

# Breast Exploratory Analysis

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# 1 Introduction

This exploratory data analysis (EDA) is the first step in our project pipeline:

1. Bayesian Hierarchical Modeling
2. Posterior Inference & Diagnostics
3. Clustering of Individual Risk Profiles

We use data from the [SEER Program](#) focused on breast cancer cases, structured across three levels:

- **Level 1 (Tumor):** Tumor-specific details (e.g., stage, size, grade)
- **Level 2 (Patient):** Demographics and marital status
- **Level 3 (Region):** County-level metro/rural designations

## 2 Data Structure and Levels

Level	Variable	Description
Tumor	stage	SEER stage: Localized, Regional, Distant
Tumor	grade	Tumor grade: 1–4 or unknown
Tumor	size	EOD Tumor Size (mm)
Tumor	site	Tumor site (ICD code)
Patient	id	Patient identifier
Patient	age	Age group at diagnosis
Patient	sex	Biological sex
Patient	raceth	Race/ethnicity
Patient	year	Year of diagnosis
Patient	marry	Marital status
Region	region	County-level metro/rural code

```
seer <- read.delim("../data/raw/breastcancer.txt", sep = "\t", header = FALSE,
stringsAsFactors = FALSE)
```

We replace “Unknown” and “Blank(s)” with NA, and then keep only complete cases:

```
seer_prime <- seer %>%
  transmute(
    id      = V1,
    region = V2,
    stage   = V3,
    age     = V4,
    sex     = V5,
    raceth  = V6,
    grade   = V7,
```

```

    size    = V10,
    year   = V11,
    marry   = V12,
    site   = V8
  )

seer_prime <- seer_prime %>%
  mutate(across(where(is.character), ~na_if(., "Unknown")))) %>%
  mutate(across(where(is.character), ~na_if(., "Blank(s))))
```

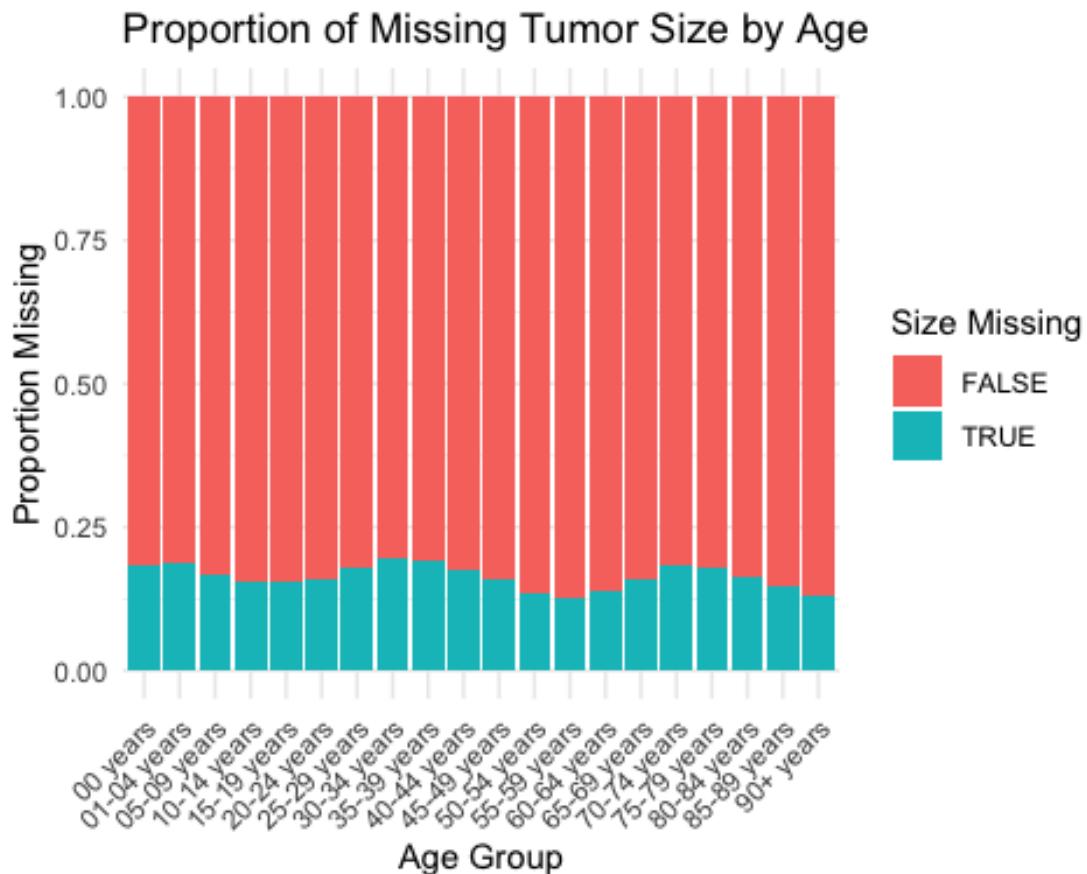
## 2.1 Is missing data more common in older patients?

```

df <- seer_prime

df <- seer_prime %>%
  mutate(size_missing = is.na(size))

ggplot(df, aes(x = age, fill = size_missing)) +
  geom_bar(position = "fill") +
  labs(title = "Proportion of Missing Tumor Size by Age",
       y = "Proportion Missing",
       x = "Age Group",
       fill = "Size Missing") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



## 2.2 Is missing data associated with Race/Ethnicity?

