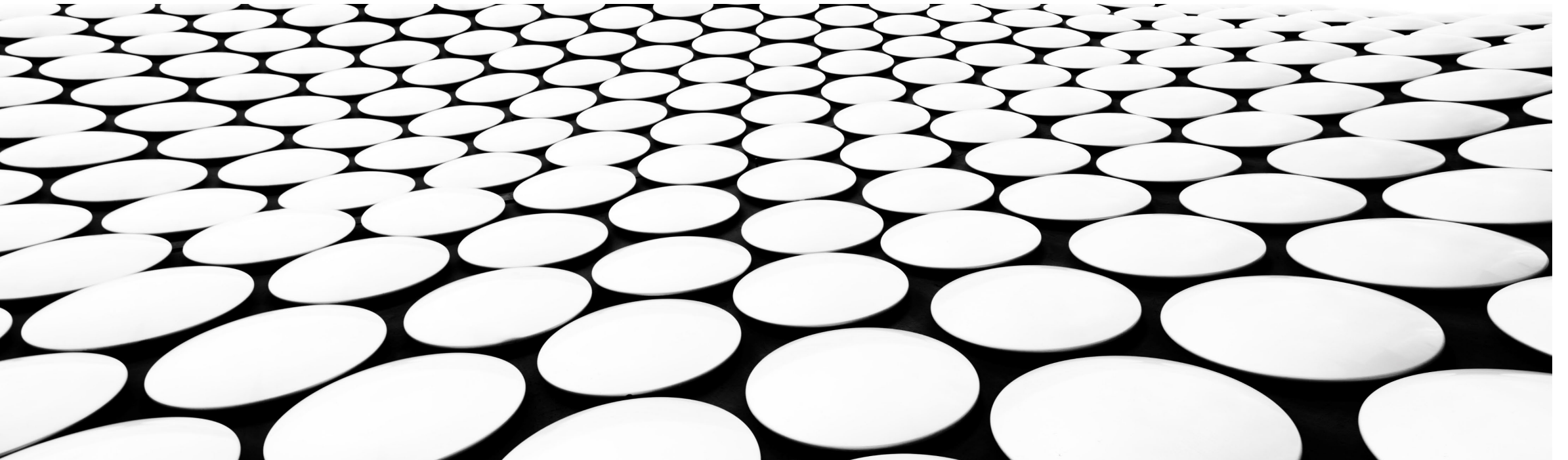
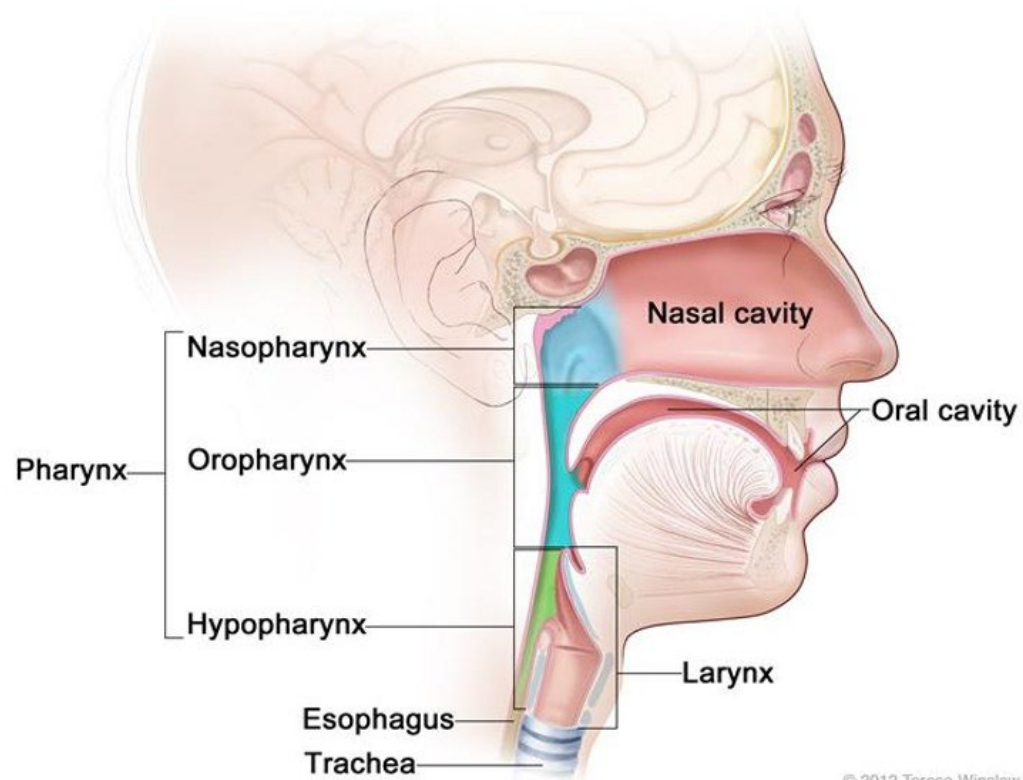

