

DATA 606 Data Project Proposal

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Data Preparation

In this project, I have chosen to work on breast cancer. There are various resources available regarding this particular topic, with the SEER being the most reliable one.

The Surveillance, Epidemiology, and End Results (SEER) Program of the National Cancer Institute (NCI) collects and publishes cancer data through a coordinated system of strategically placed cancer registries, which cover nearly 30% of the US population.

Currently, there are 18 SEER registries in the USA. This information can be found on the following website: <https://seer.cancer.gov/data/access.html>.

I have also used the following repository to assist me with this project: https://github.com/kohyarp/SEER_solid_tumor. The Database contains tons of data, the goal of my investigation will be focused only on BREAST cancer for 2011-2015 and 2019-2020. SEER has a software *STAT that I have used to import the data to a test that will be stored and used on my local computer. Additionally there is a GITHUB repository that I have used to some extent in this project. The repository is focused on all type of cancer, but my study is focused on BREAST, and I aim different question to answer. https://github.com/zgalochkina/SEER_solid_tumor

Research question

The primary question I aim to address is the survival rate of breast cancers and the influence of factors such as age, type, sex, and other parameters on this rate. Notably, a five-year threshold is commonly used to determine survival rates. Although my understanding of the rationale behind this five-year benchmark is limited, recognizing its significance has led me to divide the data into two separate datasets.

The dataset spanning from 2011-2015 assumes that the status of all patients within that period is known up to the database's current date in 2022. Additionally, I have selected the most recent data from 2019-2020 as my target years for potential correlation and regression studies to estimate survival rates.

This analysis is not scientific but rather a straightforward statistical exercise with no purpose beyond this course. However, I find the subject intriguing to investigate. I am uncertain if I will discover any significant relationships or correlations, and if found, whether they will be relevant, as I am not an expert in the field of breast cancer. My choice of topic is personal, as I have witnessed immediate family members diagnosed with this cancer, and I wish to gain a deeper understanding.

The database for 2011-2015 contains approximately 303,000 rows with 36 selected columns. I have chosen to focus solely on the 2019-2020 data, which comprises about 131,000 rows for prediction purposes. The question at hand is complex, and while I do not anticipate a definitive answer, I hope to uncover some patterns and test hypotheses, as well as engage in general data work, from tidying to cleaning.

Furthermore, I plan to explore regression analysis to determine if I can identify any linear or non-linear relationships among the critical parameters.

My knowledge of the subject is not extensive, but I am eager to learn as I progress.

Some of the general parameters to consider are as follows: * Years of diagnoses; * Age groups at diagnosis;
* Cancer type (BREAST);

Some other parameters are also available to be edited, but they are secondary.

“to be added : adding a brief literature review to provide context for my research questions and hypotheses. This could include previous studies on breast cancer survival rates, factors affecting survival, and methods used for analysis.”

```
# Replace "file.txt" with the path to your text file
directory <- "C:/Users/kohya/OneDrive/CUNY/DATA 606/DATA 606 Spring/Project"
file_2020 <- "BREAST_2019-2020-updated.csv"
file_serv <- "BREAST_2011-2015.csv"
# Complete the file path
full_path_serv <- file.path(directory, file_serv)
full_path_eval<- file.path(directory, file_2020)

BREAST_DF_serv <- read.csv(full_path_serv, header = TRUE,
                           na.strings = "NA", check.names = FALSE)
BREAST_DF_eval <- read.csv(full_path_eval, header = TRUE,
                           na.strings = "NA", check.names = FALSE)

labels_of_interest <- c("Primary Site - labeled")

# View the first few rows of the data frame
kable(head(BREAST_DF_serv, 10))
```


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your dataset. This could include summary statistics, histograms, scatter plots, or other visualizations.”

By employing Exploratory Data Analysis (EDA) methods like summary statistics and graphical representations, we aim to reveal insights that will enhance our comprehension of breast cancer outcomes and therapeutic approaches. The dataset is rich with details, encompassing variables such as the patient’s age at operation, operation year, count of positive axillary nodes detected, and survival status post-treatment.

<https://medium.com/@navamisunil174/exploratory-data-analysis-of-breast-cancer-survival-prediction-dataset-c423e4137e38>

Data collection

Describe the method of data collection. I used the SEER *STAT to collect the data and export it as a TXT to be able to import it to the R for analyses. How SEER collects the data is explained in the following page in summary:

- The SEER program collects cancer incidence data through a network of population-based cancer registries. These registries gather information on patient demographics, primary tumor site, tumor morphology, stage at diagnosis, and first course of treatment. They also follow up with patients for vital status.
- By law, these facilities are required to report new cancer cases to a central cancer registry, like a state cancer registry.
- The SEER program releases new research data annually, based on submissions from the previous year, and makes it available for public use through a data request process. This comprehensive approach ensures that the SEER database is a valuable resource for cancer research and surveillance.

<https://training.seer.cancer.gov/registration/data/collection.html>

Type of study

This will be an observational study, information is gathered for different patients and I will be evaluating the available data to present and evaluate.

“discussing potential limitations of observational studies, such as confounding variables and biases, and how you plan to address them in analysis.”

What type of study is this (observational/experiment)?

Data Source

Data is collected from SEER program and I used SEER *STAT software to glean them in a format that can be used and imported as TXT to R (Surveillance, Epidemiology, and End Results Program 2023).

“providing additional details about the specific variables included in dataset and how they were collected”

If you collected the data, state self-collected. If not, provide a citation/link.

Dependent Variable

I am still looking into the data, it seems I will have a combination of both quantitative and qualitative data to work with. For example, while the number of tumors, and survival months are qualitative. Other like race, marital status, type of cancer are categorical. I am still looking to see if I can find any qualitative data.

Categorical features, such as ‘Median household income ...’ ‘Marital Status,’ ‘Grade recode’ ‘laterality’ and ‘Radiatio recode’ and so on are represented as objects (characters).

Integer data types (int64) are assigned to ‘Patient ID,’ ‘Year of diagnosis,’ ‘total number of ...’.