```
table(df$raceth, is.na(df$size))

##
##                                     FALSE    TRUE
## American Indian/Alaska Native  40048   4775
## Asian or Pacific Islander    453003  58740
## Black                         369571  62192
## White                         3427119 685078
```

## 2.3 Is stage more likely to be missing in nonmetro rural areas?

```
df <- df %>%
  mutate(grade_missing = is.na(grade),
        region_type = factor(region))

# Proportions
prop.table(table(df$region, df$grade_missing), 1)

##
##                                     FALSE
## Counties in metropolitan areas ge 1 million pop 0.5234788
## Counties in metropolitan areas of 250,000 to 1 million pop 0.5292829
```

```

## Counties in metropolitan areas of lt 250 thousand pop      0.5255872
## Nonmetropolitan counties adjacent to a metropolitan area  0.5250781
## Nonmetropolitan counties not adjacent to a metropolitan area 0.5329171
## Unknown/missing/no match (Alaska or Hawaii - Entire State) 0.4969591
## Unknown/missing/no match/Not 1990-2023                  0.6902941
##
##                                         TRUE
## Counties in metropolitan areas ge 1 million pop          0.4765212
## Counties in metropolitan areas of 250,000 to 1 million pop 0.4707171
## Counties in metropolitan areas of lt 250 thousand pop      0.4744128
## Nonmetropolitan counties adjacent to a metropolitan area  0.4749219
## Nonmetropolitan counties not adjacent to a metropolitan area 0.4670829
## Unknown/missing/no match (Alaska or Hawaii - Entire State) 0.5030409
## Unknown/missing/no match/Not 1990-2023                  0.3097059

```

Although we did not do a statistical test for MCAR, visual and tabular inspection clearly show patterns in missingness. Tumor size by age is non-uniform, with younger and older ends having higher missing rates. Missing rates also vary by racial group, with whites having notably higher missingness.

Logistic regression is a standard method for exploring missing data mechanisms. By modeling the missingness indicator (e.g., stage\_miss) as a binary outcome and regressing it on observed variables, we can test whether missingness is related to any known covariates.

If none of the predictors are significant, this supports the MCAR assumption. But if missingness is significantly associated with observed variables (as seen here), MCAR is rejected, and MAR becomes a more reasonable assumption for downstream modeling.

```

# Create a missingness indicator for tumor size
df$stage_miss <- is.na(df$stage)

# Convert to factor if not already
df$sex <- factor(df$sex)
df$raceth <- factor(df$raceth)
df$region <- factor(df$region)
df$age <- factor(df$age)
df$marry <- factor(df$marry)
df$grade <- factor(df$grade)
df$size <- factor(df$size)

# Fit Logistic regression model to predict missingness
miss_model <- glm(stage_miss ~ sex + raceth + region + age + marry + grade +
size,
                     data = df, family = binomial)

