

Geriatric Syndrome in Older Adults with AF

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2020-01-20

SETUP

- load packages
- set figure style

```
knitr::opts_chunk$set(echo = TRUE)
```

```
## Load the libraries we will be using  
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --
```

```
## v ggplot2 3.2.1      v purrr   0.3.3  
## v tibble  2.1.3      v dplyr  0.8.3  
## v tidyr   1.0.2      v stringr 1.4.0  
## v readr   1.3.1      v forcats 0.4.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(ggthemes)
library(haven)

##### Color Palette by Paletton.com 30degrees
##### Palette URL: http://paletton.com/#uid=7070u0ksyu7hHCkmJvyuMo9zZj4

##### Color Palette by Paletton.com 150 degrees
##### Palette URL: http://paletton.com/#uid=7072m0ksyu7hHCkmJvyuMo9zZj4

## FIGURE SETTINGS
sachin_theme <- theme_bw()+
  theme(
    panel.background = element_blank(),
    axis.line = element_line(colour = "grey75"),
    panel.border = element_blank(),
    panel.grid.major.x = element_blank(),
    panel.grid.minor.x = element_blank(),
    panel.grid.major.y = element_line(color = "grey", linetype = "dotted" ),
    panel.grid.minor.y = element_blank(),
    legend.position = "none",
    axis.title=element_text(size=10)
  )

sachin_theme_leg <- theme_bw()+
  theme(
    panel.background = element_blank(),
    axis.line = element_line(colour = "grey75"),
    panel.border = element_blank(),
    panel.grid.major.x = element_blank(),
    panel.grid.minor.x = element_blank(),
    panel.grid.major.y = element_line(color = "grey", linetype = "dotted" ),
    panel.grid.minor.y = element_blank(),
    legend.position = "top",
    legend.title = element_blank(),
    axis.title=element_text(size=10)
  )
```

