BIH Berlin Institute of Health at Charité



Beyond Boundaries:
The Impact of Collaboration
BIH Scientific Symposium 2026

Digital Booklet

Table of Content

Welcome Message....3
Scientific Program....4
Abstracts – Scientific Contributed Talks....9
Poster Presentations – Titles and Presenters....13
1) Core Units....13
2) Business Divisions & Staff offices....14
3) Molecular and Genomic Mechanisms for Disease....14
4) Regenerative Medicine and Cell-Based Therapies....16
5) Data Science, AI, and Health Informatics Infrastructure....17
6) Precision Diagnostics and Therapeutic Platforms....18
Workshops....20
Panel Discussion....23
Code of Conduct....25
Floorplan – Langenbeck-Virchow Haus....28

Dear BIH Colleagues,

We are thrilled to extend a warm welcome to all members of the Berlin Institute of Health (BIH) at Charité for our internal scientific symposium with the title "Beyond Boundaries: The Impact of Collaboration".

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.

For today, we have a rich program featuring engaging talks, fascinating workshops, 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) at Charité

* Siddharth Annaldasula | Aybuge Altay | Stephania Contreras Castillo | Maria Luisa da Costa Zemsch Patricia Ebel | Luke Flanagan | Raphaela Fritsche | Jennifer Gansau | Aleksandra Laski | Claudia Marti Gifrol | Anika Neuschulz | Max Schubach | Francesca Tiso | Sven Olaf Twardziok

Wi-Fi: LVH Gäste

Password: LVH2004!

Scientific Program

08:00 am - 09:00 am	
Registration (badge pick-up) with Networking coffee	
09:00 am - 09:15 am	
Welcome Session *Chair: Max Schubach & Aybuge Altay* Introduction to the Symposium (by Organizing Committee, with PhD Net) Words of Welcome by Christopher Baum	**Lecture Hall**
Transition Time	
09:20 am - 10:05 am	
Scientific Session I **"Decoding Tumor Ecosystems and Disease Heterogeneity"** *Chair: Francesca Tiso* 1. Gräßle, S. - *"Decoding the cellular ecosystem of uveal melanoma"* 2. Jiang, Y. – *"Multi-omics mapping reveals a stromally organized immune-exhaustion ecosystem in checkpoint blockade-resistant bladder cancer"* 3. Cen, X. - *"CT-based deep embeddings Refined Patient Subtypes with Prognostic Implication of Gastric Cancer in Real-World Datasets"*	**Lecture Hall**
Workshop 1 *With: Foo Wei, Martin Braun und Jacques Ehret* *AI infrastructure at Charité/BIH: What do we have and what can we do?*	**Bernhard von Langenbeck** 1st floor
Workshop 2 *With: Peter Brunecker & Jennifer Hoos, Raphaela Fritsche, Izabela Plumbom* *Core Units*	**Rudolf Virchow** 2nd floor

Transition Time	

10:10 am - 10:40 am	
Poster Teaser Session I (20 minutes - 20 posters) *Chair: Anika Neuschulz* **Introduction Art Installation** "My Virtual Dream" - A collective, interactive multimedia installation	**Lecture Hall**
10:40 am - 11:45 am	
Poster Session I Ground floor: Core Units, Business Divisions & Staff offices 1st Floor: MG-1, MG-3, MG-5, MG-7, MG-9, MG-11, RM-1, RM-3, RM-5, RM-7, RM-9 2nd Floor: DS-2, DS-3, DS-5- DS-7, DS-9, DS-11, DS-13, PD-1, PD-3 **(with coffee break)**	**Foyer** - ground floor & 2nd floor **Wandelhalle** - 1st floor **Expertisium** - ground floor
11:45 am - 12:30 pm	
Scientific Session II **"Advanced Methodologies for Genomic and Cellular Analysis"** *Chair: Max Schubach* 1. Salomon, K. - *"Massively parallel characterization and predictive modelling of neuronal regulatory variation"* 2. Salla, M. - *"Cryo-mtscATAC-seq for single-cell mitochondrial DNA genotyping and clonal tracing in archived human tissues"* 3. Minia, I. - *"UniCap-Seq: Universal capture of transgene insertion sites for diagnostic and research purposes"*	**Lecture Hall**
Workshop 3 *With: Tina Gundlach-Hauf* *Mentoring as a Leadership Experience –Shaping Your Role as a Young Researcher*	Bernhard von Langenbeck 1st floor
Workshop 4 *With: Karin Höhne, Raphaela Fritsche, Cyril Chéret* *Mental Health @ BIH – a panel discussion*	**Rudolf Virchow** 2nd floor

12:30 pm – 02:00 pm	
Lunch Break	

02:00 pm – 02:45 pm	
Scientific Session III **"AI and Large-Scale Health Data: From Infrastructure to Clinical Application"** *Chair: Aybuge Altay* 1. Rinaldi, E. - *"Building Bridges Between Healthcare, Public Health and Research through the European Health Data Space"* 2. Zeng, W. - *"Genetic decoding reveals druggable biology implicitly learned by a medical-history foundation model"* 3. Do, M.D. - *"Modeling Multimodal 3D Brain MRI Interactions for Brain Age Prediction"*	**Lecture Hall**
Workshop 5 *With: Foo Wei Ten, Magnus Hagdorn, Sören Brinkmeier, Clemens Messerschmidt* *HPC Services at Charité/BIH*	**Bernhard von Langenbeck** 1st floor
Workshop 6 *With: Sven Friedl* *Charité BIH ARC Innovation Center (CBAIC): Impact, Not Theory – How Does My Research Make Its Way to the Patient's Bedside?*	Rudolf Virchow 2nd floor

Transition Time

02:50 pm – 03:25 pm	
Poster Teaser Session II (20 minutes – 20 posters) *Chair: Max Schubach* **BIH-Services – Speed Talks**	**Lecture Hall**

