



Organizing committee

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For any enquiry or question regarding the training workshop, please contact the training secretaries.

Resource persons



Prof. Dr. Daniel Schachtman, Director Center of Biotechnology, University of Nebraska, USA



Dr. Jean-Jack Riethoven, Head of Bioinformatics, Center of Biotechnology, University of Nebraska, USA



Dr. Tariq Shahzad, Plant Genome Mapping Lab, Center for Applied Genetic Technologies, University of Georgia, Athen, Georgia, USA



Dr. Abdul Latif Khan, Natural and Medical Sciences Research Center, University of Nizwa, Nizwa, Oman



Prof. Xiyin Wang, Professor & Dean, North China University of Science and Technology, China



Dr. Sajjad Asaf, Natural and Medical Sciences Research Center, University of Nizwa, Nizwa, Oman



Dr. Ellen Marsh, Center of Biotechnology, University of Nebraska, USA



Dr. Tapan Mohanta, Natural and Medical Sciences Research Center, University of Nizwa, Nizwa, Oman



Feb 17-20, 2019

Training Workshop on Genomics and Bioinformatics Techniques

Venue: University of Nizwa
Natural & Medical Sciences Research Center
University of Nizwa, Nizwa, Sultanate of Oman
Date: Feb 17-20, 2019



PRELIMINARY PROGRAMME OF THE TRAINING WORKSHOP

Day 1 (17/02/2019) Metagenomics

08:00-9:00 Registration and attendance

9:00-10:00 Opening ceremony

Introduction to Bioinformatics

10:00-11:00 Bioinformatics

Prof Xiyin Wang

Learning objects

1. Introduction to computational biology (Bioinformatics)
2. Online resources and biological data analysis
3. Basic tools like alignment and biological database search and retrieve data

10:30-11:00 Tea/Coffee break

Session 1: Microbiomics

11:00- 1:00 Microbiomics: soil, plant and environment

Prof. Dr. Daniel Schachtman

Learning objects

1. What is microbiome, its role and function and human use values
2. Microbial community profiling: example(s)
3. Interpret metagenomic data in biological context
4. Define a marker gene (16s rRNA, 18s rRNA, ITS1/2) and its taxonomic relevance.

1:00-14:00 Lunch

Session 2: Training on QIIME 2

2:00- 5:00 Metagenomic NGS data handling

Dr. Jean-Jack Riethoven

Learning objects

1. Reference mapping / alignment
2. Apply reference mapping to assess community structure
3. Taxonomic profiling
4. Compare taxonomic profiling using metagenomics and amplicon-based approaches
5. Functional profiling
6. Use tools to perform functional annotations of nucleic acid and protein sequences found in metagenomics datasets.
7. Ecological measurements/indexes: Alpha diversity (Chao, Simpson, etc.)
8. Understand and assess the overall quality of NGS (FastQ format) sequence reads
9. Apply a marker gene analysis workflow

Day 2 (18/02/2019) Genomics

Session 1

8:00 – 10:30 Plant genomics and chromosomal analysis

Prof. Dr. Xiyin Wang

Learning objects

1. Introduction to Next Generation Sequencing
2. Describe the recent advances in plant genomics
3. Explain the current genomics technologies and illustrate how these can be used to study gene function.
4. *De novo* assembly and functional annotation
5. Obtain and analyze information and data relating to specific genes using a number of general and plant-specific databases.
6. Analyze information from plant genomics research and recognize its potential
7. Applications in crop improvement

10:30-11:00 Tea/Coffee break

Session 2

11:00- 1:00 Genomic tools: Genotyping by sequencing

Dr. Tariq Shehzad

Learning objects

1. Population genetics
2. To understand the connection between genes and phenotypic traits, genetic mapping.
3. Need for modifying genotyping-by-sequencing (GBS)
4. To understand how genotyping-by-sequencing has facilitated large-scale population genetic analyses by providing a simpler way to survey segregating genetic variation in natural populations.
5. Bioinformatics pipelines.
6. Applications of genotyping-by-sequencing

1:00- 2:00 Lunch



Session 3

2:00-4:00 Genome *De-Novo* and reference assembly analysis

Dr. Jean-Jack Riethoven

Learning objects

1. *De-novo* assembly strategies (SSAKE, Velvet etc)
2. Understand reference assembly
3. Understand genome annotation (Structural and functional)
4. Manual and automated pipeline annotation
5. Understand Gene prediction software's
6. Understand annotation software (BLAST2GO and Manually)
7. Repeat masking
8. Genome annotation tools
9. Genome submission to NCBI

4:00-5:00 Best lab management practices for NGS Lab

Dr. Ellen Marsh

Learning objects

1. Choice of genes to be tested and choice of platforms to be used
2. Specimen handling
3. Nucleic acid extraction, quantification and storage
4. Sample labeling and identity tracking
5. Library preparation
6. Data analysis and sequence reads
7. Reporting



Day 3 (19/02/2019) Transcriptomics

Session 1

8:00 – 10:30 Total transcriptomics

Prof. Dr. Xiyin Wang

10:30-11:00 Tea/Coffee break

Session 2

11:00- 1:00 Transcriptome sequencing

Dr. Tariq Shehzad

Learning objects

1. Transcriptome sequencing and crop improvement
2. Analysis of transcript profiles
3. Expression profiling and abiotic/biotic stresses

1:00- 2:00 Lunch

Session 3

2:00-4:00 Transcriptome *De-Novo* assembly analysis

Dr. Jean-Jack Riethoven

Learning objects

1. Example workflow via Trinity
2. Methods for quality and completeness analysis of transcripts
3. Annotation of transcripts
4. Differential gene expression analysis without reference genome

Session 4

4:00-5:00 A tour at the Laboratories of Natural and Medical Sciences Research Center, University of Nizwa.



Day 4 (20/02/2019) Training practice session

Session 1

8:00 – 11:00 Training practice

Learning objects

- Form groups of three or four participants.
- Each group needs to design and deliver a 15-minute training session.
- In your groups select one of the active learning techniques (presented in workshop) that you would like to use to deliver your training session on day four.
- Groups can only select one active learning technique and can use a maximum of 5 PowerPoint slides as part of the session. Each group must choose a different activity to prepare and deliver – no two groups can select the same activity of training session.
- Each group is responsible for deciding what visual aids, resources and/or equipment are needed for their training sessions and to notify the workshop administrator and/or trainer(s).
- Each member of the group is expected to actively participate in the training session. Do not leave all the work to one person!
- Each group when not running a training session will be expected to observe the other group training sessions and provide feedback using an observation checklist (an example copies of which can be found overleaf). It is recommended that groups also refer to the checklist when designing their own training sessions.
- The trainers of this training workshop will act as observers only but will provide feedback as part of learning process.

Session 2

11:00 – 12:30 Closing remarks and certificates awarding ceremony

