



Bionano BED File Format Specification Sheet

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Bionano BED v0.1 File Format Specification Sheet

This file format specification sheet details the file format specifications for Bionano BED File Version 0.1.

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". |

| chromEnding | |
|--------------------|--|
| 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.