

The maf format alignment file starts with the following header line:

```
##maf version=? Scoring=?
```

This line specifies the version of maf format and scoring system used in this alignment (or some other information regarding this alignment.)

Then the file is composed of following alignment blocks separated by empty lines:

```
a score=????  
s genome.chr start-position sequence-size +/- chromosome-size alignment-sequence  
s genome.chr start-position sequence-size +/- chromosome-size alignment-sequence
```

Each alignment block starts with an "a" line:

```
a score=????
```

When originally computed, the score is alignment score based on alignment algorithm parameters. But after (post-)processing steps this score may not be valid any more.

Then the next line in the alignment block is an "s" line:

```
s genome.chr start-position sequence-size +/- chromosome-size alignment-sequence
```

All fields in this line are explained in details below:

's' indicate this line has alignment sequence. Each alignment block is composed of two (in case of pairwise alignment) or more of this type of lines.

genome.chr: genome assembly and chromosome information of the sequence

start-position: the position of the first base of this sequence in the chromosome

sequence-size: the number of bases in this sequence (not the length of the alignment text string, which also includes dashes)

+/-: strand information that you can ignore for now

chromosome-size: the length of the whole chromosome

alignment-sequence: the alignment text including "dashes". The lengths of alignment sequences in the same alignment block must be the same.