In [2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

In [3]:
```
data = pd.read_csv('data.csv')
```

In [4]:
```
data.head()
```

Out[4]:

	STUDYID	RPT	time	death	BMI	HEIGHTBL	WEIGHTBL	ALP	ALT	AST
0	ASC	ASC-001-0003	585	1	28.7000	172.72	85.73000	5.733341	2.944439	3.258097
1	ASC	ASC-001-0004	495	1	25.3000	171.80	74.80000	6.269096	2.708050	3.295837
2	ASC	ASC-001-0005	167	1	26.2000	167.90	73.90000	5.068904	2.639057	2.890372
3	ASC	ASC-001-0008	161	1	26.9915	166.70	83.50879	4.812184	3.761200	3.688879
4	ASC	ASC-001-0009	575	0	46.5000	175.60	143.30000	3.496508	2.944439	3.258097

5 rows × 105 columns

In [18]:
```
list(data.columns)
```

Out[18]:
```
['STUDYID',
 'RPT',
 'time',
 'death',
 'BMI',
 'HEIGHTBL',
 'WEIGHTBL',
 'ALP',
 'ALT',
 'AST',
 'CA',
 'CREAT',
 'HB',
 'LDH',
 'NEU',
 'PLT',
 'PSA',
 'TBILI',
 'TESTO',
 'WBC',
 'CREACL',
```

```
                'NA.',
                'MG',
                'PHOS',
                'ALB',
                'TPRO',
                'RBC',
                'LYM',
                'BUN',
                'CCRC',
                'GLU',
                'SYSTOLICBP',
                'DIASTOLICBP',
                'PULSE',
                'HEMAT',
                'SPEGRA',
                'LYMperLEU',
                'MONO',
                'MONOperLEU',
                'NEUperLEU',
                'POT',
                'BASOperLEU',
                'EOS',
                'EOSperLEU',
                'TARGET',
                'LYMPH_NODES',
                'KIDNEYS',
                'LUNGS',
                'LIVER',
                'PLEURA',
                'OTHER',
                'PROSTATE',
                'ORCHIDECTOMY',
                'PROSTATECTOMY',
                'LYMPHADENECTOMY',
                'BILATERAL_ORCHIDECTOMY',
                'PRIOR_RADIOTHERAPY',
                'ANALGESICS',
                'ANTI_ANDROGENS',
                'GLUCOCORTICOID',
                'GONADOTROPIN',
                'BISPHOSPHONATE',
                'CORTICOSTEROID',
                'IMIDAZOLE',
                'ACE_INHIBITORS',
                'BETA_BLOCKING',
                'HMG_COA_REDUCT',
                'ESTROGENS',
                'ANTI_ESTROGENS',
                'CEREBACC',
                'CHF',
                'DVT',
                'DIAB',
                'MI',
                'PULMEMB',
                'SPINCOMP',
                'COPD',
                'MHBLOOD',
                'MHCARD',
                'MHCONGEN',
                'MHEAR',
                'MHENDO',
                'MHGASTRO',
                'MHHEPATO',
                'MHIMMUNE',
                'MHINFECT',
```

```
 'MHINJURY',
 'MHINVEST',
 'MHMETAB',
 'MHPSYCH',
 'MHRENAL',
 'MHRESP',
 'MHSKIN',
 'MHVASC',
 'ECOG_C',
 'AGEGRP2',
 'RaceAsian',
 'RaceBlack',
 'RaceOther',
 'RaceWhite',
 'RegionAsia',
 'RegionEastEuro',
 'RegionNorthAmer',
 'RegionSouthAmer',
 'RegionWestEuro']
```

In [5]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1600 entries, 0 to 1599
Columns: 105 entries, STUDYID to RegionWestEuro
dtypes: float64(40), int64(63), object(2)
memory usage: 1.3+ MB
```

In [12]:
```
data.describe()
```

Out[12]:

	time	death	BMI	HEIGHTBL	WEIGHTBL	ALP	
count	1600.000000	1600.000000	1600.000000	1600.000000	1600.000000	1600.000000	1600.00
mean	453.798750	0.414375	28.204521	174.089024	85.506196	5.041073	3.00
std	289.693734	0.492768	4.531143	7.713103	15.834734	0.863298	0.50
min	4.000000	0.000000	15.900000	131.500000	46.000000	3.295837	1.38
25%	244.750000	0.000000	25.175000	169.200000	75.000000	4.406719	2.70
50%	387.000000	0.000000	27.700000	174.400000	84.000000	4.828314	2.95
75%	581.000000	1.000000	30.700000	179.500000	93.400000	5.494088	3.29
max	1594.000000	1.000000	54.300000	198.700000	164.700000	8.289791	5.18

8 rows × 103 columns

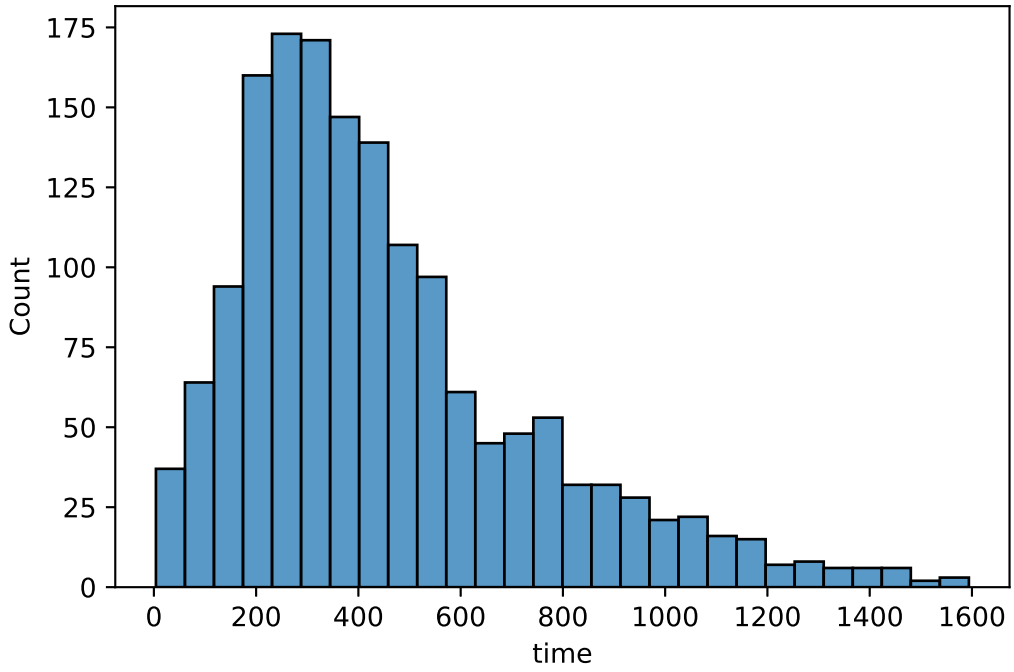
In [7]:
```
data.corr()['time'].sort_values(ascending=True)
```

Out[7]:
```
TESTO              -0.207605
ALP                -0.152988
LDH                -0.141076
NEUperLEU          -0.134277
GLU                -0.117638
                      ...
TBILI               0.160275
RegionSouthAmer     0.173898
CORTICOSTEROID      0.205400
```

