BEDTools

BED Format

- One of several file formats developed and supported by UC Santa Cruz Browser team.
- BED - Browser Extensible Data
- Simple format but has extensibility
- First 3 columns are required (chrom,start,end)
- Additional columns are (name,score,strand)

GFF Format

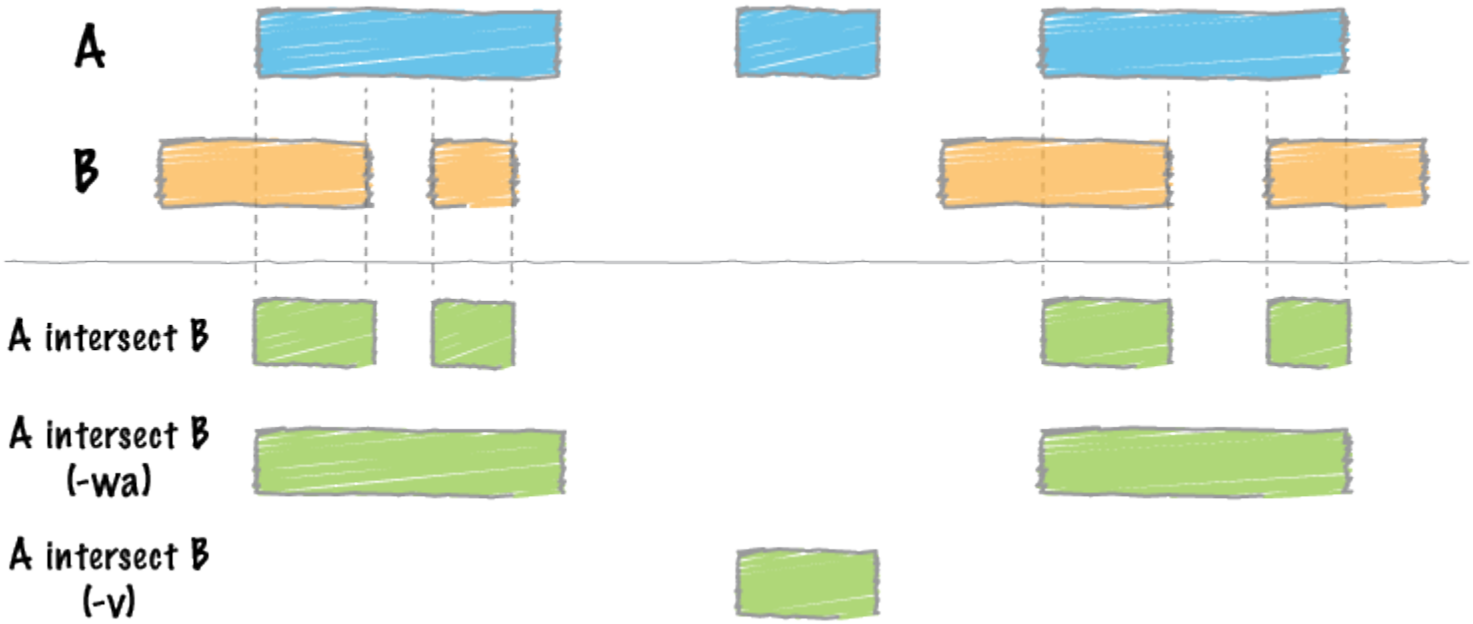
- Gene Feature Format or Generic Feature Format
- 9 columns, chromosome, source, type, start,end, score, strand, score, name

```
chr22  TeleGene enhancer  10000000  10001000  500 +  .  touch1
chr22  TeleGene promoter  10010000  10010100  900 +  .  touch1
chr22  TeleGene promoter  10020000  10025000  800 -  .  touch2
```

BEDTools

- "need for fast, flexible tools with which to compare large sets of genomic features"
- See the documentation here
- Do intersection, union of the features
- Also calculate coverage (e.g. number of SNPs or number of reads) *

