

Arioc User Guide

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Arioc User Guide

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Introduction

Arioc is a set of computer programs that carry out the alignment of short DNA sequences to a large reference sequence or genome.

There have been numerous attempts to use GPU (general-purpose graphics processing unit) hardware to accelerate the process of DNA sequence alignment – but this has turned out to be “easier said than done.” Arioc is unique because it was designed and engineered expressly to use GPU hardware to maximize the speed of DNA sequence alignment without sacrificing functionality or accuracy.

GPU acceleration of short read alignment

GPU programming requires software-development techniques that aren't needed for programs that run exclusively on a CPU. GPU hardware can run tens of thousands of threads of execution concurrently, but speed improvements in GPU software are not obtained simply by replicating source code that runs efficiently on one or two dozen CPU threads.

There are two fundamental reasons for this. One has to do with the way GPUs manage threads. In Nvidia's CUDA environment (for which Arioc is implemented), threads execute in fixed-size groups of 32, in which each thread simultaneously executes the same instruction on different data. This SIMD (single instruction, multiple data) model constrains the layout of data in memory as well as the structure of source code, so algorithms that operate efficiently in CPU threads are often suboptimal when executed in SIMD threads on a GPU. Algorithms that contain a great deal of branching logic must be carefully redesigned to accommodate SIMD parallelism.

The second, and perhaps more important, reason why GPU application speeds don't scale in direct proportion to the number of available GPU threads is that there isn't enough memory bandwidth to keep up with all those threads. Consequently, GPU programming involves writing code that conforms to a variety of memory-layout and memory-addressing constraints. This can fundamentally change assumptions that are taken for granted in algorithms that run efficiently on CPUs. Of course, memory optimization techniques are important in CPU software engineering as well, but the idiosyncrasies of GPU memory tend to dominate other considerations in choosing optimal algorithms for a GPU application.

This all means that, in practice, a 10-fold speedup in a GPU-based sequence-alignment application (compared to a multi-threaded CPU-based implementation that performs the same computational task) represents a reasonable "return on investment" [Anderson, 2011]. (A hundred-fold GPU-versus-CPU speedup would be extraordinary and make one wonder whether the corresponding CPU application had been properly optimized!) As far as Arioc is concerned, we did not release the software until we reached this 10x threshold.

How Arioc is different

The central problem in read alignment is essentially that of quantifying the similarity between two strings of symbols. This problem has attracted a great deal of attention since the early 1980s, and several successful algorithms have been developed in response. Of these, two dynamic-programming techniques — one using weighted scores for mismatches and gaps [Smith and Waterman, 1981] and the

other using Levenshtein edit distance [Ukkonen, 1983] — are the predominant algorithms in modern read aligners. Arioc uses the Smith-Waterman algorithm, which consistently finds better mappings for reads that contain multiple insertions and deletions [Wilton et al, 2015], even though it requires more computational effort than edit-distance alignment.

String similarity computations are time-consuming and use a large amount of memory. With a reference sequence the size of the human genome, it is impractical to align a read by computing similarity at every location in the entire genome. For this reason, read aligners perform a great deal of preliminary work to narrow down the number of reference-sequence locations at which they must compute alignments. This work cannot easily be reduced to a single algorithmic description. Instead, read aligners rely on heuristics and on software-engineering considerations to limit the number of reference-sequence locations they examine (and ultimately the number of string-similarity computations they perform) for each read.

It is here that GPU-based parallelism can greatly improve performance. Arioc implements a well-known technique known as "seed and extend" [Altschul, 1992] using parallel sorting and adjacent-neighbor comparisons on long, one-dimensional arrays of integers. Such operations are well suited to SIMD implementation on GPU hardware. In Arioc, GPU acceleration of this aspect of the read-alignment process is essential to obtaining high throughput.

What Arioc is (and isn't)

Arioc is a read aligner that uses GPU acceleration to find high-priority locations at which to compute alignments and then to compute them. These are the two most significant computational bottlenecks in a short-read aligner. Arioc uses GPU hardware to accelerate these computations and thereby achieve higher throughput [Wilton et al, 2015].

What Arioc does

Arioc accepts as input a large number — typically, hundreds of millions — of short sequencer reads. For each such read, Arioc reports the locations within a given reference sequence where a highly similar subsequence is found.

Ideally, Arioc would find a perfect and unique mapping for every read; there would be exactly one location in the reference sequence where each read sequence precisely matches the reference sequence. In practice, of course, many reads do not map perfectly or uniquely within a given reference sequence. For such reads, Arioc reports what it considers to be the "best" mapping (or mappings). Arioc does these things rapidly and accurately.

Nongapped and gapped alignment

For each sequencer read, Arioc first tries to find alignments that contain no gaps (insertions or deletions) and no more than a few differences between the read sequence and the reference sequence. The "spaced seed" algorithm that Arioc uses for these alignments is very fast, and Arioc's overall speed is greatly improved by identifying nongapped mappings prior to computing Smith-Waterman alignments.

Input and output data

Arioc expects FASTA-formatted reference sequences and FASTQ-formatted sequencer reads. It generates SAM-formatted output that includes an alignment score (AS) and mapping quality score (MAPQ) for every mapping it finds. Arioc's output can thus be used by any software tool that can handle alignment results from CPU-only aligners such as BWA [Li, 2013] or Bowtie 2 [Langmead and Salzberg, 2012].

Arioc has several "database-oriented" features in its implementation. One of Arioc's original design goals was to carry out read alignment on sequence data residing in relational database tables. For this reason, Arioc can create output files in the binary data format used by the Microsoft SQL Server for high-speed "bulk" input.

Arioc was designed to align large amounts of sequencer data to genomes the size of the human reference genome. If you are processing sequencer reads on a terabyte or petabyte scale, we assume that you have the CPU, GPU, memory, and disk space resources required by Arioc. We also provide a variety of parameterization options that let you tune Arioc's performance to your specific hardware and data-analysis requirements. (See [Tuning for speed and sensitivity](#), page 31.)

What Arioc does not do

Arioc is not a tool for searching a database of short sequences and ranking those sequences by their similarity to a given sequence. (CUDASW++ [Liu et al, 2013] is perhaps the best-known GPU-accelerated

tool for this.) Arioc does not operate with any sequences other than DNA; it does not understand any sequence "alphabet" other than ACGTN. It does not report SNPs or recognize structural variations. It does not do multiple sequence alignment or assemble sequencer reads in any way.

Finally, Arioc is not by any means a "simple", "turnkey", or "one size fits all" tool. Instead, Arioc exposes a variety of user-configurable parameters that let you optimize speed and sensitivity (or trade one for the other). Although this approach exposes the complexity of the read-alignment process, it provides the ability to fine-tune Arioc's performance to high-performance computing hardware and to the specific characteristics of sequencer read data.

The GPU software-development landscape continues to evolve. Since its initial release, Arioc has grown and adapted to newer, faster GPU hardware and software libraries. We think Arioc's approach to the read-alignment problem is sound, and that its accuracy and speed make it a compelling alternative to CPU-only alignment software as DNA sequencers generate ever-increasing quantities of WGS and WGBS reads to align.

Installation

Arioc is written in C++ and compiled for the Nvidia CUDA environment. The same code base is used for both Windows and Linux.

Hardware requirements

Arioc requires the following minimum hardware:

- a multi-core 64-bit Intel- or PowerPC-compatible CPU
- at least 80 gigabytes of free memory; more memory required for larger reference genomes
- enough disk space to store reference sequences, reads, and alignment results
- at least one Nvidia GPU of compute capability 3.5 or greater, with at least 5 gigabytes of GPU memory

We have tested Arioc on the following Nvidia GPU microarchitectures:

- Kepler
- Maxwell
- Pascal
- Volta
- Ampere

CUDA

The current version of Arioc was developed and tested with the following minimum CUDA versions:

- Nvidia video driver v471.11
- CUDA runtime version 11.4

We recommend using the most recent stable versions of these products to run Arioc.

Operating systems

Arioc requires a 64-bit operating system. It is compatible with the following minimum operating-system versions:

- Windows 7 (64-bit)
- Windows Server 2008 R2 datacenter
- RHEL Scientific Linux v7.2

Arioc should be compatible with more recent versions of these operating systems as well as with other recent Linux distributions.

Installation

Windows

Install using the Windows installer and the Arioc setup package (AriocSetup.msi). For source code only, unzip the Arioc.w.151.zip archive.

Linux

Unzip the Arioc.x.151.zip archive and build from source code.

Building from source code

The source code for is available in an archive whose name embodies the operating system and release version number. The Windows sources for release 1.51 are found in `Arioc.w.151.zip`; the Linux sources for the same release are in `Arioc.x.151.zip`.)

The same sources can be compiled for Windows and for Linux:

- In Windows, use Microsoft Visual Studio 2019 or later to load the Arioc solution (`Arioc.sln`). You may need to edit the associated `.vsproj` files to reference the version of the CUDA SDK installed in your development environment.
- In Linux, use GNU make and the makefile in the top-level directory of the source-code distribution. Build each Arioc binary separately:

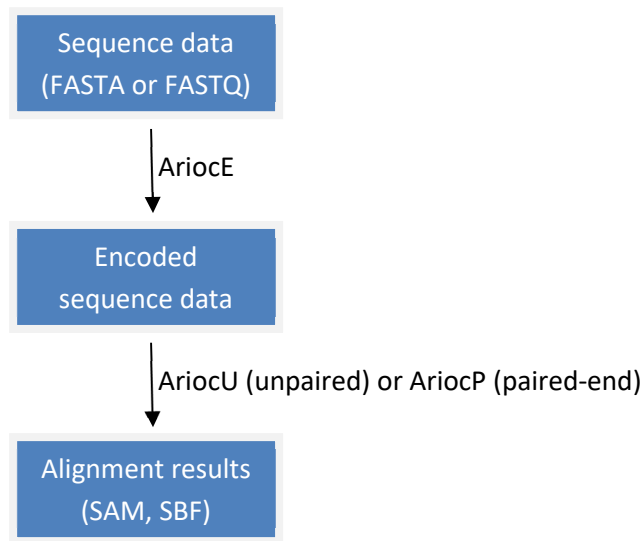
```
make clean
make AriocE
make AriocU
make AriocP
```
- You may verify your Arioc installation using the test data distributed in the `Arioc.RQA.151.zip` archive. The `readme.txt` file in that archive contains additional details.

