



Simone Ciccolella

Date of birth: 24/04/1993 | **Nationality:** Italian | **Gender:** Male | (+39) 3452882470 | Italy

● WORK EXPERIENCE

04/09/2021 – 04/10/2021 – Bratislava, Slovakia
VISITING PHD STUDENT – GENETON S.R.O.

Analysis and reconstruction of tumoral subpopulation from circulating DNA. The aim is to build populations from CNV profile of patients, with the goal to identify common patterns across patients, evolutionary history of the patient and common evolutionary paths across different patients.

01/06/2020 – 31/10/2020 – Milan, Italy
SOCIAL MEDIA MANAGER FOR SCIENTIFIC DISSEMINATION – UNIVERSITY OF MILAN-BICOCCA

Sito web ufficiale:

- Modifiche alle informazioni importante sul sito riguardanti i partner del progetto, lo scopo del progetto, gli oggetti di ricerca, ecc.
- Pubblicazioni di notizie riguardanti il progetto quali meeting ufficiali dei partner, pubblicazione di Workshop riguardanti il tema della pangenomica, ecc.
- Pubblicazioni riguardanti gli oggetti di ricerca
- Creazione e gestione di utenti

Pagine Facebook e Twitter:

- Pubblicazioni di notizie riguardanti gli oggetti di ricerca
- Pubblicazione di eventi e convegni
- Aggiornamenti in tempo reale sui convegni

Canale YouTube:

- Registrazione, editing e pubblicazione di video di spiegazione riguardanti gli oggetti di ricerca

15/10/2020 – 14/12/2020 – Bratislava, Slovakia
VISITING PHD STUDENT – GENETON S.R.O.

Analysis and reconstruction of tumoral subpopulation from circulating DNA. The aim is to build populations from CNV profile of patients, with the goal to identify common patterns across patients, evolutionary history of the patient and common evolutionary paths across different patients.

02/08/2017 – 30/10/2017 – New York City, United States
VISITING MASTER STUDENT – HAJIRASOULIHA LAB AT WEILL CORNELL MEDICAL COLLEGE

- Reconciliation of different cancer progression hypotheses
- Reconstruction of cancer progressions form Single Cell Sequencing data

New York, United States

03/2013 – 07/2017 – Novate Milanese, Italy
ASSISTANT TEACHER – MINDFLOWERING

Mathematics and Computer Science support teacher for high school students.

Novate, Italy

● EDUCATION AND TRAINING

01/11/2018 – CURRENT – Milano, Italy

PHD IN COMPUTER SCIENCE – University of Study Milano-Bicocca

EQF level 8

10/10/2016 – 24/10/2018 – Milano, Italy

MASTER OF SCIENCE IN COMPUTER SCIENCE – Università degli Studi Milano-Bicocca

Courses:

- Machine Learning: 29
- Software and data architecture: 29
- Probabilistic models for decision making: 28
- Models and Computational Theory: 28
- Bioinformatics: 30 cum laude
- Complex Systems: models and simulation: 30 cum laude
- Methods for Scientific Computing: 30 cum laude
- Computational Biology: 30 cum laude
- Data and Text Mining: 30 cum laude
- Data Warehouse: 30 cum laude
- Software Engineering: 30

Field(s) of study

- Computer Science

110/110 cum laude |

Inferring cancer progression from Single Cell Sequencing data while allowing loss of mutations | EQF level 7

18/09/2013 – 21/10/2016 – Milano, Italy

BACHELOR OF SCIENCE IN COMPUTER SCIENCE – Università degli Studi Milano-Bicocca

Courses:

- Algorithms and data structures: 30 cum laude
- Basic Calculus: 30 cum laude
- Computer Architecture: 22
- Mathematics Complements: 28
- Fundamentals of Computer Science: 30
- Programming 1: 29
- Programming 2: 28
- Software specification and design: 26
- Databases: 30
- Programming languages: 24
- Algebraic Topics for computer: 29
- Probability and statistics for computer: 28
- Operating systems and networks: 26
- Distributed Systems: 29
- Design and analysis of algorithms: 30
- Advanced data base systems: 30
- Introduction to bioinformatics: 30 cum laude
- Formal Methods: 30
- Operation Research and resource: 28

Field(s) of study

- Computer Science

110/110 cum laude |

A Linear Programming approach to reconstruct cancer phylogenies from multi-sample sequencing data |

