

ABSTRACT

Breast cancer, the most commonly diagnosed cancer among women in the USA, demands accurate survival rate estimation. This critical information plays a pivotal role in guiding patients, their families, and healthcare professionals toward informed decisions, financial planning, and personalized treatment strategies. Our project involved meticulous curation of data from over 300,000 patients (spanning 2011-2015) and rigorous exploratory analyses.

During this process, we conducted correlation, Fisher, and Chi-square analyses to identify the most crucial parameters. From the original 36 features extracted using SEER *STAT software, we pinpointed 16 essential variables. The data underwent thorough examination and preparation, including specialized encoding techniques such as one-hot. Dealing with large databases, handling missing values, and selecting the right tools were some of the challenges we encountered and valuable lessons we learned.

Subsequently, we divided the cleaned and prepared dataset and applied machine learning techniques, including random forest, logistic regression, and deep neural network. Our approach addressed complexities related to both categorical and numerical variables, as well as handling missing data. Random Forest demonstrated better accuracy and acceptable speed in predicting breast cancer patient survival rates.

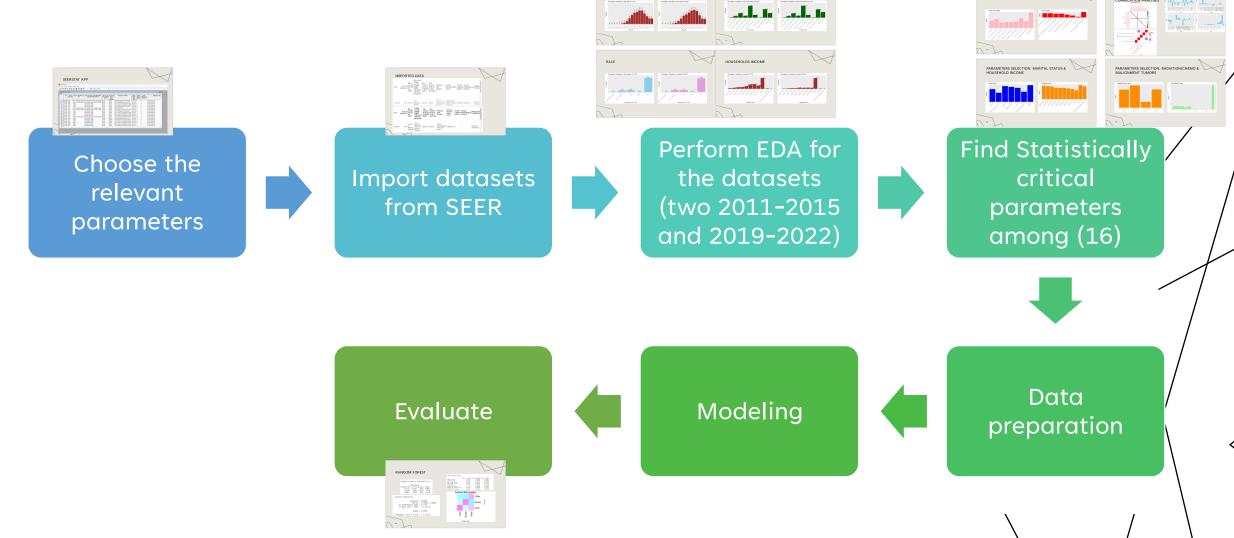
While our model is not intended for clinical use and lacks the rigor of a scientific investigation, it showcases remarkable success in estimating survival rates based on the training data. Furthermore, we extended its application to previously unseen databases from 2019-2022, comprising over 133,000 cases, allowing us to compare survival predictions against the next available dataset in the SEER program.

INTRO – WHAT & WHY

- 670,000 have lost their life to breast cancers globally in 2022 (43,700 in USA)
- Breast cancer was the most common cancer in women in 157 countries out of 185 in 2022
- Breast cancer is the most diagnosed cancer among U.S. women.
- It is also personal to me.

- Accurate survival prediction is critical for patient management
- Precise survival estimates help allocate healthcare resources effectively
- Patients and their families can make informed decisions about treatment options.
- Quality of Life Considerations
- And Economic consideration.

