

Contact Information

Davide Risso
Assistant Professor, Rita Levi Montalcini Fellow
Department of Statistical Sciences,
University of Padova
Via C. Battisti, 241
35121 Padova, Italy
E-mail: davide@stat.unipd.it
Web-site: <http://drisso.github.io>
Github: <https://github.com/drisso>

Research and Teaching Interests

Statistical methodology modeling of high-dimensional data, parametric and non-parametric regression, clustering, factor analysis and dimensionality reduction, multiple hypothesis testing, combining data from multiple sources (meta-analysis).

Genomics data analysis design and analysis of high-throughput gene expression experiments, analysis of microarray and next-generation sequencing data (RNA-seq), non-coding RNA annotation and expression quantitation.

Statistical software development visualization and statistical analysis of high-throughput genomic data, reproducible research.

Employment

2018 – present Rita Levi Montalcini Assistant Professor
Department of Statistical Sciences
University of Padova.

2018 – 2019 Adjunct Assistant Professor
Division of Biostatistics and Epidemiology,
Department of Healthcare Policy and Research,
Weill Cornell Medicine.

2017 – 2018 Assistant Professor
Division of Biostatistics and Epidemiology,
Department of Healthcare Policy and Research,
Weill Cornell Medicine.

2012 – 2016 Postdoctoral Scholar

Department of Statistics and
Division of Biostatistics, School of Public Health,
University of California, Berkeley.
Jointly supervised by Prof. Terry Speed and Prof. Sandrine Dudoit.

Education

2009 – 2012 Ph.D. in Statistics

Department of Statistical Sciences, University of Padova, Italy.
Thesis title: “Simultaneous Inference for RNA-Seq data”.
Supervisor: Prof. Monica Chiogna.
Co-supervisors: Prof. Sandrine Dudoit, Dr. Chiara Romualdi.

2005 – 2008 MSc (*Laurea Magistrale*) in “Statistics and Informatics”

Faculty of Statistical Sciences, University of Padova, Italy.
Final grade: 110 (out of 110) with honors.
Thesis (in Italian): “Analysis of gene expression data: a comparative study on the impact of normalization on statistical inference”, Supervisor: Dr. Chiara Romualdi.

2002 – 2005 BSc (*Laurea*) in “Statistics, Mathematics and Data Management”

Faculty of Mathematical, Physical and Natural Sciences, University of Genova, Italy.
Final grade: 110 (out of 110) with honors.
Thesis (in Italian): “Statistical modeling of fever episodes in neutropenic pediatric patients with cancer”, Supervisor: Dr. Vincenzo Fontana.

Teaching Experience

University of Padova

- *Computational Biostatistics and Bioinformatics* (in Italian)
MS in Statistics
Years taught: 2018 – present.
- *Multidimensional data analysis* (in Italian)
BS in Statistics
Years taught: 2019.
- *Data Mining* (in Italian)
MS in Computer Science.
Years taught: 2019.

Weill Cornell Medicine

- *Biostatistics I*
MS in Biostatistics and Data Science
Years taught: 2017.

University of California, Berkeley

- *Computational Statistics with Applications in Biology and Medicine*
PhD programs in Statistics and Biostatistics
Years taught: 2014.
- *Workshop on RNA-seq data analysis* (offered every semester)
Computational Genomics Resource Laboratory
Years taught: 2012 – 2014.

Special courses for PhD programs

- Specialist course on Statistical Analysis of RNA-Seq data. Doctoral Program in Bioinformatics.
Summer 2013; Biogem. Ariano Irpino, Italy.
- Specialist course on Statistical Inference for RNA-Seq data. Doctoral School of Statistics. University of Padova, Italy.
Summer 2012; co-taught with Sandrine Dudoit

Short courses and summer schools

- SciLifeLab / SIB Autumn School Single Cell Analysis.
October 2019; Leysin, Switzerland.
- Summer School CSAMA - Statistical Data Analysis for Genome Scale Biology.
July 2019; Bressanone, Italy.
- Winter School in Applied Bioinformatics.
January 2018; Canazei, Italy.
- Computational Genomics Approaches to Precision Medicine.
September 2016; Berlin, Germany.
- Bioinformatic Summer Course.
May 2015; University of Iowa, Iowa City, IA, USA.

Awards and Scholarships

2020-2029 National Scientific Qualification (Abilitazione Scientifica Nazionale) for Associate Professor (Settore 13/D1 - Statistica)

2018-2027 National Scientific Qualification (Abilitazione Scientifica Nazionale) for Associate Professor (Settore 05/E2 - Biologia Molecolare)

2018 Winner of the “Rita Levi Montalcini” Program for Young Researchers. Ministero dell’Istruzione dell’Università e della Ricerca, Italy.

