

Stats for LITE / light-induced transient effects

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In this document, statistical analysis of the differences observed in the data used to construct the figures are summarized. Statistical significances are denoted: '*' : $p < 0.05$; '**' : $p < 0.01$; '***' : $p < 0.001$; '****' : $p < 0.0001$; '*****' : $p < 0.00001$; 'n.s.' = not significant.

Note that timepoints of stimulation of the experiments were dependent on establishing a stable baseline and therefore, these timepoints may vary from experiment to experiment. That is reflected in the choices of timepoints on which the actual test statistics were based.

Before starting, we define some functions to extract data rows from the data frames. Every column is a cell, and rows represent the data points in the timelapse. To extract the lifetimes of all cells at a timepoint:

```
ExtractRowIntoArray <- function(df, time){  
  timeStep <- as.numeric(df[2,1]-df[1,1]) # Determine the timestep of the timelapse series  
  rowNr <- round(time/timeStep) # Calculate at which row these data are  
  nCol <- as.numeric(ncol(df))  
  Out<-as.numeric(df[rowNr,2:nCol] ) #extract the data into a numeric array  
  return(Out)  
}
```

To quantify decay rates, which is necessary when comparing data taken with dissimilar setups to avoid small systematic differences in calculated lifetimes:

```
GetDecay <-function(df, time1, time2){  
  pre <- ExtractRowIntoArray(df, time1)  
  post <- ExtractRowIntoArray(df, time2)  
  diff <- pre - post  
  return(diff)  
}
```

To get out descriptive statistics and compare significance with Wilcoxon unpaired test:

```

Stats <- function(array1, array2){
  if (missing(array1) || missing(array2)) {
    stop("Both arguments must be supplied.")
  }
  cat("Mean for: array1 ", mean(array1), "          for: array2 ", mean(array2), "\n")
  cat("Var   for: array1 ", var(array1), "          for: array2 ", var(array2), "\n")

  # Perform Wilcoxon rank-sum test
  wilcox_test_result <- wilcox.test(array1, array2)
  w <- wilcox_test_result$p.value

  p = "data do not differ significantly"
  if (w < 0.00001){
    p = "significance = ***** "
  }
  else if (w < 0.0001){
    p = "significance = **** "
  }
  else if (w < 0.001){
    p = "significance = *** "
  }
  else if (w < 0.01){
    p = "significance = ** "
  }
  else if (w < 0.05){
    p = "significance = * "
  }
  p = paste("====>>>>>>>>>      ",p,"      <<<<<<<<=====")

  return(list(Wilcox = wilcox_test_result, P = p))
}

```

For testing more than one condition, e.g. no pretreatment VS 2 min VS 4 min pretreatment, we use the Kruskal-Wallis test, which is also parameter-free:

For HeLa cells:

Compare the data of Fig. 1A (fdFLIM) to those of Fig. 1B (TCSPC). Stimulation data are taken at $t = 135$ s and return data are at $y = 475$ s in A, and at 150 s and 490 s in B. Tested is by what amount the lifetime has decayed over the indicated period, i.e. the teststatistic is the (lifetimes at 135 s - those at 475).

```
FigA <- paste(wd,"Fd_HeLa_Normal_light_Fig1A.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"1_HeLaH201_40nMIP_sustained_confocal_option2_Fig1B.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 135, 475)
B <- GetDecay(df_B, 150, 490)

S <- Stats(A, B)
```

```
## Mean for: array1  0.5628598      for: array2  0.150341
## Var  for: array1  0.01589244     for: array2  0.01902816
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 8170, p-value = 5.435e-13
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      significance = *****      <<<<<<<<====="
```

For COS7 cells:

Compare the data of Fig. 1C (fdFLIM) to those of Fig. 1D (TCSPC). Stimulation data are taken at $t = 200$ s and return data are at $y = 500$ s in A, and at 175 s and 800 s in B. Teststatistic: decay of signal over the indicated timespan. Note that in D, even after extended time, 625 s after stimulation, the TCSPC data did not decay.

```
FigA <- paste(wd,"Fd_Cos7H250_transient_plotted_till_900s_Fig1C.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"1_Cos7H250_40nMIP_sustained_confocal_Fig1D.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 200, 500)
B <- GetDecay(df_B, 175, 800)

S <- Stats(A, B)
```

```
## Mean for: array1  0.09672833      for: array2  -0.02992211
## Var  for: array1  0.005866427     for: array2  0.0004565453
```

```
print(S$Wilcox)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: array1 and array2
## W = 18761, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      significance = *****      <<<<<<<<====="
```

Figure 2. Test for differences in lifetimes upon shift to adjacent FOV.

Test statistic is the lifetime at the end of the traces in the upper graph, versus the beginning of the traces taken just after shifting the FOV (lower graph).

```
FigA <- paste(wd,"Fd_HeLa_shift_exp_part1_Fig2.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"Fd_HeLa_shift_exp_part2_Fig2.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- ExtractRowIntoArray(df_A, 230)
B <- ExtractRowIntoArray(df_B, 5)

S <- Stats(A, B)
```

```
## Mean for: array1  2.326711      for: array2  3.083313
## Var  for: array1  0.01475247    for: array2  0.003001685
```

```
print(S$Wilcox)
```

```
##
## Wilcoxon rank sum exact test
##
## data: array1 and array2
## W = 0, p-value = 5.956e-11
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      significance = *****      <<<<<<<<====="
```

Figure 3. Test for differences in transientness.

Panel A versus B, HeLa cells:

Compare the data of Fig. 3A (fdFLIM) to those of Fig. 3B (fdFLIM with ND filter). Stimulation data are taken at $t = 50$ s and return data are taken 100 s later in A, and at 115 s with return values 100 s later in B. Teststatistic: decay of signal over the indicated timespan.

```
FigA <- paste(wd,"Fd_HeLaH201_transient_Fig3A.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"Fd_HeLa_Low_light_trial2_Fig3B.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 50, 150)
B <- GetDecay(df_B, 115, 215)

S <- Stats(A, B)
```

```
## Mean for: array1  0.5802555          for: array2  0.06334511
## Var   for: array1  0.02422123          for: array2  0.01336506
```

```
print(S$Wilcox)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: array1 and array2
## W = 1796, p-value = 9.666e-14
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      significance = *****      <<<<<<<<====="
```

Panel C versus D, COS7 cells:

Compare the data of Fig. 3C (fdFLIM) to those of Fig. 3D (fdFLIM with ND filter). Stimulation data are taken at $t = 170$ s and return data are taken 800 s later in C, and at 240 s with return values 800 s later in D. Teststatistic: decay of signal over the indicated timespan.

```
FigA <- paste(wd,"Fd_Cos7_Normal_light_0.77_multiplied_Fig3C.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"Fd_Cos7_Low_light_Fig3D.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- 0.77 * GetDecay(df_A, 170, 970) # note the one-time correction factor of 0.77 for calibration mistake, see Results section.
B <- GetDecay(df_B, 240, 1040)

S <- Stats(A, B)
```

```
## Mean for: array1  0.1707775      for: array2  0.60554
## Var  for: array1  0.008313078    for: array2  0.104474
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 1963, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>      significance = *****      <<<<<<<<====="
```

Please note that a p value = 2.2×10^{-16} , which occurs several times in our tests, in R is convention to indicate that it is extremely small.

Panel E versus F, COS7 cells, with/without LED illumination:

Compare the data of Fig. 3E (TCSPC) to those of Fig. 3F (TCSPC with LED illumination). Stimulation data are taken at $t = 240$ s and return data are taken 500 s later in E, and at 200 s with return values 500 s later in F.

