

Rohit R. Jadhav

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OBJECTIVE

To seek a challenging position in the field of bioinformatics and computational biology.

EDUCATION

Doctor of Philosophy, Molecular Medicine (May 2016)

University of Texas Health Science Center at San Antonio, San Antonio, TX.

Master of Science, Bioinformatics (Dec 2011)

Indiana University, School of Informatics, Indianapolis, IN.

Bachelor of Science, Bioinformatics (May 2009)

Dr. D Y Patil Biotechnology and Bioinformatics Institute Pune, India.

POSITIONS and EMPLOYMENT

Postdoctoral Research Fellow (Jan-2017 – Present)

Department of Immunology and Rheumatology, Stanford University, Stanford, CA

(Mentor: Dr. Jorg Goronzy)

Postdoctoral Research Fellow (May-2016 – Nov-2016)

Department of Molecular Medicine, University of Texas Health Science Center, San Antonio, TX.

(Mentor: Dr. Victor X. Jin)

Research Assistant (Nov-2011 – May-2016)

Department of Molecular Medicine, University of Texas Health Science Center, San Antonio, TX.

(Mentors: Dr. Tim H-M. Huang and Dr. Victor X. Jin)

Research Assistant (Sept-2010 – Oct-2011)

Center for Computational Biology and Bioinformatics, Indiana University Purdue University, Indianapolis, IN.

(Mentor: Dr. Lang Li)

AWARDS

Pre-doctoral Fellowship (2015 – 2016)

Cancer Prevention and Research Institute of Texas Research Training Award (RP 140105)

Deans Award (2009 – 2011)

Indiana University Purdue University Indianapolis, IN.

PEER REVIEW

Ad hoc reviewer for: Bioinformatics, Scientific Reports, PLOS ONE, Journal of Molecular Biomarkers and Diagnosis, Journal of Pharmaceutical Sciences.

RESEARCH EXPERIENCE

Stanford University, Stanford, CA.

2017 – Present

Characterizing epigenetic changes in T-helper cells in aging and immune exhaustion post infection.

- Analyzed epigenetic differences using ATAC-sequencing in CD4 and CD8 Naïve and Memory cells.
- Predicted Transcription factor binding sites in differential peaks across cell types and age groups.
- Evaluated functional roles of identified TFs using pathway and network analyses.
- Investigated T-cell receptor sequence clonotype changes in these cells using TCR-sequencing data.

Identifying cancer-type-specific DNA methylomes using computational and experimental approaches.

- Designed a database for indexing and analysis of sequencing data across multiple patients.
- Implemented a hidden markov model for identification of DNA methylation patterns specific to different cancer types or subtypes from MBD-cap sequencing data.
- Validated the loci using public domain TCGA and ENCODE data sets.
- Developed a website interface for visualization of DNA methylation in large patient cohorts.

Investigating DNA methylation alterations at large gene-clusters in breast cancer patients.

- Identified gene promoters and CpG islands hypermethylated in breast cancer patients and cell lines.
- Determined 7 hypermethylated gene-clusters contributing towards lower overall patient survival.
- Identified differential expression in TCGA ER α +/- groups for Metallothionein-1 (MT-1) cluster.
- Analyzed the repression of MT-1 and the association of estrogen and DNA methylation in ER α positive and negative breast cancer cell lines.
- Evaluated invasion, proliferation properties by siRNA knock-down of genes in MT-1 gene cluster.

Analyzing epigenetic alterations resulting from environmental exposure of BPA and Genistein (GEN).

- Investigated expression, methylation in rat breast tissue with prepubertal exposure to BPA \pm GEN.
- Extracted genes with negative correlation between promoter methylation and gene expression.
- Compared the expression of identified genes in TCGA ER α +/- groups to identify potential markers.
- Investigated the markers' association with patient survival to determine group specific biomarkers.
- Identified biomarkers explaining carcinogenic properties of BPA and preventive properties of GEN.

Graduate Thesis: Epigenetic analysis of Ovarian Cancer initiating cells

- Analyzed the differences in DNA methylation, gene expression mRNA patterns in Ovarian Tumor cells, Ovarian Cancer initiating cells and normal cells.
- Integrated the information from above experiments to identify biomarkers.
- Validated the identified biomarkers with the publicly available data.

Center for Computational Biology and Bioinformatics

- Worked on analysis of High-Throughput Sequencing, Next Generation Sequencing data.
- Worked on analysis of DNA methylation, mRNA & miRNA expression data.

Implementing Algorithms in Bioinformatics

- Implemented an algorithm for Profile Hidden Markov Model which aligns a given DNA sequence with a profile provided by the user.
- Implemented an algorithm for Greedy Motif Search which searches multiple protein sequences for top 20 motifs using a greedy search algorithm.