HOW - FLOWCHART



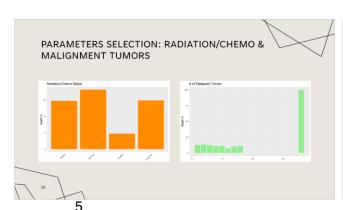
DATA DISPLAY AND PRELIMINARY ANALYSES

Survival rate 2011–2015 of 300K: 75%

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

Marital status and survival

Marital status at diagnosis	Event Population	Population	Group % in total	Death %
Divorced	4399	32214	10.61	13.66
Married (including common law)	15694	160551	52.89	9.78
Separated	544	3225	1.06	16.87
Single (never married)	7161	44678	14.72	16.03
Unknown	2774	18481	6.09	15.01
Unmarried or Domestic Partner	110	1014	0.33	10.85
Widowed	7790	43394	14.30	17.95





Principal Parameter selection

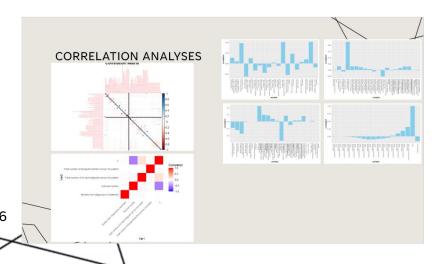
- Evaluation the data, empty, correlation analyses, normality analyses,
- Among 36 parameters 16 found critical: treatment (chemo/radiation, surgery), # tumors, months from diagnosis to treatment, race, grade, and type
- Data were analyzed using bootstrapping and random sampling to avoid the size using Chissquare and Fisher exact test
- Many collinearities were identified and removed like sex, Origin Recode, Diagnostic confirmation, ...

		\
variable	p_value	\
Race recode (W, B, AI, API)	0.0004998	Fisher
Primary Site - labeled	0.0004998	
Grade Recode (thru 2017)	0.0004998	/ Exact with
Laterality	0.0004998	simulation
Chemotherapy recode (yes, no/unk)	0.0004998	Simulation
Reason no cancer-directed surgery	0.0004998	.p.value=
Survival months flag	0.0004998	. / /
First malignant primary indicator	0.0004998	RUE due \
Marital status at diagnosis	0.0004998	to size of
Median household income inflation adj to 2021	0.0004998	10/3120 07
Age recode (<60,60-69,70+)	0.0004998	the
COD	0.0004998	
Radiation	0.0004998	s¢mple!
Rural-Urban Continuum Code	0.0011294	

HYPOTHESIS/CORRELATION EVALUATION

Summary

- Many collinearity have found and remove from the data
- Stepwise correlation analyses was performed to removed unimportant and poorly correlated parameters such as
- Both numerical and categorical data were analyzed for correlation analyses
- Dealing with categorical data was challenging specifically encoding the data for analyses



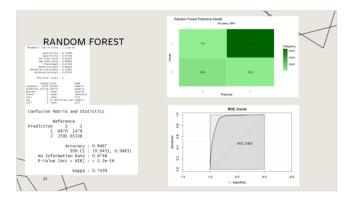
Unimportant (Total of 16)	Important (total of 16)
Different race related indicators were in the data base (all removed expect one)	(+)Months from diagnosis to treatment
Sex	(-) Total number of in situ/malignant tumors for patient
Patient ID	(-) Total number of benign/borderline tumors for patient
Year of death (the survival month exists)	Age
Sequence number	Race (W, B, AI, API)
Radiation/chemo recode (combined as one code)	Label
Year of diagnosis	Grade
Rural urban continuum	Type of tumor
	Treatment (Radiation/Surgery/Chemo)
	Income
	Marital Status

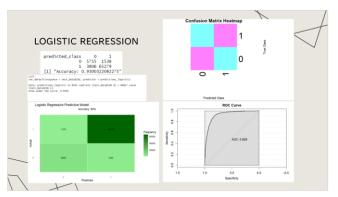
DATA ANALYSES, EVALUATION, & SUMMARY

• Summary

- Random Forest was the easiest to apply and reasonably fast
- Logistic Regression was the fast, but still accurate
- The accuracy of 94% and 93% for RF and Logistic Regression were achieved.
- Logistic regression was easier to apply compared to Random Forrest.

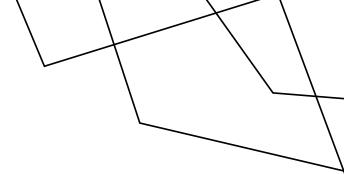
Method	Accuracy (Survival)
Logistic Regression	93%
Random Forest	94%







