

Giorgio Valentini - Curriculum vitae

Current position:

Associate Professor at the *Computer Science Department of the University of Milan* (Italy).

Education:

- Master Degree in Biology, University of Genova, Italy
- Master Degree in Computer Science, University of Genova, Italy
- PhD in Computer Science, University of Genova, Italy

Academic career:

- Researcher – Italian Institute of Matter Physics (1999) – Genova
- Post-doc researcher - Computer Science Dept., University of Milan (2003-2004)
- Assistant professor - Computer Science Dept., University of Milan (2005-2009)
- Associate professor - Computer Science Dept., University of Milan (2010 – today)
- Italian National qualification (ASN) for full professor in Computer Science (2017)

Visiting positions:

- Visiting PhD student – Department of Electrical Engineering and Computer Science, Oregon State University, USA (2001)
- Visiting researcher – Centro de Investigacion Principe Felipe, Valencia, Spain (2009)

Visiting professor:

- Department of Informatics, Aristotle University Thessaloniki, Greece (2014)
- Department of Information and Computer Science, Aalto University, Helsinki, Finland (2015) (Aalto Foundation fellowship for the project “Big data in genomics”)
- Department of Computer Science, Royal Holloway, University of London (2015)
- European Center for Living Technologies (ECLT), Venezia (2016)
- Computational Biology Group, Institut für Medizinische Genetik und Humangenetik Charité - Universitätsmedizin Berlin (2016) (DAAD fellowship for the project “Hierarchical ensemble methods for structured predictions in Biological Ontologies”).
- Departamento de Ciencia de la Computacion e Inteligencia Artificial, Universidad de Granada, Spain (2016)

Research activity

My research is on the border between Computational Biology and Artificial Intelligence and is motivated by complex bioinformatics problems. By modeling them as ML problems, I develop new, or adapt existing ML algorithms to challenging computational biology problems, with a particular interest in the emerging field of Precision and Personalized Medicine. My research interests range from the prediction of protein function, to the discovery of deleterious genetic variants associated with genetic diseases or cancer, to gene-disease prioritization and analysis of complex biomolecular networks and systems in the context of the Network Medicine.

Moreover I also pursue “pure” ML research lines, in particular in the field of ensemble methods.

More information about my research activity is available from my home page:

<http://homes.di.unimi.it/valentini>

Research projects and coordination of research groups

- Coordinator of the Computational Biology and Bioinformatics laboratory *AnacletoLab* at the Dept. of Computer Science of the University of Milan (<http://anacletoLab.di.unimi.it>).

Main international and national collaborations:

- Jackson Laboratory for Genomic Medicine, CT, USA
- BIH, Berlin Institute of Health, Germany
- Charite - Universitatamedizin Humboldt Universitat Berlin, Germany
- Computer Science dept. Royal Holloway, University of London, UK
- Computer Science dept. Aalto University, Helsinki, Finland
- European Center for Living Technologies, Venezia, Italy
- Division of Environmental Genomics and Systems Biology, Lawrence Berkeley National Laboratory, Berkeley, CA, USA
- Genomics England, UK
- Wellcome Trust Sanger and Institute of European Bioinformatics Institute (EBI) Hinxton, UK;
- Departamento de Ciencia de la Computacion e Inteligencia Artificial, Universidad de Granada, Spain

- IIT: Istituto Italiano di Tecnologia, Genova, Italy
- Ospedale S.Raffaele, Milano Italy
- Policlinico di Milano
- Istituto Nazionale Tumori, Milano, Italy
- Istituto di Ricerche Farmacologiche Mario Negri, Milano, Italy

Member or Principal Investigator (PI) of several national and international projects including

