



Naturhistoriska
riksmuseet

The Swedish Museum of Natural History is one of the leading institutions of its kind in Europe. It combines a venerable tradition and unique collections with cutting-edge research in geology, paleontology and biology.

The Department of Bioinformatics and Genetics is focused on research in computational phylogenetics, population genetics and genomics. We run a DNA sequencing facility and host several national and international infrastructures.

The Department of Bioinformatics and Genetics is looking to fill

TWO POSTDOCTORAL POSITIONS IN BAYESIAN BIODIVERSITY ANALYSIS

Tasks

The Ronquist lab at the Swedish Museum of Natural History focuses on interdisciplinary research in systematics and evolutionary biology, usually with a strong computational or methods-development component. Our software for Bayesian phylogenetic and phylogenomic inference, MrBayes (<http://mrbayes.net>) and RevBayes (<http://revbayes.com>), is widely used across the life sciences. The lab is a major partner in the Marie Skłodowska Curie Innovative Training Network BIG 4 - Biosystematics, informatics and genetics of the four major insect orders (<http://big4-project.eu>). Local students work with automated identification of insects using deep learning algorithms, metabarcoding methods development with applications to large-scale studies of island biogeography, and metabarcoding and phylogenomic approaches to the evolution of gall induction in gall wasps. Other recent research themes in the lab include dating of phylogenies with fossils, probabilistic models of morphological evolution, and novel algorithms for Bayesian phylogenetic and phylogenomic analysis.

This project, funded by the Swedish Research Council, focuses on analyses of data from massively parallel sequencing efforts using RevBayes, our R-like computing environment, and its programming language Rev. RevBayes is based on graphical model concepts, and is primarily intended for Bayesian analysis of complex evolutionary models. The successful candidate will have great freedom in formulating her or his project within this general context and the research themes of the lab. The project can be focused on method development or empirical analyses, but should include a substantial computational component.

Qualifications

We expect you to have a doctoral degree in evolutionary biology, bioinformatics, mathematics, statistics, or computer science. The PhD degree should have been received no more than three years before the deadline for applications. Regardless of your background, you should be familiar with biological research problems, be comfortable with mathematical and statistical reasoning, and have solid computational and programming skills.

We expect that you will be creative and independent while being a good team player. Fluency in spoken and written English is essential. We will pay particular attention to scientific talent and potential.

Starting date. Desired starting date is early fall 2016, but there is some flexibility in accommodating candidate preferences. The positions are for two years.

For more information about the position, contact Professor Fredrik Ronquist, Head of the Department of Bioinformatics and Genetics (fredrik.ronquist@nrm.se; +46-8 5195 4094). Trade union representative (SACO) is Anders Telenius (anders.telenius@nrm.se; +46-8 5195 5129).

The application should consist of a personal letter, a description of the planned research project (max 5 pages), and a CV. Mark your application with dnr 2.3.1-254-2016 and send it to rekrytering@nrm.se no later than **May 30, 2016**.