OMTools Manual v1.2

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Contents

1 Introduction

Optical mapping is a technique to capture specific enzyme sites on a long DNA molecule. The output data of this technology are the *optical map*, that is represented by a *tuple* (Figure 1).

Figure 1: An example of optical map. Green rectangle is the DNA backbone and the black columns are the enzyme site. The optical map can be represented as a tuple: [1518; 15487; 8455; 1350; 25188; 17845; 4948]

OMTools is a software package that provides efficient and intuitive data processing and visualization modules to handle optical mapping data.

2 Availability and Implementation

2.1 Availability

OMTools can be obtained from https://github.com/aldenleung/OMTools and released under a GPL license (See the software distribution for details).

2.2 Minimum requirements

OMTools is implemented in Java 1.8. The software has been tested on Ubuntu 14.10 and Microsoft Windows 7, 10.

2.3 Installation

All required libraries are placed in the folder lib/.

1. Compile the OMTools package in the OMTools folder:
   `javac -d bin -sourcepath src -cp "lib/*" @classes`
2. Build a runnable jar file for OMTools:
   `jar cvfm OMTools.jar manifest -C bin .`
3. Run OMTools:
   `java -jar OMTools.jar ModuleName`

3 Quick start

- `java -jar OMTools.jar FastaToOM --fastain Ecoli.fa --refmapout Ecoli.ref --enzyme BspQI`
- `java -jar OMTools.jar DataStatistics --optmapin Ecoli.ref --statout ReferenceStat.txt`
- `java -jar OMTools.jar OptMapDataGenerator --refmapin Ecoli.ref --optmapout EcoliExample.sdata --cov 100`
- `java -jar OMTools.jar DataStatistics --refmapin Ecoli.ref --optmapin EcoliExample.sdata --statout DataStat.txt`
- `java -jar OMTools.jar OMBlastMapper --refmapin Ecoli.ref --optmapin EcoliExample.sdata --optresout EcoliExample.omd --thread 2`
- `java -jar OMTools.jar ResultStatistics --refmapin Ecoli.ref --optmapin EcoliExample.sdata --optresin EcoliExample.omd --statout ResultStat.txt`
- `java -jar OMTools.jar OMView --viewrefin Ecoli.ref --viewresin EcoliExample.omd --viewregion 1:1-1000000`

4 Basic analysis procedures

Prior to the generation of optical mapping data, users are recommended to do simulation and determine the best enzyme to use. If users have sequence assembly files (e.g. short sequence contigs, long sequence scaffolds or existing reference sequences), they can perform an *in silico* digestion. Such conversion from *fasta* to *optical mapping* data can be done by using the **FastaToOM** module. Users obtain two pieces of information. First, by using the **DataStatistics** module, users can generate some basic statistics of the digested sequence. One of the most crucial number to look at is the density of enzyme sites (signal density). Data analysis in optical mapping becomes very difficult if the signal density is too high or too low (The range of "good" signal density depends on the platform used to generate optical mapping data, and users are suggested to consult the providers for more details).

Second, if the platform design is based on labeling with nicking enzyme, nicking site break can be a severe problem in continuity of optical mapping assembly. For each enzyme site, **FastaToOM** module provides the distance to the closest enzyme site. Users can predict the number of nicking site breaks by setting a distance cut-off (Again, the distance between two nicking sites that can lead to a break depends on the platform used to generate optical mapping data, and users are suggested to consult the providers for more details). In addition, if users want to complete genome assemblies using optical mapping data, looking at the location of predicted nicking site breaks at the contigs of

interest is important. It is better to avoid nicking site break near the ends of contig.

After determining the enzyme used, users can proceed to the optical mapping experiment. When users receive raw high-throughput optical mapping data, it is recommended to generate statistics on the optical mapping data using the **DataStatistics** module. Usually several criteria are of great interest - data throughput, signal density, and average molecule length. Users can then use **DataTools** module to do data processing and filtering. Sometimes, the output data is duplicated when multiple raw optical mapping files are concatenated due to some unexpected human errors. In such case, users may want to do a quick scanning by using the **DuplicatedMoleculesDetection** module and remove any duplicated molecules by using the **DuplicatedMoleculesRemover** module.

Next, one of the upstream data analysis would be alignment. **OMTools** provides several alignment modules including the **OMBlastMapper**, **OMHAMapper** and **OMFMMapper** modules. A **PairwiseAlignment** module can also help to perform pairwise alignment across multiple data sets. Users can then process and filter the alignment results by using **ResultTools** module and generate statistics using **ResultStatistics** module. Since several methods are recently published by other research groups that can perform alignment of optical mapping data, users can consider obtaining the union or intersection of alignment results from multiple methods using the **ResultMerger** module.

When it comes to development of new algorithms relating to optical mapping data, users may be interested in the simulation tools. These include **OptMapDataGenerator** module that generates optical mapping data given a reference optical map, and the **RandomReferenceGenerator** module that generates a random reference optical map. If users are developing the alignment algorithm, the **PrecisionRecallGraphDataGenerator** module generates a table that can be used for precision-recall graph generation.

Last but not least, users may want to further investigate the results and showcase some examples by visualizing the optical mapping data. **OMView** module serves as a multi-purpose visualizer on the optical mapping data for it.

Part I
Mapper

5 OMBlastMapper

Performs alignment of optical mapping data. OMBlast algorithm employs a seed-and-extend approach to align optical maps.

5.1 Common Mapper Options

`--minsig` Minimum signal of the query to align. [Default: 5]

`--minsize` Minimum size of the query to align. [Default: 50000]

`--exactmatch` Enable exact match of query to reference. Disable this option when performing self-alignment. [Default: true]

5.1.1 Overlapped Alignment Merging Module Options

`--overlapmergemode` Mode: 0: Disable merging step; 1: Merge same partial alignments; 2: Merge overlapping partial alignments [Default: 2]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--local` Enable local alignment [Default: true]

5.1.2 Result Filter Options

`--filtermode` Filter Mode. 0: No filter; 1: Filter by all the following options; 2: Filter by minimum score only [Default: 0]

`--minmatch` Minumum number of matches of a partial alignment [Default: 3]

`--maxfp` Maximum number of extra signals of a partial alignment [Default: 10000]

`--maxfn` Maximum number missing signals of a partial alignment [Default: 10000]

`--maxfpr` Maximum rate of extra signals of a partial alignment [Default: 1.0E-4]

