

Postdoctoral Research Scientist, Comparative Genomics and Phylogenomics

Chicago, IL

The Grainger Bioinformatics Center of the Science and Education Department at The Field Museum is recruiting a full-time Postdoctoral Research Associate to work on phylogenomic analyses of non-model organisms, with a focus on symbiotic fungi. We are looking for an individual with a strong interest and background in computational biology and/or bioinformatics. The position is for a term of 12 months, with the possibility for extension. Possible start date is June 1st, 2019 but is flexible.

The research entails studies on molecular evolution and diversification of non-model organisms. The successful applicant will be involved in various aspects of comparative genome analyses, including genome sequencing and analysis, phylogenomic applications, and species delimitation. Candidates should be able to demonstrate experience in phylogenetic analyses, generating and analyzing genomic datasets, competency with at least one scripting language (e.g., Perl, Python, R), and interest in applying new statistical approaches. Experience with phylogenetics and population genomics is a plus. Well-developed communication (verbal and written) and organizational skills are essential. The successful candidate will also demonstrate leadership ability to assist the PI with the direction and training of students.

The successful applicant is expected to publish at least one research paper as lead author within a year and collaborate as co-author on at least two additional research papers. Guidance will be provided following the Postdoctoral Mentoring Plan.

Please contact with questions Felix Grewe (www.felixgrewe.de, fgrewe@fieldmuseum.org)

All applicants need to include a statement of interest, CV with publication list, and contact information of 3 professional references to be considered.

Please apply at http://fieldmuseum.org/about/careers/?hireology_job_id=295741

Data Analyst

Chicago, IL

The Field Museum is recruiting a full-time Data Analyst to work on Big Data projects for the Grainger Bioinformatics Center (GBC) of the Science and Education Department. The center will be launched in June to support and enhance research in phylogenomics and biodiversity informatics. The Data Analyst conducts or assists in genome analyses or collection-based research projects and provides consultation on new and current GBC projects. In addition, the Data Analyst supports the bioinformatics Linux servers of the GBC. The position is for a term of 2 years, with the possibility for extension.

We are seeking an outstanding individual with a strong interest and background in data science and/or bioinformatics to join a diverse team of researchers working on interdisciplinary biological and ecological projects. Projects typically involve phylogenomic, biogeographic, or populations genomic research of non-model organisms. Therefore, a background in Biology and experience in processing next-generation sequence data for comparative genomics or populations genomics is a plus. The Data Analyst will discuss their involvement in projects and report to the director of the GBC.

Duties and Responsibilities

- Analysis of big data sets, mostly next-generation sequence data.
- Apply and adapt existing bioinformatics tools to analyze large, complex data sets.
- Communicate highly technical results and methods clearly.
- Interact cross-functionally with a wide variety of people and teams.
- Linux server support with help of the Field Museum's IT department, which includes but is not limited to software installation, user profile management, and problem-solving.

Qualifications

- M.Sc. in Data Science, Bioinformatics, Computer Science, Statistical Genetics or a related field at the time of start date.
- Demonstrated experience in processing and analyzing big data sets, ideally data sets of biological nature.
- 2-3 years programming experience (fluency in at least two common programming languages).
- Strong experience working in a Unix environment.
- Experience modeling genomic and phenotypic data
- Skills in Genome Analyses, such as Assembly, Annotation, Comparative Genomics, SNP detection, and Population Genomics.
- Experience in analyzing RADseq, HybSeq, UCE, and genome skimming data.
- Ability to write research publications
- Strong analytical and problem-solving skills
- Considerable collaborative skills, including the ability to interact well with collaborators
- Knowledge of machine learning methods to analyze large, complex data sets

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