

Project #1: HLA Typing from DNA and RNA assays

About Q² Solutions: Q² Solutions is a leading clinical trial laboratory services organization passionate about improving world health. The translational genomics bioinformatics department provides analysis solutions for insights from genomic data such as biomarker discovery, DNA or RNA signature identification and interpretation, immune landscape, pan-viral pipelines, pathway analyses, and more.

Purpose: The chosen applicant will gain practical work experience within an industry setting comprising individuals of diverse talents across computer science, molecular biology, statistics, and genomics. He/she will be part of a dynamic bioinformatics team, advancing the state of art in genomic data analysis with multiple projects available to apply their research and analytical skill sets to help us advance the field. The applicant will also learn principles of software development in an industry setting and the art of transitioning from research to production environments.

Project Description: Human leukocyte antigen (HLA) typing has several applications such as predicting drug safety or neoantigen burden in immunotherapeutics. We are looking to develop custom informatics for predicting HLA typing from our DNA and RNA sequencing assays. The intern will help us research latest algorithms in the field of HLA typing from sequencing assays, examine our current HLA pipeline, and recommend changes to be made to the pipeline.

Applicant Skills:

- Understanding/course work on one or more: computer programming, statistical modeling, or machine learning.
- Familiarity working in Linux/UNIX environment, including shell scripting and bash (preferred).
- Proficiency in a programming language: Python or R
- Experience giving presentations of analysis results to non-technical audiences.
- Exposure to data analysis using next generation sequencing, multi-analytic instrumentation and other *omic data (preferred).
- Appropriate verbal and written communication skills to function within a professional work environment.

Project #2: Single cell sequencing

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Purpose: The chosen applicant will gain practical work experience within an industry setting comprising individuals of diverse talents across computer science, molecular biology, statistics, and genomics. He/she will be part of a dynamic bioinformatics team, advancing the state of art in genomic data analysis with multiple projects available to apply their research and analytical skill sets to help us advance the field. The applicant will also learn principles of software development in an industry setting and the art of transitioning from research to production environments.

Project Description: Single cell sequencing technology provides digital gene expression by profiling 500 - 10,000 individual cells per sample through a microfluidic platform. We would like to enhance our single cell bioinformatics pipeline offerings in terms of doublet detection, cell annotations, and differential expression with single cell. To that end, there are several avenues available to research latest algorithms, best practices, and summarize pros and cons of each, testing on internal data, and developing / assisting in the development of a schema for testing accuracy in these settings.

Applicant Skills:

- Understanding/course work on one or more: computer programming, statistical modeling, or machine learning.
- Familiarity working in Linux/UNIX environment, including shell scripting and bash (preferred).
- Proficiency in a programming language: Python or R
- Experience giving presentations of analysis results to non-technical audiences.
- Exposure to data analysis using next generation sequencing, multi-analytic instrumentation and other *omic data (Experience with single cell sequencing data is strongly preferred).
- Appropriate verbal and written communication skills to function within a professional work environment.

Project #3: Structural Variant Algorithm Comparison

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Purpose: The chosen applicant will gain practical work experience within an industry setting comprising individuals of diverse talents across computer science, molecular biology, statistics, and genomics. He/she will be part of a dynamic bioinformatics team, advancing the state of art in genomic data analysis with multiple projects available to apply their research and analytical skill sets to help us advance the field. The applicant will also learn principles of software development in an industry setting and the art of transitioning from research to production environments.

Project Description: Genomic structural variation and associated RNA fusions are a common clinical feature known to be involved in the initiation and pathogenesis of cancer. This complex class of variants also has significant implications on therapeutic decisions and has emerging roles in evidence-based clinical applications. There is a crucial need for software to identify fusions and other structural variants accurately and precisely. We would like to perform a literature review on the latest algorithms for structural variant detection with DNA and RNA sequencing assays, evaluate our current algorithm and provide recommendations on fusion algorithms to further evaluate.

