

# Alberto J.M. Martin

## Personal Information:

- Date of birth: 08/06/1980
- Place of birth: Madrid (Spain).
- Citizenship: Spanish.

## Contact Details:

**Address:** Computational Biology Lab (DLab) Fundacion Ciencia & Vida, Santiago, Chile.

**E-mail:** ajmm@dlab.cl (proteinomano@gmail.com)

**Research Interest:** Structural Biology, Machine Learning, Graphs and Biological Networks

## Education and Experience:

- October 2013 to date, Postoc position at the Computational Biology Lab (DLab) working for Dr Tomas Perez-Acle.
- 15/01/2010 to 31/05/2013, Several research contracts at University of Padua working for Prof. Silvio C.E. Tosatto at the Biocomputing Up group (<http://protein.bio.unipd.it/>). In this time I have performed Teaching Assistant duties in the courses:
  - Bioinformatica 2 per Laurea Magistrale in Biologia Evoluzionistica : 2010-2011.
  - Bioinformatica 2 per Laurea Magistrale in Biologia Molecolare : 2010-2011.
  - Bioinformatica per Laurea Magistrale in Informatica : 2009-2010.
- 2005-2009 PhD working on Protein Potential Functions at University College of Dublin under Dr. Gianluca Pollastri supervision (<http://gruyere.ucd.ie/>). During this time I have been Senior Demonstrator of the following courses:
  - Introduction to Programming I (COMP10010) : Introduction to JAVA, 2008-2009.

- Object-Oriented Programming (COMP30070) : C++ programming, 2007-2008, 2008-2009.
- Introduction to Artificial Intelligence (COMP30030) : 2006-2007, 2007-2008.
- CS5, Bioinformatics (for H.Dip./M.Sc. in Computational Science) : 2006-2007.
- Computer Science for Engineers I (COMP10060) : Introduction to C, 2005-2006, 2006-2007, 2007-2008.

I also performed Teaching Assistant duties in this two courses:

- Connectionist Computing (COMP30230) : 2008-2009.
  - Introduction to Bioinformatics (COMP20120) : 2008-2009.
- 2005 One month working at Glaxo-Smith Kline on Malaria at the Diseases of the Developing World (D.D.W.) department at Tres Cantos, Madrid, thanks to a C.I.T.I.U.S. fellowship. During this time I had took a course on General Pharmacology (part of the grant requirements).
  - 2004 Master of Bioinformatics and Computational Biology at Universidad Complutense de Madrid (<http://www.masterbioinformatica.com/>) in which I graduated with honours. The final six months project was done at the C.M.B.I. (<http://www2.cmbi.ru.nl/>), under Prof. Gert Vriend supervision working on mutation site prediction in protein structures to increase protein stability. There I also took the following courses:
    - What If (molecular modelling package).
    - Introduction to Bioinformatics.
    - Genome browsing.
    - Sequence alignment.
    - Homology Modelling.
  - 2004 Teaching Certificate (C.A.P.) at the Universidad Complutense de Madrid (<http://www.ucm.es/>), including one month of practise in a high school teaching Biology and Environment Knowledge.
  - 2003 Four months of practise in the Continental Aquatic Ecology Laboratory, I.M.I.A. (Instituto Madrileño Investigaciones Agroalimentarias, Madrid), working on brown trout (*Salmo trutta fario*) population genetics.
  - 2003 Seminar of "Law and Biotechnology", Aliter International Business School.
  - 1998-2003 Degree in Biology, specialisation in Biochemistry and Molecular Biology at Universidad Autonoma de Madrid (<http://www.uam.es/>).

**Spoken Languages:** Spanish mother tongue. Good written and spoken English. Intermediate Italian.

**Other Skills:**

- Programming languages: C, C++, Perl. Some knowledge of shell scripting, JAVA and Octave.
- Bioinformatics tools: Molecular visualization and structure prediction software (What If, Rasmol, PYMOL, ...), CYTOSCAPE (biomolecular networks visualization and analysis), Representative protein datasets generation, ....
- Biological databases automated data mining: PDB, SwissProt/TrEMBL, DisProt, Protherm, CATH, SCOP, Pfam, ....
- Other: LaTeX, HTML.

**Hobbies:**

- Fishing, trekking and other outdoor activities.
- Reading.
- Fantasy and Science Fiction card games.

