BIH Symposium

Sparking Collaborations in Health Research

September 28-29, 2023

Digital Conference Booklet

bihealth.org

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Dear BIH Colleagues,

We are thrilled to extend a warm welcome to all members of the Berlin Institute of Health (BIH) @ Charité for our internal scientific symposium - "***Sparking Collaborations in Health Research***"

At BIH, we believe in the power of collaboration, innovation, and the exchange of ideas. Our symposium has been thoughtfully designed to provide a platform for our diverse community of health researchers to come together and forge new connections.

Over the next two days, we have a rich program featuring engaging talks, informative posters, interactive sessions, and invaluable networking opportunities. We wholeheartedly encourage the active participation of young scientists and early career researchers.

Scientific Committee & Organizing Committee*

Berlin Institute of Health (BIH) @ Charité

* Alexandra Bannach-Brown, Julie Courtiol, Natascha Drude, Dania Hamo, Jennifer Loske, Iana Lukianove, Sophie McEwen, Merrit Romeike, Somesh Sai, Anne-Christin Schöne, Summaira Yasmeen, Sija Zhou *(in alphabetical order)*

Scientific Program

Day 1 - 28.09.2023

Time	
09:00 – 09:30	**Opening** – *Registration Desk (badge pick-up)*
09:30 – 09:40	**Introduction to the Symposium** *(by Organizing Committee)*
09:40 – 09:55	**Welcome** *(by Christopher Baum)*
09:55 – 10:15	**Feedback BIH Evaluation – Christopher Baum**
10:15 – 11:00	**Scientific Contributed Talks #1** *Chair: Alexandra Bannach-Brown & Merrit Romeike*
10:15 – 10:30	EDS – Immunomics: *Somesh Sai*
10:30 – 10:45	APT – Julius Wolff: *Krishna Chander*
10:45 – 11:00	APT – Biological Design: *Gaurav Sadhnani*
11:00 – 12:30	Coffee, Networking and **Open Poster Session 1**
12:30 – 14:00	**Lunch** *(poster session remain open)*
14:00 – 14:45	**Scientific Contributed Talks #2** *Chair: Dania Hamo & Natascha Drude*
14:00 – 14:15	APT – BCRT: *Lisa-Marie Burkhardt*
14:15 – 14:30	EDS – Vascular Biomedicine: *Joseph Lim*
14:30 – 14:45	EDS – Functional Genomics: *Erika Zuljan*
14:45 – 15:00	**Introduction *"unconference"*** -what, where and why?
15:00 – 15:30	**Coffee and Networking**
15:30 – 17:00	**Unconference sessions** *(parallel sessions)* 1. Scientists Wanted – *open session* 2. Working conditions at the BIH: *Karin Höhne & Maia Salholz-Hillel* 3. Turning Cells into Solutions: Advancements in Next-Gen Therapeutics: *Gaurav Sadhnani* 4. Artificial intelligence @ BIH: *Vince Madai* 5. Healthcare data: „Confusing data in, Standardization out" – enabling healthcare data sharing for precision medicine and the role of patient involvement: *Diogo Neves, Josef Schepers, & Maik Pietzner*
17:00 – 18:30	Coffee, Networking and **Open Poster Session 2**
18:30 – 21:30	**Dinner, Get together and Networking**

Scientific Program

Day 2 – 29.09.2023

Time	
9:30 – 9:45	*Welcome, snapshots from unconference*
9:45 –10:45	**Scientific Contributed Talks #3** Chair: *Somesh Sai & Alexandra Bannach-Brown*
9:45 – 10:00	TSA – QUEST: *Clarissa F. D. Carneiro & Maria Arroyo Araujo*
10:00 – 10:15	MHDS - Digital Health: *Minh Duc Do*
10:15 – 10:30	MHDS - Data Science: *Michael Schirner & Carina Vorisek*
10:30 – 10:45	TSA – Clinical Study Center: *Stefanie Rudolph*
10:45 - 11:00	***Introduction to "workshop"*** *-what, where and why?*
11:00 - 11:15	**Coffee and Networking**
11:15 – 12:15	**Workshop** (parallel sessions) 1. Efficient communication in project environments *Tina Gundlach-Hauf* 2. Sex bias in science *Sophie van Linthout* 3. Mastering workplace diplomacy: Strengthening your inner mindset and outer behaviour *Carolin Heemann* 4. Career development and funding opportunities for PhDs and postdocs Roundtables with experts: Caroline Bacciu, *Nathalie Huber, Iwan Meij, Leif Ludwig*
12:15 - 13:45	**Lunch**
13:45 – 14:30	**Success Stories @ BIH** ***Panel Discussion with Joachim Weber, Valeria Fernandez-Vallone and Birgit Sawitzki*** Moderation: Alexandra Bannach-Brown
14:30 – 16:00	Coffee, Networking and **Open Poster Session 3**
16:00 – 16:55	**Collective Live Feedback and Award Ceremony****
16:55 – 17:00	**Closing Remarks**

Abstracts -oral presentations

Overview: Scientific Contributed Talks

Day 1 - Session #1:

1. Identifying shared transcriptional signatures in response to T2D-related environmental stressors in mouse pancreatic islet beta cells. - *Somesh Sai*
2. Characterization of Extracellular Matrix Remodeling in the Progression of Human Viral Myocarditis. - *Krishna Chander Sridhar*
3. Precision Medicine for the Skin: In situ Gene Editing Targeting Genodermatoses - *Gaurav Sadhnani*

Day 1 - Session #2:

4. Trick and TReAT - Tacrolimus Resistant Anti-viral T cell therapy. - *Lisa-Marie Burkhardt*
5. A chemical biology approach for functional perturbation studies in the vasculature. - *Joseph Lim*
6. Analysis of the tumor immune microenvironment (TIM) in advanced salivary gland cancers (SGC). - *Erika Zuljan*

Day 2 - Session #3:

7. Increasing robustness of preclinical research towards successful translation. - *Clarissa F. D. Carneiro & María Arroyo Araujo*
8. T1 weighted brain MRI predicts phenome-wide disease onset. - *Minh Duc Do*
9. Health Data Science Journey. - *Michael Schirner & Carina Vorisek*
10. German OncoLogical Data Standard (GOLD): Advancing to a Consensual Data Standard in Oncology. - *Stefanie Rudolph*

1.

