

Genomics **postdoc** to study butterfly speciation, with flexibility for the candidate to pursue their own interests within the broad goals of the project. A post-doctoral research associate position in Department of Zoology, located in Central Cambridge on Downing Street, is available from October 2014 for twenty four months, in the first instance, to work with Professor Chris Jiggins on the evolutionary genomics of adaptation and speciation in *Heliconius* butterflies, in collaboration with Dr Owen McMillan at the Smithsonian Tropical Research Institute in Panama. There are three important aspects of the position. First, we are looking for someone to work with the larger *Heliconius* community to finalize the construction of the *H. erato* genome. This genome will be the second full genome sequence available in *Heliconius*, alongside *H. erato*'s co-mimic, *H. melpomene*, and will provide a foundation for broader comparative genomic studies across the radiation. This work will primarily involve validating and improving an existing assembly using genetic linkage data. Second, we are looking for someone to produce a draft assembly of the *H. cydno* genome for comparison to the *H. melpomene* and *H. erato* genomes. The Postdoctoral Research Associate will then use these reference genomes to study adaptation and speciation in the genus. This could include demographic analysis of mimicry and speciation using coalescence-based methods to infer population history from whole-genome sequences and/or analysis of genomic rearrangements and their role in speciation, inferred from population resequence data for *H. erato* and *H. melpomene* species groups. There is considerable scope for the focus of the biological analyses to reflect the interests of the candidate. The research will primarily involve bioinformatic analysis of existing genomic sequence datasets. The successful applicant should have a Ph.D., completed or completion imminent, in evolutionary biology, bioinformatics or a related field, with a strong interest in population genomics. In addition, candidates should have experience with the manipulation and analysis of Illumina data and working knowledge of a programming language such as Python or Perl. Candidates should have a good collaborative spirit, as the work will involve close collaboration with researchers in Cambridge and Panama as well as coordination with many different labs working on *Heliconius* biology, genome assembly and genome databases. Enthusiasm, determination and the capacity to work independently are also essential. Fixed-term: The funds for this post are available for 24 months in the first instance. To apply online for this vacancy, please follow this link

<http://www.jobs.cam.ac.uk/job/4844/>

. or contact me Chris Jiggins for more information: Chris Jiggins <c.jiggins [at]

[zoo.cam.ac.uk](mailto:c.jiggins@zoo.cam.ac.uk)

> Please quote reference PF04195 on your application and in any correspondence about this vacancy. The University values diversity and is committed to equality of opportunity. The University has a responsibility to ensure that all employees are eligible to live and work in the UK.