Dario **Righelli**

Computer Scientist · Bioinformatician

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28/03/1983

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Current Position

Post-Doc   *Padua*

Department of Statistics - University of Padua   *Jan. 2020 - present*

- Main Topic: Methods Development for multi-omic Single Cell Next Generation Sequencing data analysis and integration.
- Contract type: Assegno di Ricerca - SSD: SECS-S01

Research Interests

Genomic Data Analysis   Analysis and integration of multiple bulk/single cell Next Generation Sequencing data.
Software development   solutions for visualization and analysis of high-throughput genomics data, reproducible research.

Education

PhD in Management and Information Technology
Program: Information Security and Intelligent Systems (SSD: INF01)   *Fisciano/Napoli*

Institute for Applied Mathematics (IAC-CNR) - Università degli studi di Salerno (DISA-MIS)   *2015 - 2018*

- Main Topic: Software and Methods Development for multi-omic Next Generation Sequencing data analysis and integration.
  Tutor: Dr. Angelini Claudia - Institute for Applied Mathematics "M. Picone" - National Research Council.
  Tutor: Dr. Tagliaferri Roberto - Dipartimento di Scienze Aziendali, Management & Innovation Systems.
- Title achieved on April 4th 2019.

M.Sc. in Computer Science (final grade: 110/110 - GPA: A - SSD: INF01)   *Napoli*

Università degli studi di Napoli Federico II   *2008 - 2013*

- Thesis in Bioinformatics: Feature Selection aimed to the identification of drugs mode of action: a Gene Set Enrichment Analysis (GSEA) based filter. Developed at TIGEM.
  Tutors: Prof. Nicodemi M., Prof. di Bernardo D., Dr. Napolitano F.
- From 2008 to 2011, besides to attend my Master Degree courses, I worked at Osservatorio Astronomico di Capodimonte (INAF-OAC).

B.Sc. in Computer Science (SSD: INF01)   *Napoli*

Università degli studi di Napoli Federico II   *2001 - 2008*

- Thesis in Software Engineering: The space experiment GIADA (ROSETTA mission): the data conversion problem from satellite format to standard NASA Planetary Data System (PDS) format. Developed at INAF-OAC.
  Tutors: Prof. Milano L., Prof. Colangeli L.
- I had two years break.

Experience

VOCATIONAL

Post-doc - Sofware and methods for NGS data analysis and integration   *Napoli- Italy*

Institute for Applied Mathematics (IAC-CNR)   *nov. 2018 - dic. 2019*

- Prosecution of PhD activities.
- Collaboration with Prof. Baldini (University of Naples "Federico II") on multiple Next Generation Sequencing data analysis and integration in Leduq project.
- Collaboration with Prof. Risso (University of Padua) on the comparison of multiple methods for the epigenomic data analysis.

Phd Fellow - Sofware and methods for NGS data analysis and integration   *Fisciano/Napoli- Italy*

University of Salerno (DISA-MIS) - Institute for Applied Mathematics (IAC-CNR)   *nov. 2015 - oct. 2018*

- Development of Ticorser, an R package for RNA-seq time-course data Analysis.
- Development of IntegrHO, an R-Shiny package for NGS multi-omic data analysis and integration.
- Development of easyreporting, an R package for reproducible research.
- Maintenance of RNASeqGUI, an R package for RNA-seq data Analysis.

Visiting Research Assistant - Methods for NGS data analysis and integration

New York - New York - USA

DEPARTMENT OF HEALTHCARE POLICY AND RESEARCH - WEILL CORNELL MEDICINE

oct. 2017 - apr. 2018

- Development of novel functionalities for DEScan2 R package, oriented to ATAC-seq data analysis and peak differentiation.

Research Fellow - Developer of user friendly tools aimed to NGS data analysis

Napoli- Italy

INSTITUTE FOR APPLIED MATHEMATICS (IAC-CNR)

aug. 2015 - oct. 2015

- Study, design and development of functionalities for RNASeqGUI and IntegrHO software, to analyse and integrate multiomics data.