03:25 pm – 04:30 pm	
Poster Session II Ground floor: Core Units, Business Divisions & Staff offices 1st Floor: MG-2, MG-4, MG-6, MG-8, MG-10, MG-12, RM-2, RM-4, RM-6, RM-8 2nd Floor: DS-1, DS-4, DS-6, DS-8, DS-10, DS-12, DS-14, PD-2, PD-4, PD-5 **(with coffee break)**	**Foyer** - ground floor & 2nd floor **Wandelhalle** - 1st floor **Expertisium** - ground floor
04:30 pm – 05:15 pm	
Scientific Session IV **"Translational Approaches in Regeneration, Immunotherapy & Body Composition"** *Chair: Anika Neuschulz* 1. Lim, R. - *"Targeted epigenetic engineering programs precision regulatory T cell products with antigen specificity and lineage stability"* 2. Storbeck, M. - *"Metabolic regulation of fracture healing: The role of bone marrow adipose tissue"* 3. Williamson, A. - *"Genetic architecture of fat and lean mass across body compartments in men and women"*	**Lecture Hall**
04:30 pm – 05:15 pm	
Workshop 7 *With: Laura Keßler, Valerie Bürger, Jungyeon Jung* **Implementing Patient Engagement at BIH: What does the community need?**	**Bernhard von Langenbeck** 1st floor
Workshop 8 *With: Nathalie Huber, Iwan Meij* **Discover the BIH Biomedical Innovation Academy: Spotlights on Career Support Programs and Fellows**	**Rudolf Virchow** 2nd floor
Transition Time	

05:20 pm - 06:30 pm	
5:20 - 6:10	**Lecture Hall**
Panel Discussion *With: Christopher Baum, Avner Shahal, Louise Delwen Owen Franzen* *Moderation: Aleksandra Laski* **Embracing Failure — Rethinking Error Culture in Science**	
6:10 - 6:30	
Closing Session Announcement Poster Awards	
06:30 pm - 09:00 pm	
Networking Event	**Foyer** - ground floor
"My Virtual Dream" **A collective, interactive multimedia installation**	**Expertisium** - ground floor

Abstracts – Scientific Contributed Talks

Cen, Xiaoping; Eils, Roland — Session I

CT-based deep embeddings Refined Patient Subtypes with Prognostic Implication of Gastric Cancer in Real-World Datasets — 9:20 – 10:05

Do, Minh Duc; Rheude, Tillmann; Kronenberg, Noel; Wild, Benjamin; Eils, Roland — Session III

Modeling Multimodal 3D Brain MRI Interactions for Brain Age Prediction — 2:00 – 2:45

Introduction: Current neuroimaging AI models often process MRI modalities independently or use simple fusion strategies, limiting their ability to exploit complementary biological information.
Objective: We investigate whether explicit modeling of multimodal MRI interactions improves the extraction of disease-relevant signals and biological aging patterns.
Methods: We propose a Multimodal Intra- and Cross-Context Vision Transformer (MICViT) that integrates T1-weighted, T2/FLAIR, diffusion-weighted (DWI), and susceptibility-weighted (SWI) MRI. The model combines separated local and global attention with cross-local and cross-global attention, enabling structured intra- and inter-modality information exchange across multiple spatial scales. Evaluation was performed on the UK Biobank cohort (n=41,404) using brain age prediction.
Results: MICViT achieved an MAE (Mean Absolute Error) of 2.82 ± 0.08 years, outperforming GCViT (3.34 ± 0.08) and ConvNeXt (3.53 ± 0.04) ($p<0.05$). Multimodal models consistently exceeded single-modality performance, demonstrating the value of complementary imaging information.
Conclusion: Explicit multimodal interaction modeling substantially improves MRI-based brain age prediction and provides a promising framework for future neurodegenerative disease risk stratification.

Gräßle, Sarah; Steiert, Daniel; Peuker, Caroline; Haas, Simon — Session I

Decoding the cellular ecosystem of uveal melanoma — 9:20 – 10:05

Uveal melanoma is the most common primary intraocular malignancy. To investigate how radiotherapy shapes the tumor microenvironment, we integrated single-cell RNA sequencing, surface proteomics, immune receptor profiling, and spectral flowcytometry across 200 patient samples. We identified a genotype-specific response in BAP1-deficient tumours, characterised by enhanced DNA damage, ATM pathway activation, and a senescence-associated inflammatory program. Proteomic analyses confirmed induction of senescence and DNA damage response pathways after irradiation. This state activated the cGAS–STING–interferon axis and promoted inflammatory signalling. Irradiated BAP1-mutant tumours showed increased CXCL9/10 expression in myeloid cells, CXCR3 upregulation on T cells, and infiltration of clonally expanded exhausted $CD8^+$ T cells, consistent with bystander activation. Together, our findings demonstrate that radiotherapy reprograms the UM microenvironment in a genotype-dependent manner.

Jiang, Yiheng; Eils, Roland — Session I

Multi-omics mapping reveals a stromally organized immune-exhaustion ecosystem in checkpoint blockade-resistant bladder cancer — 9:20 – 10:05

Immune-checkpoint blockade (ICB) has transformed bladder cancer (BLCA) treatment, yet many immune-infiltrated tumors remain resistant. Here, we integrated proteomic, bulk transcriptomic, single-cell and spatial transcriptomic data to define stromal features underlying ineffective antitumor immunity. Immune and stromal signals resolved three reproducible immunophenotypes: immune-activated,

immune-exhausted and non-immune. The immune-exhausted phenotype was inflamed and checkpoint-rich, but showed stromal activation, immune-evasion features and reduced benefit from anti-PD-L1 therapy. Multi-omics analyses linked this state to TGF-ß, angiogenic and WNT signaling, and identified a conserved extracellular-matrix-remodeling program involving POSTN, COL1A1, FN1 and MMP2. Single-cell and spatial analyses localized this program to POSTN+CTHRC1+ myofibroblastic CAFs at tumor boundaries, where matrix remodeling compartmentalized malignant and immune-rich regions.

Lim, Ramonique; Au Yong, Audrey; Glaser, Viktor; Saggau, Carina; Reinke, Petra; Scheffold, Alexander; Issa, Fadi; Wagner, Dimitrios L.; Kressler, Christopher; Polansky, Julia K.

