RAProject

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```
sce0 <- readRDS('toyTCRdata.rds')
sce <- clonoStats(sce0, method = 'EM')

#A<-sce0$contigs[sce0$contigs[, 'chain'] %in% c('TRA','TRB')]
for (i in 1:length(sce0$contigs)){
  #sce0$contigs[[i]]  "DFrame"  "S4Vectors"
  #sce0$contigs[[i]]<-sce0$contigs[[i]] %>% filter(chain %in% c("TRA","TRB"))
  #sce0$contigs[[i]]<-sce0$contigs[[i]][filter(sce0$contigs[[i]]$chain %in% c("TRA","TRB")),]
  sce0$contigs[[i]]<-sce0$contigs[[i]][order(sce0$contigs[[i]]$chain),]

}
```

Generate sample pool

```
samplePool=DataFrameList()
poolSize=1
for (i in 1:length(sce0$contigs)){
  if(length(sce0$contigs[[i]]$chain)==2 & sce0$contigs[[i]]$chain[1]=='TRA' & sce0$contigs[[i]]$chain[2]

    samplePool[[poolSize]]=sce0$contigs[[i]]
    poolSize=poolSize+1
  }

}
poolSize=poolSize-1
```

Functions for generate a sample

```
getClonotype<-function(clonotype_index, numberA, numberB, errorProb = .01){
    result=DataFrame()
    indexInPool=sample.int(poolSize, 3, replace=FALSE)

    if (numberA>=1){
        if(runif(1) < errorProb){
          result=rbind(result,samplePool[[indexInPool[2]]][1,])
        }else{
```

```
          result=rbind(result,samplePool[[indexInPool[1]]][1,])
        }
        numberA=numberA-1
    }
    if (numberB>=1){
        if(runif(1) < errorProb){
          result=rbind(result,samplePool[[indexInPool[3]]][2,])
        }else{
          result=rbind(result,samplePool[[indexInPool[1]]][2,])
        }

        numberB=numberB-1
    }
    while(numberA>0 | numberB>0){
        indexInPool=sample.int(poolSize, 1, replace=TRUE)
        if (numberA>=1){
            result=rbind(result,samplePool[[indexInPool]][1,])
            numberA=numberA-1
        }
        else{
            result=rbind(result,samplePool[[indexInPool]][2,])
            numberB=numberB-1
        }
    }
    return(result)

}
```

Use the functions to generate a sample with size 50

However, function 'clonoStats' is not compatible with SimpleDFrameList, how to transform SimpleDFrameList to CompressedSplitDFrameList

```
getSample <- function(samplesize){
    sample=DataFrame()
    DistributeTRA=sum(sce0$contigs[,'chain']=='TRA')
    DistributeTRB=sum(sce0$contigs[,'chain']=='TRB')
    # table(DistributeTRA,DistributeTRB)
    IndexnAnBMap=cbind(DistributeTRA,DistributeTRB)
    RandomIntegers <- sample(1:1000, samplesize, replace=T)

    barcode <- paste('cell', 1:samplesize)


    sample <- lapply(1:samplesize, function(clonotype_index){
        getClonotype(clonotype_index, IndexnAnBMap[RandomIntegers[clonotype_index],1], IndexnAnBMap[Ran
    })
    sample <- SplitDataFrameList(sample)
    sample[,'barcode'] <- barcode
    sample[,'sample'] <- 'sim'
    names(sample) <- barcode
```

```
    # sample1<-as(sample,'SplitDFrameList')
    return(sample)

}
# samplelist=getSample(SampleSize)
# EMpredicted <- clonoStats(samplelist, method = 'EM')
# UNpredicted <- clonoStats(samplelist, method = 'unique')
```

Generate hashmap. Key is clonotype in Truth(sample pool), Value is percentage of the clonotype in Truth

```
TruthPercentageMap=hashmap()

for(i in 1:poolSize){

  key=paste(samplePool[[i]]$cdr3[1],samplePool[[i]]$cdr3[2],sep=' ')

  if(is.null(TruthPercentageMap[[key]])){
    TruthPercentageMap[[key]]<-1/poolSize
  }
  else{
    TruthPercentageMap[[key]]<-TruthPercentageMap[[key]]+1/poolSize
  }