**Publications:****Peer-Reviewed Journal Articles:**

- A.J.M. Martin, I. Walsh, T. Di Domenico, I. Micetic and S.C.E. Tosatto. "PANADA: Protein Association Network Annotation, Determination and Analysis" PLoS One, 8(11): e78383, 2013.
- G. Mazzotta, A. Rossi, E. Leonardi, M. Mason, C. Bertolucci, L. Caccin, B. Spolaore, A.J.M. Martin, M. Schlichting, R. Grebler, C. Helfrich-Förster, S. Mammi, R. Costa and S.C.E. Tosatto. "Fly Cryptochrome and the Visual System". PNAS, 110(15):6163-8, 2013.
- T. Di Domenico, I. Walsh, A.J.M. Martin and S.C.E. Tosatto "MobiDB: a comprehensive database of intrinsic protein disorder annotations" Bioinformatics,28(15):2080-1, 2012.
- I. Walsh, A.J.M. Martin, T. Di Domenico and S.C.E. Tosatto. "ESpritz: accurate and fast prediction of protein disorder" Bioinformatics, 28(4):503-9, 2012.
- I. Walsh, A.J.M. Martin, T. Di Domenico, A. Vullo, G. Pollastri and S.C.E. Tosatto. "CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs". Nucleic Acids Research, 39:W190-196, 2011.
- A.J.M. Martin, M. Vidotto, F. Boscariol, T. Di Domenico, I. Walsh and S.C.E. Tosatto. "RING: Networking interacting residues, evolutionary information and energetics in protein structures" Bioinformatics, 7(14):2003-2005, 2011.

- A.J.M. Martin, C. Mirabello and G. Pollastri. “Neural Network Pairwise Interaction Fields for Protein Model Quality Assessment and Ab Initio Protein Folding” *Current Protein and Peptide Science*, 12(6):549-562, 2011.
- A.J.M. Martin, I. Walsh and S.C.E. Tosatto. “MOBI: a web server to define and visualize structural mobility in NMR protein ensembles”. *Bioinformatics* 26(22):2916-2917, 2010.
- I. Walsh, A.J.M. Martin, C. Mooney, E. Rubagotti, A. Vullo and G. Pollastri. “Ab initio and homology based prediction of protein domains by recursive neural networks”. *BMC Bioinformatics*, 10:195, 2009.
- I. Walsh, D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, G. Pollastri. “Ab initio and template-based prediction of multi-class distance maps by two-dimensional recursive neural networks”. *BMC Structural Biology*, 9:5, 2009.
- A.J.M. Martin, D. Baú, I. Walsh, A. Vullo, G. Pollastri. “Long-range information and physicality constraints improve predicted protein contact maps”. *Journal of Bioinformatics and Computational Biology*, 6(5):1001-20, 2008.
- G. Pollastri, A.J.M. Martin, C. Mooney, A. Vullo. “Accurate prediction of protein secondary structure and solvent accessibility by consensus combiners of sequence and structure information”. *BMC Bioinformatics*, 8:201, 2007.
- D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, I. Walsh, G. Pollastri. “Distill: A suite of web servers for the prediction of one-, two- and three-dimensional structural features of proteins”. *BMC Bioinformatics*, 7:402, 2006.

#### **Conference Proceedings Articles:**

- A.J.M. Martin, A. Vullo, G. Pollastri. “Neural Network Pairwise Interaction Fields for protein model quality assessment”. *Proceedings of the Learning and Intelligent OptimizatioN Conference - LION 3*. January 14-18, 2009 - Trento, Italy. Published in *Lecture Notes in Computer Science* (2009) Springer 5851:235-248.

#### **Book Chapters:**

- C. Mooney, N. Davey, A.J.M. Martin, I. Walsh, D.C. Shields and G. Pollastri. “Protein Motif Discovery and Structural Analysis“. In *Silico Tools in Gene Discovery in Springer series Methods in Molecular Biology* (vol 760). Hinchcliffe, M. and Yu, B. Eds. 2011.
- A.J.M. Martin, C. Mooney, I. Walsh and G. Pollastri. “Contact Map Prediction by Machine Learning”. In *Introduction to Protein Structure Prediction: Methods and Algorithms*. H. Rangwala and G. Karypis Eds. John Wiley & Sons, Inc. 2010.

### Conference Talks:

- “Ranking C alpha traces with Neural Network Pairwise Interaction Fields”. BITS Annual Meeting (<http://www.bioinformatics.it/>), April 14-16, 2010 - Bari, Italy.
- “Neural Network Pairwise Interaction Fields for protein model quality assessment”. Learning and Intelligent OptimizatioN Conference - LION 3. January 14-18, 2009 - Trento, Italy.

