, e.g. demonstrating the screening of several hundred thousand antibodies in a single experiment, for properties such as binding, inhibition of a drug target or even effect on a co-encapsulated target cell. His laboratory also established a personalized therapy platform enabling to test drug combinations directly on tumor biopsies (www.besttherapyforme.com). Christoph Merten is an inventor on a total of 21 patents (four of them with him as the sole inventor) and collaborates with many academic groups (e.g. The International AIDS Vaccine Initiative, EU Blueprint Consortium, Molecular Medicine Partnership Unit) and pharma companies (e.g. Roche, GSK), in Europe and the US. In 2017 he founded the antibody discovery company Velabs Therapeutics, now operating as Veraxa Biosciences (www.veraxa.de).

Dr. Jan Moritz Middeke
University Hospital Dresden
Germany

Dr. med. Jan Moritz Middeke is a specialist in internal medicine and hematology and oncology. He heads the outpatient clinic of the Department of Internal Medicine I at the University Hospital Dresden, one of the largest center for hematological malignancies in Germany. His scientific interest is therapy optimization of acute myeloid leukemia with a special focus on the integration of novel technologies.

He is co-leader of the working group “Artificial Intelligence in Cancer” at the University Hospital Dresden and the Else Kröner Fresenius Center for Digital Health. The group uses state-of-the-art computer vision to improve accuracy and usability of cancer diagnosis and machine learning to leverage the power of big data in cancer research.

Dr. Quaid Morris
Memorial Sloan Kettering
Cancer Center
USA

Quaid Morris is a Full Member in the Computational and System Biology program at Memorial Sloan Kettering Cancer Centre and he holds a CCAI chair through the Vector Institute for Artificial Intelligence (AI). Previously, he was a full professor at the University of Toronto in the Donnelly Centre with cross-appointments in Molecular Genetics and Computer Science. Quaid pursued graduate training and research in machine learning at the Gatsby Unit with Peter Dayan and Geoffrey Hinton at the University College London and obtained his PhD in Computational Neuroscience from Massachusetts Institute of Technology. His B.Sc. is in computer science, and his PDF is in computational biology with Brendan Frey and Timothy Hughes, both at the University of Toronto. Morris lab (http://www.morrislab.ai/) uses machine learning and artificial intelligence to do biomedical research, focusing on cancer evolution, post-transcriptional regulation, automated phenotyping and electronic medical records.

Prof. Olaf Ronneberger
Google DeepMind
United Kingdom

Olaf joined DeepMind in January 2016 from the University of Freiburg in Germany, where he still holds an adjunct ("außerplanmäßig") professorship for Computer Science. He's one of the pioneers of bringing modern deep learning approaches to biomedical image analysis. A neural network architecture he designed in 2015 to automatically segment biomedical images, called „u-net" is still one of the most used architectures with over 47k citations. From 2016 to 2018 he led the research in DeepMind Health bringing these powerful techniques to fields including visual loss and radiotherapy treatment. In January 2019 he joined DeepMind Science as a core member of the AlphaFold team to develop AlphaFold 2 that can predict the 3D structure of proteins with atomic accuracy such that it actually became useful for end-users. His current research focuses on protein prediction beyond the static 3D structure.

Dr. Nikolaus Schultz
Memorial Sloan Kettering
Cancer Center, USA

Nikolaus Schultz, PhD is an Attending Computational Oncologist in the Department of Epidemiology and Biostatistics and an Affiliate Member of the Human Oncology and Pathogenesis Program. Dr. Schultz also serves as Head of Knowledge Systems in the Marie-Josée and Henry R. Kravis Center for Molecular Oncology, where he leads the development of the

the cBioPortal for Cancer Genomics, a web-based resource for the analysis of complex cancer genomics data, and of OncoKB, a precision oncology knowledge base. Dr. Schultz was originally trained as a biochemist and molecular biologist, but has, since his post-doctoral training in the Computational Biology Department at MSK, transitioned towards bioinformatics and computational biology. His research focuses on identifying the genomic alterations that underlie different types of cancer. By applying existing or novel computational methods to large scale cancer genomics data sets, he aims to better understand the complex mechanisms at the gene and at the pathway level that drive tumor progression, with the ultimate goal of identifying targeted therapeutic options for cancer patients. Dr. Schultz is engaged in collaborations with multiple investigators at MSK. He has also made significant contributions to several projects of The Cancer Genome Atlas, The Human Tumor Atlas Network, AACR Project GENIE, and is an investigator in the Stand Up to Cancer Prostate Cancer Dream Team. He has a particular interest in enabling discoveries by developing novel computational methods and databases that help bridge the divide between computer scientists on one side and clinicians and researchers on the other.

