CMAP File Format Specification Sheet

Document Number: 30039

Document Revision: H

Table of Contents

Legal Notice

For Research Use Only. Not for use in diagnostic procedures.

Revision History

Revision	Notes
H	• Added additional explanation of genome map quality scores • Added text on limitations of mosaicism simulation

Introduction

The Bionano Genomics® CMAP file is a data file which provides location information for label sites within a genome map or an *in silico* digestion of a reference or sequence data. The CMAP is a tab-delimited text-based file. Although the CMAP most commonly contains data from FASTA reference digestion and a *de novo* assembly, a BNX file (which typically contains raw molecule data) can also be converted to a CMAP.

A CMAP file contains two sections: 1) the CMAP information header, which describes the format of the data, and 2) the map information block, which contains the data values. This file format specification sheet provides descriptions, with examples, of the CMAP header and map information block format of the file.

CMAP files can be opened in Excel for easy readability or in any tab-delimited, text-based editor.

Format

The CMAP file contains the following sections:

- CMAP header
    - # CMAP File Version
    - # Label Channels
    - # Nickase Recognition Site
    - # Number of Consensus Maps
    - #h
    - #f
- Map information block
    - First label site in map
    - Next label site in map (repeated for all label sites)
    - Last label site is end of map

Header Specifications

Header rows are prefixed by the pound sign (#). “*” Denotes required header line tags.

Header Line Tag	Header Line Description

# CMAP File Version:	Version of CMAP*
# Label Channels:	The number of label channels (integer)*
# Nickase Recognition Site 1:	Comma separated list of label motif recognition sequences for channel 1 followed by semicolon and channel 1 color. There can be no spaces in this string. Color is optional. This can also refer to the label recognition sequence for a non-nicking enzyme (i.e. DLE-1).
# Number of Consensus Maps:	The total number of consensus genome maps in the CMAP file (integer)
#h	The columns for each data row
#f	The numerical data type for each data column

Header Specification Details

The following tables provide the CMAP header's descriptions (including any specific formatting, limitations and requirements) and examples. CMAP currently supports up to 2 label channels. Additional columns may be present but are not defined. Certain columns may be absent in earlier versions of the CMAP format.

# CMAP File Version	
Header	# CMAP File Version:
Description	Version of CMAP, auto-generated.
Example	# CMAP File Version:<TAB>0.2

# Label Channels	
Header	# Label Channels:
Description	The number of label channels (integer). Available values are: [1, 2].
Example	# Label Channels:<TAB>1

# Nickase Recognition Site 1	
Header	# Nickase Recognition Site 1:
Description	Comma separated list of label motif recognition sequences for channel 1 followed by semicolon and channel 1 color. There can be no spaces in this string. Color is optional. This can also refer to the label recognition sequence for a non-nicking enzyme (i.e. DLE-1).
Example	# Nickase Recognition Site 1:<TAB>gctcttc,cctcagc;green_01

# Nickase Recognition Site 2 (optional)	
Header	# Nickase Recognition Site 2:

# Nickase Recognition Site 2 (optional)	
Description	Comma separated list of label motif recognition sequences for channel 2 followed by semicolon and channel 2 color. There can be no spaces in this string. Color is optional. This can also refer to the label recognition sequence for a non-nicking enzyme (i.e. DLE-1).
Example	# Nickase Recognition Site 2:<TAB>cctcagc;red_01

# Number of Consensus Maps	
Header	# Number of Consensus Maps:
Description	The total number of consensus genome maps in the CMAP file (integer).
Example	# Number of Consensus Maps:<TAB>81

