

Problem: compute overlap between BED files

Solution: `bedtools intersect -a reads.bed -b genes.bed`

This command computes the number of bases in file “B” that are covered by intervals in file “A”.

Bedtools has many utilities

Command	Function
bamtobed	Convert a BAM file to a BED file
closest	For each interval in one file, find the closest in another
overlap	Compute the overlap between intervals
merge	Merge intervals that overlap
subtract	Remove the overlapping regions from intervals

And many, many, many more functions.
Many with multiple modes of operation.