# Europass Curriculum Vitae

## Personal information


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|---|---|
| First name(s) / Surname(s) | **Giuseppe Jurman** |
| Address(es) | Fondazione Bruno Kessler<br>via Sommarive 18 – Povo<br>I-38123 Trento<br>Italy |
| Telephone(s) | +39 0461 314 523 |
| Fax(es) | +39 0461 314 591 |
| Email(s) | jurman@fbk.eu |
| Nationality(-ies) | |
| Date of birth | |


## Occupational field

Data Scientist

## Work experience

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|---|---|
| Dates | Jan 20 |
| Occupation or position held | Head of MPBA Research Unit, Fondazione Bruno Kessler |
| Dates | Jan 08 - Dec 19 |
| Occupation or position held | Senior Researcher at Fondazione Bruno Kessler, Research Unit MPBA |
| Dates | Jan 06 - Dec 07 |
| Occupation or position held | Junior Researcher at Fondazione Bruno Kessler, Research Unit MPBA |
| Dates | Jan 03 - Dec 05 |
| Occupation or position held | PostDoc Fellow at Fondazione Bruno Kessler, Research Unit MPBA |
| Dates | Jun 01 - Dec 02 |
| Occupation or position held | PostDoc Fellow at University of Trento, Department of Mathematics |
| Dates | Feb 01 - Jun 01 |
| Occupation or position held | Programmer at Netwise, snc |
| Dates | Feb 99 - Feb 01 |
| Occupation or position held | PostDoc Fellow at Center for Mathematics and Applications, Australian National University (Canberra) |

## Education and training

| | |
|---|---|
| Dates | Nov 98 |
| Title of qualification awarded | Ph. D. |
| Principal subjects | Mathematics |
| Name and type of organization providing education and training | University of Trento (Prof. A. Caranti) |
| Dates | Jul 93 |

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|---|---|
| Title of qualification awarded | M. Sc. (Laurea) |
| Principal subjects | Mathematics |
| Name and type of organization providing education and training | University of Trento (Prof. E. Ballico) |

## Language skills and competences

Mother tongue(s) **Italian**

Other language(s)

| *Self-assessment* *European level*(*) | Understanding | | Speaking | | Writing |
|---|---|---|---|---|---|
| | Listening | Reading | Spoken interaction | Spoken production | |
| **English** | C1 | C1 | C1 | C1 | C1 |

(*) *Common European Framework of Reference (CEF) level*

## Computer skills and competences

| | | |
|---|---|---|
| Programming languages | Advanced: | R, Python, PHP |
| | Intermediate: | C, SQL, Perl, Bash, Awk, Basic, Fortran, Lisp, Pascal |
| | Basic: | Matlab, Java |
| Operative Systems | Advanced: | *nix |
| | Intermediate: | OS X |
| | Basic: | Microsoft Windows |

## Research Interests

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|---|---|
| Data Science | Data Analytics, Bioinformatics, Machine Learning, Deep Learning, Computational Biology |
| Algebra | Network theory, Group theory, Lie algebras, Combinatorics |

## Teaching experience

| | |
|---|---|
| Event | WebValley FBK International Summer School |
| Role | Director |
| Year | 2009-2019 (11 editions) |

| | |
|---|---|
| Title | A telegram-bot based alerting system for metereological extreme events |
| Student | Vincenzo Caracciolo |
| Institution | B.Sc. in Computer Science, University of Trento |
| Role | Thesis Supervisor |
| Year | Ongoing |