Fall 2014 School of Public Health Committee on Teaching Excellence Award, University of California, Berkeley.

April 2013 Visiting scientist fellowship, Department of Statistical Sciences, University of Padova.

January 2012 Research award, Telethon Foundation, Italy.

January 2009 Three-year doctoral scholarship, Department of Statistical Sciences, University of Padova.

Publications

Refereed Journal Publications

1. **D. Risso**, S. M. Pagnotta (2021) Per-sample standardization and asymmetric winsorization lead to accurate clustering of RNA-seq expression profiles. *Bioinformatics*. *Online access ahead of publication*. <https://doi.org/10.1093/bioinformatics/btab091>. [Preprint: <https://doi.org/10.1101/2020.06.04.134916>].
2. S. Hicks, R. Liu, Y. Ni, E. Purdom, **D. Risso** (2021) mbcmeans: fast clustering for single cell data using mini-batch k-means. *PLoS Computational Biology* **17**:e1008625 [Open Access].
3. A. Joglekar, A. Prjibelski, A. Mahfouz, P. Collier, S. Lin, A. K. Schlusche, J. Marrocco, S. R. Williams, B. Haase, A. Hayes, J. G. Chew, N. I. Weisenfeld, M. Y. Wong, A. N. Stein, S. Hardwick, T. Hunt, Q. Wang, C. Dieterich, Z. Bent, O. Fedrigo, S. A. Sloan, **D. Risso**, E. D. Jarvis, P. Flicek, W. Luo, G. S. Pitt, A. Frankish, A. B. Smit, M. E. Ross, H. U. Tilgner (2021) A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain.. *Nature Communications* **12**:463 [Open Access].
4. M. Calgaro, C. Romualdi, L. Waldron, **D. Risso**, N. Vitulo (2020). Assessment of statistical methods from single cell, bulk RNA-seq and metagenomics applied to microbiome data. *Genome Biology* **21**:191 [Open Access].
5. M. Furnari, L. Eusebi, E. Savarino, C. Petruzzellis, G. Esposito, M. Maida, L. Ricciardiello, S. Pecere, A. Buda, M. De Bona, C. Spada, E. Di Giulio, G. Costamagna, I. Boskoski, E. Giannini, S. Angeletti, F. Barbaro, M. Brunacci, M. Cazzato, V. Corleto, M. Demarzo, E. Giambruno, G. Morreale, A. Moscatelli, M. Pesenti, L. Polese, **D. Risso**, G. Tamanini, F. Zingone (2020). Effects of SARS-CoV-2 emergency measures on high-risk lesions detection: a multicentre cross-sectional study. *Gut*. *Epub ahead of print*. [doi:10.1136/gutjnl-2020-323116](https://doi.org/10.1136/gutjnl-2020-323116).
6. D. H. Brann, T. Tsukahara, C. Weinreb, M. Lipovsek, K. Van den Berge, B. Gong, R. Chance, I. C. Macaulay, H. Chou, R. Fletcher, D. Das, K. Street, H. Roux de Bezieux, Y. Choi, **D. Risso**, S. Dudoit, E. Purdom, J. S. Mill, R. Abi Hachem, H. Matsunami, D. W. Logan, B. J. Goldstein, M. S. Grubb, J. Ngai, S. R. Datta (2020) Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. *Science Advances* **6**:eabc5801 [Open Access].
7. J. Y. Xue, Y. Zhao, J. Aronowitz, T. T. Mai, A. Vides, B. Qeriqi, D. Kim, C. Li, E. de Stanchina, L. Mazutis, **D. Risso**, P. Lito (2020). Rapid non-uniform adaptation to conformation-specific KRAS-G12C inhibition. *Nature* **577**:421-425.
8. R. A. Amezquita, A. T. L. Lun, E. Becht, V. J. Carey, L. N. Carpp, L. Geistlinger, F. Marini, K. Rue-Albrecht, **D. Risso**, C. Sonesson, L. Waldron, H. Pagès, M. Smith, W. Huber, M. Morgan, R. Gottardo, S. C. Hicks (2020). Orchestrating Single-Cell Analysis with Bioconductor. *Nature Methods* **17**:137-145. [Preprint: bioRxiv 590562; doi: <http://dx.doi.org/10.1101/590562>.]

