

## Molecular In My Pocket™ ...

# Bioinformatics: Basic File Formats Part II

## BAM, BED, and VCF (Secondary and Tertiary Analysis)

**Binary Alignment Map (BAM):** A compressed binary version of the text based Sequence Alignment/Map (SAM) format used to store sequence alignment data in a tab delimited text file. BAM files contain a header section and an alignment section. Note: certain platforms generate raw data in unmapped BAM format.

**Header Section:** It begins with an "@" and contains information about the entire file such as chromosomes, sample name, and alignment method. The optional tags are described in <http://samtools.sourceforge.net/>.

**Alignment Section:** It contains read name, read sequence, read quality, and alignment information. The rest of the fields are described in <http://samtools.sourceforge.net/>.

Common Field in Alignment Section	Field Description
QNAME	Read name.
FLAG	Alignment information about the read. The value is explained in <a href="https://broadinstitute.github.io/picard/explain-flags.html">https://broadinstitute.github.io/picard/explain-flags.html</a> .
RNAME	Chromosome the read mapped to.
POS	Position the read mapped to. The first base in a chromosome is numbered 0.
MAPQ mapping	Mapping quality.
CIGAR	Summary of the alignment. The description can be found in <a href="http://samtools.sourceforge.net/">http://samtools.sourceforge.net/</a> .
SEQ	The sequence of the read.
QUAL	The quality scores of the read.

**Example 1:** The header.

```
@HD VN:1.4
@SQ SN:chr1 LN:249250621
...
@SQ SN:chrY LN:59373566
@RG ID:sample1
@PG ID:bwa
```

Annotations for Example 1:

- Format Version: VN:1.4
- Chromosome Name & Chromosome Length: SN:chr1 LN:249250621
- Sample Name: ID:sample1
- Program Used for the Alignment: ID:bwa

**Example 2:** The alignment of a mapped bam file.

```
NB551591:7:HJT5CBGX9:3:12504:9644:16733 99 chr10 92983 60 151M = 93010 178
AGAAAAGGAGAGTTCTAGGCCACCTCCTCGGCATACCTCTCATCTCCTCCTCGGCCGTGGCCTCCTGATATTGCTGATATTCAGACACCAGGTCGTTTCATGT
TGCTCTCGGCCTCGGTGAATACCATCTCATCCATGCCTCGC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
/EEEEEEAE<6AE</AAEAEAAA<AA<< MD:Z:129T21 RG:Z:Seq01p NM:i:1 AS:i:146 XS:i:126
```

Annotations for Example 2:

- Read Name: NB551591:7:HJT5CBGX9:3:12504:9644:16733
- Alignment Information About the Read: 99
- Chromosome the Read Mapped To: chr10
- Position the Read Mapped To: 92983
- Mapping Quality: 60
- 151 Exact Matches to the Reference: 151M
- The Sequence of the Read: AGAAAAGGAGAGTTCTAGGCCACCTCCTCGGCATACCTCTCATCTCCTCCTCGGCCGTGGCCTCCTGATATTGCTGATATTCAGACACCAGGTCGTTTCATGT
- The Quality Score of the Read: /EEEEEEAE<6AE</AAEAEAAA<AA<<

### References

- [https://support.illumina.com/help/BS\\_App\\_RNASeq\\_Alignment\\_OLH\\_1000000006112/Content/Source/Informatics/BAM-Format.htm](https://support.illumina.com/help/BS_App_RNASeq_Alignment_OLH_1000000006112/Content/Source/Informatics/BAM-Format.htm)
- <http://samtools.sourceforge.net/>
- <https://genome.ucsc.edu/FAQ/FAQformat.html#format1>

**Browser Extensible Data (BED):** A text file format used to store genomic regions as coordinates and associated annotations. BED files contain a header section and a body section.

**Header section:** It is optional and begins with "browser or "track".

**Body section:** It follows the header and is whitespace or tab separated into 12 fields. The first 3 fields are required. The next 9 fields are optional and described in <https://genome.ucsc.edu/FAQ/FAQformat.html#format1>.

Common Field in Body Section	Field Description
chrom	Chromosome.
chromStart	Start coordinate on the chromosome. The first base in a chromosome is numbered 0.
chromEnd	End coordinate on the chromosome.
name (optional)	Name of the line in the BED file.
score (optional)	Score between 0 and 1000. The actual biological meaning depends on the performed experiment.
strand (optional)	DNA strand orientation.

*An Example:* The body section.

Chromosome	Start Coordinate	End Coordinate	Name of the Line	Score	DNA Strand
chr1	172628341	172628689	NM_000639.2_cds_0_0_chr1_172628342_f	0	+
chr1	172629234	172629280	NM_000639.2_cds_1_0_chr1_172629235_f	0	+
chr1	172633473	172633530	NM_000639.2_cds_2_0_chr1_172633474_f	0	+
chr1	172634761	172635156	NM_000639.2_cds_3_0_chr1_172634762_f	0	+
chr1	36931957	36932428	NM_000760.3_cds_0_0_chr1_36931958_r	0	-
chr1	36932830	36932912	NM_000760.3_cds_1_0_chr1_36932831_r	0	-
chr1	36933158	36933252	NM_000760.3_cds_2_0_chr1_36933159_r	0	-
chr1	36933422	36933563	NM_000760.3_cds_3_0_chr1_36933423_r	0	-
chr1	172628341	172628689	NM_000639.2_cds_0_0_chr1_172628342_f	0	+

**Variant Call Format (VCF) format:** The information about variants found at specific positions in a reference genome. VCF files contain a header section and a body section.

**Header section:** It begins with a "##" and lists the annotations used in the file.

**Body section:** It follows the header and is tab separated into 10 fields. The column names beginning with a "#".

Field in Body section	Field Description
CHROM	The chromosome on which the variation is called.
POS	The position of the variation on the chromosome. The first base in a chromosome is numbered 1. The vcf standard has the indel shifted to the 5' most position on the reference.
ID	The identifier of the variation.
REF	The reference allele at the position on the chromosome.
ALT	The list of alternative alleles at the position.
QUAL	A quality score associated with the given alleles.
FILTER	The filters the variation has passed.
INFO	Fields describe the variation.
FORMAT (optional)	More fields describe the variation.
SAMPLEs (optional)	The values specified in the FORMAT.

*An example:* The body section.

