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Robert Gentleman (statistician)

Robert Clifford Gentleman (born 1959) is a Canadian statistician and bioinformatician^[2] currently vice president of computational biology at 23andMe. [3][4] He is recognized, along with Ross Ihaka, as one of the originators of the R language^{[5][6]} programming and the **Bioconductor** project.^{[7][8][9]}

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Education

Gentleman was awarded a Bachelor of Science degree in mathematics from the University of British Columbia. [3] He was awarded a Ph.D. degree in Statistics from University of Washington in 1988; his thesis title was Exploratory methods for censored data.[10]

Research

Gentleman worked as a statistics professor at The University of

Auckland in the mid 1990s, where he developed the R

Robert Clifford Gentleman	
Born	1959 (age 60-61)
Alma mater	University of Washington University of British Columbia
Known for	R (programming language)
Awards	Benjamin Franklin Award (Bioinformatics)
Scientific career	
Institutions	Genentech University of Washington Harvard University The University of Auckland
Thesis	Exploratory methods for censored data (htt p://search.proquest.co m/docview/30358931 6) (1988)
Doctoral advisor	John James Crowley ^[1]

programming language alongside Ross Ihaka. [5][11] In 2001, he started work on the Bioconductor project to promote the development of open-source tools for bioinformatics and computational biology. In 2009, Gentleman joined the Genentech biotechnology corporation, where he worked as a senior director in bioinformatics and computational biology. [12][13] Gentleman joined personal genomics and biotechnology company 23 and Me as vice president in April 2015, [3] with the goal of bringing expertise on bioinformatics and computational drug discovery to the company. [4] Gentleman has also served on the board of the statistical software company Revolution Analytics (formerly known as REvolution Computing).[11]

Awards

Gentleman won the Benjamin Franklin Award in 2008, recognising his work on the R programming language, the Bioconductor project and his commitment to data and methods sharing. [14] He was made a Fellow of the International Society for Computational Biology in 2014 for his contribution to computational biology and bioinformatics.^[15] He became a fellow of the American Statistical Association in 2017. [16]

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