Dr. Itay Tirosh
Weizmann Institute
Israel

Itay Tirosh obtained his PhD from the Weizmann Institute of Science in the area of computational biology. From 2012 to 2017 he was a postdoctoral fellow at the Regev and Golub labs at the Broad Institute of MIT and Harvard, and since August 2017 he is a Senior Scientist at the Weizmann Institute of Science. The Tirosh lab is combining computational approaches and experimental single cell methods to understand the diversity of cells within human tumors, with a focus on glioma and head and neck cancers.

Dr. Adriana Tomic
University of Oxford
United Kingdom

Dr. Adriana Tomic is leading a Systems Immunology group at the University of Oxford focusing on understanding how human immune responses mediate protection and prevent severe diseases. At the interface between infection and computational biology, her research aims to transform human immunology and change the way we develop vaccines using a combination of systems-level analysis, multi-omics data integration, and artificial intelligence. Dr. Tomic is also a co-developer of SIMON, an open-source knowledge discovery platform for the application of machine learning to biomedical data. This platform has a broad application for the identification of correlates of protection in infectious diseases, autoimmunity, and cancer.

10:00 - 10:30

AI in cancer genomics

Dr. Quaid Morris, Memorial Sloan Kettering Cancer Center
New York, USA

How can you teach an artificially intelligent (AI) system to know what it doesn't know? AI systems, trained with machine learning (ML) algorithms such as Deep Neural Networks (DeepNNs), have shown incredible promise in cancer clinical decision support. Given a "training set" of data examples -- each example consisting of an input, e.g., a set of mutations detected by MSK Impact in a patient's cancer, and an associated label, e.g., breast cancer -- ML algorithms "learn" by identifying patterns in the input that are predictive of the associated label, i.e., cancer type. These patterns can then be used to label, e.g., cancers of unknown primary or to provide guidance for an uncertain pathological assessment. Designing AI systems that accurately report their uncertainty in their labelling will improve their reliability, usefulness and, hopefully, acceptance in a clinical setting.

I will discuss our work using DeepNNs to develop cancer type classifiers based on annotated somatic mutations derived from cancer DNA sequencing from two sources: MSK Impact analysis of MSK patients, and whole genome sequencing of ICGC/TCGA tumor samples. DeepNNs achieve classification accuracies 5% to 10% higher than the previous state-of-the-art, random forests, with accuracies across all cancer types in the 80-90% range, on average, and as high as 95% (or more) for common cancer types.

Unfortunately, individual DeepNNs, along with many other ML methods, are terrible at predicting how accurate their labels are, in other words, at calibrating their uncertainty estimates. This phenomenon is particularly bad for data from rare cancer types not represented in the training set: so-called "out-of-distribution" (OOD) samples. Often DeepNNs assign these OODs samples highly certain but seemingly random labels.

I will describe our work using “Deep ensembles” to compute calibrated uncertainty estimates. A Deep ensemble is a collection of DeepNNs, each trained on the same dataset but with different random initializations. We show that averaging over the outputs of the constituent DeepNNs in a Deep ensemble gives calibrated uncertainty estimates without requiring any further training. Furthermore, our Deep ensembles can identify OOD samples based on disagreement among the labels output by different members of the ensemble. Surprisingly, these approaches perform as well as, or better than, explicitly training DeepNNs to output calibrated uncertainty estimates.

In conclusion, we show that using an ensemble approach, one can transform a known weakness of DeepNNs, namely that they assign random labels to OOD samples, into a strength. As such, Deep ensembles can be used not only to make highly accurate predictions, but also well-calibrated estimates of their uncertainty in those predictions. Both of which are critical for effective clinical decision support.

10:30 - 11:00

AI in hematology: computer vision and machine learning for improved diagnosis and risk stratification

Dr. Jan Moritz Middeke, University Hospital Dresden, Germany

Artificial Intelligence (AI) has a variety of potential applications in the management of hematologic neoplasms. With its capability to make sense of large and heterogeneous data sets, Machine Learning (ML) is well suited to provide insights into disease biology using a data-driven approach or complex patient data relations utilizing clustering techniques and thus may replace hypothesis-driven approaches of data analysis. Deep learning (DL) can process medical image data and provide data-driven class predictions, especially convolutional neural nets (CNN) deliver impressive results in image classification.

