Aroon Chande
Bioinformatics Scientist

Atlanta, GA 30363
℘ (515) 981-6868
✉ mail@aroonchande.com
🖥 https://aroonchan.de
 github.com/ar0ch
in aroon-chande

Education

Aug 2017 – present	**(In progress) Ph.D. - Bioinformatics**, Georgia Institute of Technology, Atlanta, GA.
Dec 2016	**Master of Science - Bioinformatics**, Georgia Institute of Technology, Atlanta, GA.
May 2015	**Bachelor of Science - Microbiology**, University of Iowa, Iowa City, IA.
May 2013	**Bachelor of Science - Biology**, University of Iowa, Iowa City, IA.

Experience

May 2016 – Present — **Bioinformatics Scientist**, Applied Bioinformatics Laboratory, IHRC Inc, Atlanta, GA.
http://abil.ihrc.com
- Development and maintenance of analytics platforms
- Development and maintenance of custom bioinformatics databases
- Teaching bioinformatics courses

Languages used: C++/Bash/Julia/PHP/Perl/Python/R/SQL

May 2016 – Present — **Graduate Student**, Jordan Lab, Georgia Institute of Technology, Atlanta, GA.
http://jordan.biology.gatech.edu
- Studying the effects of human ancestry on disease burden in Colombia and South America
- Teaching and administrating classes in the Bioinformatics Master's program
- Development of bacterial typing schemes in collaboration with the Centers for Disease Control and Prevention

Languages used: Bash/Perl/Python/R/SQL/PHP/Julia/Rust

Aug 2015 – May 2016 — **Graduate Student Research**, Hammer Lab, Georgia Institute of Technology, Atlanta, GA.
http://www.hammerlab.biology.gatech.edu/
- Development and maintenance of *vibriocholera.com*
- *Vibrio cholerae* NGS bioinformatic analysis
- Development of webtool for Type VI Secretion System annotation

Languages used: Bash/Perl/R/Python

Dec 2011 – July 2015 — **Research Assistant**, Apicella Lab, University of Iowa, Iowa City, IA.
- Development of expression and purification protocols for NMR and x-ray crystallography study of *Haemophilus influenzae* nuclease in *E. coli*
- Screening and data collection on crystallized nuclease in-house and Synchrotron radiation (4.2.2 beamline at ALS, Berkeley)
- Biological assays for protein activity, targets and pH dependence
- Biofilm, immunoassay and confocal microscopy

Languages used: Bash/Perl

May 2011 – May 2013 — **Protein Crystallography Core Staff**, *Carver College of Medicine*, Unversity of Iowa, Iowa City, IA.
- Contracted protein purification and characterization
- User training for protein expression, purification and crystallization
- Development of custom protocols for in-house robotic liquid handlers

Languages used: Bash

Skills

Computational

Proficient	Bash, Perl, Python, R, Unix systems administration
Familiar	HTML/CSS, SQL
Learning	Julia, Rust
NGS	Whole Genome Sequencing (WGS), Whole Exome Sequences (WES), RNA-seq, microarray
'Omics	Transcriptomics, metabolomics, proteomics
Development	- Bacterial typing and identification tools using NGS data - Automated systems for bioinformatics analysis and information management
Robotics	Liquid handlers (Mosquito, TECAN, Alchemist platform), Microscopy (Rock Imager), and other programmable robotics platforms

Wet Lab

Pathogens	Collection and handling of biological samples
FPLC/HPLC	Affinity column, ionic / hydrophobic chromatography
Microscopy	Confocal, Light, SEM
Genetics	PCR and cell line mutant development

Posters and Presentations

4. **Chande, A.T.**, Norris, E.T., Moreno, A.M., Nagar, S.D., Rishishwar, L., O'Neal, K., Velex, S., Montes-Rodrigues, S., Torres, I., Medina-Rivas, M.A., Valderrama-Aguirre, A., Jordan, I.K., Gallo, J.E. (2018) Population pharmacogenomics for precision public health in Colombia. São Paulo Advanced School on Vaccines, São Paulo, Brazil.

3. **Chande, A.T.**, Wang, L., Rishishwar, L., Conley, A.B., Norris, E.T., Valderrama-Aguirre, A., Jordan, I.K. (2018) GlobAl Distribution of GEnetic Traits (GADGET): Exploring polygenic trait scores. The American Society of Human Genetics, San Diego, California.

2. **Chande A.T.**, Conley, A.B., Rowell, J., Rishishwar, L., Norris, E.T., Mariño-Ramírez, L., Valderrama-Aguirre, A., Medina-Rivas, M., Jordan, I.K. (2018) ChocoGen: Genetic ancestry and health in the Colombian Pacific. Closing the genomics research gap, McGill University, Montreal, Canada.

1. **Chande, A.T.**, Rishishwar, L., Watve, S., Jordan, I.K., Hammer, B.K. (2015). Genomic analysis of Type VI secretion systems of *Vibrio cholerae*. 10th International Conference on Bioinformatics, Atlanta, GA.

Awards and Honors

Summer 2016	**Graduate Research Award**, Jordan lab, Georgia Institute of Technology, Alanta, GA. Reclassification of Non-typeable *Haemophilus spp.*.

