Pietro Delfino

Curriculum vitae

Department of Biotechnology, University of Verona

Strada Le Grazie 15, Verona

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www.github.com/pietrod

Born April 26, 1988 - Genova

RESEARCH EXPERIENCE

May-November 2015 **Laimburg Research Center** - Researcher in the lab of Applied Genomics and Molecular Biology - Advisor: Dr. Thomas Letschka

December 2013-January 2015 **ETH Zürich** - Research Assistant at the Institute of Agricultural Sciences - Advisor: Prof. Bruno Studer

November 2012-November 2013 **Fondazione Edmund Mach** - MSc Internship in the Department of Genomics - Advisor: Dr. Daniel J. Sargent

EDUCATION

2015-present **University of Verona** - PhD Biotechnology and Bioinformatics - Tutor: Prof. Diana Bellin Title: *'Candidate-genes association study for grapevine veraison'*

2010-2013 **University of Bologna** - MSc Evolutionary Biology, graduated *cum laude* - Supervisor: Dr. Riccardo Velasco

2007-2010 **University of Genova** - BSc Medical Biotechnology - Supervisor: Prof. Ranieri Cancedda

TEACHING EXPERIENCE

2015-2016 **University of Verona** - Course 'Omics Sciences': Laboratory of RNA-Seq Data Analysis

HONORS & AWARDS

June 2016 **X International Symposium on Grapevine Physiology and Biotechnology** - Poster award winner for the section *'Advances in phenotyping, -omic technologies, large data'*

JOURNALS REVIEWED FOR

BMC Bioinformatics

PUBLICATIONS

Buti, M., Sargent, D. J., Mhelembe, K. G., **Delfino, P.**, Tobutt, K. R., & Velasco, R. (2016). Genotyping-by-sequencing in an orphan plant species *Physocarpus opulifolius* helps identify the evolutionary origins of the genus *Prunus*. *BMC Research Notes*, 9, 268. http://doi.org/10.1186/s13104-016-2069-4

SKILLS

- Languages
  - English (C1)
  - German (A1.2)

- Computer, programming, informatics
  - Unix operating systems
  - Bash scripting (intermediate)
  - R for statistics, bioinformatics - *Bioconductor*, data visualization (upper intermediate)
  - R scripting (intermediate)
  - Python (basic)
  - Version control - *Git*, *Github*
  - Reports, interactive tables, graphics and reports - *Shiny*, *Plotly*

- Bioinformatics and computational biology
  - Whole genome sequencing (*Illumina*) data analysis: quality control, alignment, variant calling, filtering, SNP functional prediction
  - Microarray data analysis
  - RNA-Seq data analysis: quality control, traditional and alignment-free methods, differential expression, gene ontology enrichment, network and pathway analysis
  - Re-analysis of published omics data from GEO and SRA databases
  - Meta-analysis and integration of genetic, genomic and transcriptomic data
  - Population genetics and genomics (phylogenetic analysis, population structure)
  - Genetic map construction from molecular markers (SSR and SNP)

- Molecular biology
  - DNA and RNA purification from animal and plant tissues
  - PCR, qPCR, High Resolution Melting (HRM)
  - Fragment analysis (capillary electrophoresis)