```
time                1.000000
RegionAsia               NaN
Name: time, Length: 103, dtype: float64
```

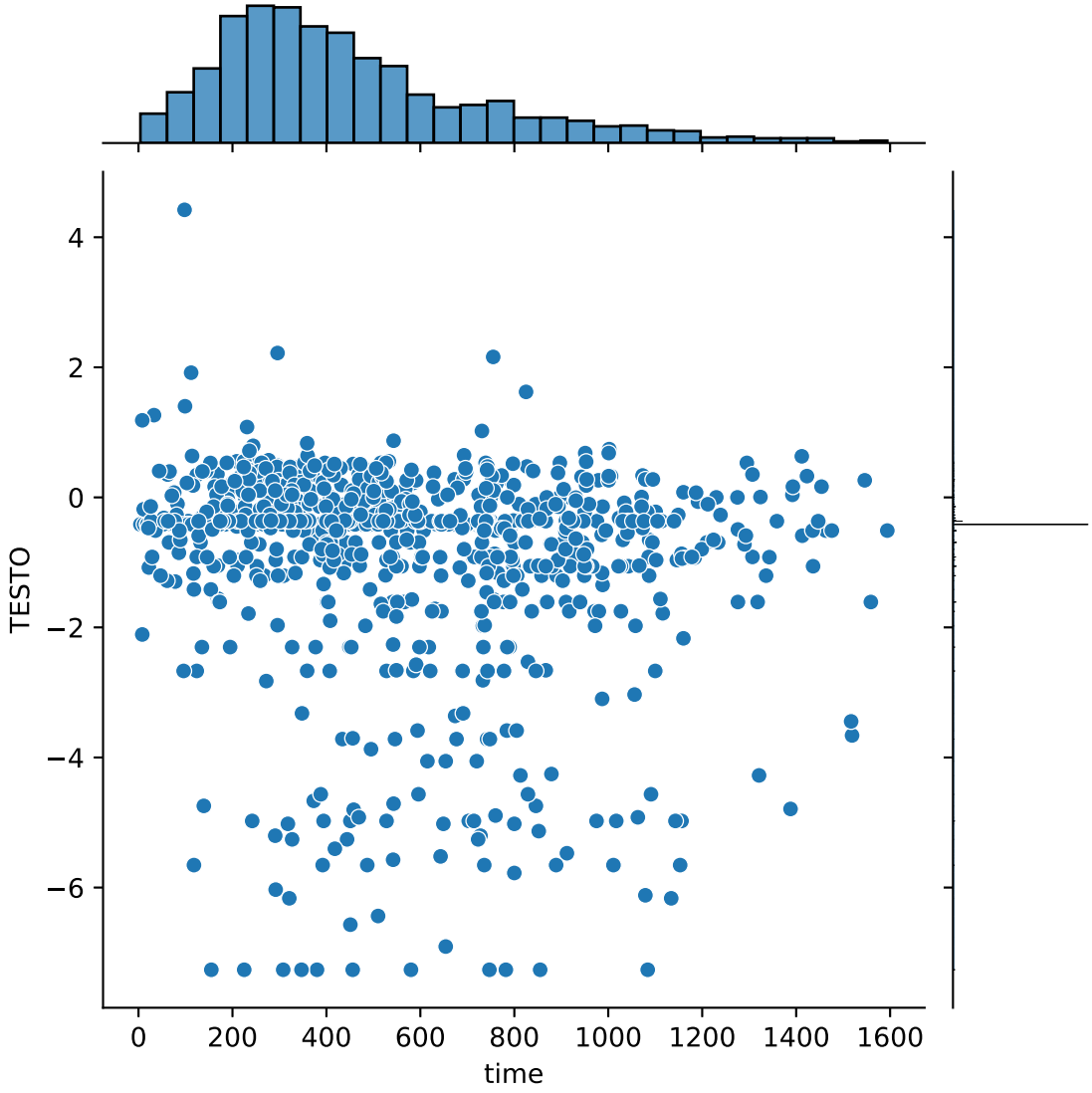
In [11]:
```
sns.histplot(data['time'])
```

Out[11]: <AxesSubplot:xlabel='time', ylabel='Count'>



In [19]:
```
sns.jointplot(x='time',y='TESTO', data=data)
```

Out[19]: <seaborn.axisgrid.JointGrid at 0x7f90885b2af0>



In [34]:
```
corr_data = data.corr()['time'].sort_values(ascending=False)
```

In [39]:
```
corr_data.head()
```

Out[39]:
```
time               1.000000
CORTICOSTEROID     0.205400
RegionSouthAmer    0.173898
TBILI              0.160275
HB                 0.149179
Name: time, dtype: float64
```

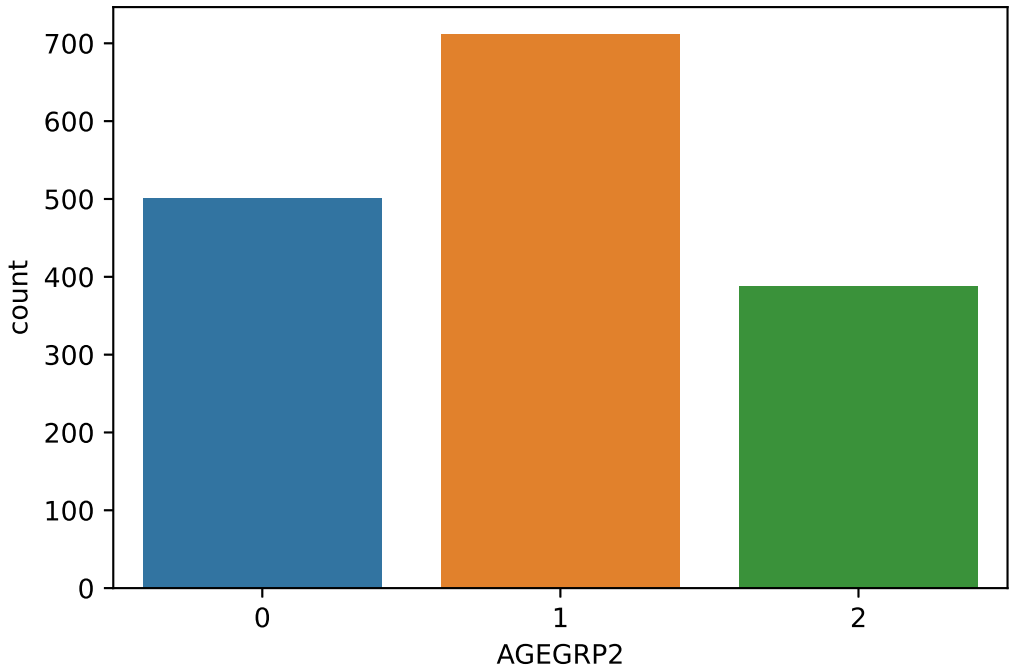
In [44]:
```
data['AGEGRP2']
```

Out[44]:
```
0       1
1       2
2       1
3       2
4       1
       ..
1595    0
1596    1
1597    0
```

```
1598    0
1599    1
Name: AGEGRP2, Length: 1600, dtype: int64
```

In [172…

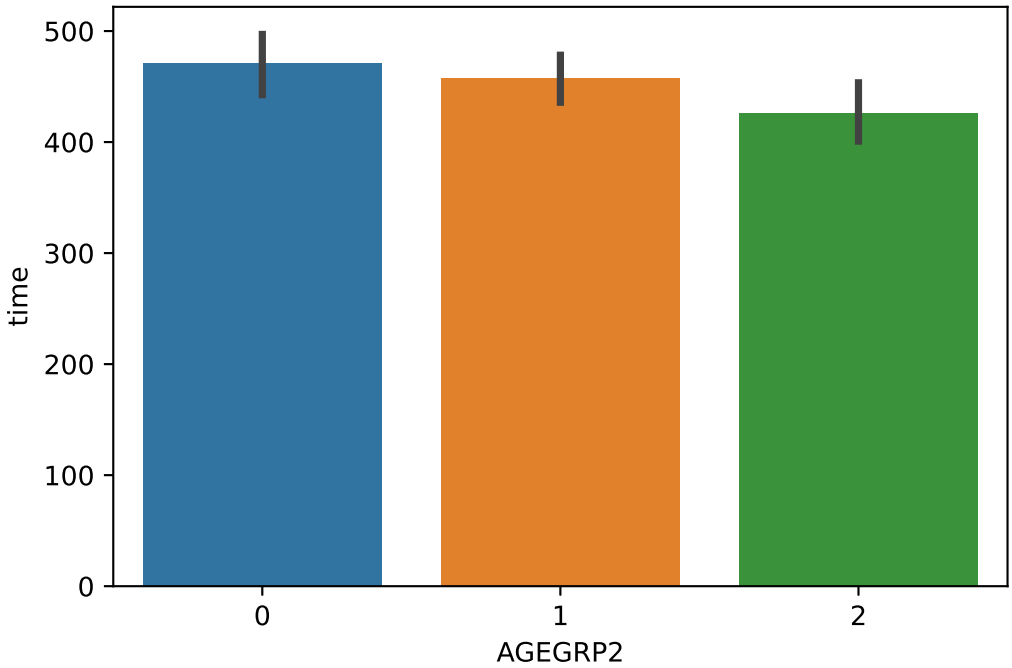
```
sns.countplot(x=data['AGEGRP2']).set_axis_labels = ('18-64','65-74','74+')
```



In [162…

```
sns.barplot(x='AGEGRP2',y='time',data=data)
```

Out[162… <AxesSubplot:xlabel='AGEGRP2', ylabel='time'>



In [71]:

```
data['BMI']
```

```
0       28.7000
```

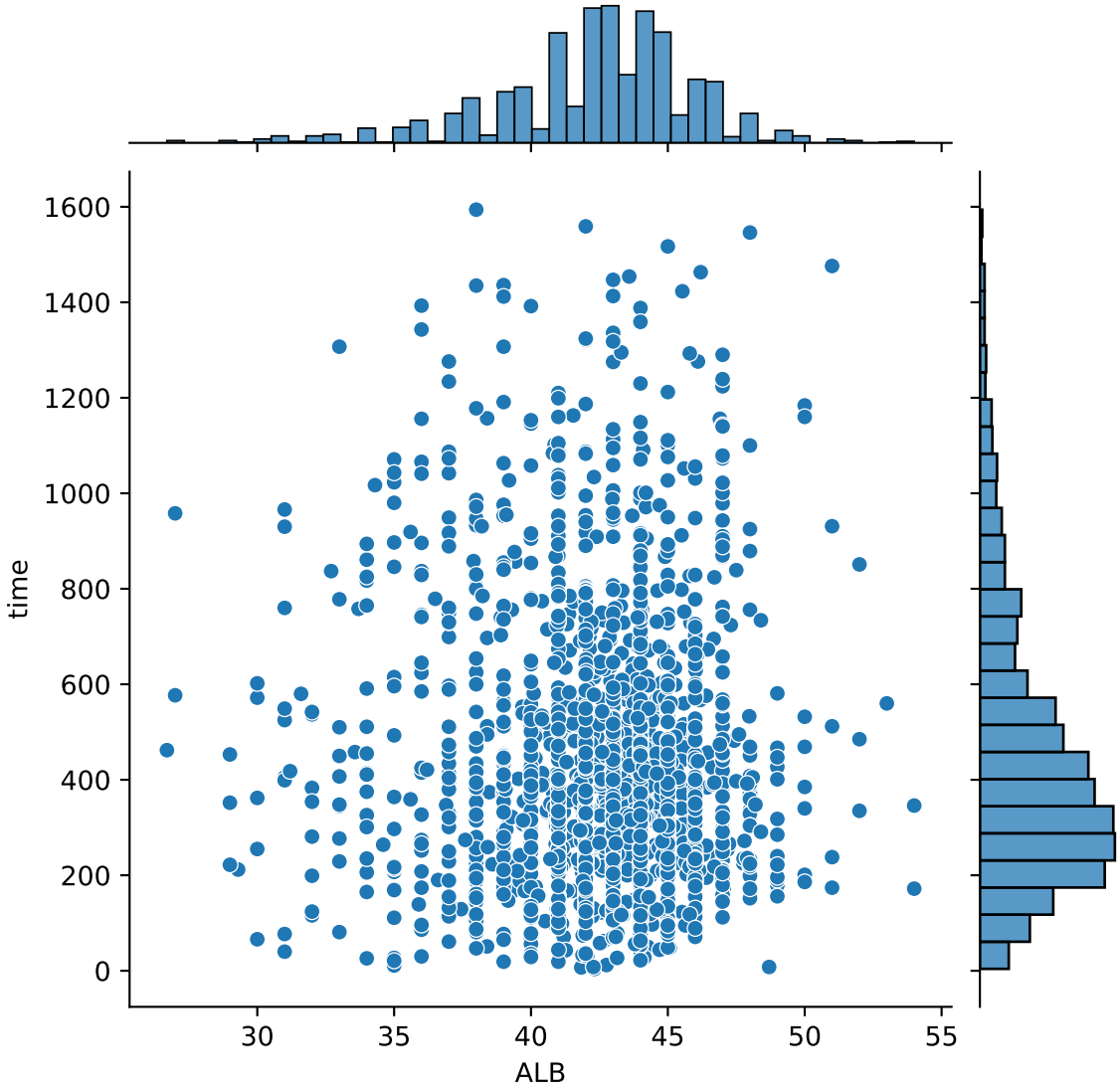
Out[71]:
```
1       25.3000
2       26.2000
3       26.9915
4       46.5000
         ...
1595    32.4000
1596    31.0000
1597    26.0000
1598    30.6000
1599    30.4000
Name: BMI, Length: 1600, dtype: float64
```

In [77]:
```
data.corr()['death'].sort_values(ascending=True)
```

Out[77]:
```
ALB              -0.238652
TESTO            -0.180615
HEMAT            -0.177278
HB               -0.153038
RBC              -0.142311
                    ...
LDH               0.206975
CORTICOSTEROID    0.211477
ALP               0.227153
death             1.000000
RegionAsia             NaN
Name: death, Length: 103, dtype: float64
```

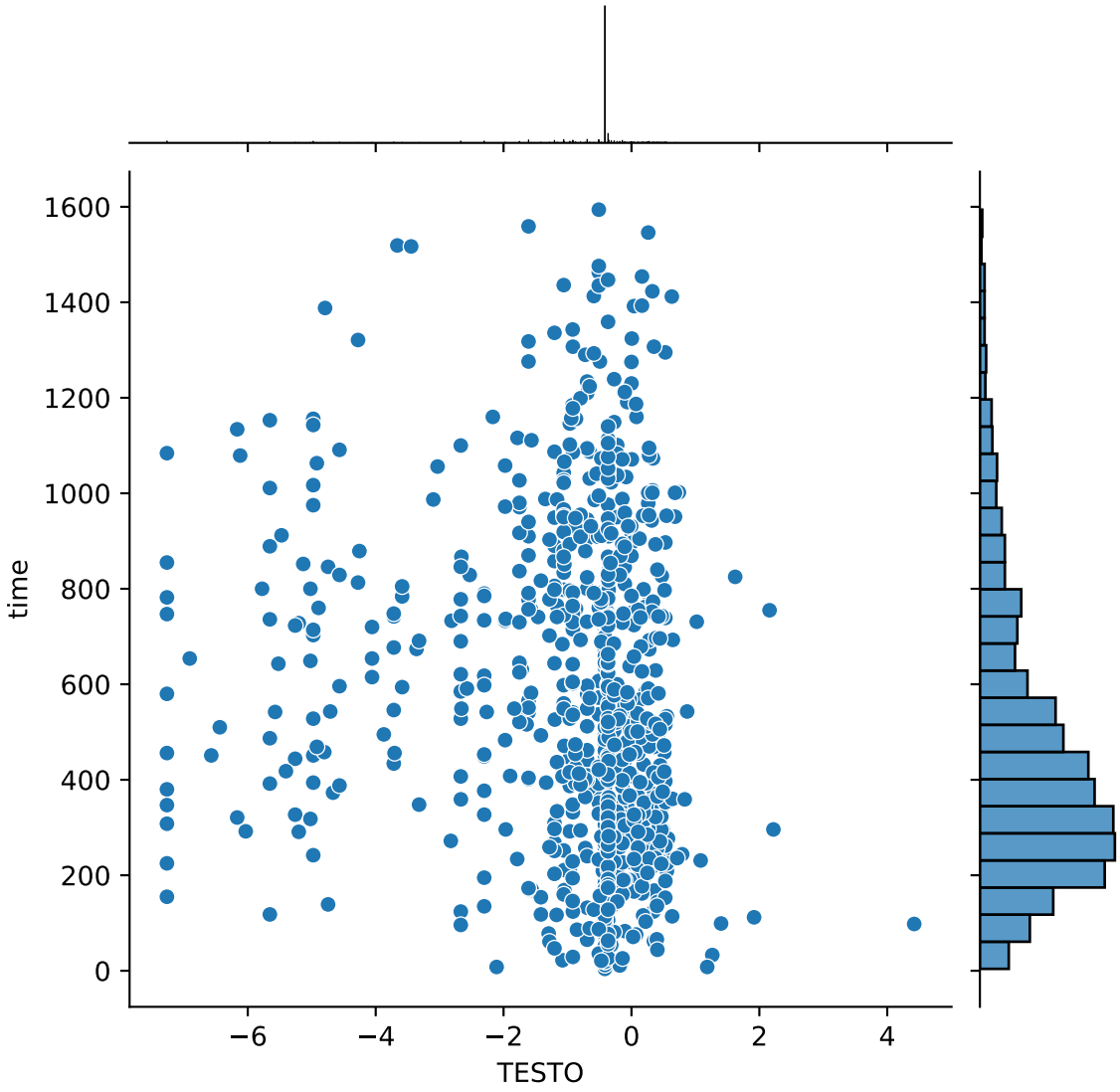
In [91]:
```
sns.jointplot(x='ALB',y='time', data=data)
```

Out[91]:
```
<seaborn.axisgrid.JointGrid at 0x7f9071eb0280>
```



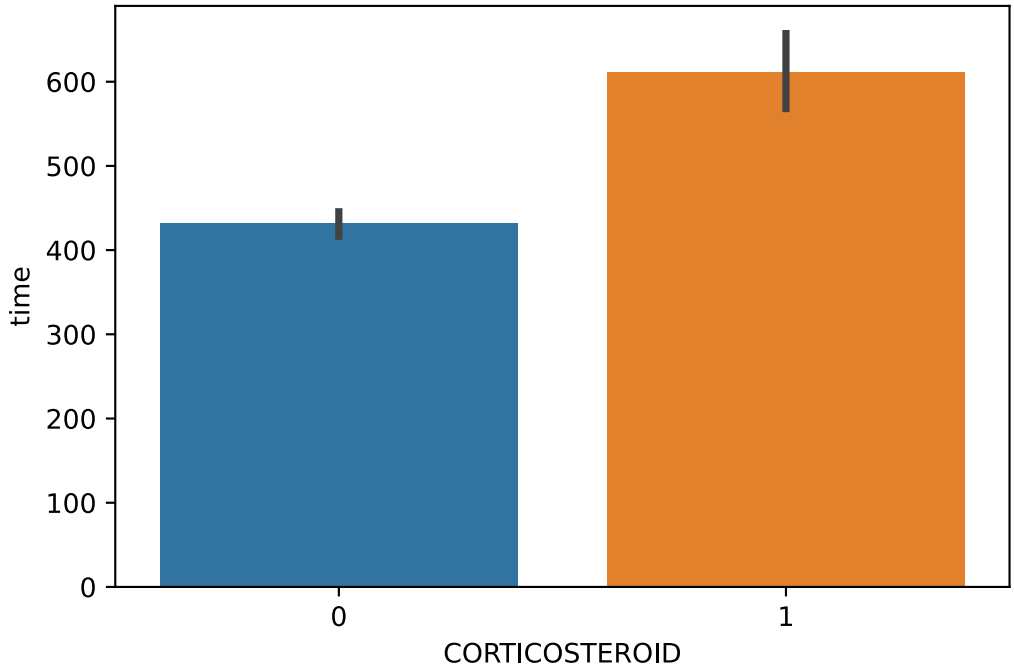
In [92]:
```
sns.jointplot(x='TESTO',y='time', data=data)
```

Out[92]:
```
<seaborn.axisgrid.JointGrid at 0x7f9072179af0>
```



In [94]:
```
sns.barplot(x='CORTICOSTEROID',y='time', data=data)
```

Out[94]:
```
<AxesSubplot:xlabel='CORTICOSTEROID', ylabel='time'>
```



Treatments

In [96]:
```
treatments =  ['ORCHIDECTOMY','PROSTATECTOMY','LYMPHADENECTOMY','BILATERAL_ORCHI
```

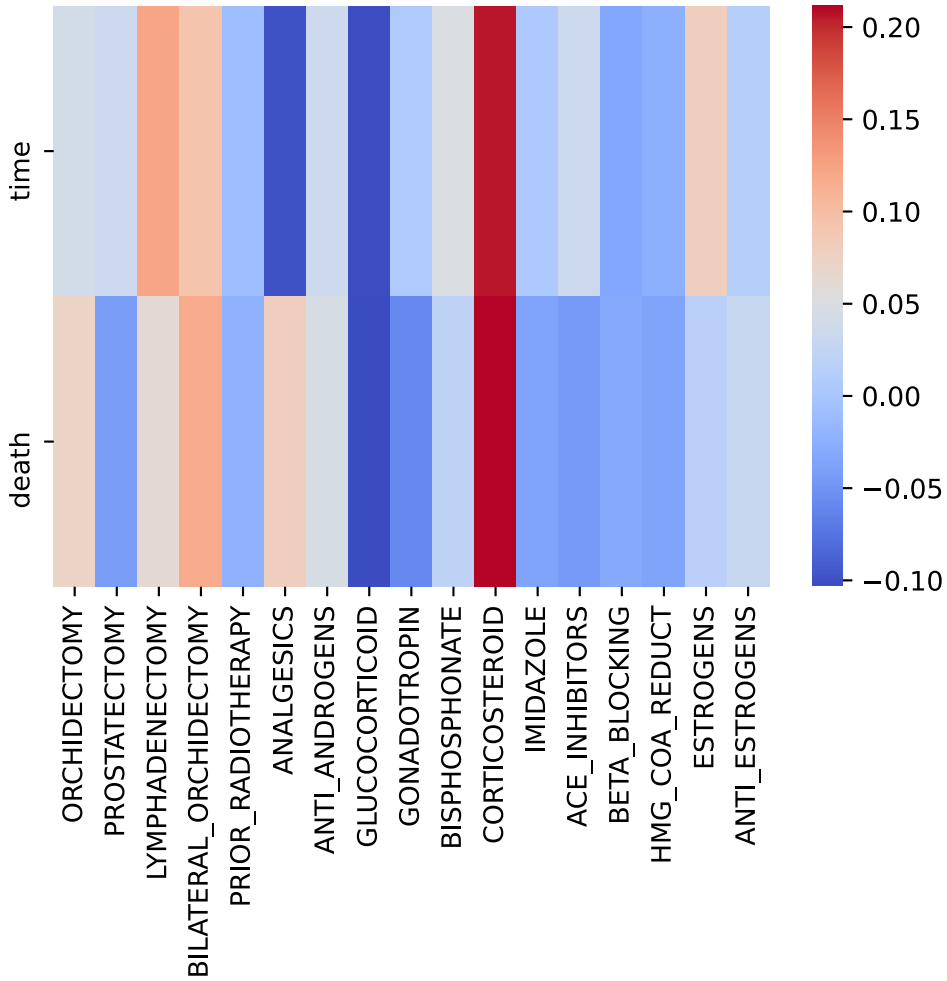
In [111…
```
data.corr()[treatments].loc[['time', 'death']]
```

Out[111…

	ORCHIDECTOMY	PROSTATECTOMY	LYMPHADENECTOMY	BILATERAL_ORCHIDECTOMY	PR
time	0.041008	0.033968	0.12393	0.094407	
death	0.073053	-0.041368	0.06353	0.118714	

In [122…
```
sns.heatmap(data.corr()[treatments].loc[['time', 'death']], cmap="coolwarm")
```

Out[122… <AxesSubplot:>



Corticosteroids seem to have greatest impact on patient outcome

Lab Values

In [128…

