Description
This intermediate-level course will provide bioinformatics training to public health laboratorians with a microbiology background. This training will give the theory and background on next generation sequencing and the fundamental analytical approaches. In addition to the theory, this course will give hands-on experience with some of the common analysis tools. Attendees are expected to complete some prerequisite materials prior to the course; participants will have access to virtual office hours with instructors and resources upon course completion.

Objectives
At the conclusion of this course, the participant will be able to:
• Understand and use in practice the basic theory behind assembly, analysis, and QC tools used in modern bioinformatics analysis
• Explain and interpret the results of these tools to laboratorians and epidemiologists.
• Discuss the strengths and weaknesses of the specific types of tools used for different pathogens and how this can impact interpretation.
• Evaluate and compare new and alternative analytical tools as they become available.

Audience
This course is intended for microbiologists who routinely generate and analyze NGS data and have some experience with basic bioinformatic analysis. Participants should have access to a Linux operating system and/or have the infrastructure in place to utilize the tools discussed in this course upon return to the laboratory.

Continuing Education
The Association of Public Health Laboratories (APHL) is approved as a provider of continuing education programs in the clinical laboratory sciences by the ASCLS P.A.C.E. Program.

Location
Centers for Disease Control and Prevention, Atlanta, GA

Security Clearance Requirements
Non-US Citizens - These courses will be held at the training laboratory on the CDC Roybal campus. Due to CDC requirements for security clearance, all non-US citizens will be asked to provide information needed to obtain clearance. Detailed instructions will be provided upon acceptance into the course. Please do not make any non-refundable travel plans until you have received confirmation of acceptance into the course and security clearance approval. The information you provide will be used for the purposes of attending this course.

Application and Registration
Application Deadline: October 9th.
• The preliminary application is to be completed online. Only completed applications received by the deadline will be considered. Application does not guarantee acceptance. If you are unable to complete the application online, email Christin Hanigan or call 240-485-2748
• Public health applicants must have approval from their state or local laboratory director to apply. Students will be selected according to the degree to which the applicant’s job description, experience, and responsibilities are consistent with the prerequisites. Priority will be given for one applicant per public health laboratory, with a second person considered on a space available basis.
• Notification of acceptance status will be sent via email after October 22nd
• All costs for this for this workshop including registration, travel support, per diem, housing etc. will be covered by APHL. Registration and logistical details will be provided upon acceptance into the course.
• Some states have lengthy travel approval processes so begin as soon as possible. Do NOT make travel arrangements until you are notified of acceptance into the course.

Questions?
Contact Christin Hanigan
Preliminary Agenda:

Day 1  Monday
Morning:
- Introduction to bacterial genomics
  - DNA replication
  - Molecular evolutionary principles
  - Variant generation
  - Chromosome vs. plasmid sequencing
- Laboratory and sequencing techniques
  - Nucleic acid extraction
  - Sanger sequencing
- Next Gen sequencing
  - Short read (Illumina)
  - Long read (PacBio, MinION)
- Quality control of NGS data
Afternoon:
- Introduction to bioinformatics analysis
  - Overview of commonly used bioinformatics tools
  - Stringing tools into pipelines
  - Ensuring pipeline reproducibility and access: introduction to github and wrappers (BioNumerics/NCBI pathogen detection)

Day 2  Tuesday
Morning:
- Introduction to the Linux environment
- Basic file handling and file permissions
- Basics of pipelining
Afternoon:
- Genome assembly
  - Bioinformatics algorithms for assembling NGS data
  - De novo genome assembly
- Sequence Alignment and Searching
  - Pairwise sequence alignment
  - Searching databases using BLAST
  - Multiple Sequence Alignment
- Whole Genome Alignment

Day 3  Wednesday
Morning:
- Multi-locus sequence typing (MLST)
- Read-to-genome mapping
- Variant calling
Afternoon:
- Pathogen Characterization and Annotation

Day 4  Thursday
Morning:
- Quality control considerations for bioinformatics analysis
- Evaluation and comparison of other bioinformatics tools
Afternoon:
- Communication and interpreting data for other users (e.g. other laboratorians, epidemiologists, etc.)
- Practical examples and hands-on exercises

Potential Faculty:
- Tiffany Hsu, Ph.D., APHL-CDC Bioinformatics Fellow, MA PHL
- Kevin Libuit, MS, Senior Informatics Scientist, VA DCLS
- Duncan MacCannell, Ph.D., Chief Science Officer, CDC OAMD
- Kelly Oakeson, Ph.D. Chief Scientist: Bioinformatics and Next Generation Sequencing UT PHL
- Scott Sammons, Bioinformatician, CDC OAMD
- Joel Sevinsky, Ph.D. Head of Molecular Science Laboratory at CO PHL
- Xiong (Sean) Wang, Ph.D., Supervisor of sequencing and bioinformatics at MN PHL

Special Needs
In compliance with the Americans with Disabilities Act (ADA), individuals seeking special accommodations should submit their request in writing at least three weeks prior to the start date of the workshop to Christin Hanigan.

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