

Cristian Del Fabbro

Bioinformatics researcher

contacts



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Cristian Del Fabbro is Assistant Researcher at the Department of Agricultural and Environmental Sciences at the University of Udine, Italy. He is also a scientific collaborator for IGA foundation (Udine, Italy). His main scientific interests are:

- programming;
- bioinformatics;
- epigenomics and methylation;
- algorithms for short read alignments.

education

- 2006–2010 **PhD in Computer Sciences** University of Udine, Italy
Thesis title: *Repeated sequences in bioinformatics: assembly, annotation and alignments.*
Supervisor: Prof. Alberto Policriti.
- 1996–2005 **Master degree in Computer Sciences** University of Udine, Italy
Thesis title: *Applicazione di tecniche di model checking all'analisi di sistemi biologici (Model checking techniques applied to the analysis of biology systems).*
Supervisor: Prof. Alberto Policriti.
Co-supervisor: Dr. Carla Piazza.

experience

- 2014–Now **Department of Agriculture and Environmental Sciences** University of Udine, Italy
Assistant Researcher
Research unit responsible for the Project “The Epigenomic Plasticity of Grapevine in Genotype by Environment (GxE) Interactions”, for the epigenetic analysis of the grapevine’s methylome.
- 2012–2014 **Istituto di Genomica Applicata** Udine, Italy
Researcher
Development of new algorithms and tools to align and analyse short read produced using Bisulfite protocol. The work was supported by “EPIGEN - progetto bandiera epigenomica” italian project.
- 2009–2011 **Department of Agriculture and Environmental Sciences** University of Udine, Italy
Post-Doc
Project, analysis, and development of alignment algorithms for short reads produced by Next Generation Sequencers.
- 2006–2011 **Istituto di Genomica Applicata** Udine, Italy
Scientific collaborator
- 2006–2009 **Department of Mathematics and Computer Sciences** University of Udine, Italy
PhD student in Computer Sciences
Development of tools for assembly, repeated sequences detection and short read alignment.
- 2005 **Department of Agriculture and Environmental Sciences** University of Udine, Italy
System administrator
DNA of trees: applications and database.
- 2002–2004 **Department of Biomedical Sciences and Technologies** University of Udine, Italy
System administrator
Server administration for web, email, print and backup services.

- 2002–2004 **Department of Mathematics and Computer Science** University of Udine, Italy
System administrator
 Computer laboratory system administrator.
- 1999–2001 **Department of Economy** University of Udine, Italy
System administrator
 Computer laboratory system administrator.

projects

- 2014–Now **The Epigenomic Plasticity of Grapevine in Genotype by Environment (GxE) Interactions**
 FIRB “Futuro in ricerca” italian project, coordinator Dr. Silvia Dal Santo, University of Verona.
 My role: *research unit responsible* (epigenetic analysis).
- 2011–Now **Epigen (Italian Flagship Project)**
 Coordinator Prof. Giuseppe Macino, La Sapienza University, Rome; research unit responsible Prof. Alberto Policriti, University of Udine.
 My role: development of novel algorithm for epigenomic alignment and analysis.
- 2010–2013 **Functional genomics, genetic improvement and innovations for the promotion of the products of the citrus industry - PON01_01623**
 Through application of functional genomics, genetic improvement-oriented, and innovative technologies, the aim is to predict the behavior of citrus’ species and varieties from the point of view of adaptability to different climatic conditions. Through genomic analysis will address the problems associated with the genetic basis of morphological characteristics, productive and adaptive species, in order to analyze together the complex genetic systems that regulate the interactions and their modulation in response to environmental stimuli. Particular attention is given to the stress and resistance of biotic and abiotic stress factors.
- 2009–2013 **DRUPOMICS - Deciphering Peach Genomics and Mas Improving in Stone Fruits Crops**
 The project is split in 3 phases. The first phase deals with genome sequencing of a peach double haploid genotype. It is carried out in cooperation with USA partners (Clemson University and the Joint Genome Institute) and is based on an integrated approach (6X Sanger and 15X 454/Solexa sequencing) that will produce sequences for a 21X genome coverage. The second phase is committed to the development of molecular tools (EST collections, genetic maps) for mapping and cloning genes/QTLs of interest for peach and apricot breeding. The major traits object of study are fruit quality and ripening and resistance to several diseases. The last phase deals with the management of information: creation of dbases, development of interactive web sites.
- 2009–2010 **Noveltree (FF7-211868)**
 NovelTree is designed to enable significant genetic improvement of tree characteristic and forest products properties to satisfy the needs (quality, quantity, sustainability, vulnerability) of the forest-based sector and consumers. The challenges facing forest geneticists and tree breeders include recognition of changing demands on forests for a wider range of high value forest products and sustainability of forest ecosystems under climate change.

