Mycobacterium tuberculosis NGS made easy: data analysis step-by-step

A capacity development initiative by TB-CAPT, PanACEA and Seq&Treat

Date: 9th-13th of January 2023

Costs: Free of charge

Location: Under https://gallantries.github.io/video-library/events/mtb-ngs/program.html

Registration: Please register to receive the links to the webinars and to participate in the hands-on trainings **here**. Registration closes on the 27th of November 2022. The number of participants is limited to 40. Registrations will be accepted on a first-come, first-served basis

About the event

TB-CAPT, PanACEA and SeqTreat are delighted to offer a series of trainings to improve basic and applied knowledge associated with next-generation sequencing (NGS) technologies and their applications in the field of tuberculosis (TB). The trainings will introduce scalable and reproducible data analysis with Galaxy. The sessions will be pre-recorded and provided in advance. They will have a strong practical component with hands-on tutorials and the possibility to interact with experts through chat and live Q&A sessions.

The goal of this workshop is to build capacity in data analysis and interpretation of NGS applied to TB. The workshop will teach participants how to:
- differentiate sequencing technologies and which ones are most commonly applied in TB (Day 1)
- implement NGS into TB laboratories (Day 1)
- do whole-genome sequence analysis (Day 2)
- detect drug resistance conferring mutations, build phylogenetic trees and infer direct transmission (Day 3)
- use different web tools dedicated to targeted analysis and what it takes to do bioinformatics (Day 4)

After the trainings all participants are expected to know how to call genomic variants, identify drug resistant mutations, use web applications designed for mycobacterium tuberculosis (M tb) and draw genetic relationships.

Who can participate?

The training series is tailored to the interests of the members of the organising projects and provides a general introduction to the topic and targets primarily TB laboratory staff and technical staff at national TB programs, clinicians and researchers at any career level, and do not require previous experience on the use of NGS.

Format

Virtual and asynchronous webinars and hands-on tutorials to be completed during the duration of the training. All training sessions will be pre-recorded and provided in advance. The hands-on tutorials can be completed at the participants own pace during each day. Live support by experts via chat and real time Q&A sessions will be provided. All materials will remain accessible and open after the event. You can choose attending the complete workshop or only selected sessions, however, certificates of attendance will be given to all participants who completed all four days of training.

Program

A preliminary program is described below, approximate time for completion of each session are provided and might differ for each participant. We suggest that you consider blocking four complete days. Experts will be available every day at times to be defined. A definitive program will be made available shortly before the event.

Day 1 – *9th of January*

Overview of NGS technologies & TB specific solutions. Implementation of NGS into TB laboratories (Trainers: Dr Andrea Cabibbe, OSR)
- Webinar 1: Overview of NGS technologies & TB specific NGS solutions (1,5h)
- Webinar 2: WHO documents on NGS for TB and implementation considerations (1,5h)
- Live Q&A session (2h)

Day 2 – *10th of January*

Mapping and variant calling of Illumina reads (Trainers: Dr Daniela Brites, Swiss TPH & Galaxy instructors)
- Webinar and hands-on tutorials: Introduction to Galaxy (1,5 h)
- Webinar and hands-on tutorials: Mapping and variant calling of Illumina reads (4h)
- 2 x Live Q&A sessions (optional): (2x1h)

Day 3 – *11th of January*

Evolutionary epidemiology: using phylogenetics to understand DR emergence and M tb transmission (Trainers: Dr Galo A. Goig)
- Webinar & hands-on: Predicting DR (1h)
- Webinar & hands-on: Clustering as proxy to transmission (1h)
- Hands-on: Inferring phylogenetic trees (1h)
- 2 x Live Q&A sessions (optional) (2x1h)

Day 4 – *12th of January*

Web tools dedicated to M tb bioinformatic analysis & Be a bioinformatician in the jungle (Trainers: Dr. Arash Ghodousi)
- Webinars: Web tools for analysis of MTBC sequenced data (1h)
- Webinar: introduction to MTBseq pipeline (30min)
- Hands-on: Data analysis using the webtools (45 min)
- Webinars: Introduction to Linux & how to use it (1h)
- Webinar: How to run programs (python, docker, singularity) (30 min)
- Hands-on: Using the bash-command (30 min)
- 2 x Live Q&A sessions (optional) (2x1h)

Day 5 (optional) – *13th of January*

Live Q&A: Discussion & Troubleshooting: 9:00-13:00 CET