Arioc runtime roadmap

There are three executable binaries in the Arioc distribution:

- AriocE: encodes sequence data
- AriocU: aligns unpaired reads
- AriocP: aligns paired end reads

Here is how they are used:



The three executables are described in detail in the sections that follow.

Arioc command-line syntax

Each of the Arioc executables obtains its runtime configuration from an XML-formatted configuration file, so the command-line syntax for running them is simple:

```
AriocE config_filename  
AriocU config_filename  
AriocP config_filename
```

where config_filename is the name of the configuration file to use.

Arioc error messages

In general, Arioc error messages contain condensed information that identifies the source-code location that detected the error, along with human-readable text that explains the nature of the error. For example, if Arioc cannot open the configuration file you specify, it emits an error message like the following:

```
44:37.416 [00001704] ApplicationException ([0x5892] AriocAppMainBase.cpp 715):  
XMLDocument::Loadfile( "AriocP.cfg" ) failed with error 3: file not found  
XML error details:  
AriocP.cfg
```

If Arioc produces an error message whose origin is not immediately apparent, you can usually find the cause of the problem by taking additional debugging and internal monitoring steps (see [Troubleshooting, page 42](#)).

Arioc input and output

Arioc writes status and error messages to the stderr device. In practice, this means that all output appears in the console by default. If you want to redirect console output to a file, use command-line redirection syntax. For example:

```
AriocU test23.cfg 2> test23.log
```

For sequence input and alignment results, Arioc uses the files you specify in the configuration (.cfg) file.

AriocE: encoding sequence data

The AriocE component transforms raw sequence data from FASTA or FASTQ format into the binary format read by the AriocU and AriocP executables. Encoded sequence data resides in separate files whose contents can be distinguished by filename extension:

- \$a21.sbf, \$a21.rc.sbf: encoded forward and reverse-complement bases (3 bits per base, 20 bases per 64-bit value)
- \$raw.sbf, \$raw.rc.sbf: ASCII representation of the sequence data (forward and reverse complement)
- \$sqm.sbf, \$sqm.rc.sbf: sequence metadata (FASTA or FASTQ description line)
- \$sqq.sbf, \$sqq.rc.sbf: sequence quality scores (for FASTQ-formatted input only)

For example, encoded sequence data for human chromosome 1 might reside in the following set of files:

```
hs_ref_GRCh38_chr1$a21.sbf
hs_ref_GRCh38_chr1$a21.rc.sbf
hs_ref_GRCh38_chr1$raw.sbf
hs_ref_GRCh38_chr1$raw.rc.sbf
hs_ref_GRCh38_chr1$sqm.sbf
hs_ref_GRCh38_chr1$sqm.rc.sbf
```

Before using the Arioc aligners, AriocU and AriocP, you must encode both a reference sequence and a set of reads to align. Encoding is a one-time-only procedure. You can re-use the encoded files for multiple invocations of either the AriocU or AriocP executables.

Encoding unpaired reads

Encoding reads with AriocE is straightforward. For each FASTA file, AriocE generates \$a21, \$raw, and \$sqm files; for FASTQ input, AriocE generates a \$sqq file as well.

The configuration file you provide to AriocE, in addition to specifying input and output filenames, contains "metadata" that is passed to the AriocU or AriocP aligners:

```
<?xml version="1.0" encoding="utf-8"?>

<AriocE>

  <dataIn sequenceType="Q">
    <file subId="1">C:\test103\i100p_1.fastq</file>
  </dataIn>

  <dataOut>
    <path>C:\BulkData\Q\Mason\test103</path>
  </dataOut>

</AriocE>
```

[Simple configuration file for AriocE \(unpaired reads\).](#)

In the XML configuration file, the sequenceType= attribute of the <dataIn> element indicates that the input sequences are to be encoded as reads. The <dataIn> element also contains one or more <file>

elements, each of which specifies the fully qualified name of an input file. Similarly, the <dataOut> element contains a <path> element that contains the fully qualified name of the output directory.

AriocE requires that you use the subId= attribute of each <file> element to assign a "subunit ID" number to each input file. (Think of the subunit ID as a chromosome number for a reference genome or a sample subset identifier for a set of reads.) The subunit ID can be any integer between 1 and 127. AriocE combines the subunit ID, the data-source ID (specified as srcId= in the <dataIn> element), and an ordinal to create a unique 64-bit integer sequence identifier for every input sequence in every file you specify.

Although it was originally intended to simplify the automation of the sequence-alignment process, the use of an XML configuration file provides flexibility in parameterization as well as an opportunity to accompany runtime parameters with human-readable documentation. Here is an example of a more complex configuration file:

```
<?xml version="1.0" encoding="utf-8"?>

<AriocE>

  <dataIn sequenceType="Q" srcId="1">
    <!-- The following rg element defines read-group attributes common to all files -->
    <rg CN="JHU PHA" DS="test 103" PL="ILLUMINA" />

    <!-- Each file is associated with different read group ID and SM attributes -->
    <file subId="1" ID="RG1" SM="sample 1: 11221">C:\test103\i100p_1.fastq</file>
    <file subId="2" ID="RG2" SM="sample 1: 11222">C:\test103\i100p_2.fastq</file>
  </dataIn>

  <dataOut>
    <path>C:\BulkData\Q\Mason\test103</path>
  </dataOut>

</AriocE>
```

Configuration file for AriocE (unpaired reads) with comments, optional parameters (XML attributes), and SAM-style read groups.

This configuration encodes two different files. It also illustrates how AriocE associates read group information with reads. The read group associated with each file is the union of the SAM-conformant read group attributes (ID, CN, DS, PL, and SM) from the <rg> and <file> elements. (The <rg> element defines read group attributes that are common to all the files; the <file> element defines attributes specific to individual files.) AriocE copies the consolidated read group attributes for each file into an associated metadata file in the output directory. The Arioc aligner (AriocU or AriocP) subsequently uses these metadata files to generate appropriate @RG headers and RG tags in SAM-formatted output.

Here is a summary of the optional XML elements and attributes that control the runtime configuration of AriocE:

Element	Attribute	Description
<AriocE>	maxDOP	Number of concurrent CPU threads
<dataIn>	srcId	Data source ID (between 0 and 4,194,303)
	QNAME	Encodes only the parenthesized fields in the FASTQ define
	SAMtags	Encodes the parenthesized fields as SAM fields
	qualityScoreBias	Bias (offset) for encoding base quality scores (33 or 64)
<rg>	ID CN DS DT FO KS LB PG PI PL PU SM	SAM read group fields (common to all input files)
<file>	SN	SAM sequence name field ID
	ID CN DS DT FO KS LB PG PI PL PU SM	SAM read group fields (merged with fields in the <rg> element)

Optional elements and attributes in the AriocE configuration file for encoding unpaired reads.

The QNAME= and SAMtags= attributes in the <dataIn> element, as well as the ID= attribute in the <rg> element, accept a simple wildcard pattern that parses subfields from the FASTQ definition line ("define") associated with each read. Each pair of parentheses in the pattern identifies a substring to extract from the define.

This technique makes it possible to generate meaningful SAM-formatted QNAME and RG (read-group) identifiers using the information in the FASTQ define for each read. For example, given a read with a CASAVA-formatted FASTQ define [Illumina, 2015]:

```
ERR037901.323683141 509.8.45.13203.181161/1
```

you can specify `<dataIn ... QNAME="(*) *(/*)">` to cause AriocE to generate the QNAME string ERR037901.323683141/1. Similarly, you can use `<rg ... ID="* (*.*).">` to associate the read with a read group whose ID is 509.8.

AriocE uses the same wildcard pattern syntax to copy one or more SAM fields from each FASTQ define into the corresponding SAM output records. Consider, for example, a FASTQ define that contains CASAVA-formatted read information, a space, and two SAM-formatted fields separated with a tab character:

```
@A112233:4127:HC3MGFFIY:2:679:9341:1024 BC:Z:ATGGTAGC+NGATCGACtabid:H:00000408
```

You could specify `SAMtags="* (*)\t"` as a <dataIn> attribute to cause AriocU or AriocP to copy the BC field into the corresponding SAM output, or simply `SAMtags="* (*)"` to copy everything after the space.

AriocE converts tabs in the define into spaces in the corresponding QNAME, so substrings extracted from the define become space-separated fields in a formatted QNAME. For example, this define:

```
@00000001/2 sx:i:13tabrx:Z:14tabpx:i:94362283tabvx:i:284
```

can be converted to the following QNAME

```
00000001/1 13 chr14 94362283 284
```

using `QNAME="(*/*)*:*:(*\t)*:*:(*\t)*:*:(*\t)*:*:(*)"` in the `<dataIn>` element. (Alternatively, the attribute string `QNAME="(*/*)sx:i:(*\t)rx:Z:(*\t)px:i:(*\t)vx:i:(*)"` would produce the same result.)

