Stroke data EDA

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Introduction

This document downloads and performs an initial view of a stroke dataset.

```
stroke <- read_csv("train_2v.csv")
```

```
## Parsed with column specification:
## cols(
##   id = col_double(),
##   gender = col_character(),
##   age = col_double(),
##   hypertension = col_double(),
##   heart_disease = col_double(),
##   ever_married = col_character(),
##   work_type = col_character(),
##   Residence_type = col_character(),
##   avg_glucose_level = col_double(),
##   bmi = col_double(),
##   smoking_status = col_character(),
##   stroke = col_double()
## )
```

```
stroke %>% glimpse
```

```
## Observations: 43,400
## Variables: 12
## $ id                <dbl> 30669, 30468, 16523, 56543, 46136, 32257, 52800, ...
## $ gender            <chr> "Male", "Male", "Female", "Female", "Male", "Fema...
## $ age               <dbl> 3, 58, 8, 70, 14, 47, 52, 75, 32, 74, 79, 79, 37,...
## $ hypertension      <dbl> 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0...
## $ heart_disease     <dbl> 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0...
## $ ever_married      <chr> "No", "Yes", "No", "Yes", "No", "Yes", "Yes", "Ye...
## $ work_type         <chr> "children", "Private", "Private", "Private", "Nev...
## $ Residence_type    <chr> "Rural", "Urban", "Urban", "Rural", "Rural", "Urb...
## $ avg_glucose_level <dbl> 95.12, 87.96, 110.89, 69.04, 161.28, 210.95, 77.5...
## $ bmi               <dbl> 18.0, 39.2, 17.6, 35.9, 19.1, 50.1, 17.7, 27.0, 3...
## $ smoking_status    <chr> NA, "never smoked", NA, "formerly smoked", NA, NA...
## $ stroke            <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
```

Initial data QA

Check id is unique and for any missing values.

Uniqueness of ID

```
stroke %>%
    count(id) %>%
    filter(n > 1)
```

```
## # A tibble: 0 x 2
## # ... with 2 variables: id <dbl>, n <int>
```

```
stroke <- stroke %>% select(-id)
```

Check for NA

Do any features have any NA?

```
# summarise_all soon to be superceded in dplyr 1.0.0
stroke %>%
    summarise_all(~sum(is.na(.))) %>%
    t
```

```
##                    [,1]
## gender                0
## age                   0
## hypertension          0
## heart_disease         0
## ever_married          0
## work_type             0
## Residence_type        0
## avg_glucose_level     0
## bmi                1462
## smoking_status    13292
## stroke                0
```

We have some missing bmi and quite a lot of missing smoking_status. Is there any obvious pattern in the missing values, or relationship between the instances?

```
stroke %>%
    mutate(bmi_na = if_else(is.na(bmi), "yes", "no")) %>%
    filter(bmi_na == "yes" | is.na(smoking_status)) %>%
    group_by(bmi_na) %>%
    count(smoking_status)
```

```
## # A tibble: 5 x 3
## # Groups:   bmi_na [2]
##   bmi_na smoking_status      n
##   <chr>  <chr>           <int>
## 1 no     <NA>            12866
## 2 yes    formerly smoked   394
## 3 yes    never smoked      306
## 4 yes    smokes            336
## 5 yes    <NA>              426
```

From the above, probably the missing BMI values are missing at random, certainly with respect to smoking, seeing as they're broadly evenly distributed with smoking status. The largest single group of missing values is that for smoking status (where BMI is not missing).

Stroke and smoking

We saw above that most of the missing values are in the smoking status column. How does this seem to relate to stroke?

```
stroke %>%
    count(smoking_status, stroke) %>%
    pivot_wider(names_from=stroke, values_from=n) %>%
    mutate(stroke_pc = 100*`1`/`0`)
```

```
## # A tibble: 4 x 4
##   smoking_status    `0`   `1` stroke_pc
##   <chr>           <int> <int>     <dbl>
## 1 formerly smoked  7272   221      3.04
## 2 never smoked    15769   284      1.80
## 3 smokes           6429   133      2.07
## 4 <NA>            13147   145      1.10
```

From the above, we see that *smokes* and *never smoked* have a similar rate of incidence of stroke, *formerly smoked* seems a bit higher, and the *NA* smoking status group a bit lower. On the face of it, there are some curious things here. How does it makes sense that "formerly smoked" has a higher incidence of stroke than *smokes*, for example? Could there be other factors involved, for example people forced to give up smoking because of another health issue or perhaps taking up unhealthy eating habits to compensate for no longer smoking?