9. M. B. Cole*, **D. Risso***, A. Wagner, D. DeTomaso, J. Ngai, E. Purdom, S. Dudoit, N. Yosef (2019). Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. *Cell Systems* **8**(4) 315-328 [Preprint: bioRxiv 235382; doi: <https://doi.org/10.1101/235382>.] (*=joint first authorship.)
10. F. Gaiti, R. Chaligne, H. Gu, R. M. Brand, S. Kothen-Hill, R. Schulman, K. Grigorev, **D. Risso**, K. Kim, A. Pastore, K. Y. Huang, A. Alonso, C. Sheridan, N. D. Omans, E. Biederstedt, K. Clement, L. Wang, J. A. Felsenfeld, E. B. Bhavsar, M. J. Aryee, J. N. Allan, R. Furman, A. Gnirke, C. J. Wu, A. Meissner and D. A. Landau (2019). Epigenetic evolution and lineage histories of chronic lymphocytic leukemia. *Nature* **569**:576-580.
11. A. Ingiosi, T. P Wintler, H. Schoch, K. G Singletary, D. Righelli, L. Roser, **D. Risso**, M. G. Frank, L. Peixoto (2019). Shank3 Modulates Sleep and Expression of Circadian Transcription Factors. *eLife* **8**:e42819 [Open Access].
12. A. Naka, J. Veit, B. Shababo, R. K. Chance, **D. Risso**, D. Stafford, B. Snyder, A. Egladyous, D. Chu, S. Sridharan, D. P. Mossing, L. Paninski, J. Ngai, H. Adesnik (2019). Complementary networks of cortical somatostatin interneurons enforce layer specific control. *eLife* **8**:e43696 [Open Access].
13. **D. Risso**, L. Purvis, R. Fletcher, D. Das, J. Ngai, S. Dudoit, E. Purdom (2018). clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. *PLOS Computational Biology* **14**(9):e1006378 [Open Access].
14. K. Street, **D. Risso**, R. B. Fletcher, D. Das, J. Ngai, N. Yosef, E. Purdom, S. Dudoit (2018). Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. *BMC Genomics*. **19**:477 [Open Access].
15. D. J. Kramer, **D. Risso**, P. Kosillo, J. Ngai, H. S. Bateup (2018). Combinatorial Expression of Grp and Neurod6 Defines Dopamine Neuron Populations with Distinct Projection Patterns and Disease Vulnerability. *eNeuro* <http://dx.doi.org/10.1523/ENEURO.0152-18.2018>.
16. K. Van den Berge, F. Perraudeau, C. Soneson, M. I. Love, **D. Risso**, JP. Vert, M. D. Robinson, S. Dudoit, L. Clement (2018). Unlocking bulk RNA-seq tools for zero inflation and single-cell applications using observation weights. *Genome Biology*. **19**:24 [Open Access].
17. **D. Risso**, F. Perraudeau, S. Gribkova, S. Dudoit, JP. Vert (2018). A general and flexible method for signal extraction from single-cell RNA-seq data. *Nature Communications* **9**:284 <http://dx.doi.org/10.1038/s41467-017-02554-5> [Open Access].
18. J. N. Koberstein, S. G. Poplawski, M. E. Wimmer, G. Porcari, C. Kao, B. Gomes, **D. Risso**, H. Hakonarson, N. R. Zhang, R. T. Schultz, T. Abel and L. Peixoto (2018). Learning-dependent chromatin remodeling highlights non-coding regulatory regions linked to autism. *Science Signaling* **11**(513). <http://dx.doi.org/10.1126/scisignal.aan6500>.
19. L. Gadye, D. Das, M. A. Sanchez, K. N. Street, A. Baudhuin, A. Wagner, M. B. Cole, Y. G. Choi, N. Yosef, E. Purdom, S. Dudoit, **D. Risso**, J. Ngai, and R. B. Fletcher (2017). Injury activates transient olfactory stem cell states with diverse lineage capacities. *Cell Stem Cell* **21** 775–790.
20. F. Perraudeau, **D. Risso**, K. Street, E. Purdom, S. Dudoit (2017). Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. *F1000Research* **6**:1158 [Open Access].

