DMM DEPARTMENT OF
MOLECULAR MEDICINE

UNIVERSITÀ
DEGLI STUDI
DI PADOVA

Via A. Gabelli 63 – I-35121 Padova, Italy

Padova, Sunday, April 15, 2018

Curriculum Vitae – Stefano Toppo

PERSONAL INFORMATION

Name: Stefano
Surname: Toppo
Date of birth: April 1, 1969
Place of birth: Venezia-Mestre (Italy)
Nationality: Italian
Address: Via M. Serao, 19 – I-35124 Padova, Italy
E-mail: stefano.toppo@unipd.it

Current position: Assistant Professor of Biochemistry (BIO/10), School of Medicine, University of Padova Department of Molecular Medicine

SCIENTIFIC EXPERIENCE

Research fields: bioinformatics, function prediction of proteins, study of protein families, protein structure prediction and analysis, study at quantum level of theory of catalytic sites, phylogeny, mass spectrometry data analysis in proteomics both identification and label free quantitation, genome sequencing data analysis, genome assembly, transcriptomics analysis and RNA-seq mapping and quantitation. Studies of viral and bacterial genomes, gene prediction, analysis of genome sequences searching for promoters, SNP and UTR regulatory regions. DNA data microarray analysis and design. Study of glutathione peroxidases at structural, computational, and phylogenetic level.

SKILLS

Informatics: different programming languages (Perl, PHP, rudiments of C and Java, SQL, scripting language), algorithms optimization, TCP/IP networking, Linux/UNIX system administration of HPC clusters. Developer of working pipelines and algorithms for data analysis and management.
Biochemistry and molecular biology: different lab techniques, project design of hypothesis driven experiments.

INTERNATIONAL RECOGNITION

Heading the MedComp group (Computational Medicine Group) http://www.medcomp.medicina.unipd.it) involved in the development of bioinformatics tools for the scientific community. Our group is reckoned as leader in automatic protein function prediction thanks to our Argot tools (http://www.medcomp.medicina.unipd.it/Argot2/ and http://www.medcomp.medicina.unipd.it/Argot2-5/) and spinoff projects as functional taxonomy (http://www.medcomp.medicina.unipd.it/funtaxis/). Our web-servers are used world-wide and produced over 87'000 reporting pages for protein function predictions in the last year (2017 google analytics report). The statistics do not take into account whole genome automatic annotations performed via REST interface. Presently we have performed more than 100 whole genome annotations. Some examples are https://kona.nhgri.nih.gov/mnemiopsis/ from NIH and the recent transcriptome analysis of an Afrotropical butterfly (Oostra, V. et al. 2018 Nat Commun. 2018).

RESEARCH FIELD OF INTEREST

1) Protein function prediction and functional taxonomy distribution
2) 3D genome and non-B DNA motifs search
3) Protein structure prediction
4) Metabolic pathway reconstruction
5) RNA-seq data analysis, differential gene expression and gene enrichment
6) Proteomics and mass spectrometry data analysis – lipidomics
7) Phylogenetic analyses

OTHER

1. Developer of web server for automatic protein structure prediction (FOX Fold eXtractor) and structural pattern recognition ranked in the TOP 20% of CASP6 experiment (Critical Assessment of Techniques for Protein Structure Prediction 2004).
2. Developer of a web server for automatic protein function prediction Argot2 (Annotation Retrieval of Gene Ontology Terms) ranked 2nd out of 56 international predictors at the CAFA experiment (Critical Assessment of Function Annotations 2012). Awarded as the best freely available tool.
3. Developer of e-commerce web sites and bank transaction platforms (2001-2002).

EDITORIAL BOARD

Current Bioinformatics (2006-present)

PEER REVIEWING ACTIVITY

(only principal activities reported)

1. Bioinformatics
2. Nucleic Acids Research
3. BMC bioinformatics
4. Antioxidant & Redox Signaling
5. Free Radical Biology and Medicine
6. Proteins
7. Proteomics
8. Current Bioinformatics
9. PlosONE
10. Plos Computational Biology
11. Bio- and Medical Informatics and Cybernetics (BMIC conference) reviewer
12. ISMB PC member and reviewer
13. Qatar National Research Fund (QNRF) reviewer.

