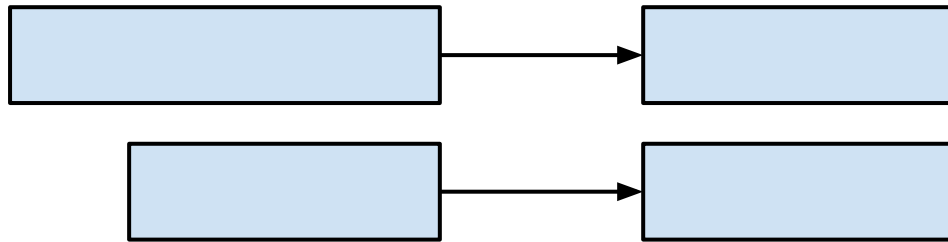
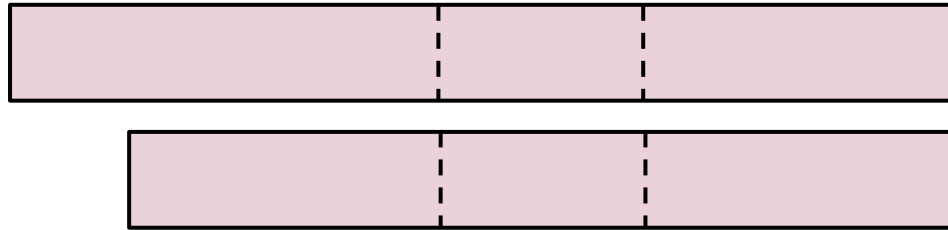


Gene model



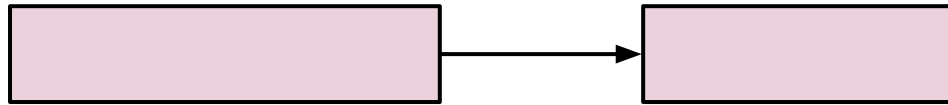
```
gene_model <- GRangesList(  
  transcript_1 = GRanges("chr1",  
    IRanges(start=c(100, 700), end=c(500, 900))),  
  transcript_2 = GRanges("chr1",  
    IRanges(start=c(200, 700), end=c(500, 900))))
```

Unspliced  
transcripts



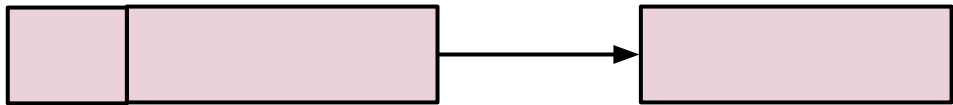
`range(gene_model)`

Gene region



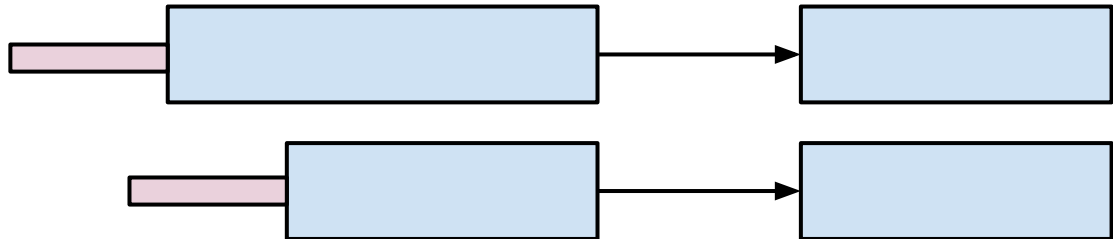
`reduce(unlist(gene_model))`

Disjoint bins



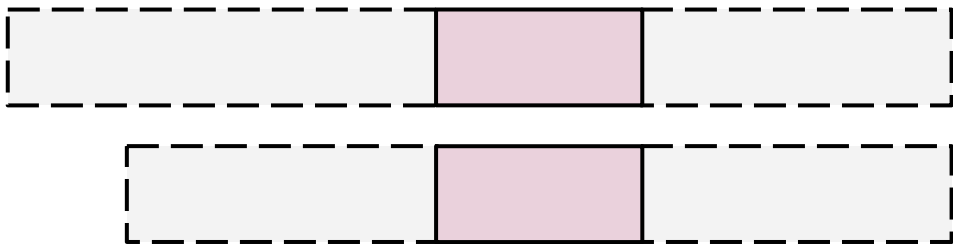
`disjoin(unlist(gene_model))`

Promoter



`flank(range(gene_model), 100)`

Introns



`psetdiff(range(gene_model), gene_model)`