2006–2010 **Structural and Functional Characterization of the Grape Genome - VIGNA (Vitis GeNome Analysis)**

The project aims to apply advanced genome analysis methods to broaden our appreciation of the genetic information contained in the grape genome. This will allow us to understand the complex genetic systems that govern developmental and physiological processes as well as mechanisms of response to environmental stimuli. Understanding these processes is fundamental to the development of new theoretical concepts and molecular tools for the evaluation and characterization of the genetic resources available to modern viticulture. The project aims to contribute to the growth of Italian and European viticulture in the 21st century in harmony with the principle that scientific knowledge should facilitate the combination of traditional methods with technological innovation.

expertises

Bioinformatics skills:

- assembly (Arachne, PCAP);
- long reads alignment (BLAST, BLAT, crossmatch);
- short reads alignment (ERNE, BWA, Bowtie2)
- transposable elements discovery and annotation (RepeatMasker, ReAS)
- methylome alignment (ERNE) and analysis (NGSTOOLS)
- development of ad-hoc scripts and programs

Programming languages:

- *Skilled level:* C++, Java, Perl, Python;
- *Basic level:* Basic, Fortran, Javascript, Mathematica, Matlab, Pascal, R, PHP, Prolog.

IT Professional skills:

- *Operating Systems:* GNU/Linux (Ubuntu, Debian, CentOS, RedHat), OSX, Windows;
- *Development software and library:* Autoconf, BOOST, Eclipse, Subversion, MPI, Mercurial;
- *Service software:* Apache, DNS, EXIM/Postifx, Mysql/Postgres, CMS, Samba, Nexentastor.

open source software (development)

ERNE <http://erne.sf.net>

ERNE (Extended Randomized Numerical alignEr) is a short string alignment package whose goal is to provide an all-inclusive set of tools to handle trimming and alignment for short (NGS-like) reads. ERNE comprises ERNE-MAP (core alignment tool/algorithm), ERNE-BS5 (bisulfite treated reads aligner, [11]), ERNE-FILTER (quality trimming and contamination filtering, [4]), and parallel version of the aligners (ERNE-PMAP and ERNE-PBS5, [5]).

LIBBIOCPP <http://libbiocpp.sf.net/>

LIBBIOCPP is a library wrote in C++ for bioinformatics people. The library provides interfaces to parse commonly used bioinformatics files (e.g., FASTA, FASTQ, SAM/BAM, WIG) and some data structure and algorithms for performe analysis (e.g., genome representations, short read analysis).

NGS-SUITE <http://ngs-suite.sf.net/>

NGS-SUITE is a set of tools (based on LIBBIOCPP) that perform a wide spectrum of statistics and analysis about NGS-like data (e.g., statistics about alignments, coverage profile creation, smallRNA trimming).

