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Description: Segminator is a fast and easy to use software which can be used for analyzing the 454 Life Sciences-Sequencing data. Features: * Reads from 454 data files can be analyzed by this software. * You can filter out the reads with Hamming distance threshold. * Hamming distance threshold may be calculated by user-defined read length, read count and required accuracy. * You can save the Hamming distance threshold report files into html format. * You can get the mutation calls of the reads by user-defined error rate threshold. * Error rate threshold may be defined by base or nucleotide counts. * At the same time, you can get the mutation calls from user-defined sequence length (default 1000bp). * Segmentminator can output sequences, read count, mutation call, etc. in two different columns. * The output data of the program can be saved into a text file, sorted and formatted in a html file. * You can set the number of threads for running. * This program can handle large 454 files with millions of reads * An example output file from Segmentminator is provided. * Segmentminator is a fast, easy to use program and will process a 454 file in less than a minute. Requirements: * A little Java knowledge will be helpful. * A single-threaded Java application is required. * Windows 64-bit * 454 Life Sciences Sequencing Data Files Comments Segminator is a handy application that can analyze the reads from your viral data set files. The program is designed to load and analyze the information from the data generated by the 454 Life Sciences platform. You can use this tool for identifying the variants of the viral population and remove the reads by using hamming distance cutoff thresholds. Segminator Description: Description: Segminator is a fast and easy to use software which can be used for analyzing the 454 Life Sciences-Sequencing data. Features: * Reads from 454 data files can be analyzed by this software. * You can filter out the reads with Hamming distance threshold. * Hamming distance threshold may be calculated by user-defined read length, read count and required accuracy. * You can save the Hamming distance threshold report files into html format. * You can get the mutation calls of the reads by user-defined error rate threshold

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Load an input file, where each line contains the read name and its position, identified as 1-based. A file may contain several types of reads, such as: Read name - A read that has been processed in the 454 Life Sciences processing. This read will be able to report Read name - A read that has been identified as not a processable read by 454 Life Sciences. Read name - A read that has not been processed because of its length. Read name - A read that has been identified as a valid sequence from the reference sequence or as a potential chimera. Read name - A read that has been filtered by Hamming distance. Read name - A read that has been filtered by quality scores. Read name - A read that has been filtered by paired ends. Read name - A read that has been filtered by subclonality. Read name - A read that has been filtered by the forward or reverse strand. Read name - A read that has been filtered by source. Read name - A read that has been filtered by a cluster of reads. Read name - A read that has been filtered by a 454 Life Sciences specific error. Read name - A read that has been filtered by quality scores. Read name - A read that has been filtered by base call quality. Read name - A read that has been filtered by self-homology (or self-duplications). Read name - A read that has been filtered by proportion. Read name - A read that has been filtered by error-rate. Read name - A

read that has been filtered by the longest substring. Read name - A read that has been filtered by the orientation. Read name - A read that has been filtered by the sublibrary. Read name - A read that has been filtered by minimum length. Read name - A read that has been filtered by the 454 Life Sciences error correction. Read name - A read that has been filtered by the 3' end of a read. Read name - A read that has been filtered by the 5' end of a read. Read name - A read that has been filtered by a mix of subclonality, quality score, and base call quality. Read name - A read that has been filtered by read count. Read name - A read that has been filtered by sequence identity. Read name - A read that has been filtered by orientation. Read 2edc1e01e8

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Segminator is a fast and easy way to find single-nucleotide polymorphisms (SNPs) and mutations in sequenced RNA or DNA 2. SVCTune-Basic 2014-09-16 17,208.20 92 SVCTune-Basic can be used as a fast and easy way to optimize the library construction and sequencing of small, as well as large, DNA fragments (100s of kb). CropGeneinfo is an online resource with information about over 10,000 plant genes. The site is searchable by gene name and description, gene family, and by gene IDs. Description: CropGeneInfo is a service for plant genomics and functional genomics researchers. It includes information about over 10,000 plant genes (including rice, wheat and barley). The database is searchable by gene name, gene family, gene description and by gene IDs. 3. Megasim 2014-03-31 3.68 1,287 Megasim allows you to explore data from next-generation sequencing technologies in a user-friendly manner. It includes the best open source alignment algorithm to align data on both the single genome as well as whole genome sequence. Genome Visualizer is an online tool that visualizes the whole genome and putative exons/introns/exons of a gene model with a color-coded display of variations. Description: Genome Visualizer is an online tool that visualizes the whole genome and putative exons/introns/exons of a gene model with a color-coded display of variations. Genome Visualizer is an online tool that visualizes the whole genome and putative exons/introns/exons of a gene model with a color-coded display of variations. Description: Genome Visualizer is an online tool that visualizes the whole genome and putative exons/introns/exons of a gene model with a color-coded display of variations. Genome Visualizer is an online tool that visualizes the whole genome and putative exons/introns/exons of a gene model with a color-coded display of variations. 4. MicroScope 2014-03-31 2.91 24,777 MicroScope is a web-based service that provides

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What's New in the?

Segminator is a powerful program, designed to analyze the 454 Life Sciences sequencing data with the goal of minimizing the risk of discarding important reads. It was designed to perform well, even on short reads, but also to be very easy to use. Creating a Segmentation File: Segminator works by creating a seg file, a text file with the format that you can use to load and analyze the data, and can be used to load the data in other tools. The Segmentation File is a text file, and has the following format: name_of_rffile*label.txt (wildcard for all files in the current directory) The labels in this file are

used to partition the reads into different regions, or segments. If no label is provided, Segmentminator will use the files extension to determine what segment they belong to. All segments are represented as a new tab on the main window. The Segmentation File should be named with a name followed by a *label.txt extension. The segmentation file may be empty, and no label will be present. If a file is not present, Segmentminator will use the default label name. If more than one label is present, Segmentminator will name them sequentially. Load the Data into the Segmentation File: After the segmentation file is created, it is loaded into the Segmentminator application. Segmentminator makes use of the read names to determine what segment they belong to. By default, the segment is labeled by the read name, but may be changed to any desired label name. Once the file is loaded, you will see the reads represented in the main window. You will notice that the segmentation file is not loaded into the main window, but will be loaded in a separate window. By default, the segmentation window will be named "seg". The reads can be accessed from the Segmentation window using the "segname" window. Verifying the Segmentation File: The segmentation file will have a label on the main window, but the segments in the Segmentation file will not be labeled. The segments in the Segmentation file are represented in a new tabbed window, which contains the files with the given names. In the Segmentation file, there are 2 columns: Read name: The read name and the corresponding position. Segment: The label assigned to the read. Sorting the Segmentation File: To sort the segments in alphabetical order, simply click on the column header. Clicking on the same column header again will reverse the order. To sort the segments in order of the read length, click on the column header, and sort by the read length. To sort by the read

System Requirements For Segminator:

OS: Windows XP/Vista/7/8 Processor: 1GHz Processor recommended (2GHz is strongly recommended) Memory: 256MB of RAM required Graphics: 128MB of Video Memory is recommended We will be hosting a first-come first-served tournament starting at 11AM PST . In the event we do not reach full capacity of players and pools are full, players will be randomly seperated by race to see which races are not represented in the tournament. Bracket Selection will occur on a first come

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