- PI of the *EU Collaborative Doctoral Partnership in Genomics and Bioinformatics*, funded by the European Commission – Joint Research Centre (2018-2022)
- PI of the project “*Developing machine learning methods for the prioritization of regulatory variants in human disease*” funded by the MIUR-DAAD Joint Mobility Program (2018-2019)
- PI of “*HyperGeV : Detection of Deleterious Genetic Variation through Hyper-ensemble Methods*” (2016-2018) , funded by CINECA and Regione Lombardia
- PI of “*HPC-SoMuC: Development of Innovative HPC Methods for the Detection of Somatic Mutations in Cancer*” (2017-2018), funded by CINECA and Regione Lombardia,
- “*Discovering Patterns in Multi-Dimensional Data*” (2016-2017) funded by Università degli Studi di Milano.
- “*Computational methods for bio-medical pattern analysis*”, funded by Università degli Studi di Milano.
- *Pattern Analysis, Statistical Modelling and Computational Learning 2 (PASCAL2)* Network of excellence, within the 7th European Framework Programme funded by the European Union (2007-2013);
- *PASCAL* Network of excellence, within the 6th European Framework Programme(2004-2006)
- *Computational methods for bio-medical pattern analysis* funded by the University of Milan (2011-2013)
- MIUR COFIN-PRIN project *Formal Languages and automata: methods, models and applications* (2003-2005)

- MIUR COFIN-PRIN project *Machine Learning Techniques for Bioinformatics: Analysis and Modeling of Functional and Structural Data of Gene Expression* (2001-2002)
- *From Bits to Information: Statistical Learning Technologies for Digital Information Management Search* – USA NSF funded project (2002).

Main Conference and workshop organization

Chair or co-chair of several conference/workshop in the field of Machine Learning and Bioinformatics, including:

- *CIBB 2018 Computational Intelligence methods for Bioinformatics and Biostatistics*, Lisboa (Portugal)
- *Workshop BigTargets at ECML-PKDD Porto* (Portugal), 2015;
- *Fourth Italian Workshop on Machine Learning and Data Mining (MLDM 2015)* at the XIV Conference of AIIA – Pisa (Italy), 2015;
- *SUEMA 2010, Third International Workshop on Supervised and Unsupervised Ensemble Methods and Their Applications* at ECML 2010, Barcelona, Spain;
- *Workshop Learning from Multiple Sources with Applications to Robotics* at NIPS 2009, Whistler, Canada, 2009;
- *SUEMA 2008*, at ECAI 2008 Patras, Greece;
- *CIBB 2007, Fourth International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Portofino, Italy

Activity as editor or referee in international journals.

Member of the editorial board or reviewer of the several bioinformatics and machine learning journals, including *Advances in Bioinformatics*, *BMC Bioinformatics*, *Bioinformatics*, *Briefings in Bioinformatics*, *IEEE ACM Trans. on Comp. Biol. and Bioinformatics*, *PLoS Computational Biology*, *PloS One*, *Scientific Reports*, *Artificial Intelligence in Medicine*, *GigaScience*, *Journal of Machine Learning Research*, *Machine Learning*, *Artificial Intelligence*, *Neurocomputing*, *Neural Networks*, *IEEE Trans on Pattern Analysis and Machine Intelligence*, *Pattern Recognition*, *IEEE Trans. on Cybernetics*, *Artificial Intelligence*, and others.

Academic teaching

Member of the *Doctoral School of Computer Science* of the University of Milano.

Advisor for tens of theses and *advisor of 8 PhD theses in Computer Science*, and *supervisor of three post-doc scholars* at the University of Milano.

I held several classes in International PhD Schools in Bioinformatics and Computer Science in several european universities and I held invited lectures in several research centers and universities.

I hold or held in the past years several courses at the University of Milan, including *Bioinformatics* (Master degree in Computer Science); *Bioinformatics Methods* (Master degree in Biomolecular Biotechnologies and Bioinformatics), *Programming Languages for Bioinformatics* (Master degree in Functional Genomics and Bioinformatics), *Bioinformatics Laboratory* (Degree in Biology), *Audio processing for Multimedia Applications* (degree in Digital Communication), *Basic Informatics courses* (degree in Medicine, degree in Humanities and Cultural Heritage). I held also the course *Functional Bioinformatics* (degree of Physics, University of Genova). From 2018 I am the responsible of the PhD Course “*Machine Learning for Genomic Medicine*” for the *Doctoral School of Computer Science* of the University of Milano, and I held a course “*Machine Learning for Personalized Medicine*” for the second level Master “*Bioinformatics and Functional Genomics*” organized by the National Institute of Molecular Genetics and University of Milan.

List of Publications

International Journals

50. M. Notaro, M. Schubach, P.N. Robinson, G. Valentini [Prediction of Human Phenotype Ontology terms by means of hierarchical ensemble methods](#), *BMC Bioinformatics*, vol. 18 (1), 2017 doi.org/10.1186/s12859-017-1854-y
49. M. Schubach, M. Re, P.N. Robinson and G. Valentini [Imbalance-Aware Machine Learning for Predicting Rare and Common Disease-Associated Non-Coding Variants](#), *Scientific Reports*, Nature Publishing, 7:2959, 2017.
48. D. Smedley, M. Schubach, J. Jacobsen, S. Kohler, T. Zemojtel, M. Spielmann, M. Jager, H. Hochheiser, N. Washington, J. McMurry, M. Haendel, C. Mungall, S. Lewis, T. Groza, G. Valentini and P.N. Robinson [A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease](#), *The American Journal of Human Genetics*, 99:3, pp.595--606, September 2016. doi.org/10.1016/j.ajhg.2016.07.005
47. Y. Jiang, P. Oron, ... G. Valentini, ... I. Friedberg and P. Radivojac [An expanded evaluation of protein function prediction methods shows an improvement in accuracy](#), *Genome Biology*, 17:184 September 2016. doi.org/10.1186/s13059-016-1037-6 [Supplementary Information](#)
46. G. Valentini, G. Armano, M. Frasca, J. Lin, M. Mesiti and M. Re [RANKS: a flexible tool for node label ranking and classification in biological networks](#), *Bioinformatics*, 32(18), September 2016. [doi:10.1093/bioinformatics/btw235](https://doi.org/10.1093/bioinformatics/btw235) [Pre-print version](#) [Supplementary Information](#)
45. M. Frasca, S. Bassis, G. Valentini [Learning node labels with multi-category Hopfield networks](#), *Neural Computing and Applications*, 27(6), pp 1677-1692, 2016 [doi:10.1007/s00521-015-1965-1](https://doi.org/10.1007/s00521-015-1965-1)
44. M. Frasca, G. Valentini [COSNet: an R package for label prediction in unbalanced biological networks](#), *Neurocomputing*, 2016. [doi:10.1016/j.neucom.2015.11.096](https://doi.org/10.1016/j.neucom.2015.11.096) [Bioconductor COSNet web site](#)
43. M. Frasca, A. Bertoni, G. Valentini [UNIPred: Unbalance-aware Network Integration and Prediction of protein functions](#), *Journal of Computational Biology*, 22(12): 1057-1074, 2015. [doi:10.1089/cmb.2014.0110](https://doi.org/10.1089/cmb.2014.0110) [Supplementary Information](#)
42. M. Mesiti, M. Re, G. Valentini [Think globally and solve locally: secondary memory-based network learning for automated multi-species function prediction](#), *GigaScience*, 3:5, 2014
41. G. Valentini, A. Paccanaro, H. Caniza, A. Romero, M. Re, [An extensive analysis of disease-gene associations using network integration and fast kernel-based gene prioritization methods](#), *Artificial Intelligence in Medicine*, Volume 61, Issue 2, pages 63-78, June 2014
40. H. Caniza, A. Romero, S. Heron, H. Yang, A. Devoto, M. Frasca, M. Mesiti, G. Valentini, A. Paccanaro, [GOssTo: a user-friendly stand-alone and web tool for calculating semantic similarities on the Gene Ontology](#), *Bioinformatics*, Vol. 30 no. 15, pages 2235-2236, 2014
39. G. Valentini, [Hierarchical Ensemble Methods for Protein Function Prediction](#), *ISRN Bioinformatics*, vol. 2014, Article ID 901419, 34 pages, 2014
38. M. Re, and G. Valentini, [Network-based Drug Ranking and Repositioning with respect to DrugBank Therapeutic Categories](#),

