Cory Brouwer, Ph.D.

	Research Description: Dr. Cory R. Brouwer is Director of the Bioinformatics Services Division and Associate Professor of Bioinformatics and Genomics at UNC Charlotte. He and his team provide a wide range of bioinformatics and computational biology services to the NCRC, UNC Charlotte and surrounding area life sciences community. Recent projects and research interests include data integration, clinical association studies, personalized medicine and the use of next generation sequencing for gene expression, variant detection and assembly.	**Email:** Cory.Brouwer@uncc.edu **Lab Website:** Bioinformatics Services Division

Xiuxia Du, Ph.D.

	Research Description: Dr. Du's research program of Metabolomics & Proteomics Bioinformatics focuses on developing computational and visual analytics algorithms for processing and analyzing mass spectrometry-based metabolomics and proteomics data and for integrating the resultant information with genomics and transcriptomics data for obtaining a systematic understanding of interactions between metabolites, enzymes, and genes.	**Email:** Xiuxia.Du@uncc.edu **Lab Website:** Du Lab

Anthony Fodor, Ph.D.

	Research Description: Dr. Fodor's research program focuses on algorithm and method development in bioinformatics. He is particularly interested in the application of new high-throughput sequencing technology to the study of complex microbial communities. Microbial ecosystems currently under study in his lab include human and mouse gut microbes, bacteria within the activated sludge of a North Carolina wastewater treatment plant and the microbial community within the South Fork of the Eel River in Mendocino County, California.	**Email:** AFodor@uncc.edu **Lab Website:** Fodor Lab

Cynthia Gibas, Ph.D.

	Research Description:	
	The Gibas research group develops methods for analysis of genomic and transcriptomic data. We are currently developing GenoSets, a suite of comparative genomic analysis tools that relies on business intelligence and visual analytics techniques. GenoSets tracks the analytic provenance of genomic data, and facilitates hypothesis-driven browsing and comparison of multiple genomes. We are currently investigating molecular evolution, gene expression, and mechanisms of pathogenicity in Vibrio vulnificus.	**Email:** CGibas@uncc.edu **Lab Website:** Gibas Lab

Jun-tao Guo, Ph.D.

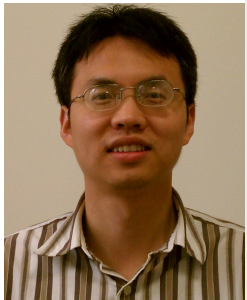|	Research Description:	
	Dr. Guo's research interests are in structural bioinformatics. More specifically, his lab focuses on developing computational methods for studying protein-DNA interactions, structure-based transcription factor binding sites (TFBS) prediction, and structural prediction of alternatively spliced protein isoforms. Dr. Guo is also interested in studying the evolution of regulatory pathways.	**Email:** JGuo4@uncc.edu **Lab Website:** Guo Lab

Dan Janies, Ph.D.

	Research Description:	
	Dr. Janies is a national principal investigator in the Tree of Life program (http://echinotol.org) of the National Science foundation and is funded by the Defense Applied Research Projects Agency. His work involves empirical studies of organismal diversity and development of software, such as Supramap (http://supramap.org). Supramap is used by public health scientists to put pathogen genomic data into context with geography and hosts. The results are akin to weather maps for disease. Dr. Janies is the director of the Bioinformatics Research Center (http://brc.uncc.edu).	**Email:** DJanies@uncc.edu **Lab Website:**

Ann Loraine, Ph.D.

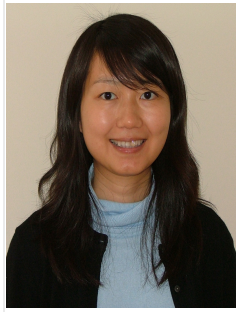|	Research Description:	
	The Loraine group is located at the North Carolina Research Campus in Kannapolis. We study: (a) Alternative splicing – effects of splicing diversity on biological systems; (b) visualization software for genomics – how software dictates what we learn from data; and (c) active learning in bioinformatics – how learning by doing transforms users into builders. Our team includes trainees and professional staff with diverse expertise, from software engineering to plant biotechnology. We provide hands-on, personalized training in diverse areas, including: molecular biology, software development, and bioinformatics data analysis.	**Email:** ALoraine@uncc.edu **Lab Website:** LoraineLab.org

Weijun Luo, Ph.D.

