

PERSONAL INFORMATION



Emanuel Weitschek

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WORK EXPERIENCE

01/09/2018–Present

Scientific Officer in Computer Science

Italian Competition Authority, Rome (Italy)

Computer science advisor on following topics: big data, machine learning, artificial intelligence, dynamic pricing, algorithmic tacit collusion, and legal informatics.

Data scientist.

01/09/2018–Present

Adjunct Professor

Uninettuno University, Rome (Italy)

Professor of Big Data, Bioinformatics, Computer Networks, and Computer Science.

20/05/2015–31/08/2018

Researcher

Uninettuno University, Rome (Italy)

Research on big data, machine learning, and bioinformatics.

Professor of following courses: Big Data, Bioinformatics, Computer Science, and Computer Networks.

Definition and supervision of the master in computer science with focus on big data.

03/06/2013–19/05/2015

Postdoctoral Researcher

Department of Engineering - Roma Tre University, Rome (Italy)

Research on big data bioinformatics.

Modeling and integration of big biomedical data.

Supervisor of bachelor and master students.

Teaching assistant for the Big Data course.

02/01/2009–31/08/2018

Research Consultant

Institute of Systems Analysis and Computer Science - National Research Council, Rome (Italy)

Research on machine learning, data mining, and bioinformatics.

Supervisor of PhD candidates and master students.

Research project manager.

Software designer and developer.

EDUCATION AND TRAINING

- 27/07/2018–Present **Associate Professor Habilitation in Computer Engineering**
Ministry of Education, University and Research, Rome (Italy)

- 01/01/2010–04/06/2013 **PhD in Computer Engineering**
Department of Engineering - Roma Tre University, Rome (Italy)
Machine learning in big data bioinformatics.
Classification of big biomedical data.

- 24/09/2009–Present **Engineering Licence**
National Council of Engineers, Rome (Italy)

- 24/02/2006–22/12/2008 **Master in Computer Engineering**
Roma Tre University, Rome (Italy)

- 01/10/2002–24/02/2006 **Bachelor in Computer Engineering**
Roma Tre University, Rome (Italy)

- 10/09/1986–01/07/2001 **German High School Diploma**
German School of Rome, Rome (Italy)

PERSONAL SKILLS

Mother tongue(s) Italian

Foreign language(s)

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
German	C2	C2	C2	C2	C2
German High School Diploma					
English	C2	C2	C2	C2	C2

Levels: A1 and A2: Basic user - B1 and B2: Independent user - C1 and C2: Proficient user
Common European Framework of Reference for Languages

Organisational / managerial skills

Scientific manager of the research contract "Extraction, integration and conversion of big biomedical data extracted from the Genomic Data Commons public database" entrusted by the Department of Electronics, Information and Bioengineering (DEIB) of the Politecnico di Milano to the Uninettuno Telematic University within the project ERC Advanced Grant 693174 "Data Driven Genomic Computing". The research contract lasted from 22 September 2017 to 22 March 2018 and enabled two collaboration grants to be activated for research, development and data integration activities.

Scientific manager of the work unit called "WP5 - Genomic Data Analytics" of the PRIN research project "Data-Centric Genomic Computing (GenData 2020)" [grant number 2010RTFWBH]. The main outcomes were the design and implementation of numerous methods and software for the analysis of genomic and clinical Big Data.

Scientific manager of the Cineca project entitled "A new multiple rule-based classification method for big next generation sequencing data of cancer" (BIGBIOCL) [grant number HP10CTJZAM]. The project allowed to get 50 thousand computational hours on the parallel computing resources of the Cineca. The participants in the project were 2 doctoral students and a computer scientist. The project led to the publication of the article F. Celli, F. Cumbo, E. Weitschek: Classification of Large DNA Methylation Datasets for Identifying Cancer Drivers. *Big Data Research*, 13:21-28, 2018.

Supervisor of more than 50 master and bachelor **theses** on big data, machine learning, and bioinformatics.

Co-supervisor of 3 **PhD students** and 1 post doctoral researcher.

Participation to several national and international **research projects** on data mining, software engineering, and bioinformatics.

