PhD position in Ancient DNA Bioinformatics
Statistical and Computational Biology Group, Prof. Wegmann, University of Fribourg, Switzerland

Who we are
We are a young, international, interdisciplinary and enthusiastic research group at the University of Fribourg, Switzerland, aiming at understanding the evolutionary and ecological processes shaping the realm of biological diversity we see today. To achieve this, we design and develop new statistical and computational approaches, and apply them to big data from many biological fields. A current focus of the lab is on dedicated tools for ancient DNA (aDNA) bioinformatics and their use to study past human societies.

Your tasks
We develop ATLAS (https://bitbucket.org/wegmannlab/atlas), a dedicated tool to conduct bioinformatic analyses from raw-sequence data to population genomics. We seek a highly motivated PhD student to extend the machine learning models of ATLAS for genotyping, in particular regarding post-mortem damage and recalibration, and to support the analysis of ancient DNA data within larger consortia.

The position is fully funded with a competitive salary for four years, with the possibility to extend by one additional year. The successful candidate should ideally start in Summer 2022. The project does not involve lab work, unless specifically desired by the candidate.

What we offer
We offer a stimulating research environment, well embedded in the strong bioinformatic community in western Switzerland. We are part of the Swiss Institute of Bioinformatics (SIB) and boost excellent research facilities, including state-of-the-art high-performance computational infrastructures. Fribourg is a lively university town with pleasant surroundings (such as the Alps) and an excellent quality of life. It is located only 20 minutes from the capital of Switzerland, Bern, and just a little over an hour from Geneva and Zürich. While some knowledge of German or French is beneficial for living in Switzerland, it is not essential. The working language in our lab and institute is English.

What you bring
You should have a master degree in bioinformatics, computational biology, evolutionary biology, computer science, statistics, physics or a related field, and a strong interest to acquire new skills in programming (C++ and R) and statistical inference, for which we are happy to provide state-of-the-art training. Experience in programming is not strictly required, but a plus. Good knowledge of written and spoken English is expected.

How to apply
To receive full consideration, apply before May 15 2022 at https://forms.gle/7ehFod3uo59CizNx8 with a single PDF file including
- a cover letter with a brief summary of your previous research and motivation for the position,
- a Curriculum Vitae,
- copies of degree certificates and list of coursework, including grades,
- names, addresses and emails of two professional references.

Further information on our lab:
- http://www.wegmannlab.com
- https://www.sib.swiss/daniel-wegmann-group

Recent papers on the topic
- Link et al. (2017) Atlas: analysis tools for low-depth and ancient samples.
- Kousathanas et al. (2017) Inferring heterozygosity from ancient and low coverage genomes.
- Burger et al.(2020) Low prevalence of lactase persistence in bronze age europe indicates ongoing strong selection over the last 3,000 years.
- Broushaki et al. (2016) Early neolithic genomes from the eastern fertile crescent.
- Hofmanová et al. (2016) Early farmers from across europe directly descended from neolithic aegeans.