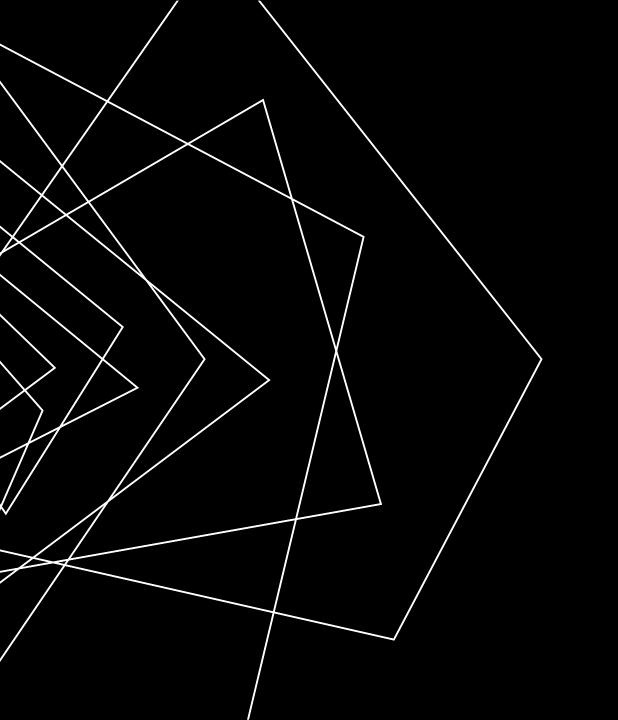
CONCLUSION



- A combined categorical and numerical data collected by SEER can be used for survival prediction of breast cancer with acceptable accuracy of 94%.
- Random Forest Simplicity: Opt for user-friendly models like Random Forest.
- Logistic regression is a powerful and reliable tool for a quick and relatively accurate survival rate estimate
- Correlation analyses of the large database including categorical data is challenging
- For this sort of problem Neural Network did not offer a better result than random Forrest.

REFERENCES:

- [1] SEER (https://seer.cancer.gov/data/access.html)
- [2] zgalochkina/SEER_solid_tumor: R code for SEER data analysis of solid tumor in different populations (github.com)
- [3] XAI_Healthcare_eXplainable_AI_in_Healthcare.pdf (upc.edu)
- [4] Pargen, F., Pfisterer, F., Thomas, J., Bischl, B.: Regularized target encoding out performs traditional methods in supervised machine learning with high cardinality features. Computational Statistics 37(5), 2671–2692 (Nov 2022)
- [5] American Cancer Society Breast Cancer Survival Rates
- GitHub: <u>koohpi/Breast_Cancer_Survival_Project</u>: A <u>non-scientific project for breast cancer survival rate estimate in women based on SEER DB (github.com)</u>
- Rpub: RPubs Breast Cancer Survival Rate With SEER



THANK YOU

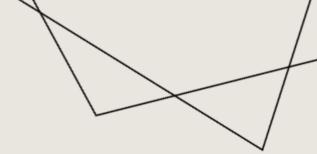
Koohyar Pooladvand koohyar.pooladvand69@cuny.spsmail.edu

IMPORTED DATA

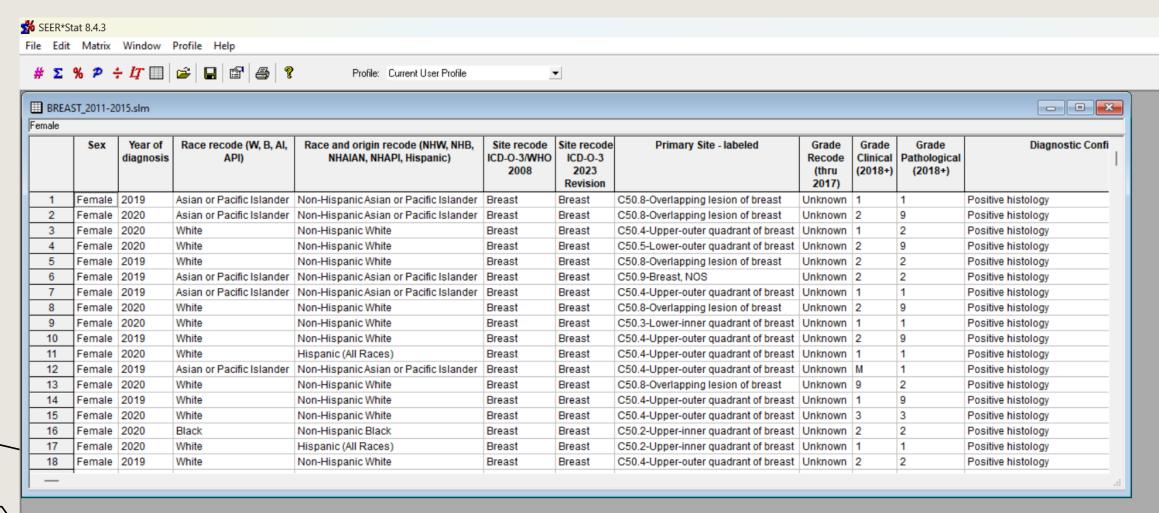
Sex	Race Year of recode diagnosis (W, B, AI, API)	Race and origin recode (NHW, NHB, NHAIAN, NHAPI, Hispanic)	ICD-O-	ICD-O-	labeled	Recode (thru	Grade Clinical (2018+)	Pathological	Diagno Confir
Female	2015 White	Non- Hispanic White	Breast	Breast	C50.4- Upper-outer quadrant of	Moderately differentiated; Grade II	Blank(s)	Blank(s)	Positive histolog
		aniain							

