



Marco Chierici

Current position

Senior researcher at Fondazione Bruno Kessler (Trento, Italy), MPBA Research Unit.

Research activity

Integration of artificial intelligence (i.e., deep learning) in computational biology workflows; tutorial/tutoring activity in machine learning for life sciences; development of high-end bioinformatic workflows for data science.

Education

2007 **Ph.D. in Bioengineering**, *Università di Padova*, Italy.

2003 **Master's Degree in Electronic Engineering (Biomedical track)**, *Università di Padova*, Italy.

Other

2002 **Doctor of Musical Arts in Composition ("diploma di composizione")**, *Conservatorio di musica "A. Pedrollo"*, Vicenza, Italy.

1999 **Doctor of Musical Arts in Piano ("diploma di pianoforte")**, *Conservatorio di musica "A. Pedrollo"*, Vicenza, Italy.

Skills and competences

- Operating systems: MacOS, Linux, Windows
- Programming languages: Python, Bash
- Statistical computing: R and Bioconductor
- Bioinformatics software: short read alignment (e.g., BWA, Bowtie, STAR, TopHat, cufflinks, kallisto); genomic assembly (e.g., SOAPdenovo, Ray, ABySS); metagenomics quantification (e.g., QIIME, kaiju); utility suites (e.g., SAMtools, BEDtools, HTSeq); variant calling (e.g., freebayes, GATK)
- Machine learning frameworks: scikit-learn, PyTorch
- High performance computing and cloud-based data analysis environments: Grid Engine, Slurm, DNAnexus, Microsoft Azure
- Workflow management systems: Snakemake, Nextflow
- Container platforms: Singularity, Docker

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- Productivity: L^AT_EX, Microsoft Office suite
- Meta-languages: HTML, SQL
- Skilled in web design and web site development

Languages

Italian	Mother tongue	
English	Proficient	<i>C2 (reading), C1 (writing, speaking, reading)</i>

Experience

2017–present **Member of the faculty board**, *Doctoral course in Cognitive Sciences, Università di Trento, Trento, Italy.*

2007–present **Researcher**, *Fondazione Bruno Kessler (MPBA research unit), Trento, Italy.*

Main activities and responsibilities:

- Responsible for the bioinformatics workflows and high-performance computing pipelines for functional genomics and metagenomics
- Developer of Python software implementing machine learning Data Analysis Protocols adherent to the FDA MAQC/SEQC guidelines, with focus on deep learning
- Advisor of two graduate MSc students, working on machine learning methods for predictive toxicology (2018, 2019)
- Coordinator of the activity of a junior researcher, focusing on the bioinformatic and statistical analysis of epigenetic data from high-throughput platforms (2016–2018)
- Advisor of a PhD student, developing metagenomic pipelines integrating predictive profiling methods and complex networks for the analysis of deep sequencing microbiome data (2014–2017)
- Collaboration with University of Milano and Ospedale Bassini (Prof. Alberico Catapano, Dr. Andrea Baragetti) on bioinformatics and artificial intelligence methods for the integration of biomedical imaging, omics markers and clinical data for cardiovascular risk prediction (2019–ongoing)
- Collaboration with Ospedale Pediatrico Bambino Gesù, Rome (Dr. Doriana Fruci) on studying the impact of tumor-infiltrating lymphocytes on neuroblastoma patient risk-stratification (2016–present)
- Collaboration with University of Trento, ODFlab (Dr. Paola Venuti) and Ospedale Pediatrico Bambino Gesù, Rome (Dr. Lorenza Putignani) on a project exploring the interactions between microbiota and gut::brain axis in Autism Spectrum Disorders (2014–2020)
- Collaboration with Ospedale Pediatrico Bambino Gesù, Rome (Dr. Lorenza Putignani) on the study of gut microbial communities in pediatric patients with Inflammatory Bowel Diseases (2013–2016)
- Collaboration with Ospedale Pediatrico Bambino Gesù, Rome (Dr. Anna Alisi) on finding mechanisms of gene expression modulation in hepatocellular carcinoma (2016–2017)

- Active participation to international working groups and face-to-face meetings: MAQC-II (2008–2010), SEQC phase 1 and 2 (2008–present), the FANTOM consortium (2010–2014)
- Coordinator of the activity of a PhD student regarding the study and development of algorithms and software for Next Generation Sequencing, with a particular focus on plant genomics (2010–2011)
- Software developer in R/Bioconductor and Python/C environments for the analysis of high-throughput mass spectrometry data, in collaboration with Dr. Pietro Franceschi (FEM) (2007–2012)
- Supervisor of a young biotechnologist in activities regarding the study and development of algorithms and software for Next Generation Sequencing (2008–2012)

