Dr. Richard Durbin

Richard Durbin works in computational genetics and bioinformatics at the Department of Genetics at the University of Cambridge. His first degree was in mathematics, followed by a PhD at the Laboratory of Molecular Biology in Cambridge, a postdoc on neural modelling, and then 25 years in genomics at the Wellcome Trust Sanger Institute, prior to moving to Cambridge University in 2017. He has played significant roles in multiple genome sequencing projects, including co-leading the 1000 Genomes Project to map human sequence variation. His current research is focused on genome variation and genome evolution, as well as on methods for processing population scale whole genome sequencing data. He has also made contributions to biological sequence analysis, including developing methods for sequence alignment using Hidden Markov models and suffix array methods, and developing genomic databases including Pfam, Ensembl, and TreeFam. Richard is a Member of EMBO and a Fellow of the Royal Society.