The event indicator refers to the death and the time registered is either the time-to-event (when the individual eventually dies) or the time-to-censorship (the event is not observed), measured in months.

```
# Find unique values in each column
# Apply function to find unique values for each column

unique_values <- data.frame(unique = apply(BREAST_DF_surv, 2, function(x) length(unique(x))), colnames = )

# Check for NULL values
any_null <- any(sapply(BREAST_DF_surv, is.null))

# Check for NA values
any_na <- any(sapply(BREAST_DF_surv, is.na))

# Check if there are any NULL or NA values
if (any_null || any_na) {
  print("The data frame contains NULL or NA values.")
} else {
  print("The data frame does not contain any NULL or NA values.")
}
```

```
## [1] "The data frame does not contain any NULL or NA values."
```

```
has_na_character <- any(sapply(BREAST_DF_surv, function(x) any(x == "NA"))))

if (has_na_character) {
  print("The data frame contains character values of 'NA'.")
} else {
  print("The data frame does not contain character values of 'NA'.")
}
```

```
## [1] "The data frame does not contain character values of 'NA'."
```

Data tidying

Upon exploring the data, it seems data might have an empty column, in this data-based, the empty values are filled with “Blanks”. Thus, in this section, I first explore if there is any column which is entirely empty, then will remove it and if there are others which have some empty values filled with “blanked” I will repalced them with “NA” which is handled better in dplyr and tidyverse.

```
# There are cells in the DF that contianes "Blank(s) which is literally NA, first I want to find if the

#look for columns with all "Blank(s)" values
Empty_column <- BREAST_DF_surv %>%
  dplyr::summarise(dplyr::across(everything(), ~all(. == "Blank(s)"))) %>%
  as.logical() %>%
  unlist()
```

```
# Get the names of columns with all cells containing "Blank(s)"
blank_column_names <- names( BREAST_DF_surv)[Empty_column]
```

```
# Print the column names with all cells containing "Blanks"
print(blank_column_names)
```

```
## [1] "Grade Clinical (2018+)"
## [2] "Grade Pathological (2018+)"
## [3] "Scope of reg lymph nd surg (1998-2002)"
## [4] "Tumor Size Summary (2016+)"
```

```
#remove those empty column from thr DF
BREAST_DF_surv <- BREAST_DF_surv[, !names(BREAST_DF_surv) %in% blank_column_names]
BREAST_DF_eval <- BREAST_DF_eval[, !names(BREAST_DF_eval) %in% blank_column_names]
```

```
#Then let's see if there is any cell in the remaining that might still have "Blank(s)", if so replace it
```

```
#This code first replaces all occurrences of "Blank(s)" with an empty string "", and then uses na_if()
```

```
BREAST_DF_surv <- BREAST_DF_surv %>%
  mutate_if(is.character, ~ifelse(. == "Blank(s)", "", .)) %>% # For character columns
  mutate_if(is.numeric, ~ifelse(. == "", as.numeric(NA), .)) # For numeric columns
```

```
# Now, empty character cells are replaced with NA
```

```
BREAST_DF_surv <- BREAST_DF_surv %>%
  mutate_if(is.character, na_if, "")
```

```
#same to be done for eval dataset
```

```
BREAST_DF_eval <- BREAST_DF_eval %>%
  mutate_if(is.character, ~ifelse(. == "Blank(s)", "", .)) %>% # For character columns
  mutate_if(is.numeric, ~ifelse(. == "", as.numeric(NA), .)) # For numeric columns
```

```
# Now, empty character cells are replaced with NA
```

```
BREAST_DF_eval <- BREAST_DF_eval %>%
  mutate_if(is.character, na_if, "")
```

```
#Change characters to numerics
```

```
BREAST_DF_surv$`Months from diagnosis to treatment` <- as.numeric(BREAST_DF_surv$`Months from diagnosis to treatment`)
BREAST_DF_surv$`Survival months` <- as.numeric(BREAST_DF_surv$`Survival months`)
```

```
## Warning: NAs introduced by coercion
```

```
BREAST_DF_surv$`Total number of in situ/malignant tumors for patient` <-
  as.numeric(BREAST_DF_surv$`Total number of in situ/malignant tumors for patient`)
```

```
## Warning: NAs introduced by coercion
```

```
BREAST_DF_surv$`Total number of benign/borderline tumors for patient` <-
  as.numeric(BREAST_DF_surv$`Total number of benign/borderline tumors for patient`)
#Change the character to numeric in Eval dataset too
BREAST_DF_eval$`Months from diagnosis to treatment` <- as.numeric(BREAST_DF_eval$`Months from diagnosis
BREAST_DF_eval$`Survival months` <- as.numeric(BREAST_DF_eval$`Survival months`)
```

Warning: NAs introduced by coercion

```
BREAST_DF_eval$`Total number of in situ/malignant tumors for patient` <-
  as.numeric(BREAST_DF_eval$`Total number of in situ/malignant tumors for patient`)
```

Warning: NAs introduced by coercion

```
BREAST_DF_eval$`Total number of benign/borderline tumors for patient` <-
  as.numeric(BREAST_DF_eval$`Total number of benign/borderline tumors for patient`)

# View the structure of the data frame
#str(BREAST_DF_surv)
skimr::skim(BREAST_DF_surv)
```

Table 3: Data summary

Name	BREAST_DF_surv
Number of rows	303557
Number of columns	32
Column type frequency:	
character	25
numeric	7
Group variables	None

Variable type: character

skim_variable	n_miss- ing	com- plete_rate	min	max	empty	n_unique	whites- pace
Sex	0	1	6	6	0	1	0
Race recode (W, B, AI, API)	0	1	5	29	0	5	0
Race and origin recode (NHW, NHB, NHAIAN, NHAPI, Hispanic)	0	1	18	42	0	6	0
Site recode ICD-O-3/WHO 2008	0	1	6	6	0	1	0
Site recode ICD-O-3 2023 Revision	0	1	6	6	0	1	0
Primary Site - labeled	0	1	12	36	0	9	0
Grade Recode (thru 2017)	0	1	7	38	0	5	0
Diagnostic Confirmation	0	1	7	57	0	9	0
Laterality	0	1	24	53	0	5	0
Chemotherapy recode (yes, no/unk)	0	1	3	10	0	2	0
Radiation recode	0	1	12	53	0	8	0

skim_variable	n_miss- ing	com- plete_rate	min	max	empty	n_unique	whites- pace
Reason no cancer-directed surgery	0	1	15	76	0	8	0
Survival months flag	0	1	61	73	0	5	0
COD to site recode	0	1	5	55	0	87	0
First malignant primary indicator	0	1	2	3	0	2	0
Sequence number	0	1	16	60	0	13	0
Marital status at diagnosis	0	1	7	30	0	7	0
Median household income inflation adj to 2021	0	1	8	38	0	11	0
Rural-Urban Continuum Code	0	1	38	60	0	7	0
Age recode (<60,60-69,70+)	0	1	9	11	0	18	0
Race and origin (recommended by SEER)	0	1	21	21	0	1	0
Year of death recode	0	1	4	21	0	11	0
SEER other cause of death classification	0	1	16	55	0	4	0
RX Summ-Systemic/Sur Seq (2007+)	0	1	16	55	0	8	0
Origin recode NHIA (Hispanic, Non-Hisp)	0	1	23	27	0	2	0

Variable type: numeric

skim_variable	n_miss- ing	com- plete_rate	mean	sd	p0	p25	p50	p75	p100	hist
Year of diagnosis	0	1.00	2013.04	1.42	2011	2012	2013	2014	2015	
Months from diagnosis to treatment	15843	0.95	1.13	1.14	0	0	1	2	24	
Survival months	1290	1.00	74.22	29.88	0	62	78	97	119	
Total number of in situ/malignant tumors for patient	3	1.00	1.36	0.65	1	1	1	2	20	
Total number of benign/borderline tumors for patient	0	1.00	0.01	0.09	0	0	0	0	5	
Patient ID	0	1.00	32479919167852417309	17852417309	16624923538965403536503287749					
Year of follow-up recode	0	1.00	2018.90	2.14	2011	2019	2020	2020	2020	

```
skimr::skim(BREAST_DF_eval)
```

