Dario Ghersi

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Education

Postdoctoral Training, Princeton University, 2010-2014

Ph.D. Computational Biology, Mount Sinai/New York University, 2010

M.D. University of Genoa, Italy, 2004, 110/110 *Summa Cum Laude*

Awards

American-Italian Cancer Foundation Postdoctoral Fellowship, 2011-2013

NBCR Scholarship, 2007, University of California, San Diego

Medal for academic achievements, 2004, University of Genoa

Research Experience

Assistant Professor of Biomedical Informatics — 2014-present
School of Interdisciplinary Informatics — University of Nebraska at Omaha
Development of computational methods to study immunoinformatics and cancer genomics datasets. Structural bioionformatics of protein binding.

Postdoctoral Fellow — 2010-2014
Mona Singh — Princeton University
Development of computational methods for the analysis of protein interactions and their alterations in pathology.

PhD Student — 2006-2010
Roberto Sanchez — Mount Sinai School of Medicine
Development of computational methods to detect and characterize protein binding sites

Research Assistant — 2004-2005
Franco Celada — NYU Medical Center
Mathematical modeling of the immune system with a multiagent-based simulator. Development of routines to model crossreactivity in T cell-mediated immune response to viral infections.

Teaching Experience

Courses taught at the University of Nebraska at Omaha: BIOI-1000 "Introduction to Bioinformatics", BIOI-2000 "Foundations of Bioinformatics", BMI-8850 "Biomedicine for the Nonmedical Professional" (newly developed course), BMI-8300 "Public Health Genomics" (newly developed course), BMI-8020 "Linear Algebra with Applications in Biomedical Informatics" (newly developed course).

Thesis advisor of five MS students, dissertation advisor of one doctoral student at UNO.

Co-mentor of over ten undergraduate students (summer internships and senior independent research) at Princeton University, 2010-2013.

First-author publications

Ghersi D, Parakh A, Mezei M, "Comparison of a quantum random number generator with pseudo-random number generators for their use in molecular Monte Carlo simulations", *Journal of Computational Chemistry*, 2017, 10.1002/jcc.25065

Ghersi D, Sanchez R, "Recovering bound forms of protein structures using the Elastic Network Model and Molecular Interaction Fields", *7th ACM Conference on Bioinformatics* 2016

Ghersi D, Mosca R, "Computational approaches for identifying and characterizing binding sites in protein structures", book chapter, *CRC Handbook of Computational Biology* 2015 (accepted)

Ghersi D, Singh M, "molBLOCKS: a suite to break down small molecules into fragments and analyze their distribution", *Bioinformatics* 2014, 10.1093/bioinformatics/btu173

Ghersi D, Singh M, "Interaction-based discovery of functionally important genes in cancers", *Nucleic Acids Research* 2013, 10.1093/nar/gkt1305

Ghersi D, Singh M, "Disentangling the complex relationship between function, network features and disease: an application to cancer and Mendelian disorders", *BMC Systems Biology* 2013, 7:5

Ghersi D, Sanchez R, "Automated Identification of Binding Sites for Phosphorylated Ligands in Protein Structures", *Proteins* 2012, 80:2347-58

Ghersi D, Sanchez R, "Beyond structural genomics: computational approaches for the identification of ligand binding sites in protein structures", *Journal of Structural and Functional Genomics* 2011, 12(2):109

Ghersi D, Sanchez R, "`EasyMIFs` and `SiteHound`: tools for the identification of ligand-binding sites in protein structures", *Bioinformatics* 2009, 25(23):3185-6

Ghersi D, Sanchez R, "Improving accuracy and efficiency of blind protein-ligand docking by focusing on predicted binding sites", *Proteins* 2009, 4(2):417-24

Other publications

Munro D, Ghersi D, Singh M, "Two critical positions in zinc finger domains are heavily mutated in three human cancer types", *PLOS Computational Biology* 2018, doi.org/10.1371/journal.pcbi.1006290