Encoding paired end reads

The AriocE configuration file for paired end reads uses the same parameters as the configuration file for unpaired reads, but it uses an additional XML attribute (`mate=`) to indicate the files in which mate 1 and mate 2 are found.

```
<?xml version="1.0" encoding="utf-8"?>

<AriocE>

  <dataIn sequenceType="Q">
    <file subId="1" mate="1">C:\test103\paired\i100p_1.fastq</file>
    <file subId="1" mate="2">C:\test103\paired\i100p_2.fastq</file>
  </dataIn>

  <dataOut>
    <path> C:\BulkData\Q\Mason\test103</path>
  </dataOut>

</AriocE>
```

Simple configuration file for AriocE (paired end reads).

Multiple input files

It is possible to encode multiple input files (or, more exactly, pairs of input files) by using the `subId=` and `mate=` attributes of the `<file>` element:

```
<?xml version="1.0" encoding="utf-8"?>

<AriocE>

  <dataIn sequenceType="Q" srcId="110114">
    <file subId="5" mate="1">E:\yh110114\s_5_1_sequence.txt</file>
    <file subId="5" mate="2">E:\yh110114\s_5_2_sequence.txt</file>
    <file subId="6" mate="1">E:\yh110114\s_6_1_sequence.txt</file>
    <file subId="6" mate="2">E:\yh110114\s_6_2_sequence.txt</file>
    <file subId="7" mate="1">E:\yh110114\s_7_1_sequence.txt</file>
    <file subId="7" mate="2">E:\yh110114\s_7_2_sequence.txt</file>
  </dataIn>

  <dataOut>
    <path>C:\BulkData\Q\yh110114</path>
  </dataOut>

</AriocE>
```

Configuration file for AriocE (paired end reads) with multiple input files and optional parameters.

Nevertheless, you should exercise caution when you encode multiple input files (or pairs of input files) because AriocE cannot recognize different layouts among the input files. For example, files that

originate from different sequencer runs may have different define layouts or may use a different bias to encode base quality scores (e.g., 33 for Sanger, 64 for Illumina v1.3 and later).

Encoding a reference sequence

Encoding a reference sequence or genome is like encoding reads in that AriocE creates binary files that encode the sequence data and metadata. In addition, for a reference sequence or genome, AriocE builds a set of lookup tables (hash tables) that are used in both AriocU and AriocP.

Input files

AriocE accepts reference sequence files in FASTA format only. Each reference sequence file should be identified with a distinct "subunit ID" (subId=) attribute in the AriocE configuration file.

When a FASTA file contains only one reference sequence, you should specify the sequence name (corresponding to the SN tag in a @SQ record in SAM/BAM format) explicitly in the .cfg file:

```
<file subId="1" SN="chr1">chr1.fna</file>
<file subId="2" SN="chr2">chr2.fna</file>
<file subId="3" SN="chr3">chr3.fna</file>
```

When a FASTA file contains multiple sequences, AriocE extracts the sequence name for each sequence in the file from the FASTA define for that sequence. In this case, AriocE uses a parenthesized wildcard specification (see above, page 13) to parse each define, and you must use the same field-formatted layout for every define in the file. For example, given a reference sequence with the following FASTA-formatted define:

```
>acc|GENBANK|AF338823.1|linear|Possum adenovirus 1
```

you can specify `<file ... SN="*|*|(*)">` to cause AriocE to associate the SN string AF338823.1 with this reference sequence.

Two-pass encoding

AriocE encodes each sequence and then indexes the encoded sequence. Encoding involves the transformation of the original ASCII character set used in FASTA or FASTQ format into a bit-packed representation where each base is represented using only three bits; the sequence is thus encoded as a sequence of 8-byte (64-bit) integers, each of which contains 21 3-bit fields.

At every location in each reference sequence, the encoder extracts a "seed", that is, a short subsequence (either 84 bases for nongapped alignment or about 20-30 bases for gapped alignment). The seed length and pattern are specified in the AriocE configuration file. A numerical hash function is applied to each seed and the reference-sequence location is appended to a list of such locations for the seed's hash value. Other configuration-file parameters control the number of bits in a hash value (and thus the size of the hash table) as well as the maximum number of reference-sequence locations recorded for a given hash value.

AriocE builds hash tables in two passes. The reason is that both the AriocU (unpaired) and AriocP (paired end) aligners implement a pipeline in which nongapped alignments for each read are computed prior to gapped alignments. The aligners use different hash tables for nongapped (spaced-seed) alignment and for gapped (seed-and-extend) alignment. This means that you must execute AriocE twice

to fully encode a reference sequence. The idea is to make it possible to use AriocE multiple times to create hash tables with different characteristics and then choose among those hash tables when you execute the AriocU or AriocP aligners.

Here is an example of an AriocE configuration file that builds a nongapped (spaced seed) hash table for the human reference genome:

```
<?xml version="1.0" encoding="utf-8"?>
<AriocE seed="ssi84_2_30" maxJ="*">
  <dataIn sequenceType="R" srcId="0" filePath="/dss004/R/GRCh38.p6" AS="GRCh38"
uriPath="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000001405.21_GRCh38.p6/GCA_000001405.21_GR
Ch38.p6_assembly_structure/Primary_Assembly/assembled_chromosomes/FASTA">
    <file SN="chr1" subId="1">chr1.fna</file>
    <file SN="chr2" subId="2">chr2.fna</file>
    <file SN="chr3" subId="3">chr3.fna</file>
    <file SN="chr4" subId="4">chr4.fna</file>
    <file SN="chr5" subId="5">chr5.fna</file>
    <file SN="chr6" subId="6">chr6.fna</file>
    <file SN="chr7" subId="7">chr7.fna</file>
    <file SN="chr8" subId="8">chr8.fna</file>
    <file SN="chr9" subId="9">chr9.fna</file>
    <file SN="chr10" subId="10">chr10.fna</file>
    <file SN="chr11" subId="11">chr11.fna</file>
    <file SN="chr12" subId="12">chr12.fna</file>
    <file SN="chr13" subId="13">chr13.fna</file>
    <file SN="chr14" subId="14">chr14.fna</file>
    <file SN="chr15" subId="15">chr15.fna</file>
    <file SN="chr16" subId="16">chr16.fna</file>
    <file SN="chr17" subId="17">chr17.fna</file>
    <file SN="chr18" subId="18">chr18.fna</file>
    <file SN="chr19" subId="19">chr19.fna</file>
    <file SN="chr20" subId="20">chr20.fna</file>
    <file SN="chr21" subId="21">chr21.fna</file>
    <file SN="chr22" subId="22">chr22.fna</file>
    <file SN="chrX" subId="23">chrX.fna</file>
    <file SN="chrY" subId="24">chrY.fna</file>
    <file SN="chrMT" subId="25">
uriPath="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000001405.21_GRCh38.p6/GCA_000001405.21_GR
Ch38.p6_assembly_structure/non-nuclear/assembled_chromosomes/FASTA">chrMT.fna</file>
  </dataIn>
  <dataOut>
    <path>/dss004/BulkData/R/NCBI/GRCh38.p6</path>
  </dataOut>
</AriocE>
```

Configuration file for AriocE (reference sequences) for a nongapped (spaced seed) hash table.

To build the corresponding gapped (spaced seed) hash tables, change the parameters specified in the XML attributes of the <AriocE> element and re-execute AriocE:

```
<AriocE seed="hsi20_0_30" maxJ="200">
```


Here is a list of additional configuration-file parameters for reference-sequence encoding:

Element	Attribute	Description																				
<AriocE>	maxDOP	Number of concurrent CPU threads																				
	gpuMask	Bits corresponding to GPU devices																				
	maxJ	Maximum hash table bucket size ("big bucket" threshold)																				
	seed	One of the following values: <table><thead><tr><th></th><th>Seed width</th><th>Mismatches</th><th>Hash bits</th></tr></thead><tbody><tr><td>ssi84_2_bb</td><td>84</td><td>2</td><td>bb between 29 and 32</td></tr><tr><td>ssi84_2_bb_CT</td><td>84</td><td>2</td><td>bb between 29 and 32</td></tr><tr><td>hsiww_0_bb</td><td>ww between 18 and 42</td><td>0</td><td>bb between 29 and 32</td></tr><tr><td>hsiww_0_bb_CT</td><td>ww between 18 and 42</td><td>0</td><td>bb between 29 and 32</td></tr></tbody></table> <p>Examples: seed="ssi84_2_30" seed="hsi21_0_32" seed="hsi25_0_31_CT"</p>		Seed width	Mismatches	Hash bits	ssi84_2_bb	84	2	bb between 29 and 32	ssi84_2_bb_CT	84	2	bb between 29 and 32	hsiww_0_bb	ww between 18 and 42	0	bb between 29 and 32	hsiww_0_bb_CT	ww between 18 and 42	0	bb between 29 and 32
		Seed width	Mismatches	Hash bits																		
ssi84_2_bb	84	2	bb between 29 and 32																			
ssi84_2_bb_CT	84	2	bb between 29 and 32																			
hsiww_0_bb	ww between 18 and 42	0	bb between 29 and 32																			
hsiww_0_bb_CT	ww between 18 and 42	0	bb between 29 and 32																			
<dataIn>	srcId	Data source ID (between 0 and 4,194,303)																				
	AS	SAM genome assembly identifier (common to all input files)																				
	filePath	Parent directory for files specified in <file> elements																				
	uriPath	Original URI for reference sequences (copied to the UR field in the @SQ records in SAM-formatted output)																				
<file>	SN	Reference-sequence subunit (chromosome) name (e.g., "chr1")																				
	AS	SAM genome assembly identifier (overrides AS in <dataIn>)																				
	uriPath	Original URI for reference sequence (overrides uriPath in <dataIn>)																				
	TP	Reference-sequence topology: "linear" (default) or "circular"																				

Optional elements and attributes in the AriocE configuration file for encoding reference sequences or a genome.