Diabetic Proteins Repository

- Built a simple and efficient interface to be used by scientists working on Diabetes.
- Used different repositories like Uniprot, KEGG, Drug Bank for information collection.
- Collected & Integrated information for proteins, pathways & drugs related to Diabetes.
- Created a database and interface for the information representation.

Decision support system for clinicians prescribing antibiotics

- Built an interface to be used by physicians while prescribing antibiotics to patients.
- Collected data for symptoms, diagnosis and antibiotics for different diseases.
- Integrated information into a database with corresponding tables and relationships.
- Created a user interface for simple and efficient use by the physicians.

Dr. D Y Patil Biotechnology and Bioinformatics Institute Pune, India

2008 - 2009

Undergraduate Thesis: Sequence, Structure and Phylogenetic Analysis of GH Family 10, 11

Xylanases in Fungi

- The comparative study of the Fungal Glycosyl Hydrolase Family 10 and 11 xylanases.
- Identified and selected xylanases unique to the GH Families 10 and 11 from Fungi.
- Compiled and curated the molecular data for the components of the Families 10 and 11
- Performed Sequence and Structure Alignment of the residues.
- Performed molecular Phylogenetic study to get an insight into the evolutionary trend of xylanases belonging to these Families in Fungi.

MENTORING EXPERIENCE

University of Texas Health Science Center at San Antonio, San Antonio, TX

Bioinformatics Mentor

- Mentored other graduate students with statistical and bioinformatics applications for data analysis in various projects

Indiana University, School of Informatics, Indianapolis, IN.

Teaching Assistant

- Worked as a teaching assistant for graduate course in Introduction to Informatics.
- Conducted lectures on introduction to programming languages and databases.
- Assisted on evaluations of assignments and examinations.

INTERNSHIP/ OTHER EXPERIENCE

Indiana University, School of Informatics, Indianapolis, IN.

Website Developer, University Information Technology Services

2009 - 2010

- Worked with the Podcasting team.
- Worked on development of Administrator interface in Perl, Java, Asp.Net and C#.

University Information Technology Services

Summer 2010

- Developed interfaces in .NET and Perl-CGI.
- Worked with XML, HTML, JavaScript.
- Worked on implementing client and server side cookies in Java Script and Perl.

INVITED PRESENTATIONS

“Epigenetic analysis following combinatorial exposure to bisphenol A and genistein reveals their mammary cancer predisposition properties” CPRIT's fourth Innovations in Cancer Prevention and Research Conference, Austin, TX. November 2015

“Genome-wide DNA methylation analysis reveals estrogen-mediated epigenetic repression of metallothionein-1 gene cluster in breast cancer.” The 7th Annual Terry M. Mikiten Graduate Student Research Forum, San Antonio, TX. June 2015.

“Model-based Analysis of Group Differential Enriched Patterns in Cancer.” ICBP Multi-scale Cancer Systems Biology Symposium, Houston, TX. April 2015.