Participation to national and international projects:

- I-REACT, H2020-DRS-2015 - Improving Resilience to Emergencies through Advanced Cyber Technologies (2016–2019)
- ENPADASI - European Nutritional Phenotype Assessment Data Sharing Initiative and FOOTBALL (JPI HDHL 2015–2017): Biomarkers in nutrition and health (2016–2017)
- CCM2015 - Il modello One-Health per il contenimento delle resistenze microbiche di possibile origine zoonosica in sanità pubblica (2015–2017)
- CCM2014 - Fiducia del pubblico nei programmi vaccinali e le sue necessità informative (2015–2017)
- CCM2012 - Ottimizzazione del processo di gestione del paziente complesso sul territorio: modelli di presa in carico e gestione della multimorbidità attraverso una piattaforma di integrated care (2012–2014)
- AXonomiX - Identifying the translational networks altered in motor neuron diseases (Grande Progetto Ricerca 2012 - PAT) (2013–2017)
- HIPERDART, FP7-HEALTH-2007-B - Development of high performance diagnostic array replication technology (2009–2012)
- ISITAD, Progetto di ricerca finalizzata Ministero della Salute bando 2007 - Innovative strategies for depression treatment: novel pharmacological targets and preclinical studies for the personalization of therapy (2008–2010)

Workshops and conferences

- 2019 Scientific instructor, WebValley international summer school, Casez (TN)
- 2019 Local organizing team, 3rd Annual Massive Analysis and Quality Control Society Conference, Riva del Garda (TN), Apr 8-10
- 2016 Co-organizer, 1st international workshop on deep learning for precision medicine, Riva del Garda (TN), Sep 23
- 2014 Scientific instructor, WebValley international summer school, San Lorenzo in Banale (TN)
- 2010 Co-organizer and instructor, Next-generation Sequencing for Biomedical Omics, Ivano Fracena (TN)

- 2009 Scientific instructor, WebValley international summer school, Luserna (TN)
2008 Local organizing team, International workshop MGED11, Riva del Garda (TN)

Talks and training activity

- talk *Artificial intelligence and life sciences: challenges and cutting-edge applications in computational biology*. New Frontiers in Research, Diagnostics and Therapies, Trieste, December 2019
- talk *Machine learning for computational biology*. Università degli studi di Milano, October 2019
- tutorial *An introduction to machine learning*. Bayer AG, Berlin, July 2019
- tutorial *Machine learning from scratch*. EMBO practical course “Population genomics: Background, tools and programming”. Procida (NA), April 2019
- talk *Predictive models: principles and case studies*. Machine learning: applications to clinical and psychological research, Rovereto (TN), 2019
- talk *Deep learning for predictive toxicology*. OpenTox USA 2018, Durham (NC), 2018
- talk *Machine learning for the biomedical researcher* (with N. Bussola). WebValley 2018 International Summer School, Casez (TN), 2018
- tutorial *The data analysis plan: intro to unbiased pipelines for binary classification*. ELIXIR-IIB Training course on Machine Learning for Biologists. San Michele all’Adige (TN), 2017
- talk *Machine learning for the working (biomedical) researcher* (with A. Zandonà). Web-Valley 2016 International Summer School, San Lorenzo Dorsino (TN), 2016
- talk *Integrating MIC co-occurrence networks in the analysis of NGS Metagenomics data*. The XV Annual FGED Meeting, Seattle, WA, USA, 2013
- talk *Pipelines for next-generation sequencing data analysis*. GMPF Bioinformatics Summer School, Fondazione Edmund Mach, 2012
- tutorial *A crash course on next-generation sequencing data analysis*. FBK, 2012
- tutorial *Short read alignment, analysis and visualization*. ANIS3 Alp Nano-bio International School, Vipiteno, 2012
- tutorial *Computational tools, alignment strategies and bioinformatics challenges in Next-Generation Sequencing data analysis*. EMBO practical course on Analysis of High-Throughput Sequencing Data. EMBL-EBI, Hinxton, Cambridge, UK, October 2011
- talk *Computational tools for next-generation sequencing*. Bioinformatica e genetica in medicina, Genova, Italy, April 2011
- talk *High-throughput platforms for functional genomics: computational tools and challenges*. Burg Randeck Workshop, Regensburg, Germany, 2010
- tutorial *Computational tools for next-generation sequencing: from nucleotides to functional genomics*. Next-Generation Sequencing for Biomedical Omics, Ivano Fracena (TN), 2010
- talk *High-throughput platforms*. FBK-EURAC joint meeting, Trento, 2010

