Senior Scientist, Computational Biology, Genetics

We Are Genetic Navigators bringing together passionate, creative and dedicated professionals to join a rapidly-growing startup on our mission to translate novel genetic insights into lifesaving medicines. We are integrating human genetics and functional genomics to decode the mysteries of genetic modifiers, leading us to new medicines we'll develop for a range of severe diseases.

We are seeking a computational biologist/statistical geneticist to join our organization. The successful candidate will contribute to the design of robust genetic association and gene interaction studies, develop workflows/pipelines for association analyses and other statistical genetics techniques, and perform analyses on large-scale genetic datasets. In addition, the candidate will integrate results from functional genomics screens with human genetics and contribute to interpretation of results with the goal of identifying new therapeutic targets.

Your Role in Navigating The Maze:
- You will lead analyses of large-scale public human genetics datasets (UKBioBank, etc.) to identify genetic modifiers of disease.
- Integrate multiple data sources and develop tools to identify and validate candidate therapeutic targets.
- You will work as part of a diverse cross-functional team at Maze.
- Contribute directly to the development of novel disease modifying therapeutics.

Your Navigation Tools:
- Ph.D. or a Master's degree with significant relevant experience in bioinformatics / computational biology and the biologic interpretation of human genetic data.
- Candidates with a B.S. in computer science with 5+ years applied experience in genetics research will also be considered.
- Proficiency in the management and analysis of large datasets, including those derived from SNP arrays and next-generation sequencing platforms, is ideal.
- Ability to analyze large-scale genomic association studies in complex genetic diseases including correcting for population stratification and imputation of genotypes, solidly understand software development (Perl, Python), and to possess a strong computational/statistical background (R) is highly desirable.
- Experience with expression quantitative trait loci (eQTL) datasets and other approaches to identify functional variants, causality inference approaches (co-localization or mendelian randomization) to link functional variants in the human genome to association signals, or CRISPR screen analysis is a plus.

If you're ready to **Enter The Maze**, send your resume to careers@mazetx.com.