Identifying shared transcriptional signatures in response to T2D-related environmental stressors in mouse pancreatic islet beta cells

Somesh Sai[1,2,3*], Matthew Wortham[4*] and Maike Sander[2]

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[*]These authors contributed equally

The endocrine pancreas regulates glucose homeostasis through the secretion of metabolic hormones, including insulin. In response to increased metabolic demand, β-cells can enhance insulin production to counter insulin resistance. However, chronic exposure to cellular and molecular stressors leads to progressive β-cell dysfunction, resulting in glucose intolerance and type 2 diabetes (T2D). Despite multiple single-cell RNA sequencing (scRNAseq) datasets, no consensus exists on β-cell populations or pathways related to dysfunction in different conditions. By jointly analyzing multiple datasets from several mouse models, we compiled an atlas of pancreatic β-cells exposed to environments mimicking T2D defects. We integrated over 100,000 cells from seven models varying in body composition, glycemic status, and insulin demand. Through this atlas, we identified an enriched "compensating" state associated with increased insulin demand as well as a "stressed-immature" state enriched during hyperglycemia. While the "compensating" state exhibited increased β-cell workload and preservation of β-cell maturity, the "stressed-immature" state was associated with increased workload and loss of maturity. Altogether, these observations suggest that successful β-cell adaptation to increased insulin demand corresponds to maturity preservation during enhanced workload. Identifying pathways linked to β-cell workload and maturity loss lays the basis for mechanistic studies, making this resource invaluable for understanding β-cell failure in T2D.

2.

Characterization of Extracellular Matrix Remodeling in the Progression of Human Viral Myocarditis

Krishna Chander Sridhar[1], Julia Mehl[1], Mario Thiele[1], Sophie Van Linthout[2,3], Carsten Tschöpe[2,3], Viola Vogel[4] and Georg N. Duda*[1,2]

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[2]Berlin Institute of Health Center for Regenerative Therapies (BCRT), Charité - Universitätsmedizin Berlin.

[3]German Centre for Cardiovascular Research (DZHK).

[4]Laboratory of Applied Mechanobiology, ETH Zürich

Viral myocarditis is the inflammation of the myocardium resulting from a viral infection. Mechanistic research on viral myocarditis pathogenesis has so far focused on molecular mechanisms and to a lesser degree on the role of the extracellular matrix (ECM) signatures. Here, we analyzed the ECM niche during inflammation progression focusing on the inflammatory microenvironment. Thereby, immunohistochemical (IHC) analyses were performed on endomyocardial biopsies from patients (N=41) at the different stages of disease progression – acute myocarditis, inflammatory dilated cardiomyopathy (DCMi) and dilated cardiomyopathy (DCM) to characterize the local immune cell composition and ECM-changes. Using a fibronectin-binding peptide mechanosensor FnBPA5, the tensional states of fibronectin fibers were studied. Using second harmonic generation (SHG) microscopy the presence of collagen I deposits was quantified. IHC analysis also revealed the presence of CD68+ macrophages in the inflamed tissues. Interestingly, relaxed Fn fibers were largely found in areas of tissues with high macrophage concentration. Spatial proximity analysis confirmed a preferential localization of relaxed Fn fibers in close proximity to areas of high macrophage concentration in sites of ongoing inflammation. Further, SHG analysis showed collagen I bundles at exactly these sites. The proximal localization of macrophages, relaxed Fn fibers and dense collagen bundles indicated clearly distinct spots of matrix remodeling and hints at a tight interplay between immune cells and ECM.

3.

Precision Medicine for the Skin: In situ Gene Editing Targeting Genodermatoses

J Bolsoni[1], D Liu[1], F Mohabatpour[1], GG Sadhnani[2], DC Apaydin[2], J Leung[3], E Jan[3], JA Kulkarni[4], P Cullis[3] and S Hedtrich[1,2,5,6*]

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Autosomal Recessive Congenital Ichthyosis (ARCI) encompasses a group of severe skin conditions characterized by abnormal keratinization processes. These disorders arise due to single mutations in several genes, with one of the most affected enzymes being Transglutaminase-1 (TGM-1). Gene editing tools have a considerable therapeutic potential to target and correct these single mutations. Nevertheless, intraepidermal delivery of gene editing tools remains challenging due to the skin's restrictive barrier, even in diseased states. All treatment regimens for ARCI are restricted to symptom management rather than long-lasting cures. The Hedtrich Lab has developed a non-viral in situ TGM-1 gene editing approach to bridge this treatment gap, which combines a potent pharmacological carrier (lipid nanoparticle) with physical modulation of the skin barrier (i.e., laser ablation or microneedles) to deliver gene editing tools. We have assessed the safety and efficacy of our approach in 2D and 3D human skin models and achieved in situ editing rates of ≥ 10% without inducing pro-inflammatory cytokine release. We are currently developing ARCI-diseased skin models to aid the preclinical evaluation of our ATMP. Aided by SPARK-BIH, we aim to tackle regulatory hurdles and enter phase I/II clinical trials by the end of 2025.

