

# Bed file

## Bed : Browser Extensible Data

### Specifications

Officially none,  
but UCSC browser propose one that can be used :  
<http://www.genome.ucsc.edu/FAQ/FAQformat.html#format1>  
Most prog (I've used) consider only the 3 first column  
(seq\_id, start, end).

### Warning :

UCSC spec. use 0-based coordinates, half-open region, not all  
prog consider this.

### Samples

#### S1

```
chr7 127471196 127472363  
chr7 127472363 127473530  
chr7 127473530 127474697
```

#### S2

```
chr7 0 1 base_une
```

### Recommended library

?

# Recommended tools

bedops : <https://bedops.readthedocs.io>

bedtools : [bedtools.readthedocs.io](http://bedtools.readthedocs.io)

## Comments

- Spec seems to imply that `start < end`, but as it is not strictly forbidden, I use “`seq end start`” to a feature on the opposite strand.
- To load data I used a personal class `RegionLink` that aims to manage file like “`chrom,start,end <=> chrom',start',end'`”  
It can be found in [https://gitlab.inria.fr/sletort/Brassica\\_scripts/blob/master/lib/RegionLink.py](https://gitlab.inria.fr/sletort/Brassica_scripts/blob/master/lib/RegionLink.py)
- Bedops propose the format `starch` which is a `gzip` bed with an integrated index, which is great to work and save space.