Undersampling the majority class repeatedly generates some consistent results wrt age and may implicate smoking, depending on the composition of the groups.

Modeling stroke risk using all available features

We balance the dataset, which means undersampling the non-stroke group, and perform logistic regression.

```
set.seed(47)
complete_cases <- stroke %>%
    filter(complete.cases(.))
run_glm <- function() {
    glm(stroke ~ ., family=gaussian, complete_cases %>%
            group_by(stroke) %>%
            sample_n(min(group_size(.)))) %>%
    summary
}

print(run_glm())
```

```
##
## Call:
## glm(formula = stroke ~ ., family = gaussian, data = complete_cases %>%
##     group_by(stroke) %>% sample_n(min(group_size(.))))
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.01983  -0.32604   0.04539   0.29950   1.03111
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  -0.2561585  0.1591742  -1.609 0.107843
## genderMale                  0.0133074  0.0264136   0.504 0.614498    
## age                         0.0135245  0.0008441  16.022  < 2e-16 ***
## hypertension                0.0799254  0.0322678   2.477 0.013403 *  
## heart_disease               0.1237507  0.0395916   3.126 0.001821 ** 
## ever_marriedYes            -0.0791385  0.0374892  -2.111 0.035004 *  
## work_typeGovt_job          -0.0981213  0.1550050  -0.633 0.526854    
## work_typeNever_worked      -0.1346361  0.3272353  -0.411 0.680835    
## work_typePrivate           -0.1143959  0.1519900  -0.753 0.451821    
## work_typeSelf-employed     -0.0667985  0.1546680  -0.432 0.665912    
## Residence_typeUrban         0.0034897  0.0251281   0.139 0.889572    
## avg_glucose_level           0.0009122  0.0002438   3.742 0.000192 ***
## bmi                        -0.0009332  0.0019730  -0.473 0.636315    
## smoking_statusnever smoked  0.0046084  0.0300202   0.154 0.878025    
## smoking_statussmokes        0.0510177  0.0365439   1.396 0.162981    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for gaussian family taken to be 0.1703464)
## 
##     Null deviance: 274.00  on 1095  degrees of freedom
## Residual deviance: 184.14  on 1081  degrees of freedom
## AIC: 1187.4
## 
## Number of Fisher Scoring iterations: 2
```

```
print(run_glm())
```

```
## 
## Call:
## glm(formula = stroke ~ ., family = gaussian, data = complete_cases %>% 
##     group_by(stroke) %>% sample_n(min(group_size(.))))
## 
## Deviance Residuals: 
##      Min        1Q    Median        3Q       Max  
## -1.04153  -0.32763   0.05888   0.31348   1.06084  
## 
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                -0.2309899  0.1285544  -1.797 0.072642 .  