Highly-Specialized Training Fellow in Bioinformatics (PON - SSD: MED04)

Napoli- Italy

UNIVERSITÀ DI NAPOLI FEDERICO II - INSTITUTE FOR APPLIED MATHEMATICS (IAC-CNR)

jul. 2014 - jul. 2015

- Study, design and development of novel functionalities for RNASeqGUI software, for the analysis of RNA-seq data.

Research Fellow - Netview Project Developer

Napoli- Italy

TELETHON INSTITUTE OF GENETICS AND MEDICINE (TIGEM)

feb. 2014 - jun. 2014

- Update and development of novel functionalities for the Netview Project, a web tool for Human and Mouse genome correlation visualization.

Master Thesis Internship

Napoli- Italy

TELETHON INSTITUTE OF GENETICS AND MEDICINE (TIGEM)

apr. 2013 - dec. 2013

- Thesis Title: Feature Selection aimed to the identification of drugs Mode of Action: a Gene Set Enrichment Analysis filter.
- Design of a feature selection method for the gene enrichment analysis, in R language, developing a multicore parallel algorithm for cluster machines.

Research Fellow - Developmental support of a calculation code for GIADA data analysis

Napoli - Italy

OSSERVATORIO ASTRONOMICO DI CAPODIMONTE (INAF-OAC - SSD: FIS05)

dec. 2008 - feb. 2011

- Refining and development of novel functionalities for the MaGx-Converter, C++ software aimed to convert GIADA data, instrument part of ROSETTA mission.

Bachelor Thesis Internship

Napoli - Italy

OSSERVATORIO ASTRONOMICO DI CAPODIMONTE (INAF-OAC)

sep. 2007 - jun. 2008

- Thesis title: The space experiment GIADA (ROSETTA mission): the data conversion problem from satellite format to standard NASA Planetary Data System (PDS) format
- Study, design and development of MaGx-Converter software, a graphical user interface in C++ aimed to convert GIADA data, instrument part of ROSETTA mission.

OTHERS

System Administrator

Napoli - Italy

INSTITUTE FOR APPLIED MATEMATICS (IAC-CNR)

jul. 2014 - present

- System administrator of a 12 nodes cluster with Rocks distribution based on CentOS Linux.
- Administration of other machines running Ubuntu Linux operative distribution.

Website Administrator

Napoli - Italy

INSTITUTE FOR APPLIED MATEMATICS (IAC-CNR)

dec. 2014 - present

- Website development and administration internal websites and organized conferences.

Videogame developer - HIM the dark plane

Napoli - Italy

INDEPENDENT

2006

- Design and development of a videogame in C++ and OpenGL. A 3D puzzle game inspired to the popular 2D flash game Road Block.

Awards and Scholarships

jul. 2018	**Travel Grant**, Bioconductor travel fellowship.	*Napoli - Toronto*
jan. 2018	**Travel Grant**, EPIGEN travel fellowship.	*Napoli - New York*
jun. 2016	**Best poster award**, 13th Annual Meeting of the Bioinformatics ITalian Society (BITS)	*Fisciano (SA) - Italy*
nov. 2015	**Three-year doctoral scholarship**, DISA-MIS - University of Salerno	*Fisciano (SA) - Italy*
jul. 2014	**One-year highly-specialized training in bioinformatics (PON)**, University of Napoli Federico II	*Napoli - Italy*

Publications

Published

[1] **Dario Righelli**, John Koberstein, Nancy Zhang, Claudia Angelini, Lucia Peixoto, and Davide Risso. Differential Enriched Scan 2 (DEScan2): a fast pipeline for broad peak analysis. *PeerJ*, nov 2018.

[2] Valerio Costa*, **Dario Righelli***, Francesco Russo, Piergiuseppe De Berardinis, Claudia Angelini, and Luciana D'Apice. Distinct antigen delivery systems induce dendritic cells' divergent transcriptional response: New insights from a comparative and reproducible computational analysis. *International Journal of Molecular Sciences*, 2017.

[3] Francesco Russo*, **Dario Righelli***°, and Claudia Angelini. Advantages and limits in the adoption of reproducible research and R-tools for the analysis of omic data. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 2016.

