Luminex_DataAnalysis

Elise Viox

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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.

```r
#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	2.0666402	10.786574
A	w	1.9098910	9.316363
A	p	1.4034626	10.569711
A	s	-0.3181182	10.141705
A	sw	2.7347088	10.630005
A	sb	1.8254144	9.551700
B	un	2.5588003	9.371376
B	w	2.6566757	8.473509
B	p	1.7264005	12.029697
B	s	4.0961240	9.861062
B	sw	2.0819004	8.136102
B	sb	2.8774627	11.459936
C	un	3.2282185	10.758087
C	w	2.5824330	10.027787
C	p	1.8640119	10.584482
C	s	1.7811960	10.586150
C	sw	1.9265060	9.706217
C	sb	-0.3001023	11.328602

Split table by donor

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

donor	stim	ifng	tnfa
A	un	2.0666402	10.786574
A	w	1.9098910	9.316363
A	p	1.4034626	10.569711
A	s	-0.3181182	10.141705
A	sw	2.7347088	10.630005
A	sb	1.8254144	9.551700

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

donor	stim	ifng	tnfa
B	un	2.558800	9.371376
B	w	2.656676	8.473509
B	p	1.726401	12.029697
B	s	4.096124	9.861062
B	sw	2.081900	8.136102
B	sb	2.877463	11.459936

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

donor	stim	ifng	tnfa
C	un	3.2282185	10.758087
C	w	2.5824330	10.027787
C	p	1.8640119	10.584482
C	s	1.7811960	10.586150
C	sw	1.9265060	9.706217
C	sb	-0.3001023	11.328602

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.

```r
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	-0.1567492	-1.4702115
A	p	-0.6631776	-0.2168629
A	s	-2.3847584	-0.6448692
A	sw	0.6680686	-0.1565693
A	sb	-0.2412258	-1.2348739
B	un	0.0000000	0.0000000
B	w	0.0978755	-0.8978672
B	p	-0.8323998	2.6583208
B	s	1.5373238	0.4896861
B	sw	-0.4768999	-1.2352742
B	sb	0.3186625	2.0885603
C	un	0.0000000	0.0000000
C	w	-0.6457856	-0.7302998
C	p	-1.3642066	-0.1736049
C	s	-1.4470226	-0.1719367
C	sw	-1.3017126	-1.0518698
C	sb	-3.5283209	0.5705153

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