- rNA** <http://iga-rna.sf.net>
rNA (randomized Numerical Aligner, [13]) is a short string alignment tool to trim and align reads. There is also a parallel version optimized for MPI-based clusters [6]. rNA is no more maintained: the code was exported and improved in ERNE software.
- GAM** <http://services.appliedgenomics.org/software/gam/>
GAM (Genomic Assembler Merger, [2]) is a software tool to integrate two different assemblies (produced using Sanger long reads) and improves the overall quality of the genome sequences by merging them.

teaching

- 2012/13 **Technology and design of computer systems and telecommunications** (G.Bearzi High School, Udine, Italy)
- 2012/13 **Laboratory of Computer Systems and Networking** (G.Bearzi High School, Udine, Italy)
- 2012/13 **Laboratory of Algorithms and Data structures** (Department of Computer Science, University of Udine, Italy)
- 2012/13 **Laboratory of Computer Systems and Networking** (G.Bearzi High School, Udine, Italy)
- 2011/12 **Laboratory of Algorithms and Data structures** (Department of Computer Science, University of Udine, Italy)
- 2011/12 **Laboratory of Computer Systems and Networking** (G.Bearzi High School, Udine, Italy)
- 2010/11 **Laboratory of Algorithms and Data structures** (Department of Computer Science, University of Udine, Italy)
- 2009/10 **Bioinformatics** (interfaculty course, University of Trieste, Italy)
- 2008/09 **Informatic** (Biotechnology interfaculty course, University of Udine, Italy)
- 2007/08 **Informatic** (Biotechnology interfaculty course, University of Udine, Italy)

other activities

- 2015 Organization and speaker for the workshop **On top of genomics**
- 2013 Organization of the **BITS Annual Meeting 2013**
- 2012 Organization of the **BCI 2012 (Biology, Computation and Information)** summer school
- 2012 Organization and speaker for the **NGS Training Workshop 2012 - Data Crunching: from hell to heaven**
- 2011 Organization of the **IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis**
- 2010 Organization of the **BCI 2010 (Biology, Computation and Information)** summer school
- 2008 Organization of the **BCI 2008 (Biology, Computation and Information)** summer school
- 2007 Organization of the **BCI 2007 (Biology, Computation and Information)** summer school
- 2006 Organization of the **BCI 2006 (Biology, Computation and Information)** summer school

reviewer

Bioinformatics (Oxford University Press)

<http://bioinformatics.oxfordjournals.org>

BMC Bioinformatics (BioMed Central)

<http://www.biomedcentral.com/bmcbioinformatics>

ICBEB (International Conference on Biomedical Engineering and Biotechnology)

<http://www.icbeb.org/>

International Journal of Genomics (Hindawi)

<http://www.hindawi.com/journals/ijg/>

contests

1997–2000 ACM International Collegiate Programming Contest: University of Ulm (Germany, 1997), University of Valladolid (Spain, 1998), University of Valladolid (Spain, 1999) - best rank: 3, University of Porto (Portogallo, 2000).

1995 Italian mathematics contest, Bocconi university, Milano (Italy). Final rank: 8.

summary

Cristian Del Fabbro formation starts as computer scientist but since 2005, with its Master Degree thesis (“Applicazione di tecniche di model checking all’analisi di sistemi biologici” - “Model checking techniques applied to the analysis of biology systems”) taken at University of Udine, he approached to the bioinformatics area. In 2006 he started the PhD student program in the University of Udine and it was involved in the first steps of the preparation of IGA’s laboratory: LIMS (Laboratory Information Management System), computational services, system administrator, and—last but not least—bioinformatics research for the IGA. In its four years as PhD computer science student and in the following 2 years as post-doc (either in University of Udine) he was involved in a lot of aspect of biological data manipulation, computation and analysis, from the “old-era” generation sequencers (ABI3730) to the Next Generation Sequencers (Illumina).

In 2010 he defends its PhD thesis “Repeated sequences in bioinformatics: assembly, annotation and alignments” a summary of its experiences in genome assembly, transposable elements detection and annotation, and short reads aligners. As post-doc he continued to work, principally, on the enhancement of short reads aligners. He worked on a tool called rNA (randomized Numerical Aligner, [13]) that it is able to efficiently and accurately aligns DNA/RNA short reads. He worked also on a distributed version of rNA, called mrNA [6] that can take advantages of cluster of computer.

