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# A) Retrieve data from Cufflinks
cuffDB <- readCufflinks(dir='./cuffdiff_output/', rebuild=TRUE, gtfFile='./cuff-merge/merged.gtf') # create SQL database via cummeRbund

mySpliceRList <- prepareCuff(cuffDB) # Extract data from SQL database

# B) Identify ORFs and annotate PTCs in transcripts
require("BSgenome.Hsapiens.UCSC.hg19",character.only = TRUE) # load genome sequence

ucscCDS <- getCDS(selectedGenome="hg19", repoName="UCSC") # Get annotated ORFs

mySpliceRList <- annotatePTC(mySpliceRList, ucscCDS, Hsapiens) # Analyze ORFs

# C) Analyze alternative splicing in transcripts
mySpliceRList <- spliceR(mySpliceRList, compareTo='preTranscript', filters= 'isoOK')

# D) Create GTF file
generateGTF(mySpliceRList, filters="isoOK", filePrefix='./outputPaht/outputName')
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