summary(miss_model)

```

```

## Call:
## glm(formula = stage_miss ~ sex + raceth + region + age + marry +
##      grade + size, family = binomial, data = df)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -3.1834 -0.2965 -0.2107 -0.0537  4.6368
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                -3.342e-01   1.131e+00  -0.300 0.76477
## sexMale                     1.072e-01   4.788e-02  2.240 0.25140
## racethAsian or Pacific Islander  2.072e-02   6.914e-02  0.300 0.76477
## racethBlack                  -4.788e-01   6.914e-02 -7.000 0.00000
## racethWhite                  -6.914e-02   1.594e-01 -0.440 0.66044
## regionCounties in metropolitan areas of 250,000 to 1 million pop -4.161e-02   5.517e-01 -0.075 0.94154
## regionCounties in metropolitan areas of lt 250 thousand pop       -2.610e-02   1.746e-01 -0.150 0.88100
## regionNonmetropolitan counties adjacent to a metropolitan area   -3.532e-02   1.746e-01 -0.200 0.81100
## regionNonmetropolitan counties not adjacent to a metropolitan area -4.719e-03   1.746e-01 -0.027 0.97277
## regionUnknown/missing/no match (Alaska or Hawaii - Entire State)  1.594e-01   1.746e-01  0.900 0.36000
## regionUnknown/missing/no match/Not 1990-2023                      -5.517e-01   1.746e-01 -3.130 0.00000
## age01-04 years                   1.746e-02   1.746e-01  0.010 0.99000
## age05-09 years                  -6.052e-02   1.746e-01 -0.034 0.96000
## age10-14 years                  -6.301e-02   1.746e-01 -0.035 0.95000
## age15-19 years                  -8.425e-02   1.746e-01 -0.048 0.90000
## age20-24 years                  -1.677e-01   1.746e-01 -0.095 0.80000
## age25-29 years                  -2.168e-01   1.746e-01 -0.124 0.70000
## age30-34 years                  -2.608e-01   1.746e-01 -0.149 0.60000
## age35-39 years                  -2.702e-01   1.746e-01 -0.154 0.55000

```

## age40-44 years	-2.780e
+00	
## age45-49 years	-2.757e
+00	
## age50-54 years	-2.857e
+00	
## age55-59 years	-2.881e
+00	
## age60-64 years	-2.981e
+00	
## age65-69 years	-3.079e
+00	
## age70-74 years	-3.109e
+00	
## age75-79 years	-3.121e
+00	
## age80-84 years	-3.074e
+00	
## age85-89 years	-3.013e
+00	
## age90+ years	-2.913e
+00	
## marryMarried (including common law)	-1.080e
-01	
## marrySeparated	-2.218e
-02	
## marrySingle (never married)	-1.074e
-03	
## marryUnmarried or Domestic Partner	-1.354e
-01	
## marryWidowed	5.563e
-02	
## gradeModerately differentiated; Grade II	3.028e
+00	
## gradeNK cell; natural killer cell (1995+)	1.382e
+00	
## gradeNull cell; non T-non B	1.907e
+00	
## gradePoorly differentiated; Grade III	3.400e
+00	
## gradeT-cell	1.335e
+00	
## gradeUndifferentiated; anaplastic; Grade IV	3.878e
+00	
## gradeWell differentiated; Grade I	3.293e
+00	
## size10	1.099e
+00	
## size11	-1.202e
-01	

## size12	-4.207e
-01	
## size13	-1.178e
+00	
## size14	-1.149e
+00	
## size15	-7.817e
-01	
## size16	-1.542e
+01	
## size17	-1.540e
+01	
## size18	-1.531e
+01	
## size19	1.427e
-03	
## size20	-1.151e
-02	
## size21	-3.988e
+00	
## size22	-3.577e
+00	
## size23	-3.827e
+00	
## size24	-2.221e
+00	
## size25	4.253e
-01	
## size26	1.371e
-02	
## size27	2.452e
-02	
## size28	-3.100e
+00	
## size29	-1.559e
+01	
## size30	1.621e
-01	
## size31	3.673e
+00	
## size32	-4.749e
-01	
## size33	-3.079e
+00	
## size34	1.110e
+00	
## size35	-8.326e
-01	
## size36	-3.526e
+00	

## size37	-1.539e
+01	
## size38	-1.580e
+01	
## size40	4.476e
-01	
## size41	-5.124e
-01	