USING A MACHINE LEARNING STRATEGY TO PREDICT CANCER PATIENT OUTCOME BASED ON CLINICAL AND MOLECULAR FEATURES

TOM BELBIN



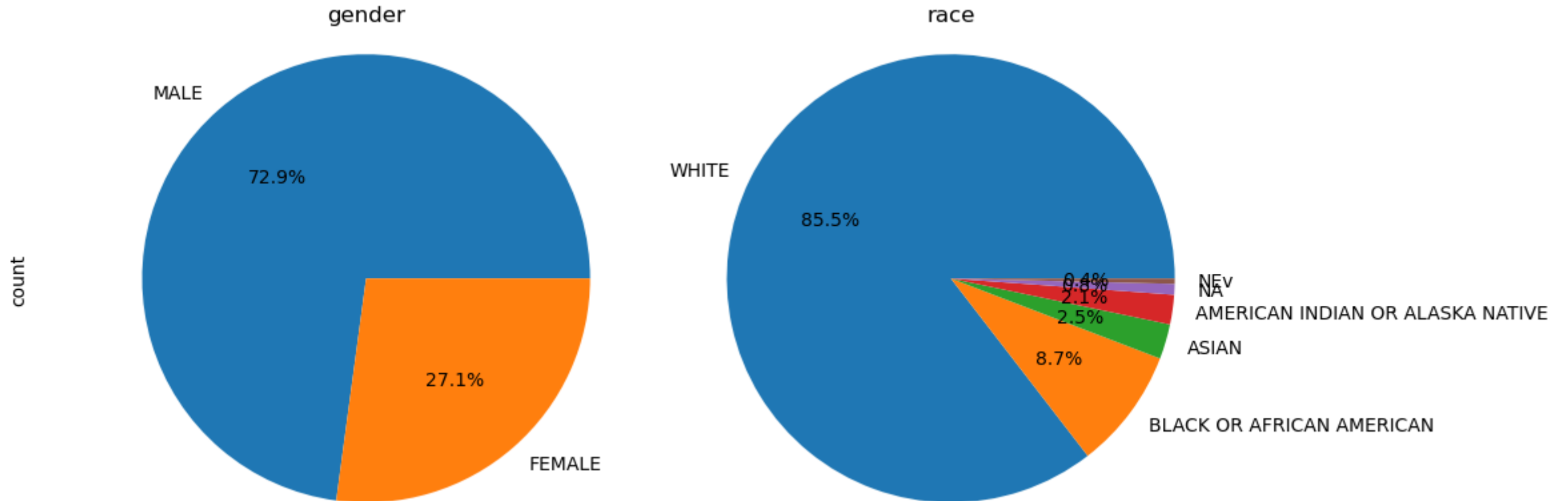
HEAD AND NECK CANCER



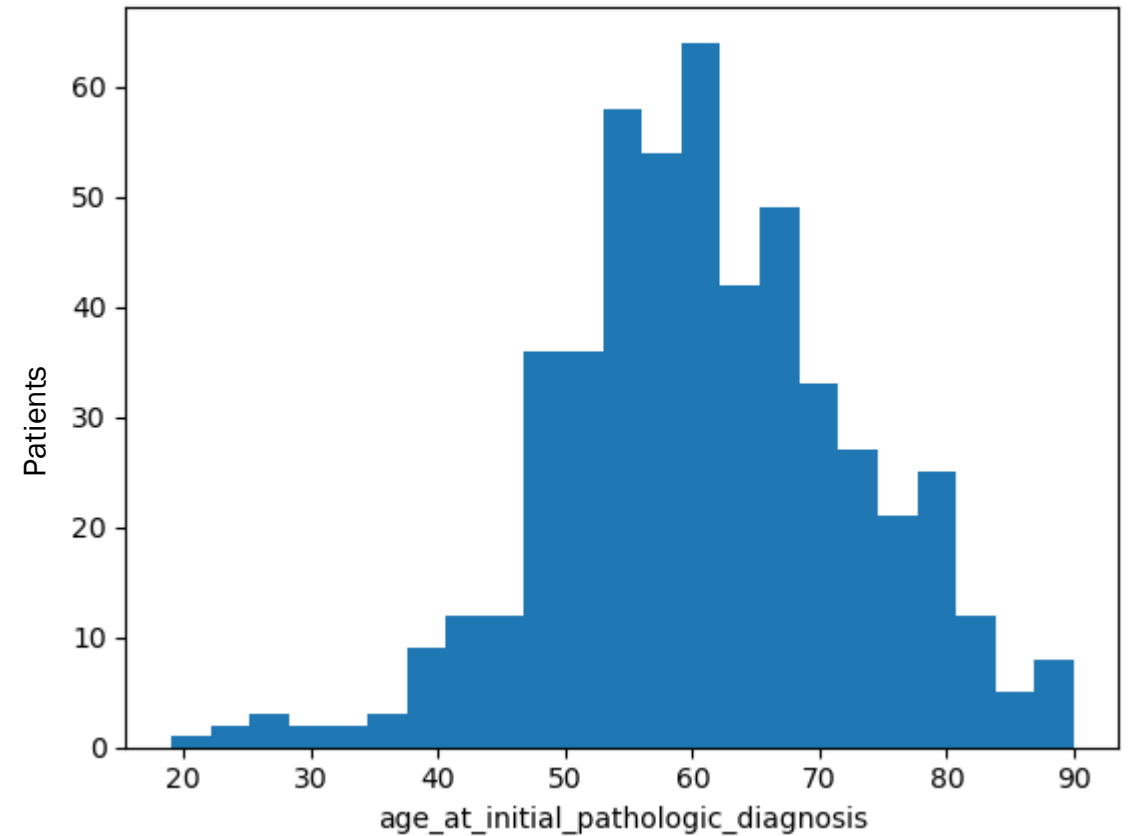
