

Probability density functions on patient and cell line proteomics, all values, long data format

The aim of this analysis is to compare the probability density functions of the phosphoproteomic data for cell lines and patient samples.

Data import

```
data_read<-read.table("Merged_Fold_change_all_values.txt",sep="\t",header=TRUE)
library(reshape2)
names(data_read)
```

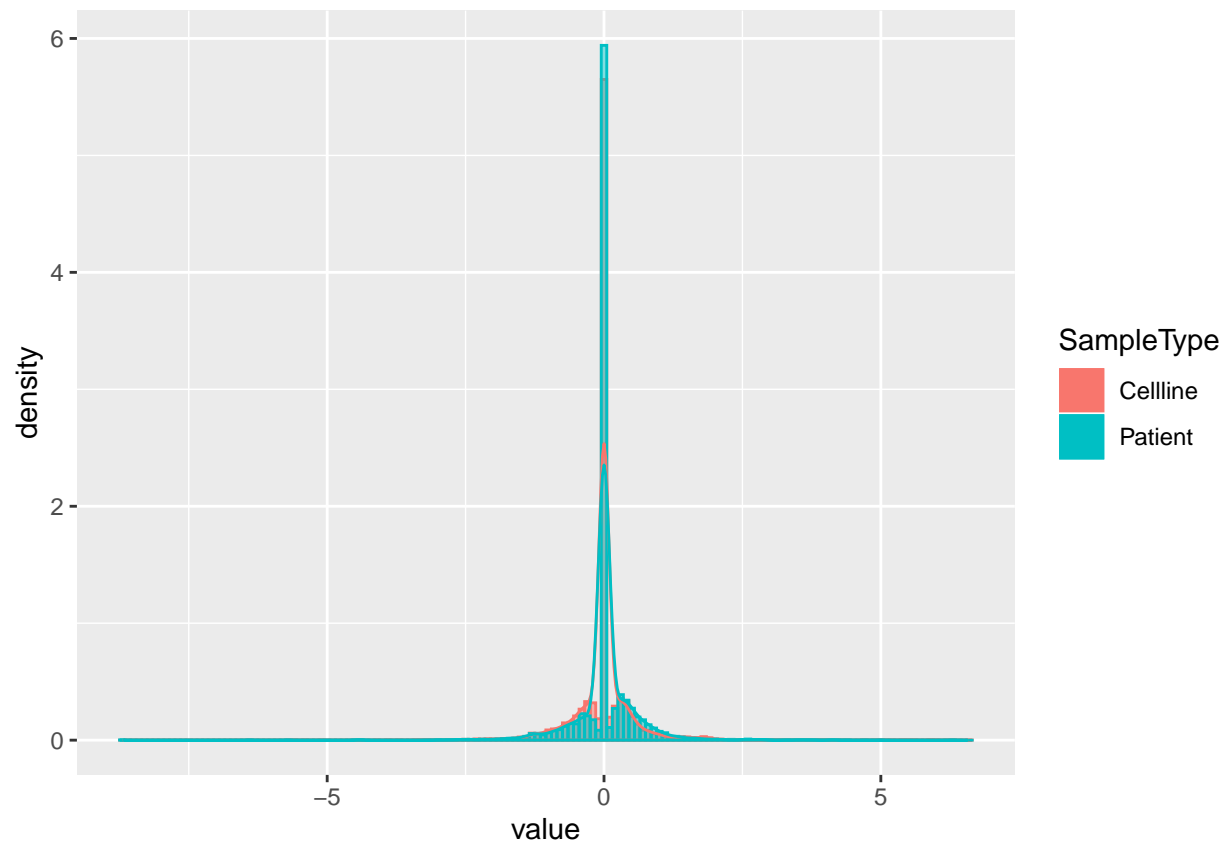
```
## [1] "SampleType"      "SampleID"      "Drug"          "AKT308"
## [5] "AKT473"          "ATF2"          "AXL"           "bCATENIN"
## [9] "CHK1"           "CHK2"          "cJUN"          "cKIT"
## [13] "cMET"           "cRAF"          "EGFR"          "ERK.MAPK"
## [17] "FAK"            "FGFR1"         "FGFR2"         "FGFR3"
## [21] "FLT3"           "GSK3a"         "GSK3B"         "HER2"
## [25] "HER3"           "HER4"          "HSP27"         "HSP27.total."
## [29] "IGF1R"          "IGF1R..pan.TYR." "IR"           "IR..pan.TYR."
## [33] "IRS1"           "JAK1"          "JNK"           "LCK"
## [37] "MEK1"           "MSK1"          "mTOR"          "NFkB"
## [41] "p38"            "p53"           "p70S6K"        "PDGFRa"
## [45] "PDGFRb"         "PRAS40"        "PTEN"          "Rb"
## [49] "RET"            "RPS6"          "SRC"           "STAT1"
## [53] "STAT3"          "STAT5A.B"      "TSC2"          "VEGFR2"
```

```
data<-melt(data_read, id.vars=c("SampleType", "SampleID", "Drug"))
names(data)
```

```
## [1] "SampleType" "SampleID"   "Drug"       "variable"   "value"
```

PDF

```
library(ggplot2)
p<-ggplot(data, aes(value, color=SampleType)) +
  geom_histogram(position="identity", binwidth=0.1, aes(y=..density.., fill=SampleType), alpha=0.5) +
  geom_density()
p
```



T test

```
cellline<-subset(data, data$SampleType=="Cellline")
patient<-subset(data, data$SampleType=="Patient")
t.test(cellline$value,patient$value)
```

```
##
##  Welch Two Sample t-test
##
## data:  cellline$value and patient$value
## t = -2.707, df = 8436, p-value = 0.006804
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.052995962 -0.008478895
## sample estimates:
##  mean of x    mean of y
## 0.0001645765 0.0309020050
```