In [3]:

```
#importing required libraries
import pandas as pd
import matplotlib.pyplot as plt
import tabulate
import seaborn as sns
from sklearn.preprocessing import LabelEncoder
from sklearn.decomposition import PCA
from imblearn.over_sampling import SMOTE
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import accuracy_score, recall_score, precision_score
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from sklearn.svm import SVC
from sklearn.preprocessing import StandardScaler
from imblearn.over_sampling import RandomOverSampler
from sklearn.metrics import confusion_matrix
from scipy.cluster.hierarchy import dendrogram, linkage,fcluster
import numpy as np
from lifelines import KaplanMeierFitter
from lifelines.utils import median_survival_times
from lifelines import CoxPHFitter
```

In [3]:

```
#read data
data= pd.read_csv("G:\\My Drive\\Ryerson\\Capstone\\METABRIC_RNA_Mutation.csv\\METABRIC_RNA_Mutation.csv", sep=",")
```

```
C:\Users\mdaum\AppData\Local\Temp\ipykernel_13744\2593902994.py:2: DtypeWarning: Columns (678,688,690,692) have mixed types. Specify dtype option on import or set low_memory=False.
  data= pd.read_csv("G:\\My Drive\\Ryerson\\Capstone\\METABRIC_RNA_Mutation.csv\\METABRIC_RNA_Mutation.csv", sep=",")
```

In [46]:

```
#seperating clinical attributes and converting into categorical variables
df_clinical =data.iloc[:, 1:31]
categorical_variables= ["type_of_breast_surgery","cancer_type","cancer_type_detailed","cellularity","chemotherapy","pam50_+_claudin-low_subtype","cohort","er_status_measured_by_ihc",
"er_status","neoplasm_histologic_grade","her2_status_measured_by_snp6","her2_status","tumor_other_histologic_subtype","hormone_therapy","inferred_menopausal_state","integrative_cluster",
"primary_tumor_laterality","oncotree_code","overall_survival","pr_status","radio_therapy","3-gene_classifier_subtype","tumor_stage","death_from_cancer"]
for i in categorical_variables:
    df_clinical[i] =df_clinical[i].astype("category")
print(df_clinical.dtypes)
```

```
age_at_diagnosis                 float64
type_of_breast_surgery          category
cancer_type                     category
cancer_type_detailed            category
cellularity                     category
chemotherapy                    category
pam50_+_claudin-low_subtype     category
cohort                          category
er_status_measured_by_ihc       category
er_status                       category
neoplasm_histologic_grade       category
her2_status_measured_by_snp6    category
her2_status                     category
tumor_other_histologic_subtype  category
hormone_therapy                 category
inferred_menopausal_state       category
integrative_cluster             category
primary_tumor_laterality        category
```

```
lymph_nodes_examined_positive      float64
mutation_count                     float64
nottingham_prognostic_index        float64
oncotree_code                     category
overall_survival_months            float64
overall_survival                  category
pr_status                         category
radio_therapy                     category
3-gene_classifier_subtype         category
tumor_size                         float64
tumor_stage                       category
death_from_cancer                 category
dtype: object
```

Making a new dataframaame for the treatments.

In [47]:

```
treatmentList = ["type_of_breast_surgery", "chemotherapy", "hormone_therapy", "radio_therapy"]
dfTreatments = df_clinical[treatmentList].copy()  # Create a copy of the DataFrame

dfTreatments.loc[:, "type_of_breast_surgery"] = dfTreatments["type_of_breast_surgery"].apply(lambda x: 1 if "MASTECTOMY" in str(x) else 0)
dfTreatments.rename(columns={'type_of_breast_surgery': 'masectomy'}, inplace=True)
dfTreatments.head()
```

Out[47]:

	masectomy	chemotherapy	hormone_therapy	radio_therapy
0	**1**	**0**	**1**	**1**
1	**0**	**0**	**1**	**1**
2	**1**	**1**	**1**	**0**
3	**1**	**1**	**1**	**1**
4	**1**	**1**	**1**	**1**

Dropping columns from the clinical df which are unnecessary and have low variability, and then concatenating with the treatment df

In [48]:

```
#seperating genetic data
df_genetic =data.iloc[:, 31:520]
```

In [49]:

```
col_to_remove =["type_of_breast_surgery", "cancer_type","cancer_type_detailed","chemotherapy","cohort","hormone_therapy","radio_therapy"]
df_clinical=df_clinical.drop(columns=col_to_remove)
df_for_treatment_prediction =pd.concat([df_clinical,dfTreatments,df_genetic],axis=1)
df_for_treatment_prediction.dtypes
```

Out[49]:

```
age_at_diagnosis                 float64
cellularity                     category
pam50_+_claudin-low_subtype     category
er_status_measured_by_ihc       category
er_status                       category
                                   ...
tnk2                             float64
tulp4                            float64
ugt2b15                          float64
ugt2b17                          float64
ugt2b7                           float64
Length: 516, dtype: object
```

In [50]:

```
#encoding categogical data


categorical_variables= ["masectomy","cellularity","chemotherapy","pam50_+_claudin-low_subtype","er_status_measured_by_ihc",
"er_status","neoplasm_histologic_grade","her2_status_measured_by_snp6","her2_status","tumor_other_histologic_subtype","hormone_therapy","inferred_menopausal_state","integrative_cluster",
"primary_tumor_laterality","oncotree_code","overall_survival","pr_status","radio_therapy","3-gene_classifier_subtype","tumor_stage","death_from_cancer"]


label_encoder = LabelEncoder()
for i in categorical_variables:
    df_for_treatment_prediction[i] =label_encoder.fit_transform(df_for_treatment_prediction[i])

original_df_for_treatment_prdiction=df_for_treatment_prediction.copy(deep=True)
df_for_treatment_prediction =df_for_treatment_prediction.dropna(axis=0)
```

PCA for feature selection

In [51]:

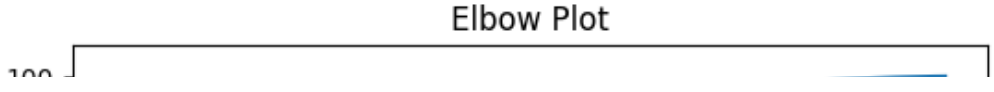
```
#using PCA for feature selection


# Create a PCA object with the desired number of components
np.random.seed(42)
pca = PCA(n_components="mle",svd_solver="full",random_state=42)

# Perform PCA on the dataset
pca_for_treatment_prediction = pca.fit_transform(df_for_treatment_prediction)

# Access the explained variance ratio of each component
explained_variance = np.cumsum(pca.explained_variance_ratio_*100)
n_components=pca.n_components_
print(explained_variance)
```