EQF level 6

09/2007 – 07/2012 – Milano, Italy

DIPLOMA DI MATURITÀ SCIENTIFICA – Liceo Scientifico Statale Piero Bottoni

EQF level 4

● LANGUAGE SKILLS

Mother tongue(s): ITALIAN

Other language(s):

| | UNDERSTANDING | | SPEAKING | | WRITING |
|----------------|---------------|---------|-------------------|--------------------|---------|
| | Listening | Reading | Spoken production | Spoken interaction | |
| ENGLISH | C2 | C2 | C1 | C1 | C1 |

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

● PUBLICATIONS

Publications - Journals

- Sarwan Ali, Simone Ciccolella, Lorenzo Lucarella, Gianluca Della Vedova, Murray D Patterson. **Simpler and faster development of tumor phylogeny pipelines.** *Journal of Computation Biology*, to appear.
- Simone Ciccolella, Murray Patterson, Paola Bonizzoni, Gianluca Della Vedova. **Effective Clustering for Single Cell Sequencing Cancer Data.** *IEEE J Biomed Health Inform.* 2021 May 18;PP. doi: 10.1109/JBHI.2021.3081380.
- Simone Ciccolella, Camir Ricketts, Mauricio Soto Gomez, Murray Patterson, Dana Silverbush, Paola Bonizzoni, Iman Hajirasouliha, Gianluca Della Vedova. **Inferring Cancer Progression from Single Cell Sequencing while allowing loss of mutations.** *Bioinformatics*, <https://doi.org/10.1093/bioinformatics/btaa722>.
- Simone Ciccolella, Giulia Bernardini, Luca Denti, Paola Bonizzoni, Marco Previtali, Gianluca Della Vedova, **Triplet-based similarity score for fully multilabeled trees with poly-occurring labels,** *Bioinformatics*, <https://doi.org/10.1093/bioinformatics/btaa676>
- Simone Ciccolella, Mauricio Soto Gomez, Murray D. Patterson, Gianluca Della Vedova, Iman Hajirasouliha & Paola Bonizzoni. **gpps: an ILP-based approach for inferring cancer progression with mutation losses from single cell data.** *BMC Bioinformatics* 21, 413 (2020). <https://doi.org/10.1186/s12859-020-03736-7>
- Malikić S, Mehrabadi FR, Ciccolella S, Rahman MK, Ricketts C, Haghshenas E, Seidman D, Hach F, Hajirasouliha I, Sahinalp SC. **PHISCS: a combinatorial approach for subperfect tumor phylogeny reconstruction via integrative use of single-cell and bulk sequencing data.** *Genome Res.* 2019 Nov;29(11):1860-1877. doi: 10.1101/gr.234435.118. Epub 2019 Oct 18. PMID: 31628256; PMCID: PMC6836735.
- Bonizzoni P, Ciccolella S, Vedova GD, Soto M. **Does Relaxing the Infinite Sites Assumption Give Better Tumor Phylogenies? An ILP-Based Comparative Approach.** *IEEE/ACM Trans Comput Biol Bioinform.* 2019 Sep-Oct;16(5):1410-1423. doi: 10.1109/TCBB.2018.2865729. PMID: 31603766.
- P. Bonizzoni, S. Ciccolella, G. Della Vedova, and M. Soto. **Beyond Perfect Phylogeny: Multisample Phylogeny Reconstruction via ILP.** *ACM-BCB 2017.*

● DRIVING LICENCE

Driving Licence: B

● CONFERENCES AND SEMINARS

Conferences

- 19th European Conference on Computational Biology, 2020, Barcelona, Spain (Virtual)
- 24th Annual International Conference RECOMB, 2020. Verona, Italy (Virtual)
- RECOMB-Computational Cancer Biology (CCB), 2020. Verona, Italy (Virtual). **Presenting author.**
- SCANGEN: Single-cell cancer genomics, special session of ISMB (the main Conference in Bioinformatics), 2018. Chicago, IL, USA. **Presenting author.**
- Cancer Development And Complexity, 2018. Como, Italy. **Presenting author.**
- 22nd Annual International Conference RECOMB, 2018. Paris, France.
- RECOMB-Computational Cancer Biology (CCB), 2018. Paris, France. **Presenting author.**
- 8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), 2017. Boston, MA, USA. **Presenting author.**
- 17th Workshop on Algorithms in Bioinformatics (WABI), 2017. Boston, MA, USA.
- Cancer Development And Complexity, 2017. Como, Italy.
- Workshop on Graph Assembly Algorithms for omics data, 2016. Milano, Italy.