

Input BAMs + list
files partitioning
genome

s1.bam list1.list
s2.bam + list2.list
s3.bam list3.list



bam2gvcf



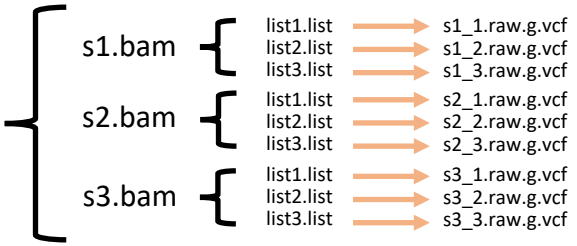
gvcf2DB



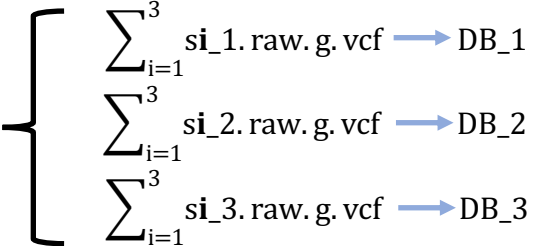
DB2vcf



gatherVcfs



scattered by sample,
scattered by list file



gathered by sample,
scattered by list file



scattered by list file



gathered by list file