

Luca Denti

✉ lidenti92@gmail.com | 🏠 lidenti.github.io | 🐙 github.com/lidenti

RESEARCH INTERESTS

My research activity focuses on developing algorithms and data structures for processing and analyzing WGS 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).

EDUCATION

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| Doctor of Philosophy in Computer Science | Nov. 2016 – Oct. 2019 |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</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 | |
| Master’s Degree in Computer Science | Nov. 2014 – Oct. 2016 |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</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 | |
| Bachelor’s Degree in Computer Science | Oct. 2011 – Oct. 2014 |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</i> |
| <ul style="list-style-type: none">• Thesis: “Development of an enhanced Petri Net simulator”• Supervisors: Dr. Luca Bernardinello, Prof. Lucia Pomello | |

AWARDS

- Best Poster Award, RECOMB2018

OPEN SOURCE SOFTWARE

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|---|----------------------------|
| 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

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|---|-----------------------|
| Postdoctoral Researcher | March 2022 – Present |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</i> |
| <ul style="list-style-type: none">• Supervisor: Prof. Paola Bonizzoni | |
| Postdoctoral Researcher | Sep. 2020 – Feb. 2022 |
| <i>Institut Pasteur</i> | <i>Paris, France</i> |
| <ul style="list-style-type: none">• Supervisor: Dr. Rayan Chikhi | |
| Research Fellowship (8 months) | Jan. 2020 – Aug. 2020 |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</i> |
| <ul style="list-style-type: none">• Project: “Algorithms to detect alternative splicing events”• Supervisor: Dr. Yuri Pirola | |
| Professional partnership (14 days) | Nov. 2019 |
| <i>University of Milano - Bicocca</i> | <i>Milan, Italy</i> |
| <ul style="list-style-type: none">• Computer Science Lab and DNA Analysis 2019 | |

Visiting Period

Life Sciences and Health group, CWI

- Supervisor: Leen Stougie

Feb. 2019 – Apr. 2019

Amsterdam, The Netherlands

Visiting Period

Life Sciences and Health group, CWI

- Supervisor: Alexander Schönhuth

Oct. 2018 – Dec. 2018

Amsterdam, The Netherlands

Substitute teaching (8 hours) - Computer Science

High School “B. Russell”

Dec. 2017

Garbagnate Milanese, Italy

Professional partnership (2 months)

University of Milano - Bicocca

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

2017

Milan, Italy

Activity of data entry on CRM

Dos&Donts S.r.l.

2013

Rho, Italy

TEACHING EXPERIENCE

Teaching assistant

University of Milano - Bicocca

2016 – Present

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

University of Milano - Bicocca

2016 – Present

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 †.

10. † 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)
9. 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)
8. 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)
7. 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)
6. 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)
5. L. Denti*, M. Previtali*, G. Bernardini, A. Schönhuth, P. Bonizzoni. MALVA: genotyping by Mapping-free ALlele detection of known VARIants. *Iscience* (2019)
4. 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

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

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

paola.bonizzoni@unimib.it

rayan.chikhi@pasteur.fr

aschoen@cebitec.uni-bielefeld.de