Luminex_DataAnalysis

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October 31, 2018

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 "fake1" 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)
fake1<-as.data.table(cbind(donor, stim, ifng, tnfa))
fake1$ifng=as.numeric(as.character(fake1$ifng))
fake1$tnfa=as.numeric(as.character(fake1$tnfa))

#Print "fake1" and "fake2" datatables
library(knitr)
kable(fake1)</pre>
```

donor	stim	ifng	tnfa
A	un	5.135134	11.284392
A	w	2.993568	11.237697
A	p	1.242304	10.199650
A	\mathbf{s}	1.851270	7.820466
A	sw	3.160695	9.455148
A	sb	2.782952	9.070787
В	un	1.293589	9.551887
В	W	2.336140	8.681582
В	p	2.465959	11.372807
В	\mathbf{s}	2.183786	9.003924
В	sw	1.111685	8.983659
В	sb	1.976339	10.436547
\mathbf{C}	un	3.390056	13.127995
\mathbf{C}	w	1.298728	12.260930
\mathbf{C}	p	1.532007	8.938962
\mathbf{C}	\mathbf{s}	2.090289	9.771697
\mathbf{C}	sw	1.261252	10.324381
С	sb	1.337989	10.502982

```
#Write "fake1" csv
setwd("/Users/eviox/Documents/Emory_IMP/Rotations/Day_Lab/Luminex/FakeData/")
write.csv(fake1,"fake1.csv")

#Create "fake2" datatable
donor<-c(rep("D", 6), rep("E",6), rep("F",6))
stim<-rep(c("un","w","p","s","sw","sb"),3)
ifng<-rnorm(18, 2)
tnfa<-rnorm(18, 10)
fake2<-as.data.table(cbind(donor,stim,ifng,tnfa))
fake2$ifng=as.numeric(as.character(fake2$ifng))
fake2$tnfa=as.numeric(as.character(fake2$tnfa))

#Print "fake2"
library(knitr)
kable(fake2)</pre>
```

donor	stim	ifng	tnfa
D	un	2.3464536	9.729142
D	w	2.4074203	9.045107
D	p	1.2158856	10.392932
D	\mathbf{s}	3.2306417	9.413768
D	sw	2.6038645	10.487950
D	sb	1.8973273	10.735175
\mathbf{E}	un	1.9027319	10.568300
\mathbf{E}	w	2.9638790	11.080846
\mathbf{E}	p	1.4411480	8.957203
\mathbf{E}	\mathbf{s}	1.8566001	8.236116
\mathbf{E}	sw	0.5942901	10.630849
\mathbf{E}	sb	1.9571775	10.487071
\mathbf{F}	un	2.6401058	11.721516
\mathbf{F}	w	2.6740841	10.399720
\mathbf{F}	p	2.3797991	9.465059
\mathbf{F}	\mathbf{s}	1.2863356	11.391298
\mathbf{F}	sw	4.6461456	9.954923
\mathbf{F}	sb	3.3595321	10.994076

```
#Write "fake2" csv
setwd("/Users/eviox/Documents/Emory_IMP/Rotations/Day_Lab/Luminex/FakeData/")
write.csv(fake2, "fake2.csv")
library(data.table)
file_names <- dir("/Users/eviox/Documents/Emory_IMP/Rotations/Day_Lab/Luminex/FakeData/")
setwd("/Users/eviox/Documents/Emory_IMP/Rotations/Day_Lab/Luminex/FakeData/")
fakecombined <- do.call(rbind,lapply(file_names,read.csv))
fakecombined$X <- NULL</pre>
```

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)
#Redefine donor (since previously defined for generating fake data)
donor<-fakecombined$donor
fakesplit<- split(fakecombined, donor)
kable(fakesplit$A)</pre>
```

donor	stim	ifng	tnfa
A	un	5.135134	11.284392
A	w	2.993568	11.237697
A	p	1.242304	10.199650
A	\mathbf{s}	1.851270	7.820466
A	sw	3.160695	9.455148
A	sb	2.782952	9.070787