STEERING COMMITEEE

1. Executive Member of the International Grapevine Genome Project at Istituto Agrario San Michele all’Adige (2005-2007)
2. DATA-ENABLED LIFE SCIENCES ALLIANCE (DELSA http://delsaglobal.org) steering committee member (2013-2017)

MEMBER OF SCIENTIFIC SOCIETY

1. BITS (Bioinformatics Italian Society) (2004-present)
2. ISCB (International Society for Computational Biology) (2012-present)

LECTURES AND SEMINARS

Invited speaker at over 30 meetings and international/national conferences/courses. Most recent talks are reported (2012-2016):

SCIENTIFIC AWARDS

1. Awarded as the best protein function prediction server (Argot2) available for the scientific community. CAFA 2012 (Critical Assessment of Function Annotations) 2012 – Automated

Function Prediction Special Interest Group (AFP-SIG) of ISMB conference Long Beach LA July, 15-17, 2012 selected talk.

TEACHING ACTIVITIES

1. 2014-present Padova (Italy) holder of “Laboratory activities” course in the second-level degree in Medical Biotechnology (School of Medicine - University of Padova). (held in English)
2. 2017-present Padova (Italy) holder of “Informatica e bioinformatica” course in the first-level degree in Biologia (School of Science - University of Padova).
3. 2011-present Padova (Italy) holder of “Proteomics and Bioinformatics” course in the second-level degree in Medical Biotechnology (School of Medicine - University of Padova). (held in English)
4. 2011-2014 Padova (Italy) holder of “Struttura e Funzione delle Proteine” course in the “Pietro D’Abano” degree in Medicine (Faculty of Medicine - University of Padova). (held in English)
5. 2011-2014 Padova (Italy) holder of “Boinformatica” course in the “Curriculum Biomedico” and “Pietro D’Abano” degree in Medicine (School of Medicine - University of Padova). (held in English)
6. 2010-2016 Padova (Italy) holder of “Boinformatica” course in the “Curriculum Biomedico” degree in Medicine (School of Medicine - University of Padova).
7. 2009-2010 Padova (Italy) holder of “Proteomica e bioinformatica” course in the second-level degree in Medicine Biotechnology (School of Medicine - University of Padova).
8. September 12-16, 2011 Padova (Italy) AACSE summer school of Algorithms and Architectures for Computational Science And Engineering
9. 2003 – 2008 Padova (Italy) holder of "Laboratorio biochimica strutturale e proteomica" course in the second-level degree in Medicine Biotechnology (School of Medicine - University of Padova).
10. November 28-30, 2005 Salsomaggiore Terme (Parma) (Italy) 2nd part: Tutorial on "Bioinformatic management of EST projects" for PhD students in an "Advanced course of bioinformatic applied to genetic improvement of plants" organized by "Società Italiana di Genetica Agraria" (SIGA)
11. May 2-4, 2005 Salsomaggiore Terme (Parma) (Italy) 1st part: Tutorial on "Bioinformatic management of EST projects" for PhD students in an "Advanced course of bioinformatic applied to genetic improvement of plants" organized by "Società Italiana di Genetica Agraria" (SIGA)
12. 2003 – 2004 Padova (Italy) Holder of "Bioinformatica I" course in the first-level degree in (Faculty of Science MM.FF.NN. - University of Padova)
13. 2001 – 2002 Holder of "Bioinformatica I" course in the first-level degree in Molecular Biology (Faculty of Science MM.FF.NN. - University of Padova)

14. 2001 – 2002 Padova (Italy) Integrative teaching activity for "Laboratory of Bioinformatics" in the first-level degree in Molecular Biology and Biological Science (Faculty of Science MM.FF.NN. - University of Padova)
15. May 6-8, 2002 Roma (Italy) Lesson on "Analysis and annotation of DNA sequences" for The "Microarray Course" at "Istituto Superiore della Sanità"
16. 1996 Padova (Italy) two days course on "Internet and Medicine" for physicians at CNR Padova
17. 1996 Padova (Italy) one week couse on "Large Scale DNA Sequencing"
18. practical activity" for ERASMUS students at CRIBI biotechnology center

BIBLIOMETRICS AND PUBLICATONS

1. Update March 2018
    a. Web Of Science:
        i. h-index: 24
        ii. Total citations: 3519
    b. Scopus
        i. h-index: 26
        ii. Total citations: 3938
    c. Google Scholar
        i. h-index: 31
        ii. Total citations: 5690
2. Total peer reviewed papers: 80
3. Letter: 1
4. Book chapters: 3
5. Published interviews: 2
6. Abstracts: over 200 in international conferences

