



Bioinformatics Expert

The Position

Earli is currently seeking high-caliber bioinformatics expert candidates with strong capabilities in oncology (cancer genomics), statistics and AI / ML.

About Earli

Earli Inc. has a large mission: to detect and then cure cancer at its earliest stages, effortlessly and painlessly. In other words, we aim to make cancer a benign experience. Our science is based on a new method of detecting, localizing and then treating cancer, developed by Dr. Sam Gambhir, who runs Stanford's Canary Center for Early Cancer Detection. Earli is starting what we believe will be a new era of "synthetic biomarkers." Rather than relying on hard-to-detect natural biomarkers in blood samples, Earli's technology *forces* cancer cells, if they exist, to produce non-human molecules they otherwise would not naturally make. As a result, such synthetic biomarkers are readily detectable and are easily quantified. The same platform can be used to localization and treatment. Other diseases beyond cancer, are potentially also diagnosable and treatable with this novel approach. Earli is financed by some of the best venture capital firms in Silicon Valley and China. We are currently based in the West Coast's prime biotech hub in South San Francisco. More information can be found at www.earli.com.

Who You Are

- You share our same sense of dedication, scientific passion and entrepreneurial spirit.
- You are technically gifted, with great hands on experience.
- You work well in a fast-paced and extremely focused startup environment.
- You are not only smart, but clever and constantly think outside the box.
- You are able to make logical decisions in an instant when there is little time to evaluate.
- You are a natural communicator and relationship builder.
- You stay calm under high pressure and stress.

- You have the ability to multi-task in a serious way, with an extreme attention to detail.
- You become a representative of the core DNA of the company through who you are and how you contribute.

Primary Responsibilities

- Develop and implement algorithms to appropriately cluster patient tumor gene expression data, and identify gene expression fingerprints within these clusters.
- Analyze results data (reporters) from animal and human samples on rather small data sets (in the hundreds), using small dataset approaches to AI for pattern fingerprinting, and statistical tools for validation.
- Establish methods for the retrieval, processing, cleaning and normalization of gene expression data from large public oncology databases (e.g. GTEx, TCGA, ICGC, CPTAC)
- Develop appropriate shrinkage models to identify statistically relevant signal from noise, and cross-compare and correct for data from varying sources.
- Create pipelines to generate effective data visualizations to communicate and summarize findings for both high-level executives and lab members focused on cell and molecular biology.
- Identify and propose models that are empirically testable by biologists both *in vitro* and *in vivo*.
- Develop the actual code, run algorithms in the cloud

Required Experience, Knowledge and Skills

- Very strong education in mathematics, statistics, or bioinformatics with a minimum of 4-6 years of relevant industry experience applying quantitative approaches to clinical data, with a focus on cancer genomics
- Demonstrated ability to integrate heterogeneous data sources and perform multivariate analysis of integrated datasets on large and small datasets.

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- Proven expertise in the development and/or implementation of algorithms to distill, analyze and interpret complex datasets with breadth and depth, and experience encompassing both supervised and unsupervised learning algorithms (AI/ML)
- Experience in computational biology research on a wide variety of molecular profiling platforms, including Total RNA/mRNA profiling, mutational profiling, DNA copy number quantification, epigenetic profiling and proteomics.
- Familiar with various cancer genomics consortium efforts, tools and databases.
- Hands-on expertise in algorithmic implementation, statistical programming and data manipulation, using e.g. R/Bioconductor and contemporary, open-source bioinformatics tools and database structures, and running systems in the cloud.
- Track record of peer-reviewed publications in top-tier scientific journals.
- Proven problem-solving skills, collaborative nature and adaptability across disciplines.
- Excellent verbal communication and interpersonal skills are required
- Must be able to multi-task, manage multiple projects simultaneously
- Ability to think independently and fully integrate into a high-achieving team environment

Preferred Experience, Knowledge and Skills

- MS or PhD degree preferred but will consider other degrees, contingent on strong relevant experience
- Demonstrated experience in the development of novel mathematical and statistical algorithms for gene expression data analysis
- Demonstrated experience in the publication of software packages and libraries for data analyses
- Experience within the field of gene regulation and epigenetics (DNA methylation, histone modification, etc.)
- Understanding of molecular biology assays and appropriate experimental designs for wet lab hypothesis testing

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- Understanding of the regulation of mRNA expression (e.g. transcription initiation, transcription elongation, miRNA, mRNA structure, etc.)
- Experience with the regulation and analysis of gene regulatory networks

If you are interested in applying, please attach a CV or have a well developed LinkedIn profile for us to be able to assess your background.

We look forward to hearing from you!