

## ANN E. LORAINÉ

Concord, NC 28085 ◦ 205-789-2048 ◦ [aloraine@gmail.com](mailto:aloraine@gmail.com) ◦ <https://www.linkedin.com/in/annloraine/>

### OBJECTIVE

---

Use my data analysis, software, and project management skills to support researchers & developers.

### SKILLS

---

#### SCIENTIFIC

- RNA-Seq, CHIP-Seq, and microarray data analysis using R, RStudio, knitr, Bioconductor
- Analysis pipeline building and testing using HPC compute clusters & cloud resources
- Writing and editing research reports, technical documentation, training materials, funding proposals

#### SOFTWARE

- Languages: Java, python, R, perl, shell
- Tools: Maven, Sonatype Nexus, OSGi, Docker, git, Bitbucket pipelines, Jira
- Databases: MySQL, MySQL Workbench

### WORK EXPERIENCE

---

**UNC Charlotte Department of Bioinformatics and Genomics, Kannapolis, NC** Feb. 2008 – Present  
Associate Professor

- Lead research team investigating topics in genomics, software design, visualization.
- Design, develop, deploy, and support visualization and data analysis software.
- Recruit, interview, train, and manage student and staff software experts.
- Administer, maintain, and improve IT infrastructure of research group.
- Write technical documentation for developers and end users.
- Develop and teach programming and statistics courses.
- Raise external funding to support research (NIH, NSF).
- Review funding proposals for NIH, NSF, Genome BC.

**University of Alabama at Birmingham Dept. of Biostatistics** Sep. 2004 – Jan. 2008  
Assistant Professor

- Taught statistical bioinformatics, UNIX, R programming.
- Developed genetic variation database for NIH-funded population genetics project.
- Wrote articles on alternative splicing, microarray data analysis.

**Neomorphic/Affymetrix, Inc, Emeryville, CA** Nov. 1999 – Jul. 2003  
Bioinformatics Scientist

- Wrote GUI-based annotation software (Java) for The Institute for Genomic Research.
- Co-developed probe set annotation pipeline, deployed as NetAffx support Web site.
- Supported researchers developing genotyping applications for Affymetrix microarrays.
- Developed algorithms and software for analysis of alternative splicing.
- Showed that alternative splicing frequently modifies conserved protein domains.
- Wrote articles and content for patent applications on visualization, annotation, alternative splicing.

### EDUCATION

---

**University of California at Berkeley**, Ph.D. Molecular and Cell Biology Aug. 1990 – Dec. 1996  
**University of Texas at Austin**, BA Plan II (Honors liberal arts), BS Zoology Aug. 1984 – Dec. 1989

### LINKS

---

- Products - <http://bitbucket.org/lorainelab>, <https://bitbucket.org/aloraine>
- Publications - <http://scholar.google.com/citations?user=dg3fgysAAAAJ>
- Presentations - <http://www.slideshare.net/AnnLorraine>