4.

Trick and TReAT - Tacrolimus Resistant Anti-viral T cell therapy

Lisa-Marie Burkhardt[1], Lukas Ehlen[2], Niklas Wiese[1], Claudia Beltran Mestres[1], Dr. Anna-Catharina Michaela Krebs[2], Ugarit Daher[2,4,5], Janine Arndt[2], Melanie Rothe[1], Andy Römhild[1], Harald Stachelscheid[5], Hans-Dieter Volk[3], Petra Reinke[1], Michael Schmueck-Henneresse[2] and Leila Amini[1,2]

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Patients suffering from end-stage organ failure require solid organ transplantation (SOT) and life-long treatment with immunosuppressive drugs. This results in the patients' vulnerability to virus infections causing transplant rejection, morbidity and mortality. Current antiviral drug treatments are not sufficient and show toxic side effects. This is why, adoptive anti-viral T cell Therapy is highlighted as novel, promising approach.

In the TReAT project, we manufacture Tacrolimus resistant (Tac-res.) anti-viral T-cells for clinical application using a GMP compliant process. These novel gene-edited Tac-res. anti-viral T-cells are built by gene editing with a vector-free Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-Cas9-based protocol. To confirm the safety and efficacy of these anti-viral T-cell products (TCPs), we had the unique chance to set up a human co-culture platform. For this, patient derived lung organoids and immune cells can be combined in an autologous system, as we have access to primary lung tissue and blood samples from the same patient. We are now integrating TCPs into the lung platform for safety and efficacy testing. Finally, this human-derived platform holds the potential to yield valuable pre-clinical data on TCPs and pave their way into the clinic.

5.

A chemical biology approach for functional perturbation studies in the vasculature

Joseph Lim[1,2], Jorge Andrade[1,2] and Michael Potente[1,2]

[1]Angiogenesis and Metabolism Laboratory, Berlin Institute of Health at Charité – Universitätsmedizin Berlin, Germany

[2]Angiogenesis and Metabolism Laboratory, Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany

Genetic tools for manipulating gene expression play pivotal roles in biomedical research. Particularly, the Cre-loxP technology has revolutionized our understanding of genes and pathways that govern organ development, growth, and regeneration. However, these systems have inherent limitations such as the irreversibility of the genetic perturbation that curtail mechanistic and translatable insights. To overcome these shortcomings, we utilized a chemical biology tool known as the dTAG system. This approach pairs a cell-permeable heterobifunctional degrader of FKBP12^{F36V} (dTAG) with expression of a FKBP12^{F36V} fused protein of interest, thereby allowing exclusive degradation through an induced proximity interaction. To test the applicability of this technology for in vivo studies, we targeted FOXO1 – a disease-relevant transcription factor with essential roles in the vascular and immune system. We found that FOXO1-FKBP12^{F36V} is rapidly depleted following treatment with nanomolar concentrations of dTAG compound. This perturbation is reversible because withdrawal of the dTAG compound led to full recovery of the FOXO1 protein. By extending our analysis to cells derived from *Foxo1-FKBP12*^{F36V} knock-in mice, we validated the highly efficient ablation of FOXO1 signaling in these cells. Together, our data show that the dTAG system is a novel approach for precise control of protein abundance, whose temporal dynamics enable high-resolution analysis of protein functions. We postulate that coupling this technology with spatially-resolved analysis methods will provide unprecedented insights into (patho-)physiological roles of master regulators such as FOXO transcription factors.

6.

Analysis of the tumor immune microenvironment (TIM) in advanced salivary gland cancers (SGC)

Erika Zuljan, Eric Blanc, Benjamin von der Emde, Iris Piwonski, Frederick Klauschen, Inge Tinhofer, Andreas Mock, Peter Horak, Ulrich Keller, Konrad Klinghammer, Stefan Fröhling, Sebastian Ochsenreither, Ulrich Keilholz, Damian T. Rieke and Dieter Beule

Salivary gland cancers (SGC) are rare and heterogeneous tumors. Among SGC, Adenoid cystic carcinoma (ACC) is the second most common histology and is characterized by an immune depleted microenvironment. Advanced SGC lack established treatment options and show poor response to immunotherapy. The aim of this study is to characterize the tumor immune microenvironment (TIME) in advanced SGC, with a focus on ACC, to identify potential therapeutic strategies.

Advanced SGC from the DKTK MASTER program were sequenced for bulk RNA-seq (n=95), Exome (n=55), Genome (n=50) and single cell RNAseq (n=13). Results were validated immunohistochemically (n=14).

RNA-seq immune deconvolution showed an overall lower immune cell infiltration in ACC compared to other SGC entities. A small subset of ACC showed high immune infiltration. TMB in ACC was significantly lower than in other SGC and was not associated with inflammation. No association was found between inflammation and clinical parameters. The immune checkpoint VTCN1 was found to be significantly overexpressed in ACC. Single cell RNAseq is being analyzed to validate the results from bulk RNA seq.

These data suggest an immune-high subgroup in advanced ACC. A clinical trial of a VTCN1-directed therapy is ongoing.

7.