Table 6: Data summary

Name	BREAST_DF_eval
Number of rows	131395
Number of columns	32
Column type frequency:	
character	25
numeric	7
Group variables	None

Variable type: character

skim_variable	n_miss- ing	com- plete_rate	min	max	empty	n_unique	whites- pace
Sex	0	1	6	6	0	1	0
Race recode (W, B, AI, API)	0	1	5	29	0	5	0
Race and origin recode (NHW, NHB, NHAIAN, NHAPI, Hispanic)	0	1	18	42	0	6	0
Site recode ICD-O-3/WHO 2008	0	1	6	6	0	1	0
Site recode ICD-O-3 2023 Revision	0	1	6	6	0	1	0
Primary Site - labeled	0	1	12	36	0	9	0
Grade Recode (thru 2017)	0	1	7	7	0	1	0
Diagnostic Confirmation	0	1	7	57	0	9	0
Laterality	0	1	24	53	0	5	0
Chemotherapy recode (yes, no/unk)	0	1	3	10	0	2	0
Radiation recode	0	1	12	53	0	8	0
Reason no cancer-directed surgery	0	1	15	76	0	8	0
Survival months flag	0	1	61	73	0	5	0
COD to site recode	0	1	5	55	0	67	0
First malignant primary indicator	0	1	2	3	0	2	0
Sequence number	0	1	16	60	0	16	0
Marital status at diagnosis	0	1	7	30	0	7	0
Median household income inflation adj to 2021	0	1	8	38	0	11	0
Rural-Urban Continuum Code	0	1	38	60	0	7	0
Age recode (<60,60-69,70+)	0	1	9	11	0	17	0
Race and origin (recommended by SEER)	0	1	21	21	0	1	0
Year of death recode	0	1	4	21	0	3	0
SEER other cause of death classification	0	1	16	55	0	4	0
RX Summ-Systemic/Sur Seq (2007+)	0	1	16	55	0	8	0
Origin recode NHIA (Hispanic, Non-Hisp)	0	1	23	27	0	2	0

Variable type: numeric

skim_variable	n_miss- ing	com- plete_rate	mean	sd	p0	p25	p50	p75	p100	hist
Year of diagnosis	0	1.00	2019.48	0.50	2019	2019	2019	2020	2020	
Months from diagnosis to treatment	6807	0.95	1.26	1.18	0	1	1	2	24	
Survival months	537	1.00	11.07	7.05	0	5	11	17	23	
Total number of in situ/malignant tumors for patient	11	1.00	1.31	0.62	1	1	1	1	50	
Total number of benign/borderline tumors for patient	0	1.00	0.01	0.09	0	0	0	0	2	
Patient ID	0	1.00	331370471820379812750	168966936734406099942763289421						
Year of follow-up recode	0	1.00	2019.98	0.14	2019	2020	2020	2020	2020	

What is the response variable? Is it quantitative or qualitative?

Independent Variable(s)

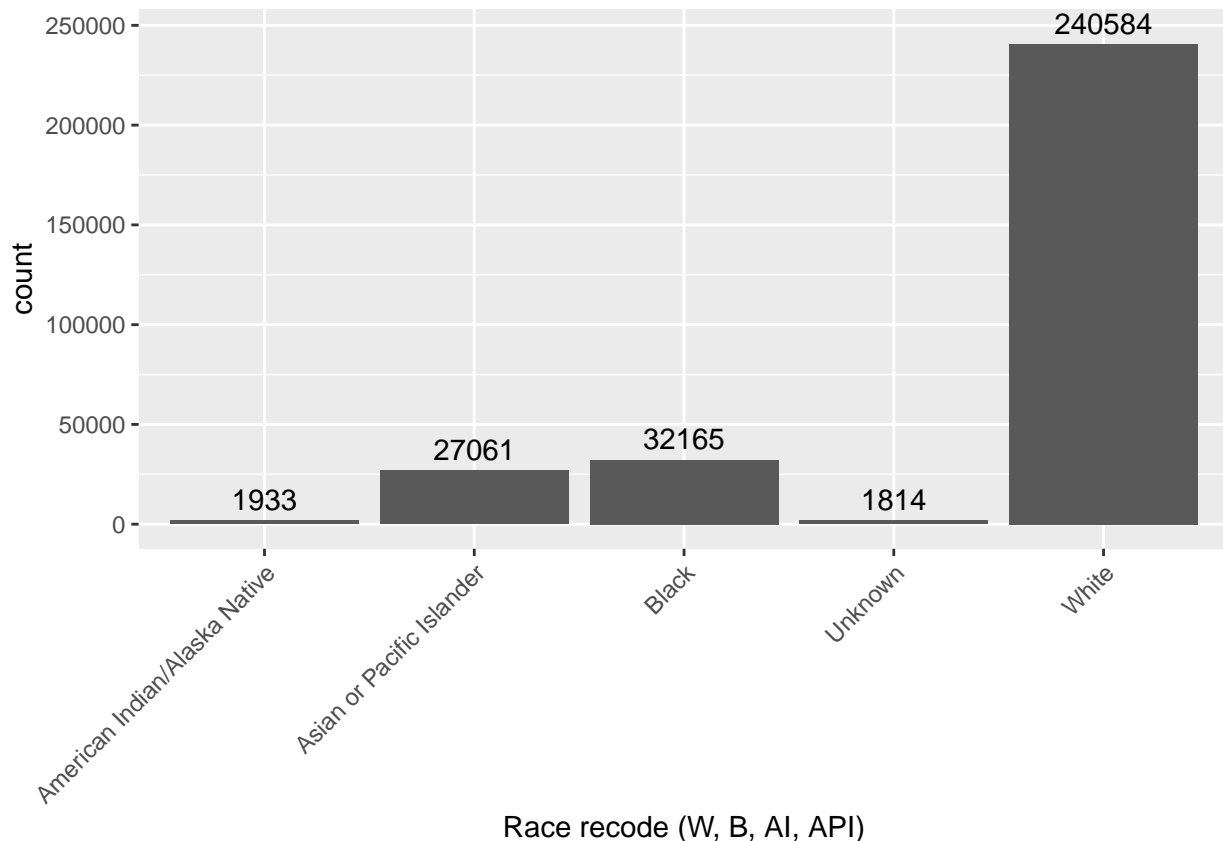
Relevant summary statistics

Provide summary statistics for each the variables. Also include appropriate visualizations related to your research question (e.g. scatter plot, boxplots, etc). This step requires the use of R, hence a code chunk is provided below. Insert more code chunks as needed.

```
#find column name to use later if needed
DF_col_names <- colnames(BREAST_DF_surv)

#Find unique values in `Race recode (W, B, AI, API)` column
uniques_races <- unique(BREAST_DF_surv$`Race recode (W, B, AI, API)`)

# use ggplot to plot the race information
BREAST_DF_surv |>
  ggplot(mapping = aes(x=`Race recode (W, B, AI, API)`) +
    geom_bar(stat = "count") +
    theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
    geom_text(aes(label = after_stat(count)), stat = "count", vjust = -0.5) +
    ylim(0, 246000)
```