In 2012 he became a member of the “EPIGEN - progetto bandiera epigenomica” project whose aim is to discover and analyse the role of the epigenetic modifications between individuals. Within this project he contributed to the realization of the ERNE (Extended Randomized NumErical - <http://erne.sf.net>) suite of aligners program. In the suite it is presented the ERNE-BS5 aligner [11]. ERNE-BS5 is a short read aligner able to align reads produced using BS-seq protocol.

In 2013 he won a FIRB - “Futuro in ricerca” grant for the project “The Epigenomic Plasticity of Grapevine in Genotype by Environment (GxE) Interactions”, a joint work of three research units with different expertise. Together with Silvia Del Santo (project coordinator, University of Verona) and Irene Perrone (University of Turin), the transcriptome and methylome of two grapevine varieties will be sequenced and analyzed to detect the modifications induced by the climate changes.

He contributed to the assembly and the analysis of several genomes: barley, citrus [14], grapevine [8, 9], maize, peach [12], poplar, and many more.

links

University home page

<http://people.uniud.it/page/cristian.delfabbro>

Linkedin 

<http://it.linkedin.com/in/delfabbro>

Google Scholar

<http://http://scholar.google.it/citations?user=-jBq0cQAAAAA>

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<http://www.scopus.com/authid/detail.url?authorId=22133929400>

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<http://orcid.org/0000-0001-8189-6192>

ResearchID (ID:C-5523-2014)