Running BEDtools: intersect

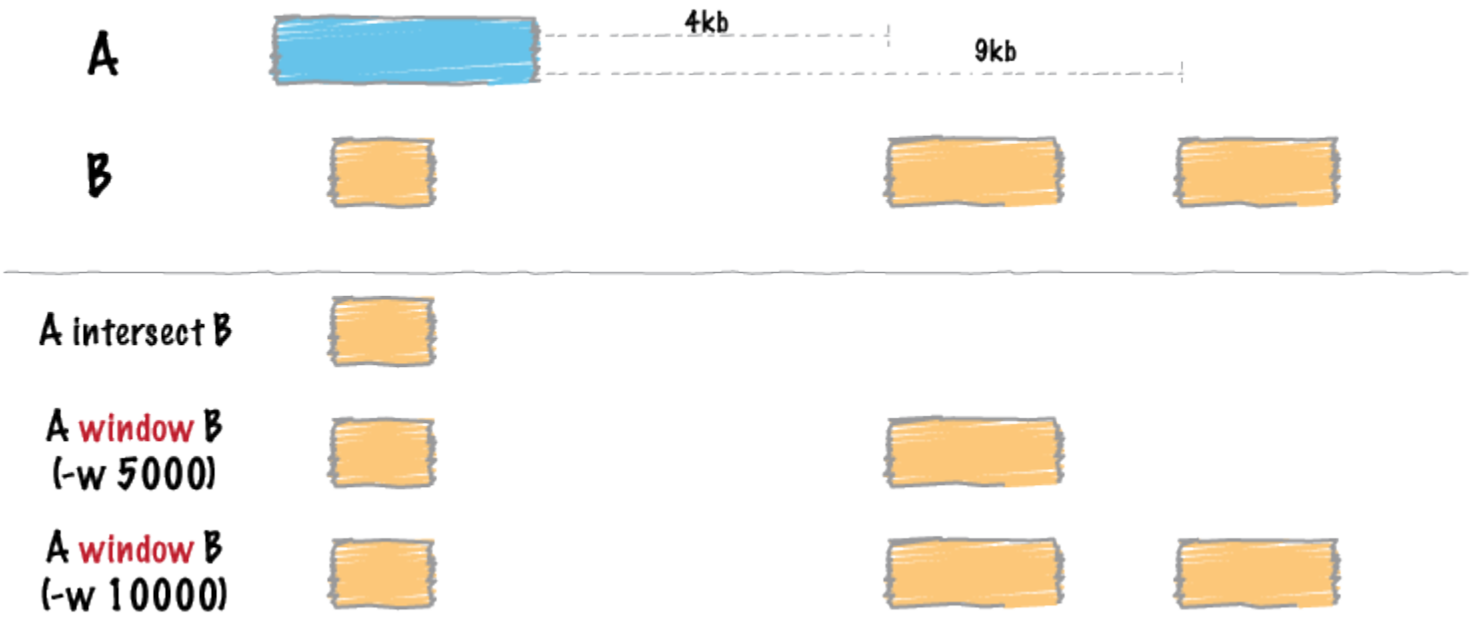


Look for overlaps

```
# report the SNPs which overlap genes
$ cd /shared/gen220/data_files/features/
$ bedtools intersect -a HEG4.SNPs.vcf -b  rice_chr6.gff
$ bedtools intersect -a HEG4.SNPs.vcf -b rice_chr6_genesonly.gff
# report the same but print out the gene feature too - use the -wo option
```

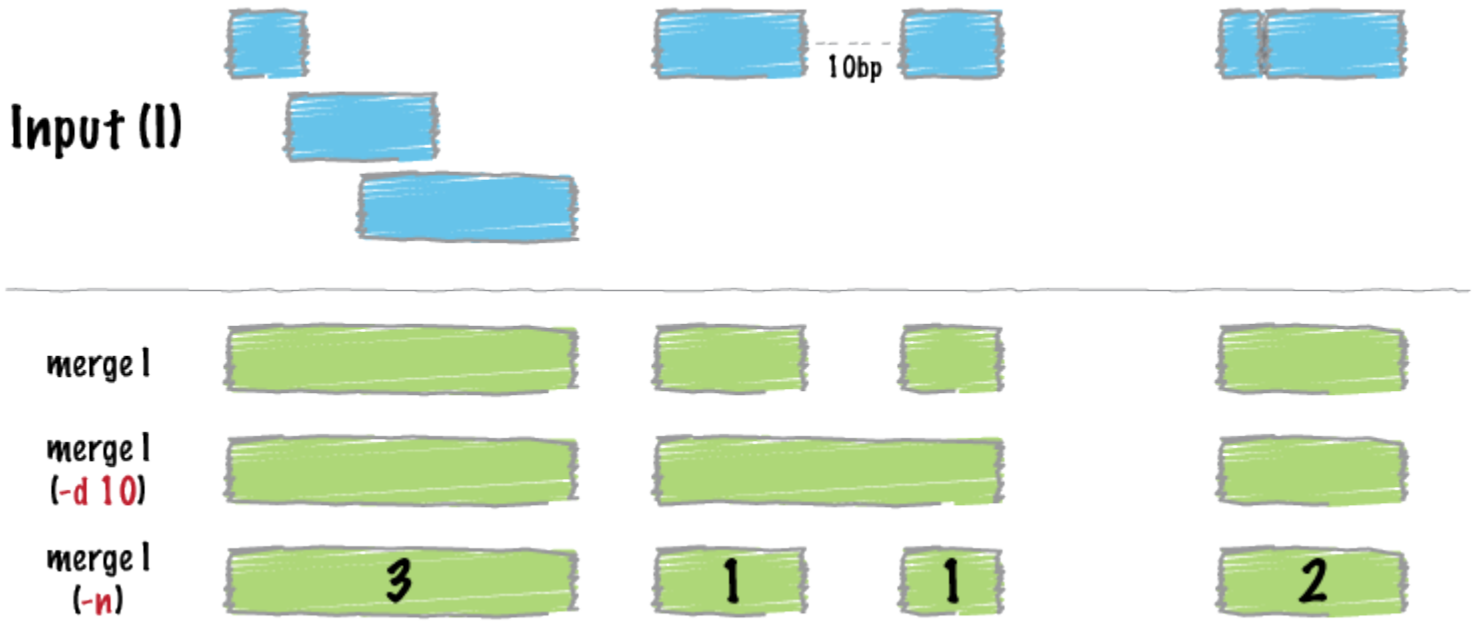
```
$ bedtools intersect -a HEG4.SNP.vcf -b rice_chr6.gff -wo
# report the gene features which don't have SNPs
```

BEDtools: window



Can do the same thing as intersect but allows the features to be 'grown'.

BEDtools: merge



Merge features that are nearby (or overlapping). Useful for NGS reads and merging coverage

BEDtools: muticov

- "eports the count of alignments from multiple position-sorted and indexed BAM files that overlap intervals in a BED file. Specifically, for each BED interval provided, it reports a separate count of overlapping alignments from each BAM file."
- So calculate the coverage, by reads, of features

  $ bedtools multicov -bams HEG4.tophat.bam -bed rice_chr6_genesonly.gff