Intro to ALL data for Bioc monograph

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1 Introduction

This document is for authors of the Bioc monograph, it just goes over various aspects of the ALL data. Example analyses can be added here for illustration.

2 Attachment and data list

```
> library(ALL)
> data(ALL)
> show(ALL)

ExpressionSet (storageMode: lockedEnvironment)
assayData: 12625 features, 128 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: 01005 01010 ... LAL4 (128 total)
  varLabels: cod diagnosis ... date last seen (21 total)
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
  pubMedIds: 14684422 16243790
Annotation: hgu95av2
```

3 Tables and graphs for phenodata

```
> print(summary(pData(ALL)))

     cod              diagnosis            sex           age                BT
 Length:128         Length:128         F    :42   Min.   : 5.00   B2     :36
```

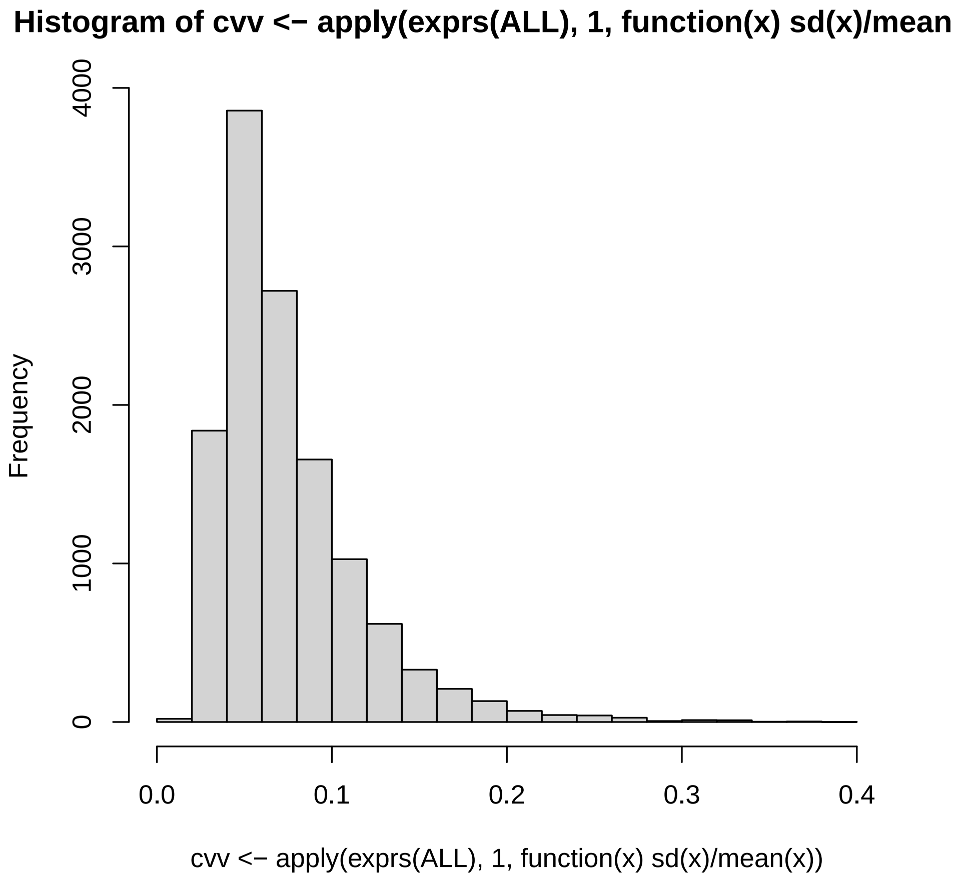
```
 Class :character   Class :character   M   :83   1st Qu.:19.00   B3     :23
 Mode  :character   Mode  :character   NA's: 3   Median :29.00   B1     :19
                                                 Mean   :32.37   T2     :15
                                                 3rd Qu.:45.50   B4     :12
                                                 Max.   :58.00   T3     :10
                                                 NA's   :5       (Other):13
 remission      CR              date.cr           t(4;11)
 CR  :99   Length:128         Length:128         Mode :logical
 REF :15   Class :character   Class :character   FALSE:86
 NA's:14   Mode  :character   Mode  :character   TRUE :7
                                                 NA's :35


  t(9;22)        cyto.normal        citog              mol.biol
 Mode :logical   Mode :logical   Length:128         ALL1/AF4:10
 FALSE:67        FALSE:69        Class :character   BCR/ABL :37
 TRUE :26        TRUE :24        Mode  :character   E2A/PBX1: 5
 NA's :35        NA's :35                           NEG     :74
                                                    NUP-98  : 1
                                                    p15/p16 : 1

   fusion protein   mdr          kinet       ccr           relapse
 p190     :17     NEG :101   dyploid:94   Mode :logical   Mode :logical
 p190/p210: 8     POS : 24   hyperd.:27   FALSE:74        FALSE:35
 p210     : 8     NA's:  3   NA's   : 7   TRUE :26        TRUE :65
 NA's     :95                             NA's :28        NA's :28


 transplant          f.u             date last seen
 Mode :logical   Length:128         Length:128
 FALSE:91        Class :character   Class :character
 TRUE :9         Mode  :character   Mode  :character
 NA's :28
```

```
> hist(cvv <- apply(exprs(ALL),1,function(x)sd(x)/mean(x)))
```



```
> ok <- cvv > .08 & cvv < .18
> fALL <- ALL[ok,]
> show(fALL)
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 3841 features, 128 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: 01005 01010 ... LAL4 (128 total)
  varLabels: cod diagnosis ... date last seen (21 total)
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
  pubMedIds: 14684422 16243790
Annotation: hgu95av2
```

```
> allx2 <- data.frame(t(exprs(fALL)), class=ALL$BT)
```

```
> library(rpart)
> rp1 <- rpart(class~.,data=allx2)
> plot(rp1)
> text(rp1)
```