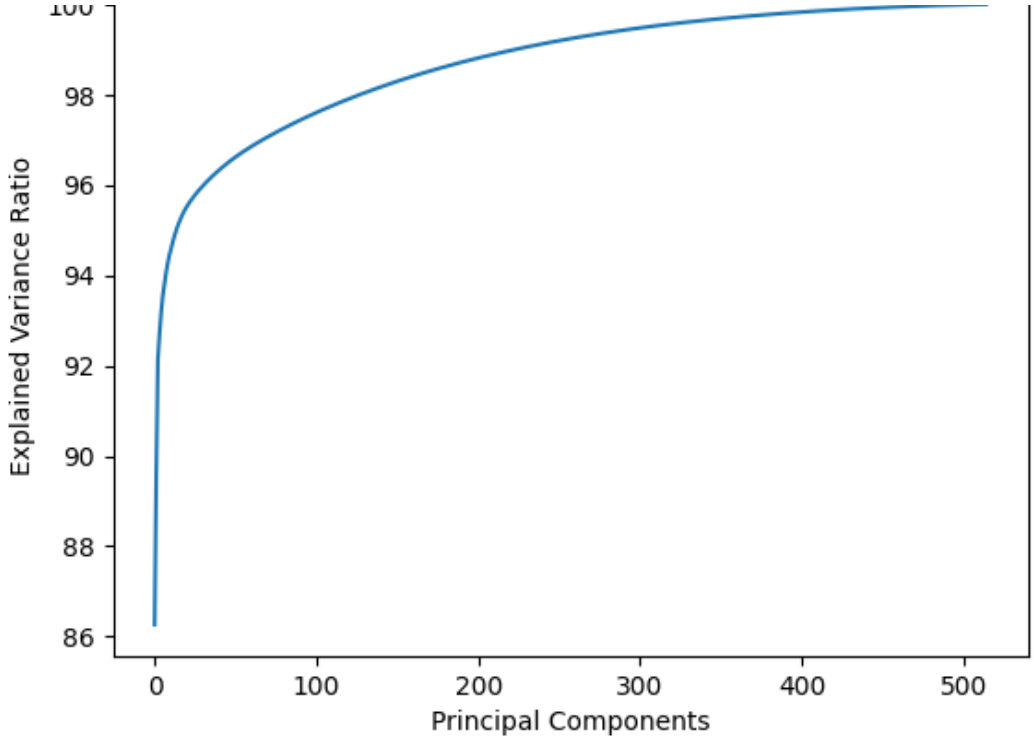
```
[86.26548932 89.58858375 92.12567196 92.69380581 93.16223109 93.53745828
 93.80313947 94.04045826 94.25374924 94.42859958 94.57170435 94.71327469
 94.84245924 94.96095107 95.06821237 95.16180081 95.24722538 95.32847041
 95.40370877 95.4686744  95.5288229  95.58483262 95.63735813 95.68739843
 95.73550147 95.78083651 95.82508605 95.86839257 95.90953978 95.94958743
 95.98867101 96.02656571 96.06397575 96.10068324 96.13668657 96.17223371
 96.20582174 96.23904607 96.27199691 96.30391525 96.33521149 96.366328
 96.39667114 96.42686437 96.45558923 96.48407497 96.51242971 96.54016434
 96.56684688 96.59317876 96.61929483 96.64499644 96.67012181 96.69474874
 96.71899128 96.74273078 96.76619517 96.78958561 96.81238597 96.83482761
 96.85704109 96.87891268 96.90056246 96.92206204 96.94337578 96.9645974
 96.98556528 97.00608191 97.02644869 97.04668257 97.06668357 97.08640302
 97.10602172 97.12558402 97.14507506 97.16447553 97.18349279 97.20241757
 97.22125746 97.23995827 97.25852715 97.27696174 97.29535142 97.31349788
 97.33159762 97.349579   97.3674217  97.3851925  97.40271604 97.42015028
 97.43747907 97.45466973 97.47162096 97.48847397 97.50518729 97.52182961
 97.53839594 97.55486008 97.57115526 97.5873559  97.60346543 97.61949539
 97.63545521 97.65128252 97.66702257 97.68257548 97.69804869 97.7133991
 97.72871375 97.74392164 97.759008   97.77405354 97.78905457 97.80396119
 97.81874079 97.83339112 97.84791717 97.86243122 97.87684274 97.89119508
 97.90547692 97.91968009 97.93383734 97.94776585 97.96163026 97.97544068
 97.98918731 98.00286986 98.01640745 98.02987359 98.04332549 98.05666201
 98.06996069 98.08317381 98.09625863 98.1092741  98.12228102 98.13519414
 98.14798808 98.16070381 98.17335127 98.18594529 98.19850918 98.21098567
 98.22338787 98.23566395 98.24788982 98.2600577  98.27214661 98.28419119
 98.29617681 98.30809549 98.3198675  98.33162984 98.34335943 98.35501981
 98.36659024 98.37809782 98.3895025  98.40085778 98.41210291 98.42328977
 98.43446746 98.44546252 98.45638369 98.46728773 98.47816777 98.48891735
 98.49961009 98.51022444 98.52081142 98.53135938 98.54183652 98.55223397
 98.56258668 98.5729245  98.58314344 98.59330207 98.60342866 98.61349169
```

```
 98.62349975 98.63342313 98.64324828 98.65304099 98.66282767 98.67250708
 98.68208445 98.69162809 98.70112809 98.71056876 98.71997218 98.72932507
 98.73863345 98.7478725  98.75706831 98.76622744 98.77528388 98.78427954
 98.79320129 98.80210392 98.81092436 98.8196905  98.82842457 98.83713247
 98.84574932 98.85432055 98.86287384 98.87135217 98.87980085 98.88817353
 98.8965092  98.90480511 98.91307562 98.92132882 98.92956831 98.93769883
 98.94578306 98.95383728 98.9618541  98.96985872 98.97778469 98.98568007
 98.99352901 99.00135017 99.00911154 99.01682996 99.02451725 99.03217469
 99.03973113 99.04725066 99.05472136 99.06210632 99.06945232 99.07677278
 99.08407486 99.09132775 99.09856094 99.1057212  99.11283208 99.11993383
 99.12697328 99.13398537 99.14093059 99.14779436 99.15462653 99.16141286
 99.16813402 99.17484666 99.18151937 99.18817093 99.19479292 99.20137158
 99.20791401 99.21442433 99.22087697 99.22726229 99.23363357 99.23995749
 99.24625261 99.25251424 99.25874463 99.26494892 99.27109953 99.27724115
 99.28331554 99.2893284  99.29529009 99.30122749 99.30711809 99.31295485
 99.31877382 99.32458535 99.33033548 99.33605864 99.34175438 99.34743262
 99.35307421 99.35867108 99.36424178 99.36979854 99.37526928 99.3806971
 99.38611222 99.39150264 99.39686569 99.40221201 99.40747835 99.41272013
 99.41793256 99.42311348 99.42828158 99.433407   99.43851701 99.44355589
 99.448574   99.45358167 99.45851811 99.46344368 99.4683355  99.47318374
 99.47802074 99.48282837 99.48757791 99.49231704 99.49699668 99.50164899
 99.50628399 99.51091125 99.51548533 99.52003772 99.52455858 99.52903986
 99.5335066  99.53795851 99.54236134 99.54672543 99.55104966 99.55535884
 99.55964975 99.56391242 99.56814193 99.57234218 99.5765262  99.58068211
 99.58477964 99.5888555  99.59289327 99.5969202  99.60090511 99.6048767
 99.60881357 99.61272574 99.61661618 99.62049132 99.62434665 99.62817957
 99.63200315 99.63578624 99.63955425 99.64329628 99.64701709 99.65070699
 99.65434688 99.65796177 99.6615663  99.66516184 99.66871217 99.67224261
 99.67575649 99.67924556 99.68270487 99.68614186 99.68954725 99.6929119
 99.69626619 99.69958935 99.70290744 99.70621555 99.70948724 99.71274023
 99.71597759 99.71920952 99.72241746 99.72559959 99.72876748 99.7319146
 99.73503401 99.73813552 99.74120411 99.74424679 99.74728427 99.75029501
 99.75327825 99.7562512  99.7592026  99.76212351 99.76502617 99.76791662
 99.77079163 99.77364725 99.77647835 99.77928582 99.78208035 99.7848535
 99.78761729 99.79036645 99.79308857 99.79579802 99.79848099 99.80115714
 99.80379992 99.80641504 99.80902654 99.81159877 99.81416314 99.81670684
 99.81924605 99.82176274 99.82426244 99.82672721 99.8291669  99.83159722
 99.8340126  99.83640745 99.83877876 99.8411316  99.84347457 99.84579575
 99.84810205 99.85039632 99.85265902 99.8549009  99.85713073 99.85934097
 99.86153508 99.8637076  99.86586183 99.86799625 99.87012595 99.87224107
 99.87433281 99.87642251 99.8784864  99.88054993 99.88259562 99.88460044
 99.88660159 99.88859135 99.89056882 99.89250673 99.89443483 99.89635903
 99.89825231 99.90013081 99.90199827 99.90385026 99.90567784 99.90749268
 99.90929197 99.91107763 99.912842   99.91459729 99.91633221 99.91804049
 99.91974175 99.92143381 99.92311721 99.92479086 99.92642868 99.92805256
 99.92966258 99.93123944 99.93280617 99.93435777 99.93589768 99.9374219
 99.9389309  99.94043728 99.94192147 99.94339771 99.94485481 99.94629473
 99.94773004 99.94915753 99.95056908 99.95196527 99.95335853 99.95473106
 99.95610165 99.95744871 99.95878086 99.96009726 99.96137903 99.96263668
 99.96388268 99.96511847 99.9663387  99.96754496 99.96874904 99.96992993
 99.97108524 99.97223605 99.97337564 99.9744986  99.97559894 99.97669556
 99.97777611 99.97882471 99.97986489 99.98088237 99.98189135 99.98289231
 99.98388895 99.98486709 99.98582908 99.98677896 99.98769922 99.98860405
 99.98949465 99.99036993 99.99123256 99.99207149 99.99287919 99.99366641
 99.99443953 99.99520294 99.99592688 99.99662461 99.99726743 99.99784892
 99.99837375 99.99881222 99.99920924 99.99952116 99.99980433]
```

In [52]:

```
#plotting the variance to see choose the no of components

# Plot the explained variance ratio

plt.plot(explained_variance)
plt.xlabel('Principal Components')
plt.ylabel('Explained Variance Ratio')
plt.title('Elbow Plot')
plt.show()
```





From the plot it seems almost 100% of the variability can be explained by 300 principal components. As a result we will use 300 components for future training.

