



Title: Lead Statistical Geneticist
Department: Computational Genome Analytics
Reporting to: Vice President, Head of Genomics
Location: Cambridge, MA

Company Overview:

Goldfinch is a biotechnology company that is singularly focused on discovering and developing precision therapies for patients with kidney disease. Goldfinch has built the Kidney Genome Atlas™ (KGA), a comprehensive patient registry comprising a combination of genomic data, including whole genome and exome sequences, bulk and single-cell RNA sequences, and epigenetic and clinical patient profiles alongside a human biology platform that is harnessing advances in stem cell science to develop and apply human organoid models. We are building on recent breakthroughs in genetics and human biology to generate an unparalleled understanding of the biological pathways that drive kidney disease. Goldfinch Bio is uniquely positioned to translate these discoveries into new therapies that target the molecular causes for diseases of the kidney and bring new therapeutics to a severely underserved patient population.

The Role: We are looking for a highly collaborative, experienced Statistical Geneticist to play a central role in the continued development of the Kidney Genome Atlas (KGA) and the analysis of KGA data to drive the discovery of novel drug targets, genomic and phenotypic biomarkers for patient stratification, and insights into the underlying molecular mechanisms of disease. We seek an independent, hands-on analyst with the desire and potential to build and ultimately lead a small team and strong genetics network to support the success of the Computational and Genome Analytics team at Goldfinch.

The successful candidate will join an interdisciplinary team of bioinformaticians, computational biologists, and software engineers working in a pioneering and collaborative environment alongside our biology and drug discovery colleagues. This person will be a leader in statistical genetics and responsible for designing and implementing robust analysis plans, building analysis workflows/pipelines, developing statistical and computational methods and performing analyses on large scale integrating data sets, and interpreting the data to help develop therapeutic hypotheses for new kidney disease treatments.

Job Responsibilities Include:

- Researching, adapting, and implementing cutting edge analytical and statistical genetics approaches for analyses and interpretation of proprietary and publicly available genomic data.
- Identifying and developing new strategic statistical genetics initiatives to meet group and company goals
- Developing and documenting statistical and computational genomics analysis plans to interrogate whole-exome and whole-genome sequence data in combination with other genomic and phenotypic data with the KGA to enable the identification of causal genetic determinants of disease.
- Conducting robust statistical and computational genomics analyses, for common and rare variants, genome-wide epigenetic association studies, and integrative genomic studies that incorporate sequence and expression data, analysis of RNAseq data for calculating eQTLs and differential gene expression
- Fine mapping and locus dissection to assist in target identification, including leveraging public and proprietary genomic functional annotations and implementation of Bayesian methods for constructing credible sets of variants



- Interpretation and communication of key findings as they relate to the goals of Goldfinch Bio's drug discovery and development strategies.
- Providing analytical insights and contributing to the design of additional population based genomic studies for the continued development of the KGA
- Curation of new public and proprietary genomic data as it is added to the KGA (e.g. ChIPseq, histone marks), including rigorous examination of batch effects
- Providing genetics and genomics insight into target identification, nomination and validation packages in collaboration with wet lab biologists and clinical scientists to leverage genetic findings in the design of functional validation and clinical trials.
- Some supervisory experience of interns, contractors, and vendor management

Qualifications/Experience:

- Ph.D. in Statistical Genetics, Human Genetics, Genetic Epidemiology, Statistics, Computational Biology, Bioinformatics, or related subject and >5+ years Post-Doctoral training or equivalent experience.
- Demonstrated ability to analyze next generation sequencing data, with a particular focus on whole genome and/or whole exome sequencing data in large populations.
- Demonstration of technical and project leadership in the field
- Demonstration of independent problem solving in complex cross functional projects
- Proficiency in Python, R and Linux is required; experience with Hail is preferred.
- Proven ability to work independently and in a team environment
- Excellent written and verbal communication skills and the ability to clearly articulate and explain complicated results to a senior leadership/Board of Director-level audience
- Track record of peer-reviewed publications in top-tier scientific journals.
- Strong drive with a desire to make an impact on kidney disease.

Preferred technical experience in addition to the above:

- Experience with Genome Analysis Toolkit (GATK) and/or similar variant calling pipelines
- Experience operating in a cloud platform (Preferably AWS)
- Experience with version control, electronic notebooks (Jupyter or other)
- Experience using containerization technologies (Docker or other) for reproducible research
- Experience working with controlled access data from public repositories, such as a dbGaP and the UK BioBank
- Experience with Mendelian Randomization and/or multi-phenotype analyses a plus
- Experience operating in a large-scale, distributed computing environment