```
lab_values = [
 'ALP',
 'ALT',
 'AST',
 'CA',
 'CREAT',
 'HB',
 'LDH',
 'NEU',
 'PLT',
 'PSA',
 'TBILI',
 'TESTO',
 'WBC',
 'CREACL',
 'NA.',
 'MG',
 'PHOS',
 'ALB',
 'TPRO',
 'RBC',
 'LYM',
 'BUN',
```

```
 'CCRC',
 'GLU']
```

In [130…

```
data.corr()[lab_values].loc[['time', 'death']]
```

Out[130…

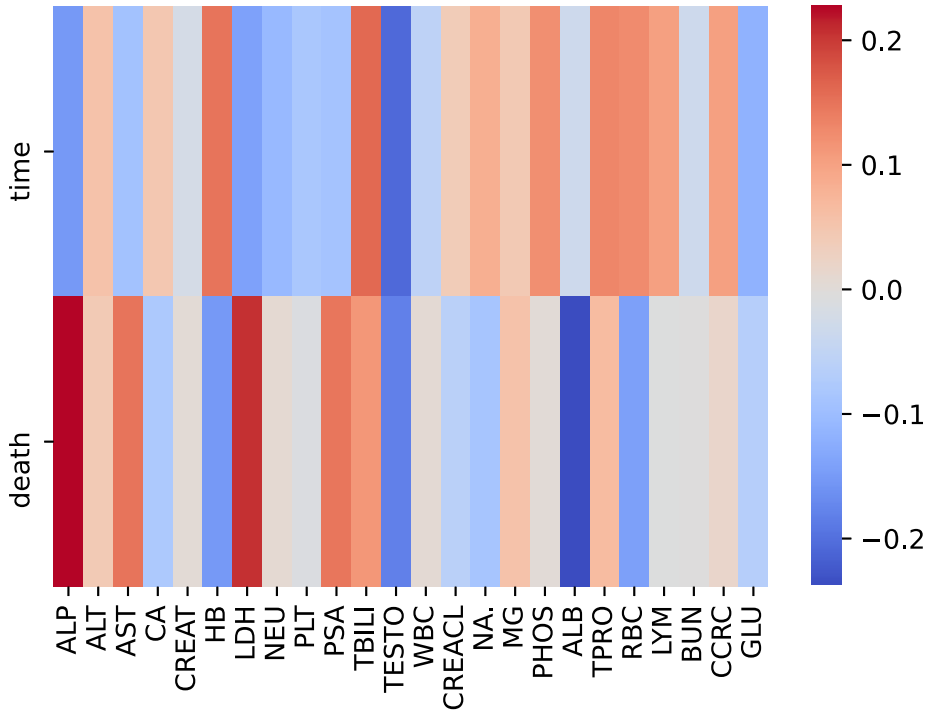
	ALP	ALT	AST	CA	CREAT	HB	LDH	NEU	
time	-0.152988	0.055176	-0.092459	0.048479	-0.021601	0.149179	-0.141076	-0.107470	-0.(
death	0.227153	0.041613	0.149438	-0.079346	0.003589	-0.153038	0.206975	0.008491	-0.(

2 rows × 24 columns

In [131…

```
sns.heatmap(data.corr()[lab_values].loc[['time', 'death']], cmap="coolwarm")
```

Out[131… <AxesSubplot:>



Lesions

In [132…

```
lesions = [
 'TARGET',
 'LYMPH_NODES',
 'KIDNEYS',
 'LUNGS',
 'LIVER',
 'PLEURA',
 'OTHER',
 'PROSTATE'
]
```

In [134…

```
data.corr()[lesions].loc[['time', 'death']]
```

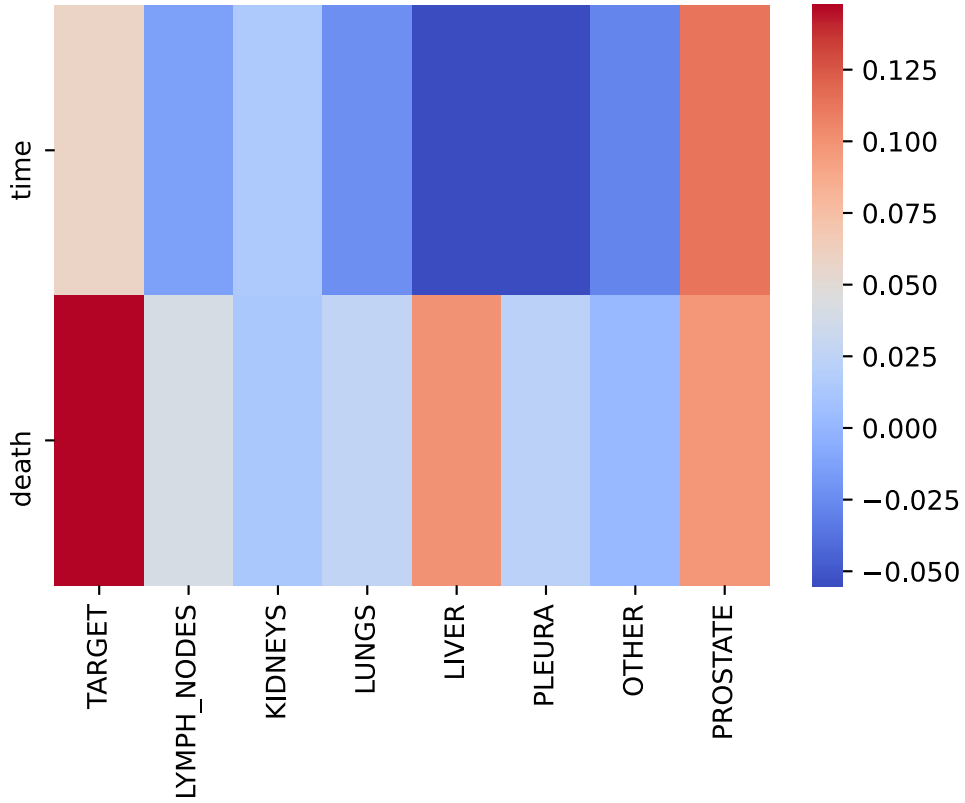
Out[134…

	TARGET	LYMPH_NODES	KIDNEYS	LUNGS	LIVER	PLEURA	OTHER	PROSTA
time	0.058253	-0.013224	0.014979	-0.023299	-0.054362	-0.054945	-0.027685	0.1140
death	0.147467	0.040938	0.013785	0.026993	0.100168	0.023198	0.002114	0.0982

In [136…

```
sns.heatmap(data.corr()[lesions].loc[['time', 'death']], cmap="coolwarm")
```

Out[136… <AxesSubplot:>



In [151…

```
data[lesions].sum()
```

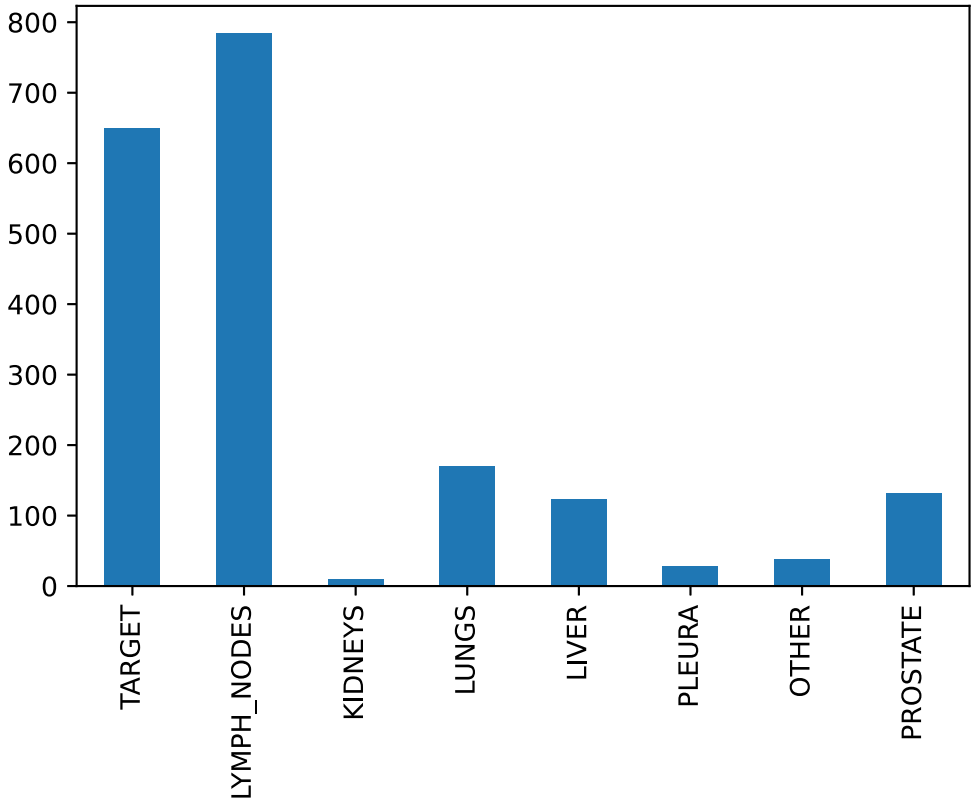
Out[151…

```
TARGET         649
LYMPH_NODES    784
KIDNEYS         10
LUNGS          170
LIVER          123
PLEURA          28
OTHER           38
PROSTATE       132
dtype: int64
```

In [160…

