PUBLICATIONS

Emerging bioinformatics approaches for analysis of NGS-derived coding and non-coding RNAs in neurodegenerative diseases
Guffanti A., Simchovitz A. & Soreq A.
Frontiers in Cellular Neuroscience 8 Article 89 (2014)

BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach
Riebler A., Menigatti M., Song, J. Z., Statham A.L., Stirzaker C., Mahmud N., Mein C. A., Clark S. J. & Robinson M. D. Genome Biology 15(2):R35 (2014)

h5vc: scalable nucleotide tallies with HDF5
Pyl P. T., Gehring J., Fischer B. & Huber W. Bioinformatics Published online 5 Feb (2014)

Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages
Ohnishi Y., Huber W., Tsumura A., Kang M., Xenopoulos P., Kurimoto K., Oleś A.K., Araúzo-Bravo M. J., Saitou M., Hadjantonakis A-K. & Hiiragi T.
Nature Cell Biology 16:27-37 (2014)

Improved variational Bayes inference for transcript expression estimation
Papastamoulis P., Hensman J., Glaus P. & Rattray M.
Statistical Applications in Genetics and Molecular Biology 13(2):203-216 (2014)

Accounting for technical noise in single-cell RNA-seq experiments
Brennecke P., Anders S., Kim J.K., Kołodziejczyk A.A., Zhang X., Proserpio V., Baying B., Benes V., Teichmann S.A, Marioni J.C, & Heisler M.G.
Nature Methods 10:1093-1095 (2013)

Hierarchical Bayesian modelling of gene expression time series across irregularly sampled replicates and clusters
Hensman J., Lawrence N. D. & Rattray M.
BMC Bioinformatics 14:252 (2013)

Count-based differential expression analysis of RNA sequencing data using R and Bioconductor
Anders S., McCarthy D. J., Chen Y., Okoniewski M., Smyth G. K., Huber W. & Robinson M. D.
Nature Protocols 8:1765-1786 (2013)

Drift and conservation of differential exon usage across tissues in primate species
Reyes A., Anders S., Weatheritt R.J., Gibson T. J., Steinmetz L. M., & Huber W.
PNAS 110(38):15377-15382 (2013)

The RADIANT Consortium

Principal Investigator	Partner Institution
University of Manchester UK	Prof. Magnus Rattray (Scientific Coordinator)
Genomatix Software GmbH, Germany	Dr. Korbinian Grote
Genomnia, Italy	Dr. Alessandro Guffanti
European Molecular Biology Laboratory, Germany	Dr. Wolfgang Huber
Telethon Institute of Genetics and Medicine, Italy	Dr. Diego di Bernardo
Institute Italiano di Tecnologia, Italy	Dr. Mattia Pelizzola
ARMINES, France	Dr. Jean-Philippe Vert
University of Zurich, Switzerland	Prof. Mark Robinson
University of Cambridge, UK	Prof. Simon Tavaré
University of Sheffield UK	Prof. Neil Lawrence

Scientific Advisory Board

Prof. David Balding
Genetics Institute, University College London

Prof. Vingron
Max Plank Institute for Molecular Genetics

Dr. Magnus Nordborg
Gregor Mendel Institute of Molecular Plant Biology

Dr. Sophie Schbath
Institut National de la Recherche Agronomique

RADIANT

RADIANT is a research project funded by the 7th Framework Programme of the European Commission. The project started in December 2012 and brings together ten project partners from five European countries. The aim of the RADIANT project is to develop new statistical analysis tools for solving open problems in next generation sequencing (NGS) data analysis.

NGS is a rapidly evolving family of technologies with many applications, including genetics of both rare and common diseases, understanding disease mechanism progression. RADIANT aims to provide an integrated computational framework for NGS data analysis that is robust and user-friendly, and provide tools to benchmark experimental protocols and statistical methods. The project will establish training materials and an extensive training programme for the rapid dissemination of these new tools to the biomedical community.

http://radiant-project.eu

RADIANT stands for Rapid Development and Distribution of Statistical Tools for High-Throughput Sequencing.

The project consists of work packages around three themes: Analysis, Integration and Dissemination.

Analysis

WP1 Improved Read Mapping

WP2 Genomic Variations

WP3 Counts and Regions

WP4 Methylation Data Analysis

WP5 Transcriptome Expression

Integration

WP6 Genome, Epigenome, Transciptome

WP7 Systems Biology of Gene Regulation

WP8 Visualisation

Dissemination

WP9 Scientific Publishing

WP10 Benchmarking

WP11 Training

For more information about the project visit the RADIANT website:
http://radiant-project.eu

PROJECT OUTPUT

SOFTWARE

DESeq2

Differential gene expression analysis based on the negative binomial distribution
Estimate variance-mean dependence in count data from high-throughput sequencing assays and test for differential expression based on a model using the negative binomial distribution.
Authors: Love M., Anders S., & Huber W.

BiocStyle

Provides standard formatting styles for Bioconductor documents.
Authors: Morgan M., Oleś A. & Huber, W.

Repitools

Epigenomic tools for the analysis of enrichment-based epigenomic data. Features include summarization and visualization of epigenomic data across promoters according to gene expression context, finding regions of differential methylation/binding and BayMeth for quantifying methylation.
Authors: Robinson M., Strbenac D., Statham A., & Riebler A.

Meetings/Training

Computational statistics for genome biology, Brixen, Italy

RADIANT has been involved this intensive week-long course on current approaches in statistical and computational analysis of large-scale experiments. Members of the RADIANT team delivered lectures on the 2013 course, and will be doing so again on the course in June, 2014.

RADIANT Workshop at ECCB'14, Strasbourg, France 6-7 September 2014

Analysis of differential isoform usage by RNA-seq: statistical methodologies and open software workshop. Bringing together leading researchers working on computational tools for exploring differential isoform usage to explore different approaches to method benchmarking.

Genomic Workshop at MASAMB 2014

RADIANT sponsored workshop on mathematical and computational aspects of dealing with big data at the MASAMB (Mathematical and Statistical Aspects of Molecular Biology) workshop, April 2014.

RADIANT 2nd General Meeting, January 2014

RADIANT held its 2nd General Meeting at the Institute Marie Curie, Paris on 9-10 January. Participants included members of the RADIANT consortium, Sasa Jenko, RADIANT EC Project Officer, members of the Scientific Advisory Board, and Peter Fraser, invited speaker from The Babraham Institute Cambridge.

European Bioconductor Developers Meeting, December 2013

2013 European Bioconductor Developers Meeting, hosted by The University of Cambridge. The meeting was aimed at bioinformaticians, programmers and software engineers who contribute to the Bioconductor project,or are interested in developing packages for Bioconductor.

SIG Frontiers in Somatic Variant Calling, Workshop at the EMBL Cancer Genomics Conference, November 2013

RADIANT sponsored workshop bringing together computational biologists directly involved in designing, benchmarking and applying somatic variant calling.

This project has received funding from the European Union's Seventh Framework Programme for Research, Technological Development and Demonstration under Grant Agreement no 305626.