Teststatistic: decay of signal over the indicated timespan.

```
FigA <- paste(wd,"1_Cos7H250_40nMIP_sustained_confocal_Fig3E.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"4_Cos7H250_40nMIP_transient_confocal_option_3_Fig3F.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 240, 740)
B <- GetDecay(df_B, 200, 700)

S <- Stats(A, B)
```

```
## Mean for: array1  0.009542691      for: array2  0.7517311
## Var  for: array1  0.0004993614    for: array2  0.003570755
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 5, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>>      significance = *****      <<<<<<<<<====="
```

Figure 5D. Comparison of rescue by ascorbic acid:

Data in the presence of a.a. are compared to control, i.e. the data of Figure 3F. Teststatistic: decay of signal over the indicated timespan. Data from both 3F and 5D are taken at 200 s and 500 s later.

```
FigA <- paste(wd,"4_Cos7H250_40nMIP_transient_confocal_option_3_Fig3F.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"8_Cos7H250_40nMIP_sustained_AA_rescue_confocal_option2_Fig5D.csv",sep="") #
get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 200, 700)
B <- GetDecay(df_B, 200, 700)

S <- Stats(A, B)
```

```
## Mean for: array1  0.7517311      for: array2  0.009667909
## Var   for: array1  0.003570755      for: array2  0.0004493405
```

```
print(S$Wilcox)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: array1 and array2
## W = 240378, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>>      significance = *****      <<<<<<<<<====="
```

Figure 6. Decay rates under various conditions.

Figure 6A:

Following uncaging of cAMP, lifetime values decay from a level that depends on the previous baseline. For fair comparison, because breakdown is exponential, we compare decay speed starting at identical lifetimes within the cAMP decay curve, i.e. we test significance between peak 1 Vs 2, peak 2 vs 3 and peak 1 vs 3 at timepoints 55 s, 355 s and 786 s for peak 1, 2 and 3, respectively. Note that correction for multiple testing was not necessary because as expected, these data are not significantly different.


```
FigA <-paste(wd,"10_caged_experiment_data_Fig6A.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')

A <- GetDecay(df_A, 65, 165)
B <- GetDecay(df_A, 380, 480)
C <- GetDecay(df_A, 800, 900)

S <- Stats(A, B)
```

```
## Mean for: array1  0.1801871      for: array2  0.1852731
## Var  for: array1  0.001433976    for: array2  0.001145625
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 2462, p-value = 0.4292
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>      data do not differ significantly      <<<<<<<====="
```

```
S <- Stats(A, C)
```

```
## Mean for: array1  0.1801871      for: array2  0.1845844
## Var  for: array1  0.001433976    for: array2  0.001240754
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 2524, p-value = 0.5837
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>      data do not differ significantly      <<<<<<<====="
```

```
S <- Stats(B, C)
```

```
## Mean for: array1  0.1852731      for: array2  0.1845844
## Var   for: array1  0.001145625    for: array2  0.001240754
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 2724, p-value = 0.8174
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>      data do not differ significantly      <<<<<<<====="
```

Figure 6B. Comparison of the effect of blue light given before or during stimulation with isoproterenol:

Blue light given before IsoP does not affect cAMP generation. Increase in lifetime is detected as the difference of baseline values at $t = 50$ and stimulated values at $t = 500$, as compared to control data taken from Fig. 3E at $t = 100$ s and $t = 550$ s. Teststatistic: increase in signal upon IsoP administration.

```
FigA <- paste(wd,"1_Cos7H250_40nMIP_sustained_confocal_Fig3E.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"10_Cos7H250_40nMIP_shining_light_before_stimulation_Fig6B.csv",sep="") # get data
df_B  <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 100, 550)
B <- GetDecay(df_B, 50, 500)

S <- Stats(A, B)
```

```
## Mean for: array1  -0.8673886      for: array2  -0.7825448
## Var   for: array1  0.004172273    for: array2  0.003477725
```

```
print(S$Wilcox)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  array1 and array2
## W = 41338, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```



```
FigA <- paste(wd,"11_Cos7H250_250nMAdre_in_FB_only_Fig7C.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"11_Cos7H250_250nMAdre_in_FB_LED_2mins_Fig7D.csv",sep="") # get data
df_B <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 200, 800)
B <- GetDecay(df_B, 200, 800)

