Bionano BED File Format Specification Sheet

Document Number: 30164

Document Revision: B

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Revision History

	Notes
A	Initial document release
B	Fix hyperlink to BED specification

Introduction

A BED (Browser Extensible Data) file, typically tab-delimited, contains a list of genomic regions. There are three required fields, which specify the regions of the interest, and additional optional fields. All rows in the BED file are expected to contain the same number of fields. The format for the BED files that Bionano uses is generally consistent with that described on the UCSC Genome Browser website (https://genome.ucsc.edu/FAQ/FAQformat#format1). Exceptions are noted below. Currently, BED files are used for annotating structural variant calls. BED files can be opened in Excel or any text editor for easy readability and editing.

Each BED file entry contains information about a genomic region. This file format specification sheet provides descriptions, with examples, of the fields in the BED file.

Format

The BED file contains a three required fields: chrom, chromStart, and chromEnd. Additional optional fields include: name, score, strand, thickStart, thickEnd, and itemRgb. The BED files that Bionano provides currently contain no header lines.

Example

1	1	10000	gap	1	+	1	10000	100,0,150
1	207667	257666	gap	2	+	207667	257666	100,0,150
1	297969	347968	gap	3	+	297969	347968	100,0,150
1	535989	585988	gap	4	+	535989	585988	100,0,150
1	2702782	2746290	gap	5	+	2702782	2746290	100,0,150
1	12954385	13004384	gap	6	+	12954385	13004384	100,0,150
1	16799164	16849163	gap	7	+	16799164	16849163	100,0,150
1	121976460	122026459	gap	8	+	121976460	122026459	100,0,150
1	125184588	143184587	gap	9	+	125184588	143184587	100,0,150
1	223558936	223608935	gap	10	+	223558936	223608935	100,0,150
1	228558365	228608364	gap	11	+	228558365	228608364	100,0,150
1	248946423	248956422	gap	12	+	248946423	248956422	100,0,150

Field Specifications

The following table provides brief descriptions for each field. The data is grouped per genomic region represented in the BED file. Each group includes three required fields (the chromosome, the chromosome start, and the chromosome end for the region of interest) and additional fields.

Fields	Field Descriptions
chrom	Name of the chromosome, scaffold, or contig
chromStart	Starting position
chromEnd	Ending position
name	Name
score	Score (not used for visualization)
strand	Strand/orientation (not used for visualization)
thickStart	Starting position (not used for visualization)

thickEnd	Ending position (not used for visualization)
itemRgb	Display color in RGB space

Field Specification Details

The following tables provide details and examples for each field (including any specific formatting, limitations and requirement).

chrom	
Description	Name of the chromosome, scaffold, or contig. This should be numeric. There should be no “chr” prefix. This field is required.
Example	For example, “1” and “2”.

chromStart	
Description	Starting position. This should be numeric. This field is required.
Example	For example, “100”.

chromEnd	
Description	Ending position. This should be numeric. This field is required.
Example	For example, “10000”.

name	
Description	Name or type. This can be any string. Currently, three types of regions are recognized for annotating structural variant calls: “gap”, “common”, and “segdupe”.
Example	For example, “gap” and “common”.

score	
Description	Score. This can be any numeric value. This is currently used as a region ID field. The UCSC definition requires that the range be between 0 and 1000. Bionano does not enforce this requirement. This field is not used for visualization.
Example	For example, “1”.

strand	
Description	Strand. This can be either “+” or “-“. This field is not used for visualization.
Example	For example, “+”.

thickStart	
Description	Starting position. This should be numeric but is currently considered a dummy field. It is expected to be consistent with chromStart. This field is not used for visualization.
Example	For example, “100”.

thickEnd	
Description	Ending position. This should be numeric but is currently considered a dummy field. It is expected to be consistent with chromEnd. This field is not used for visualization.
Example	For example, “10000”.

itemRgb	
Description	Display color in RGB space. An RGB value should be in the form “R, G, B”. The three-color components are comma-delimited.
Example	For example, “100,0,150”.

Note: Additional fields may be present.