

# Disease Burden Analysis

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## Initializing

```
library(mosaic)
library(tidyverse)
library(lubridate)
library(ggplot2)
library(readxl)
library(writexl)
library(plotly)
library(dplyr)
library(readr)
library(here)
library(rvest)
library(purrr)
library(conflicted)
conflict_prefer("max", "mosaic")
conflict_prefer("filter", "dplyr")
conflict_prefer("select", "dplyr")
conflict_prefer("summarize", "dplyr")
conflict_prefer("mean", "mosaic")

## Adjust!
knitr::opts_knit$set(root.dir = here::here())
```

## Loading Data

```

Cardiovascular_Disease_Mortality_Burden_path <- here("Data_Raw/Disease_Mortality_Burden", "H
Cardiovascular_Disease_Mortality_Burden <- read_xlsx(Cardiovascular_Disease_Mortality_Burden

Liver_Disease_Mortality_Burden_path <- here("Data_Raw/Disease_Mortality_Burden", "Heart_Liver
Liver_Disease_Mortality_Burden <- read_xlsx(Liver_Disease_Mortality_Burden_path, sheet = 1)

Kidney_Disease_Mortality_Burden_path <- here("Data_Raw/Disease_Mortality_Burden", "Heart_Liver
Kidney_Disease_Mortality_Burden <- read_xlsx(Kidney_Disease_Mortality_Burden_path, sheet = 1)
# Source: https://www.cdc.gov/nchs/has/contents2020-2021.htm#Table-SlctMort

```

```

HRSA_National_Data_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_National_Data <- read_xlsx(HRSA_National_Data_path, sheet = 2)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

HRSA_State_Data_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_State_Data <- read_xlsx(HRSA_State_Data_path, sheet = 3)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

HRSA_Donor_Demographics_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_Donor_Demographics <- read_xlsx(HRSA_Donor_Demographics_path, sheet = 4)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

HRSA_Candidate_Registration_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_Candidate_Registration <- read_xlsx(HRSA_Candidate_Registration_path, sheet = 7)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

HRSA_Waitlist_Removal_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_Waitlist_Removal <- read_xlsx(HRSA_Waitlist_Removal_path, sheet = 9)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

HRSA_Recipient_Demographics_path <- here("Data_Raw/Organ_Transplant", "Organ_Donation_and_Transplantation
HRSA_Recipient_Demographics <- read_xlsx(HRSA_Recipient_Demographics_path, sheet = 10)
# Source: https://data.hrsa.gov/data/download?data=organ#organ

```

## Cleaning Data

### Disease mortality burden by organ v sex and race

```
Sexes <- c("Male", "Female")
Races <- c("White only", "Black or African American only", "Asian or Pacific Islander only", "Hispanic or Latino")

# Renaming columns
Cardiovascular_Disease_Mortality_Burden_Columns <- as.character(Cardiovascular_Disease_Mortality_Burden_Columns)
Cardiovascular_Disease_Mortality_Burden_Columns[is.na(Cardiovascular_Disease_Mortality_Burden_Columns)] <- "All"
Cardiovascular_Disease_Mortality_Burden_Columns <- make.unique(Cardiovascular_Disease_Mortality_Burden_Columns)
# make.unique appends a sequence of numbers to make the column names unique
colnames(Cardiovascular_Disease_Mortality_Burden) <- Cardiovascular_Disease_Mortality_Burden_Columns

Cardiovascular_Disease_Mortality_Burden <- Cardiovascular_Disease_Mortality_Burden |>
  rename(Characteristic = "Sex and cause of death\\1") |>
  select(Characteristic, `1997`\\3:`2019`\\4`)

# Removing irrelevant data
Cardiovascular_Disease_Mortality_Burden <- Cardiovascular_Disease_Mortality_Burden[c(6, 26, 46, 66, 86, 106, 126, 146, 166, 186, 206, 226, 246, 266, 286, 306, 326, 346, 366, 386, 406, 426, 446, 466, 486, 506, 526, 546, 566, 586, 606, 626, 646, 666, 686, 706, 726, 746, 766, 786, 806, 826, 846, 866, 886, 906, 926, 946, 966, 986, 1006, 1026, 1046, 1066, 1086, 1106, 1126, 1146, 1166, 1186, 1206, 1226, 1246, 1266, 1286, 1306, 1326, 1346, 1366, 1386, 1406, 1426, 1446, 1466, 1486, 1506, 1526, 1546, 1566, 1586, 1606, 1626, 1646, 1666, 1686, 1706, 1726, 1746, 1766, 1786, 1806, 1826, 1846, 1866, 1886, 1906, 1926, 1946, 1966, 1986, 2006, 2026, 2046, 2066, 2086, 2106, 2126, 2146, 2166, 2186, 2206, 2226, 2246, 2266, 2286, 2306, 2326, 2346, 2366, 2386, 2406, 2426, 2446, 2466, 2486, 2506, 2526, 2546, 2566, 2586, 2606, 2626, 2646, 2666, 2686, 2706, 2726, 2746, 2766, 2786, 2806, 2826, 2846, 2866, 2886, 2906, 2926, 2946, 2966, 2986, 3006, 3026, 3046, 3066, 3086, 3106, 3126, 3146, 3166, 3186, 3206, 3226, 3246, 3266, 3286, 3306, 3326, 3346, 3366, 3386, 3406, 3426, 3446, 3466, 3486, 3506, 3526, 3546, 3566, 3586, 3606, 3626, 3646, 3666, 3686, 3706, 3726, 3746, 3766, 3786, 3806, 3826, 3846, 3866, 3886, 3906, 3926, 3946, 3966, 3986, 4006, 4026, 4046, 4066, 4086, 4106, 4126, 4146, 4166, 4186, 4206, 4226, 4246, 4266, 4286, 4306, 4326, 4346, 4366, 4386, 4406, 4426, 4446, 4466, 4486, 4506, 4526, 4546, 4566, 4586, 4606, 4626, 4646, 4666, 4686, 4706, 4726, 4746, 4766, 4786, 4806, 4826, 4846, 4866, 4886, 4906, 4926, 4946, 4966, 4986, 5006, 5026, 5046, 5066, 5086, 5106, 5126, 5146, 5166, 5186, 5206, 5226, 5246, 5266, 5286, 5306, 5326, 5346, 5366, 5386, 5406, 5426, 5446, 5466, 5486, 5506, 5526, 5546, 5566, 5586, 5606, 5626, 5646, 5666, 5686, 5706, 5726, 5746, 5766, 5786, 5806, 5826, 5846, 5866, 5886, 5906, 5926, 5946, 5966, 5986, 6006, 6026, 6046, 6066, 6086, 6106, 6126, 6146, 6166, 6186, 6206, 6226, 6246, 6266, 6286, 6306, 6326, 6346, 6366, 6386, 6406, 6426, 6446, 6466, 6486, 6506, 6526, 6546, 6566, 6586, 6606, 6626, 6646, 6666, 6686, 6706, 6726, 6746, 6766, 6786, 6806, 6826, 6846, 6866, 6886, 6906, 6926, 6946, 6966, 6986, 7006, 7026, 7046, 7066, 7086, 7106, 7126, 7146, 7166, 7186, 7206, 7226, 7246, 7266, 7286, 7306, 7326, 7346, 7366, 7386, 7406, 7426, 7446, 7466, 7486, 7506, 7526, 7546, 7566, 7586, 7606, 7626, 7646, 7666, 7686, 7706, 7726, 7746, 7766, 7786, 7806, 7826, 7846, 7866, 7886, 7906, 7926, 7946, 7966, 7986, 8006, 8026, 8046, 8066, 8086, 8106, 8126, 8146, 8166, 8186, 8206, 8226, 8246, 8266, 8286, 8306, 8326, 8346, 8366, 8386, 8406, 8426, 8446, 8466, 8486, 8506, 8526, 8546, 8566, 8586, 8606, 8626, 8646, 8666, 8686, 8706, 8726, 8746, 8766, 8786, 8806, 8826, 8846, 8866, 8886, 8906, 8926, 8946, 8966, 8986, 9006, 9026, 9046, 9066, 9086, 9106, 9126, 9146, 9166, 9186, 9206, 9226, 9246, 9266, 9286, 9306, 9326, 9346, 9366, 9386, 9406, 9426, 9446, 9466, 9486, 9506, 9526, 9546, 9566, 9586, 9606, 9626, 9646, 9666, 9686, 9706, 9726, 9746, 9766, 9786, 9806, 9826, 9846, 9866, 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35626, 35646, 35666, 35686, 35706, 35726, 35746, 35766, 35786, 35806, 
```

```

1 All          0.00278  0.00271  0.00266  0.00258  0.00249  0.00245  0.00236
2 Male         0.00350  0.00339  0.00331  0.0032   0.00308  0.00303  0.00292
3 Female       0.00225  0.00221  0.00218  0.00211  0.00205  0.00200  0.00194
4 White only   0.00276  0.00269  0.00264  0.00256  0.00247  0.00242  0.00234
5 Black or African Am~ NA      NA      0.00337  0.00328  0.00323  0.00317  0.00310
6 Asian or Pacific Is~ NA      NA      0.00156  0.00146  0.00140  0.00139  0.00132
7 Hispanic or Latino 0.00206  0.00203  0.00206  0.00196  0.00194  0.00189  0.00182
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>

```

```

Cardiovascular_Disease_Mortality_Burden_Sex <- Cardiovascular_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Sexes)) |>
  rename(Sex = Characteristic)

print(Cardiovascular_Disease_Mortality_Burden_Sex)

```

```

# A tibble: 2 x 24
  Sex      `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004` `2005`
  <chr>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Male    0.00350  0.00339  0.00331  0.0032   0.00308  0.00303  0.00292  0.00274  0.00268
2 Female  0.00225  0.00221  0.00218  0.00211  0.00205  0.00200  0.00194  0.00182  0.00178
# i 14 more variables: `2006` <dbl>, `2007` <dbl>, `2008` <dbl>, `2009` <dbl>,
#   `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>, `2014` <dbl>,
#   `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>, `2019` <dbl>

```

```

Cardiovascular_Disease_Mortality_Burden_Race <- Cardiovascular_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Races)) |>
  rename(Race = Characteristic)

print(Cardiovascular_Disease_Mortality_Burden_Race)

```

```

# A tibble: 4 x 24
  Race      `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 White only 0.00276  0.00269  0.00264  0.00256  0.00247  0.00242  0.00234  0.00220
2 Black or Af~ NA      NA      0.00337  0.00328  0.00323  0.00317  0.00310  0.00291
3 Asian or Pa~ NA      NA      0.00156  0.00146  0.00140  0.00139  0.00132  0.00123
4 Hispanic or~ 0.00206  0.00203  0.00206  0.00196  0.00194  0.00189  0.00182  0.00169
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,

```

```
# `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
# `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
# `2019` <dbl>
```

```
# Renaming columns
Liver_Disease_Mortality_Burden_Columns <- as.character(Liver_Disease_Mortality_Burden[3, ])
Liver_Disease_Mortality_Burden_Columns[is.na(Liver_Disease_Mortality_Burden_Columns)] <- "NA"
Liver_Disease_Mortality_Burden_Columns <- make.unique(Liver_Disease_Mortality_Burden_Columns)
# make.unique appends a sequence of numbers to make the column names unique
colnames(Liver_Disease_Mortality_Burden) <- Liver_Disease_Mortality_Burden_Columns

Liver_Disease_Mortality_Burden <- Liver_Disease_Mortality_Burden |>
  rename(Characteristic = "Sex and cause of death\\1") |>
  select(Characteristic, `1997`\\3:`2019`\\4`)

# Removing irrelevant data
Liver_Disease_Mortality_Burden <- Liver_Disease_Mortality_Burden[c(14, 35, 56, 97, 137, 217,

# Updating characteristics for "Chronic liver disease and cirrhosis"
Liver_Disease_Mortality_Burden[1, "Characteristic"] <- "All"
Liver_Disease_Mortality_Burden[2, "Characteristic"] <- "Male"
Liver_Disease_Mortality_Burden[3, "Characteristic"] <- "Female"
Liver_Disease_Mortality_Burden[4, "Characteristic"] <- "White only"
Liver_Disease_Mortality_Burden[5, "Characteristic"] <- "Black or African American only"
Liver_Disease_Mortality_Burden[6, "Characteristic"] <- "Asian or Pacific Islander only"
Liver_Disease_Mortality_Burden[7, "Characteristic"] <- "Hispanic or Latino"

# Cleaning year names
colnames(Liver_Disease_Mortality_Burden) <- gsub("\\\\\\\\[0-9]$", "", colnames(Liver_Disease_Mo

Liver_Disease_Mortality_Burden <- Liver_Disease_Mortality_Burden |>
  mutate(across(`1997`:`2019`, ~ as.numeric(.x) / 100000))

print(Liver_Disease_Mortality_Burden)
```

```
# A tibble: 7 x 24
```