```
data[lesions].sum().plot(kind='bar')
```

Out[160… <AxesSubplot:>



BMI - Height/Weight

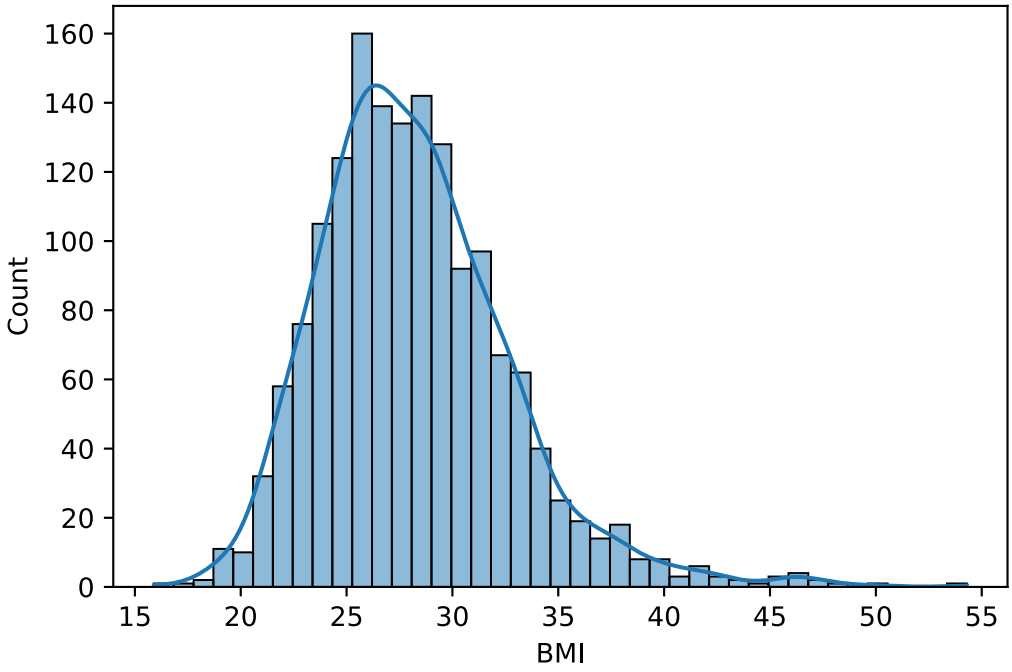
In [178…