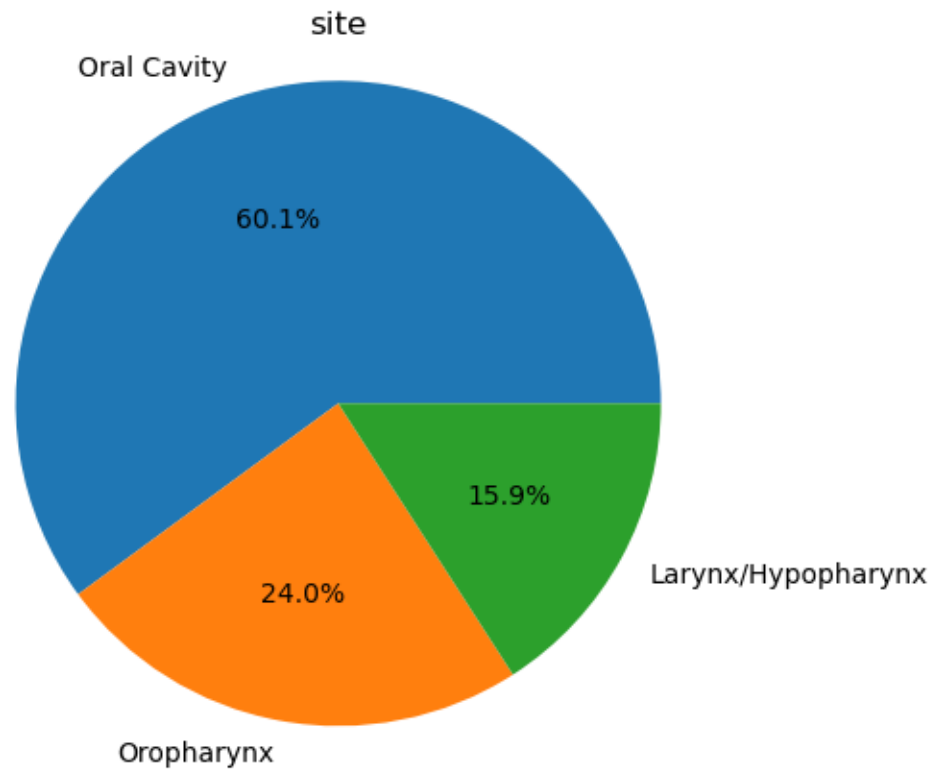
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- Tobacco use, alcohol consumption, HPV infection
- Surgery, radiation therapy, chemotherapy
- Speech, swallowing
- Recurrence
- 5-yr survival
- Biomarkers?

