In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:

```
df = pd.read_csv(r'C:\Users\91701\Desktop\livr prediction/cirrhosis.csv',index_col='ID')
df.head()
```

Out[2]:

ID	N_Days	Status	Drug	Age	Sex	Ascites	Hepatomegaly	Spiders	Edema	Bilirubi
1	400	D	D-penicillamine	21464	F	Y	Y	Y	Y	14.
2	4500	C	D-penicillamine	20617	F	N	Y	Y	N	1.
3	1012	D	D-penicillamine	25594	M	N	N	N	S	1.
4	1925	D	D-penicillamine	19994	F	N	Y	Y	S	1.
5	1504	CL	Placebo	13918	F	N	Y	Y	N	3.

In [3]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 418 entries, 1 to 418
Data columns (total 19 columns):
 #   Column         Non-Null Count  Dtype  
---  ------         --------------  -----  
 0   N_Days         418 non-null    int64  
 1   Status         418 non-null    object 
 2   Drug           312 non-null    object 
 3   Age            418 non-null    int64  
 4   Sex            418 non-null    object 
 5   Ascites        312 non-null    object 
 6   Hepatomegaly   312 non-null    object 
 7   Spiders        312 non-null    object 
 8   Edema          418 non-null    object 
 9   Bilirubin      418 non-null    float64
 10  Cholesterol    284 non-null    float64
 11  Albumin        418 non-null    float64
 12  Copper         310 non-null    float64
 13  Alk_Phos       312 non-null    float64
 14  SGOT           312 non-null    float64
 15  Tryglicerides  282 non-null    float64
 16  Platelets      407 non-null    float64
 17  Prothrombin    416 non-null    float64
 18  Stage          412 non-null    float64
dtypes: float64(10), int64(2), object(7)
memory usage: 65.3+ KB
```

In [4]:

```
df.describe()
```

Out[4]:

	N_Days	Age	Bilirubin	Cholesterol	Albumin	Copper	Alk_Ph
count	418.000000	418.000000	418.000000	284.000000	418.000000	310.000000	312.0000
mean	1917.782297	18533.351675	3.220813	369.510563	3.497440	97.648387	1982.6557
std	1104.672992	3815.845055	4.407506	231.944545	0.424972	85.613920	2140.3888
min	41.000000	9598.000000	0.300000	120.000000	1.960000	4.000000	289.0000
25%	1092.750000	15644.500000	0.800000	249.500000	3.242500	41.250000	871.5000
50%	1730.000000	18628.000000	1.400000	309.500000	3.530000	73.000000	1259.0000
75%	2613.500000	21272.500000	3.400000	400.000000	3.770000	123.000000	1980.0000
max	4795.000000	28650.000000	28.000000	1775.000000	4.640000	588.000000	13862.4000

In [5]:

```
df.isna().sum()
```

Out[5]:

```
N_Days             0
Status             0
Drug             106
Age                0
Sex                0
Ascites          106
Hepatomegaly     106
Spiders          106
Edema              0
Bilirubin          0
Cholesterol      134
Albumin            0
Copper           108
Alk_Phos         106
SGOT             106
Tryglicerides    136
Platelets         11
Prothrombin        2
Stage              6
dtype: int64
```

Here we have two types of numerical and categorical

lets deal with numerical data

In [6]:

```
df.select_dtypes(include=(['int64', 'float64'])).isna().sum()
```

Out[6]:

```
N_Days             0
Age                0
Bilirubin          0
Cholesterol      134
Albumin            0
Copper           108
Alk_Phos         106
SGOT             106
Tryglicerides    136
Platelets         11
Prothrombin        2
Stage              6
dtype: int64
```

In [7]:

```
df.select_dtypes(include=(['int64', 'float64'])).isna().sum()
df_num_col = df.select_dtypes(include=(['int64', 'float64'])).columns
for c in df_num_col:
    df[c].fillna(df[c].median(), inplace=True)

df.select_dtypes(include=(['int64', 'float64'])).isna().sum()
```

Out[7]:

```
N_Days          0
Age             0
Bilirubin       0
Cholesterol     0
Albumin         0
Copper          0
Alk_Phos        0
SGOT            0
Tryglicerides   0
Platelets       0
Prothrombin     0
Stage           0
dtype: int64
```

for the categorical data

In [8]:

```
df.select_dtypes(include=('object')).isna().sum()
```

Out[8]:

```
Status          0
Drug          106
Sex             0
Ascites       106
Hepatomegaly  106
Spiders       106
Edema           0
dtype: int64
```

In [9]:

```
df_cat_col = df.select_dtypes(include=('object')).columns
for c in df_cat_col:
    df[c].fillna(df[c].mode().values[0], inplace=True)

df.select_dtypes(include=('object')).isna().sum()
```

Out[9]:

```
Status          0
Drug            0
Sex             0
Ascites         0
Hepatomegaly    0
Spiders         0
Edema           0
dtype: int64
```

In [10]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 418 entries, 1 to 418
Data columns (total 19 columns):
 #   Column         Non-Null Count  Dtype
---  ------         --------------  -----
 0   N_Days         418 non-null    int64
 1   Status         418 non-null    object
 2   Drug           418 non-null    object
 3   Age            418 non-null    int64
 4   Sex            418 non-null    object
 5   Ascites        418 non-null    object
 6   Hepatomegaly   418 non-null    object
 7   Spiders        418 non-null    object
 8   Edema          418 non-null    object
 9   Bilirubin      418 non-null    float64
 10  Cholesterol    418 non-null    float64
 11  Albumin        418 non-null    float64
 12  Copper         418 non-null    float64
 13  Alk_Phos       418 non-null    float64
 14  SGOT           418 non-null    float64
 15  Tryglicerides  418 non-null    float64
 16  Platelets      418 non-null    float64
 17  Prothrombin    418 non-null    float64
 18  Stage          418 non-null    float64
dtypes: float64(10), int64(2), object(7)
memory usage: 65.3+ KB
```

EDA part

In [11]:

```
df['Stage'].value_counts()
```

Out[11]:

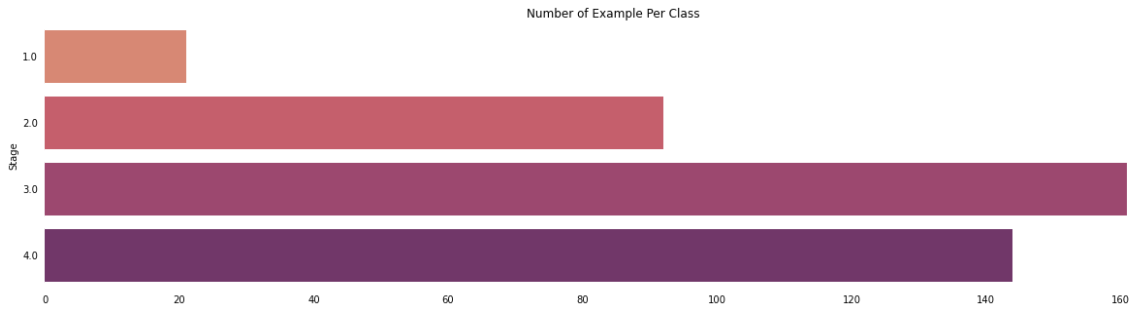
```
3.0    161
4.0    144
2.0     92
1.0     21
Name: Stage, dtype: int64
```

In [12]:

```
plt.figure(figsize=(21,5))
sns.countplot(y=df['Stage'], palette="flare", alpha=1.0, )
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Number of Example Per Class')
```

Out[12]:

```
Text(0.5, 1.0, 'Number of Example Per Class')
```



Extracting essential inputs(features) and output(Target)

In [13]:

```
df['Stage'] = np.where(df['Stage'] == 4,1,0)
```

relation with disease(Target vs input feature)