```
body_measures = [
 'BMI',
 'HEIGHTBL',
 'WEIGHTBL'
]
```

In [189…

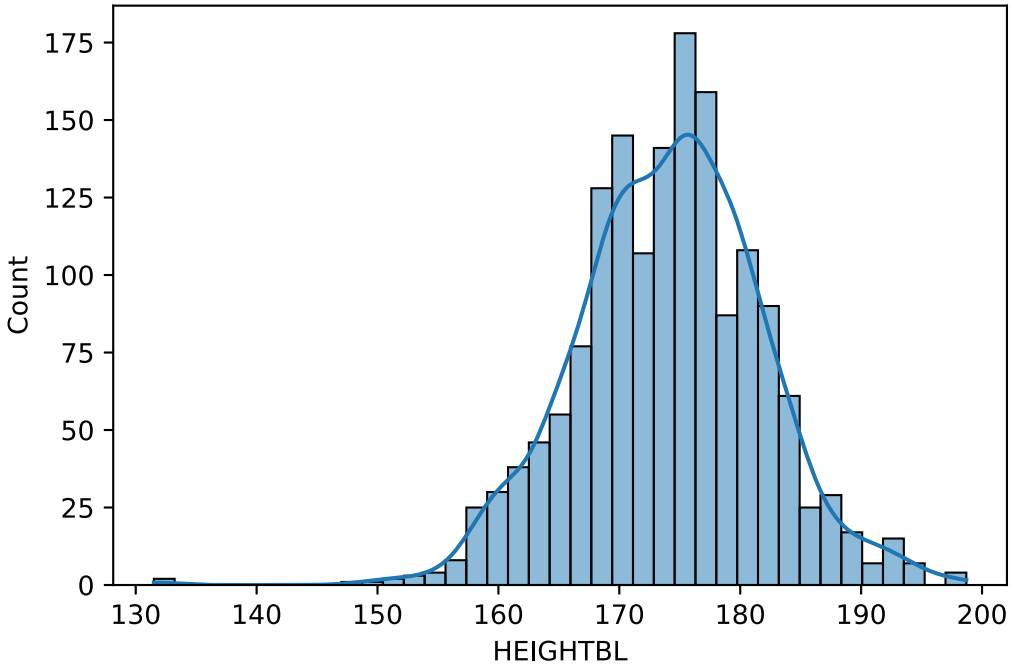
```
sns.histplot(data['BMI'], kde=True)
```

Out[189… <AxesSubplot:xlabel='BMI', ylabel='Count'>



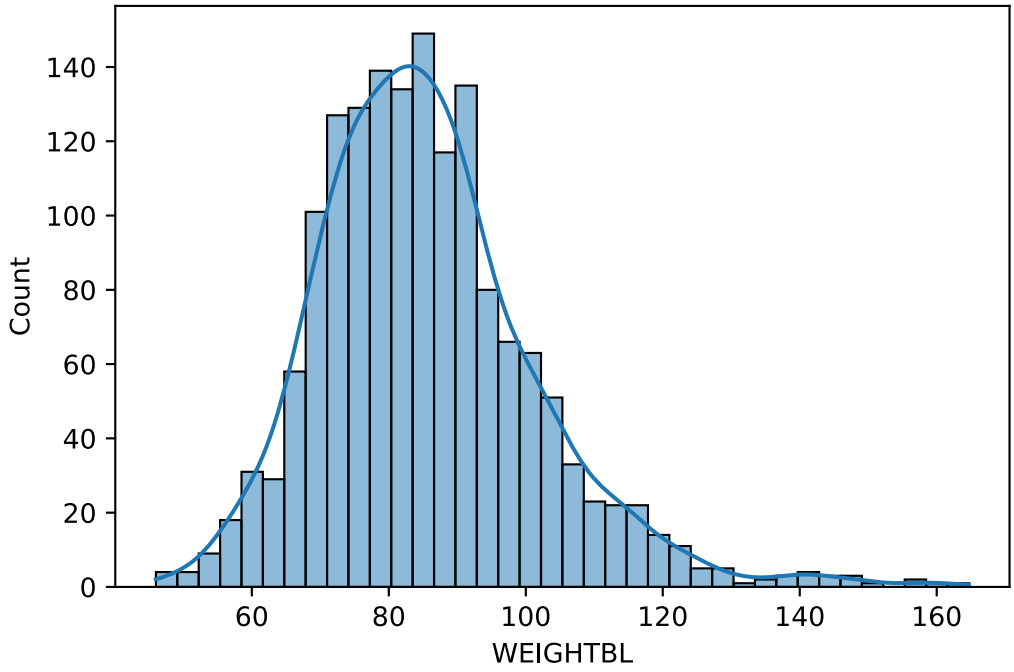
In [190…
```
sns.histplot(data['HEIGHTBL'], kde=True)
```

Out[190… <AxesSubplot:xlabel='HEIGHTBL', ylabel='Count'>



In [191…
```
sns.histplot(data['WEIGHTBL'], kde=True)
```

Out[191… <AxesSubplot:xlabel='WEIGHTBL', ylabel='Count'>



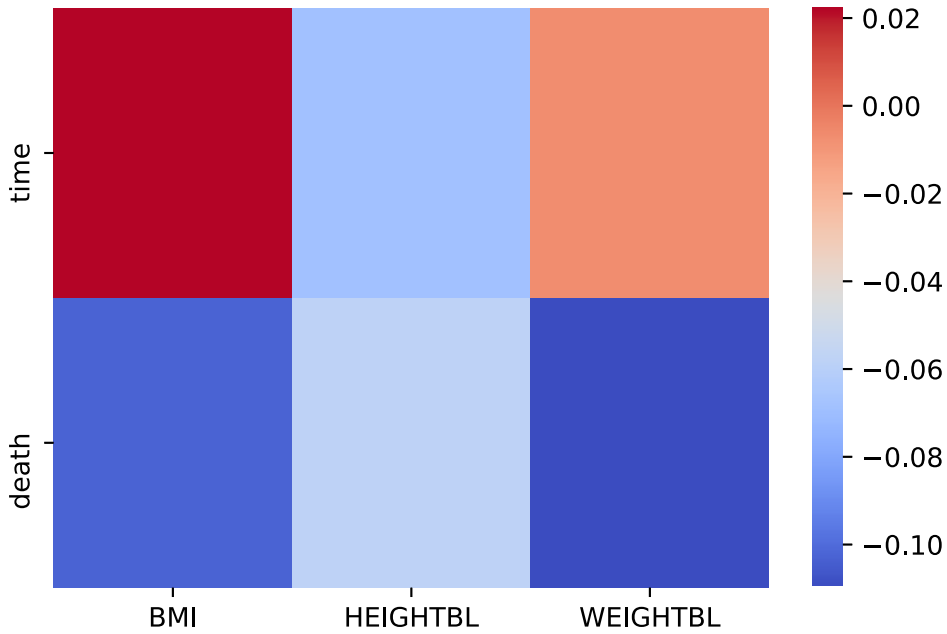
In [195…
```
data.corr()[body_measures].loc[['time','death']]
```

Out[195…

	BMI	HEIGHTBL	WEIGHTBL
time	0.022269	-0.068792	-0.006945
death	-0.102690	-0.057813	-0.109833

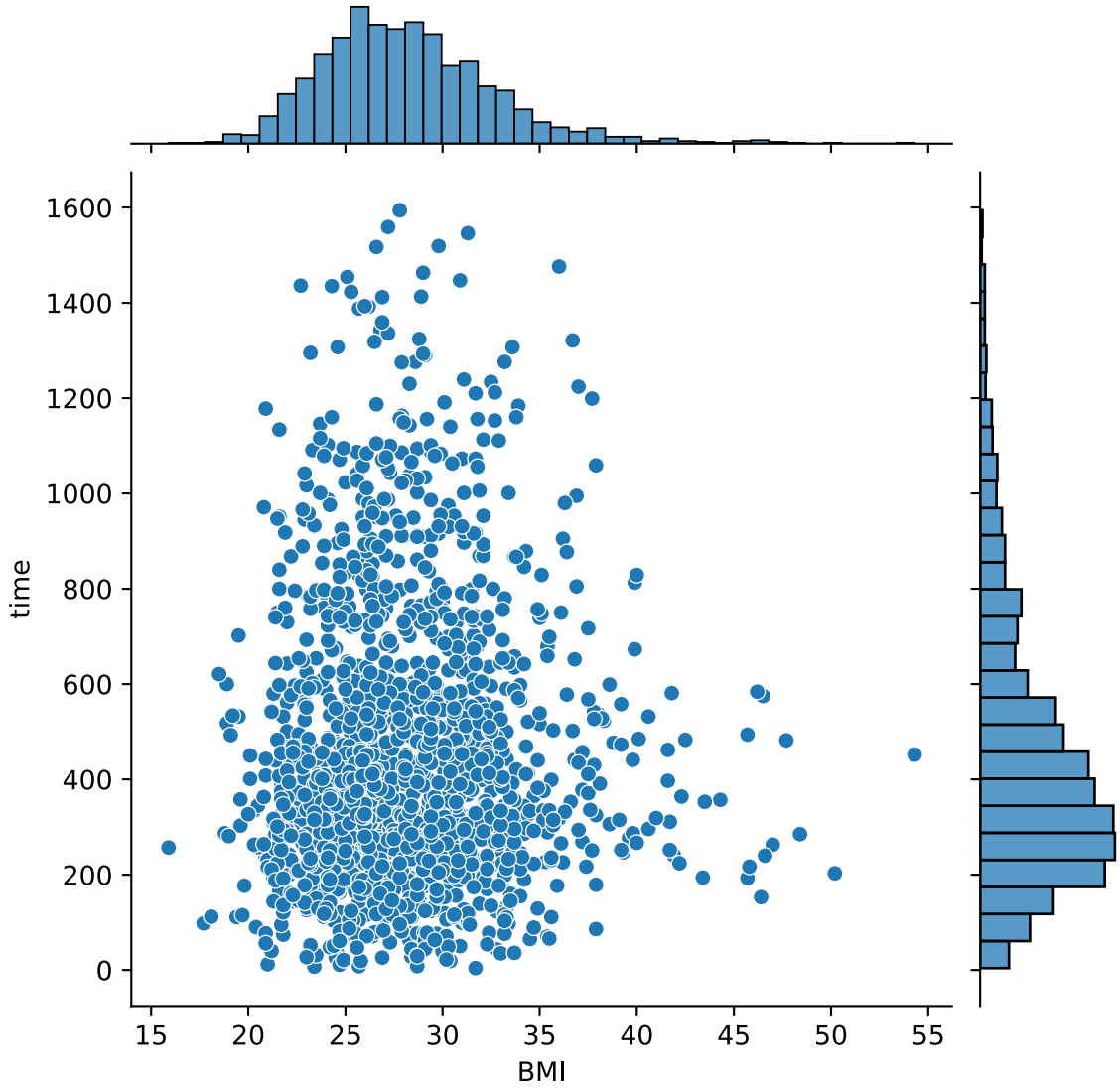
In [196…
```
sns.heatmap(data.corr()[body_measures].loc[['time', 'death']], cmap="coolwarm")
```

Out[196… <AxesSubplot:>



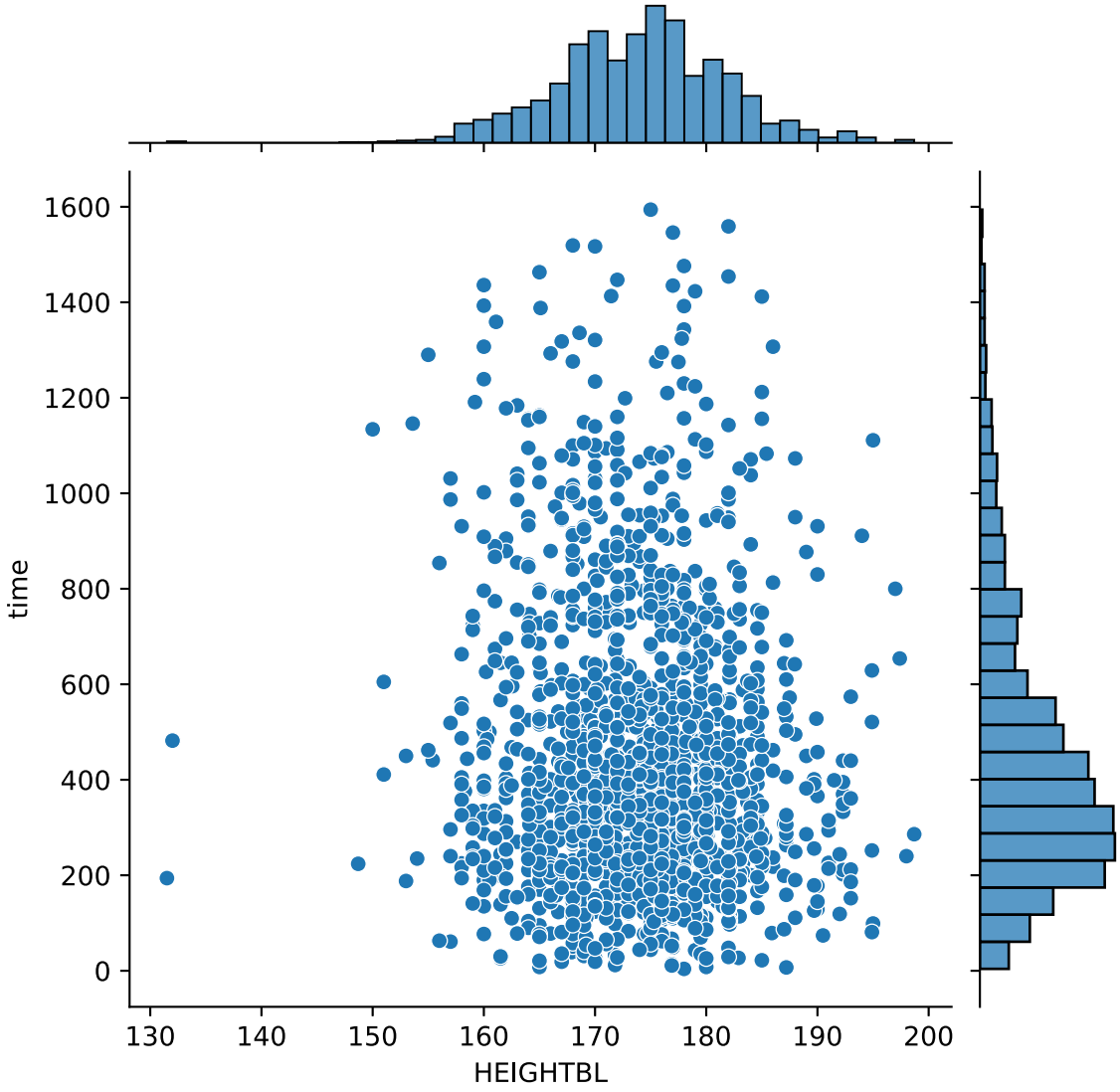
In [197…
```
sns.jointplot(x='BMI',y='time',data=data)
```

Out[197… <seaborn.axisgrid.JointGrid at 0x7f907df85700>



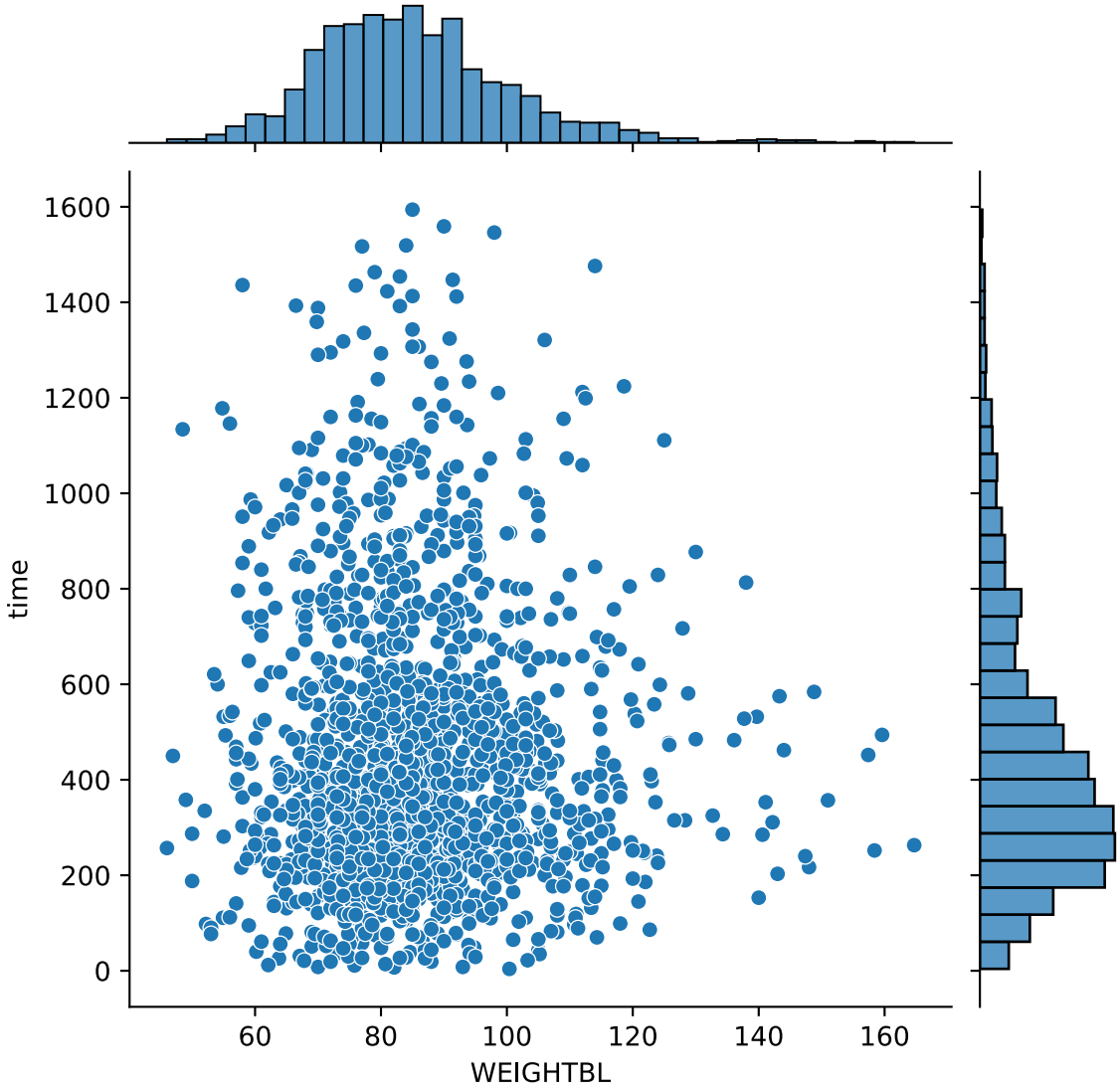
In [198…
```
sns.jointplot(x='HEIGHTBL',y='time',data=data)
```

Out[198… <seaborn.axisgrid.JointGrid at 0x7f907e34ccd0>



In [199…
```
sns.jointplot(x='WEIGHTBL',y='time',data=data)
```

Out[199…
```
<seaborn.axisgrid.JointGrid at 0x7f907e55b3a0>
```



Medical History — Diseases

In [200…

