UPPSALA
UNIVERSITET

PhD Student position available:
Computational Genetics, Uppsala University

The Department of Medical Biochemistry and Microbiology at Uppsala University seeks a PhD student candidate in Computational Genetics in the research group of Örjan Carlborg.

The selected candidate will be offered a full time four year employment at Uppsala University. The position comes with salary and full benefits of being a Swedish University employee. Up to 20% teaching can be requested annually, in which case the position will be prolonged to five years. The PhD program includes a total of 30 credits (20 weeks) of courses, a few obligatory and most optional, the rest of the program is own research. More information on the PhD program can be found at http://www.imbim.uu.se/Education/Postgraduate+education/information-and-documents/. The starting date is flexible, but the initial plan is for admission during the fall semester of 2018. Review of applications will start immediately and will continue until a suitable candidate has been found.

The research group focus is on studying the genetics of complex traits with a particular emphasis on non-additive genetic inheritance in polygenic genetic architectures. An interdisciplinary, interspecies approach is used, where new genetic models, statistical methods, and bioinformatics approaches are developed to explore experimental data from a range of species – from yeast to plants and domestic animals. We always attempt to make use of the most powerful experimental data available and therefore obtain it from a variety of sources including public repositories, collaborators or by generating it ourselves. This PhD-student project is an important part in this effort and will be performed in this strong, inter-disciplinary research environment. You can find more information about our group at http://katalog.uu.se/organisation/?orgId=X38:50 . During the studies, the PhD candidate will have full access to state of art computing resources and training programs provided by SciLife & Uppsala University. Limited travel funding for attending conference and summer schools are available within the program.

The first half (2 years) of this PhD project is to work with the Virginia lines – a chicken population developed during a long-term (60 year) bi-directional, single-trait selection experiment. This is an excellent model to study the genetic basis of long-term selection response on an adaptive trait that is highly polygenic. Earlier work has shown that selection has acted on a complex genetic architecture including loci with either tightly linked adaptive variants, multiple segregating haplotypes and/or interactions between loci. The PhD student will be involved in efforts to map and model the genetic architectures of the adaptive trait in and its contributions to the long-term selection responses. A valuable resource to the project is a new dataset including approximately 4000 phenotyped, pedigreed and individually low-coverage sequenced individuals from a 19 generation deep advanced intercross line between the divergently selected lines. The later half (2 years) of the project will be decided depending on the interest and competence of the admitted PhD student, and could therefore involve, for example, detailed explorations of specific genetic mechanisms via analyses of data from other species or data simulations, or more focus on development of new models and methods for trait mapping or modeling of genotype-to-phenotype mappings.

Qualifications
MSc in Bioinformatics, Statistics, Computational biology, Quantitative/Population/Evolutionary genetics or similar qualifications is a requirement. If the degree is not complete at the deadline of applications, it should be indicated when it is estimated to be obtained.

Given the analytical content of the project, it is a merit to have good knowledge and experience of both genetics and informatics. This can be shown through earlier research experience in the field. Programming is an important tool in the project and therefore you should have experience in programming in e.g. R, C++, Fortran, Perl, Python or Java. You should have excellent English abilities, both orally and in writing. If you are a mathematician/statistician/computer scientist, complementary knowledge in genetics or genomics is meriting. Knowledge in mathematics/statistics/computer science is in the same way meriting if your exam is in biology.

The letter of interest, including a description of your formal qualifications together with any questions about the PhD project, should be directed to Prof. Örjan Carlborg, Department of Medical Biochemistry and Microbiology, Uppsala University; orjan.carlborg@imbim.uu.se.

Selected references of relevance to the project are:
1. Carlborg, Ö., Jacobsson, L., Åhgren, P., Siegel, P. & Andersson, L. Epistasis and the release of genetic variation during long-term selection. Nat Genet 38, 418–420 (2006).
2. Le Rouzic, A., Siegel, P. B. & Carlborg, Ö. Phenotypic evolution from genetic polymorphisms in a radial network architecture. BMC Biol. 5, 50 (2007).
3. Johansson, A. M., Pettersson, M. E., Siegel, P. B. & Carlborg, Ö. Genome-wide effects of long-term divergent selection. PLoS Genet 6, e1001188 (2010).
4. Pettersson, M., Besnier, F., Siegel, P. B. & Carlborg, Ö. Replication and explorations of high-order epistasis using a large advanced intercross line pedigree. PLoS Genet 7, e1002180 (2011).
5. Sheng, Z., Pettersson, M. E., Honaker, C. F., Siegel, P. B. & Carlborg, Ö. Standing genetic variation as a major contributor to adaptation in the Virginia chicken lines selection experiment. Genome Biol. 16, 219 (2015).
6. Zan, Y. et al. Artificial Selection Response due to Polygenic Adaptation from a Multilocus, Multiallelic Genetic Architecture. Mol Biol Evol 34, 2678–2689 (2017).
7. Forsberg, S. K. G., Bloom, J. S., Sadhu, M. J., Kruglyak, L. & Carlborg, Ö. Accounting for genetic interactions improves modeling of individual quantitative trait phenotypes in yeast. Nat Genet 49, 497–503 (2017).
8. Forsberg, S. K. G. & Carlborg, Ö. On the relationship between epistasis and genetic variance heterogeneity. Journal of Experimental Biology doi:doi:10.1093/jxb/erx283

Örjan Carlborg
Professor in Computational Genomics
Uppsala University

Mailing address:
Department of Medical Biochemistry and Microbiology, Genomics
Box 582
SE-751 23 Uppsala
Sweden

Visiting address:
Uppsala biomedical centre BMC (D11 room 311e)
Husargatan 3
SE-751 23 Uppsala
Sweden

Email: orjan.carlborg@imbim.uu.se
Phone: +46-18-4714592
Web: http://www.uu.se
http://www.imbim.uu.se/Research/+Genomics/carlborg--rjan/?languageId=1
Facebook: http://www.facebook.com/pages/Computationalgenetics/174216822622706
Twitter: @OrjanGenetiker @Uppsalauni
LinkedIn: https://www.linkedin.com/in/örjan-carlborg-822913135