Luminex_DataFormatting

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R Markdown

Format Data

I wrote this script to format Luminex raw data in an "R friendly" format. I originally started with the Luminex raw data summary tab file generated by MagPix software. I created a new header for the table that combined cytokine names with their respective units of concentration, removed "unknown" sample entries from the table, and renamed the "Analyte..Sample" column to "Sample." For analyte concentrations below and above the limit of detection, I removed the special characters "<|>|↓"" in the cells. Therefore, concentrations that exceeded the upper limit of detection will now read as being the value of the upper limit and concentrations that were below the lower limit of detection will now read as being the lower limit. ##Load Data

```
library(knitr)
library(kableExtra)
library(data.table)
setwd("/Users/eviox/Documents/Emory_IMP/Rotations/Day_Lab")
test<-read.csv("Luminex_Practice.csv", header=TRUE, skip=4, sep=",")
kable(test) %>% kable_styling(latex_options="scale_down")
```

X.Location	Analyte..Sample	GM.CSF	IFNg	IL.10	IL.17a	IL.22	IP.10	MIP.1b	TNFa	X	X.1
		pg/ml	pg/ml	pg/ml	pg/ml	pg/ml	pg/ml	pg/ml	pg/ml		NA
1A3	1	<9.63↓	<1.86↓	1.06	<0.07↓	<0.03↓	209.38	22.75	0.03		NA
1B3	11	<9.63↓	<1.86↓	1.73	<0.07↓	<0.03↓	246.15	13.28	0.18		NA
1C3	21	26.9	69.74	3.58	4.71	<0.03↓	8228	41.5	13.15		NA
1D3	31	38.11	31.66	1.62	<0.07↓	<0.03↓	2786	58.4	6.91		NA
1E3	41	<9.63↓	14.35	2.57	<0.07↓	<0.03↓	1042	22.63	2.11		NA
1F3	51	139.49	464.3	6.69	24.97	<0.03↓	2216	234.67	10.44		NA
1G3	unstim	<9.63↓	19.15	1.13	<0.07↓	<0.03↓	197.47	33.68	0.38	See IFNg sheet	NA
1H3	Unknown24	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A4	2	<9.63↓	<1.86↓	1.62	<0.07↓	<0.03↓	197.68	10.51	<0.00↓		NA
1B4	12	<9.63↓	<1.86↓	0.96	<0.07↓	<0.03↓	136.47	25.29	<0.00↓		NA
1C4	22	<9.63↓	<1.86↓	0.86	<0.07↓	<0.03↓	212.09	29.43	<0.00↓		NA
1D4	32	<9.63↓	3.18	1.5	<0.07↓	<0.03↓	641.03	9.87	0.4		NA
1E4	42	79.07	175.32	1.97	2.45	<0.03↓	7560	140.68	26.2		NA
1F4	52	134.61	276.88	4.89	3.5	<0.03↓	7107	184.39	31.35		NA
1H4	Unknown32	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A5	3	<9.63↓	<1.86↓	1.17	<0.07↓	<0.03↓	199.54	24.15	0.03		NA
1B5	13	<9.63↓	<1.86↓	0.76	<0.07↓	<0.03↓	196.52	32.3	<0.00↓		NA
1C5	23	<9.63↓	<1.86↓	1.73	0.52	<0.03↓	198.15	14.45	0.26		NA
1D5	33	<9.63↓	<1.86↓	1.17	<0.07↓	<0.03↓	198.84	19.56	0.33		NA
1E5	43	<9.63↓	2.6	1.17	<0.07↓	<0.03↓	310.03	14.73	0.26		NA
1F5	53	<9.63↓	2.88	1.17	<0.07↓	<0.03↓	218.67	12.98	0.11		NA
1H5	Unknown40	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A6	4	<9.63↓	2.32	1.5	<0.07↓	<0.03↓	196.52	13.28	0.11		NA
1B6	14	<9.63↓	<1.86↓	0.96	<0.07↓	<0.03↓	153.02	33.29	<0.00↓		NA
1C6	24	<9.63↓	3.48	1.06	<0.07↓	<0.03↓	338.03	25.29	0.26		NA
1D6	34	<9.63↓	2.32	1.28	<0.07↓	<0.03↓	336.88	16.41	0.18		NA
1E6	44	<9.63↓	5.42	0.86	<0.07↓	<0.03↓	204.49	37.13	0.18		NA