}
```

Get Variation Distance

```
getDistance<-function(predicted){

  clonotypes=clonoNames(predicted)
  abundance=clonoAbundance(predicted)
  SumAbundance=sum(abundance)
  distance=0
  seen <- hashmap()
  for(i in 1:length(abundance)){
    if(is.null(TruthPercentageMap[[clonotypes[i]]])){
      distance=distance+abundance[i]/SumAbundance
    }
    else{
      seen[[clonotypes[i]]]<-TruthPercentageMap[[clonotypes[i]]]
      distance=distance+abs(abundance[i]/SumAbundance-TruthPercentageMap[[clonotypes[i]]])
    }
  }

  distance=distance+Reduce("+", values(TruthPercentageMap)) -Reduce("+", values(seen))
  return(distance)
}
```

Calculate distances for samples

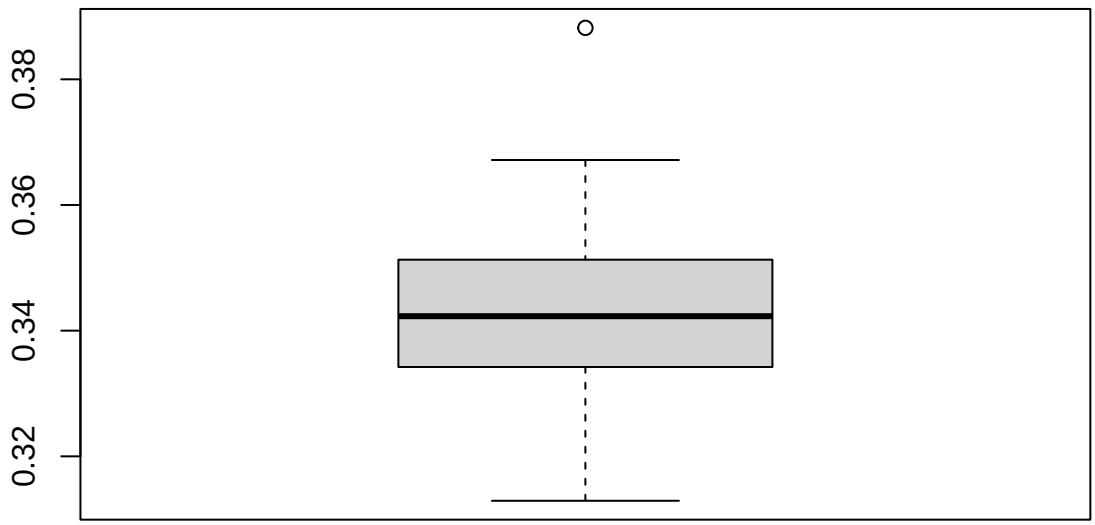
```
DistanceListFromEM=c()
DistanceListFromUN=c()
for(i in 1:50){
  samplelist=getSample(2000)
  EMpredicted <- clonoStats(samplelist, method = 'EM')
  distance1=getDistance(EMpredicted)
  DistanceListFromEM[i]=distance1
  UNpredicted <- clonoStats(samplelist, method = 'unique')
  distance2=getDistance(UNpredicted)
  DistanceListFromUN[i]=distance2
  print(i)
}
```