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|---|---|
| Student | Ylenia Giarratano |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2016 |

| | |
|---|---|
| Title | Techniques of integration for high-throughput omics data |
| Student | Lucia Trastulla |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2016 |

| | |
|---|---|
| Title | Theoretical and algorithmic solutions for null models in network theory |
| Student | Andrea Gobbi |
| Institution | Doctoral Programme in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2013 |
| | |
| Title | Distances and Stability in Biological Network Theory |
| Student | Roberto Visintainer |
| Institution | Doctoral Programme in Information and Communication Technology, University of Trento |
| Role | Thesis Supervisor |
| Year | 2013 |
| | |
| Title | Biological network inference via DTW & correlation measures from time-course data |
| Student | Marco Ferrarini |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2012 |
| | |
| Title | Algebraic reconstruction of gene regulatory networks |
| Student | Andrea Gobbi |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2010 |
| | |
| Title | Algebraic reconstruction of gene regulatory networks |
| Student | Andrea Gobbi |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2010 |
| | |
| Title | Feature ranking and classification of molecular data based on discriminant analysis methods |
| Student | Roberto Visintainer |
| Institution | M.Sc. in Telecommunications Engineering, University of Trento |
| Role | Thesis Supervisor |
| Year | 2008 |
| | |
| Title | Algebraic and combinatorial techniques for stability algorithms on ranked data |
| Student | Andrea Gobbi |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2008 |
| | |
| Title | Studio di algoritmi algebrici per la stabilitá predittiva di signature molecolari per dati genomici ad alta dimensione |
| Student | Martina Rossi |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2008 |
| | |
| Title | Metodi algebrici per la bioinformatica: codici ECOC in problemi multiclasse con costi non uniformi |

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|---|---|
| Student | Irene Oliani |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2005 |
| | |
| Title | Algoritmi permutazionali per la sintesi di profili molecolari |
| Student | Stefano Maragnoli |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2005 |
| | |
| Title | Indicatori algebrici di stabilitá per liste ordinate in diagnostica molecolare |
| Student | Alessia Peretti |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Thesis Supervisor |
| Year | 2005 |
| | |
| Course | Data Visualization Lab |
| Institution | M. Sc. Data Science, University of Trento |
| Role | Lecturer |
| Year | 2018/19 |
| | |
| Course | Data Visualization Lab |
| Institution | M. Sc. Data Science, University of Trento |
| Role | Lecturer |
| Year | 2018/19 |
| | |
| Course | Data Mining |
| Institution | M. Sc. Computer Science, Free University of Bolzano |
| Role | Lecturer |
| Year | 2016/17 |
| | |
| Course | Algebra I |
| Course | Statistical Machine Learning |
| Institution | ICT International Doctorate School, University of Trento |
| Role | Lecturer |
| Year | 2005/06 |
| | |
| Course | Algebra I |
| Institution | M.Sc. in Mathematics, University of Trento |
| Role | Assistant |
| Year | 2001/02 |
| | |
| Course | Algebra II |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Assistant |
| Year | 2001/02 |
| | |
| Course | Galois Theory |
| Institution | B.Sc. in Mathematics, University of Trento |
| Role | Assistant |

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|---|---|
| Year | 2001/02 |
| Course | Introduction to Lie algebras |
| Institution | M.Sc. in Mathematics, Australian National University |
| Role | Lecturer |
| Year | 2000 |
| Course | Calculus II |
| Institution | B.Sc. in Informatic Engineering, University of Trento |
| Role | Assistant |
| Year | 1997/98 |
| Course | Calculus |
| Institution | B.Sc. in Economics, University of Trento |
| Role | Assistant |
| Year | 1996/97 |
| Course | Calculus |
| Institution | B.Sc. in Economics, University of Trento |
| Role | Assistant |
| Year | 1995/96 |

## Publications

| | |
|---|---|
| **$h$-index (Google Scholar)** | 25 |
| OrcID | orcid.org/0000-0002-2705-5728 |
| ScopusID | 6602367398 |

Refereed Journals

D. Chicco and G. Jurman.
The advantages of the Matthews correlation coefficient (MCC) over F1 score and accuracy in binary classification evaluation.
*BMC Genomics*, 21(6):6, 2020

G. Franch, G. Jurman, L. Coviello, M. Pendesini, and C. Furlanello.
MASS-UMAP: Fast and Accurate Analog Ensemble Search in Weather Radar Archives.
*Remote Sensing*, 11(24):2922, 2019

