

```
countGenomicOverlaps(query, subject,  
    type = "any", "start", "end", "within", "equal"),  
    resolution = "none", "divide", "uniqueDisjoint"),  
    ignore.strand = FALSE)
```

All reads have a total hit value of 1.
In the case of split reads, each read fragment has a fraction of the whole. If a split read has 5 fragments, each fragment has 0.25 of a hit to contribute to the subject it hits.

read/read fragment hit 1 subject

read/read fragment hit 1 > subject

Hit value is assigned to the subject

resolution

none

divide

uniqueDisjoint

All multi-hit reads are dropped

Hit value is divided evenly among all subjects hit

Hit value is assigned to the subject with unique disjoint interval that is hit by the read. If none exists, no hit is assigned.