



PLEASE POST

Data Content Manager and Curation Group Leader, Saccharomyces Genome Database, Department of Genetics, Stanford University

Department of Genetics has an excellent opportunity available for a motivated and experienced Biocurator with proven management skills. The successful candidate will be an essential member of the *Saccharomyces* Genome Database project with the following roles: (1) identifying and creating annotations that represent experimental results describing the biological role of gene products in the budding yeast *S. cerevisiae*, (2) overseeing the data content, web presence and outreach for the project, (3) managing Biocurators and Data Wranglers, Ph.D.-level scientists who identify and annotate experimental data and process high-throughput datasets, respectively, from peer-reviewed literature, and (4) collaborating and coordinating with software engineers, system engineers, and database administrators to specify and develop software and tools to visualize and search these data.

As an active Biocurator, this individual will identify and extract results from scientific literature in diverse biological fields, capture these data using controlled vocabularies and ontologies, compile scholarly summaries of the peer-reviewed literature, and refine genomic maps. As Data and Content Manager, this individual will define the goals for the incorporation and presentation of experimental results. This individual will also define the outreach efforts including the helpdesk as well as creating and maintaining tutorials and online help provided by the project. Additionally, this individual will coordinate and prioritize tasks for the Biocurators and Data Wranglers. Therefore, the successful candidate must understand experimental methods, data processing and analysis methods, and inferences that can be applied to both single-gene experimentation and high-throughput analyses. In addition, the successful candidate will define and maintain processes that evaluate and verify the accuracy of these data, applying judgment and evaluating the experiment data, not as a peer-reviewer, but to determine if the results reported are appropriate for the database.

As an integral member of the academic research community, this individual will need to understand how the scientific community wants to search and access diverse data types in order to advise on the specification and development of new search and analysis tools. Additionally, the successful candidate will be responsible for describing and designing educational material that will help these researchers use the tools developed by the project.

Tasks will include the maintenance and specification of pipelines and curation processes to identify scientific literature that describe experimental findings for the budding yeast in diverse fields, including genetics, genomics, cellular and molecular biological studies as well as the integration of these data into databases maintained by the Stanford project. Additional tasks will include the specification of curatorial processes, data models, meta-data, and analysis and search tools used for the display of these data. Knowledge of classical and contemporary experimental methodology, analysis of experimental results, large genomic datasets and their analysis is

expected. Experience with communicating scientific information via an online portal is required. Previous experience should include cellular and molecular biology or genetics laboratory work. The applicant should have knowledge of high-throughput sequencing technologies that identify RNA transcripts, transcription factor binding sites, histone modification, methylated regions, and SNPs as well as understanding of their computational analysis. Experience with comparative genomics is desirable. An advanced education in biology is required to facilitate the assessment of experimental details and to successfully evaluate quality control of novel experimental data. The successful candidate must be able to learn and work independently, yet collaborate effectively with co-workers. Previous experience working in an academic environment is a plus.

The successful candidate will work at Stanford University in Palo Alto, California. This position will work on model organism projects funded by the National Institutes of Health. Compliance with and support of University and government health & safety regulations & policies is required.

Required:

- An advanced PhD level degree in genetics, genomics, cellular biology, molecular biology or an equivalent is required and 5 years of related experience. Experience with high-throughput methodologies and their analysis is required. The ability to create scripts and process data via state of the art tools is desired.
- Technical expertise in genetics, cell biology, molecular biology.
- Experience in management of scientists coordinating their tasks, goals, professional growth, and fostering group morale.
- Experience with data quality assessment.
- Excellent verbal and written communication skills.
- Experience with literature curation methodologies
- Knowledge of the interconnectedness of complex biological data types
- Proficiency in communicating an understanding of genetics details.
- Experience in the application of ontologies for biological annotation.
- Knowledge of current experimental procedures and their application in the study of biology including possible errors and boundaries of what can be described by the use of these methods
- Knowledge of principals and practices of data analysis as applied to experimental results.

Desired:

- Knowledge of principles and practices of computational biological as applied to genomics.
- Experience in use of Perl or Python.
- Experience with specification of relational data models.
- Knowledge of modern high-throughput genomics and proteomics experiments and their data types.
- Experience with specification of metadata for biological data.

Contact J. Michael Cherry (cherry@stanford.edu) for more information or apply for Stanford University Job ID 50628 at: http://stanfordcareers.stanford.edu/job-search