Bioinformatis PhD Position in Gene Expression Evolution of Fireflies

I invite applications for one doctoral position in my research group at the GeoBio-Center of the Ludwig-Maximilians-Universität (LMU), München. The position is part of the DFG SPP "Genomic Basis of Evolutionary Innovations (GEvol)" (https://g-evol.com) which means that you will be part of a large network consisting of 17 projects with 1-2 doctoral students in each project. The topic of our project is gene expression evolution in fireflies (https://g-evol.uni-muenster.de/projectpage/#AnkerFireflies). You will be jointly supervised by Sebastian Höhna (https://hoehnalab.github.io) and Ana Catalán (https://www.anacatalan-evolution.com/). This is a research-only PhD position funded for 3 years (no classes and teaching required but possible). The starting date is flexible between 1st July 2023 and 1st January 2024. This project focuses on gene expression data analysis. Therefore, we strongly encourage evolutionary biologists with a keen interest in bioinformatics/statistics or bioinformaticians with a keen interest in evolutionary biology to apply.

A major part of the wide phenotypic diversity that we observe today can be explained by changes in gene expression. Changes in gene expression have been successfully linked to the variation of different trait types. One of the most extreme differences among species are sexually dimorphic traits, many of which can be linked to sex-biased gene expression. In fireflies, sexual dimorphism has evolved several times independently, which makes fireflies an excellent study system for repeated evolution. In this project we want to explore: Which are the selective pressures acting on gene expression divergence? Are the same genes differentiated for other sexually dimorphic species or does each species have their own set of sex-specific genes? We will try to address this question using RNA-seq of ~15 firefly species from ~6 genera (3 with extreme sexual dimorphism) and performing specific hypothesis tests within a statistical phylogenetic framework. These phylogenetic models will be newly developed within this project.

Your tasks will include:
- Performing bioinformatic analyses to assemble the sex- and tissue-specific gene expression dataset (e.g., Genome and transcriptome *de-novo* assemblies, population genetics, genome wide orthology assessment)
- Implementing our new approach (e.g., as an R package) for gene expression evolution
- Performing simulation studies (e.g., using available R packages)
- Leading and performing the statistical analysis of gene expression evolution
- Writing research articles
- Presenting your work at international conferences

Your required skills:
- A Master's degree or equivalent in Evolutionary Biology, Bioinformatics or a similar field.
- Good communication skills in English
- Good written and oral skills in English
- Highly motivated and independent working

- Basic knowledge in statistical analysis (e.g., a first course in statistical analyses using R)

What we offer:
- Being part of a large network of genome evolution in insects (https://g-evol.com)
- Training in genomics and statistical analysis
- Opportunities to participate at international workshops and conferences
- Working at the LMU Munich, one of Germany's and Europe's top Universities
- standard LMU salary scheme for doctoral students
- benefits such as health care, 30 days of vacation per year, pension, unemployment insurance, child support (if applicable) and parental leave.

LMU Munich is an equal opportunity employer. The University continues to be very successful in increasing the number of female faculty members and strongly encourages applications from female candidates. LMU Munich intends to enhance the diversity of its faculty members. Furthermore, disabled candidates with essentially equal qualifications will be given preference.

Any questions should be directed to Sebastian Höhna (hoehna@lmu.de) or Ana Catalán (catalan@bio.lmu.de). Applications, including a cover letter which states your motivation and research idea (1 page), current CV and names and contact details of two referees should be sent to Sebastian Höhna by the deadline of 31 March 2023.