

Hamed Bostan

Ph.D. in Computational Biology and Bioinformatics
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OBJECTIVE	Pursuing research and development in Computational Biology and Bioinformatics internationally.
PERSONAL INFORMATION	Name: Hamed Surname: Bostan
EDUCATIONAL SUMMARY	<p><u>Postgraduate</u></p> <ul style="list-style-type: none">• 2015: Ph.D. in Computational Biology and Bioinformatics (<i>SPOT-ITN Marie Curie fellow: EU Grant agreement no. 289220</i>). Title of Thesis: Bioinformatics strategies for Genomics: Examples and approaches for Tomato (Vote: Optimum).• 2010: Master of Computer Science, <i>Universiti Teknologi Malaysia</i>, Malaysia. Title of Thesis: Neural Network for Prediction of Cysteine Disulphide Bridge Connectivity in Proteins (Grade 4/4). <p><u>Undergraduate</u></p> <ul style="list-style-type: none">• 2008: Bachelor of Software Engineering, <i>Maybod University</i>, Yazd, Iran. Title of Thesis: Development of a multi-purpose form builder and report generator Portal for e-questionnaires (Grade 20/20).• 2002: High School Diplomas in Mathematics and Physics, <i>Sama High School</i>, Yazd, Iran.
RESEARCH INTERESTS	<ul style="list-style-type: none">• Integrative Biology and Comparative Genomics (Bioinformatics)• Genome Assembly and Finishing• Gene Prediction, Annotation and Curation• NGS Data Analysis and Large Scale Gene Expression Profiling• Development of Bioinformatics Tools and Pipelines• Biological Databases• Artificial Neural Network and Evolutionary Algorithms, and their implementation in real world problems such as biological systems

**PROFESSIONAL
EXPERIENCES
AND
ACHIEVEMENTS**

Plant for Human Health Institute (PHHI), NC Research Campus

(2016-present)

As a bioinformatician and a post-doctoral research scholar, focused in the development of bioinformatics tools and strategies in bio-projects. The interests are in high-throughput “omics” data analysis and modeling, method development for data processing and integration, and establishing biological databases and platforms for data exchanges. Currently working on blueberry and also involved in other vegetable crop genome assembly and finishing projects which aim to assemble high quality genomes, annotate and investigate them using data produced from different high-throughput techniques such as PacBio, Oxford Nanopore, 10X Genomics, Dovetail, RNA-Seq etc. Moreover, also involved in the identification of genes playing role in the accumulation of nutritionally important metabolites such as anthocyanin, or carotenoids in fruit and vegetable genomes.

University of Naples “Federico II”

(2012-2015)

Marie Curie Ph.D. fellow in Computational Biology and Bioinformatics in *Solanaceae* Pollen Thermotolerance-Initial Training Network (SPOT-ITN) Project entitled “Development and modelling of Gene Networks implied in tomato pollen Heat Shock Response (HSR) and thermos-tolerance” ([Reference](#)).

- Development of an efficient data management system with the aim of:
 - Establishing standards for data exchange and integration,
 - Setting up the most adequate methodologies and platforms for reconciliation of manifold resources available in different data levels allowing the biological system modelling.
- Implementation of suitable methods and automated analytical pipelines for different genomics data processing (from raw data to results) such as RNA-seq, MACE, Chip-Seq and small-RNAs analyses pipelines.
- Setting up different web platforms as the data representation layer (such as *NexGenEx-Tom*, *NextEpiEx-Tom*, *GenomeBrowser* etc.) aligned with the objectives of the research ([Reference](#)).
- Comparative analyses among heat sensitive and tolerant genotypes with the final goals of:
 - Attempting to identify genes implied in the heat shock response, possibly inferring on the involved regulatory networks and,
 - Integrating different data levels (e.g. small-RNAs, epigenomics, gene expression, proteomics and metabolomics) aiming for the modelling of the biological system underlying the mechanism in pollen HSR and thermos-tolerance.