`--maxfnr` Maximum rate of missing signals of a partial alignment [Default: 0.5]

`--minscore` Minimum score of a partial alignment [Default: 0.0]

`--minsubfragratio` Minimum subfragment ratio of a partial alignment [Default: 0.0]

`--minsigratio` Minimum aligned signal ratio of a partial alignment [Default: 0.0]

`--trimmode` Trim Mode. 0: Trim mode disabled; 1: Trim mode enabled [Default: 0]

`--maxtrim` Maximum number of trimming steps of a partial alignment [Default: 5]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

5.1.3 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence (uniqueness) of the final alignment [Default: 0.4]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

5.1.4 Result Reader Options

`--optresin` Input alignment result file for re-alignment

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

5.2 OMBlastMapper Options

`--local` Enable local alignment [Default: true]

`--meas` Measurement error [Default: 500]

`--ear` Error acceptable range (Scaling error tolerance) [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--falselimit` Maximum number of consecutive extra/missing signals [Default: 5]

`--maxseedno` Maximum similar seed number on query [Default: 10]

5.2.1 Seeding Options

`--seedingmode` Seeding mode: 1: Optimized for long k-mer (usually for k larger than 10); 2: Optimized for short k-mer (usually for k smaller than or equal to 10); -1: Auto-selection. [Default: -1]

`--k` Kmer length. [Default: 3]

`--maxnosignal` Maximum no signal region between signals for seeding. [Default: 10000000]

5.3 Multi-thread Options

`--thread` Number of threads [Default: 1]

5.4 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

5.5 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

5.6 Result Writer Options

`--optresout` Output alignment result file [Required]

`--optresoutformat` Result file format -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

`--writeunmap` Write discarded or unmapped molecules. [Default: true]

`--multiple` Write multiple maps for a molecule. [Default: true]

`--writeinfo` Write information of a molecule. [Default: true]

6 OMHAMapper

Performs alignment of optical mapping data. OMHA algorithm employs a heuristic approach to align optical maps.

6.1 Common Mapper Options

`--minsig` Minimum signal of the query to align. [Default: 5]

`--minsize` Minimum size of the query to align. [Default: 50000]

`--exactmatch` Enable exact match of query to reference. Disable this option when performing self-alignment. [Default: true]

6.1.1 Overlapped Alignment Merging Module Options

`--overlapmergemode` Mode: 0: Disable merging step; 1: Merge same partial alignments; 2: Merge overlapping partial alignments [Default: 2]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--local` Enable local alignment [Default: true]

6.1.2 Result Filter Options

`--filtermode` Filter Mode. 0: No filter; 1: Filter by all the following options; 2: Filter by minimum score only [Default: 0]

`--minmatch` Minumum number of matches of a partial alignment [Default: 3]

`--maxfp` Maximum number of extra signals of a partial alignment [Default: 10000]

`--maxfn` Maximum number missing signals of a partial alignment [Default: 10000]

`--maxfpr` Maximum rate of extra signals of a partial alignment [Default: 1.0E-4]

`--maxfnr` Maximum rate of missing signals of a partial alignment [Default: 0.5]

`--minscore` Minimum score of a partial alignment [Default: 0.0]

`--minsubfragratio` Minimum subfragment ratio of a partial alignment [Default: 0.0]

`--minsigratio` Minimum aligned signal ratio of a partial alignment [Default: 0.0]

`--trimmode` Trim Mode. 0: Trim mode disabled; 1: Trim mode enabled [Default: 0]

`--maxtrim` Maximum number of trimming steps of a partial alignment [Default: 5]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

6.1.3 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence (uniqueness) of the final alignment [Default: 0.4]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

6.1.4 Result Reader Options

`--optresin` Input alignment result file for re-alignment

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

6.2 OMHAMapper Options

`--local` Enable local alignment [Default: true]

`--localstart` Local start pos for alignment, 0: starts at every signal (exhausive), x: starts at first x signals, -x: starts without last x signals. [Default: 0]

`--scorefilter` Primary score filter during alginment [Default: 30]

`--deg` Degeneracy of close signals to handle resolution error. [Default: 1500]

`--meas` Measurement error [Default: 500]

`--ear` Error acceptable range (Scaling error tolerance) [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--falselimit` Max consecutive false signals [Default: 5]

6.3 Multi-thread Options

`--thread` Number of threads [Default: 1]

6.4 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

6.5 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

6.6 Result Writer Options

`--optresout` Output alignment result file [Required]

`--optresoutformat` Result file format -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

`--writeunmap` Write discarded or unmapped molecules. [Default: true]

`--multiple` Write multiple maps for a molecule. [Default: true]

`--writeinfo` Write information of a molecule. [Default: true]

7 OMFMMapper

Performs alignment of optical mapping data. OMFM algorithm employs an indexing approach to align optical maps.

7.1 Common Mapper Options

`--minsig` Minimum signal of the query to align. [Default: 5]

`--minsize` Minimum size of the query to align. [Default: 50000]

`--exactmatch` Enable exact match of query to reference. Disable this option when performing self-alignment. [Default: true]

7.1.1 Overlapped Alignment Merging Module Options

`--overlapmergemode` Mode: 0: Disable merging step; 1: Merge same partial alignments; 2: Merge overlapping partial alignments [Default: 2]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--local` Enable local alignment [Default: true]

7.1.2 Result Filter Options

`--filtermode` Filter Mode. 0: No filter; 1: Filter by all the following options; 2: Filter by minimum score only [Default: 0]

`--minmatch` Minumum number of matches of a partial alignment [Default: 3]

`--maxfp` Maximum number of extra signals of a partial alignment [Default: 10000]

`--maxfn` Maximum number missing signals of a partial alignment [Default: 10000]

`--maxfpr` Maximum rate of extra signals of a partial alignment [Default: 1.0E-4]

`--maxfnr` Maximum rate of missing signals of a partial alignment [Default: 0.5]

`--minscore` Minimum score of a partial alignment [Default: 0.0]

`--minsubfragratio` Minimum subfragment ratio of a partial alignment [Default: 0.0]

`--minsigratio` Minimum aligned signal ratio of a partial alignment [Default: 0.0]

`--trimmode` Trim Mode. 0: Trim mode disabled; 1: Trim mode enabled [Default: 0]

`--maxtrim` Maximum number of trimming steps of a partial alignment [Default: 5]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

7.1.3 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence (uniqueness) of the final alignment [Default: 0.4]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