Most of these parameters are self-evident, but the seed= and maxJ= values deserve careful attention.

seed=. The seed= value for the nongapped hash table should generally be ssi84_2_30 (seed width 84, up to 2 mismatches, 30-bit hash values). For the gapped hash table, a seed width of 20 or 21 bits is usually appropriate for WGS reads, whereas a 25-bit seed width is generally a better choice for bisulfite-treated (WGBS) reads.

For both WGS and WGBS reads, there is a tradeoff between hash table size and the number of hash-value bits: 29-bit hash values require a 2.5GB table and the table size doubles with each additional bit in

the hash value. If enough memory is available, "wider" hash values and correspondingly larger hash tables may provide up to 5% additional speed and about 0.5% additional sensitivity.

maxJ=. Because it limits the number of reference-sequence locations associated with a seed, the maxJ= parameter trades speed for sensitivity during read alignment. For the nongapped hash table, however, this effect is barely noticeable, so you can usually specify maxJ="*" to indicate that the maximum size of a hash table bucket is unlimited.

In contrast, the value of maxJ= has a tangible effect on the sensitivity of seed-and-extend (gapped) read alignment. In general, maximum throughput is obtained with a value of about 16 (but with less sensitivity), whereas maximum sensitivity can be achieved by using values of 200 and up (but with a corresponding decrease in throughput).

When encoding a genome such as the human genome that contains numerous repetitive regions, AriocE uses the limit specified by maxJ= to optimize the hash table by pruning repetitive regions of the genome where adjacent seeds hash to "big buckets". This optimization improves throughput significantly with very little decrease in sensitivity for reads that map to repetitive regions.

maxDOP=. The maxDOP= value controls the number of concurrent threads AriocE uses for encoding and validating reference sequences. Additional threads generally cause AriocE to run faster due to increased parallelism. Since AriocE's default behavior is to use all available CPU threads, there is usually no reason to specify maxDOP= explicitly unless you wish to "reserve" CPU resources for another concurrently executing program.

gpuMask=. The gpuMask= parameter is a bit mask (specified as a hexadecimal value) that indicates which GPU device is to be used by AriocE for sorting hash-table bins. Each bit in the parameter corresponds to a GPU device identifier. Because AriocE uses only one GPU for sorting, only one bit in the parameter should be set. If gpuMask= is omitted or specified as zero, AriocE uses CPU threads to sort.

TP=. Certain reference sequences (e.g., human mitochondrial chromosome, bacteriophage lambda, EBV) have circular topology. When you specify TP="circular", AriocE encodes these reference sequences in a way that enables AriocU and AriocP to report read mappings that straddle the origin of the reference sequence. This can improve mapping coverage near the origin of a circular reference sequence, although not all software tools can recognize the SAM representation of such mappings.

Output directory layout

The output from each invocation of AriocE should occupy a single directory that contains encoded sequence files as well as a subdirectory for each hash table. If, for example, you run AriocE twice (once for a nongapped hash table and once for a gapped hash table) and configure it to write its output to a directory named /GRCh38, the resulting directory layout would look like this:

/GRCh38	encoded reference sequence files (*.sbf)
/GRCh38/ssi84_2_30	LUTs for nongapped (spaced seed) aligner
/GRCh38/hsi20_0_30	LUTs for gapped (seed-and-extend) aligner

If you use a set of previously encoded reference sequence files, ensure that the directory structure follows this pattern. The lookup tables for both the nongapped and the gapped aligner must reside in subdirectories of the directory that contains the encoded reference sequences, and the subdirectory names must correspond to the "seed" strings that describe their format, seed width, and hash-value size.

AriocU: aligning unpaired reads

Before running AriocU, use AriocE to encode a reference sequence and hash tables (see [AriocE: encoding sequence data, page 11](#)).

To run AriocU, use a configuration file that specifies where to find encoded reference-sequence and read files, where to write alignment-result files, and how to parameterize the aligner:

```
<?xml version="1.0" encoding="utf-8"?>

<AriocU gpuMask="0x00000001" batchSize="64k">

  <R>C:\BulkData\R\NCBI\GRCh38.p6</R>

  <nongapped seed="ssi84_2_30" maxJ="*" />

  <gapped seed="hsi20_0_30" maxJ="200" Wmxgs="2_6_5_3" Vt="400"/>

  <Q filePath="C:\BulkData\Q\mason\test203">
    <unpaired subId="1">
      <file>i250p_1</file>
    </unpaired>
  </Q>

  <A overwrite="true">
    <sam report="mu">C:\BulkData\A\mason</sam>
  </A>

</AriocU>
```

Simple configuration file for AriocU.

Each of the XML elements in the configuration file controls a different aspect of the read-alignment pipeline:

- <AriocU>: GPU devices, GPU memory, and CPU threads
- <R>: encoded reference sequence files
- <nongapped>: seed type for nongapped alignments
- <gapped>: seed type and scoring parameters for gapped alignments
- <Q>: encoded read files
- <A>: output files and formats

The following table summarizes the basic configuration parameters:

Element	Attribute	Description
<AriocU>	gpuMask	Bits corresponding to GPU devices
	batchSize	Number of reads per batch per GPU
	maxDOP	Number of concurrent CPU threads
<nongapped>	seed	Seed used for AriocE nongapped reference-sequence encoding
	maxJ	Per-seed maximum number of reference-genome locations at which to compute nongapped alignments
<gapped>	seed	Seed used for AriocE gapped reference-sequence encoding
	maxJ	Per-seed maximum number of reference-genome locations at which to compute gapped alignments
	Wmxgs	Smith-Waterman scoring parameters
	Vt	Minimum reportable alignment score
	AtO	Minimum number of overall (nongapped + gapped) proper mappings per read (see Tuning for speed and sensitivity, page 31)
<unpaired>	subId	Subunit ID used for AriocE read encoding
<Q>	filePath	Directory path for Q sequence (FASTQ) files
	subRate	Expected per-base substitution rate (percentage)
<A>	overwrite	"true" to overwrite existing result file(s)
	cigarFormat	=XIDS [default], MIDS, or MID
	mdFormat	standard: [default] conforms with SAM format specification regex compact: omits placeholder 'O' characters for adjacent mismatches
	mapqVersion	0: [default] ($0 \leq \text{MAPQ} \leq 60$) 1: Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$) 2: Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$), optimized for AriocU 3: BWA model ($0 \leq \text{MAPQ} \leq 60$)
	maxAperRead	Maximum number of output records per read
	seedDepth	Limits the number of seed iterations (see Tuning for speed and sensitivity, page 31)
	maxAperFile	Maximum number of read alignments per output file
	xmClip	"true": [default] exclude soft-clipped bases from SAM XM (methylation context) field "false": include soft-clipped bases in XM
	xmBQS	Base quality score threshold for SAM XM methylation contexts
<sam> <sbF>	report	Alignment result type(s) to report in SAM or SBF format in the specified output directory

XML elements and attributes in the AriocU configuration file.

Some of these configuration parameter values are self-evident, but others demand careful attention:

gpuMask=. The gpuMask= parameter is a bit mask (specified as a hexadecimal value) that indicates which GPU device(s) are to be used by AriocU. Each bit in the parameter corresponds to a GPU device identifier. If there is only one GPU in the computer, the value of gpuMask= should be 1. To run AriocU on two or more GPUs, set the corresponding bits in gpuMask=. For example, to use GPUs 0, 1, and 2, specify gpuMask="0x0007".

batchSize=. The batchSize= parameter determines how many reads AriocU can process concurrently per GPU. Batch sizes are limited by available GPU memory, but the amount of GPU memory needed to compute alignments cannot be precisely predicted because it depends on the number of Smith-Waterman computations AriocU must perform in its search for satisfactory mappings for every read — and this is something you don't know until you try it.

With some data, we have observed overall speed increases up to 10% with well-chosen batch sizes, but batch size has less effect on speed than other runtime configuration parameters (see [Tuning for speed and sensitivity, page 31](#)). If you do want to try to find an optimal batch size for your data, start with a batch size of about 64K. If AriocU runs without memory-allocation errors, increase the batch size and re-run AriocU until it runs out of GPU memory or until its throughput does not improve with increasing batch size.

The batchSize= parameter may be specified either as a positive integer (e.g., "25000") or as a multiple of 1024 (e.g., "128K").

maxDOP=. AriocU uses CPU threads for file input/output and for post-processing alignment data (computing mapping qualities, formatting alignment results, and so on). If you omit maxDOP=, AriocU uses as many CPU threads as are available. You should specify a value for maxDOP= only if you wish to reserve CPU threads for a task other than AriocU.

Wmxgs=. This parameter specifies four Smith-Waterman scoring parameters as non-negative integers separated by commas or underscores. The four values indicate the score for a match, mismatch, gap open, and gap space respectively. For example, "2,6,5,3" means match=+2; mismatch=-6; gap open=-5; gap space=-3.