Disease Stage Across Gender

Ascites proportion across Stages

Medications prescribed across Stages

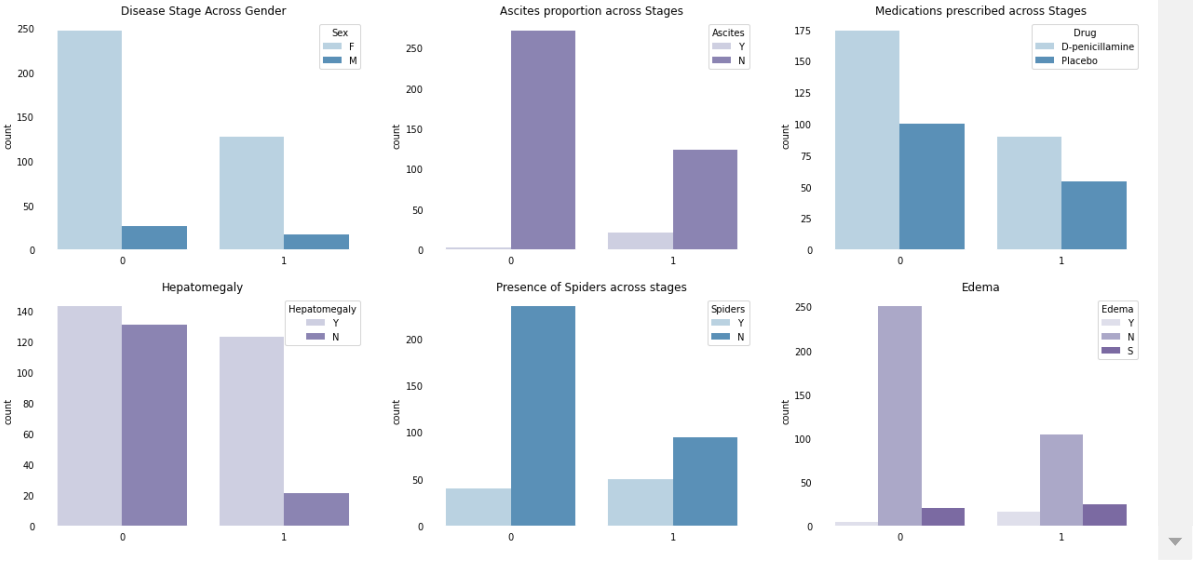
Hepatomegaly

Presence of Spiders across stages

Edema

In [14]:

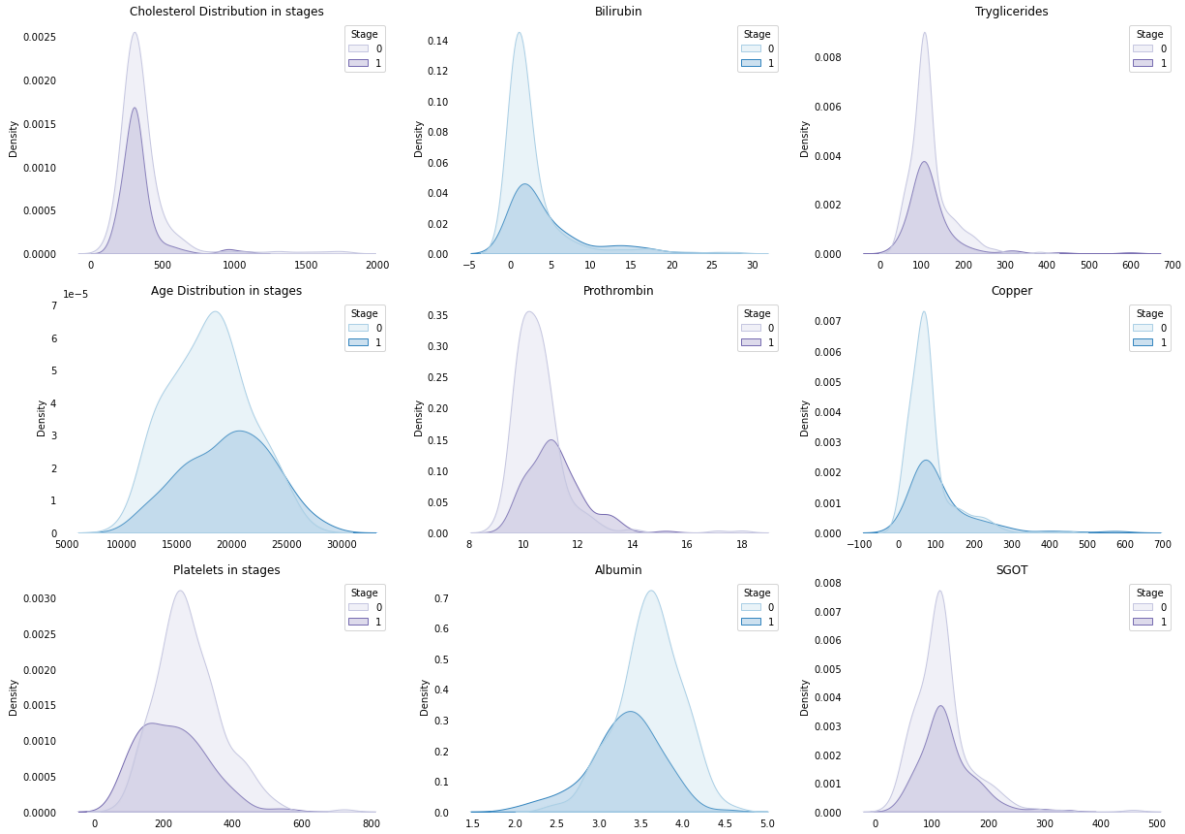
```
plt.figure(figsize=(21.2,10))

plt.subplot(2,3,1)
sns.countplot(x=df['Stage'], hue=df['Sex'], palette='Blues', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Disease Stage Across Gender')

plt.subplot(2,3,2)
sns.countplot(x=df['Stage'], hue=df['Ascites'], palette='Purples', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Ascites proportion across Stages')

plt.subplot(2,3,3)
sns.countplot(x=df['Stage'], hue=df['Drug'], palette='Blues', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Medications prescribed across Stages');

plt.subplot(2,3,4)
sns.countplot(x=df['Stage'], hue=df['Hepatomegaly'], palette='Purples', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Hepatomegaly');

plt.subplot(2,3,5)
sns.countplot(x=df['Stage'], hue=df['Spiders'], palette='Blues', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Presence of Spiders across stages');

plt.subplot(2,3,6)
sns.countplot(x=df['Stage'], hue=df['Edema'], palette='Purples', alpha=0.9)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Edema');
```