1F6	54	<9.63↓	2.05	1.39	<0.07↓	<0.03↓	283.09	8.2	0.11		NA
1H6	Unknown48	<9.63↓	4.75	1.73	1.05	11.51	12.58	4.97	0.78		NA
1A7	5	11.76	25.17	1.28	<0.07↓	<0.03↓	2012	40.43	3.81		NA
1B7	15	<9.63↓	5.76	1.12	<0.07↓	<0.03↓	236.39	29	0.7		NA
1C7	25	1058	1787	3.97	9.18	16.81	>8308↑	538.3	50.19		NA
1D7	35	24.22	45.03	1.39	<0.07↓	<0.03↓	1758	47	2.7		NA
1E7	45	130.15	290.53	1.17	<0.07↓	<0.03↓	923.66	129.12	9.27		NA
1F7	55	<9.63↓	3.18	0.76	<0.07↓	<0.03↓	208.25	27.29	0.11		NA
1H7	Unknown56	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A8	6	107.91	142.75	1.85	<0.07↓	<0.03↓	3259	208.4	18.96		NA
1B8	16	<9.63↓	6.11	1.5	<0.07↓	<0.03↓	318	10.83	<0.00↓		NA
1C8	26	182.29	266.17	2.33	3.23	<0.03↓	6123	108.01	12.42		NA
1D8	36	623.76	1070	3.2	3.84	12.83	>8308↑	109.86	29.53		NA
1E8	46	2028	4480	3.71	4.71	85.17	>8308↑	1888	127.98		NA
1F8	56	1433	1398	6.35	20.75	34.29	>8308↑	1338	58.26		NA
1H8	Unknown64	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A9	7	<9.63↓	4.42	0.96	<0.07↓	<0.03↓	211.42	29.43	0.18		NA
1B9	17	<9.63↓	4.1	1.17	<0.07↓	<0.03↓	167.61	7.68	0.11		NA
1C9	27	609.69	719.22	2.57	7.98	27.52	>8308↑	403.43	40.6		NA
1D9	37	13.25	42.61	1.06	<0.07↓	<0.03↓	600.79	19.94	0.92		NA
1E9	47	177.97	145.7	1.97	0.87	0.05	5156	131.93	22.42		NA
1F9	57	154.99	214.15	3.33	4.71	<0.03↓	>8308↑	42.38	19.25		NA
1G9	PHA	975.47	9252	117.08	390.53	42.11	6433	3970	81.48		NA
1H9	Unknown72	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A10	8	<9.63↓	2.05	1.28	<0.07↓	<0.03↓	127.53	8.88	<0.00↓		NA
1B10	18	<9.63↓	2.32	0.96	<0.07↓	<0.03↓	173.06	21.79	<0.00↓		NA
1C10	28	9.9	17.92	1.39	<0.07↓	<0.03↓	703.28	14.73	0.85		NA
1D10	38	<9.63↓	10.11	1.73	<0.07↓	<0.03↓	346.05	10.19	0.7		NA
1E10	48	21.93	50.66	1.5	0.34	<0.03↓	3872	55.03	6.18		NA
1F10	58	<9.63↓	12.02	0.96	<0.07↓	<0.03↓	807.11	30.47	1		NA
1H10	Unknown80	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A11	9	<9.63↓	<1.86↓	1.06	<0.07↓	<0.03↓	192.4	8.88	<0.00↓		NA
1B11	19	<9.63↓	3.79	0.96	<0.07↓	<0.03↓	227.99	11.77	<0.00↓		NA
1C11	29	150.09	247.85	4.89	2.45	<0.03↓	>8308↑	80.03	33.77		NA
1D11	39	<9.63↓	6.11	1.17	<0.07↓	<0.03↓	686.08	19.31	0.85		NA
1E11	49	<9.63↓	8.62	1.62	<0.07↓	<0.03↓	809.21	22.51	0.85		NA
1F11	59	80.47	245.74	3.58	9.01	<0.03↓	2367	125.64	14.76		NA
1H11	Unknown88	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
1A12	10	<9.63↓	2.05	1.06	<0.07↓	<0.03↓	178.53	17.75	<0.00↓		NA
1B12	20	<9.63↓	<1.86↓	0.76	<0.07↓	<0.03↓	182.45	18.79	<0.00↓		NA
1C12	30	12.5	17.92	2.82	<0.07↓	<0.03↓	1711	22.99	2.11		NA
1D12	40	<9.63↓	3.18	1.17	<0.07↓	<0.03↓	647.7	13.57	0.33		NA
1E12	50	<9.63↓	17.92	1.06	<0.07↓	<0.03↓	347.96	24.61	0.63		NA
1F12	60	97.46	246.09	4.36	11.75	<0.03↓	4781	96.27	16.88		NA
1H12	Unknown96	<9.63↓	<1.86↓	<0.51↓	<0.07↓	<0.03↓	<0.63↓	<0.28↓	<0.00↓		NA
Notes:											NA
Red-higher than maxDC, Black-Lower than minDC, Blue-between maxDC and minDC;											NA
NAN-Curve Fitting Failed; N/A-Data marked out; ND-missing original data											NA

