Integer Sequences - Statistical Analysis

E. Ajao, M. C. Gîrjău, A. Lee

We are investigating whether there is any significant difference in the performance/accuracy of UMAD with single-point crossover and UMAD with no crossover.

```
# read in data
data <- readRDS("data/clean.Rds")

data %>%
  group_by(sequence, has_crossover) %>%
  summarize(success_rate = mean(found_solution),
            avg_generations = mean(generations_taken),
            avg_runtime = mean(time_taken),
            avg_error = mean(best_error),
            avg_size = mean(avg_size)) %>%
  kable(booktabs = TRUE, digits = 2, linesep = "", align = "lrrrrrr",
        col.names = c("Sequence", "Has Crossover", "Success Rate", "Mean Generations",
                      "Mean Runtime", "Mean Error", "Mean Size")) %>%
  kable_styling(latex_options = "hold_position")
```

Sequence	Has Crossover	Success Rate	Mean Generations	Mean Runtime	Mean Error	Mean Size
:A000292	FALSE	0.00	300.00	4272747.04	26.31	20.97
:A000292	TRUE	0.00	300.00	5253421.36	26.06	28.03
:A037270	FALSE	0.49	228.76	5049518.51	211.18	21.36
:A037270	TRUE	0.48	229.60	3670713.52	195.72	24.83
:A114241	FALSE	0.00	300.00	2649490.87	423.67	24.86
:A114241	TRUE	0.00	300.00	2870666.38	415.66	30.20
:A168392	FALSE	0.00	300.00	3834728.97	12.53	23.02
:A168392	TRUE	0.06	291.34	4807402.77	11.23	28.10
:simple	FALSE	1.00	14.45	61252.36	0.00	13.17
:simple	TRUE	1.00	9.65	33147.59	0.00	12.41

```
prop.test(c(48 + 6 + 100, 49 + 100), c(1000, 1000), alternative = "l") # overall
```

```
    2-sample test for equality of proportions with continuity correction

data:  c(48 + 6 + 100, 49 + 100) out of c(1000, 1000)
X-squared = 0.062234, df = 1, p-value = 0.5985
alternative hypothesis: less
95 percent confidence interval:
 -1.00000000  0.03237327
sample estimates:
prop 1 prop 2
 0.154  0.149
```

```r
prop.test(c(6, 0), c(100, 100), alternative = "g") # just for :A16839
```

```
    2-sample test for equality of proportions with continuity correction

data:  c(6, 0) out of c(100, 100)
X-squared = 4.2955, df = 1, p-value = 0.01911
alternative hypothesis: greater
95 percent confidence interval:
 0.01093689 1.00000000
sample estimates:
prop 1 prop 2
  0.06   0.00
```