Disease Stage Across Gender
Sex
F
M
count
Ascites proportion across Stages
Ascites
Y
N
count
Medications prescribed across Stages
Drug
D-penicillamine
Placebo
count
Hepatomegaly
Hepatomegaly
Y
N
count
Presence of Spiders across stages
Spiders
Y
N
count
Edema
Edema
Y
N
S
count

In [15]:

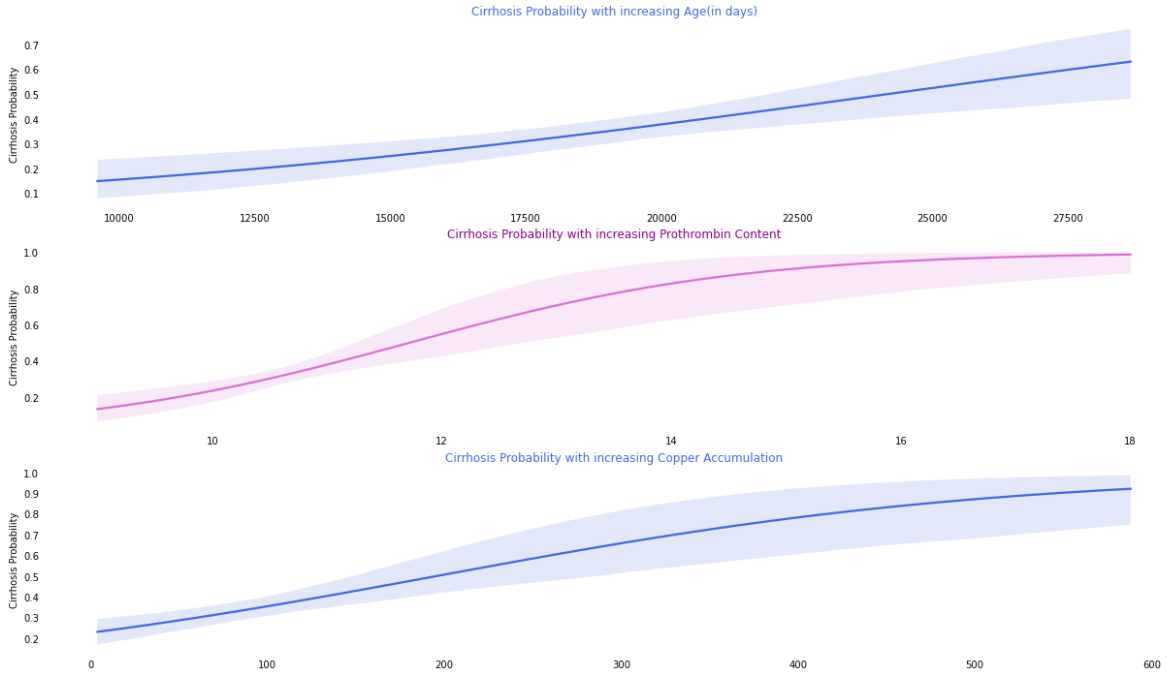
```
plt.figure(figsize=(20.6,15))

plt.subplot(3,3,1)
sns.kdeplot(df['Cholesterol'], hue=df['Stage'], fill=True, palette='Purples')
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Cholesterol Distribution in stages');

plt.subplot(3,3,2)
sns.kdeplot(df['Bilirubin'], hue=df['Stage'], fill=True, palette='Blues', common_norm=True)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Bilirubin');

plt.subplot(3,3,3)
sns.kdeplot(df['Tryglicerides'], hue=df['Stage'], fill=True, palette='Purples', common_norm
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Tryglicerides');

plt.subplot(3,3,4)
sns.kdeplot(df['Age'], hue=df['Stage'], fill=True, palette='Blues', common_norm=True)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Age Distribution in stages');

plt.subplot(3,3,5)
sns.kdeplot(df['Prothrombin'], hue=df['Stage'], fill=True, palette='Purples', common_norm=T
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Prothrombin');

plt.subplot(3,3,6)
sns.kdeplot(df['Copper'], hue=df['Stage'], fill=True, palette='Blues', common_norm=True)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Copper');

plt.subplot(3,3,7)
sns.kdeplot(df['Platelets'], hue=df['Stage'], fill=True, palette='Purples')
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Platelets in stages');

plt.subplot(3,3,8)
sns.kdeplot(df['Albumin'], hue=df['Stage'], fill=True, palette='Blues', common_norm=True)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('Albumin');

plt.subplot(3,3,9)
```

```
sns.kdeplot(df['SGOT'], hue=df['Stage'], fill=True, palette='Purples', common_norm=True)
sns.despine(top=True, right=True, bottom=True, left=True)
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('')
plt.title('SGOT');
```