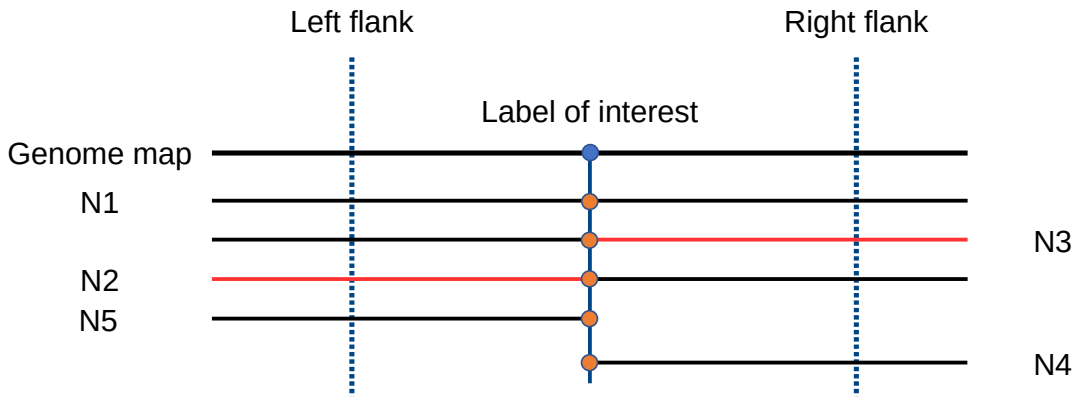
#h		
Header	#h	
Description	Defines the columns for each data row in #h rows:	
	CMapId	Map ID, ordinal number
	ContigLength	Map length in basepairs
	NumSites	Total number of label sites in map
	SiteID	Label ID, ordinal number
	LabelChannel	Label channel of label sites The last LabelChannel field of each map is always 0.
	Position	Position of label on map [0-based from map start] in basepairs
	StdDev	Theoretical standard deviation in bases of label site interval between the current and next site. Value will be 0 for FASTA digestion of a reference.
	Coverage	Weighted coverage of aligned molecules across an interval. The values may be fractional. How much an alignment to a map contributes to the weighted coverage depends on whether the alignment is unique to that particular map. If a molecule aligns equally well to two maps, it would contribute 0.5 in coverage to each of the maps. Since Solve 3.5, coverage refers to the interval between the current and the next label. The header of the CMAP now includes a comment on whether coverage is based on the interval between labels.
	Occurrence	Number of molecules with a label aligned to a given label. This is also weighed. If a molecule spans an interval but its labels do not align to the label of interest, it would contribute to coverage but not occurrence. Generally, occurrence should be less than coverage. However, this may not be true in corner cases.
	ChimQuality	Percent of molecules that align to both sides of the label out of all molecules that align on either side near this label.
	SegDupL	See Note.
	SegDupR	See Note.
	FragileL	See Note.
	FragileR	See Note.
	OutlierFrac	Fraction of number of molecules with internal outlier which overlaps this site.
	ChimNorm	This is the quantity (N1+N2+N3) described below.
	Mask	64-bit hex value: each bit flags a possible attribute for each label. See below for currently used flags.
Example	#h CmapId<TAB>ContigLength<TAB>NumSites<TAB>SiteID<TAB> LabelChannel<TAB>Position<TAB>StdDev<TAB>Coverage<TAB>Occurrence<TAB> ChimQuality<TAB>SegDupL<TAB>SegDupR<TAB>FragileL<TAB>FragileR<TAB>OutlierFrac<TAB>ChimNorm <TAB>Mask	

#f	
Header	#f
Description	Defines the numerical data type for each data column.
Example	#f<TAB>int<TAB>float<TAB>int<TAB>int<TAB>int<TAB>float<TAB>float<TAB>float <TAB>float<TAB>float<TAB>float<TAB>float<TAB>float<TAB>float<TAB>float<TAB>float<TAB>Hex

Genome map quality scores

Based on the molecule-to-genome map alignment, we compute the following genome map quality scores for each label of the genome map. In the example below, N1-N5 are representative molecules which align to the genome map. They all contain the label of interest, for which the score is computed. The numbers may be fractional, since coverage is typically weighted (a molecule that aligns to 2 regions of the genome gets a weight of 0.5 for each location).

- First, the following quantities are computed for each label in the genome map. For N2 through N5, up to two missing and one extra label are allowed next to the label for which the score is computed.
- N1: the number of molecules which align over both left and right flanks. Each flank is 36 kbp (see CovTrimLen in refineFinal section of optArguments.xml)
- N2/N3: number of molecules which align on one flank, but have an endoutlier (unaligned portion, shown in red below) which spans the second flank.
- N4/N5: same as N2/N3 but no endoutlier is present
- The genome map quality scores are defined by the following (they are expressed as fractions):
    - ChimQuality = N1/(N1+N2+N3)
    - SegDupL = N2/(N1+N2+N3)
    - SegDupR = N3/(N1+N2+N3)
    - FragileL = N4/(coverage)
    - FragileR = N5/(coverage)



Genome map label attributes encoded in Mask column

The following bits are currently used to flag attributes of labels in the genome map (the default bit value is 0):

