

# Europass Curriculum Vitae



## Personal information

First name(s) / Surname(s)

**Giuseppe Jurman**

Address(es)

### Home

via Canaletta 21/D  
I-38049 Altopiano della Vigolana (Trento)  
Italy

### Work

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Email(s)

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Nationality(-ies)

Italian

Date of birth

June, the 7th 1970

## Occupational field

Data Scientist

## Work experience

Dates  
Occupation or position held  
Dates  
Occupation or position held  
Dates  
Occupation or position held  
Dates  
Occupation or position held  
Dates  
Occupation or position held  
Dates  
Occupation or position held

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

## Education and training

Dates  
Title of qualification awarded  
Principal subjects

Nov 98  
Ph. D.  
Mathematics

Name and type of organization providing education and training

Dates

Title of qualification awarded

Principal subjects

Name and type of organization providing education and training

University of Trento (Prof. A. Caranti)

Jul 93

M. Sc. (Laurea)

Mathematics

University of Trento (Prof. E. Ballico)

## Language skills and competences

Mother tongue(s)

Other language(s)

*Self-assessment  
European level<sup>(\*)</sup>*

**English**

**Italian**

Understanding		Speaking		Writing
Listening	Reading	Spoken interaction	Spoken production	
C1	C1	C1	C1	C1

<sup>(\*)</sup> Common European Framework of Reference (CEF) level

## Computer skills and competences

Programming languages

Operative Systems

Advanced: R, Python, PHP

Intermediate: C, SQL, Perl, Bash, Awk, Basic, Fortran, Lisp, Pascal

Basic: Matlab, Java

Advanced: \*nix

Intermediate: OS X

Basic: Microsoft Windows

## Research Interests

Data Science

Algebra

Data Analytics, Bioinformatics, Machine Learning, Deep Learning, Computational Biology

Network theory, Group theory, Lie algebras, Combinatorics

## Teaching experience

Event

Role

Year

WebValley FBK International Summer School

Director

2009-2019 (11 editions)

Title

Student

Institution

Role

Year

Deep learning solutions for metagenomics data

Ylenia Giarratano

M.Sc. in Mathematics, University of Trento

Thesis Supervisor

Ongoing

Title

Student

Institution

Role

Year

Techniques of integration for high-throughput omics data

Lucia Trastulla

M.Sc. in Mathematics, University of Trento

Thesis Supervisor

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 stabilit� 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
Student	Irene Olini
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 stabilità 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 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
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)**

20

OrCID

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ScopusID

6602367398

Refereed Journals

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

A. Bizzego, N. Bussola, M. Chierici, V. Maggio, M. Francescato, 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.  
*Oncolmmunology*, 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. Francescato, M. Chierici, S. Rezvan Dezfouli, 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. Francescato, 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.

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*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.

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*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.  
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- A. Barla, G. Jurman, S. Riccadonna, M. Chierici, S. Merler, and C. Furlanello.  
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- S. Paoli, G. Jurman, D. Albanese, S. Merler, and C. Furlanello.  
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*International Journal of Approximate Reasoning*, 47(1):58–69, 2008
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*Journal of Integrative Bioinformatics*, 4(3):74, 2007
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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.  
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*Journal of Algebra*, 284(2):435–461, 2005



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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.  
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Differential network analysis and graph classification: a glocal approach.  
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- 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
- 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.  
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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.  
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- G. Jurman, R. Visintainer, and C. Furlanello.  
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*Frontiers in Artificial Intelligence and Applications*, 226:227–234, 2011
- G. Jurman, S. Riccadonna, R. Visintainer, and C. Furlanello.  
Canberra Distance on Ranked Lists.  
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- 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
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- B. Caprile, S. Merler, C. Furlanello, and G. Jurman.  
Exact bagging with k-nearest neighbour classifiers.  
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Preprints

- 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
- G. Mangioni, G. Jurman, and M. De Domenico.  
Multilayer flows in molecular networks identify biological modules in the human proteome.  
arXiv:1801.10144, 2018
- A. Bizzego, N. Bussola, M. Chierici, M. Cristoforetti, M. Francescato, V. Maggio, G. Jurman, and C. Furlanello.  
Evaluating reproducibility of AI algorithms in digital pathology with DAPPER.  
biorXiv:340646
- V. Maggio, M. Chierici, G. Jurman, and C. Furlanello.  
A multiobjective deep learning approach for predictive classification in Neuroblastoma.  
arXiv:1711.08198, 2017
- C. Furlanello, M. De Domenico, G. Jurman, and N. Bussola.  
Towards a scientific blockchain framework for reproducible data analysis.  
arXiv:1707.06552, 2017
- M. Cristoforetti, G. Jurman, A. Nardelli, and C. Furlanello.  
Towards meaningful physics from generative models.  
arXiv:1705.09524, 2017
- F. Iorio, A. Gobbi, T. Cokelaer, M.B. Faura, G. Jurman, and J. Saez Rodriguez.  
Efficient randomization of biological networks while preserving functional characterization of individual nodes.  
bioRxiv-doi:10.1101/069245, 2016
- M. Cristoforetti, M. Guerini, G. Jurman, and C. Furlanello.  
Community dynamics in connected time-dependent multilayer networks.  
arXiv:1511.03447, 2015
- G. Jurman.  
Seasonal Linear Predictivity in National Football Championships.  
arXiv:1511.06262, 2015
- M. Mina, G. Jurman, and C. Furlanello.  
CIDER: a pipeline for detecting waves of coordinated transcriptional regulation in gene expression time-course data.  
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bioRxiv-doi:10.1101/008433, 2014
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Entropy Dynamics of of Community Alignment of the Italian Parliament Time-Dependent Network.  
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- T. Furlanello, M. Cristoforetti, C. Furlanello, and G. Jurman.  
Sparse Predictive Structure of Deconvolved Functional Brain Networks.  
arXiv:1310.6547, 2013
- A. Barla, S. Riccadonna, S. Masecchia, M. Squillario, M. Filosi, G. Jurman, and C. Furlanello.  
Evaluating sources of variability in pathway profiling.  
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D. Albanese, R. Visintainer, S. Merler, S. Riccadonna, G. Jurman, and C. Furlanello.  
mlpy: Machine Learning Python.  
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M. Chierici, G. Jurman, M. Roncador, and C. Furlanello.  
Single-base mismatch profiles for NGS samples.  
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G. Jurman, S. Riccadonna, R. Visintainer, and C. Furlanello.  
Biological network comparison via Ipsen-Mikhailov distance.  
arXiv:1109.0220, 2011

G. Jurman.  
(Finite) presentations of Bi-Zassenhaus loop algebras.  
arXiv:1004.1482v1, 2010

Ph.D. Thesis

G. Jurman.  
*On graded Lie algebras in characteristic two.*  
PhD thesis, University of Trento, Italy, 1998

### (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
Venue	Comano Terme (I)
Date	Oct 2015
Title	Thresholding Pearson coexpression networks
Venue	Janssen 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

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)
<b>Professional Memberships</b>	
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

Giuseppe Jurman

Trento, May, the 23<sup>rd</sup> 2019

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)