**TMBstable Installation Guide**

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1. Document Overview

This guide delineates a step-by-step protocol for the installation of TMBstable software, a bioinformatics tool engineered for high-throughput genomic sequencing data variant analysis. This document caters to system administrators, bioinformatics engineers, and other professionals in computational biology.

1. Installation Prerequisites

Prior to initiating the TMBstable installation, ensure that your computational environment adheres to the following criteria:

* + Operating System: CentOS Linux 7.9.2009 (Core) or a compatible variant.
  + Required Python Libraries: Refer to the TMBatable deployment guide for a detailed enumeration.
  + Adequate storage capacity for both installation and extensive data processing activities.

1. Software Acquisition

TMBstable can be obtained from the following GitHub repository: <https://github.com/hello-json/TMBstable>. Clone or download the repository to a designated location within your system's architecture.

1. Installation Procedure

4.1 System Configuration

* + - Update your system to its most current state to ensure optimal compatibility and security.
    - Install Python, if it is not preexisting, to create an appropriate runtime environment.
    - Implement the installation of Python libraries as prescribed in the TMBatable deployment guide.

4.2 Repository Cloning

* + - Execute the command git clone https://github.com/hello-json/TMBstable.git to clone the TMBstable repository onto your local machine.

4.3 Installation Execution

* + - Navigate to the cloned TMBstable directory.
    - Given TMBstable's Python-based architecture, no further installation steps are necessitated.

1. Installation Verification

To validate the successful installation of TMBstable, execute the following command in the terminal: **python workFlow.py -h**. A successful installation is indicated by the emergence of the following output, elucidating the usage information and options for TMBstable:  
  
usage: workFlow.py [-h] -b BAM\_FILE -d INI\_INFO\_DIR -g REFGENOME -m SNP\_METAMODEL -n SV\_METAMODEL -w SNP\_WINDOW -r INIREPEATFILEDIR -o OUTFILEDIR

optional arguments:

-h, --help show this help message and exit

-b BAM\_FILE, --bam\_file BAM\_FILE

input the bam file, e.g., sample.bam

-d INI\_INFO\_DIR, --ini\_info\_dir INI\_INFO\_DIR

input the ini\_info\_dir, e.g., ini\_info/

-g REFGENOME, --refGenome REFGENOME

input the refGenome file, e.g., refGenome/hg19.fa

-m SNP\_METAMODEL, --snp\_metaModel SNP\_METAMODEL

the snp meta model file directory, e.g., Nsnp\_134.m

-n SV\_METAMODEL, --sv\_metaModel SV\_METAMODEL

the sv meta model file directory, e.g., Nsv\_2567.m

-w SNP\_WINDOW, --snp\_window SNP\_WINDOW

the snp window size, e.g., 1000000

-r INIREPEATFILEDIR, --iniRepeatFileDir INIREPEATFILEDIR

the repeat file directory, e.g., hg19RepeatFile/rmsk.txt

-o OUTFILEDIR, --outFileDir OUTFILEDIR

the output file directory, e.g., myresult/TMBstable.vcf

Adhering to these procedures should culminate in the successful installation of TMBstable. This guide is designed to facilitate a seamless installation process for users within the domain of computational biology. It is imperative to meticulously follow the provided guidelines and ensure all prerequisites are met prior to installation. Should any issues arise during the installation, consult the troubleshooting section of the TMBatable deployment guide or the TMBstable GitHub repository for further assistance.