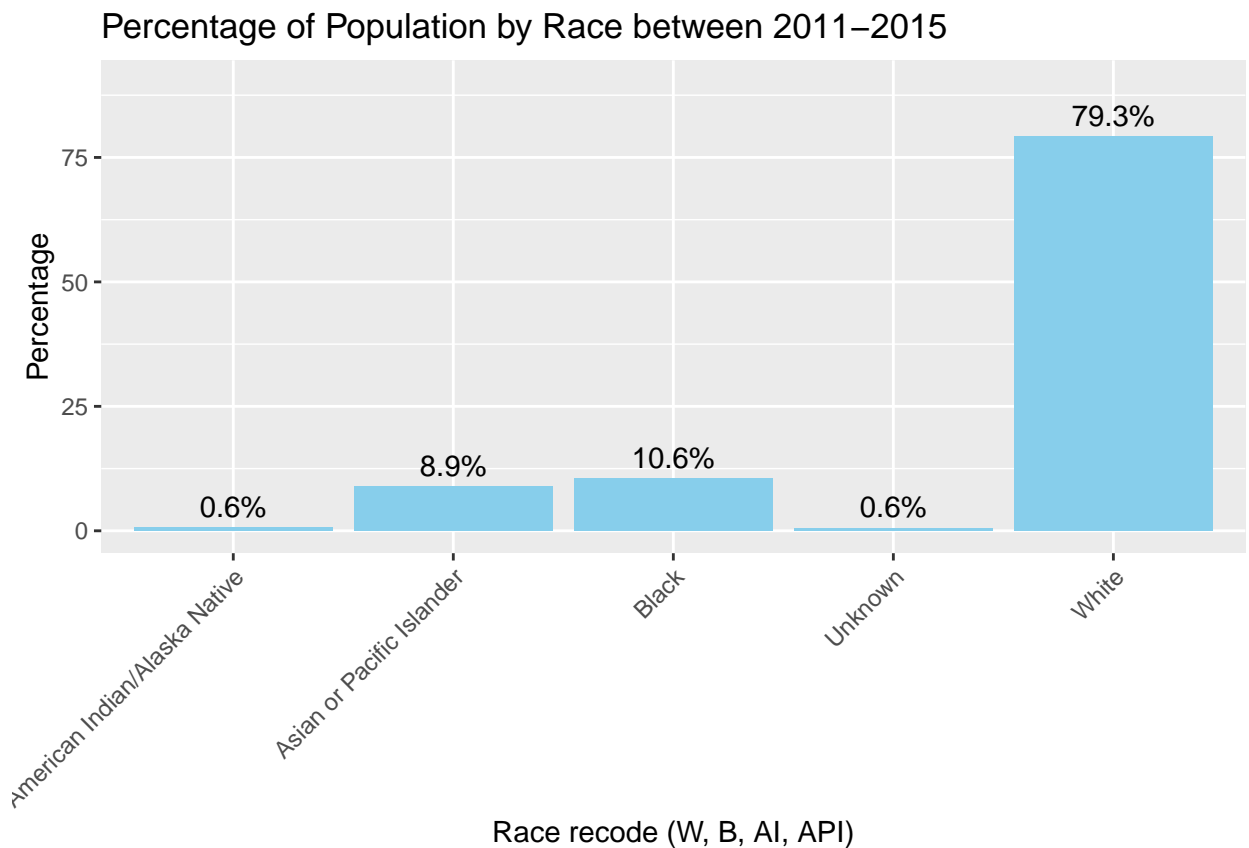
```
#we want to compare the percentage of the different race in the eval and survival data, thus i use sumam
#find percentage of race for the survival
BREAST_DF_perc_surv <- BREAST_DF_surv %>%
```

```

group_by(`Race recode (W, B, AI, API)` )>%
dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
ungroup() %>% # Ungroup the data
mutate(total_count = sum(count)) %>% # Calculate total count
mutate(percentage = count / total_count * 100) # Calculate percentage using total count

# Plot the percentages
ggplot(BREAST_DF_perc_surv, aes(x = `Race recode (W, B, AI, API)`, y = percentage)) +
  geom_bar(stat = "identity", fill = "skyblue") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), vjust = -0.5, color = "black") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  labs(title = "Percentage of Population by Race between 2011-2015", x = "Race recode (W, B, AI, API)",

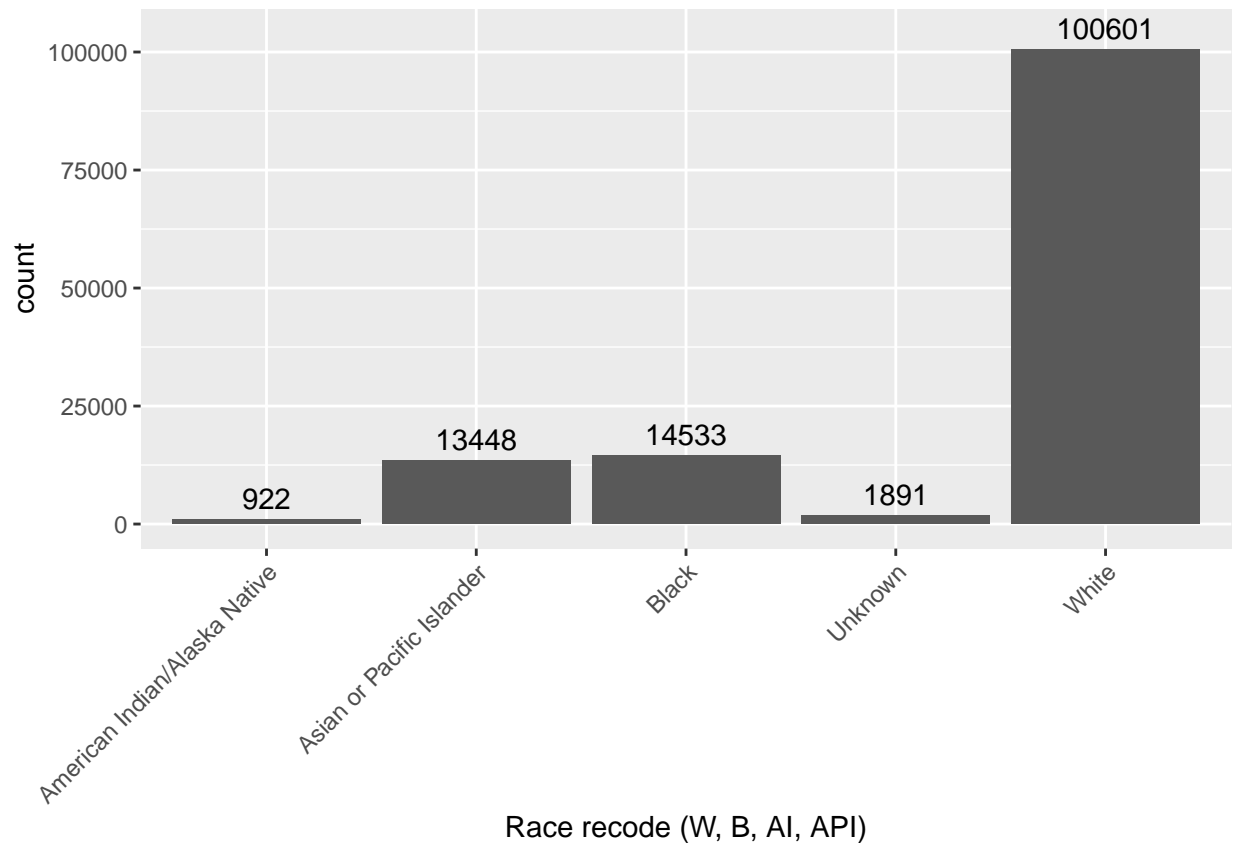
```



```