Vt=. This parameter indicates the minimum reportable Smith-Waterman alignment score. You can specify Vt= in one of two ways: as a non-negative integer threshold score (e.g., "100") or as a function of read length described in a Bowtie-style function parameter: "[LSG],b,a", where the initial letter indicates the function type (L: linear; S: square root; G: natural log), b is a constant term and a is the coefficient. For example, Vt="S,75,2.5" specifies a reportable alignment score threshold of $75 + 2.5 * \sqrt{\text{read_length}}$.

subRate=. Arioc uses the value of the optional subRate= parameter to fine-tune the computation of MAPQ values for mapqVersion="0" (see below). The substitution rate is specified as a percentage, e.g., subRate="0.25" (that is, a nominal substitution rate of 0.25%) could be appropriate for Illumina paired end WGS reads.

mapqVersion=. The mapqVersion= parameter specifies the computational model that AriocU uses to generate mapping quality (MAPQ) scores for reads:

- mapqVersion="0": [default] a probabilistic model using exponentiated scores in a partition function ($0 \leq \text{MAPQ} \leq 60$) [Frith, 2020]
- mapqVersion="1": Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$)
- mapqVersion="2": Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$), optimized for AriocU
- mapqVersion="3": BWA model ($0 \leq \text{MAPQ} \leq 60$)

See the Arioc source-code distribution for details.

maxAperRead=. The maxAperRead= parameter limits the number of alignment-result records output by AriocU. This is independent of the AtO= parameter whose purpose is to establish a minimum number of proper mappings to compute for each read. (This may exceed the number of proper mappings to report.) Thus, for example, you might use AtO="2" (to increase accuracy by searching for at least two proper mappings for every read) and maxAperRead="1" (to report only the primary mapping for each read, regardless of how many proper mappings were found).

xmClip=. When computing BS-seq alignments, setting xmClip="true" causes Arioc to exclude soft-clipped bases from methylation context analysis. This parameter is true by default. (See Additional SAM output fields for BS-seq reads, [page 40](#).)

xmBQS=. For each cytosine base (methylated or unmethylated) in BS-seq alignments, Arioc uses the value of xmBQS= as a threshold for determining whether to report CpG, CHG, and CHH methylation contexts. When either the cytosine or one of the adjoining bases in the read sequence has a sub-threshold base quality score, Arioc reports only an "unknown" methylation context. (See Additional SAM output fields for BS-seq reads, [page 40](#).)

report=. Use the report= parameter to filter reported alignment results. You can use any combination of m (mapped) and u (unmapped). For example, to report both mapped and unmapped results in the same SAM file, use a <sam> element with report="mu". To report the same results to two separate SAM files, use two <sam> elements, one with report="m" and one with report="u".

AriocP: aligning paired end reads

You must use AriocE to encode a reference sequence and hash tables (see [AriocE: encoding sequence data, page 11](#)) before you run AriocP.

The AriocP configuration file resembles the one that AriocU uses. The important differences have to do with parameters that control the alignment of paired end reads:

```
<?xml version="1.0" encoding="utf-8"?>

<AriocP gpuMask="0x00000001" batchSize="48k">

  <R>/BulkData/R/NCBI/GRCh38.p6</R>

  <nongapped seed="ssi84_2_30" maxJ="*" />

  <gapped seed="hsi20_0_30" maxJ="200" Wmxgs="2,6,5,3" Vt="100" />

  <Q filePath="/BulkData/Q/mason/test103">
    <paired subId="1">
      <file>i100p_1</file>
      <file>i100p_2</file>
    </paired>
  </Q>

  <A overwrite="true" pairOrientation="c" pairCollision="oc">
    <sam report="cdru">/BulkData/A/mason</sam>
  </A>

</AriocP>
```

Simple configuration file for AriocP.

Each of the XML elements in the configuration file controls a different aspect of the read-alignment pipeline:

- <AriocP>: GPU devices, GPU memory, and CPU threads
- <R>: encoded reference sequence files
- <nongapped>: seed type for nongapped alignments
- <gapped>: seed type and scoring parameters for gapped alignments
- <Q>: encoded read files
- <A>: output files and formats

The following table summarizes the basic configuration parameters:

Element	Attribute	Description
<AriocP>	gpuMask	Bits corresponding to GPU devices
	batchSize	Number of reads per batch per GPU
	maxDOP	Number of concurrent CPU threads
<nongapped>	seed	Seed used for AriocE nongapped reference-sequence encoding
	maxJ	Per-seed maximum number of reference-genome locations at which to compute nongapped alignments
<gapped>	seed	Seed used for AriocE gapped reference-sequence encoding
	maxJ	Per-seed maximum number of reference-genome locations at which to compute gapped alignments
	Wmxgs	Smith-Waterman scoring parameters
	Vt	Minimum reportable alignment score
	Vtw	Vt for low-scoring mates
	AtO	Minimum number of overall (nongapped + gapped) proper mappings per read (see Tuning for speed and sensitivity, page 31)
	subId	Subunit ID used for AriocE read encoding
<Q>	filePath	Directory path for Q sequence (FASTQ) files
	subRate	Expected per-base substitution rate (percentage)
<A>	overwrite	"true" to overwrite existing result file(s)
	pairFragmentLength	Distance between the ends of a paired end mapping
	pairOrientation	Specifies the relative orientation (convergent/divergent/same) of the mates in a pair.
	pairCollision	Indicates whether mates may overlap, cover, or dovetail.
	cigarFormat	=XIDS [default], MIDS, or MID
	mdFormat	standard: [default] conforms with SAM format specification regex compact: omits placeholder 'O' characters
	mapqVersion	0: [default] ($0 \leq \text{MAPQ} \leq 60$) 1: Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$) 2: Bowtie 2 model ($0 \leq \text{MAPQ} \leq 44$), optimized for AriocP 3: BWA model ($0 \leq \text{MAPQ} \leq 60$)
	maxAperRead	Maximum number of output records per read
	seedDepth	Limits the number of seed iterations (see Tuning for speed and sensitivity, page 31)
	maxAperFile	Maximum number of read alignments per output file
	xmClip	"true": [default] exclude soft-clipped bases from SAM XM (methylation context) field "false": include soft-clipped bases in XM
	xmBQS	Base quality score threshold for SAM XM methylation contexts
	report	Alignment result type(s) to report in SAM or SBF format in the specified output directory

XML elements and attributes in the AriocP configuration file.

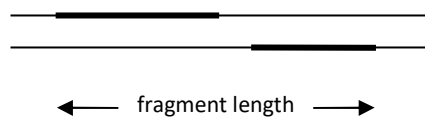
Most of the AriocP configuration parameters control the same behaviors as they do with AriocU. The important differences are related to the management of paired end alignments:

Vt=. The Vt= parameter is the minimum reportable alignment score for each individual mate in a pair, not the combined alignment scores for both mates.

Vtw=. The optional Vtw= parameter specifies a minimum reportable alignment score to be used when AriocP computes a gapped alignment for a mate whose opposite mate has a high-scoring mapping. This lets AriocP report mappings for pairs where one mate maps with a low alignment score in a region of high variability and the opposite mate maps with a high alignment score. This can provide additional sensitivity for the detection of variants in hard-to-map regions of the genome.

Specify Vtw= as an integer value or as a Bowtie-style function (see [page 22](#)).

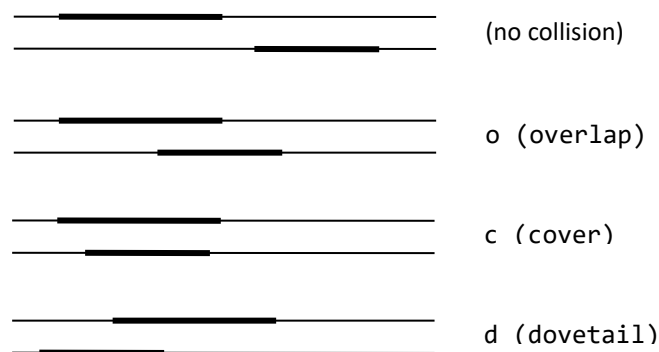
pairFragmentLength=. The pairFragmentLength= parameter specifies a range of acceptable fragment-length values. AriocP computes the pair fragment length as a SAM TLEN, that is, the number of mapped reference-sequence positions between the first ("upstream") mapped base and the last ("downstream") mapped base in a pair of mappings:



pairOrientation=. This parameter specifies the expected orientation of the mates in a pair:

- convergent: the "upstream" mate (that is, the mate at the lower-numbered location on the reference sequence) maps to the forward strand and the opposite mate maps to the reverse-complement strand
- divergent: the upstream mate maps to the reverse-complement strand and the opposite mate to the forward strand
- same: both mates map to the same strand

pairCollision=. The pairCollision= parameter indicates whether the mappings of a pair of mates may overlap, cover, or dovetail each other:



report=. The report= parameter value can be any combination of the following (similar to Bowtie's paired end alignment result categories):

- c (concordant): both mates in a pair have reportable mappings and meet the user-specified constraints for orientation and fragment length
- d (discordant): each mate has a unique mapping, but the mappings do not meet the user-specified paired end constraints
- r (rejected): both mates have mappings and at least one of the mates has two or more mappings, but no combination of the mappings meets the user-specified paired end constraints
- u (unmapped): one or both mates have no reportable mapping

You can write alignment results to two, three, or four different files by using multiple <sam> elements, each with a different, mutually exclusive subset of the four alignment-result categories.

Alignment results

Both AriocU and AriocP can generate alignment results in two different formats: SAM [SAM/BAM Format Specification Working Group, 2017] and SBF (the binary format that the Microsoft SQL Server uses for "native" bulk inserts). The <sam> and <sbf> elements in the configuration file control whether the Arioc aligners emit results in SAM, SBF, or both formats.

SAM results

The Arioc aligners emit the following tab-separated fields. (See the SAM optional fields specification document for details):

Field name	Description
QNAME	Query-sequence (read) metadata
FLAG	Flag bits
RNAME	Reference sequence name
POS	Mapping position
MAPQ	Mapping quality
CIGAR	CIGAR string
RNEXT	Opposite mate reference sequence name
PNEXT	Opposite mate mapping position
TLEN	Paired end fragment length
SEQ	Query sequence
QUAL	Phred-scaled base quality scores
AS	Alignment score
XS	Second-highest alignment score
YS	Opposite mate alignment score
NM	Edit distance
MD	MD string
YT	Alignment result category
Na	Number of distinct mappings found by the aligner
Nb	Number of maximum-score Smith-Waterman mappings
RG	Read group
c3	Triplet complexity score
id	Unique sequence identifier
af	Aligner flags
qf	Query flags

Tab-separated fields in Arioc SAM files.