## genderMale                  0.0242324  0.0265943   0.911 0.362400    
## age                         0.0130166  0.0008643  15.060  < 2e-16 ***
## hypertension                0.1085631  0.0327666   3.313 0.000953 ***
## heart_disease               0.1277511  0.0395171   3.233 0.001263 ** 
## ever_marriedYes            -0.0503513  0.0375954  -1.339 0.180756    
## work_typeGovt_job          -0.1581656  0.1283303  -1.232 0.218035    
## work_typeNever_worked      -0.0492383  0.2671162  -0.184 0.853787    
## work_typePrivate           -0.1422922  0.1240072  -1.147 0.251449    
## work_typeSelf-employed     -0.1292618  0.1277775  -1.012 0.311948    
## Residence_typeUrban         0.0289548  0.0252591   1.146 0.251919    
## avg_glucose_level           0.0008353  0.0002504   3.336 0.000878 ***
## bmi                         0.0002146  0.0019329   0.111 0.911599    
## smoking_statusnever smoked -0.0469770  0.0306347  -1.533 0.125456    
## smoking_statussmokes        0.0191133  0.0373637   0.512 0.609072    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## (Dispersion parameter for gaussian family taken to be 0.1733751)
## 
##     Null deviance: 274.00  on 1095  degrees of freedom
## Residual deviance: 187.42  on 1081  degrees of freedom
## AIC: 1206.7
## 
## Number of Fisher Scoring iterations: 2
```

```r
print(run_glm())
```

```
## 
## Call:
## glm(formula = stroke ~ ., family = gaussian, data = complete_cases %>% 
##     group_by(stroke) %>% sample_n(min(group_size(.))))
## 
## Deviance Residuals: 
##      Min        1Q    Median        3Q       Max  
## -0.95564  -0.30725   0.05161   0.29418   1.05987  
## 
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)               -0.1947513  0.1215472  -1.602 0.109388    
## genderMale                 0.0062660  0.0259661   0.241 0.809357    
## age                        0.0144178  0.0008497  16.968  < 2e-16 ***
## hypertension               0.1223461  0.0324092   3.775 0.000169 ***
## heart_disease              0.0952517  0.0382928   2.487 0.013016 *  
## ever_marriedYes           -0.0792282  0.0370255  -2.140 0.032592 *  
## work_typeGovt_job         -0.1488065  0.1226230  -1.214 0.225193    
## work_typePrivate          -0.1478148  0.1183145  -1.249 0.211812    
## work_typeSelf-employed    -0.1395757  0.1222013  -1.142 0.253632    
## Residence_typeUrban        0.0060401  0.0248372   0.243 0.807906    
## avg_glucose_level          0.0007434  0.0002419   3.073 0.002173 ** 
## bmi                       -0.0026782  0.0018359  -1.459 0.144908    
## smoking_statusnever smoked -0.0076359  0.0297879  -0.256 0.797735    
## smoking_statussmokes       0.0825829  0.0366399   2.254 0.024402 *  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for gaussian family taken to be 0.167373)
## 
##     Null deviance: 274.0  on 1095  degrees of freedom
## Residual deviance: 181.1  on 1082  degrees of freedom
## AIC: 1167.1
## 
## Number of Fisher Scoring iterations: 2
```