Sex	Race Year of (W, B, diagnosis AI, API)	NHR	ICD-O-	ICD-O-	labeled	(thru	Grade Clinical (2018+)	Pathological	Diagnostic Confirmat
Female	Asian 2019 or Pacific Islander	Pacific	Breast	Breast	C50.8- Overlapping lesion of breast	Unknown	1	1	Positive histology

1

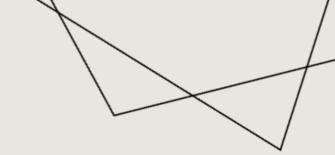


SEERSTAT APP

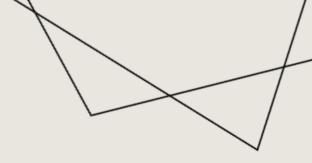


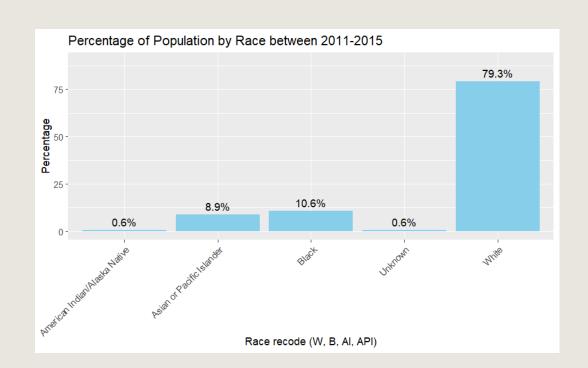


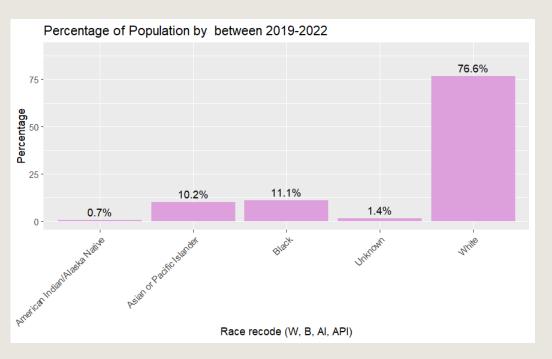
— Data Summary —	
Name Number of rows Number of columns	Values BREAST_DF_surv_clean 303557 18
Column type frequency: factor numeric	14 4
Group variables — Data Summary ————	None
Name Number of rows Number of columns	Values BREAST_DF_eval_clean 131395 17
Column type frequency: factor numeric	13 4
Group variables	None



