

Luminex_DataAnalysis

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R Markdown

Analyze Data

Subtract out unstimulated values

Generate Practice Luminex Data

A practice table was created with data similar to what we might obtain from running Luminex.

```
#Create "fake" datatable
library(knitr)
library(data.table)
donor<-c(rep("A", 6), rep("B",6), rep("C",6))
stim<-rep(c("un", "w", "p", "s", "sw", "sb"),3)
ifng<-rnorm(18, 2)
tnfa<-rnorm(18,10)
fake<-as.data.table(cbind(donor,stim,ifng,tnfa))
fake$ifng=as.numeric(as.character(fake$ifng))
fake$tnfa=as.numeric(as.character(fake$tnfa))
#Print "fake" datatable
library(knitr)
kable(fake)
```

donor	stim	ifng	tnfa
A	un	1.688526	9.593895
A	w	1.870233	9.212677
A	p	3.793762	11.328438
A	s	4.777702	10.325315
A	sw	1.444837	10.383912
A	sb	1.094972	11.694451
B	un	2.779554	8.335728
B	w	2.852028	8.060091
B	p	1.597759	9.767544
B	s	1.702800	9.378159
B	sw	1.904133	10.627053
B	sb	1.431957	9.208255
C	un	1.425050	9.186655
C	w	1.612393	9.564590
C	p	1.776426	9.368215
C	s	2.926851	9.547829
C	sw	1.829877	9.515927
C	sb	3.741753	11.553834

Subtract out unstimulated values

I wrote a function called “subtractun” that pulls the unstimulated value for each cytokine from each donor and subtracts it from the respective stim values for the respective cytokine.

The function uses the 1) split, 2) apply, 3) combine sequence to 1) generate data tables for each individual donor, 2) apply the subtraction of the unstim to the respective cytokines for those donors, and 3) take these newly calculated values for individual donors and combine them into a data table containing all donor values.

The subtractun function will be applied only to the numeric columns of a datatable as specified by the “numeric.only” function. In the case of luminex data, this ensures that the function will only be applied to cytokine data.

Split table by donor

```
library(knitr)
y<- split(fake, donor)
kable(y$A)
```

donor	stim	ifng	tnfa
A	un	1.688526	9.593895
A	w	1.870233	9.212677
A	p	3.793762	11.328438
A	s	4.777702	10.325315
A	sw	1.444837	10.383912
A	sb	1.094972	11.694451

```
kable(y$B)
```

donor	stim	ifng	tnfa
B	un	2.779554	8.335728
B	w	2.852028	8.060091
B	p	1.597759	9.767544
B	s	1.702800	9.378159
B	sw	1.904133	10.627053
B	sb	1.431957	9.208255

```
kable(y$C)
```

donor	stim	ifng	tnfa
C	un	1.425050	9.186655
C	w	1.612393	9.564590
C	p	1.776426	9.368215
C	s	2.926851	9.547829
C	sw	1.829877	9.515927
C	sb	3.741753	11.553834

```
subtractun<-function (datatable) {
  #Split datatable by donor
```

```

y<- split(datatable, donor)
#Write function that will select numeric columns of datatable
numeric.only <- function(X,...){
  returnCols <- names(X)
  a<-sapply(X, is.numeric)
  print(returnCols[a == "TRUE"])
}
#Apply numeric.only function to datatable
for (x in numeric.only(datatable)){
  #Subtract out unstim value from respective stim cytokine values
  newcolumn<-unlist(lapply(y,function(g)
    (g[,..x]- as.matrix(subset(g[,..x], g$stim=="un"))[1,1])
  ))
  #Create new datatable with unstim subtractions applied to all donors
  datatable[,x] <- newcolumn}
  datatable
}

#Apply subtractun function to datatable of interest
newfake<-subtractun(fake)

## [1] "ifng" "tnfa"

library(knitr)
kable(newfake)

```

donor	stim	ifng	tnfa
A	un	0.0000000	0.0000000
A	w	0.1817069	-0.3812184
A	p	2.1052361	1.7345431
A	s	3.0891757	0.7314201
A	sw	-0.2436887	0.7900172
A	sb	-0.5935541	2.1005555
B	un	0.0000000	0.0000000
B	w	0.0724742	-0.2756363
B	p	-1.1817943	1.4318165
B	s	-1.0767539	1.0424316
B	sw	-0.8754212	2.2913259
B	sb	-1.3475973	0.8725280
C	un	0.0000000	0.0000000
C	w	0.1873431	0.3779348
C	p	0.3513762	0.1815607
C	s	1.5018004	0.3611744
C	sw	0.4048266	0.3292719
C	sb	2.3167028	2.3671793

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.