LAVANYA RISHISHWAR

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⭐ SUMMARY

- Bioinformaticist with seven years of strong bioinformatics research and teaching experience
- Worked and published research articles on a number of different topics
- Specialize in pipeline development and handling of large scale datasets
- Managed and trained a small team of bioinformaticians and students
- Proficient programmer, web developer and data visualization enthusiast

💼 PROFESSIONAL EXPERIENCE

Applied Bioinformatics Laboratory (ABiL, *abil.ihrc.com*), Atlanta, GA, USA   Aug 2014 – Present
Position: Team Lead
- Founding member of ABiL, helped establish the company from ground up
- Managed a small team of full-time and part-time bioinformaticians
- Developed and deployed bioinformatics workflows internally and for clients
- Developed and delivered 40+ bioinformatics training to CDC branch managers, scientists and epidemiologists
- Over 1,500 hours of bioinformatics teaching experience
- Worked with clients to establish project objectives, timeline and deliverables
- Drafted numerous proposals, grants and company expansion plans
- Designed and developed ABiL advertisement materials, brochure and website
- Interviewed and recruited bioinformaticians

School of Biological Sciences, Georgia Institute of Technology, Atlanta, GA, USA   Aug 2011 – Present
Position: Graduate Assistant (Research and Teaching)
- Worked on and managed various independent and collaborative projects
- Coordinated lab resources and HPC environment
- Taught programming course to graduate students, faculty and visiting scholars
- Mentored and trained 23 graduate students and visiting scholars in carrying out bioinformatics research
- Planned, organized and executed international training courses in Latin America
- Worked with the director of the Bioinformatics Graduate Program in program development and related activities

Department of Computer Science, University of Hong Kong, Hong Kong, China   Dec 2010 – Jan 2011
Position: Student Research Assistant
- Tasked with the development of an efficient algorithm for finding maximum parsimonious tree for given phylogenetic profiles having linkages
- Developed in-house assembly graph visualization software for the mapping of mate pairs in the genome for then ongoing project on genome assembly: IDBA

🎓 EDUCATION

Doctor of Philosophy (Bioinformatics)   Jan 2013 – Nov 2016
Georgia Institute of Technology, Atlanta, GA, USA   (Expected)
Advisor: I. King Jordan
Thesis title: Population Genomics of Human Polymorphic Transposable Elements

Master of Science (Bioinformatics)   Aug 2011 – Dec 2012
Georgia Institute of Technology, Atlanta, GA, USA

Bachelor of Technology (Bioinformatics)   Jul 2007 – May 2011
Maulana Azad National Institute of Technology, Bhopal, India

PUBLICATIONS

21. Clayton, E.A., Wang, L., **Rishishwar, L.**, Wang, J., McDonald, J.F., Jordan, I.K. Dynamics of transposable element expression and insertion in cancer. *In revision*. Journal: *Front. Mol. Biosci.*

20. Hu, F., **Rishishwar, L.**, Sivadas, A., Mitchell, G., Jordan, I.K., Murphy, T., Gilsdorf, J., Mayer, L. and Wang, X. Comparative genomic analysis of *Haemophilus haemolyticus* and non-typeable *Haemophilus influenzae* and a new testing scheme for their discrimination. *In revision*. Journal: *J. Clin. Micro.*

19. Gupta, A., Jordan, I.K., **Rishishwar, L.** (2016). stringMLST: a fast k-mer based tool for multi locus sequence typing. *Bioinformatics*. In Press.

18. Orata, F.D., Xu, Y., Gladney, L.M., **Rishishwar, L.**, Case, R.J., Boucher, Y., Jordan, I.K., Tarr, C.L. (2016). Characterization of clinical and environmental isolates of *Vibrio cidicii sp. nov.*, a close relative of *Vibrio navarrensis*. *Int J Syst Evol Microbiol*. doi: 10.1099/ijsem.0.001327.

17. **Rishishwar, L.**, Mariño-Ramírez, L., and Jordan, I.K. (2016). Benchmarking Computational Tools for Polymorphic Transposable Element Detection. *Brief Bioinform*. doi: 10.1093/bib/bbw072.

16. **Rishishwar, L.**, Kraft, C.S., and Jordan, I.K. (2016). Population genomics of reduced vancomycin susceptibility in *Staphylococcus aureus*. *mSphere*. 1: e00094-16

15. Hemme, C.L., Green, S.J., **Rishishwar, L.**, Prakash, O., Pettenato, A., Chakraborty, R., Deutchbauer, A.M., Van Nostrand, J.D., Wu, L., He, L., Jordan, I.K., Hazen, T.C., Arkin, A.P., Kostka, J.E. and Zhou, J. (2016). Lateral gene transfer in a heavy metal-contaminated groundwater microbial community. *mBio*. 7: e02234-15