21. C. Vallejos*, **D. Risso***, A. Scialdone*, S. Dudoit, J. Marioni (2017). Challenges in the normalization of single-cell RNA sequencing datasets. *Nature Methods* **14** 565–571 <http://dx.doi.org/10.1038/nmeth.4292>. (*=joint first authorship.)
22. R. B. Fletcher, D. Das, L. Gadye, K. N. Street, A. Baudhuin, A. Wagner, M. B. Cole, Q. Flores, Y. G. Choi, N. Yosef, E. Purdom, S. Dudoit, **D. Risso** and J. Ngai (2017). Deconstructing olfactory stem cell trajectories at single-cell resolution. *Cell Stem Cell* **20** 817–830 <http://dx.doi.org/10.1016/j.stem.2017.04.003>.
23. Y. J. Choi*, C. Lin*, **D. Risso***, S. Chen, T. A. Kim, M. H. Tan, J. B. Li, Y. Wu, C. Chen, Z. Xuan, T. Macfarlan, W. Peng, S. Y. Kim, T. P. Speed and L. He (2017). Deficiency of microRNA *miR-34a* expands cell fate potential in pluripotent stem cells. *Science*. **355**. <http://dx.doi.org/10.1126/science.aag1927>. (*=joint first authorship.)
24. J. R. Gerstner, J. N. Koberstein, A. J. Watson, N. Zaperro, **D. Risso**, T. P. Speed, M. G. Frank and L. Peixoto (2016). Removal of unwanted variation reveals novel patterns of gene expression linked to sleep homeostasis in murine cortex. *BMC Genomics*, **17(Suppl 8)**:727 [Open Access].
25. S. G. Poplawski, L. Peixoto, G. S. Porcari, M. E. Wimmer, A. G. McNally, K. Mizuno, K. P. Giese, S. Chatterjee, J. N. Koberstein, **D. Risso**, T. P. Speed and T. Abel (2016). Contextual fear conditioning induces differential alternative splicing. *Neurobiology of Learning and Memory*, **134**, 221-235.
26. M. Revelli, F. Paparo, L. Bacigalupo, C. Puppo, M. Furnari, C. Conforti, G. A. Binda, E. Savarino, **D. Risso**, G. A. Rollandi (2016). Comparison of computed tomography and magnetic resonance imaging in the discrimination of intraperitoneal and extraperitoneal rectal cancer: initial experience. *Clinical Imaging*, **40**(1), 57-62.
27. L. Peixoto, **D. Risso**, S. G. Poplawski, M. E. Wimmer, T. P. Speed, M. A. Wood, T. Abel (2015). How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. *Nucleic Acids Research*, **43**(16), 7664-7674.
28. **D. Risso**, J. Ngai, T.P. Speed and S. Dudoit (2014). Normalization of RNA-seq data using factor analysis of control genes or samples. *Nature Biotechnology*, **32**, 896-902.
29. T. Ferreira, S.R. Wilson, J. Choi, **D. Risso**, S. Dudoit, T.P. Speed and J. Ngai (2014). Silencing of odorant receptor gene expression by G protein $\beta \gamma$ signaling ensures the expression of one odorant receptor per olfactory sensory neuron. *Neuron*, **81**, 847-859.
30. **D. Risso**, K. Schwartz, G. Sherlock, S. Dudoit (2011). GC-content normalization for RNA-Seq data. *BMC Bioinformatics*, **12**, 480. [Open Access]
31. P. Martini, **D. Risso**, G. Sales, C. Romualdi, G. Lanfranchi, S. Cagnin (2011). Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. *BMC Bioinformatics*, **12**, 92. [Open Access]
32. R. De Bin, **D. Risso** (2011). A novel approach to the clustering of microarray data via nonparametric density estimation. *BMC Bioinformatics*, **12**, 49. [Open Access]
33. **D. Risso**, M.S. Massa, M. Chiogna, C. Romualdi (2009). A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. *Bioinformatics*, **25**(20), 2685-2691.

34. A. Bisognin, A. Coppe, F. Ferrari, **D. Risso**, C. Romualdi, S. Bicciato, S. Bortoluzzi (2009). A-MADMAN: annotation-based microarray data meta-analysis tool. *BMC Bioinformatics*, **10**, 201 [Open Access].
35. M. Chiogna, M.S. Massa, **D. Risso**, C. Romualdi (2009). A comparison on effects of normalisations in the detection of differentially expressed genes. *BMC Bioinformatics*, **10**, 61 [Open Access].

Book Chapters and Proceedings

1. **D. Risso** (2021). Normalization of Single-Cell RNA-Seq Data. In Ernesto Picardi (ed.), *RNA Bioinformatics*, Methods in Molecular Biology, vol. 2284, Springer, New York.
2. T. K. Hue Nguyen, M. Chiogna, and **D. Risso** (2020). Graphical models for count data: an application to single-cell RNA sequencing. In A. Pollice, N. Salvati, F. Schirripa Spagnolo (Editors) *Book of Short Papers SIS 2020*. Pearson, Italy.
3. **D. Risso** (2019). Advantages of Modeling Zero-Inflation in scRNA-Seq Data. In *Proceedings of the 2018 Joint Statistical Meetings*. Alexandria, VA: American Statistical Association.
4. **D. Risso**, J. Ngai, T.P. Speed and S. Dudoit (2014). The role of spike-in standards in the normalization of RNA-seq. In D. Nettleton and S. Datta (Editors) *Statistical Analysis of Next Generation Sequence Data*. Springer, New York. http://link.springer.com/chapter/10.1007/978-3-319-07212-8_9.
5. **D. Risso**, G. Sales, C. Romualdi, M. Chiogna (2013). A hierarchical Bayesian model for RNA-Seq data. In Grigoletto, Lisi, Petrone (Editors) *Complex Models and Computational Methods in Statistics*. Springer-Verlag, Italy. http://link.springer.com/chapter/10.1007/978-88-470-2871-5_17.