RACE



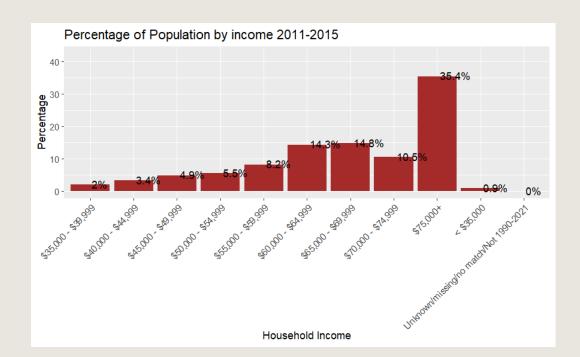


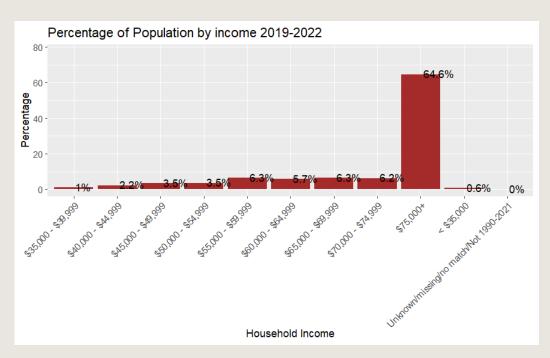


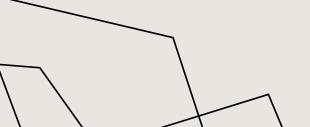




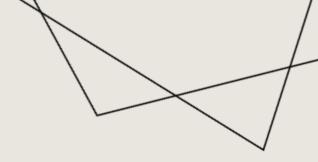
HOUSEHOLDS INCOME

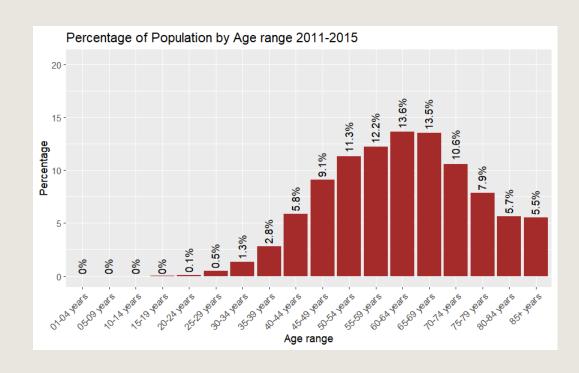


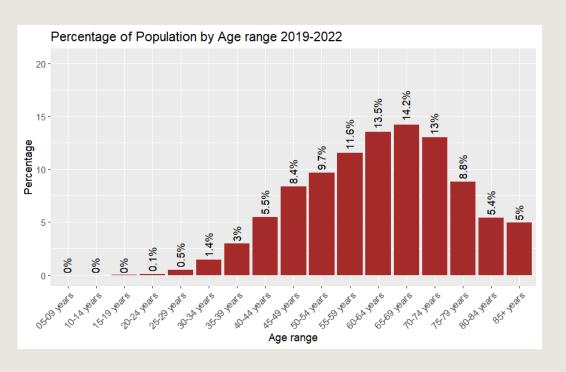




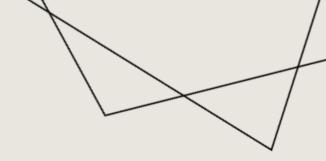




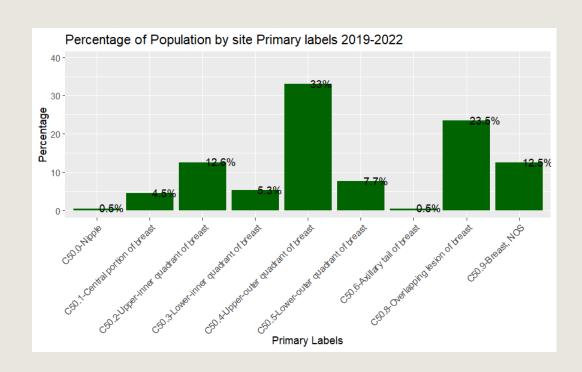


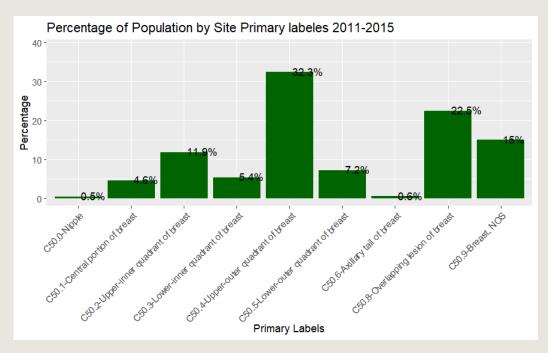