Characteristic <chr>	`1997` <dbl>	`1998` <dbl>	`1999` <dbl>	`2000` <dbl>	`2001` <dbl>	`2002` <dbl>	`2003` <dbl>
1 All	9.5 e-5	9.3 e-5	9.60e-5	9.5 e-5	9.5 e-5	9.40e-5	9.3 e-5
2 Male	1.34e-4	1.32e-4	1.35e-4	1.34e-4	1.32e-4	1.29e-4	1.3 e-4
3 Female	6.1 e-5	6 e-5	6.1 e-5	6.20e-5	6.30e-5	6.30e-5	6 e-5
4 White only	8.80e-5	8.70e-5	9 e-5	9 e-5	9 e-5	9 e-5	9 e-5

```

5 Black or African Am~ NA      NA      1.02e-4 9.60e-5 9.40e-5 8.5 e-5 8.40e-5
6 Asian or Pacific Is~ NA      NA      3.7 e-5 3.5 e-5 3.5 e-5 3.20e-5 3 e-5
7 Hispanic or Latino    1.65e-4 1.61e-4 1.61e-4 1.65e-4 1.59e-4 1.57e-4 1.49e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>

```

```

Liver_Disease_Mortality_Burden_Sex <- Liver_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Sexes))

```

```
print(Liver_Disease_Mortality_Burden_Sex)
```

```

# A tibble: 2 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 Male          0.000134 1.32e-4 1.35e-4 1.34e-4 1.32e-4 1.29e-4 1.3e-4 1.24e-4
2 Female        0.000061 6 e-5 6.1 e-5 6.20e-5 6.30e-5 6.30e-5 6 e-5 5.90e-5
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>

```

```

Liver_Disease_Mortality_Burden_Race <- Liver_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Races))

```

```
print(Liver_Disease_Mortality_Burden_Race)
```

```

# A tibble: 4 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 White only    8.80e-5 8.70e-5 9 e-5 9 e-5 9 e-5 9 e-5 9 e-5
2 Black or African Am~ NA      NA      1.02e-4 9.60e-5 9.40e-5 8.5 e-5 8.40e-5
3 Asian or Pacific Is~ NA      NA      3.7 e-5 3.5 e-5 3.5 e-5 3.20e-5 3 e-5
4 Hispanic or Latino    1.65e-4 1.61e-4 1.61e-4 1.65e-4 1.59e-4 1.57e-4 1.49e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>

```

```

# Renaming columns
Kidney_Disease_Mortality_Burden_Columns <- as.character(Kidney_Disease_Mortality_Burden[3, ])
Kidney_Disease_Mortality_Burden_Columns[is.na(Kidney_Disease_Mortality_Burden_Columns)] <- "1"
Kidney_Disease_Mortality_Burden_Columns <- make.unique(Kidney_Disease_Mortality_Burden_Columns)
# make.unique appends a sequence of numbers to make the column names unique
colnames(Kidney_Disease_Mortality_Burden) <- Kidney_Disease_Mortality_Burden_Columns

Kidney_Disease_Mortality_Burden <- Kidney_Disease_Mortality_Burden |>
  rename(Characteristic = "Sex and cause of death\\1") |>
  select(Characteristic, `1997`\\3:`2019`\\4`)

# Removing irrelevant data
Kidney_Disease_Mortality_Burden <- Kidney_Disease_Mortality_Burden[c(21, 42, 63, 104, 144, 205)]

# Updating characteristics for "Chronic liver disease and cirrhosis"
Kidney_Disease_Mortality_Burden[1, "Characteristic"] <- "All"
Kidney_Disease_Mortality_Burden[2, "Characteristic"] <- "Male"
Kidney_Disease_Mortality_Burden[3, "Characteristic"] <- "Female"
Kidney_Disease_Mortality_Burden[4, "Characteristic"] <- "White only"
Kidney_Disease_Mortality_Burden[5, "Characteristic"] <- "Black or African American only"
Kidney_Disease_Mortality_Burden[6, "Characteristic"] <- "Asian or Pacific Islander only"
Kidney_Disease_Mortality_Burden[7, "Characteristic"] <- "Hispanic or Latino"

# Cleaning year names
colnames(Kidney_Disease_Mortality_Burden) <- gsub("\\\\\\\\[0-9]$", "", colnames(Kidney_Disease_Mortality_Burden))

Kidney_Disease_Mortality_Burden <- Kidney_Disease_Mortality_Burden |>
  mutate(across(`1997`:`2019`, ~ as.numeric(.x) / 100000))

print(Kidney_Disease_Mortality_Burden)

```

```

# A tibble: 7 x 24
  Characteristic    `1997`    `1998`    `1999`    `2000`    `2001`    `2002`    `2003`
  <chr>            <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
1 All             9.60e-5  9.8 e-5  1.3 e-4  1.35e-4  1.41e-4  1.44e-4  1.47e-4
2 Male           1.25e-4  1.26e-4  1.65e-4  1.69e-4  1.76e-4  1.8 e-4  1.82e-4
3 Female         8.10e-5  8.2 e-5  1.11e-4  1.15e-4  1.21e-4  1.23e-4  1.25e-4
4 White only     8.80e-5  9 e-5   1.15e-4  1.2 e-4  1.25e-4  1.29e-4  1.3 e-4
5 Black or African Am~ NA      NA      2.88e-4  2.91e-4  3.01e-4  3.05e-4  3.14e-4
6 Asian or Pacific Is~ NA      NA      9.8 e-5  8.40e-5  9.1 e-5  8.90e-5  8.10e-5
7 Hispanic or Latino 7.4 e-5  7.70e-5 1.2 e-4  1.18e-4  1.25e-4  1.2 e-4  1.31e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,

```

```
# `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
# `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
# `2018` <dbl>, `2019` <dbl>
```

```
Kidney_Disease_Mortality_Burden_Sex <- Kidney_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Sexes))

print(Kidney_Disease_Mortality_Burden_Sex)
```

```
# A tibble: 2 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 Male          1.25e-4 1.26e-4 1.65e-4 1.69e-4 1.76e-4 1.8 e-4 1.82e-4 1.78e-4
2 Female        8.10e-5 8.2 e-5 1.11e-4 1.15e-4 1.21e-4 1.23e-4 1.25e-4 1.25e-4
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
# `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
# `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
# `2019` <dbl>
```

```
Kidney_Disease_Mortality_Burden_Race <- Kidney_Disease_Mortality_Burden |>
  filter(Characteristic %in% c(Races))

print(Kidney_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 White only    8.80e-5 9 e-5 1.15e-4 1.2 e-4 1.25e-4 1.29e-4 1.3 e-4
2 Black or African Am~ NA NA 2.88e-4 2.91e-4 3.01e-4 3.05e-4 3.14e-4
3 Asian or Pacific Is~ NA NA 9.8 e-5 8.40e-5 9.1 e-5 8.90e-5 8.10e-5
4 Hispanic or Latino 7.4 e-5 7.70e-5 1.2 e-4 1.18e-4 1.25e-4 1.2 e-4 1.31e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
# `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
# `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
# `2018` <dbl>, `2019` <dbl>
```

## Donor Living Status (only applicable to livers and kidneys)



```

Categories <- c("1 - Donor Type", "0 - Total")
Donor_Living_Status <- c("Deceased Donor", "Living Donor")

# Filtering for just data on living status
Donor_Living_Status <- HRSA_Donor_Demographics |>
  filter(Category %in% Categories) |>
  select(`Donor Type Filter`, `Donor Count`) |>
  rename(Status = `Donor Type Filter`,
          Count = `Donor Count`) |>
  mutate(Count = as.numeric(Count))

# Saving total value
All <- Donor_Living_Status$Count[Donor_Living_Status$Status == "Grand Total"]

# Add proportion column
Donor_Living_Status <- Donor_Living_Status |>
  mutate(Proportion = (Count / All))

print(Donor_Living_Status)

```

```

# A tibble: 3 x 3
  Status      Count Proportion
  <chr>      <dbl>     <dbl>
1 Grand Total 122783      1
2 Deceased Donor 83854    0.683
3 Living Donor 38929    0.317

```

## Recipient Demographic Data

```

Heart_Recipients <- HRSA_Recipient_Demographics |>
  filter(`Organ Transplanted` == "Heart") |>
  select(`Transplant Year`: `Distinct Recipients with Other Insurance Payment Sources`)

# Generating proportions from counts
Heart_Recipients <- Heart_Recipients |>
  mutate(across(`Total Distinct Recipients`: `Distinct Recipients with Other Insurance Payment
                ~ as.numeric(.x))) |>
  mutate(across(`Male Distinct Recipients`: `Distinct Recipients with Other Insurance Payment
                ~ .x / `Total Distinct Recipients`,

```

```

      .names = "Prop_{.col}"))

# Renaming Prop_ variables
Heart_Recipients <- Heart_Recipients |>
  rename_with(
    .fn = ~ paste0(gsub(" Distinct Recipients", "", .x)),
    .cols = `Prop_Male Distinct Recipients`:`Prop_Distinct Recipients with Other Insurance P
  ) |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male:`Prop_Distinct Recipients with Otl

print(Heart_Recipients)

```

```

# A tibble: 6 x 24
  `Transplant Year` `Donor Type`   `Organ Transplanted` Prop_Male Prop_Female
      <dbl> <chr>           <chr>           <dbl>     <dbl>
1         2019 Deceased Donor Heart         0.694     0.306
2         2020 Deceased Donor Heart         0.715     0.285
3         2021 Deceased Donor Heart         0.719     0.281
4         2022 Deceased Donor Heart         0.713     0.287
5         2023 Deceased Donor Heart         0.707     0.293
6         2024 Deceased Donor Heart         0.721     0.279
# i 19 more variables: `Prop_Distinct Recipients with Age Not Reported` <dbl>,
#   Prop_Pediatric <dbl>, `Prop_Age 18-30` <dbl>, `Prop_Age 31-40` <dbl>,
#   `Prop_Age 41-50` <dbl>, `Prop_Age 51-60` <dbl>, `Prop_Age 61+` <dbl>,
#   Prop_White <dbl>, Prop_Black <dbl>, Prop_Hispanic <dbl>, Prop_Asian <dbl>,
#   `Prop_American Indian` <dbl>, `Prop_Native Hawaiian` <dbl>,
#   Prop_Multiracial <dbl>,
#   `Prop_Distinct Recipients with Medicare Advantage Payment Source` <dbl>, ...

```

```

Organs <- c("Liver", "Kidney")

Deceased_Organ_Recipients <- HRSA_Recipient_Demographics |>
  filter(`Organ Transplanted` %in% Organs,
    `Donor Type` == "Deceased Donor")

Living_Organ_Recipients <- HRSA_Recipient_Demographics |>
  filter(`Organ Transplanted` %in% Organs,
    `Donor Type` == "Living Donor")

Deceased_v_Living_Organ_Recipients <- rbind(Deceased_Organ_Recipients, Living_Organ_Recipients)

```

```

Deceased_v_Living_Organ_Recipients <- Deceased_v_Living_Organ_Recipients |>
  select(`Transplant Year`: `Distinct Recipients with Other Insurance Payment Sources`)

# Generating proportions from counts
Deceased_v_Living_Organ_Recipients <- Deceased_v_Living_Organ_Recipients |>
  mutate(across(`Total Distinct Recipients`: `Distinct Recipients with Other Insurance Payment Sources`,
    ~ as.numeric(.x))) |>
  mutate(across(`Male Distinct Recipients`: `Distinct Recipients with Other Insurance Payment Sources`,
    ~ .x / `Total Distinct Recipients`,
    .names = "Prop_{.col}"))

# Renaming Prop_ variables
Deceased_v_Living_Organ_Recipients <- Deceased_v_Living_Organ_Recipients |>
  rename_with(
    .fn = ~ paste0(gsub(" Distinct Recipients", "", .x)),
    .cols = `Prop_Male Distinct Recipients`: `Prop_Distinct Recipients with Other Insurance Payment Sources`
  )

print(Deceased_v_Living_Organ_Recipients)

```

```

# A tibble: 24 x 46
  `Transplant Year` `Donor Type` `Organ Transplanted` Total Distinct Recipi~1
      <dbl> <chr>          <chr>                                <dbl>
1      2019 Deceased Donor Kidney                                16521
2      2019 Deceased Donor Liver                                 8263
3      2020 Deceased Donor Kidney                                17574
4      2020 Deceased Donor Liver                                 8291
5      2021 Deceased Donor Kidney                                18683
6      2021 Deceased Donor Liver                                 8547
7      2022 Deceased Donor Kidney                                19621
8      2022 Deceased Donor Liver                                 8807
9      2023 Deceased Donor Kidney                                21034
10     2023 Deceased Donor Liver                                 9863
# i 14 more rows
# i abbreviated name: 1: `Total Distinct Recipients`
# i 42 more variables: `Male Distinct Recipients` <dbl>,
#   `Female Distinct Recipients` <dbl>,
#   `Distinct Recipients with Age Not Reported` <dbl>,
#   `Pediatric Distinct Recipients` <dbl>,
#   `Age 18-30 Distinct Recipients` <dbl>, ...