Preprints and Technical Reports

- M. Borella, G. Martello, **D. Risso**, C. Romualdi (2021) PsiNorm: a scalable normalization for single-cell RNA-seq data. *bioRxiv* <https://doi.org/10.1101/2021.04.07.438822>.
- D. Righelli, L. M. Weber, H. L. Crowell, B. Pardo, L. Collado-Torres, S. Ghazanfar, A. T. L. Lun, S. C. Hicks, **D. Risso** (2021) SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor. *bioRxiv* <https://doi.org/10.1101/2021.01.27.428431>.
- T. K. H. Nguyen, K. Van den Berge, M. Chiogna, **D. Risso** (2020). Structure learning for zero-inflated counts, with an application to single-cell RNA sequencing data. *arXiv* <http://arxiv.org/abs/2011.12044>.
- H. Roux de Bezieux, K. Street, S. Fischer, K. Van den Berge, R. Chance, **D. Risso**, J. Gillis, J. Ngai, E. Purdom, S. Dudoit (2020) Improving replicability in single-cell RNA-Seq cell type discovery with Dune. *bioRxiv* <https://doi.org/10.1101/2020.03.03.974220>.
- Z. Yao, H. Liu, F. Xie, S. Fischer, A. S. Boeshaghi, R. S. Adkins, A. I. Aldridge, S. A. Ament, A. Pinto-Duarte, A. Bartlett, M. M. Behrens, K. Van den Berge, D. Bertagnolli, T. Biancalani, H. Corrada Bravo, T. Casper, C. Colantuoni, H. Creasy, K. Crichton, M. Crow, N. Dee, E. L. Dougherty, W. I. Doyle, S. Dudoit, R. Fang, V. Felix, O. Fong, M. Giglio, J. Gillis, J. Goldy, M. Hawrylycz, H. Roux de Bezieux, B. R. Herb, R. Hertzano, X. Hou, Q. Hu, J. Crabtree, J. Kancherla, M. Kroll, K. Lathia, Y. E. Li, J. D. Lucero, C. Luo, A. Mahurkar, D. McMillen, N. Nadaf, J. R. Nery, S. Niu, J. Orvis, J. K. Osteen, T. Pham, O. Poirion, S. Preissl, E. Purdom, C. Rimorin, **D. Risso**, A. C. Rivkin, K. Smith, K. Street, J.

- Sulc, T. N. Nguyen, M. Tieu, A. Torkelson, H. Tung, E. D. Vaishnav, V. Svensson, C. R. Vanderburg, V. Ntranos, C. van Velthoven, X. Wang, O. R. White, Z. J. Huang, P. V. Kharchenko, L. Pachter, J. Ngai, A. Regev, B. Tasic, J. D. Welch, J. R. Ecker, E. Z. Macosko, B. Ren, BRAIN Initiative Cell Census Network (BICCN), H. Zeng, E. A. Mukamel (2020). An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types *bioRxiv* <https://doi.org/10.1101/2020.02.29.970558>.
- D. Righelli, J. Koberstein, N. Zhang, C. Angelini, L. Peixoto, **D. Risso** (2018). Differential Enriched Scan 2 (DEScan2): a fast pipeline for broad peak analysis. *PeerJ Preprints* 6:e27357v1 <https://doi.org/10.7287/peerj.preprints.27357v1>.
 - R. De Bin, **D. Risso** (2010). Clustering via nonparametric density estimation: an application to microarray data. *WP 3-2010. Department of Statistical Sciences, University of Padova*.

