

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

N.unique :128	N.unique :115	M :83	1st Qu.:19.00	B3 :23
N.blank : 0	N.blank : 0	NAs: 3	Median :29.00	B1 :19
Min.nchar: 4	Min.nchar: 8		Mean :32.37	T2 :15
Max.nchar: 5	Max.nchar: 10		3rd Qu.:45.50	B4 :12
	NAs : 2		Max. :58.00	T3 :10
			NAs :5	(Other):13

remission	CR	date.cr	t(4;11)	t(9;22)
CR :99	Length :128	Length :128	Mode :logical	Mode :logical
REF:15	N.unique : 4	N.unique : 92	FALSE:86	FALSE:67
NAs:14	N.blank : 0	N.blank : 0	TRUE :7	TRUE :26
	Min.nchar: 2	Min.nchar: 8	NAs :35	NAs :35
	Max.nchar: 18	Max.nchar: 10		
	NAs : 7	NAs : 31		

cyto.normal	citog	mol.biol	fusion protein	mdr
Mode :logical	Length :128	ALL1/AF4:10	p190 :17	NEG:101
FALSE:69	N.unique : 15	BCR/ABL :37	p190/p210: 8	POS: 24
TRUE :24	N.blank : 0	E2A/PBX1: 5	p210 : 8	NAs: 3
NAs :35	Min.nchar: 6	NEG :74	NAs :95	
	Max.nchar: 20	NUP-98 : 1		
	NAs : 35	p15/p16 : 1		

kinet	ccr	relapse	transplant	f.u
dyploid:94	Mode :logical	Mode :logical	Mode :logical	Length :128
hyperd.:27	FALSE:74	FALSE:35	FALSE:91	N.unique : 11
NAs : 7	TRUE :26	TRUE :65	TRUE :9	N.blank : 0
	NAs :28	NAs :28	NAs :28	Min.nchar: 3
				Max.nchar: 17
				NAs : 28

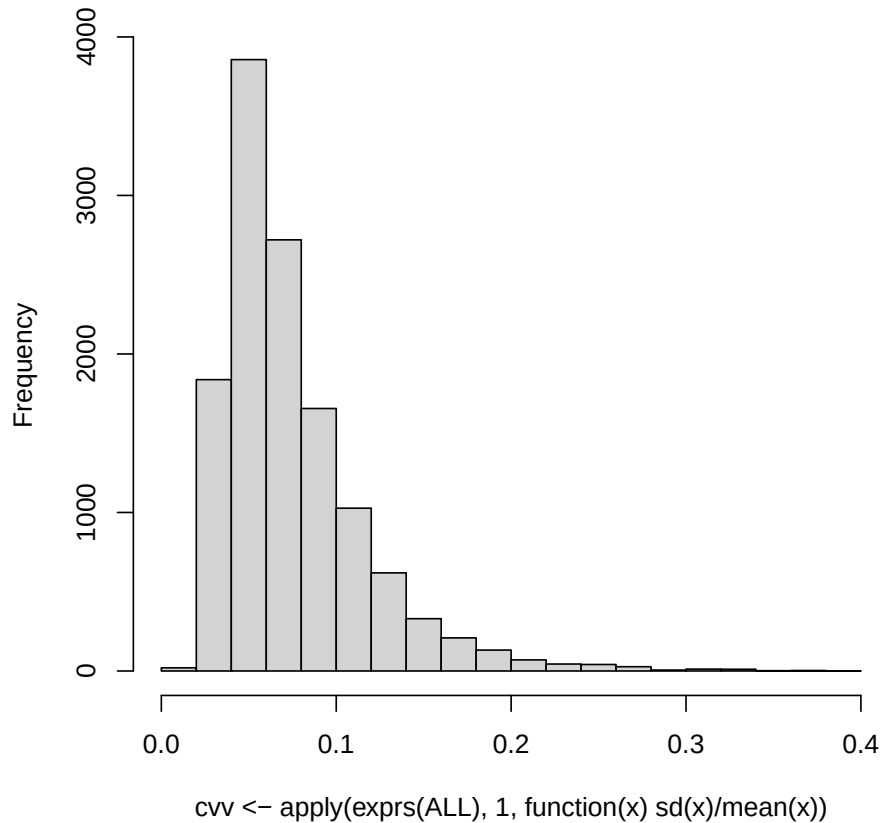
```

date last seen
Length :128
N.unique : 87
N.blank : 0
Min.nchar: 8
Max.nchar: 15
NAs : 35

```

```
> 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)

```

