

metagenome  
fastq



$10^7$ /sample

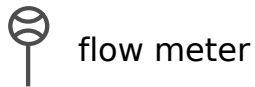


assembly

contigs



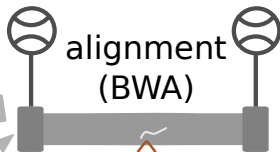
Legend



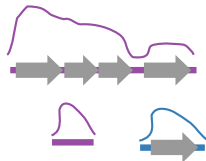
fastq



$10^7$ /sample



alignment  
(BWA)



count  
(htseq-count)

Gene	Reads
A1	10
A2	8
A3	7
B1	7

reference DNA