- IEEE ACM Transactions on Computational Biology and Bioinformatics* 10(6), pp. 1359-1371, Nov-Dec 2013 [IEEE link](#) [Supplemental Material](#)
37. I. Cattinelli, G. Valentini, E. Paulesu, A. Borghese [A Novel Approach to the Problem of Non-uniqueness of the Solution in Hierarchical Clustering](#), *IEEE Transactions on Neural Networks and Learning Systems* 24(7) pp.1166-1173, July 2013
36. M. Frasca, A. Bertoni, M. Re, and G. Valentini, [A neural network algorithm for semi-supervised node label learning from unbalanced data](#), *Neural Networks* 43, pp.84-98, July 2013 [Science Direct link](#)
35. M. Re, M. Mesiti and G. Valentini, [A Fast Ranking Algorithm for Predicting Gene Functions in Biomolecular Networks](#), *IEEE ACM Transactions on Computational Biology and Bioinformatics* 9(6) pp. 1812-1818, 2012. [IEEE link](#)
34. A. Beghini, F. Corlazzoli, L. Del Giacco, M. Re, F. Lazzaroni, M. Brioschi, G. Valentini, F. Ferrazzi, A. Ghilardi, M. Righi, M. Turrini, M. Mignardi, C. Cesana, V. Bronte, M. Nilsson, E. Morra and R. Cairoli, [Regeneration-associated Wnt signaling is activated in long-term reconstituting AC133bright acute myeloid leukemia cells](#), *Neoplasia* 14:12, pp. 1236-1248, 2012
33. M. Re and G. Valentini [Cancer module genes ranking using kernelized score functions](#) *BMC Bioinformatics* 13 (Suppl 14): S3, 2012.
32. N. Cesa-Bianchi, M. Re, G. Valentini, [Synergy of multi-label hierarchical ensembles, data fusion, and cost-sensitive methods for gene functional inference](#), *Machine Learning*, vol.88(1), pp. 209-241, 2012. [Springer link](#)
31. M. Re, M. Mesiti, G. Valentini, [Drug repositioning through pharmacological spaces integration based on networks projection](#), *EMBnet.journal*, vol 18, Supplement A, pp.30-31, *BITS 2012, Bioinformatics Italian Society Meeting*, Catania, Italy, 2012.
30. M. Frasca, A. Bertoni, G. Valentini, [Regularized Network-Based Algorithm for Predicting Gene Functions with High-Imbalanced Data](#), *EMBnet.journal*, vol 18, Supplement A, pp.41,42, *BITS 2012, Bioinformatics Italian Society Meeting*, Catania, Italy, 2012.
29. G. Valentini, [True Path Rule hierarchical ensembles for genome-wide gene function prediction](#), *IEEE ACM Transactions on Computational Biology and Bioinformatics*, vol.8 n.3 pp. 832-847, 2011. [IEEE CS Digital library](#)
28. M. Muselli, A. Bertoni, M. Frasca, A. Beghini, F. Ruffino, and G. Valentini, [A mathematical model for the validation of gene selection methods](#), *IEEE ACM Transactions on Computational Biology and Bioinformatics*, vol.8 n.5 pp. 1385-1392, 2011. [IEEE CS Digital library](#)
27. M. Re, G. Valentini, [Noise tolerance of Multiple Classifier Systems in data integration-based gene function prediction](#), [Supplementary Information](#) *Journal of Integrative Bioinformatics*, 7(3):139, 2010
26. M. Re, G. Valentini, [Simple ensemble methods are competitive with state-of-the-art data integration methods for gene function prediction](#) *Journal of Machine Learning Research*, W&C Proceedings, vol.8: Machine Learning in Systems Biology, pp. 98-111, 2010.
25. N. Cesa-Bianchi, G. Valentini, [Hierarchical cost-sensitive algorithms for genome-wide gene function prediction](#), *Journal of Machine Learning Research*, W&C Proceedings, vol.8: Machine Learning in Systems Biology, pp.14-29, 2010.
24. M. Re, G. Valentini, [Integration of heterogeneous data sources for gene function prediction](#)