[4] Francesco Russo, **Dario Righelli**, and Claudia Angelini. Advancements in RNASeqGUI towards a Reproducible Analysis of RNA-Seq Experiments. *BioMed Research International*, 2016.

[5] Lucio Di Filippo, **Dario Righelli**, Miriam Gagliardi, Maria Rosaria Matarazzo, and Claudia Angelini. HiCeekR: a novel Shiny app for Hi-C data analysis. *Frontiers in Genetics*, 2019.

[6] Ashley M Ingiosi, Hannah Schoch, Taylor Wintler, Kristan G Singletary, **Dario Righelli**, Leandro G Roser, Elizabeth Medina, Davide Risso, Marcos G Frank, and Lucia Peixoto. Shank3 modulates sleep and expression of circadian transcription factors. *eLife*, 2019.

[7] James Hong, Mahmood Chamankhah, Anna Badner, **Dario Righelli**, Priscilla Chan, Claudia Angelini, and Michael Fehlings. Dual time course RNA-seq reveals levelspecific neurovascular response after cervical and thoracic spinal cord injury. *Journal of Neurotrauma*, 2017.

[8] Mario Alessandro Russo, Francesco Guarino, Monica Franzese, **Dario Righelli**, Giovanni Improta, Claudia Angelini, and Maria Triassi. A novel shiny platform for the geo-spatial analysis of large amount of patient data. Technical report, PeerJ Preprints, 2017.

[9] Daniela Savi, Stefano Schiavetto, Nicholas J. Simmonds, **Dario Righelli**, and Paolo Palange. Effects of Lumacaftor/Ivacaftor on physical activity and exercise tolerance in three adults with cystic fibrosis. *Journal of Cystic Fibrosis*, pages 1–5, 2019.

[10] Claudia Angelini, **Dario Righelli**, and Francesco Russo. Reproducible Research in the era of Next Generation Sequencing: current approaches, examples and future perspectives. *EMBnet.journal*, 2015.

Please note that * means equally contributing authors and ° means corresponding author.

Preprints

Time Course RNA-Seq analysis on Mouse Spinal Cord Injury.
- Active collaboration with Dr. Fehlings's group of University Health Network at University of Toronto, on RNA-Seq study on Mouse spinal cord injury neuronal activity.

Reliable and reproducible epigenomic enrichment data analysis using Bioconductor.
- Authors: **Righelli Dario**, Johnson Ben, Angelini Claudia, Triche Timothy Jr., Peixoto Lucia, Risso Davide.

easyreporting: an S4 class for reproducible research handling.
- Authors: **Righelli Dario**, Angelini Claudia.
- Ref: https://github.com/drighelli/easyreporting/ (Bioconductor Accepted)

ticorser: an R package for Time Course RNA-Seq Analysis.
- Authors: **Righelli Dario**, Hong James, Fehlings Michael, Angelini Claudia.

IntegrHO: Integration of High-throughput Omics data.
- Development of a Shiny Graphical User Interface for multi-omics data analysis and integration
- Authors: **Righelli Dario**, Angelini Claudia.

ROBIN: Robustness in Networks.
- An R package for checking robustness of community detection methods in Networks.
- Ref: https://cran.r-project.org/web/packages/robin/index.html Authors: Valeria Policastro, Dario Righelli, Luisa Cutillo, Italia De Feis, Annamaria Carissimo.

Contributions in Conferences

Oral Contribution as Speaker @ EuroBioC 2019   *Brussels, Belgium*

Epigenomic Enrichment Analysis using Bioconductor   *dec. 2019*
- Authors: **Righelli Dario**, Johnson Ben, Angelini Claudia, Triche Tim, Peixoto Lucia, Risso Davide.

Poster @ BBCC/NetTab 2019   *Fisciano, Italy*

EasyReporting: the R6 class for implementing Reproducible Research   *nov. 2019*
- Authors: **Righelli Dario**, Angelini Claudia.