ADDITIONAL INFORMATION

Publications

International peer reviewed journals

E. Cappelli, G. Felici, E. Weitschek: Combining DNA methylation and RNA sequencing data of cancer for supervised knowledge extraction. *BioData Mining*, 11:22, 2018. Impact Factor: 2.07

E. Weitschek, S. Di Lauro, E. Cappelli, P. Bertolazzi, G. Felici: CamurWeb: a classification software and a large knowledge base for gene expression data of cancer. *BMC Bioinformatics*, 19(S10):354, 2018. Impact Factor: 3.11

G. Fiscon*, E. Weitschek*, A. Cialini, G. Felici, P. Bertolazzi, S. De Salvo, A. Bramanti, P. Bramanti, M.C. De Cola: Combining EEG signal processing with supervised methods for Alzheimer's patients classification. *BMC Medical Informatics and Decision Making*, 18:35, 2018. Impact Factor: 2.36 *(equal contributors)

F. Celli, F. Cumbo, E. Weitschek: Classification of Large DNA Methylation Datasets for Identifying Cancer Drivers. *Big Data Research*, 13:21-28, 2018.

F. Previtali, P. Bertolazzi, G. Felici, E. Weitschek: A novel method and software for automatically classifying Alzheimer's disease patients by magnetic resonance imaging analysis. *Computer Methods and Programs in Biomedicine*, 143:89-95 2017. Impact Factor: 2.5.

F. Cumbo*, G. Fiscon*, S. Ceri, M. Masseroli, E. Weitschek*: TCGA2BED: extracting, extending, integrating, and querying The Cancer Genome Atlas. *BMC Bioinformatics*, 18:6, 2017. Impact Factor: 2.5 *(equal contributors).

G. Fiscon*, E. Weitschek*, E. Cella, A. Lo Presti, M. Giovanetti, M. Babakir-Mina, M. Ciotti, M. Ciccozzi, A. Pierangeli, P. Bertolazzi, G. Felici: MISSEL: a method to identify a large number of small species-specific genomic subsequences and its application to viruses classification. *BioData Mining*, 9:38, 2016. Impact Factor: 1.64 *(equal contributors).

V. Cestarelli*, G. Fiscon*, G. Felici, P. Bertolazzi, E. Weitschek*: CAMUR: Knowledge extraction from RNA-seq cancer data through equivalent classification rules. *Bioinformatics*, 32(5): 697-704, 2016. Impact Factor: 5.0 *(equal contributors).

P. Bertolazzi, G. Felici, P. Festa, G. Fiscon, E. Weitschek: Integer programming models for feature selection: new extensions and a randomized solution algorithm. *European Journal of Operational Research*, 250(2):389-399, 2016. Impact Factor: 2.36

K. Wilkins, ..., G. Fiscon, E. Weitschek, M. Ciccozzi, P. Bertolazzi, G. Felici, et. al: A novel feature selection method to extract multiple adjacent solutions for viral genomic sequences classification - Highlights from the 11th ISCB Student Council Symposium 2015. *BMC Bioinformatics*, 7(3):203, 2016. Impact Factor: 2.57

D. Santoni, E. Weitschek, G. Felici: Optimal discretization and selection of features by association rates of joint distributions. *RAIRO Operational Research*, 50(2):437-449, 2016. Impact Factor: 0.33

E. Weitschek*, F. Cunial, G. Felici: LAF: Logic Alignment Free and its application to bacterial genomes classification. *BioData Mining*, 8(1):39, 2015. Impact Factor: 2.02.

E. Weitschek, D. Santoni, G. Fiscon, M.C. De Cola, P. Bertolazzi, G. Felici: Next generation sequencing reads comparison with an alignment-free distance. *BMC Research Notes*, 7:869, 2014.

D. Polychronopoulos*, E. Weitschek*, S. Dimitrieva, P. Bucher, G. Felici, Y. Almirantis: Classification of selectively constrained DNA elements using feature vectors and rule-based classifiers. *Elsevier Genomics*, 104(2):79-86, 2014. Impact Factor: 2.8 *(joint first authors).

E. Weitschek*, G. Fiscon*, G. Felici: Supervised DNA Barcodes species classification: analysis, comparisons, and results. *BioData Mining*, 7(1):4, 2014. Impact Factor: 1.54 *(joint first authors).

E. Weitschek, R. van Velzen, G. Felici, P. Bertolazzi: BLOG 2.0: a software system for character-based species classification with DNA Barcode sequences. What it does, how to use it. *Molecular ecology resources*, 13(6):1043-1046, 2013. Impact Factor: 7.4.