In this talk, I will give an overview of the current research on the use of different ML methods in hematology, with a special focus on analysis of large-scale complex data sets of AML patients and its potential to improve risk stratification. Further, I will talk about recent developments in the use of computer vision for cytomorphology, still one of the most important diagnostic tool in hematology, and the potential to fundamentally change research and routine diagnostic approaches. Using myeloid malignancies as an example, topics such as un-/supervised Learning, different source of data and potentially pitfalls and limitations will be discussed.

11:00 - 11:30

Towards clinical decision support in oncology: Data integration, outcome models, and intuitive software

Dr. Nikolaus Schultz, Memorial Sloan Kettering Cancer Center, USA

With the recent adoption of clinical sequencing of tumor samples as part of routine cancer care, we are now in a position to retrospectively analyze genomic and clinical data from cancer patients to identify predictors of outcome and treatment response. At Memorial Sloan Kettering Cancer Center (MSK), tumor samples are sequenced as part of routine care using MSK-IMPACT, a targeted sequencing panel that covers >500 genes and can identify somatic and germline mutations, copy-number alterations, as well as select rearrangements and gene fusions. To date, tumor samples from >70,000 patients have been sequenced, and genomic alterations identified in these tumors are used to guide targeted therapies by using OncoKB, MSK's precision oncology knowledge base. All sequencing results are made available internally to MSK investigators using the cBioPortal for Cancer Genomics, a web based system for the visualization and analysis of complex cancer genomics data and matching clinical annotation. The abstraction of clinical data for these patients remains a bottleneck, and we are developing methods based on natural language processing (NLP) and machine learning (ML) to automatically derive these data from the electronic health records at scale. The resulting data will enable the identification of biomarkers for treatment sensitivity and resistance, as well as the development of more complex outcome models. For example, a recent analysis of 25,000 tumor samples from 50 tumor types revealed that oncogenic alteration frequency and chromosomal instability are increased in metastases, but that the correlations between chromosomal instability and metastatic burden depend on cancer type. As the data set grows and clinical data mining improves, we expect to be able develop outcome models that can be used in clinical care.

13:30 - 14:00

Dissecting intra-tumor heterogeneity by single cell RNA-seq

Dr. Itay Tirosh, Weizmann Institute, Israel

Each tumor is composed of diverse malignant, immune and stromal cells that interact with one another and collectively determine tumor biology and clinical phenotypes. Over the past nine years, we have been applying single cell RNA-seq (scRNA-seq) to diverse clinical tumor samples to comprehensively characterize the cellular diversity within tumors and explore the function of distinct tumor subpopulations. In this talk, I will describe our work on specific cancer types (e.g. glioma) and our pan-cancer integrative analysis of intra-tumor heterogeneity (ITH). We identify consistent patterns of heterogeneity across tumors, including expression meta-programs, consisting of dozens of genes that are coordinately upregulated in subpopulations of cells within many tumors. The meta-programs cover diverse cellular processes including both generic (e.g. cell cycle and stress) and lineage-specific patterns that influence metastasis, response to treatments and other tumor phenotypes. The improved understanding of ITH will help to understand tumor biology and to design improved therapeutic strategies such as combination treatments and differentiation therapies.

14:00 - 14:30

SIMON says: Deciphering the human immune responses using machine learning

Dr. Adriana Tomic, University of Oxford, United Kingdom

Over the past years, technological advances have enabled the generation of large amounts of data at multiple scales. Monitoring of these features is particularly important in biomedical sciences, as they serve to advance knowledge about the mechanism of health and disease, as well as to predict clinical outcomes well in advance of their occurrence. Despite the major clinical and economic consequences of these approaches, due to the lack of powerful analytical tools that are accustomed to the average biomedical researcher, translation of such knowledge has been extremely slow.