Figure: Relationship between AC use and geriatric syndrome count

- analysis done in SAS and saved in dataset thinner_ame.sas7dbat
- imported to R to create figure

```
### read in data
library(haven)
ame <- read_sas("C:/Users/sachi/Box Sync/AF frailty/tables and figures/thinner_ame.sas7bdat",
  NULL)

### Add in reference rows
library(tibble)
toadd_names <- c("Falls", "ADL", "IADL", "Cognitive function", "Incontinence")
toadd_levels <- c("No falls (ref)", "No ADL impairment (ref)", "No IADL impairment (ref)", "No cognitive impairmen
t (ref)", "Not incontinent (ref)")
ame <- add_row(ame, syndrome = toadd_names, Diff = 0, LL = 0, UL = 0, level = toadd_levels)

### create factors for syndrome and lables so that we get the right order
ame$syndrome <- as.factor(ame$syndrome)
ame$syndrome <- factor(ame$syndrome, levels = c("Falls", "ADL", "IADL", "Cognitive function", "Incontinence"))
color_level5 <- c("#FB6549", "#35B862", "#32829D", "#D53E80", "#FBA449")
color_sig <- c("#696969", "#157696")

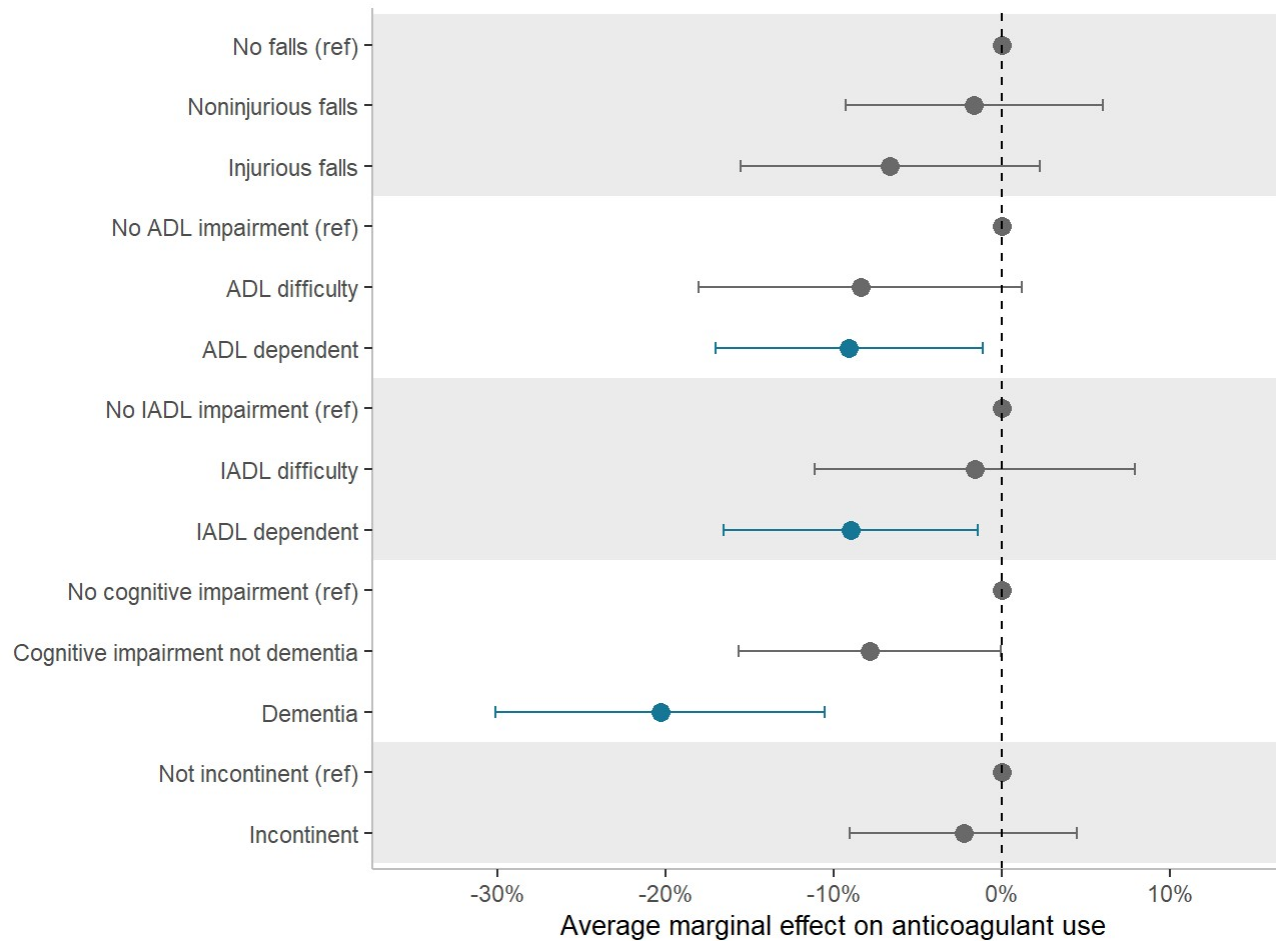
ame$level <- as.factor(ame$level)
ame$level <- factor(ame$level, levels = c("No falls (ref)", "Noninjurious falls", "Injurious falls", "No ADL impair
ment (ref)", "ADL difficulty", "ADL dependent", "No IADL impairment (ref)", "IADL difficulty", "IADL dependent", "
No cognitive impairment (ref)", "Cognitive impairment not dementia", "Dementia", "Not incontinent (ref)", "Inconti
nent"))

### Add columns to aid in the shading of the figure
ame <- ame %>% mutate(Xn=as.numeric(fct_rev(level)))
shade_cat <- c("Falls", "IADL", "Incontinence")
ame <- mutate(ame, shade = ifelse(syndrome %in% shade_cat, "gray", "white"))