<http://www.researcherid.com/rid/C-5523-2014>

publications

- [1] K. R. Bradnam, J. N. Fass, A. Alexandrov, P. Baranay, M. Bechner, I. Birol, S. Boisvert, J. A. Chapman, G. Chapuis, R. Chikhi, H. Chitsaz, W.-C. Chou, J. Corbeil, **C. Del Fabbro**, T. R. Docking, R. Durbin, D. Earl, S. Emrich, P. Fedotov, N. A. Fonseca, G. Ganapathy, R. A. Gibbs, S. Gnerre, E. Godzaridis, S. Goldstein, M. Haimel, G. Hall, D. Haussler, J. B. Hiatt, I. Y. Ho, J. Howard, M. Hunt, S. D. Jackman, D. B. Jaffe, E. Jarvis, H. Jiang, S. Kazakov, P. J. Kersey, J. O. Kitzman, J. R. Knight, S. Koren, T.-W. Lam, D. Lavenier, F. Laviolette, Y. Li, Z. Li, B. Liu, Y. Liu, R. Luo, I. Maccallum, M. D. Macmanes, N. Maillat, S. Melnikov, D. Naquin, Z. Ning, T. D. Otto, B. Paten, O. S. Paulo, A. M. Phillippy, F. Pina-Martins, M. Place, D. Przybylski, X. Qin, C. Qu, F. J. Ribeiro, S. Richards, D. S. Rokhsar, J. G. Ruby, S. Scalabrin, M. C. Schatz, D. C. Schwartz, A. Sergushichev, T. Sharpe, T. I. Shaw, J. Shendure, Y. Shi, J. T. Simpson, H. Song, F. Tsarev, F. Vezzi, R. Vicedomini, B. M. Vieira, J. Wang, K. C. Worley, S. Yin, S.-M. Yiu, J. Yuan, G. Zhang, H. Zhang, S. Zhou, and I. F. Korf, "Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species," *Gigascience*, vol. 2, p. 10, Jul 2013.
- [2] A. Casagrande, **C. Del Fabbro**, S. Scalabrin, and A. Policriti, "GAM: Genomic Assemblies Merger: A Graph Based Method to Integrate Different Assemblies," *Bioinformatics and Biomedicine, IEEE International Conference on*, vol. 0, pp. 321–326, 2009.
- [3] **C. Del Fabbro**, A. Policriti, M. Morgante, and N. Vitacolonna, "TEA: a Transposable Elements Annotator," *Proceedings of The 2009 International Conference on Bioinformatics and Computational Biology*, vol. 2, pp. 528–535, July 2009.
- [4] **C. Del Fabbro**, S. Scalabrin, M. Morgante, and F. M. Giorgi, "An Extensive Evaluation of Read Trimming Effects on Illumina NGS Data Analysis," *PLoS one*, vol. 8, no. 12, p. e85024, 2013.
- [5] **C. Del Fabbro**, F. Tardivo, and A. Policriti, "A Parallel Algorithm for the Best k-mismatches Alignment Problem," *Proceedings of 2014 22nd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing (PDP2014)*, vol. 0, pp. 586–589, February 12–14 2014.
- [6] **C. Del Fabbro**, F. Vezzi, and A. Policriti, "mrNA: The MPI Randomized Numerical Aligner," *Bioinformatics and Biomedicine, IEEE International Conference on*, vol. 0, pp. 139–142, 2011.
- [7] F. M. Giorgi, **C. Del Fabbro**, and F. Licausi, "Comparative study of RNA-seq- and Microarray-derived coexpression networks in Arabidopsis thaliana," *Bioinformatics*, vol. 29 (6), pp. 717–724, 2013.
- [8] O. Jaillon, J.-M. Aury, B. Noel, A. Policriti, C. Clepet, A. Casagrande, N. Choisne, S. Aubourg, N. Vitulo, C. Jubin, A. Vezzi, F. Legeai, P. Huguency, C. Dasilva, D. Horner, E. Mica, D. Jublot, J. Poulain, C. Bruyère, A. Billault, B. Segurens, M. Gouyvenoux, E. Ugarte, F. Cattonaro, V. Anthouard, V. Vico, **C. Del Fabbro**, M. Alaux, G. D. Gaspero, V. Dumas, N. Felice, S. Paillard, I. Juman, M. Moroldo, S. Scalabrin, A. Canaguier, I. L. Clainche, G. Malacrida, E. Durand, G. Pesole, V. Laucou, P. Chatelet, D. Merdinoglu, M. Delledonne, M. Pezzotti, A. Lecharny, C. Scarpelli, F. Artiguenave, M. E. Pè, G. Valle, M. Morgante, M. Caboche, A.-F. Adam-Blondon, J. Weissenbach, F. Quétier, P. Wincker, and French-Italian Public Consortium for Grapevine Genome Characterization, "The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla," *Nature*, vol. 449, pp. 463–467, Sep 2007.