Universiti Teknologi Malaysia

(2011-2012)

Research assistant in Bioinformatics Research Laboratory (BIRG), Faculty of Biosciences and Bioengineering, *Universiti Teknologi Malaysia*.

- In charge of the analyses for:
 - The prediction of *Dengue Fever* based on the patient symptoms using Machine Learning approaches,
 - Artificial Neural Networks modelling of dengue fever outbreak based on climate factors and detected cases.
- Involved in “Protein-protein interaction mapping in the human brain” data processing, implementation and design of SVM and Neural Network (under

”Development of Dementia Brain (DBrain) Multi-Agents Using Gene, Protein and Drug Platforms on Bio-Grid with New SOA for Diagnostic, Therapeutics and Treatment for Ageing and Active People” project, vote number: 79910).

Universiti Teknologi Malaysia

2009-2010

Master project at the faculty of Computer Science and Information Systems in coloration with faculty of Bioscience and Bioengineering under the title of: “Neural Network for Prediction of Cysteine Disulphide Bridge Connectivity in Proteins”

- Generation of protein sequence database and the adjacent amino acid residues of Cysteine for 67000 protein structures from Protein Databank Files (PDB).
- Design and optimize Neural Network models for prediction of disulphide bridge connectivity state of protein.
- Purify all existing PDB Files downloaded on January 2010 to a new version of Purified Protein Databank (PPDB) for further structural references and optimized processes.
- Development and implementation of several software applications relevant to biological information processes and descriptor generation.

Algorithm Co.

2002-2008

2005-2008: Head of Programming Team (Full-time)

- In charge of several different database analyses, windows and web software application design, implementation and testing.

2002-2005: Programmer (Part-time)

- Holding .net programming courses (C#.net, Vb.net and ASP.net) and contributing in some windows and web software application designs and implementation.

Published († indicates co-first author)

- Tranchida-Lombardo, V., Aiese-Cigliano, R., Anzar, I., Landi, S., Colantuono, C., **Bostan, H.**, Palombieri, S., Termolino, P., Aversano, R., Batelli, G., Cammareri, M., Carputo, D., Chiusano, M.L., Conicella, C., Consiglio, F., D’agostino, N., De Palma, M., Di Matteo, A., Grandillo, S., Tucci, M., Sanseverino, W., and Grillo, S. “*Whole-genome re-sequencing of two Italian tomato landraces reveals sequence variations in genes associated with stress tolerance, fruit quality and long shelf-life traits*”. *DNA Research* (Accepted on October 20, 2017).
- Ellison, S., Senalik, D., **Bostan, H.**, Iorizzo, M., & Simon, P. (2017). “*Fine Mapping, Transcriptome Analysis, and Marker Development for Y2, the Gene That Conditions β -Carotene Accumulation in Carrot (*Daucus carota* L.)*”. *G3: Genes, Genomes, Genetics*, 7(8), 2665-2675.
- Ambrosone, A., Batelli, G., **Bostan, H.**, D’Agostino, N., Chiusano, M.L., Perrotta, G., Leone, A., Grillo, S. and Costa, A., 2016. “*Distinct gene networks drive differential response to abrupt or gradual water deficit in potato*”. *Gene*, 597, pp.30-39.
- Ambrosino, L.†, **Bostan, H.**†, Ruggieri, V. and Chiusano, M.L., 2016. “*Bioinformatics resources for pollen*”. *Plant reproduction*, pp.1-15.
- Iovieno, P., Punzo, P., Guida, G., Mistretta, C., Van Oosten, M.J., Nurcato, R., **Bostan, H.**, Colantuono, C., Costa, A., Bagnaresi, P. and Chiusano, M.L., 2016.

“Transcriptomic Changes Drive Physiological Responses to Progressive Drought Stress and Rehydration in Tomato”. *Frontiers in Plant Science*, 7.

