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 an exceptional computational biologist/statistical geneticist to join our organization. The successful candidate will lead human genetic modifier screens utilizing genome-wide association techniques including correcting for population stratification, single variant and gene burden association methods, and polygenic scores.

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.
- Coordinate with external collaborators and work as part of a cross-functional team.
- Integrate multiple data sources and develop tools to identify and validate candidate therapeutic targets.
- You will contribute directly to the development of novel disease modifying therapeutics.

Your Navigation Tools:

- Ph.D. or 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 3+ years applied experience in genetics research will also be considered.
- Proficient in the management and analysis of large datasets, including those derived from SNP arrays and next-generation sequencing platforms, is ideal.
- Experience in the analysis of large-scale genomic association studies in complex genetic diseases including correcting for population stratification and imputation of genotypes, a solid understanding of software development (Perl, Python), and a strong computational/statistical background (R) is highly desirable.
- Experience with causality inference approaches (co-localization or mendelian randomization) to link functional variants in the human genome to association signals or analysis of CRISPR screens is a plus.

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