



## Francesca Finotello, Ph.D.

### PERSONAL DATA

Name	Francesca Finotello
Year of Birth	1985
Nationality	Italian
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### RESEARCH INTERESTS

Implementation of computational methods for the analysis of Next-generation Sequencing data, with application to human health. Main case studies:

- Investigation of complex and genetic diseases through RNA-seq and exome sequencing;
- Study of the human microbiome in chronic diseases and cancer through 16S sequencing;
- Assembly of human pathogens from whole-genome sequencing.

### WORKING EXPERIENCE

December 2013 – present

Postdoctoral fellow at the Department of Information Engineering, University of Padova, Italy. Grant funded by the European Commission: "Development of algorithms and tools for Next-Generation Sequencing data analysis".  
Advisor: Prof. Barbara Di Camillo.

Development of computational methods for the analysis of Next-Generation Sequencing data and application to the study of complex diseases. Ongoing projects: characterization of gene expression and SNPs from "static" and time-course RNA-seq data; study of the human microbiome in healthy and pathological individuals and reconstruction of bacterial co-occurrence networks.

June 2010 – January 2011

Research assistant at the Department of Information Engineering, University of Padova, Italy. Project: "Comparative analysis of genomic assemblers".  
Advisor: Prof. Gianna Maria Toffolo.

Comparative analysis of methods for the assembly of pyrosequencing data from whole-genome sequencing. Optimization of analysis pipelines for the reconstruction of bacterial genomes from pyrosequencing data.

## EDUCATION

- 2011 – 2014  
PhD in Bioengineering, Department of Information Engineering, University of Padova, Italy.  
Advisor: Dr. Barbara Di Camillo  
Thesis: "Computational methods for the analysis of gene expression from RNA sequencing data".  
Development of computational methods for the quantification of gene expression *via* RNA-seq and application to the study of complex diseases. Main tasks: experimental design, bioinformatics and statistical analysis, computational methods development and implementation.
- 2007 – 2009  
Master's Degree in Bioengineering, Department of Information Engineering, University of Padova, Italy.  
Grade: 110/110 *cum Laude*.  
Advisor: Prof. Gianna Maria Toffolo.  
Thesis: "Complete comparative analysis of algorithms for whole genome shotgun assembly".
- 2004 – 2007  
Bachelor's Degree in Biomedical Engineering, Department of Information Engineering, University of Padova, Padova, Italy.  
Grade: 107/110.  
Advisor: Prof. Alfredo Ruggeri.  
Thesis: "Feature extraction and classification methods for automatic karyotyping".

## TEACHING EXPERIENCE

- 2012 and 2013  
Teaching support for the MD course "Bioingegneria per la Genomica".  
Department of Information Engineering, University of Padova, Italy.
- 2013  
"RNA-seq data analysis" tutorial, within the MD course "Bioingegneria per la Genomica".  
May 28 and June 4, 2013. Department of Information Engineering, University of Padova, Italy.
- 2013  
Teaching support for the MD course "Elaborazione di Segnali Biologici".  
Department of Information Engineering, University of Padova, Italy.
- 2004 – 2009  
Private lessons of mathematics for high school students.

## RESEARCH PROJECTS

- Progetto di Ricerca di Ateneo (PRAT): "Models of RNA sequencing data variability for quantitative transcriptomics" (CPDA101217).  
Role: Junior investigator.
- Progetto di dottorato CARIPARO: "RNA sequencing for quantitative transcriptomics".  
Role: Junior investigator.
- IMI Call topic: The Innovative Medicines Initiative, European Project, SUMMIT: "SURrogate markers for Micro- and Macro-vascular hard endpoints for Innovative diabetes Tools" (EU-IMI 115006).  
Role: Junior investigator.

## VISITING FELLOWSHIPS

- June 2013 – November 2013  
Centro Nacional de Investigaciones Cardiovasculares (CNIC), Madrid, Spain.  
Advisor at CNIC: Dr. Fátima Sánchez Cabo.  
Development and implementation of computational pipelines for the analysis of RNA-seq and exome sequencing data, and application to the study of spinal muscular atrophy.

June 2011,  
April and October 2012

Clinical Research Centre (CRC), Lund University, Malmö, Sweden.  
Advisor at CRC: Prof. Leif Groop.

Optimization of methods for the analysis of exome sequencing data from diabetic patients (SUMMIT project)  
Transcriptomics analysis of RNA-seq and exome sequencing data from human pancreatic islets.

## GRANTS AND AWARDS

- 2014 Winner of the "Best Poster Award" at "NETTAB 2014, from structural bioinformatics to integrative systems biology", with the poster: "Reverse engineering the human microbiota".
- 2014 Winner of the "Marco Ramoni's doctoral research award" with the PhD thesis: "Computational methods for the analysis of gene expression from RNA sequencing data".
- 2014 Finalist in the "GNB Young Researchers Award" of the Fourth National Congress of Bioengineering.
- 2013 Awarded with "Premio Città Impresa" for young entrepreneurs, researchers and innovators.
- 2012 Finalist in "Start Cup Veneto - Competition for innovative business ideas" with the idea: "*Mindtrack*, a portable device for drivers' drowsiness detection".
- 2011 CARIPARO Foundation's grant for a 3 years PhD Scholarship on research theme: "RNA sequencing for quantitative transcriptomics".
- 2003 Awarded with "Premio studente atleta" for proficient students and athletes.

## PUBLICATIONS

### JOURNAL PAPERS

- 2014 T. Sanavia, **F. Finotello**, B. Di Camillo. "FunPat: function-based pattern analysis on RNA-seq time series data". BMC Bioinformatics (in print).
- 2014 **F. Finotello** and B. Di Camillo. "Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis". Briefings in Functional Genomics, Briefings in Functional Genomics, published ahead of print on September 18, 2014 doi:10.1093/bfgp/elu035.
- 2014 J. Fadista, P. Vikman, E. Ottosson Laakso, I. Mollet, P. Osmark, J. Esguerra, J. Taneera, C. Ladenvall, K. Hansson, **F. Finotello**, U. Krus, B. Di Camillo, O. Hansson, L. Eliasson, A. Rosengren, E. Renström, C. B. Wollheim, L. Groop. "Global transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism". Proceedings of the National Academy of Sciences, published ahead of print on September 8, 2014, doi:10.1073/pnas.1402665111.
- 2013 **F. Finotello**, E. Lavezzo, L. Bianco, L. Barzon, P. Mazzon, P. Fontana, S. Toppo, B. Di Camillo. "Reducing bias in RNA sequencing data: a novel approach to compute counts". BMC Bioinformatics 15(1):1-12, 2014. Highly accessed.
- 2013 E. Lavezzo, S. Toppo, E. Franchin, B. Di Camillo, **F. Finotello**, M. Falda, R. Manganelli, G. Palù, L. Barzon. "Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitidis outbreak". BMC Infectious Diseases 13(1):554, 2013. Highly accessed.
- 2012 **F. Finotello**, E. Lavezzo, P. Fontana, D. Peruzzo, A. Albiero, L. Barzon, M. Falda, B. Di Camillo, S. Toppo. "Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data". Briefings in Bioinformatics, 13(3):269-280, 2012.

ABSTRACTS AND  
SHORT PAPERS

- 2010 E. Lavezzo, S. Toppo, L. Barzon, C. Cobelli, B. Di Camillo, **F. Finotello**, E. Franchin, D. Peruzzo, G.M. Toffolo, M. Trevisan, G. Palù. "Draft genome sequences of two *Neisseria meningitidis* serogroup C clinical isolates". *Journal of bacteriology*, 192(19):5270-5271, 2010.
- 2014 G. Baruzzo, **F. Finotello**, E. Lavezzo, A. Serafini, R. Provvedi, S. Toppo, L. Barzon, R. Manganelli, B. Di Camillo. "Benchmarking RNA-seq mapping strategies for paired-end reads". NETTAB 2014, from structural bioinformatics to integrative systems biology, October 15-17, 2014, Turin, Italy.
- 2014 **F. Finotello**, E. Lavezzo, S. Toppo, L. Barzon, B. Di Camillo. "Reverse engineering the human microbiota". NETTAB 2014, from structural bioinformatics to integrative systems biology, October 15-17, 2014, Turin, Italy.
- 2014 **F. Finotello**, E. Lavezzo, A. Zandonà, S. Toppo, L. Barzon, B. Di Camillo. "Modelling differences and interactions in the human microbiota". GNB 2014, IV National Congress of Bioengineering, June 25-27, 2014. Pavia, Italy. Oral communication.
- 2014 T. Sanavia, **F. Finotello**, B. Di Camillo. "FunPat: a function-based pattern analysis framework for RNA-seq time-series data". GNB 2014, IV National Congress of Bioengineering, June 25-27, 2014. Pavia, Italy.
- 2014 A. Benguría, **F. Finotello**, S. Callejas, R. Álvarez, F. Sánchez-Cabo, B. Di Camillo, C. Hernández-Chico, A. Dopazo. "Analysis of whole blood transcriptome of Spinal Muscular Atrophy patients using RNA-seq". Next Generation Sequencing Conference 2014, June 2-4, 2014. Barcelona, Spain.
- 2014 M. Scarpa, L. Barzon, G. Costanzi, E. Lavezzo, **F. Finotello**, F. Erroi, L. Dallagnese, S. Basato, P. Brun, S. Toppo, B. Di Camillo, C. Castoro, and I. Castagliuolo. "Colonic microbiota and gene methylation in colonic carcinogenesis" In DDW2014, Digestive Disease Week, May 4-6, 2014. Chicago, Illinois, USA.
- 2014 T. Sanavia, **F. Finotello**, B. Di Camillo. "FunPat: a function-based pattern analysis pipeline for RNA-seq time-series data". In BITS annual meeting 2014, February 26-28, 2014. Rome, Italy. Oral communication.
- 2012 **F. Finotello**, E. Lavezzo, L. Barzon, P. Fontana, S. Toppo, B. Di Camillo. "Characterization and reduction of biases in RNA sequencing data". In IDAMAP, Intelligent data analysis in biomedicine and pharmacology, November 22, 2012. Pavia, Italy. Oral communication.
- 2012 **F. Finotello**, E. Lavezzo, L. Barzon, P. Mazzon, P. Fontana, S. Toppo, B. Di Camillo. "A strategy to reduce technical variability and bias in RNA sequencing data". *EMBnet. journal*, 18(B):pp-65, 2012. Oral communication in NETTAB 2012, November 14-16, 2012. Como, Italy.
- 2012 **F. Finotello**, E. Lavezzo, L. Barzon, P. Fontana, A. Si-Ammour, S. Toppo, B. Di Camillo. "RNA sequencing data: biases and normalization". *EMBnet. journal*, 18(A), p-99. In BITS 2012, IX Annual Meeting of the Bioinformatics Italian Society Meeting Abstracts, May 2-4, 2012. Catania, Italy.
- 2012 **F. Finotello**, E. Lavezzo, L. Barzon, P. Fontana, A. Si-Ammour, S. Toppo, B. Di Camillo. "Comparison of parametric methods for detecting differential expression in RNA sequencing data". In Third National Congress of Bioengineering, June 26-29, 2012. Rome, Italy.
- 2010 **F. Finotello**, D. Peruzzo, E. Lavezzo, B. Di Camillo, G. M. Toffolo, C. Cobelli, S. Toppo. "Complete and comparative analysis of algorithms for whole genome shotgun assembly". In BITS 2010, VII Annual meeting of the Bioinformatics Italian Society, April 14-16, 2010. Bari, Italy. Oral communication.

## OTHER RESEARCH ACTIVITIES

- 2014 **Reviewer** for BMC Research Notes.
- 2010 – 2014 Participation to more than 20 **workshops, congresses and courses**.
- 2012 – present **Co-advisor** of 4 MD and PhD students. Defended theses:
- 2013 Alessandro Zandonà , MD thesis: "Metagenomics methods for microbiome analysis: application to patients affected by chronic obstructive pulmonary disease and colon cancer".  
Department of Information Engineering, University of Padova, Italy.  
Advisor: Barbara Di Camillo.
- 2012 Andrea Apolloni, MD thesis: "Comparison of statistical methods for detecting differential expression in RNA sequencing data".  
Department of Information Engineering, University of Padova, Italy.  
Advisor: Barbara Di Camillo.

## LANGUAGES

ITALIAN	mother tongue
ENGLISH	fluent
SPANISH	intermediate (speaking, reading); basic (writing)
FRENCH	basic

## INFORMATICS SKILLS

- OS Windows, Mac OS X, Linux.
- Programming languages and software tools Java (basic), Perl (expert), C (basic), HTML (basic), CSS (basic), JavaScript (basic), D3 (basic), Bash (good), SQL (basic), R (expert), MATLAB (expert), Office (expert), LaTeX (expert), Saam II (basic), LabVIEW (basic).
- Expert user of software tools for NGS data analysis: read mapping and assembly, analysis of differential gene expression from RNA-seq data, variant calling and genotyping, metagenomics.
- Basic experience in PCR and microarray data analysis.
- Intermediate experience in statistics and R-based statistical packages.