Increasing robustness of preclinical research towards successful translation

Clarissa F. D. Carneiro[1,2], María Arroyo Araujo[1,2], Natascha Drude[1,2], Ulf Tölch[1,2] and Ulrich Dirnagl[1]

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[2]AG Tölch, QUEST center

Many preclinical studies fail to translate in humans despite promising results. Besides the complex and poorly understood pathology to account for some of the failures, most preclinical evidence lacks the robustness required for successful translation. The DECIDE (Decision-Enabling Confirmation of Innovative Discoveries and Exploratory Evidence) project accompanies 12 multicenter confirmatory projects across Germany aiming to develop a framework for the preclinical research process. With the evidence generated by the participating laboratories complemented by simulation approaches and multi-stakeholder workshops, we have been investigating how robust and trustworthy the confirmatory replication projects are, and how informative their results are considering their translational goals. Currently, we are comparing the different versions of experimental protocols to describe how the strategies change across the translational pathway. Next, we will compare the effect sizes and statistical significance of exploratory and confirmatory experiments. Lastly, we will evaluate how the knowledge claim is updated by the confirmatory results.

In conclusion, the DECIDE project is conducting several studies engaging with groups around Germany with the goal of strengthening the research quality of preclinical studies.

8.

T1 weighted brain MRI predicts phenome-wide disease onset

Minh Duc Do[1], Benjamin Wild[1], Marc-Andre Schulz[2] and Roland Eils[1,3,*]

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Radiographic imaging has fundamentally revolutionized medicine by providing non-invasive insights into the human anatomy, thus playing a vital role in medical diagnostics. Sonography, X-ray, computer tomography, and magnet resonance imaging (MRI) are crucial tools used to substantiate suspected diagnoses based on a patient's symptoms or to assess the extent of radiological correlates of various symptoms. However, the success of such symptom-oriented diagnoses is limited by radiologists' experience in recognizing a signal visible to the human eye. While radiological imaging is used as a reactive diagnostic tool to detect morphological manifestations of advanced-stage disease, the potential for early diagnosis and benefit for preventive medical treatment of most diseases is largely unknown. In this study, we examine the predictive potential of brain MRI to stratify the onset risk for 73 neurological, psychiatric, neuro-hemodynamic, and neuro-degenerative diseases. Furthermore, we performed a phenome-wide analysis for 688 endpoints, including non-brain-related diseases. Specifically, we have trained a three-dimensional ResNet-based neural network to learn disease-specific risk states from 48,451 T1-weighted brain MRI scans from the UK Biobank (UKBB). The results suggest the model can stratify the onset risk for most investigated diseases, surpassing basic demographic predictors like age and sex in outcome prediction for most of the 73 endpoints studied. This study demonstrates that T1-weighted brain MRI scans can reveal a potential radiological manifestation that is not recognizable to the human eye at an early stage before a clinical-symptomatic presentation. This understanding of radiological diagnostics could revolutionize treatment strategies, including early interventions against preventable diseases and early disease diagnosis to slow disease progression and broadly improve patient outcomes.

In future research, aggregating several MRI sequence types can potentially reveal a better predictive performance across the investigated endpoints, and integrating temporal information from follow-up brain MRIs may further increase the predictive performance. We have not yet exhausted the potential of classical optimization approaches in deep learning, and better model architectures such as Vision Transformers and extensive data augmentation could achieve better predictive outcomes.

9.

Health Data Science Journey

Schirner M, Vorisek C, Wirth F, Wunderlich T, Miron G, Gütig R, Meisel C, Poikela M, Prasser F, Ritter P and Thun S

Health Data Science Center (HDSC)

We demonstrate our approach at the Health Data Science Center for clinical discovery science. The increasing availability of 'physiomes' of patients through digital monitoring, sensor and wearable technologies offers opportunities for a transformation of diagnostics and therapy in many fields. To univocally and unambiguously define and extend existing data elements we use terminologies that are specified within the Fast Healthcare Interoperability (HL7 FHIR) profiles. Making these data available for research purposes and enabling data sharing across different institutions is an integral part of reproducible research. As part of this process, we develop innovative community-oriented tools, which cover a broad spectrum from agile data loading processes to self-service analytics and data anonymization, and which are published as open-source software. Our research includes investigating what kind of methods and tools might best help patients to overcome trust and privacy issues. We recently developed a first use case of human digital twin simulations using the trusted infrastructure developed at the BIH. With novel learning algorithms for spiking neural networks, we discover predictive features in unsegmented high-dimensional data streams that support decisions for the benefit of patients.

10.

German OncoLogical Data Standard (GOLD): Advancing to a Consensual Data Standard in Oncology

Stefanie Rudolph, Liudmila Lysyakova, Julian Sass, Andrea Essenwanger, Marie Chantal Kühn, Laura Purfürst, Sharen Nicole Heinig, Sylvia Thun and Christof von Kalle

The project "German OncoLogical Data Standard," abbreviated as GOLD, was initiated to bridge the gap between data used in research and patient care, ultimately generating tangible benefits for patients. So far, various initiatives and project datasets have included partially identical or similar data fields. This leads to duplicated efforts in data management at different stages of a patient's journey, requiring unnecessary additional input and effort. It can also result in treatment errors, for instance, if crucial data is not machine-readable due to technical incompatibilities. In the GOLD project, data fields from various (inter)national data set formats across the entire oncological patient journey have been merged in terms of content into curated parameter groups (CPG), involving professionals from both research and patient care. Using the CPG, machine-readable codes for semantic concepts such as SNOMED CT, LOINC, and ICD10, and the existing profiles of the open-source data exchange standard "HL7 Fast Healthcare Interoperability Resources" (FHIR) were analyzed. Based on all available information, the most suitable FHIR profiles as a GOLD standard were proposed. We are convinced that harmonized definitions of all relevant data parameters for an oncological patient journey can be developed to create tangible value for patients through improved data exchange.

Posters -Number and Titles

All Sessions (Day 1 & 2)*:

*These posters are provided by the BIH Core facilities and will be available throughout the whole symposium to ensure that you have the chance to explore the possibilities for your projects.

