

Luca Denti

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RESEARCH INTERESTS

My research activity focuses on developing heuristics and tools for processing and analyzing sequencing data. My interests are in the field of transcriptome analysis (spliced alignment and alternative splicing events quantification) and genomic variations analysis (genotyping of SNPs and indels as well as structural variations discovery). In short, I really like bioinformatics and programming languages.

POSTIONS

Postdoctoral Researcher <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Supervisor: Prof. Paola Bonizzoni	March 2022 – Present <i>Milan, Italy</i>
Postdoctoral Researcher <i>Institut Pasteur</i> <ul style="list-style-type: none">Supervisor: Dr. Rayan Chikhi	Sep. 2020 – Feb. 2022 <i>Paris, France</i>
Research Fellowship <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Supervisor: Dr. Yuri Pirola	Jan. 2020 – Aug. 2020 <i>Milan, Italy</i>

EDUCATION

Doctor of Philosophy in Computer Science <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Thesis: “Algorithms for analyzing genetic variability from Next-Generation Sequencing data”Supervisors: Prof. Paola Bonizzoni, Dr. Raffaella Rizzi, Dr. Marco Previtali	Nov. 2016 – Oct. 2019 <i>Milan, Italy</i>
Master’s Degree in Computer Science <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Thesis: “A new algorithmic approach for the approximate alignment of a string to a graph”Supervisors: Prof. Paola Bonizzoni, Dr. Raffaella Rizzi	Nov. 2014 – Oct. 2016 <i>Milan, Italy</i>
Bachelor’s Degree in Computer Science <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Thesis: “Development of an enhanced Petri Net simulator”Supervisors: Dr. Luca Bernardinello, Prof. Lucia Pomello	Oct. 2011 – Oct. 2014 <i>Milan, Italy</i>

AWARDS

- Premio Giovani Talenti 2022, Università degli Studi di Milano - Bicocca
- Best Poster Award, RECOMB2018

EXPERIENCE

Professional partnership <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Computer Science Lab and DNA Analysis 2019	Nov. 2019 <i>Milan, Italy</i>
Substitute teaching (8 hours) - Computer Science <i>High School “B. Russell”</i>	Dec. 2017 <i>Garbagnate Milanese, Italy</i>
Research collaboration <i>University of Milano - Bicocca</i> <ul style="list-style-type: none">Pattern matching on pangenomeSupervisor: Prof. Paola Bonizzoni	2017 <i>Milan, Italy</i>

RESEARCH PROJECTS

PANGAIA: Pan-genome Graph Algorithms and Data Integration

Funding: EU Horizon 2020, RISE Marie Skłodowska-Curie Action

Role: administrative and research

OPEN SOURCE SOFTWARE

SVDSS C++	github.com/Parsoa/SVDSS
PingPong C++	github.com/Parsoa/PingPong
ASGAL C++, Python	asgal.algolab.eu
MALVA C++	algolab.github.io/malva
Shark C++	github.com/AlgoLab/shark
MALVIRUS Snakemake, Python, Bash	algolab.github.io/MALVIRUS
ppvcf C++	ldenti.github.io/ppvcf

TEACHING

Teacher

University of Milano - Bicocca

Milan, Italy

- Algorithms and Data Structure - Laboratory, *B.Sc. in Computer Science* (a.y. 2021/2022)

Seminars

University of Milano - Bicocca

Milan, Italy

- Analysis and visualization of NGS data (Bioinformatics, *M.Sc. in Computer Science* (a.y. 2021/2022))
- Analysis and visualization of NGS data (Bioinformatics, *M.Sc. in Computer Science* (a.y. 2020/2021))
- FMD-Index and SMEMs (Bioinformatics, *M.Sc. in Computer Science* (a.y. 2017/2018))

Teaching assistant

University of Milano - Bicocca

Milan, Italy

- Programming Language Laboratory, *B.Sc. in Statistics* (a.y. 2019/2020)
- Foundations of Computer Science, *M.S. in Data Science* (a.y. 2019/2020)
- Design and Analysis of Algorithms, *B.Sc. in Computer Science* (a.y. 2016/2017, 2017/2018, 2018/2019, 2019/2020)
- Algorithms and Data Structure, *B.Sc. in Computer Science* (a.y. 2016/2017, 2019/2020)

Supervision activities

University of Milano - Bicocca

Milan, Italy

- Co-supervisor of 11 B.Sc. theses in Computer Science

PUBLICATIONS

Joint first/last authors are indicated with *. Any preprint is marked with a †.

