

Luca Denti

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EDUCATION

Doctor of Philosophy in Computer Science

Nov. 2016 – Oct. 2019

University of Milano - Bicocca

Milan, Italy

- Thesis: “Algorithms for analyzing genetic variability from Next-Generation Sequencing data”
- Supervisors: Prof. Paola Bonizzoni, Dr. Raffaella Rizzi, Dr. Marco Previtali

Master’s Degree in Computer Science

Nov. 2014 – Oct. 2016

University of Milano - Bicocca

Milan, Italy

- Thesis: “A new algorithmic approach for the approximate alignment of a string to a graph”
- Supervisors: Prof. Paola Bonizzoni, Dr. Raffaella Rizzi

Bachelor’s Degree in Computer Science

Oct. 2011 – Oct. 2014

University of Milano - Bicocca

Milan, Italy

- Thesis: “Development of an enhanced Petri Net simulator”
- Supervisors: Dr. Luca Bernardinello, Prof. Lucia Pomello

AWARDS

- Best Poster Award, RECOMB2018

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++

lidenti.github.io/ppvcf

EXPERIENCE

Postdoctoral Researcher

March 2022 – Present

University of Milano - Bicocca

Milan, Italy

- Supervisor: Prof. Paola Bonizzoni

Postdoctoral Researcher

Sep. 2020 – Feb. 2022

Institut Pasteur

Paris, France

- Supervisor: Dr. Rayan Chikhi

Research Fellowship (8 months)

Jan. 2020 – Aug. 2020

University of Milano - Bicocca

Milan, Italy

- Project: “Algorithms to detect alternative splicing events”
- Supervisor: Dr. Yuri Pirola

Professional partnership (14 days)

Nov. 2019

University of Milano - Bicocca

Milan, Italy

- Computer Science Lab and DNA Analysis 2019

Visiting Period

Feb. 2019 – Apr. 2019

Life Sciences and Health group, CWI

Amsterdam, The Netherlands

- Supervisor: Leen Stougie

Visiting Period

Oct. 2018 – Dec. 2018

Life Sciences and Health group, CWI

Amsterdam, The Netherlands

- Supervisor: Alexander Schönhuth

Substitute teaching (8 hours) - Computer Science*High School "B. Russell"*

Dec. 2017

*Garbagnate Milanese, Italy***Professional partnership (2 months)***University of Milano - Bicocca*

2017

Milan, Italy

- Pattern matching on pangenome
- Supervisor: Prof. Paola Bonizzoni

Activity of data entry on CRM*Dos&Donts S.r.l.*

2013

*Rho, Italy***TEACHING EXPERIENCE****Teaching assistant**

2016 – Present

*University of Milano - Bicocca**Milan, Italy*

- Programming Language Laboratory, *Bachelor's Degree in Statistics* (a.y. 2019/2020)
- Foundations of Computer Science, *Master's Degree in Data Science* (a.y. 2019/2020)
- Design and Analysis of Algorithms, *Bachelor's Degree in Computer Science* (a.y. 2016/2017, 2017/2018, 2018/2019, 2019/2020)
- Algorithms and Data Structure, *Bachelor's Degree in Computer Science* (a.y. 2016/2017, 2019/2020)

Cosupervisor of undergraduate final project

2016 – Present

*University of Milano - Bicocca**Milan, Italy*

- Detecting novel exons with enhanced splicing graphs, C++ implementation (a.y. 2019/20)
- Greedy MEM-based alignment to splicing graphs (a.y. 2019/20)
- Read alignment to a multi-gene splicing graph (a.y. 2018/19)
- Detecting novel exons with enhanced splicing graphs, python implementation (a.y. 2018/19)
- Detection of Local Splicing Variation via alignment to a splicing graph (a.y. 2017/18)
- Comparison of tools for alternative splicing analysis (a.y. 2017/18)
- Comparison of tools for read alignment (a.y. 2016/17)

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)
- 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)
- † S. Ciccolella*, L. Denti*, P. Bonizzoni, G. Della Vedova, Y. Pirola*, and M. Previtali*. MALVIRUS: an integrated web application for viral variant calling. *bioRxiv* (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)
- S. Beretta, L. Denti, M. Previtali. Network Properties. *Encyclopedia of Bioinformatics and Computational Biology* (2019)
- 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)
- 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

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 VArants. BITS2019
2. MALVA: genotyping by Mapping-free ALlele detection of known VArants. 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 VArants. RECOMB2019
1. ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. RECOMB2018

PROFESSIONAL ACTIVITIES

Peer-Reviewer

Journals:

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

Conferences:

- ITAT (2021), RECOMB (2021), WABI (2019,20), ISBRA (2018,20), BIBM (2018), BICOB (2018), SPIRE (2017), ICCS (2017)

TECHNICAL SKILLS

Languages: C/C++, Python, 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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