- talk *Replicability in high-throughput functional genomics: pipelines & data analysis protocols*. Università di Padova, 2009
- talk *Selecting predictive biomarkers on high-throughput molecular data*. Rosetta Biosoftware, Seattle, WA, USA, 2008
- tutorial *Machine Learning Methods for Predictive Proteomics*. 3S Biology Summer School, Trento, 2008

Ph.D. Thesis

- title *Estimation of hepatic glucose production by deconvolution: a novel method assessed on simulated and IVGTT & Meal data*
- supervisors Prof. Gianna Toffolo, Prof. Giuseppe De Nicolao

M.Sc. Thesis

- title *Metodi di deconvoluzione per la stima della produzione epatica di glucosio*
- supervisor Prof. Gianna Toffolo

List of publications

- Chierici M, Francescatto M, Bussola N, Jurman G, and Furlanello C. "Predictability of drug-induced liver injury by machine learning". In: *Biology Direct* 15.1 (2020), p. 3.
- Bizzego A, Bussola N, Salvalai D, Chierici M, Maggio V, Jurman G, and Furlanello C. "Integrating deep and radiomics features in cancer bioimaging". In: *2019 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*. July 2019, pp. 1–8. DOI: 10.1109/CIBCB.2019.8791473.
- Bizzego A, Bussola N, Chierici M, Maggio V, Francescatto M, Cima L, Cristoforetti M, Jurman G, and Furlanello C. "Evaluating reproducibility of AI algorithms in digital pathology with DAPPER". In: *PLoS computational biology* 15.3 (2019), e1006269.
- Boldrini R, De Pasquale MD, Melaiu O, Chierici M, Jurman G, Benedetti MC, Salfi NC, Castellano A, Collini P, Furlanello C, et al. "Tumor-infiltrating T cells and PD-L1 expression in childhood malignant extracranial germ-cell tumors". In: *Oncolmmunology* 8.2 (2019), e1542245.
- Polano M, Chierici M, Dal Bo M, Gentilini D, Di Cintio F, Baboci L, Gibbs DL, Furlanello C, and Toffoli G. "A Pan-Cancer Approach to Predict Responsiveness to Immune Checkpoint Inhibitors by Machine Learning". In: *Cancers* 11.10 (2019), p. 1562.
- Chierici M, Giulini M, Bussola N, Jurman G, and Furlanello C. "Machine learning models for predicting endocrine disruption potential of environmental chemicals". In: *Journal of Environmental Science and Health, Part C* (2018), pp. 1–15.
- Fioravanti D, Giarratano Y, Maggio V, Agostinelli C, Chierici M, Jurman G, and Furlanello C. "Phylogenetic convolutional neural networks in metagenomics". In: *BMC bioinformatics* 19.2 (2018), p. 49.
- Francescatto M, Chierici M, Dezfooli SR, Zandonà A, Jurman G, and Furlanello C. "Multi-omics integration for neuroblastoma clinical endpoint prediction". In: *Biology direct* 13.1 (2018), p. 5.
- Maggio V, Chierici M, Jurman G, and Furlanello C. "Distillation of the clinical algorithm improves prognosis by multi-task deep learning in high-risk Neuroblastoma". In: *PLoS ONE* 13.12 (2018), e0208924.