Session IV
4:30 – 5:15

Targeted epigenetic engineering programs precision regulatory T cell products with antigen specificity and lineage stability

Minia, Igor; Gaebler, Christian; Ibrahim, Daniel

Session II
11:45 – 12:30

UniCap-Seq: Universal capture of transgene insertion sites for diagnostic and research purposes

The rapid adoption of engineered cell products, including CAR-T cells and gene-edited therapies, has created a growing need for methods that simultaneously assess transgene integration sites, structural integrity, and clonal composition. Current approaches typically address only one of these parameters or rely on complex PCR-based workflows that introduce bias and limit scalability. Here, we present UniCap-Seq (Universal Capture Sequencing), a long-read sequencing approach that combines programmable target capture with Nanopore sequencing to simultaneously map integration sites, characterize transgene integrity, and estimate clonal abundance. The platform is adaptable to diverse integration systems, including lentiviral vectors, transposons, and targeted genome editing approaches. UniCap-Seq has been validated in an HIV reporter cell line and applied to a CD19 CAR-T cell product. Ongoing studies are extending the method to CRISPR/Cas9-edited cells and Sleeping Beauty transposon systems, establishing UniCap-Seq as a versatile tool for genomic safety assessment and gene therapy quality control.

Rinaldi Eugenia; Salgado, Eduardo; Thun, Sylvia

Session III
2:00 – 2:45

Building Bridges Between Healthcare, Public Health and Research through the European Health Data Space

The EHDS establishes a framework for both the primary and secondary use of health data. While these domains are governed by distinct processes, their effective interaction depends on the ability to exchange and interpret health information in a consistent and interoperable manner.
Within the European project xShare, the BIH/Charité team collaborates with public health authorities, standards organisations, healthcare providers, and research institutions across Europe to harmonise health datasets and support the reuse of health data for public health and research. Particular focus is placed on cancer surveillance, antimicrobial resistance, and healthcare-associated infections.
By combining expertise in digital medicine, clinical research, public health, and interoperability, the project contributes to the adoption of HL7 FHIR, SNOMED CT, and LOINC and supports the development of the European Electronic Health Record Exchange Format. The work demonstrates how collaboration across disciplines, organisations, and countries is essential for building interoperable and reusable European health data ecosystems.

Salla, Maren; Obermayer, Benedikt; Cotta, Marie; Friebel, Ekaterina; Beule,Dieter; Radbruch, Helena; Capper, David; Heppner, Frank; Liu, Ilon; Ludwig, Leif S.

Session II
11:45 – 12:30

Cryo-mtscATAC-seq for single-cell mitochondrial DNA genotyping and clonal tracing in archived human tissues

High-throughput clonal tracing of primary human samples relies on naturally occurring barcodes, such as somatic mitochondrial DNA (mtDNA) mutations detected via single-cell ATAC-seq (mtscATAC-seq). Fresh-frozen clinical specimens preserve tissue architecture but compromise cell integrity, thereby precluding their use in multiomic approaches such as mitochondrial genotyping at single-cell resolution. Here, we introduce Cryo-mtscATAC-seq, a broadly applicable method for diverse pathophysiological contexts to isolate nuclei with their associated mitochondria ("CryoCells") from frozen samples for high-throughput clonal analysis. We applied Cryo-mtscATAC-seq to the neurodegenerated human brain, glioblastoma (GBM), pediatric neuroblastoma, and human aorta, and implemented mitobender, a computational tool to reduce ambient mtDNA in single-cell assays. Our approach revealed regional clonal gliogenesis and microglial expansions in amyotrophic lateral sclerosis (ALS), persistence of oligodendrocyte progenitor cell (OPC)-like clones in GBM recurrence, mtDNA depth heterogeneity after neuroblastoma chemotherapy, and oligoclonal proliferation of smooth muscle cells in human aorta. In conclusion, Cryo-mtscATAC-seq broadly extends mtDNA genotyping to archival frozen specimens across tissue types, opening new avenues for investigation of cell state-informed clonality in human health and disease.

Salomon, Kilian; Schubach Max; Kircher, Martin

Session II
11:45 – 12:30

Massively parallel characterization and predictive modelling of neuronal regulatory variation

Most disease-linked genetic variants lie outside genes, in DNA that regulates when and how much genes are transcribed. We tested thousands of candidate regulatory regions and tens of thousands of variants located within them in humans, measuring their effect on transcription in neurons. Regions with measurable effects on transcription not previously known to be active in brain tissue showed mostly weaker-than-random activity, suggesting that these predominantly reduce transcription in neurons. For individual variants, significant effects were observed at similar rates across the allele frequency (AF) range. Detectability of variant effects depended more on regional activity than on AF. Models predicting variant effects trained on our experimental data outperformed general-purpose models, while those based on chromatin accessibility performed well only within open regions. Together, these findings show that existing regulatory annotations and variant frequency alone cannot reliably identify high-impact variation, underscoring the value of experimental testing.

Storbeck, Mareen; Schmidt-Bleek, Katharina

Session IV
4:30 – 5:15

Metabolic regulation of fracture healing: The role of bone marrow adipose tissue

Delayed fracture healing increases in metabolic disorders like obesity, characterized by chronic low-grade inflammation, reduced adiponectin signalling, and expansion of bone marrow adipose tissue (BMAT). Although BMAT can occupy up to 70% of the marrow cavity in adult long bones, its role in fracture healing remains largely unexplored. This study investigates how BMAT and adiponectin signalling influence bone regeneration under different metabolic conditions.
Female mice were fed a high-fat diet for eight weeks before femoral osteotomy, with subgroups receiving AdipoRon, an adiponectin receptor agonist, during two weeks of healing. Bone formation, lipid profiles, and immune populations were assessed through interdisciplinary collaborations.

Obese mice showed increased BMAT, reduced bone formation, altered lipid profiles, and immune cell shifts. AdipoRon restored bone regeneration without altering BMAT volume, suggesting BMAT expansion is not the primary driver of impaired healing. Reduction of pro-inflammatory immune populations points to immunomodulation as the more decisive mechanism.