	Research Description:	
	Dr. Luo conducts research across a broad range of topics in bioinformatics and biostatistics. His major research interests include:computational method development and implementation; high throughput genomic, expression and metabolomics data analysis, big data analytics and high performance computing. He collaborates with scientists from numerous research institutions studying complex diseases and processes using systems biology approach. He also works on translational bioinformatics, i.e. direct applications of high throughput omics technologies and bioinformatics in clinic, like disease prevention, diagnosis, and personalized medicine.	**Email:** Weijun.Luo@uncc.edu **Lab Website:** Bioinformatics Services Division

Jessica Schlueter, Ph.D.

	Research Description:	
	Dr. Schlueter's research program is focused on plant genomics and understanding genome structure to improve crops. Current projects include an NSF-funded program to sequence the hexaploid oat genome, understanding ozone stress tolerance in soybeans, miRNA profiling in oats and soybeans, and developing genetic tools for Yaupon, a native North American tea plant.	**Email:** JSchluet@uncc.edu **Lab Website:**

Wei Sha, Ph.D.

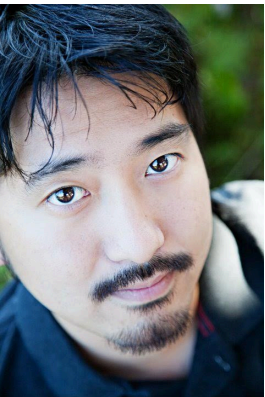|	Research Description:	
	Dr. Sha's research interest is in high throughput data analysis, especially in statistical analysis of SNP data, "-omics" data and clinical trial data. She collaborates with biologists and medical professionals in a variety of research areas, including nutrition science, cancer biology, pediatric pulmonology, etc. She provides experimental design, performs power and sample size estimation, develops randomization schemes, and conducts statistical analysis in these projects. Dr. Sha is also interested in developing novel statistical methods for "–omics" data analysis.	**Email:** wsha@uncc.edu **Lab Website:**

Mindy Shi, Ph.D.

	Research Description:	
	Shi Lab at UNC Charlotte is a computational systems biology lab, focusing on the design and development of tools and algorithms to solve large-scale computational problems in biomedical research and big data health. Specifically, we are developing computational approaches/pipelines to integrate and analyze large-scale (epi)genomic, expression, interaction, language, and cultural data sets to investigate complex diseases and infectious diseases. We are also developing techniques to preserve genetic privacy in human genomic data.	**Email:** x.shi@uncc.edu **Lab Website:** Shi Lab

ZhengChang Su, Ph.D.

	Research Description:	
	Dr. Su's research focus is on computational inference and modeling of regulatory networks/pathways. His work involves the characterization and modeling of transcriptional regulatory networks in prokaryotic and eukaryotic cells. Other interests include molecular modeling and simulation of protein/membrane complexes.	**Email:** ZcSu@uncc.edu **Lab Website:** Su Lab

Jennifer Weller, Ph.D.

Research Description:

Dr. Weller's research interests include the management, integration, analysis and mining of high-throughput datasets, specifically of nucleic acids. Each molecule has structural as well as sequence characteristics that affect the measurement process – correct biological interpretation requires that other factors be accounted for. My lab works at understanding the influence of structure and either mitigating by wet-lab procedures or compensating with computational methods. We have worked with several groups at the Carolinas Health Center to identify blood biomarkers for ovarian cancer and ALS, with the goal of producing robust companion assays for assigning treatment regimens. We have been working with collaborators at Wake Forest University to develop platforms that allow identification of proteins that bind to specific nucleic acid motifs, such as aptamers and transcription factor binding sites.

Email:

JWeller2@uncc.edu

Lab Website:

Weller Lab

Research Description:

Dr. Sung's research program focuses on understanding microbial genome evolution and architecture. His current research includes developing theoretical, computational, and molecular techniques to understand the evolution of genome architecture and mutation rate in microbes, with a focus on microbial pathogens and multi-chromosomal bacteria. In addition, Dr. Sung seeks to understand the distribution of fitness effects of deleterious mutations within these organisms. Current projects include developing microbial mutation-accumulation lines in controlled microfluidic chambers, large-scale high-throughput sequencing and data analysis of mutational properties in microbes, and high-throughput competition assays using droplet-digital PCR technology.

Email:

wsung@uncc.edu

Lab Website: