

# 7 Packages for Efficient Data Science with R

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June 22, 2017

**“Progress isn’t made by early risers. It’s made by lazy men trying to find easier ways to do something.” — Robert A. Heinlein**

In this presentation I am going to discuss some tricks, techniques, and packages that will improve your data science game by making you and your R code more efficient.

By *efficiency* I am not just talking about algorithmic speed and data structure complexity, but I am also considering efficiency in the broader sense of the term to encompass programmer and engineering productivity. As Gillespie and Lovelace (2016) note, *efficiency* can include programming idioms, IDEs, coding conventions, development processes, and even community support – all things that can greatly improve the speed and ease of “doing” data science.

Efficiency is especially important for R - a language that is notoriously flexible in its ability to solve problems in multiple ways. This issue is compounded when one considers the thousands of packages that are available on **CRAN**, **Bioconductor**, and **Github**. R’s flexibility is both a blessing and curse. It is a blessing because it affords you the tools to write code specific to your individual needs. It is a curse because (a) it makes it more likely that you will choose a sub-optimal solution to your problem and (b) it makes it more likely that another scientist or team mate (and possibly your own *future self*) will not understand your code, making it more difficult to maintain and extend.

In the following sections, on a case by case basis, I will briefly introduce a problem or challenge relating to common data science tasks. I will illustrate how these problems might be tackled in base R or other common packages. Next, I will show you what I think is a preferred solution – one that makes for more effective and efficient code, especially in a *production* environment *collaborating* with other engineers and scientists. Rather than reinventing the wheel, I will show you what I have found are the most useful packages and techniques for solving common tasks balancing the needs of computational and engineering efficiency with code expressiveness.

## 1. Benchmarking

In a production environment, for real-time applications, it is often important to determine the most optimal way to write a function so as to reduce processing time. For large blocks of code we can rely on the R profiler to identify performance bottlenecks, but we often need a quick, agile approach to identifying the most efficient solution among several alternatives.

**What is the quickest method to subset a data.frame to a single cell?**

(a). `df[row, col]` (b). `df[row, "col_name"]` (c). `df$col_name[row]`

**SOLUTION #1.1 - A naive approach is to take time stamps. The following approach is inaccurate because (a) it relies on a single trial to compute the run time and (b) it prints the result of the subset operation to the console (which in fact takes up the bulk of the processing time).**

```
df_1 <- data.frame(num = sample(x = 1:100, size = 100, replace = TRUE),
  ltr = sample(x = letters, size = 100, replace = TRUE))

s_time <- Sys.time()
df_1[10, 2]

## [1] n
## Levels: a b c d e f g h i j k l m n o p q r s t u v w x y z

e_time <- Sys.time()
difftime(e_time, s_time, units = "secs")

## Time difference of 0.001963139 secs
```

**SOLUTION #1.2 - a better approach is to conduct multiple trials on each subset operation using `system.time()` with a loop around the function call. This provides a more reliable estimate of processing time.**

```
system.time(for (i in 1:10000) {
  df_1[10, 2]
})

##      user  system elapsed
##    0.16    0.00    0.15

system.time(for (i in 1:10000) {
  df_1[10, "ltr"]
})

##      user  system elapsed
##    0.14    0.00    0.14

system.time(for (i in 1:10000) {
  df_1$ltr[10]
})

##      user  system elapsed
##    0.11    0.00    0.11
```

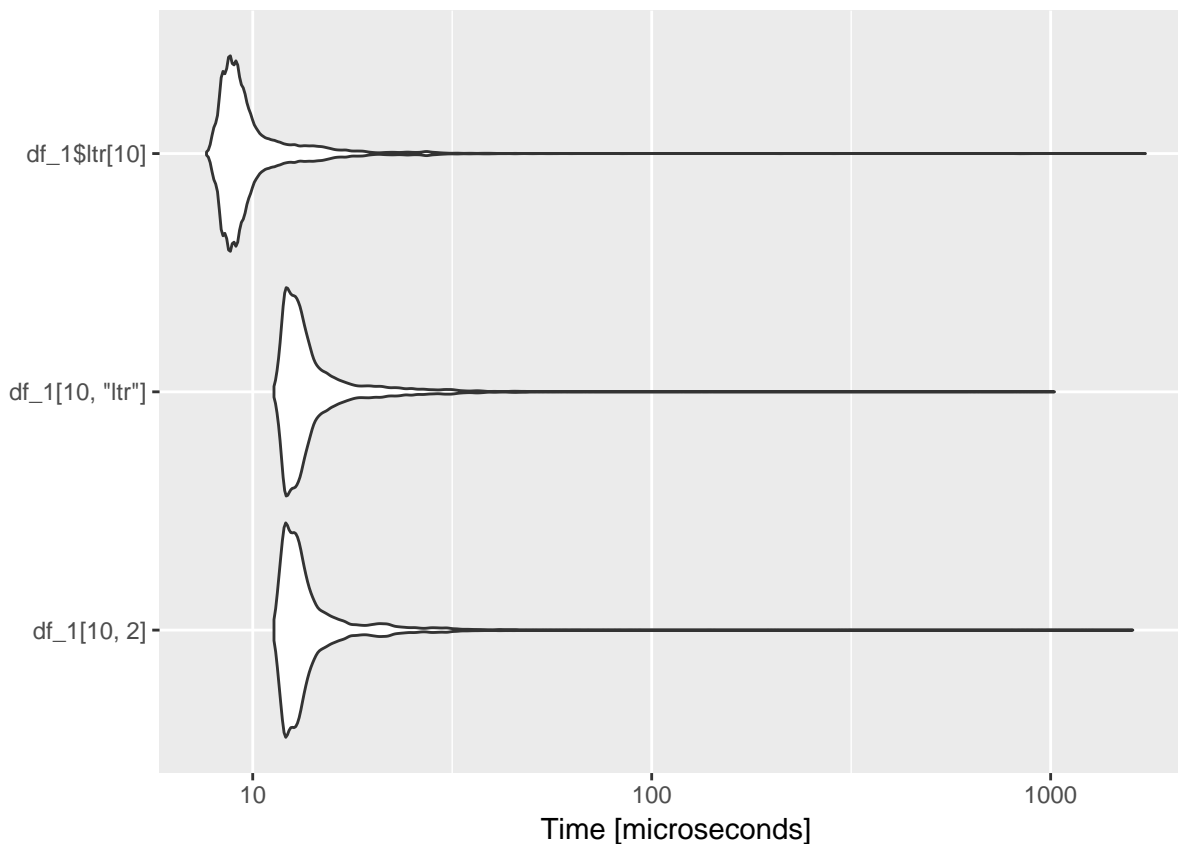
**PREFERRED SOLUTION #1.3** - Use `{microbenchmark}` to benchmark small pieces of source code. Makes it easy to evaluate multiple expressions and provides easy-to-understand summary of results.

```
library(microbenchmark)
(m <- microbenchmark(df_1[10, 2], df_1[10, "ltr"], df_1$ltr[10],
  times = 10000))

## Unit: microseconds
##      expr      min       lq     mean  median      uq      max  neval  cld
## df_1[10, 2] 11.305 12.035 15.32990 12.765 14.223 1607.109 10000   b
## df_1[10, "ltr"] 11.305 12.399 15.14608 13.129 14.587 1022.540 10000   b
## df_1$ltr[10]  7.658  8.753 10.85743  9.118 10.212 1728.180 10000   a
```

**BONUS** - the results of `microbenchmark()` play nicely with package `{ggplot2}`.

```
ggplot2::autoplot(m)
```



## 2. Reading Data

There are numerous ways to read/write various data formats into R. My goto these days is package `{readr}` because it is quick, easy to use, and has functions for reading flat files in a variety of common formats (e.g., csv, tsv, logs, tables). For large data.frames, `{readr}` functions approach the speeds of `data.table::fread()` (Fig. 1).

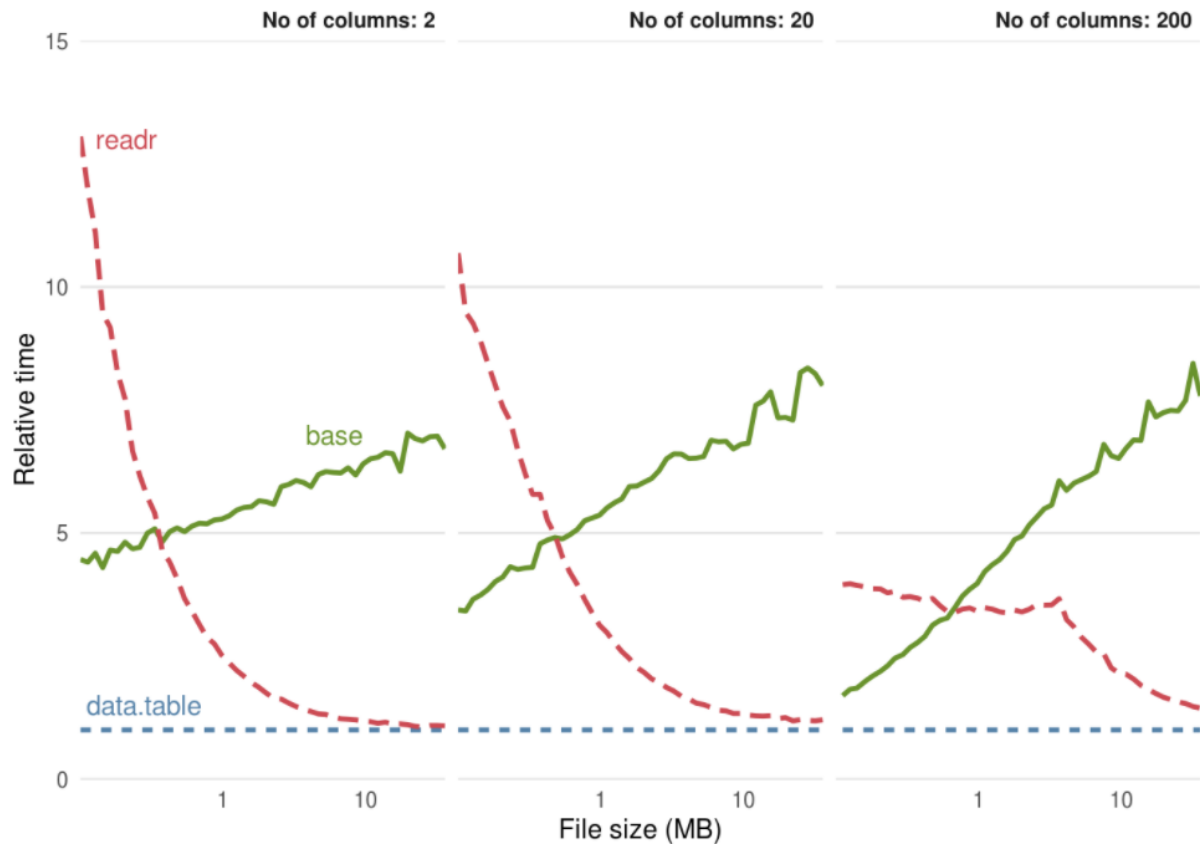


Figure 1: Benchmarks of base, data.table, and readr approaches for reading CSV files. Source: Gillespie & Lovelace (2016)

### PREFERRED SOLUTION #2.1 - Use `{readr}`.

```
file_name <- "data/texas_census.csv"
df_2 <- readr::read_csv(file_name)
```

```
## Parsed with column specification:
## cols(
##   GEOID = col_integer(),
##   SUMLEV = col_character(),
##   STATE = col_integer(),
##   COUNTY = col_character(),
##   CBSA = col_integer(),
##   CSA = col_integer(),
##   NECTA = col_character(),
```

```
## CNECTA = col_character(),
## NAME = col_character(),
## POP100 = col_integer(),
## HU100 = col_integer(),
## POP100.2000 = col_integer(),
## HU100.2000 = col_integer(),
## P001001 = col_integer(),
## P001001.2000 = col_integer()
## )
```

{readr} prints out a handy column specification that can be easily copied, pasted, and modified for a subsequent call, appropriately mapping column names to specified data types. In this example, **GEOID** shouldn't be an integer it should be a factor.

