TaBSAP Documentation

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Contents

User Guide - v1.0.2 A pipeline to analyze the data obtained from targeted bisulfite sequencing through the ion-torrent platform.

TaBSAP is a pipeline to map bisulfite treated sequencing reads to a genome of interest and perform methylation calls in a single step and enables a researcher to analyze the methylation levels of their samples straight away. It's main features are:

-Bisulfite mapping and methylation calling in one single step

-Supports single-end read alignments

-Alignment seed length, number of mismatches etc. are adjustable

-The output gives heatmap with categories.

1.1 Minimum System Requirements

1.1.1 Project Name: TaBS-Pipe

1.1.2 Project Homepage: https://github.com/pradyumnasagar/TaBSAP

1.1.3 Operating System: 64 bit Unix-like OS/ Linux Distributions(Ubuntu, CentOS, RHEL,etc.),Windows (with cygwin and R in cygwin).

1.1.4 Programming Language: SHELL Scripting.

1.1.5 Recommended System Requirement: 4GB RAM, 64 bit unix/linux OS.

1.1.6 Other Requirements: R, Pheatmap package for R,fastx toolkit(for 32 bit System), Dos2Unix.

1.1.7 License: MIT License.

CHAPTER 2

Installation:

Install the requirements Download the pipeline or clone the Pipeline in your Linux system with git Open Terminal

To download

wget https://github.com/pradyumnasagar/TaBSAP/archive/v1.0.2.zip

unzip v1.0.2.zip

cd v1.0.2

To Clone

git clone https://github.com/pradyumnasagar/TaBSAP.git

cd TaBSAP

Copy all the fastq files to fastq folder and Unconverted reference to reference folder Run the pipeline and follow the ON-Screen Instructions ./start.sh