Statistical Analyisis of viral load data

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The data report below outlines the statistical tests of significance with viral load data from the heterozygous CC lines (F/N + N/f) and the null lines (N/N).

```
# load dplyr for data transformations

library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.2.5
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
# display my entire session info
sessionInfo()
```

```
## R version 3.2.3 (2015-12-10)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 14393)
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] dplyr_0.5.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.8    digest_0.6.11   rprojroot_1.1   assertthat_0.1
##  [5] R6_2.2.0       DBI_0.5-1       backports_1.0.4 magrittr_1.5
##  [9] evaluate_0.10  stringi_1.1.2   rmarkdown_1.3   tools_3.2.3
## [13] stringr_1.1.0  yaml_2.1.14     htmltools_0.3.5 knitr_1.15.1
## [17] tibble_1.2
```

```
# load qpcr data
qpcr_data <- read.csv(file="C:\\gale_lab\\oas1b_manuscript\\revisions\\qpcr_data_4_ttests.csv",
header=T)

#Evaluate which fields we are interested in

names(qpcr_data)
```

```
## [1] "Mating"       "Outcome"      "UNC_ID"       "Oas1b_status"
## [5] "Virus"        "Tissue"       "Timepoint"    "fc.mean"
```

```
# We will first filter by spleen tissue

qpcr_spleen <- filter(qpcr_data, Tissue=="Spleen")

# Next filter by Oas1b status

qpcr_spleen_NF_FN_NN <- filter(qpcr_spleen, Oas1b_status %in% c("Null+Functional","Functional+Nu
ll", "Null+Null"))

# Pool heterozgous data

qpcr_spleen_NF_FN <- filter(qpcr_spleen, Oas1b_status %in%
c("Null+Functional","Functional+Null"))

# Pool null spleen data

qpcr_spleen_NN <- filter(qpcr_spleen, Oas1b_status %in% c("Null+Null"))

qpcr_spleen_NF_FN_NN <- filter(qpcr_spleen, Oas1b_status %in% c("Null+Functional","Functional+Nu
ll", "Null+Null"))

# perform student t-test on viral spleen data

t.test(qpcr_spleen_NF_FN$fc.mean,qpcr_spleen_NN$fc.mean)
```

```
##
##  Welch Two Sample t-test
##
## data:  qpcr_spleen_NF_FN$fc.mean and qpcr_spleen_NN$fc.mean
## t = -0.65543, df = 292.5, p-value = 0.5127
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -33.18763  16.60523
## sample estimates:
## mean of x mean of y
##  51.26664  59.55784
```

```
# They do not appear signifcant in the spleen

# next filter by day 4 post infection

qpcr_spleen_NF_FN_D4 <- filter(qpcr_spleen_NF_FN, Timepoint==4)

qpcr_spleen_NN_D4 <- filter(qpcr_spleen_NN, Timepoint==4)

# perform student t-test on viral spleen data at day 4 post infection

t.test(qpcr_spleen_NF_FN_D4$fc.mean,qpcr_spleen_NN_D4$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:  qpcr_spleen_NF_FN_D4$fc.mean and qpcr_spleen_NN_D4$fc.mean
## t = -0.74464, df = 73.637, p-value = 0.4589
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   -87.65483  39.96524
## sample estimates:
## mean of x mean of y
##   107.3096   131.1544
```

#They are not distinctly significant day 4 post infection either

Lets compare the two heterozygous CC lines in the spleen with all timepoints (2,4,7,12) inor der to give us greater statistical power

```
qpcr_spleen_NF <- filter(qpcr_spleen, Oas1b_status %in% c("Null+Functional"))

qpcr_spleen_FN <- filter(qpcr_spleen, Oas1b_status %in% c("Functional+Null"))

t.test(qpcr_spleen_NF$fc.mean,qpcr_spleen_FN$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:  qpcr_spleen_NF$fc.mean and qpcr_spleen_FN$fc.mean
## t = 0.3956, df = 118.21, p-value = 0.6931
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   -24.67300  36.99195
## sample estimates:
## mean of x mean of y
##   54.62636  48.46688
```

###

```
# next filter by day 7 post infection

qpcr_spleen_NF_FN_D7 <- filter(qpcr_spleen_NF_FN, Timepoint==7)

qpcr_spleen_NN_D7 <- filter(qpcr_spleen_NN, Timepoint==7)


# perform student t-test on viral spleen data at day 7 post infection


t.test(qpcr_spleen_NF_FN_D7$fc.mean,qpcr_spleen_NN_D7$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:   qpcr_spleen_NF_FN_D7$fc.mean and qpcr_spleen_NN_D7$fc.mean
## t = -0.032616, df = 48.701, p-value = 0.9741
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   -18.41387  17.82577
## sample estimates:
## mean of x mean of y
##   17.73181  18.02586
```

```r
#They are not distinctly significant day 7 post infection either


#Lets look at the viral brain qPCR


qpcr_brain <- filter(qpcr_data, Tissue=="Brain")


# Next filter by Oas1b status


qpcr_brain_NF_FN <- filter(qpcr_brain, Oas1b_status %in% c("Null+Functional","Functional+Null"))

# Null

qpcr_brain_NN <- filter(qpcr_brain, Oas1b_status %in% c("Null+Null"))

# Hetero

qpcr_brain_NF_FN_NN <- filter(qpcr_brain, Oas1b_status %in% c("Null+Functional","Functional+Null", "Null+Null"))

# perform student t-test on viral brain data

t.test(qpcr_brain_NF_FN$fc.mean,qpcr_brain_NN$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:   qpcr_brain_NF_FN$fc.mean and qpcr_brain_NN$fc.mean
## t = -2.109, df = 128.39, p-value = 0.03689
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   -9613.9006  -306.6125
## sample estimates:
## mean of x mean of y
##   143.6763 5103.9329
```

```
# this p value of 0.03689 meetings our criteria (p-value <=.05) and therefore shows significance


# Next lets filter by timepoint. Day 7 and 12 post infection

qpcr_brain_NF_FN_D7 <- filter(qpcr_brain_NF_FN, Timepoint==7)


qpcr_brain_NF_FN_D12 <- filter(qpcr_brain_NF_FN, Timepoint==12)

# Null

qpcr_brain_NN_D7 <- filter(qpcr_brain_NN, Timepoint==7)


qpcr_brain_NN_D12 <- filter(qpcr_brain_NN, Timepoint==12)

#perform student t-test on viral brain data at day 7 post infection


t.test(qpcr_brain_NF_FN_D7$fc.mean,qpcr_brain_NN_D7$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:  qpcr_brain_NF_FN_D7$fc.mean and qpcr_brain_NN_D7$fc.mean
## t = -1.4545, df = 45.362, p-value = 0.1527
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2703.3604   435.8828
## sample estimates:
##  mean of x  mean of y
##   61.45759 1195.19636
```

```
#perform student t-test on viral brain data at day 12 post infection


t.test(qpcr_brain_NF_FN_D12$fc.mean,qpcr_brain_NN_D12$fc.mean)
```

```
##
##   Welch Two Sample t-test
##
## data:  qpcr_brain_NF_FN_D12$fc.mean and qpcr_brain_NN_D12$fc.mean
## t = -2.0146, df = 35.083, p-value = 0.05166
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -32872.3115    124.3175
## sample estimates:
##  mean of x  mean of y
##   385.8939 16759.8909
```

```
# this p value of 0.05 meetings our criteria (p-value <=.05) and therefore shows significance
```