Bioinformatics Software Developer –
Antimicrobial Resistance in Bacterial Genomes

The Beiko lab at Dalhousie University is seeking a software developer to extend the ARETE project pipeline (https://github.com/fmaguire/arete/) which aims to identify mobile genetic elements in bacterial genomes, and trace their pathways of gene transfer between genomes and across multiple habitats. ARETE is a collaboration between researchers at multiple Canadian universities and government labs (Agriculture and Agri-Food Canada and the Public Health Agency of Canada).

Further development of ARETE will include the incorporation of additional bioinformatics tools, deployment across multiple platforms, and production of visualizations of genomic neighbourhoods, gene content, and trajectories of lateral gene transfer.

The following are essential skills for the position:

- At least a Master's degree in bioinformatics, computer science, or related area
- Experience in cross-platform development (e.g., git/github), and testing, including in the Linux environment
- Coding experience in either Python or R, with links to public repositories such as Github
- Experience with scientific visualization tools (e.g., matplotlib, seaborn, shiny, ggplot2)
- Research experience in a collaborative environment
- Good interpersonal skills and ability to collaborate remotely

The following are highly desirable:

- Experience with bioinformatics software tools and biological sequence databases
- Familiarity with the R statistical software package
- Experience with workflow development in Galaxy, Nextflow, or other tools
- Experience with packaging (conda/docker) deployment

The developer will have the opportunity to be a named author / co-author on ARETE publications. Flexible working arrangements, including part-time appointment, remote work, and flexible working hours, are possible for highly qualified candidates.

The position is funded until September 2022.

Prospective applicants should send a covering letter and academic CV to rbeiko@dal.ca.