P. Brown, The RELISH Consortium, and Y. Zhou.
Large expert-curated database for benchmarking document similarity detection in biomedical literature search.
*Database*, 2019:baz085, 2019

G. Jurman.
Seasonal Linear Predictivity in National Football Championships.
*Big Data*, 7:21–34, 2019

A. Bizzego, N. Bussola, M. Chierici, V. Maggio, M. Francescatto, L. Cima, M. Cristoforetti, G. Jurman, and C. Furlanello.
Evaluating reproducibility of AI algorithms in digital pathology with DAPPER.
*PLOS Computational Biology*, 15(3):e1006269, 2019

M. Chierici, M. Giulini, N. Bussola, G. Jurman, and C. Furlanello.
Machine learning models for predicting endocrine disruption potential of environmental chemicals.
*Journal of Environmental Science and Health. Part C, Environmental Carcinogenesis & Ecotoxicology Reviews*, 36:237–251, 2019

R. Boldrini, M. D. De Pasquale, O. Melaiu, M. Chierici, G. Jurman, M. C. Benedetti, N. C. Salfi, A. Castellano, P. Collini, C. Furlanello, V. Pistoia, L. Cifaldi, M. Terenziani, and D. Fruci.
Tumor-infiltrating T cells and PD-L1 expression in childhood malignant extracranial germ-cell tumors.
*OncoImmunology*, 8(2):e1542245, 2019

D. Fioravanti, Y. Giarratano, V. Maggio, C. Agostinelli, M. Chierici, G. Jurman, and C. Furlanello.
Phylogenetic convolutional neural networks in metagenomics.
*BMC Bioinformatics*, 19(S2):49, 2018

V. Maggio, M. Chierici, G. Jurman, and C. Furlanello.
Distillation of the clinical algorithm improves prognosis by multi-task deep learning in high-risk Neuroblastoma.
*PLOS ONE*, 13(12):e0208924, 2018

G. Mangioni, G. Jurman, and M. De Domenico.
Multilayer flows in molecular networks identify biological modules in the human proteome.
*IEEE Transactions on Network Science and Engineering*, Early Access:1, 2018

N.M. Rad, S.M. Kia, C. Zarbo, T. van Laarhoven, G. Jurman, P. Venuti, E. Marchiori, and C. Furlanello.
Deep learning for automatic stereotypical motor movement detection using wearable sensors in autism spectrum disorders.
*Signal Processing*, 144:180–191, 2018

M. Francescatto, M. Chierici, S Rezvan Dezfooli, A. Zandoná, G. Jurman, and C. Furlanello.
Multi-omics integration for neuroblastoma clinical endpoint prediction.
*Biology Direct*, 13(1):5, 2018

G. Jurman, V. Maggio, I. Landi, M. Francescatto, M. Chierici, M. De Domenico, and C. Furlanello.
omicsCNN: a general deep learning framework for omics data modeling and classification.
*Human Genomics*, 12(S1):38, 2018

O. Melaiu, M. Mina, M. Chierici, R. Boldrini, G. Jurman, P. Romania, V. D'Alicandro, M.C. Benedetti, A. Castellano, T. Liu, C. Furlanello, F. Locatelli, and D. Fruci.
PD-L1 is a therapeutic target of the Bromodomain inhibitor JQ1 and, combined with HLA class I, a promising prognostic biomarker in neuroblastoma.
*Clinical Cancer Research*, 23(15):4462–4472, 2017

G. Jurman.
Metric projection for dynamic multiplex networks.
*Heliyon*, 2(7):e00136, 2016

S. Riccadonna, G. Jurman, R. Visintainer, M. Filosi, and C. Furlanello.
DTW-MIC Coexpression Networks from Time-Course Data.
*PLOS ONE*, 11(3):e0152648, 2016

M. Mina, S. Magi, G. Jurman, M. Itoh, H. Kawaji, T. Lassmann, E. Arner, A.R.R. Forrest, P. Carninci, Y. Hayashizaki, C.O. Daub, The FANTOM Consortium, M. Okada-Hatakeyama, and C. Furlanello.
Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells.
*Nature Scientific Report*, 5:11999, 2015