1. Bit 0 (Value 1) is set for end labels to mark a broken end when a genome map is broken at an ambiguous CMPR (complex multi-path region). See Bionano Solve Theory of Operation: Structural Variant Calling (PN# 30110) for detail.
2. Bit 1 (Value 2) is set for end labels to mark the end of an alternate allele map (similar to assembly graph bubbles). Typically, such a map consists of the alternate region plus 300 kbp at either end of the shared homozygous region. They are generated when haplotype-aware assembly is performed. For a haplotype –aware assembly, most of these alternate maps are assigned to one of the two allelic maps, but any alternate maps that could not be assigned to either of the two dominant alleles will have their ends marked with this Bit 1.
3. Bit 2 (Value 4) is set for all labels in a region that is a suspected CMPR (complex multi-path region): these are genome map regions that closely resemble regions in other genome maps (other than the matching allelic map pair) and could be mediated by segmental duplications. By default, such regions over 140 kbp are likely to be broken with both pieces sharing the CMPR region and the broken ends marked with Bit 0 (see above). We also provide the option to not break them. Currently, CMPR regions under 140 kbp are NOT broken but marked with Bit 2.
4. Bit 3 (Value 8) is used in Hybrid Scaffold to mark ends derived from a Bionano genome map.
5. Bit 4 (Value 16 OR 0x10) is used in Hybrid Scaffold to mark ends derived from an NGS sequence (or sequence scaffold).

Note that a hybrid scaffold can have one end derived from a Bionano genome map *and* the other end derived from an NGS sequence. During Hybrid Scaffold, Mask bits 3 and 4 are used to prevent merging scaffold ends that are both derived from NGS sequence.

Genome map information block specification

The data is grouped per each genome map represented in the CMAP file. Each group starts with the first label site, followed by each label site in the map, and ends with the map length. Each group follows this convention:

- Genome map information block
  - First label site in map
  - Next label site in map [repeated for all label sites]
  - End location of genome map. This position encodes the final coordinates of the map.

Example

```
# CMAP File Version:    0.2
# Label Channels:       1
# Nickase Recognition Site 1:   cttaag;green_01
# Number of Consensus Maps:     459
# Values corresponding to intervals (StdDev, HapDelta) refer to the interval between current site and next site
#h CMapId      ContigLength    NumSites        SiteID  LabelChannel    Position        StdDev  Coverage        Occurrence      ChimQuality     SegDupL
   SegDupR FragileL        FragileR        OutlierFrac     ChimNorm        Mask
#f int  float   int     int     int     float   float   float   float   float   float   float   float   float   float   float   Hex
182     58474736.7      10235   1       1       58820.9 35.4    13.5    13.5    -1.00   -1.00   -1.00   3.63    0.00    0.00    -1.00   0
182     58474736.7      10235   2       1       70333.1 36.5    13.6    13.6    -1.00   -1.00   -1.00   0.00    0.00    0.00    -1.00   0
182     58474736.7      10235   3       1       84845.3 30.7    14.6    13.7    -1.00   -1.00   -1.00   0.31    0.00    0.00    -1.00   0
182     58474736.7      10235   4       1       87470.9 36.7    14.6    14.6    -1.00   -1.00   -1.00   0.31    0.00    0.04    -1.00   0
182     58474736.7      10235   5       1       106152.6        34.9    14.6    14.5    -1.00   -1.00   -1.00   0.00    0.00    0.10    -1.00   0
182     58474736.7      10235   6       1       119659.3        30.7    14.6    13.2    100.00  0.00    0.00    0.03    0.00    0.00    13.64   0
182     58474736.7      10235   7       1       122330.5        29.9    15.1    14.1    96.66   3.34    0.00    5.33    0.00    0.00    14.99   0
```

Technical Assistance

For technical assistance, contact Bionano Genomics Technical Support.

You can retrieve documentation on Bionano products, SDS's, certificates of analysis, frequently asked questions, and other related documents from the Support website or by request through e-mail and telephone.

Type	Contact
Email	**support@bionanogenomics.com**
Phone	**Hours of Operation:** **Monday through Friday, 9:00 a.m. to 5:00 p.m., PST** **US: +1 (858) 888-7600**
Website	**www.bionanogenomics.com/support**

Bionano Genomics, Inc.
9540 Towne Centre Drive, Suite 100
San Diego, CA 92121