- Ruggieri, V., **Bostan, H.**, Barone, A., Frusciante, L. and Chiusano, M.L., 2016. *“Integrated bioinformatics to decipher the ascorbic acid metabolic network in tomato”*. *Plant Molecular Biology*, pp.1-16.
- Ambrosino L.†, **Bostan H.**†, Di Salle P., Mara Sangiovanni², Vigilante A. and Chiusano M.L. (2015). *“pATsi: paralogs and singleton genes from Arabidopsis thaliana”*. *BMC Bioinformatics*.
- **Bostan, H.** and Chiusano, M. L. (2015). *“NexGenEx-Tom: a gene expression platform to investigate the functionalities of the tomato genome”*. *BMC Plant Biology*, 15(1), 48.
- Bokszczanin K., Krezdorn N., Fragkostefanakis S., Müller, S., Rycak, L., Chen Y.Y., Hoffmeier K., Kreutz J., Paupière M., Chaturvedi P., Iannacone R., Müller F., **Bostan H.**, Chiusano M.L., Scharf K.D., Rotter B., Schleiff E. and Winter P., (2015). *“Identification of novel small ncRNAs in pollen of tomato”*. *BMC Genomics*.
- Bokszczanin K., **Bostan H.**, Bovy A., Chaturvedi P., Chiusano M.L., Firon N., Iannacone R., Jegadeesan S., Klaczynski K., Li H., Marina C., Muller F., Paul P., Paupiere M., Pressman E., Rieu I., Scharf K., Schleiff E., Heusden A.W., Virezen W., Weckwerth W., Winter P., and Fragkostefanakis S., (2013). *“Perspectives on deciphering mechanisms underlying plant heat stress response and thermotolerance”*, *Frontiers in Plant Science* 4.
- **Bostan, H.**, Salim, N., Hussein, Z. A., Klappa, P., and Shamsir, M. S. (2012). *“CMD: A Database to Store the Bonding States of Cysteine Motifs with Secondary Structures”*. *Advances in Bioinformatics*.

Presentations, conferences and preceding

- **Asharfi, H., and Bostan, H.**, *“Using SMRT Iso-Seq Sequencing to Dissect Polyploid Transcriptomes: Lessons Learned from Tetra- and Hexaploid Blueberries”*, Pacbio User Group Meeting (UGM), Genomics Resource Center, Institute for Genome Sciences, University of Maryland, Baltimore, USA. June 28, 2017 (co-oral presentation).
- Iorizzio, M., Zielinski, K., **Bostan, H.**, Senalik, D., Cavagnaro, P., Lila, M.A. and Simon, P.W., *“Leveraging Genetic and Genomic Resources to Link Anthocyanin Genetics and Nutrigenomics in Carrot and Blueberry”*, Plant and Animal Genome conference, San Diego, USA. January 14-18, 2017 (oral presentation).
- Tranchida-Lombardo, V., Aiese-Cigliano, R., Anzar I., Landi, S., Palombieri, S., Colantuono, C., **Bostan, H.**, Termolino, P., Aversano, R., Batelli, G., Cammareri, M., Carputo, D., Chiusano, M.L., Conicella, C., Consiglio, F., D’agostino, N., De Palma, M., Di Matteo, A., Grandillo, S., Tucci, M., Sanseverino, W., and Grillo, S. *“Whole-genome Re-sequencing of two Tomato Landraces Reveals Sequence Variations Underpinning Key Economically Important Traits”*. *Proceedings of the LX SIGA Annual Congress*, Catania, Italy. September 13-16, 2016. ISBN: 978-88-904570-6-7 (poster).
- **Bostan, H.** and Chiusano, M.L., *“Reconciliation and Integration: an essential step towards the modelling of biological systems starting from omics data”*, Sorrento, Italy, March 18-22, 2015 (oral presentation).