```

```
Deceased_v_Living_Liver_Recipients <- Deceased_v_Living_Organ_Recipients |>
  filter(`Organ Transplanted` == "Liver") |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male:`Prop_Distinct Recipients with Otl

print(Deceased_v_Living_Liver_Recipients)
```

```
# A tibble: 12 x 24
```

	`Transplant Year`	`Donor Type`	`Organ Transplanted`	Prop_Male	Prop_Female
	<dbl>	<chr>	<chr>	<dbl>	<dbl>
1	2019	Deceased Donor	Liver	0.635	0.365
2	2020	Deceased Donor	Liver	0.629	0.371
3	2021	Deceased Donor	Liver	0.626	0.374
4	2022	Deceased Donor	Liver	0.625	0.375
5	2023	Deceased Donor	Liver	0.612	0.388
6	2024	Deceased Donor	Liver	0.599	0.401
7	2019	Living Donor	Liver	0.515	0.485
8	2020	Living Donor	Liver	0.515	0.485
9	2021	Living Donor	Liver	0.476	0.524
10	2022	Living Donor	Liver	0.517	0.483
11	2023	Living Donor	Liver	0.508	0.492
12	2024	Living Donor	Liver	0.442	0.558

```
# i 19 more variables: `Prop_Distinct Recipients with Age Not Reported` <dbl>,
#   Prop_Pediatric <dbl>, `Prop_Age 18-30` <dbl>, `Prop_Age 31-40` <dbl>,
#   `Prop_Age 41-50` <dbl>, `Prop_Age 51-60` <dbl>, `Prop_Age 61+` <dbl>,
#   Prop_White <dbl>, Prop_Black <dbl>, Prop_Hispanic <dbl>, Prop_Asian <dbl>,
#   `Prop_American Indian` <dbl>, `Prop_Native Hawaiian` <dbl>,
#   Prop_Multiracial <dbl>,
#   `Prop_Distinct Recipients with Medicare Advantage Payment Source` <dbl>, ...
```

```
# Note: Pancreases are almost exclusively harvested from deceased donors, so excluding them
```

```
Deceased_v_Living_Kidney_Recipients <- Deceased_v_Living_Organ_Recipients |>
  filter(`Organ Transplanted` != "Liver") |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male:`Prop_Distinct Recipients with Otl

print(Deceased_v_Living_Kidney_Recipients)
```

```
# A tibble: 12 x 24
```

	`Transplant Year`	`Donor Type`	`Organ Transplanted`	Prop_Male	Prop_Female
	<dbl>	<chr>	<chr>	<dbl>	<dbl>
1	2019	Deceased Donor	Kidney	0.601	0.399

```

2          2020 Deceased Donor Kidney          0.610          0.390
3          2021 Deceased Donor Kidney          0.605          0.395
4          2022 Deceased Donor Kidney          0.607          0.393
5          2023 Deceased Donor Kidney          0.599          0.401
6          2024 Deceased Donor Kidney          0.594          0.406
7          2019 Living Donor Kidney            0.629          0.371
8          2020 Living Donor Kidney            0.631          0.369
9          2021 Living Donor Kidney            0.627          0.373
10         2022 Living Donor Kidney            0.620          0.380
11         2023 Living Donor Kidney            0.628          0.372
12         2024 Living Donor Kidney            0.640          0.360
# i 19 more variables: `Prop_Distinct Recipients with Age Not Reported` <dbl>,
#   Prop_Pediatric <dbl>, `Prop_Age 18-30` <dbl>, `Prop_Age 31-40` <dbl>,
#   `Prop_Age 41-50` <dbl>, `Prop_Age 51-60` <dbl>, `Prop_Age 61+` <dbl>,
#   Prop_White <dbl>, Prop_Black <dbl>, Prop_Hispanic <dbl>, Prop_Asian <dbl>,
#   `Prop_American Indian` <dbl>, `Prop_Native Hawaiian` <dbl>,
#   Prop_Multiracial <dbl>,
#   `Prop_Distinct Recipients with Medicare Advantage Payment Source` <dbl>, ...

```

## Exploratory Data Analysis

### Disease Mortality Burden

#### Cardiovascular Disease Mortality Burden

```
print(Cardiovascular_Disease_Mortality_Burden_Sex)
```

```

# A tibble: 2 x 24
  Sex      `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004` `2005`
  <chr>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Male    0.00350 0.00339 0.00331 0.0032  0.00308 0.00303 0.00292 0.00274 0.00268
2 Female  0.00225 0.00221 0.00218 0.00211 0.00205 0.00200 0.00194 0.00182 0.00178
# i 14 more variables: `2006` <dbl>, `2007` <dbl>, `2008` <dbl>, `2009` <dbl>,
#   `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>, `2014` <dbl>,
#   `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>, `2019` <dbl>

```

```

Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data <- Cardiovascular_Disease_Mortality_Bu
  select(Sex, `2010`:`2019`) |>
  pivot_longer(cols = `2010`:`2019`,

```

```

      names_to = "Year",
      values_to = "Prevalence") |>
mutate(
  Prevalence = as.numeric(Prevalence),
  Year = Year
)

print(Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data)

```

```

# A tibble: 20 x 3
  Sex    Year Prevalence
  <chr> <chr>    <dbl>
1 Male  2010    0.00225
2 Male  2011    0.00218
3 Male  2012    0.00215
4 Male  2013    0.00215
5 Male  2014    0.00211
6 Male  2015    0.00212
7 Male  2016    0.00209
8 Male  2017    0.00209
9 Male  2018    0.00208
10 Male 2019    0.00205
11 Female 2010    0.00143
12 Female 2011    0.00139
13 Female 2012    0.00136
14 Female 2013    0.00134
15 Female 2014    0.00132
16 Female 2015    0.00134
17 Female 2016    0.00130
18 Female 2017    0.00130
19 Female 2018    0.00128
20 Female 2019    0.00126

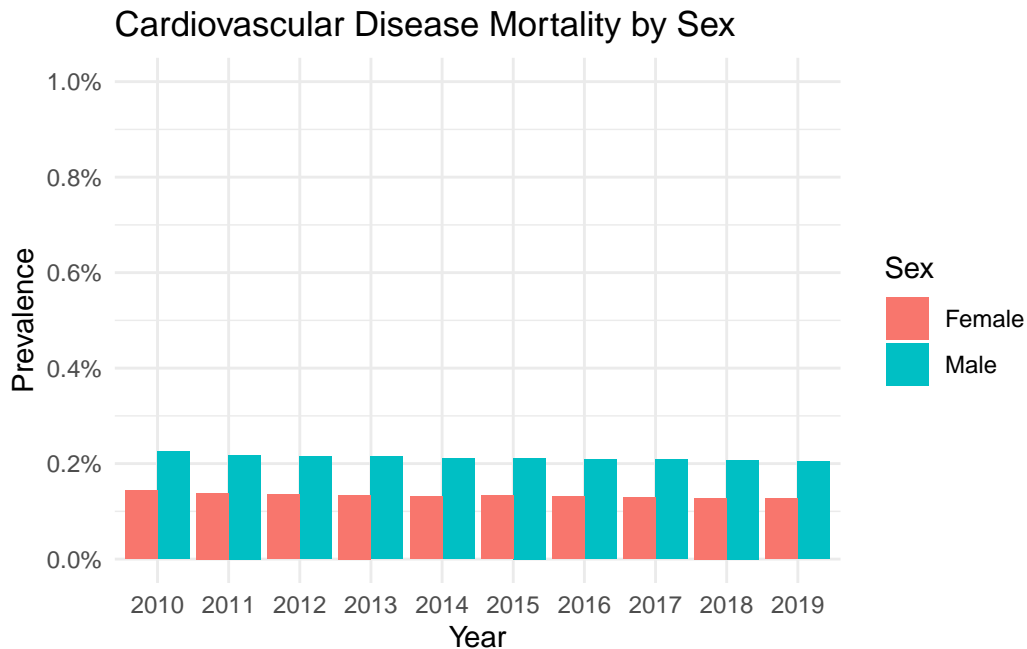
```

```

ggplot(Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data, aes(x = Year, y = Prevalence,
  geom_col(position = "dodge") +
scale_y_continuous(
  limits = c(0, 0.01),
  breaks = seq(0, 0.01, by = 0.002),
  labels = scales::percent_format(accuracy = 0.1)
) +
  labs(title = "Cardiovascular Disease Mortality by Sex",

```

```
y = "Prevalence",
x = "Year") +
theme_minimal()
```



```
print(Cardiovascular_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Race      `1997`  `1998`  `1999`  `2000`  `2001`  `2002`  `2003`  `2004`
  <chr>      <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1 White only 0.00276 0.00269 0.00264 0.00256 0.00247 0.00242 0.00234 0.00220
2 Black or Af~ NA      NA      0.00337 0.00328 0.00323 0.00317 0.00310 0.00291
3 Asian or Pa~ NA      NA      0.00156 0.00146 0.00140 0.00139 0.00132 0.00123
4 Hispanic or~ 0.00206 0.00203 0.00206 0.00196 0.00194 0.00189 0.00182 0.00169
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>
```

```
Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data <- Cardiovascular_Disease_Mortality_Burden_Race
select(Race, `2010`:`2019`) |>
pivot_longer(cols = `2010`:`2019`,
```

```

      names_to = "Year",
      values_to = "Prevalence") |>
mutate(
  Prevalence = as.numeric(Prevalence),
  Year = Year
)

print(Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data)

```

```

# A tibble: 40 x 3
  Race      Year Prevalence
  <chr>    <chr>    <dbl>
1 White only 2010      0.00180
2 White only 2011      0.00176
3 White only 2012      0.00172
4 White only 2013      0.00172
5 White only 2014      0.00170
6 White only 2015      0.00172
7 White only 2016      0.00169
8 White only 2017      0.00169
9 White only 2018      0.00168
10 White only 2019      0.00168
# i 30 more rows

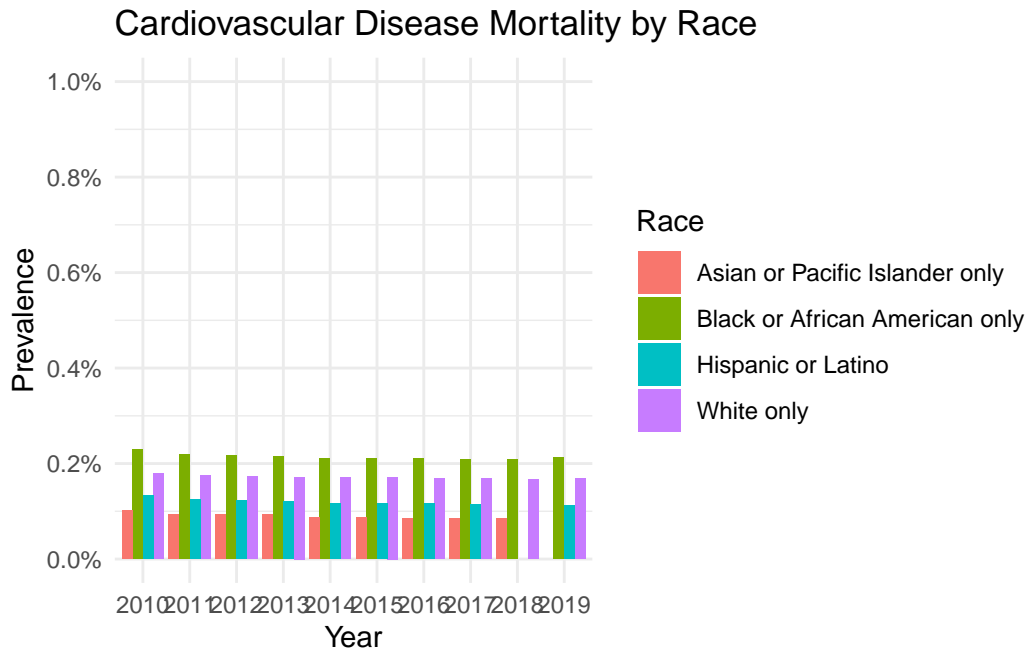
```

```

ggplot(Cardiovascular_Disease_Mortality_Burden_Sex_Plot_Data, aes(x = Year, y = Prevalence, )) +
  geom_col(position = "dodge") +
scale_y_continuous(
  limits = c(0, 0.01),
  breaks = seq(0, 0.01, by = 0.002),
  labels = scales::percent_format(accuracy = 0.1)
) +
  labs(title = "Cardiovascular Disease Mortality by Race",
       y = "Prevalence",
       x = "Year") +
  theme_minimal()

```





### Liver Disease Mortality Burden

```
print(Liver_Disease_Mortality_Burden_Sex)
```

```
# A tibble: 2 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 Male          0.000134 1.32e-4 1.35e-4 1.34e-4 1.32e-4 1.29e-4 1.3e-4 1.24e-4
2 Female        0.000061 6 e-5 6.1 e-5 6.20e-5 6.30e-5 6.30e-5 6 e-5 5.90e-5
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
# `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
# `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
# `2019` <dbl>
```

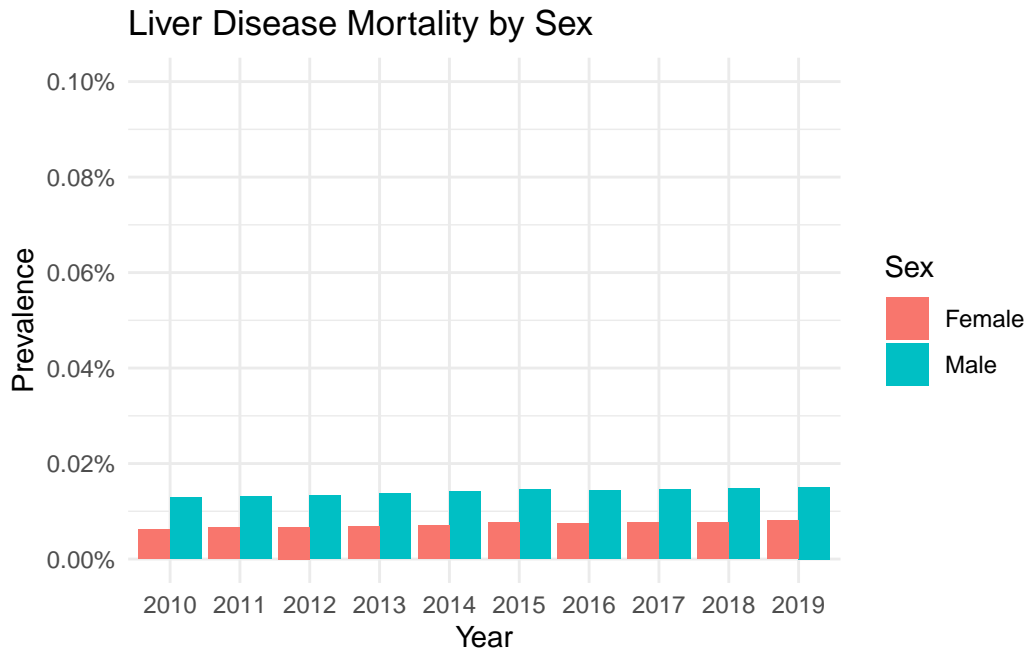
```
Liver_Disease_Mortality_Burden_Sex_Plot_Data <- Liver_Disease_Mortality_Burden_Sex |>
  select(Characteristic, `2010`:`2019`) |>
  rename(Sex = Characteristic) |>
  pivot_longer(cols = `2010`:`2019`,
               names_to = "Year",
               values_to = "Prevalence") |>
```

```
mutate(
  Prevalence = as.numeric(Prevalence),
  Year = Year
)

print(Liver_Disease_Mortality_Burden_Sex_Plot_Data)
```

```
# A tibble: 20 x 3
  Sex      Year Prevalence
  <chr>   <chr>     <dbl>
1 Male   2010     0.000129
2 Male   2011     0.000131
3 Male   2012     0.000134
4 Male   2013     0.000138
5 Male   2014     0.000141
6 Male   2015     0.000145
7 Male   2016     0.000143
8 Male   2017     0.000145
9 Male   2018     0.000147
10 Male  2019     0.000151
11 Female 2010     0.000062
12 Female 2011     0.000066
13 Female 2012     0.000067
14 Female 2013     0.000068
15 Female 2014     0.000071
16 Female 2015     0.000076
17 Female 2016     0.000075
18 Female 2017     0.000076
19 Female 2018     0.000077
20 Female 2019     0.00008
```

```
ggplot(Liver_Disease_Mortality_Burden_Sex_Plot_Data, aes(x = Year, y = Prevalence, fill = Sex)) +
  geom_col(position = "dodge") +
  scale_y_continuous(
    limits = c(0, 0.001),
    breaks = seq(0, 0.001, by = 0.0002),
    labels = scales::percent_format(accuracy = 0.01)
  ) +
  labs(title = "Liver Disease Mortality by Sex",
       y = "Prevalence",
       x = "Year") +
  theme_minimal()
```



```
print(Liver_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Characteristic      `1997`      `1998`      `1999`      `2000`      `2001`      `2002`      `2003`
  <chr>              <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
1 White only        8.80e-5    8.70e-5    9.0e-5     9.0e-5     9.0e-5     9.0e-5     9.0e-5
2 Black or African Am~ NA          NA          1.02e-4    9.60e-5    9.40e-5    8.5e-5     8.40e-5
3 Asian or Pacific Is~ NA          NA          3.7e-5     3.5e-5     3.5e-5     3.20e-5    3.0e-5
4 Hispanic or Latino 1.65e-4    1.61e-4    1.61e-4    1.65e-4    1.59e-4    1.57e-4    1.49e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>
```

```
Liver_Disease_Mortality_Burden_Race_Plot_Data <- Liver_Disease_Mortality_Burden_Race |>
  select(Characteristic, `2010`:`2019`) |>
  rename(Race = Characteristic) |>
  pivot_longer(cols = `2010`:`2019`,
               names_to = "Year",
               values_to = "Prevalence") |>
  mutate(
    Prevalence = as.numeric(Prevalence),
```

```

    Year = Year
  )

print(Liver_Disease_Mortality_Burden_Race_Plot_Data)

```

```

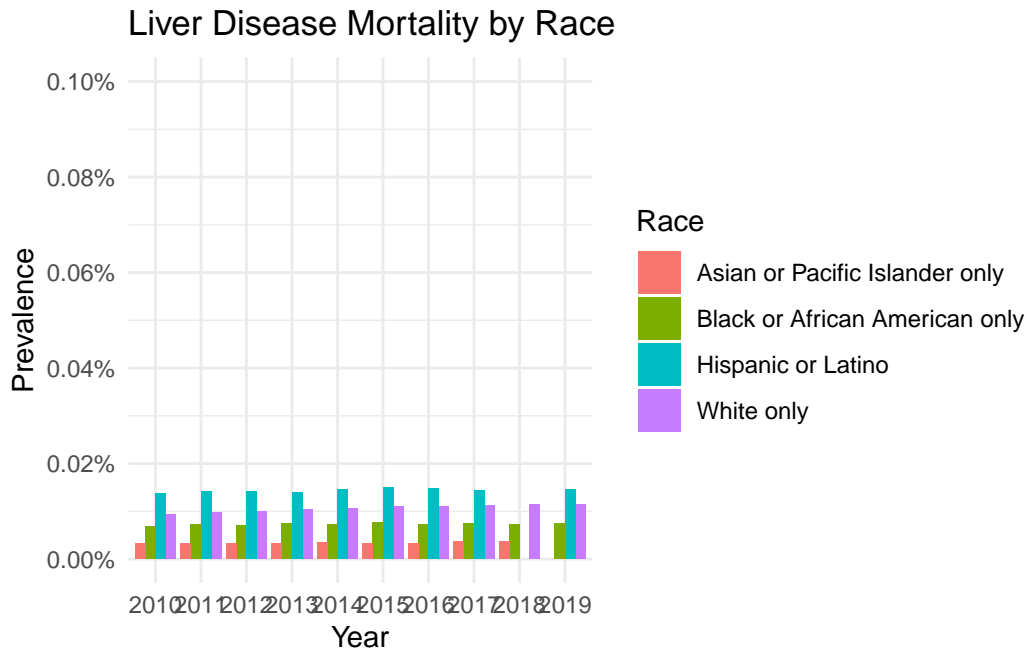
# A tibble: 40 x 3
  Race      Year Prevalence
  <chr>    <chr>     <dbl>
1 White only 2010    0.000094
2 White only 2011    0.000097
3 White only 2012    0.0001
4 White only 2013    0.000103
5 White only 2014    0.000106
6 White only 2015    0.000111
7 White only 2016    0.00011
8 White only 2017    0.000113
9 White only 2018    0.000114
10 White only 2019    0.000115
# i 30 more rows

```

```

ggplot(Liver_Disease_Mortality_Burden_Race_Plot_Data, aes(x = Year, y = Prevalence, fill = Race)) +
  geom_col(position = "dodge") +
  scale_y_continuous(
    limits = c(0, 0.001),
    breaks = seq(0, 0.001, by = 0.0002),
    labels = scales::percent_format(accuracy = 0.01)
  ) +
  labs(title = "Liver Disease Mortality by Race",
       y = "Prevalence",
       x = "Year") +
  theme_minimal()

```



## Kidney Disease Mortality Burden

```
print(Kidney_Disease_Mortality_Burden_Sex)
```

```
# A tibble: 2 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 Male          1.25e-4 1.26e-4 1.65e-4 1.69e-4 1.76e-4 1.8 e-4 1.82e-4 1.78e-4
2 Female        8.10e-5 8.2 e-5 1.11e-4 1.15e-4 1.21e-4 1.23e-4 1.25e-4 1.25e-4
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>
```

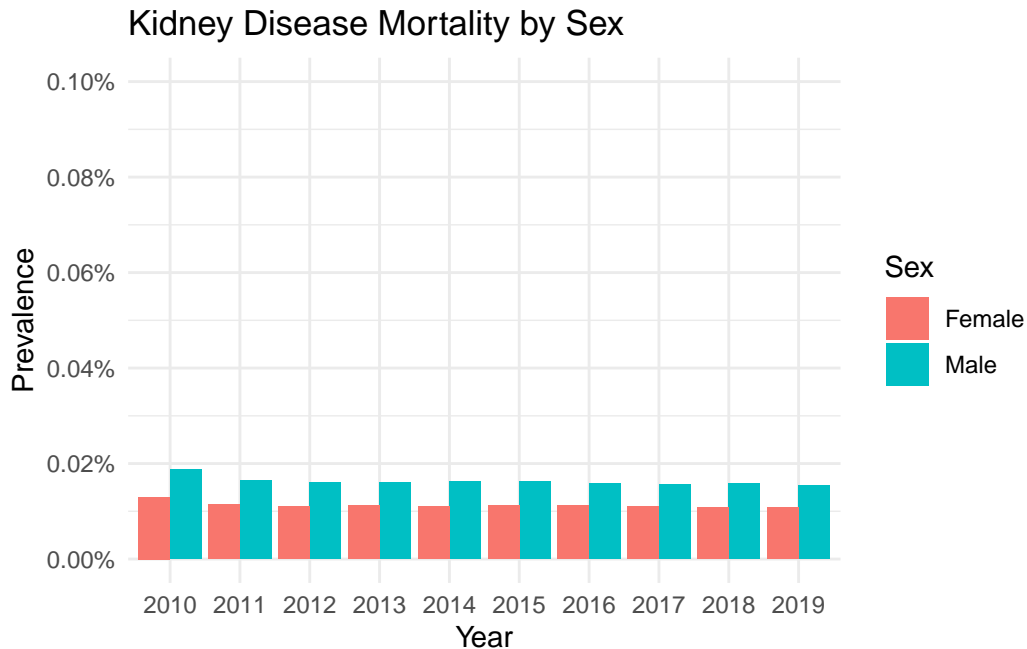
```
Kidney_Disease_Mortality_Burden_Sex_Plot_Data <- Kidney_Disease_Mortality_Burden_Sex |>
  select(Characteristic, `2010`:`2019`) |>
  rename(Sex = Characteristic) |>
  pivot_longer(cols = `2010`:`2019`,
               names_to = "Year",
               values_to = "Prevalence") |>
```

```
mutate(
  Prevalence = as.numeric(Prevalence),
  Year = Year
)

print(Kidney_Disease_Mortality_Burden_Sex_Plot_Data)
```

```
# A tibble: 20 x 3
  Sex      Year Prevalence
  <chr>   <chr>     <dbl>
1 Male   2010      0.000187
2 Male   2011      0.000165
3 Male   2012      0.00016
4 Male   2013      0.000161
5 Male   2014      0.000162
6 Male   2015      0.000163
7 Male   2016      0.000159
8 Male   2017      0.000157
9 Male   2018      0.000158
10 Male  2019      0.000154
11 Female 2010      0.00013
12 Female 2011      0.000114
13 Female 2012      0.000111
14 Female 2013      0.000113
15 Female 2014      0.000111
16 Female 2015      0.000113
17 Female 2016      0.000112
18 Female 2017      0.000111
19 Female 2018      0.000108
20 Female 2019      0.000107
```

```
ggplot(Kidney_Disease_Mortality_Burden_Sex_Plot_Data, aes(x = Year, y = Prevalence, fill = Sex)) +
  geom_col(position = "dodge") +
  scale_y_continuous(
    limits = c(0, 0.001),
    breaks = seq(0, 0.001, by = 0.0002),
    labels = scales::percent_format(accuracy = 0.01)
  ) +
  labs(title = "Kidney Disease Mortality by Sex",
       y = "Prevalence",
       x = "Year") +
  theme_minimal()
```



```
print(Kidney_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Characteristic      `1997`      `1998`      `1999`      `2000`      `2001`      `2002`      `2003`
  <chr>              <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
1 White only        8.80e-5    9.0e-5    1.15e-4    1.2e-4    1.25e-4    1.29e-4    1.3e-4
2 Black or African Am~ NA          NA          2.88e-4    2.91e-4    3.01e-4    3.05e-4    3.14e-4
3 Asian or Pacific Is~ NA          NA          9.8e-5     8.40e-5    9.1e-5     8.90e-5    8.10e-5
4 Hispanic or Latino 7.4e-5     7.70e-5    1.2e-4     1.18e-4    1.25e-4    1.2e-4     1.31e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>
```

```
Kidney_Disease_Mortality_Burden_Race_Plot_Data <- Kidney_Disease_Mortality_Burden_Race |>
  select(Characteristic, `2010`:`2019`) |>
  rename(Race = Characteristic) |>
  pivot_longer(cols = `2010`:`2019`,
               names_to = "Year",
               values_to = "Prevalence") |>
  mutate(
    Prevalence = as.numeric(Prevalence),
```

```

    Year = Year
  )

print(Kidney_Disease_Mortality_Burden_Race_Plot_Data)

```

```

# A tibble: 40 x 3
  Race      Year Prevalence
  <chr>    <chr>    <dbl>
1 White only 2010    0.000138
2 White only 2011    0.000122
3 White only 2012    0.000119
4 White only 2013    0.000121
5 White only 2014    0.000121
6 White only 2015    0.000122
7 White only 2016    0.000119
8 White only 2017    0.000117
9 White only 2018    0.000116
10 White only 2019    0.000116
# i 30 more rows

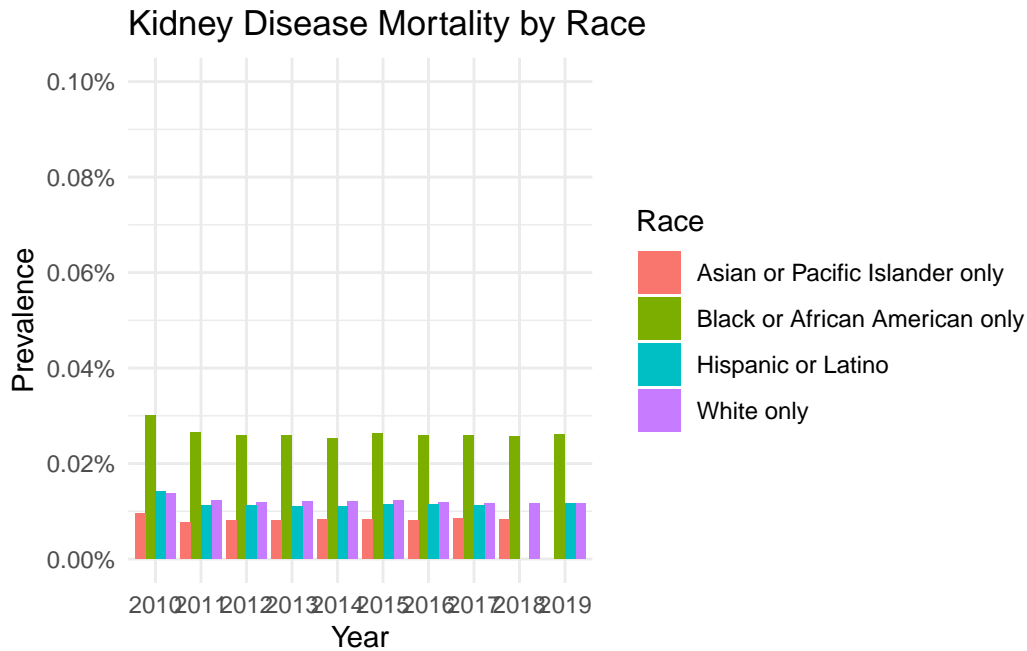
```

```

ggplot(Kidney_Disease_Mortality_Burden_Race_Plot_Data, aes(x = Year, y = Prevalence, fill = Race)) +
  geom_col(position = "dodge") +
  scale_y_continuous(
    limits = c(0, 0.001),
    breaks = seq(0, 0.001, by = 0.0002),
    labels = scales::percent_format(accuracy = 0.01)
  ) +
  labs(title = "Kidney Disease Mortality by Race",
       y = "Prevalence",
       x = "Year") +
  theme_minimal()

```



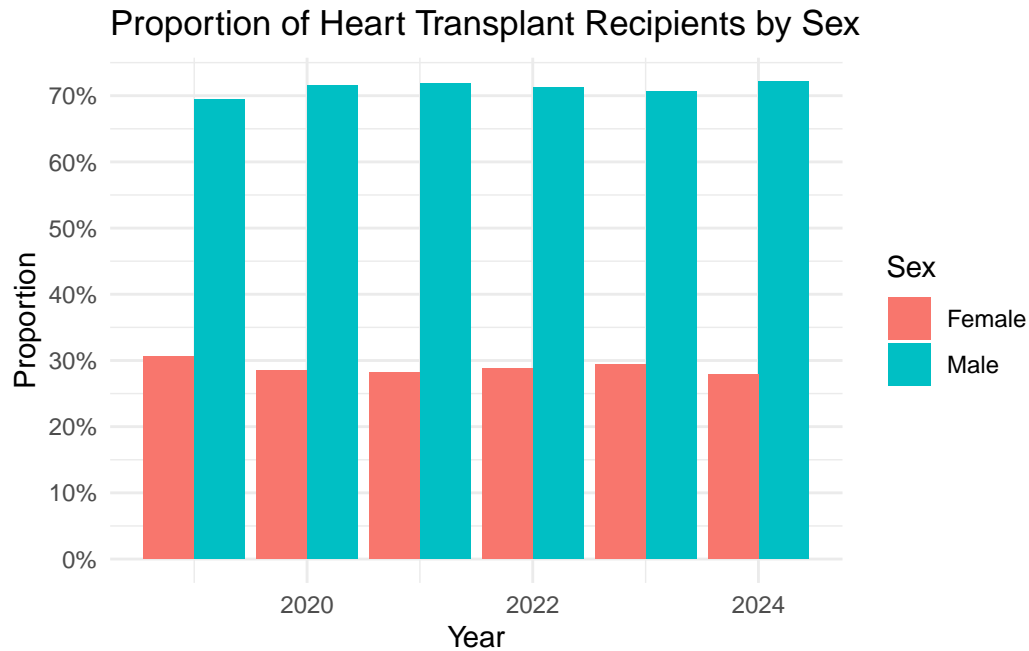


## Organ Allocation

### Heart Allocation

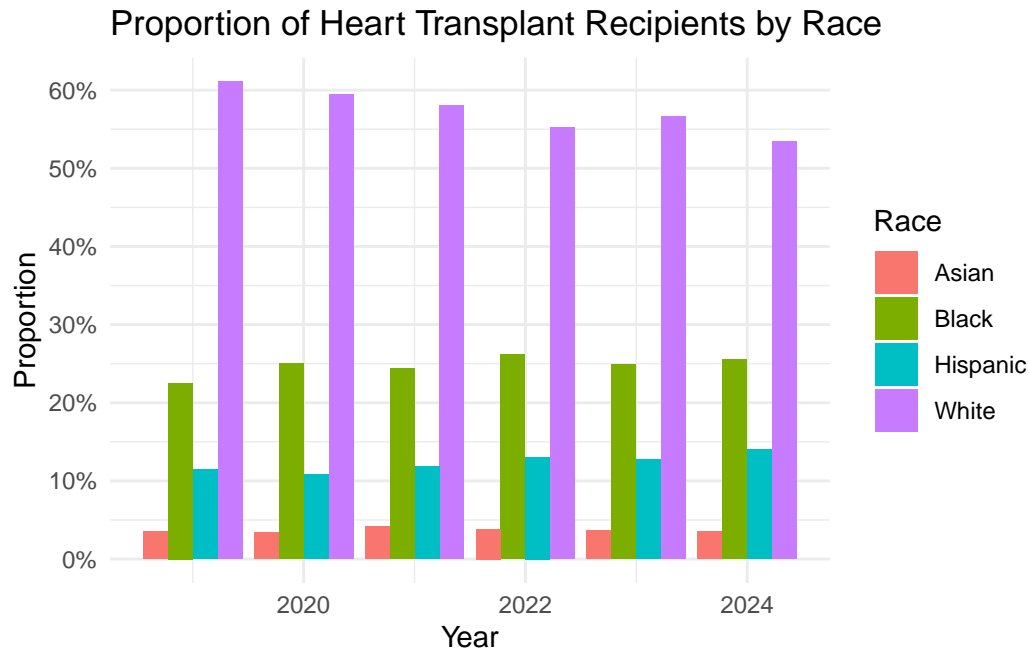
```
Heart_Plot_Sex_Data <- Heart_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male, Prop_Female) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Sex",
               values_to = "Proportion") |>
  mutate(Sex = str_remove(Sex, "Prop_"))

ggplot(Heart_Plot_Sex_Data, aes(x = `Transplant Year`, y = Proportion, fill = Sex)) +
  geom_col(position = "dodge") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Heart Transplant Recipients by Sex",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```



```
Heart_Plot_Race_Data <- Heart_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_White:Prop_Multiracial) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Race",
               values_to = "Proportion") |>
  mutate(Race = str_remove(Race, "Prop_")) |>
  filter(!Race %in% c("Multiracial", "Native Hawaiian", "American Indian"))

