

# White Rice vs. Brown Rice

In this report, I'm using data from <https://fdc.nal.usda.gov/index.html> to present a comparison of the nutritional value of brown rice vs. white rice. For information on this API look here. <https://fdc.nal.usda.gov/api-guide.html>

My API key is stored in .Renviron in my home directory using .Renviron as data\_gov\_api\_key

Here are two functions written to fetch the information.

## Search Functions

```
library(curl)
library(jsonlite)

get_food_data <- function(x) {
  # make sure to bookend with quotes
  x <- paste0("\"", x, "\"")
  get_food_url <- "https://api.nal.usda.gov/fdc/v1/foods/search"
  query_terms = c(
    paste("query", URLencode(x), sep = "="),
    paste("dataType", "Survey (FNDDS)", sep = "="),
    paste("pageSize", "200", sep = "=")
  )
  query_string = paste(query_terms, collapse = "&")
  url <- paste(get_food_url, query_string, sep = "?")
  # print(url)

  curl_h <- new_handle()
  handle_setheaders(curl_h, 'X-API-Key' = Sys.getenv("data_gov_api_key"))
  con <- curl(url, handle = curl_h)
  out <- readLines(con)
  close(con)
  fromJSON(out)[[5]]
}

get_food_by_fdcId <- function(id) {
  get_food_url <- "https://api.nal.usda.gov/fdc/v1/food"
  url <- paste(get_food_url, id, sep = "/")
  # print(url)

  curl_h <- new_handle()
  handle_setheaders(curl_h, 'X-API-Key' = Sys.getenv("data_gov_api_key"))
  con <- curl(url, handle = curl_h)
  out <- readLines(con)
  close(con)
  fromJSON(out)
}
```

## Retrieve Data

```
rice <- c(
  white="Rice, white, cooked, fat not added in cooking",
  brown="Rice, brown, cooked, fat not added in cooking"
)

shortNames <- c("white", "brown")
white.df <- get_food_data(rice["white"])
brown.df <- get_food_data(rice["brown"])

ids <- c(white.df$fdcId, brown.df$fdcId)

foodItems <- lapply(ids, get_food_by_fdcId)
```

## Initial Inputs

```
library(dplyr)
library(kableExtra)

white_rice_ingredients <- foodItems[[1]]$inputFoods %>%
  transmute(
    ingredient=ingredientDescription,
    portion=portionDescription,
    grams=ingredientWeight
  )
brown_rice_ingredients <- foodItems[[2]]$inputFoods %>%
  transmute(
    ingredient=ingredientDescription,
    portion=portionDescription,
    grams=ingredientWeight
  )
```

Table 1: White Rice Ingredients			Table 2: Brown Rice Ingredients		
ingredient	portion	grams	ingredient	portion	grams
Rice, white, long-grain, regular, enriched, cooked	1 cup	158.000	Rice, brown, long-grain, cooked	1 cup	195.000
Salt, table	1 teaspoon	1.002	Salt, table	1 teaspoon	1.002

## Compare Nutrients

```
library(dplyr)
library(knitr)
library(xtable)

portions <- unlist(lapply(foodItems, function(x) {x$foodPortions$portionDescription[1]}))
names(portions) <- shortNames

white.nutrients.df <- white.df$foodNutrients[[1]] %>%
  transmute(nutrient=nutrientName, value=value, unit=unitName)
```

Table 3: Nutrient List

nutrient	white	brown
Energy	129.000	122.000
Water	68.010	69.910
Carbohydrate, by difference	27.990	25.450
Protein	2.670	2.730
Fiber, total dietary	0.400	1.600
Total lipid (fat)	0.280	0.960
Fatty acids, total monounsaturated	0.087	0.367
18:1	0.086	0.363
Fatty acids, total saturated	0.077	0.259
Fatty acids, total polyunsaturated	0.076	0.364
16:0	0.069	0.197
18:2	0.062	0.353
Sugars, total including NLEA	0.050	0.240
18:3	0.013	0.011
18:0	0.005	0.022
14:0	0.002	0.009
16:1	0.001	0.001

```

brown.nutrients.df <- brown.df$foodNutrients[[1]] %>%
  transmute(nutrient=nutrientName,value,unit=unitName)

combined.df <- full_join(
  white.nutrients.df, brown.nutrients.df,
  by="nutrient", suffix=c(".white",".brown")
) %>%
  filter(
    unit.brown=="G" |
    unit.white == "G" |
    unit.brown == "KCAL" |
    unit.white == "KCAL"
  ) %>%
  filter(value.brown > 0, value.white > 0) %>%
  arrange(desc(value.white)) %>%
  rename(white=value.white, brown=value.brown) %>%
  select(nutrient, white, brown)

kable(combined.df, format = "latex", label="Table 3",
  caption="Nutrient List", booktabs = TRUE)

```

## Calories

```

compared.df <-data.frame(
  rbind(combined.df$white, combined.df$brown),
  row.names = shortNames)
names(compared.df) <- combined.df$nutrient

grams <- colSums(combined.df[2:6,2:3], na.rm=TRUE)

```

```
print(grams)
```

```
## white brown  
## 99.35 100.65
```

```
barplot(compared.df$Energy, main = "Calories", names.arg=shortNames)
```



Nutrients by Mass

```
barplot(height=as.matrix(compared.df[,2:6]),names.arg=c("Water", "Carbohydrates", "Protein", "Fiber", "Lipids"),  
        legend=TRUE)
```