**SOME
OUTREACH
ACTIVITIES**

- **Bostan, H.** and Chiusano, M.L., "*SPOT-ITN Data Sharing and Bioinformatics Platform*". Goethe University of Frankfurt, Germany. December 8, 2015 (oral presentation).
- **Bostan, H.** and Chiusano, M.L., "*A tutorial to the SPOT-ITN Data Sharing and Bioinformatics Platform*". University of Vienna, Austria. November 4, 2014 (oral presentation).
- **Bostan, H.**, Ambrosino, L., Ruggieri, V., Chiusano, M.L., "*Characterization of Derivative Relationship between Tomato and Grapevine: A Key Step to Investigate Fruit Development in the Two Species*". 3rd Annual Conference of the COST ACTION FA1106 on Fleshy fruit research, Chania, Crete. September 21-24, 2014 (oral presentation).
- Ruggieri, V., **Bostan, H.**, Barone, A., Frusciante, L., Chiusano, M.L., "*Integrating omics for Tomato Ascorbic Acid Pathway*". Proceedings of the 58th Italian Society of Agricultural Genetics Annual Congress Alghero, Italy. September 15-18, 2014 ISBN 978-88-904570-4-3 (poster).
- **Bostan, H.**, Colontuono, C., Chiusano, M.L., "*Tomato Genome Annotation: Genome peculiarities or miss-annotation*". BITs Annual Meeting, Rome, Italy. February 23, 2014 (poster).
- **Bostan, H.** and Chiusano, M.L., "*Development of a bioinformatics platform for gene expression analysis in tomato: A first step to investigate pollen peculiarities*". 2nd SPOT-ITN conference, Arnhem, Netherlands. November 2, 2013 (oral presentation and poster).
- Ruggieri, V., **Bostan, H.**, Chiusano, M.L., "*Integrated Bioinformatics: A key step towards the annotation of metabolic pathways. An example for ascorbic acid in tomato*". COST ACTION FA1106 Quality Fruit, Crete, Greece. March 24, 2013 (poster).
- **Bostan, H.** and Chiusano, M.L., "*Development of a bioinformatics platform for gene expression analysis in tomato: A first step to investigate pollen peculiarities*". Computational Biology and Bioinformatics, Avelino, Italy. June 28, 2013 (oral presentation).
- Sabetian, S.F.J., Lau, C., **Bostan, H.**, Valipour, A.R. and Shamsir, M.S., "*Construction and analysis of the protein-protein interaction network for the spermatozoa*". The eighth international conference on bioinformatics of genome regulation and structure/systems biology (BGRS/SB'12), Novosibirsk, Russia, June 25–29, 2012 (oral presentation).
- **Bostan, H.** and Shamsir, M.S., "*Mining for dictionary definition for disulphide bond formation using sequence pattern recognition and motif detection*". 15th Biological Science Graduate Congress, University of Malaya. December 15-17, 2010 (oral presentation).
- Scientist for a day, "Suspect Identification, paternity and maternity test and disease diagnostics using genetic variation and single nucleotide polymorphism (SNP)". Organizer: Douglas Vernon, Plant for Human Health Institute, NCSU. October 8, 2017 (workshop).
- Chinese group visit to PHHI, "Brief insights to bioinformatics and its impact on biological science progress". Organizer: NC State Global Training Initiative. Plant for Human Health Institute, NCSU. August 8, 2017 (oral presentation).

- STEMersion by Cabarrus County Schools, “A brief journey though the Bioinformatics Analysis (DNA Assembly)”. Organizer: Brenda Eason. Plant for Human Health Institute, NCSU. June 26, 2017 (oral presentation).
- Computational Biology and Bioinformatics: Market potentials and challenges. Organizer: Hamid Reza Ghomi. Yazd Scientific and Technology Park (YSTP), Yazd, Iran. January 2, 2016 (oral presentation).
- Computational Biology and Bioinformatics: “Omics” based techniques for deciphering and modelling the mechanism underlying a biological system. Organizer: Vahid Abootalebi. Department of Electrical and Computing, University, Yazd, Iran. December 23, 2015 (oral presentation).

Major Programming, Scripting and Data-basing Skills

- Microsoft VB.net, C#.net and ASP.net
- Java and JSP
- PHP
- Python
- R
- MS SQL and MySQL

Languages

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| • Persian | Native or bilingual proficiency |
| • English | Professional working proficiency |
| • Italian | Limited working proficiency |