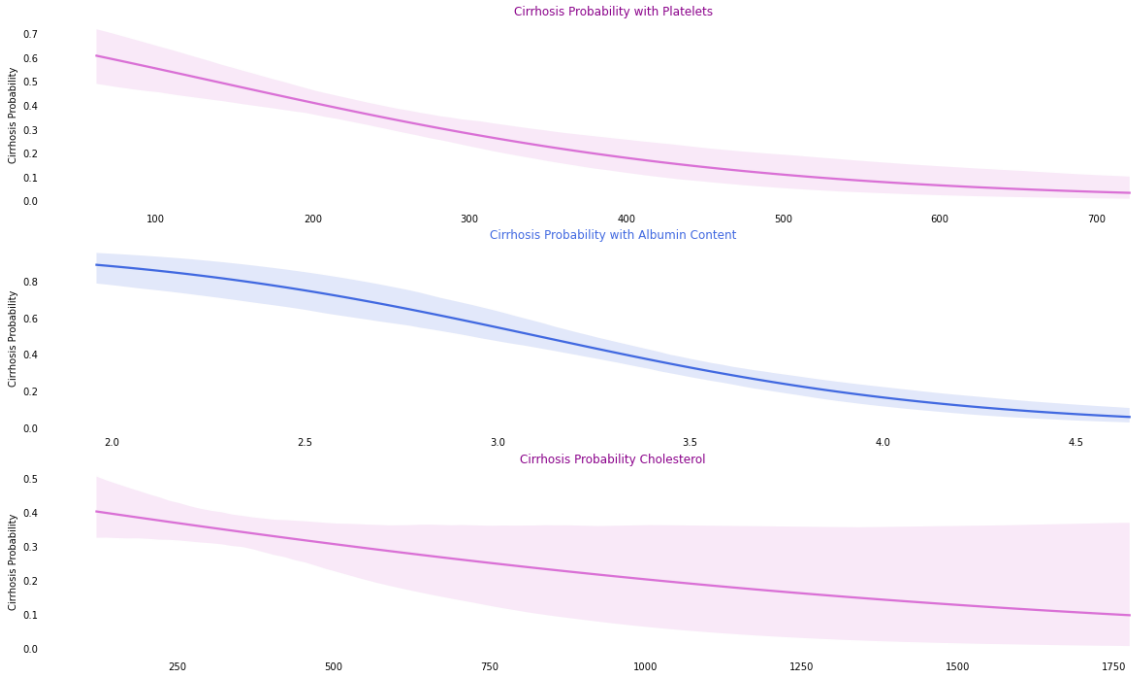
In [16]:

```
#title Regression Plots of Positive Correlated Features.
plt.figure(figsize=(21,12))

plt.subplot(3,1,1)
sns.regplot(x=df['Age'], y=df['Stage'], scatter=False, logistic=True, color='royalblue')
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability with increasing Age(in days)'), color='royalblue'

plt.subplot(3,1,2)
sns.regplot(x=df['Prothrombin'], y=df['Stage'], scatter=False, logistic=True, color='orchid
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability with increasing Prothrombin Content'), color='dar

plt.subplot(3,1,3)
sns.regplot(x=df['Copper'], y=df['Stage'], scatter=False, logistic=True, color='royalblue')
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability with increasing Copper Accumulation'), color='roy
```