E. Weitschek, A.L. Presti, G. Drovandi, G. Felici, M. Ciccozzi, M. Ciotti, P. Bertolazzi: Human polyomaviruses identification by logic mining techniques. *Virology journal*, 9(1):1-6, 2012. Impact Factor: 2.04.

R. van Velzen, E. Weitschek, G. Felici, F.T. Bakker: DNA barcoding of recently diverged species: relative performance of matching methods. *PLoS one*, 7(1):e30490, 2012. Impact Factor: 3.73.

M.C. De Cola, G. Felici, D. Santoni, E. Weitschek: Filtering with alignment free distances for high throughput DNA reads assembly. *EMBNET journal*, 18(B):23-25, 2012.

I. Arisi, M. D'Onofrio, R. Brandi, A. Felsani, S. Capsoni, G. Drovandi, G. Felici, E. Weitschek, P. Bertolazzi, A. Cattaneo: Gene expression biomarkers in the brain of a mouse model for Alzheimer's disease: mining of microarray data by logic classification and feature selection. *Journal of Alzheimer's Disease*, 24(4):721-738, 2011. Impact Factor: 4.17.

P. Bertolazzi, G. Felici, E. Weitschek: Learning to classify species with barcodes. *BMC Bioinformatics*, 10(Suppl 14), S7, 2009 Impact Factor: 3.02.

Conference proceedings

E. Weitschek, F. Cumbo, E. Cappelli, G. Felici, P. Bertolazzi: Classifying Big DNA Methylation Data: A Gene-Oriented Approach. International Conference on Database and Expert Systems Applications, 138-149, Communications in Computer and Information Science, 903:138-149, 2018

F. Cumbo, E. Weitschek, P. Bertolazzi, G. Felici: IRIS-TCGA: an information retrieval and integration system for genomic data of cancer. Lecture Notes in Bioinformatics vol. 10477, Computational Intelligence Methods for Bioinformatics and Biostatistics, Springer, October, 2017.

E. Cappelli, E. Weitschek: Extending the Genomic Data Model and the Genometric Query Language with Domain Taxonomies. Lecture Notes in Computer Science vol. 10360, International Conference on Web Engineering, pp. 567-574, Springer, Cham, Rome (Italy), June, 2017.

D. Assante, C. Fornaro, E. Weitschek, M. Castro, et al. Smart open online tool for adaptive education on Cloud Computing. In Global Engineering Education Conference (EDUCON), pp. 1183-1186. IEEE, Athens (Greece), April, 2017.

E. Weitschek, F. Cumbo, E. Cappelli, G. Felici: Genomic data integration: A case study on next generation sequencing of cancer. In Database and Expert Systems Applications (DEXA), 27th International Workshop on Biological Knowledge Discovery, IEEE, Porto (Portugal), September, 2016.

F. Cumbo, E. Weitschek, P. Paci, T. Colombo, P. Bertolazzi, G. Felici: IRIS-TCGA: an information retrieval and integration system for cancer genomic data. In 13th international meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB), pp.178-183, A Bracciali, D Gilbert, G MacKenzie (Eds.), Stirling (UK), August, 2016.

E. Weitschek, G. Fiscon, V. Cestarelli, P. Bertolazzi, G. Felici: LAF Barcoding: classifying DNA Barcode multi-locus sequences with feature vectors and supervised approaches. In Twelfth international meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB), pp.1-6, ISBN: 9788890643798, Naples (Italy), September, 2015

E. Weitschek, G. Fiscon, G. Felici, P. Bertolazzi: GELA: a software tool for the analysis of gene expression data. In Database and Expert Systems Applications (DEXA), 26th International Workshop on Biological Knowledge Discovery, pp. 31-35, ISSN: 1529-4188/15, doi: 10.1109/DEXA.2015.26,

IEEE, Valencia (Spain), September, 2015.

E. Weitschek, G. Fiscon, P. Bertolazzi, G. Felici: Classifying DNA barcode multi-locus sequences with feature vectors and supervised approaches. GENOME, 58(5), pp. 295-295, doi:10.1139/gen-2015-0087, Ottawa (Canada), August, 2015.

G. Fiscon*, E. Weitschek*, G. Felici, P. Bertolazzi, S. de Salvo, P. Bramante, M.C. De Cola: Alzheimer's disease patients classification through EEG signals processing. In Proceedings of SSCI 2014 - IEEE Symposium Series on Computational Intelligence and Data Mining, pp. 105-112. IEEE, 2014.