## size42	1.254e
+00	
## size43	2.357e
+00	
## size44	-1.540e
+01	
## size45	5.495e
-01	
## size46	-9.219e
-02	
## size47	-7.049e
-01	
## size48	-1.547e
+01	
## size49	-1.548e
+01	
## size50	-1.469e
+00	
## size51	-3.809e
+00	
## size52	-1.961e
+00	
## size53	-1.815e
+00	
## size54	-1.262e
+00	
## size55	-1.616e
+01	
## size56	-1.566e
+01	
## size57	-1.559e
+01	
## size58	-1.548e
+01	
## size59	-1.551e
+01	
## size60	2.163e
+00	
## size61	-1.565e
+01	
## size62	-4.792e
+00	

## size63	-1.555e
+01	
## size64	-1.572e
+01	
## size65	-1.545e
+01	
## size66	-1.544e
+01	
## size67	-1.544e
+01	
## size68	-1.562e
+01	
## size69	-1.554e
+01	
## size70	-1.094e
+00	
## size71	-1.585e
+01	
## size72	-1.566e
+01	
## size73	-1.564e
+01	
## size74	-1.559e
+01	
## size75	-1.549e
+01	
## size76	-1.547e
+01	
## size77	-1.568e
+01	
## size78	-1.555e
+01	
## size79	-1.548e
+01	
## size80	-6.651e
-01	
## size90	1.359e
+00	
## size98	6.779e
+00	
## size99	1.723e
+00	
##	Std. Err
ror	
## (Intercept)	1.087e
-01	
## sexMale	8.255e
-03	
## racethAsian or Pacific Islander	4.742e
-02	

## racethBlack	4.803e
-02	
## racethWhite	4.612e
-02	
## regionCounties in metropolitan areas of 250,000 to 1 million pop	9.622e
-03	
## regionCounties in metropolitan areas of lt 250 thousand pop	1.640e
-02	
## regionNonmetropolitan counties adjacent to a metropolitan area	1.659e
-02	
## regionNonmetropolitan counties not adjacent to a metropolitan area	1.695e
-02	
## regionUnknown/missing/no match (Alaska or Hawaii - Entire State)	9.020e
-02	
## regionUnknown/missing/no match/Not 1990-2023	6.510e
-02	
## age01-04 years	1.026e
-01	
## age05-09 years	1.071e
-01	
## age10-14 years	1.017e
-01	
## age15-19 years	9.791e
-02	
## age20-24 years	9.785e
-02	
## age25-29 years	9.478e
-02	
## age30-34 years	9.262e
-02	
## age35-39 years	9.037e
-02	
## age40-44 years	8.872e
-02	
## age45-49 years	8.770e
-02	
## age50-54 years	8.724e
-02	
## age55-59 years	8.703e
-02	
## age60-64 years	8.698e
-02	
## age65-69 years	8.698e
-02	
## age70-74 years	8.704e
-02	
## age75-79 years	8.713e
-02	
## age80-84 years	8.736e
-02	

## age85-89 years	8.801e
-02	8.984e
## age90+ years	
-02	
## marryMarried (including common law)	1.328e
-02	
## marrySeparated	4.058e
-02	
## marrySingle (never married)	1.569e
-02	
## marryUnmarried or Domestic Partner	8.086e
-02	
## marryWidowed	1.678e
-02	
## gradeModerately differentiated; Grade II	4.547e
-02	
## gradeNK cell; natural killer cell (1995+)	1.920e
-01	
## gradeNull cell; non T-non B	3.335e
-01	
## gradePoorly differentiated; Grade III	4.532e
-02	
## gradeT-cell	5.384e
-02	
## gradeUndifferentiated; anaplastic; Grade IV	4.631e
-02	
## gradeWell differentiated; Grade I	4.635e
-02	
## size10	1.329e
-01	
## size11	5.099e
-01	
## size12	2.336e
-01	
## size13	3.583e
-01	
## size14	1.784e
-01	
## size15	1.990e
-01	
## size16	1.695e
+02	
## size17	4.053e
+02	
## size18	9.019e
+02	
## size19	9.638e
-02	
## size20	2.957e
-02	

## size21	2.430e
-01	
## size22	7.184e
-02	
## size23	1.328e
-01	
## size24	1.012e
-01	
## size25	4.118e
-02	
## size26	5.072e
-02	
## size27	1.697e
-02	
## size28	4.088e
-01	
## size29	3.092e
+02	
## size30	1.328e
-02	
## size31	2.710e
-02	
## size32	6.896e
-02	
## size33	1.340e
-01	
## size34	1.186e
-01	
## size35	2.476e
-01	
## size36	4.096e
-01	
## size37	8.031e
+01	
## size38	5.563e
+02	
## size40	1.398e
-02	
## size41	2.996e
-02	
## size42	2.618e
-02	
## size43	3.944e
-02	
## size44	9.959e
+01	
## size45	4.494e
-02	
