The University of Groningen offers a
4-year PhD studentship
On
Complex Trait Analysis

What?	Four-year bursary **PhD position**, fully funded
When?	Available from January 2008
Where?	Groningen Bioinformatics Centre, University of Groningen, The Netherlands

Groningen Bionformatics Centre

The Groningen Bioinformatics Centre (GBiC) is a member of the Groningen Biomolecular Sciences and Biotechnology Institute (GBB) in the Faculty of Mathematics and Natural Sciences of the University of Groningen. The group is truly multidisciplinary and studies a variety of problems in bioinformatics and statistical genetics. It routinely provides analytical support to experimentalists ranging from molecular cell biologists to evolutionary ecologists.

Job description

Project 1: The aim of this PhD position is to help unravel the genetic basis of agriculturally/evolutionary important traits using association- and linkage mapping approaches. The prospective student will be involved in the analysis of data from a large, densely genotyped natural collection of the flowering plant *Arabidopsis thaliana* and a novel multi-family panel of *recombinant* inbred lines. The nature and magnitude of these data will provide an unprecedented high-resolution picture of the genetic variation underlying complex phenotypes and will make it possible to systematically integrate information from natural as well as experimental populations. The task is to build an analytical/computational framework to facilitate such an integrative analysis. As an extension, different types of –omics data will be collected from these populations, which will then be used to reconstruct the molecular networks that link genetic variation to phenotypic variation.

Project 2: DNA methylation is an epigenetic mechanism that leads to changes in gene expression which can be inherited through mitosis, and even through meiosis in some instances. The impact of differential methylation on the variability in complex quantitative traits at the population level is an area of research that is vastly under-explored. The aim of this novel project is to map methylation loci that influence complex phenotypes using tiling array technology. The student will be involved in the computer implementation of statistical methods and is also expected to make creative contributions to the conceptual development of this project.

Requirements

You are a university graduate at MSc level in one of the following disciplines: bioinformatics, statistics, computer science, mathematics, theoretical biology, quantitative genetics, physics, or mathematics. You are expected to have an excellent academic record (supply a list of examination marks from your university study) and be curious, creative and ambitious. You should be able to write scientific articles and reports (to be proven by your graduation thesis or another comparable report) and be fluent in the English language.

Additional information and applications

You can apply for this job until we have found a suitable candidate. For further information and direct applications please contact:

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