EXPLORATORY ANALYSIS OF THE TCGA HNSCC COHORT



EXPLORATORY ANALYSIS OF THE TCGA HNSCC COHORT



EXPLORATORY ANALYSIS OF THE TCGA HNSCC COHORT

Lymph nodes of the head and neck

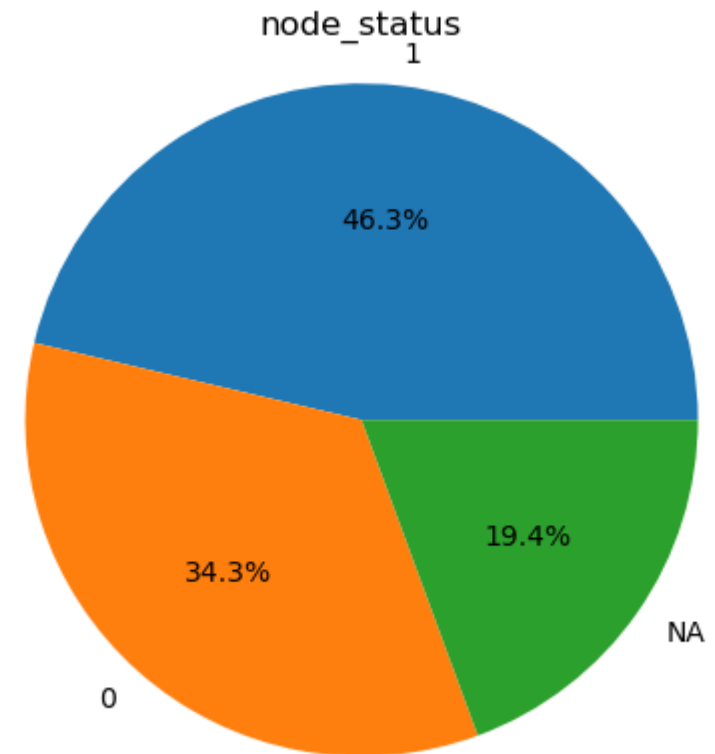
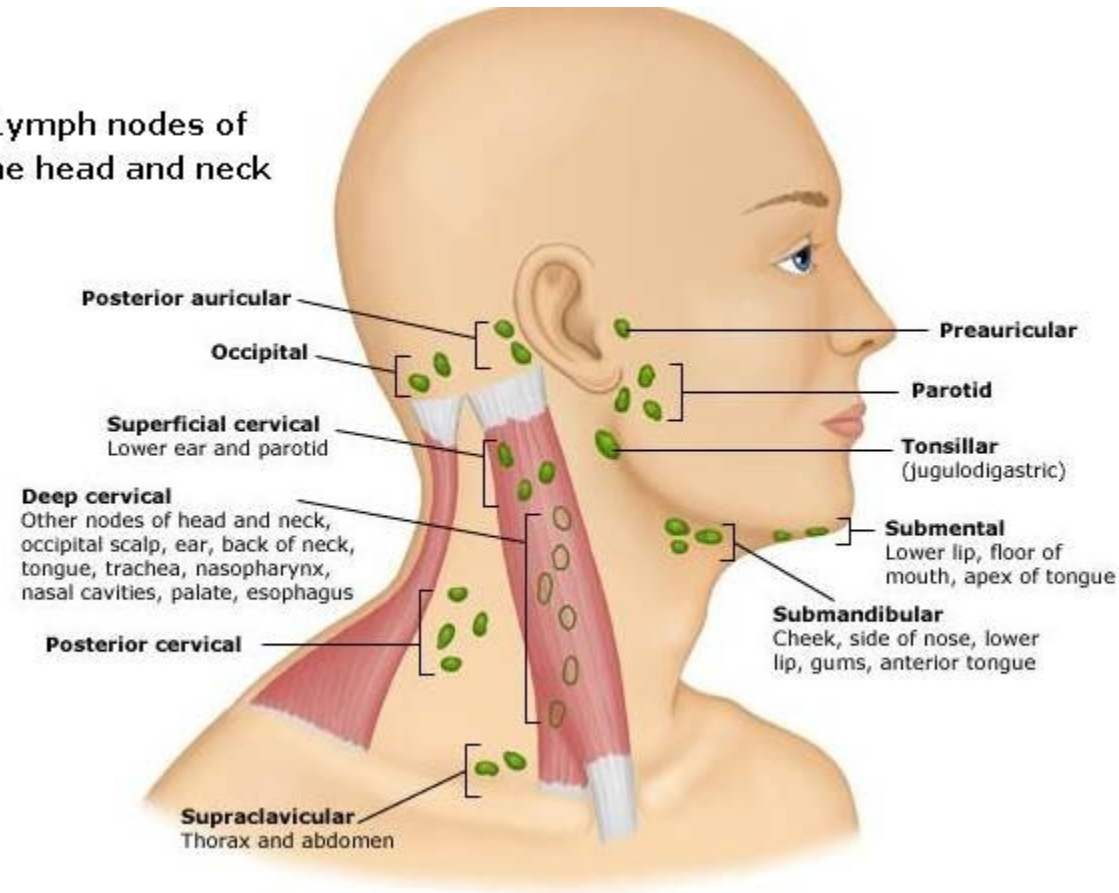


Table 1. HNSCC patient characteristics by tumor site							
		Oral Cavity		Oropharynx		Larynx	
		N=310		N=82		N=124	
		N	%	N	%	N	%
Gender							
	Male	206	66.5	69	84.1	101	81.5
	Female	104	33.5	13	15.9	23	18.5
Race							
	White	266	85.8	76	92.7	99	79.8
	Black or African American	20	6.5	6	7.3	19	15.3
	Asian	10	3.2	0	0	1	0.8
	American Indian or Alaska Native	1	0.3	0	0	1	0.8
	Information not available	13	4.2	0	0	4	3.2
Ethnicity							
	Hispanic/Latino	16	5.2	3	3.7	5	4
	Non-Hispanic/Latino	269	86.8	76	92.7	109	87.9
	Information not available	25	8.1	3	3.7	10	8.1
Smoking							
	Ever smoker	215	69.4	56	68.3	113	91.1
	Lifelong non-smoker	86	27.7	25	30.5	8	6.5
	Information not available	9	2.9	1	1.2	3	2.4
HPV Status							
	HPV +	31	10	56	68.3	11	8.9
	HPV -	278	89.7	26	31.7	112	90.3
	Indeterminate	1	0.3	0	0	1	0.8
Vital Status							
	Alive	197	63.5	69	84.1	82	66.1
	Deceased	113	36.5	13	15.9	42	33.9
Nodal Status							
	Positive	147	47.4	34	41.5	58	46.8
	Negative	119	38.4	16	19.5	42	33.9
	Information not available	44	14.2	32	39	24	19.4
Pathologic Tumor Stage							
	Stage I	19	6.1	4	4.9	2	1.6
	Stage II	56	18.1	10	12.2	12	9.7
	Stage III	52	16.8	9	11.0	14	11.3
	Stage IV	160	51.6	28	34.1	79	63.7
	Information not available	23	7.4	31	37.8	17	13.7