- Gnani D, Romito I, Artuso S, Chierici M, De Stefanis C, Panera N, Crudele A, Ceccarelli S, Carcarino E, D'Oria V, et al. "Focal adhesion kinase depletion reduces human hepatocellular carcinoma growth by repressing enhancer of zeste homolog". In: *Cell Death and Differentiation* 24 (2017), pp. 889–902.
- Melaiu O, Mina M, Chierici M, Boldrini R, Jurman G, Romania P, D'Alicandro V, Benedetti MC, Castellano A, Liu T, et al. "PD-L1 is a therapeutic target of the bromodomain inhibitor JQ1 and, combined with HLA class I, a promising prognostic biomarker in neuroblastoma". In: *Clinical Cancer Research* 23.15 (2017), pp. 4462–4472.
- Mortera SL, Del Chierico F, Vernocchi P, Rosado MM, Cavola A, Chierici M, Pieroni L, Urbani A, Carsetti R, Lante I, et al. "Monitoring perinatal gut microbiota in mouse models by mass spectrometry approaches: parental genetic background and breastfeeding effects". In: *Frontiers in Microbiology* 7 (2016).
- De Mariano M, Gallesio R, Chierici M, Furlanello C, Conte M, Garaventa A, Croce M, Ferrini S, Tonini GP, and Longo L. "Identification of GALNT14 as a novel neuroblastoma predisposition gene". In: *Oncotarget* 6.28 (2015), p. 26335.
- Zhang W, Yu Y, Hertwig F, Thierry-Mieg J, Zhang W, Thierry-Mieg D, Wang J, Furlanello C, Devanarayan V, Cheng J, et al. "Comparison of RNA-seq and microarray-based models for clinical endpoint prediction". In: *Genome biology* 16.1 (2015), p. 133.
- De Mariano M, Gallesio R, Chierici M, Furlanello C, Conte M, Garaventa A, Tonini G, and Longo L. "GALNT14 as a novel candidate gene for neuroblastoma predisposition". In: *Advances in Neuroblastoma Research Association*. 2014.
- Gallesio R, De Mariano M, Chierici M, Stigliani S, Scaruffi P, Coco S, Furlanello C, Longo L, and Tonini G. "Exome sequencing suggests candidate genes associated with aggressiveness of stage 4 neuroblastoma patients". In: *Advances in Neuroblastoma Research Association*. 2014.
- The FANTOM Consortium. "A promoter-level mammalian expression atlas". In: *Nature* 507 (2014), pp. 462–470.
- The SEQC/MAQC-III Consortium. "A comprehensive assessment of RNA-Seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium". In: *Nature Biotechnology* (2014).
- Wang C, Gong B, Bushel P, Thierry-Mieg J, Thierry-Mieg D, Xu J, Fang H, Hong H, Shen J, Su Z, et al. "The concordance between RNA-Seq and microarray data depends on chemical treatment and transcript abundance". In: *Nature Biotechnology* (2014).
- Corneo P, Pellegrini A, Cappellin L, Roncador M, Chierici M, Gessler C, and Pertot I. "Microbial community structure in vineyard soils across altitudinal gradients and in different seasons". In: *FEMS Microbiology Ecology* 84.3 (2013), pp. 588–602.
- Chierici M, Albanese D, Franceschi P, and Furlanello C. "TOFwave: Reproducibility in Biomarker Discovery from time-of-flight Mass Spectrometry Data". In: *Molecular Biosystems* 8 (2012), pp. 2845–2849.
- Longo L, De Mariano M, Chierici M, Roncador M, Furlanello C, and Tonini G. "Identification of familial neuroblastoma associated genes by whole exome sequencing". In: *Advances in Neuroblastoma Research Association*. 2012.
- Chierici M, Jurman G, Roncador M, and Furlanello C. *Single-base mismatch profiles for next-generation sequencing samples*. Preprint (arXiv:1109.1108). 2011.
- Gandolfi F, Malagoli Tagliazucchi G, Albanese D, Chierici M, Furlanello C, and Bicciato S. "A wavelet-based approach for the analysis of exon-array data". In: *BITS*. 2011.

