Webinar Sesi Perkongsian Latihan Luar Negara Bil. 1 / 2025

Joint FAO/IAEA Programme
Nuclear Techniques in Food and Agriculture

Training Course for

Veterinary Diagnostic Laboratory Network (VETLAB)

Next Generation Sequencing (NGS) and Nanopore Sequencing Applications For the Detection and Characterization of Pathogens

IAEA Laboratories, Seibersdorf, Austria
18 to 29 November 2024

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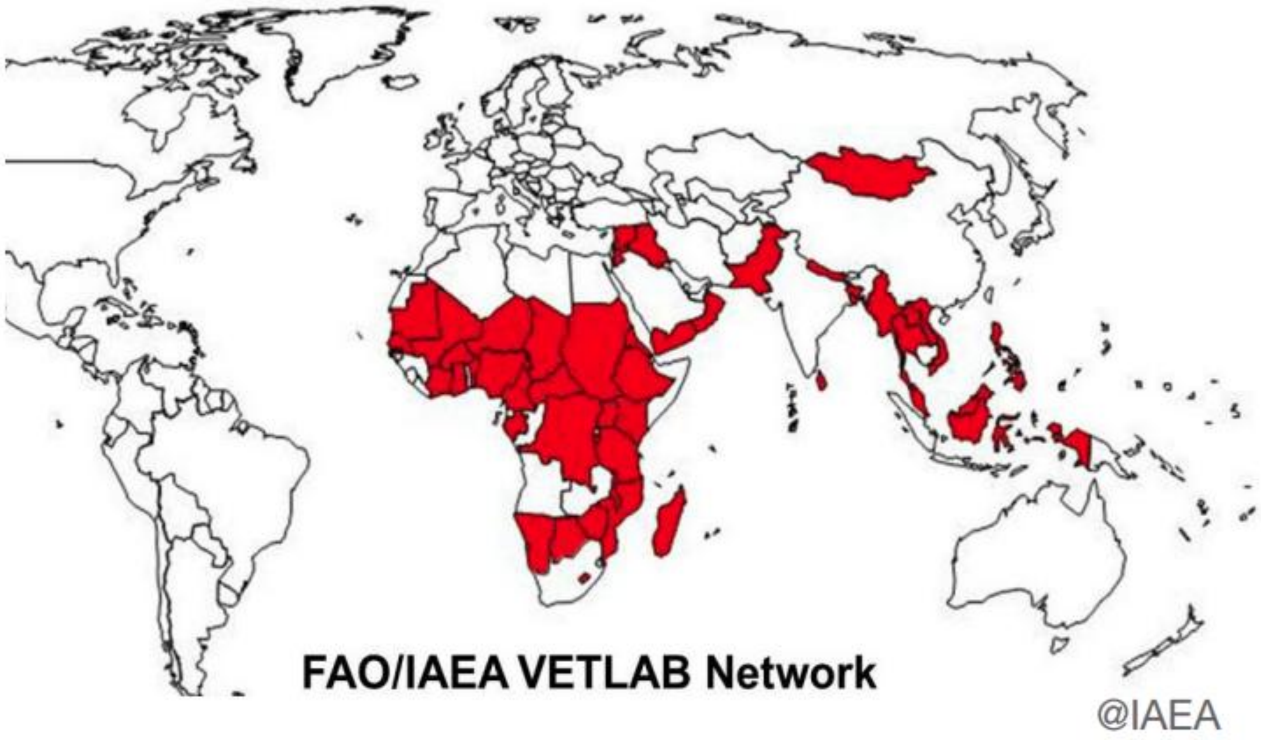
PENGENALAN KURSUS



To strengthen the **Veterinary Diagnostic Laboratory Network (VETLAB)** partners' capacities for using **new sequencing technologies** and **bioinformatics tools** in the characterization and molecular surveillance of major pathogens causing transboundary animal diseases and zoonoses.