Here are some additional details about the SAM fields reported by AriocU and AriocP:

RNAME: By default, the Arioc aligners use a 3-digit decimal string in RNAME. This numerical identifier corresponds to the subId= parameter that you associate with each reference sequence at the time the sequence is encoded (see Encoding a reference sequence, [page 15](#)). The metadata associated with each reference sequence (that is, in the original FASTA file for the reference sequence) appears in the rm= field of the corresponding @SQ record in the SAM file.

You can override this default behavior by running AriocE with a configuration file that specifies an SN= value (for example, a chromosome name) in each <file> element in the .cfg file. (See the example on [page 16](#)).

YT: AriocP assigns a 2-character "mapping type" (based on the YT field in Bowtie 2) to each SAM record:

YT	Description
CP	Concordant (meets user-specified criteria for mate orientation and fragment length)
DP	Discordant (unique mapping that does not meet user-specified criteria for orientation and fragment length)
RP	Rejected (both mates mapped without meeting user-specified criteria for orientation and fragment length, and one or both mates had multiple mappings)
UP	Unmapped (one or both mates unmapped)

[Paired end mapping types reported by AriocP.](#)

Na: Because the Arioc aligners evaluate potential alignments in parallel, the number of mappings they discover may be significantly greater than the number of mappings they report. The Na field indicates the total number of distinct mappings that were found by the aligner.

Nb: In the scoring matrix computed for Smith-Waterman alignment, two or more different cells may contain the same maximum alignment score. The Nb field records the number of different cells that contained the same maximum score for the reported mapping.

c3: The c3 field contains a "triplet complexity" score for a FASTQ read sequence. This score estimates the information content of a read sequence as a weighted sum of the counts of each three-base triplet in the sequence based on the technique used in DUST [Morgulis et al, 2006]:

$$\text{sum}((c_t * (c_t - 1)) / 2)$$

The score is normalized to the sequence length and represented as a phred score. Low-complexity sequences have lower c3 scores; 95% of randomly generated short reads from the human reference genome have c3 scores between 45 and 60. See the AriocE source code distribution for details.

id: The AriocE encoder assigns a unique 64-bit sequence identifier to each sequence it reads from a FASTA or FASTQ file. The AriocU and AriocP aligners emit this unique identifier in the id field. The identifiers are assigned in the order in which they are encountered in the input FASTA or FASTQ file, although this ordering is not preserved in SAM output.

af, qf: These fields contain status flags used internally by the Arioc aligners.

SBF results

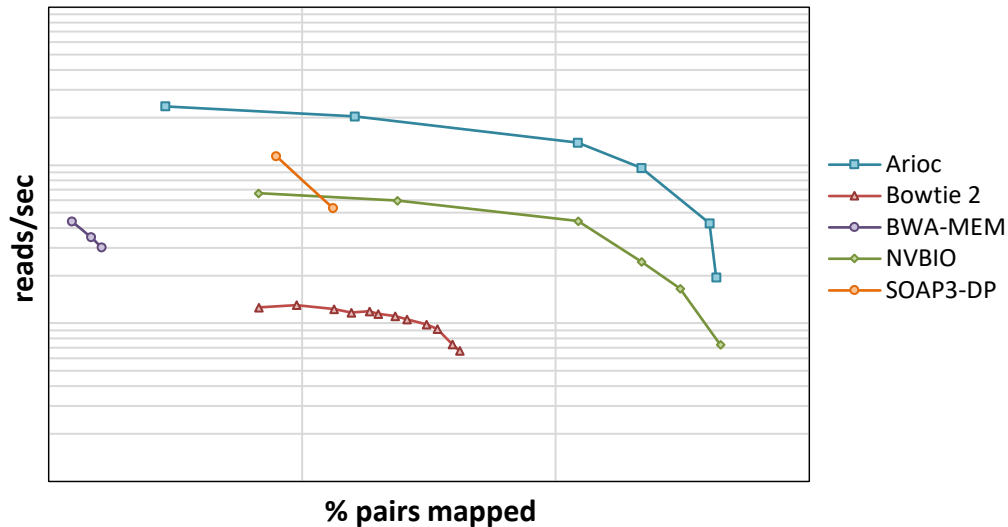
The binary format of SBF files generated by the Arioc aligners corresponds to the following SQL table definition (where N is a placeholder for a user-specified maximum size for variable-length strings):

```
create table AriocSBFTable
( qname  varchar(N)      not null,
  flag    smallint       not null,
  rname    smallint       not null,
  pos      int           not null,
  mapq     tinyint       not null,
  cigar    varchar(N)    not null,
  rnext     smallint      not null,
  pnext     int           not null,
  tlen      int           not null,
  seq       varchar(N)    not null,
  qual      varbinary(N)  not null,
  sqId      bigint        not null,
  V         smallint      not null,
  XS        smallint      not null,
  NM        smallint      not null,
  MD        varchar(N)    not null,
  NA        smallint      not null,
  NB        smallint      not null,
  RG        smallint      not null,
  af        smallint      not null,
  qf        smallint      not null
)
```

SQL table definition corresponding to the Arioc SBF file format.

Tuning for speed and sensitivity

Like other short-read aligners, Arioc exhibits a decrease in speed when you configure it for higher sensitivity. To discover acceptable mappings for read sequences that contain larger numbers of mismatches and indels, the aligner computes more alignments and therefore runs more slowly:



The simplest way to mitigate this is to use more capable hardware! Increasing the number of GPU threads available to Arioc increases overall throughput. You can accomplish this either by using multiple GPU devices or by running Arioc on newer GPU hardware with a larger number of compute cores and a higher degree of parallelism.

Before you process multiple samples with Arioc, we recommend that you perform a few test runs to establish a reasonable balance between speed and sensitivity. Arioc supports a variety of parameters you can use to control the tradeoff between speed and sensitivity.

The configuration files distributed with Arioc contain settings for reference-sequence encoding (AriocE) and alignment (AriocU, AriocP) that are reasonable for the human reference genome and for typical Illumina whole-genome sequencing (WGS) reads. You can use these settings as a starting point to adjust Arioc's performance to the reference genome you are using and to the content of your own sequencer reads.

The verboseMask= and maxQ= parameters

The verboseMask= parameter (used with the <AriocE>, <AriocU>, or <AriocP> element) controls the amount of detail in the output of each of the Arioc executables. Specify the parameter value as a 32-bit hexadecimal bitmap:

Bit	Hexadecimal	Description
31	0x80000000	Output to stderr
30	0x40000000	Output to Windows debugger
29	0x20000000	Emit timestamps
11	0x00000800	Trace main loop iterations
10	0x00000400	Trace file open/close
9	0x00000200	Trace CUDA (GPU) memory management
8	0x00000100	Trace host (CPU) memory management
4	0x00000010	Detailed trace
3	0x00000008	Basic trace
2	0x00000004	Detailed performance metrics
1	0x00000002	Basic performance metrics
0	0x00000001	Banners and exceptions

Bit flags in the `verboseMask=` parameter.

For performance tuning, use `verboseMask=0xE0000807` to see time-stamped intermediate results and summary timings.

The `readId=` parameter (used with the `<Q>` element) limits read alignment computation to a specified subset of the input reads. For example, `<Q readId="0-999" ...>` causes only the first 1,000 input reads (or pairs) to be aligned.

Tuning for sensitivity

Arioc finds more high-scoring mappings when it evaluates potential alignments at more reference-sequence locations. Here are several ways to broaden Arioc's "search space":

AriocE: The parameters provided in the sample configuration files for AriocE represent a reasonable starting point for encoding the lookup tables used by AriocU and AriocP, but you can adjust the tradeoff between speed and sensitivity by choosing alternative values for those parameters.

maxJ=. Build the seed-and-extend lookup table (hash table) with a higher value for `maxJ=` to increase sensitivity at the expense of speed. The `maxJ=` parameter affects "big bucket" hash values, that is, seeds that derive from highly repetitive regions and that are therefore associated with many reference-sequence locations. Increasing `maxJ=` causes AriocU and AriocP to compute more potential alignments for reads that contain "big bucket" seeds.

Increasing `maxJ=` has no effect on most hash table buckets because seeds that are not associated with highly repetitive regions of the reference hash to comparatively few reference-sequence locations. Thus, with increased `maxJ=`, AriocU and AriocP find additional mappings primarily for a few noisy reads. (By "noisy", we mean that a read contains so many mismatches and indels that only a few of its seeds remain intact. When those intact seeds happen to be associated with "big buckets" in the hash table, the aligner is more likely to find a mapping when you use a larger value for `maxJ=`.)

AriocU and AriocP spend more time evaluating additional seed locations when they use a seed-and-extend hash table built with larger values for `maxJ=` in AriocE. For example, with the human reference genome, speed starts to decrease sharply with `maxJ=` values above 500 or 1000, with relatively small improvements in sensitivity. With a larger, highly repetitive reference such as the bread wheat genome, a `maxJ=` value of 100 or less may provide a better tradeoff between speed and sensitivity.

This effect is much less noticeable with the spaced-seed (nongapped) lookup table because the spaced-seed alignment algorithm is much faster than the Smith-Waterman algorithm used in Arioc's seed-and-extend (gapped) aligner. (More about this below.) If you do not notice a significant improvement in speed by limiting `maxJ=` for the spaced-seed lookup table, then simply use `maxJ="*"` in AriocE.

seed=. AriocE supports a variety of seeds of different widths and bit encodings. The first part of each seed name specifies the number of bases in the seed; the third part of the seed name specifies the number of bits used to encode a seed's hash value. For example, `seed="hsi20_0_30"` represents 20-base seeds encoded using 30-bit hash values.