Williamson, Alice; Langenberg, Claudia

Session IV
4:30 – 5:15

Genetic architecture of fat and lean mass across body compartments in men and women

Adiposity and fat distribution both contribute to the development of diverse diseases and understanding their genetic architecture can identify the mechanisms linking different body sizes and types to disease risk.
Here, we lead a collaboration of researchers from 9 international institutions to study genetic variation underlying segmental fat and lean mass across body compartments using whole-body dual X-ray absorptiometry (DEXA) scans.
We identify 679 independent genetic signals at p<5x10-8 in genome-wide meta-analyses of up to 74,554 individuals, ~50% of which were specific to fat distribution, i.e. independent of overall body size. Systematic molecular and clinical follow up provided insights into candidate novel genes and pathways contributing to both differences in body composition and disease risk.
This is the first large-scale study to identify the complex genetic architecture of both fat and lean mass distribution across the rare and common allelic spectrum. This study demonstrates the value in going beyond simple measures to investigate the genetic mechanisms influencing body composition.

Zeng, Wenhuan; Kohleick, Leonhard; Zoodsma Martijn; Wild, Benjamin; Langenberg, Claudia; Pietzner, Maik

Session III
2:00 – 2:45

Genetic decoding reveals druggable biology implicitly learned by a medical-history foundation model

Individual health trajectories and lifetime morbidity are likely influenced by genetic factors beyond disease-specific susceptibility but remain difficult to study through traditional GWAS. Deep learning models using transformer architectures can predict health trajectories from electronic health records but lack interpretability and biological grounding. Here, we reimplemented the GPT-2-based Delphi-2M model in 501,939 UK Biobank participants to generate 120 individual-level embeddings representing diagnosis-based health trajectories. Phenome-wide analyses across >1,800 traits revealed that embeddings captured disease domains and implicitly encoded risk factors, including body composition, deprivation, biomarkers, and genetically inferred ancestry. GWAS in 441,189 European individuals revealed modest but significant SNP heritability across embeddings. Fine-mapping identified 434 genome-wide significant variant–embedding associations across 151 loci and 98 embeddings, with pleiotropic signals implicating cholesterol metabolism and immune regulation. Most loci overlapped GWAS Catalog findings, with strong enrichment for asthma, lipids, education, and BMI. These results demonstrate genetics as an orthogonal approach for interpreting clinically relevant deep learning models.

Poster Presentations – Titles and Presenters

1) Core Units

Foyer, ground floor

Title, Author	Poster #
Biobank	
How the central biobank (ZeBanC) can support translational research Merz, Myriam	CU - 5
Core Unit Bioinformatics (CUBI)	
Supporting researchers with bioinformatics and data analysis expertise: Scientific Services, Standardized Processing & User Empowerment	CU - 8
Core Unit pluripotent Stem Cells and Organoids (CUSCO)	
Enabling Robust Human hiPSC and Organoid Models for Translational Research Vallone, Valeria	CU - 3
Genomics	
Genomics Platform: Expertise. Technology. Solutions.	CU - 9
Cytometry	
Flow & Mass Cytometry - BIH Cytometry Core Facility Kunkel, Desiree	CU - 6
Imaging Mass Spectrometry	
Accelerating the translation of molecular insights into clinically relevant diagnostic and therapeutic assay	CU - 7
Metabolomics	
From Experimental Design to Data Interpretation: Metabolomics Services for Researchers Fritsche, Raphaela	CU - 4
Proteomics	
Advanced Proteomics for Biomarker and Therapeutic Target Discovery	CU - 10
Research IT	
Data Integration Center and Health Data Platform: Scalable Research Data Services for the Charité and BIH Ecosystem Hoos, Jennifer	CU - 1
Research IT	
Data Integration Center and Health Data Platform: Scalable Research Data Services for the Charité and BIH Ecosystem Seidel, Florian	CU - 2

2) Business Divisions & Staff offices

Expertisium, ground floor

	Poster #
Communication Head: Pflüger, Konstanze	CM - 5
Team Legal & Compliance Team Lead: Zimmer, Jens	CM - 6
Team Personnel Team lead: Hoppe, Melanie	CM - 8
Regulatory Affairs Head: Conrad, Christoph	CM - 9
Strategic Science Management Heads: Haubold, Kathrin, Weber, Joachim	CM – 7
National Strategy GCT & Berlin Center for Gene and Cell Therapies Gallus, Christian	CM - 4
Building National Infrastructures for Rare Diseases to Advance Research and Patient Care Hartung, Mara	CM - 3
Berlin Long-term Observation of Vascular Events (BeLOVE) as a Research Platform for Cardiovascular Disease: Longitudinal Data, Biosamples, and Multi-Omics for the Scientific Community Rohrpasser-Napierkowski, Ira	CM – 2
Medical Computational Research Environment From Secure Data Access to Scientific Impact: MediCoRE and the EHDS Schönrath, Katharina	CM - 1

3) Molecular and Genomic Mechanisms for Disease

Wadelhalle, 1st floor

Author, Title	Poster #
Braun, Julian; Kaeferstein, Isabel; Pohlmann-Krappitz, Dominika; Winterhalter, Sibylle, Thiel, Andreas **T-cell-mediated autoimmunity in Birdshot Uveitis**	MG – 10 Afternoon
Brumhard, Sophia; Hiller, Anna, Sander, Leif **Comparative analysis of innate immune responses to COVID-19 vaccine platforms and their relevance for T cell activation**	MG – 11 Morning