A. Gobbi and G. Jurman.
A null model for Pearson correlation networks.
*PLOS ONE*, 10(6):e0128115, 2015

D. Fay, A.W. Moore, K. Brown, M. Filosi, and G. Jurman.
Graph metrics as summary statistics for Approximate Bayesian Computation with application to network model parameter estimation.
*IMA Journal of Complex Networks*, 3:52–83, 2015

M. Filosi, R. Visintainer, S. Riccadonna, G. Jurman, and C. Furlanello.
Stability Indicators in Network Reconstruction.
*PLOS ONE*, 9(2):e89815, 2014

A. Gobbi, F. Iorio, K.J. Dawson, D.C. Wedge, D. Tamborero, L.B. Alexandrov, N. Lopez-Bigas, M.J. Garnett, G. Jurman, and J. Saez-Rodriguez.
Fast randomization of large genomics datasets while preserving alteration counts.
*Bioinformatics*, 30(17):i617–i623, 2014

C. Wang, B. Gong, P.R. Bushel, J. Thierry-Mieg, D. Thierry-Mieg, J. Xu, H. Fang, H. Hong, J. Shen, Z. Su, J. Meehan, X. Li, L. Yang, H. Li, P.P. Labaj, D.P. Krell, D. Megherbi, S. Gaj, F. Calment, J. van Delft, J. Kleinjans, A. Sherer, V. Devanarayan, J. Wang, Y. Yang, H.-R. Qian, L.J. Lancashire, M. Bessarabova, Y. Nikolsky, C. Furlanello, M. Chierici, D. Albanese, G. Jurman, S. Riccadonna, M. Filosi, R. Visintainer, K.K. Zhang, J. Li, J.-H. Hsieh, D.L. Svoboda, J.C. Fuscoe, Y. Deng, L. Shi, R.S. Paules, S.S. Auerbach, and W. Tong.
The concordance between RNA-Seq and microarray data depends on chemical treatment and transcript abundance.
*Nature Biotechnology*, 32(9):926–932, 2014

The Fantom5 Consortium.
A promoter-level mammalian expression atlas.
*Nature*, 507:462–470, 2014

D. Albanese, M. Filosi, R. Visintainer, S. Riccadonna, G. Jurman, and C. Furlanello.
minepy and minerva: a C engine for the MINE suite and its Python, R and MATLAB wrappers.
*Bioinformatics*, 29(3):407–408, 2013

S. Merler and G. Jurman.
A combinatorial model of malware diffusion via Bluetooth connections.
*PLOS ONE*, 8(3):e59468, 2013

R. Sanz-Pamplona, A. Berenguer, D. Cordero, S. Riccadonna, X. Solé, M. Crous-Bou, E. Guinó, X. Sanjuan, S. Biondo, A. Soriano, G. Jurman, G. Capella, C. Furlanello, and V. Moreno.
Clinical value of prognosis gene expression signatures in colorectal cancer: a systematic review.
*PLOS ONE*, 7(11):e48877, 2012

B. di Camillo, T. Sanavia, M . Martini, G. Jurman, C. Furlanello, F. Sambo, A. Barla, M. Squillario, G. Toffolo, and C. Cobelli.
Effect of size and heterogeneity of samples on biomarker discovery: synthetic and real data assessment.
*PLOS ONE*, 7(3):e32200, 2012

G. Jurman, S. Riccadonna, and C. Furlanello.
A comparison of MCC and CEN error measures in multi-class prediction.
*PLOS ONE*, 7(8):e41882, 2012

G. Jurman, S. Riccadonna, R. Visintainer, and C. Furlanello.
Algebraic Comparison of Partial Lists in Bioinformatics.
*PLOS ONE*, 7(5):e36540, 2012

M. Grimaldi, R. Visintainer, and G. Jurman.
RegnANN: Reverse Engineering Gene Networks using Artificial Neural Networks.
*PLOS ONE*, 6(12):e28646, 2011