BREAST_DF_eval |>
  ggplot(mapping = aes(x=`Race recode (W, B, AI, API)`)) +
  geom_bar(stat = "count") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  geom_text(aes(label = after_stat(count)), stat = "count", vjust = -0.5) +
  ylim(0, 104000)

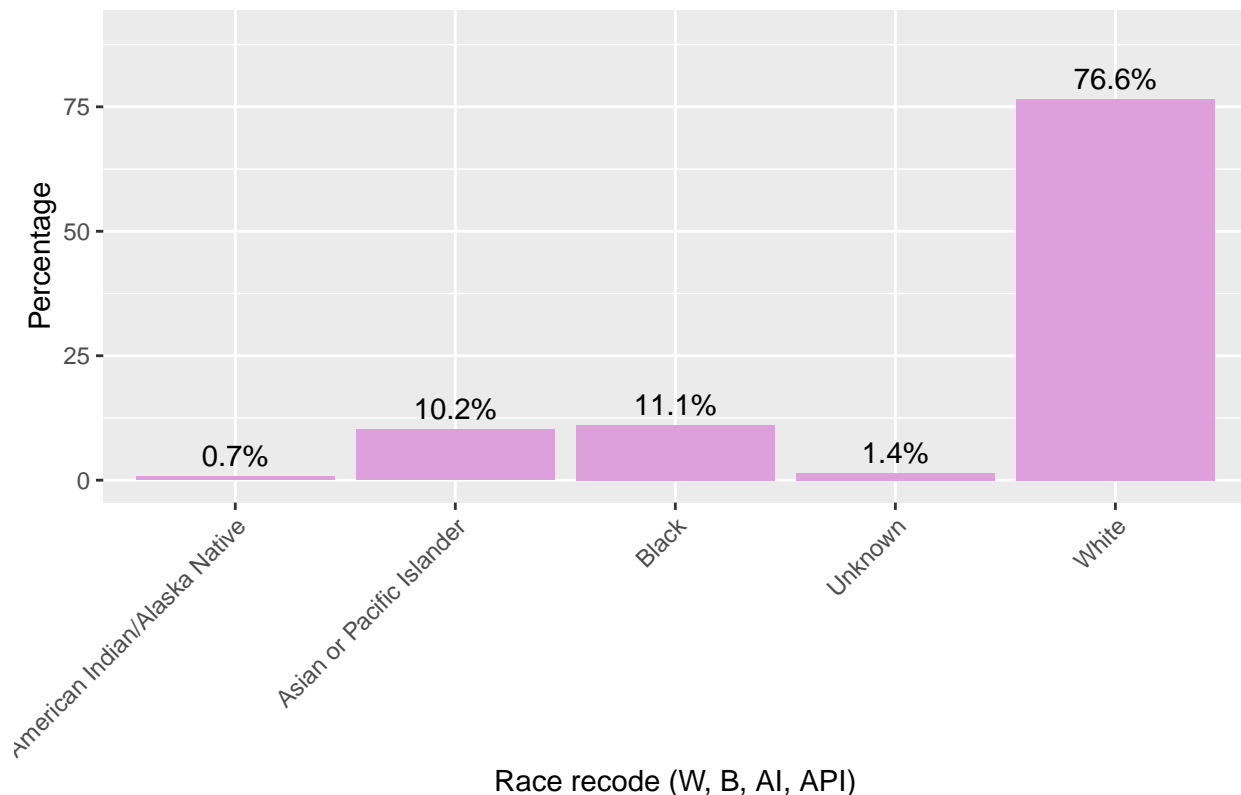
```



```
BREAST_DF_perc_eval <- BREAST_DF_eval %>%
  group_by(`Race recode (W, B, AI, API)`) %>%
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(total_count = sum(count)) %>% # Calculate total count
  mutate(percentage = count / total_count * 100) # Calculate percentage using total count

# Plot the percentages
ggplot(BREAST_DF_perc_eval, aes(x = `Race recode (W, B, AI, API)`, y = percentage)) +
  geom_bar(stat = "identity", fill = "plum") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), vjust = -0.5, color = "black") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  labs(title = "Percentage of Population by between 2019-2022", x = "Race recode (W, B, AI, API)", y =
```