- Roncador M, Chierici M, Filosi M, Visintainer R, Jurman G, and Furlanello C. "Developing pipelines for predictive biomarkers from metagenomics next-generation sequencing data". In: *International Conference on Environmental OMICS*. Guangzhou, 2011.
- Chierici M, Miclaus K, Vega S, and Furlanello C. "An interactive effect of batch size and composition contributes to discordant results in GWAS with the CHIAMO genotyping algorithm". In: *The Pharmacogenomics Journal* 10.4 (2010), pp. 355–363.
- Hong H, Shi L, Su Z, Ge W, Jones W, Czika W, Miclaus K, Lambert C, Vega S, Zhang J, et al. "Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples". In: *The Pharmacogenomics Journal* (2010).
- Miclaus K, Chierici M, Lambert C, Zhang L, Vega S, Hong H, Yin S, Furlanello C, Wolfinger R, and Goodsaid F. "Variability in GWAS analysis: the impact of genotype calling algorithm inconsistencies". In: *The Pharmacogenomics Journal* 10.4 (2010), pp. 324–335.
- Miclaus K, Wolfinger R, Vega S, Chierici M, Furlanello C, Lambert C, Hong H, Zhang L, Yin S, and Goodsaid F. "Batch effects in the BRLMM genotype calling algorithm influence GWAS results for the Affymetrix 500K array". In: *The Pharmacogenomics Journal* 10.4 (2010), pp. 336–346.
- Zhang L, Yin S, Miclaus K, Chierici M, Vega S, Lambert C, Hong H, Wolfinger R, Furlanello C, and Goodsaid F. "Assessment of variability in GWAS with CRLMM genotyping algorithm on WTCCC Coronary Artery Disease". In: *The Pharmacogenomics Journal* 10.4 (2010), pp. 347–354.
- Chierici M, Roncador M, Paoli S, Jurman G, and Furlanello C. "Comparing UHTS pipelines for SNP discovery from RNA-Seq data". In: *MGED* 12. 2009.
- Miclaus K, Chierici M, Hong H, Furlanello C, Vega S, Lambert C, Wolfinger R, Zhang L, Yin S, Pacanowski M, and Goodsaid F. "Evaluating the effects of batch composition and size on BRLMM and CHIAMO genotype calls for the Affymetrix 500K Array". In: *59th American Society of Human Genetics conference*. Honolulu, USA, 2009.
- "Sources of variability in the analysis of GWAS data". In: *Cold Spring Harbor Laboratory / Wellcome Trust conference on Pharmacogenomics & personalized medicine*. Hinxton, UK, 2009.
- Pillonetto G, De Nicolao G, Chierici M, and Cobelli C. "Fast algorithms for nonparametric population modeling of large data sets". In: *Automatica* 45.1 (2009), pp. 173–179.
- Barla A, Jurman G, Riccadonna S, Merler S, Chierici M, and Furlanello C. "Machine learning methods for predictive proteomics". In: *Briefings in Bioinformatics* 9.2 (2008), p. 119.
- Cogo P, Simonato M, Toffolo G, Stefanutti G, Chierici M, Cobelli C, Ori C, and Carnielli V. "Dexamethasone therapy in preterm infants developing bronchopulmonary dysplasia: effect on pulmonary surfactant disaturated-phosphatidylcholine kinetics". In: *Pediatric Research* 63.4 (2008), pp. 433–437.
- Chierici M, Toffolo G, Basu R, Rizza R, and Cobelli C. "Postprandial Endogenous Glucose Production from a Single Tracer Labeled Meal: Validation against a Triple Tracer Protocol". In: *Diabetes* 56 (2007), p. 155.
- Cogo P, Simonato M, Toffolo G, Stefanutti G, Chierici M, Cobelli C, Ori C, and Carnielli V. "Dexamethasone therapy in preterm infants with developing bronchopulmonary dysplasia: effect on pulmonary surfactant disaturated-phosphatidylcholine kinetics". In: *Neonatology* 91.4 (2007), pp. 327–328.
- Cogo P, Toffolo G, Ori C, Vianello A, Chierici M, Gucciardi A, Cobelli C, Baritussio A, and Carnielli V. "Surfactant disaturated-phosphatidylcholine kinetics in acute respiratory distress syndrome by stable isotopes and a two compartment model". In: *Respiratory Research* 8.1 (2007), p. 13.
- De Nicolao G, Pillonetto G, Chierici M, and Cobelli C. "Efficient nonparametric population modeling for large data sets". In: *Proceedings of the American Control Conference*. 2007, pp. 2921–2926.

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- Cogo P, Toffolo G, Ori C, Vianello A, Chierici M, Gucciardi A, Cobelli C, Baritussio A, and Carnielli V. "Surfactant Disaturated Phosphatidylcholine Kinetics in Human Adults with Acute Respiratory Distress Syndrome using Stable Isotopes". In: *Biology of the neonate* 89 (2006), p. 344.
- Chierici M, Toffolo G, Basu R, Rizza R, and Cobelli C. "Effect of Age and Gender on Glucose Production During Intravenous Glucose Tolerance Test". In: *Diabetologia*. Vol. 48. 2005, A226.

Declaration

I hereby declare that the above mentioned information is correct up to my knowledge and I bear the responsibility for its correctness.

Date: March 27, 2020

Place: Vicenza



Marco Chierici