```
mhDisease =  ['CEREBACC',
 'CHF',
 'DVT',
 'DIAB',
'MI',
 'PULMEMB',
 'SPINCOMP',
 'COPD']
```

In [202…

```
data[mhDisease].sum()
```

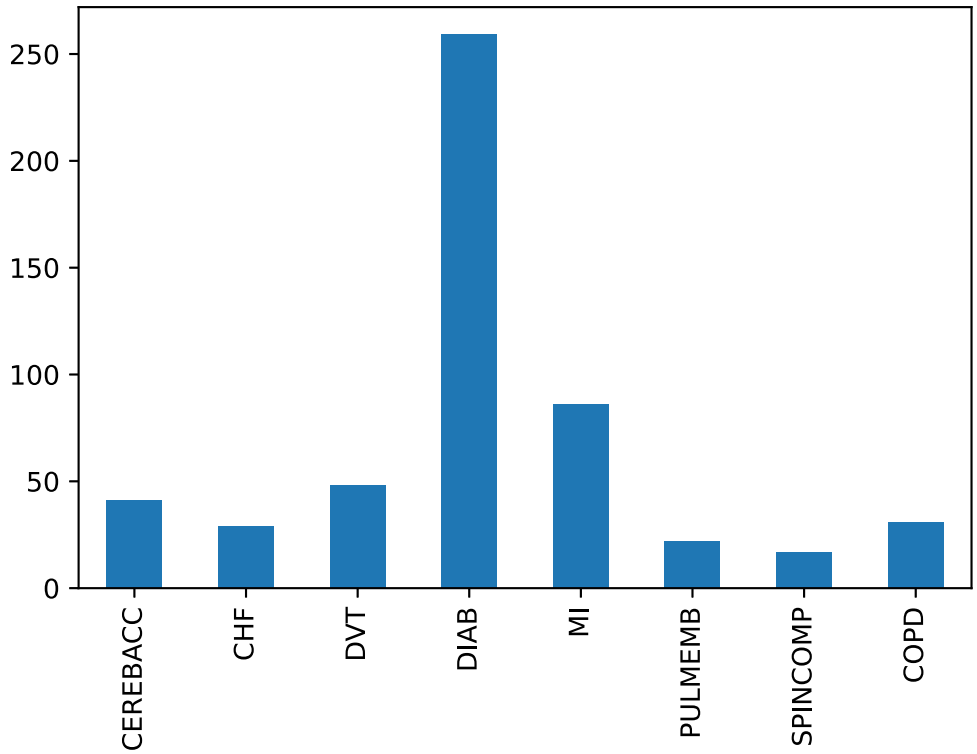
Out[202…

```
CEREBACC     41
CHF          29
DVT          48
DIAB        259
MI           86
PULMEMB      22
SPINCOMP     17
```

```
COPD          31
dtype: int64
```

In [203…
```
data[mhDisease].sum().plot(kind='bar')
```

Out[203… <AxesSubplot:>



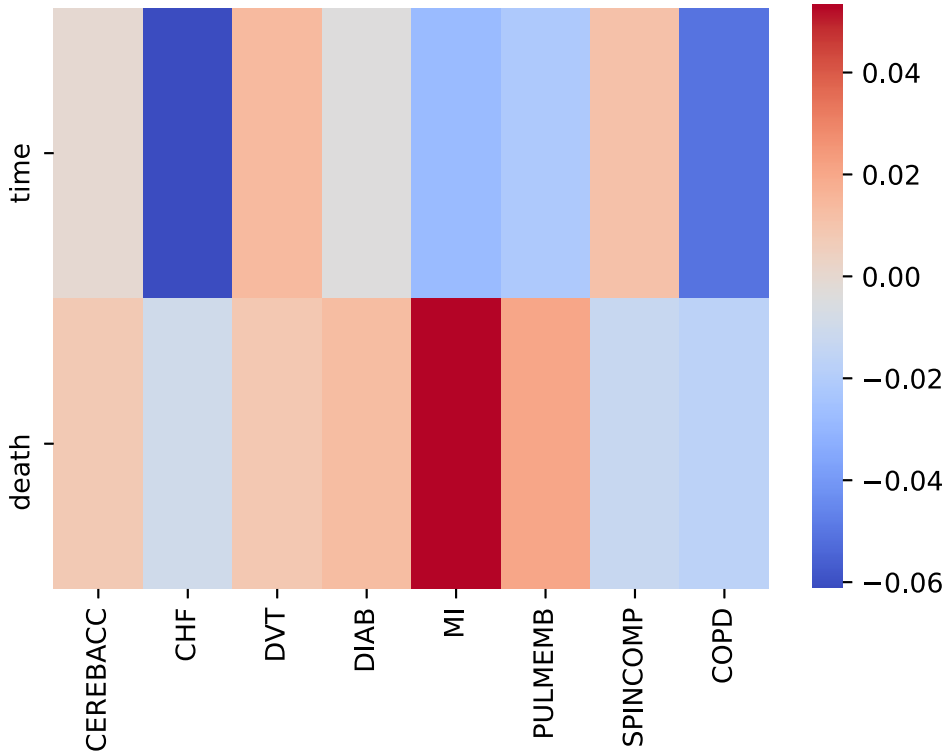
In [205…
```
data.corr()[mhDisease].loc[['time','death']]
```

Out[205…

	CEREBACC	CHF	DVT	DIAB	MI	PULMEMB	SPINCOMP	COPD
time	-0.000611	-0.061331	0.013545	-0.004294	-0.028801	-0.022101	0.011144	-0.050834
death	0.008115	-0.009671	0.008256	0.012665	0.052678	0.020524	-0.012924	-0.016988

In [207…
```
sns.heatmap(data.corr()[mhDisease].loc[['time','death']], cmap='coolwarm')
```

Out[207… <AxesSubplot:>



Medical History - Body System

In [217…

```
mhBody = ['MHBLOOD',
 'MHCARD',
 'MHCONGEN',
 'MHEAR',
 'MHENDO',
 'MHGASTRO',
 'MHHEPATO',
 'MHIMMUNE',
 'MHINFECT',
 'MHINJURY',
 'MHINVEST',
 'MHMETAB',
 'MHPSYCH',
 'MHRENAL',
 'MHRESP',
 'MHSKIN',
 'MHVASC']
```

In [219…

```
data[mhBody].sum()
```

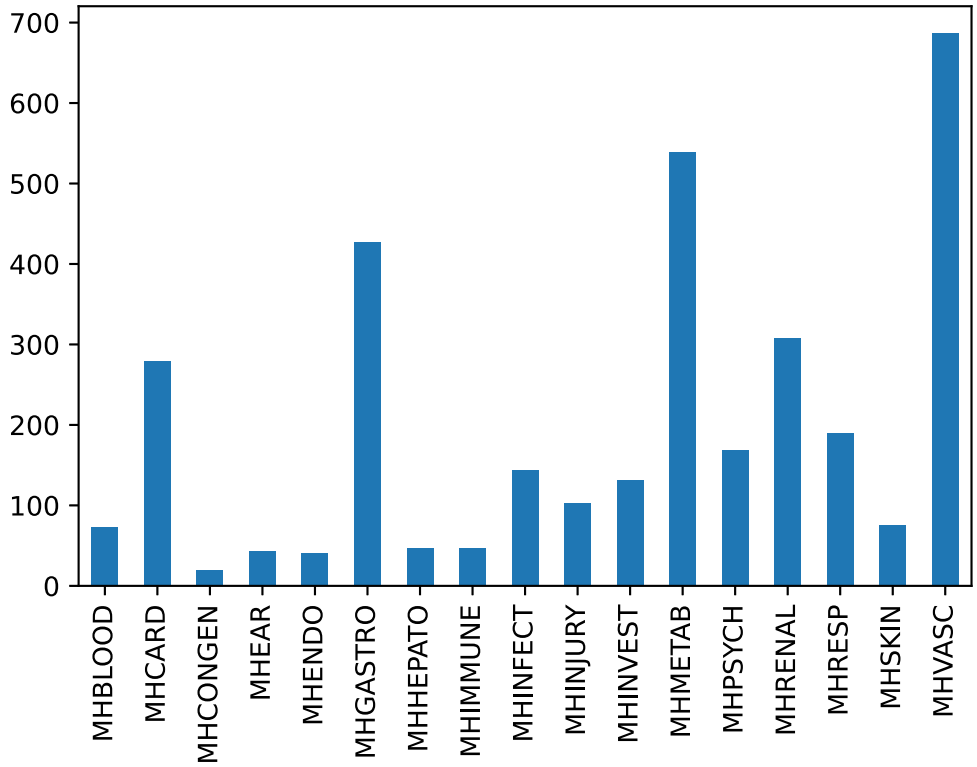
Out[219…

```
MHBLOOD      73
MHCARD      279
MHCONGEN     19
MHEAR        43
MHENDO       40
MHGASTRO    427
MHHEPATO     46
MHIMMUNE     46
MHINFECT    144
MHINJURY    103
```

