

ABBAS (ADRIAN) SALAVATY

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SKILLS

- **Bioinformatics and Systems Biology:** Genomics (cancer genomics), Epigenomics (familiar with epigenetic modifications/gene regulation), NGS data analysis, Transcriptomics (RNA-seq and microarray data analysis), Proteomics (protein sequence and structure analysis), Interactomics, Investigation of protein-protein interactions, visualization and analysis of biological networks, homology modelling, function prediction, ...
- **Programming languages and skills:** R, R package development, Shiny app development, Python, Linux and command-line-based high performance computing (HPC)
- **Machine learning (ML):** Supervised ML, Unsupervised ML, Familiar with both classical (*e.g.* SVM, Random Forest, Decision Tree) and modern (neural network-based) ML models, Dimension reduction, Feature selection/extraction
- **Statistics:** Biostatistics, Data mining, Meta-analysis
- **Scientific writing:** Reference manager (EndNote, Mendeley, Citavi)
- **Computer skills:** MS Office, Adobe Photoshop, Adobe Illustrator

CERTIFICATES

- Learning Python
LinkedIn Learning May 2021
- Workshop on Application of Next-Generation Sequencing in Cancer Diagnosis and Management
Isfahan University of Medical Sciences, Department of Genetics and Molecular Biology
OMICS™ October 2015
BGI Tech Isfahan, Iran
- Bioinformatics Workshop June 2014
Shahid Chamran University of Ahvaz Ahvaz, Iran

DEVELOPMENTS

- **AutoClone: Calculation of distances (clonality) based on color features**
URL: <https://autoclone.erc.monash.edu/>
Monash University 2021

- Influential Software Package web portal**
 URL: <https://influential.erc.monash.edu/>
 ExIR Shiny app
 IVI Shiny app
 Monash University 2021
- influential: Identification and Classification of the Most Influential Nodes**
 R package, released on CRAN
 CRAN link: <https://cran.r-project.org/package=influential>
 Website: <https://asalavaty.github.io/influential/>
 GitHub repo: <https://github.com/asalavaty/influential>
 Experimental-data-based Integrative Ranking (ExIR)
 Integrated Value of Influence (IVI)
 SIR model-based Influence Ranking (SIRIR)
 Monash University 2020-2021

EDUCATION

- Ph.D. in Medicine** 2019-2022
 Australian Regenerative Medicine Institute, Monash University Melb, AUS
 PhD thesis: Identification of commonalities in clonal selection during normal and cancer tissue development using bioinformatics and systems biology techniques
- Master of Science in Biology-Biochemistry** 2016-2018
 University of Kashan Kashan, Iran
 Master thesis: Functional analysis and annotation of lung adenocarcinoma prognostic long non-coding RNAs
 GPA: 3.82/4
- Bachelor of Science in Genetics** 2011-2015
 Shahid Chamran University of Ahvaz Ahvaz, Iran
 GPA: 3.72/4

PROFESSIONAL EXPERIENCES

Affiliations

- The Systems Biology Institute Australia 2019-present
- Professional Member of Cancer Epigenetics Society (ID Number: 1537) 2018-present
- Member of Young Researchers and Elite Club, Iran 2016-present
- Research fellow (Bioinformatician), Al-Zahra Medical Genetics Laboratory, Isfahan, Isfahan, Iran 2015-2018
- Member of National Elites Foundation, Iran 2015-present

- Member of Complex Biological Systems Alliance (CBSA), 2015-present
a global non-profit research consortium

Editorial and reviewer

- Reviewer, Frontiers in Genetics 2020
- Reviewer, Journal of Rare Diseases Research & Treatment 2017
- Reviewer, Molecular Neurobiology 2017
- Editor, AMOR: Advances in Modern Oncology Research 2015-2019
- Reviewer, MOJPB: MedCrave Online Journal of Proteomics & Bioinformatics 2014-2016

Teaching experiences

- TA of Introduction to Bioinformatics (BMS5021) 2021
Monash University Melbourne, Australia
- TA of Genomics and its applications (GEN3040) 2020-2021
Monash University Melbourne, Australia
- Cancer Systems Biology Workshop 2018
Tehran University of Medical Sciences Tehran, Iran
- Manuscript Writing Workshop 2016
University of Kashan Kashan, Iran
- Secondary school-level courses in English language 2015
Ghalamchi Educational Foundation Isfahan, Iran

AWARDS AND HONORS

- Awardee of the Best Oral Talk Based on People's Choice
COMBINE-ABACBS Student Symposium 2021
- Awardee of the Best Student Oral Talk
Victorian Cancer Bioinformatics Symposium 2021
- Awardee of Australia's Global Talent Permanent Residency Visa
Data Science sector 2020
- Ph.D. scholarship from Monash University, (awarded and taken up) 2018
- Ph.D. scholarship from the Vancouver Prostate Center, University of British Columbia, (offered, but not taken up) 2018
- Ph.D. scholarship from Griffith University, (offered, but not taken up) 2018
- Ph.D. scholarship from the John Curtin School of Medical Research, Australian National University, (offered, but not taken up) 2018
- Ranked 2nd among all M.Sc. students in Biochemistry, University of Kashan 2018
- Ranked among the top 4% of participants in the
National University Entrance Exam, Iran 2011

GRANTS

Monash Data Futures Institute Seed Grants - AI and Data Science for Monash Global Challenges.
Finding the right targets: most influential nodes in complex networks

Chief investigators: Ramialison, Currie, Dowe

August 2021

Abbas Salavaty is a named investigator in this grant .

