

BIOGRAPHICAL SKETCH

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NAME: Davide Cittaro

eRA COMMONS USER NAME (credential, e.g., agency login): CITTARODAVIDE

POSITION TITLE: Researcher

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Università di Milano, Milan, Italy	M.Sc.	04/2002	Biotechnology
Università di Milano-Bicocca, Milan, Italy	1 st level Professional Master's Programme	06/2003	Bioinformatics
Università di Torino, Turin, Italy	PhD	12/2010	Computational Biology
Italian Institute of Technology, Milan, Italy	Postdoctoral	09/2011	Bioinformatics

A. Personal Statement

I have a long-lasting expertise in bioinformatics, with a specific experience on analysis of Next Generation Sequencing data. My working experience has always been focused on the analysis of high-throughput data, covering a wide range of applications. I have been working on NGS data since 2009, with a specific focus on the analysis of molecular mechanisms underlying DNA damage and its implications in cancer development. I have been coordinating the Bioinformatics Unit for five years (2011-2016) at the Center for Translational Genomics and Bioinformatics (now Center for Omics Sciences), within San Raffaele Scientific Institute. As coordinator, I've been supervising several projects focused on genome, epigenome and transcriptome characterization in cellular models and in primary human samples. Since 2017 I am coordinator of the Laboratory for Advanced Methods in Bioinformatics and Data Analysis (λ -lab) at San Raffaele Hospital; I am developing novel tools to investigate multiple omics at single cell level I have contributed to the development of scGET-seq, a novel and powerful method to study chromatin dynamics in single cells. In 2024 I was appointed the role of Assistant Professor of Bioinformatics at UniSR (Milan).

Citations:

- Giansanti V, Tang M, **Cittaro D** — Fast analysis of scATAC-seq data using a predefined set of genomic regions. *F1000Research* 2020, 9:199. doi:10.12688/f1000research.22731.2
- Tedesco M, Giannese F, Lazarevic D, Giansanti V, Rosano D, Monzani S, Catalano I, Grassi E, Zanella E, Botrugno O, Morelli L, Panina Bordignon P, Caravagna G, Bertotti A, Martino G, Aldrichetti L, Pasqualato S, Trusolino L, **Cittaro D**, Tonon G — Chromatin Velocity reveals epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. *Nat Biotechnol.* 2022 Feb 40(2):235-244. doi: 10.1038/s41587-021-01031-1
- Morelli L, Giansanti V, **Cittaro D**. — Nested Stochastic Block Models applied to the analysis of single cell data. *BMC Bioinformatics.* 2021 Nov 30;22(1):576. doi: 10.1186/s12859-021-04489-7
- Giansanti V, Giannese F, Botrugno OA, Gandolfi G, Balestrieri C, Antoniotti M, Tonon G, **Cittaro D** — Scalable Integration of Multiomic Single Cell Data Using Generative Adversarial Networks. *Bioinformatics.* 2024 May 2. doi: 10.1093/bioinformatics/btae300.

5. Perelli L, Zhang L, Mangiameli S, Giannese F, Mahadevan KK, Peng F, Citron F, Khan H, Le C, Gurreri E, Carbone F, Russell AJC, Soeung M, Lam TNA, Lundgren S, Marisetty S, Zhu C, Catania D, Mohamed AMT, Feng N, Augustine JJ, Sgambato A, Tortora G, Draetta GF, Tonon G, Futreal A, Giuliani V, Carugo A, Viale A, Kim MP, Heffernan TP, Wang L, Kalluri R, **Cittaro D**, Chen F, Genovese G — Evolutionary fingerprints of epithelial-to-mesenchymal transition. *Nature*. 2025 Mar 5. doi: 10.1038/s41586-025-08671-2

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2003-2005	Fellow, Proteomic Unit, FIRC Institute for Molecular Oncology, Milano, Italy
2005-2009	System Administrator, European Institute of Oncology, Milano, Italy
2009-2011	Data Analyst, European Institute of Oncology, Milano, Italy
2011	Postdoctoral Fellow, Italian Institute of Technology, Milano, Italy
2011-2017	Head of Bioinformatics, San Raffaele Hospital, Milano, Italy
2017- Present	Area coordinator, San Raffaele Hospital, Milano, Italy
2024- Present	Assistant Professor in Bioinformatics, Università Vita-Salute San Raffaele, Milano, Italy