We repeated the undersampling a couple of times above because we'd noticed some variability in the results for different samples drawn from the majority class. Age is pretty consistently strongly significant. This is no great surprise for stroke risk. Hypertension and heart disease, and particularly average glucose level, are also frequently implicated. The signs of their coefficients are all intuitive as well; they are positive contributors to stroke risk.

We should pause here before continuing to dive into inference. We don't know how the data were sampled and we have multiple potentially confounding variables, especially categorical ones. We should stress that we are still exploring potential relationships amongst the variables, rather than attempting a rigorous statistical inference. There is a hint that smoking may be a risk factor for stroke.

We have some encouraging, and plausible, patterns, but we should remember the words of Ronald Fisher:

> To consult the statistician after an experiment is finished is often merely to ask him to conduct a post mortem examination. He can perhaps say what the experiment died of.

Hypertension is binary, as is heart disease, and themselves are imbalanced:

```
stroke %>% count(hypertension)
```

```
## # A tibble: 2 x 2
##   hypertension     n
##          <dbl> <int>
## 1            0 39339
## 2            1  4061
```

```
stroke %>% count(heart_disease)
```

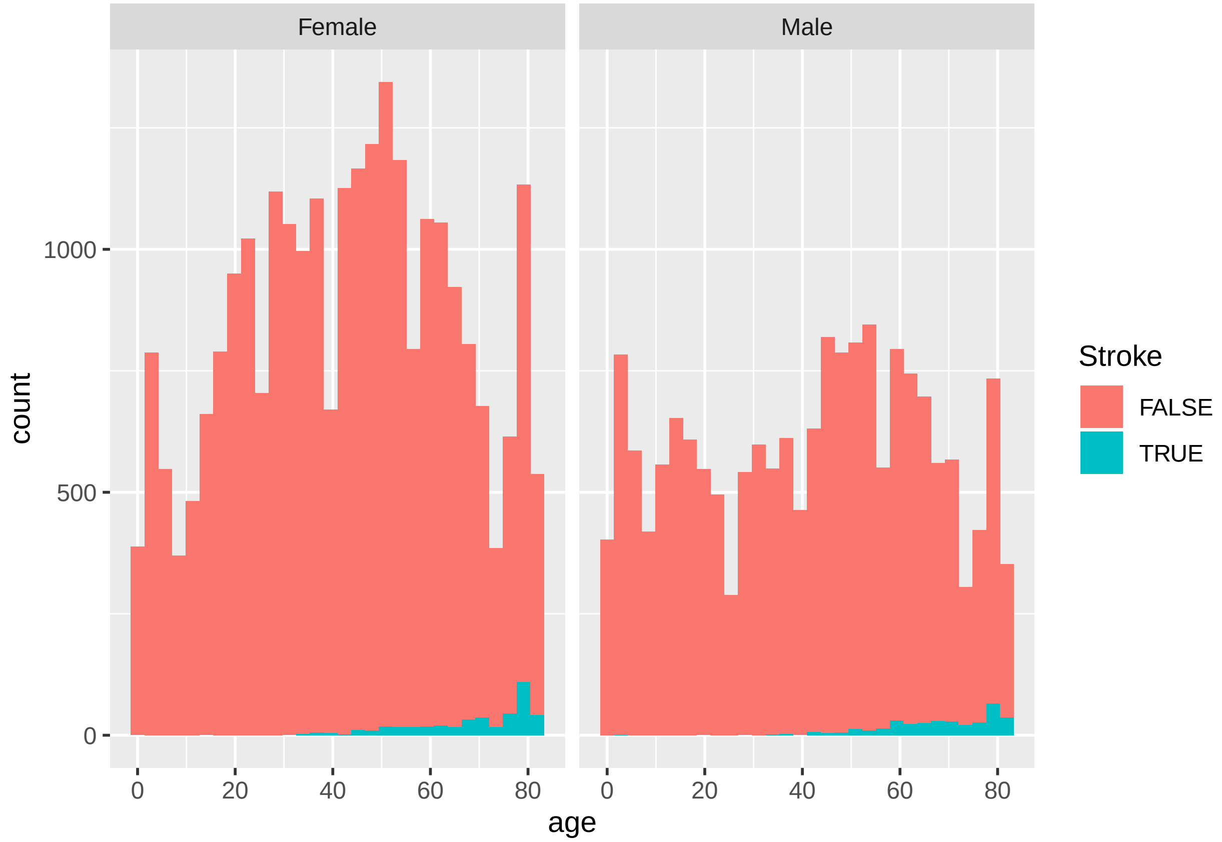
```
## # A tibble: 2 x 2
##   heart_disease     n
##           <dbl> <int>
## 1             0 41338
## 2             1  2062
```