The MicroArray Quality Control (MAQC) Consortium.
The MAQC-II Project: A comprehensive study of common practices for the development and validation of microarray-based predictive models.
*Nature Biotechnology*, 28(8):827–838, 2010

W. Shi, M. Bessarabova, D. Dosymbekov, Z. Dezso, T. Nikolskaya, M. Dudoladova, T. Serebryiskaya, A. Bugrim, R.J. Brennan, R. Shah, J. Dopazo, M. Chen, Y. Deng, T Shi, G. Jurman, C. Furlanello, R.S. Thomas, J.C. Corton, W. Tong, L. Shi, and Y. Nikolsky.
Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes.
*The Pharmacogenomics Journal*, 10:310–323, 2010

G. Guzzetta, G. Jurman, and C. Furlanello.
A machine learning pipeline for quantitative phenotype prediction from genotype data.
*BMC Bioinformatics*, 11(Supp.8):S3, 2010

M. Avitabile, G. Jurman, and S. Mattarei.
The structure of thin Lie algebras with characteristic two.
*International Journal of Algebra and Computation*, 20(6):731–768, 2010

J.P.A. Ioannidis, D.B. Allison, C.A. Ball, I. Coulibaly, X. Cui, Culhane. A.C., M. Falchi, C. Furlanello, L. Game, G. Jurman, T. Mehta, J. Mangion, M. Nitzberg, G.P. Page, E. Petretto, and V. van Noort.
Repeatability of published microarray gene expression analyses.
*Nature Genetics*, 41(2):499–505, 2009

G. Jurman, S. Merler, A. Barla, S. Paoli, A. Galea, and C. Furlanello.
Algebraic stability indicators for ranked lists in molecular profiling.
*Bioinformatics*, 24(2):258–264, 2008

A. Barla, G. Jurman, S. Riccadonna, M. Chierici, S. Merler, and C. Furlanello.
Machine learning methods for predictive proteomics.
*Briefings in Bioinformatics*, 9(2):119–128, 2008

S. Paoli, G. Jurman, D. Albanese, S. Merler, and C. Furlanello.
Integrating gene expression profiling and clinical data.
*International Journal of Approximate Reasoning*, 47(1):58–69, 2008

S. Riccadonna, G Jurman, S. Merler, S. Paoli, A. Quattrone, and C. Furlanello.
Supervised classification of combined copy number and gene expression data.
*Journal of Integrative Bioinformatics*, 4(3):74, 2007

M. Cannataro, A. Barla, R. Flor, A. Gallo, G. Jurman, S. Merler, S. Paoli, G. Tradigo, P. Veltri, and Furlanello.
A grid environment for high-throughput proteomics.
*IEEE Transactions on Nanobioscience*, 6(2):117–123, 2007

M.L. Ciofi degli Atti, C. Rizzo, A Bella, M. Massari, M. Iannelli, A. Lunelli, A. Pugliese, J. Ripoll, P. Manfredi, G. Scalia Tomba, S. Merler, G. Jurman, and C. Furlanello.
Modelling scenarios of diffusion and control of pandemic influenza, italy.
*Eurosurveillance*, 12(1):E070104.2, 2007

C. De Pittá, L. Tombolan, G. Albiero, F. Sartori, C. Romualdi, G. Jurman, M. Carli, C. Furlanello, G. Lanfranchi, and A. Rosolen.
Gene expression profiling identifies potential relevant genes in alveolar rhabdomyosarcoma pathogenesis and discriminates PAX3-FKHR positive and negative tumors.
*International Journal of Cancer*, 118(11):2772–2781, 2006

C. Furlanello, S. Merler, and G. Jurman.
Combining feature selection and DTW for time-varying functional genomics.
*IEEE Transactions on Signal Processing*, 54(6):2436–2443, 2006

S. Merler and G. Jurman.
Terminated Ramp - Support Vector Machine: a nonparametric data dependent kernel.
*Neural Networks*, 19:1597–1611, 2006

