Opportunity Title: Bioinformatics Analysis/Computational Biology Internship
Opportunity Reference Code: USDA-APHIS-2022-0061

Organization	U.S. Department of Agriculture (USDA)
Reference Code	USDA-APHIS-2022-0061
How to Apply	*Connect with ORISE...on the GO!* Download the new ORISE GO mobile app in the Apple App Store or Google Play Store to help you stay engaged, connected, and informed during your ORISE experience and beyond!

A complete application consists of:

- An application
- Transcript(s) – For this opportunity, an unofficial transcript or copy of the student academic records printed by the applicant or by academic advisors from internal institution systems may be submitted. All transcripts must be in English or include an official English translation. Click here for detailed information about acceptable transcripts.
- A current resume/CV, including academic history, employment history, relevant experiences, and publication list
- Two educational or professional recommendations. At least one recommendation must be received in order for the mentor to view your application.

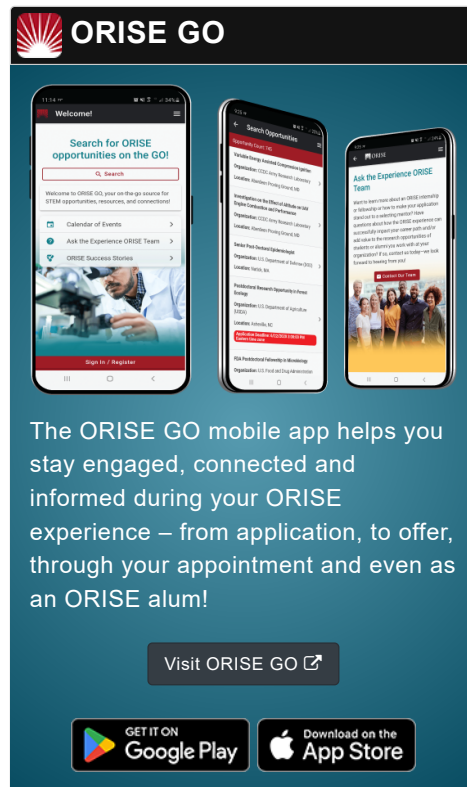All documents must be in English or include an official English translation.

Application Deadline	2/23/2022 3:00:00 PM Eastern Time Zone
Description	***Applications are reviewed on a rolling-basis.***

APHIS Office/Lab and Location: A research opportunity is currently available with the U.S. Department of Agriculture (USDA), Foreign Animal Disease Diagnostic Laboratory (FADDL) at the Plum Island Animal Disease Center located in Orient, New York or the National Bio-and Agro-Defense Facility located in Manhattan, Kansas (possible remote). These facilities diagnose and response to Foreign Animal Disease (FAD) threats to the United States.

Research Project: Recently FADDL has expanded its diagnostic capabilities to include next-generation sequencing technologies using Illumina and Oxford Nanopore sequencing platforms. FADDL utilizes these instruments to produce large amounts of data toward detection and epidemiological characterization of whole viral genomes for the FAD viruses of concern. Activities include but are not limited to:

- Process and analyze genomic datasets using the Linux command line on a distributed HPC system
- Program novel software in Shell, Python, C++ or a similar language to extract diagnostic information from genomic data
- Develop standard operating procedures for genomic diagnostics using their developed software tools
- Summarize, report, and present the results of their work to their mentors and to FADDL at large
- Participate in FADDL team meetings around bioinformatics support for the FADDL diagnostic mission

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Learning Objectives: The selected fellow will learn to analyze and develop novel methods for the analysis of large genomic and epidemiological datasets. The fellow will learn from and collaborate remotely alongside FADDL's experienced team of data scientists, computational biologists, microbiologists and veterinary epidemiologists to develop cutting-edge genomic analytical methods and software. The candidate will learn to work in a High-Performance Computing cluster (HPC) environment and to develop software in the context of bioinformatics analysis, and become proficient to optimize analytical pipelines for diagnostic and epidemiological workflows.

Mentor(s): The mentor for this opportunity is Roger Barrette (roger.w.barrette@usda.gov). If you have questions about the nature of the research please contact the mentor.

Anticipated Appointment Start Date: January 2022. Start date is flexible and will depend on a variety of factors.

Appointment Length: The appointment will initially be for one year but may be renewed upon recommendation of APHIS and is contingent on the availability of funds.

Level of Participation: The appointment is full-time.

Participant Stipend: The participant(s) will receive a monthly stipend as support for their living and other expenses during this appointment. **The annual stipend rate will be determined upon selection and will range between $50,000 and $70,000. Relocation expenses are not available. Candidates will be eligible to receive a health insurance allowance.**

Citizenship Requirements: This opportunity is available to U.S. citizens only.

ORISE Information: This program, administered by ORAU through its contract with the U.S. Department of Energy (DOE) to manage the Oak Ridge Institute for Science and Education (ORISE), was established through an interagency agreement between DOE and APHIS. Participants do not become employees of USDA, APHIS, DOE or the program administrator, and there are no employment-related benefits. Proof of health insurance is required for participation in this program. Health insurance can be obtained through ORISE.

This is an equal opportunity program open to all qualified individuals without regard to race, color, age, sex, religion, national origin, mental or physical disability, genetic information, sexual orientation, or covered veteran's status.

Questions: Please visit our Program Website. After reading, if you have additional questions about the application process please email USDA-APHIS@orau.org and include the reference code for this opportunity.

Qualifications

The qualified candidate should have received a bachelor's degree in one of the relevant fields.

Preferred skills:

- Fluency in programming small software applications using an open-source programming language (e.g. Python, C++,

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    Bash)
- Familiarity with the Linux command line and operating system
- A basic understanding of genomic data produced by next-generation sequencers (FASTA/FASTQ format files, SAM files, etc.)
- A basic understanding of microbiology (e.g. DNA/RNA, types of viruses, gene translation)
- Proficiency in technical writing, oral communication, interpersonal and organizational skills, and critical thinking skills used to analyze and interpret data
- Flexibility and motivation to complete assigned tasks in a remote work environment
- Eagerness to learn from peers and to work in a scientific team environment
- Proficiency using basic word processing and data management software
- Specific experience analyzing Illumina and/or Oxford Nanopore sequencing data
- Knowledge of bioinformatics pipeline languages (e.g. Nextflow) and containerization software (e.g. Singularity)
- An understanding of genomes, how they are annotated, and the national databases that maintain them (e.g. NCBI GenBank)
- Experience working with HPC systems
- A code portfolio demonstrating the above skill

Eligibility Requirements

- **Citizenship:** U.S. Citizen Only
- **Degree:** Bachelor's Degree.
- **Discipline(s):**
  - **Computer, Information, and Data Sciences** (17 👁)
  - **Life Health and Medical Sciences** (48 👁)
  - **Mathematics and Statistics** (11 👁)