ame <- mutate(ame, significant = ifelse(round(UL,2) < 0, "sig", "notsig"))

### Create figure

library(stringr)
```

```
fig_ac_x_gs_ame <- ggplot(data=ame, aes(y=Diff, x=fct_rev(level), group = syndrome)) +  
  geom_rect(aes(xmin=Xn-0.5, xmax = Xn+0.5, ymin = -Inf, ymax= Inf, fill = shade),  
    alpha = 0.3, stat="identity", show.legend = FALSE) +  
    scale_fill_manual(values = alpha(c("gray", "white"), 0.3)) +  
  geom_point(aes(color = significant), size=3)+  
  geom_errorbar(aes(ymin=LL, ymax=UL, width = 0.2, color=significant)) +  
  scale_x_discrete(name="") +  
  scale_y_continuous(name = "Average marginal effect on anticoagulant use",  
    limits = c(-0.35,0.15),  
    breaks = c(seq(from = -0.3, to = 0.1, by = 0.1)),  
    labels = scales::percent_format(accuracy = 1)) +  
  scale_color_manual(values = color_sig)+  
  theme(  
    panel.background = element_blank(),  
    axis.line = element_line(colour = "grey75"),  
    panel.border = element_blank(),  
    panel.grid.major.y = element_blank(),  
    panel.grid.minor.x = element_blank(),  
    panel.grid.major.x = element_blank(),  
    panel.grid.minor.y = element_blank(),  
    legend.position = "none",  
    legend.title = element_blank(),  
    axis.title=element_text(size=10),  
    plot.caption = element_text(hjust = +0, face = "italic"),  
    plot.title = element_text(hjust = +1)  
  ) +  
  
  geom_hline(yintercept = 0, linetype ="dashed") +  
  coord_flip()  
  
fig_ac_x_gs_ame
```



```
ggsave("C:/Users/sachi/Box Sync/AF frailty/tables and figures/fig gs x ac ame.png", width = 7, height = 4)
```

