

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

```

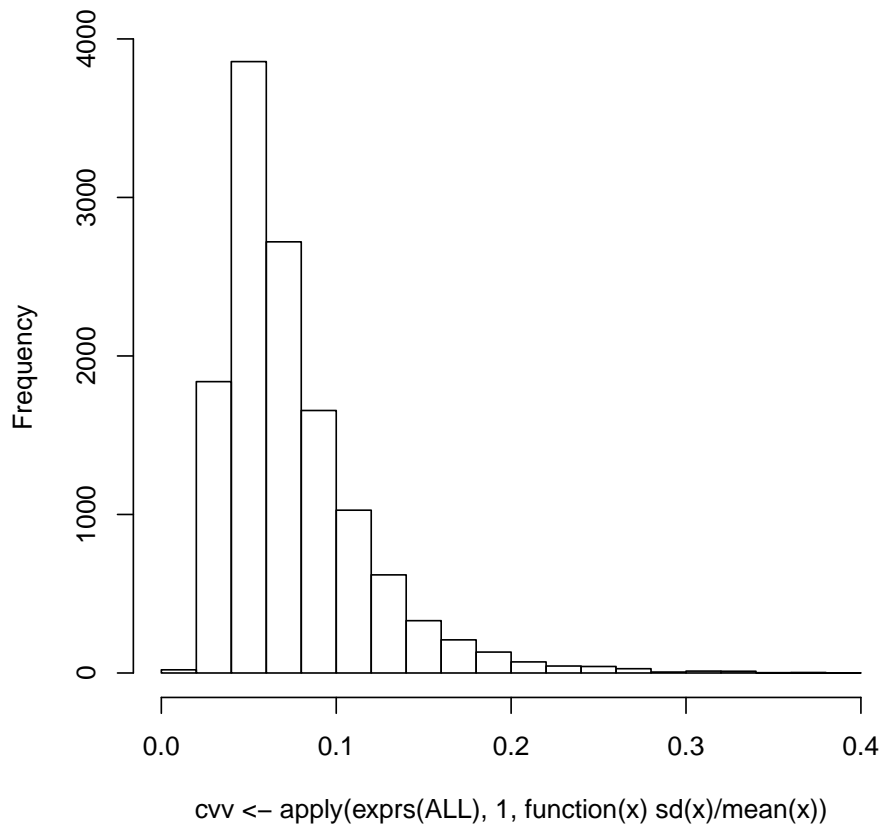
```

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)))
```

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)
```