**PREFERRED SOLUTION #2.2** Use {readr} with *revised* column specification if you need to read in data multiple times (e.g., a nightly process dumps a CSV file that needs to be processed).

```
lvls <- unique(df_2$GEOID)

library(readr)
df_2 <- read_csv(file_name, col_types = cols(GEOID = col_factor(levels = lvls),
  SUMLEV = col_character(), STATE = col_integer(), COUNTY = col_character(),
  CBSA = col_integer(), CSA = col_integer(), NECTA = col_character(),
  CNECTA = col_character(), NAME = col_character(), POP100 = col_integer(),
  HU100 = col_integer(), POP100.2000 = col_integer(), HU100.2000 = col_integer(),
  P001001 = col_integer(), P001001.2000 = col_integer()))

class(df_2$GEOID)
```

```
## [1] "factor"
```

Once I've preprocessed and cleaned my data.frame, I then store the data as a binary R object. This facilitates collaboration by ensuring that all team members are using *exactly the same data* (as opposed to using a CSV file that may be read and mapped differing data types).

**PREFERRED SOLUTION #2.3** - After initial formatting, store data.frame as an R object with saveRDS() for subsequent I/O and to facilitate collaboration.

```
saveRDS(df_2, file = "data/texas_census_cleaned_df.Rds")
cleaned_df_2 <- readRDS(file = "data/texas_census_cleaned_df.Rds")
head(cleaned_df_2)
```

```
## # A tibble: 6 x 15
##   GEOID SUMLEV STATE COUNTY CBSA CSA NECTA CNECTA NAME
##   <fctr> <chr> <int> <chr> <int> <int> <chr> <chr> <chr>
## 1 48155 050 48 155 99999 999 <NA> <NA> Foard County
## 2 48011 050 48 011 11100 999 <NA> <NA> Armstrong County
## 3 48025 050 48 025 13300 999 <NA> <NA> Bee County
## 4 48195 050 48 195 99999 999 <NA> <NA> Hansford County
## 5 48205 050 48 205 99999 999 <NA> <NA> Hartley County
## 6 48415 050 48 415 43660 999 <NA> <NA> Scurry County
## # ... with 6 more variables: POP100 <int>, HU100 <int>, POP100.2000 <int>,
```

```
## # HU100.2000 <int>, P001001 <int>, P001001.2000 <int>
```

**BONUS - Binary formats are fast!** Reading and writing from binary formats is also much quicker than storing it as a CSV (Fig. 2).

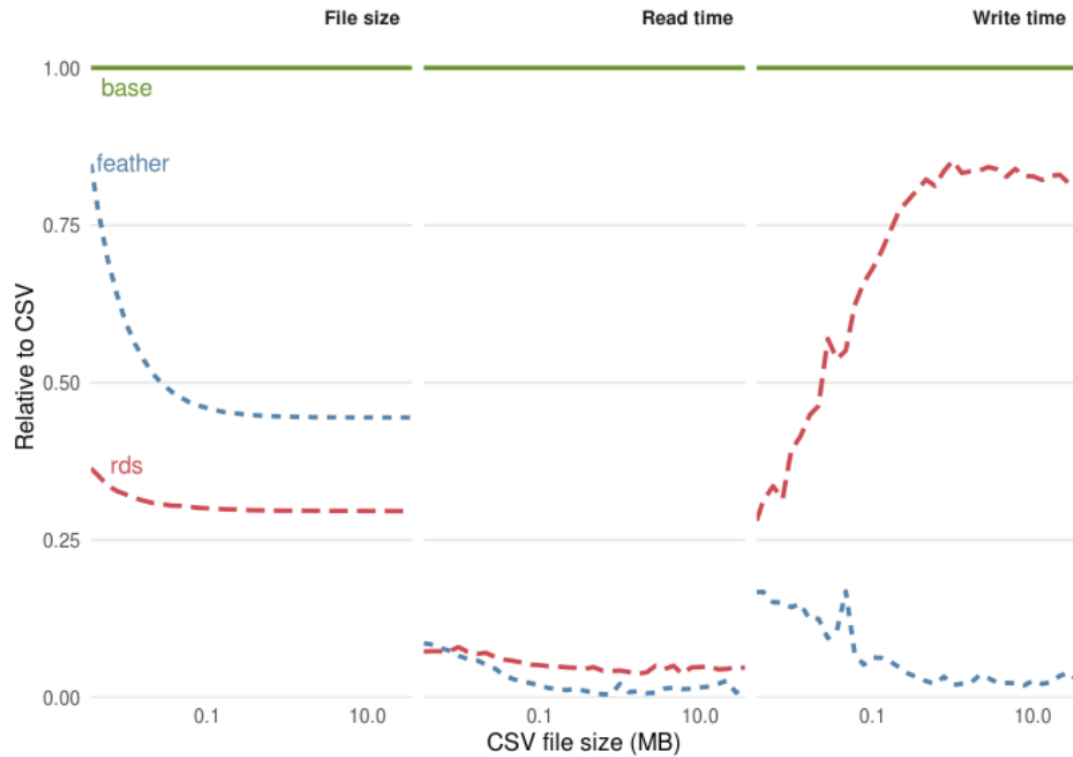


Figure 2: Comparison of the performance of binary formats for reading and writing datasets with 20 columns with the plain-text format CSV. Source: Gillespie & Lovelace (2016)

### 3. String Formatting

For string formatting in base R, the most common approaches are `paste()` and `sprintf()`—both ungainly options that make your code difficult to read and debug.

**SOLUTION #3.1 - Use `paste()`.** Makes for difficult to read code, often requiring use of different separators to deal with sentence boundaries.

```
name <- "Brandon"
age <- 45
age_units <- "years"
weight <- 162.5
weight_units <- "pounds"

paste(name, "is", age, paste0(age_units, "."), "He weighs", weight,
      paste0(weight_units, "!"))
```

```
## [1] "Brandon is 45 years. He weighs 162.5 pounds!"
```

**SOLUTION #3.2 - Use `sprintf()`.** Difficult to remember formatting codes; Difficult to interpret long strings (e.g., complex SQL statement) requiring you to visually map variables at end of construct to embedded placeholders.

```
sprintf("%s is %i %s. He weighs %3.1f %s!", name, age, age_units,
      weight, weight_units)
```

```
## [1] "Brandon is 45 years. He weighs 162.5 pounds!"
```

**PREFERRED SOLUTION #3.3 - Use package `{glue}`.** Reads like a sentence, easy to interpret.

```
library(glue)
glue("{name} is {age} {age_units}. He weighs {weight} {weight_units}!")
```

```
## Brandon is 45 years. He weighs 162.5 pounds!
```

**BONUS - Use an environment to evaluate your variables with `glue()`.**

```
person <- new.env()
person$name = "Fred"
person$age = 28
person$age_units = age_units
person$weight = 185
person$weight_units = weight_units
ls(person)
```

```
## [1] "age"          "age_units"    "name"         "weight"
## [5] "weight_units"
```

```
glue::glue("{name} is {age} {age_units}. He weighs {weight} {weight_units}!",
  .envir = person)
```

## Fred is 28 years. He weighs 185 pounds!



## 4. Complex Expressions

R always passes by value. It never passes by reference. There are two types of people: those who understand the preceding paragraph and those who don't. If you don't understand it, then R is right for you — it means that R is a safe place. - The R Inferno (Burns, 2011)

Because R passes *by value* (rather than *by reference*), complex expressions are formed by creating (1) nested function call stacks that are difficult to interpret (because they are “read” inside-to-out), or (2) by reassigning function calls to temporary variables thus introducing the opportunity for bugs. As a typical data science example, consider an NLP data pipeline that transforms unstructured text (e.g., tweets) into a structured bag-of-words representation.

```
## Define some text manipulation functions
remove_punc <- function(s) {
  gsub("[[:punct:]]", "", s)
}

tokenize <- function(s, split_str) {
  stringr::str_split(s, split_str)
}

same_case <- function(s, case) {
  if (case == "upper") {
    toupper(s)
  } else if (case == "lower") {
    tolower(s)
  } else {
    s
  }
}

splitSubHash <- function(s) {
  # pat <- '(\W|^)\#(\w+)'
  pat <- "(\W|^)\#[a-zA-Z][\w]*"
  sub <- "\\1HASHTAG \\2"
  gsub(pat, sub, s)
}

splitMention <- function(s) {
  pat <- "(\W|^)(@)(\w+)"
  sub <- "\\1MENTION \\3"
  gsub(pat, sub, s)
}

subURL <- function(s) {
  pat <- "http[s]?://(?:[a-zA-Z]|[0-9]|[$-_@.&+]|!*\\(\\),|(?:%[0-9a-fA-F][0-9a-fA-F]))+"
  sub <- "URL"
  gsub(pat, sub, s)
}

stripNonAscii <- function(s) {
  pat <- "[^\001-\177]+"
  sub <- " "
  gsub(pat, sub, s)
}
```

```

}

remove_extraspaces <- function(s) {
  stringr::str_replace(gsub("\\s+", " ", stringr::str_trim(s)),
    "B", "b")
}

```

**SOLUTION #4.1 - Use nested functions.** Extremely difficult to read, especially when functions take multiple arguments.

```

## Let's transform a tweet into a useable list of tokens
s <- "@foobar 'Developers who use spaces make more money than those who use tabs' https://stackoverflow.com/questions/11111111"

tokenize(remove_extraspaces(remove_punc(subURL(splitSubHash(splitMention(same_case(stripNonAscii(s),
  case = "lower"))))))), split_str = " ")

## [[1]]
## [1] "MENTION"      "foobar"      "developers"  "who"         "use"
## [6] "spaces"       "make"        "more"        "money"       "than"
## [11] "those"        "who"         "use"         "tabs"        "URL"
## [16] "HASHTAG"      "rstats"

```

**SOLUTION #4.2 - Assign to temporary variables.** More interpretable than nesting, but still unwieldy and easy to make mistakes.

```

s1 <- stripNonAscii(s)
s2 <- same_case(s1, case = "lower")
s3 <- splitMention(s2)
s4 <- splitSubHash(s3)
s5 <- subURL(s4)
s6 <- remove_punc(s5)
s7 <- remove_extraspaces(s6)
tokenize(s7, split_str = " ")

## [[1]]
## [1] "MENTION"      "foobar"      "developers"  "who"         "use"
## [6] "spaces"       "make"        "more"        "money"       "than"
## [11] "those"        "who"         "use"         "tabs"        "URL"
## [16] "HASHTAG"      "rstats"

```

**PREFERRED SOLUTION #4.3 - Use {magrittr} pipe %>%.** Statement read naturally from left-to-right (or top-to-bottom) by feeding output from LHS of %>% to 1st arg of RHS function.

```

library(magrittr)

s %>% stripNonAscii() %>% same_case(case = "lower") %>% splitMention() %>%
  splitSubHash() %>% subURL() %>% remove_punc() %>% remove_extraspaces() %>%
  tokenize(split_str = " ")

## [[1]]

```

```
## [1] "MENTION"      "foobar"      "developers"  "who"         "use"
## [6] "spaces"       "make"        "more"        "money"       "than"
## [11] "those"        "who"         "use"         "tabs"        "URL"
## [16] "HASHTAG"      "rstats"
```

## 5. Data Munging

There are numerous functions available in base R for common data carpentry tasks like filtering, selecting, sorting, and summarizing (e.g., `order()`, `subset()`, `aggregate()`). Most use standard evaluation that make for long, unwieldy statements, and the differing syntax makes them difficult to remember and they often do not play well together.

```
weapons_df <- tibble::tribble(~name, ~weapon, "Luke Skywalker",  
  "lightsaber", "C-3P0", "none", "R2-D2", "none", "Darth Vader",  
  "lightsaber", "Leia Organa", "blaster", "Obi-Wan Kenobi",  
  "lightsaber", "Chewbacca", "bowcaster", "Han Solo", "blaster",  
  "Greedo", "blaster", "Boba Fett", "blaster")
```

```
df_5 <- dplyr::starwars  
df_5 %>% head()
```

```
## # A tibble: 6 x 13  
##           name height  mass hair_color skin_color eye_color  
##           <chr>  <int> <dbl>    <chr>    <chr>    <chr>  
## 1 Luke Skywalker  172    77    blond    fair     blue  
## 2      C-3P0      167    75    <NA>    gold    yellow  
## 3      R2-D2      96    32    <NA> white, blue red  
## 4   Darth Vader   202   136    none    white    yellow  
## 5   Leia Organa   150    49    brown    light    brown  
## 6    Owen Lars   178   120 brown, grey light     blue  
## # ... with 7 more variables: birth_year <dbl>, gender <chr>,  
## #   homeworld <chr>, species <chr>, films <list>, vehicles <list>,  
## #   starships <list>
```

In the Star Wars franchise, among all characters of known gender and mass GE 75, what is the difference in mean height between blaster users and lightsaber wielders?

**SOLUTION #5.1 (partial) - Using base.** Complex, hard to figure out where to start with lots of opportunities for introducing bugs.

```
## filter  
df_5a <- df_5[!is.na(df_5$gender), ]  
df_5b <- df_5a[df_5a$mass >= 75, ]  
  
## select  
df_5c <- df_5b[, c("name", "height")]  
  
## left join  
df_5c$weapon <- NA  
res <- sapply(1:nrow(df_5c), function(i) {  
  (nm <- df_5c$name[i])  
  (idx <- which(weapons_df$name == nm))  
  if (length(idx) == 0) {  
    NA  
  } else {  
    weapons_df$weapon[idx]  
  }  
})
```

```
df_5c$weapon <- res

## try to summarize
tb <- table(df_5c$height, df_5c$weapon)
head(tb, n = 10)

##
##      blaster bowcaster lightsaber
##  165         0         0         0
##  170         0         0         0
##  172         0         0         1
##  175         0         0         0
##  177         0         0         0
##  178         0         0         0
##  180         1         0         0
##  182         0         0         1
##  183         1         0         0
##  185         0         0         0

## Ugh! Going to stop Way too complex, there has got to be a
## better approach!
```

**SOLUTION #5.2 (not shown)** - Use `{sqldf}` for a straight SQL implementation. Better, but does not allow syntax checking nor does it facilitate agile interactive analysis.

**PREFERRED SOLUTION #5.3** - Use `{dplyr}` with `{magrittr}` `%>%`. Easy to read, easy to chain together expressions. Complex expressions build up in a natural sequence that facilitates interactive analysis.

```
library(magrittr)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following object is masked from 'package:glue':
##
##      collapse

## The following objects are masked from 'package:stats':
##
##      filter, lag

## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union

weapon_height <- df_5 %>% left_join(weapons_df) %>% filter(!is.na(gender) &
  mass >= 75 & weapon %in% c("blaster", "lightsaber")) %>%
  select(name, height, weapon) %>% group_by(weapon) %>% summarize(mean_height = mean(height)) %>%
  mutate(height_diff = mean_height[weapon == "blaster"] - mean_height[weapon ==
    "lightsaber"])

## Joining, by = "name"
```

```
weapon_height
```

```
## # A tibble: 2 x 3
##   weapon mean_height height_diff
##   <chr>      <dbl>      <dbl>
## 1 blaster   181.5000    -3.833333
## 2 lightsaber 185.3333    -3.833333
```

## 6. Model Results

Output from various ML algorithms take myriad forms making it difficult to create data processing pipelines.

```
## Fit a model
lm_fit <- lm(Petal.Width ~ ., data = iris[, 1:4])

## Fit a different model
glm_fit <- glm(am ~ wt, mtcars, family = "binomial")

## Useful summary for reading, but not so useful for
## computational processing
summary(lm_fit)

##
## Call:
## lm(formula = Petal.Width ~ ., data = iris[, 1:4])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.60959 -0.10134 -0.01089  0.09825  0.60685
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.24031    0.17837  -1.347    0.18
## Sepal.Length -0.20727    0.04751  -4.363 2.41e-05 ***
## Sepal.Width   0.22283    0.04894   4.553 1.10e-05 ***
## Petal.Length  0.52408    0.02449  21.399 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.192 on 146 degrees of freedom
## Multiple R-squared:  0.9379, Adjusted R-squared:  0.9366
## F-statistic: 734.4 on 3 and 146 DF,  p-value: < 2.2e-16
```

Suppose we want to programmatically fit a model to some data and select all terms that are significant at  $p < 0.01$  so that we can pass the terms on to some other downstream process in our data pipeline.