Percentage of Population by between 2019–2022

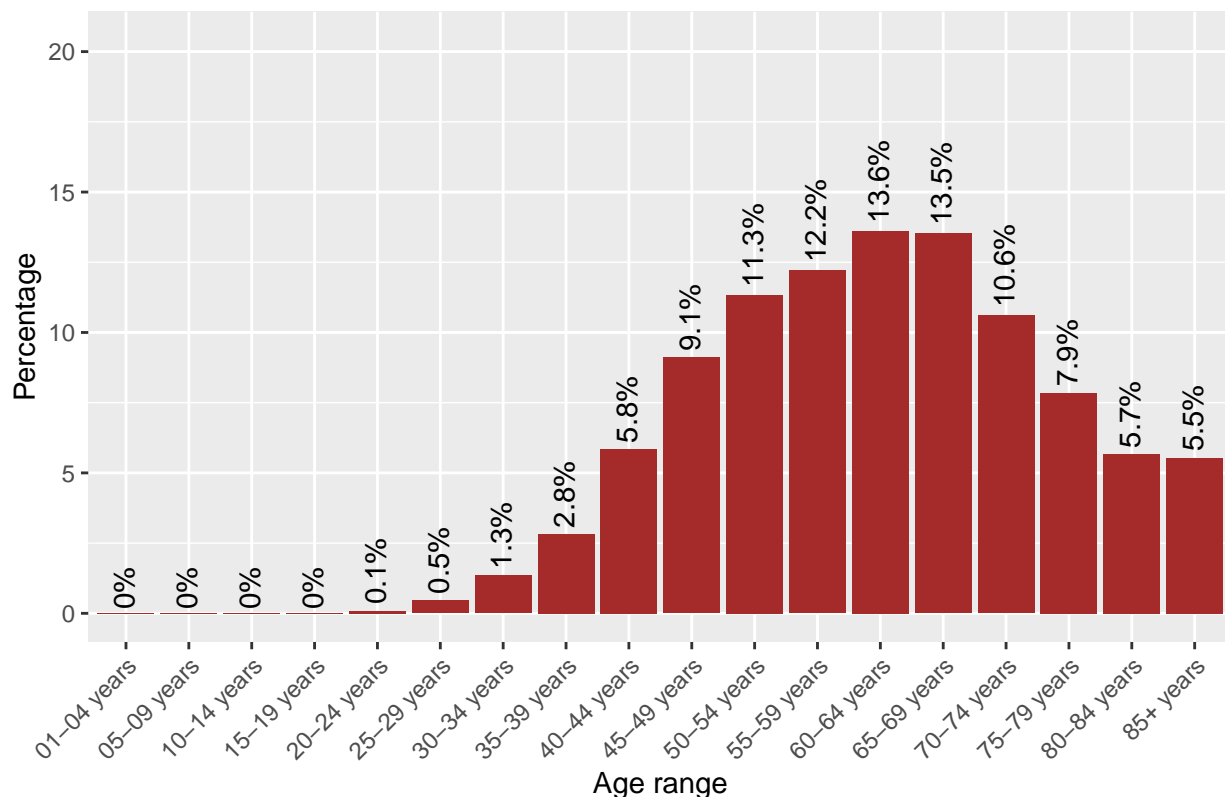


```
# In this section I want to focus on the age and see if age matetrs, same sets of data is going to be p
#find percentage of race for the survival
#find ubique values for column ratted to age
uniques_ages <- unique(BREAST_DF_surv[29])

BREAST_DF_age_perc_surv <- BREAST_DF_surv %>%
  dplyr::group_by(`Age recode (<60,60-69,70+)`) %>%
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(total_count = sum(count)) %>% # Calculate total count
  mutate(percentage = count / total_count * 100) # Calculate percentage using total count

perc_max <- max(BREAST_DF_age_perc_surv$percentage)
# Plot the percentages
ggplot(BREAST_DF_age_perc_surv, aes(x = `Age recode (<60,60-69,70+)`, y = percentage)) +
  geom_bar(stat = "identity", fill = "brown") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), hjust = -0.1, vjust = 0.4, color = "black")
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +labs(title = "Percentage of Population by Age",
    x = "Age range",
    y = "Percentage") +
  ylim(0, round(1.5 * perc_max, 1))
```

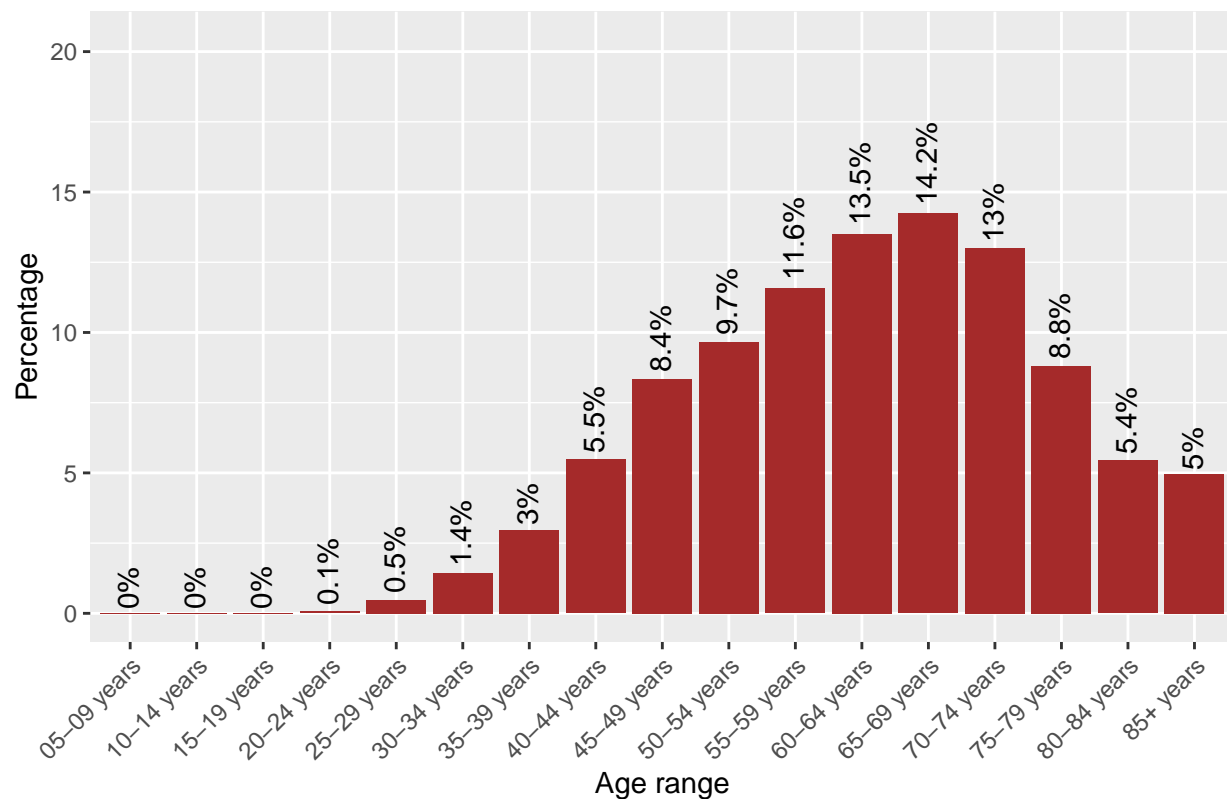
Percentage of Population by Age range 2011–2015



```
# In this section we do the same analyses for Eval dta based on age
BREAST_DF_age_perc_eval <- BREAST_DF_eval %>%
  dplyr::group_by(`Age recode (<60,60-69,70+)`) %>%
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(total_count = sum(count)) %>% # Calculate total count
  mutate(percentage = count / total_count * 100) # Calculate percentage using total count

# Plot the percentages
ggplot(BREAST_DF_age_perc_eval, aes(x = `Age recode (<60,60-69,70+)`, y = percentage)) +
  geom_bar(stat = "identity", fill = "brown") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), hjust = -0.1, vjust = 0.4, color = "black")
theme(axis.text.x = element_text(angle = 45, hjust = 1)) + labs(title = "Percentage of Population by Age range",
  x = "Age range",
  y = "Percentage") +
ylim(0, round(1.5 * perc_max, 1))
```