Software

- **RUVSeq**: Remove Unwanted Variation from RNA-Seq Data. *R/Bioconductor package*.
Role: author, maintainer.
Release: <http://bioconductor.org/packages/RUVSeq>
Development: <https://github.com/drisso/RUVSeq>
- **EDASeq**: Exploratory Data Analysis and Normalization for RNA-Seq. *R/Bioconductor package*.
Role: author, maintainer.
Release: <http://bioconductor.org/packages/EDASeq>
Development: <https://github.com/drisso/EDASeq>
- **zinbwave**: Zero-Inflated Negative Binomial-based Wanted Variation Extraction. *R/Bioconductor package*.
Role: author, maintainer.
Release: <http://bioconductor.org/packages/zinbwave>
Development: <https://github.com/drisso/zinbwave>
- **SingleCellExperiment**: S4 class for storing data from single-cell experiments. *R/Bioconductor package*.
Role: author, maintainer.
Release: <http://bioconductor.org/packages/SingleCellExperiment>
Development: <https://github.com/drisso/SingleCellExperiment>
- **clusterExperiment**: Techniques for comparing clusterings of single-cell sequencing data *R/Bioconductor package*.
Role: author.
Release: <http://bioconductor.org/packages/clusterExperiment>
Development: <https://github.com/epurdom/clusterExperiment>
- **scone**: Single-Cell Overview of Normalized Expression. *R/Bioconductor package*.
Role: author, maintainer.
Release: <http://bioconductor.org/packages/scone>
Development: <https://github.com/YosefLab/scone>
- **DEScan2**: Integrated peak and differential caller, specifically designed for broad epigenomic signals. *R/Bioconductor package*.
Role: author.

Release: <http://bioconductor.org/packages/DEScan2>
Development: <https://github.com/drighelli/DEScan2>

- **mbkmeans**: K-means clustering for large single-cell datasets. *R/Bioconductor package*.
Role: author, maintainer.
Release: <https://bioconductor.org/packages/mbkmeans>
Development: <https://github.com/drisso/mbkmeans>
- **NewWave**: Negative binomial model for scRNA-seq. *R/Bioconductor package*.
Role: author.
Release: <https://bioconductor.org/packages/NewWave>
Development: <https://github.com/fedeago/NewWave>
- **SpatialExperiment**: S4 Class for Spatial Experiments handling. *R/Bioconductor package*.
Role: author.
Release: <https://bioconductor.org/packages/SpatialExperiment>
Development: <https://github.com/drighelli/SpatialExperiment>

Presentations

Invited Presentations and Seminars

February 18, 2021 PRBB Computational Biology Seminar, Barcelona Biomedical Research Park, Spain (virtual seminar).

Title: Multivariate analysis of single-cell and spatial transcriptomic data.

December 10, 2019 European Bioconductor Meeting, Bruxelles, Belgium.

Title: Efficient and scalable analysis of single-cell RNA-seq data using Bioconductor.

November 11, 2019 iBRIGHT 2019 - Integrative Biostatistics Research For Imaging Genomics, and High-throughput Technologies in Precision Medicine. MD Anderson Cancer Center, Houston, TX, USA.

Title: *Efficient Clustering of Large Single-cell Datasets*.

May 17, 2019 University of Ghent, Statistics for Single-Cell RNA-seq Data Analysis Symposium.

Title: *Count Models for Single-Cell RNA-Seq and Metagenomics Data*.

August 21, 2018 Johns Hopkins University, Bloomberg School of Public Health.

Title: *Dimensionality Reduction and Clustering for Single-Cell RNA-Seq Data*.

Jul 28 – Aug 2, 2018 Joint Statistical Meetings, Vancouver, Canada. Invited Session 318 – *Advances on the Analysis of Single-Cell Sequencing Data*.

Title: *General and Flexible Methods for Signal Extraction from Single-Cell RNA-Seq Data*.

July 7, 2018 Guest Lecturer, Cold Spring Harbor Laboratory, New York.

Title: Statistical methods for single-cell RNA-seq.

May 17–20, 2018 International Indian Statistical Association Conference, Gainesville, FL.

Title: *General and flexible model for signal extraction and differential expression of single-cell RNA-seq*.

August 24, 2017 New York Genome Center.

Title: *Statistical challenges in single-cell RNA-seq: normalization and dimensionality reduction*.