- [using Decision Templates and ensembles of learning machines](#),
Neurocomputing, 73:7-9 pp. 1533-37, 2010 [doi:10.1016/j.neucom.2009.12.012](https://doi.org/10.1016/j.neucom.2009.12.012)
23. M. Mesiti, E. Jimenez-Ruiz, I. Sanz, R. Berlanga-Llavori, P. Perlasca, G. Valentini and D. Manset, [XML-Based Approaches for the Integration of Heterogeneous Bio-Molecular Data](#)
BMC Bioinformatics 10:(S12)S7, 2009
 22. R. Avogadri, M. Brioschi, F. Ferrazzi, M. Re, A. Beghini, and G. Valentini, [A stability-based algorithm to validate hierarchical clusters of genes](#),
International Journal of Knowledge Engineering and Soft Data Paradigms, 1(4), pp. 318-330, 2009
 21. G. Valentini, R. Tagliaferri, F. Masulli, [Computational Intelligence and Machine Learning in Bioinformatics](#)
Artificial Intelligence in Medicine 45(2), pp. 91-96, 2009
 20. R. Avogadri, G. Valentini, [Fuzzy ensemble clustering based on random projections for DNA microarray data analysis](#)
Artificial Intelligence in Medicine 45(2), pp. 173-183, 2009
 19. G. Pavesi, G. Valentini, [Classification of co-expressed genes from DNA regulatory regions](#),
Information Fusion 10(3), pp. 233-241, 2009
 18. A. Bertoni, G. Valentini, [Discovering multi-level structures in bio-molecular data through the Bernstein inequality](#)
BMC Bioinformatics 9(Suppl 2):S4, 2008
 17. G. Valentini, N. Cesa-Bianchi, [HCGene: a software tool to support the hierarchical classification of genes](#),
Bioinformatics, 24(5), pp. 729-731, 2008. [HCGene web-site](#)
 16. F. Ruffino, M. Muselli, G. Valentini, [Gene expression modelling through positive Boolean functions](#),
International Journal of Approximate Reasoning, 47(1), pp. 97-108, 2008.
 15. A. Bertoni, G. Valentini, [Model order selection for biomolecular data clustering](#),
BMC Bioinformatics, vol.8, Suppl.3, 2007. [Mosclust web-site](#)
 14. G. Valentini, [Mosclust: a software library for discovering significant structures in bio-molecular data](#).
Bioinformatics 23(3):387-389, 2007.
 13. G. Valentini, F. Ruffino, [Characterization of Lung tumor subtypes through gene expression cluster validity assessment](#),
RAIRO - Theoretical Informatics and Applications, 40:163-176, 2006.
 12. A. Bertoni, G. Valentini, [Randomized maps for assessing the reliability of patients clusters in DNA microarray data analyses](#),
Artificial Intelligence in Medicine 37(2):85-109 2006, [Science Direct access](#)
 11. G. Valentini, [Clusterv: a tool for assessing the reliability of clusters discovered in DNA microarray data](#),
Bioinformatics 22(3):369-370, 2006. [Clusterv web-site](#)
 10. G. Valentini, [An experimental bias-variance analysis of SVM ensembles based on resampling techniques](#),
IEEE Transactions on Systems, Man and Cybernetics, Part B vol.35(6) pp. 1252-1271, 2005
[IEEE Explore access](#)
 9. P. Campadelli, E. Casiraghi, G. Valentini, [Support Vector Machines for candidate nodules classification](#),
Neurocomputing vol.68 pp. 281-289, 2005 [Science Direct access](#)
 8. A. Bertoni, R. Folgieri, G. Valentini, [Bio-molecular cancer prediction with random subspace ensembles of Support Vector Machines](#),