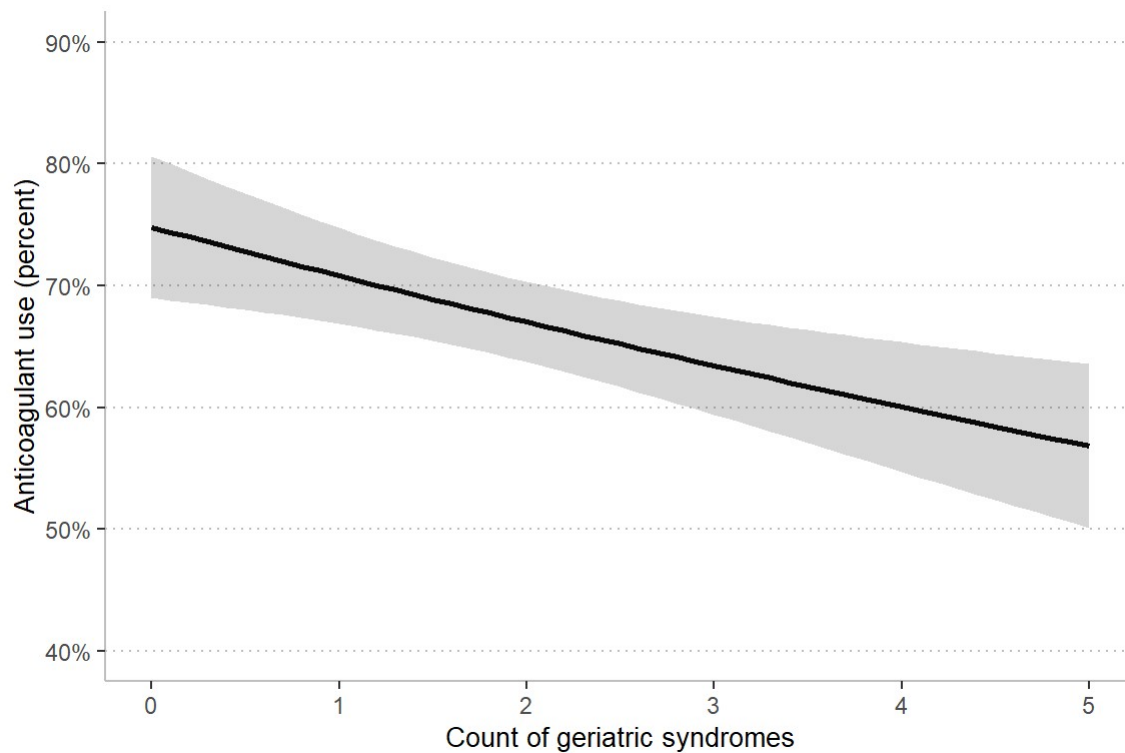
Figure AC use by geriatric count

- analysis done in sas and saved to gs_count_x_ac.sas7dbat
- sas output saved to dataset and imported to R

```
library(haven)
GS_count <- read_sas("C:/Users/sachi/Box Sync/AF frailty/tables and figures/gs_count_x_ac.sas7bdat",
  NULL)

fig_ac_x_gscount <- ggplot(data = GS_count, mapping = aes(x = GERI_SYN_COUNT, y = Estimate )) +
  geom_line(size=1) +
  geom_ribbon(aes(ymin=Lower, ymax=Upper), alpha =0.2) +
  scale_x_continuous(name = "Count of geriatric syndromes") +
  scale_y_continuous(name = "Anticoagulant use (percent)", labels = scales::percent_format(accuracy =
1), limits = c(0.4,0.9), breaks = c(seq(from = 0.4, to = 0.9, by = .10))) +
  sachin_theme_leg

fig_ac_x_gscount
```



```
ggsave("C:/Users/sachi/Box Sync/AF frailty/tables and figures/fig_ac_x_gscount.png", width = 6, height = 4)
```

Cohort flow diagram


```

library (DiagrammeR)

# Define some sample data
data <- list(a=10364, b=9249, c=4882, d=779, e = 776)
flow <- DiagrammeR::grViz("
digraph graph2 {

graph [layout = dot, fontsize = 11]

# node definitions with substituted label text
node [shape = rectangle, width = 1, fontname = Arial]
a [label = '@@1']
b [label = '@@2']
c [label = '@@3']
d [label = '@@4']
1 [label = '@@5']
2 [label = '@@6']
3 [label = '@@7']
4 [label = '@@8']
5 [label = '@@9']

a -> b -> c -> d

d -> {1,2,3,4,5}

}

[1]: paste0('65+ at 2014 HRS interview\\n', '(n = ', data$a, ')')
[2]: paste0('Agreed to Medicare claims linkage\\n', '(n = ', data$b, ')')
[3]: paste0('Enrolled in Medicare Part A and B for 24\\n', 'consecutive months before 2014 interview\\n', '(n = ',
data$c, ')')
[4]: paste0('Met claims definition for atrial fibrillation\\n', '(n = ', data$d, ')')
[5]: paste0('Falls prevalence\\n', 'measure excludes\\n', '3 missing falls data\\n', '(n=776)\\n', ' \\n', ' \\n',
'Falls and AC\\n', 'analysis excludes\\n', 'an additional\\n', '3 missing AC data\\n', '(n=773)')
[6]: paste0('ADL prevalence\\n', 'measure excludes\\n', '3 missing ALD data\\n', '(n=776)\\n', ' \\n', ' \\n', 'AD
L and AC\\n', 'analysis excludes\\n', 'an additional\\n', '3 missing AC data\\n', '(n=773)')

```

```
[7]: paste0('IADL prevalence\\n', 'measure\\n', '(n=779)\\n', ' \\n', ' \\n', ' \\n', 'IADL and AC\\n', 'analysis
excludes\\n', '3 missing AC data\\n', '(n=776)\\n', ' \\n')
[8]: paste0('Cognition prevalence\\n', 'measure\\n', '(n=779)\\n', ' \\n', ' \\n', ' \\n', 'Cognition and AC\\n', '
anlalysis excludes\\n', '3 missing AC data\\n', '(n=776)\\n', ' \\n')
[9]: paste0('Incontinence prevalence\\n', 'measure excludes\\n', '3 missing\\n', 'incontinence data\\n', '(n=77
6)\\n', ' \\n', 'Incontinence and AC\\n', 'analysis excludes\\n', 'an additional\\n', '2 missing AC data\\n', '(n=77
4)')
")
```

flow