C. Contributions to Science

1. My early work is related to the study of proteome by means of Mass Spectrometry. In this context I have devised a method to study protein-protein interactions from the analysis of fragmentation spectra of crosslinked proteins. This method has been applied to help resolving the structure of Ndc80/Spc25 complex, a protein complex hard to be resolved by X-ray crystallography.
 - a. Maiolica A, **Cittaro D**, Borsotti D, Sennels L, Ciferri C, Tarricone C, Musacchio A and Rappsilber J — Structural analysis of multi-protein complexes by cross-linking, mass spectrometry and database searching. *Mol Cell Proteomics*. 2007 Dec;6(12):2200-11.
 - b. Petrovic A, Pasqualato S, Dube P, Santaguida S, **Cittaro D**, Monzani S, Massimiliano L, Keller J, Tarricone A, Maiolica A, Stark H, Musacchio A. — The MIS12 complex is a protein interaction hub for outer kinetochore assembly. *J Cell Biol*. 2010 Sep 6;190(5):835-52
2. I have contributed to the analysis of diffuse epigenetic signals by implementing Digital Signal Processing techniques. This approach has been then proven useful for the analysis of broad-source signals which cannot be analyzed by standard methods in epigenome analysis, such as peak calling. This approach has been applied to the analysis of DNA replication mechanisms in eukaryotic cells and heterochromatin assembly.
 - a. Dellino GI, **Cittaro D**, Piccioni R, Luzi L, Banfi S, Segalla S, Cesaroni M, Mendoza-Maldonado R, Giacca M, Pelicci PG. — Genome-wide mapping of human DNA-replication origins: levels of transcription at ORC1 sites regulate origin selection and replication timing. *Genome Res*. 2013 Jan;23(1):1-11
 - b. Rondinelli B, Rosano D, Antonini E, Frenquelli M, Montanini L, Huang D, Segalla S, Yoshihara K, Amin SB, Lazarevic D, The BT, Verhaak RG, Futreal PA, Di Croce L, Chin L, **Cittaro D**, Tonon G. — Histone demethylase JARID1C inactivation triggers genomic instability in sporadic renal cancer. *J Clin Invest*. 2016 Nov 1;126(11):4387. doi: 10.1172/JCI91191
3. My latest work has been focused on technological development in single cell analysis. I contributed to the invention of a novel technology (scGET-seq), a multimodal approach useful to study chromatin dynamics by mapping of accessible and compact chromatin. Moreover, I have developed computational approaches for effective analysis of single cell data.
 - a. Giansanti V, Tang M, **Cittaro D** — Fast analysis of scATAC-seq data using a predefined set of genomic regions. *F1000Research* 2020, 9:199. doi:10.12688/f1000research.22731.2
 - b. Tedesco M, Giannese F, Lazarevic D, Giansanti V, Rosano D, Monzani S, Catalano I, Grassi E, Zanella E, Botrugno O, Morelli L, Panina Bordignon P, Caravagna G, Bertotti A, Martino G, Aldrighetti L, Pasqualato S, Trusolino L, **Cittaro D**, Tonon G — Chromatin Velocity reveals

epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. *Nat Biotechnol.* 2022 Feb 40(2):235-244. doi: 10.1038/s41587-021-01031-1

- c. Morelli L, Giansanti V, **Cittaro D**. — Nested Stochastic Block Models applied to the analysis of single cell data.. *BMC Bioinformatics.* 2021 Nov 30;22(1):576. doi: 10.1186/s12859-021-04489-7
- d. **Cittaro D**, Lazarević D, Tonon G, Giannese F — Analyzing genomic and epigenetic profiles in single cells by hybrid transposase (scGET-seq). *Star Prot.* 2023 Jun; 4(2) 102176. doi: 10.1016/j.xpro.2023.102176.
- e. Giansanti V, Giannese F, Botrugno OA, Gandolfi G, Balestrieri C, Antoniotti M, Tonon G, **Cittaro D** — Scalable Integration of Multiomic Single Cell Data Using Generative Adversarial Networks. *Bioinformatics.* 2024 May 2. doi: 10.1093/bioinformatics/btae300.

Complete list of Published Work in MyBibliography:

<https://www.ncbi.nlm.nih.gov/myncbi/10ol-VtgJtNk8/bibliography/public/>