Combine Cytokine name with units of concentration for new column names

```
n <- names(test)
row1 <- as.matrix (test[1,])
new_head<- paste(n, row1, sep= "_")
colnames(test)<- (c(new_head))
```

Find "Unknown" analyte sample entries, remove row from data set

```
test$Analyte..Sample_[grepl("Unknown",test$Analyte..Sample_)]<-""
```

Rename “Analyte..Sample”" column to “Sample”

```
library(dplyr)
test2<- rename(test, Location=X.Location_, Sample=Analyte..Sample_)%>%
  filter(Sample!="")%>%
  select(-X_,-X.1_NA)
```

Find analyte concentrations below and above the limit of detection, delete “<”“,”>“”, “↓” characters

```
library(knitr)
library(kableExtra)
library(data.table)
test3<- data.frame(lapply(test2,function(x) {
  gsub("<|>|↓","", x)
}))
kable(test3) %>% kable_styling(latex_options="scale_down")
```

Location	Sample	GM.CSF__pg.ml	IFNg__pg.ml	IL.10__pg.ml	IL.17a__pg.ml	IL.22__pg.ml	IP.10__pg.ml	MIP.1b__pg.ml	TNFa__pg.ml
1A3	1	9.63	1.86	1.06	0.07	0.03	209.38	22.75	0.03
1B3	11	9.63	1.86	1.73	0.07	0.03	246.15	13.28	0.18
1C3	21	26.9	69.74	3.58	4.71	0.03	8228	41.5	13.15
1D3	31	38.11	31.66	1.62	0.07	0.03	2786	58.4	6.91
1E3	41	9.63	14.35	2.57	0.07	0.03	1042	22.63	2.11
1F3	51	139.49	464.3	6.69	24.97	0.03	2216	234.67	10.44
1G3	unstim	9.63	19.15	1.13	0.07	0.03	197.47	33.68	0.38
1A4	2	9.63	1.86	1.62	0.07	0.03	197.68	10.51	0.00
1B4	12	9.63	1.86	0.96	0.07	0.03	136.47	25.29	0.00
1C4	22	9.63	1.86	0.86	0.07	0.03	212.09	29.43	0.00
1D4	32	9.63	3.18	1.5	0.07	0.03	641.03	9.87	0.4
1E4	42	79.07	175.32	1.97	2.45	0.03	7560	140.68	26.2
1F4	52	134.61	276.88	4.89	3.5	0.03	7107	184.39	31.35
1A5	3	9.63	1.86	1.17	0.07	0.03	199.54	24.15	0.03
1B5	13	9.63	1.86	0.76	0.07	0.03	196.52	32.3	0.00
1C5	23	9.63	1.86	1.73	0.52	0.03	198.15	14.45	0.26
1D5	33	9.63	1.86	1.17	0.07	0.03	198.84	19.56	0.33
1E5	43	9.63	2.6	1.17	0.07	0.03	310.03	14.73	0.26
1F5	53	9.63	2.88	1.17	0.07	0.03	218.67	12.98	0.11
1A6	4	9.63	2.32	1.5	0.07	0.03	196.52	13.28	0.11
1B6	14	9.63	1.86	0.96	0.07	0.03	153.02	33.29	0.00
1C6	24	9.63	3.48	1.06	0.07	0.03	338.03	25.29	0.26