7 The BIH Bioportal Single Cells – *Markus Morkel*

Core units; Primary Tissue; Single Cell; FFPE; Pathology

13 BIH Proteomics core unit – *Marieluise Kirchner, Matthias Ziehm, Philipp Mertins*

Proteomics; Mass Spectrometry; Olink; Biomarkers; Therapeutic Targets

25 – *Josef Schepers*

35 From ATMP Characterization to Spatial Tissue Assessment. How specialized mass spectrometry-based technologies can support clinical translational projects. – *Oliver Klein*

Spatial Omics; Mass Spectrometry Imaging; Extracellular matrix; ATMP; Translation

40 Genomics Core Unit – *Ulrike Krüger, Thomas Conrad, Marten Jäger, Tatiana Borodina, Cornelius Fischer, Janine Altmüller*

Genomics; Single-cell technology; Spatial biology; Long-read sequencing; Next Generation Sequencing

49 BIH Cytometry Core Facility - Flow & Mass Cytometry – *Desiree Kunkel*

Core Facility; Flow Cytometry; Mass Cytometry; Imaging Mass Cytometry; Full Spectrum Flow Cytometry

54 Central Biobank - *Alexandra Stege, Jenny Schlesinger, Dana Briesemeister*

Biobanking; Core Facility; Storage of biosamples; clinical studies; sample processing

75 People and Organizational Development - *Carolin Heemann*

Trainings; Coachings; Mediation; Team Building; Leadership

Day 1 – Morning Session (11:00-12:30):

1 Spatio-temporal correlation structure in human intracranial EEG: hierarchy and perturbations – *Paul Mueller*

Spatio-temporal correlation; Intracranial EEG; Anti-seizure medication; Cortical hierarchy; Brain Criticality

4 - *Christian Meisel*

10 MINIscR-seq - A miniaturized platform for high-throughput single-cell RNA sequencing for precision medicine – *Agata Rakszewska*

Single-cell analysis; Long-read sequencing; Transcriptomics; Bioinformatics; Method development

16 Opening the BLACK BOX: The social innovation of implementing an electronic laboratory notebook – *Christiane Wetzel*

responsible research; indicators; intervention; electronic laboratory notebook; social innovation

19 Preclinical Systematic Reviews and Meta-Analyses: Using Evidence Synthesis to Support Translation – *Torsten Rackoll*

Systematic Reviews; Meta-Analysis; Preclinical; Translation; Support

22 Calcitonin Gene-Related Peptide Alpha Promotes Inflammation and Stabilizes Bone Homeostasis in Age-Related Osteoarthritis – *Alexander Hildebrandt*

Calcitonin Gene-Related Peptide Alpha; Osteoarthritis; Pain Perception; Cartilage; Joint Disease

28 Commonly mutated driver genes in primary mucinous ovarian carcinoma – *Francesca Tiso*

Mucinous ovarian carcinoma; NGS; cancer genomics; Targeted DNA sequencing; Driver mutations

31 Novel Candidate Disease Gene for Familial Hyperaldosteronism – *Janek Haus*

Primary Aldosteronism; Adrenal Gland; Hypertension; Familial Hyperaldosteronism; Rare variants

34 Deep Learning-based Multimodal Learning for Risk Prediction – *Tillmann Rheude*

Deep Learning; Multimodal Learning; Machine Learning; Survival Analysis; Risk Prediction

37 Immunomodulatory placental-expanded, mesenchymal stromal cells ameliorates cartilage degeneration in knee primary osteoarthritis – *Sijia Zhou*

Cartilage; Mesenchymal stromal cells; Cell therapy; Immunomodulation; Inflammation

43 Systems biology of metabolic host-pathogen interactions – *Johannes Hartl*

Microbial metabolism; Proteomics/Metabolomics; Fungal pathogens; Antimicrobial resistance; Functional genomics

46 – *Olivia Debnath*

52 Multiscale Co-Simulation of TheVirtualBrain with NEST, ANNachy and NetPyNE (NEURON) spiking networks – *Dionysios Perdikis*

TheVirtualBrain; Co-Simulation; spiking networks; multiscale; modeling

55 Insights into the mechanobiological regulation of tissue regeneration processes through in silico approaches – *Sara Checa*

Mechanobiology; Regeneration; Computer Modeling; Finite element Models; Agent-based models

58 Interoperability Services for a FAIR Digital Health System – *Sylvia Thun*

Data Infrastructure; FAIR; Interoperability; Digital Health; Terminologies

61 Self-Supervised Representation Learning for Medical Images – *Nabil Jabareen*

Self-Supervised Learning; Deep Learning; Medical imaging; Representation Learning; Magnetic Resonance Imaging

64 BIH Digital Health Accelerator - *David John Murphy*

Digital health; Innovation; Funding; Translation; Clinically-validated solution

67 Deciphering molecular effects of triple therapy in children with cystic fibrosis by single-cell transcriptomics – *Jennifer Loske*

cystic fibrosis; single cell RNA analysis; upper airway cells; treatment-induced changes; children

70 DNA methylome and scRNA sequencing of nasal cells from COVID-19 patients reveal long-term impact on expression of genes involved in ciliary function – *Marey Messingschlager*

COVID-19; post-infection follow-up; whole-genome enzymatic methyl-seq; scRNA-seq; nasopharynx

73 Dissecting genotype-phenotype relationships in acute myeloid leukemias by cohort-scale multi-layered single-cell approaches – *Sarah Gräßle*

Single-cell analysis; Immune microenvironment; Leukemia; Cancer classification; Large patient cohort

