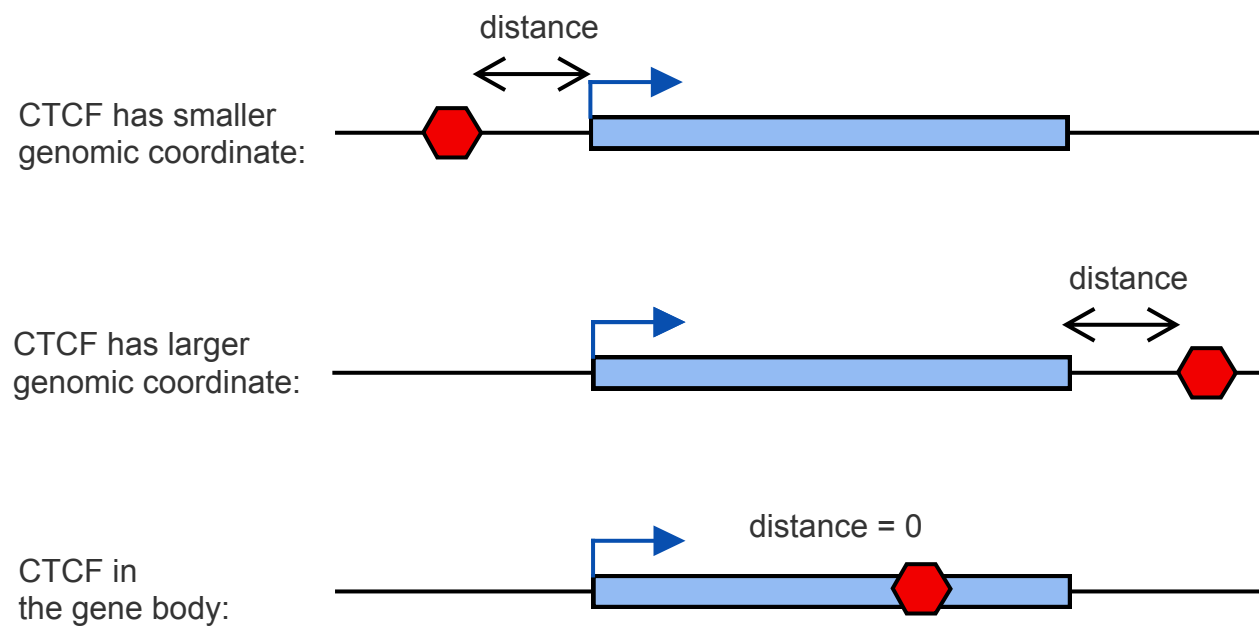


entry of the genes table (genes):