- Neurocomputing* vol. 63C pp. 535-539, 2005 [Science Direct access](#)
7. G. Valentini, T. G. Dietterich, [Bias-variance analysis of Support Vector Machines for the development of SVM-based ensemble methods](#), *Journal of Machine Learning Research*, 5(Jul) pp. 725--775, 2004, MIT Press, [JMLR link](#)
 6. F. Masulli, G. Valentini, [An experimental analysis of the dependence among codeword bit errors in ECOC learning machines](#). *Neurocomputing* 57 pp. 189-214, 2004, [science direct link](#)
 5. G. Valentini, M. Muselli and F. Ruffino, [Cancer recognition with bagged ensembles of Support Vector Machines](#), *Neurocomputing* 56 pp. 461-466, 2004, [science direct link](#)
 4. F. Masulli, G. Valentini, [Effectiveness of output coding decomposition schemes in ensemble and monolithic learning machines](#). *Pattern Analysis and Applications* 6 pp. 285-300, 2003.
 3. G. Valentini, [Gene expression data analysis of human lymphoma using Support Vector Machines and Output Coding ensembles](#). *Artificial Intelligence in Medicine* 26(3) pp 283-306, 2002
 2. G. Valentini, F. Masulli, [NEUROObjects: an object-oriented library for neural network development](#), *Neurocomputing* 48(1-4) pp. 623-646 , 2002, [science direct link](#)
 1. M. Pardo, G. Sberveglieri, A.Taroni, F. Masulli, G. Valentini [Decompositive classification models for electronic noses](#). *Anal. Chim. Acta* (446) pp. 223-232, 2001.

Edited Books

5. O. Okun, G. Valentini, M. Re (eds.), [Ensembles in Machine Learning Applications](#), *Studies in Computational Intelligence*, vol. 373 Springer, ISBN: 978-3-642-22909-1, 2011.
4. O. Okun, M. Re, G. Valentini (eds.), [Proceedings of the the Third Workshop on Supervised and Unsupervised Ensemble Methods and Their Applications \(SUEMA\)](#), European Conference on Machine Learning, Barcelona, Spain, 2010.
3. O. Okun, G. Valentini (eds.), [Applications of Supervised and Unsupervised Ensemble Methods](#), *Studies in Computational Intelligence*, vol. 245 Springer, ISBN: 978-3-642-03998-0, 2010.
2. O. Okun, G. Valentini (eds.), [Proceedings of the the Second Workshop on Supervised and Unsupervised Ensemble Methods and Their Applications \(SUEMA\)](#), European Conference on Artificial Intelligence, University of Patras, Greece, ISBN: 978-960-89282-2-0, 2008.
1. O. Okun, G. Valentini (eds.), [Supervised and Unsupervised Ensemble Methods and their Applications](#), *Studies in Computational Intelligence*, vol. 126 Springer, ISBN: 978-3-540-78980-2, 2008.

Proceedings of International Conferences and book chapters

- 78.A. Petrini, M. Schubach, M. Re, M. Frasca, M. Mesiti, G. Grossi, T. Castrignano', P.N. Robinson, G. Valentini [Parameters tuning boosts hyperSMURF predictions of rare deleterious non-coding genetic variants](#), *PeerJ Preprints* 5:e3185v1, 2017 presented at Methods, tools & platforms for Personalized Medicine in the Big Data Era - NETTAB 2017, Palermo, Italy
- 77.M. Schubach, M. Re, P.N. Robinson, G. Valentini [Variant relevance prediction in extremely imbalanced training sets](#), *F1000Research* 2017, 6(*ISCB Comm J*):1392 (poster) (doi: 10.7490/f1000research.1114637.1),

