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

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
- Bedops propose the format starch which is a gzip bed with an integrated index, which is greatto work and save space.