SlopMap 1.3.0 (2013-05-18)

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0.1 Introduction

SlopMap is a software application tool for quick and flexible identification of similar sequences using exact k-mer matching.

0.2 Download and Installation

You can download from the following websites:

1. From project site on the Bitbucket: `https://bitbucket.org/izhbannikov/slopmap/get/master.zip` (or use `git clone https://izhbannikov@bitbucket.org/izhbannikov/slopmap.git` command).

2. From IBEST GRC web site: `http://cores.ibest.uidaho.edu/software/slopmap`

Unpack downloaded file. Go to unpacked folder. Type "make clean", than "make". bin directory contains SlopMap executable.

0.3 Usage

- Paired-end Illumina

```
./slopmap -1 <PE1 filename> -2 <PE1 filename> -l <Library name> -o <Output prefix> [-k <KMER SIZE> -d <DISTANCE> -t <THRESHOLD>]
```

- Single-end Illumina

```
./slopmap -U <SE filename> -l <Library name> -o <Output prefix> [-k <KMER SIZE> -d <DISTANCE> -t <THRESHOLD>]
```

- Roche 454

```
./slopmap -454 <454 filename> -l <Library name> -o <Output prefix> [-k <KMER SIZE> -d <DISTANCE> -t <THRESHOLD>]
```

Default parameters:
```
-k <KMER SIZE> 11
-d <DISTANCE> 5 (distance between two consecutive kmers)
-t <THRESHOLD> 0.75
```

0.4 Examples

- Paired-end Illumina

```
./slopmap -1 <SlopMap HOME>/test_data/SmallTestIllumina_R1.fastq.gz -2 <SlopMap HOME>/test_data/SmallTestIllumina_R2.fastq.gz -o test -l <SlopMap HOME>/test_data/vectors.fasta -t 0.9
```

- Single-end Illumina

```
./slopmap -U <SlopMap HOME>/test_data/SmallTestIllumina_R1.fastq.gz -o test -l <SlopMap HOME>/test_data/vectors.fasta -t 0.83 -d 3
```

- Roche 454

```
./slopmap -454 <SlopMap HOME>/test_data/Small454Test.sff -o test -l <SlopMap HOME>/test_data/vectors.fasta -t 0.56 -k 14
```

0.5 Conclusion

For any questions please contact Ilya via the following email: zhba3458@vandals.uidaho.edu