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
Semi-supervised learning for molecular profiling.
*IEEE Transactions on Computational Biology and Bioinformatics*, 2(2):110–118, 2005

G. Jurman.
Graded Lie algebras of maximal class, III.
*Journal of Algebra*, 284(2):435–461, 2005

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
Methods for predictive classification and molecular profiling from DNA microarray data.
*Italian Heart Journal*, 5(1):199–202, 2004

G. Jurman.
A family of simple Lie algebras in characteristic two.
*Journal of Algebra*, 271(2):454–481, 2004

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
Control of selection bias in microarray data analysis.
*Minerva Biotecnologica*, 15(4):217–222, 2003

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
Entropy-Based Gene Ranking without Selection Bias for the Predictive Classification of Microarray Data.
*BMC Bioinformatics*, 4:54, 2003

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
An accelerated procedure for recursive feature ranking on microarray data.
*Neural Networks*, 16(5–6):641–648, 2003

M. Avitabile and G. Jurman.
Diamonds in thin Lie algebras.
*Bollettino della Unione Matematica Italiana B*, 4(3):597–608, 2001

A. Caranti and G. Jurman.
Quotients of maximal class of thin Lie algebras. The odd characteristic case.
*Communications in Algebra*, 28(12):5741–5748, 1999

G. Jurman.
Quotients of maximal class of thin Lie algebras. The case of characteristic two.
*Communications in Algebra*, 28(12):5749–5789, 1999

Book Chapters

G. Jurman, M. Filosi, R. Visintainer, S. Riccadonna, and C. Furlanello.
*Stability in GRN inference*, volume 786 of *Methods in Molecular Biology*, pages 323–346.
Springer, 2019

G. Jurman, M. Filosi, S. Riccadonna, R. Visintainer, and C. Furlanello.
Differential network analysis and graph classification: a glocal approach.
In A. Rogato, V. Zazzu, and M. Guarracino, editors, *Dynamics of Mathematical Methods in Biology – Bringing Math to Life*, page 268. Springer, 2016

A. Barla, G. Jurman, R. Visintainer, M. Squillario, M. Filosi, S. Riccadonna, and C. Furlanello.
A Machine Learning Pipeline for Discriminant Pathways Identification.
In N. Kasabov, editor, *Springer Handbook of Bio-/Neuroinformatics*. Springer, 2013

Proceedings

C. Furlanello, G. Jurman, C. Dolci, R. Villani, E. Gadotti, and P. Venuti.
Talents and technology: training the artificial intelligence generation.
In *Proc. IV Talent Education 2019*, pages 21–35. MIB, 2019

N.M. Rad, S.M. Kia, C. Zarbo, G. Jurman, P. Venuti, and C. Furlanello.
Stereotypical motor movement detection in dynamic feature space.
In IEEE, editor, *Proceedings Workshop Data Mining in Human Activity Analysis in International Conference in Data Mining (ICDM DHAA 2016)*, page in press, 2016

G. Jurman, R. Visintainer, M. Filosi, S. Riccadonna, and C. Furlanello.
The HIM glocal metric and kernel for network comparison and classification.
In *Proceedings IEEE International Conference on Data Science and Advanced Analytics (DSAA'2015)*. IEEE, 2015

N.M. Rad, A. Bizzego, S.M. Kia, G. Jurman, P. Venuti, and C Furlanello.
Convolutional Neural Networks for Stereotypical Motor Movements Detection in Autism.
Online Proceedings of NIPS 2015 Workshop on Machine Learning and Interpretation in Neuroimaging (MLINI 2015) http://arxiv.org/html/1605.04435, 2015.
Paper MLINI/2015/13 – arXiv:1511.01865

A. Barla, G. Jurman, R. Visintainer, M. Squillario, M. Filosi, S. Riccadonna, and C. Furlanello.
A Machine Learning Pipeline for Discriminant Pathways Identification.
In E. Biganzoli, A. Vellido, F. Ambrogi, and R. Tagliaferri, editors, *Computational Intelligence Methods for Bioinformatics and Biostatistics*, volume 7548 of *Lecture Notes in Computer Science*, pages 36–48. Springer, 2012