### Conference/Workshop abstracts:

- CSpritz: Modeling protein disorder using CSpritz in CASP10. I. Walsh, A.J.M. Martin, T. Di Domenico and S.C.E. Tosatto. 10<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Gaeta, Italy December 9-12, 2012.
- Analysis and prediction of non-globular proteins. T. Di Domnico, I. Walsh, A.J.M. Martin, F. Sirocco, E. Leonardi and S.C.E. Tosatto. Segundo Congreso Argentino de Bioinformatica y Biologia Computacional, Cordoba, Argentina May 11-13, 2011.
- Distill\_NNPIF. A.J.M. Martin, 9<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar Conference Center, Pacific Grove, California, December 5-9, 2010.
- DISTILLF. A.J.M. Martin and G. Pollastri. 8<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Cagliari, Sardinia, Italy December 3-7, 2008.
- Distill, Shandy, Punch: draft protein structures by machine learning. D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, I. Walsh and G. Pollastri. 8<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Cagliari, Sardinia, Italy December 3-7, 2008.
- Distill, Draft protein structures by machine learning. D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, I. Walsh, S. Tosatto, Gianluca Pollastri. 7<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar Conference Center, Pacific Grove, California, November 26-30, 2006
- DISTILLFM, A Filtering Approach for Improved Modelling of Predicted Contact Maps. A.J.M. Martin, A. Vullo and G. Pollastri. 7<sup>th</sup> edition of the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar Conference Center, Pacific Grove, California, November 26-30, 2006

### Conference/Workshop posters:

- T. Di Domenico, A.J.M. Martin, I. Walsh and S.C.E. Tosatto. “MobiDB: a database of intrinsically disordered proteins”. ISMB/ECCB 2011, Vienna, Austria.

- I. Walsh, A.J.M. Martin, T. Di Domenico and S.C.E. Tosatto. “Spritz: Protein disorder prediction for genomes and insights into protein function”. ISMB/ECCB 2011, Vienna, Austria.
- A.J.M. Martin, I. Walsh, S.C.E. Tosatto. “MOBI: a web server to define and visualize structural mobility in NMR protein ensembles”. Critical Assessment of Techniques for Protein Structure Prediction (CASP9), Asilomar, California, U.S.A. 2010.
- M. Vidotto, A.J.M. Martin, F. Boscaroli, I. Walsh, S.C.E. Tosatto. “Networking interacting residues, evolutionary conservation and energetics in protein structures”. ECCB 2010, Ghent, Belgium.
- A.J.M. Martin, A. Vullo, G. Pollastri. “Neural Network Pairwise Interaction Fields for protein model quality assessment”. ISMB/ECCB 2009, Stockholm, Sweden.
- A.J.M. Martin, D. Baú , C. Mooney, C. Roche, E. Rubagotti, A. Vullo, I. Walsh, G. Pollastri. “Protein Structural Features Prediction And Modelling Of  $C_{\alpha}$  Traces Through Predicted Structural Constraints”. Critical Assessment of Techniques for Protein Structure Prediction (CASP8), Cagliari, Sardinia, Italy 2008.
- C. Mooney, A.J.M. Martin, A. Vullo, G. Pollastri. “Exploiting similarity to proteins of known structure leads to improved protein structural motif prediction”. ISMB/ECCB 2007, Vienna, Austria.
- C. Roche, D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, I. Walsh, G. Pollastri, “High-Throughput Comparative Modelling of Protein Structures by Machine Learning” Microsoft Research Summer School 2007.
- D. Baú, A.J.M. Martin, C. Mooney, A. Vullo, I. Walsh, G. Pollastri. “Modelling of protein  $C_{\alpha}$  traces through residue contact maps predicted by machine learning”. Critical Assessment of Techniques for Protein Structure Prediction (CASP7), Asilomar, California, U.S.A. 2006.
- A.J.M. Martin, A. Vullo, G. Pollastri. “A Filtering Approach for Improved Modelling of Predicted Contact Maps”. ISMB 2006, Fortaleza, Brazil.

**Other:**

Reviewer for Journal of Biological Systems (2012)

Reviewer for Amino Acids (2011).

Co-reviewer for Proteins (2011).

Co-reviewer for ECCB 2010, Bioinformatics.

Co-reviewer for ISMB 2010, Bioinformatics.

Co-reviewer for ISMB 2009, Bioinformatics.

Co-reviewer for ISMB 2007, Bioinformatics.