Post-doc in statistical genetics - Roslin Institute, University of Edinburgh

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http://www.biometricsociety.net/2015/02/06/post-doc-in-statistical-genetics-roslin-institute-university-of-edinburgh/

Files:

http://bayesian.org/sites/default/files/femnOZ09p

Genetic analysis of infectious disease outbreaks in livestock populations

Post-doc position in the Division of Genetics and Genomics, The Roslin Institute and R(D)SVS, The University of Edinburgh, Scotland, UK.

A post-doc position in statistical genetics is available at the Roslin Institute to determine host genetic influences underlying infectious disease outbreaks in livestock populations. The successful candidate will contribute to two international collaborative projects aiming to determine the genetic basis of infectious disease outbreaks in aquaculture. In particular, we will analyse epidemiological data from diverse fish disease challenge experiments generated within these projects with the aim to quantify genetic susceptibility, infectivity and tolerance of fish to diseases of major importance to the aquaculture industry. The knowledge will be utilized to design new genetic disease control strategies. For this purpose we will implement and further develop a variety of state-of-the art inference methods in statistical genetics applied to time to infection or death as well as to cross-sectional and longitudinal binary disease data, including MCMC methods for quantitative genetics models of infection dynamics recently developed by our team. The work will be carried out in close collaboration with quantitative geneticists and aquaculture specialists in the UK, Spain and Norway. The post-doc will also contribute to the development and application of mathematical simulation models and experimental designs to assess how host genetics affects disease spread and impact in genetically diverse livestock populations.

Qualifications:

The post-holder must have a PhD in a mathematical or statistical discipline with a substantial quantitative component (e.g. mathematics, statistics, theoretical biology or physics, quantitative genetics), together with evidence of skills and training in mathematical modelling and statistical inference.

Essential requirements:

•   Experience of Bayesian statistics, Markov chain Monte Carlo or related techniques for statistical inference of dynamic processes.

•   Excellent programming skills and experience in writing computational code for analysing or modelling dynamic processes.

• Experience in a range of statistical techniques for mixed model analyses of multivariate data. A track record of research outputs, publications in peer reviewed scientific journals and presentations at scientific conferences.

• Excellent written and verbal communication skills; ability to communicate findings to other researchers with different research backgrounds.

The ideal candidate for this post will further have:

• Experience in statistical analysis of genetic or epidemiological data.

• Basic knowledge of quantitative genetics applied to livestock

• A strong interest in multi-disciplinary research and in acquiring new skills.

• Experience in collaboration with scientists from other disciplines.

Application Details:

This post is available immediately from a mutually agreed start date.

Initially the post will be a 16 months full-time contract (or longer part-time position) with a potential for longer-term extension (funding dependent).

If interested, please follow the instructions for "Application procedure" on the Edinburgh website:

https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=032488

The closing date for applications is February 27th 2015. Please send also a current CV, letter of interest, and contact information for 3 references to Dr. Andrea Doeschl- Wilson (andrea.wilson@roslin.ed.ac.uk) by 27. February 2015. If you have questions about the post, us or our work, please contact Dr Andrea Doeschl Wilson (phone +44 -131 – 651 9224 or above email).

Some relevant publications:

Lipschutz-Powell D. et al. 2013. A unifying theory for genetic epidemiological analysis of binary disease data. Genetics Selection Evolution. 46:15

Doeschl-Wilson A.B and Kyriazakis I (2012). Should we aim for genetic improvement in host resistance or tolerance to infectious pathogens?

Editorial to special research topic: Should we aim for genetic improvement of host resistance or tolerance to infectious disease. (eds. Doeschl-Wilson A.B.

and Kyriazakis I.). Front. Gene. 3:272. doi: 10.3389/fgene.2012.00272

Lipschutz-Powell D. et al. 2012. Are we capturing the full heritable variation underlying disease prevalence? PLoS One. 7(6): e39551.

doi:10.1371/journal.pone.0039551

Doeschl-Wilson A.B et al. (2011) Implications of host genetic variation on the risk and prevalence of infectious diseases transmitted through the environment. Genetics. 188: 683-693. doi:10.1534/genetics.110.12562

We are looking forward to hearing from you!

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