Bioconductor case studies

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Monografía

Bioconductor software has become a standard tool for the analysis and comprehension of data from high-throughput genomics experiments. Its application spans a broad field of technologies used in contemporary molecular biology. In this volume, the authors present a collection of cases to apply Bioconductor tools in the analysis of microarray gene expression data. Topics covered include @* import and preprocessing of data from various sources @* statistical modeling of differential gene expression @* biological metadata @* application of graphs and graph rendering @* machine learning for clustering and classification problems @* gene set enrichment analysis Each chapter of this book describes an analysis of real data using hands-on example driven approaches. Short exercises help in the learning process and invite more advanced considerations of key topics. The book is a dynamic document. All the code shown can be executed on a local computer, and readers are able to reproduce every computation, figure, and table. The authors of this book have longtime experience in teaching introductory and advanced courses to the application of Bioconductor software. Florian Hahne is a Postdoc at the Fred Hutchinson Cancer Research Center in Seattle, developing novel methodologies for the analysis of high-throughput cell-biological data. Wolfgang Huber is a research group leader in the European Molecular Biology Laboratory at the European Bioinformatics Institute in Cambridge. He has wide-ranging experience in the development of methods for the analysis of functional genomics experiments. Robert Gentleman is Head of the Program in Computational Biology at the Fred Hutchinson Cancer Research Center in Seattle, and he is one of the two authors of the original R system. Seth Falcon is a member of the R core team and former project manager and developer for the Bioconductor project

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Título: Bioconductor case studies Florian Hahne [and others]

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Descripción física: 1 online resource (x, 283 pages) illustrations (some color)

Mención de serie: Use R!

Bibliografía: Includes bibliographical references (pages 271-275) and index

Contenido: The ALL data set -- R and Bioconductor introduction -- Processing affymetrix expression data -- Two color arrays -- Fold changes, log-ratios, background correction, shrinkage estimation and variance stabilization --

Easy differential expression -- Differential expression -- Annotation and metadata -- Supervised machine learning -- Unsupervised machine learning -- Using graphs for interactome data -- Graph layout -- Gene set enrichment analysis -- Hypergeometric testing used for gene set enrichment analysis -- Solutions to exercises -- References -- Index

Materia Título preferido: Bioconductor (Computer file) Bioconductor (Computer file)

Materia: Bioinformatics R (Computer program language) Bioinformatics R (Computer program language) Bioinformatik R Programm

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