To address these challenges, we have developed SIMON, a knowledge discovery software to facilitate the application of over 180 state-of-the-art machine learning algorithms to high-dimensional biomedical data. With an easy-to-use graphical user interface, standardized pipelines, an automated approach for machine learning, and other statistical analysis methods, SIMON helps to identify optimal algorithms and provides a resource that empowers non-technical and technical researchers to identify crucial patterns in biomedical data. We demonstrate the accuracy, ease of use, and power of our software on biomedical datasets containing transcriptome, microbiome, cytometry, and multi-omics data, and identify signatures of protection that track with favorable patient outcomes in diseases and vaccine responses to influenza, meningococcus, respiratory syncytial virus, Salmonella typhi, and current SARS-CoV-2. These examples illustrate useful insights into biological mechanisms that can be achieved for the identification of correlates of protection using SIMON and help to guide further analysis of the biomedical data. Overall, SIMON is a powerful software platform for data mining that facilitates pattern recognition and knowledge extraction from high-quality, heterogeneous and multi-omics biological and clinical data.

14:30 - 15:00

Clinical intelligent systems in the wild?

Prof. Lena Maier-Hein, German Cancer Research Center, Germany

Machine learning has begun to revolutionize almost all areas of health research. Success stories cover a wide variety of application fields ranging from radiology and gastroenterology all the way to mental health. Strikingly, however, solutions that perform favorably in research generally do not translate well to clinical practice, and little attention is being given to learning from failures. Focusing on biomedical image analysis as a key area of health-related machine learning, this talk will present pitfalls, caveats and recommendations related to machine learning-based biomedical image analysis. As a particular highlight, it will cover novel solutions for some of the current roadblocks, which have been compiled based on the input of hundreds of image analysis researchers worldwide.

15:00 - 15:30

The deep learning architecture of AlphaFold

Prof. Olaf Ronneberger, Google DeepMind, United Kingdom

AlphaFold is the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated it in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14), demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm. In this talk I will describe the key components of the deep learning architecture of AlphaFold, and provide some insights into what we think are the critical design choices that made it work.

16:00 - 16:30

Droplet microfluidics in antibody discovery and personalized cancer therapy

Prof. Christoph Merten, EPFL, Switzerland

We have developed droplet microfluidic screening platforms enabling rapid identification of optimal drug cocktails for personalized cancer therapy[1]. In these systems, patient's tumor cells are encapsulated into tiny droplets surrounded by oil, together with systematic drug combinations that are tested for their efficacy. Due to the miniaturized assay volumes, the amount of cells that can be obtained from a single biopsy, is sufficient to screen tens to hundreds of treatment conditions in functional assays, each with lots of replicates. Results are available within 24h after surgery at consumables costs of less than 150 US$ per screen. The power of this platform has been demonstrated using cancer cell lines, xenograft mouse models and even human tumor biopsies. We are now translating the technology into a robust and easy to use diagnostic device (www.besttherapyforme.com), integrate transcriptomic readouts[2] and start first-in-human studies. In parallel to this, we have developed fully integrated droplet-based microfluidic platforms for the screening of therapeutic antibodies[3,4]. In these systems tiny aqueous droplets (picoliter volumes) surrounded by oil serve as independent assay vessels. The technology allows the direct screening of several hundred thousand primary, non-immortalized murine or even human B-cells for the secretion of antibodies that do not just bind to a drug target, but functionally inhibit it. Taken together this opens the way for many new approaches in drug discovery, including personalized immunotherapy or the use of antibodies to control cellular pathways at will.

1. Eduati, F. et al. A microfluidics platform for combinatorial drug screening on cancer biopsies. *Nat Commun* **9**, 2434 (2018).
2. Mathur, L. et al. Combi-seq for multiplexed transcriptome-based profiling of drug combinations using deterministic barcoding in single-cell droplets. *Nat Commun* **13**, 4450 (2022).
3. El Debs, B., Utharala, R., Balyasnikova, I.V., Griffiths, A.D. & Merten, C.A. Functional single-cell hybridoma screening using droplet-based microfluidics. *Proc Natl Acad Sci* U S A **109**, 11570-11575 (2012).
4. Shembekar, N., Hu, H., Eustace, D. & Merten, C.A. Single-Cell Droplet Microfluidic Screening for Antibodies Specifically Binding to Target Cells. *Cell Rep* **22**, 2206-2215.