PUBLICATIONS, PRESENTATIONS, AND ABSTRACTS

Publications (Google Scholar Citations = 499)

- **Salavaty A**, Ramialison M, Currie P. Integrated Value of Influence: An Integrative Method for the Identification of the Most Influential Nodes within Networks. *Patterns*. August 2020. PMID: 33205118
- **Salavaty A**, Rezvani Z, Najafi A. Survival analysis and functional annotation of long non-coding RNAs in lung adenocarcinoma. *Journal of Cellular and Molecular Medicine*. June 2019. PMID: 31211495
- **Salavaty A**, Movahedi Motlagh F, Barabadi M, Cheshomi H, Dehghan Esmatabadi MJ, Shahmoradi M, Soleimanpour-lichaei HR. Potential role of RAB6C-AS1 long noncoding RNA in different cancers. *Journal of Cellular Physiology*. August 2018. PMID: 30076712
- **Salavaty A**, Rezvani Z, Najafi A. Long non-coding RNA LINC00987 may function as a tumor suppressor in lung adenocarcinoma. *F1000Research*. May 2018. DOI: 10.12688/f1000research.14785.1
- **Salavaty A**, Mohammadi N, Shahmoradi M, Naderi Soorki M. Bioinformatic analysis of circadian expression of oncogenes and tumor suppressor genes. *Bioinformatics and Biology Insights*. December 2017. PMID: 29276378
- Hajjari M, Sadeghi I, **Salavaty A**, Nasiri H, Birgani MT. Tissue Specific Expression Levels of Apoptosis Involved Genes Have Correlations with Codon and Amino Acid Usage. *Genomics & Informatics*. 14(4):234-240. December 2016. PMID: 28154517
- Sedghi M, Esfandiari E, Fazel-Najafabadi E, Salehi M, **Salavaty A**, Fattahpour S, Dehghani L, Nouri N, Mokarian F. Genomic rearrangement screening of the BRCA1 from seventy Iranian high-risk breast cancer families. *Journal of Research in Medical Sciences*. 21:95. November 2016. PMID: 28163741
- Hajjari M, **Salavaty A**, Crea F, Shin YK. The potential role of PHF6 as an oncogene: a genotranscriptomic/proteomic meta-analysis. *Tumor Biology*. 37:5317-5325. April 2016. PMID: 26561469
- **Salavaty A**. Carcinogenic effects of circadian disruption: an epigenetic viewpoint. *Chinese Journal of Cancer*. 34-38. June 2015. PMID: 26253128

- Hajjari M, **Salavaty A**. *HOTAIR: an oncogenic long non-coding RNA in different cancers. Cancer Biology & Medicine*. 12:1-9. March 2015. PMID: 25859406

Manuscripts submitted for publication

- **Salavaty A**, Ramialison M, Currie P. ExIR: a versatile one-stop model for the extraction, classification, and prioritization of candidate genes from experimental data. *Submitted to the BIB*.

Presentations and abstracts

- Oral presentation: **Salavaty A**, Ramialison M, Currie P. Identification, classification, and prioritization of most influential players in normal biological processes and diseases.
 - COMBINE-ABACBS Student Symposium November 2021
 - Victorian Cancer Bioinformatics Symposium October 2021
 - Oz Single Cell – PERTH September 2021
 - ANZSCDB August 2021
- ISMB/ECCB conference alliance July 2021
 - Virtual
 - E-Poster and Short Talk: **Salavaty A**, Ramialison M, Currie P. Identification, classification, and prioritization of most influential players in normal biological processes and diseases.
 - E-Poster and Short Talk: **Salavaty A**, Ramialison M, Currie P. Identification of the most influential nodes involving all topological dimensions of a network.
- Global Meet on Nanomedicine & Healthcare November 2017
 - New Orleans, USA
 - E-Poster: **Salavaty A**, Shahmoradi M. Application of nanobioinformatics in drug design and delivery systems. *Biol Med Case Rep*. DOI: 10.13140/RG.2.2.24092.39043
- Global Meet on Nanomedicine & Healthcare November 2017
 - New Orleans, USA
 - E-Poster: **Salavaty A**, Shahmoradi M. Application of nanobioinformatics in drug design and delivery systems. *Biol Med Case Rep*. DOI: 10.13140/RG.2.2.24092.39043
- 5th International Conference on Proteomics & Bioinformatics September 2015
 - OMICS Group, Valencia, Spain
 - Abstract: **Salavaty A**, Hajjari M. Meta-analysis of RAG2 using a genotranscriptomic/proteomic approach: suggestive of its oncogenic role. *Journal of Proteomics & Bioinformatics*. 8:88. October 2015. DOI: 10.4172/0974-276X.S1.077

Books

- Co-translator of “Next Generation Sequencing Technologies in Medical Genetics” book
ISBN: 978-600-356-502-9; National Bibliography Number (NBN): 4282468
Shahid Chamran University of Ahvaz 2015
Supervisor: Dr. Maryam Naderi Soorki

RESEARCH INTERESTS

- Bioinformatics and systems biology analysis of cancer initiation/progression causes
- Cancer stem cells
- Epigenetic basis of carcinogenesis
- Development of tools and packages for the identification, classification, prioritization, and visualization of biological molecules