- [9] E. Mica, V. Piccolo, M. Delledone, A. Ferrarini, M. Pezzotti, C. Casati, **C. Del Fabbro**, G. Valle, A. Policriti, M. Morgante, G. Pesole, M. E. Pe, and D. S. Horner, "Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in *Vitis vinifera*," *BMC Genomics*, vol. 11, p. 109, Feb 2010.
- [10] E. Mica, V. Piccolo, M. Delledone, A. Ferrarini, M. Pezzotti, C. Casati, **C. Del Fabbro**, G. Valle, A. Policriti, M. Morgante, G. Pesole, M. E. Pe, and D. S. Horner, "High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in *Vitis vinifera*," *BMC Genomics*, vol. 10, p. 558, Nov 2009.
- [11] N. Prezza, **C. Del Fabbro**, F. Vezzi, E. De Paoli, and A. Policriti, "ERNE-BS5: Aligning BS-treated Sequences by Multiple Hits on a 5-letters Alphabet," *Proceedings of The 2012 ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2012)*, vol. 0, pp. 12–19, 2012. ISBN: 978-1-4503-1670-5.
- [12] I. Verde, A. G. Abbott, S. Scalabrin, S. Jung, S. Shu, F. Marroni, T. Zhebentyayeva, M. T. Dettori, J. Grimwood, F. Cattonaro, A. Zuccolo, L. Rossini, J. Jenkins, E. Vendramin, L. A. Meisel, V. Decroocq, B. Sosinski, S. Prochnik, T. Mitros, A. Policriti, G. Cipriani, L. Dondini, S. Ficklin, D. M. Goodstein, P. Xuan, **C. Del Fabbro**, V. Aramini, D. Copetti, S. Gonzalez, D. S. Horner, R. Falchi, S. Lucas, E. Mica, J. Maldonado, B. Lazzari, D. Bielenberg, R. Pirona, M. Miculan, A. Barakat, R. Testolin, A. Stella, S. Tartarini, P. Tonutti, P. Arús, A. Orellana, C. Wells, D. Main, G. Vizzotto, H. Silva, F. Salamini, J. Schmutz, M. Morgante, and D. S. Rokhsar, "The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution," *Nature Genetics*, vol. 45, pp. 487–494, 2013.
- [13] F. Vezzi, **C. Del Fabbro**, A. I. Tomescu, and A. Policriti, "rNA: a Fast and Accurate Short Reads Numerical Aligner," *Bioinformatics*, vol. 28, pp. 123–124, January 2012.
- [14] G. A. Wu, S. Prochnik, J. Jenkins, J. Salse, U. Hellsten, F. Murat, X. Perrier, M. Ruiz, S. Scalabrin, J. Terol, M. A. Takita, K. Labadie, J. Poulain, A. Couloux, K. Jabbari, F. Cattonaro, **C. Del Fabbro**, S. Pinosio, A. Zuccolo, J. Chapman, J. Grimwood, F. R. Tadeo, L. H. Estornell, J. V. Muñoz-Sanz, V. Ibanez, A. Herrero-Ortega, P. Aleza, J. Pérez-Pérez, D. Ramón, D. Brunel, F. Luro, C. Chen, W. G. Farmerie, B. Desany, C. Kodira, M. Mohiuddin, T. Harkins, K. Fredrikson, P. Burns, A. Lomsadze, M. Borodovsky, G. Reforgiato, J. Freitas-Astúa, F. Quetier, L. Navarro, M. Roose, P. Wincker, J. Schmutz, M. Morgante, M. A. Machado, M. Talon, O. Jaillon, P. Ollitrault, F. Gmitter, and D. Rokhsar, "Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication," *Nature Biotechnology*, Jun 2014.

oral presentations

- [15] E. De Paoli, **C. Del Fabbro**, M. Celii, S. Pinosio, M. Miculan, F. Marroni, G. Di Gaspero, and M. Morgante, "Single-base resolution of the grapevine methylome reveals the epigenomic landscape of a perennial fruit crop," in *SIGA 2013*, (Foggia, Italy), September 16-19, 2013.
- [16] **C. Del Fabbro**, "An Algorithmic Analysis Pipeline for Next Generation Sequencers," in *BCI 2008*, (Trieste, Italy), September 9, 2008.
- [17] **C. Del Fabbro**, "Illumina pipeline for primary data analysis," in *Second IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis*, (Udine, Italy), September 6-9, 2011.
- [18] **C. Del Fabbro**, "Alignment to a reference," in *Second IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis*, (Udine, Italy), September 6-9, 2011.
- [19] **C. Del Fabbro**, "Sequence Analysis Pipeline," in *Workshop on HT-resequencing in Populus*, (Udine, Italy), May 12-14, 2010.
- [20] **C. Del Fabbro**, "Experience with GRAPE at IGA," in *Workshop on Populus*, (Rome, Italy), March 16, 2009.
- [21] **C. Del Fabbro**, "Tour e classificazione dei principali strumenti di allineamento (per sequenze corte) - Tour and classification of the principal alignment software (for short

