## Presentation Helper Code

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```
library(dplyr); library(ggplot2); library(survival); library(survminer)
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
##
## Loading required package: ggpubr
##
## Attaching package: 'survminer'
## The following object is masked from 'package:survival':
##
##
       myeloma
data_path <- "C:/Users/jhirs/Documents/Projects/Consulting22_Dementia/data"</pre>
output_path <- "C:/Users/jhirs/Documents/Projects/Consulting22_Dementia/Outputs/"</pre>
load(file.path(data_path, "Analysis Data.RData"))
load(file.path(output_path, "FinalModelingData.RData"))
cv1age + site + gender + apo4 + educ + faminc + race*any_work
knitr::kable(head(
  df2|>
      dem_year, dementia, cv1age, site, gender, apo4, educ, faminc, race, any_work
    ) |>
    rename(
      `ID` = habcid,
      `Onset Year` = dem_year,
      `Dementia` = dementia,
      `Age` = cv1age,
```

## Adding missing grouping variables: 'habcid'

ID	Onset Year	Dementia	Age	Study Site	Gender	Apoe4	Education	Income	Race	Work Status
1001	9	1	73	1	2	0	3	1	1	0
1003	3	1	73	1	1	0	2	2	1	1
1005	3	1	77	1	1	0	2	2	1	1
1006	9	1	75	1	1	1	2	4	1	0
1007	9	1	71	1	1	0	2	2	2	1
1008	8	1	73	1	2	0	2	4	1	0