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RANDOM FOREST CLASSIFIER FOR NODAL STATUS PREDICTION

```
# build model
# define random forest regressor model
from sklearn.ensemble import RandomForestClassifier

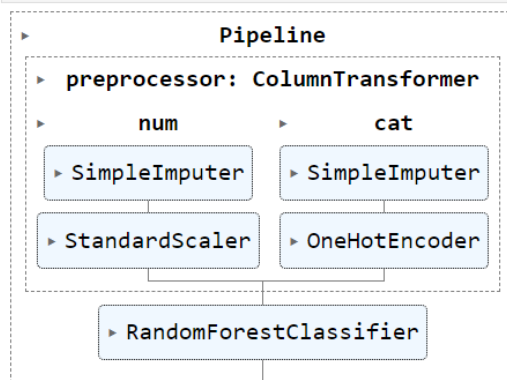
number_of_trees = 100 # set the number of trees in the forest
model = RandomForestClassifier(n_estimators=number_of_trees, random_state=42) # define model.
# n_estimators is the hyperparameter that we tune as necessary
model_name = 'hnscc' # put a name for your model to input to the Pipeline function
```

```
# define full model
```

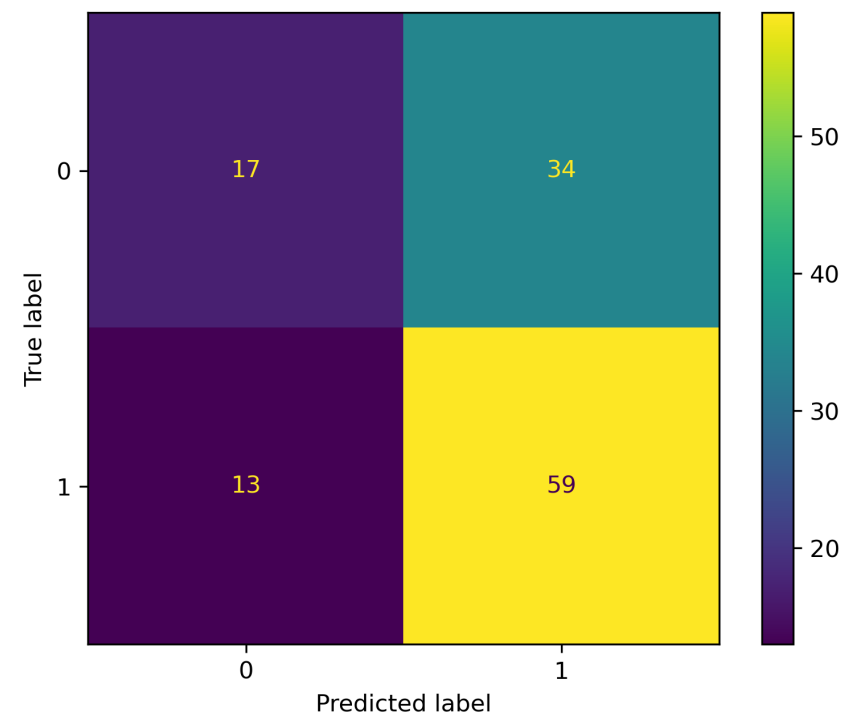
```
full_model = Pipeline(steps=[('preprocessor', preprocessor),
                              (model_name, model)])
```

```
# fit model to data
```