Publications

15. Bernardy, E.E., Petit, R.A., Moller, A.G., Blumenthal, J.A., McAdam, A.J., Priebe, G.P., **Chande, A.T.**, Rishishwar, L., Jordan, I.K., Read, T.D., Goldberg, J.B. (2019) Whole-Genome Sequences of Staphylococcus aureus Isolates from Cystic Fibrosis Lung Infections. Microbiol Resour Announc 8 (3), e01564-18 doi: 10.1128/MRA.01564-18 PubMed: 30687841

14. Crisan C.V.*, **Chande A.T.***, Williams K., Raghuram V., Rishishwar L., Steinbach G., Yunker P., Jordan I.K., Hammer B.K. (2019) Analysis of *Vibrio cholerae* genomes using a novel bioinformatic tool identifies new, active Type VI Secretion System gene clusters. bioRxiv. doi: 10.1101/526723

13. **Chande, A.T.**, Wang, L., Rishishwar, L., Conley, A.B., Norris, E.T., Valderrama-Aguirre, A., Jordan, I.K. (2018) GlobAl Distribution of GEnetic Traits (GADGET) web server: polygenic trait scores worldwide. Nucleic Acids Research. doi: 10.1093/nar/gky415. PubMed: 29788182

12. Cho, C.*, **Chande, A.T.***, Gakhar, L., Hunt, J., Ketterer, M. R., Apicella, M. A. (2018) Characterization of a nontypeable Haemophilus influenzae Thermonuclease. PLoS One. doi: 10.1371/journal.pone.0197010. PubMed: 29746527

11. Medina-Cordoba, L.K., **Chande, A.T**, Rishishwar, L., Mayer, L.W., Mariño-Ramírez, L., Valderrama-Aguirre, L., Valderrama-Aguirre, A., Kostka, J.E, Jordan, I.K. (2018). Genome sequences of 15 Klebsiella spp. isolates from sugarcane fields in Colombia's Cauca Valley. Genome Announcements. doi: 10.1128/genomeA.00104-18. PubMed: 29567732

10. **Chande, A.T.**, Rowell, J., Rishishwar, L., Conley, A.B., Norris, E.T., Valderrama-Aguirre, A., Medina-Rivas, M., Jordan, I.K. (2017). Influence of genetic ancestry and socioeconomic status on type 2 diabetes in the diverse Colombian populations of Chocó and Antioquia. Scientific Reports. doi: 10.1038/s41598-017-17380-4. PubMed: 29215035

9. Dale, R., Grüning, B., Sjödin, A., Rowe, J., Chapman, B. A., Tomkins-Tinch, C. H., . . . **Chande, A. T.**, . . . Köster, J. (2017). Bioconda: A sustainable and comprehensive software distribution for the life sciences. bioRxiv. doi: 10.1101/207092

8. Espitia, H, **Chande, A. T.**, Jordan, I. K., Rishishwar, L. (2017). Method of sequence typing with in silico aptamers from a Next Generation Sequencing platform. Patent Pending.

7. Post, D. M. B., Slütter, B., Schilling, B., **Chande, A. T**., Rasmussen, J. A., Jones, B. D., . . . Apicella, M. A. (2017). Characterization of Inner and Outer Membrane Proteins from Francisella tularensis Strains LVS and Schu S4 and Identification of Potential Subunit Vaccine Candidates. mBio, 8(5). doi: 10.1128/mBio.01592-17. PubMed: 29018123

6. Topaz, N., Mojib, N., **Chande, A. T.**, Kubanek, J., & Jordan, I. K. (2017). RampDB: a web application and database for the exploration and prediction of receptor activity modifying protein interactions. Database, 2017, bax067-bax067. doi: 10.1093/database/bax067. PubMed: 29220456

5. Norris, E. T., Rishishwar, L., Wang, L., Conley, A. B., **Chande, A. T.**, Dabrowski, A. M., . . . Jordan, I. K. (2017). Assortative mating on ancestry-variant traits in admixed Latin American populations. bioRxiv. doi: 10.1101/177634

4. Post, D. M. B., Schilling, B., Reinders, L. M., D'Souza, A. K., Ketterer, M. R., Kiel, S. J., . . . **Chande, A. T.**, . . . Gibson, B. W. (2017). Identification and characterization of AckA-dependent protein acetylation in Neisseria gonorrhoeae. PLoS One, 12(6), e0179621. doi: 10.1371/journal.pone.0179621. PubMed: 28654654

3. Watve, S. S., **Chande, A. T.**, Rishishwar, L., Mariño-Ramírez, L., Jordan, I. K., & Hammer, B. K. (2016). Whole-Genome Sequences of 26 Vibrio cholerae Isolates. Genome Announcements, 4(6). doi: 10.1128/genomeA.01396-16. PubMed: 28007852

2. Cho, C.*, **Chande, A.***, Gakhar, L., Bakaletz, L. O., Jurcisek, J. A., Ketterer, M., . . . Apicella, M. A. (2015). Role of the Nuclease of Nontypeable Haemophilus influenzae in Dispersal of Organisms from Biofilms. Infection and Immunity, 83(3), 950-957. doi: 10.1128/iai.02601-14. PubMed: 25547799

1. Apicella, M.A., Gakhar, L., **Chande, A.T.** Novel Thermonuclease from Haemophilus Influenzae and Uses Thereof in Industry and Scientific Research. Patent Pending.

Manuscripts in preparation

1. **Chande, A.T.**, Rishshwar, L., Conley, A.B.m Valderrama-Aguirre, A., Medina-Rivas, M., Jordan, I.K. (2019) Ancestry effects on type 2 diabetes genetic risk inference in Hispanic/Latino populations. Genes.