Predicting the suitability of CHEMOTHERAPY as a treatment option. As Chemotherapy has imbalanced sampling, SMOTE and ROSE resampling techniques are used. And the results are compared.

In [53]:

```
#predicting chemotherapy using SMOTE .
# Load the dataset and split into features (X) and target variable (y)
X = df_for_treatment_prediction.drop(columns=['chemotherapy'])
y = df_for_treatment_prediction['chemotherapy']

scaler = StandardScaler()
scaled_X = scaler.fit_transform(X)

# Apply PCA for dimensionality reduction
pca = PCA(n_components=300)
X_pca = pca.fit_transform(scaled_X)



# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_pca, y, test_size=0.3, random_stat
e=42)

# Initialize d SMOTE resampling methods

smote = SMOTE()

# Apply the resampling method to the training set

X_train_resampled, y_train_resampled = smote.fit_resample(X_train, y_train)

# Train a Random Forest classifier
rf_classifier = RandomForestClassifier()
rf_scores = cross_val_score(rf_classifier, X_train_resampled, y_train_resampled, cv=10,
scoring='accuracy')

print("Random Forest Classifier Cross-Validation Scores:")
print(rf_scores)
print("Mean Accuracy:", rf_scores.mean())

# Train a Gradient Boosting classifier
```

```
gb_classifier = GradientBoostingClassifier()
gb_scores = cross_val_score(gb_classifier, X_train_resampled, y_train_resampled, cv=10,
scoring='accuracy')

print("Gradient Boosting Classifier Cross-Validation Scores:")
print(gb_scores)
print("Mean Accuracy:", gb_scores.mean())

# Train an SVM classifier
svm_classifier = SVC()
svm_scores = cross_val_score(svm_classifier, X_train_resampled, y_train_resampled, cv=10
, scoring='accuracy')

print("SVM Classifier Cross-Validation Scores:")
print(svm_scores)
print("Mean Accuracy:", svm_scores.mean())
```

```
Random Forest Classifier Cross-Validation Scores:
[0.91747573 0.87864078 0.9368932  0.98543689 0.99514563 0.99029126
 0.98543689 0.98543689 0.99512195 0.9902439 ]
Mean Accuracy: 0.9660123135211934
Gradient Boosting Classifier Cross-Validation Scores:
[0.86407767 0.83495146 0.89320388 0.90291262 0.91747573 0.94174757
 0.90776699 0.9368932  0.95609756 0.93170732]
Mean Accuracy: 0.9086834004262373
SVM Classifier Cross-Validation Scores:
[0.93203883 0.92718447 0.95145631 0.95145631 0.96116505 0.97572816
 0.95631068 0.95631068 0.9804878  0.96097561]
Mean Accuracy: 0.955311390007104
```

In [54]:

```
#predicting chemotherapy using ROSE
# Load the dataset and split into features (X) and target variable (y)
X = df_for_treatment_prediction.drop(columns=['chemotherapy'])
y = df_for_treatment_prediction['chemotherapy']

scaler = StandardScaler()
scaled_X = scaler.fit_transform(X)

# Apply PCA for dimensionality reduction
pca = PCA(n_components=300)
X_pca = pca.fit_transform(scaled_X)

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_pca, y, test_size=0.3, random_stat
e=42)

# Initialize the ROSE  resampling method

RandomOverSampler = RandomOverSampler()

# Apply the resampling method to the training set

X_train_resampled, y_train_resampled = RandomOverSampler.fit_resample(X_train, y_train)

# Train a Random Forest classifier
rf_classifier = RandomForestClassifier()
rf_scores = cross_val_score(rf_classifier, X_train_resampled, y_train_resampled, cv=10,
scoring='accuracy')

print("Random Forest Classifier Cross-Validation Scores:")
print(rf_scores)
print("Mean Accuracy:", rf_scores.mean())

# Train a Gradient Boosting classifier
gb_classifier = GradientBoostingClassifier()
gb_scores = cross_val_score(gb_classifier, X_train_resampled, y_train_resampled, cv=10,
scoring='accuracy')

print("Gradient Boosting Classifier Cross-Validation Scores:")
print(gb_scores)
```

```
print("Mean Accuracy:", gb_scores.mean())

# Train an SVM classifier
svm_classifier = SVC()
svm_scores = cross_val_score(svm_classifier, X_train_resampled, y_train_resampled, cv=10
, scoring='accuracy')

print("SVM Classifier Cross-Validation Scores:")
print(svm_scores)
print("Mean Accuracy:", svm_scores.mean())
```

```
Random Forest Classifier Cross-Validation Scores:
[0.97572816 0.97572816 1.         1.         0.99029126 0.99514563
 1.         1.         1.         0.99512195]
Mean Accuracy: 0.9932015155103006
Gradient Boosting Classifier Cross-Validation Scores:
[0.93203883 0.93203883 0.96601942 0.93203883 0.91747573 0.93203883
 0.94174757 0.94174757 0.93658537 0.92195122]
Mean Accuracy: 0.9353682216433816
SVM Classifier Cross-Validation Scores:
[0.94660194 0.9368932  0.95145631 0.94660194 0.92718447 0.96116505
 0.95145631 0.96601942 0.95121951 0.95121951]
Mean Accuracy: 0.9489817665166944
```

The ROSE algorithm gives slightly better accuracy

Predicting death_from_cancer

In [56]:

```
#scaling the data
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df_for_treatment_prediction)


X = df_for_treatment_prediction.drop(columns=['death_from_cancer'])
y = df_for_treatment_prediction['death_from_cancer']


pca = PCA(n_components=300)
X_pca = pca.fit_transform(scaled_X)



# Splitting the data into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X_pca, y, test_size=0.3, random_stat
e=42)

# Random Forest Classifier
rf_classifier = RandomForestClassifier(random_state=42)
rf_classifier.fit(X_train, y_train)
rf_predictions = rf_classifier.predict(X_test)

# Gradient Boosting Classifier
gb_classifier = GradientBoostingClassifier(random_state=42)
gb_classifier.fit(X_train, y_train)
gb_predictions = gb_classifier.predict(X_test)

# Support Vector Machine (SVM) Classifier
svm_classifier = SVC(random_state=42)
svm_classifier.fit(X_train, y_train)
svm_predictions = svm_classifier.predict(X_test)

# Evaluation
print("Random Forest Classifier:")
print("Accuracy:", accuracy_score(y_test, rf_predictions))
print("Recall:", recall_score(y_test, rf_predictions, average='macro'))
print("Precision:", precision_score(y_test, rf_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, rf_predictions))
```

```
print()

print("Gradient Boosting Classifier:")
print("Accuracy:", accuracy_score(y_test, gb_predictions))
print("Recall:", recall_score(y_test, gb_predictions, average='macro'))
print("Precision:", precision_score(y_test, gb_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, gb_predictions))
print()

print("Support Vector Machine (SVM) Classifier:")
print("Accuracy:", accuracy_score(y_test, svm_predictions))
print("Recall:", recall_score(y_test, svm_predictions, average='macro'))
print("Precision:", precision_score(y_test, svm_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, svm_predictions))
```

```
Random Forest Classifier:
Accuracy: 0.6213768115942029
Recall: 0.41255251588370256
Precision: 0.40987104370769434
Confusion Matrix:
[[122  15  49   0]
 [ 49  13  71   0]
 [ 15   9 208   0]
 [  0   0   1   0]]

Gradient Boosting Classifier:
Accuracy: 0.7192028985507246
Recall: 0.508694915821255
Precision: 0.510356699751861
Confusion Matrix:
[[138  37  11   0]
 [ 46  55  32   0]
 [ 16  12 204   0]
 [  0   0   1   0]]

Support Vector Machine (SVM) Classifier:
Accuracy: 0.8242753623188406
Recall: 0.5965934197284088
Precision: 0.5956809249458476
Confusion Matrix:
[[140  44   2   0]
 [ 43  86   4   0]
 [  1   2 229   0]
 [  0   0   1   0]]
```

```
c:\Users\mdaum\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\metrics\
_classification.py:1344: UndefinedMetricWarning: Precision is ill-defined and being set t
o 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this
behavior.
  _warn_prf(average, modifier, msg_start, len(result))
c:\Users\mdaum\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\metrics\
_classification.py:1344: UndefinedMetricWarning: Precision is ill-defined and being set t
o 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this
behavior.
  _warn_prf(average, modifier, msg_start, len(result))
c:\Users\mdaum\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\metrics\
_classification.py:1344: UndefinedMetricWarning: Precision is ill-defined and being set t
o 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this
behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

Predicting overall survival

In [57]:

```
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df_for_treatment_prediction)

X = df_for_treatment_prediction.drop(columns=['overall_survival'])
```

```
y = df_for_treatment_prediction['overall_survival']

pca = PCA(n_components=300)
X_pca = pca.fit_transform(scaled_X)



# Splitting the data into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X_pca, y, test_size=0.3, random_stat
e=42)

# Random Forest Classifier
rf_classifier = RandomForestClassifier(random_state=42)
rf_classifier.fit(X_train, y_train)
rf_predictions = rf_classifier.predict(X_test)

# Gradient Boosting Classifier
gb_classifier = GradientBoostingClassifier(random_state=42)
gb_classifier.fit(X_train, y_train)
gb_predictions = gb_classifier.predict(X_test)

# Support Vector Machine (SVM) Classifier
svm_classifier = SVC(random_state=42)
svm_classifier.fit(X_train, y_train)
svm_predictions = svm_classifier.predict(X_test)

# Evaluation
print("Random Forest Classifier:")
print("Accuracy:", accuracy_score(y_test, rf_predictions))
print("Recall:", recall_score(y_test, rf_predictions, average='macro'))
print("Precision:", precision_score(y_test, rf_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, rf_predictions))
print()

print("Gradient Boosting Classifier:")
print("Accuracy:", accuracy_score(y_test, gb_predictions))
print("Recall:", recall_score(y_test, gb_predictions, average='macro'))
print("Precision:", precision_score(y_test, gb_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, gb_predictions))
print()

print("Support Vector Machine (SVM) Classifier:")
print("Accuracy:", accuracy_score(y_test, svm_predictions))
print("Recall:", recall_score(y_test, svm_predictions, average='macro'))
print("Precision:", precision_score(y_test, svm_predictions, average='macro'))
print("Confusion Matrix:")
print(confusion_matrix(y_test, svm_predictions))
```

```
Random Forest Classifier:
Accuracy: 0.7373188405797102
Recall: 0.6910560344827585
Precision: 0.8162753361428858
Confusion Matrix:
[[314   6]
 [139  93]]

Gradient Boosting Classifier:
Accuracy: 0.8786231884057971
Recall: 0.8668642241379311
Precision: 0.8844340621338942
Confusion Matrix:
[[301  19]
 [ 48 184]]

Support Vector Machine (SVM) Classifier:
Accuracy: 0.9873188405797102
Recall: 0.9866918103448276
Precision: 0.9872759639114779
Confusion Matrix:
[[317   3]
```

```
[  4 228]]
```

Clustering the genetic data

In [58]:

```
from sklearn.cluster import KMeans
from sklearn import metrics
from sklearn.metrics import adjusted_rand_score

X=df_for_treatment_prediction.iloc[:,27:].values # takeing only the genetic data
y=df_for_treatment_prediction["death_from_cancer"]


k = 4 # Number of clusters
kmeans = KMeans(n_clusters=k, random_state=0 )
kmeans.fit_predict(X)

from sklearn.metrics import adjusted_rand_score
ari = adjusted_rand_score(kmeans.labels_, y)
print("Adjusted Rand Index (ARI):", ari)
```

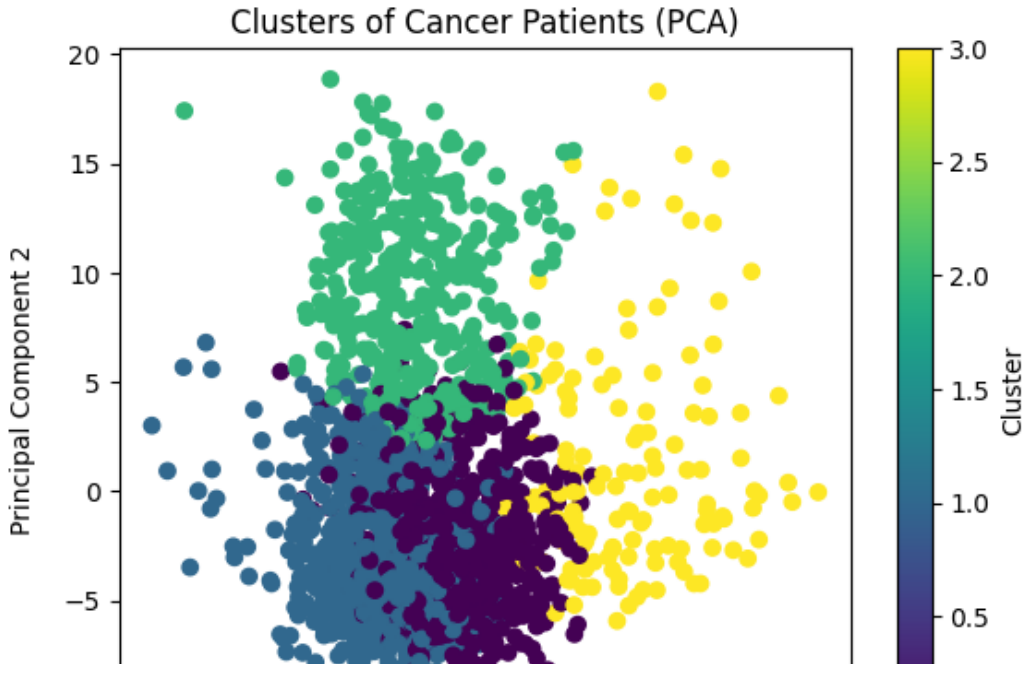
```
Adjusted Rand Index (ARI): 0.02056935376078903
```

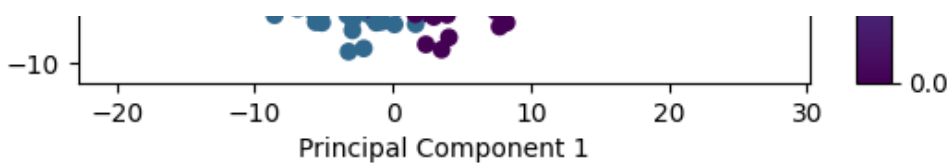
```
c:\Users\mdaum\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\cluster\
_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto
' in 1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
```

As random labelings have an ARI close to 0.0. 1.0 stands for perfect match. It seems the clustering is random in regards to "death_from_cancer"

In [59]:

```
#plotting the clusters


# Perform PCA to reduce dimensionality to 2
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X)

# Plotting the scatter plot
plt.scatter(X_pca[:, 0], X_pca[:, 1], c=kmeans.labels_, cmap='viridis')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.title('Clusters of Cancer Patients (PCA)')
plt.colorbar(label='Cluster')
plt.show()
```

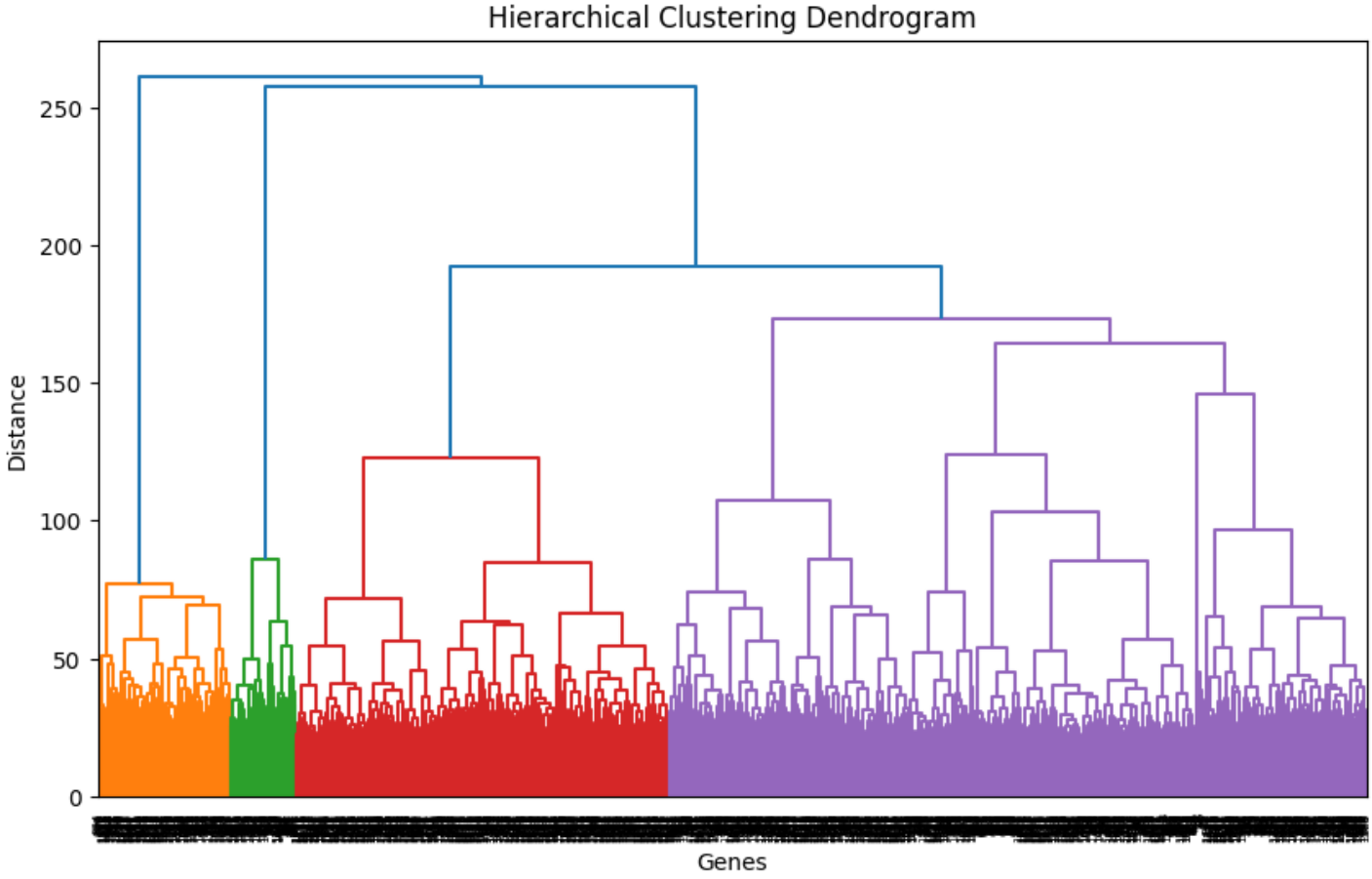




Hierarchicalclustering of the genetic data

In [60]:

```
# Perform hierarchical clustering
Z = linkage(X, method='ward')

# Plot the dendrogram
plt.figure(figsize=(10, 6))
dendrogram(Z)
plt.xlabel('Genes')
plt.ylabel('Distance')
plt.title('Hierarchical Clustering Dendrogram')
plt.show()


# Assign cluster labels based on the dendrogram
threshold = 50  # Adjust the threshold as needed
cluster_labels = fcluster(Z, t=threshold, criterion='distance')

# Calculate Adjusted Rand Index (ARI)
ari = adjusted_rand_score(y, cluster_labels)
print("Adjusted Rand Index (ARI):", ari)
```




```
Adjusted Rand Index (ARI): 0.0038828343198253528
```

Survival Analysis

In [61]:

```
#Creating a df for survival analysis
df_survival = pd.concat([df_clinical["overall_survival_months"],df_clinical["overall_sur
vival"]],axis = 1)
```

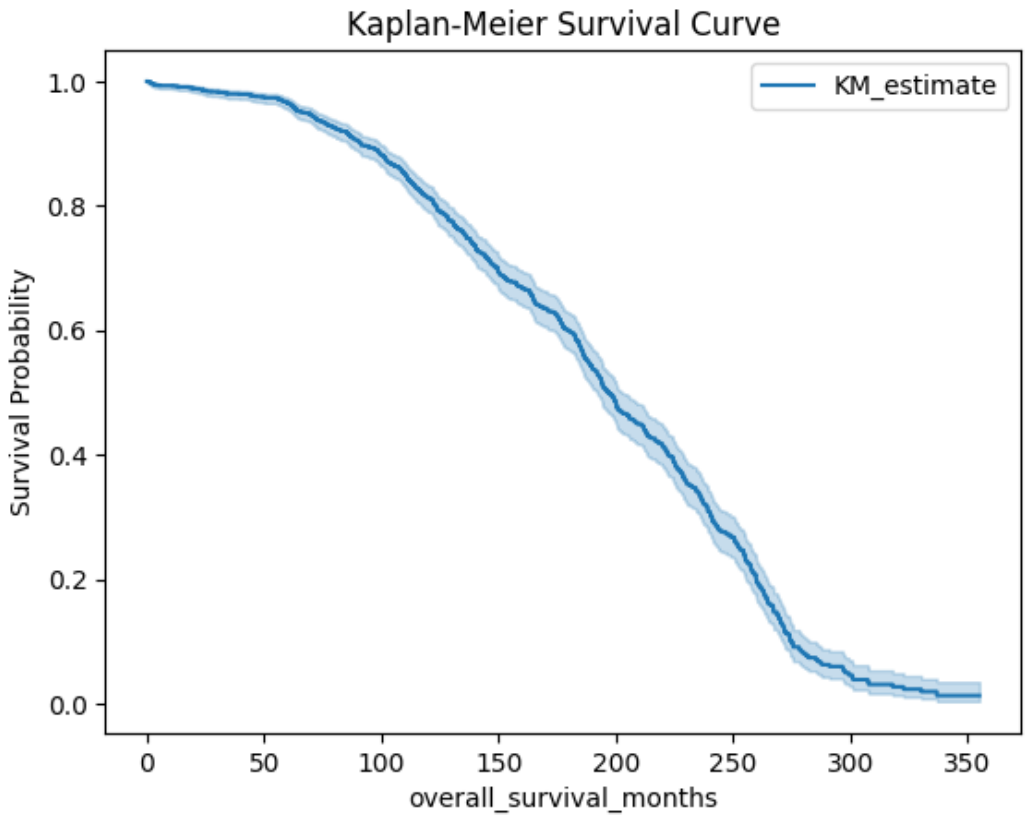
```
df_survival.head
```

Out[61]:

```
<bound method NDFrame.head of       overall_survival_months overall_survival
0                  140.500000                1
1                   84.633333                1
2                  163.700000                0
3                  164.933333                1
4                   41.366667                0
...                       ...              ...
1899               196.866667                1
1900                44.733333                0
1901               175.966667                0
1902                86.233333                0
1903               201.900000                0

[1904 rows x 2 columns]>
```

In [62]:

```
#plotting survival curve

kmf = KaplanMeierFitter()
kmf.fit(df_survival['overall_survival_months'], event_observed=df_survival['overall_survi
val'])

kmf.plot()
plt.xlabel('overall_survival_months')
plt.ylabel('Survival Probability')
plt.title('Kaplan-Meier Survival Curve')
plt.show()
```



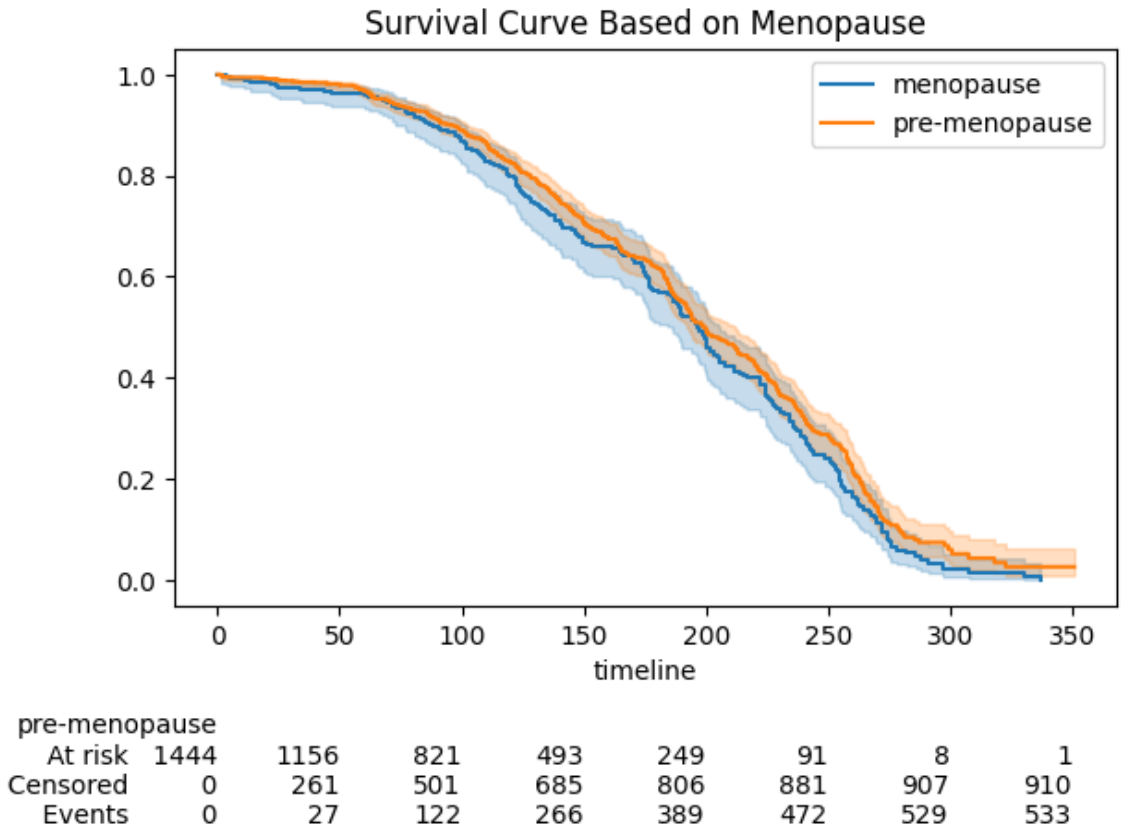
In [63]:

```
#evaluating the effect of menopause on overal survival
ax = plt.subplot(111)
menopause = (df_for_treatment_prediction["inferred_menopausal_state"] == 1)
kmf.fit(durations = df_for_treatment_prediction["overall_survival_months"][menopause], ev
ent_observed = df_for_treatment_prediction["overall_survival"][menopause], label = "meno
pause")
kmf.plot_survival_function(ax = ax)
kmf.fit(df_for_treatment_prediction["overall_survival_months"][~menopause], event_observe
d = df_for_treatment_prediction["overall_survival"][~menopause], label = "pre-menopause"
```

```
)
kmf.plot_survival_function(ax = ax, at_risk_counts = True)
plt.title("Survival Curve Based on Menopause")
```

Out[63]:

```
Text(0.5, 1.0, 'Survival Curve Based on Menopause')
```



pre-menopause								
At risk	1444	1156	821	493	249	91	8	1
Censored	0	261	501	685	806	881	907	910
Events	0	27	122	266	389	472	529	533

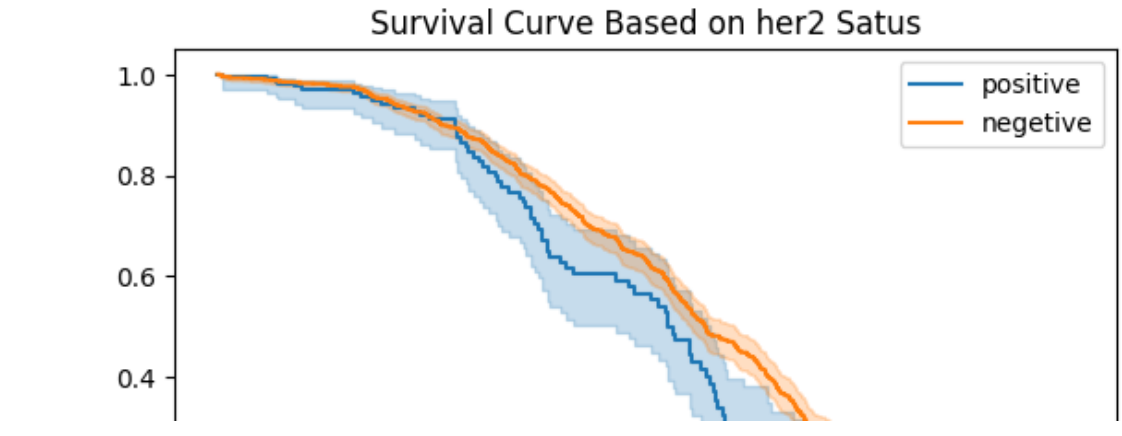
it shows a litte bit more suvival probability in premenopausal women.

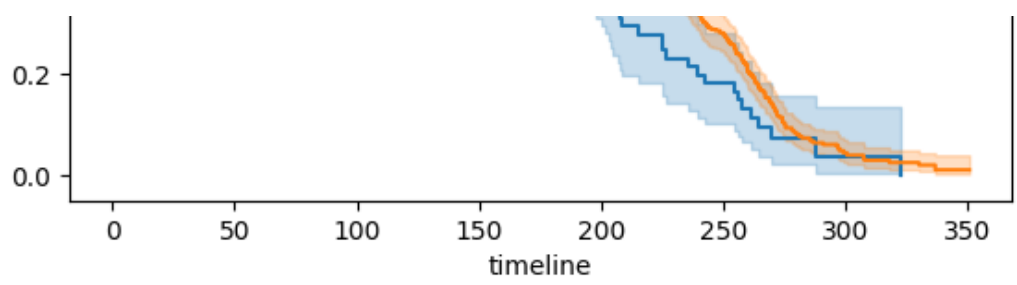
In [64]:

```
#evaluating effect of her2 status on survival

ax = plt.subplot(111)
positive = (df_for_treatment_prediction["her2_status"] == 1)
kmf.fit(durations = df_for_treatment_prediction["overall_survival_months"][positive], eve
nt_observed = df_for_treatment_prediction["overall_survival"][positive], label = "positiv
e")
kmf.plot_survival_function(ax = ax)
kmf.fit(df_for_treatment_prediction["overall_survival_months"][~positive], event_observed
= df_for_treatment_prediction["overall_survival"][~positive], label = "negetive")
kmf.plot_survival_function(ax = ax, at_risk_counts = True)
plt.title("Survival Curve Based on her2 Satus")
```

Out[64]:

```
Text(0.5, 1.0, 'Survival Curve Based on her2 Satus')
```





negetive							
At risk	1613	1318	965	608	327	127	10	1
Censored	0	260	504	690	816	899	926	929
Events	0	35	144	315	470	587	677	683

her2 negetive patients have a better probability of survival.

In [65]:

```
#finding out the median survival month
median_ = kmf.median_survival_time_
median_confidence_interval_ = median_survival_times(kmf.confidence_interval_)
print(median_,median_confidence_interval_)
```

```
199.9666667      negetive_lower_0.95  negetive_upper_0.95
0.5           193.966667           211.733333
```

Survival Regression - Cox's proportional hazard model

Cox model is a semi parametric model. The real advantage of Cox Proportional Hazards regression is that you can still fit survival models without knowing (or assuming) the distribution.

In [68]:

```
#encoding categorixal variables in the clinical df
new_survival_df =df_for_treatment_prediction.iloc[:, :27]