1D6	34	9.63	2.32	1.28	0.07	0.03	336.88	16.41	0.18
1E6	44	9.63	5.42	0.86	0.07	0.03	204.49	37.13	0.18
1F6	54	9.63	2.05	1.39	0.07	0.03	283.09	8.2	0.11
1A7	5	11.76	25.17	1.28	0.07	0.03	2012	40.43	3.81
1B7	15	9.63	5.76	1.12	0.07	0.03	236.39	29	0.7
1C7	25	1058	1787	3.97	9.18	16.81	8308↑	538.3	50.19
1D7	35	24.22	45.03	1.39	0.07	0.03	1758	47	2.7
1E7	45	130.15	290.53	1.17	0.07	0.03	923.66	129.12	9.27
1F7	55	9.63	3.18	0.76	0.07	0.03	208.25	27.29	0.11
1A8	6	107.91	142.75	1.85	0.07	0.03	3259	208.4	18.96
1B8	16	9.63	6.11	1.5	0.07	0.03	318	10.83	0.00
1C8	26	182.29	266.17	2.33	3.23	0.03	6123	108.01	12.42
1D8	36	623.76	1070	3.2	3.84	12.83	8308↑	109.86	29.53
1E8	46	2028	4480	3.71	4.71	85.17	8308↑	1888	127.98
1F8	56	1433	1398	6.35	20.75	34.29	8308↑	1338	58.26
1A9	7	9.63	4.42	0.96	0.07	0.03	211.42	29.43	0.18
1B9	17	9.63	4.1	1.17	0.07	0.03	167.61	7.68	0.11
1C9	27	609.69	719.22	2.57	7.98	27.52	8308↑	403.43	40.6
1D9	37	13.25	42.61	1.06	0.07	0.03	600.79	19.94	0.92
1E9	47	177.97	145.7	1.97	0.87	0.05	5156	131.93	22.42
1F9	57	154.99	214.15	3.33	4.71	0.03	8308↑	42.38	19.25
1G9	PHA	975.47	9252	117.08	390.53	42.11	6433	3970	81.48
1A10	8	9.63	2.05	1.28	0.07	0.03	127.53	8.88	0.00
1B10	18	9.63	2.32	0.96	0.07	0.03	173.06	21.79	0.00
1C10	28	9.9	17.92	1.39	0.07	0.03	703.28	14.73	0.85
1D10	38	9.63	10.11	1.73	0.07	0.03	346.05	10.19	0.7
1E10	48	21.93	50.66	1.5	0.34	0.03	3872	55.03	6.18
1F10	58	9.63	12.02	0.96	0.07	0.03	807.11	30.47	1
1A11	9	9.63	1.86	1.06	0.07	0.03	192.4	8.88	0.00
1B11	19	9.63	3.79	0.96	0.07	0.03	227.99	11.77	0.00
1C11	29	150.09	247.85	4.89	2.45	0.03	8308↑	80.03	33.77
1D11	39	9.63	6.11	1.17	0.07	0.03	686.08	19.31	0.85
1E11	49	9.63	8.62	1.62	0.07	0.03	809.21	22.51	0.85
1F11	59	80.47	245.74	3.58	9.01	0.03	2367	125.64	14.76
1A12	10	9.63	2.05	1.06	0.07	0.03	178.53	17.75	0.00
1B12	20	9.63	1.86	0.76	0.07	0.03	182.45	18.79	0.00
1C12	30	12.5	17.92	2.82	0.07	0.03	1711	22.99	2.11
1D12	40	9.63	3.18	1.17	0.07	0.03	647.7	13.57	0.33
1E12	50	9.63	17.92	1.06	0.07	0.03	347.96	24.61	0.63
1F12	60	97.46	246.09	4.36	11.75	0.03	4781	96.27	16.88