7.1.4 Result Reader Options

`--optresin` Input alignment result file for re-alignment

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

7.2 OMFMMapper Options

`--meas` Measurement error [Default: 500]

`--ear` Error acceptable range (Scaling error tolerance) [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--rfalselimit` Max consecutive false signals on reference [Default: 5]

`--qfalselimit` Max consecutive false signals on query [Default: 5]

`--cfalselimit` Max consecutive false signals on both reference and query [Default: 5]

`--minalignscore` Minimum score at alignment stage [Default: 20]

7.2.1 Seeding Options

`--seedingmode` Seeding mode: 1: Optimized for long k-mer (usually for k larger than 10); 2: Optimized for short k-mer (usually for k smaller than or equal to 10); -1: Auto-selection. [Default: -1]

`--k` Kmer length. [Default: 3]

`--maxnosignal` Maximum no signal region between signals for seeding. [Default: 10000000]

7.3 Multi-thread Options

`--thread` Number of threads [Default: 1]

7.4 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

7.5 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

7.6 Result Writer Options

`--optresout` Output alignment result file [Required]

`--optresoutformat` Result file format -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

`--writeunmap` Write discarded or unmapped molecules. [Default: true]

`--multiple` Write multiple maps for a molecule. [Default: true]

`--writeinfo` Write information of a molecule. [Default: true]

8 PairwiseAlignment

Performs pairwise alignment of data files based on OMBlastMapper. Input multiple data files for pair-wise alignment between each pair of them.

8.1 Common Mapper Options

`--minsig` Minimum signal of the query to align. [Default: 5]

`--minsize` Minimum size of the query to align. [Default: 50000]

`--exactmatch` Enable exact match of query to reference. Disable this option when performing self-alignment. [Default: true]

8.1.1 Overlapped Alignment Merging Module Options

`--overlapmergemode` Mode: 0: Disable merging step; 1: Merge same partial alignments; 2: Merge overlapping partial alignments [Default: 2]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--local` Enable local alignment [Default: true]

8.1.2 Result Filter Options

`--filtermode` Filter Mode. 0: No filter; 1: Filter by all the following options; 2: Filter by minimum score only [Default: 0]

`--minmatch` Minumum number of matches of a partial alignment [Default: 3]

`--maxfp` Maximum number of extra signals of a partial alignment [Default: 10000]

`--maxfn` Maximum number missing signals of a partial alignment [Default: 10000]

`--maxfpr` Maximum rate of extra signals of a partial alignment [Default: 1.0E-4]

`--maxfnr` Maximum rate of missing signals of a partial alignment [Default: 0.5]

`--minscore` Minimum score of a partial alignment [Default: 0.0]

`--minsubfragratio` Minimum subfragment ratio of a partial alignment [Default: 0.0]

`--minsigratio` Minimum aligned signal ratio of a partial alignment [Default: 0.0]

`--trimmode` Trim Mode. 0: Trim mode disabled; 1: Trim mode enabled [Default: 0]

`--maxtrim` Maximum number of trimming steps of a partial alignment [Default: 5]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

8.1.3 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence (uniqueness) of the final alignment [Default: 0.4]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

8.1.4 Result Reader Options

`--optresin` Input alignment result file for re-alignment

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

8.2 OMBlastMapper Options

`--local` Enable local alignment [Default: true]

`--meas` Measurement error [Default: 500]

`--ear` Error acceptable range (Scaling error tolerance) [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--falselimit` Maximum number of consecutive extra/missing signals [Default: 5]

`--maxseedno` Maximum similar seed number on query [Default: 10]

8.2.1 Seeding Options

`--seedingmode` Seeding mode: 1: Optimized for long k-mer (usually for k larger than 10); 2: Optimized for short k-mer (usually for k smaller than or equal to 10); -1: Auto-selection. [Default: -1]

`--k` Kmer length. [Default: 3]

`--maxnosignal` Maximum no signal region between signals for seeding. [Default: 10000000]

8.3 Multi-thread Options

`--thread` Number of threads [Default: 1]

8.4 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

8.5 Pairwise alignment options

`--output` output prefix [Required]

`--rerun` Rerun even if the result file exists [Default: false]

Part II
Simulation

9 OptMapDataGenerator

Generates simulated data from the reference.

9.1 Reference Reader Options

`--refmapin` Input reference map file

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

9.2 Multiple Reference Reader Options

`--refmaplistin` Input reference map file list with ratio

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

9.3 Data Generator Options

`--rsln` Resolution error [Default: 1200]

`--meas` Measurement error [Default: 500]

`--fsize` Average fragment size [Default: 200000]

`--fubound` Size upper boundary, inclusive [Default: 1000000]

`--flbound` Size lower boundary, inclusive [Default: 100000]

`--median` Median for scale [Default: 1.0]

`--scalesd` SD for scale [Default: 0.04]

`--subound` Scale upper boundary, inclusive [Default: 1.3]

`--slbound` Scale lower boundary, inclusive [Default: 0.7]

`--fpr` false positive rate [Default: 1.0E-5]

`--fnr` false negative rate [Default: 0.1]

`--seed` Random seed

`--indelsize` Random Insertion/Deletion size [Default: 0]

`--inversionmode` Inversion mode. 0: no inversion. 1: inversion of second half [Default: 0]

`--cov` Coverage of data output [Default: 10.0]

`--moleno` Number of molecules to be generated. Overriding coverage option if set to a positive number [Default: -1]

9.4 Data Writer Options

`--optmapout` Output optical map file [Required]

`--optmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

10 RandomReferenceGenerator

Generates random reference maps by shuffling the order of segments in the input reference maps.

10.1 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

10.2 Reference Writer Options

`--refmapout` Output reference map file [Required]

`--refmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

Part III
Fasta Tools

11 FastaToOM

Performs *in silico* digestion on DNA sequence.

11.1 Stream Fasta Reader Options

`--fastain` fasta input file [Required]

11.2 Enzyme Input Options

`--enzyme` Built-in enzymes [BspQI, BbvCI, AlwI, BsmAI, BstNBI, BsmI, BsrDI, BssSI, BtsI]

`--enzymestring` Enzyme sequence (e.g. GCTCTTC)

11.3 Reference Writer Options

`--refmapout` Output reference map file [Required]

`--refmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

11.4 Nicking Site Break Prediction Options

`--nsbout` Potential nicking site breaks output (The prediction is useful for nicking enzyme-based data only)

Part IV
Data Tools

12 DataTools

Provides basic functions for filtering and processing optical mapping data

12.1 Data Tools Options

`--idprefix` Add a prefix to all ids

`--idmodify` Convert all ids to x .. x + n - 1 (x: input value, n: number of optical maps in the data file). A negative value disables this function. [Default: -1]

`--idmodifylog` Log file containing the id conversions

`--fix` Fix the data (negative signal-to-signal distance correction and etc.) [Default: true]

`--condense` Merge multiple signals closer than parameter into one signal [Default: 0]

`--removeseg` Remove segments smaller than the parameter [Default: -1]

`--minsize` Data with minimum size to retain [Default: 0]

`--minsig` Data with minimum signal to retain [Default: 0]

`--dataid` List of Data ID to be extracted

`--region` List of regions to be extracted.

`--shift` Shift forward (right) x bp (Assume circular) [Default: 0]

`--randdata` Number of random data to be extracted

`--seed` Seed used in random data extraction

`--concat` Concatenate all data entries into single entry. -1: not activated; Non-negative value: space (segment without any signal) between each data entry. Ignore any data modification functions [Default: -1]

12.1.1 ConcatInfo Reader Options

`--concatin` ConcatInfo file input.

12.1.2 ConcatInfo Writer Options

`--concatout` ConcatInfo file output.

12.1.3 Low complexity filtering

`--lowcom` Retain/Remove molecules with low complexity -1: Retain Low Complexity; 0: Do nothing; 1: Retain High Complexity [Default: 0]

`--maxdensity` Maximum density per 100kbp to filter [Default: 25.0]

`--maxseed` Maximum seed to filter [Default: 5]

12.2 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

12.3 Data Writer Options

`--optmapout` Output optical map file [Required]

`--optmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

13 DataStatistics

Generates statistics of the data file.

13.1 DataStatistics Options

`--statout` Statistics output [Required]

13.2 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

13.3 Reference Reader Options

`--refmapin` Input reference map file

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

14 DuplicatedMoleculesDetection

Detects duplicated molecules in an optical map data set. Duplicated molecules contain same number of total segment, and the difference between size of each segment is very small (usually smaller than 100 bp)

14.1 Multithread Seeding Options

`--meas` Measuring Errors. Usually it is much smaller than normal measuring errors in discovering duplicated molecules [Default: 100]

`--ear` Error acceptable range [Default: 0.0]

`--thread` Number of threads [Default: 1]

14.2 Seeding Options

`--seedingmode` Seeding mode: 1: Optimized for long k-mer (usually for k larger than 10); 2: Optimized for short k-mer (usually for k smaller than or equal to 10); -1: Auto-selection. [Default: -1]

`--k` Kmer length. [Default: 3]

`--maxnosignal` Maximum no signal region between signals for seeding. [Default: 10000000]

14.3 Duplicated Molecules Detecting Options

`--dupout` Files containing duplicated molecules [Required]

`--minseg` Minimum segments to be considered duplicated [Default: 15]

14.4 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

15 DuplicatedMoleculesRemover

Removes detected duplicated molecules from the data file

15.1 Duplicated Molecules Remover Options

`--dupin` Files containing duplicated molecules [Required]

15.2 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

15.3 Data Writer Options

`--optmapout` Output optical map file [Required]

`--optmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

Part V
Alignment Tools

16 ResultTools

Provides basic functions for filtering and processing alignment results

16.1 Result Reader Options

`--optresin` Input alignment result file [Required]

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

16.2 Result Writer Options

`--optresout` Output alignment result file

`--optresoutformat` Result file format -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

`--writeunmap` Write discarded or unmapped molecules. [Default: true]

`--multiple` Write multiple maps for a molecule. [Default: true]

`--writeinfo` Write information of a molecule. [Default: true]

16.3 Reference Reader Options

`--refmapin` Input reference map file

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

16.4 Data Reader Options

`--optmapin` Input optical map file

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

16.5 Data Output Options

`--mapout` Mapped molecules output

`--unmapout` Unmapped molecules output

`--optmapoutformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

16.6 Result Tools Options

`--disinvalid` Discard invalid results. [Default: true]

`--conf` Recalculating result confidence [Default: false]

`--dataid` List of Data ID to be extracted

`--region` Region in chrN:start-end or chrN:start format

`--refnamemodify` Modify the reference name according to the target file in format: src\tTarget

`--dataremoval` Remove result with query names in the file

`--joinresult` Represent partial alignments in one alignment (The gap is filled with extra and missing signals). Only works on partial alignments with indel relationship [Default: false]

16.6.1 Results Breaker Option

`--breakermode` Mode 0: Disable the breaking function; 1: Break the alignment at query/reference segment with size deviating too much, into multiple partial alignments [Default: 0]

`--meas` Measurement error [Default: 500]

`--ear` Error acceptable range (Scaling error tolerance) [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

16.6.2 Result Filter Options

`--filtermode` Filter Mode. 0: No filter; 1: Filter by all the following options; 2: Filter by minimum score only [Default: 0]

`--minmatch` Minumum number of matches of a partial alignment [Default: 3]

`--maxfp` Maximum number of extra signals of a partial alignment [Default: 10000]

`--maxfn` Maximum number missing signals of a partial alignment [Default: 10000]

`--maxfpr` Maximum rate of extra signals of a partial alignment [Default: 1.0E-4]

`--maxfnr` Maximum rate of missing signals of a partial alignment [Default: 0.5]

`--minscore` Minimum score of a partial alignment [Default: 0.0]

`--minsubfragratio` Minimum subfragment ratio of a partial alignment [Default: 0.0]

`--minsigratio` Minimum aligned signal ratio of a partial alignment [Default: 0.0]

`--trimmode` Trim Mode. 0: Trim mode disabled; 1: Trim mode enabled [Default: 0]

`--maxtrim` Maximum number of trimming steps of a partial alignment [Default: 5]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

16.6.3 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence [Default: 0.0]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

16.6.4 Lift Over Options

`--liftoverin` Input liftOver file, Format: chromosome\t coordinate\t size\n

16.7 Simulated Results Analysis Options

`--rocout` Output a table for ROC curve plotting

17 ResultMerger

Merges alignment results from different alignment methods

17.1 Result Reader Options

`--optresin` Input alignment result file [Required]

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

17.2 Result Merger Options

`--resultkey` Keys (names) to represent the result files [Required]

`--gapallowed` Gaps allowed between results [Default: 0]

`--analyzeall` Analyze only if the query is present in all results [Default: false]

`--prefix` Output file prefix [Required]

`--outtype` Output file type [Default: .omd]

18 ResultStatistics

Generates statistics for alignment results

18.1 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

18.2 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

18.3 Result Reader Options

`--optresin` Input alignment result file [Required]

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

18.4 Result Stat Options

`--checkstrand` Checking strand for correctness [Default: true]

`--covout` Coverage output (Under construction)

`--statout` Statistics output

19 PrecisionRecallGraphDataGenerator

Generates a data table for precision recall graphs. This module assumes one alignment (it can contain multiple partial alignments) per one query. You need to use the same alignment joining module parameters if the alignment file is generated by OMTools mapper. If you are using other alignment tools, set alignmentjoinmode as 0.

19.1 Reference Reader Options

`--refmapin` Input reference map file [Required]

`--refmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

19.2 Data Reader Options

`--optmapin` Input optical map file [Required]

`--optmapinformat` -1: Auto-detected from file extension; 0: Reference Standard Format (REF) (Equivalent to SILICO format); 1: fasta-01 format (FA01); 2: Spots File Format (SPOTS); 3: Molecule Standard Format (DATA); 4: Molecule Simulation Format (SDATA); 5: BNX File Format (BNX); 6: CMAP File Format (CMAP); 7: SOMA opt format (OPT); 8: SOMA silico format (SILICO) (Equivalent to REF format); 9: OpGen XML Format; 10: Valouev data format; 11: Maligner maps format; [Default: -1]

`--bnxsnr` BNX SNR filter value [Default: 3.0]

19.3 Result Reader Options

`--optresin` Input alignment result file [Required]

`--optresinformat` -1: Auto-detected from file extension; 0: OM Alignment Format (OMA); 1: OM Detailed Alignment Format (OMD); 2: XMAP format (XMAP); 3: Valouev et al. format; 4: SOMA v2 Unique Match Format; 5: Twin PSL Format; 6: Maligner ALN Format; [Default: -1]

19.4 Alignment Joining Options

`--alignmentjoinmode` Mode. 0: No joining. 1: Standard indel joining. 2: Standard indel-inv joining. 3. Standard transloc joining [Default: 0]

`--closeref` The maximum distance (reference) between two partial alignments to be joined [Default: 250000]

`--closefrag` The maximum distance (query) between two partial alignments to be joined [Default: 250000]

`--minmatch` Minimum matching signals to be considered as a valid partial alginment. [Default: 3]

`--maxtrim` Maximum trimming steps for a partial alignment [Default: 5]

`--trimear` Scaling error tolerance during trimming [Default: 0.1]

`--match` Score for matching signal [Default: 5]

`--fpp` Penalty for extra signal [Default: 2]

`--fnp` Penalty for missing signal [Default: 2]

`--indelp` Penalty for joining partial alignments with indel relationship [Default: 10]

`--invp` Penalty for joining partial alignments with inversion relationship [Default: 30]

`--transp` Penalty for joining partial alignments with translocation relationship [Default: 50]

`--localpenalty` Enable local-alignment penalty for the final alignment (treated as global alignment) [Default: false]

`--minjoinscore` Minimum score of the joined final alignment [Default: 30]

`--minconf` Minimum confidence (uniqueness) of the final alignment [Default: 0.4]

`--minjoinedfragratio` Minimum ratio of aligned length against query length [Default: -1.0]

`--minjoinedsigratio` Minimum ratio of number of aligned signals against total number of query signals [Default: -1.0]

`--overlapalign` Allow overlapping final alignments to be output [Default: true]

`--maxalignitem` Maximum number of final alignments output. -1: No limit on the number of final alignments [Default: 1]

19.5 Precision Recall Graph Options

`--prgout` Precision recall graph table output [Required]

`--checkstrand` Checking strand for correctness [Default: true]

`--sortstrat` Sort by "score" or "confidence" [Default: score]

Part VI
Visualization

20 OMView

Visualizes optical mapping data. OMView provides a GUI to visualize optical mapping data for different purposes.

20.1 Data Loading

`--viewrefin` Load references

`--viewmapin` Load molecules

`--viewresin` Load alignment results

`--viewcblin` Load collinear blocks

`--viewcboin` Load collinear blocks (order)

`--viewcbcin` Load collinear blocks (color)

`--viewannoin` Load annotations

20.2 View Opening

`--viewregion` Show a specific region on a regional view

`--viewanchor` Show a specific anchor on an anchor view

`--viewalignment` Show a specific alignment

`--viewma` Automatically open multiple alignment view [Default: false]

`--viewmolecule` Automatically open molecule view [Default: false]

`--viewsave` Save views to specific location instead of starting OMView

`--viewsaveformat` Formats of image to be saved. [svg; png; jpg;] [Default: png]

20.3 View Settings

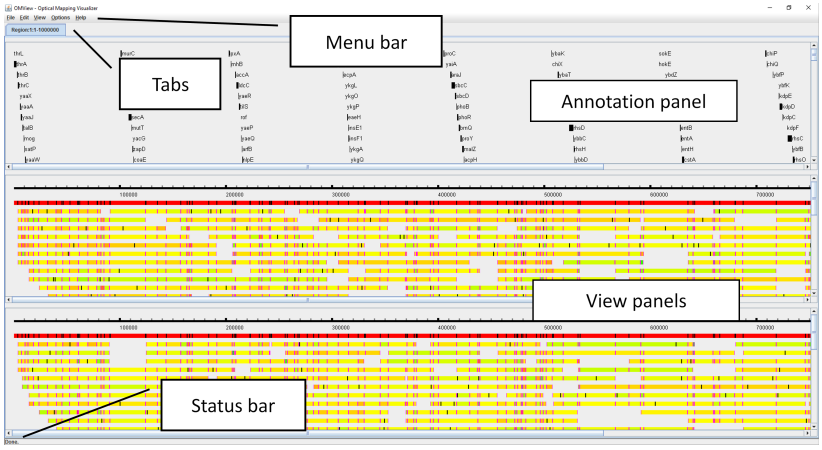
`--viewbreakresult` Enable Result Breaker [Default: false]

20.4 Help

`--help` Display help menu

20.5 Visualization Procedures

20.5.1 Layout of OMView

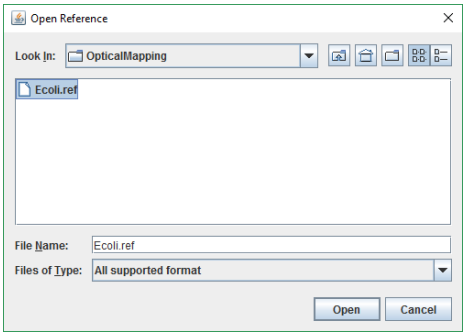


20.5.2 Load required data

There are two ways to load data into OMView: (1) Load datasets from the menu option and (2) Drag and drop data sets into the program.

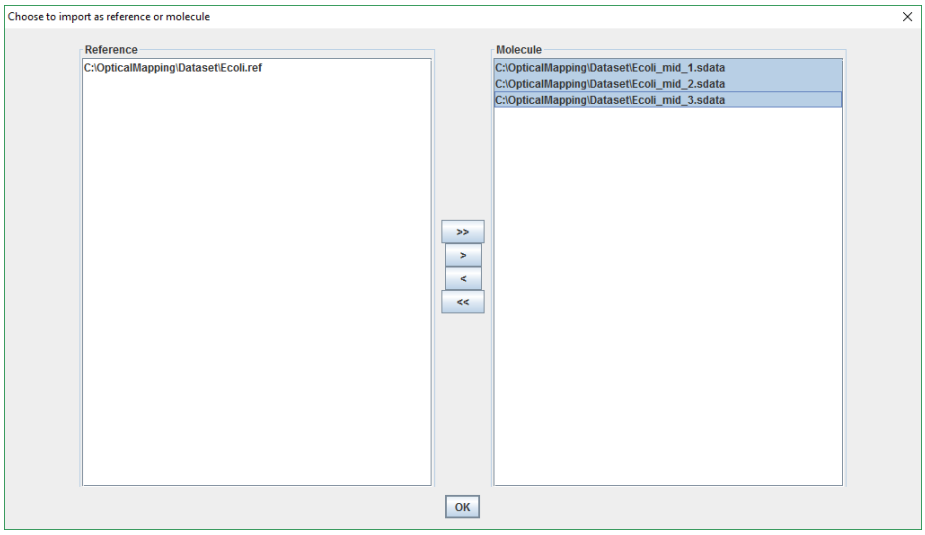
Note: Users must load the reference and molecule files first before loading other files (Alignment, annotations and multiple alignments files)

Select data files from menu After choosing the data file to loaded (**File→Load**) select the target file and click **Open**.



Drag and drop datasets Multiple files can be dragged and dropped into the program at the same time.

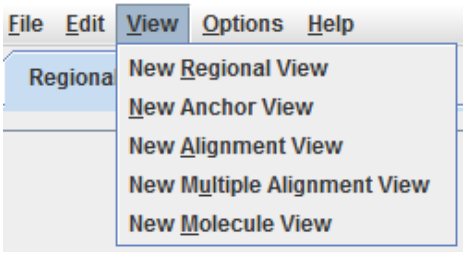
Since the formats for reference and molecule files are the same, users need to specify whether the files are loaded as reference or molecules.



File dependency

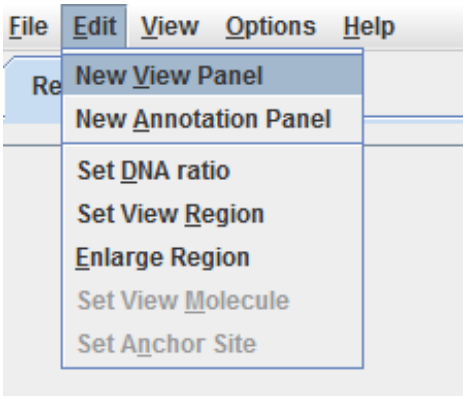
- Reference and molecules: No requirements on other data files. Note that the reference ID should not be duplicated among all reference files. Similarly, molecule ID should not be duplicated.
- Alignments: Require references and molecules (If alignment file contains molecule information, the loading of molecule file is not needed)
- Annotations: Require reference
- Multiple alignments: Require molecules

20.5.3 Starting a view



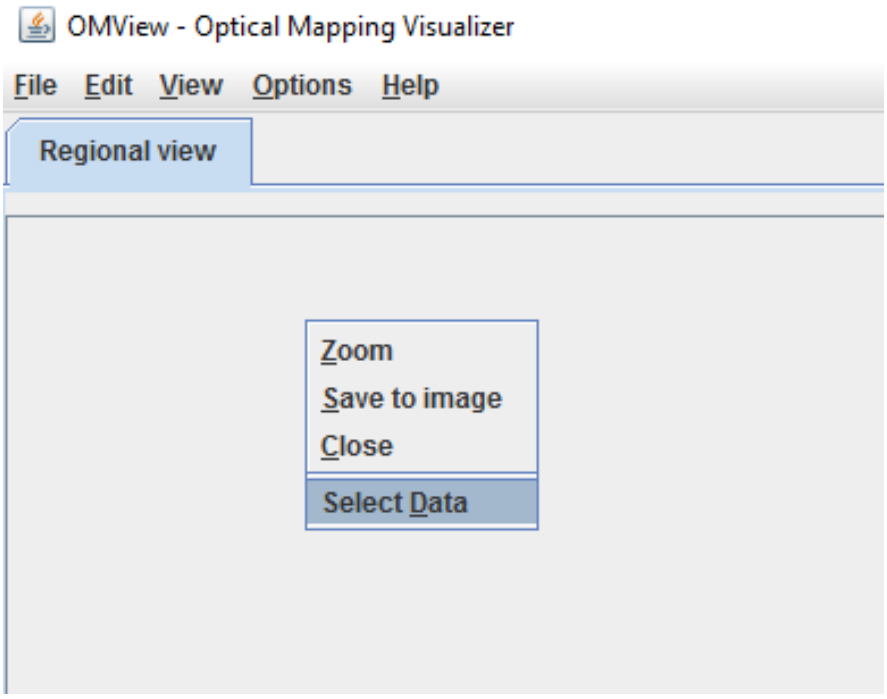
Users can open new view tabs under the menu **View**. By default, OMView will initialize with a new blank regional view.

Each tab contains a view panel by default. Some views support visualization of more than one view panels (regional view, anchor view and molecule view)



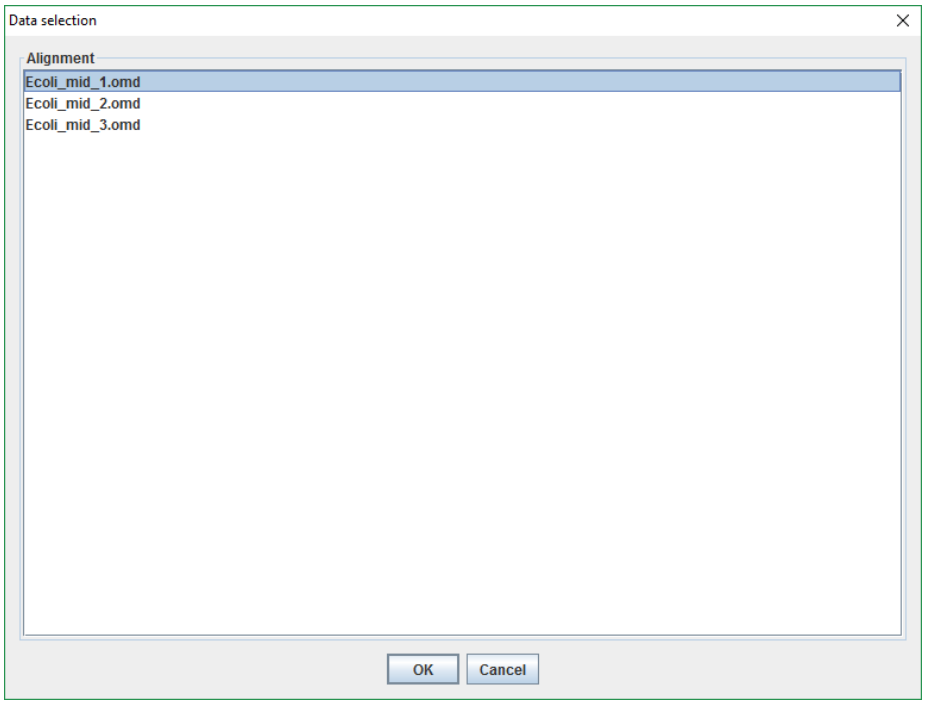
and annotation panels (regional view and anchor view) in the same tab. Users can insert new panels under the menu **Edit**.

20.5.4 Select data in the view panel



From the right click menu for each view panel, choose **Select Data** to select the data to be displayed.

A dialog will open for users to choose the data. Note that if more than one set of alignment results are loaded in the same view panel, make sure their



respective molecule IDs are distinct.

20.5.5 Procedures on specific views

Regional view Regional view displays alignments as an overview at a selected region.

After opening a regional view tab, set the target region as X:NNNNNN-NNNNNN (**Edit** → **Set View Region**). A reference (red rectangle) with signals (black vertical bars) should appear.

Note: The reference name should be consistent with that in the dataset. A common mistake in setting the region is messing up the reference name "chr1" or "1".

After selecting the alignments and annotations, the results will be displayed in the view panels. Aligned portion of molecules are shown in a color spectrum (from green to red depending on the scaling factor from 0.5 to 1.5, where yellow implies scaling factor 1) with pink and black signals indicating mapped or unmapped signals.

Move the cursor on the signal to display its information. To display details of alignment of a certain molecule, simply click on the target molecule and a new alignment view tab will be created. To view all molecules aligned to a specific reference signal, click on that signal to create a new anchor view.

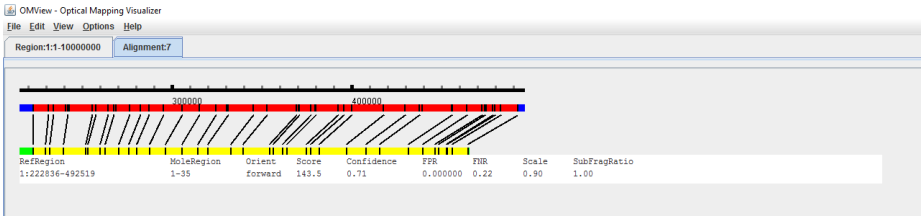
Example: (Reference) Ecoli.ref, Ecoli_mid_1.omd, Ecoli_mid_2.omd, Ecoli_mid_3.omd, Ecoli.gff

Anchor view Anchor view displays alignments that match selected signals to validate structural variations

The procedure of setting is similar to that in regional view. After opening the anchor view tab, set the anchor site as X:NNNNNN-NNNNNN (**Edit**-¿**Set Anchor Site**). Note that the anchor site must represent the position of one or two signals. Users can set the region as X:NNNNNN-NNNNNN (**Edit**-¿**Set Region**). By default region is set to 200 kbp away from the anchor sites.

Example: (Reference) Ecoli.ref, Ecoli_mid_1.omd, Ecoli_mid_2.omd, Ecoli_mid_3.omd, Ecoli.gff

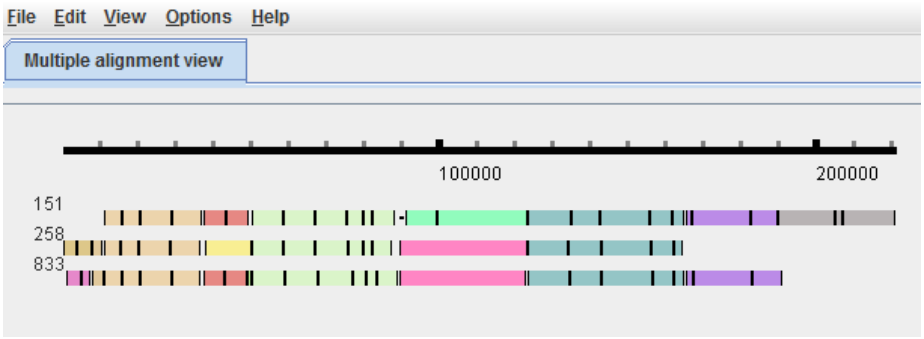
Alignment view Alignment view displays alignment detail of a single molecule.



In alignment view, set the molecule ID to view the details of an alignment (**Edit** $\rightarrow$ **Set View Molecule**). Users will receive a warning message if an alignment does not exist for the selected molecule.

