

# 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
phenoData
  sampleNames: 01005, 01010, ..., LAL4 (128 total)
  varLabels and varMetadata description:
    cod: Patient ID
    diagnosis: Date of diagnosis
    ...: ...
    date last seen: date patient was last seen
    (21 total)
featureData
  featureNames: 1000_at, 1001_at, ..., AFFX-YEL024w/RIP1_at (12625 total)
  fvarLabels and fvarMetadata description: 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    : 5.00      (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 :35          NA's :28          NA's :28

```

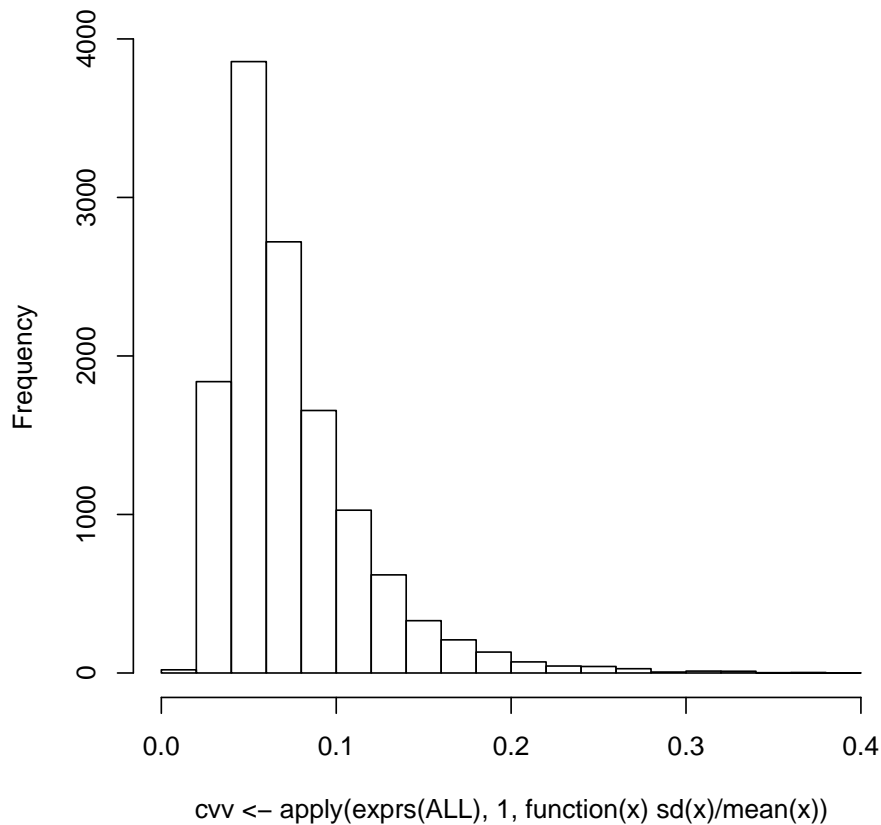
```

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 > 0.08 & cvv < 0.18
> fALL <- ALL[ok, ]
> show(fALL)
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 3841 features, 128 samples
  element names: exprs
phenoData
  sampleNames: 01005, 01010, ..., LAL4 (128 total)
  varLabels and varMetadata description:
    cod: Patient ID
    diagnosis: Date of diagnosis
    ...: ...
    date last seen: date patient was last seen
    (21 total)
featureData
  featureNames: 1005_at, 1007_s_at, ..., AFFX-YEL024w/RIP1_at (3841 total)
```

fvarLabels and fvarMetadata description: 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)
```

