CURRICULUM VITAE et STUDIORUM

of Prof. Marco Botta

Education:

1987: graduated, with laude, in Computer Science at Universita` di Torino. His Laurea thesis title was: *Development of a system for Incremental Machine Learning*.

1993: Ph. D. in Computer Science from Universita` di Torino. Thesis title*: WHY: A Tool for the Acquisition and Refinement of a Diagnostic Knowledge Base*.

Nov. 1992 – Oct 2001: *assistant professor* at the Faculty of Mathematical, Physical and Natural Sciences of the Universita` di Torino, Italy. He is affiliated to the Dipartimento di Informatica of the same University.

Current Position:

Since Nov. 2001, Marco Botta is an *associate professor* of Computer Science at the Faculty of Mathematical, Physical and Natural Sciences of the Universita` di Torino, Italy. He is affiliated to the Dipartimento di Informatica of the same University.

Research activity:

Marco Botta research activity was mainly focused on artificial intelligence topics and, in particular, on machine learning problems. In his early research years he mainly studied and developed new methods for learning concepts from instances. Such methods were oriented both to the construction of knowledge bases for expert systems and to their refinement.

Since 1996 his research activity has been devoted to the integration of symbolic and subsymbolic learning approaches with the aim of combining the expressive power of first-order logic with the refinement mechanisms that are typical of a connectionist approach. This research is currently being carried on. So far, it has lead to the design of two systems (FONN, NTR) that are able to refine a Horn-clause rule base by means of connectionist techniques.

Since 2002 he is also interested in bioinformatics research and has developed many collaborations with biologists on several topics, such as protein folding prediction, microarray data analysis, and more recently transcription factor binding sites prediction. In particular, he is currently developing algorithms for the discovery of sparse events in long sequences of data, using Hierarchical Hidden Markov Models, that have been applied to several domains such as user profiling, network log analysis and web log analysis, DNA and RNA sequence analysis.

In 2009 and 2010 he has been a visitor researcher at the Computing lab of the University of Cambridge, where he collaborated with Prof. Pietro Lio` on bioinformatics topics.

He published over 80 papers in international journals, international conference proceedings and international book chapters. A selected list of recent papers is included in this curriculum.

Teaching activity:

Marco Botta was responsible of the lab course "Computer Systems Architectures" in the years 1992-1995 and of the lab course on "Operating systems" thereafter. In the years 1990-1993 he gave seminars on artificial intelligence topics at the Master on Computer Science and Automation, organized by Corep (Consortium for research and permanent education, Torino, Italy). He also gave several lectures on computer programming in C, C++ and Java. In 1996-97 he taught a course on "Programming languages", and in 1997-98 he taught "Software

Engineering". Between 2001 and 2006 he taught a course on "Operating System Concepts" and one on "Artificial Intelligence and Machine Learning". Since the academic year 2003/2004 he teaches a course on "Bioinformatics" for the Laurea degrees in Molecular Biology, in Neurobiology, and in Computer Science. Finally, in 2007/2008 he taught a lab course on "Network Applications". In 20010/2011 he taught a lab course on "Operating System Concepts" and a course on Networks and Distributed Systems.

Marco Botta's selected list of recent publications

International Journals:

1. F. Cordero, M. Botta, R. A. Calogero (2007) "Microarray data analysis and mining approaches", **Briefings in Functional Genomics and Proteomics**, doi: 10.1093/bfgp/elm034, pp. 265-281.

2. Botta M, Haider S, Leung IX, Lio P, Mozziconacci J. (2010) "Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide" **Molecular Systems Biology**;6:426.PMID: 21045820

International Book Chapters:

3. Ugo Galassi, Marco Botta, Lorenza Saitta (2009) **Structured Hidden Markov Model versus String Kernel Machines for Symbolic Sequence Classification,** in Jacek Koronacki, Zbigniew W. Ras, Slawomir T.Wierzchon, Janusz Kacprzyk, Advances in Machine Learning I, Springer, Berlin / Heidelberg, pp. 275- 295.

International Conference Proceedings:

4. Visconti A., Cordero F., Botta M., Calogero R.A (2010) **Gene Ontology rewritten for computing gene functional similarity**, Conferences on Complex, Intelligent and Software Intensive Systems, February 15th – 18th, 2010, Krakow, Poland.

5. M. Botta, G. Negro (2010) **Multiple Sequence Alignment with Genetic Algorithms**, LNCS 6160, revised selected papers from Computational Intelligence Methods for Bioinformatics and Biostatistics 6th International Meeting, CIBB 2009, Genoa, Italy, pp. 206-214.

6. Cordero F., Visconti A., Botta M. (2009) **A new protein motif extraction framework based on constrained co-clustering,** ACM Press, New York, 24th Annual ACM Symposium on Applied Computing, March 8-12 2009, Honolulu, Hawaii.

7. F. Cordero, R. G. Pensa, A. Visconti, D. Ienco, M. Botta (2009) **Ontology-driven Co-clustering of Gene Expression Data,** LECTURE NOTES IN ARTIFICIAL INTELLIGENCE , pp. 426- 435, Vol. 5883/2009, 11th Conference of the Italian Association for Artificial Intelligence AI*IA 2009, December 9-12, 2009, Reggio Emilia, Italy.