## size46	1.127e
-01	

## size47	1.451e
-01	
## size48	1.130e
+02	
## size49	9.241e
+01	
## size50	2.069e
-02	
## size51	1.235e
-01	
## size52	1.113e
-01	
## size53	1.291e
-01	
## size54	1.477e
-01	
## size55	6.384e
+01	
## size56	9.745e
+01	
## size57	6.735e
+01	
## size58	1.641e
+02	
## size59	1.335e
+02	
## size60	1.632e
-02	
## size61	5.557e
+01	
## size62	1.000e
+00	
## size63	1.240e
+02	
## size64	3.113e
+02	
## size65	3.200e
+02	
## size66	3.550e
+02	
## size67	1.407e
+02	
## size68	1.064e
+03	
## size69	1.098e
+03	
## size70	9.287e
-02	
## size71	1.010e
+02	

## size72	2.306e
+02	
## size73	5.484e
+02	
## size74	9.089e
+02	
## size75	2.051e
+02	
## size76	8.429e
+02	
## size77	5.694e
+02	
## size78	1.226e
+03	
## size79	2.897e
+03	
## size80	1.102e
-01	
## size90	4.737e
-02	
## size98	4.528e
-02	
## size99	6.904e
-02	
##	
## (Intercept)	z value
## sexMale	-30.744
## racethAsian or Pacific Islander	13.695
## racethBlack	0.437
## racethWhite	-9.969
## regionCounties in metropolitan areas of 250,000 to 1 million pop	-1.499
## regionCounties in metropolitan areas of lt 250 thousand pop	-4.325
## regionNonmetropolitan counties adjacent to a metropolitan area	-1.592
## regionNonmetropolitan counties not adjacent to a metropolitan area	-2.129
## regionUnknown/missing/no match (Alaska or Hawaii - Entire State)	-0.278
## regionUnknown/missing/no match/Not 1990-2023	1.767
## age01-04 years	-0.085
## age05-09 years	0.170
## age10-14 years	-5.653
## age15-19 years	-6.195
## age20-24 years	-8.604
## age25-29 years	-17.140
## age30-34 years	-22.877
## age35-39 years	-28.157
## age40-44 years	-29.899
## age45-49 years	-31.336
## age50-54 years	-31.434
## age55-59 years	-32.749
## age60-64 years	-33.097
## age65-69 years	-34.275
	-35.399

## age70-74 years	-35.720
## age75-79 years	-35.815
## age80-84 years	-35.182
## age85-89 years	-34.237
## age90+ years	-32.428
## marryMarried (including common law)	-8.131
## marrySeparated	-0.547
## marrySingle (never married)	-0.068
## marryUnmarried or Domestic Partner	-1.674
## marryWidowed	3.315
## gradeModerately differentiated; Grade II	66.583
## gradeNK cell; natural killer cell (1995+)	7.195
## gradeNull cell; non T-non B	5.719
## gradePoorly differentiated; Grade III	75.008
## gradeT-cell	24.799
## gradeUndifferentiated; anaplastic; Grade IV	83.753
## gradeWell differentiated; Grade I	71.056
## size10	8.275
## size11	-0.236
## size12	-1.801
## size13	-3.288
## size14	-6.441
## size15	-3.929
## size16	-0.091
## size17	-0.038
## size18	-0.017
## size19	0.015
## size20	-0.389
## size21	-16.411
## size22	-49.788
## size23	-28.811
## size24	-21.951
## size25	10.327
## size26	0.270
## size27	1.445
## size28	-7.583
## size29	-0.050
## size30	12.202
## size31	135.551
## size32	-6.886
## size33	-22.978
## size34	9.359
## size35	-3.363
## size36	-8.606
## size37	-0.192
## size38	-0.028
## size40	32.011
## size41	-17.101
## size42	47.895
## size43	59.749

## size44	-0.155
## size45	12.228
## size46	-0.818
## size47	-4.860
## size48	-0.137
## size49	-0.168
## size50	-70.973
## size51	-30.839
## size52	-17.627
## size53	-14.064
## size54	-8.549
## size55	-0.253
## size56	-0.161
## size57	-0.232
## size58	-0.094
## size59	-0.116
## size60	132.510
## size61	-0.282
## size62	-4.791
## size63	-0.125
## size64	-0.051
## size65	-0.048
## size66	-0.043
## size67	-0.110
## size68	-0.015
## size69	-0.014
## size70	-11.782
## size71	-0.157
## size72	-0.068
## size73	-0.029
## size74	-0.017
## size75	-0.076
## size76	-0.018
## size77	-0.028
## size78	-0.013
## size79	-0.005
## size80	-6.036
## size90	28.680
## size98	149.717
## size99	24.953
##	Pr(> z )
## (Intercept)	< 2e-1
6 ***	< 2e-1
