**TMBstable Testing Documentation**

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1. Overview

This document delineates the testing procedure for TMBstable, a bioinformatics tool designed for the high-throughput analysis of genomic variants. The testing protocol outlined herein utilizes computational biology terminologies and is intended for professionals adept in bioinformatics and genomic data analysis.

1. Testing Prerequisites
   * Ensure Python runtime environment is properly installed.
   * Verify the presence of all required Python libraries as specified in the TMBstable installation guide.
   * Confirm availability of sufficient computational resources to handle the intensive data processing.
2. Input Data Specification
   * TMBstable requires BAM file format input for sequencing data analysis.
   * Test data for this procedure is located at <https://github.com/hello-json/TMBstable> under the directory codesAndData/testData/sample.bam.
3. Test Command Execution
   * + Example command:   
       python workFlow.py -b sample.bam -d /ini\_info/ -g /refGenome/hg19.fa -m Nsnp\_134.m -n Nsv\_2567.m -w 1000000 -r /hg19RepeatFile/rmsk.txt -o /myresult/TMBstable.vcf
     + This command runs TMBstable with specified parameters including BAM file, initialization info directory, reference genome file, SNP and SV meta-model files, window size for SNP analysis, repeat file directory, and output file directory.
4. Output File Format and Interpretation
   * The output of TMBstable is a VCF (Variant Call Format) file, specifically TMBstable.vcf, conforming to the VCFv4.2 standard.
   * The VCF file format contains the following columns:

* CHROM: The chromosome number where the variant is located.
* POS: The position of the variant on the chromosome.
* ID: A unique identifier for the variant, if available.
* REF: The reference base(s) at the variant site.
* ALT: The alternate base(s) observed at the variant site.
* QUAL: Quality score of the variant call.
* FILTER: Filter status of the variant, indicating if it passes quality thresholds.
* INFO: Additional information about the variant, such as allele frequency, depth of coverage, and other annotations.
* FORMAT: Format of the data in the genotype fields.
* unknown: Sample-specific genotype information, detailing the genotype of the sample and additional metrics like genotype quality, depth, and allele count.

1. Testing and Validation
   * Execute the test command and monitor the process for successful completion.
   * Validate the output TMBstable.vcf file for correct format adherence and the presence of expected genomic variant data.
   * Cross-reference output data with known genomic databases or previously analyzed data sets for accuracy verification.
2. Troubleshooting and Debugging
   * In case of errors or unexpected results, consult the TMBstable installation guide and GitHub repository.
   * Analyze log files and error messages for debugging and identifying potential issues.

This testing documentation provides an guide for the testing of TMBstable. The aim is to ensure the reliability and accuracy of TMBstable in processing and analyzing complex genomic sequencing data sets.