Day 1 – Evening Session (17:00-18:30):

8 Tolerogenic DC-10 cells are marked by cytoplasmic accumulation of vesicles

– *Tomislav Kostevc*

Dendritic cells; DC-10; Vesicles; TEM; Proteomics

11 A Novel Computational Tool to Identify DNA Repair Malfunction for Disease Prognosis – *Benedikt Obermayer*

Class-switch recombination; Long-read sequencing; DNA repair deficiency; Immune repertoir; Machine learning

12 Opening the BLACK BOX: The three stages of translating education into responsible research practices - *Sarah Wendt*

responsible research; interventions; training transfer; work environment; transfer support

14 Machine learning of electronic health records across population cohorts for applications in phenome-wide disease prediction – *Leylanur Bodur*

Machine Learning; Population Cohort Studies; Electronic Health Records; Risk Modeling; Disease Prediction

17 Machine learning of genetic risk for common diseases across population studies – *Julius Upmeier zu Belzen*

Machine Learning; Genetics; Polygenic Risk Score; Interpretability; Gene Ontology

20 Empowering Future Clinical Research – *Johanna Nothacker*

Clinical trial; Trial prototyping; Data curation; Broad consent; Patient finder

23 Role of an unexplored extracellular matrix protein in myocarditis – *Sophie van Linthout*

Myocarditis; inflammation; liquid chromatography-mass spectrometry; extracellular matrix; fibroblast

26 – *Marieke Voß*

29 – *Eldar Abdullaev*

32 Cord blood DNA methylation pattern predicts food allergy development later in children´s life – *Laura Matzner*

Food allergy; Epigenetics; DNA Methylation; Birth cohorts; Targeted Sequencing

38 2D or not 2D? Investigating the third dimension in spatial transcriptomics data – *Sebastian Tiesmeyer*

Spatial transcriptomics; quality control; cell typing; cell segmentation; computational biology

41 Fully integrated pipeline for hPSC quality control data analysis with SNP arrays – *Nicolai von Kügelgen*

Pluripotent stem cells; quality control; bioinformatic pipeline; SNP array; copy number variantion

44 Implementing Responsible Research Assessments for Appointments at the BUA – No Chance without Collaborations – *Fabian Hempel*

Research assessment reform; Evidence-based science management; Implementation; Appointments of professors; Collaborations

47 – *Harald Wagener*

50 IP Management: Patents & Licenses – *Claudia Keil-Dieckmann*

Invention; patent; license; startup; translation

53 The Virtual Brain Ontology - a computational knowledge framework and semantic web approach for building and sharing reproducible brain network models – *Leon Martin*

Brain Simulation; Semantic Web; Knowledge Framework; Metadata Schema; Automatic Programming

56 Health data at your fingertips: A framework for data exploration, analysis, and visualization – *Lena Baum*

Health data; self-service analytics; data exploration; data analysis and visualization; hypothesis generation

59 Match & Connect. International Startup Partnerships. – *Verena Benz*

Connecting external start-ups; Networking Service; Access to clinical expertise; Co-development; Israel Innovation Authority

62 Charité BIH Innovation (CBI) - joint technology transfer of Charité and BIH – *Thomas Gazlig*

Translational mindset; Patient benefits; Increasing impact; Innovation journey;Services & Consultations

65 SPARK-BIH Program – *Tanja Rosenmund*

Academic Innovation; funding; support by expert network; therapy, diagnostics and medical device; development translation

68 Promoting anti-discriminatory measures to foster Diversity, Equity and Inclusion at BIH - initiatives and progress – *Karin Höhne*

Positive working environment; equal treatment; prevention of discrimination and conflicts; Equality Diversity Inclusion; First Contact Points

71 Exploring the potential of unmasked epitopes: rational antigen design for effective subunit vaccines against human and animal viruses - *Emre Mert Ipekoglu*

EBV; Viral Vaccines; Neutralizing antibodies; Antigen design; Epitope masking

74 Beyond Conventional Histopathology: Unraveling Spatial Complexity Using Light-Sheet Microscopy – *Rose Behncke*

3D Histopathology; Lightsheet Microscopy; 3D Imaging and Analysis; Fluorescent H&E (Hämatoxylin and Eosin) and Vascular network; Nanobodies as a new diagnostic marker

Day 2 – 14:30-16:00:

2 Aging and viral evolution impair dominant pan-coronavirus-reactive immunity against SARS-CoV-2 – *Andreas Thiel*

Aging; T cells; Adaptive Immunity; SARS-CoV-2; vaccination

3 A Trustworthy AI Reality-Check: The Lack of Transparency of Artificial Intelligence Products in Healthcare – *Jana Fehr*

Artificial Intelligence; trustworthy AI; AI Ethics; medical AI; Transparency

5 Integration and modeling of clinical and molecular data of patients suffering from non-small cell lung carcinoma – *Karl Kraft*

NSCLC; Data Integration; Personalized Medicine; Molecular Tumor Board; Patient Similarity Measures

6 Proteogenomic landscape of multiple myeloma – *Valeriia Sapozhnikova*

Multiple myeloma;Proteomics;Clinal Proteomics;Risk Signatures;Therapeutic Targets

9 – *Daniel Ibrahim*

15 Diffsurv: Differentiable sorting for censored time-to-event data – *Benjamin Wild*

Survival analysis; Risk stratification; Machine Learning; Algorithmic Supervision; Time-to-event-data