## sexMale	< 2e-1
6 ***	
## racethAsian or Pacific Islander	0.66215
1	
## racethBlack	< 2e-1
6 ***	

## racethWhite	0.13383
9	
## regionCounties in metropolitan areas of 250,000 to 1 million pop	1.53e-0
5 ***	
## regionCounties in metropolitan areas of lt 250 thousand pop	0.11149
0	
## regionNonmetropolitan counties adjacent to a metropolitan area	0.03324
3 *	
## regionNonmetropolitan counties not adjacent to a metropolitan area	0.78071
1	
## regionUnknown/missing/no match (Alaska or Hawaii - Entire State)	0.07714
8 .	
## regionUnknown/missing/no match/Not 1990-2023	0.93245
8	
## age01-04 years	0.86496
7	
## age05-09 years	1.58e-0
8 ***	
## age10-14 years	5.84e-1
0 ***	
## age15-19 years	< 2e-1
6 ***	
## age20-24 years	< 2e-1
6 ***	
## age25-29 years	< 2e-1
6 ***	
## age30-34 years	< 2e-1
6 ***	
## age35-39 years	< 2e-1
6 ***	
## age40-44 years	< 2e-1
6 ***	
## age45-49 years	< 2e-1
6 ***	
## age50-54 years	< 2e-1
6 ***	
## age55-59 years	< 2e-1
6 ***	
## age60-64 years	< 2e-1
6 ***	
## age65-69 years	< 2e-1
6 ***	
## age70-74 years	< 2e-1
6 ***	
## age75-79 years	< 2e-1
6 ***	
## age80-84 years	< 2e-1
6 ***	
## age85-89 years	< 2e-1
6 ***	

## age90+ years	< 2e-1
6 ***	
## marryMarried (including common law)	4.24e-1
6 ***	
## marrySeparated	0.58469
9	
## marrySingle (never married)	0.94543
1	
## marryUnmarried or Domestic Partner	0.09410
7 .	
## marryWidowed	0.00091
8 ***	
## gradeModerately differentiated; Grade II	< 2e-1
6 ***	
## gradeNK cell; natural killer cell (1995+)	6.24e-1
3 ***	
## gradeNull cell; non T-non B	1.07e-0
8 ***	
## gradePoorly differentiated; Grade III	< 2e-1
6 ***	
## gradeT-cell	< 2e-1
6 ***	
## gradeUndifferentiated; anaplastic; Grade IV	< 2e-1
6 ***	
## gradeWell differentiated; Grade I	< 2e-1
6 ***	
## size10	< 2e-1
6 ***	
## size11	0.81373
0	
## size12	0.07169
0 .	
## size13	0.00101
0 **	
## size14	1.19e-1
0 ***	
## size15	8.53e-0
5 ***	
## size16	0.92751
8	
## size17	0.96969
7	
## size18	0.98645
3	
## size19	0.98818
3	
## size20	0.69695
3	
## size21	< 2e-1
6 ***	

## size22	< 2e-1
6 ***	< 2e-1
## size23	< 2e-1
6 ***	< 2e-1
## size24	< 2e-1
6 ***	< 2e-1
## size25	< 2e-1
6 ***	< 2e-1
## size26	0.78697
8	
## size27	0.14851
4	
## size28	3.38e-1
4 ***	
## size29	0.95978
5	
## size30	< 2e-1
6 ***	< 2e-1
## size31	< 2e-1
6 ***	< 2e-1
## size32	5.72e-1
2 ***	
## size33	< 2e-1
6 ***	< 2e-1
## size34	< 2e-1
6 ***	< 2e-1
## size35	0.00077
1 ***	
## size36	< 2e-1
6 ***	< 2e-1
## size37	0.84808
0	
## size38	0.97733
9	
## size40	< 2e-1
6 ***	< 2e-1
## size41	< 2e-1
6 ***	< 2e-1
## size42	< 2e-1
6 ***	< 2e-1
## size43	< 2e-1
6 ***	< 2e-1
## size44	0.87711
9	
## size45	< 2e-1
6 ***	< 2e-1
## size46	0.41316
9	
## size47	1.18e-0
6 ***	

## size48	0.89113
4	
## size49	0.86695
8	
## size50	< 2e-1
6 ***	
## size51	< 2e-1
6 ***	
## size52	< 2e-1
6 ***	
## size53	< 2e-1
6 ***	
## size54	< 2e-1
6 ***	
## size55	0.80013
7	
## size56	0.87234
4	
## size57	0.81690
8	
## size58	0.92485
5	
## size59	0.90748
7	
## size60	< 2e-1
6 ***	
## size61	0.77820
6	
## size62	1.66e-0
6 ***	
## size63	0.90022
7	
## size64	0.95971
8	
## size65	0.96148
8	
## size66	0.96530
8	
## size67	0.91266
5	
## size68	0.98828
7	
## size69	0.98871
4	
## size70	< 2e-1
6 ***	
## size71	0.87531
9	
## size72	0.94586
3	