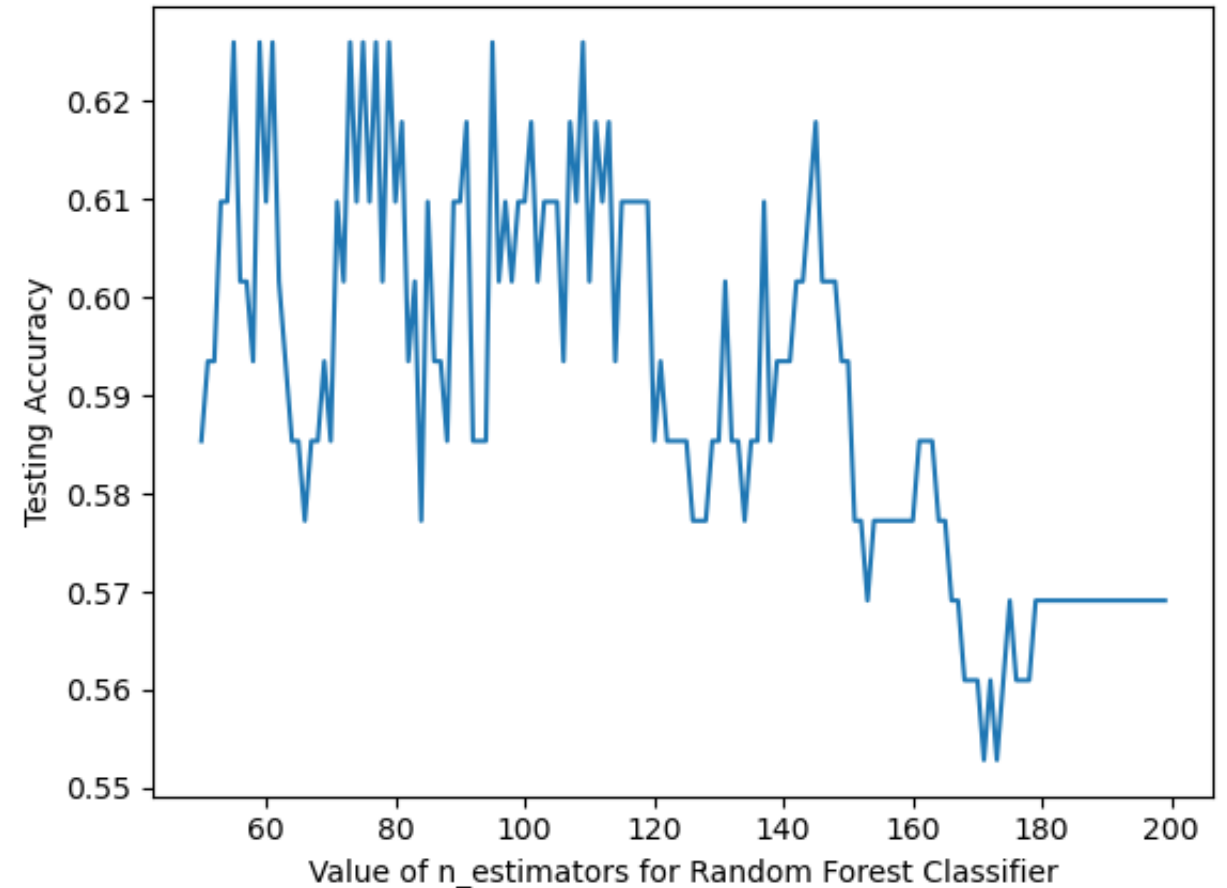
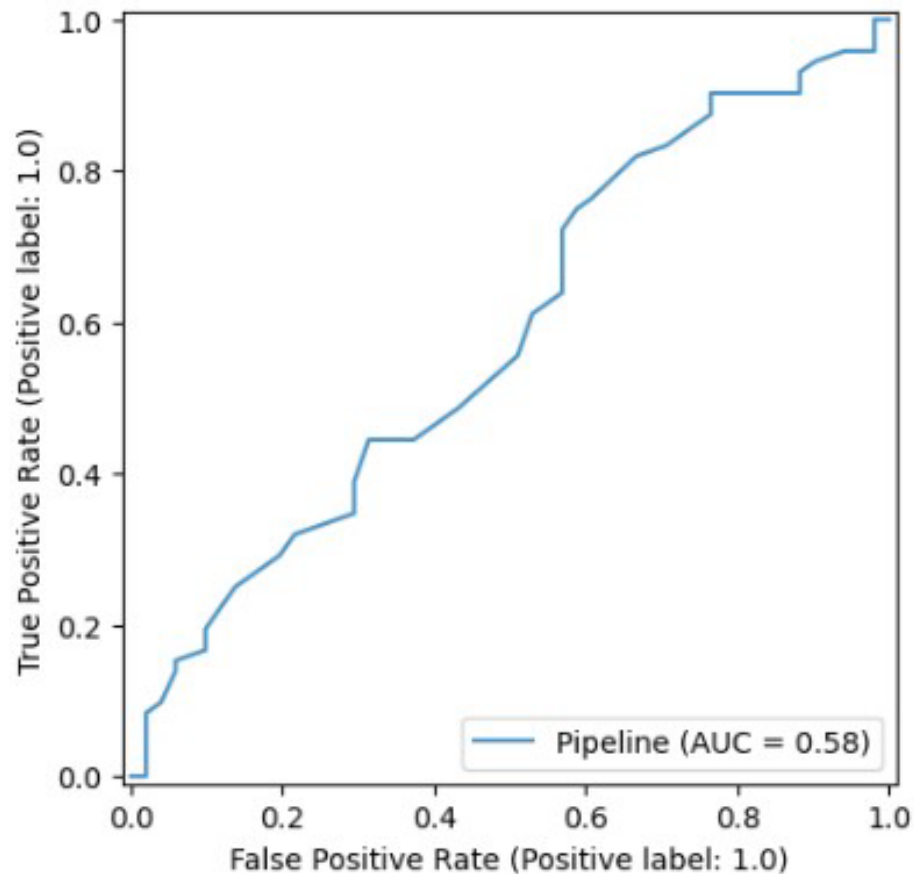
```
full_model.fit(X_train, y_train)
```