In [17]:

```
#@title Regression Plots of negatively correlated Features.
plt.figure(figsize=(21,12))

plt.subplot(3,1,1)
sns.regplot(x=df['Platelets'], y=df['Stage'], scatter=False, logistic=True, color='orchid')
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability with Platelets'), color='darkmagenta');

plt.subplot(3,1,2)
sns.regplot(x=df['Albumin'], y=df['Stage'], scatter=False, logistic=True, color='royalblue'
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability with Albumin Content'), color='royalblue');

plt.subplot(3,1,3)
sns.regplot(x=df['Cholesterol'], y=df['Stage'], scatter=False, logistic=True, color='orchid
sns.despine(fig=None, ax=None, top=True, right=True, left=True, bottom=True, offset=None, t
plt.tick_params(axis='both', which='both', bottom=False, top=False, left=False)
plt.xlabel('');
plt.ylabel('Cirrhosis Probability');
plt.setp(plt.title('Cirrhosis Probability Cholesterol'), color='darkmagenta') ;
```



preprocessing

In [18]:

```
# replacing catagorical data with intigers.
df['Sex'] = df['Sex'].replace({'M':0, 'F':1})                                  # Male : 0 , F
df['Ascites'] = df['Ascites'].replace({'N':0, 'Y':1})                          # N : 0, Y : 1
df['Drug'] = df['Drug'].replace({'D-penicillamine':0, 'Placebo':1})            # D-penicillam
df['Hepatomegaly'] = df['Hepatomegaly'].replace({'N':0, 'Y':1})                # N : 0, Y : 1
df['Spiders'] = df['Spiders'].replace({'N':0, 'Y':1})                          # N : 0, Y : 1
df['Edema'] = df['Edema'].replace({'N':0, 'Y':1, 'S':-1})                      # N : 0, Y : 1
df['Status'] = df['Status'].replace({'C':0, 'CL':1, 'D':-1})                   # 'C':0, 'CL':
```

In [19]:

```
X = df.drop(['Status', 'N_Days', 'Stage'], axis=1)
y = df.pop('Stage')
```

In [20]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 418 entries, 1 to 418
Data columns (total 18 columns):
 #   Column         Non-Null Count  Dtype  
---  ------         --------------  -----  
 0   N_Days         418 non-null    int64  
 1   Status         418 non-null    int64  
 2   Drug           418 non-null    int64  
 3   Age            418 non-null    int64  
 4   Sex            418 non-null    int64  
 5   Ascites        418 non-null    int64  
 6   Hepatomegaly   418 non-null    int64  
 7   Spiders        418 non-null    int64  
 8   Edema          418 non-null    int64  
 9   Bilirubin      418 non-null    float64
 10  Cholesterol    418 non-null    float64
 11  Albumin        418 non-null    float64
 12  Copper         418 non-null    float64
 13  Alk_Phos       418 non-null    float64
 14  SGOT           418 non-null    float64
 15  Tryglicerides  418 non-null    float64
 16  Platelets      418 non-null    float64
 17  Prothrombin    418 non-null    float64
dtypes: float64(9), int64(9)
memory usage: 78.2 KB
```

Model selection

In [21]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import StratifiedKFold

log_model = LogisticRegression(max_iter=5000, solver='saga')
skf = StratifiedKFold(n_splits=10, random_state=1, shuffle=True)

acc=[]
def training(train, test, fold_no):
  X_train = train
  y_train = y.iloc[train_index]
  X_test = test
  y_test = y.iloc[test_index]
  log_model.fit(X_train, y_train)
  score = log_model.score(X_test,y_test)
  acc.append(score)
  print('For Fold {} the accuracy is {}'.format(str(fold_no),score))
```

