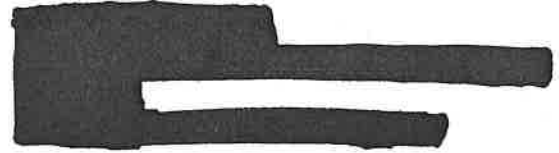


GAZELLE (GHAZALEH) TAHERZADEH

15th September, 2019

CONTACT INFORMATION

School of Information and
Communication Technology, Griffith
University, Gold Coast, QLD, Australia.



APPOINTMENTS

- PhD

RESEARCH BACKGROUND

- **Bioinformatics & Computational Biology**

Structural biology, Protein function prediction, Protein binding site prediction, Post Translational Modification prediction, Feature Selection and Feature Extraction

- **Learning from Data**

Pattern Recognition and Classification, Machine Learning, Data Analysis/Mining, Discriminative Training and Error Minimization, Statistics, Algorithms.

EDUCATION

- **Ph.D.**, Bioinformatics and Computational Biology, Griffith University, Gold Coast, Queensland, Australia, (2014- 2018)
- **M.Sc.**, Artificial Intelligence, University of Malaya, Selangor, Malaysia, (2011-2013)
- **B.Sc.**, Software Engineering, Multi Media University, Cyberjaya, Malaysia (2007-2011)

HIGHLIGHTS

- Griffith University Higher Degree Research scholarship (GUPRS)
- Griffith University International Postgraduate Research Scholarship (GUIPRS)
- Travel Grant Award to attend ISMB 2017 Conference
- Silver Medal in PECIPTA 2013 (International Conference and Exposition on Invention of Institution of Higher Learning).
- Dean List Award in 2008 (Multimedia University)

JOURNALS

- J1. Taherzadeh, G., Dehzangi, A., Golchin, M., Zhou, Y., & Campbell, M. P. (2019). SPRINT-Gly: predicting N-and O-linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. *Bioinformatics*.
- J2. Dehzangi, A., López, Y., Taherzadeh, G., Sharma, A., & Tsunoda, T. (2018). SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. *Molecules*, 23(12), 3260.
- J3. Zhao, H., Taherzadeh, G., Zhou, Y., & Yang, Y. (2018). Computational Prediction of Carbohydrate-Binding Proteins and Binding Sites. *Current protocols in protein science*, 94(1), e75.
- J4. Taherzadeh, G., Yang, Y., Xu, H., Xue, Y., Liew, A. W. C., & Zhou, Y. (2018). Predicting lysine-malonylation sites of proteins using sequence and predicted structural features. *Journal of computational chemistry*, 39(22), 1757-1763.
- J5. Dehzangi, A., Lopez, Y., Lal, S. P., Taherzadeh, G., Sattar, A., Tsunoda, T., & Sharma, A. (2018). Improving

succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. *PLoS one*, 13(2), e0191900.

- J6. López, Y., Sharma, A., Dehzangi, A., Lal, S. P., Taherzadeh, G., Michaelson, J., Sattar, A. & Tsunoda, T. (2018). Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. *BMC Genomics Journal*, 19(1), 923.
- J7. Guruge, I., Taherzadeh, G., Zhan, J., Zhou, Y., and Yang, Y. (2018). B-factor profile prediction for RNA flexibility using support vector machines. *J. Comput. Chem.* 39(8), 407-411.
- J8. Taherzadeh, G., Zhou, Y., Liew, A., Yang, Y. (2017). Structure-based prediction of protein-peptide binding regions using Random Forest. *Bioinformatics*, 34(3), 477-484.
- J9. Dehzangi, A., López, Y., Lal, S. P., Taherzadeh, G., Michaelson, J., Sattar, A. & Sharma, A. (2017). PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. *Journal of Theoretical Biology*, 425, 97-102.
- J10. López, Y., Dehzangi, A., Lal, S. P., Taherzadeh, G., Michaelson, J., Sattar, A. & Sharma, A. (2017). SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. *Analytical Biochemistry*, 527, 24-32.
- J11. Taherzadeh, G., Zhou, Y., Liew, A. W. C., & Yang, Y. (2016). Sequence-based prediction of protein-carbohydrate binding sites using support vector machines. *Journal of chemical information and modeling*, 56(10), 2115-2122.
- J12. Taherzadeh, G., Yang, Y., Zhang, T., Liew, A. W. C., & Zhou, Y. (2016). Sequence-based prediction of protein-peptide binding sites using support vector machine. *J. Comput. Chem.*, 37(13), 1223-1229.

SUBMITTED

- S1. Abrahams, J., Taherzadeh, G., Jarvas, J., Guttman, A., Zhou, Y., & Campbell, M. (2019) Recent Advances in Glycoinformatic Platforms for Glycomics and Glycoproteomics. *Current opinion in structural biology review*.

BOOK CHAPTERS

- B1. H. Zhao, G. Taherzadeh, Y. Zhou, and Y. Yang, "Computational prediction of carbohydrate-binding proteins and binding sites.", in *Current Protocols in Protein Science*, edited by G. Taylor, Chapter 2, in press, Wiley, Hoboken, NJ, 2018.