18 Joint forces of targeted and non-targeted imaging techniques to unravel tissue heterogeneity – *Marta Grzeski*

Mass spectrometry; spatial; imaging; antibodies; multiplex

21 Determining the role of transcription factors involved in human liver cell plasticity – *Marta Cagna*

Liver regeneration; Cell plasticity; Bipotent cells; Cholangiocyte organoids; Forward programmed hepatocytes

24 International interoperability standards facilitate data exchange in multi-cohort research projects – *Eugenia Rinaldi*

Interoperability; semantic standards; terminology; data exchange; multy-country study

27 Development of a multi organ on chip system to model the gut-lung axis - *Alessandro Bentivogli*

Microphysiological systems; Disease modelling; Gut-lung axis; Organ crosstalk; 3D models

30 – *Shashwat Sahay*

33 Extracellular Matrix Remodeling in Atopic Dermatitis as a Putative Contributor to the Atopic March - *Dana Sophie Wörz*

Atopic Dermatits; Atopic March; Extracellular Matrix Remodeling; Human Disease Models; Inter-epithelial crosstalk

36 Dissecting regulatory function by Hi-C, MPRAs and sequence modeling – *Pia Keukeleire*

Bioinformatics; MPRA; Hi-C; regulatory genomics; sequence modeling

39 Sex Differences in Ischaemic Stroke: Leveraging Systematic Review for Enhanced Translational Insights – *Sofija Vojvodic*

Sex; Sex differences; Ischaemic stroke; Systematic review; Translation

42 Peering into the Black Box: Literature Mining and Feature Remapping to Identify Biological Mechanisms Underpinning Machine Learning Prediction in Psychosis – *Jaskiret Dhindsa*

Machine Learning; Psychosis; Explainable AI; Omics Data; Semantic Knowledge

45 Towards Clinical Practice: Biomarker Discovery and Clinical Applications Using Targeted and Untargeted Proteomics Approaches – *Oliver Lemke*

Biomarker Discovery; High-throughput Proteomics; Quantitative Protein Panel Assay; Machine Learning & Multi-parametric Regression; COVID-19

48 WESkit, a user-friendly workflow execution service – *Valentin Schneider-Lunitz*

GA4GH WES API; workflow; container; cloud; cluster

51 Towards a comprehensive understanding of residual privacy risks in anonymous health data – *Mehmed Halilovic*

Health data; data sharing; privacy protection; anonymization; synthetization

57 DNA replication speed regulates heterochromatic DNA hypomethylation during T cell aging – *Dania Hamo*

DNA Methylation; T cells; DNA replication speed; cellular aging; Heterochromatin

60 Data Management in Multidisciplinary Research: environMENTAL - *Marcel Jentsch*

Data Management; Data Life Cycle; Mental Health; Environment; FAIR

63 Charité BIH Innovation – Detect & Dispatch and Idea Office – *Elisabeth Krenkler*

Service; Guidance; Support; Ideation; Translational Journey

66 – *Martin Braun*

69 Adding An Additional Dimension to Routine Clinical Diagnostics - Development of Nanobody-based 3D Imaging for Histopathological Analyses – *Nils Hansmeier*

Histopathology; 3D Imaging; Nanobodies; Clinical Diagnostics; Wholemount Stainings

72 BeLOVE- a platform for translational cardiovascular disease research – *Joachim Weber*

Cardiovascular disease; stroke; diabetes; multi-omics; trial-ready cohort

76 Decoding multi-omic signatures: from single cells to patient stratifcation – *Suharto Banerjee*

Single cell genomics; Deep learning; Natural language processing; Structural variation; Diagnostic karyotyping

77 Unravelling the clonal dynamics of somatic mutations to learn mechanisms of treatment resistance – *Benedict Monteiro*

Genomics; Bioinformatics; Somatic mutation; Clonal evolution; Inflammatory disease

Unconference Session - Day 1:

What is an unconference?

"Unlike traditional conferences, an unconference is a participant-oriented meeting where the attendees decide on the agenda, discussion topics, and themes. The informal and flexible program allows participants to suggest topics of their own interest and choose to attend sessions accordingly. The aim is for researchers from diverse disciplines to grow their network, and work collaboratively on topics of common interest."

Budd et al., 2015 - doi: 10.1371/journal.pcbi.1003905

How to participate?

1. Attend the topic that interests you the most.
2. Introduce yourself at the table you are seated at.
3. During the session, participants collaboratively determine the specific session topics. Co-chairs will facilitate you when you have sat down.
4. Participants are encouraged to share their experiences. There is a focus on conversations and discussions, rather than prepared presentations.

1) Scientist wanted

Description: Scientist wanted sessions are an opportunity to briefly introduce an aspect of your project where you are missing specific expertise or would like consultation from someone at BIH. More information below.

2) Working conditions at the BIH - *what is needed to create a positive working environment*

Description: Together with the scientists at the symposium, we would like to discuss about existing (power) structures and inequalities and how to overcome exclusion mechanisms so that everyone working and doing research at the BIH can reach their full potential. Scientific excellence needs diversity and people with various backgrounds and experiences, and we must make sure, that we create structures and shape a working culture, which is inclusive and supportive for everyone.

Leading team: Karin Höhne (Equal Opportunities Officer) and Maia Salholz-Hillel (PhD Student)
Contact: karin.hoehne@bih-charite.de , maia.salholz-hillel@bih-charite.de

3) Turning Cells into Solutions: Advancements in Next-Gen Therapeutics

Description: Next generation therapeutics such as nucleic acid delivery, protein-based targeted therapeutics and cell therapies have encountered a substantial market boom in the past 15 – 20 years, with multiple strategies successfully translating from bench-side to bed. In this session, we not only want to spark collaborations between BIH scientists working on groundbreaking therapies, but also initiate intriguing discussions,

ultimately aiming that all participants are able to expand their (theoretical or experimental) horizons.

