

pairDistance

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SYNOPSIS

To collect information about distance in paired-end reads.

```
./bin//pair_distance chr13.fa reads.fa -o:pd.cfg
```

To display distribution chart of distances (Fig. 1).

```
./SView/Sview -type PE
```

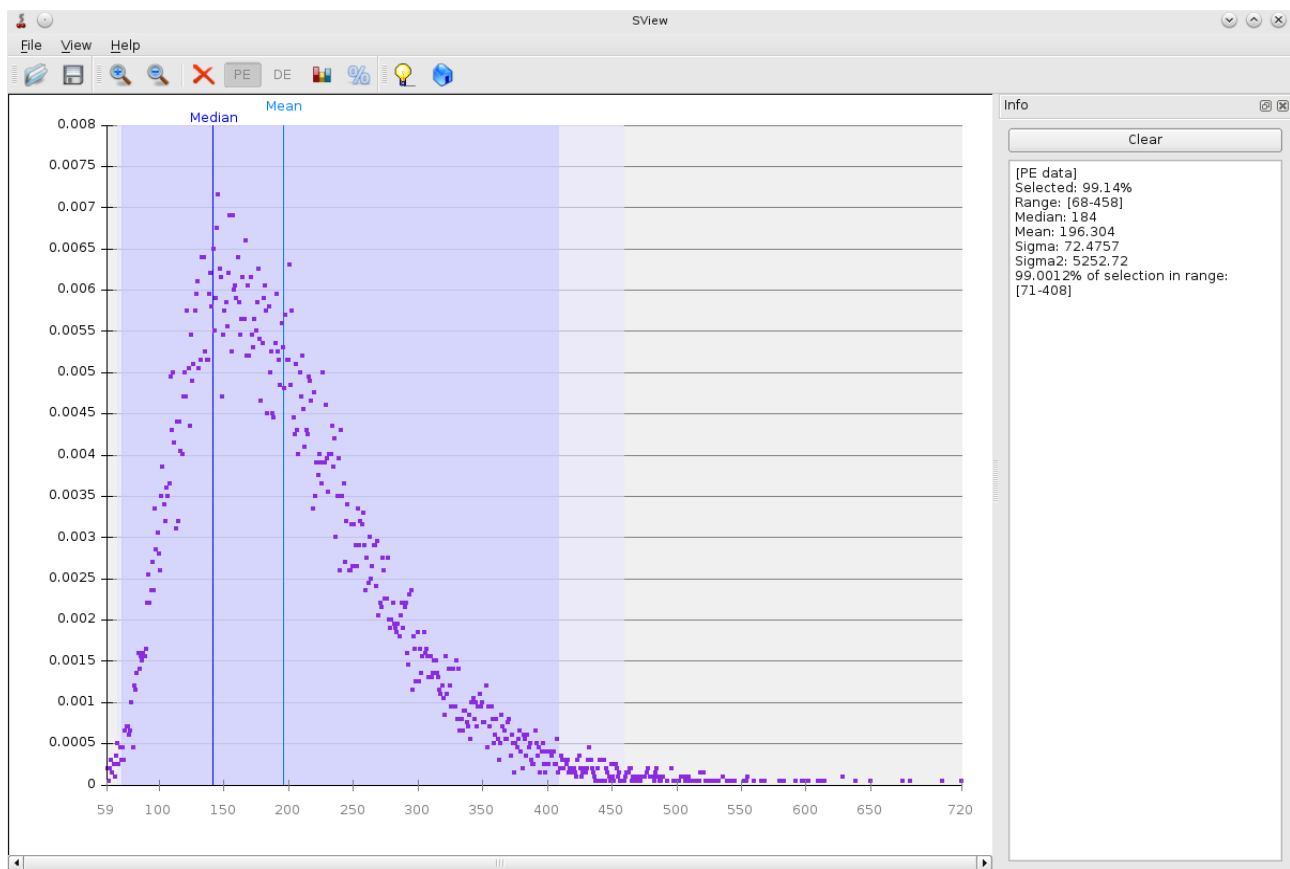


Fig. 1 Result of the visualization.

DESCRIPTION

Here we describe the programs for collecting, analyzing and visualizing distances within paired-end reads. *Pair_distance* program attempts to align reads on contigs and collects statistical data on distance between reads. Then, a user can load that data into visualization program *SView* than select a region on a curve and get parameters of distribution.

COMMANDS AND OPTIONS

./pair_distance *contig.fna reads.fna -o:config [options],*

where:

contig.fna - *fasta file with one or more genomic contigs.*

reads.fna - *fasta file with paired-end reads, sequences of paired reads should be in order even/odd.*

pair_distance options:

- PE_only - selects data for "PE" reads only
- MP_only - selects data for "MP" reads only
- DE_only - selects data for "distance ends" reads only with very long distances (>1K bp) between ends.

A name of an output file is the same as a name of input with added ".distance" extension.

./SView -type PE|MP|DE <options>

Sview is a QT-based GUI program for analysis and visualization of distance data on paired-end reads. User must specify type of paired reads before loading a data file.

-type PE|MP|DE - specifies reads type.

-in "data.bin" - loads file with data in binary format. User can also specify a datafile in menu "File"

-out "result.txt" - specifies name of an output file. If name isn't specified, an output will be printed in stdout.

User can navigate a distribution curve with a mouse wheel and use Ctrl-mouse wheel to zoom in and out. Statistic data is printed in an info window if a representative part of curve is selected by clicking and dragging a mouse pointer. For "PE" and "DE" reads, user must select a single area. In case of "MP" reads, user can switch between types of area by pressing "PE" and "DE" buttons in

a toolbar.

User can save an output by pressing a button on a toolbar or by using "File→Save" menu command.

LICENSE AND CITATION

pairDistance is free for academic usage. For commercial licensing, please inquire to softberry@softberry.com.