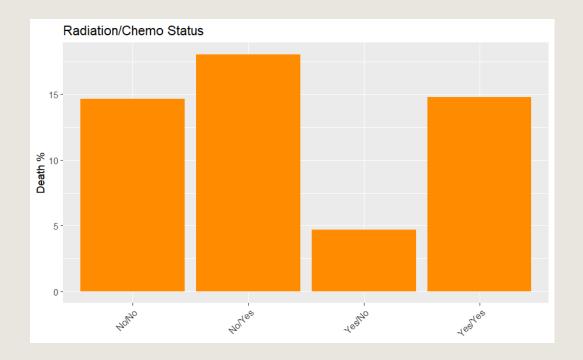


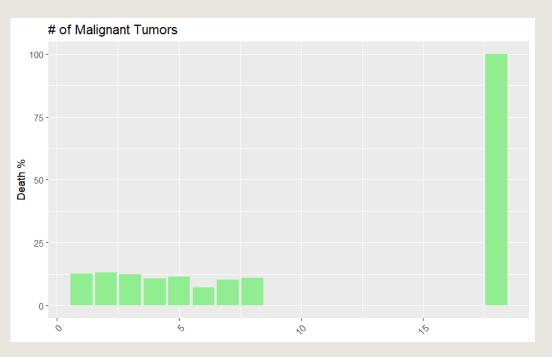
CANCER PRIMARY SITE LABELS





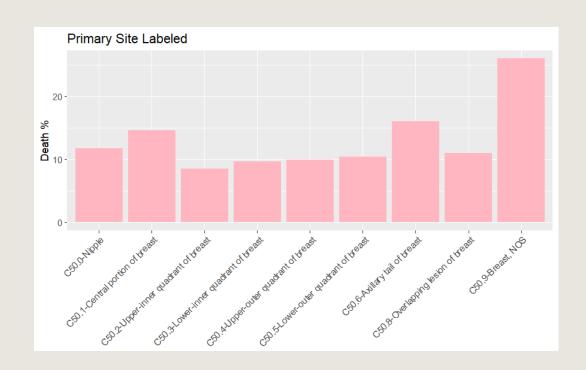
PARAMETERS SELECTION: RADIATION/CHEMO & MALIGNMENT TUMORS

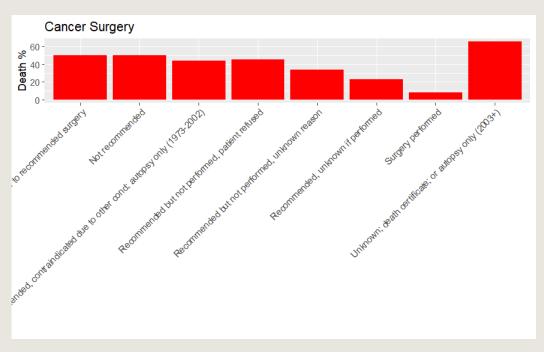




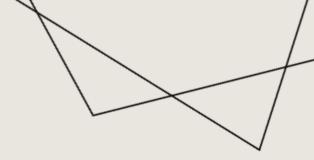


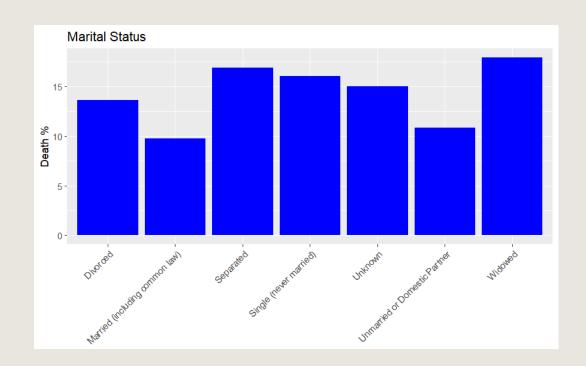
PARAMETERS SELECTION: PRIMARY SITE & SURGERY

