# Evolving Event-driven Programs with SignalGP: Statistics

Here, we provide fully detailed statistical test results, including the R code used to generate them. Across experiments, we performed a Kruskal-Wallis rank sum test to determine if a set was significant, and if significant, we performed a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons. See the paper for full context.

Each post-hoc Dunn's test was performed using the FSA package.

```
library(FSA)
```

```
## ## FSA v0.8.17. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related book.
```

We'll set our significance threshold to 0.05.

# Changing Environment Problem

In this section, we give the statistical details for the Changing Environment Problem broken down by environment-size.

First, we'll load the fitness data.

```
ce_ff_data <- read.csv("../data/chg_env/mt_final_fitness.csv")</pre>
```

A note about how treatments are named within the data: treatment names describe the parameters and their values used when running the experiment. Parameters and their values are adjacent in the name, and parameter-value combinations are separated by underscores. For example, ED1\_AS1\_ENV2\_TSK0 indicates that event-driven (ED) signals were enabled (1), active sensors (AS) were enabled (1), and there were two environments states. In other words, ED1\_AS1\_ENV2\_TSK0 indicates the two-state environment combined treatment. The trailing TSK0 can be ignored.

Okay, next we'll partition out different subsets of the data.

```
# two-state environment
# -- overall data --
ce_ff_data_2 <- ce_ff_data[grep("_ENV2_", ce_ff_data$treatment),]</pre>
ce_ff_data_2 <- ce_ff_data_2[ce_ff_data_2$analysis == "fdom",]</pre>
ce_ff_data_2$treatment <- relevel(ce_ff_data_2$treatment, ref="ED1_AS1_ENV2_TSK0")</pre>
# -- teasing apart combined treatment data --
ce_tff_data_2 <- ce_ff_data[grep("ED1_AS1_ENV2_", ce_ff_data$treatment),]</pre>
ce_tff_data_2$treatment <- relevel(ce_tff_data_2$treatment, ref="ED1_AS1_ENV2_TSK0")</pre>
# four-state environment
# -- overall data --
ce_ff_data_4 <- ce_ff_data[grep("_ENV4_", ce_ff_data$treatment),]</pre>
ce_ff_data_4 <- ce_ff_data_4[ce_ff_data_4$analysis == "fdom",]</pre>
ce ff data 4\$treatment <- relevel(ce ff data 4\$treatment, ref="ED1 AS1 ENV4 TSKO")
# -- teasing apart combined treatment data --
ce_tff_data_4 <- ce_ff_data[grep("ED1_AS1_ENV4_", ce_ff_data$treatment),]</pre>
ce_tff_data_4$treatment <- relevel(ce_tff_data_4$treatment, ref="ED1_AS1_ENV4_TSKO")</pre>
# eight-state environment
```

```
# -- overall data --
ce_ff_data_8 <- ce_ff_data[grep("_ENV8_", ce_ff_data$treatment),]
ce_ff_data_8 <- ce_ff_data_8[ce_ff_data_8$analysis == "fdom",]
ce_ff_data_8$treatment <- relevel(ce_ff_data_8$treatment, ref="ED1_AS1_ENV8_TSKO")
# -- teasing apart combined treatment data --
ce_tff_data_8 <- ce_ff_data[grep("ED1_AS1_ENV8_", ce_ff_data$treatment),]
ce_tff_data_8$treatment <- relevel(ce_tff_data_8$treatment, ref="ED1_AS1_ENV8_TSKO")

# sixteen-state environment
# -- overall data --
ce_ff_data_16 <- ce_ff_data[grep("_ENV16_", ce_ff_data$treatment),]
ce_ff_data_16 <- ce_ff_data_16[ce_ff_data_16$analysis == "fdom",]
ce_ff_data_16$treatment <- relevel(ce_ff_data_16$treatment, ref="ED1_AS1_ENV16_TSKO")
# -- teasing apart combined treatment data --
ce_tff_data_16 <- ce_ff_data[grep("ED1_AS1_ENV16_", ce_ff_data$treatment),]
ce_tff_data_16$treatment <- relevel(ce_tff_data_16$treatment, ref="ED1_AS1_ENV16_TSKO")</pre>
```

#### Two-state Environment

# Run the Kruskal-Wallis rank sum test

#### **Overall Results**

##

##

```
kw_fit_ce_2 <- kruskal.test(fitness ~ treatment, data=ce_ff_data_2)
kw_fit_ce_2

##

## Kruskal-Wallis rank sum test
##

## data: fitness by treatment
## Kruskal-Wallis chi-squared = 283.26, df = 2, p-value < 2.2e-16

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

# Run the post-hoc Dunn's test.
dt_ce_2 <- dunnTest(fitness~treatment, data=ce_ff_data_2, method="bonferroni")
dt_ce_2

## Dunn (1964) Kruskal-Wallis multiple comparison</pre>
```

P.unadj

Z

```
Combined Treatment Re-evaluations
```

P.adj

## 1 1.204471e-47 ## 2 1.204471e-47 ## 3 1.000000e+00

p-values adjusted with the Bonferroni method.