- reads),” in *Corso su "STRUMENTI BIOINFORMATICI PER L'ANALISI DELLA STRUTTURA E DELLA FUNZIONE DEL GENOMA"*, (Volterra, Italy), June 17, 2009. (invited speaker).
- [22] **C. Del Fabbro**, “Introduction to the Unix Environment,” in *IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis*, (Udine, Italy), June 13-16, 2011.
- [23] **C. Del Fabbro**, “Illumina pipeline for primary data analysis,” in *IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis*, (Udine, Italy), June 13-16, 2011.
- [24] **C. Del Fabbro**, “Alignment to a reference,” in *IGA Summer School 2011. Next Generation Sequencing: from samples to data analysis*, (Udine, Italy), June 13-16, 2011.
- [25] **C. Del Fabbro**, “ERNE-BS5: Aligning BS-treated Sequences by Multiple Hits on a 5-letters Alphabet,” in *Next Generation Sequencing & Epigenomics, fourth Bari workshop*, (Bari, Italy), December 5-7, 2012.
- [26] **C. Del Fabbro**, “Allineamento di sequenze nell’era dei NGS - Sequence alignment in the NGS era,” in *Corso su "BIOINFORMATICA APPLICATA ALLA GENOMICA AGRARIA"*, (Salsomaggiore Terme, Italy), April 12 and 19, 2009. (invited speaker).
- [27] **C. Del Fabbro**, “ERNE-BS5: Aligning BS-treated Sequences by Multiple Hits on a 5-letters Alphabet,” in *The 2012 ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2012)*, (Orlando, Florida, USA), 2012.
- [28] **C. Del Fabbro**, C. Cattonaro, A. Policriti, and M. Morgante, “Automatic Identification Of Transposable Elements,” in *BITS 2007 Meeting*, (Naples, Italy), April 27, 2007.
- [29] **C. Del Fabbro**, D. Copetti, A. Brindisi, A. Policriti, and M. Morgante, “Combining Evidences For Repeats Annotation,” in *BCI 2007*, (Trieste, Italy), July 4, 2007.
- [30] **C. Del Fabbro**, E. De Paoli, N. Prezza, M. Celii, M. Morgante, and A. Policriti, “ERNE-BS5: Aligning BS-treated Sequences by Multiple Hits on a 5-letters Alphabet,” in *BITS Annual Meeting 2013*, (Udine, Italy), May 21-23, 2013.
- [31] **C. Del Fabbro** and C. Piazza, “Preprocessing Biochemical Traces,” in *BCI 2004*, (Dobbiaco, Italy), September 25, 2004.
- [32] **C. Del Fabbro** and A. Policriti, “In silico annotation of repeated sequences in Grape genome,” in *VIGNA meeting*, (Padova, Italy), March 13, 2007.
- [33] **C. Del Fabbro**, A. Policriti, M. Morgante, and N. Vitacolonna, “TEA: a Transposable Elements Annotator,” in *The 2009 International Conference on Bioinformatics and Computational Biology*, (Las Vegas, USA), July 13-16, 2009.
- [34] **C. Del Fabbro**, A. Vezzi, and A. Policriti, “mrNA: the MPI randomized Numerical Aligner,” in *Proceedings of 2011 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2011)*, (Atlanta, Georgia), November 12-15, 2011.
- [35] A. Lunardon, **C. Del Fabbro**, E. De Paoli, T. Hardcastle, C. Forestan, S. Farinati, and S. Varotto, “Analysis of small RNA populations of maize leaves following abiotic stress treatments,” in *SIGA 2013*, (Foggia, Italy), September 16-19, 2013.
- [36] N. Vitacolonna, **C. Del Fabbro**, and A. Policriti, “TEA: a Transposable Elements Annotator,” in *One day BITS meeting*, (Rome, Italy), July 4, 2008.

posters

- [37] C. Cattonaro, **C. Del Fabbro**, and The French-Italian Public Consortium for Grapevine Genome Characterization, “Application of Illumina Genome Analysis platform and Whole Transcriptome Analysis for grape genome annotation,” in *Illumina Usermeeting 2008*, (Rottach-Egern, Germany), May 8-9, 2008.
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