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Sandrine Dudoit is Professor of Biostatistics and Statistics at the University of California, Berkeley. Professor Dudoit's methodological research interests regard high-dimensional inference and include exploratory data analysis (EDA), visualization, loss-based estimation with cross-validation (e.g., density estimation, regression, model selection), and multiple hypothesis testing. Much of her methodological work is motivated by statistical inference questions arising in biological research and, in particular, the design and analysis of high-throughput microarray and sequencing gene expression experiments, e.g., single-cell transcriptome sequencing (RNA-Seq) for discovering novel cell types and for the study of stem cell differentiation. Her contributions include: exploratory data analysis, normalization and expression quantitation, differential expression analysis, class discovery, prediction, inference of cell lineages, integration of biological annotation metadata (e.g., Gene Ontology (GO) annotation). She is also interested in statistical computing and, in particular, reproducible research. She is a founding core developer of the Bioconductor Project (<http://www.bioconductor.org>), an open-source and open-development software project for the analysis of biomedical and genomic data.

Professor Dudoit is a co-author of the book *Multiple Testing Procedures with Applications to Genomics* and a co-editor of the book *Bioinformatics and Computational Biology Solutions Using R and Bioconductor*. She is Associate Editor of three journals, including *The Annals of Applied Statistics* and *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. Professor Dudoit was named Fellow of the American Statistical Association in 2010 and Elected Member of the International Statistical Institute in 2014.

Professor Dudoit obtained a Bachelor's degree (1992) and a Master's degree (1994) in Mathematics from Carleton University, Ottawa, Canada. She first came to UC Berkeley as a graduate student and earned a PhD degree in 1999 from the Department of Statistics. Her doctoral research, under the supervision of Professor Terence P. Speed, concerned the linkage analysis of complex human traits. From 1999 to 2000, she was a postdoctoral fellow at the Mathematical

Sciences Research Institute, Berkeley. Before joining the Faculty at UC Berkeley in July 2001, she underwent two years of postdoctoral training in genomics in the laboratory of Professor Patrick O. Brown, Department of Biochemistry, Stanford University. Her work in the Brown Lab involved the development and application of statistical methods and software for the analysis of microarray gene expression data.