```

## size73          0.97724
8
## size74          0.98631
2
## size75          0.93979
7
## size76          0.98535
7
## size77          0.97803
7
## size78          0.98988
4
## size79          0.99573
6
## size80          1.58e-0
9 ***
## size90          < 2e-1
6 ***
## size98          < 2e-1
6 ***
## size99          < 2e-1
6 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 873451  on 2035845  degrees of freedom
## Residual deviance: 559836  on 2035731  degrees of freedom
##   (3113162 observations deleted due to missingness)
## AIC: 560066
##
## Number of Fisher Scoring iterations: 17

```

The missingness in stage is likely not MCAR, because missingness depends significantly on several observed variables (e.g., sex, raceth, region, age, marry, grade, size). Therefore, it's reasonable to assume MAR (Missing at Random) for modeling purposes.

## 2.4 Selecting Complete Cases

```

seer_prime <- seer_prime %>%
  filter(complete.cases(.))

total_cases <- nrow(seer)
complete_cases <- nrow(seer_prime)
percent_complete <- round(100 * complete_cases / total_cases, 2)

cat("Complete cases:", complete_cases, "out of", total_cases,
  sprintf("(%.2f%% complete)\n", percent_complete))

```

```
## Complete cases: 209123 out of 5149008 (4.06% complete)
```

we have 209123 cases to work with (4.06% of the whole thing) after removing “Unknown” and “Blank(s)” Values.

Further cleaning is done via tabling all variables.

## 2.5 Cancer Site

We want to filter for top ten cancer sites (breast, lung, etc). We exclude 998 and 999 because they are unknown. The code is structured so we can switch sites.

```
seer_prime <- seer_prime %>%
  filter(!(site %in% c("998", "999")))

top_sites <- seer_prime %>%
  count(site, sort = TRUE) %>%
  slice_head(n = 10)

seer_prime <- seer_prime %>%
  filter(site %in% top_sites$site)

table(seer_prime$site)

##
##  010  012  015  018  020  025  030  035  040  050
## 4269 3940 5738 3284 5440 4994 6046 3768 4953 4415
```

## 2.6 Region

REGION: collapse and recode into ordered, interpretable regional factors, removes the Alaska/Hawaii “unknown” entries.

```
seer_prime <- seer_prime %>%
  mutate(
    region = case_when(
      str_detect(region, "1 million") ~ "Large",
      str_detect(region, "lt 250") | str_detect(region, "250,000") ~ "Small",
      str_detect(region, "adjacent") | str_detect(region, "not adjacent") ~ "Nonmetro",
      TRUE ~ NA_character_
    ),
    region = factor(region, levels = c("Large", "Small", "Nonmetro"))
  )
table(seer_prime$region)

##
##      Large     Small Nonmetro
##      39835     2410     4497
```

## 2.7 Tumor Stage

STAGE: restrict to tumors that are invasive (drop In situ, Unknown/unstaged).

```
seer_prime <- seer_prime %>%
  mutate(
    stage = case_when(
      stage %in% c("Localized", "Regional", "Distant") ~ stage,
      TRUE ~ NA_character_
    ),
    stage = factor(stage, levels = c("Localized", "Regional", "Distant"))
  )
table(seer_prime$stage)

##
## Localized   Regional   Distant
##       26446      13382      3918
```

## 2.8 Tumor Grade

GRADE: extract numeric grade 1–4; drop cell-line entries (“B-cell”, “T-cell” etc.). Convert them to Start (1/2) and End (3/4) since our model is logistic