14. Medina Rivas, M.A., Norris, E.T., **Rishishwar, L.**, Conley, A.B., Medrano Trochez, C., Valderrama-Aguirre, A., Vannberg, F.O., Mariño-Ramírez, L., and Jordan, I.K. (2016). El Chocó Colombia: a hotspot of human biodiversity. *Rev. Biodivers. Neotrop*. 6: 45-54

13. **Rishishwar, L.**, Conley, A.B., Vidakovic, B. and Jordan, I.K. (2015). A combined evidence Bayesian method for human ancestry inference applied to Afro-Colombians. *Gene*. 574: 345-351

12. **Rishishwar, L.**, Tellez Villa, C.E. and Jordan, I.K. (2015). Transposable element polymorphisms recapitulate human evolution. *Mob. DNA*. 6: 21

11. **Rishishwar, L.**, Conley, A.B., Wigington, C.H., Wang, L., Valderrama-Aguirre, A. and Jordan, I.K. (2015). Ancestry, admixture and fitness in Colombian genomes. *Sci. Rep.* 5: 12376

10. Gladney, L.M., Katz, L., Knipe, K.M., Rowe, L., Conley, A.B., **Rishishwar, L.**, Mariño-Ramírez, L., Jordan, I.K., Tarr, C.L. (2014). Genome Sequences of *Vibrio navarrensis*, a Potential Human Pathogen. *Genome Announcements*. 2(6): e01188-14.

9. **Rishishwar, L.**, Petit, R., Kraft, C.S., Jordan, I.K. (2014). A genome sequence based discriminator for vancomycin-intermediate *Staphylococcus aureus*. *J Bacteriol*. 196(5): 940-948

8. Sebastian, A., **Rishishwar, L.**, Wang, J., Bernard, K.F., Conley, A.B., McCarty, N.A., Jordan, I.K. (2013). Origin and evolution of the cystic fibrosis transmembrane regulator protein R domain. *Gene*. 523(2):137-46

7. **Rishishwar, L.**, Katz, L.S., Sharma, N.V., Rowe, L., Frace, M., Dolan Thomas, J., Harcourt, B.H., Mayer, L.W., Jordan, I.K. (2012). The genomic basis of a polyagglutinating isolate of *Neisseria meningitidis*. *J Bacteriol*. 194(20): 5649-5656.

6. **Rishishwar, L.**, Varghese, N., Tyagi, E., Harvey, S.C., Jordan, I.K., McCarty, N.A. (2012). Relating the disease mutation spectrum to the evolution of the cystic fibrosis transmembrane conductance regulator (CFTR). *PLoS One*, 7(8): e42336.

5. Kostka, J.E., Green, S.J., **Rishishwar, L.**, Prakash, O., Katz, L.S., Marino-Ramirez, L., Jordan, I.K., Watson, D.B., Brown, S.D., Palumbo, A.V., Brooks, S.C. (2012). Genome sequences for six Rhodanobacter strains isolated from soils and the terrestrial subsurface with variable denitrification capabilities. *J Bacteriol*. 194(16): 4461.

4. **Rishishwar, L.**, Pant, B., Pant, K., Pardasani, K.R. (2011). Mining Genomic Patterns in *Mycobacterium tuberculosis* H37Rv Using a Web Server Tuber-Gene. *Genomic Proteomics Bioinformatics*, 9(4-5): 171-178.

3. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R. (2011). Support Vector Machine Based Method for Lyases Classification and Prediction. *OJB*, 12(1): 1-8.

2. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R. (2010). Support Vector Machine Approach for Isomerases Prediction Problem. *CiiT Int J of Data Mining Knowledge Engg*. doi: DMKE052010005.

1. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R. (2010). ProCoS - PROtein COmposition Server. *Bioinformation.* 5(5): 227.

BOOK CHAPTERS

1. Green, S., **Rishishwar, L.**, Prakash, O., Jordan, I., Kostka, J. (2013) Insights into environmental microbial denitrification from integrated metagenomic, cultivation and genomic analyses. In *Encyclopedia of Metagenomics*, (Nelson, K. eds.) Springer, Berlin.