16:30 - 17:00

Predicting adaptive immunity using systems immunology and machine learning

Dr. Victor Greiff, University of Oslo, Norway

Adaptive immune receptor repertoires (AIRRs) are natural and very specific diagnostics and therapeutics. The challenge is to understand how specificity is encoded in AIRRs. I will show how we address this challenge using experimental, computational, and machine learning methods. Specifically, I will present recent work of the lab on antibody-antigen binding prediction, AIRR-based prediction of immune state, personalized biases in VDJ recombination, and benchmarking of mass-spectrometry-based antibody profiling.

17:00 - 17:30

Philosophy of AI for health

Dr. Ignacio Mastroleo, University of Buenos Aires, Argentina

Solid analytical work in philosophy has clearly defined the real possibility of existential harm to humanity by general artificial intelligence (AI) and argued that existential risk prevention is a global priority. Such existential risk scenarios of a "super AI" exterminating humankind have a rich and powerful attraction to our imagination. In contrast, here I claim that the main practical aim of the philosophy of AI for health should be the study of non-existential risks of AI health interventions, including AI scientific health claims (see Figure 1). I will call this "the duty to study the non-existential risks of AI health interventions". To support this duty, I will argue that harm to individuals, groups, or populations with AI health interventions is not just a probability that may happen in the future but is instead a reality already happening in the present, with consequences for our understanding of traditional duties and something that can be averted or minimized with simple safeguards. The Surgisphere database scandal during the COVID-19 pandemic illustrates the first point. The AI scientific claims —published in The Lancet and NEJM, based on a fraudulent global database that allegedly used AI/ML to automate processes— made governments and the World Health Organization (WHO) change their health policy with harmful results. If this argument is sound, three traditional duties of health professions gain a new meaning in the philosophy of AI for health. First, the duty to care brings support to the main idea of this presentation that the philosophy of AI for health should prioritize the study of non-existential risks, as we prioritize some patients to emergency care over research in medicine. Second, once we know of non-existential risks, the duty to do no harm justifies implementing appropriate safeguards in the work of health professionals (e.g. medicine, nursing, pharmacy, and public health) and data scientists who are currently developing and using AI health interventions. Third, the duty of justice states that we should redress

unfair inequalities related to AI health interventions, such as improving AI education for health professionals and the national government's capacity to evaluate AI scientific claims—usually from low- and middle-income countries that are at a higher risk of non-existential harms. Finally, I will share some examples of simple appropriate safeguards (e.g., SPIRIT-AI guidelines for clinical trial presentations, support from WHO) and attempt to address general objections to its implementation such as futility, stifling the benefits of health innovation, and trade secret confidentiality.

Intensity Scope	Endurable	Terminal
Personal	Misinformation leading to a chronic condition (e.g. ivermectin for COVID19)	Misinformation leading to death (e.g. ivermectin for COVID19)
Local	Misuse of scarce resources (e.g. mandating ivermectin for COVID19)	Morbidity rate caused by misuse of scarce resources (e.g. using ambulances to deliver ivermectin kits for COVID19)
Global	Mistrust in scientific research	"Super AI" exterminates humanity (existential risk)

Figure 1. Typology and examples of risks of AI health intervention

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[1] Adapted from Figure 1 in Bostrom, N. (2002). Existential risks: Analyzing human extinction scenarios and related hazards. *Journal of Evolution and Technology, 9.*

MISSION

Connecting investigators and other visionaries aiming to boost cancer research with the help of modern AI methods. Bringing together leading experts from interdisciplinary fields such as physicians, computer scientists, cell and molecular biologists, as well as from pharma and the med-tech industry. We are exploring new pathways in cancer treatment with AI together. Our common goal: push the boundaries of what is possible. Joining forces, we can learn to cure cancer.

AIM OF THE CONFERENCE

The theme of the symposium is AI-assisted cancer research, and our aim is to present the states-of-the art in cancer diagnosis, prognosis, and treatment with data-driven methods. Our goal is to identify high-impact research directions, and to connect experts from academia and industry, in order to foster collaborations and translation into clinical practice.

SCIENTIFIC BOARD

Prof. Dr. Mascha Binder
CRIION Scientific Director Clinical Oncology & University Hospital Halle

Prof. Dr. Joschka Boedecker
CRIION Scientific Director AI & Department of Computer Science, University of Freiburg

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CEO Mertelsmann Foundation & Medical Center, University of Freiburg

Prof. Dr. Robert Zeiser
CRIION Scientific Director Translational Oncology & Medical Center, University of Freiburg

GENERAL INFORMATION

Event Location

Otto-Krayer-Haus
Alberstr. 25 | 79104 Freiburg im Breisgau | Germany

Price

100 € physicians and scientists | 300 € industry | students are free

You can either join the meeting on site or online.
Lectures will be recorded and available after the event.