Percentage of Population by Age range 2019–2022

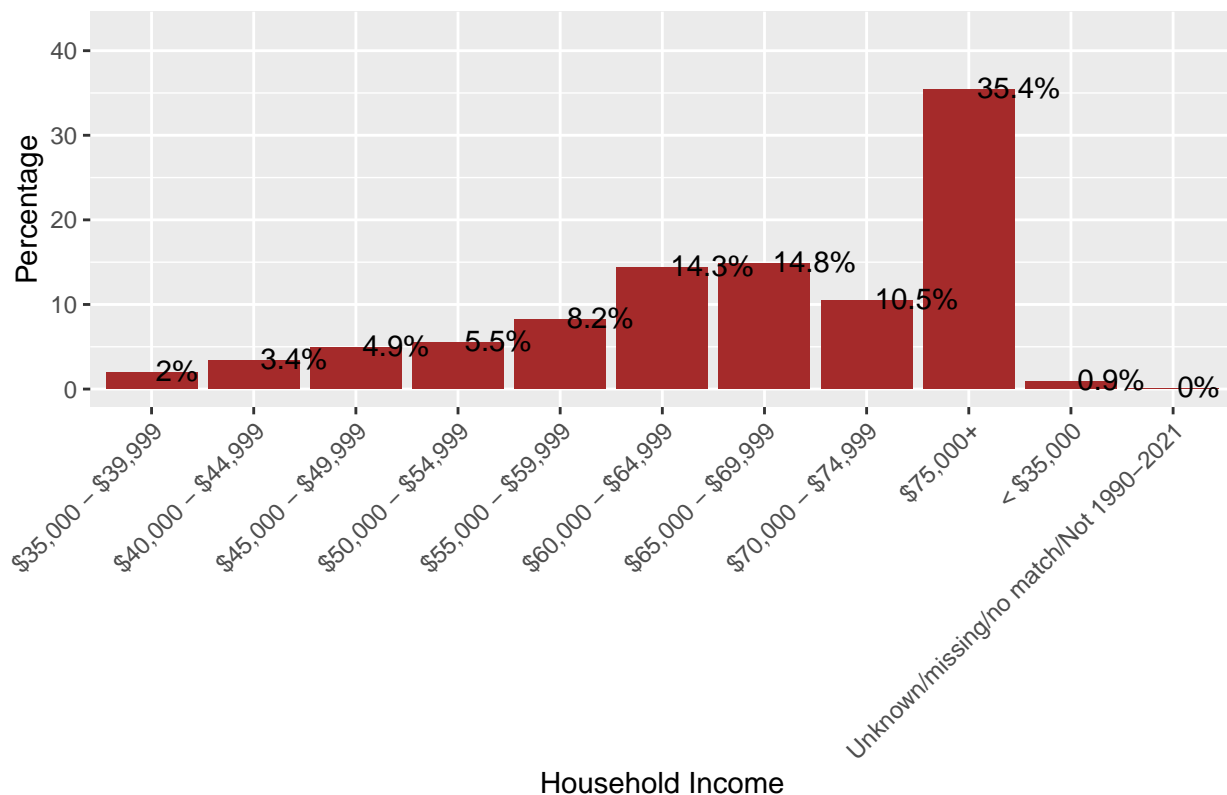


```
# In this section, we do the analyses on household income}
#find unique values for column ratted to age
uniques_householdes <- unique(BREAST_DF_surv[27])

BREAST_DF_income_perc_surv <- BREAST_DF_surv %>% dplyr::group_by(`Median household income inflation adj
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(total_count = sum(count)) %>% # Calculate total count
  mutate(percentage = count / total_count * 100) # Calculate percentage using total count

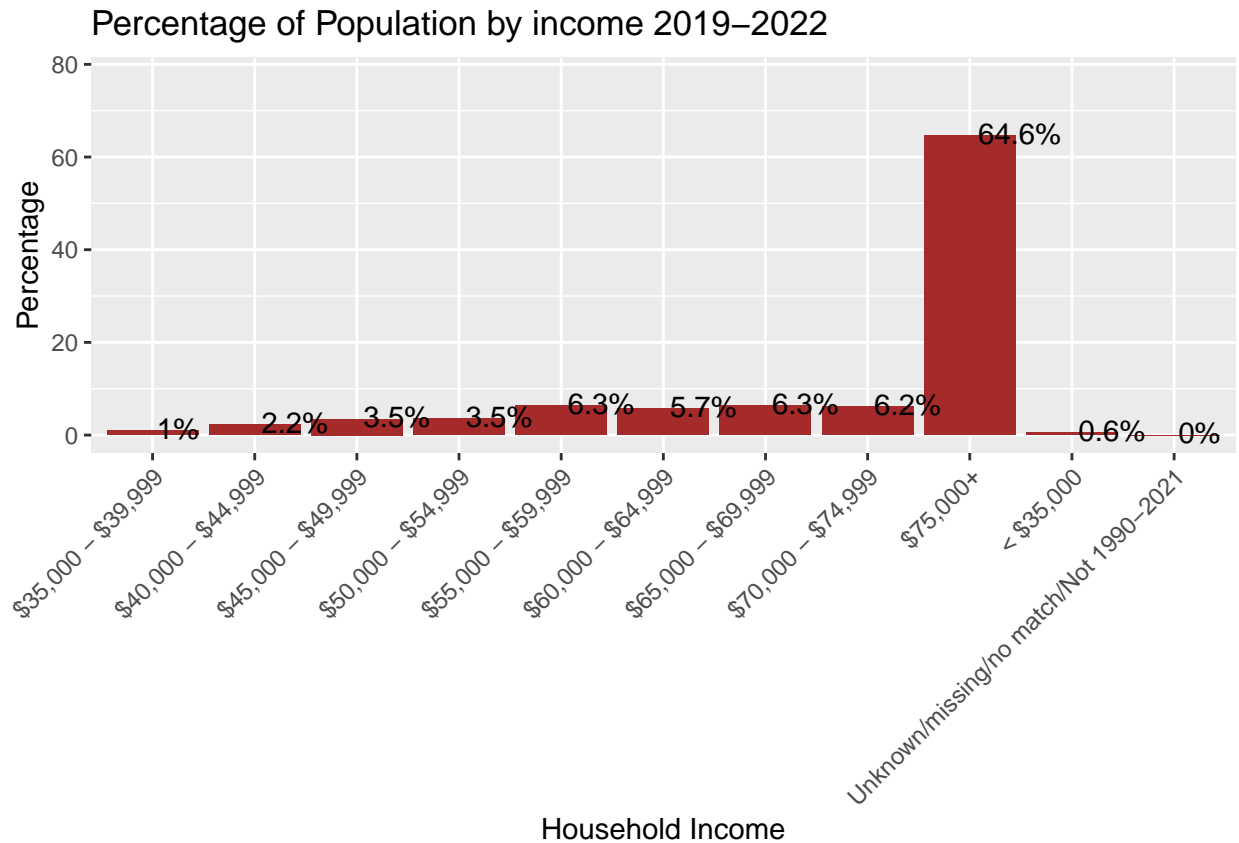
perc_max <- max(BREAST_DF_income_perc_surv$percentage) # Plot the percentages
ggplot(BREAST_DF_income_perc_surv, aes(x = `Median household income inflation adj to 2021`, y = percent
  geom_bar(stat = "identity", fill = "brown") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), hjust = -0.1 , vjust = 0.4, color = "black"
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  labs(title = "Percentage of Population by income 2011-2015", x = "Household Income", y = "Percentage"
  ylim(0, 1.2*perc_max)
```


