

T test for each row

Ishack

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```
data = read.csv("original_data.csv") # import the dataset
head(data)
```

```
##      Gene.Symbol      Division      Category QE1_Jo_Exp1_AOCS1
## 1      ALB Non-ECM Protein  Non-ECM Protein      37623.12
## 2      POSTN Core matrisome ECM Glycoproteins      29567.72
## 3      POSTN Core matrisome ECM Glycoproteins      29564.63
## 4  HIST1H2BB Non-ECM Protein  Non-ECM Protein      26814.03
## 5      AHSG Non-ECM Protein  Non-ECM Protein      25752.90
## 6      VIM Non-ECM Protein  Non-ECM Protein      24976.30
##  QE1_Jo_Exp1_G33 QE1_Jo_Exp1_G164 QE1_Jo_Exp1_G342 QE1_Jo_Exp1_G351
## 1      40166.904      352347.5090      924.2543      733.3503
## 2      34018.336      212.4495      43512.8320      48251.9929
## 3      34018.336      188.1493      43511.1663      48247.2426
## 4      4382.611      283.5868      2258.9506      987.5856
## 5      18890.483      1833.1177      257.6850      233.0221
## 6      40067.900      467.2290      26315.5844      47464.7515
##  QE1_Jo_Exp1_G369
## 1      1324.5012
## 2      37954.5521
## 3      37949.7421
## 4      2777.5721
## 5      479.1749
## 6      37981.5538
```

```
data = subset(data,data$Category!="Non-ECM Protein")
genename = data[, 1]
Gene.Symbol = as.data.frame(genename)
```

```
data$Division <- data$Category <- data$Gene.Symbol <- NULL

pValues <- apply(data, 1, function(x) t.test(x[2:4],x[5:7])$p.value)
pValues = as.data.frame(pValues)

PvData = data.frame(gene=Gene.Symbol,pValues=pValues)
head(PvData)
```

##	genename	pValues
## 2	POSTN	0.32416156
## 3	POSTN	0.32428628
## 19	PRSS1	0.78892014
## 28	COL3A1	0.89373457
## 40	SERPINH1	0.05691749
## 43	PLOD1	0.43697109