REFERENCES

1. Giuliodori A, Beffagna G, Marchetto G, Fornetto C, Vanzi F, **Toppo S**, Facchinello N, Santimaria M, Vettori A, Rizzo S, Della Barbera M, Pilichou K, Argenton F, Thiene G, Tiso N, Basso C: **Loss of cardiac Wnt/beta-catenin signalling in Desmoplakin-deficient AC8 zebrafish models is rescuable by genetic and pharmacological intervention**. *Cardiovascular research* 2018.
2. Formentin E, Sudiro C, Perin G, Riccadonna S, Barizza E, Baldoni E, Lavezzo E, Stevanato P, Sacchi GA, Fontana P, **Toppo S**, Morosinotto T, Zottini M, Lo Schiavo F: **Transcriptome and Cell Physiological Analyses in Different Rice Cultivars Provide New Insights Into Adaptive and Salinity Stress Responses**. *Frontiers in plant science* 2018, **9**:204.

3. Berselli M, Lavezzo E, **Toppo S***: **NeSSie: a tool for the identification of approximate DNA sequence symmetries**. *Bioinformatics* 2018.
4. Zaccarin M, Bosello-Travain V, Di Paolo ML, Falda M, Maiorino M, Miotto G, Piccolo S, Roveri A, Ursini F, Venerando R, **Toppo S***: **Redox status in a model of cancer stem cells**. *Archives of biochemistry and biophysics* 2017, **617**:120-128.
5. Perrone R, Lavezzo E, Riello E, Manganelli R, Palu G, **Toppo S***, Provvedi R, Richter SN: **Mapping and characterization of G-quadruplexes in Mycobacterium tuberculosis gene promoter regions**. *Scientific reports* 2017, **7**(1):5743.
6. Delfino-Machin M, Madelaine R, Busolin G, Nikaido M, Colanesi S, Camargo-Sosa K, Law EW, **Toppo S**, Blader P, Tiso N, Kelsh RN: **Sox10 contributes to the balance of fate choice in dorsal root ganglion progenitors**. *Plos One* 2017, **12**(3):e0172947.
7. Cozza G, Rossetto M, Bosello-Travain V, Maiorino M, Roveri A, **Toppo S**, Zaccarin M, Zennaro L, Ursini F: **Glutathione peroxidase 4-catalyzed reduction of lipid hydroperoxides in membranes: The polar head of membrane phospholipids binds the enzyme and addresses the fatty acid hydroperoxide group toward the redox center**. *Free radical biology & medicine* 2017, **112**:1-11.
8. Bianco L, Riccadonna S, Lavezzo E, Falda M, Formentin E, Cavalieri D, **Toppo S**, Fontana P: **Pathway Inspector: a pathway based web application for RNAseq analysis of model and non-model organisms**. *Bioinformatics* 2017, **33**(3):453-455.
9. Tolomeo AM, Carraro A, Bakiu R, **Toppo S**, Place SP, Ferro D, Santovito G: **Peroxiredoxin 6 from the Antarctic emerald rockcod: molecular characterization of its response to warming**. *Journal of comparative physiology B, Biochemical, systemic, and environmental physiology* 2016, **186**(1):59-71.
10. Piccirillo A, Lavezzo E, Niero G, Moreno A, Massi P, Franchin E, **Toppo S**, Salata C, Palu G: **Full Genome Sequence-Based Comparative Study of Wild-Type and Vaccine Strains of Infectious Laryngotracheitis Virus from Italy**. *Plos One* 2016, **11**(2):e0149529.
11. Parmeggiani F, Barbaro V, De Nadai K, Lavezzo E, **Toppo S**, Chizzolini M, Palu G, Parolin C, Di Iorio E: **Identification of novel X-linked gain-of-function RPGR-ORF15 mutation in Italian family with retinitis pigmentosa and pathologic myopia**. *Scientific reports* 2016, **6**:39179.
12. Lavezzo E, Masi G, **Toppo S**, Franchin E, Gazzola V, Sinigaglia A, Masiero S, Trevisan M, Pagni S, Palu G, Barzon L: **Characterization of Intra-Type Variants of Oncogenic Human Papillomaviruses by Next-Generation Deep Sequencing of the E6/E7 Region**. *Viruses* 2016, **8**(3):79.
13. Lavezzo E, Falda M, Fontana P, Bianco L, **Toppo S***: **Enhancing protein function prediction with taxonomic constraints--The Argot2.5 web server**. *Methods* 2016, **93**:15-23.
14. Lavezzo E, Barzon L, **Toppo S**, Palu G: **Third generation sequencing technologies applied to diagnostic microbiology: benefits and challenges in applications and data analysis**. *Expert review of molecular diagnostics* 2016, **16**(9):1011-1023.
15. Jiang Y, Oron TR, Clark WT, Bankapur AR, D'Andrea D, Lepore R, Funk CS, Kahanda I, Verspoor KM, Ben-Hur A, Koo da CE, Penfold-Brown D, Shasha D, Youngs N, Bonneau R, Lin A, Sahraeian SM, Martelli PL, Profiti G, Casadio R, Cao R, Zhong Z, Cheng J, Altenhoff A, Skunca N, Dessimoz C, Dogan T, Hakala K, Kaewphan S, Mehryary F, Salakoski T, Ginter F, Fang H, Smithers B, Oates M, Gough J, Toronen P, Koskinen P, Holm L, Chen CT, Hsu WL, Bryson K, Cozzetto D, Minneci F, Jones DT, Chapman S, Bkc D, Khan IK, Kihara D, Ofer D, Rappoport N, Stern A, Cibrian-Uhalte E, Denny P,