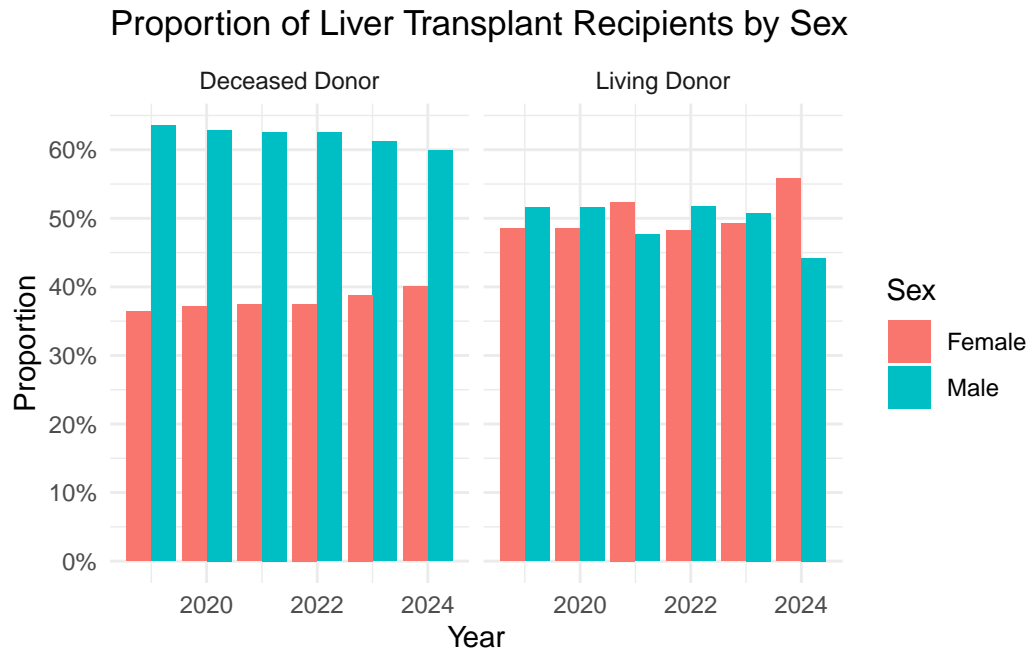
ggplot(Heart_Plot_Race_Data, aes(x = `Transplant Year`, y = Proportion, fill = Race)) +
  geom_col(position = "dodge") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Heart Transplant Recipients by Race",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```



## Liver Allocation

```
Liver_Plot_Sex_Data <- Deceased_v_Living_Liver_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male, Prop_Female) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Sex",
               values_to = "Proportion") |>
  mutate(Sex = str_remove(Sex, "Prop_"))

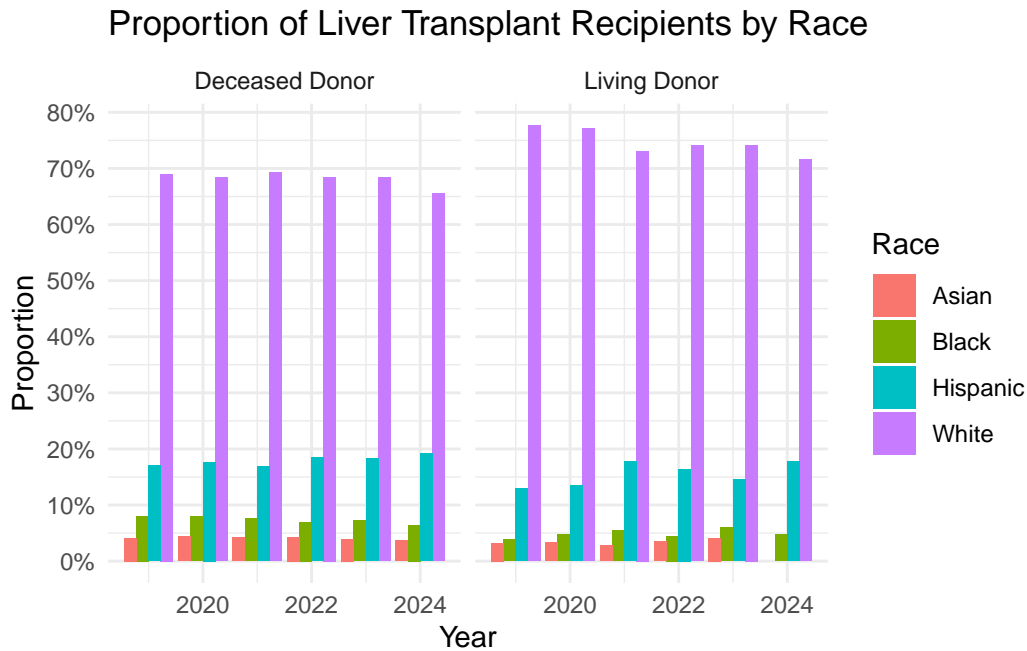
ggplot(Liver_Plot_Sex_Data, aes(x = `Transplant Year`, y = Proportion, fill = Sex)) +
  geom_col(position = "dodge") +
  facet_wrap(~ `Donor Type`) +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Liver Transplant Recipients by Sex",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```



# It appear that males get deceased donor kidneys more often than females

```
Liver_Plot_Race_Data <- Deceased_v_Living_Liver_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_White:Prop_Multiracial) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Race",
               values_to = "Proportion") |>
  mutate(Race = str_remove(Race, "Prop_")) |>
  filter(!Race %in% c("Multiracial", "Native Hawaiian", "American Indian"))

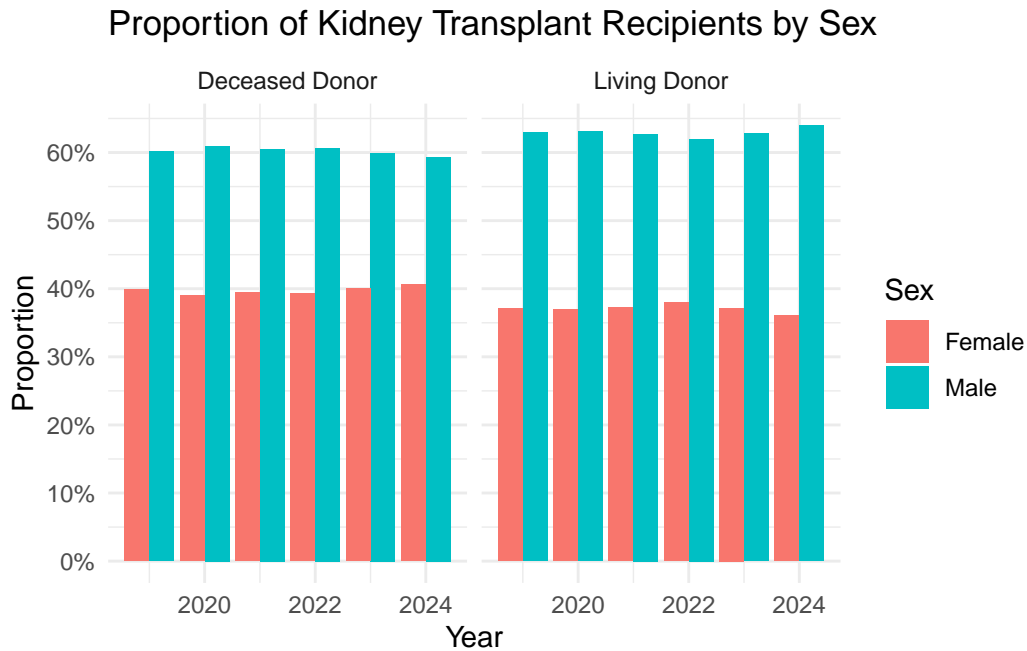
ggplot(Liver_Plot_Race_Data, aes(x = `Transplant Year`, y = Proportion, fill = Race)) +
  geom_col(position = "dodge") +
  facet_wrap(~ `Donor Type`) +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Liver Transplant Recipients by Race",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```



## Kidney Allocation

```
Kidney_Plot_Sex_Data <- Deceased_v_Living_Kidney_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_Male, Prop_Female) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Sex",
               values_to = "Proportion") |>
  mutate(Sex = str_remove(Sex, "Prop_"))

ggplot(Kidney_Plot_Sex_Data, aes(x = `Transplant Year`, y = Proportion, fill = Sex)) +
  geom_col(position = "dodge") +
  facet_wrap(~ `Donor Type`) +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Kidney Transplant Recipients by Sex",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```

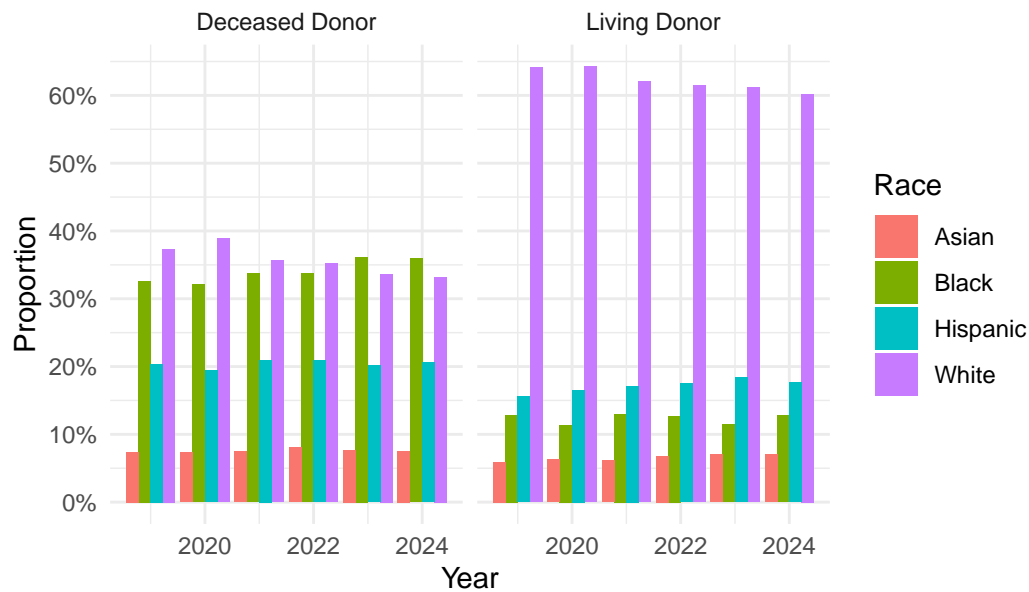


# It appear that males get deceased donor kidneys more often than females

```
Kidney_Plot_Race_Data <- Deceased_v_Living_Kidney_Recipients |>
  select(`Transplant Year`:`Organ Transplanted`, Prop_White:Prop_Multiracial) |>
  pivot_longer(cols = starts_with("Prop_"),
               names_to = "Race",
               values_to = "Proportion") |>
  mutate(Race = str_remove(Race, "Prop_")) |>
  filter(!Race %in% c("Multiracial", "Native Hawaiian", "American Indian"))

ggplot(Kidney_Plot_Race_Data, aes(x = `Transplant Year`, y = Proportion, fill = Race)) +
  geom_col(position = "dodge") +
  facet_wrap(~ `Donor Type`) +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1), breaks = seq(0, 1, by = 0.1)) +
  labs(title = "Proportion of Kidney Transplant Recipients by Race",
       y = "Proportion",
       x = "Year") +
  theme_minimal()
```

## Proportion of Kidney Transplant Recipients by Race



## Testing

Are there sex differences in disease mortality by organ system?

