



UNIVERSITY OF GOTHENBURG



Post-doctoral position in Marine Genomics/Bioinformatics

at the Department of Chemistry and Molecular Biology and the Centre for Marine Evolutionary Biology (CeMEB)

The department

Research and graduate education at the Department of Chemistry and Molecular biology comprise a wide scientific field from the atomic and molecular levels all the way through cells to intact organisms. Much of the phenomena studied here impact on our natural environment and living systems. We participate in undergraduate programs in chemistry, molecular biology, medicinal chemistry, biology, marine sciences, pharmacy, genomics, bioinformatics and systems biology. For more information about the department see: www.cmb.gu.se/english.

The research group

The research group where this post-doc position is placed is engaged in various marine projects with emphasis on functional genomics of osmoregulation and signalling in unicellular eukaryotes like the yeasts *Saccharomyces cerevisiae* and the marine yeast *Debaryomyces hansenii*, the diatom *Skeletonema marinoi*, and the barnacle *Balanus improvisus*. In this barnacle cloning and functional characterization of genes encoding octopamine receptors, pheromones, aquaporins and Na/K-ATPases have been conducted. The group is also in charge of genome sequencing projects of eight marine organisms. This is part of an activity within CeMEB that is called IMAGO that aims at building an infrastructure based on novel marine model organisms that are well adapted to explore essential questions in ecology and evolution. For more information about the involved research group see the home page of Anders Blomberg: www.cmb.gu.se/personal/blomberg-anders.

The centre for marine evolutionary biology – CeMEB

The post-doc employed will be part of highly active research consortium at the University of Gothenburg (CeMEB). The Linnaeus Centre for Marine Evolutionary Biology, CeMEB, brings together a broad expertise in biology. The main focus is on evolutionary processes and mechanisms in marine species and populations. The goal is to increase our understanding of how marine organisms adapt to new environmental conditions, for example changing seawater pH, temperature and salinity. CeMEB started in July 2008, when the consortium was selected for a ten year Linnaeus grant that was awarded by the Swedish Research Councils. For more information about CeMEB: www.cemeb.science.gu.se.

Job assignments

The project is part of the CeMEB ambitions to establish eight marine organisms as potent marine genetic model system as part of the Infrastructure for Marine Model Organisms

(IMAGO; www.cemeb.science.gu.se/research/imago-marine-genome-projects). An essential step in this process is to finalize the genome sequence of these eight organisms. We currently have in the order of one tera-base of sequence information in total, mainly based on next generation sequencing platform Illumina, providing a rich source of sequence information based on short reads. We are currently in the process of complementing this source by alternative NGS technologies, e.g. PacBio, and other means to improve the assembly process. In several of the genome projects various novel approaches for genome assembly are currently being tested and optimised, and for some genomes we are now approaching a phase of finalizing and publishing. This two-years post-doc position (with an option of one additional year) aims at supporting annotation and publication, both in scientific journals as well as in local and central databases, of these marine genomes. The work will also include analysis of RAD-sequencing and RNA-seq data. One important aspect of the position is to work closely with the responsible researchers for the various organisms in order to explore the genome sequences for interesting and novel genes and features.

Qualifications/eligibility

We are looking for a highly motivated person with a doctoral degree in bioinformatics or in another relevant area where the research has been focused on sequenced-based analysis. Earlier experience of working with large amounts of NGS sequence data is a necessary requirement.

Criteria/assessment

The qualified candidate shall have experience with the major techniques in Bioinformatics. In addition, you must have used Linux/Unix systems as well as programming in script-based language, such as Perl and/or Python. It is furthermore a merit if you have used or created databases for handling and analyses of sequence data, or if you have earlier experience of analysis of data on population genomics. Understanding of biological evolution and evolutionary processes, extracted from sequence data, is also a merit. The work will to a large extent mean various ways of interacting with researchers outside your own field of expertise, and therefore it is necessary that you have good communication skills. Earlier experience with genome projects is an asset.

For further information please contact

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Professor Kerstin Johansson, e-post: kerstin.johannesson@bioenv.gu.se

Head of Department Per Sunnerhagen, e-post: Per.Sunnerhagen@cmb.gu.se

The application and how to apply

The application shall include:

- Cover letter with an explanation of why you apply for the position
- CV including scientific publications
- Copy of exam certificate
- Two referees (name, telephone no, relation)

For more information and how to apply online see:

http://www.gu.se/english/about_the_university/announcements-in-the-job-application-portal/?languageId=0&disableRedirect=true&id=19144&Dnr=592082&Type=E

Application with reference number: **PER 2014/14**

The application must be received **no later than 4th of February 2014**