Applicant Skills:

- Understanding/course work on one or more: computer programming, statistical modeling, or machine learning.
- Familiarity working in Linux/UNIX environment, including shell scripting and bash (preferred).
- Proficiency in a programming language: Python or R
- Experience giving presentations of analysis results to non-technical audiences.
- Exposure to data analysis using next generation sequencing, multi-analytic instrumentation and other *omic data (preferred).
- Appropriate verbal and written communication skills to function within a professional work environment.

Project #4: Immune Landscape Signatures

About Q² Solutions: Q² Solutions is a leading clinical trial laboratory services organization passionate about improving world health. The translational genomics bioinformatics department provides analysis solutions for insights from genomic data such as biomarker discovery, DNA or RNA signature identification and interpretation, immune landscape, pan-viral pipelines, pathway analyses, and more.

Purpose: The chosen applicant will gain practical work experience within an industry setting comprising individuals of diverse talents across computer science, molecular biology, statistics, and genomics. He/she will be part of a dynamic bioinformatics team, advancing the state of art in genomic data analysis with multiple projects available to apply their research and analytical skill sets to help us advance the field. The applicant will also learn principles of software development in an industry setting and the art of transitioning from research to production environments.

Project Description: Interplay between various immune cell activities in human tumors contributes to patient responses to treatment with checkpoint inhibitors or other immunotherapies as well as overall patient outcomes. The Immune Landscape Signature Scores, derived from RNA sequencing, can be used to determine immunogenic status of solid tumors. These signatures can also be used in a single- or multi-factor analysis of treatment response and survival. We would like to look at association of Q² Solutions developed immune landscape signatures with responses to immunotherapy using publicly available clinical data using statistical methods. Additionally, we would like to understand the indications in which immune landscape signatures help understand variation in survival (while controlling for factors like age, gender, etc.).

Applicant Skills:

- Understanding/course work on one or more: computer programming, statistical modeling, or machine learning.
- Familiarity working in Linux/UNIX environment, including shell scripting and bash (preferred).
- Proficiency in a statistical programming language: SAS or R
- Experience giving presentations of analysis results to non-technical audiences.
- Exposure to survival-related data analysis including Kaplan-Meier and Proportional Hazards regression methods (preferred).
- Appropriate verbal and written communication skills to function within a professional work environment.

Project #5: UMI tools assessment

About Q² Solutions: Q² Solutions is a leading clinical trial laboratory services organization passionate about improving world health. The translational genomics bioinformatics department provides analysis solutions for insights from genomic data such as biomarker discovery, DNA or RNA signature identification and interpretation, immune landscape, pan-viral pipelines, pathway analyses, and more.

Purpose: The chosen applicant will gain practical work experience within an industry setting comprising individuals of diverse talents across computer science, molecular biology, statistics, and genomics. He/she will be part of a dynamic bioinformatics team, advancing the state of art in genomic data analysis with multiple projects available to apply their research and analytical skill sets to help us advance the field. The applicant will also learn principles of software development in an industry setting and the art of transitioning from research to production environments.

Project Description: Unique molecular indices (UMI) are molecular tags used in sequencing that allow us to improve the accuracy of sequencing results by reducing PCR errors and biases. We are interested in assessing UMI tools on our datasets and understand the performance of UMI tools on datasets generated from different sequencing platforms. The intern will help us assess the tools through proficient pipeline analysis in nextflow, summarize the analyses, and provide recommendations on which tool(s) to use for UMI applications.

Applicant Skills:

- Understanding/course work on one or more: computer programming, statistical modeling, or machine learning.
- Familiarity working in Linux/UNIX environment, including shell scripting and bash (preferred).
- Proficiency in a programming language: Python or R
- Experience giving presentations of analysis results to non-technical audiences.
- Exposure to data analysis using next generation sequencing, multi-analytic instrumentation and other *omic data (preferred).
- Appropriate verbal and written communication skills to function within a professional work environment.