#cox model
cph = CoxPHFitter()
cph.fit(new_survival_df, duration_col='overall_survival_months', event_col='overall_survival')
cph.print_summary()
```

model	**lifelines.CoxPHFitter**
duration col	**'overall_survival_months'**
event col	**'overall_survival'**
baseline estimation	**breslow**
number of observations	**1839**
number of events observed	**764**
partial log-likelihood	**-4272.43**
time fit was run	**2023-06-22 20:17:44 UTC**

	coef	exp(coef)	se(coef)	coef lower 95%	coef upper 95%	exp(coef) lower 95%	exp(coef) upper 95%	cmp to	z	p	-log2(p)
age_at_diagnosis	0.03	1.03	0.01	0.02	0.04	1.02	1.04	0.00	4.88	<0.005	19.84
cellularity	-0.02	0.98	0.04	-0.10	0.06	0.91	1.06	0.00	-0.52	0.60	0.73
pam50_+_claudin-low_subtype	0.01	1.01	0.02	-0.03	0.06	0.97	1.06	0.00	0.60	0.55	0.86
er_status_measured_by_ihc	0.04	1.05	0.15	-0.24	0.33	0.79	1.39	0.00	0.31	0.76	0.40

	coef	exp(coef)	se(coef)	coef lower 95%	coef upper 95%	exp(coef) lower 95%	exp(coef) upper 95%	cmp to	z	p	log2(p)
er_status	-0.23	0.79	0.17	-0.56	0.09	0.57	1.10	0.00	-1.41	0.16	2.66
neoplasm_histologic_grade	-0.14	0.87	0.06	-0.26	-0.01	0.77	0.99	0.00	-2.16	0.03	5.03
her2_status_measured_by_snp6	-0.05	0.95	0.06	-0.18	0.07	0.84	1.08	0.00	-0.82	0.41	1.28
her2_status	0.18	1.20	0.17	-0.16	0.52	0.86	1.68	0.00	1.06	0.29	1.78
tumor_other_histologic_subtype	-0.01	0.99	0.03	-0.07	0.04	0.93	1.04	0.00	-0.45	0.65	0.62
inferred_menopausal_state	0.30	1.35	0.13	0.05	0.56	1.05	1.75	0.00	2.31	0.02	5.59
integrative_cluster	-0.02	0.99	0.01	-0.04	0.01	0.96	1.01	0.00	-1.16	0.25	2.01
primary_tumor_laterality	0.12	1.12	0.07	-0.02	0.25	0.98	1.28	0.00	1.70	0.09	3.47
lymph_nodes_examined_positive	0.01	1.01	0.02	-0.02	0.05	0.98	1.05	0.00	0.71	0.48	1.06
mutation_count	-0.05	0.95	0.01	-0.08	-0.03	0.93	0.97	0.00	-4.06	<0.005	14.31
nottingham_prognostic_index	-0.11	0.90	0.06	-0.21	0.00	0.81	1.00	0.00	-1.89	0.06	4.10
oncotree_code	-0.00	1.00	0.04	-0.08	0.07	0.92	1.08	0.00	-0.12	0.91	0.14
pr_status	-0.09	0.91	0.10	-0.28	0.09	0.75	1.10	0.00	-0.99	0.32	1.64
3-gene_classifier_subtype	-0.05	0.96	0.04	-0.12	0.03	0.89	1.03	0.00	-1.24	0.22	2.21
tumor_size	0.00	1.00	0.00	-0.01	0.01	0.99	1.01	0.00	0.19	0.85	0.23
tumor_stage	0.09	1.09	0.03	0.03	0.14	1.03	1.15	0.00	3.20	<0.005	9.49
death_from_cancer	3.07	21.60	0.19	2.70	3.44	14.94	31.23	0.00	16.34	<0.005	196.85
masectomy	-0.02	0.98	0.10	-0.22	0.17	0.81	1.19	0.00	-0.22	0.83	0.27
chemotherapy	0.55	1.73	0.13	0.30	0.79	1.35	2.21	0.00	4.35	<0.005	16.19
hormone_therapy	0.62	1.86	0.09	0.44	0.80	1.56	2.22	0.00	6.87	<0.005	37.22
radio_therapy	0.17	1.18	0.11	-0.05	0.38	0.95	1.47	0.00	1.51	0.13	2.92

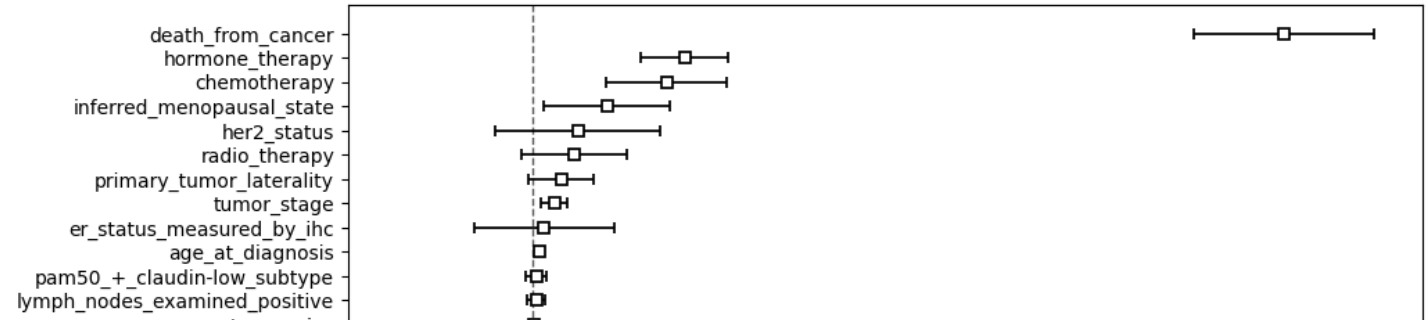
Concordance	0.79
Partial AIC	8594.87
log-likelihood ratio test	807.32 on 25 df
-log2(p) of ll-ratio test	509.79

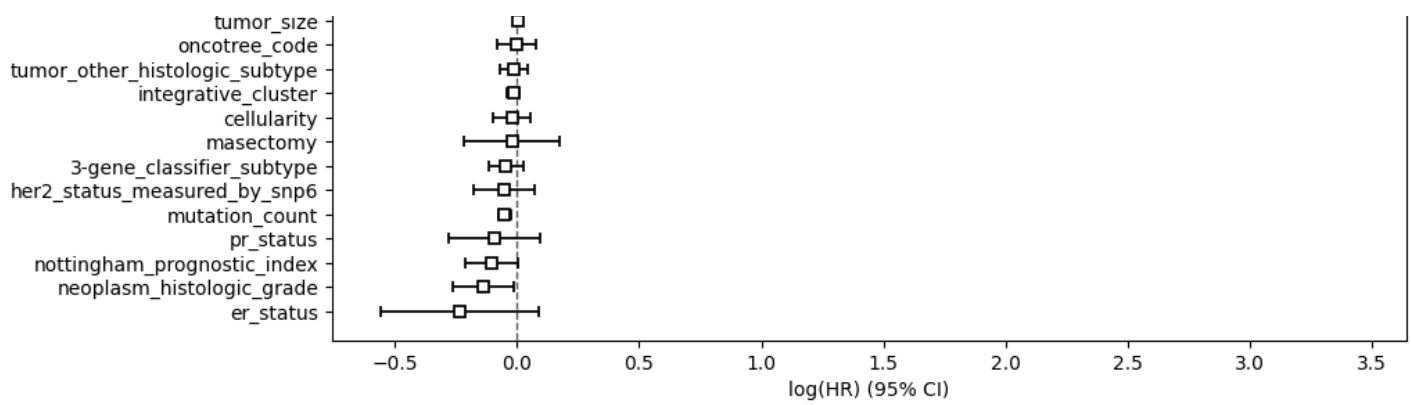
In [69]:

```
plt.subplots(figsize = (10, 6))
cph.plot()
```

Out[69]:

```
<AxesSubplot: xlabel='log(HR) (95% CI)'>
```



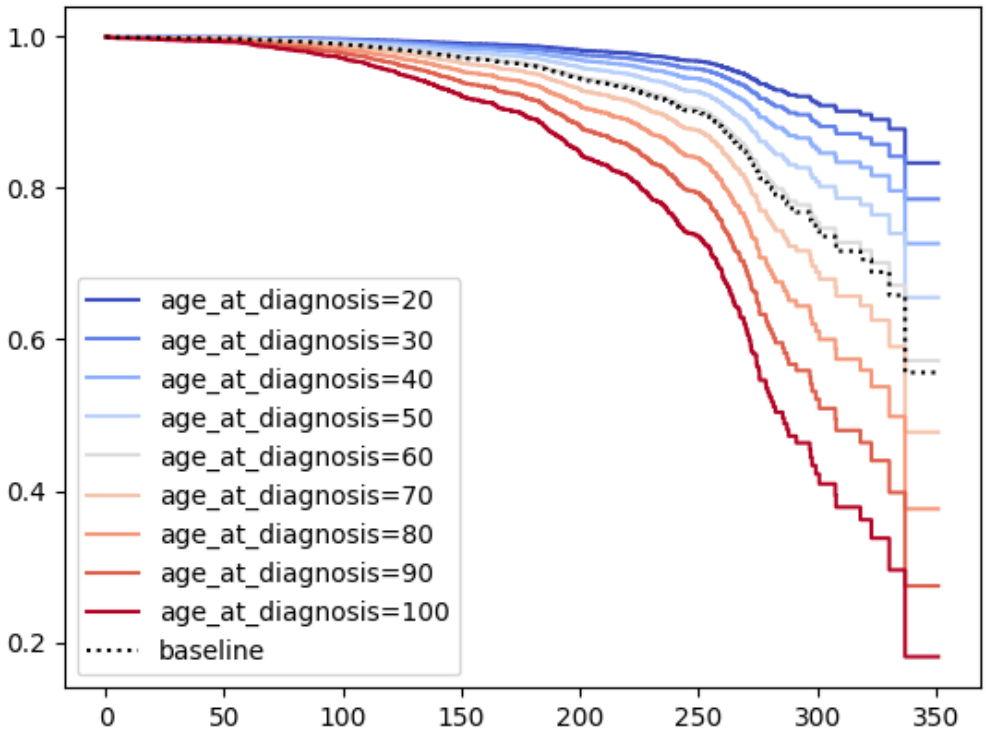


In [70]:

```
#effect of age at diagnosis on overall survival probability
cph.plot_partial_effects_on_outcome(covariates = 'age_at_diagnosis', values = [20,30,40,
50, 60, 70, 80,90,100], cmap = 'coolwarm')
```

Out[70]:

```
<AxesSubplot: >
```



In [71]:

```
cph.check_assumptions(new_survival_df, p_value_threshold = 0.05)
```

```
The ``p_value_threshold`` is set at 0.05. Even under the null hypothesis of no violations
, some
covariates will be below the threshold by chance. This is compounded when there are many
covariates.
Similarly, when there are lots of observations, even minor deviances from the proportiona
l hazard
assumption will be flagged.

With that in mind, it's best to use a combination of statistical tests and visual tests t
o determine
the most serious violations. Produce visual plots using ``check_assumptions(..., show_plo
ts=True)``
and looking for non-constant lines. See link [A] below for a full example.
```

null_distribution	chi squared
degrees_of_freedom	1

model	**<lifelines.CoxPHFitter: fitted with 1839 total...**
test_name	**proportional_hazard_test**

		test_statistic	p	-log2(p)
3-gene_classifier_subtype	**km**	0.71	0.40	1.32
	rank	1.15	0.28	1.81
age_at_diagnosis	**km**	0.05	0.82	0.29
	rank	0.02	0.88	0.18
cellularity	**km**	0.65	0.42	1.25
	rank	0.41	0.52	0.93
chemotherapy	**km**	0.70	0.40	1.31
	rank	0.25	0.62	0.70
death_from_cancer	**km**	6.36	0.01	6.42
	rank	6.61	0.01	6.62
er_status	**km**	0.53	0.46	1.11
	rank	0.66	0.42	1.26
er_status_measured_by_ihc	**km**	0.21	0.65	0.63
	rank	0.51	0.48	1.07
her2_status	**km**	0.31	0.58	0.79
	rank	0.24	0.63	0.67
her2_status_measured_by_snp6	**km**	0.00	0.96	0.06
	rank	0.00	0.98	0.04
hormone_therapy	**km**	0.02	0.88	0.18
	rank	0.01	0.93	0.10
inferred_menopausal_state	**km**	0.10	0.75	0.42
	rank	0.06	0.80	0.32
integrative_cluster	**km**	0.18	0.67	0.58
	rank	0.29	0.59	0.77
lymph_nodes_examined_positive	**km**	0.38	0.54	0.89
	rank	0.25	0.61	0.70
masectomy	**km**	0.00	0.97	0.04
	rank	0.02	0.89	0.17
mutation_count	**km**	8.18	<0.005	7.88
	rank	6.62	0.01	6.63
neoplasm_histologic_grade	**km**	0.55	0.46	1.12
	rank	0.26	0.61	0.70
nottingham_prognostic_index	**km**	0.11	0.74	0.43
	rank	0.10	0.76	0.40
oncotree_code	**km**	1.30	0.25	1.97
	rank	1.22	0.27	1.89
pam50_+_claudin-low_subtype	**km**	0.25	0.62	0.69
	rank	0.06	0.80	0.32
pr_status	**km**	0.22	0.64	0.64
	rank	0.11	0.75	0.42
primary_tumor_laterality	**km**	0.52	0.47	1.08
	rank	0.72	0.40	1.34

		test_statistic	p	-log2(p)
radio_therapy	km	0.77	0.38	1.40
	rank	0.70	0.40	1.31
tumor_other_histologic_subtype	km	0.60	0.44	1.19
	rank	0.65	0.42	1.25
tumor_size	km	0.91	0.34	1.55
	rank	0.62	0.43	1.21
tumor_stage	km	3.84	0.05	4.32
	rank	2.18	0.14	2.84

```
1. Variable 'mutation_count' failed the non-proportional test: p-value is 0.0042.

   Advice 1: the functional form of the variable 'mutation_count' might be incorrect. Tha
t is, there
may be non-linear terms missing. The proportional hazard test used is very sensitive to i
ncorrect
functional forms. See documentation in link [D] below on how to specify a functional form
.

   Advice 2: try binning the variable 'mutation_count' using pd.cut, and then specify it
in
`strata=['mutation_count', ...]` in the call in `.fit`. See documentation in link [B] bel
ow.

   Advice 3: try adding an interaction term with your time variable. See documentation in
link [C]
below.


2. Variable 'tumor_stage' failed the non-proportional test: p-value is 0.0500.

   Advice 1: the functional form of the variable 'tumor_stage' might be incorrect. That i
s, there
may be non-linear terms missing. The proportional hazard test used is very sensitive to i
ncorrect
functional forms. See documentation in link [D] below on how to specify a functional form
.

   Advice 2: try binning the variable 'tumor_stage' using pd.cut, and then specify it in
`strata=['tumor_stage', ...]` in the call in `.fit`. See documentation in link [B] below.

   Advice 3: try adding an interaction term with your time variable. See documentation in
link [C]
below.


3. Variable 'death_from_cancer' failed the non-proportional test: p-value is 0.0102.

   Advice 1: the functional form of the variable 'death_from_cancer' might be incorrect.
That is,
there may be non-linear terms missing. The proportional hazard test used is very sensitiv
e to
incorrect functional forms. See documentation in link [D] below on how to specify a funct
ional form.

   Advice 2: try binning the variable 'death_from_cancer' using pd.cut, and then specify
it in
`strata=['death_from_cancer', ...]` in the call in `.fit`. See documentation in link [B]
below.

   Advice 3: try adding an interaction term with your time variable. See documentation in
link [C]
below.


---
[A]  https://lifelines.readthedocs.io/en/latest/jupyter_notebooks/Proportional%20hazard%2
```

```
0assumption.html
[B]  https://lifelines.readthedocs.io/en/latest/jupyter_notebooks/Proportional%20hazard%2
0assumption.html#Bin-variable-and-stratify-on-it
[C]  https://lifelines.readthedocs.io/en/latest/jupyter_notebooks/Proportional%20hazard%2
0assumption.html#Introduce-time-varying-covariates
[D]  https://lifelines.readthedocs.io/en/latest/jupyter_notebooks/Proportional%20hazard%2
0assumption.html#Modify-the-functional-form
[E]  https://lifelines.readthedocs.io/en/latest/jupyter_notebooks/Proportional%20hazard%2
0assumption.html#Stratification
```

Out[71]:

```
[]
```

In [5]:

```
#seperating mutation data
df_mutation =data.iloc[:,520:]
```