```
print(Cardiovascular_Disease_Mortality_Burden_Sex)
```

```
# A tibble: 2 x 24
  Sex    `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004` `2005`
  <chr>   <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Male   0.00350 0.00339 0.00331 0.0032  0.00308 0.00303 0.00292 0.00274 0.00268
2 Female 0.00225 0.00221 0.00218 0.00211 0.00205 0.00200 0.00194 0.00182 0.00178
# i 14 more variables: `2006` <dbl>, `2007` <dbl>, `2008` <dbl>, `2009` <dbl>,
#   `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>, `2014` <dbl>,
#   `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>, `2019` <dbl>
```

```
# Pivoting to long
Cardiovascular_Disease_Mortality_Burden_Sex_Test <- Cardiovascular_Disease_Mortality_Burden_Sex
pivot_longer(
  cols = `1997`:`2019`,
```

```

    names_to = "Year",
    values_to = "Prevalence"
  )

print(Cardiovascular_Disease_Mortality_Burden_Sex_Test)

```

```

# A tibble: 46 x 3
  Sex    Year Prevalence
  <chr> <chr>     <dbl>
1 Male  1997     0.00350
2 Male  1998     0.00339
3 Male  1999     0.00331
4 Male  2000     0.0032
5 Male  2001     0.00308
6 Male  2002     0.00303
7 Male  2003     0.00292
8 Male  2004     0.00274
9 Male  2005     0.00268
10 Male 2006     0.00255
# i 36 more rows

```

```

# Hypotheses:
# H0: Mean cardiovascular disease mortality is the same for males and females.
# H1: Mean cardiovascular disease mortality differs between males and females.

```

```

ANOVA_Cardiovascular_Disease_Mortality_Burden_Sex <- aov(as.numeric(Prevalence) ~ Sex, data = data)

summary(ANOVA_Cardiovascular_Disease_Mortality_Burden_Sex)

```

```

          Df    Sum Sq Mean Sq F value    Pr(>F)
Sex          1 9.450e-06 9.45e-06    52.6 4.88e-09 ***
Residuals    44 7.905e-06 1.80e-07
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# Conclusion: Cardiovascular disease mortality is significantly higher among males than females.

```

```

print(Liver_Disease_Mortality_Burden_Sex)

```

```

# A tibble: 2 x 24

```



```

Characteristic  `1997`  `1998`  `1999`  `2000`  `2001`  `2002`  `2003`  `2004`
<chr>           <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1 Male          0.000134 1.32e-4 1.35e-4 1.34e-4 1.32e-4 1.29e-4 1.3e-4 1.24e-4
2 Female        0.000061 6.1e-5 6.1e-5 6.20e-5 6.30e-5 6.30e-5 6.1e-5 5.90e-5
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>

```

```

# Pivoting to long
Liver_Disease_Mortality_Burden_Sex_Test <- Liver_Disease_Mortality_Burden_Sex |>
  pivot_longer(
    cols = `1997`:`2019`,
    names_to = "Year",
    values_to = "Prevalence"
  ) |>
  rename(Sex = Characteristic)

print(Liver_Disease_Mortality_Burden_Sex_Test)

```

```

# A tibble: 46 x 3
  Sex   Year Prevalence
<chr> <chr>   <dbl>
1 Male 1997    0.000134
2 Male 1998    0.000132
3 Male 1999    0.000135
4 Male 2000    0.000134
5 Male 2001    0.000132
6 Male 2002    0.000129
7 Male 2003    0.00013
8 Male 2004    0.000124
9 Male 2005    0.000124
10 Male 2006    0.000121
# i 36 more rows

```

```

# Hypotheses:
# H0: Mean liver disease mortality is the same for males and females.
# H1: Mean liver disease mortality differs between males and females.

ANOVA_Liver_Disease_Mortality_Burden_Sex <- aov(as.numeric(Prevalence) ~ Sex, data = Liver_D
summary(ANOVA_Liver_Disease_Mortality_Burden_Sex)

```

```

      Df    Sum Sq   Mean Sq F value Pr(>F)
Sex      1 5.393e-08 5.393e-08   928.9 <2e-16 ***
Residuals 44 2.550e-09 6.000e-11
---

```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Conclusion: Liver disease mortality is significantly higher among males than females.
```

```
print(Kidney_Disease_Mortality_Burden_Sex)
```

```

# A tibble: 2 x 24
  Characteristic `1997` `1998` `1999` `2000` `2001` `2002` `2003` `2004`
  <chr>          <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Male          1.25e-4 1.26e-4 1.65e-4 1.69e-4 1.76e-4 1.8 e-4 1.82e-4 1.78e-4
2 Female          8.10e-5 8.2 e-5 1.11e-4 1.15e-4 1.21e-4 1.23e-4 1.25e-4 1.25e-4
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>

```

```

# Pivoting to long
Kidney_Disease_Mortality_Burden_Sex_Test <- Kidney_Disease_Mortality_Burden_Sex |>
  pivot_longer(
    cols = `1997`:`2019`,
    names_to = "Year",
    values_to = "Prevalence"
  ) |>
  rename(Sex = Characteristic)

print(Kidney_Disease_Mortality_Burden_Sex_Test)

```

```

# A tibble: 46 x 3
  Sex   Year Prevalence
  <chr> <chr>    <dbl>
1 Male 1997    0.000125
2 Male 1998    0.000126
3 Male 1999    0.000165
4 Male 2000    0.000169
5 Male 2001    0.000176
6 Male 2002    0.00018
7 Male 2003    0.000182

```

```

8 Male 2004 0.000178
9 Male 2005 0.000181
10 Male 2006 0.000183
# i 36 more rows

```

```

# Hypotheses:
# H0: Mean kidney disease mortality is the same for males and females.
# H1: Mean kidney disease mortality differs between males and females.

ANOVA_Kidney_Disease_Mortality_Burden_Sex <- aov(as.numeric(Prevalence) ~ Sex, data = Kidney)

summary(ANOVA_Kidney_Disease_Mortality_Burden_Sex)

```

```

              Df      Sum Sq   Mean Sq F value    Pr(>F)
Sex              1 3.079e-08 3.079e-08   133.6 6.36e-15 ***
Residuals       44 1.014e-08 2.300e-10
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# Conclusion: Kidney disease mortality is significantly higher among males than females.

```

Conclusions: Males die from cardiovascular, liver, and kidney disease at higher rates than females.

## Are there racial differences in disease mortality by organ system?

### Cardiovascular

```

print(Cardiovascular_Disease_Mortality_Burden_Race)

# A tibble: 4 x 24
  Race      `1997`  `1998`  `1999`  `2000`  `2001`  `2002`  `2003`  `2004`
<chr>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
1 White only 0.00276 0.00269 0.00264 0.00256 0.00247 0.00242 0.00234 0.00220
2 Black or Af~ NA      NA      0.00337 0.00328 0.00323 0.00317 0.00310 0.00291
3 Asian or Pa~ NA      NA      0.00156 0.00146 0.00140 0.00139 0.00132 0.00123
4 Hispanic or~ 0.00206 0.00203 0.00206 0.00196 0.00194 0.00189 0.00182 0.00169
# i 15 more variables: `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,

```

```
# `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
# `2019` <dbl>
```

```
# Pivoting to long
Cardiovascular_Disease_Mortality_Burden_Race_Test <- Cardiovascular_Disease_Mortality_Burden
  pivot_longer(
    cols = `1997`:`2019`,
    names_to = "Year",
    values_to = "Prevalence"
  )

print(Cardiovascular_Disease_Mortality_Burden_Race_Test)
```

```
# A tibble: 92 x 3
  Race      Year Prevalence
  <chr>    <chr>    <dbl>
1 White only 1997      0.00276
2 White only 1998      0.00269
3 White only 1999      0.00264
4 White only 2000      0.00256
5 White only 2001      0.00247
6 White only 2002      0.00242
7 White only 2003      0.00234
8 White only 2004      0.00220
9 White only 2005      0.00215
10 White only 2006      0.00204
# i 82 more rows
```

```
# Hypotheses:
# H0: Mean cardiovascular disease mortality is the same across racial groups
# H1: Mean cardiovascular disease mortality differs between at least one pair of racial groups

ANOVA_Cardiovascular_Disease_Mortality_Burden_Race <- aov(as.numeric(Prevalence) ~ Race, data=
summary(ANOVA_Cardiovascular_Disease_Mortality_Burden_Race)
```

```
      Df    Sum Sq  Mean Sq F value Pr(>F)
Race    3 2.431e-05 8.103e-06   60.5 <2e-16 ***
Residuals 82 1.098e-05 1.340e-07
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
6 observations deleted due to missingness
```

```
# Conclusion: There are significant differences in cardiovascular disease mortality between a
```

```
Tukey_Cardiovascular_Mortality_Race <- TukeyHSD(ANOVA_Cardiovascular_Disease_Mortality_Burden
print(Tukey_Cardiovascular_Mortality_Race)
```

```
Tukey multiple comparisons of means
 95% family-wise confidence level
```

```
Fit: aov(formula = as.numeric(Prevalence) ~ Race, data = Cardiovascular_Disease_Mortality_Burden)
```

```
$Race
```

	diff
Black or African American only-Asian or Pacific Islander only	0.0014412571
Hispanic or Latino-Asian or Pacific Islander only	0.0004319000
White only-Asian or Pacific Islander only	0.0009475304
Hispanic or Latino-Black or African American only	-0.0010093571
White only-Black or African American only	-0.0004937267
White only-Hispanic or Latino	0.0005156304
	lwr
Black or African American only-Asian or Pacific Islander only	0.0011413973
Hispanic or Latino-Asian or Pacific Islander only	0.0001353832
White only-Asian or Pacific Islander only	0.0006540992
Hispanic or Latino-Black or African American only	-0.0013021526
White only-Black or African American only	-0.0007833969
White only-Hispanic or Latino	0.0002294222
	upr
Black or African American only-Asian or Pacific Islander only	0.0017411170
Hispanic or Latino-Asian or Pacific Islander only	0.0007284168
White only-Asian or Pacific Islander only	0.0012409617
Hispanic or Latino-Black or African American only	-0.0007165617
White only-Black or African American only	-0.0002040565
White only-Hispanic or Latino	0.0008018386
	p adj
Black or African American only-Asian or Pacific Islander only	0.0000000
Hispanic or Latino-Asian or Pacific Islander only	0.0014510
White only-Asian or Pacific Islander only	0.0000000
Hispanic or Latino-Black or African American only	0.0000000
White only-Black or African American only	0.0001442
White only-Hispanic or Latino	0.0000550

Conclusions: There are significant differences in cardiovascular disease mortality among racial

groups: - Asian or Pacific Islander people die of cardiovascular disease at significantly lower rates than their counterparts - Latine cardiovascular disease mortality is higher than that of Asian people, but lower than that of White and Black people - Black people experience significantly highest rates of cardiovascular disease mortality than their counterparts

## Liver

```
print(Liver_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Characteristic      `1997`      `1998`      `1999`      `2000`      `2001`      `2002`      `2003`
  <chr>              <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
1 White only        8.80e-5    8.70e-5    9.0e-5    9.0e-5    9.0e-5    9.0e-5    9.0e-5
2 Black or African Am~ NA          NA          1.02e-4    9.60e-5    9.40e-5    8.5e-5    8.40e-5
3 Asian or Pacific Is~ NA          NA          3.7e-5    3.5e-5    3.5e-5    3.20e-5    3.0e-5
4 Hispanic or Latino 1.65e-4    1.61e-4    1.61e-4    1.65e-4    1.59e-4    1.57e-4    1.49e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
#   `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
#   `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
#   `2018` <dbl>, `2019` <dbl>
```

```
# Pivoting to long
Liver_Disease_Mortality_Burden_Race_Test <- Liver_Disease_Mortality_Burden_Race |>
  pivot_longer(
    cols = `1997`:`2019`,
    names_to = "Year",
    values_to = "Prevalence"
  ) |>
  rename(Race = Characteristic)

print(Liver_Disease_Mortality_Burden_Race_Test)
```

```
# A tibble: 92 x 3
  Race      Year Prevalence
  <chr>    <chr>      <dbl>
1 White only 1997      0.000088
2 White only 1998      0.000087
3 White only 1999      0.00009
4 White only 2000      0.00009
5 White only 2001      0.00009
```

```

6 White only 2002      0.00009
7 White only 2003      0.00009
8 White only 2004      0.000087
9 White only 2005      0.000087
10 White only 2006     0.000086
# i 82 more rows

```

```

# Hypotheses:
# H0: Mean liver disease mortality is the same across racial groups
# H1: Mean liver disease mortality differs between at least one pair of racial groups

ANOVA_Liver_Disease_Mortality_Burden_Race <- aov(as.numeric(Prevalence) ~ Race, data = Liver_
summary(ANOVA_Liver_Disease_Mortality_Burden_Race)

```

```

          Df      Sum Sq   Mean Sq F value Pr(>F)
Race         3 1.403e-07 4.678e-08   644.8 <2e-16 ***
Residuals    82 5.950e-09 7.000e-11
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
6 observations deleted due to missingness

```

```

# Conclusion: There are significant differences in liver disease mortality between among at

```

```

Tukey_Liver_Mortality_Race <- TukeyHSD(ANOVA_Liver_Disease_Mortality_Burden_Race)
print(Tukey_Liver_Mortality_Race)

```

```

Tukey multiple comparisons of means
 95% family-wise confidence level

```

```

Fit: aov(formula = as.numeric(Prevalence) ~ Race, data = Liver_Disease_Mortality_Burden_Race)

```

```

$Race
                                diff
Black or African American only-Asian or Pacific Islander only 4.397143e-05
Hispanic or Latino-Asian or Pacific Islander only             1.138091e-04
White only-Asian or Pacific Islander only                     6.287826e-05
Hispanic or Latino-Black or African American only             6.983766e-05
White only-Black or African American only                     1.890683e-05
White only-Hispanic or Latino                                -5.093083e-05

