FAI Report Analysis

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Introduction

This document includes the R code used to analyse the data in the statistical briefing 'Nothing to See Here'. Not all data was analysed; the focus was on the statistical significance of findings.

Set-up

```
library(tidyverse) library(broom)
```

Analysis

Findings by whether family was involved

The code used to set-up the data and run the analysis is below:

```
df_family <tribble(
      ~n_finding, ~n_total, ~family,
      21, 81, "involved", #
      10, 115, "not involved"
   )

res_fam <df_family %>% mutate(family =
fct_rev(family)) %>%
glm( cbind(n_finding, n_total - n_finding) ~ family, data = ., family = "binomial"
) %>% tidy()
   %>%
   mutate(est_exp = exp(estimate), ci_low_exp = exp(estimate - 1.96 *
               std.error), ci_upp_exp = exp(estimate + 1.96 * std.error),
               p.value = round(p.value, 4))

res_fam
```

```
## # A tibble: 2 x 8
##      term                estimate std.error statistic p.value est_exp ci_low_exp ci_upp_exp
##      <chr>                  <dbl>     <dbl>     <dbl>   <dbl>   <dbl>      <dbl>      <dbl>
## 1 (Intercept)               -2.35     0.331     -7.11 0          0.0952     0.0498     0.182
## 2 familyinvolved             1.30     0.417      3.12 0.0018     3.67       1.62       8.32
```

The results show that having a family involved is associated with a higher probability of a finding being reached. The p-value for this difference is 0.0018, which is statistically significant at the conventional 0.05 level. This means that it would be unusual to this large a difference in the proportion of FAIs with findings when family are/are not involved if there was no real difference in the rate of findings between these two conditions. The odds ratio for the difference is 3.675 - our best guess is that FAIs when there is a family involved are around 3.7 times more likely to have a decision, although the data are consistent with a difference as low as 1.6 or as high as 8.3.

Change over time

```
df_time <tribble(
   ~year, ~n_finding, ~n_total,
   "2005-08", 6, 40, # please also check these
   "2011-14", 12, 36,
   "2012-15", 10, 45,
   "2016-19", 10, 85
)

res_time <df_time %>% mutate(year = fct_rev(year)) %>% # compare other periods to 2016-2019
glm( cbind(n_finding, n_total - n_finding) ~ year, data = ., family = "binomial"
) %>% tidy() %>% mutate(est_exp = exp(estimate), ci_low_exp = exp(estimate - 1.96 *
   std.error), ci_upp_exp = exp(estimate + 1.96 * std.error), p_adj =
   as.vector(stats::p.adjust(p.value, method = "holm")), p.value = round(p.value, 4), p_adj
   = round(p_adj, 4)
               ) %>% select(-statistic)
res_time
```

```
## # A tibble: 4 x 8
##   term                estimate std.error p.value est_exp ci_low_exp ci_upp_exp p_adj
##   <chr>                  <dbl>     <dbl>   <dbl>   <dbl>      <dbl>      <dbl> <dbl>
## 1 (Intercept)           -2.01      0.337  0       0.133      0.0689     0.258  0
## 2 year2012-15            0.762     0.492  0.121   2.14       0.817      5.62   0.242
## 3 year2011-14            1.32      0.488  0.0068  3.75       1.44       9.76   0.0203
## 4 year2005-08            0.280     0.556  0.614   1.32       0.445      3.94   0.614
```

Here we compare the probability of an FAI having a finding in three different periods (2005-08, 2011-14 and 2012-15) to the probability of an FAI having a finding in 2016-19. In these three periods, the different in the probability of a finding is statistically significant between 2011-14 and 2016-19, with FAIs in 2011-14 being more likely to have a finding. The p.value for this difference is 0.0068. This is statistically significant, even when accounting for potential bias arising from making multiple comparisons. This means that it would be unusual to this large a difference in the proportion of FAIs with findings between 2011-14 and 2016-19 if there was no real difference in the rate of findings between these two periods. However, the periods 2005-08 and 2012-15 do not show statistically significant differences in the rate of findings compared to 2016-19. It is possible that the statistically significant difference observed here is a function of the time periods used.

