Title: Director, Bioinformatics  
Reports to: Chief Data Officer  
Department: Bioinformatics  
Location: Norwalk, CT

Job Summary
The Multiple Myeloma Research Foundation is seeking a talented, self-motivated Bioinformatics expert to join our team to participate in leading edge research in translational Informatics. The successful applicant will have formal training in bioinformatics with outstanding project management skills. They will be part of an interdisciplinary team that designs and prototypes computational tools that improve the detection and interpretation of disease-relevant variants, which ultimately lead to better therapeutic options in a personalized medicine context. A key responsibility of this position will be exploring and promoting novel informatics methodologies into clinical practice. As an example, this may include the integration and standardization of large genomic datasets, means to bridge disparate data sets (e.g., EHR/EMR, Genomic, Claims, etc.) and the application of machine learning and statistical techniques to enable decision-making. In addition, the role will have responsibilities to lead major portfolio(s) of informatics work, standing up entire systems while working in the context of a matrixed team.

Essential Duties and Responsibilities
- Apply state-of-the-art computational methods to analyze large-scale whole genome, and/or high dimensional immunologic data (e.g., CyTOF, proteomics) and exome sequence data to support data analysis in genetic studies a plus
- Architect, create, maintain, extend, update bioinformatics pipelines (such as for RNAseq, CyTOF, DNA, EHR and/or other bioinformatic data types)
- Architect means of integrating or connecting disparate data sets that are linked
- Improve robust and highly automated computational pipelines
- Create, curate, manipulate and perform analytics on connected data sets that include EHR/EMR, genomics, proteomic, patient reported outcomes and medical insurance (claims) data
- Lead a research project(s) in either human genetics or bioinformatics method development.
- Analyze EHR/EMR-based data sets, with an ability to create and work with patient cohorts
- A working knowledge of standardized terminology and vocabularies such as ICD-10, SNOMed, MEDDRA, and RxNorm (a plus)
- Architect/design data visualization tools for use by patients, clinicians and researchers
- Identify and validate innovative approaches to improve the quality and efficiency of the processing and analysis of -omics data (a plus)
- Maintain current awareness of emerging approaches and methods in computational biology
Director, Bioinformatics
Norwalk, CT

Required Qualifications

• Formal Informatics training in healthcare/life sciences with a minimum of a Master's in Bioinformatics, Biostatistics, Computational Biology, or related disciplines required; PhD or other terminal degree, a plus.
• Alternatively, an MD with clinical/healthcare Informatics degree or post-doctoral fellowship will also be considered.
• Minimum of 8 years demonstrated experience working with big data (biologic data – scRNA Seq, CyTOF, and other bioinformatics data sets); high-throughput sequencing data, EHR/EMR data analysis or method development
• A working understanding of standardized vocabularies (as noted above)
• Experience in using R and/or R Studio
• Prior experience working in a life science, academic medical center environment, or a health plan Informatics group.
• Strong project management skills – evidence of successfully leading large, complex projects to delivery, on time and on budget
• Ability to build and foster solid relationships both internally and externally with matrix team members
• Strong systems and creative thinking, excellent problem-solving skills
• Excellent verbal and written communication skills; the ability to interface effectively with scientists and clinicians to communicate/discuss results and ideas.
• Google Cloud and/or AWS experience a plus
• Strong experimental design (prototyping) abilities
• Excellent presentation skills

Desirable Qualifications

• Knowledge of genomic data repositories relevant to clinical genetics
• Strong working knowledge of scripting in a Unix environment,
• Programming fluency with at least one general-purpose programming language (such as Python, Perl or Swift, MySQL and one language for scientific computing (such as R or MATLAB).
• Knowledge of various Informatics techniques that may extend to (but not limited to) population health, clinical data cohort generation and use, quality initiatives, genetics, and molecular biology a plus
• Confluence (a plus)
• Desire to stay on the leading edge of discoveries in the field of personalized medicine