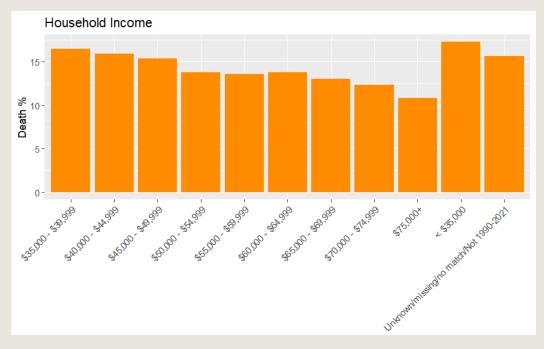


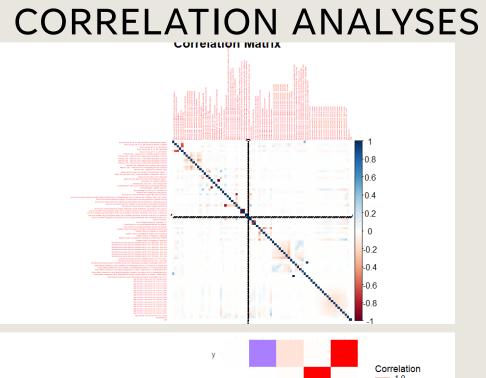


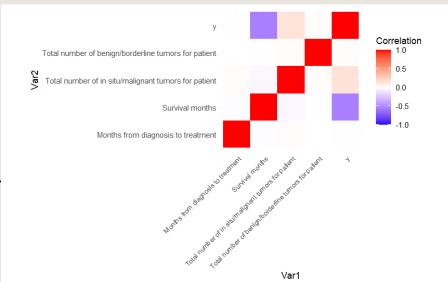


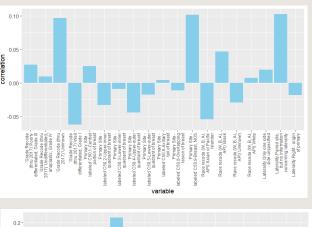


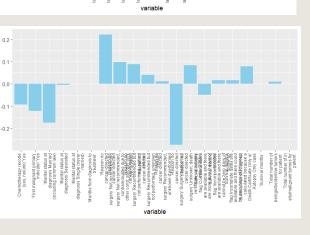


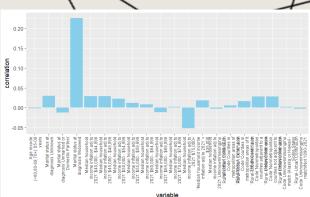


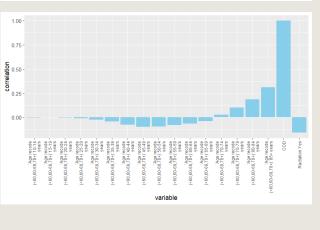












RANDOM FOREST

Confusion Matrix and Statistics

Reference

Prediction Alive Breast Other Alive 173595 6943 10682 Breast 2662 14334 4729 Other 1923 4220 11079

Overall Statistics

Accuracy : 0.8646

95% CI: (0.8632, 0.866)

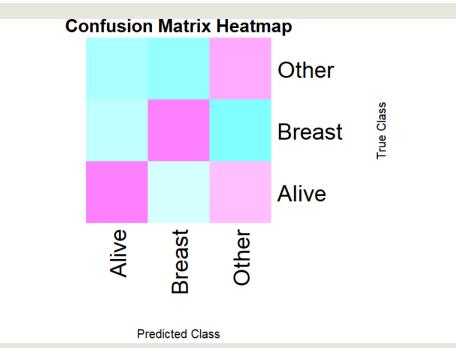
No Information Rate : 0.7741 P-Value [Acc > NIR] : < 2.2e-16

Kappa: 0.5992

Mcnemar's Test P-Value : < 2.2e-16

Statistics by Class:

	Class: Alive	Class: Breast	Class: Other
Sensitivity	0.9743	0.56218	0.41823
Specificity	0.6610	0.96389	0.96984
Pos Pred Value	0.9078	0.65979	0.64331
Neg Pred Value	0.8823	0.94645	0.92763
Prevalence	0.7741	0.11078	0.11509
Detection Rate	0.7542	0.06228	0.04813
Detection Prevalence	0.8308	0.09439	0.07482
Balanced Accuracy	0.8176	0.76304	0.69404



RANDOM FOREST

```
Sensitivity: 0.72900
           Specificity: 0.97786
        Pos Pred Value: 0.82495
        Neg Pred Value: 0.96186
            Prevalence: 0.12518
        Detection Rate: 0.09126
  Detection Prevalence: 0.11062
     Balanced Accuracy: 0.85343
       'Positive' Class : 1
         Length Class
                                  Mode
response 76378 factor
                                  numeric
predictor 152756 matrix
                                  numeric
percent
              1 -none-
                                  logical
levels
              2 -none-
                                  character
rocs
              1 -none-
                                  list
              1 mv.multiclass.auc numeric
auc
call
              3 -none-
                                  call
```

Mcnemar's Test P-Value : < 2.2e-16

Confusion Matrix and Statistics

Reference

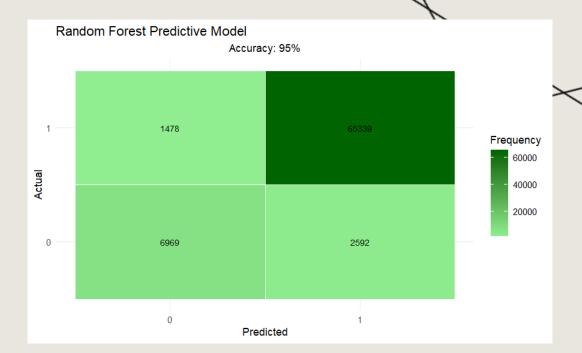
Prediction 1 2 1 6970 1479 2 2591 65338

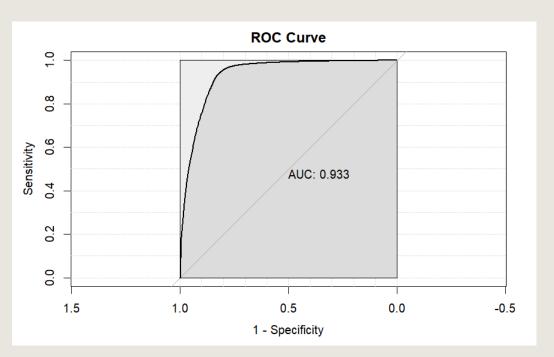
Accuracy: 0.9467

95% CI: (0.9451, 0.9483)

