

## NITheCS COLLOQUIUM: Multi-Omics and Spatial Single Cell Methods for Precision Medicine of Blood Cancers

Dr Wolfgang Huber (European Molecular Biology Laboratory, Germany)

Monday, 24 April 2023 | 16h00 – 17h00 SAST

Attend online

### ABSTRACT

While the arsenal of anti-tumour therapies is expanding, responses to therapy can vary highly from patient to patient. Our research aims at contributing to prediction of response for optimal therapy selection, as well as at molecular understanding of resistances, for possible exploitation in improving treatments e.g. by combination.

To this end, we employ systematic multi-omics characterisation of large patient-derived lymphoid tumour cohorts, ex-vivo drug response assays, laboratory models of microenvironmental interactions at different levels of complexity, single-cell sequencing of transcriptomes, and spatial single cell omics of tumours in their native lymph node microenvironment. We use various statistical approaches of multi-omics data integration, including multi-omics factor analysis (MOFA), to discover prognostic markers suitable for follow-up clinical study, and mechanistic hypotheses suitable for molecular biological follow-up. I will report on recent examples in CLL and B-NHL, which exemplify feasibility and success of the approach.

### BIOGRAPHY

Dr Wolfgang Huber received a PhD in Statistical Physics in 1998 from the University of Freiburg, Germany. He then conducted postdoctoral research at the IBM Almaden Research Center in San Jose, USA, and at the German Cancer Research Centre (DKFZ) in Heidelberg, Germany.

From 2004 to 2009, he served as research group leader at the European Bioinformatics Institute (EBI) of the European Molecular Biology Laboratory (EMBL) in Cambridge, UK. In 2009, he was appointed research group leader at EMBL's laboratories in Heidelberg. Since 2011, he has been an EMBL Senior Scientist.

Dr Huber is a co-director of the Molecular Medicine Partnership Unit, a joint venture between EMBL and the Faculty of Medicine of the University Hospital in Heidelberg. He also co-chairs the EMBL's Transversal Theme in Theory. He is a co-founder of the Bioconductor Project, a large international collaboration on open-source software for computational biology.

With Susan Holmes, he co-authored the textbook, '*Modern Statistics for Modern Biology*'.



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