Ehrlich R, Ghersi D, "Analyzing T cell receptor alpha/beta usage in binding to the pMHC", *IEEE BIBM* 2017 (Conference proceedings)

Castiglione F, Ghersi D, Celada F, "In-Silico analysis of the "memory anti-naïve" effect in anti-viral cross-reactive responses", *IEEE BIBM* 2017 (Conference proceedings)

Chirravuri Venkata R, Ghersi D, "Biological pathway data formats and standards", book chapter, *Elsevier Encyclopedia of Bioinformatics*, 2017 (in press)

Chirravuri Venkata R, Ghersi D, "Biological pathway analysis", book chapter, *Elsevier Encyclopedia of Bioinformatics*, 2017 (in press)

Sharma A, Ali H, Ghersi D, "Cluster analysis of biological networks", book chapter, *Elsevier Encyclopedia of Bioinformatics*, 2017 (in press)

Aslan A, Watkin L, Gil A, Mishra R, Clark F, Welsh R, Ghersi D, Luzuriaga K, Selin LK, "Severity of Acute Infectious Mononucleosis Correlates with Cross-Reactive Influenza CD8 T-Cell Receptor Repertoires", *mBIO*, 2017, 10.1128/mBio.01841-17.

Watkin L, Mishra R, Gil A, Aslan N, Ghersi D, Luzuriaga K, Selin LK, "Unique influenza A cross-reactive memory CD8 T-cell receptor repertoire has a potential to protect against EBV seroconversion", *Journal of Allergy and Clinical Immunology*, 2017, S0091.

Song I, Gil A, Mishra R, Ghersi D, Selin LK, Stern L, "Broad TCR repertoire and diverse structural solutions for recognition of an immunodominant $CD8^+$ T cell epitope", *Nature Structural & Molecular Biology* 2017, 24:395

Scott McGrath and Dario Ghersi, "Building towards Precision Medicine: empowering medical professionals for the next revolution", *BMC Medical Genomics* 2016, 9:23

Sunandini Sharma, Kritika Karri, Ishwor Thapa, Dhundy Bastola, and Dario Ghersi, "Identifying enriched drug fragments as possible candidates for metabolic engineering", *BMC Medical Genomics* 2016, 9(Suppl 2):46

Balasubramanya A, Thapa I, Bastola D, Ghersi D, *IEEE BIBM 2015* (Conference proceedings)

Pritykin Y, Ghersi D, Singh M, "Genome-wide Detection and Analysis of Multifunctional Genes", *PLOS Computational Biology* (2015), 10.1371/journal.pcbi.1004467

Chakravarty S, Ghersi D, Sanchez R, "Systematic Assessment of Accuracy of Comparative Model of Proteins Belonging to Different Structural Fold Classes", *J Mol Mod* 2011, 17(11):2831

Calcagno C, Puzone R, Pearson YE, Cheng Y, Ghersi D, Selin LK, Welsh RM, Celada F "Computer simulations of heterologous immunity: highlights of an interdisciplinary cooperation", *Autoimmunity* 2011, 44(4):304

Zhang Q, Chakravarty S, Ghersi D, Plotnikov AN, Sanchez R, Zhou MM, "Biochemical Profiling of Histone Binding Selectivity of the Yeast Bromodomain Family", *PLoS One* 2010, 5(1):e8903

Hernandez M, Ghersi D, Sanchez R, "SITEHOUND-web: a server for ligand binding site identification in protein structures", *Nucleic Acids Research* 2009, 37(Web Server issue): W413-W416

Cheng Y, Ghersi D, Calcagno C, Selin LK, Puzone R, Celada F, "A discrete computer model of the immune system reveals competitive interactions between the humoral and cellular branch and between cross-reacting memory and naive responses", *Vaccine* 2009, 27(6):833-45

Bahl K, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Selin LK, Welsh RM "IFN-induced attrition of CD8 T cells in the presence or absence of cognate antigen during the early stages of viral infections", *J Immunol* 2006, 176(7):4284-95

Cornberg M, Chen AT, Wilkinson LA, Brehm MA, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Welsh RM, Selin LK "Narrowed TCR repertoire and viral escape as a consequence of heterologous immunity", *J Clin Invest* 2006, 116(5):1443-56

Selin LK, Cornberg M, Brehm MA, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Welsh RM "CD8 memory T cells: cross-reactivity and heterologous immunity", *Semin Immunol* 2004 16(5):335-47

Invited Talks

"Computational approaches to characterize antiviral immune responses", Big Data Statistical Methodology Workshop, Omaha, NE, 2018.