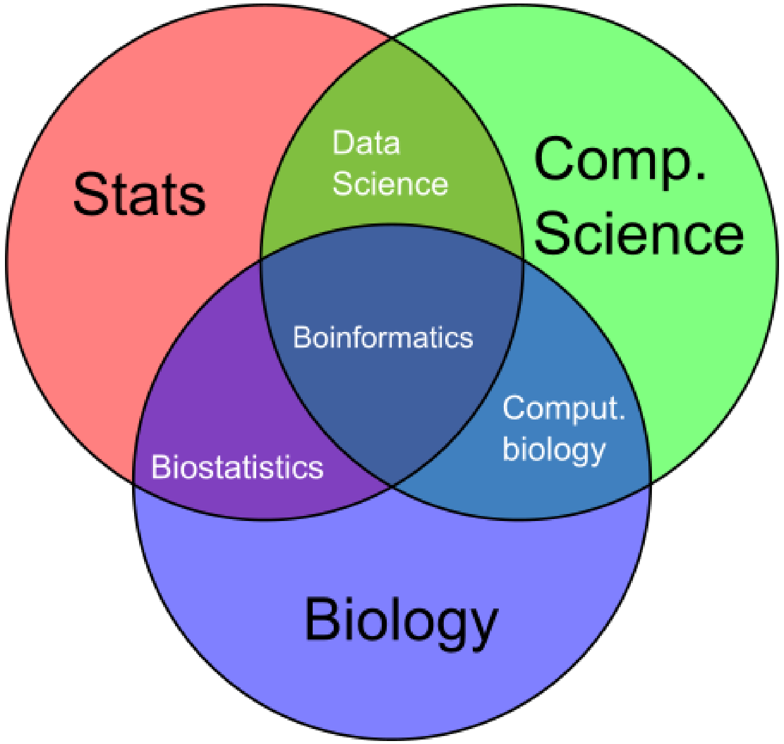
NEW SEQUENCING TECHNOLOGY

1. Advanced **method** used to **determine the sequence of DNA or RNA** molecules.
2. Reading the **genetic code** of organisms, **explore**, **analyze** and **provide information.**

First generation	Second generation (next generation sequencing)	Third generation
Sanger sequencing Maxam and Gilbert Sanger chain termination	454, Solexa, Ion Torrent, Illumina	PacBio Oxford Nanopore
Infer nucleotide identity using dNTPs, then visualize with electrophoresis	High throughput from the parallelization of sequencing reactions	Sequence native DNA in real time with single-molecule resolution
500–1,000 bp fragments	~50–500 bp fragments	Tens of kb fragments, on average

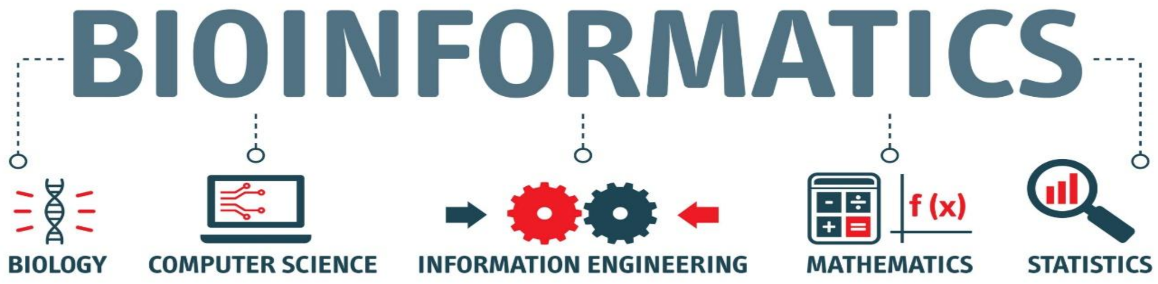
NEXT GENERATION SEQUENCING (NGS)

BIOINFORMATICS



Bioinformatics adalah **aplikasi teknologi berkomputer** yang digunakan dalam **pengurusan maklumat/data biologi** termasuklah **menganalisa**, **meninterpretasi** serta penciptaan dan penyelenggaraan **pengkalan data** maklumat biologi.

Gabungan beberapa bidang seperti statistik, sains komputer, dan biologi.

