

Five Postdoctoral Fellowships – Centre for Biodiversity Genomics

The Centre for Biodiversity Genomics (CBG) at the University of Guelph has global leadership in the development and application of DNA-based identification systems for eukaryotes with a focus on the animal kingdom. Based in a 50,000 ft² facility, its unique research capacity reflects the coupling of one of Canada's largest genomics platforms with a workforce that includes world-class expertise in biodiversity science, DNA sequencing, and informatics (visit biodiversitygenomics.net for further details). The CBG seeks five highly qualified postdoctoral fellows to join and strengthen a vibrant research and innovation group. Applicants for these positions must possess a passion for problem solving, the ability to work in a team, and a strong publication record. Ideally, candidates should bring prior experience in biodiversity genomics and in scripting (e.g. Perl, Python, R). These positions have the potential for extension beyond an initial two-year term, subject to annual performance reviews. Applications will be reviewed as they are received. Please send your curriculum vitae, the names of three potential referees, and PDF copies of your two most relevant publications to: <mailto:CBGfellowship@bioiversitygenomics.net>

Multi-species Population Genetics/Genomics

High-throughput sequencing (HTS) of taxon assemblages makes it possible to test hypotheses relating to regional patterns of demographic stability, isolation, and admixture. The successful applicant will join a team developing multi-taxa population genomic models to understand community assembly, colonization, and vicariance based on population-level sequencing data collected across entire taxonomic assemblages. Desirable Background: proficiency with methods in community population genetics; statistical skills; experience in analysing large-scale genetic/genomic data.

Species Distribution Modelling and Spatial Mapping

Large data sets generated by HTS can address current challenges in Species Distribution Modelling while extended matrix regression models (e.g. generalized dissimilarity modelling) can analyse and predict spatial patterns of turnover in community composition. The successful applicant will have a unique opportunity to combine metabarcoding results with ancillary information, such as trait data, to develop process-based models that can identify the functional composition of any location and map expected distributions of ecosystem functions and services. Desirable Background: proficiency with GIS software (ideally ArcGIS); statistical analysis in R; experience in distribution modelling and with predictive algorithms.

Mito-nuclear Interactions

Functional incompatibility between mitochondrial- and nuclear-encoded components of the co-adapted gene complex responsible for oxidative phosphorylation is increasingly recognized as an important cause of post-zygotic isolation. The CBG holds DNA extracts from nearly 400,000 species, providing an exceptional resource for examining nuclear-mitochondrial interactions among both closely allied and distantly related taxa. The successful applicant will use these DNA extracts and our genomics facility to extend understanding of the interactions between nuclear and mitochondrial gene products. Desirable Background: molecular background such as primer design and PCR optimization; HTS and sequence analysis; statistical skills; experience in analysing large-scale genetic/genomic data; experience with technologies such as genome skimming and target enrichment as well as combinations of both (e.g. Hyb-Seq).

Bioinformatics/Phylogenomics

Our team has initiated a collaboration that will strengthen two informatics platforms (BOLD, mBRAVE) developed at the CBG with platforms to support phylogenetic analysis and global ecosystem modelling. The successful applicant will join the implementation team to develop methods for estimating divergence times from DNA barcodes, as well as multi-gene and genome-scale datasets as well as the empirical analysis of large molecular datasets to test hypotheses relating to rates of speciation and molecular evolution. Desirable Background: proficiency with phylogenetic and phylogenomic methods; statistical skills; experience in analysing large-scale genetic/genomic data; proficiency in programming and the use of compute clusters; experience in other programming languages.

Molecular Evolution

About 5% of known species possess deep ‘intraspecific’ divergences at mitochondrial markers (including the DNA barcode region). These cases have several possible explanations; each taxon may represent an assemblage of young species or the deep divergence may truly represent variation in a single species that has arisen as a consequence of the merger of phylogeographic isolates or through rate acceleration. The successful applicant will do broad scans of sequence divergence in the nuclear genome, advancing our understanding of species ages and boundaries thereby helping to discriminate between these alternatives. Desirable Background: molecular background such as primer design and PCR optimization; HTS and sequence analysis; statistical skills; experience in analysing large-scale genetic/genomic data; experience with technologies such as RAD sequencing and genome skimming.

At the University of Guelph, fostering a culture of inclusion is an institutional imperative. The University invites and encourages applications from all qualified individuals, including from groups that are traditionally underrepresented in employment, who may contribute to further diversification of our Institution.