A. Barla, G. Jurman, R. Visintainer, M. Squillario, M. Filosi, S. Riccadonna, and C. Furlanello.
A machine learning pipeline for discriminant pathways identification.
In *Proc. CIBB 2011*, 2011

G. Jurman, R. Visintainer, and C. Furlanello.
An introduction to spectral distances in networks.
*Frontiers in Artificial Intelligence and Applications*, 226:227–234, 2011

G. Jurman, S. Riccadonna, R. Visintainer, and C . Furlanello.
Canberra Distance on Ranked Lists.
In *Proceedings Advances in Ranking NIPS 2009 Workshop*, pages 22–27. NIPS, 2009

S. Merler, M. Ajelli, G. Jurman, C. Furlanello, C. Rizzo, A. Bella, M. Massari, and M.L. Ciofi degli Atti.
Modeling influenza pandemic in Italy: an individual based approach.
In *Proceedings. ICISS 2007*. ISTAT, 2007

S. Merler, G. Jurman, and C. Furlanello.
Deriving the Kernel from Training Data.
In *Proceedings MCS 2007*, volume 4472 of *Lecture Notes in Computer Science*, pages 32–41. Springer, 2007

S. Merler, G. Jurman, C. Furlanello, C. Rizzo, A. Bella, M. Massari, and M.L. Ciofi degli Atti.
Strategies for containing an influenza pandemic: the case of Italy.
In *Proceedings Bionetics 2006*, page 11. IEEE, 2006

A. Barla, B. Irler, S. Merler, G. Jurman, S. Paoli, and C. Furlanello.
Proteome profiling without selection bias.
In *Proceedings IEEE/CBMS 2006*, pages 941–946. IEEE, 2006

S. Paoli, G. Jurman, D. Albanese, S. Merler, and C. Furlanello.
Semisupervised Profiling of Gene Expressions and Clinical Data.
In *Proceedings WILF 2005*, volume 3849 of *Lecture Notes in Computer Science*, pages 284–289. Springer, 2006

S. Merler, C. Furlanello, and G. Jurman.
Machine learning on historic air photographs for mapping risk of unexploded bombs.
In *Proceedings ICIAP 2005*, volume 3617 of *Lecture Notes in Computer Science*, pages 735–742. Springer, 2005

B. Caprile, S. Merler, C. Furlanello, and G. Jurman.
Exact bagging with k-nearest neighbour classifiers.
In *Proceedings MCS 2004*, volume 3077 of *Lecture Notes in Computer Science*, pages 72–81. Springer, 2004

C. Furlanello, M. Serafini, S. Merler, and G. Jurman.
Gene selection and classification by entropy-based recursive feature elimination.
In *Proceedings of IJCNN 2003*, pages 3077–3082. IEEE, 2003

Preprints

L. Coviello, M. Cristoforetti, G. Jurman, and C. Furlanello.
In-field grape berries counting for yield estimation using dilated CNNs.
arXiv:1909.12083, 2019

N. Bussola, A. Marcolini, V. Maggio, G. Jurman, and C. Furlanello.
Not again! Data Leakage in Digital Pathology.
arXiv:1909.06539, 2019

G. Mangioni, G. Jurman, and M. De Domenico.
Multilayer flows in molecular networks identify biological modules in the human proteome.
arXiv:1801.10144, 2018

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G. Lami, M. Cristoforetti, G. Jurman, C. Furlanello, and T. Furlanello.
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T. Furlanello, M. Cristoforetti, C. Furlanello, and G. Jurman.
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arXiv:1109.0220, 2011