- June 25–28, 2017** The Western North American Region of the International Biometric Society (WNAR).
Title: *ZINB-WaVE: A general and flexible method for signal extraction from single-cell RNA-seq data.*
- September 12–23, 2016** Computational Genomics Approaches to Precision Medicine, Berlin, Germany.
Title: *Normalization and clustering of single-cell RNA-seq data.*
- August 18–21, 2016** International Indian Statistical Association Conference, Corvallis, OR.
Title: *Normalization, clustering, and differential expression of single-cell RNA-seq data.*
- July 15, 2015** National Research Council (CNR), Napoli, Italy.
Title: *Identification of sub-population of neurons by single-cell RNA sequencing.*
- May 18–20, 2015** Bioinformatic Summer Course, Division of Bioinformatics, Iowa Institute of Human Genetics, University of Iowa, Iowa City, IA, USA.
Title: *Statistical Analysis of RNA-seq.*
- March 28–31, 2015** The Association of Biomolecular Resource Facilities Annual Meeting (ABRF 2015), St. Louis, MO, USA.
Title: *RNA-seq Normalization and Batch Effect Removal.*
- February 11, 2014** Division of Biostatistics, School of Public Health, University of California, Berkeley.
Title: *Normalization of RNA-Seq Data.*
- October 24, 2013** Statistics and Genomics Seminar, University of California, Berkeley.
Title: *The Role of Spike-In Standards in the Normalization of RNA-Seq.*
- Aug 11 – 16, 2013** Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine, Banff, AB, Canada.
Title: *The Role of Spike-in Standards in the Normalization of RNA-seq.*
- May 13, 2013** Department of Statistics, University of Padova, Italy.
Title: *Can we use spike-in sequences to normalize RNA-Seq data?*
- Jan 13, 2012** Symposium: *Computational Sciences and Bioinformatics*, Padova, Italy.
Title: *From data normalization to regulatory networks.*
- Contributed Presentations**
- Jul 27 – 31, 2020** BioC 2020: Where Software and Biology Connect (virtual meeting).
Title: Bench pressing differential abundance methods for microbiome data.
- Jul 27 – Aug 1, 2019** Joint Statistical Meetings, Denver, CO. Section on Statistics in Genomics and Genetics, Session 453 – *Advantages of Modeling Zero-Inflation in scRNA-Seq Data.*
- June 25, 2019** BioC 2019: Where Software and Biology Connect, New York, NY, USA.
Title: Analysis of large single-cell RNA-seq datasets in R/Bioconductor
- April 10, 2019** BRAIN Initiative Cell Census Network (BICCN) Meeting, Bethesda, MD
Title: *Mini-atlas RNA-seq: cluster resolution and reproducibility*
- March 28, 2018** ENAR Spring Meeting, Atlanta, GA
Title: *ZINB-WaVE: A General and Flexible Method for the Supervised and Unsupervised Analysis of Single-Cell RNA-Seq.*

- August 2, 2017** NYQB'17: Making use of emerging technologies; Cold Spring Harbor Laboratory, NY
 Title: *A general and flexible method for signal extraction from single-cell RNA-seq data.*
- Jul 30 – Aug 4, 2016** Joint Statistical Meetings, Chicago, IL. Section on Statistics in Genomics and Genetics, Session 593 – *Batch Effects in Genomics Data.*
 Title: *Accounting for Sample Quality and Other Unwanted Effects in Single-Cell RNA-Seq Data.*
- June 25, 2016** BioC 2016: Where Software and Biology Connect, Stanford, CA, USA.
 Title: Workshop: Analysis of single-cell RNA-seq data with R and *Bioconductor*.
 Workshop material: <https://github.com/drisso/bioc2016singlecell>.
- November 5–6, 2015** Program in Quantitative Genomics Conference 2015: *Single-cell Genomics: Technology, Analysis, and Applications*, Harvard T.H. Chan School of Public Health, Boston, MA, USA.
 Title: *Quality control, exploration, and normalization of single-cell RNA-seq data.* (poster)
- July 10–14, 2015** 23rd Annual International Conference on Intelligent Systems for Molecular Biology / 14th European Conference on Computational Biology (ISMB/ECCB 2015), Dublin, Ireland.
 Title: *Power gain: how normalization affects reproducibility and biological insight of RNA-seq studies in neuroscience.* (poster) [doi: [10.7490/f1000research.1110164.1](https://doi.org/10.7490/f1000research.1110164.1)]
- January 12–13, 2015** European Bioconductor Developers' Meeting, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.
 Title: *Removing unwanted variation from RNA-seq data.*
- Jul 29 – Aug 2, 2012** Joint Statistical Meetings, San Diego, CA. Section on Statistical Computing, Session 224 – *Statistical and Computational Challenges in Metagenomic Analysis of Next-Generation Sequencing Data.*
 Title: *Normalization and Differential Expression in RNA-Seq.*
- Sept 19–21, 2011** 7th Conference on Statistical Computation and Complex Systems (SCo2011), Padova, Italy.
 Title: *A hierarchical Bayesian model for RNA-Seq data.*
- July 28, 2011** Bioconductor Developers' Meeting (BioC 2011), Fred Hutchinson Cancer Research Center, Seattle, WA, USA.
 Title: *EDASeq: Exploratory Data Analysis and Quality Control for RNA-Seq data.*

Grants

Current

- CZF2019-002443
 Bioconductor for the analysis and comprehension of the Human Cell Atlas
 Chan Zuckerberg Foundation
 2019 – 2022
 Role: co-P.I.
- U24 CA 180996-07
 Cancer Genomics: Integrative and Scalable Solutions in R/Bioconductor
 National Cancer Institute
 2019 – 2024
 Role: co-I.