E. Weitschek, F. Cunial, G. Felici: Classifying bacterial genomes on k-mer frequencies with compact logic formulas. In Database and Expert Systems Applications (DEXA), 25th International Workshop on Biological Knowledge Discovery, pp. 69-73. IEEE, 2014.

E. Weitschek, G. Felici, P. Bertolazzi: Clinical data mining: problems, pitfalls and solutions. In Database and Expert Systems Applications (DEXA), 24th International Workshop on Biological Knowledge Discovery, pp. 90-94. IEEE, 2013.

E. Weitschek, G. Felici, P. Bertolazzi: Mala: A microarray clustering and classification software. In Database and Expert Systems Applications (DEXA), 23rd International Workshop on Biological Knowledge Discovery, pp. 201-205. IEEE, 2012.

G. Felici, E. Weitschek: Mining logic models in the presence of noisy data. In International Symposium on Artificial Intelligence and Mathematics, 2012

Book chapters

G. Fiscon, E. Weitschek: String-Matching and Alignment Algorithms for Finding Motifs in NGS data. In Algorithms for Next-Generation Sequencing Data (Techniques, Approaches, and Applications), Elloumi M (Ed.), Mourad Elloumi Eds, Springer, ISBN 978-3-319-59824-6, 2017.

E. Weitschek, G. Fiscon, V. Fustaino, G. Felici, P. Bertolazzi: Clustering and Classification Techniques for Gene Expression Profiles Pattern Analysis. In Pattern Recognition in Computational Molecular Biology: Techniques and Approaches, Mourad Elloumi, Costas S. Iliopoulos, Jason T. L. Wang and Albert Y. Zomaya Editors, Wiley Book Series on Bioinformatics: Computational Techniques and Engineering, Wiley-Blackwell, New Jersey, USA (Publisher), ISBN 978-1118893685, 2015.

Technical reports

E. Weitschek, G. Fiscon, V. Fustaino, G. Felici, P. Bertolazzi: Analysis of microarray and RNA-sequencing gene expression profiles through clustering and classification techniques. IASI-CNR, R. 14-11, 2014

G. Fiscon, E. Weitschek, P. Bertolazzi, M.C. De Cola, S. De Salvo S, P. Bramanti, G. Felici: EEG signals analysis to detect Alzheimer's disease patients. IASI-CNR, R. 14-10, 2014

E. Weitschek, I. Arisi, G. Felici, P. Bertolazzi,. Knowledge extraction in clinical data. IASI-CNR, R. 13-20, 2013.

E. Weitschek, G. Felici, P. Bertolazzi: Microarray Logic Analyzer Software. IASI-CNR, R. 13-18, 2013.

E. Weitschek, G. Fiscon, G. Felici: Supervised Learning Meets DNA Barcoding Species Classification. IASI-CNR, R. 13-16, 2013.

E. Weitschek, D. Polychronopoulos, Y. Almirantis, G. Felici: Conserved non coding elements classification. IASI-CNR, R. 13-15, 2013.

E. Weitschek, D. Santoni, M.C. De Cola, G. Felici: About similarity of DNA reads. IASI-CNR, R. 13-17, 2013.

G. Felici, E. Weitschek: Mining Logic Models in the Presence of Noisy Data. IASI-CNR, R. 11-25, 2011.

E. Weitschek, R. van Velzen, G. Felici: Species classification using DNA Barcode sequences: A comparative analysis. IASI-CNR, R. 11-07, 2011.

P. Bertolazzi, G. Felici, E. Weitschek, G. Drovandi, A. Lo Presti, M. Ciccozzi, M. Ciotti: Human Polyomaviruses genome analysis by logic mining techniques, IASI-CNR, R. 10-23, 2010.

PhD Thesis

E. Weitschek: Logic mining techniques for biological data analysis and classification. Roma Tre University, 2013.

Reviver for following journals

- [Information](#)
- [Computers in biology and medicine](#)
- [Bioinformatics](#)
- [PeerJ](#)
- [Biotechnology Progress](#)
- [BioData Mining](#)
- [International Journal of Environmental Research and Public Health](#)
- [The Computer Journal](#)
- [Methods in Ecology and Evolution](#)
- [Plos One](#)
- [Health Informatics Journal](#)
- [Molecular Ecology Resources](#)
- [Wiley Series in Bioinformatics](#)
- [Springer books](#)
- [DEXA 2017](#) (BIOKDD program committee)
- [DEXA 2016](#) (BIOKDD program committee)
- [DEXA 2015](#) (BIOKDD program committee)
- [DEXA 2014](#) (BIOKDD program committee)

Conferences

E. Weitschek: Computational methods to analyze biological big data. International Conference on Bioinformatics and Computational Biology (BBCC2017). **Naples (Italy)**, 2017.