Stroke and age

The relationship between stroke risk and age is clear in the histograms below:

```
stroke %>%
    filter(gender != "Other") %>%
    ggplot() +
    geom_histogram(aes(x = age, fill = stroke==1)) +
    facet_wrap(~gender) +
    labs(fill="Stroke")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

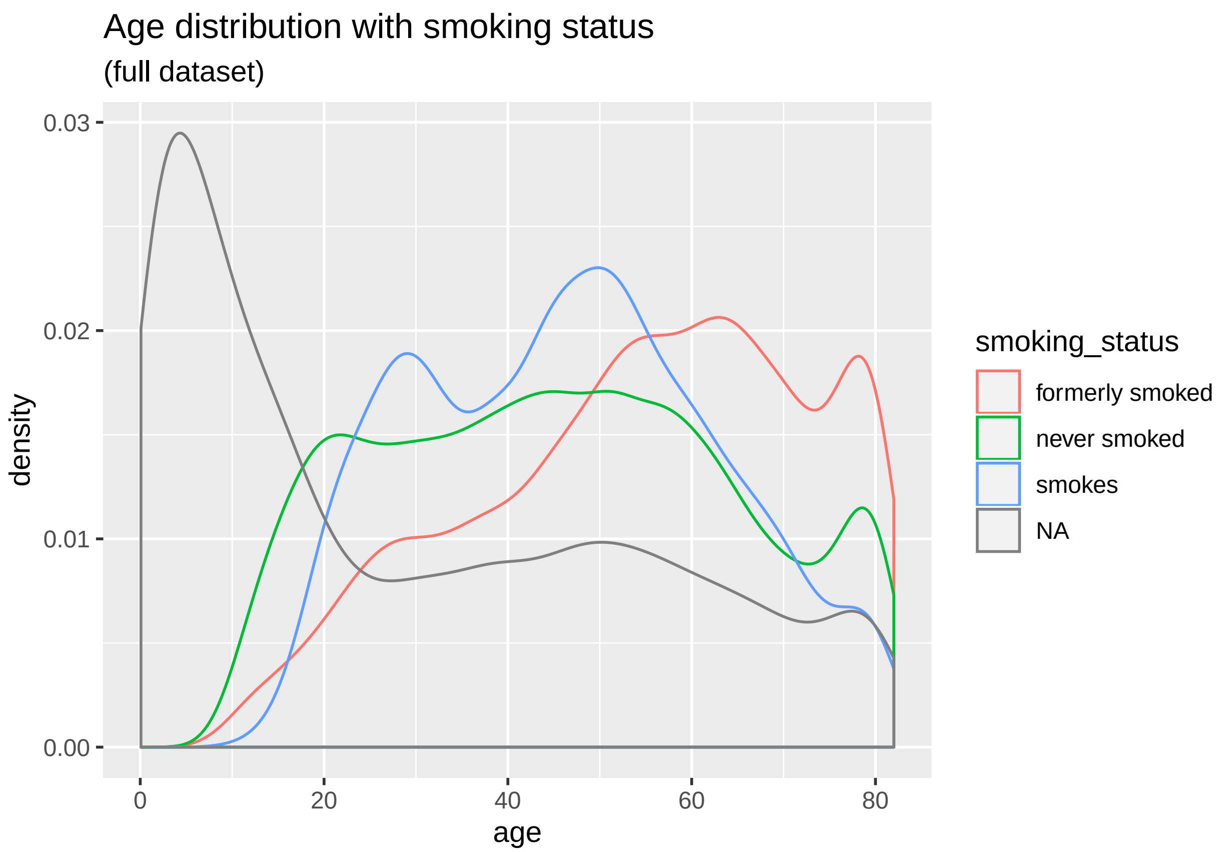


We have more women than men, perhaps up to twice as many. The age distribution for men is fairly flat, whereas for women there seem to be more weight in the middle but fairly symmetric. The increasing prevalence of stroke with age is clear.

Age and smoking

Now we return to looking at smoking status. We suggested above that there might be an occasional sign of a relationship between smoking status and stroke, but we saw a very clear signal that stroke risk was age related. Is there a relationship between age and smoking status?

```
stroke %>%
    ggplot() +
    geom_density(aes(x = age, colour = smoking_status)) +
    labs(title="Age distribution with smoking status",
         subtitle="(full dataset)")
```



The distributions above contain much detail we can now put into perspective. The missing values for smoking status are clearly dominated by children. This makes total sense. It's quite intuitive that the data pertaining to children did not include a smoking status. This also means that simply omitting samples missing a smoking status is fundamentally flawed because this is to greatly bias the data away from younger people. If the desire was to model stroke risk only for adults, that's one thing, but then this should be explicitly done on age, not accidentally by smoking status.

We can see another clear pattern as well. The category of ex-smokers ("formerly smoked") is heavily weighted to older ages. Again, this is an intuitive result given a moment's thought. In order to be a former smoker, one must first have been a smoker. A 20 year old has had only a few potential smoking years, whereas a 60 year old has many years of opportunity to be a smoker before giving up.

The young, below the early twenties, who have never smoked, dominate those who do smoke. This effect alone would bias the group who've never smoked to be younger, and so at less age-related risk of stroke. Having said that, both the *never smoked* and *formerly smoked* groups have an uptick at the oldest ages that is lacking in the *smokes* group. This could perhaps be a survival bias. It's not impossible that the suppression of the oldest ages from the smoking group might even make smoking appear protective of a stroke in some cases; the truth, of course, would be closer to the fact that smokers die of smoking-related disease before the stroke risk ramps up.

In short, there seem some powerful interactions between age and smoking status.

Can we further illustrate the linkage between age and smoking status wrt stroke risk?

Firstly, with a bit of trial and error, we found a partitioning of the data that suggested a mildly significant effect of smoking:

```r
set.seed(100)
cc_balanced <- complete_cases %>%
    group_by(stroke) %>%
    sample_n(min(group_size(.)))
glm(stroke ~ age + smoking_status,
    family=gaussian, cc_balanced) %>%
    summary
```

```
##
## Call:
## glm(formula = stroke ~ age + smoking_status, family = gaussian,
##     data = cc_balanced)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9174  -0.3260   0.1233   0.2775   1.0925
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                -0.3829560  0.0472681  -8.102 1.44e-15 ***
## age                         0.0154113  0.0006597  23.360  < 2e-16 ***
## smoking_statusnever smoked -0.0331415  0.0289850  -1.143   0.2531
## smoking_statussmokes        0.0674830  0.0364413   1.852   0.0643 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1651324)
##
##     Null deviance: 274.00  on 1095  degrees of freedom
## Residual deviance: 180.32  on 1092  degrees of freedom
## AIC: 1142.4
##
## Number of Fisher Scoring iterations: 2
```

So taking just age and smoking status (from the complete cases data) we see a slight suggestion of a positive risk from being a smoker compared to being a former smoker. Although the p-value is quite high, the sign associated with having never smoked is negative, which is in the intuitive direction, but the data really can't be said to provide sufficient evidence for this.

```
set.seed(100)
cc_balanced <- complete_cases %>%
    group_by(stroke) %>%
    sample_n(min(group_size(.)))
glm(stroke ~ age * smoking_status,
    family=gaussian, cc_balanced) %>%
    summary
```

```
##
## Call:
## glm(formula = stroke ~ age * smoking_status, family = gaussian,
##     data = cc_balanced)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9482  -0.3261   0.1190   0.2810   1.0819
##
## Coefficients:
```

```
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    -0.3836295  0.0895914  -4.282 2.02e-05 ***
## age                             0.0154220  0.0013844  11.139  < 2e-16 ***
## smoking_statusnever smoked     -0.0156065  0.1026565  -0.152    0.879
## smoking_statussmokes            0.0039135  0.1306149   0.030    0.976
## age:smoking_statusnever smoked -0.0003111  0.0016191  -0.192    0.848
## age:smoking_statussmokes        0.0011764  0.0021772   0.540    0.589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1653402)
##
##     Null deviance: 274.00  on 1095  degrees of freedom
## Residual deviance: 180.22  on 1090  degrees of freedom
## AIC: 1145.8
##
## Number of Fisher Scoring iterations: 2
```

By now including interactions between age and smoking status, the p-values associated with smoking are huge. Whilst we may intuit that smoking could be a stroke risk, my gut feeling is that in this dataset, smoking status is largely acting as a proxy for age. We can demonstrate this another way by modelling age on smoking status:

```
set.seed(100)
glm(age ~ smoking_status,
    family=gaussian,
    complete_cases %>%
        group_by(smoking_status) %>%
        sample_n(min(group_size(.)))) %>%
summary
```