Organisation

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Further Information

www.intelligent-oncology.org/events/

FOR YOUR NOTES:

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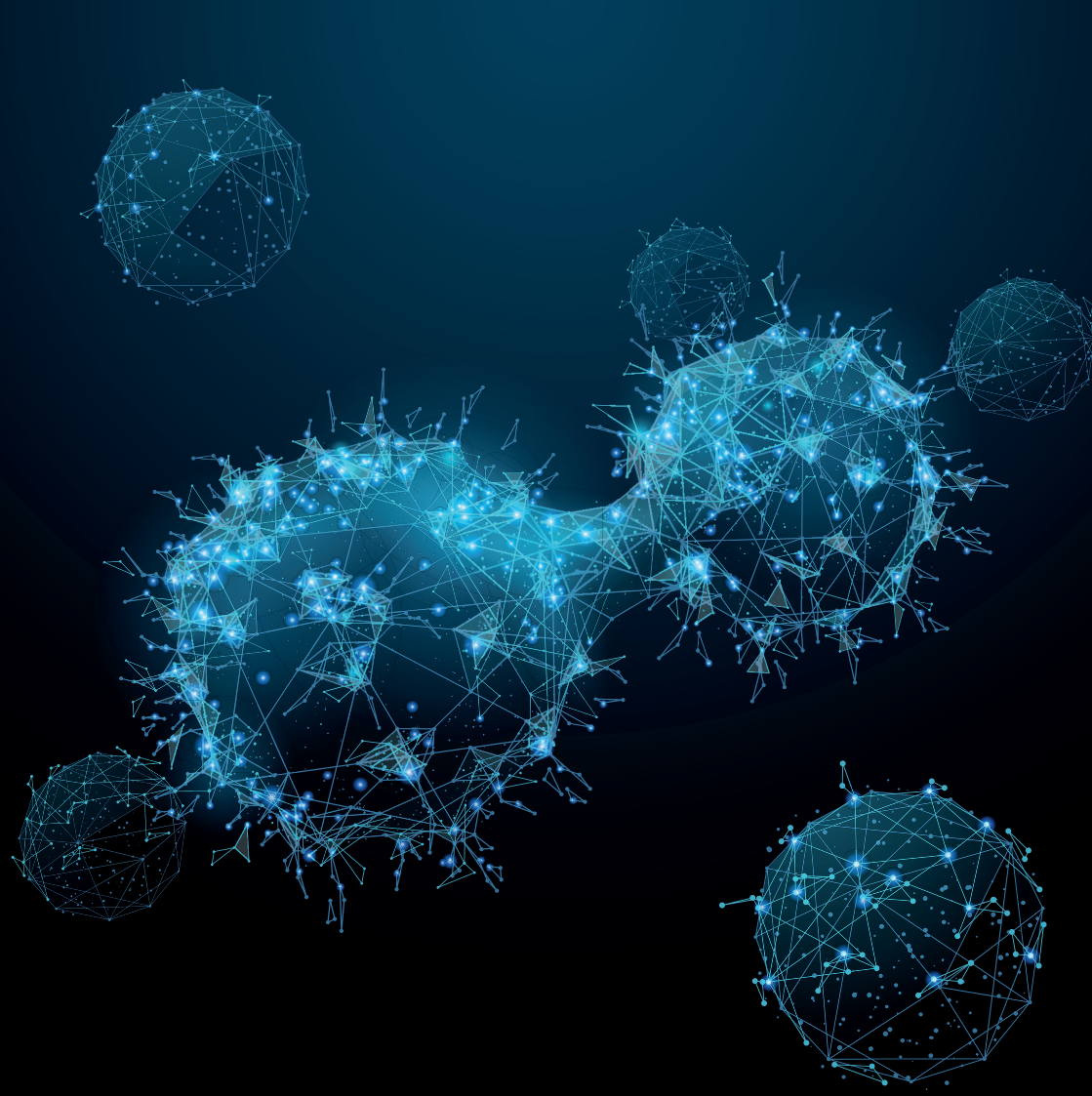

Thank you very much for joining!