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Ph.D. Thesis

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## (Selected) Invited talks

| | |
|---|---|
| Title | Towards a scientific blockchain framework for reproducible data analysis |
| Venue | BlockNet Workshop - NetSci 2018, Paris (F) |
| Date | June 2018 |
| Title | Differential network analysis and graph classification: a glocal approach |
| Venue | Altschuler & Wu Lab, UCSF, San Francisco (US) |
| Date | May 2016 |
| Title | Differential network analysis and graph classification: a glocal approach |
| Event | Bringing Maths to Life (BMTL) 2015 |
| Venue | Naples (I) |
| Date | Oct 2015 |
| Title | Microbial Communities & Individual Health Trajectories |
| Event | Microbiota: salute, terme e alimentazione 2015 |

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|---|---|
| Venue | Comano Terme (I) |
| Date | Oct 2015 |
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| Title | Thresholding Pearson coexpression networks |
| Venue | Jannsen J& J Pharmaceutical Companies, Philadelphia (US) |
| Date | May 2015 |
| | |
| Title | Applications of streaming data environments for health and safety |
| Event | Streaming Analytics Advanced Technologies (SAAT) 2014 |
| Venue | Bournemouth (UK) |
| Date | Mar 2014 |
| | |
| Title | Network biology & network medicine |
| Event | Copenhagenomics CPHx 2012 |
| Venue | Copenhagen (DK) |
| Date | Jun 2012 |

## Reviewing Activity

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| Journal | Artificial Intelligent |
| | Bioinformatics |
| | BMC Bioinformatics |
| | Briefings in Bioinformatics |
| | Chemometrics and Intelligent Laboratory Systems |
| | Computational Biology and Chemistry |
| | Computational and Structural Biotechnology Journal |
| | Computer Methods and Programs in Biomedicine |
| | Entropy |
| | Journal of Complex Networks |
| | Journal of Pharmacological and Toxicological Methods |
| | Plos One |
| | Scientific Data |
| | Sensors |
| | Statistical Applications in Genetics and Molecular Biology |
| | The Computer Journal |
| | Transactions on Computational Biology and Bioinformatics |
| | Transactions on Neural Networks and Learning Systems |
| | |
| Conferences | ACM-SIAM Symposium on Discrete Algorithms (SODA) |
| | ACM SIGKDD Conferences on Knowledge Discovery and Data Mining |
| | Bringing Maths to Life |
| | European Conference on Computational Biology (ECCB) |
| | IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB) |
| | IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB) & International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB) |
| | IARIA Data Analytics |
| | IEEE International Conference on Healthcare Informatics (ICHI) |
| | International Conference on Bioinformatics Models, Methods and Algorithms |
| | International Workshop on Multiple Classifier Systems (MCS) |
| | Neural Information Processing Systems (NIPS) |

## Professional Memberships

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|---|---|
| Academic Boards | Doctoral Committee, ICT International Doctoral School, University of Trento, 2019-ongoing |
| Academic Boards | Doctoral Committee, PhD in Smart Computing, Universities of Florence, Pisa, Siena and Bruno Kessler Foundation, 2015-2017 |
| | Management Committee, M.Sc. in Data Science, University of Trento |
| Conference Boards | Local Organizer, 3st International MAQC Conference 2019 |
| | Workshop Organizers, 1st International Workshop on Deep Learning for Precision Medicine, in conjunction with ECML-PKDD 2016 |
| | Program Committee, International Conference on Bioinformatics Models, Methods and Algorithms, 2012-2017 |
| | Program Committee, IEEE International Conference on Healthcare Informatics 2015 |
| | Program Committee, IAPR International Conference on Pattern Recognition in Bioinformatics & International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics 2013 |
| | Program Committee, IAPR International Conference on Pattern Recognition in Bioinformatics 2012 |
| | Organizing Committee, 11th MGED International Meeting of the Microarray and Gene Expression Data Society 2008 |

Trento, January, the 25$^{th}$ 2020

Autorizzo il trattamento dei miei dati personali ai sensi del D.lgs. 196 del 30 giugno 2003

Acconsento alla pubblicazione del mio CV in ottemperanza alle disposizioni di legge dettate in materia di trasparenza (D.Lgs. 33/2013)