Comparison

## 1 EDO\_AS1\_ENV2\_TSK0 - ED1\_AS0\_ENV2\_TSK0 -14.57562 4.014904e-48 ## 2 EDO\_AS1\_ENV2\_TSK0 - ED1\_AS1\_ENV2\_TSK0 -14.57562 4.014904e-48 ## 3 ED1 AS0 ENV2 TSK0 - ED1 AS1 ENV2 TSK0 0.00000 1.000000e+00

```
# Run the Kruskal-Wallis rank sum test
kw_ce_comb_2 <- kruskal.test(fitness ~ analysis, data=ce_tff_data_2)
kw_ce_comb_2
##
## Kruskal-Wallis rank sum test
##
## data: fitness by analysis
## Kruskal-Wallis chi-squared = 283.27, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
# Run the post-hoc Dunn's test.
dt_ce_comb_2 <- dunnTest(fitness~analysis, data=ce_tff_data_2, method="bonferroni")
dt_ce_comb_2
## Dunn (1964) Kruskal-Wallis multiple comparison
##
     p-values adjusted with the Bonferroni method.
##
                                    Ζ
                  Comparison
                                           P.unadj
                                                           P.adj
## 1
           fdom - no_sensors 0.00000 1.000000e+00 1.000000e+00
## 2
           fdom - no_signals 14.57563 4.014092e-48 1.204228e-47
## 3 no_sensors - no_signals 14.57563 4.014092e-48 1.204228e-47
```

#### Four-state Environment

### Overall Results

```
# Run the Kruskal-Wallis rank sum test
kw_fit_ce_4 <- kruskal.test(fitness ~ treatment, data=ce_ff_data_4)
kw_fit_ce_4
##
## Kruskal-Wallis rank sum test
##
## data: fitness by treatment
## Kruskal-Wallis chi-squared = 283.26, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
comparisons.
# Run the post-hoc Dunn's test.
dt_ce_4 <- dunnTest(fitness~treatment, data=ce_ff_data_4, method="bonferroni")</pre>
dt_ce_4
## Dunn (1964) Kruskal-Wallis multiple comparison
     p-values adjusted with the Bonferroni method.
##
                                 Comparison
                                                     Z
                                                            P.unadj
##
## 1 EDO AS1 ENV4 TSKO - ED1 AS0 ENV4 TSKO -14.57561 4.015039e-48
## 2 EDO_AS1_ENV4_TSK0 - ED1_AS1_ENV4_TSK0 -14.57561 4.015039e-48
## 3 ED1_AS0_ENV4_TSKO - ED1_AS1_ENV4_TSKO
                                             0.00000 1.000000e+00
##
            P.adj
## 1 1.204512e-47
```

```
## 2 1.204512e-47
## 3 1.000000e+00
```

#### **Combined Treatment Re-evaluations**

```
# Run the Kruskal-Wallis rank sum test
kw_ce_comb_4 <- kruskal.test(fitness ~ analysis, data=ce_tff_data_4)
kw_ce_comb_4
##
## Kruskal-Wallis rank sum test
##
## data: fitness by analysis
## Kruskal-Wallis chi-squared = 283.27, df = 2, p-value < 2.2e-16
According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple</pre>
```

comparisons.
# Run the post-hoc Dunn's test.
dt\_ce\_comb\_4 <- dunnTest(fitness~analysis, data=ce\_tff\_data\_4, method="bonferroni")
dt ce comb 4</pre>

```
## Dunn (1964) Kruskal-Wallis multiple comparison
## p-values adjusted with the Bonferroni method.
## Comparison Z P.unadj P.adj
## 1 fdom - no_sensors 0.00000 1.000000e+00 1.000000e+00
## 2 fdom - no_signals 14.57564 4.013687e-48 1.204106e-47
## 3 no_sensors - no_signals 14.57564 4.013687e-48 1.204106e-47
```

## **Eight-state Environment**

## **Overall Results**

```
# Run the Kruskal-Wallis rank sum test
kw_fit_ce_8 <- kruskal.test(fitness ~ treatment, data=ce_ff_data_8)
kw_fit_ce_8
##
## Kruskal-Wallis rank sum test
##
## data: fitness by treatment
## Kruskal-Wallis chi-squared = 273.26, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
# Run the post-hoc Dunn's test.
dt_ce_8 <- dunnTest(fitness~treatment, data=ce_ff_data_8, method="bonferroni")
dt_ce_8
## Dunn (1964) Kruskal-Wallis multiple comparison</pre>
```

## p-values adjusted with the Bonferroni method.

```
## 1 EDO_AS1_ENV8_TSKO - ED1_AS0_ENV8_TSKO -14.2165237 7.235911e-46
## 2 EDO_AS1_ENV8_TSKO - ED1_AS1_ENV8_TSKO -14.4131139 4.279713e-47
## 3 ED1_AS0_ENV8_TSKO - ED1_AS1_ENV8_TSKO -0.1965902 8.441483e-01
## P.adj
## 1 2.170773e-45
## 2 1.283914e-46
## 3 1.000000e+00
```