chrom start end strand

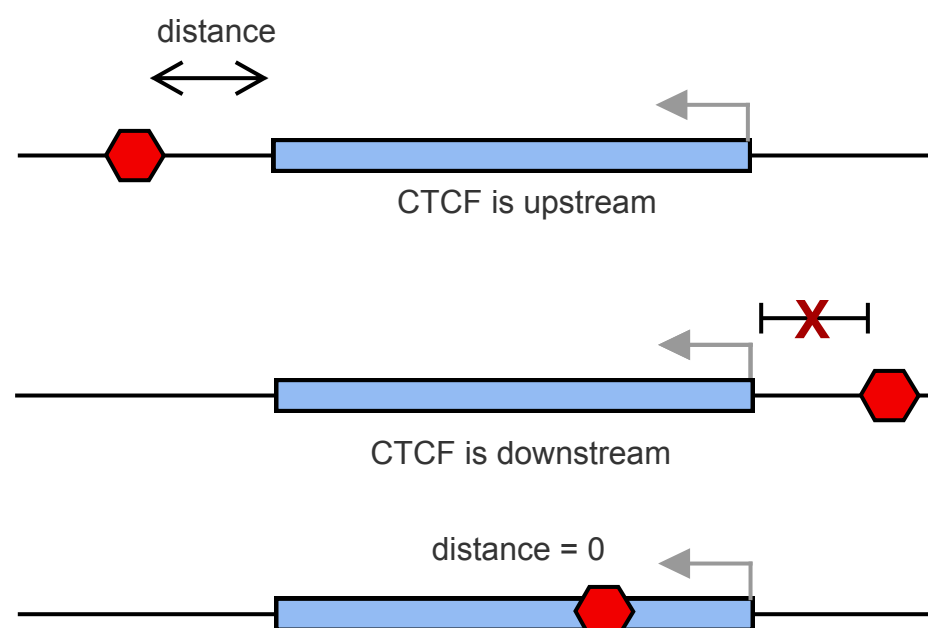
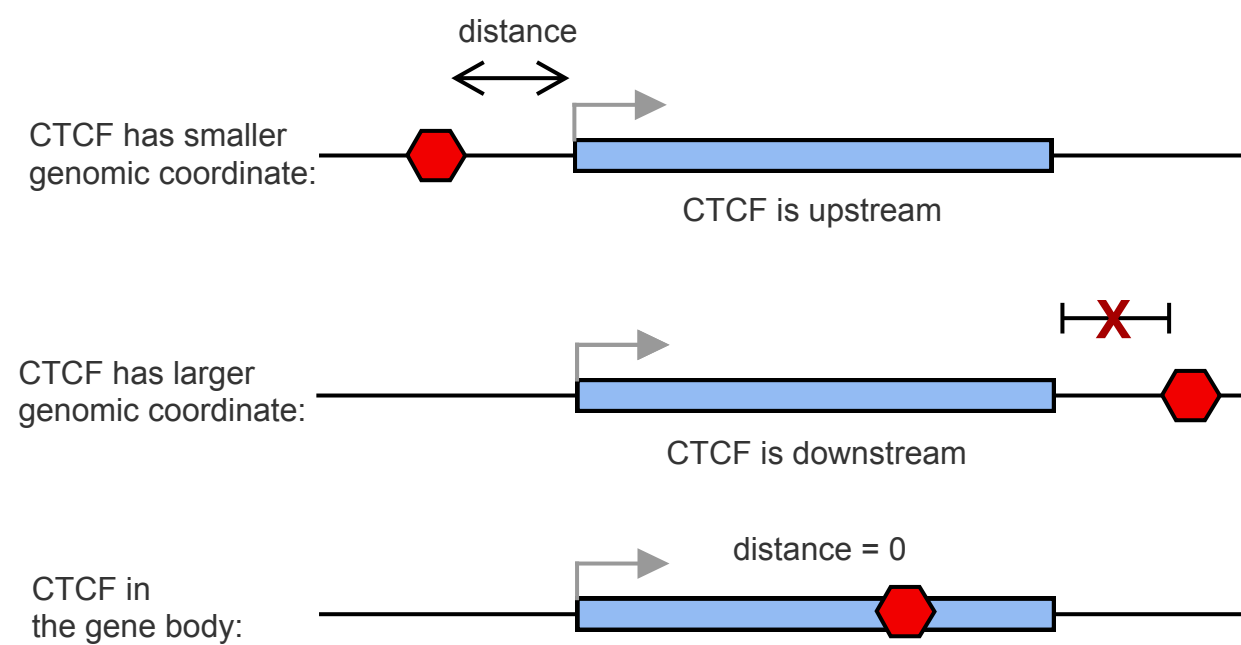
entry of the CTCF table (ctcf_peaks):