Castro, Marco; Potente, Michael **Modelling Cerebral Cavernous Malformations using human iPSC-derived vascular organoids**	MG – 4 Afternoon
Cotta, Marie **Deciphering neuroblastoma heterogeneity via single-cell epigenomics**	MG – 6 Afternoon
Grammatikaki, Aliki; Beule, Dieter **NB single cell heterogeneity emerges as a combination of embryonic and cancer programs shaped by CNAs**	MG -2 Afternoon
Huang, Kaixin; Ishaque, Naveed **Subclonal chromosomal alterations and the spatial-functional architecture of IDH-wildtype glioblastoma**	MG – 5 Morning
Keukeleire, Pia; Kircher, Martin **Capture-C MPRA: A high-throughput method to simultaneously characterize promoter interactions and regulatory activity**	MG – 9 Morning
Nagar, Ritika; Hitzler, Sebastian; Losch, Lea; Wulsten, Dag; Bader, Jakob; Duda, Georg; Jahn, Denise **Three-Point Bending as a Reliable and Efficient Method for Biomechanical Assessment of Mouse Femurs**	MG – 7 Morning
Özerdem, Ceren; Haas, Simon **Deciphering and targeting the principles of neuroblastoma metastasis to the bone marrow**	MG – 8 Afternoon
Pappritz, Kathleen; Tschöpe, Carsten; Knöll, Ralph; Van Linthout, Sophie **Permanent phosphorylation of the sarcomeric myosin light chain 2 drives sarcomere-dependent myocardial remodeling and innate immune activation**	MG – 12 Afternoon
Suresh, Athira; Zhang, Yang; Benjanin, Bella; Yu, Kunyuan; Hass, Simon; Potente, Michael **Endothelial FOXO signaling governs bone marrow niche homeostasis**	MG – 1 Morning
Uluvar, Burulca; Pietzner, Maik **A proteogenomic framework defines the pharmacogenomics and long-term safety of proton pump inhibitors**	MG – 3 Morning

4) Regenerative Medicine and Cell-Based Therapies

Wadelhalle, 1st floor

Author, Title	Poster #
Brinster, Sophia; Schmieder, Karen; Oktay, Zeynep; Iwert, Christina; Duda, Georg; Wolf, Jana; Sawitzki, Birgit **How aging rewires danger sensing in the immune system**	RM – 1 Morning
Condric, Antonela; Losch, Lea; Rahmani, Adibeh; Fuchs, Melanie; Jahn, Denise **Characterization of circadian rhythms in murine bone**	RM – 5 Morning
Herzberg, Charlotte; Na, Il-Kang **Restoring T-Cell Fitness for Improved CAR T Therapies**	RM – 3 Morning
Liabeuf, Dylan; Conrad, Liam; Behncke, Rose Yinghan; Wang, Haoxin; Haep, Nils; Sauer, Igor Maximilian; Hägerling, René; Ishaque, Naveed; Vallier, Ludovic **From Regenerative Niches to Organ Reconstruction: A Multi-Scale Framework for Human Liver Regeneration**	RM – 9 Morning
Meß, Ann-Kathrin; Schmidt-Bleek, Katharina **Regulatory T cells and the bone - lymph node axis in fracture repair**	RM – 2 Afternoon
Peitsch, Cornelia; Textor, Martin; Yang, Mingxing; Lauterbach, Luis; Lugo, Shirley; Hamo, Dania; Geißler, Sven; Polansky, Julia **Improving the therapeutic potential of mesenchymal stromal cell products for bone regeneration using epigenetic editing**	RM – 8 Afternoon
Roussou, Efthalia; Benjanin, Bella; Özerdem, Ceren; Kazezian, Vartan; Bolander, Johanna; Haas, Simon **In Vitro Skeletal Progenitor Populations Enable Modeling of Cellular Interplay During Early Human Fracture Healing**	RM – 7 Morning
Schiele, Phillip; Na, Il-Kang **Epigenetic Engineering of Adoptive T-Cell Therapies to Overcome Tumor-Induced Dysfunction**	RM – 4 Afternoon
Zampeta, Kalliopi; Henze, Larissa; Thiel, Andreas; Loyal, Lucie **Detection of antigen-specific T cells with high avidity in melanoma**	RM – 6 Afternoon

5) Data Science, AI, and Health Informatics Infrastructure

Foyer, 2nd floor

Author, Title	Poster #
Flanagan, Luke; Roller, Roland; Poikela, Maija **Anonymization of free text and dialogue to enable data sharing**	DS – 6 Afternoon
Giguelay, Ambre; Nitsch, Lena; Kautz, Pauline; Liebold, Janet; Oevermann, Lena; Frick, Mareike; Damm, Frederik; Satpathy, Ansuman T.; Lareau, Caleb A.; Ludwig, Leif S. **Mitochondrial DNA mosaicism and clonality in human hematopoietic aging and regeneration**	DS – 10 Afternoon
Halilovic, Mehmed; Abu Attieh, Hammam; Prasser, Fabian **FLAME: Privacy-Preserving Federated Analytics for Collaborative Medical Research**	DS – 7 Morning
Herzler, Florian; Jabareen, Nabil; Lukassen, Sören; the FACE consortium **Balancing accuracy and data privacy in AI-based holter ECG analysis - the FACE project**	DS – 12 Afternoon
Jentsch, Marcel; Polemiti, Elli; Twarziok, Sven O. **CLUES A Comprehensive Workflow for Integrating Geospatial Data in Biomedical Research**	DS – 5 Morning
Johns, Marco; Prasser, Fabian **Charité Cohort Finder: A Digital Patient Search Engine for Study Planning and Feasibility**	DS – 1 Afternoon
Kranz, Dominik D.; Terziev, Robert; Łukomski, Michał; Krumm, Laura; Meisel, Christian **From Raw EEG to Clinical Answers: A Biosignal-Language Model for Routine EEG Interpretation**	DS – 3 Morning
Lindequist, Björn; Prasser, Fabian **PCOR-MII: Interoperable Integration of Patient-Reported Outcomes into the Data Infrastructure of University Medical Centers**	DS – 9 Morning
Schneider-Lunitz, Valentin; Kraatz, Landfried; Strubel, Philipp; Twardziok, Sven; Eils, Roland **WESkit: A de.NBI service for high-throughput workflow execution**	DS – 4 Afternoon

Heinig, Sharen Nicole; Rönnefarth, Maria; Ehret, Jacques; Ruhm, Loreen; Ten, Foo-Wie; Braun, Martin; Wagner, Harald; von Kalle, Christof; Rudolph, Stefanie; Nothacker, Johanna **CSC Trial Agent - From Idea to Data: An Agentic Architecture for the Clinical Trial Life Cycle**	DS – 8 Afternoon
Rotter Sophia; Tölch, Ulf **Preclinical Confirmatory Studies: An innovative approach to foster collaboration and enhance translation**	DS – 14 Afternoon
Steinhaus, Robin; Robinson, Peter N.; Seelow, Dominik **FABIAN-variant 2026: improved prediction of the effects of DNA variants on transcription factor binding**	DS – 13 Morning
Upmeier zu Belzen, Julius; Arnoldt, Lucas; Wild, Benjamin; Eils, Roland **An omnigenic interpretable neural network architecture for the human genome**	DS – 11 Morning
Yerunkar, Samruddhi; Strech, Daniel **A scalable semi-automated approach to assess terminated clinical trials: A meta-research study at university medical centres**	DS – 2 Morning