CONFERENCES

- C1. Taherzadeh, G., Loo, C. K., & Chaw, L. T. (2015). A Novel Hybrid SP-QPSO Algorithm Using CVT for High Dimensional Problems. In *Advances in Global Optimization* (pp. 347-354). Springer, Cham.
- C2. Taherzadeh, G., & Loo, C. K. (2014, October). Comparison of Applying Centroidal Voronoi Tessellations and Levenberg-Marquardt on Hybrid SP-QPSO Algorithm for High Dimensional Problems. In *International Conference in Swarm Intelligence* (pp. 332-341). Springer, Cham.
- C3. Taherzadeh, G., & Loo, C. K. (2013, August). Image Classification Using Optimized Synergetic Neural Network. In *FIRA RoboWorld Congress* (pp. 170-180). Springer, Berlin, Heidelberg.
- C4. Taherzadeh, G., Karimi, R., Ghobadi, A., & Beh, H. M. (2011, February). Evaluation of online signature verification features. In *Advanced Communication Technology (ICACT), 2011 13th International Conference on* (pp. 772-777). IEEE.
- C5. Taherzadeh, G., Karimi, R., Ghobadi, A., Amoli, P. V., & Mirjalili, S. (2011). Categorizing Global and local features of On-line signature verification using DTW and Fuzzy logic. In *Proceedings of the 2011 International Conference on Security Management, SAM 2011, Las Vegas, Nevada, USA*.
- C6. Amoli, P. V., Ghobadi, A. R., Taherzadeh, G., Karimi, R., & Maham, S. (2011). New detection technique using correlation of network flows for NIDS. In *Proceedings of the 2011 International Conference on Security Management, SAM 2011, Las Vegas, Nevada, USA*.
- C7. Taherzadeh, G., Karimi, R., Ghobadi, A., & Beh, H. M. (2010). Optimized Features Set for On-line Signature Verification. In *International Conference on Test and Measurement* (pp. 48-53).

PRESENTATIONS and POSTERS

- P1. Taherzadeh, G., Zhou, Y., Liew, A. W. C., & Yang, Y. "Structure-based prediction of protein-peptide binding regions using Random Forest". Presented at *Function Special Interest Group (Function-SIG)(ISMB) 2017*.

PROFESSIONAL EXPERIENCE

Joi invent (October 2018- Present)

- Research and development team (Analysit programmer)

STEM Educator

- *Workshop developer* (April- July 2018)

PhD Student

Griffith University (April 2014- May 2018)

- Developing webserver for protein function predictions from protein structure and sequence.
- *SPRINT*: Designed and developed structure and sequence-based prediction of protein-peptide binding sites and regions using machine learning techniques (Supervised and Unsupervised learning).
Available: <http://sparks-lab.org/server/SPRINT-Str>
Available: <http://sparks-lab.org/server/SPRINT/>
- *SPRINT-CHB*: Designed and developed sequence-based prediction of protein-carbohydrate binding sites using machine learning techniques.
Available: <http://sparks-lab.org/server/SPRINT-CBH/>
- *SPRINT-Mal*: Designed and developed prediction of Post Translational Modifications (Lysine-Malonylation sites) using machine learning techniques.
Available: <http://sparks-lab.org/server/SPRINT-Mal/>
- *SPRINT-Gly*: Designed and developed prediction of N- and O-linked glycosylations in human and mouse proteins.
Available: <http://sparks-lab.org/server/SPRINT-Gly/>
- *RNAflex*: Designed and developed B-factor profile prediction for RNA flexibility using machine learning techniques.
Available: <http://sparks-lab.org/server/RNAflex/>

Research Assistant

University of Malaya (May 2013 – December 2013)

Advanced Robotic Lab.

- Designed Creative Learning for Emotional Expression of Robot Partners Using Interactive Particle Swarm Optimization.
- Part of developing “Baby Monitoring System” project.

TEACHING EXPERIENCE

- 2018 Griffith University, Gold Coast, Queensland, Australia.
Teaching Assistant: Discrete mathematics Course
- 2012-2013 University of Malaya, Kuala Lumpur, Malaysia.
Teacher Assistant: Advance Programming
- 2009-2010 Multimedia University, Cyberjaya, Malaysia.
Tutor: Fundamental of programming & Advanced programming

MENTORING & ADVISING

School of Information and Communication Technology, Griffith University , 2017

- I have mentored honor student working on summer project in Bioinformatics and Computational Biology.

Soha Sdn. Bhd Company, Malaysia, 2013- 2014.

SERVICES

- Training undergraduate students in their internship program.
- Reviewer of Journal of Chemical Information and Modeling
- Reviewer of BMC-Bioinformatics Journal
- Reviewer at The World Scientific and Engineering Academy and Society (WSEAS)

VOLUNTEER ACTIVITIES

- Working as a student committee member in PRICAI/PRIMA2014 Conference.
- Director of funding and grants in Gold Coast Association of Postgraduates, Griffith University (2014 – 2016).
- Director of events in Gold Coast Association of Postgraduates, Griffith University (2017 – 2018).
- President of Iranian Student Association in Griffith University 2012-2014.
- Vice president of Ladies in Technology, Engineering, and Science, Griffith University (2015-2017).
- Member of Managerial board of Iranian Society of Gold Coast and Iranian Women Activity (2015-2018).

SKILLS

- Programming in C/C++, R, Python, Matlab
- WEKA Meta Classifiers
- Computational Biology and Bioinformatics
- Pattern Recognition and Classification tools
- Discrete Mathematics, Data Structure & Algorithms, Engineering Mathematics, Statistics
- AI methods: pruning and analysis
- PyMol, Numerical Calculation, Linux, Windows

REFERENCES

Dr. Yaoqi Zhou

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Institute for Glycomics, Griffith University
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Dr. Alan Wee-Chung Liew

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School of Information and Communication Technology, Griffith University
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