

Introduction

In this tutorial we provide a basic overview of Spectre's graphing and violin plot options, with statistical analysis included.

```
library('Spectre')
package.load()

sum.dat <- Spectre::demo.sum
sum.dat
```

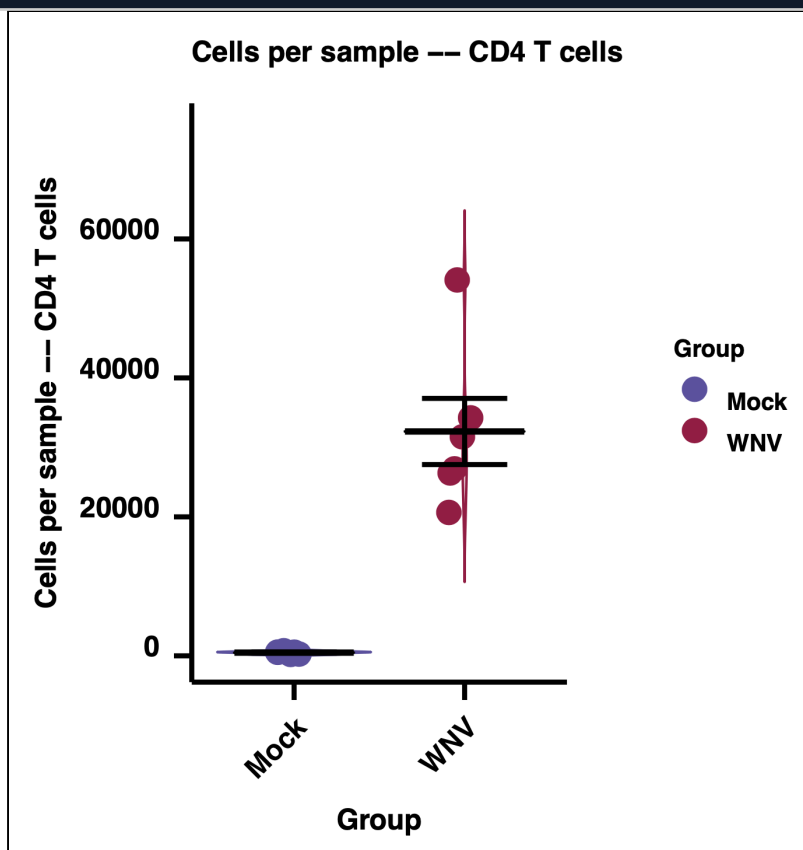
```
      Sample Group Batch Cells per sample -- CD4 T cells Cells per sample -- CD8 T cells Cells per
sample -- Infil Macrophages ...
  1: 01_Mock_01 Mock      A              734.6282              2696.9910
2143.504 ...
  2: 02_Mock_02 Mock      B              506.0006              1037.9500
2536.490 ...
  3: 03_Mock_03 Mock      B              540.5026              1003.7905
2470.869 ...
  4: 04_Mock_04 Mock      A              252.2882              404.8345
1965.501 ...
  5: 05_Mock_05 Mock      A              201.5021              549.5512
2198.205 ...
  6: 06_Mock_06 Mock      B              531.5886              1308.5259
4722.961 ...
  7: 07_WNV_01 WNV       A            54094.7075             50529.2479
605738.162 ...
  8: 08_WNV_02 WNV       B            20636.9741             23901.9282
674243.824 ...
  9: 09_WNV_03 WNV       A            26314.1446             34814.6759
678792.425 ...
10: 10_WNV_04 WNV       A            26910.2796             32397.4082
652559.687 ...
11: 11_WNV_05 WNV       B            31520.7836             36292.8545
644041.191 ...
12: 12_WNV_06 WNV       A            34251.3184             37500.6658
645714.590 ...
```

```
as.matrix(names(sum.dat))
```

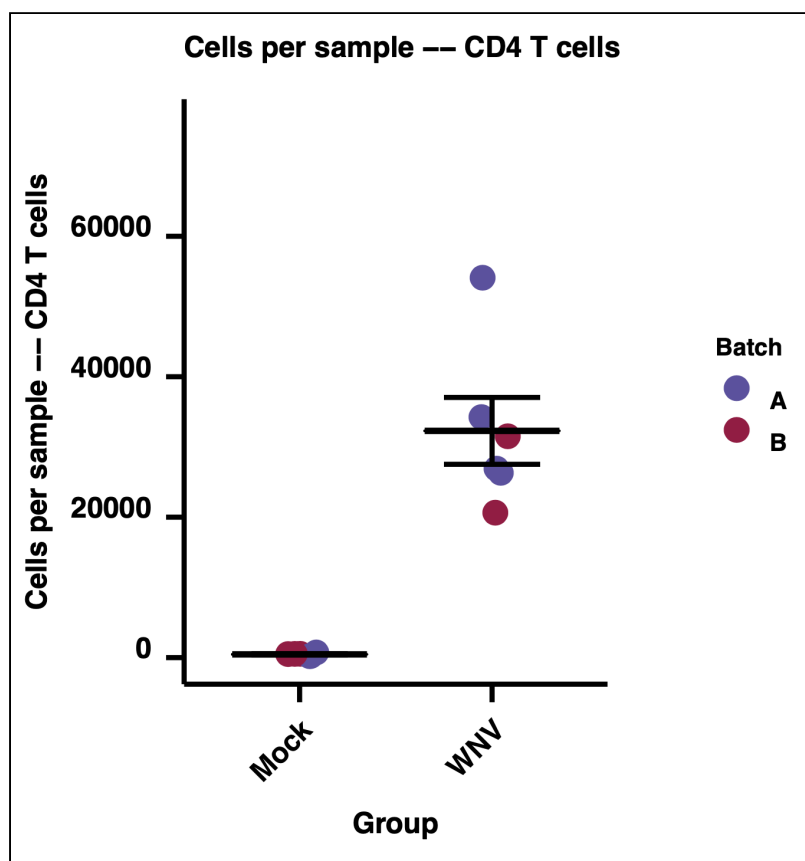
```
      [,1]
[1,] "Sample"
[2,] "Group"
[3,] "Batch"
[4,] "Cells per sample -- CD4 T cells"
[5,] "Cells per sample -- CD8 T cells"
[6,] "Cells per sample -- Infil Macrophages"
[7,] "Cells per sample -- Microglia"
[8,] "Cells per sample -- Neutrophils"
[9,] "Cells per sample -- NK cells"
[10,] "Percent Ly6C_asinh positive -- CD4 T cells"
[11,] "Percent Ly6C_asinh positive -- CD8 T cells"
[12,] "Percent Ly6C_asinh positive -- Infil Macrophages"
[13,] "Percent Ly6C_asinh positive -- Microglia"
[14,] "Percent Ly6C_asinh positive -- Neutrophils"
[15,] "Percent Ly6C_asinh positive -- NK cells"
```

```
getwd()
```

```
make.autograph(dat = sum.dat,  
  x.axis = 'Group',  
  y.axis = 'Cells per sample -- CD4 T cells')
```



```
make.autograph(dat = sum.dat,  
  x.axis = 'Group',  
  y.axis = 'Cells per sample -- CD4 T cells',  
  colour.by = 'Batch',  
  violin = FALSE)
```



```
make.autograph(dat = sum.dat,  
  x.axis = 'Group',  
  y.axis = 'Cells per sample -- CD4 T cells',  
  grp.order = c('WNV', 'Mock'))
```

