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")
```

```
ga_a <- import("a.bam")
cov_gr <- GRanges(coverage(granges(ga_a)))
```

```
gr_b <- import("b.bed")
pairs <- findOverlapPairs(cov_gr, gr_b,
                          ignore.strand = TRUE)
pintersect(pairs, ignore.strand = TRUE)
```