Type of death

```
df_type <tribble(
   ~type, ~n_total, ~ n_finding,
   "self-inflicted", 73, 17,
   "drugs", 22, 6,
   "total", 196, 32,
   "other", 196 - 73 - 22, 32 - 17 - 6
) %>% filter(type != "total")

res_type <df_type %>% mutate(type = fct_relevel(type, # make other deaths the reference
category
                                                "other", "self-inflicted", "drugs")) %>%
   glm( cbind(n_finding, n_total - n_finding) ~ type, data = ., family = "binomial"
   ) %>% tidy() %>% mutate(est_exp = exp(estimate), ci_low_exp = exp(estimate - 1.96 *
   std.error), ci_upp_exp = exp(estimate + 1.96 * std.error), p_adj =
   as.vector(stats::p.adjust(p.value, method = "holm")), p.value = round(p.value, 4), p_adj
   = round(p_adj, 4)
            ) %>% select(-statistic)
res_type
```

```
## # A tibble: 3 x 8
##   term                    estimate std.error p.value est_exp ci_low_exp ci_upp_exp p_adj
##   <chr>                      <dbl>     <dbl>   <dbl>   <dbl>      <dbl>      <dbl> <dbl>
## 1 (Intercept)               -2.32      0.349 0          0.0978     0.0493      0.194 0
## 2 typeself-infl~             1.13      0.446 0.0111     3.10       1.30        7.43  0.0221
## 3 typedrugs                  1.34      0.593 0.0234     3.83       1.20       12.2   0.0234
```

Comparing the probability of an FAI having a finding based on the the type of death, both deaths that were self-inflicted and those involving drugs were more likely to have a finding than other types of deaths. Both these comparisons are statistically significant at the 0.05 level. Again, this means that it would be unusual to this large a difference in the proportion of FAIs with findings between other types of deaths and those which were self-inflicted or involved drugs if there was no real difference in the rate of findings between FAIs for other types of deaths and self-inflicted or drug-involved deaths. Despite the statistical significance of these differences, there is still considerable uncertainty as to their size. For self-inflicted deaths, the point-estimate of the odds-ratio is 3.103, but with 95% confidence intervals as low as 1.295 and as high as 7.434. This means that the data are compatible with a wide range plausible differences in the rate of findings between self-inflicted deaths and other types of deaths; but that it is unlikely that there is no difference between self-inflicted deaths and other kinds of death.

Sheriffdom

```
df_sher <tribble(
      ~n_finding, ~n_total, ~sheriff,
      4, 41, "lothian",
      11, 53, "tayside"
   )

res_sher <glm( cbind(n_finding, n_total - n_finding) ~ sheriff, data = df_sher, family = "binomial"
) %>% tidy() %>% mutate(est_exp = exp(estimate), ci_low_exp =
   exp(estimate - 1.96 * std.error), ci_upp_exp = exp(estimate + 1.96 *
   std.error), p.value = round(p.value, 4))

res_sher
```

```
## # A tibble: 2 x 8
##   term                estimate std.error statistic p.value est_exp ci_low_exp ci_upp_exp
##   <chr>                  <dbl>     <dbl>     <dbl>   <dbl>   <dbl>      <dbl>      <dbl>
## 1 (Intercept)           -2.22      0.526     -4.23   0       0.108      0.0385     0.303
## 2 sherifftayside         0.885     0.626      1.41   0.157   2.42       0.710      8.26
```

This comparison just focuses on the rate of findings between the two Sheriffdoms with the most FAIs and the largest difference in the number of findings. These are the conditions most likely to show a statistically significant difference. The p.value for the difference is 0.1574, which is not statistically significant at the conventional 0.05 level. This means that it would not be unusual to see this size of difference in the number FAIs with decisions between Sherrifdoms with this number of FAIs if there was no difference in their rate of reaching decisions.

Notes

- The relatively small number of cases makes it harder for us to distinguish between variation by chance vs variation due to systematic differences. A non-statistically-significant difference might still be due to systematic differences, but we there may not be enough data to confirm this with much certainty.
- Differences between Sheriffdoms might be hard to rule out differences consistent with chance (see above analysis) but the non-statistically-significant finding above doesn't mean that there aren't differences in practice (just that we don't have strong quantitative evidence to evaluate these differences).
- The report includes a discussion of the problems from censoring of time-to-report for reports that haven't been published yet. There might be some scope to do more analysis of this - this is a common problem particularly in medical studies, and there's a pretty established methodology (survival analysis) to account for it (where AFAIUI sample sizes aren't too different).