<table>
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<th>Job Title</th>
<th>Bioinformatician</th>
<th>Bioinformatician II</th>
<th>Bioinformatician III</th>
<th>Sr Bioinformatician</th>
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<td>Bioinformatician</td>
<td>MC2200</td>
<td>MC2201</td>
<td>MC2202</td>
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**Position Summary**
Under the direction of a member of the faculty, the Bioinformatician is responsible for the design, development, evaluation and iterative modification of a technical infrastructure to expedite the quantitative evaluation of data resulting from studies that are laboratory based. The position will entail the establishment and maintenance of applicable in-house bioinformatics resources and interaction with individual lab members on customized research projects, as well independent projects that are solely computational.

**Essential Functions**

**Scope**
- **Establish general bioinformatics resources for day-to-day use by members of the laboratory**
- In collaboration with a faculty member, generate customized programming solutions to improve user interaction with available bioinformatics resources
- Assist in the implementation of programs for microarray analysis, high-throughput sequencing data analysis, cis regulatory motif identification, and multi-genome protein motif searches
- Local establishment and customization of model organism genomic databases and tools for batch sequence analysis utilizing these resources
- *Integrate and present study results in support of laboratory members*
- *Provide tabular and written summaries of approaches and analyses in a form suitable for inclusion in manuscripts or grant applications, as well as media for presentation at scientific meetings*
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**Essential Functions**

**Scope**
- Implement and adapt programs for microarray analysis, high-throughput sequencing data analysis, cis regulatory motif identification, and multi-genome protein motif searches
- Independently develop, implement and maintain custom-designed computational solutions relevant for ongoing lab-based projects.
- Independently develop, implement and maintain computational methods for meta-analysis of data generated in the lab as well as publicly available data.
- Independently execute a scientific computational project (e.g. a project that can result in a first author publication)
- Local establishment and customization of model organism genomic databases and tools for batch sequence analysis utilizing these resources.
- Design and implement reusable bioinformatics analysis pipelines for processing next-generation sequencing, microarray, genomics, proteomics and chemogenomics data.
- Develop computational methods/pipelines with high performance computing clusters
- Collaborate closely with PIs and their lab members on research projects and provide training and support for bioinformatics resources.
- Participate in the oral presentation of all project findings and abstracts including participation in periodic project status meetings and presentation of final project deliverables.
- Develop novel methods for data analysis, as well as independent projects that are solely computational.

**Required Qualifications**
- BS in computer science, or equivalent experience 3-5 years of related experience
- BS in computer science, equivalent experience 1-2 years of related experience
- Strong background in statistical methodology, software languages and computer systems (Perl, C++, R, MySQL, etc.) Experience in writing basic search algorithms and the ability to generate new algorithms and programs for custom data manipulation and analysis.
- Master's degree in Computer Science, a related computational discipline, or equivalent experience 3-5 years of bioinformatics-related research experience
- Proven research record such as co-authorship on peer-reviewed publications.

**FLSA Status**
- Exempt

**Promotional Process**
- Requisition or In-family Promotion from Bioinformatician
- Requisition or In-family Promotion from Bioinformatican II
- Requisition or In-family Promotion from Bioinformatican III

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