In [22]:

```
fold_no = 1
for train_index,test_index in skf.split(X, y):
  train = X.iloc[train_index,:]
  test = X.iloc[test_index,:]
  training(train, test, fold_no)
  fold_no += 1
print()
print('Logestic Regression Mean Accuracy = ', np.mean(acc))
```

```
For Fold 1 the accuracy is 0.6904761904761905
For Fold 2 the accuracy is 0.7857142857142857
For Fold 3 the accuracy is 0.6190476190476191
For Fold 4 the accuracy is 0.6666666666666666
For Fold 5 the accuracy is 0.8095238095238095
For Fold 6 the accuracy is 0.6666666666666666
For Fold 7 the accuracy is 0.6904761904761905
For Fold 8 the accuracy is 0.7380952380952381
For Fold 9 the accuracy is 0.7317073170731707
For Fold 10 the accuracy is 0.6341463414634146

Logestic Regression Mean Accuracy =  0.7032520325203252
```

In [23]:

```
from sklearn.metrics import classification_report
log_model_predict = log_model.predict(test)
log_model_predict_proba = log_model.predict_proba(test)

print(classification_report(y.iloc[test_index], log_model_predict))
```

```
              precision    recall  f1-score   support

           0       0.70      0.78      0.74        27
           1       0.45      0.36      0.40        14

    accuracy                           0.63        41
   macro avg       0.58      0.57      0.57        41
weighted avg       0.62      0.63      0.62        41
```

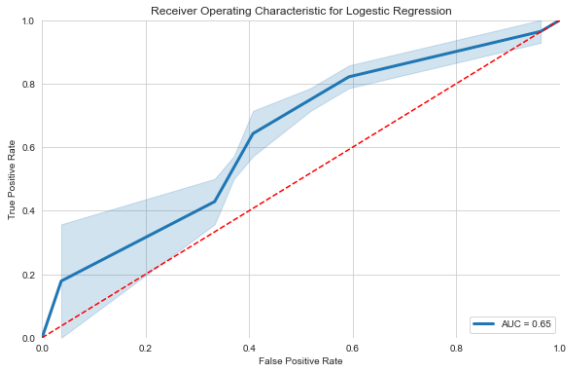
In [24]:

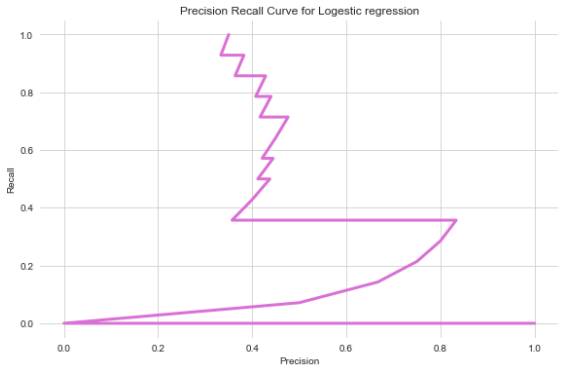
```
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve, auc

fpr, tpr, threshold = roc_curve(y.iloc[test_index], log_model_predict_proba[:,1])
roc_auc = auc(fpr, tpr)

print('AUC : ', roc_auc_score(y.iloc[test_index], log_model_predict_proba[:,1]))
```

```
AUC :  0.6507936507936508
```

In [25]:

```
sns.set_style('whitegrid')
plt.figure(figsize=(21,6))

plt.subplot(1,2,1)
plt.title('Receiver Operating Characteristic for Logestic Regression')
sns.lineplot(x=fpr, y=tpr, label = 'AUC = %0.2f' % roc_auc, palette='purple', linewidth=3)
plt.legend(loc = 'lower right')
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0, 1])
plt.ylim([0, 1])
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.tick_params(left=False, bottom=False)
sns.despine(top=True, bottom=True, left=True)

# calculate precision-recall curve
from sklearn.metrics import precision_recall_curve, f1_score
precision, recall, thresholds = precision_recall_curve(y.iloc[test_index], log_model_predic

plt.subplot(1,2,2)
plt.plot(precision, recall, linewidth=3, color='orchid')
sns.despine(top=True, bottom=True, left=True)
plt.xlabel('Precision')
plt.ylabel('Recall')
plt.title('Precision Recall Curve for Logestic regression');
```