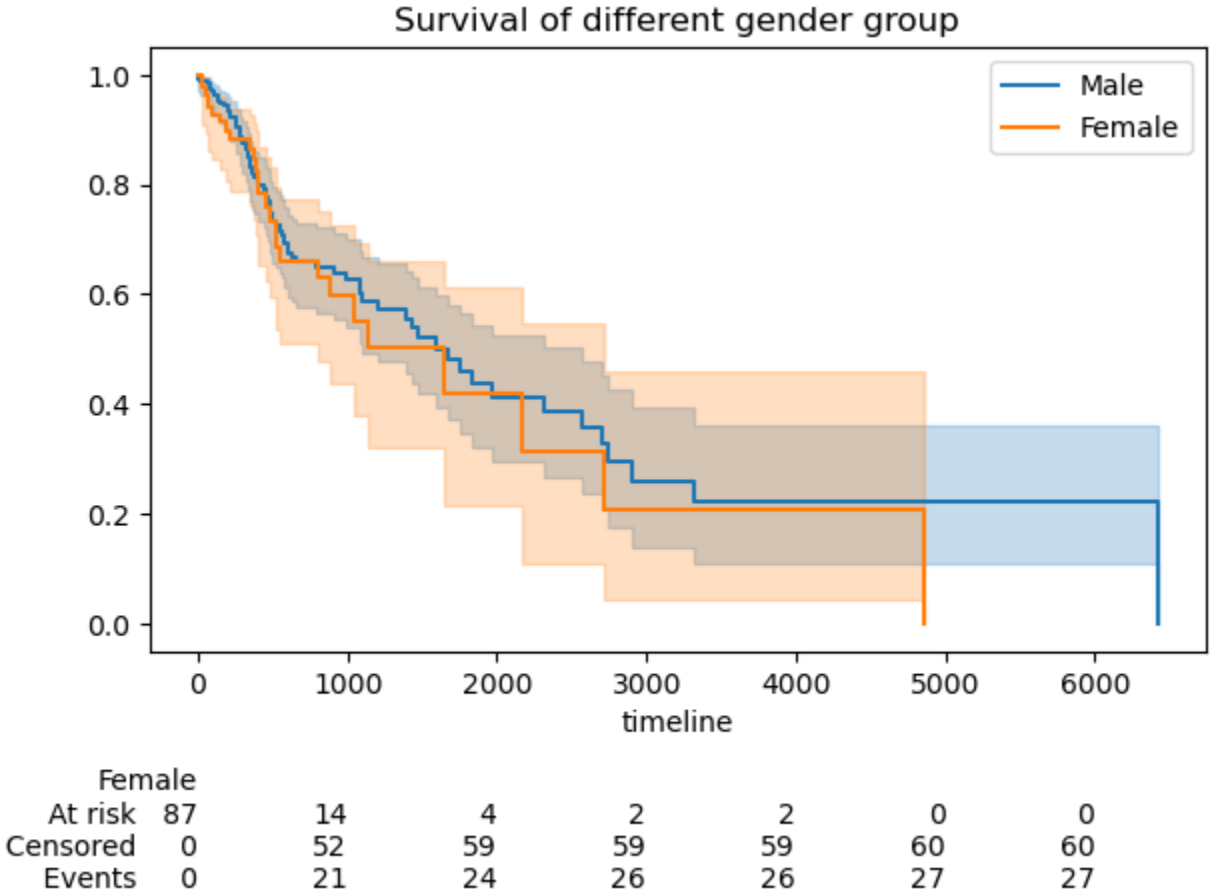
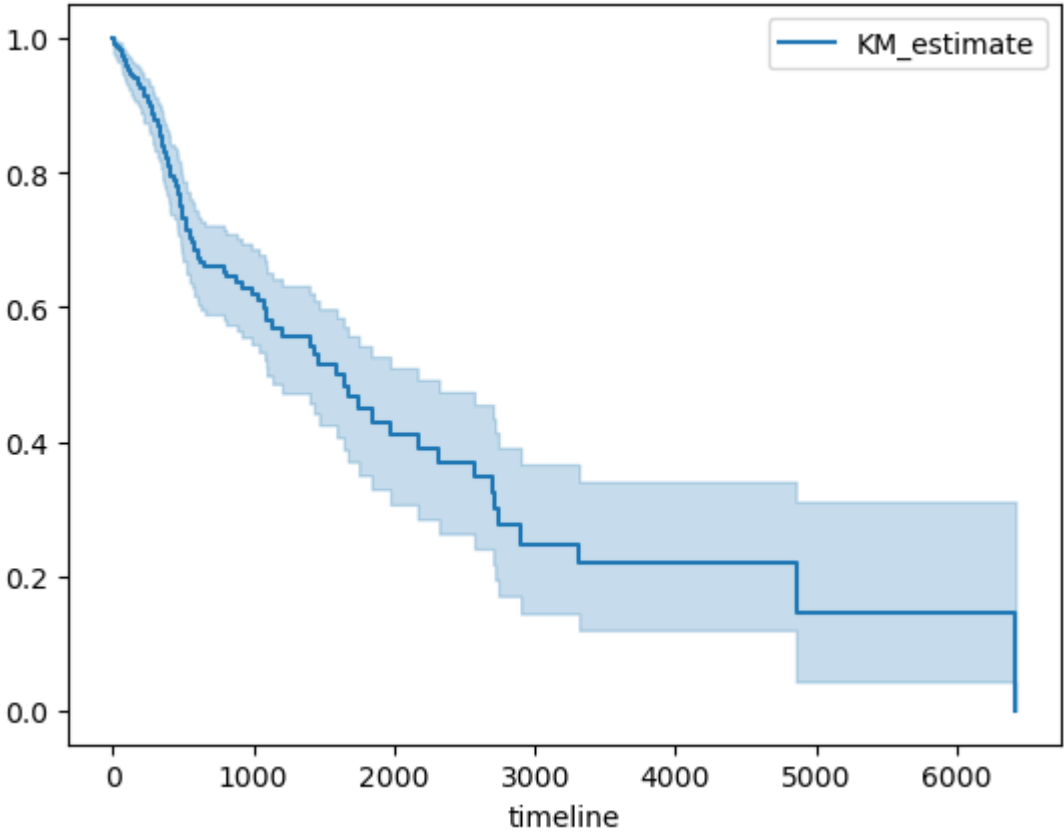
Accuracy: 0.62
Precision: 0.63
Recall: 0.82



