## **Requirements from trainees**

- Affiliated with a national research programs or universities in Oman and GCC
- Currently engaged in biosciences or medical sciences and planning to implement next generation sequencing methods in research
- A minimum of MSc in biological sciences
- •Good working knowledge of written and spoken English
- Basic skills with computers
- Must bring their laptops for training

## Training delivery modules and facilities

- Online material, databases and related articles
- Course modules and materials on each topic
- Theory lectures
- Practical skills on supercomputing facilities at USA
- Tasks, analysis and evaluation
- Wi-Fi and internet
- Food (lunch and Coffee)
- Accommodation is not included
- Pick & Drop from specific hotels around the University of Nizwa

## Workshop fee

- Online distance learning 100 US\$
- Participants: Students (260US\$ or 100/-OMR) Faculty/staff/post-doc (150/-OMR)

# Important date

Last call for registration 1st of Feb 2018

# **Key Course topics**

- Soil and plant microbiome
- Whole genome sequencing and analysis
- Transcriptomic analysis
- Metagenomic analysis of soil data set(microbiome)
- Plant physiological and genomic interactions

## **Expected skills outcomes**

- Understanding genomic and
- transcriptomics data sets
- Analysis techniques for next generationbased sequence data
- Learning command-based OMICs tool for genome annotation, architecture, gene composition, sequence alignments, trimming, filtering, de novo assembly, digital gene expressions



## Introduction

Genomics involves the study of genes, gene functions and whole genomes of organisms, and incorporates elements from genetics. It deals with the systematic use of genome information, associated with other data, to provide answers in biology, medicine, and industry. Genomics uses a combination of molecular biology, DNA sequencing methods, and bioinformatics to sequence, assemble, and analyze the structure and function of genomes. Bioinformatics is the application of computational tools to organize, analyze and visualize biological data. It is an interdisciplinary research area at the interface between computer science and biological science.

# Training objectives

• To build capacities of researchers / scientists / students in bioinformatics tools for analyzing genomic sequence data to understand microbial communities, genome annotation, and gene expression analysis.

• To establish a group of researchers / scientists / students to develop and establish future joint projects on bioinformatics and genome sequence analysis.







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



## **Organizing committee**

#### Training Mentor:

Prof. Dr. Ahmed Al-Harrasi. Vice Chancellor for Research, Graduate Studies and External Affairs. University of Nizwa, Nizwa Tel (office): +968-25446328 Email: aharrasi@unizwa.edu.om

#### Training coordinator:

Dr. Abdul Latif Khan. Associate Professor at Natural and Medical Sciences Research Center. University of Nizwa, Nizwa Oman Tel (office): +968-25446358 Mobile: +968-95486703 Email: abdullatif@unizwa.edu.om

Training Secretaries:

Mr. Ahmed Al-Rawahi. Research assistant at Natural and Medical Sciences Research Center, University of Nizwa, Nizwa Tel (office): +968-25446974 Mobile: +968-95192191 Email: ahmed.alrawahi@unizwa.edu.om

Mr. Omar Al-Sudairy, Research assistant at Natural and Medical Sciences Research Center. University of Nizwa, Nizwa Tel (office): 25446512 Mobile: +968-94484734 Email: omaralsudairy@unizwa.edu.om

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



Riethoven, Head of Bioinformatics. Center of Biotechnology, University of Nebraska, USA

Dr. Abdul Latif Khan,

Natural and Medical

Sciences Research

Center, University of

Nizwa, Nizwa, Oman



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

Prof. Xiyin Wang,

North China

China

Professor & Dean,

and Technology,

University of Science



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



Biotechnology, University of Nebraska, USA



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









## 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

#### 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

**Dr. Jean-Jack Riethoven** 

#### Learning objects

- 1. What is microbiome, it 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

#### 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

**Prof Xiyin Wang** 

## Day 2 (18/02/2019) Genomics

#### Session 1

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

#### 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

**Prof. Dr. Xivin Wang** 

#### 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. Jea Learning objects

**Dr. Jean-Jack Riethoven** 

- 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 Learning objects

Dr. Ellen Marsh

- 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	
<ol> <li>Transcriptome sequencing and crop improvement</li> <li>Analysis of transcript profiles</li> <li>Expression profiling and abiotic/biotic stresses</li> </ol>	
1:00- 2:00 Lunch	
Session 3	
2:00-4:00 Transcriptome <i>De-Novo</i> assembly analysis Learning objects	Dr. Jean-Jack Riethoven
<ol> <li>Example workflow via Trinity</li> <li>Methods for quality and completeness analysis of transcripts</li> <li>Annotation of transcripts</li> <li>Differential gene expression analysis without reference genome</li> </ol>	

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