#### **Combined Treatment Re-evaluations**

```
# Run the Kruskal-Wallis rank sum test
kw_ce_comb_8 <- kruskal.test(fitness ~ analysis, data=ce_tff_data_8)
kw_ce_comb_8
##
## Kruskal-Wallis rank sum test
##
## data: fitness by analysis
## Kruskal-Wallis chi-squared = 290.92, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
# Run the post-hoc Dunn's test.
dt_ce_comb_8 <- dunnTest(fitness~analysis, data=ce_tff_data_8, method="bonferroni")
dt_ce_comb_8

## Dunn (1964) Kruskal-Wallis multiple comparison

## p-values adjusted with the Bonferroni method.

## Comparison Z P.unadj P.adj

## 1 fdom - no_sensors 0.00000 1.000000e+00 1.000000e+00

## 2 fdom - no_signals 14.77117 2.247789e-49 6.743368e-49

## 3 no_sensors - no_signals 14.77117 2.247789e-49 6.743368e-49</pre>
```

## Sixteen-state Environment

## **Overall Results**

```
# Run the Kruskal-Wallis rank sum test
kw_fit_ce_16 <- kruskal.test(fitness ~ treatment, data=ce_ff_data_16)
kw_fit_ce_16

##
## Kruskal-Wallis rank sum test
##
## data: fitness by treatment
## Kruskal-Wallis chi-squared = 199.38, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
# Run the post-hoc Dunn's test.
dt_ce_16 <- dunnTest(fitness~treatment, data=ce_ff_data_16, method="bonferroni")</pre>
dt_ce_16
## Dunn (1964) Kruskal-Wallis multiple comparison
     p-values adjusted with the Bonferroni method.
##
                                   Comparison
                                                                P.unadj
## 1 EDO_AS1_ENV16_TSK0 - ED1_AS0_ENV16_TSK0 -12.1256145 7.727836e-34
## 2 ED0_AS1_ENV16_TSK0 - ED1_AS1_ENV16_TSK0 -12.3285843 6.355345e-35
## 3 ED1_AS0_ENV16_TSK0 - ED1_AS1_ENV16_TSK0 -0.2029699 8.391586e-01
##
            P.adj
## 1 2.318351e-33
## 2 1.906603e-34
## 3 1.000000e+00
```

#### Combined Treatment Re-evaluations

```
# Run the Kruskal-Wallis rank sum test
kw_ce_comb_16 <- kruskal.test(fitness ~ analysis, data=ce_tff_data_16)
kw_ce_comb_16

##
## Kruskal-Wallis rank sum test
##
## data: fitness by analysis
## Kruskal-Wallis chi-squared = 207.01, df = 2, p-value < 2.2e-16</pre>
```

According to our Kruskal-Wallis rank sum test, at least one treatment is significantly different from the other treatments. Thus, we'll perform a post-hoc Dunn's test, applying a Bonferroni correction for multiple comparisons.

```
# Run the post-hoc Dunn's test.
dt_ce_comb_16 <- dunnTest(fitness~analysis, data=ce_tff_data_16, method="bonferroni")
dt_ce_comb_16
## Dunn (1964) Kruskal-Wallis multiple comparison
##
     p-values adjusted with the Bonferroni method.
##
                                    Z
                                                           P.adj
                  Comparison
                                           P.unadj
## 1
           fdom - no sensors 0.00000 1.000000e+00 1.000000e+00
## 2
           fdom - no_signals 12.46013 1.231736e-35 3.695207e-35
## 3 no_sensors - no_signals 12.46013 1.231736e-35 3.695207e-35
```

## Distributed Leader Election Problem

In this section, we give the statistical details for the distributed leader election problem.

First, we'll load the fitness data.

```
election_data <- read.csv("../data/election/final_fitness.csv")
# Run the Kruskal-Wallis rank sum test.
elec_kw <- kruskal.test(max_fitness ~ treatment, data=election_data)
elec_kw</pre>
```

```
##
## Kruskal-Wallis rank sum test
##
## data: max_fitness by treatment
## Kruskal-Wallis chi-squared = 103.25, df = 2, p-value < 2.2e-16
# Run the post-hoc Dunn's test.
elec_dt <- dunnTest(max_fitness~treatment, data=election_data, method="bonferroni")</pre>
elec_dt
## Dunn (1964) Kruskal-Wallis multiple comparison
    p-values adjusted with the Bonferroni method.
##
                                            Comparison
## 1
       EventDriven_MsgForking - Imperative_MsgForking 9.681599 3.610247e-22
## 2 EventDriven_MsgForking - Imperative_MsgNonForking 7.512422 5.804340e-14
## 3 Imperative_MsgForking - Imperative_MsgNonForking -2.169177 3.006924e-02
            P.adj
## 1 1.083074e-21
## 2 1.741302e-13
## 3 9.020771e-02
```