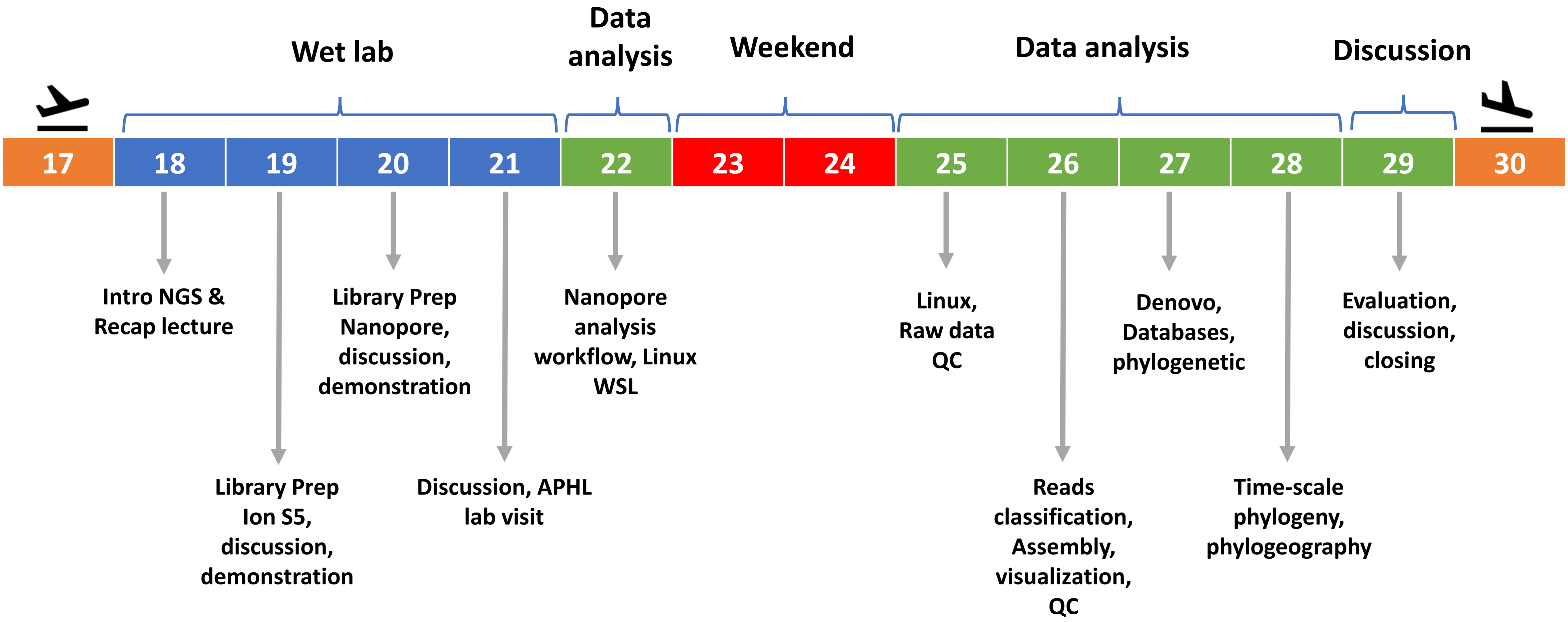


PENGAJAR & PESERTA KURSUS

1. Charles E. LAMIEN, APHL, IAEA
2. Irene MEKI, APHL, IAEA
3. Bharani SETTYPALI, APHL, IAEA
4. William DUNDON, APHL, IAEA
5. Bo LIU, APHL, IAEA
6. Taichiro TAKEMURA APHL, IAEA
7. Vincent APPIAH, University of Ghana
8. Anna Signe FOMSGAARD, Institut Pasteur du Cambodge, Cambodia
9. Tommy LAM, Hong Kong University
10. Zoe SONG, Hong Kong University

1. Ms Dimpho Tladi, Botswana
2. Mr Abel Wade, Cameroon
3. Ms Esther Guladys Kougang, Cameroon
4. Ms Aregitu Mekuriaw Arega, Ethiopia
5. Mr Getachew Abichu Duressa, Ethiopia
6. Mr Daniel Nana Yaw Tawiah-Yingar, Ghana
7. Mr Audi Tri Harsono, Indonesia
8. Ms Diana NURJANAH, Indonesia
9. Ms Lestari, Indonesia
10. Mr Mohammad Masrin Bin Azami, Malaysia
11. Mr Batdolgor Tserendorj, Mongolia
12. Mr Aissa Saidi, Morocco
13. Ms Hasnae Zekhnini, Morocco
14. Ms Josephina Ndamonako Kambode, Namibia
15. Ms Aida Diop, Senegal
16. Ms Kultyarat Bhakha, Thailand
17. Ms Nalinee Hongchumpon, Thailand
18. Ms Salma Ben Yahia Barbria, Tunisia
19. Ms Thi Vui Dam, Viet Nam
20. Mr George Dautu, Zambia