**SOLUTION #6.1 - Figure out the structure of the results, craft a “solution”, and extend to cover all use cases (i.e. the models your pipeline will support).**

```
library(magrittr)
library(dplyr)
## Examine the structure of this particular output
str(lm_fit, max.level = 1, vec.length = 2, give.attr = FALSE)

## List of 12
## $ coefficients : Named num [1:4] -0.24 -0.207 0.223 0.524
## $ residuals    : Named num [1:150] -0.0163 0.0537 0.0201 -0.0832 -0.0593 ...
## $ effects      : Named num [1:150] -14.6888 7.6104 2.5293 -4.1078 -0.0638 ...
## $ rank         : int 4
## $ fitted.values: Named num [1:150] 0.216 0.146 0.18 0.283 0.259 ...
## $ assign       : int [1:4] 0 1 2 3
```

```
## $ qr          :List of 5
## $ df.residual  : int 146
## $ xlevels      : Named list()
## $ call         : language lm(formula = Petal.Width ~ ., data = iris[, 1:4])
## $ terms        :Classes 'terms', 'formula' language Petal.Width ~ Sepal.Length + Sepal.Width + Pet
## $ model        :'data.frame': 150 obs. of 4 variables:

df_6 <- as.data.frame(coef(summary(lm_fit))) ## figure out how to access it
filt_df <- df_6[df_6$`Pr(>|t|)` <= 0.01, ] ## identify the appropriate column
(sig_terms <- row.names(filt_df)) ## extract terms

## [1] "Sepal.Length" "Sepal.Width" "Petal.Length"

## Looks good, let's wrap in a function that we can apply to
## all model fits

get_sigterms <- function(fit) {
  df <- as.data.frame(coef(summary(fit))) ## figure out how to access it
  filt_df <- df[df$`Pr(>|t|)` <= 0.01, ] ## identify the appropriate column
  (sig_terms <- row.names(filt_df)) ## extract terms
  return(sig_terms)
}

get_sigterms(lm_fit) ## Great it works

## [1] "Sepal.Length" "Sepal.Width" "Petal.Length"

get_sigterms(glm_fit) ## Hmmm... really no significant terms?

## character(0)

coef(summary(glm_fit)) ## Oh, the column has a different name...

##          Estimate Std. Error   z value    Pr(>|z|)
## (Intercept) 12.04037   4.509706  2.669879 0.007587858
## wt          -4.02397   1.436416 -2.801396 0.005088198

## better add a switch statement... (and repeat for every
## case)
```

**PREFERRED SOLUTION #6.2 – Use package {broom}.** Transforms disparate results into a standardized data.frame format.

```
lm_fit %>% broom::tidy() %>% filter(p.value <= 0.01) %>% select(term)

##          term
## 1 Sepal.Length
## 2 Sepal.Width
## 3 Petal.Length

glm_fit %>% broom::tidy() %>% filter(p.value <= 0.01) %>% select(term)

##          term
## 1 (Intercept)
## 2          wt
```



## 7. Variable Caching

The newest technique I've added to my arsenal for writing efficient R code is variable caching. When properly done, it can drastically improve the performance of your programs and improve the user experience. The idea of caching is simple: if a computationally expensive function is called multiple times with the same arguments, you can do the computation once, and then store a local copy or cache that is quickly returned whenever that function is called with the same argument list. Package `{memoise}` offers an elegant, easy-to-implement solution to variable caching.

```
library(microbenchmark)

my_func <- function(a1, a2) {
  Sys.sleep(0.1) ## Sleep for 1/10th a second to mimic heavy computation
}
```

**SOLUTION #7.1 - Just deal with it.** User has to wait while heavy computations takes place.

```
for (i in 1:100) {
  my_func("foo", "bar")
}
```

**PREFERRED SOLUTION #7.2 - Use package `{memoise}`.** Elegant, no custom code, provides mechanisms for clearing caches.

```
library(memoise)

mem_my_func <- memoise(my_func)

microbenchmark(my_func("foo", "bar"), mem_my_func("foo", "bar"),
  unit = "ms")

## Unit: milliseconds
##           expr           min           lq         mean        median
##   my_func("foo", "bar") 100.055394 100.2371835 100.47649 100.372294
## mem_my_func("foo", "bar")   0.171397   0.5667005   2.62104   1.034575
##           uq         max neval cld
## 100.664032 101.3183   100    b
##   1.559703 101.8423   100    a

## Bonus you can use Google Drive or Drop Box to share the
## cache among colleagues gdc <- cache_filesystem('~/.Google
## Drive/.rcache') mrunif <- memoise(runif, cache = gdc)
## mrunif(20) # Results stored in Google Drive .rcache folder
## which will be synced between computers.
```

## **Thank you to our sponsor Booz Allen Hamilton**

For more information on writing efficient R code, I direct you to Gillespie and Lovelace's excellent book *Efficient R Programming* (2016) published by O'Reilly Media. You can read my full review of their book on RStudio's R Views Blogs. A useful discussion of the quirks and pitfalls of R that can impact the efficiency of your code, is Patrick Burn's *The R Inferno* (2011).

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