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

```r
> 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

```r
> 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)
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.biolog
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
                      p190/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(x))

> 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
eperimentData: 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)