6) Precision Diagnostics and Therapeutic Platforms

Foyer, 2nd floor

Author, Title	Poster #
Augustin, Stine; Kreßler, Christopher; Finke, Marcel; Hamm, Frederik; Tasgin, Toros; Crooks, Gay; Notarangelo, Luigi; von Bernuth, Horst; Polansky, Julia; Dinges, Sarah **Artificial Thymic Organoids guide therapy decisions in inborn T-cell defects**	PD – 1 Morning
Föhr, Annika; Abdullaev, Eldar T.; Armann, Regine; Rosnev, Stanislav; Annaldasula, Siddharth; Knödler, Maren; Benary, Manuela; Kübler, Kirsten; **Sample-Level Tissue-of-Origin Inference for Cancers of Unknown Primary**	PD – 3 Morning
Hübner, Miriam; Thun, Sylvia **Achieving precision medicine by closing the gender data gap – development of gender-specific healthcare applications**	PD – 5 Afternoon
Mutithu, Daniel; Grzeski, Marta; Brüning, Ulrike; Trajkovski, Sarah; Elsayed, Hager; Steinfelder, Svenja; Klein, Oliver; Kirwan, Jennifer **Spatial localisation of metabolomics and lipidomics biomarkers across multiple organs using DESI and MALDI Imaging**	PD – 4 Afternoon

Simó Vesperinas, Inés; Haas, Simon

MHC-II-mediated CD4 T cell engagement overcomes the differentiation block in acute myeloid leukemia

PD – 2
Afternoon

Workshops

No.	Title & Abstract	Time & Room
1	**AI infrastructure at Charité/BIH: What do we have and what can we do?** *With: Foo Wei, Martin Braun und Jacques Ehret* This workshop will provide insights into selected AI-related infrastructures currently available at Charité and BIH, with a particular focus on local and secure LLM infrastructures, compute environments and tools that can support AI-driven research and innovation. Through illustrative use cases from research and clinical contexts, participants will explore how locally hosted LLMs can already be leveraged for data-driven and translational projects. The session will also open a discussion on future collaboration opportunities to further strengthen the AI ecosystem across Charité and BIH. Designed as an interactive exchange, the workshop invites participants to share ideas, discuss needs, and identify potential synergies and future directions together.	9:20 am – 10:05 am Bernhard von Langenbeck 1st floor
2	**Core Units** *With: Peter Brunecker & Jennifer Hoos, Raphaela Fritsche, Izabela Plumbom* This workshop will present talks from Core Units Genomics, Core Unit Metabolomics and Core Unit Research IT. Join this workshop to learn more about these Core Units as they present a talk about the work of the Core Unit and the services they offer. • Research IT: "CURIT - reinvent regularly" • Genomics: Current developments in Genomics • Metabolomics: "DESI metabolic imaging and more: Potential to bring metabolomics to the clinic"	9:20 am – 10:05 am Rudolf Virchow 2nd floor
3	**Mentoring as a Leadership Experience -Shaping Your Role as a Young Researcher** *With: Tina Gundlach-Hauf* This interactive workshop is designed for researchers who are gaining their first experience in guiding and supervising students and wish to actively shape their leadership role. We will discuss how to competently support others without losing focus of your own responsibilities. To this end, we will reflect on mentoring as a leadership process, communication and feedback in mentoring relationships, and fostering the mentees' independence. The goal is to develop a confident and reflective self-image that strengthens your own position while simultaneously creating a supportive learning environment for others.	11:45 am – 12:30 pm Bernhard von Langenbeck 1st floor
4	**Mental Health @ BIH - a panel discussion** *With: Karin Höhne, Raphaela Fritsche, Cyril Chéret* The "Embrace Diversity" survey last year showed, that more than half of BIH employees experienced mental health struggles or	11:45 am – 12:30 pm Rudolf Virchow 2nd floor

suffered from depression or anxiety symptoms at some point in their training.
At the very start of 2026, BIH partnered with Dragonfly Mental Health, a nonprofit organization dedicated to cultivating excellent mental health among academics worldwide. Together we formed a Mental Health Culture Committee at BIH, composed of representatives from different status groups and from diverse work areas. One goal of our work is to increase Mental Health Literacy among BIH members and raise awareness for the topic.
With the panel discussion at the BIH symsposium with scientists at different career stages we would like to openly address some of the mental health struggles in an academic career and invite the participants to share their perspectives and discuss approaches how to better support each other at the BIH.

5 **HPC Services at Charité & BIH**

2:00 pm – 2:45 pm

Bernhard von Langenbeck

1st floor

With: Foo Wei Ten, Magnus Hagdorn, Sören Brinkmeier, Clemens Messerschmidt

Have you ever wanted a way to perform data analyses but didn't have the tools to do it? Maybe you needed a more powerful computer, more storage, or access to software or pipelines you can't set-up. High-performance computing (HPC) resources are a potential solution for you. There are three HPC resources within Charité and BIH, from the GB IT Scientific Computing; CUBI (Core Unit Bioinformatics), and AG Eils' Cloud & IT teams. Join this workshop to learn more about each of these resources, how they might be useful for you, and how to apply for access. There will be Q&A for you to talk directly with the HPC service providers about your needs.

6 **Charité BIH ARC Innovation Center (CBAIC): Impact, Not Theory - How Does My Research Make Its Way to the Patient's Bedside?**

2:00 pm – 2:45 pm

Rudolf Virchow

2nd floor

With: Sven Friedl

The Charité BIH ARC Innovation Center (CBAIC) is the new central point of contact for all employees who want to translate their research into practical applications. To this end, we bring together research, clinical practice, and external partners to systematically shorten the path from idea to clinical implementation.
In this 45-minute interactive workshop, we'll present the CBAIC's services, but above all, we want to spark a conversation. Participants are invited to bring their questions about intellectual property (IP), technology transfer, and clinical innovations, such as:

- Who owns my idea?
- Science or commercialization—do I have to choose?
- Is my research actually ready for commercialization? Who can help me with this?
- Technology transfer: Career killer or career booster?
- Technology transfer is such a luxury! — When am I supposed to find the time for that?