E. Weitschek, S. Di Lauro, E. Cappelli, G. Felici, P. Bertolazzi: CAMUR-Web, a classification software and a big knowledge base for gene expression data of cancer. 14th annual meeting of the Bioinformatics Italian Society (BITS). **Cagliari (Italy)**, 2017.

E. Weitschek, G. Fiscon, P. Bertolazzi, G. Felici: MISSEL: A new genetic feature selection algorithm to compute multiple adjacent solutions for the classification of dna sequences. 18th free workshop on metaheuristics for a better world. **Rome (Italy)**, 2017.

E. Weitschek: Genomic Big Data Management, Integration, and Mining. Data Driven Innovation Open Summit. **Rome (Italy)**, 2017.

E. Weitschek, F. Cumbo, E. Cappelli, G. Felici: Integrating and analyzing big next generation sequencing data of cancer. Nettab 2016 Workshop. **Rome (Italy)**, 2016.

F. Cumbo, E. Weitschek, G. Felici, P. Bertolazzi: IRIS-TCGA: an information retrieval and integration system for cancer genomic data. In 13th international meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB). **Stirling (UK)**, 2016.

E. Weitschek, F. Cumbo, E. Cappelli, G. Felici: Genomic data integration: A case study on next generation sequencing of cancer. Database and Expert Systems Applications (DEXA), 27th International Workshop on Biological Knowledge Discovery. **Porto (Portugal)**, 2016.

- S. Ceri, M. Masseroli, E. Weitschek: Genomic Big Data Management, Modeling and Computing (special session). Intelligent Systems for Molecular Biology (ISMB) 2016. **Orlando (Florida, USA)**, 2016.
- E. Weitschek: TCGA2BED and CAMUR for cancer NGS data processing. Intelligent Systems for Molecular Biology (ISMB) 2016. **Orlando (Florida, USA)**, 2016.
- F. Cumbo, G. Fiscon, S. Ceri, M. Masseroli, E. Weitschek: TCGA2BED: converting and querying The Cancer Genome Atlas. Bioinformatics Italian Society (BITS) 2016. **Salerno (Italy)**, 2016.
- V. Cestarelli, G. Fiscon, P. Bertolazzi, G. Felici, E. Weitschek: Extraction of multiple rule-based models to classify RNA-seq cancer data. Bringing Maths To Life (BMTL) **Naples (Italy)**, 2015.
- E. Weitschek, G. Fiscon, V. Cestarelli, P. Bertolazzi, G. Felici: LAF Barcoding: classifying DNA Barcode multi-locus sequences with feature vectors and supervised approaches. In Twelfth international meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB). **Naples (Italy)**, 2015.
- E. Weitschek, G. Fiscon, G. Felici, P. Bertolazzi: GELA: a software tool for the analysis of gene expression data. Database and Expert Systems Applications (DEXA), 26th International Workshop on Biological Knowledge Discovery. **Valencia (Spain)**, 2015.
- E. Weitschek, G. Fiscon, P. Bertolazzi, G. Felici: Classifying DNA barcode multi-locus sequences with feature vectors and supervised approaches. 6th International Barcode of Life Conference. **Guelph, Toronto (Canada)**, 2015.
- E. Weitschek, G. Fiscon, G. Felici: Extracting multiple adjacent classification solutions from viral genomic sequences with a MIP feature selection technique. European conference for Operational Research. **Glasgow (Scotland, UK)**, 2015.
- G. Fiscon, E. Weitschek, P. Bertolazzi, G. Felici: Novel feature selection-based method to extract equivalent adjacent solutions to classify viral genome sequences. Intelligent Systems for Molecular Biology. **Dublin (Ireland, UK)**, 2015.
- G. Fiscon, E. Weitschek, G. Felici, P. Bertolazzi, S. De Salvo, P. Bramante, M.C. De Cola: Alzheimer's disease patients classification through EEG signals processing. SSCI 2014 - IEEE Symposium Series on Computational Intelligence and Data Mining. **Orlando, USA**, 2014.
- G. Fiscon, E. Weitschek, M.C. De Cola, S. De Salvo, P. Bramanti, P. Bertolazzi, G. Felici: EEG signals analysis to detect Alzheimer's disease patients (Poster). Bringing Math To Life Workshop. **Naples, Italy**, 2014.
- E. Weitschek, G. Fiscon, G. Felici, P. Bertolazzi: From structural bioinformatics to integrative systems biology. Nettare 2014 Workshop. **Turin, Italy**, 2014.
- E. Weitschek, F. Cunial, G. Felici: Classifying bacterial genomes on k-mer frequencies with compact logic formulas. Database and Expert Systems Applications (DEXA), 25th International Workshop on Biological Knowledge Discovery. IEEE. **Munich, Germany**, 2014.
- E. Weitschek, G. Felici Rule based analysis of genomic sequences. CBBM 2014, IV EURO WG Conference on Operational Research in Computational Biology, Bioinformatics and Medicine. **Biedrusko (Poznan), Poland**, 2014.
- E. Weitschek, G. Fiscon, G. Felici: Supervised DNA Barcode species classification: analysis, comparison and results. 5th International Barcode of Life Conference. **Kunming, China**, 2013.
- E. Weitschek, G. Felici, P. Bertolazzi: Clinical data mining: problems, pitfalls and solutions. In Database and Expert Systems Applications (DEXA), 2013 24th International Workshop on Biological Knowledge Discovery. IEEE. **Prague, Czech Republic**, 2013.
- E. Weitschek, D. Santoni, M.C. De Cola, G. Felici: On the validity of alignment free distance for DNA reads comparison. (Poster). Intelligent Systems for Molecular Biology. **Berlin, Germany**, 2013.
- E. Weitschek, M.C. De Cola, D. Santoni, G. Felici: Filtering with alignment free distances for high