- presented at the 25th International Conference on Intelligent Systems for Molecular Biology (ISMB), Prague 2017
76. M. Notaro, M. Schubach, P.N. Robinson, G. Valentini [Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions](#), *CIBB 2017, The 14th International Conference on Bioinformatics and Biostatistics*, Cagliari, Italy, 2017.
75. M. Frasca, J.F. Fontaine, G. Valentini, M. Mesiti, M. Notaro, D. Malchiodi and M.A. Andrade-Navarro [Disease Genes must Guide Data Source Integration in the Gene Prioritization Process](#), *CIBB 2017, The 14th International Conference on Bioinformatics and Biostatistics*, Cagliari, Italy, 2017.
74. J. Lin, M. Mesiti, M. Re and G. Valentini [Within network learning on big graphs using secondary memory-based random walk kernels](#), *Complex Networks & Their Applications V: Proceedings of the 5th International Workshop on Complex Networks and their Applications (COMPLEX NETWORKS 2016)*, Studies in Computational Intelligence, Springer, pp. 235-245, 2017, doi.org/10.1007/978-3-319-50901-3_19
73. P. Perlasca, G. Valentini, M. Frasca, M. Mesiti [Multi-species Protein Function Prediction: Towards Web-based Visual Analytics](#), *Proceedings of the 18th International Conference on Information Integration and Web-based Applications & Services*, Singapore, ACM, New York, USA pp. 1-5, 2016. doi.org/10.1145/3011141.3011222
72. H. Su, G. Valentini, S. Szedmak and J. Rousu [Transport Protein Classification through Structured Prediction and Multiple Kernel Learning](#), *NIPS Workshop on Machine Learning in Computational Biology (MLCB) & Machine Learning in Systems Biology (MLSB) 2015* - Montreal, Canada, December 2015
71. P.N. Robinson, M. Frasca, S. Kohler, M. Notaro, M. Re, G. Valentini, [A hierarchical ensemble method for DAG-structured taxonomies](#), *Multiple Classifier Systems - MCS 2015* - Gunzburg, Germany *Lecture Notes in Computer Science*, vol. 9132, pp. 15-36, Springer, 2015
70. G. Valentini, S. Kohler, M. Re, M. Notaro, P.N. Robinson, [Prediction of human gene - phenotype associations by exploiting the hierarchical structure of the Human Phenotype Ontology](#), *3rd International Work-Conference on Bioinformatics and Biomedical Engineering - IWBBIO 2015*, Granada, Spain *Lecture Notes in Bioinformatics*, vol. 9043, pp. 66-77, Springer, 2015
69. M. Re, M. Mesiti, G. Valentini, [An automated pipeline for multi-species protein function prediction from the UniProt Knowledgebase](#), *Automated Function Prediction SIG 2014* - ISMB 2014, Boston, USA
68. M. Re, M. Mesiti, G. Valentini, [On the Automated Function Prediction of Big Multi-Species Networks](#), *Network Biology SIG 2014* - ISMB 2014, Boston, USA
67. M. Frasca, A. Bertoni, G. Valentini [An unbalance-aware network integration method for gene function prediction](#), *MLSB 2013 - Machine Learning for Systems Biology*, Berlin, 2013
66. G. Valentini, A. Paccanaro, H. C. Vierci, A. E. Romero, M. Re, [Network integration boosts disease gene prioritization](#), *Network Biology SIG 2013* - ISMB 2013, Berlin
65. M. Mesiti, M. Re, G. Valentini [Scalable Network-based Learning Methods for Automated Function Prediction based on the Neo4j Graph-database](#), *Automated Function Prediction SIG 2013* - ISMB 2013, Berlin

