

We seek a dedicated and talented person to join Hans Ellegren's research group at the Evolutionary Biology Centre, Uppsala University, Sweden (<http://www.ieg.uu.se/evolutionsbiologi/ellegren-se/?languageld=1>) as

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bioi

informatician

We work with large-scale genomic approaches to general evolutionary questions such as speciation, DNA sequence evolution and sex chromosome evolution. Our main study system is birds and we have sequenced and assembled the flycatcher genome in house (Ellegren et al 2012 Nature 491:756-760), and were part of the large avian phylogenomics consortium (Jarvis et al 2014 Science 346:1320-1331). By whole-genome re-sequencing of large population samples of different flycatcher species we gather extensive amounts of SNP data and use these for population genomic analyses. The bioinformatician, who will be fully integrated with the research group, will work with genome assembly and detection of structural variation using data from NGS-technologies that provide long (>10 kb) reads. She/he will also be responsible for curation of flycatcher genome sequence data and participate in research projects. The position is initially for one year but can be extended.

It can also

be combined with PhD studies

Suitable background is a BSc or MSc in, for example, bioinformatics or computer science. Experience from working with NGS-data in UNIX environment is of merit, as is familiarity with relevant programming languages (e.g. Perl, Python). To apply for the position, please visit the Uppsala University web site for Open Positions and log in and register your application at <http://uu.se/en/about-uu/join-us/details/?positionId=73431>

Closing date for the application is Sep 20. Please feel free to contact me at Hans.Ellegren@ebc.uu.se

with any questions. Our research group consists of some 15 scientists, including PhD students, post-docs and bioinformaticians. The research is funded by the European Research Council (ERC), Knut and Alice Wallenbergs Foundation and the Swedish Research Council. The venue for the position, the Evolutionary Biology Centre, is situated in central Uppsala. The working atmosphere is international with the great majority of PhD students and post-docs recruited from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Local platforms for high-performance computational analyses (

<https://www.uppmax.uu.se/uppnex>

), NGS, SNP genotyping and proteomic analyses (

<http://www.scilifelab.se>

) ensure immediate access to state-of-the-art technology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful and easy accessible surroundings conveniently situated close to Stockholm. The Ellegren group is part of the Department of Evolutionary Biology (

<http://www.ieg.uu.se/evolutionary-biology/>

), which is a branch of the larger Department of Ecology and Genetics (

<http://www.ieg.uu.se/?languageld=1>

). The Department of Evolutionary Biology houses 8 independent research groups and about 25 PhD students, 25 postdocs, and several bioinformaticians. A common theme is that we address key questions in evolutionary biology, like speciation, local adaptation, life history evolution, genome and molecular evolution, using genomic approaches. We have tight connections with several other research groups in the Department of Ecology and Genetics within the Evolutionary Biology Centre. Professor Hans Ellegren Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvdžgen 18D SE-752 36 Uppsala Sweden Email:

Hans.Ellegren@ebc.uu.se

LAB WEB PAGE:

<http://www.ieg.uu.se/evolutionsbiologi/ellegren-se/?languageld=1>

Two post-doctoral positions in population genomics

Two two-year post-doctoral positions are available in the Ellegren

lab at the Evolutionary Biology Centre, Uppsala University, Sweden (<http://www.ieg.uu.se/evolutionsbiologi/ellegren-se/?languageld=3D1>

). Two positions are broadly defined as population genomics (presented below) and one as molecular evolution, although there is some extent of overlap both in terms of concepts and data used among the positions. 1. Population genomics We use flycatchers of the genus *Ficedula* to study evolutionary processes related to the evolution of heterogeneous genomic landscapes of species differentiation (e.g. Ellegren et al 2012 *Nature* 491:756-760). There is increasing evidence that genomic regions with elevated differentiation ('differentiation islands') can evolve by processes unrelated to speciation. For example, the concept of linked selection, which is particularly pronounced in low-recombining regions, will locally reduce the effective population size and thereby enhance genetic drift of segregating variants. Pursuing these studies using haplotype-based statistics and NGS-data from sequencing platforms generating long reads is one possible direction of research for the post-doc. Other directions include, for example, demographic analyses and studies of the recombination landscape. The specific questions to be addressed will be decided in dialogue with the successful candidate and will depend on her/his interests and background. Recent publications from the group relating to the project include Nadachowska-Brzyska et al 2015 *Current Biology* 25:1375-1380; Nater et al 2015 *Systematic Biology*, in press; Smeds et al. 2015 *Nature Communications* 6:7330; Suh et al 2015 *PLoS Biology* 13:1002224. 2. Population genomics The wolf was once widespread in Scandinavia, as well as in other parts of Europe, but long-term persecution led to its extinction by the 1960s. Two animals founded a new population in Sweden in the 1970s and a limited number of immigrants have subsequently become integrated with the population and it has grown to several hundreds of individuals. The population is highly inbred (inbreeding coefficient of newborns is currently 0.25 on average) and there are signs of inbreeding depression. We are now conducting whole-genome re-sequencing of 100 animals sampled from throughout the

time period since the new population was founded. The post-doc will be responsible for analysing these data with the aims of investigating the rate of allelic loss, the extent and distribution of genomic regions identical-by-descent, the genomic contribution of each founder to the extant population, and to compare genetic relationships derived from the pedigree and genome sequence data. Several other research questions can apply as well. The project is a collaboration with Grimso Wildlife Research Station of the Swedish University of Agricultural Sciences. Suitable background to these position is a PhD geared toward evolutionary biology, population genetics, or bioinformatics. Experience from bioinformatic analyses of next-generation sequencing data is of merit. Depending on the direction of research to be taken, experience of demographic modeling, molecular evolutionary analyses or conservation biology could also be of merit. Start date is flexible, ideally before January 1, 2016. The positions can be extended for up to two more years. For full consideration, please send application materials by September 18, 2015. Interested candidates should submit the following to

Hans.Ellegren@ebc.uu.se

- a cover letter stating research interests, - CV, including publication record - a short (1-2 page) description of research accomplishments, - email addresses and phone numbers of three references Please feel free to contact me at the above email address with questions. The venue for the positions, the Evolutionary Biology Centre, is situated in central Uppsala. The working atmosphere is international with the great majority of PhD students and post-docs recruited from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Local platforms for high-performance computational analyses (

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