

NGS Bioinformatics

Pathogen variant calling practical assignment

Module topic: Pathogen variant calling

Contact session title: inferring genetic relatedness

Trainer: Narender, Jon

Participant: <write your name here>

Date: <write today's date here>

Inferring genetic relatedness

Introduction

All information is found in practical material. We will use this document to answer the questions.

Please note

- **Hand-in information** please upload your completed assignment to the Vula 'Assignments' tab. Take note of the final hand-in date for each assignment, which will be indicated on Vula.

Session 3: Genetic relatedness

Q 3.1: What is the length of the alignment in "snpsitesOut.fa" file?

<start typing your answer here>

Q 3.2: What is the pairwise SNP difference between the following pairs: MD001-- repMD001 and NC_00962.3 – MD001?

<start typing your answer here>

Q3.3 : What is the pairwise SNP difference for following pairs:

- a) MD001-MD003:
- b) MD012-MD024:
- c) MD003-MD012:
- d) MD001-MD024:

Q3.4 : Report the resistance conferring variant identified for the following isolate drug combination: (record the position/coordinate and the mutation identified in the cases where isolates are resistant)

Isolate	Drug	Gene	Position	Genotype (R/S)
MD003	Isoniazid	<i>katG</i>		
MD003	Streptomycin	<i>rpsL</i>		
MD012	Rifampicin	<i>rpoB</i>		
MD012	Fluoroquinolone	<i>gyrA</i>		
MD024	Isoniazid	<i>katG</i>		
MD024	Streptomycin	<i>rpsL</i>		
MD024	Rifampicin	<i>rpoB</i>		
MD024	Fluoroquinolone	<i>gyrA</i>		