64. H. C. Vierci, A. E. Romero, S. Heron, H. Yang, M. Frasca, M. Mesiti, G. Valentini and A. Paccanaro [GOssTo & GOssToWeb: user-friendly tools for calculating semantic similarities on the Gene Ontology](#), *Bio-Ontologies SIG 2013 - ISMB 2013*, Berlin
63. M. Re, M. Mesiti, G. Valentini [Comparison of early and late omics data integration for cancer modules gene ranking](#), *NETTAB 2012 Workshop on Integrated Bio-Search*, Como 14-16 November, 2012.
62. M. Re and G. Valentini [Random walking on functional interaction networks to rank genes involved in cancer](#) *2nd Artificial Intelligence Applications in Biomedicine Workshop*, in: AIAI 2012 - Artificial Intelligence Applications and Innovations, pp. 66-75, *IFIP AICT Series*, Springer, 2012
61. M. Re, G. Valentini [Large Scale Ranking and Repositioning of Drugs with Respect to DrugBank Therapeutic Categories](#), [slides](#)
In: L. Bleris et al. (Eds.): International Symposium on Bioinformatics Research and Applications (ISBRA 2012), Dallas, USA, *Lecture Notes in Bioinformatics* vol.7292, pp. 225-236, Springer, 2012.
60. M. Re, G. Valentini, [Ensemble methods: a review](#),
In: *Advances in Machine Learning and Data Mining for Astronomy*, Chapman & Hall Data Mining and Knowledge Discovery Series, Chap. 26, pp. 563-594, 2012.
59. M. Re, G. Valentini [Genes prioritization with respect to Cancer Gene Modules using functional interaction network data](#), *NETTAB 2011 Workshop on Clinical Bioinformatics*, Pavia 12-14 October, 2011.
58. A. Bertoni, M. Frasca, G. Valentini [COSNet: a Cost Sensitive Neural Network for Semi-supervised Learning in Graphs](#),
In: "Machine Learning and Knowledge Discovery in Databases". European Conference, ECML PKDD 2011, Athens, Greece, Proceedings, Part I, *Lecture Notes in Artificial Intelligence*, vol. 6911, pp.219-234, Springer, 2011.
57. A. Rozza, G. Lombardi, M. Re, E. Casiraghi, G. Valentini and P. Campadelli [A Novel Ensemble Technique for Protein Subcellular Location Prediction](#),
In: "Ensembles in Machine Learning Applications", *Studies in Computational Intelligence* vol. 373, pp. 151-167, Springer, 2011
56. M. Frasca, A. Bertoni, G. Valentini [A cost-sensitive neural algorithm to predict gene functions using large biological networks](#),
Network Biology SIG: On the Analysis and Visualization of Networks in Biology, ISMB 2011, Wien
55. A. Bertoni, M. Re, F. Sacca, G. Valentini [Identification of promoter regions in genomic sequences by 1-dimensional constraint clustering](#),
Frontiers in Artificial Intelligence and Applications, vol. 234, *Neural Nets WIRN11 - Proceedings*, pp. 162-169, 2011.
54. A. Rozza, G. Lombardi, M. Re, E. Casiraghi, and G. Valentini, [DDAG K-TIPCAC: an ensemble method for protein subcellular localization](#),
Proc. of the Third Edition of SUEMA, pp. 75-84, ECML, Barcelona, Spain, 2010.
53. N. Cesa-Bianchi, M. Re, G. Valentini, [Functional Inference in FunCat through the Combination of Hierarchical Ensembles with Data Fusion Methods](#),
ICML Workshop on learning from Multi-Label Data MLD'10, Haifa, Israel, pp.13-20, 2010
52. A. Bertoni, M. Frasca, G. Grossi, G. Valentini, [Learning functional linkage networks with a cost-sensitive approach](#),
Neural Networks - WIRN 2010, IOS Press, pp. 52-61, 2010
51. M. Re, G. Valentini, [An experimental comparison of Hierarchical Bayes and True Path Rule](#)

- [ensembles for protein function prediction](#),
In: (N. El Gayar, J. Kittler and F. Roli, Eds) Ninth International Workshop on Multiple Classifier Systems MCS 2010, *Lecture Notes in Computer Science*, vol. 5997, pp. 294-303, Springer, 2010.
50. N. Cesa-Bianchi, G. Valentini, [Hierarchical cost-sensitive algorithms for genome-wide gene function prediction](#),
Machine Learning in Systems Biology, Proceedings of the Third international workshop, Ljubljana, Slovenia, pp. 25-34, 2009.
49. M. Re, G. Valentini, [Simple ensemble methods are competitive with state-of-the-art data integration methods for gene function prediction](#),
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