```

	lwr
Black or African American only-Asian or Pacific Islander only	3.699234e-05
Hispanic or Latino-Asian or Pacific Islander only	1.069078e-04
White only-Asian or Pacific Islander only	5.604879e-05
Hispanic or Latino-Black or African American only	6.302299e-05
White only-Black or African American only	1.216490e-05
White only-Hispanic or Latino	-5.759218e-05
	upr
Black or African American only-Asian or Pacific Islander only	5.095052e-05
Hispanic or Latino-Asian or Pacific Islander only	1.207104e-04
White only-Asian or Pacific Islander only	6.970773e-05
Hispanic or Latino-Black or African American only	7.665233e-05
White only-Black or African American only	2.564876e-05
White only-Hispanic or Latino	-4.426948e-05
	p adj
Black or African American only-Asian or Pacific Islander only	0
Hispanic or Latino-Asian or Pacific Islander only	0
White only-Asian or Pacific Islander only	0
Hispanic or Latino-Black or African American only	0
White only-Black or African American only	0
White only-Hispanic or Latino	0

Conclusions: There are significant differences in liver disease mortality among racial groups:  
- Asian or Pacific Islander people have significantly lower liver disease mortality rates than all other racial groups  
- Latines have significantly higher liver disease mortality rates than all other racial groups  
- Black people have significantly higher liver disease mortality rates than Asians or Pacific Islanders, but lower than Latines and Whites

## Kidney

```
print(Kidney_Disease_Mortality_Burden_Race)
```

```
# A tibble: 4 x 24
  Characteristic    `1997`    `1998`    `1999`    `2000`    `2001`    `2002`    `2003`
  <chr>            <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
1 White only      8.80e-5  9.0e-5  1.15e-4  1.2e-4  1.25e-4  1.29e-4  1.3e-4
2 Black or African Am~ NA      NA      2.88e-4  2.91e-4  3.01e-4  3.05e-4  3.14e-4
3 Asian or Pacific Is~ NA      NA      9.8e-5  8.40e-5  9.1e-5  8.90e-5  8.10e-5
4 Hispanic or Latino  7.4e-5  7.70e-5  1.2e-4  1.18e-4  1.25e-4  1.2e-4  1.31e-4
# i 16 more variables: `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>,
```



```
# `2008` <dbl>, `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>,
# `2013` <dbl>, `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>,
# `2018` <dbl>, `2019` <dbl>
```

```
# Pivoting to long
Kidney_Disease_Mortality_Burden_Race_Test <- Kidney_Disease_Mortality_Burden_Race |>
  pivot_longer(
    cols = `1997`:`2019`,
    names_to = "Year",
    values_to = "Prevalence"
  ) |>
  rename(Race = Characteristic)

print(Kidney_Disease_Mortality_Burden_Race_Test)
```

```
# A tibble: 92 x 3
  Race      Year Prevalence
  <chr>    <chr>    <dbl>
1 White only 1997    0.000088
2 White only 1998    0.00009
3 White only 1999    0.000115
4 White only 2000    0.00012
5 White only 2001    0.000125
6 White only 2002    0.000129
7 White only 2003    0.00013
8 White only 2004    0.000129
9 White only 2005    0.000131
10 White only 2006    0.000132
# i 82 more rows
```

```
# Hypotheses:
# H0: Mean kidney disease mortality is the same across racial groups
# H1: Mean kidney disease mortality differs between at least one pair of racial groups

ANOVA_Kidney_Disease_Mortality_Burden_Race_Test <- aov(as.numeric(Prevalence) ~ Race, data =
summary(ANOVA_Kidney_Disease_Mortality_Burden_Race_Test)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Race	3	4.999e-07	1.666e-07	636.5	<2e-16 ***
Residuals	82	2.150e-08	2.600e-10		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
6 observations deleted due to missingness

# Conclusion: There are significant differences in kidney disease mortality between among at

```
Tukey_Kidney_Mortality_Race <- TukeyHSD(ANOVA_Kidney_Disease_Mortality_Burden_Race_Test)
print(Tukey_Kidney_Mortality_Race)
```

Tukey multiple comparisons of means  
95% family-wise confidence level

Fit: aov(formula = as.numeric(Prevalence) ~ Race, data = Kidney\_Disease\_Mortality\_Burden\_Race)

\$Race

	diff
Black or African American only-Asian or Pacific Islander only	1.977667e-04
Hispanic or Latino-Asian or Pacific Islander only	3.150909e-05
White only-Asian or Pacific Islander only	3.505652e-05
Hispanic or Latino-Black or African American only	-1.662576e-04
White only-Black or African American only	-1.627101e-04
White only-Hispanic or Latino	3.547431e-06
	lwr
Black or African American only-Asian or Pacific Islander only	1.845086e-04
Hispanic or Latino-Asian or Pacific Islander only	1.839884e-05
White only-Asian or Pacific Islander only	2.208269e-05
Hispanic or Latino-Black or African American only	-1.792033e-04
White only-Black or African American only	-1.755177e-04
White only-Hispanic or Latino	-9.107036e-06
	upr
Black or African American only-Asian or Pacific Islander only	2.110247e-04
Hispanic or Latino-Asian or Pacific Islander only	4.461935e-05
White only-Asian or Pacific Islander only	4.803035e-05
Hispanic or Latino-Black or African American only	-1.533119e-04
White only-Black or African American only	-1.499026e-04
White only-Hispanic or Latino	1.620190e-05
	p adj
Black or African American only-Asian or Pacific Islander only	0.0000000
Hispanic or Latino-Asian or Pacific Islander only	0.0000001
White only-Asian or Pacific Islander only	0.0000000
Hispanic or Latino-Black or African American only	0.0000000

White only-Black or African American only	0.0000000
White only-Hispanic or Latino	0.8826521

Conclusions: There are significant differences in kidney disease mortality between among racial groups: - Black people have significantly higher kidney disease mortality than all other racial groups - Asian individuals have significantly lower kidney disease mortality than all other racial groups - White and Latine groups have insignificantly differing kidney disease mortalities

## Do males receive organs in accordance with their disease mortality burdens?

```
Sex_Organ_Plots <- list(Heart_Plot_Sex_Data, Liver_Plot_Sex_Data, Kidney_Plot_Sex_Data)
Organ_Names <- c("Heart", "Liver", "Kidney")

# Hypotheses:
# H0: Males and females receive approximately the same proportion of donor Xs
# H1: Males and females do not receive approximately the same proportion of donor Xs

Organ_Recipient_Sex_ANOVA_Results <- map2(Sex_Organ_Plots, Organ_Names, # Iterates over two
      function(df, organ) {
        model <- aov(Proportion ~ Sex, data = df)
        cat("\n====", organ, "====\n") # Prints header
        print(summary(model))
        return(summary(model))
      }
    )
```

==== Heart ====

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Sex	1	0.5364	0.5364	5575	4.53e-15 ***
Residuals	10	0.0010	0.0001		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

==== Liver ====

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Sex	1	0.08168	0.08168	17.09	0.000435 ***
Residuals	22	0.10517	0.00478		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
==== Kidney ====
              Df Sum Sq Mean Sq F value Pr(>F)
Sex              1  0.3221   0.3221    1426 <2e-16 ***
Residuals       22  0.0050   0.0002
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
names(Organ_Recipient_Sex_ANOVA_Results) <- Organ_Names
# To look up results in this format: Organ_Recipient_Sex_ANOVA_Results$ORGAN
```

Conclusions: Males receive donor hearts, livers, and kidneys at higher rates than females. This is an indicator of equitable allocation in accordance with disease mortality burden.

## Do people of different races receive hearts, livers, and kidneys at different rates?

```
Race_Organ_Plots <- list(Heart_Plot_Race_Data, Liver_Plot_Race_Data, Kidney_Plot_Race_Data)

# Hypotheses:
# H0: Racial groups receive approximately the same proportion of donor organs
# H1: At least one racial group receives a different proportion of donor organs

Organ_Recipient_Race_ANOVA_Results <- map2(
  Race_Organ_Plots,
  Organ_Names,
  function(df, organ) {
    model <- aov(Proportion ~ Race, data = df)
    cat("\n====", organ, "====\n") # FIXED: use 'organ' not 'race'
    print(summary(model))
    return(summary(model))
  }
)
```

```
==== Heart ====
              Df Sum Sq Mean Sq F value Pr(>F)
Race              3  0.9947   0.3316    1219 <2e-16 ***
Residuals       20  0.0054   0.0003
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

==== Liver ====
      Df Sum Sq Mean Sq F value Pr(>F)
Race      3  3.590   1.1967    2197 <2e-16 ***
Residuals 43  0.023   0.0005
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
1 observation deleted due to missingness

==== Kidney ====
      Df Sum Sq Mean Sq F value    Pr(>F)
Race      3  1.124   0.3746    45.53 1.52e-13 ***
Residuals 44  0.362   0.0082
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
names(Organ_Recipient_Race_ANOVA_Results) <- Organ_Names
```

Conclusions: At least one racial group receives a different proportion of organs than all other racial groups for hearts, livers, and kidneys.

## Do people of different races receive equitable proportions of hearts, livers, and kidneys?

```

Organ_Recipient_Race_Tukey_Results <- map2(
  Race_Organ_Plots,
  Organ_Names,
  function(df, organ) {
    model <- aov(Proportion ~ Race, data = df)
    cat("\n==== Tukey HSD for", organ, "====\n")
    tukey_result <- TukeyHSD(model)
    print(tukey_result)
    return(tukey_result)
  }
)

```

```

==== Tukey HSD for Heart ====
Tukey multiple comparisons of means
95% family-wise confidence level

```

```
Fit: aov(formula = Proportion ~ Race, data = df)
```

```
$Race
```

	diff	lwr	upr	p adj
Black-Asian	0.21058497	0.18393809	0.23723186	0e+00
Hispanic-Asian	0.08654537	0.05989848	0.11319225	1e-07
White-Asian	0.53626218	0.50961530	0.56290907	0e+00
Hispanic-Black	-0.12403961	-0.15068649	-0.09739272	0e+00
White-Black	0.32567721	0.29903033	0.35232409	0e+00
White-Hispanic	0.44971682	0.42306993	0.47636370	0e+00

```
==== Tukey HSD for Liver ====
```

```
Tukey multiple comparisons of means  
95% family-wise confidence level
```

```
Fit: aov(formula = Proportion ~ Race, data = df)
```

```
$Race
```

	diff	lwr	upr	p adj
Black-Asian	0.02345158	-0.002583258	0.04948642	0.0908427
Hispanic-Asian	0.12939900	0.103364164	0.15543384	0.0000000
White-Asian	0.67634043	0.650305596	0.70237527	0.0000000
Hispanic-Black	0.10594742	0.080484850	0.13141000	0.0000000
White-Black	0.65288885	0.627426281	0.67835143	0.0000000
White-Hispanic	0.54694143	0.521478859	0.57240400	0.0000000

```
==== Tukey HSD for Kidney ====
```

```
Tukey multiple comparisons of means  
95% family-wise confidence level
```

```
Fit: aov(formula = Proportion ~ Race, data = df)
```

```
$Race
```

	diff	lwr	upr	p adj
Black-Asian	0.16144985	0.06258170	0.2603180	0.0004349
Hispanic-Asian	0.11723340	0.01836525	0.2161015	0.0143692
White-Asian	0.41892917	0.32006102	0.5177973	0.0000000
Hispanic-Black	-0.04421645	-0.14308459	0.0546517	0.6337654
White-Black	0.25747933	0.15861118	0.3563475	0.0000001
White-Hispanic	0.30169577	0.20282763	0.4005639	0.0000000

```
names(Organ_Recipient_Race_Tukey_Results) <- Organ_Names
```

Conclusions: General: - Whites receive significantly more hearts, livers, and kidneys than their counterparts - Asians and Pacific Islanders receive significantly fewer hearts and kidneys than their counterparts

Hearts:

- Latines receive significantly more hearts than Asians, but significantly fewer than Blacks

Livers:

- There is no statistically significant difference in livers received by Asians and Blacks
- Latines received significantly more livers than Asians and Pacific Islanders and Blacks

Kidneys:

- There is no statistically significant difference in kidneys received by Latines and Blacks