chrom start end



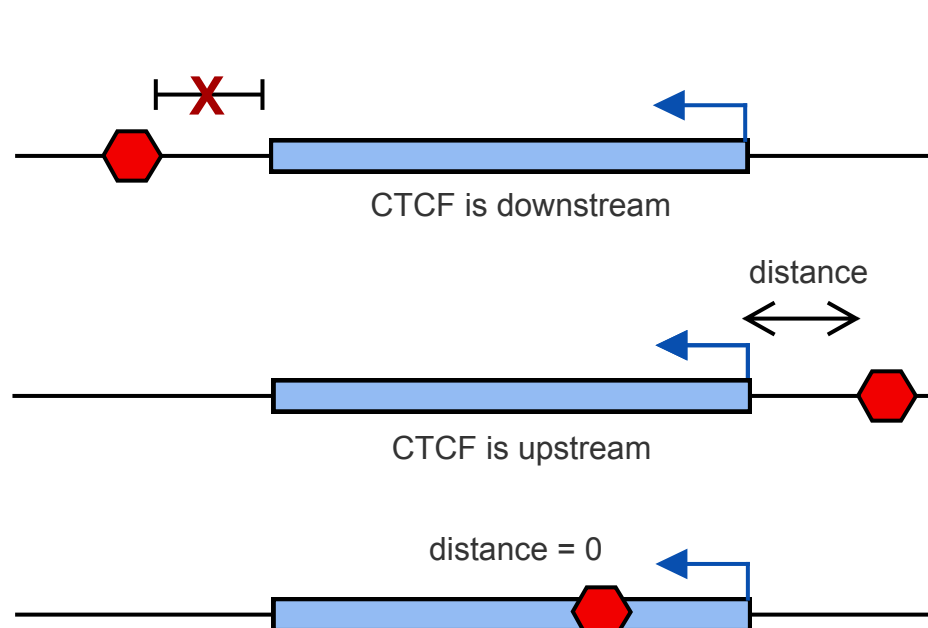
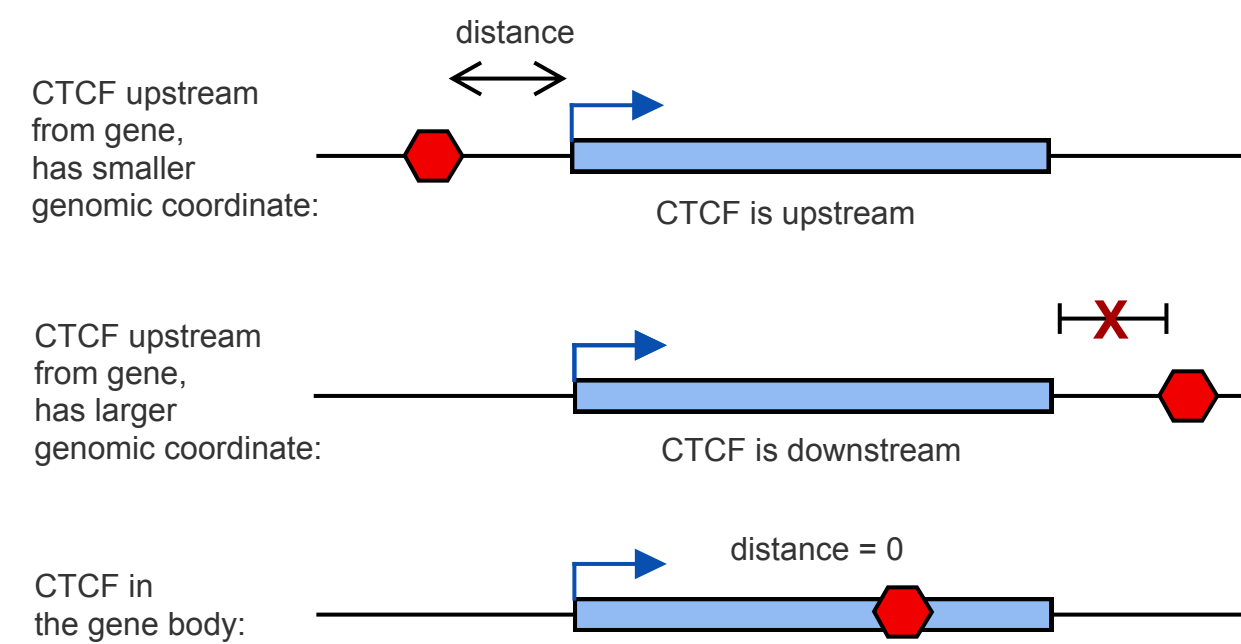
```
bioframe.closest(ctcf_peaks, genes,
                 ignore_overlaps=False,
                 ignore_upstream=False,
                 ignore_downstream=False,
                 direction_col=None)
```

- upstream/downstream direction is defined by genomic coordinates
- direction of the gene does not matter



```
bioframe.closest(ctcf_peaks, genes,
                 ignore_overlaps=False,
                 ignore_upstream=False,
                 ignore_downstream=True,
                 direction_col=None)
```

- upstream/downstream direction is defined by genomic coordinates
- direction of the gene does not matter



```
bioframe.closest(ctcf_peaks, genes,
                 ignore_overlaps=False,
                 ignore_upstream=False,
                 ignore_downstream=True,
                 direction_col='strand')
```

- upstream/downstream direction is defined by the strand of the gene
- direction of the gene matters