throughput DNA reads assembly. 26th European Conference on Operational Research. **Rome, Italy**, 2013.

M.C. De Cola, G. Felici, D. Santoni, E. Weitschek: next generation sequencing reads filtering with alignment free distances (Poster). 4th Bari Workshop: Next Generation Sequencing & Epigenomics. **Bari, Italy**, 2012

E. Weitschek, G. Felici, P. Bertolazzi: Mala: A microarray clustering and classification software. In Database and Expert Systems Applications (DEXA), 2012 23rd International Workshop on Biological Knowledge Discovery (pp. 201-205). IEEE. **Vienna, Austria**, 2012.

E. Weitschek, M.C. De Cola, G. Drovandi, G. Felici, P. Bertolazzi: Alignment free high throughput DNA reads filtering with GPGPU computing (Poster). Intelligent Systems for Molecular Biology . **Long Beach, USA**, 2012.

E. Weitschek, R. van Velzen, G. Felici: Species classification with DNA Barcode sequences. DNA Barcoding: quali prospettive per l'Italia. **Modena, Italy**, 2012.

E. Weitschek, R. van Velzen, G. Felici: Species classification using DNA Barcode sequences: A comparative analysis. 4th International Barcode of Life Conference. **Adelaide, Australia**, 2011.

E. Weitschek, G. Felici, P. Bertolazzi: DMB: novel software tools for logic data mining in bioinformatics. Intelligent Systems for Molecular Biology. **Vienna, Austria**, 2011.

E. Weitschek, G. Felici, G. Drovandi, P. Bertolazzi: Updates in logic mining for bioinformatics. AIRO Winter 2011 International Conference. **Cortina D'Ampezzo, Italy**, 2011

E. Weitschek: BLOG 2.0: a DNA Barcoding classification software. Second meeting of the DNA barcode of life data analysis working group. **Chicago, USA**, 2011.

I. Arisi, M. D'Onofrio, R. Brandi, A. Cattaneo, G. Drovandi, G. Felici, E. Weitschek, P. Bertolazzi, S. Brancorsini, S. Ercolani, F. Mangialasche, P. Mecocci: New diagnostic model for the early diagnosis of Alzheimer's Disease and other dementias, based on Logic Mining of clinical variables (Poster). 10th International Conference on Alzheimer's & Parkinson's Diseases. **Barcelona, Spain**, 2011.

E. Weitschek: BLOG: a DNA Barcoding classification software. First meeting of the DNA barcode of life data analysis working group. **Chicago, USA**, 2009.

Citations **Scopus database**

H-Index: 12

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