Recent technological breakthroughs in high throughput biological profiling methods have been the driving force behind advances in precision and personalized medicine. In particular, we have seen the success adoption of genome, transcriptome and epigenome profiling for diagnosis, predictive outcomes, and therapy recommendations for disease. However, multi-faceted heterogeneity represents a major challenge – disease, patient and sample heterogeneity introduce additional complexity in unraveling the molecular determinants of health and disease.

To successfully implement efficient pipelines and workflows for precision medicine, there is also a need for advancing data automation and integration, computational infrastructure, personalized model systems, and applications of artificial intelligence and machine learning.

In this talk I will present some of our recent efforts to unravel heterogeneity in human disease and a general overview how the newly established Digital Health Centre at the Berlin Institute of Health and Charite University Hospital is contributing to the effort of advancing the field of precision medicine. Specific topics covered will include low cost tumor diagnostics using DNA sequence and methylation data, implications of tumor evolution on precision medicine, analysis of in-situ transcriptomics data, and drug screening in ex-vivo models.