```
## [1] 1
## [1] 2
## [1] 3
## [1] 4
## [1] 5
## [1] 6
## [1] 7
## [1] 8
## [1] 9
## [1] 10
## [1] 11
## [1] 12
## [1] 13
## [1] 14
## [1] 15
## [1] 16
## [1] 17
## [1] 18
## [1] 19
## [1] 20
## [1] 21
## [1] 22
## [1] 23
## [1] 24
## [1] 25
## [1] 26
## [1] 27
## [1] 28
## [1] 29
## [1] 30
## [1] 31
## [1] 32
## [1] 33
## [1] 34
## [1] 35
## [1] 36
## [1] 37
```

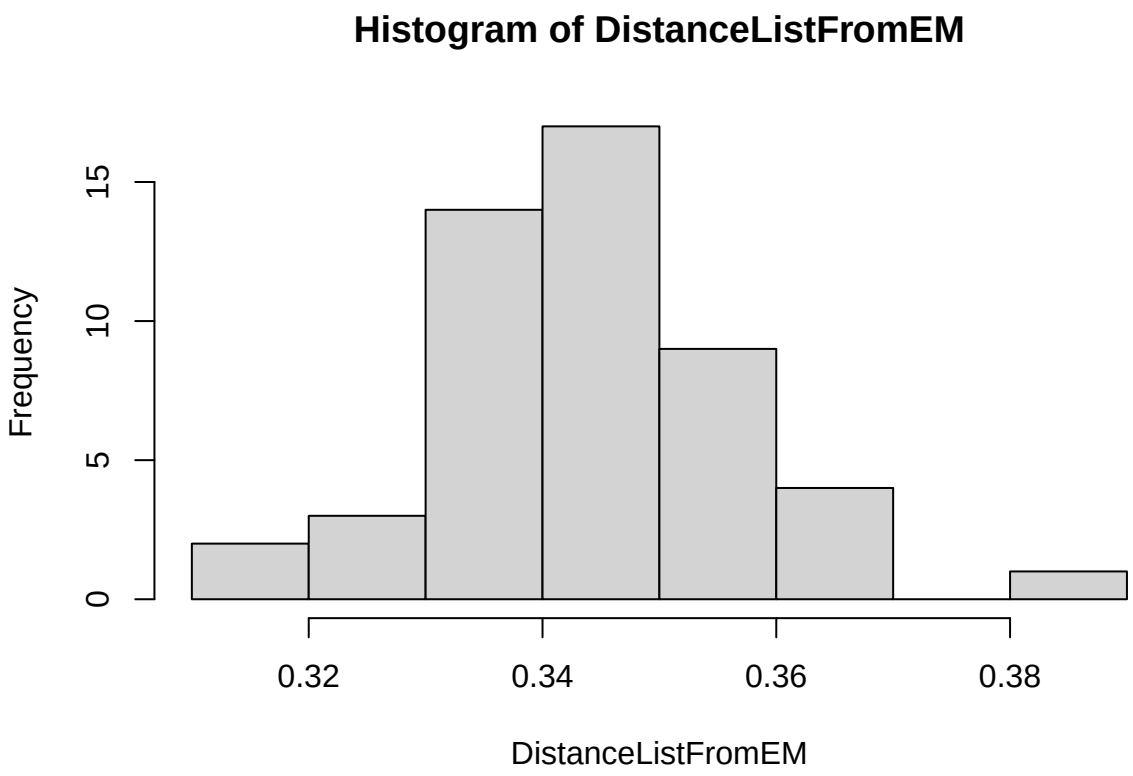
```
## [1] 38
## [1] 39
## [1] 40
## [1] 41
## [1] 42
## [1] 43
## [1] 44
## [1] 45
## [1] 46
## [1] 47
## [1] 48
## [1] 49
## [1] 50
```