Poster @ BBCC/NetTab 2019
Napoli, Italy

ROBIN: AN R PACKAGE FOR VALIDATION OF COMMUNITY ROBUSTNESS.
nov. 2019

- Authors: Policastro Valeria, **Righelli Dario**, De Feis Italia, Cutillo Luisa, Carissimo Annamaria.

Poster @ 12th IBS-Italian Region conference
Napoli, Italy

ROBIN: AN R PACKAGE FOR VALIDATION OF COMMUNITY ROBUSTNESS.
jul. 2019

- Authors: Policastro Valeria, **Righelli Dario**, De Feis Italia, Cutillo Luisa, Carissimo Annamaria.

Oral Contribution @ Women in Networks (WIN) Workshop 2019
University of Leeds, UK

ROBIN: AN R PACKAGE FOR VALIDATION OF COMMUNITY ROBUSTNESS.
feb. 2019

- Authors: Policastro Valeria, **Righelli Dario**, De Feis Italia, Cutillo Luisa, Carissimo Annamaria.

Oral Contribution as Speaker @ BBCC 2018
Naples, Italy

DIFFERENTIAL ENRICHED SCAN 2 (DESCAN2): A FAST PIPELINE FOR BROAD PEAK ANALYSIS.
Nov. 2018

- Authors: **Righelli Dario**, Koberstein John, Gomes Bruce, Nancy Zhang, Angelini Claudia, Peixoto Lucia, Risso Davide.

Poster @ North American Cystic Fibrosis Conference
Denver, Colorado, USA

DEPRESSION, ANXIETY AND HEALTH-RELATED QUALITY OF LIFE RELATIONSHIP: FINDINGS FROM AN ITALIAN SAMPLE.
oct. 2018

- Authors: Graziano Sonia, Fabiana Ciciriello, **Dario Righelli**, Lucidi Vincenzina, Tabarini Paola.

Oral Contribution as Speaker @ BioC 2018
Toronto, Canada

DIFFERENTIAL ENRICHED SCAN 2 (DESCAN2): A FAST PIPELINE FOR BROAD PEAK ANALYSIS.
jul. 2018

- Authors: **Righelli Dario**, Koberstein John, Gomes Bruce, Nancy Zhang, Angelini Claudia, Peixoto Lucia, Risso Davide.

Oral Contribution as Speaker @ 15th Annual Meeting of the Bioinformatics ITalian Society
Turin, Italy

DIFFERENTIAL ENRICHED SCAN 2 (DESCAN2): A FAST PIPELINE FOR BROAD PEAK ANALYSIS
jun. 2018

- Authors: **Righelli Dario**, Koberstein John, Gomes Bruce, Nancy Zhang, Angelini Claudia, Peixoto Lucia, Risso Davide.

Poster @ 14th Annual Meeting of the Bioinformatics ITalian Society
Cagliari, Italy

TICORSE: TIME COURSE RNA-SEQ ANALYSIS TOOLKIT
jul. 2017

- Authors: **Righelli Dario**, Angelini Claudia.

Oral Contribution as Speaker @ EMBnet and NETTAB 2016
Rome, Italy

A SHINY BASED TOOL FOR NGS DATA INTEGRATION IN REPRODUCIBLE SPIRIT.
oct. 2016

- Authors: **Righelli Dario**, Franzese Monica, Angelini Claudia.

Poster @ 13th Annual Meeting of the Bioinformatics ITalian Society (BITS)
Fisciano (SA), Italy

INTEGRHO A SOFTWARE TO ANALYSE AND INTEGRATE NGS DATA IN REPRODUCIBLE RESEARCH SPIRIT.
jun. 2016

- Authors: **Righelli Dario**, Franzese Monica, Angelini Claudia
- Best Poster Award 2016

Poster @ Bioinformatica e Biologia Computazionale in Campania
Avellino, Italy

NOVEL BIOINFORMATICS TOOLS FOR NGS DATA ANALYSIS AND INTEGRATION.
dec. 2015

- Authors: **Righelli Dario**, Franzese Monica, Russo Francesco, Di Filippo Lucio, Angelini Claudia

Poster @ Statistical Methods for Omics Data Integration and Analysis 2015
Valencia, Spain