```
##
## Call:
## glm(formula = age ~ smoking_status, family = gaussian, data = complete_cases %>%
##     group_by(smoking_status) %>% sample_n(min(group_size(.))))
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -44.345  -14.139    0.655   13.655   36.861
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 54.3445     0.2267  239.72   <2e-16 ***
## smoking_statusnever smoked  -9.2056     0.3206  -28.71   <2e-16 ***
## smoking_statussmokes        -8.2702     0.3206  -25.80   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 319.9704)
##
##     Null deviance: 6295077  on 18677  degrees of freedom
## Residual deviance: 5975447  on 18675  degrees of freedom
## AIC: 160750
##
## Number of Fisher Scoring iterations: 2
```

This shows us highly significant effects. On average, those who smoke are 8 years younger than those who are former smokers, and those who have never smoked tend to be younger still. Given the powerful effect of age on stroke risk, we clearly have the potential for smoking status to be a proxy (potentially false) risk factor for stroke.

It is quite possible that smoking status has some predictive power in addition to other features, but we have to admit we don't really see any evidence of it in this exploration. Given the quantity of samples missing a smoking status, we should be far more comfortable dropping this feature than dropping the samples with missing smoking status.

Age and work type

Another set of relationships worth exploring is that of age and work type. We naturally dislike features that are vague or lack orthogonality. What do we mean by the latter? Firstly, the data dictionary defines *work_type* as "Type of occupation". What are these types?

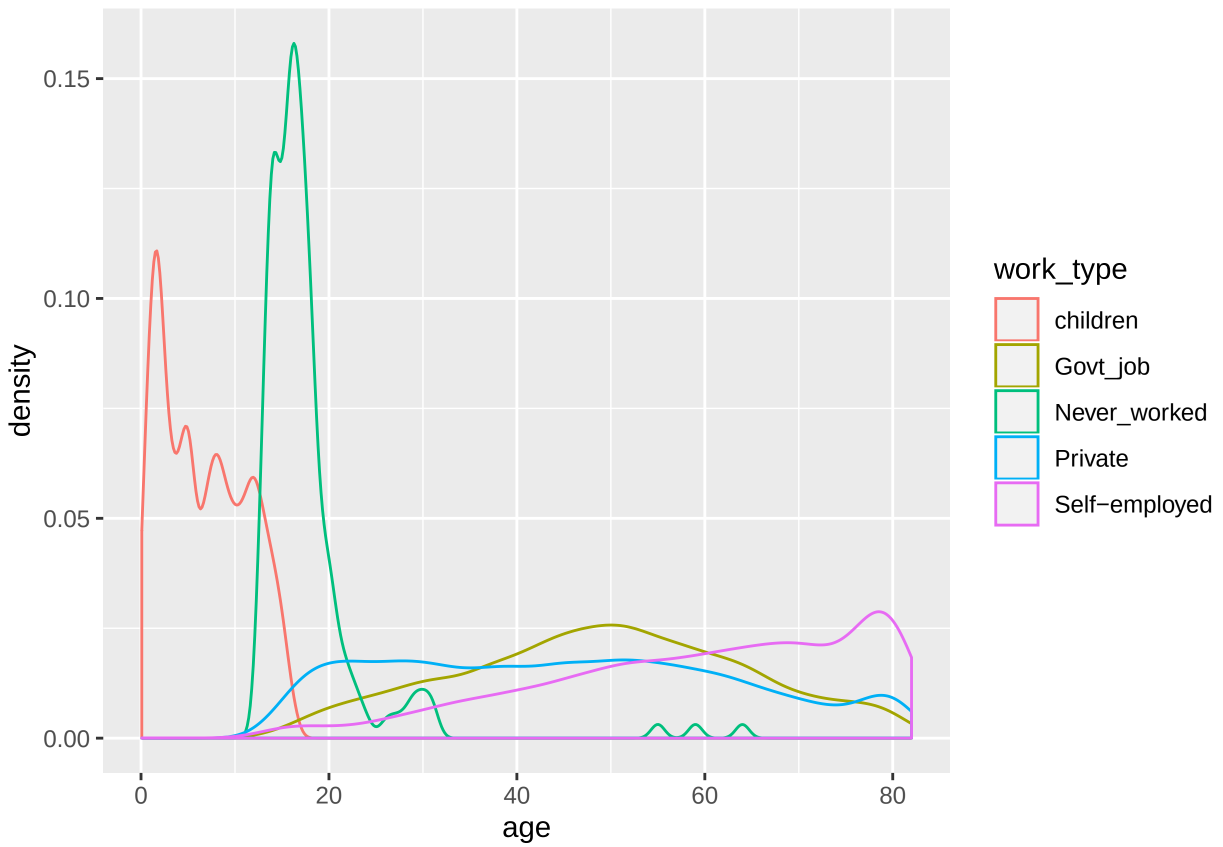
```r
stroke %>%
    count(work_type) %>%
    kable(caption="Work type counts in dataset")
```

Table 1: Work type counts in dataset

work_type	n
children	6156
Govt_job	5440
Never_worked	177
Private	24834
Self-employed	6793

One of the types is *children*. Does this mean the occupation is someone who works with children? Or does it mean the subjects themselves are children? We can check this by looking at the distribution of age with respect to *work_type*:

```r
stroke %>%
    ggplot(aes(x = age, colour=work_type)) +
    geom_density()
```



The answer now is clear that *children* means the subject is a child, not that they work with children. Knowing that work type just tells us that the subject is younger than around 18. Similarly, the vast bulk of those listed as *never_worked* are below the age of 20 or so. To know these work types is to essentially know the subject is young and, as we have clearly seen in the earlier exploration, age is the dominant risk factor. These work types are highly unlikely to contain additional predictive power. They are also not orthogonal to the other work types. Everyone at age 50, whether they're in a government job or the private sector, or self-employed was once a child. They may very well have likely also never worked before the age of 20.

In this feature, we have both a strong age component and also do not have a means to fundamentally distinguish separate groups of people. There is further uncertainty regarding this feature. Is it what the subject was doing at the time of being surveyed? We cannot assume that's the only work type they've ever done. The self-employed category is biased towards older age. Why is there no *retired* category? Is everyone in this population working until they drop?

This feature might be of interest if we better understood what it actually meant and if we wanted to, say, understand stroke risk for people over 60 and take into account whether they still worked, and in what kind of job, or had retired. In short, the *work_type* feature seems very much to be one that should be held back pending clarification about what it's actually measuring.

Appendix

Session info

```
sessionInfo()
```

```
## R version 3.6.3 (2020-02-29)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Linux Mint 19.3
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.7.1
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.7.1
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8        LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8    LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] knitr_1.26      forcats_0.4.0   stringr_1.4.0   dplyr_0.8.3
##  [5] purrr_0.3.3     readr_1.3.1     tidyr_1.0.0     tibble_2.1.3
##  [9] ggplot2_3.2.1   tidyverse_1.3.0 rmarkdown_2.0   nvimcom_0.9-78
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_0.2.5 xfun_0.11        haven_2.2.0      lattice_0.20-40
##  [5] colorspace_1.4-1 vctrs_0.2.1      generics_0.0.2   htmltools_0.4.0
##  [9] yaml_2.2.0       utf8_1.1.4       rlang_0.4.2      pillar_1.4.3
## [13] withr_2.1.2      glue_1.3.1       DBI_1.1.0        dbplyr_1.4.2
## [17] modelr_0.1.5     readxl_1.3.1     lifecycle_0.1.0  munsell_0.5.0
## [21] gtable_0.3.0     cellranger_1.1.0 rvest_0.3.5      evaluate_0.14
## [25] labeling_0.3     fansi_0.4.0      highr_0.8        broom_0.5.3
## [29] Rcpp_1.0.3       scales_1.1.0     backports_1.1.5  jsonlite_1.6
## [33] farver_2.0.1     fs_1.3.1         hms_0.5.2        digest_0.6.23
## [37] stringi_1.4.3    grid_3.6.3       cli_2.0.0        tools_3.6.3
## [41] magrittr_1.5     lazyeval_0.2.2   crayon_1.3.4     pkgconfig_2.0.3
## [45] zeallot_0.1.0    xml2_1.2.2       reprex_0.3.0     lubridate_1.7.4
## [49] assertthat_0.2.1 httr_1.4.1       rstudioapi_0.10  R6_2.4.1
## [53] nlme_3.1-144     compiler_3.6.3
```