Visualize

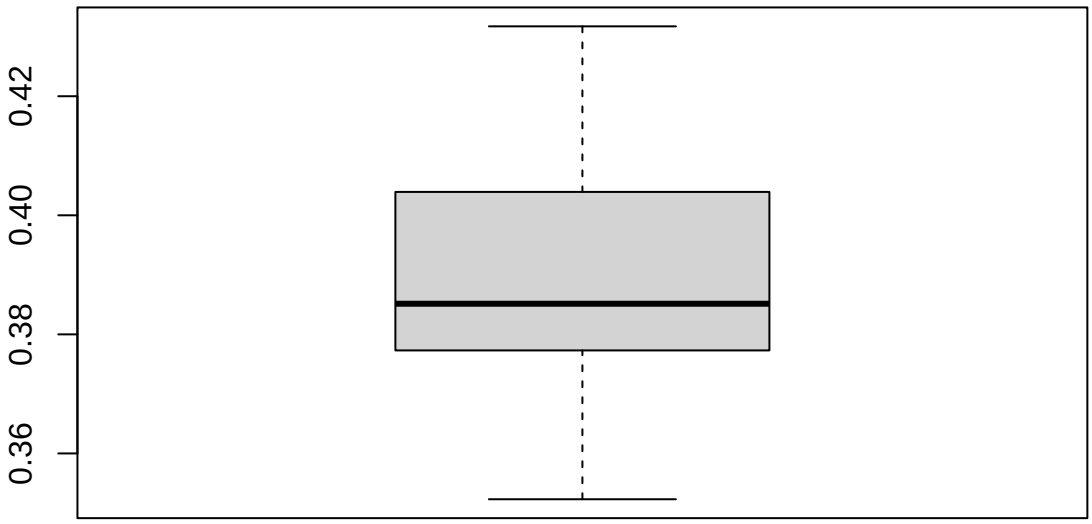
```
boxplot(DistanceListFromEM)
```



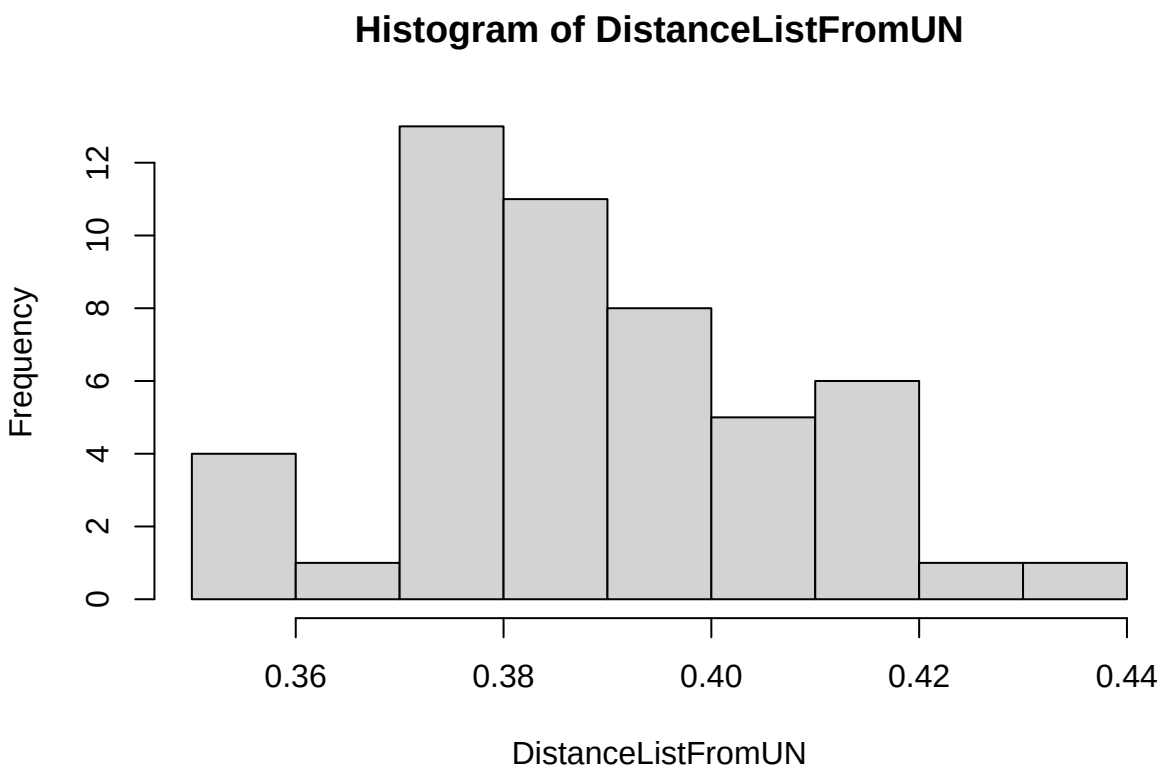

```
hist(DistanceListFromEM)
```




```
boxplot(DistanceListFromUN)
```




```
hist(DistanceListFromUN)
```




```
print(median(DistanceListFromEM))
```

```
## [1] 0.3423002
```

```
print(median(DistanceListFromUN))
```

```
## [1] 0.3851499
```

```
print(mean(DistanceListFromEM))
```

```
## [1] 0.3438032
```

```
print(mean(DistanceListFromUN))
```

```
## [1] 0.3883685
```