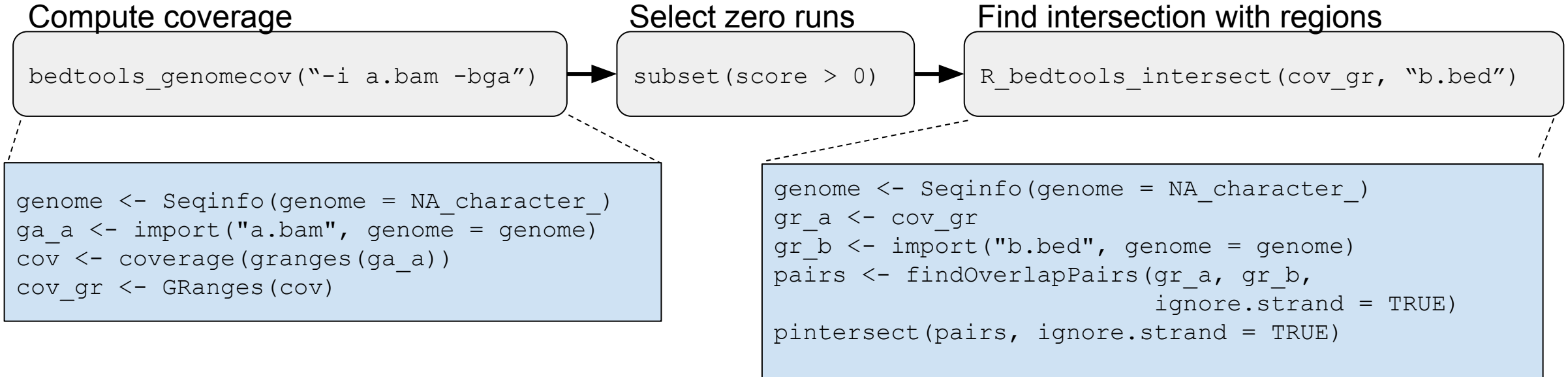
Compute coverage
bedtools_genomecov("-i a.bam -bga")
Select zero runs
subset(score > 0)
Find intersection with regions
R_bedtools_intersect(cov_gr, "b.bed")
genome <- Seqinfo(genome = NA_character_)
ga_a <- import("a.bam", genome = genome)
cov <- coverage(granges(ga_a))
cov_gr <- GRanges(cov)
genome <- Seqinfo(genome = NA_character_)
gr_a <- cov_gr
gr_b <- import("b.bed", genome = genome)
pairs <- findOverlapPairs(gr_a, gr_b,
ignore.strand = TRUE)
pintersect(pairs, ignore.strand = TRUE)