In [26]:

```
from sklearn.model_selection import StratifiedKFold
from xgboost import XGBClassifier
skf = StratifiedKFold(n_splits=10, random_state=1, shuffle=True)
model = XGBClassifier(learning_rate=0.75, max_depth=3, random_state=1, gamma=0, eval_metric

acc=[]
def training(train, test, fold_no):
  X_train = train
  y_train = y.iloc[train_index]
  X_test = test
  y_test = y.iloc[test_index]
  model.fit(X_train, y_train)
  score = model.score(X_test,y_test)
  acc.append(score)
  print('For Fold {} the accuracy is {}'.format(str(fold_no),score))

fold_no = 1
for train_index,test_index in skf.split(X, y):
  train = X.iloc[train_index,:]
  test = X.iloc[test_index,:]
  training(train, test, fold_no)
  fold_no += 1
print()
print('XGboost model Mean Accuracy = ', np.mean(acc))
```

```
For Fold 1 the accuracy is 0.7857142857142857
For Fold 2 the accuracy is 0.7619047619047619
For Fold 3 the accuracy is 0.6428571428571429
For Fold 4 the accuracy is 0.7380952380952381
For Fold 5 the accuracy is 0.7619047619047619
For Fold 6 the accuracy is 0.7142857142857143
For Fold 7 the accuracy is 0.7142857142857143
For Fold 8 the accuracy is 0.7619047619047619
For Fold 9 the accuracy is 0.6829268292682927
For Fold 10 the accuracy is 0.7804878048780488

XGboost model Mean Accuracy =  0.7344367015098723
```

In [27]:

```
from sklearn.metrics import classification_report
XGB_model_predict = model.predict(test)
XGB_model_predict_proba = model.predict_proba(test)

print(classification_report(y.iloc[test_index], XGB_model_predict))
```

```
              precision    recall  f1-score   support

           0       0.82      0.85      0.84        27
           1       0.69      0.64      0.67        14

    accuracy                           0.78        41
   macro avg       0.76      0.75      0.75        41
weighted avg       0.78      0.78      0.78        41
```

In [30]:

```
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve, auc

fpr, tpr, threshold = roc_curve(y.iloc[test_index], XGB_model_predict_proba[:,1])
roc_auc = auc(fpr, tpr)

print('AUC : ', roc_auc_score(y.iloc[test_index], XGB_model_predict_proba[:,1]))
```

```
AUC :  0.738095238095238
```

In [33]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 418 entries, 1 to 418
Data columns (total 18 columns):
 #   Column         Non-Null Count  Dtype  
---  ------         --------------  -----  
 0   N_Days         418 non-null    int64  
 1   Status         418 non-null    int64  
 2   Drug           418 non-null    int64  
 3   Age            418 non-null    int64  
 4   Sex            418 non-null    int64  
 5   Ascites        418 non-null    int64  
 6   Hepatomegaly   418 non-null    int64  
 7   Spiders        418 non-null    int64  
 8   Edema          418 non-null    int64  
 9   Bilirubin      418 non-null    float64
 10  Cholesterol    418 non-null    float64
 11  Albumin        418 non-null    float64
 12  Copper         418 non-null    float64
 13  Alk_Phos       418 non-null    float64
 14  SGOT           418 non-null    float64
 15  Tryglicerides  418 non-null    float64
 16  Platelets      418 non-null    float64
 17  Prothrombin    418 non-null    float64
dtypes: float64(9), int64(9)
memory usage: 78.2 KB
```

In [38]:

```
prediction = model.predict((np.array([[90,
                                       89,
                                       65,
                                       90,
                                       80,
                                       5.0,
                                       150,90,
                                       89,
                                       65,
                                       90,
                                       80,
                                       5.0,
                                       150,
                                      100,
                                      120]])))
print("liver cirrhosis prediction :", prediction)
if prediction == 1:
    print("the patient has liver cirrhosis")
else:
    print("the patient has no liver cirrhosis")
```

```
liver cirrhosis prediction : [1]
the patient has liver cirrhosis
```

In [ ]: