

=====

AgilentReadTrimmer

=====

AgilentReadTrimmer is a tool for removing adaptor sequences from targeted high-throughput sequencing data. It utilizes paired-end information by looking at the 5' overlap of both mates, as well as searching for an expected adaptor motif via a semi-global alignment.

AgilentReadTrimmer is implemented in Java.

License

=====

(This is the MIT license.)

Copyright (c) 2013 Magnus Isaksson, Ashutosh, Barbara Novak, (Agilent Technologies)

Permission is hereby granted, free of charge, to any person obtaining a copy of this software and associated documentation files (the "Software"), to deal in the Software without restriction, including without limitation the rights to use, copy, modify, merge, publish, distribute, sublicense, and/or sell copies of the Software, and to permit persons to whom the Software is furnished to do so, subject to the following conditions:

The above copyright notice and this permission notice shall be included in all copies or substantial portions of the Software.

THE SOFTWARE IS PROVIDED "AS IS", WITHOUT WARRANTY OF ANY KIND, EXPRESS OR IMPLIED, INCLUDING BUT NOT LIMITED TO THE WARRANTIES OF MERCHANTABILITY, FITNESS FOR A PARTICULAR PURPOSE AND NONINFRINGEMENT. IN NO EVENT SHALL THE

AUTHORS OR COPYRIGHT HOLDERS BE LIABLE FOR ANY CLAIM, DAMAGES OR OTHER LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM, OUT OF OR IN CONNECTION WITH THE SOFTWARE OR THE USE OR OTHER DEALINGS IN THE SOFTWARE.

#### Dependencies

=====

Depends on the Picard framework (<http://picard.sourceforge.net>,  
Apache License V2.0, MIT License)

#### Installation of existing JAR file

=====

Copy the jar file that matches your java JRE to your local disk.

#### Installation From Source

=====

AgilentReadTrimmer's deployment is currently based on Apache Ant and Ivy. To build a runnable jar-file:

1) Enter extracted, or checked out, source code folder.

```
$ cd AgilentReadTrimmer
```

2) Execute Ant.

```
$ ant
```

3) To create a jar-file (file will be located in "AgilentReadTrimmer/jar").

```
$ ant jar
```

Running

```
=====
```

Example 1 (provides usage for AgilentReadTrimmer):

```
$ java -jar AgilentReadTrimmer.jar
```

Example 2 (trims standard Illumina multiplexing adaptors):

```
$ java -jar AgilentReadTrimmer.jar -m1 mate1.fastq.gz -m2 mate2.fastq.gz -o results/trimmed_
```

Example 3 (trims SureSelect QXT adaptors):

```
$ java -jar AgilentReadTrimmer.jar -m1 mate1.fastq.gz -m2 mate2.fastq.gz -o results/trimmed_ -qxt
```