

### BED file format

| Column             | e.g.           | Definition                                 |
|--------------------|----------------|--|
| <b>chrom</b>       | <i>Sc112.1</i> | <STR> name of chromosome/scaffold          |
| <b>start</b>       | <i>2134</i>    | <INT> start position of feature            |
| <b>end</b>         | <i>2565</i>    | <INT> end position of feature              |
| <b>name</b>        | <i>gene123</i> | <STR> name of feature                      |
| <b>score</b>       | <i>544</i>     | <NUM> score for the feature e.g. bit score |
| <b>strand</b>      | <i>+</i>       | <+/-.> strand on which feature is located  |
| <b>thickStart</b>  | <i>2235</i>    |  |
| <b>thickEnd</b>    | <i>2489</i>    |  |
| <b>itemRgb</b>     | <i>255,0,0</i> |  |
| <b>blockCount</b>  | <i>2</i>       |  |
| <b>blockSizes</b>  | <i>150,80</i>  |  |
| <b>blockStarts</b> | <i>0,2333</i>  |  |

### GFF vs BED indexing

|     |    |   |         |         |     |     |
|-----|----|---|---------|---------|-----|-----|
| GFF | ┌1 | 2 | 3┐      | 4       | ... |     |
|     |    | G | - - - A | - - - T | C   | ... |
| BED | ┌0 | 1 | 2       | ┌3      | ... |     |

#### gff > bed:

```
bed_start = gff_start - 1,
bed_end = gff_end
```

#### bed > gff:

```
gff_start = bed_start + 1,
gff_end = bed_end
```

### getfasta

```
$ bedtools getfasta [OPTIONS] -fi <input FASTA> -bed
<BED/GFF/VCF>
```

#### options

- fo** Specify an output file name. By default, output goes to stdout.
- name** Use the "name" column in the BED file for the FASTA headers in the output FASTA file.
- tab** Report extract sequences in a tab-delimited format instead of in FASTA format.
- bedOut** Report extract sequences in a tab-delimited BED format instead of in FASTA format.

### getfasta (cont)

- s** Force strandedness. If the feature occupies the antisense strand, the sequence will be reverse complemented. Default: strand information is ignored.
- Given BED12 input, extract and concatenate the sequences from the BED "blocks" (e.g., exons)

### maskfasta

```
$ bedtools maskfasta [OPTIONS] -fi <input FASTA> -bed
<BED/GFF/VCF> -fo <output FASTA>
```

#### OPTIONS

- Soft-mask (that is, convert to lower-case bases) the FASTA sequence. By default, hard-masking (that is, conversion to Ns) is performed.
- mc** Replace masking character. That is, instead of masking with Ns, use another character.

```
FASTA ACTGATCATGATACATGATACCATTAGGATACAATA
BED      ██████████ ██████████ ██████████
FASTA ' ACTGATNNNNNATACATGNNNNNNATTAGNNNNNAATA
```