JADUAL KURSUS



KANDUNGAN KURSUS - Makmal

Ion GeneStudio S5

Ion Chef (Library Prep)

1. DNA fragmentation
2. Adapter ligation
3. Size selection
4. PCR amplification
5. Template preparation and loading
6. Sequencing

R10

Nanopore MinIon

Mk1b

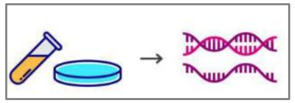
Native barcoding kit (1-24 BC)

1. DNA repair
2. Barcode ligation
3. Adapter ligation
4. Cleanup
5. Flow cell preparation and loading
6. Sequencing

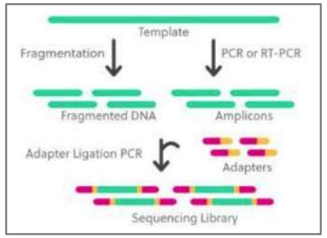
Bento Lab

- 4 in 1 lab.
- Compact, all-in-one molecular biology workstation
- Gel electrophoresis, Transilluminator, Thermocycler, Centrifuge

KANDUNGAN KURSUS – Analisa data

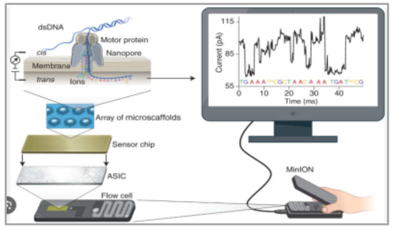


Sample Preparation

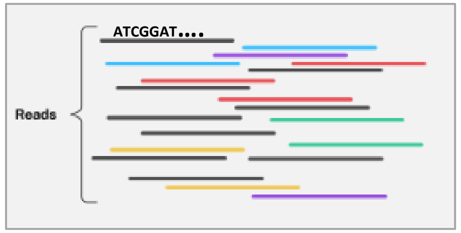


Library Preparation

Wet Laboratory



Sequencing

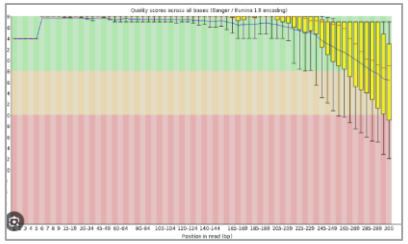


Raw reads

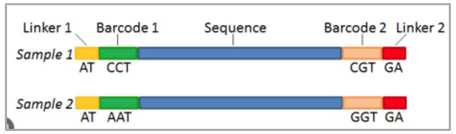
Complete Sequence / WGS

Dry Laboratory / Computing

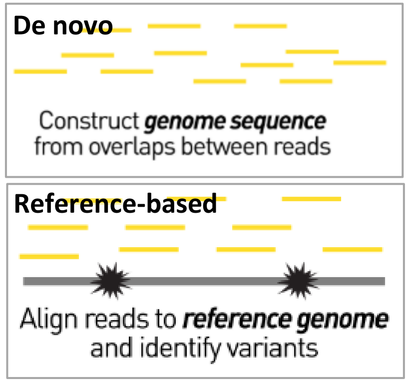
Raw Metagenomic



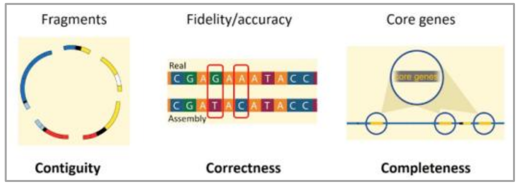
QC check



Trim & filtering



Assembly



QC

WGS

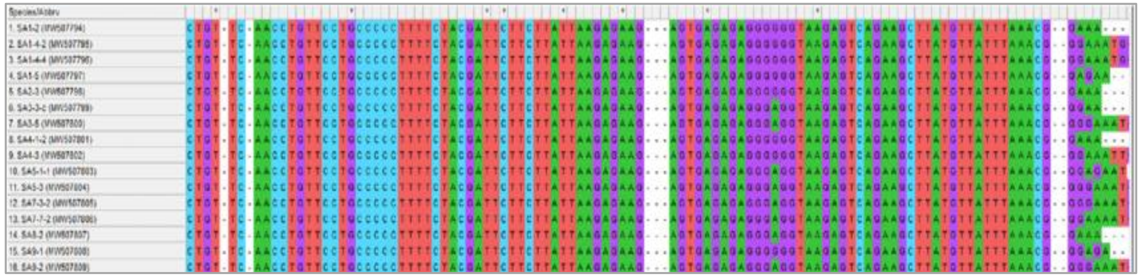