If you want to increase the aligner's ability to find mappings for reads that contain a significant number of differences from the reference genome – that is, with an "error rate" of 5% or more – you can increase sensitivity by using shorter seeds (with, of course, a tangible decrease in speed). Conversely, reads with typical Illumina error rates of 1% or less can be aligned with high sensitivity using longer seeds (21 bases or higher).

You can also encode the reference lookup tables (hash tables) with up to 32-bit hash values. Larger hash values (and their correspondingly larger lookup tables) provide additional sensitivity because there are fewer hash collisions. You should use the largest hash tables that fit into available memory.

AriocU, AriocP: To obtain greater sensitivity from the AriocU and AriocP aligners, you can increase the value of any or all of the following parameters:

Element	Attribute	Description
<nongapped>	<code>maxJ</code>	Per-seed maximum number of reference-genome locations at which to compute nongapped alignments
<gapped>	<code>maxJ</code>	Per-seed maximum number of reference-genome locations at which to compute gapped alignments
	<code>At0</code>	Per-read threshold for overall (nongapped + gapped) proper mappings
	<code>seedDepth</code>	Number of seed iterations

Configuration parameters useful for AriocU and AriocP performance tuning.

To understand how to use these parameters, consider how the AriocU and AriocP aligners process each read.

First, the aligner uses periodic spaced seeds to find nongapped mappings that contain no more than two mismatches. The value of `maxJ=` sets an upper limit on the number of reference-genome locations at which the aligner computes nongapped mappings (see above). Higher `At0=` values cause the aligner to compute alignments until it finds a greater number of proper mappings. In this way, the aligner may

discover additional high-scoring mappings for hard-to-map reads that contain multiple indels. The additional mappings may also improve the accuracy of the aligner's mapping quality (MAPQ) estimates because the aligner computes a lower MAPQ score for reads with multiple high-scoring mappings.

After searching for nongapped mappings, the aligner uses seed-and-extend to find gapped mappings for the remaining reads (i.e., those that do not have the minimum number of proper mappings). For each such read, the aligner iteratively chooses seeds, starting with the set of seeds that are immediately adjacent to each other. (For example, with 20nt seeds, the aligner starts with the seeds at positions 0, 20, 40... in the read). If none of these seeds leads to a successful mapping, the seed interval is halved and the new set of seeds is evaluated.

With typical seed sizes, six such "interval halving" iterations are needed to evaluate every possible seed location in the read. You can alter this behavior by setting the `seedDepth=` parameter, which limits the number of seed iterations to a number between 1 and 6. The Arioc aligners run significantly faster with smaller values of `seedDepth=`, but they also find fewer high-scoring mappings for reads that contain multiple differences from the reference genome. Also, as read length increases, more seeds are generated in each iteration, so you may find that fewer seed iterations are needed to find enough mappings for longer reads.

Arioc abandons the search for seed-and-extend mappings for a read when it discovers at least the configured number of high-scoring mappings. Again, Arioc keeps searching for higher-scoring mappings until it finds at least the number of mappings specified in `AtO=` (or until it runs out of seeds).

Because Arioc computes potential alignments in parallel, it cannot strictly respect the value specified for `AtO=`. For example, even with the default setting of `AtO="1"`, Arioc often finds multiple high-scoring mappings for many reads because those mappings are all discovered in parallel.

AriocP: For paired-end reads, you can use the `Vtw=` parameter to specify a minimum reportable alignment score for the special case where one mate of a pair maps may map within a region of high variability in the reference genome. This lets AriocP report mappings in "hard-to-map" regions where one mate maps only with an exceptionally low alignment score and the opposite, high-scoring mate "anchors" the overall paired mapping.

A reasonable value for `Vtw=` is roughly 15% of the alignment score for a perfect mapping. This obviously permits AriocP to report mappings with a considerable number of mismatches and/or indels, but in general this special case occurs infrequently enough that there should be little adverse effect on overall speed.

Tuning for speed

Arioc runs faster when it searches for fewer mappings. In general, choosing lower values for the same set of tuning parameters leads to higher throughput.

AriocE: Build the seed-and-extend hash table with a lower value for `maxJ=`. This causes AriocE to be more aggressive in identifying "big bucket" regions of the reference genome and pruning the hash table accordingly. You can use values for `maxJ=` as low as 16 and still obtain acceptable alignment results with AriocU and AriocP.

AriocU, AriocP: The AriocU and AriocP aligners also require the `maxJ=` parameter. (Use `maxJ=` on the `<nongapped>` and `<gapped>` elements in the configuration file.) In the aligners, `maxJ=` specifies a limit to the number of reference-sequence locations that the aligners examine for each seed. Changing `maxJ=` has little effect when used with the nongapped aligner (which is very fast anyway) but using lower values for `maxJ=` can tangibly increase the speed of the gapped aligner.

You can also increase throughput by using smaller values for the `seedDepth=` and `At0=` parameters.

- `seedDepth`: AriocU and AriocP iterate through overlapping subsets of the seeds for each read sequence. By limiting the number of iterations, you limit the number of reference-sequence locations at which each read can potentially be mapped.
- `At0`: this parameter specifies the minimum number of overall (nongapped plus gapped) mappings that AriocU or AriocP must find for a read before it stops computing alignments for the read. The default value (`At0="1"`) favors speed but can overestimate MAPQ for some reads that actually have two or more high-scoring mappings. Consider using larger values if you prefer to avoid this inaccuracy or if you want the aligner to report secondary mappings for such reads.

As you decrease these parameter values, you may notice that speed is limited by factors other than the intrinsic speed of the aligners. Disk I/O bandwidth and contention for the PCIe bus can each limit overall throughput, especially when you run AriocU or AriocP on multiple GPUs.

Multiple input files

It is possible to align multiple input files (or, more exactly, pairs of input files) by using the `subId=` and `mate=` attributes of the `<paired>` or `<unpaired>` element in the configuration file. This may provide a marginal improvement in overall speed because GPU initialization, which takes several minutes in some computers, is performed only once.

Nevertheless, you should exercise caution when you align multiple input files (or pairs of input files) because AriocE cannot recognize different layouts among the input files. For example, files that originate from different sequencer runs may use a different bias to encode base quality scores (e.g., 33 for Sanger, 64 for Illumina v1.3 and later), but AriocU and AriocP cannot recognize this on the fly.

It is preferable simply to encode and align one sequencer run at a time.

Extra ("X") parameters

AriocU and AriocP recognize several additional configuration parameters that may be useful for optimizing performance with certain hardware configurations.

The X parameters are documented in file `Xparams.txt` in the `Arioc.RQA.zip` archive.

GPU-specific builds

More recent iterations of the Nvidia GPU microarchitecture support a more powerful instruction set than do older Nvidia GPUs. Nvidia identifies instruction set versions with an identifier it calls the "compute capability." For example, the Kepler K80 device, released in 2014, has compute capability 3.7, whereas the V100 GPU, released in 2017, has compute capability 7.0. (Complete lists of compute capabilities for all CUDA-enabled Nvidia GPUs are available online.)

To ensure broad hardware compatibility, the makefile shipped with the Linux distribution of Arioc specifies that the Nvidia compiler generate code that targets an older (lower-numbered) compute capability. If you will be using Arioc with a GPU with a more recent (higher-numbered) compute capability, you can build AriocU and AriocP specifically for that hardware by specifying an additional parameter, `CUDA_CC`, on the make command line. For example, to target V100 GPUs, you could build AriocP like this:

```
make AriocP CUDA_CC=70
```

The resulting executable binary will be incompatible with GPU devices that do not support the targeted compute capability, but it may run up to 5% faster on the same GPU device than a binary that is built for an older (lower-numbered) compute capability.

Tuning for variant calling

Arioc can be used in a variant-calling toolchain with results comparable to those obtained with aligners such as BWA-MEM or Bowtie 2. For example, here are typical results with GIAB HG002 "difficult-to-map regions" using the GATK v4.2.6.1 HaplotypeCaller, GATK VariantFiltration with recommended "generic" filtration parameters, and hap.py:

BWA-MEM2 v2.2.1				
Type	Filter	METRIC.Recall	METRIC.Precision	METRIC.F1_Score
INDEL	ALL	0.991472	0.989025	0.990247
INDEL	PASS	0.991431	0.989787	0.990608
SNP	ALL	0.992490	0.984448	0.988453
SNP	PASS	0.989958	0.992017	0.990987
Arioc v1.51				
Type	Filter	METRIC.Recall	METRIC.Precision	METRIC.F1_Score
INDEL	ALL	0.991882	0.989013	0.990445
INDEL	PASS	0.991832	0.989840	0.990835
SNP	ALL	0.992938	0.984200	0.988549
SNP	PASS	0.989979	0.992634	0.991305

For a given set of whole genome sequencing reads, Arioc, BWA, and Bowtie generally produce the same set of alignments. However, the aligners differ in details that can influence the performance of downstream variant callers:

Alignment scores for hard-to-align mates: Short-read sequences that vary considerably from the reference genome generally contain many mismatches and/or indels – but such mappings may be of particular interest for variant calling. You can cause AriocP to report such mappings for mates whose opposite mate has a high alignment score by specifying the `Vtw=` parameter (see page 26.)

Alignment scoring weights can influence variant calling performance: In high-variability, hard-to-map regions that contain numerous mismatches, small adjustments to scoring weights can affect variant-calling recall and precision. For example, using `Wmxgs="2,8,5,3"` penalizes mismatches more than Arioc's default "2,6,5,3" does; with HG002 and GRCh38, using this higher mismatch penalty weight results in incrementally improved precision at the cost of a slight decrease in runtime speed.

MAPQ computation: Mapping quality (MAPQ), the probability that a given read is mapped to the wrong place in the reference genome, is an essential component in computing the probability that a variant is correctly reported. However, every short-read aligner computes MAPQ using a probabilistic model that is heuristically "tuned" to the details of the aligner's implementation.