- † L. Denti*, P. Khorsand*, P. Bonizzoni, F. Hormozdiari, R. Chikhi. Improved structural variant discovery in hard-to-call regions using sample-specific string detection from accurate long reads. *bioRxiv* (2022)
- S. Ciccolella*, L. Denti*, P. Bonizzoni, G. Della Vedova, Y. Pirola*, and M. Previtali*. MALVIRUS: an integrated web application for viral variant calling. *BMC Bioinformatics* (2022)
- P. Khorsand*, L. Denti*, Human Genome Structural Variant Consortium, P. Bonizzoni, R. Chikhi, F. Hormozdiari. Comparative genome analysis using sample-specific string detection in accurate long reads. *Bioinformatics Advances* (2021)
- L. Denti*, Y. Pirola*, M. Previtali*, T. Ceccato, G. Della Vedova, R. Rizzi, P. Bonizzoni. Shark: fishing relevant reads in an RNA-Seq sample. *Bioinformatics* (2020)
- S. Ciccolella, G. Bernardini, P. Bonizzoni, M. Previtali, G. Della Vedova. Triplet-based similarity score for fully multi-labeled trees with poly-occurring labels. *Bioinformatics* (2020)
- L. Denti*, M. Previtali*, G. Bernardini, A. Schönhuth, P. Bonizzoni. MALVA: genotyping by Mapping-free ALlele detection of known VARIants. *Iscience* (2019)
- S. Beretta, L. Denti, M. Previtali. Graph Theory and Definitions. *Encyclopedia of Bioinformatics and Computational Biology* (2019)

3. S. Beretta, L. Denti, M. Previtali. Network Properties. Encyclopedia of Bioinformatics and Computational Biology (2019)
2. L. Denti, R. Rizzi, S. Beretta, G. Della Vedova, M. Previtali, P. Bonizzoni. ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. BMC Bioinformatics (2018)
1. S. Beretta, P. Bonizzoni, L. Denti, M. Previtali, R. Rizzi. Mapping RNA-seq data to a transcript graph via approximate pattern matching to a hypertext. International Conference on Algorithms for Computational Biology. Springer (2017)

TALKS, POSTERS, SCHOOLS, AND VISITS

Invited talks:

1. Structural Variations Discovery from Specific Strings. Nov. 9, 2022. Comenius University (Tomas Vinar)

Talks:

6. Comparative genome analysis using sample-specific string detection in accurate long reads. HiTSeq2021
5. Comparative genome analysis using sample-specific string detection in accurate long reads. DSB2021
4. Dynamic quasi-minimal perfect hash function for k-mers. DSB2020
3. MALVA: genotyping by Mapping-free ALlele detection of known VARIants. BITS2019
2. MALVA: genotyping by Mapping-free ALlele detection of known VARIants. RECOMBSEQ2019
1. Mapping RNA-seq data to a transcript graph via approximate pattern matching to a hypertext. AlCoB2017

Posters:

2. MALVA: genotyping by Mapping-free ALlele detection of known VARIants. RECOMB2019
1. ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. RECOMB2018

Research visits:

4. Geneton (Bratislava, Slovakia). Dr. Tomas Szemes - Aug/Nov, 2022
3. Institut Pasteur (Paris, France). Dr. Rayan Chikhi - Dec, 2019
2. Centrum Wiskunde & Informatica (Amsterdam, The Netherlands). Prof. Leen Stougie - Feb/Apr, 2019
1. Centrum Wiskunde & Informatica (Amsterdam, The Netherlands). Prof. Alexander Schönhuth - Oct/Dec, 2018

Schools:

2. Intensive School on Cellular Automata (ACRI school) / Como (Italy) / 2018
1. International School on Mathematics (Graph Theory, Algorithms and Applications) / Erice (Italy) / 2017

PROFESSIONAL ACTIVITIES

Committee

Organizing committee member of:

- PhD School “Introduction to Pangenomics” 2022

Reviewer

Journals:

- Algorithms for Molecular Biology / Bioinformatics / F1000Research / Nucleic Acids Research

Conferences:

- APBC 2022 / BIBM 2022,2018 / BICOB 2018 / ICCS 2017 / ISBRA 2021,2020,2018 / ITAT 2021 / RECOMB 2021 / RECOMB-CG 2022 / RECOMBSEQ 2022,2021 / SPIRE 2017 / WABI 2022,2020,2019

TECHNICAL SKILLS

Languages: C/C++, Python, Rust, Java, Bash, L^AT_EX

Frameworks: Snakemake

Developer Tools: Git, Docker

Libraries: biopython, gffutils, pysam, pandas, NumPy, Matplotlib, Seaborn

REFERENCES

Prof. Paola Bonizzoni, University of Milano - Bicocca

Dr. Rayan Chikhi, Institut Pasteur

Prof. Alexander Schönhuth, University of Bielefeld

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