S <- Stats(A, B)
```

```
## Mean for: array1  0.04289268      for: array2  0.714335
## Var   for: array1  0.003814529      for: array2  0.001846706
```

```
print(S$Wilcox)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: array1 and array2
## W = 0, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
print(S$P)
```

```
## [1] "====>>>>>>      significance = *****      <<<<<<<<====="
```

Panel E versus F: Prostaglandin with and without LED illumination.

Drop in lifetime is detected as the difference of values at $t = 240$ and 500 s later. Teststatistic: decay of signal after stimulation.

```
FigA <- paste(wd,"11_Cos7H250_200nMPGE-1_in_FB_only_Fig7E.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
FigB <- paste(wd,"11_Cos7H250_200nMPGE-1_in_FB_LED_2mins_Fig7F.csv",sep="") # get data
df_B <- read.csv(FigB, sep = ',')

A <- GetDecay(df_A, 240, 740)
B <- GetDecay(df_B, 240, 740)

S <- Stats(A, B)
```

```
## Mean for: array1  0.1733938      for: array2  0.1718793
## Var   for: array1  0.002606596      for: array2  0.002635679
```

```
print(S$Wilcox)
```

```
## [1] "====>>>>>> data do not differ significantly <<<<<<====="
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>>      significance = *****      <<<<<<<<====="
```

Panel 8E vs 8F vs control: 7A: Norepinephrin with 0 s (control), 2 min or 6 min of LED illumination:

Absolute lifetimes at t = 300 are compared, noting that between these experiments, stimulation was identical timepoints. Teststatistic: lifetime value.

```
FigA <- paste(wd,"11_Cos7H250_200nMNE_in_FB_only_Fig7A.csv",sep="") # get data
df_A  <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- list(array1 = A)

FigA <- paste(wd,"T0455_13_Cos7H250_200nMNE_degradation_2mins_eppie_Fig8E.csv",sep="") # get
data
df_A  <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- append(dataList, list(array2 = A))

FigA <- paste(wd,"T0405_13_Cos7H250_200nMNE_degradation_6mins_eppie_Fig8F.csv",sep="") # get
data
df_A  <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- append(dataList, list(array3 = A))

S <- StatsKruskal(dataList)
```

```
## Mean  3.124143      Var  0.008663382
## Mean  3.011552      Var  0.009681888
## Mean  2.77395       Var  0.01050768
```

```
print(S$kruskal)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: list_of_arrays
## Kruskal-Wallis chi-squared = 1409.4, df = 2, p-value < 2.2e-16
```

```
print(S$P)
```

```
## [1] "====>>>>>>>>>      significance = *****      <<<<<<<<====="
```

Panel 7C vs 8G vs 8H: Adrenalin with 0 s (control), 2 min or 6 min of LED illumination:

Absolute lifetimes at $t = 300$ are compared, noting that between these experiments, stimulation was at identical timepoints. Teststatistic: lifetime value.

```
FigA <- paste(wd,"11_Cos7H250_250nMAdre_in_FB_only_Fig7C.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- list(array1 = A)

FigA <- paste(wd,"T0340_13_Cos7H250_250nMAdre_degradation_2mins_eppie_Fig8G.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- append(dataList, list(array2 = A))

FigA <- paste(wd,"T0425_13_Cos7H250_250nMAdre_degradation_6mins_eppie_Fig8H.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 300)
dataList <- append(dataList, list(array3 = A))

S <- StatsKruskal(dataList)
```

```
## Mean  3.279348      Var  0.0005154811
## Mean  3.265813      Var  0.001822629
## Mean  2.674917      Var  0.01261923
```

```
print(S$kruskal)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  list_of_arrays
## Kruskal-Wallis chi-squared = 1141.3, df = 2, p-value < 2.2e-16
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      significance = *****      <<<<<<<<====="
```

Panel 7E vs 8I vs 8J: Prostaglandin with 0 s (control), 2 min or 6 min of LED illumination:

Absolute lifetimes at timepoint of maximum stimulation are compared. Teststatistic: lifetime value.