Example: (Reference) Ecoli.ref, Ecoli_mid_1.omd

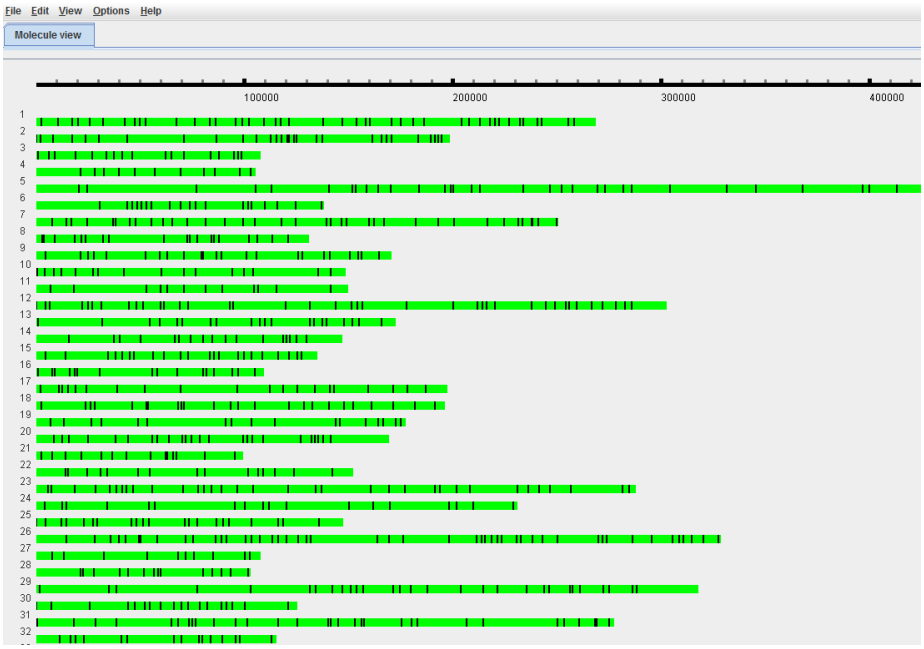
Multiple alignment view Multiple alignment view displays the multiple alignments of all queries for genomic comparison.



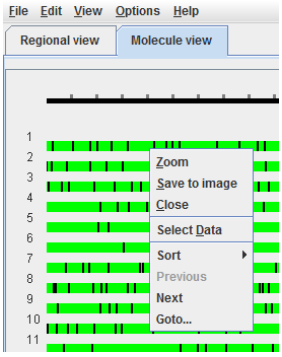
Multiple alignment view displays automatically once you set the data. If the color file (.cbc) is not provided, random color will be assigned to the collinear blocks.

Right click to sort and manipulate the multiple alignments. Users could save the current multiple alignment after the manipulation. A counting function is also available and the statistics is output in the console.

Example: (Molecule) Ecoli_MA.sdata, Ecoli_MA.cbl, Ecoli_MA.cbo, Ecoli_MA.cbc



Molecule view In molecule view, a panel displays a page that contains 100 molecules. Go to another page using the right click menu items Previous, Next, and Goto. A sorting function is also available to sort the molecules by molecule size, number of signals in the molecules, or molecule name.

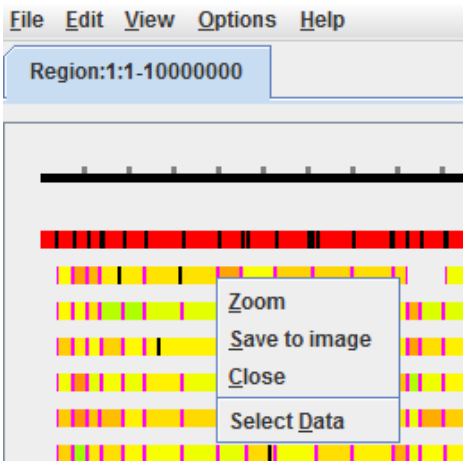


Example: (Molecule) Ecoli_mid_1.sdata

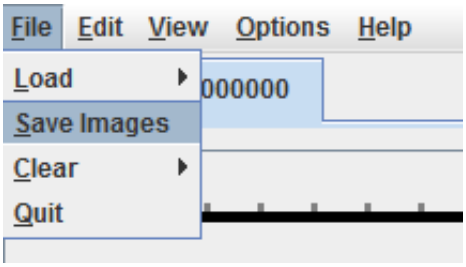
20.5.6 Export image

Images could be exported in individual panels or multiple panels in SVG, PNG and JPG formats.

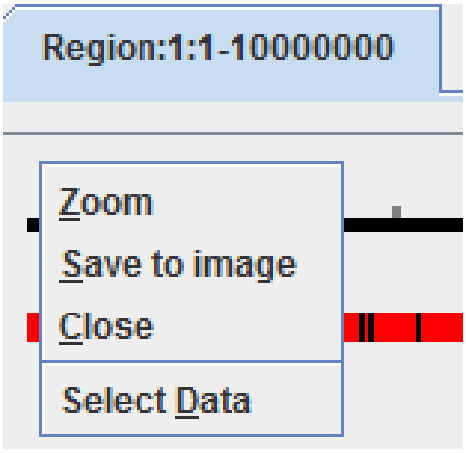
Individual panel From the right click menu, users could select Save to image to save the current view panel.



All panels under the same tab Users could select the menu File-¿Save images to save all view panels in the current tab to a single image.



20.5.7 Closing tabs and panels



To close the tab, click the tab with middle mouse button. To close the view panel, right click on the panel and select close.

20.6 Frequently Asked Questions (FAQs)

Q: Can I choose multiple items at the same time to import reference or select data?

A: Yes. Hold the control key when you choose multiple items.

Q: I loaded all the files including references, molecules and alignment results but don't see anything. Whats wrong?

A: To visualize the reference and the alignment results, (1) you have to select the data in the view panel (**Select Data** from the right click menu); and (2) a view region must be set by **Edit→Set View Region**.

Q: I set view region or anchor site to visualize my data, but get the error of Reference not found. Whats wrong? A: The most common cause for the error is an incorrect input of a reference name. Note for the difference between "chr1" "Chr1", "CHR1", and "1".

Q: Why is the file loading speed very slow after loading half of my data?

A: Ensure that you have enough memory to store all the data. Use the parameter Xmx to allocate more memory to Java machine. Dont load too many data into an OMView instance if your machine does not have enough memory.

Q: The loading speed of regional view is slow.

A: Try to limit the range of region. Usually a region larger than 1 Mbp takes some time to completely load.

Q: What formats does OMView accept?

A: Reference and molecule file formats: REF, FA01, SPOTS, DATA, SDATA, BNX, CMAP, OPT, SILICO, and OpGen XML
Alignment result formats: OMA, OMD, XMAP, Valouev et al., SOMA v2 Unique Match, and Twin PSL
Annotation formats: BED, GVF, and OSV