Leading team: Gaurav Sadhnani (PhD student, Hedtrich group)
Contact: gaurav-girish.sadhnani@charite.de

4) Artificial intelligence @ BIH

Description: This session aims to connect researchers on AI topics to enhance collaboration and streamline activities across BIH on how AI tools are used in our work.

Leading team: Vince Madai (Project Leader, Responsible Algorithms)
Contact: vince_istvan.madai@bih-charite.de

5) Healthcare data: „Confusing data in, Standardisation out“ – enabling healthcare data sharing for precision medicine and the role of patient involvement

Description: This unconference session aims to discuss themes of enabling healthcare data sharing using privacy-preserving techniques, implementing secure data-sharing platforms, precise documentation for utilizing precision medicine techniques, and strategies to increase patient involvement.

Leading team: Diogo Neves, Josef Schepers, Maik Pietzner (Medical Informatics & Computational Medicine)
Contact: diogo-telmo.neves@bih-charite.de , josef.schepers@bih-charite.de , maik.pietzner@bih-charite.de

Workshops - Day 2:

What are the workshops about?

Workshops are for active conversations about the state of research and on topics to improve our scientific world.

1) Efficient communication in project environments

Tina Gundlach-Hauf (Head of Team Organisation)
Contact: tina.gundlach-hauf@bih-charite.de

Description: This session will discuss the importance and challenges of communication strategies in research projects. You will learn about appropriate tools for communication set-ups in projects to foster transparency and project success and a strategy on how to deal with stakeholders.

2) Sex bias in science

Sophie van Linthout
Contact: sophie.van-linthout@bih-charite.de

Description: Participants will gain insight into sex biases in scientific research and its implications. A current example will be discussed.

3) Mastering workplace diplomacy: Strengthening your inner mind-set and outer behaviour

Carolin Heemann (Personnel Development Officer)
Contact: carolin.heemann@bih-charite.de

Description: Participants will get a short insight into navigating challenging workplace scenarios by strengthening their mindset and establish a growth-oriented perspective, additionally to using communication skills to fine-tune their outward behaviour, enabling them to foster constructive dialogue, and transform workplace tensions into opportunities for growth and collaboration.

4) Career development and funding opportunities for PhDs and postdocs

Caroline Bacciu (Berlin University Alliance, Promoting Talent), Nathalie Huber (Head of BIH Biomedical Innovation Academy; Head of Clinician Scientist Office), Iwan Meij (Head of BIH Biomedical Innovation Academy; Head of BIH Application and Reporting Portal), Leif Ludwig (Emmy Noether Group Leader)
Contact: caroline.bacciu@berlin-university-alliance.de, nathalie.huber@bih-charite.de, iwan.meij@bih-charite.de, leif.ludwig@bih-charite.de

Description: Participants will be introduced to structures supporting career development for clinician scientists, PhD students and postdocs. Questions and further information can be discussed in small groups. Also first-hand experience of the transition from early career researcher to independence will be shared.

Code of Conduct

During this event, we want to strengthen the scientific community at the BIH and grow a community of contributors sharing their experiences and scientific insight.

In the interest of fostering an open and welcoming environment, we as organizers pledge to make participation in the **BIH Symposium 2023** a kind and harassment-free experience for everyone, regardless of age, body size, disability, ethnicity, sex characteristics, gender identity and expression, level of experience, education, socio-economic status, nationality, personal appearance, race, religion, or sexual identity and orientation.
We hope to host an event in which differing and diverse experiences and viewpoints are taken into account equally, and without judgement from other participants.
Sharing content in this event can only be done with the specific consent of the person who wrote/created the given content.

Examples of behavior that contributes to creating a positive environment include:

- Being welcoming and respectful/considerate of others
- Being respectful of differing viewpoints and experiences
- Gracefully accepting constructive criticism
- Showing empathy towards other community members
- Add trigger-warnings if your contribution includes personal stories about e.g., (power) abuse. Be mindful that your stories affect others around you.

Examples of avoidable behavior:

- Ironic and sarcastic comments as well as non-obvious jokes
- Use of UAs (unnecessary abbreviations :D)

Examples of unacceptable behavior by participants include:

- The use of sexualized language or imagery and unwelcome sexual attention or advances
- Trolling, insulting/derogatory comments, and personal or political attacks
- Public or private harassment
- Publishing others' private information, such as a physical or electronic address, without explicit permission
- Other conduct which could reasonably be considered inappropriate in a professional setting

The organizers are responsible for clarifying the standards of acceptable behavior and are expected to take appropriate and fair corrective action in response to any instances of unacceptable behavior.

Organizers have the right and responsibility to remove participants that are not aligned to this Code of Conduct, or to ban temporarily or permanently any participant for other behaviors that they deem inappropriate, threatening, offensive, or harmful.

Scope: This Code of Conduct applies during the BIH symposium 2023 and subsequent resource creation process, and within all project spaces and formats (scientific talks, unconference, workshop, poster sessions, BIH success stories).

Instances of abusive, harassing, or otherwise unacceptable behavior may be reported by contacting the organizer-team at bih-symposium@bih-charite.de. All complaints will be reviewed and will result in a response that is deemed necessary and appropriate to the circumstances. The organizers are obligated to maintain confidentiality with regard to the reporter of an incident. Further details of specific enforcement policies may be posted separately.

This Code of Conduct is adapted from the Contributor Covenant, version 1.4, available at https://www.contributor-covenant.org/version/1/4/code-of-conduct.html

Floorplan GINN Hotel