Percentage of Population by income 2011–2015



```
#In this section we do the same analyses for Eval data based on age
BREAST_DF_income_perc_eval <- BREAST_DF_eval %>%
  dplyr::group_by(`Median household income inflation adj to 2021`) %>%
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(total_count = sum(count)) %>% # Calculate total count
  mutate(percentage = count / total_count * 100) # Calculate percentage using total count

#Plot the percentages
perc_max <- max(BREAST_DF_income_perc_eval$percentage)
ggplot(BREAST_DF_income_perc_eval, aes(x = `Median household income inflation adj to 2021`, y = percentage)) +
  geom_bar(stat = "identity", fill = "brown") +
  geom_text(aes(label = paste0(round(percentage, 1), "%")), hjust = -0.1, vjust = 0.4, color = "black") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  labs(title = "Percentage of Population by income 2019-2022", x = "Household Income", y = "Percentage")
ylim(0, 1.2*perc_max)
```



*# In this section I want to focus on the cause of death, COD, and investigate whether those who have had
find percentage of deceased due to breast cancer
find unique values for column related to age*

```
uniques_CODs <- unique(BREAST_DF_surv[20])
DF_col_names[20]
```

```
## [1] "Total number of in situ/malignant tumors for patient"
```

check if the column `COD to site recode` has value of Alive or Breast meaning they are still alive or

```
BREAST_DF_surv <- BREAST_DF_surv %>%
  mutate(COD = ifelse(`COD to site recode` %in% c("Alive", "Breast"), `COD to site recode`, "Other"))

BREAST_DF_COD_perc_surv <- BREAST_DF_surv %>%
  dplyr::group_by(COD) %>%
  dplyr::summarise(count = dplyr::n()) %>% # Calculate count per group
  ungroup() %>% # Ungroup the data
  mutate(`Total Count` = sum(count)) %>% # Calculate total count
  mutate(Population = round(count / `Total Count` * 100), 2) # Calculate percentage using total count

kable(BREAST_DF_COD_perc_surv)
```

COD	count	Total Count	Population
Alive	228221	303557	75
Breast	38472	303557	13
Other	36864	303557	12

```
# Let's first group by the number of tumor and find how many in the population have those and then among them
BREAST_DF_TNoT_perc_surv <- BREAST_DF_surv %>%
  dplyr::group_by(`Total number of in situ/malignant tumors for patient`) %>%
  dplyr::add_count() %>%
  filter(COD == "Breast") %>%
  dplyr::summarise(`Event Population` = n(),
    Population = dplyr::first(n)) # Use `first()` to extract the total count in each group

# Do simple math to find the percentage of the group in the population and then the percentage of the death
BREAST_DF_TNoT_perc_surv$`Group % in total` <- round(BREAST_DF_TNoT_perc_surv$Population/sum(BREAST_DF_TNoT_perc_surv$Population), 2)
BREAST_DF_TNoT_perc_surv$`Death %` <- round(BREAST_DF_TNoT_perc_surv$`Event Population`/BREAST_DF_TNoT_perc_surv$Population, 2)

kable(BREAST_DF_TNoT_perc_surv)
```

Total number of in situ/malignant tumors for patient	Event Population	Population	Group % in total	Death %
1	27314	217122	71.53	12.58
2	8945	68082	22.43	13.14
3	1808	14579	4.80	12.40
4	322	2996	0.99	10.75
5	68	595	0.20	11.43
6	9	126	0.04	7.14
7	3	29	0.01	10.34
8	2	18	0.01	11.11
18	1	1	0.00	100.00

```
# Let's focus on the treatment, There are two types of treatment and can be a 4 combination, as follows:
BREAST_DF_surv <- BREAST_DF_surv %>%
  mutate(Radiation = ifelse(`Radiation recode` %in% c("None/Unknown", "Refused (1988+)", "Recommended, unknown", "Not recommended"), "None/Unknown", "Refused (1988+)", "Recommended, unknown", "Not recommended"))

#use DPLYR to filter based on two parameters chemotherapy and radiation therapy and evaluate the death
BREAST_DF_RNC_perc_surv <- BREAST_DF_surv %>%
  dplyr::group_by(Radiation, `Chemotherapy recode (yes, no/unk)`) %>%
  dplyr::add_count() %>%
  filter(COD == "Breast") %>%
  dplyr::summarise(`Event Population` = n(),
    Population = dplyr::first(n)) # Use `first()` to extract the total count in each group

## `summarise()` has grouped output by 'Radiation'. You can override using the
## `.groups` argument.
```

```
#knowign the population calcualte the gorup rate and death rate in each group
BREAST_DF_RNC_perc_surv$`Group % in total` <- round(BREAST_DF_RNC_perc_surv$Population/sum(BREAST_DF_RNC_perc_surv$Population))

BREAST_DF_RNC_perc_surv$`Death %` <- round(BREAST_DF_RNC_perc_surv$`Event Population`/BREAST_DF_RNC_perc_surv$Population)

kable(BREAST_DF_RNC_perc_surv)
```

Radiation	Chemotherapy recode (yes, no/unk)	Event Population	Popula- tion	Group % in total	Death %
No/Un- known	No/Unknown	15684	107012	35.25	14.66
No/Un- known	Yes	9929	54966	18.11	18.06
Yes	No/Unknown	3731	79926	26.33	4.67
Yes	Yes	9128	61653	20.31	14.81

#next let's look into the surgery and the survival rate and whether it might have been critical or not.

Results of the exploratory data analysis

In this section, we look into some exploratory data analysis such as

- Cause of death of those who have had cancer
- Total number of tumors (Malignant or Benign)
- Radiation and chemotherapy
- Marital Status

We looked into the population and then among the population how many survived the cancer. Later we will run some analyses to see whether those were important or deciding factors or not.

Surveillance, Epidemiology, and End Results Program. 2023. “SEER*stat Database: Incidence - SEER Research Data, 8 Registries, Nov 2021 Sub (1975-2020) - Linked to County Attributes - Time Dependent (1990-2020) Income/Rurality, 1969-2020 Counties.” National Cancer Institute, DCCPS, Surveillance Research Program, released April 2023, based on the November 2022 submission. <https://seer.cancer.gov/data/citation.html>.