The workshop offers insight into the structured innovation ecosystem at Charité and BIH and highlights key points of contact, people to reach out to, and support services.

7 **Implementing Patient Engagement at BIH: What does the community need?**

4:30 pm – 5:15 pm

Bernhard von Langenbeck

1st floor

With: Laura Keßler, Valerie Bürger, Jungyeon Jung

Patient and stakeholder engagement (PSE) is gaining increasing importance in research, but how can it be successfully implemented in practice at BIH? This workshop offers a compact introduction to PSE, followed by an interactive exchange with participants to identify the community's actual needs and how existing resources can be integrated for full impact.

After a short input presentation, participants work in small groups on three key questions: What do institutions need in order to successfully implement PSE? How can existing resources and initiatives for patients and patient representatives be reused and implemented across BIH, and how can researchers and patient representatives find each other? Results are shared and discussed in a joint plenary session, with a focus on concrete next steps for advancing the implementation of PSE at BIH. Whether you are just starting to think about PSE or already have experience with it, this workshop is a chance to help shape how patient engagement moves forward at BIH: Bring your questions, ideas, and needs!

Format: Short input talk, small-group work, plenary discussion
Target audience: All staff and stakeholders interested in strengthening patient engagement at BIH - researchers, science support, administration, and beyond.

8 **Discover the BIH Biomedical Innovation Academy: Spotlights on Career Support Programs and Fellows**

4:30 pm – 5:15 pm

Rudolf Virchow

2nd floor

With: Nathalie Huber, Iwan Meij

The BIH Biomedical Innovation Academy (BIA) supports early-career researchers through a range of career development programs for Clinician Scientists, Medical Scientists, and other emerging translational researchers. But who are the young career researchers benefiting from these programs, and what research projects are they pursuing? This session offers a great opportunity to discover the breadth of research conducted by fellows across BIA's different funding programs. Following a brief introduction to the BIA portfolio and its career support opportunities, fellows from various career stages and different funding lines will present their research, providing insights into both their scientific work and their experiences within the BIA programs. Whether you are a student exploring research careers, an early-career researcher looking for funding opportunities, or simply interested in cutting-edge translational research, this session provides an excellent opportunity to learn about the BIA community, exchange ideas, and connect with researchers from different career stages across BIH.

Panel Discussion

5:20 pm – 6:30 pm

Lecture Hall

Embracing Failure — Rethinking Error Culture in Science

With: Christopher Baum, Avner Shahal, Louise Delwen Owen Franzen

Moderation: Aleksandra Laski

Every researcher and entrepreneur has experienced it: an experiment that failed, a rejected grant, a project that led nowhere, a product that found no market, or a decision that proved wrong. Yet in academia and entrepreneurship, failure and mistakes are rarely discussed openly — they can feel like a career risk, a threat to credibility, or evidence of poor judgment.

How we deal with mistakes is also shaped by institutional and organizational culture. How should supervisors and founders respond to errors by employees, doctoral researchers and team members? How fair are peer review, funding and hiring processes — and what happens when these forms of evaluation fail? How can teams distinguish between responsible experimentation, avoidable mistakes and systemic failures? And how can institutions create a culture in which setbacks are acknowledged, discussed and used for learning rather than hidden?

This panel brings together BIH colleagues from academia and entrepreneurship to reflect on personal experiences and explore how failure can be addressed more openly, fairly and constructively — at the individual, team and institutional levels.

My Virtual Dream

An immersive neurofeedback performance

- What if your brain could become part of the evening's performance? -

My Virtual Dream (MVD) is a collective, interactive multimedia installation at the intersection of neuroscience, brain simulation, art, and technology. Four participants, the *dreamers*, wear wireless EEG headsets while entering their personalized dream world. Their brain activity is continuously translated into evolving dreams in real time.

MVD is linked to The Virtual Brain (TVB), an open-source platform for full-brain simulation. It uses real-time brain-computer interface and neurofeedback, specifically it uses EEG frequency-band relationships to estimate the dreamers' state at any given moment: the theta/alpha and beta/alpha ratio are used as a proxy for weather the dreamers are relaxed or focused. These signals are translated into the behavior of each dreamer's avatar and into the audiovisual environment.

However, this is not simply individual neurofeedback. Dreamers influence one another. Their combined brain states determine which of the possible dream scenes unfold, while their brain activity is influenced by external stimuli. The result is a closed-loop system in which brain activity shapes the environment, the environment feeds back into the participants, and the collective state of the group helps determine what happens next. No two dreams are quite the same.

Step into the experiment with an open mind and discover what happens when the brain becomes both the dreamer and the interface.

An interactive multimedia installation by
Jay Palmer, Prof. Dr. Petra Ritter, and the team of
the Brain Simulation Section



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 2026 welcoming, safe, and equitable for all. We are committed to fostering an environment that respects and promotes the dignity, rights, and contributions of all individuals, regardless of characteristics including age, personal appearance, visible or invisible disability, ethnicity, sex or gender, gender identity and expression, sexual identity and orientation, level of experience, education, socio-economic status, race, caste, color, neurodiversity, language, philosophy or religion, nationality, national or social origin or other status.

The same privileges of participation are extended to everyone who participates in good faith and in accordance with this Covenant.

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.

Encouraged Behaviors

While acknowledging differences in social norms, we all strive to meet our community's expectations for positive behavior. We also understand that our words and actions may be interpreted differently than we intend based on culture, background, or native language.

