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	0.7596654	9.958882
A	w	5.1247673	11.377720
A	p	2.4705963	9.030101
A	s	2.7576538	8.994454
A	sw	2.0571398	10.213432
A	sb	2.3673422	9.798246
B	un	2.1298393	9.804421
B	w	1.4881478	10.057633
B	p	1.0254435	9.691318
B	s	1.8692274	8.988050
B	sw	1.3086453	10.336213
B	sb	2.1178839	11.514145
C	un	1.9645604	9.826070
C	w	0.0751685	11.174305
C	p	2.9423855	9.652364
C	s	-0.1464763	9.249670
C	sw	1.5490459	9.759217
C	sb	1.0703551	9.806964

Split table by donor

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

donor	stim	ifng	tnfa
A	un	0.7596654	9.958882
A	w	5.1247673	11.377720
A	p	2.4705963	9.030101
A	s	2.7576538	8.994454
A	sw	2.0571398	10.213432
A	sb	2.3673422	9.798246

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

donor	stim	ifng	tnfa
B	un	2.129839	9.804421
B	w	1.488148	10.057633
B	p	1.025443	9.691318
B	s	1.869227	8.988050
B	sw	1.308645	10.336213
B	sb	2.117884	11.514145

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

donor	stim	ifng	tnfa
C	un	1.9645604	9.826070
C	w	0.0751685	11.174305
C	p	2.9423855	9.652364
C	s	-0.1464763	9.249670
C	sw	1.5490459	9.759217
C	sb	1.0703551	9.806964

Subtract out unstimulated values

I wrote a function called "subtractun"" that pulls the unstim 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.

```
for (i in 1:ncol(fake)){
  if(is.numeric(fake[[i]])){
    subtractun<-function (datatable,column) {
      #Split full data table into smaller data tables for each individual donor
      y<- split(datatable, donor)
      #Subtract out unstim
      newcolumn<-unlist(lapply(y,function(g)
```

```
        (g[,..column]- as.matrix(subset(g[,..column], g$stim=="un"))[1,1])
      ))
      ##Merge donor and stim condition to create new sample ID
      ###newsampleid<- paste(donor, stim, sep= "_")
      #Create new datatable with unstim substractions applied to all donors
      datatable[,column] <- newcolumn
      datatable
    }
  }
}
```

```
newnewfake<-subtractun(fake,"tnfa")
newnewnewfake<-subtractun(newnewfake,"ifng")
library(knitr)
kable(newnewnewfake)
```

donor	stim	ifng	tnfa
A	un	0.0000000	0.0000000
A	w	4.3651018	1.4188382
A	p	1.7109309	-0.9287805
A	s	1.9979883	-0.9644281
A	sw	1.2974744	0.2545504
A	sb	1.6076768	-0.1606358
B	un	0.0000000	0.0000000
B	w	-0.6416914	0.2532129
B	p	-1.1043957	-0.1131030
B	s	-0.2606119	-0.8163706
B	sw	-0.8211939	0.5317927
B	sb	-0.0119554	1.7097248
C	un	0.0000000	0.0000000
C	w	-1.8893919	1.3482358
C	p	0.9778251	-0.1737058
C	s	-2.1110367	-0.5763999
C	sw	-0.4155146	-0.0668530
C	sb	-0.8942053	-0.0191057

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