kable(fakesplit\$B)

	donor	stim	ifng	tnfa
7	В	un	1.293589	9.551887
8	В	w	2.336140	8.681582
9	В	p	2.465959	11.372807
10	В	\mathbf{s}	2.183786	9.003924
11	В	sw	1.111685	8.983659
12	В	sb	1.976339	10.436547

kable(fakesplit\$C)

	donor	stim	ifng	tnfa
13	С	un	3.390056	13.127995
14	\mathbf{C}	w	1.298728	12.260930
15	\mathbf{C}	p	1.532007	8.938962
16	\mathbf{C}	\mathbf{s}	2.090289	9.771697
17	\mathbf{C}	sw	1.261252	10.324381
18	С	sb	1.337989	10.502982

kable(fakesplit\$D)

	donor	stim	ifng	tnfa
19	D	un	2.346454	9.729142
20	D	w	2.407420	9.045107
21	D	p	1.215886	10.392932
22	D	\mathbf{s}	3.230642	9.413768
23	D	sw	2.603864	10.487950
24	D	sb	1.897327	10.735175

kable(fakesplit\$E)

	donor	stim	ifng	tnfa
25	Е	un	1.9027319	10.568300
26	\mathbf{E}	w	2.9638790	11.080846
27	\mathbf{E}	p	1.4411480	8.957203
28	\mathbf{E}	\mathbf{s}	1.8566001	8.236116
29	\mathbf{E}	sw	0.5942901	10.630849
30	\mathbf{E}	sb	1.9571775	10.487071

kable(fakesplit\$F)

	donor	stim	ifng	tnfa
31	F	un	2.640106	11.721516
32	\mathbf{F}	w	2.674084	10.399720
33	\mathbf{F}	p	2.379799	9.465059
34	\mathbf{F}	\mathbf{s}	1.286336	11.391298
35	\mathbf{F}	sw	4.646146	9.954923
36	\mathbf{F}	sb	3.359532	10.994076

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

}

[1] "ifng" "tnfa"

library(knitr)
kable(newfake)

donor	stim	ifng	tnfa
A	un	0.0000000	0.0000000
A	w	-2.1415658	-0.0466941
A	p	-3.8928303	-1.0847420
A	s	-3.2838643	-3.4639255
A	sw	-1.9744388	-1.8292432
A	sb	-2.3521822	-2.2136047
В	un	0.0000000	0.0000000
В	w	1.0425513	-0.8703055
В	p	1.1723695	1.8209196
В	s	0.8901972	-0.5479630
В	sw	-0.1819045	-0.5682288
В	sb	0.6827498	0.8846596
\mathbf{C}	un	0.0000000	0.0000000
\mathbf{C}	w	-2.0913288	-0.8670644
\mathbf{C}	p	-1.8580498	-4.1890327
\mathbf{C}	s	-1.2997668	-3.3562978
\mathbf{C}	sw	-2.1288040	-2.8036138
\mathbf{C}	sb	-2.0520673	-2.6250131
D	un	0.0000000	0.0000000
D	w	0.0609666	-0.6840349
D	p	-1.1305681	0.6637906
D	\mathbf{s}	0.8841881	-0.3153732
D	sw	0.2574108	0.7588085
D	sb	-0.4491263	1.0060333
\mathbf{E}	un	0.0000000	0.0000000
\mathbf{E}	w	1.0611471	0.5125467
\mathbf{E}	p	-0.4615839	-1.6110963
\mathbf{E}	\mathbf{s}	-0.0461318	-2.3321833
\mathbf{E}	sw	-1.3084418	0.0625497
\mathbf{E}	$^{\mathrm{sb}}$	0.0544456	-0.0812288
F	un	0.0000000	0.0000000
F	w	0.0339782	-1.3217957
F	p	-0.2603067	-2.2564568
\mathbf{F}	\mathbf{s}	-1.3537702	-0.3302182
\mathbf{F}	sw	2.0060398	-1.7665934
F	sb	0.7194263	-0.7274396

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