

# 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	1.5113992	9.807327
A	w	2.4856359	9.248165
A	p	2.7239211	10.527961
A	s	1.4220725	9.753966
A	sw	1.1472618	8.786866
A	sb	1.3792708	10.176871
B	un	2.3062838	10.424934
B	w	1.7273622	12.569366
B	p	3.1918904	11.705108
B	s	0.4447401	10.267100
B	sw	0.4700931	9.198517
B	sb	2.6553355	10.429650
C	un	3.7515018	10.535765
C	w	1.5444065	10.057914
C	p	2.4073224	11.060441
C	s	1.6032928	8.958578
C	sw	3.1705278	10.817782
C	sb	2.3408988	8.734096

## 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	1.511399	9.807327
A	w	2.485636	9.248165
A	p	2.723921	10.527961
A	s	1.422073	9.753966
A	sw	1.147262	8.786866
A	sb	1.379271	10.176871

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

donor	stim	ifng	tnfa
B	un	2.3062838	10.424934
B	w	1.7273622	12.569366
B	p	3.1918904	11.705108
B	s	0.4447401	10.267100
B	sw	0.4700931	9.198517
B	sb	2.6553355	10.429650

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

donor	stim	ifng	tnfa
C	un	3.751502	10.535765
C	w	1.544407	10.057914
C	p	2.407322	11.060441
C	s	1.603293	8.958578
C	sw	3.170528	10.817782
C	sb	2.340899	8.734096

```
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	0.9742368	-0.5591621
A	p	1.2125220	0.7206335
A	s	-0.0893266	-0.0533615
A	sw	-0.3641373	-1.0204609
A	sb	-0.1321283	0.3695437
B	un	0.0000000	0.0000000
B	w	-0.5789216	2.1444323
B	p	0.8856066	1.2801737
B	s	-1.8615437	-0.1578334
B	sw	-1.8361908	-1.2264168
B	sb	0.3490517	0.0047162
C	un	0.0000000	0.0000000
C	w	-2.2070953	-0.4778516
C	p	-1.3441795	0.5246754
C	s	-2.1482090	-1.5771870
C	sw	-0.5809740	0.2820168
C	sb	-1.4106030	-1.8016699

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