Foulger RE, Hieta R, Legge D, Lovering RC, Magrane M, Melidoni AN, Mutowo-Meullenet P, Pichler K, Shypitsyna A, Li B, Zakeri P, ElShal S, Tranchevent LC, Das S, Dawson NL, Lee D, Lees JG, Sillitoe I, Bhat P, Nepusz T, Romero AE, Sasidharan R, Yang H, Paccanaro A, Gillis J, Sedeno-Cortes AE, Pavlidis P, Feng S, Cejuela JM, Goldberg T, Hamp T, Richter L, Salamov A, Gabaldon T, Marcet-Houben M, Supek F, Gong Q, Ning W, Zhou Y, Tian W, Falda M, Fontana P, Lavezzo E, **Toppo S**, Ferrari C, Giollo M, Piovesan D, Tosatto SC, Del Pozo A, Fernandez JM, Maietta P, Valencia A, Tress ML, Benso A, Di Carlo S, Politano G, Savino A, Rehman HU, Re M, Mesiti M, Valentini G, Bargsten JW, van Dijk AD, Gemovic B, Glisic S, Perovic V, Veljkovic V, Veljkovic N, Almeida ESDC, Vencio RZ, Sharan M, Vogel J, Kansakar L, Zhang S, Vucetic S, Wang Z, Sternberg MJ, Wass MN, Huntley RP, Martin MJ, O'Donovan C, Robinson PN, Moreau Y, Tramontano A, Babbitt PC, Brenner SE, Linial M, Orengo CA, Rost B, Greene CS, Mooney SD, Friedberg I, Radivojac P: **An expanded evaluation of protein function prediction methods shows an improvement in accuracy**. *Genome biology* 2016, **17**(1):184.

16. Falda M, Lavezzo E, Fontana P, Bianco L, Berselli M, Formentin E, **Toppo S***: **Eliciting the Functional Taxonomy from protein annotations and taxa**. *Scientific reports* 2016, **6**:31971.
17. Orian L, Mauri P, Roveri A, **Toppo S***, Benazzi L, Bosello-Travain V, De Palma A, Maiorino M, Miotto G, Zaccarin M, Polimeno A, Flohe L, Ursini F: **Selenocysteine oxidation in glutathione peroxidase catalysis: an MS-supported quantum mechanics study**. *Free radical biology & medicine* 2015, **87**:1-14.
18. Maiorino M, Bosello-Travain V, Cozza G, Miotto G, Roveri A, **Toppo S**, Zaccarin M, Ursini F: **Understanding mammalian glutathione peroxidase 7 in the light of its homologs**. *Free radical biology & medicine* 2015, **83**:352-360.
19. Bosello-Travain V, Forman HJ, Roveri A, **Toppo S**, Ursini F, Venerando R, Warnecke C, Zaccarin M, Maiorino M: **Glutathione peroxidase 8 is transcriptionally regulated by HIFalpha and modulates growth factor signaling in HeLa cells**. *Free radical biology & medicine* 2015, **81**:58-68.
20. Barzon L, Papa A, Lavezzo E, Franchin E, Pacenti M, Sinigaglia A, Masi G, Trevisan M, Squarzon L, **Toppo S**, Papadopoulou E, Nowotny N, Ulbert S, Piralla A, Rovida F, Baldanti F, Percivalle E, Palu G: **Phylogenetic characterization of Central/Southern European lineage 2 West Nile virus: analysis of human outbreaks in Italy and Greece, 2013-2014**. *Clin Microbiol Infect* 2015, **21**(12):1122 e1121-1110.
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and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. *Omics-a Journal of Integrative Biology* 2014, **18**(1):10-14.