"Computational Approaches in Cancer Genomics and Heterologous Immunity", Dept. of Biochemistry, University of Nebraska Medical Center, 2017.

"From mutations to drugs: a computational perspective", South Dakota State University, Brookings, SD, 2016.

"Omics in biomedicine: bridging the gap between statistical analysis and mechanistic interpretation", Big Data for Health and Medicine Workshop, Omaha, NE, 2016.

"Making life computable: the challenges of data-driven biology", ETS, Princeton, NJ, 2013.

"Protein interactions: from molecules to networks", Nanyang Technological University, Singapore, 2012.

"Increasing accuracy and speed of protein-ligand docking approaches", University of Sheffield, U.K., 2009.

"Computational approaches to detect and exploit protein binding sites", Cold Spring Harbor, NY, 2008.

Service

Chair of the Biomedical Informatics Graduate Program Committee at UNO, 2018 – present

Chair of the Bioinformatics Undergraduate Program Committee at UNO, 2016 – 2018

Member of the Doctoral Program Committee in Biomedical Informatics at UNO, 2015 – present

NIH grant review panelist for the GCAT (Genomics, Computational Biology and Technology) study session, 2018 – present

Member of the University Committee for the Advancement of Teaching at UNO, 2018 – present

Member of the University Committee on Research and Creative Activity at UNO, 2015 – 2018

Referee for *PLoS Computational Biology*, *Nucleic Acids Research*, *Bioinformatics*, *IEEE Transactions on Computational Biology and Bioinformatics*, *BioMed International*, *Journal of Chemoinformatics*.

Software Development

FunSet – for performing Gene Ontology enrichment analysis calculations and visualization (in collaboration with Dr. Matt Hale). (`https://github.com/thecodingdoc/GOUtil`, `http://funset.uno`)

molBLOCKS – for breaking down small molecules into fragments and analyzing their composition (`http://compbio.cs.princeton.edu/molblocks`)

CanBind – for exploring protein binding sites mutated in human cancers (`http://canbind.princeton.edu`)

fcsampling – for carrying out functionally-constrained sampling (`http://compbio.cs.princeton.edu/fcsampling`)

EasyMIFs and **SiteHound** – for computing Interaction Energy Maps and performing binding site identification in protein structures (`http://sitehound.sanchezlab.org`)

Skills

Programming languages: C/C++, Python, R, Lisp, Octave/Matlab, Mathematica

Operating systems: Linux, Mac OS X, Windows

Database design and implementation (MySQL)

Software: MODELLER (comparative modeling), AutoDock (molecular docking)

References

Prof. Mona Singh, (`mona@cs.princeton.edu`), Dept. of Computer Science and Lewis-Sigler Institute for Comparative Genomics, Princeton University, Princeton, NJ, Tel. +1 609-258-7059

Prof. Roberto Sanchez (`roberto.sanchez@mssm.edu`), Dept. of Structural and Chemical Biology, Mount Sinai School of Medicine, New York, NY, Tel. +1 212-659-8648

Prof. Ming-Ming Zhou (`ming-ming.zhou@mssm.edu`), Dept. of Structural and Chemical Biology, Mount Sinai School of Medicine, Tel. +1 212-659-8652

Prof. Franco Celada (`franco.celada@nyumc.org`), Dept. of Pathology, Hospital for Joint Diseases, NYU, New York, NY, Tel. +1 212-598-6507