```
seer_prime <- seer_prime %>%
  mutate(
    grade = case_when(
      str_detect(grade, "I\$") ~ "1",
      str_detect(grade, "II\$") ~ "2",
      str_detect(grade, "III\$") ~ "3",
      str_detect(grade, "IV\$") ~ "4",
      TRUE ~ NA_character_
    ),
    grade = case_when(
      grade %in% c("1", "2") ~ "Start",
      grade %in% c("3", "4") ~ "End",
      TRUE ~ NA_character_
    ),
    grade = factor(grade, levels = c("Start", "End"), ordered = FALSE)
  )
table(seer_prime$grade)

##
## Start   End
## 42877  3650
```

## 2.9 Tumor Size

SIZE: Making this numeric and then filtering implausible values, we can bin these (“≤20mm”, “21–50mm”, “51–100mm”, “>100mm”) if needed.

```

seer_prime <- seer_prime %>%
  mutate(
    size = as.numeric(size),
    size = ifelse(size > 0 & size <= 200, size, NA)
  )
summary(seer_prime$size)

##      Min. 1st Qu. Median      Mean 3rd Qu.      Max.      NA's
##    10.00   23.00  30.00    34.66  44.00   99.00   6305

```

## 2.10 Marital Status

MARRY: Making this binary, only married or unmarried.

```

seer_prime <- seer_prime %>%
  mutate(
    marry = case_when(
      str_detect(marry, "Married") ~ "Married",
      TRUE ~ "Unmarried"
    ),
    marry = factor(marry)
  )
table(seer_prime$marry)

##
##      Married Unmarried
##        28032     18815

```

## 2.11 Race

Recode RACETH to be three levels

```

seer_prime <- seer_prime %>%
  mutate(
    raceth = case_when(
      raceth == "White" ~ "W",
      raceth == "Black" ~ "B",
      TRUE ~ "O"
    ),
    raceth = factor(raceth, levels = c("W", "B", "O"))
  )
table(seer_prime$raceth)

##
##      W      B      O
##  36288  3978  6581

```

## 2.12 Complete Summary of available data

Seeing how many cases are available now:

```

seer_prime <- seer_prime %>% filter(complete.cases(id, region, stage, age, sex, raceth, grade, size, site, marry, year))
cat("Remaining complete cases:", nrow(seer_prime), "\n")
## Remaining complete cases: 37530

```

## 3 Hierachal Encoding

To do hierachal models in R, identifiers must be encoded as numeric integers (e.g., 1, 2, ..., N) for levels like REGION and ID.

```

seer_prime <- seer_prime %>%
  mutate(
    regionid = as.integer(factor(region)),
    patientid = as.integer(factor(id)))
)

```

Setting factor and checking data structure.

```

seer_prime <- seer_prime %>%
  mutate(
    age = factor(age),
    sex = factor(sex),
    raceth = factor(raceth),
  )

```

Inspect the data:

```

str(seer_prime)

## 'data.frame': 37530 obs. of 13 variables:
## $ id      : int 1028 1034 1152 2172 4489 5518 9181 9314 9415 10092 ...
## $ region   : Factor w/ 3 levels "Large","Small",...: 1 1 1 1 1 1 1 1 1 1 ...
## ...
## $ stage    : Factor w/ 3 levels "Localized","Regional",...: 1 1 1 1 1 1 1 1 2 1 2 ...
## $ age      : Factor w/ 20 levels "00 years","01-04 years",...: 14 16 17 19 15 13 17 18 18 17 ...
## $ sex      : Factor w/ 2 levels "Female","Male": 1 2 2 2 1 1 1 1 1 1 ...
## $ raceth   : Factor w/ 3 levels "W","B","O": 1 2 1 3 1 2 3 1 3 1 ...
## $ grade    : Factor w/ 2 levels "Start","End": 1 1 1 2 1 1 1 1 2 1 ...
## $ size     : num 30 30 38 27 22 49 22 50 27 27 ...
## $ year     : int 2017 2016 2016 2017 2017 2016 2017 2017 2017 2016 ...
## $ marry    : Factor w/ 2 levels "Married","Unmarried": 1 2 1 2 2 2 1 1 2 2 ...
## $ site     : chr "020" "025" "035" "020" ...
## $ regionid: int 1 1 1 1 1 1 1 1 1 ...
## $ patientid: int 1 2 3 4 5 6 7 8 9 10 ...

```

## 4 Saving Final Data

Code here so you can save it as CSV: 37530 observations of 13 variables

```
write.csv(seer_prime, "../data/clean/seer_nov13.csv", row.names = FALSE)
```