

THE GIS

Andrew Teschendorff is currently a Principal Investigator at the Shanghai Institute of Nutrition and Health, part of the Chinese Academy of Sciences, leading a lab in Computational Systems Epigenomics, with a research focus on aging and cancer-risk. He trained as a Mathematical Physicist at the University of Edinburgh (1990-1995) and Cambridge University (1996-2000) where he obtained his PhD. From 2003 to 2008 he held Cambridge-MIT and Isaac Newton Fellowships to conduct research in Statistical Cancer Genomics at the University of Cambridge. From 2008 to 2013 he held the Heller Research Fellowship at the UCL Cancer Institute in London. In 2013 he moved to Shanghai where he is currently a PI at the CAS Key Lab of Computational Biology, part of the Shanghai Institute for Nutrition and Health. From 2015 to 2019 he held an International Newton Fellowship from the Royal Society in association with the Shanghai Institute of Nutrition and Health. His research focuses on DNA methylation, in aging, cancer-risk and cancer itself. To attain this goal, we have been developing computational methods that address some of the key emerging challenges, such as how to infer cell-type specific DNAm changes from large bulk-tissue genome datasets, how to identify stem-like cells in preneoplastic lesions from RNA-seq data, or how to identify disrupted regulatory networks in aging at single-cell resolution. In this talk I will describe 4 different computational methods for analyzing DNAm data.