24. Kolker E, Ozdemir V, Martens L, Hancock W, Anderson G, Anderson N, Aynacioglu S, Baranova A, Campagna SR, Chen R, Choiniere J, Dearth SP, Feng WC, Ferguson L, Fox G, Frishman D, Grossman R, Heath A, Higdon R, Hutz MH, Janko I, Jiang L, Joshi S, Kel A, Kemnitz JW, Kohane IS, Kolker N, Lancet D, Lee E, Li W, Lisitsa A, Llerena A, Macnealy-Koch C, Marshall JC, Masuzzo P, May A, Mias G, Monroe M, Montague E, Mooney S, Nesvizhskii A, Noronha S, Omenn G, Rajasimha H, Ramamoorthy P, Sheehan J, Smarr L, Smith CV, Smith T, Snyder M, Rapole S, Srivastava S, Stanberry L, Stewart E, **Toppo S**, Uetz P, Verheggen K, Voy BH, Warnich L, Wilhelm SW, Yandl G: **Toward more transparent and reproducible omics studies through a common metadata checklist and data publications**. *Big Data* 2014, **1**(4):196-201.
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28. Militello V, Lavezzo E, Costanzi G, Franchin E, Di Camillo B, **Toppo S**, Palu G, Barzon L: **Accurate human papillomavirus genotyping by 454 pyrosequencing**. *Clin Microbiol Infec* 2013, **19**(10):E428-E434.
29. Lavezzo E, **Toppo S**, Franchin E, Di Camillo B, Finotello F, Falda M, Manganelli R, Palu G, Barzon L: **Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak**. *BMC infectious diseases* 2013, **13**:554.
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33. Barzon L, Lavezzo E, Costanzi G, Franchin E, **Toppo S**, Palu G: **Next-generation sequencing technologies in diagnostic virology**. *J Clin Virol* 2013, **58**(2):346-350.
34. Frasson I, Lavezzo E, Franchin E, **Toppo S**, Barzon L, Cavallaro A, Richter SN, Palu G: **Antimicrobial Treatment and Containment Measures for an Extremely Drug-Resistant Klebsiella pneumoniae ST101 Isolate Carrying pKPN101-IT, a Novel Fully Sequenced bla(KPC-2) Plasmid**. *J Clin Microbiol* 2012, **50**(11):3768-3772.
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38. Barzon L, Pacenti M, Franchin E, Squarzon L, Lavezzo E, **Toppo S**, Martello T, Cattai M, Cusinato R, Palu G: **Novel West Nile virus lineage 1a full genome sequences from human cases of infection in north-eastern Italy, 2011**. *Clin Microbiol Infec* 2012, **18**(12):E541-E544.
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Koepke T, Jiwan D, Schaeffer S, Krishnan V, Wu C, Chu VT, King ST, Vick J, Tao Q, Mraz A, Stormo A, Stormo K, Bogden R, Ederle D, Stella A, Vecchietti A, Kater MM, Masiero S, Lasserre P, Lespinasse Y, Allan AC, Bus V, Chagne D, Crowhurst RN, Gleave AP, Lavezzo E, Fawcett JA, Proost S, Rouze P, Sterck L, **Toppo S**, Lazzari B, Hellens RP, Durel CE, Gutin A, Bumgarner RE, Gardiner SE, Skolnick M, Egholm M, Van de Peer Y, Salamini F, Viola R: **The genome of the domesticated apple (Malus x domestica Borkh.)**. *Nat Genet* 2010, **42**(10):833-839.

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