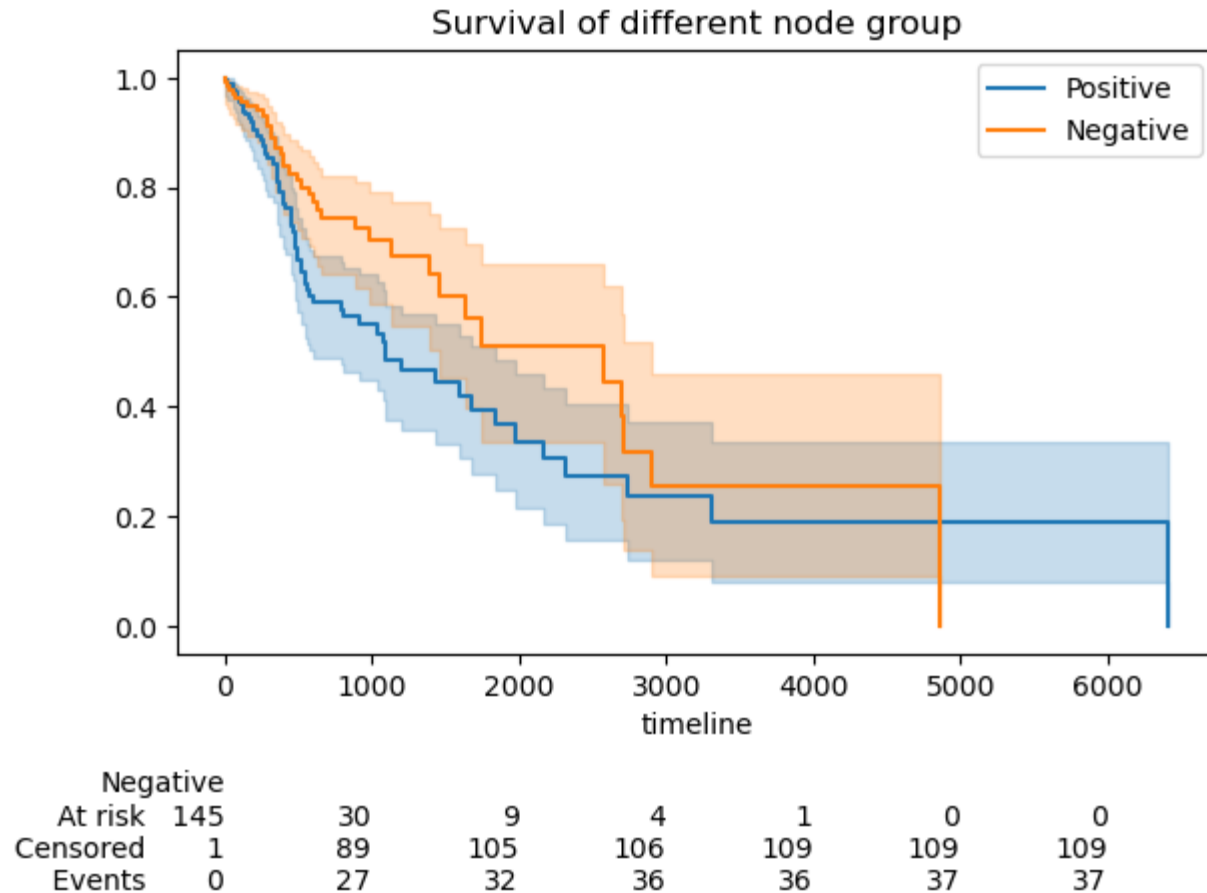
EXPANDING THE NUMBER OF TREES DID NOT IMPROVE PERFORMANCE OF THE NODAL METASTASIS CLASSIFIER



WHAT ABOUT PATIENT SURVIVAL?



NODAL STATUS ARE SIGNIFICANTLY ASSOCIATED WITH POOR OUTCOME



- Nodal metastasis
- Age
- History of other malignancy

FUTURE DIRECTIONS

- Re-try RF classifier with new features (much high feature set, other molecular measurements, etc.)
- Repeat survival analysis with many more features
- Is node-negative REALLY node-negative? Is RF classifier calling them node-positive for a reason?
- Try other ML approaches

Accuracy: 0.62
Precision: 0.63
Recall: 0.82