PUBLICATIONS

1. **R. R. Jadhav**, Victor X Jin. "Model based analysis of group differential enriched patterns (MAGDEP)." (under preparation).
2. **R. R. Jadhav**, Julia Santucci-Pereira, Yao Vickie Wang, Joseph Liu, Theresa D. Nguyen, Jun Wang, Sarah Jenkins, Jose Russo, Tim H-M Huang, Victor X Jin and Coral A. Lamartiniere. (2017). "DNA Methylation Targets Influenced by Bisphenol A and/or Genistein Are Associated with Survival Outcomes in Breast Cancer Patients." Genes (Basel) 8(5).
3. Clarie E. Gustafson, Qian Qi, Jessica Hutter Sanders, Sheena Gupta, **R. R. Jadhav**, Evan W. Newell, Holden Maecker, Cornelia M. Weyand, Jorg J. Goronzy (2017). "Checkpoint Function of CD85j in CD8 T Cell Aging." Front Immunol. 8: 692.
4. **R. R. Jadhav**, Yao Vickie Wang, Ya-Ting Hsu, Joseph Liu, Dawn Garcia, Zhao Lai, Tim H-M Huang, Victor X Jin (2016). "Methyl-binding DNA capture sequencing for patient tissues." J Vis Exp, 116.
5. **R. R. Jadhav**, Zhenqing Ye, Rui-Lan Huang, Joseph Liu, Pei-Yin Hsu, Leticia B. Rangel, Hung-Cheng Lai, Juan Carlos Roa, Nameer B. Kirma, Tim Hui-Ming Huang, Victor X. Jin (2015). "Genome-wide DNA methylation analysis reveals estrogen-mediated epigenetic repression of metallothionein-1 gene cluster in breast cancer." Clin Epigenetics. 7(1):13.
6. Yao Vickie Wang, **R. R. Jadhav**, Joseph Liu, Yidong Chen, Ian M. Thompson, Dean A. Troyer, Javier Hernandez, Huidong Shi, Robin J. Leach, Tim H-M Huang, and Victor X Jin (2016). "Roles of Distal and Genic Methylation in the Development of Prostate Tumorigenesis Revealed by Genome-wide DNA Methylation Analysis." Sci Rep, 6, 22051.
7. Aaron M. Horning, Julius A. Awe, Chiou-Miin Wang, Joseph Liu, Zhao Lai, Vickie Yao Wang, **R. R. Jadhav**, Anna D. Louie, Chun-Lin Lin, Jeff Saranchuk, Darrel Drachenberg, Tad Kroczak, Yidong Chen, Victor X. Jin, Sherry L. Abboud-Werner, Robin J. Leach, Javier Hernandez, Ian M. Thompson, Chun-Liang Chen, Sabine Mai, and Tim Hui-Ming Huang (2015). "DNA methylation screening of primary prostate tumors identifies SRD5A2 and CYP11A1 as candidate markers for assessing risk of biochemical recurrence" Prostate, 75(15), 1790-1801.
8. Hsu, Y. T., F. Gu, Y. W. Huang, J. Liu, J. Ruan, R. L. Huang, C. M. Wang, C. L. Chen, **R. R. Jadhav**, H. C. Lai, D. G. Mutch, P. J. Goodfellow, I. M. Thompson, N. B. Kirma and T. H. Huang (2013). "Promoter hypomethylation of EpCAM-regulated bone morphogenetic protein gene family in recurrent endometrial cancer." Clin Cancer Res 19(22): 6272-6285.
9. Chen, C. L., D. Mahalingam, P. Osmulski, **R. R. Jadhav**, C. M. Wang, R. J. Leach, T. C. Chang, S. D. Weitman, A. P. Kumar, L. Sun, M. E. Gaczynska, I. M. Thompson and T. H. Huang (2013). "Single-cell analysis of circulating tumor cells identifies cumulative expression patterns of EMT-related genes in metastatic prostate cancer." Prostate 73(8): 813-826.
10. Huang, T. T., C. B. Gonzales, F. Gu, Y. T. Hsu, **R. R. Jadhav**, C. M. Wang, S. W. Redding, C. E. Tseng, C. C. Lee, I. M. Thompson, H. R. Chen, T. H. Huang and N. B. Kirma (2013). "Epigenetic deregulation of the anaplastic lymphoma kinase gene modulates mesenchymal characteristics of oral squamous cell carcinomas." Carcinogenesis 34(8): 1717-1727.
11. Sawant, D. V., S. Sehra, E. T. Nguyen, **R. R. Jadhav**, K. Englert, R. Shinnakasu, G. Hangoc, H. E. Broxmeyer, T. Nakayama, N. B. Perumal, M. H. Kaplan and A. L. Dent (2012). "Bcl6 controls the Th2 inflammatory activity of regulatory T cells by repressing Gata3 function." J Immunol 189(10): 4759-4769.

PUBLISHED ABSTRACTS

1. Hsu YT, Gu F, Huang YW, Liu J, Ruan JH, Huang RL, Wang CM, Chen CL, **Jadhav RR**, Wang Y, et al: EpCAM-mediated hypomethylation of BMP and cell adhesion genes is associated with advanced endometrial cancer. Cancer Res 2014, 74.
2. Chen C-L, Osmulski P, Mahalingam D, Horning AM, **Jadhav RR**, Louie AD, Wang C-M, Huang TH-M: Epithelial-to-mesenchymal markers of circulating tumor cells for detection of castration-resistant prostate cancer. Cancer Res 2014, 74:5588-5588.
3. Balch C, **Jadhav R**, Fang F, Pilrose J, Li M, Shen C, Li L, Huang TH, Nephew KP: Systems biology identification of processes/pathways facilitating the development of high-grade serous ovarian cancer. Cancer Res 2012, 72:5206-5206.

TECHNICAL & LABORATORY SKILLS

Programming Languages/Scripting Languages:

R, Perl, Python, Matlab, C, C++, Java, Visual Basic, SQL, DBMS, C#, Asp.Net.

Database Applications:

SQL, PL/SQL, Access, Database Design and Architecture

Operating Systems/Platforms:

NET, Computer Fundamentals, Networking, UNIX and Windows, LINUX, MAC.

INDUSTRIAL TRAINING

Serum Institute of India Pvt. Ltd Pune.

2008

Design & Production of Bacterial vaccine

Certificate courses

2007-2009

C, C++, Java and Advanced Java

COMMUNITY SERVICE

- Volunteer, Blood Donor
- Member, Indian Student Association and Maharashtra Mandal

INTERESTS

Table - Tennis Team member, Dr. D. Y. Patil Biotechnology and Bioinformatics Institute
Won singles and doubles tournaments at college and district level in Table Tennis
Team Member, additional sports (CrossFit, Swimming, Cricket, Badminton etc.)

LANGUAGES

English : Fluent.
Hindi : Fluent.
Marathi : Fluent.
German : Conversational.