1 → 2 → 3 → 4 → 5 → 6

Remove: Host DNA, Barcode, Adapter, Low quality reads

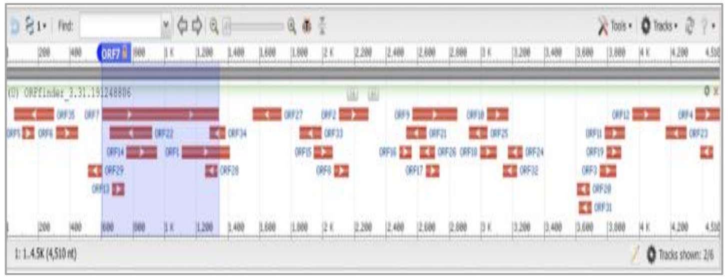
Downstream analysis

KANDUNGAN KURSUS – Analisa data

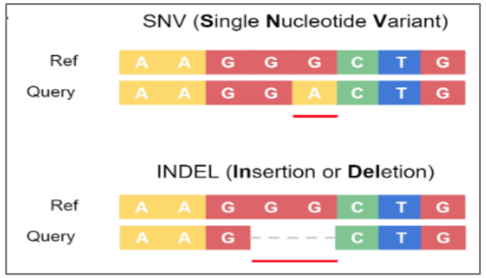
Downstream analysis



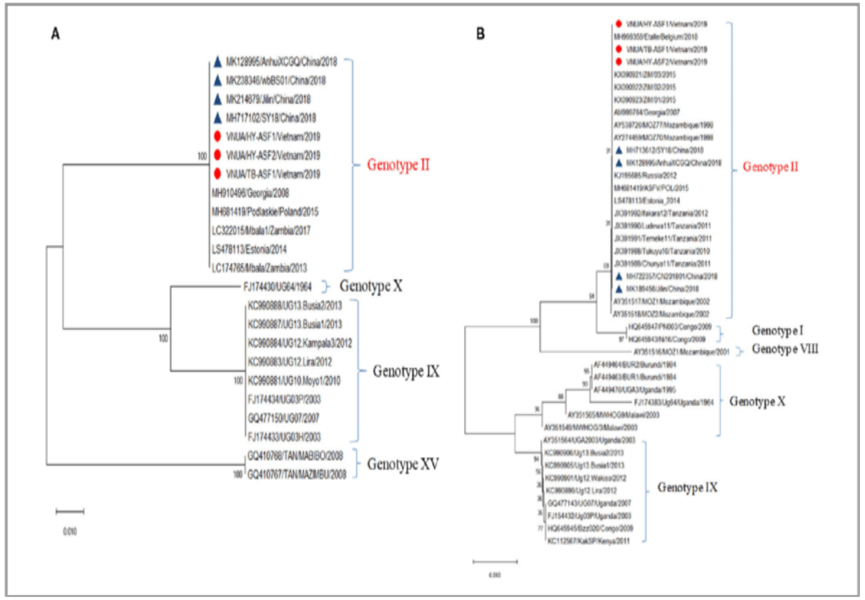
Alignment



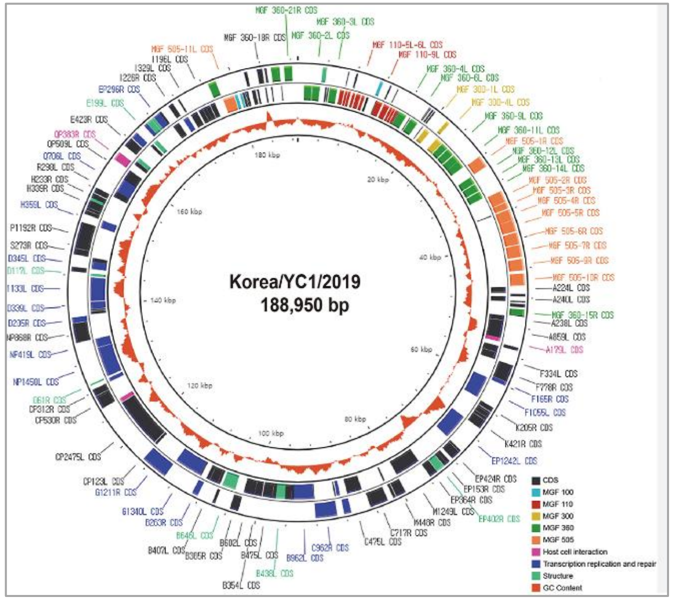
ORF finder



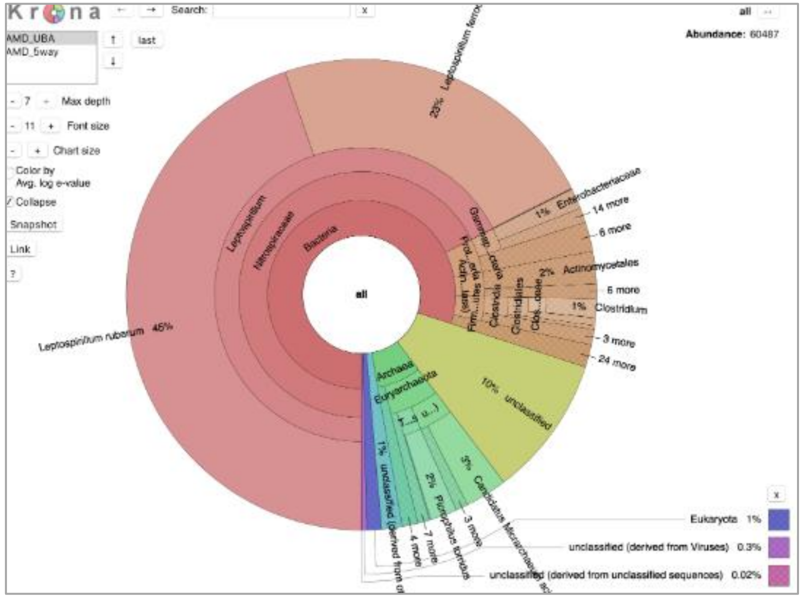
Variant



Phylogenetics



Gene Annotation



Metagenomic Classification

KANDUNGAN KURSUS – Analisa data

Nucleotide Databases

EMBL
European Molecular Biology Laboratory

ndb NUCLEIC ACID DATABASE

NCBI
GenBank

GSA
Genome Sequence Archive

NCBI
dbSNP

DDBJ
DNA Data Bank of Japan

Kursus Analisa Bioinformatik - IAEA

Beginner	Intermediate	Advanced	Trainer
2023	**2024**	**2025**	**2026**
20 Nov – 1 Dec 2023 VETLAB Next Generation Sequencing (NGS) Bioinformatics And Molecular Phylogeny	**18 -29 Nov 2024** VETLAB Next Generation Sequencing (NGS) and Nanopore Sequencing Applications For the Detection and Characterization of Pathogens	**10 – 21 Nov 2025** VETLAB Next Generation Sequencing (NGS) Applications and Bioinformatics	**TBC** VETLAB Next Generation Sequencing (NGS) Train the Trainers

- Concept of NGS
- NGS Equipment
- Library preparation
- Understanding analysis workflow
- Bioinformatics file format
- Type of data analysis
- Setting up analysis environment
- Open-source resources
- Databases
- Quality control
- Analysis tools & software
- Linux & CLI
- Basic analysis

- Recap
- Update on current NGS technologies
- Metagenomic data classification & analysis.
- Build analysis pipeline
- Analysis based on single-end and paired-end data
- Phylogenetics
- Time-scaled & Phylogeography
- Genome local database setup
- Genome annotation
- Variant analysis
- Quality control
- Data visualization
- Analysis tools & software
- Linux, CLI & Scripting

PENAMBAHBAIKAN KEPADA JABATAN

1. Meningkatkan pengetahuan dan kepakaran dalam teknologi dan kaedah analisa bioinformatic / NGS.
2. Mewujudkan jalinan kerjasama (networking) di kalangan pakar dan peserta kursus.
3. Mewujudkan idea-idea baru yang boleh diaplikasikan pada aktiviti R&D yang boleh memberi impak kepada jabatan.
4. Berkongsi ilmu dan skil yang diperoleh kepada kakitangan jabatan melalui seminar / bengkel.

TERIMA KASIH