Completed

- 2018-183201
Statistical Analysis and Comprehension of the Human Cell Atlas in R /Bioconductor
Chan Zuckerberg Initiative
2018 – 2019
Role: P.I.
- U01 MH105979
Classification of Cortical Neurons by Single Cell Transcriptomics (Ngai J., PI)
National Institutes of Health / NIMH
2014 – 2017
Role: post-doc.
- U19 MH114830
A Comprehensive Whole-Brain Atlas of Cell Types in the Mouse. (Zeng H., PI)
National Institutes of Health / NIMH
2017 – 2018
Role: co-I.

Professional Memberships

American Statistical Association (ASA): Member since 2012.

Italian Statistical Society (SIS): Member since 2020.

Professional Service

Editorial Service

- **Guest Editor**, PLoS Computational Biology, Frontiers in Oncology (editorial: <https://doi.org/10.3389/fonc.2020.01768>).
- **Reviewer** for international journals, including *Science*, *Annals of Applied Statistics*, *Biostatistics*, *Biometrics*, *Briefings in Bioinformatics*, *Bioinformatics*, *Genome Biology*, *Nature Biotechnology*, *Nature Communications*, *BMC Bioinformatics*, *BMC Genomics*, *Computational Statistics and Data Analysis*, *RNA*, *PLoS Computational Biology*, *PLoS ONE*, *F1000 Research*, *Statistical Methods & Applications*.

Conferences

2020 Member of the Organizing Committee

EuroBioc2020: The European Bioconductor Conference (virtual).

2020 Session Chair

SIS 2020: 50th Scientific Meeting of the Italian Statistical Society.

2020 Member of the Program Committee

ERUM2020 Conference.

2019 Member of the Program Committee

ISMB/ECCB Conference.

2018 Member of the Program Committee

ISMB Conference.

2018 Session Chair

ENAR Spring Meeting, Joint Statistical Meetings.

2017 Member of the Program Committee

ISMB/ECCB Conference (High Throughput Sequencing Algorithm and Applications)

2015, 2017, 2019 Member of the Program Committee

Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB).

Working groups

2017 – 2020 Member of the mini-atlas data-analysis working group

BRAIN Initiative Cell Census Network (BICCN). National Institutes of Health.

2017 – 2020 Member of the analysis working group

TCGA Center for Cancer Genomics Tumor Deconvolution and Immunogenicity

2015 – 2016 Member of the data-analysis sub-working group

BRAIN Initiative Cell Census Consortium (BICCC). National Institutes of Health.

Thesis committees

• **PhD Supervisor**

Erika Banzato, Department of Statistical Sciences, University of Padova (XXXV Cycle).

• **Member of the thesis committee**

Natalie Davidson, Weill Cornell Graduate School of Medical Sciences, New York, USA.
Koen Van den Berge, Ghent University, Belgium.

• **Member of the ACE committee**

Aditya Deshpande, Tri-I Program in Computational Biology and Medicine, New York, USA.
Kofi Gyan, Tri-I Program in Computational Biology and Medicine, New York, USA.
Mervin Fansler, Tri-I Program in Computational Biology and Medicine, New York, USA.

• **Member of the Scientific Evaluation Committee**

INCIPIIT: Innovative Life Science PhD Programme in South Italy (Cofund Marie Skłodowska-Curie Actions).

• **MS Thesis Supervisor (Laurea Magistrale)**

- 2018/2019: Giulia Brunelli, Federico Agostinis, Caterina Ciampanelli, Fabrizio Panzacchi, Clara Bagatin, Giuseppa Tomasello, Matteo Borella.
- 2019/2020: Elena Zuin, Lorenzo Negro.

• **BS Thesis Supervisor (Laurea Triennale)**

- 2019/2020: Benedetta Dal Sasso

University service

- **Department Coordinator for the Italian Evaluation of Research Quality 2015-2019 (VQR)**
Department of Statistical Sciences, University of Padova.
- **Member of the Scientific Committee**
Department of Statistical Sciences, University of Padova
Since 4/2019.
- **Member of the Teaching Board**
PhD Program in Statistics,
Department of Statistical Sciences, University of Padova
Since 10/2019.

Science Outreach

- Oct. 20, 2020** World Statistics Day
Covid 19: a che punto siamo? (in Italian)
- Oct. 15, 2020** Galileo Festival
Un po' di statistica fa bene alla salute (in Italian)
- Sept. 27, 2019** VenetoNight: Researcher's Night
A conversation on statistics and its applications. (in Italian)