

# Intro to ALL data for Bioc monograph

VJ Carey

April 28, 2022

## 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              NA's :0                  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 :0           NA's :0              NA's :28           NA's :28

```

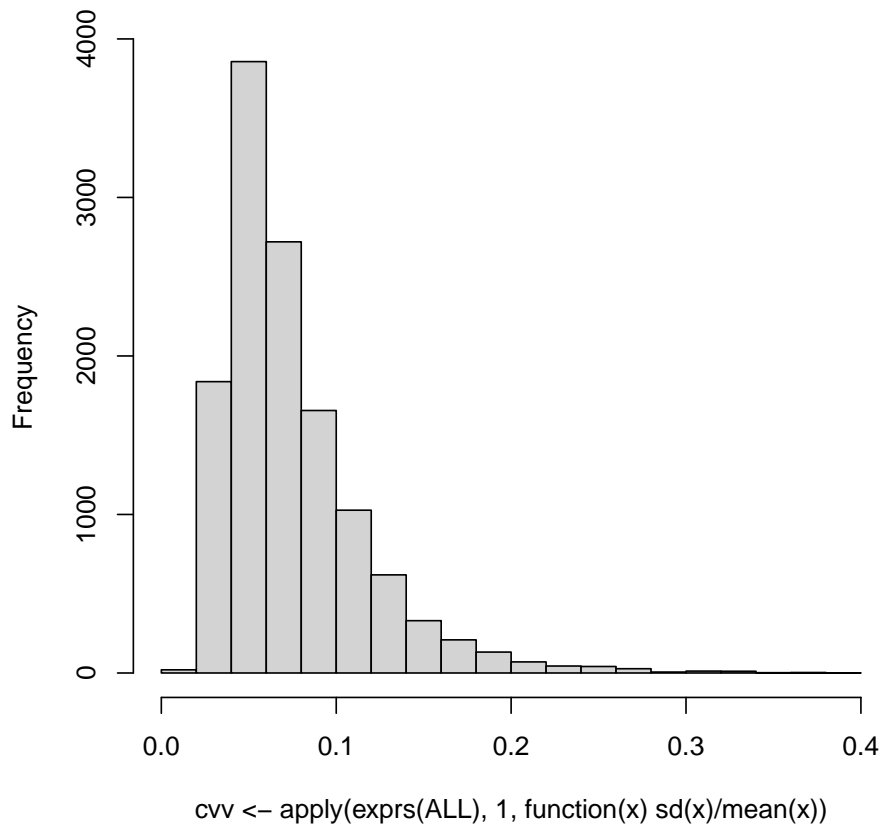
```

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)))
```

### Histogram of `cvv <- apply(exprs(ALL), 1, function(x) sd(x)/mean`



```
> 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)
```