MANUSCRIPTS IN PREPRATION

11. **Rishishwar, L.**, Conley, A.B., Rogowski, K.K., Jiménez-Madrid, J.H., Valderrama-Aguirre, A., Jordan, I.K., Vannberg, F.V. Differential diagnosis of syndromic versus non-syndromic developmental delay in a Colombian patient using whole genome sequence analysis.
10. **Rishishwar, L.**, Wang, L., Wang, J., Yi, S.V., Lachance, J. Jordan, I.K. polymorphic transposable elements are selected in human populations.
9. **Rishishwar, L.** and Jordan, I.K. Human evolution, admixture and the feasibility of mitochondrial replacement
8. Wang, L., **Rishishwar, L.**, Mariño-Ramírez, L., Jordan, I.K. Human population-specific gene expression and transcriptional network modification with polymorphic transposable elements.
7. Norris, E.T., **Rishishwar, L.**, Pentz, J.T., Wang, X., Mayer, L.W., Jordan, I.K. The genomic basis of capsule switching in the Hajj clone of *Neisseria meningitidis*.
6. Chande, A.T., **Rishishwar, L.**, Watve, S., Jordan, I.K., Hammer, B.K. Characterizing novel T6SS in environmental isolates of *Vibrio cholerae*.
5. Watve, S., Chande, A.T., **Rishishwar, L.**, Bernardy, E.E., Mariño-Ramírez, L., Jordan, I.K., Hammer, B.K. Whole genome sequence of 24 environmental *Vibrio cholerae* isolates.
4. Sepúlveda-Torres, L.d.C., **Rishishwar, L.**, Rogers, M.L., Ríos-Olivares, E., Jordan, I.K., Boukli, N., Cubano, L.A. A Decade of Drug Resistance and Associated Mutations in a Population of HIV-1+ Puerto Ricans: 2002 – 2011
3. Aguirre, A., **Rishishwar, L.**, Galloway, R., Hoffmaster, A., Jordan, I.K., Gallo, J.E. Phylogenomic studies of the pathogenic bacteria *Leptospira interrogans* serovars Icterohaemorrhagiae and Copenhageni reveals no differences between them.
2. Gaby, J.C., **Rishishwar, L.,** Valderrama-Aguirre, L.C., Green, S.J., Valderrama-Aguirre, A., Jordan, I.K., Kostka, J.E. Diazotroph community analysis via a high-throughput nifH amplicon sequencing and analysis pipeline
1. **Rishishwar, L.,** Green, S.J., Prakash, O., Katz, L.S., Jordan, I.K., Kostka, J.E. Comparative genomics of denitrifying and non-denitrifying bacteria from the genus Rhodanobacter.

POSTERS AND CONFERENCE PAPERS

7. Cubano, L., Roger, M.L., **Rishishwar, L.,** Sepúlveda-Torres, L.d.C., Ríos-Olivares, E., Jordan, I.K., Boukli, N. (2016). Decade Long Study in HIV-1+ Puerto Ricans Finds Reduction in Average Drug Resistance Per Individual, Changes in Antiretroviral Medication Resistances and Shifts in Mutations Expression. *The FASEB Journal*. 30(1 Supplement):925.14-.14.
6. **Rishishwar, L.,** Kraft, C.S., Jordan, I.K. (2015). "Population genomics of reduced vancomycin susceptibility in *Staphylococcus aureus*". 10th International Conference on Bioinformatics, Atlanta, GA.
5. **Rishishwar, L.**, Tellez Villa, C.E. and Jordan, I.K. (2015). "Transposable element polymorphisms recapitulate human evolution". Mobile DNA In Mammalian Genomes. West Palm, FL.
4. **Rishishwar, L.**, Conley, A.B., Valderrama-Aguirre, A., Jimenez-Madrid, J.H., Vannberg, F.O., Jordan, I.K. (2013) "Ancestry, admixture & selection in Colombian genomes". Genome Biology & Bioinformatics. Atlanta, GA.
3. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R. (2010) "A Multi Class Support Vector Machine for Predicting Enzyme Classes". Asia Pacific Bioinformatics Conference. Banglore, India.
2. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R., (2010). Support Vector Machines Based Method for Oxidoreductases Classification and Prediction. 1st IFIP Conference on Bioinformatics. Surat, India.
1. **Rishishwar, L.**, Mishra, N., Pant, B., Pant, K., Pardasani, K.R., (2010). Predicting Enzyme Subclasses of Oxidoreductases Using AAC. 5th World Congress at Cellular & Molecular Biology. Indore, India.

🏆 AWARDS AND HONORS

• Wayne and Willa Kerr Award for Best Graduate Student Paper for fall 2015.
• Leland Jackson Endowment Summer Research and Travel Fellowship for the summer 2014 (Georgia Tech, Atlanta)
• Young Scientist Award for Oral Presentation in the 1st International IFIP conference held at SVNIT, Surat (India)
• Meritorious Scholarship by MANIT for the academic year of 2010-11

🔧 TECHNICAL SKILLS

Programming Languages:
• Proficient in Perl & Bash
• Statistical languages & data visualization: R and MATLAB
• Previous experience with C/C++, Java, Python
Web Development and Databases: HTML/CSS, PHP, SQL and JavaScript
Bioinformatics:
• Experience working with genomes from many life forms
• Next Generation Sequence (NGS) analysis workflows: DNA-seq (Whole genome/Exome), RNA-seq, MNase-seq
• Computational genomics/transcriptomics: Quality assessment, assembly/mapping, gene prediction, annotation, variant detection and comparative analysis
• Genome visualization/alignment: Circos, Cytoscape, CGView, IGV, J/GBrowse, Mauve
• Experience with metagenomics
• Developing machine learning tools for extraction and analysis of patterns in genomic data
Graphic designing: Adobe CS6/CC package
OS Platforms: Windows and *-nix based environments