

# Aroon Chande

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## 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: Bash/Perl/R/Python/C++/HTML/CSS/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/R/Python
- 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 *vibrio*cholera.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, University 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 C/C++, HTML, CSS, SQL

NGS DNA-seq, RNA-seq, microarray

'Omics Analysis of metabolomics and 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

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, Atlanta, GA.  
Reclassification of Non-typeable *Haemophilus spp.*

## Publications

13. **Chande, A.T.**, Wang, L., Rishishwar, L., Conley, A.B., Norris, E.T., Valderrama-Aguirre, A., Jordan, I.K. (2018) GlobAI Distribution of GENetic Traits (GADGET) web server: polygenic trait scores worldwide. Nucleic Acids Research. doi: 10.1093/nar/gky415
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
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
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
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., SiĀijtter, 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
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
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., DāŹSouza, 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
3. Watve, S. S., **Chande, A. T.**, Rishishwar, L., MariŹso-RamŹrez, 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
2. Cho, C., **Chande, A.**, Gakhar, L., Bakaletz, L. O., Jurgisek, 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
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.**, Crisan, C., Rishishwar, L., Watve, S., Jordan, I.K., Hammer, B.K. Computational characterization of Type VI Secretion Systems in Vibrio cholerae