No Information Rate : 0.8748 P-Value [Acc > NIR] : < 2.2e-16

Kappa: 0.7439





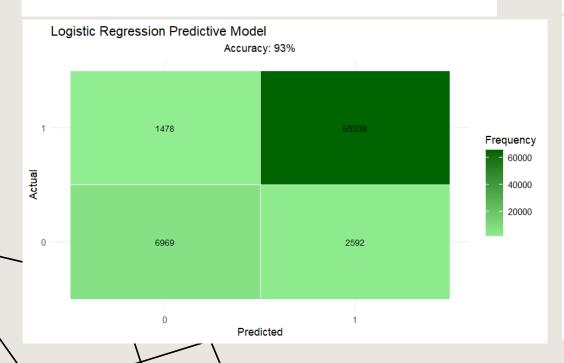
LOGISTIC REGRESSION

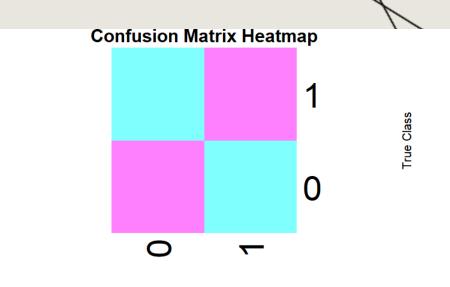
predicted_class 0 1 0 5755 1538 1 3806 65279 [1] "Accuracy: 0.9300322082275"

Call:
roc.default(response = test_data\$COD, predictor = predictions_logistic)

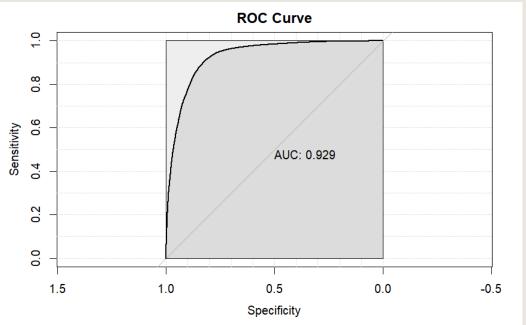
Data: predictions_logistic in 9561 controls (test_data\$COD 0) < 66817 cases (test_data\$COD 1).

Area under the curve: 0.9291



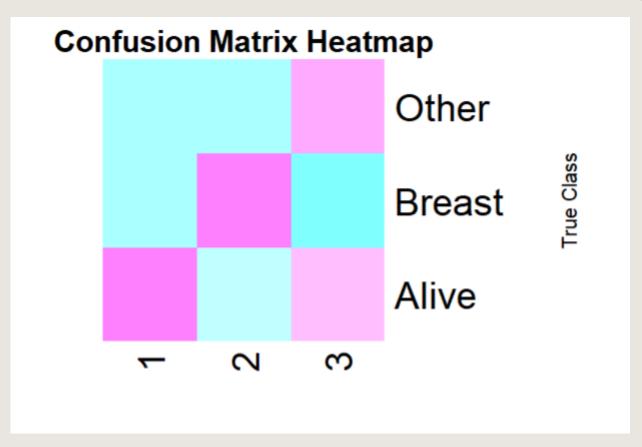








predicted_class 1 2 3 Alive 170984 5537 9856 Breast 4044 15950 5887 Other 3152 4010 10747 [1] "Accuracy: 0.858859002376535"



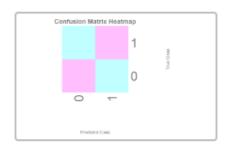


GRADIENT BOOSTING

```
[1] "Length of gredicted_class:"
[1] 76278
[1] "Length of test_data5000:"
[1] 76278
[1] "Confusion Matrix:"

predicted_class 0 1 0 0 4028 2108 1 2109 7008
[1] "Accuracy: 0.94280199439153"

R Console
```



- [1] "Length of predicted_class:"
- [1] 76378
- [1] "Length of test_data\$COD:"
- [1] 76378
- [1] "Confusion Matrix:"

```
predicted_class 0 1
0 64628 2198
1 2189 7363
```

[1] "Accuracy: 0.94256199429155"