```
FigA <- paste(wd,"11_Cos7H250_200nMPGE-1_in_FB_only_Fig7E.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 180)
dataList <- list(array1 = A)

FigA <- paste(wd,"T0406_13_Cos7H250_200nMPGE-1_degradation_2mins_eppie_Fig8I.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 180)
dataList <- append(dataList, list(array2 = A))

FigA <- paste(wd,"T0406_13_Cos7H250_200nMPGE-1_degradation_6mins_eppie_Fig8J.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 200)
dataList <- append(dataList, list(array3 = A))

S <- StatsKruskal(dataList)
```

```
## Mean  3.086965      Var  0.008278756
## Mean  3.082212      Var  0.01244308
## Mean  3.089186      Var  0.006797883
```

```
print(S$kruskal)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  list_of_arrays
## Kruskal-Wallis chi-squared = 0.021175, df = 2, p-value = 0.9895
```

```
print(S$P)
```

```
## [1] "====>>>>>>>      data do not differ significantly      <<<<<<<<====="
```

Figure 10. Effects of Folic acid.

Panel A vs B vs C: Isoproterenol stimulation with 0 s (control), 2 min and 6 min of exposure to LED light:

Responses after stimulation, just before addition of forskolin are compared. Teststatistic: lifetime value.


```
FigA <- paste(wd,"14_Cos7H250_40nMIP_degradation_0mins_eppie_HBS++_FA_Fig10A.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 400)
dataList <- list(array1 = A)

FigA <- paste(wd,"T0425_14_Cos7H250_40nMIP_degradation_2mins_eppie_HBS++_FA_Fig10B.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 400)
dataList <- append(dataList, list(array2 = A))

FigA <- paste(wd,"T0531_14_Cos7H250_40nMIP_degradation_6mins_eppie_HBS++_FA_Fig10C.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 400)
dataList <- append(dataList, list(array3 = A))

S <- StatsKruskal(dataList)
```

```
## Mean  3.279881          Var  0.0004879474
## Mean  3.114069          Var  0.014296
## Mean  2.71332           Var  0.007782577
```

```
print(S$kruskal)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: list_of_arrays
## Kruskal-Wallis chi-squared = 1524.1, df = 2, p-value < 2.2e-16
```

```
print(S$P)
```

```
## [1] "====>>>>>>      significance = *****      <<<<<<<<====="
```

Panel E vs F vs G: Isoproterenol in saline with folic acid w/wo LED illumination, and rescue by inclusion of ascorbic acid:

Responses after stimulation and upon subsequent exposure to LED light are compared. Teststatistic: lifetime value.

```
FigA <- paste(wd,"15_Cos7H250_40nMIP_sustained_LED_2mins_HBS+_only_cut_to_997s_Fig10E.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 750)
dataList <- list(array1 = A)

FigA <- paste(wd,"15_Cos7H250_40nMIP_LED_2mins_HBS+_FA_option3_Fig10F.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 750)
dataList <- append(dataList, list(array2 = A))

FigA <- paste(wd,"15_Cos7H250_40nMIP_sustained_LED_2mins_HBS+_FA_AA_RESCUE_cut_to_997s_Fig10G.csv",sep="") # get data
df_A <- read.csv(FigA, sep = ',')
A <- ExtractRowIntoArray(df_A, 750)
dataList <- append(dataList, list(array3 = A))

S <- StatsKruskal(dataList)
```

```
## Mean  3.267984      Var  0.001180006
## Mean  2.581877      Var  0.01052889
## Mean  3.261728      Var  0.0009009804
```

```
print(S$kruskal)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: list_of_arrays
## Kruskal-Wallis chi-squared = 1402.8, df = 2, p-value < 2.2e-16
```

```
print(S$P)
```

```
## [1] "====>>>>>>      significance = *****      <<<<<<<====="
```