SOME NOVEL TOOLS FOR NGS DATA ANALYSIS INSPIRED FROM REPRODUCIBLE RESEARCH.
may. 2015

- Authors: **Righelli Dario**, Franzese Monica, Russo Francesco, Angelini Claudia

Oral Contribution @ CIBB 2015
Napoli, Italy

A WALKING TOUR IN REPRODUCIBLE RESEARCH AND BIG DATA MANAGEMENT WITH RNASEQGUI AND R.
may. 2015

- Authors: Russo Francesco, **Righelli Dario**, Angelini Claudia

Oral Contribution @ SeqAHEAD 2015
Bratislava, Slovakia

REPRODUCIBLE RESEARCH IN THE ERA OF NEXT GENERATION SEQUENCING: CURRENT APPROACHES, EXAMPLES ...
may. 2015

- Authors: Angelini Claudia, **Righelli Dario**, Russo Francesco

Poster @ RECOMB 2013
Toronto, Ontario, Canada

ELUCIDATION OF THE MODE OF ACTION OF CORRECTORS FOR THE CYSTIC FIBROSIS MUTANT GENE ...
nov. 2013

- Authors: Napolitano Francesco, Carrella Diego,**Righelli Dario**, Galietta Luis J. V., di Bernardo Diego

Software

RNASeqGUI	<u>Devel/Maint</u>: A graphical interface for NGS RNA-Seq data analysis. *http://bioinfo.na.iac.cnr.it/RNASeqGUI/*
DEScan2	<u>Devel/Maint</u>: A tool for NGS ChIP-Seq/Atac-Seq peak differentiation analysis. *https://bioconductor.org/packages/release/bioc/html/DEScan2.html*
ticorser	<u>Devel/Maint</u>: A tool for NGS RNA-Seq time-course data analysis. *https://github.com/drighelli/ticorser*
IntegrHO	<u>Devel/Maint</u>: A tool for NGS data analysis and integration. *https://github.com/drighelli/integrho*
easyreporting	<u>Devel/Maint</u>: A tool for Reproducible Research handling. *https://github.com/drighelli/easyreporting*
HiCeekR	<u>Auth</u>: A graphical interface for Hi-C data analysis. *https://github.com/lucidif/hiceekr*
ROBIN	<u>Auth</u>: An R package for validation of community robustness in Networks. *https://cran.r-project.org/web/packages/robin/index.html*

Courses Teached/Organized

nov. 2019	**Teacher @ Single Cell RNA-seq tutorial**, NETTAB/BBCC 2019, University of Salerno	*Fisciano, Italy*
Oct. 2019	**Teacher @ Bulk RNA-seq Differential Expression Workflow**, R/Bioconductor Meetup - National Research Council	*Naples, Italy*
Apr. 2019	**Teacher @ RNA-seq Differential Expression Analysis**, University of Salerno	*Fisciano, Salerno, Italy*
Oct. 2018	**Teacher @ R-Package Creation Tutorial**, R/Bioconductor Meetup - National Research Council	*Naples, Italy*
since Oct. 2018	**Organizer @ R/Bioconductor Meetup**, National Research Council	*Naples, Italy*

Science Dissemination (Outreach)

2016-2018	**Pint of Science**, Part of organization neapolitan team for Pint of Science international event.	*Napoli*
2017-2018	**Tempesta di Cervelli**, Part of science dissemination neapolitan team for Tempesta di Cervelli.	*Napoli*
May. 2017	**Futuro Remoto**, Part of IAC-CNR team on brain modeling with 3D-printing, Scientific speed dating.	*Napoli*
Oct. 2015	**Futuro Remoto**, Part of IAC-CNR team on DNA extraction from fruits.	*Napoli*