With these considerations in mind, we agree to behave mindfully toward each other and act in ways that center our shared values, including:

1. Respecting the purpose of our community, our activities, and our ways of gathering
2. Engaging kindly and honestly with others
3. Respecting different viewpoints and experiences
4. Taking responsibility for our actions and contributions
5. Gracefully giving and accepting constructive feedback
6. Committing to repairing harm when it occurs
7. Behaving in other ways that promote and sustain the well-being of our community

Specific examples include:

- Being welcoming and respectful/considerate of others
- Gracefully accepting constructive criticism
- Showing empathy towards other community members
- Adding trigger warnings if your contribution includes personal stories about e.g., (power) abuse, being 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)

Restricted Behaviors

We agree to restrict the following behaviors in our community. Instances, threats, and promotion of these behaviors are violations of this Code of Conduct:

1. **Harassment and discrimination.** Ignoring expressed boundaries, unwanted personal attention, or characterizing anyone based on immutable traits — including insulting or demeaning comments about a person or group.
2. **Sexualization.** Intimacy that is inappropriate for the context of our community.
3. **Endangerment.** Causing, encouraging, or threatening violence or other harm.
4. **Violating privacy.** Sharing someone's personal information without their permission.
5. **Misconduct.** Impersonating others (including to evade enforcement), failing to credit sources, promoting commercial content outside community norms, or irresponsibly sharing content that depicts or describes the above behaviors.

Reporting an Issue

Tensions can occur between community members even when they are trying their best to collaborate. Not every conflict represents a code of conduct violation, and this Code of Conduct reinforces encouraged behaviors and norms that can help avoid conflicts and minimize harm.

When an incident does occur, it is important to report it promptly. To report a possible violation, contact the organizer team at bih-symposium@bih-charite.de. All complaints will be reviewed and investigated, 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.



In addition, **First Contact Points (FCPs)** will be present at the event. If a concrete situation arises during the event where there is a need to talk, you are welcome to approach them at any time. The FCPs can be identified by their buttons.

An overview of all FCP contact addresses is available in the BIH intranet:

https://www.bihealth.org/de/ueber/werte/gutes-miteinander/fcp

Addressing and Repairing Harm

Organizers have the right and responsibility to remove, edit, or reject comments, contributions, and other content that are not aligned to this Code of Conduct, and will communicate reasons for moderation decisions when appropriate.

Scope

This Code of Conduct applies during the BIH Symposium 2026 and subsequent resource creation process, and within all project spaces and formats (scientific talks, unconference, workshop, poster sessions, BIH success stories).

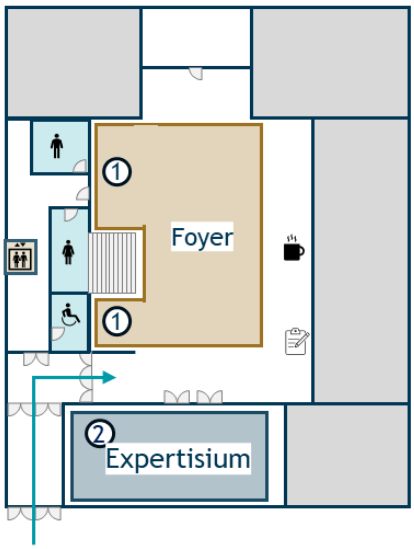
Organizers may take appropriate and fair corrective action in response to any instances of unacceptable behavior, including removing participants that are not aligned to this Code of Conduct, or to ban temporarily or permanently any participant for behaviors deemed inappropriate, threatening, offensive, or harmful. This enforcement framework is intended as a guideline and does not limit the ability of organizers to use their discretion and judgment, in keeping with the best interests of our community.

Further details of specific enforcement policies may be posted separately.

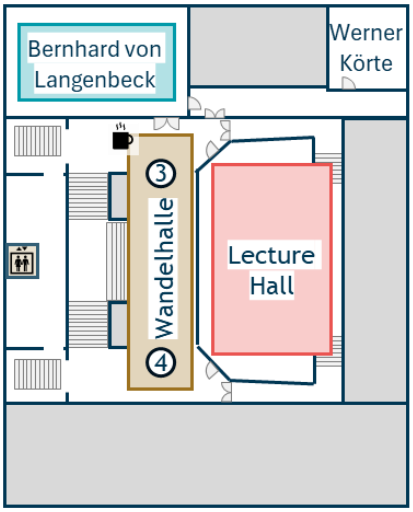
This Code of Conduct is adapted from the **Contributor Covenant,** version 3.0, permanently available at https://www.contributor-covenant.org/version/3/0/code_of_conduct/

Floorplan - Langenbeck-Virchow Haus

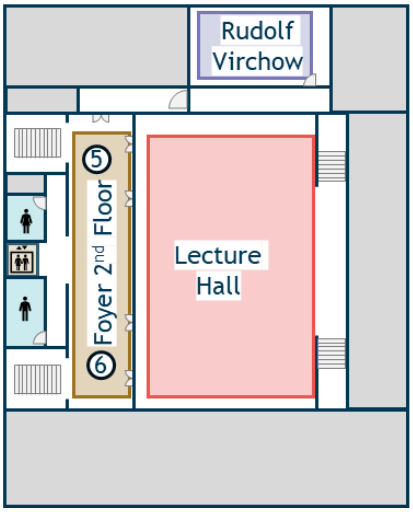
Ground Floor



1st Floor



2nd Floor



Ground Floor

Registration

Foyer	Poster session ① Core Units
Expertisium	Poster session ② Business Divisions & Staff offices

1st Floor

Lecture Hall	Scientific Sessions I - IV Poster Teaser I & II Overview Core Units Highlight Session
Wandelhalle	Poster session ③ Molecular and Genomic Mechanisms for Disease ④ Regenerative Medicine and Cell-Based Therapies
Bernhard von Langenbeck	Workshop 1 Workshop 3 Workshop 5 Workshop 7

2nd Floor

Lecture Hall	Scientific Sessions I - IV Poster Teaser I & II Overview Core Units Highlight Session
Foyer 2nd Floor	Poster session ⑤ Data Science, AI, and Health Informatics Infrastructure ⑥ Precision Diagnostics and Therapeutic Platforms
Rudolf Virchow	Workshop 2 Workshop 4 Workshop 6 Workshop 8

Registration	Ground Floor	Elevator
Coffee	Ground Floor 1st Floor	
Toilets	Ground Floor 2nd Floor	