Arioc's MAPQ model has been validated with a recent version (v4.2.6.1) of the GATK HaplotypeCaller using reads and variant-call references for HG002 and Arioc's default MAPQ model (`mapqVersion="0"`). To fine-tune Arioc's MAPQ model, you can specify the `subRate=` parameter in the AriocU or AriocP configuration file to indicate the expected base substitution rate in your short-read data. (The "substitution rate" is the overall percentage of bases in read sequences that are expected to differ from

the corresponding bases in the reference genome.) By default, Arioc uses `subRate="0.25"` (0.25%). You can confirm the actual substitution rate for properly mapped reads by examining Arioc's output.

TLEN distribution: The fragment lengths for paired-end mappings (reported in the TLEN field in SAM/BAM format) typically have a right-skewed, non-symmetric distribution, so it is important to verify that you configure AriocP with an appropriate range of TLEN values.

Arioc's default criteria for proper (concordant) mappings include a minimum TLEN of 0 and a maximum TLEN of 1000 (`pairFragmentLength="0-1000"`). Although these are acceptable TLEN criteria for most Illumina paired-end sequencing experiments, they are not universally optimal. If the configured range is too large for the actual distribution of fragment lengths in the reads, AriocP reports a certain number of proper mappings that should be considered outliers; if the range is too small, AriocP reports too few proper mappings (and runs slower as it searches for mappings that fall within the fragment-length range).

AriocP's output includes several TLEN-related statistics that help you confirm that you are using an appropriate range for the `pairFragmentLength=` parameter:

TLEN mean and standard deviation	Compare with expected mean and standard deviation
TLEN distribution	TLEN histogram for all pairs considered by the aligner as being potential proper (concordant) mappings, regardless of whether they are ultimately reported as proper mappings
TLEN-discordant pairs	Number and percentage of mappings not classified as concordant because TLEN was outside the range specified in the <code>pairFragmentLength=</code> parameter; should generally be $\leq 0.01\%$

BS-seq alignment

The Arioc aligners natively support alignment of bisulfite-treated DNA reads. By "natively" we mean that the additional logic involved in computing BS-seq alignments is integrated into Arioc. Although this approach allows for significant GPU acceleration of the code as well as increased sensitivity [Wilton et al., 2017], Arioc nevertheless aligns BS-seq reads several times more slowly than it does non-bisulfite-treated reads of similar length.

Arioc's BS-seq functionality is compatible with that of the Bismark aligner [Krueger and Andrews, 2011]. In particular, AriocU and AriocP produce SAM-formatted output that is recognized by Bismark's downstream processing tools, so Arioc is functionally compatible with Bismark in a BS-seq read-processing workflow.

Preparing for BS-seq alignment

In terms of sequencer output, bisulfite-treated DNA sequences represent a six-letter alphabet using only five letters, so T in a BS-seq read may represent either cytosine or thymine in the original DNA sequence:

	original DNA	sequencer read
adenine	A	A
cytosine	C	T
methylcytosine	C _m	C
guanine	G	G
thymine	T	T
(unknown)	N	N

The Arioc aligners use hash tables in which the reference sequence (genome) is similarly encoded. They then disambiguate Ts in each mapped sequence by comparing them to the corresponding base in the original reference sequence.

To encode the reference sequence for BS-seq alignment, specify a CT-converted seed type in the seed= attribute of the <AriocE> element when you execute AriocE. For example, the following creates a gapped (spaced seed) hash table with seeds of length 25:

```
<AriocE seed="hsi25_0_30_CT" maxJ="200">
```

(See also Encoding a reference sequence, [page 15](#).)

Running the aligner

When executed using CT-converted hash tables, the Arioc aligners use CT-converted lookup tables to identify reference genome alignment locations, compute mappings, and report methylcytosines in context. The following configuration file illustrates how to accomplish this:

```
<?xml version="1.0" encoding="utf-8"?>
<AriocU gpuMask="0x0007" batchSize="8K" verboseMask="0xE0000007">

  <R>C:\data\raid5-2\BulkData\R\NCBI\GRCh38.p6\maxJ 2048</R>

  <nongapped seed="ssi84_2_30_CT" maxJ="*" />

  <gapped seed="hsi25_0_30_CT" maxJ="200" Wmxgs="2_6_5_3" Vt="L,-50,2" />

  <Q filePath="C:\data\data2\BulkData\Q\Sherman">
    <unpaired srcId="1" subId="1">
      <file>test00</file>
    </unpaired>
  </Q>

  <A overwrite="true" cigarFormat="MIDS">
    <sam report="mu">C:\data\data2\BulkData\A\Sherman</sam>
  </A>

</AriocU>
```

BS-seq configuration file for AriocU.

In the above example, the `cigarFormat`= attribute of the `<A>` element specifies the SAM CIGAR encoding style recognized by Bismark's `bismark_methylation_extractor`.

Additional SAM output fields for BS-seq reads

When computing BS-seq alignments, Arioc emits three additional fields in SAM-formatted output:

Field name	Description
XM	Methylation context map
XR	Reference-sequence encoding (always CT)
XG	Read sequence encoding (CT or GA)

Additional tab-separated fields in Arioc SAM files for BS-seq alignments.

These three fields are modeled after the identically named fields in SAM output from the Bismark read aligner. Although the format of each field in Arioc SAM output matches the Bismark format, there are small differences in the way the fields are generated.

The XM field is a character map of the position of each methylcytosine (C_m) identified by the read aligner. For each mapped read, Arioc encodes the methylation context for each cytosine by examining the two symbols that follow it in the read sequence:

XM encoding	methylation context	symbols following C
Z, z	CpG	G
H, h	CAG, CTG, CCG	AA AC AT CA CC CT TA TC TT
X, x	CHG	AG CG TG
U, u	unknown	N AN CN TN (or end of read)

Uppercase letters (ZHXU) represent methylcytosine. Lowercase letters (zhxu) represent unmethylated cytosine.

Arioc differs from Bismark in that AriocP and AriocU determine methylation context exclusively by examining the read sequence, whereas Bismark always uses the corresponding reference sequence and ignores the bases in the read that follow each cytosine. Consequently, there are observable differences between the XM maps generated by Bismark and by Arioc for identically mapped reads:

- If a cytosine appears at the end of a read sequence, Arioc cannot determine a methylation context for it and therefore reports it as U or u.
- Where the read sequence contains a variation from the reference genome (mismatch or indel), Arioc may report a different methylation context than Bismark would. This can happen due to true biological variation, but it can also occur in bases associated with low base quality scores (BQS). The `xmBQS=` parameter specifies the BQS threshold at which Arioc reports each methylation context. If you specify a non-zero threshold value for `xmBQS=`, Arioc will report a methylation context as "unknown" if any of the corresponding bases in the read sequence have sub-threshold BQS.

Arioc also gives you the option to exclude or include soft-clipped bases in the analysis of methylation context:

```
CIGAR 69M6S  
reference ATGCTAATCATAAATCATATTAATTTAATCATTTATGCACATTATAACAATATTACTATCAATAAACT  
read      ATGTTAATTATAAATGTATTAATTTAATTTATGTATATTATAAATAATATTATTATTATAATAAATTCTCCN  
Arioc XM ..h...h...z.....h....h.h.....h..h...h...h..  
Bismark XM ..h...h...h.....h....h.h.....h..h...h...u.
```

For the methylation context highlighted in yellow, Arioc's XM map contains z (unmethylated C in CpG context) because Arioc uses the read sequence to determine the methylation context; Bismark would report h (unmethylated C in CHH context) because it uses the reference sequence to infer the methylation context. In the soft-clipped region highlighted in green, both Arioc and Bismark exclude the methylated Cs from the XM map.

In Arioc, you can override this behavior and include soft-clipped Cs by specifying `xmClip="false"` in the `<A>` element of the Arioc configuration file:

```

reference ATGCTAATCATAAATCATATTAATTTAATCATTTATGCACATTATAAACAATATTACTATCAATAAACT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
read      ATGTTAATTATAAAATTGTATTAATTTAATTATTTATGTATATTATAAAATAATATTATTATTAATAAAATT CCTCCN
Arioc XM ...h...h.....z.....h.....h.h.....h.....h.....h..h.....h HH UU

```

Although Arioc does not use the same approach as Bismark to index the reference genome for computing BS-seq alignments, it emits XG and XR fields for each mapped read that correspond to those generated by Bismark. This maintains compatibility with the `bismark methylation extractor` tool.

In practice, with high-quality BS-seq reads, both Bismark and Arioc produce nearly identical methylation context calls. The optional `xmClip=` and `xmBQS=` parameters should not be used unless downstream analysis indicates that Arioc's default behavior does not lead to optimal methylation context calls.

Troubleshooting

We test each Arioc release against full-size human WGS and WGBS data samples to validate its functionality and measure its performance, but we cannot guarantee that the software is entirely free from bugs and other problems with functionality. Here are some suggestions for troubleshooting problems you encounter with the Arioc software:

- Ensure that Arioc operates correctly with the sample reference and read data that we provide. These data are downloadable in the `Arioc.RQA.151.zip` archive. You should be able to complete an end-to-end test of the software (AriocE, AriocU, and AriocP) in 10 to 15 minutes.
- Use the `verboseMask=` parameter to generate trace and debugging information. A setting of `verboseMask="0xE0000007"` is a good place to start.
- Do a debug build of the Arioc software and add additional `verboseMask=` flags to obtain more detailed trace information (see [Tuning for speed and sensitivity, page 31](#)).
- Use the public source-code repository (<https://github.com/RWilton/Arioc>) to let us know about the problem. You may also contact us directly (richard.wilton@jhu.edu).

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