Schools and Courses

sep. 2019	**Network inference in biology and disease - EMBO workshop - 4 days**, Telethon Institute of Genetics and Medicine	*Napoli, Italy*
June. 2018	**MixOmics Advanced Workshop - 2 days**, Université d'Evry and Institute for Plant Science Saclay	*Saclay, Paris, France*
sep. 2016	**Computational Genomics Approaches to Precision Medicine - 15 days**, Berlin Institute for Medical Systems Biology, Max Delbruck Center	*Berlin, Germany*
jul. 2016	**International Summer School in Computational Intelligence and Data Analysis - 5 days**, Dipartimento di Scienze Aziendali Management Innovation Systems - University of Salerno	*Fisciano (SA), Italy*
sep. 2015	**STATegra Summer School in Omics Data Integration - 7 days**,	*Benicassim, Spain*
apr. 2015	**Statistical Learning - Stanford online course**, Stanford University - Exam passed with Distinction	*Stanford, Online*
mar. 2015	**The Genomic of Gene Expression RNA-Seq Course - 7 days**, Centro de Investigation Principe Felipe	*Valencia, Spain*
nov. 2014	**A crash course on Python - 3 days**, Istituto di Calcolo e Reti ad Alte Prestazioni - National Research Council	*Napoli, Italy*

Collaborations and Affiliations

since jul. 2014	**Active Collaboration: Dr. Angelini Claudia**, Istituto per le Applicazioni del Calcolo - Consiglio Nazionale delle Ricerche Development of novel tools for Bioinformatics
since dec. 2018	**Active Collaboration: Prof. Baldini Antonio**, Dipartimento di Medicina molecolare e Biotecnologie mediche - Università Federico II di Napoli Analysis of ChIP-seq, ATAC-seq, RNA-seq for studying the role of Tbx1 transcription factor.
since nov. 2017	**Active Collaboration: Dr. Peixoto Lucia**, Elon S. Floyd College of Medicine, Washington State University Analysis of RNA-seq for investigating the regulating mechanisms of Autism Spectrum Disorder.
may. 2018	**Active Collaboration: Dr. Graziano Sonia**, Ospedale Pediatrico Bambino Gesù, IRCSS. Analysis of psychological state of Cystic Fibrosis patients.
since jun. 2016	**Member of: Bioinformatic ITalian Society (BITS)**, link: http://bioinformatics.it
since jan. 2017	**Member of: Istituto Nazionale di Alta Matematica (INdAM)**, link: http://www.altamatematica.it

Technical Skills

INFORMATICS

Operative Systems	Linux (Debian, Ubuntu, CentOS), OS-X, Rocks cluster, Windows.
Programming Languages	R, C/C++, PHP, Python, UML, Objective-C, Pascal.
Other Languages	HTML4/5, CSS, JavaScript, Bash Shell, XML, VoiceXML, Matlab.
Graphic Libraries	R-Shiny, GTK+, WxWidgets, OpenGL.
Databases	MySQL, Access, Oracle.
Document Systems	Latex, Office Packages (MS, Libre, Open).
Version Control	Git, SVN, Eclipse CVS.
Graphical Tools	Photohsop, GIMP2, Illustrator, Inkscape, Lightroom.
Computer Networks	Equipment, Cabling, Configuration.

BIOINFORMATICS

Data Analysis	RNA-seq, RNA-seq time-course, ChIP-seq, ATAC-seq, Sono-seq, Hi-C.
Biological Databases	DAVID, Ensembl/biomart, KEGG, GEO, BLAST, Connectivity Map, Molecular Signature Database (MSigDB), Genome Browser, MANTRA, Netview.
R Packages	ggplot2, tidyverse, filehash, RGtk2, RMySql, doParallel, foreach, snow, Shiny, htmlwidgets, plotly.
Bioconductor R Packages	biomaRt, Graphite, RDAVIDWebService, Gage, ReportingTools, NOISeq, DESeq2, Rsamtools, BiocParallel, MASigPro, limma:voom, edgeR, ChIPpeakAnno, RUVSeq, GenomiRanges, DelayedArray, MultyAssayExperiment, summarizedExperiment.
Other Tools	Cytoscape, samtools, bedtools, FastQC, Cufflinks, Tuxedo pipeline, Trinity, HISAT, STAR, DeepTools.

Languages

Italian	Mother Tongue
English	Fluent (C1)
Spanish	Elementary (A2)