```
MHINVEST    131
MHMETAB     539
MHPSYCH     168
MHRENAL     307
MHRESP      190
MHSKIN       75
MHVASC      686
dtype: int64
```

In [218…
```
data[mhBody].sum().plot(kind='bar')
```

Out[218… <AxesSubplot:>



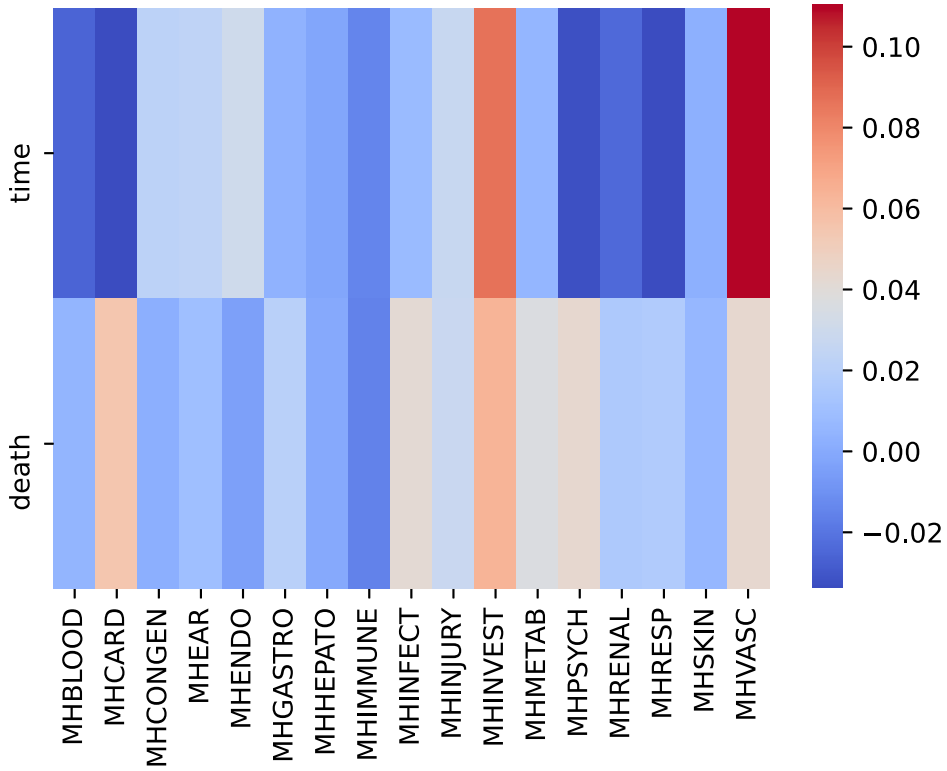
In [220…
```
data.corr()[mhBody].loc[['time','death']]
```

Out[220…

	MHBLOOD	MHCARD	MHCONGEN	MHEAR	MHENDO	MHGASTRO	MHHEPATO	MHIMM
time	-0.025828	-0.033762	0.021613	0.023002	0.030149	0.003517	-0.002399	-0.01
death	0.004564	0.054803	0.001486	0.009272	-0.004673	0.020256	-0.000465	-0.01

In [221…
```
sns.heatmap(data.corr()[mhBody].loc[['time','death']], cmap='coolwarm')
```

Out[221… <AxesSubplot:>



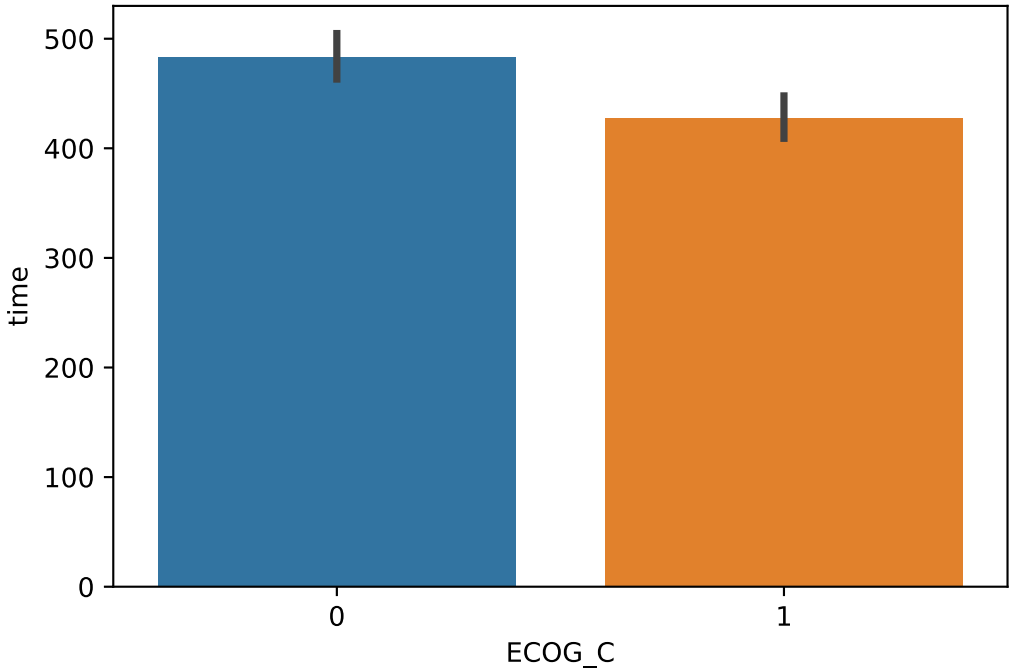
Baseline Patient Performance Status

In [224…
```
data.corr()['ECOG_C'].loc[['time','death']]
```

Out[224…
```
time    -0.096396
death    0.109507
Name: ECOG_C, dtype: float64
```

In [227…
```
sns.barplot(x='ECOG_C',y='time',data=data)
```

Out[227…
```
<AxesSubplot:xlabel='ECOG_C', ylabel='time'>
```



Race

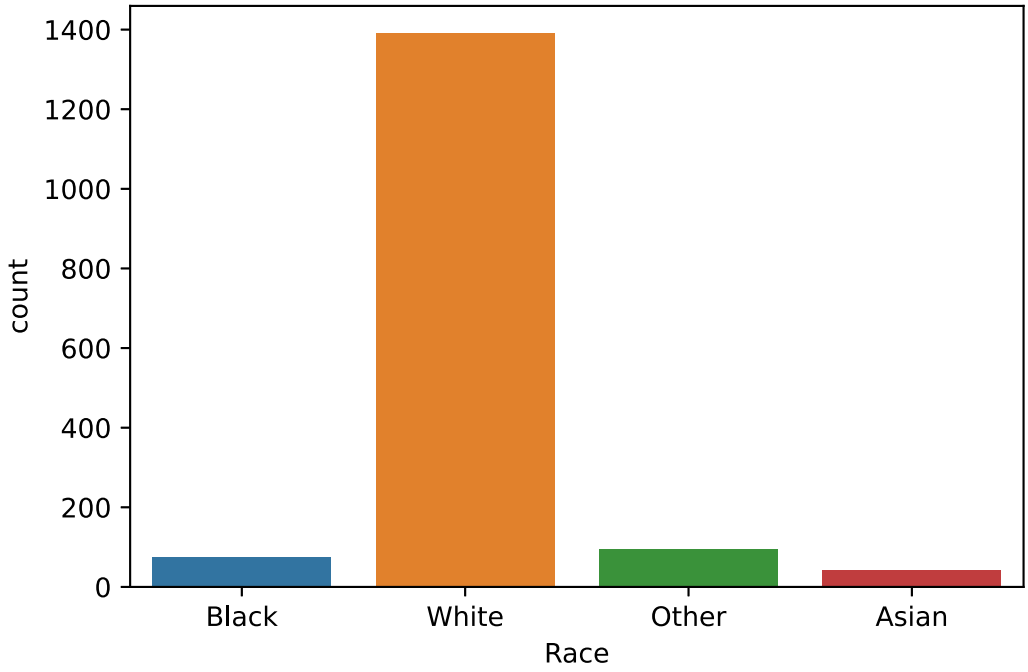
In [229…
```
race = ['RaceAsian',
 'RaceBlack',
 'RaceOther',
 'RaceWhite']
```

In [259…
```
def get_race(data):
    if data['RaceWhite'] == 1:
        return 'White'
    elif data['RaceBlack'] == 1:
        return 'Black'
    elif data['RaceAsian'] == 1:
        return 'Asian'
    else:
        return 'Other'
```

In [260…
```
data['Race'] = data[race].apply(get_race, axis=1)
```

In [274…
```
sns.countplot(x='Race',data=data)
```

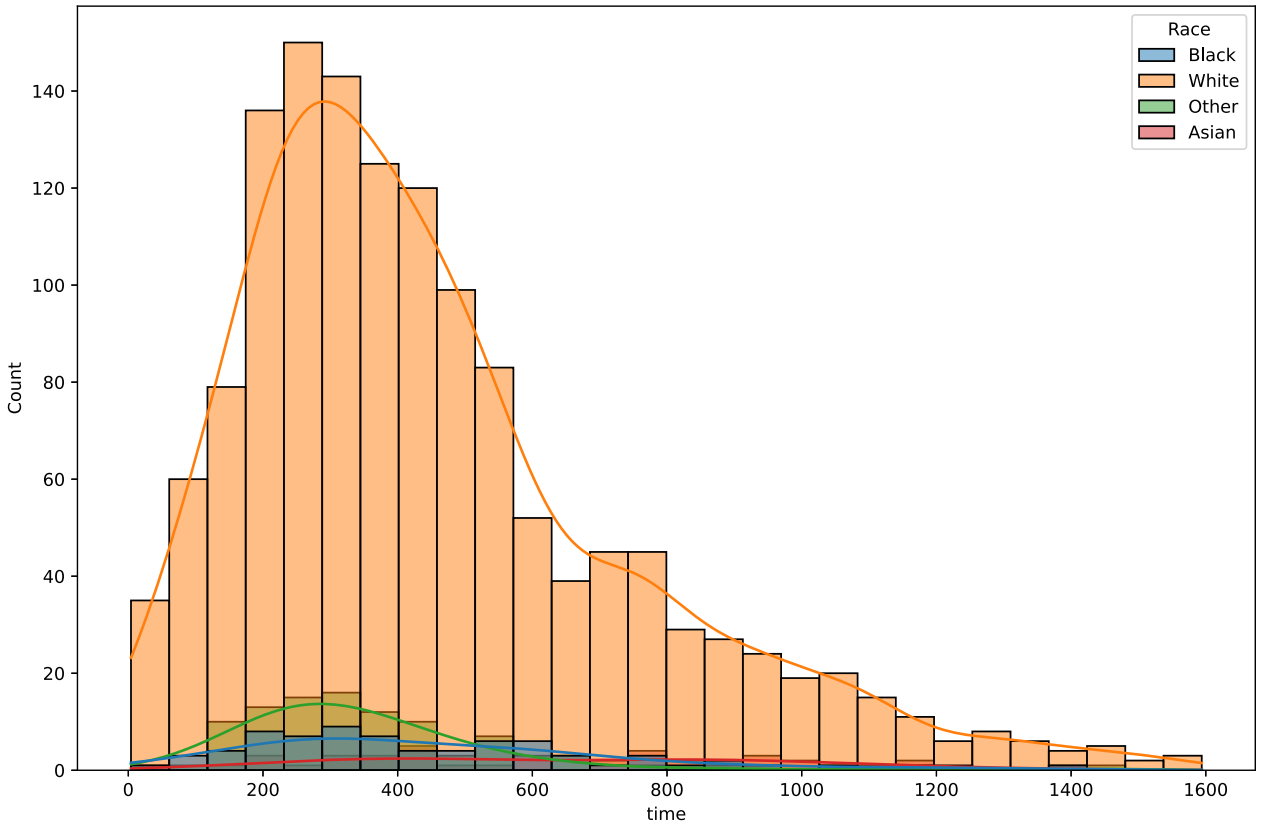
Out[274… <AxesSubplot:xlabel='Race', ylabel='count'>



In [277…

```
plt.figure(figsize=(12,8))
sns.histplot(x='time',data=data, hue='Race', kde=True)
```

Out[277… <AxesSubplot:xlabel='time', ylabel='Count'>



In [291…

```
data.corr()[race].loc[['time','death']]
```

Out[291…

	RaceAsian	RaceBlack	RaceOther	RaceWhite

	RaceAsian	RaceBlack	RaceOther	RaceWhite
time	0.112981	0.000800	-0.009367	0.008313
death	0.080378	-0.034214	-0.057938	0.060187

Region

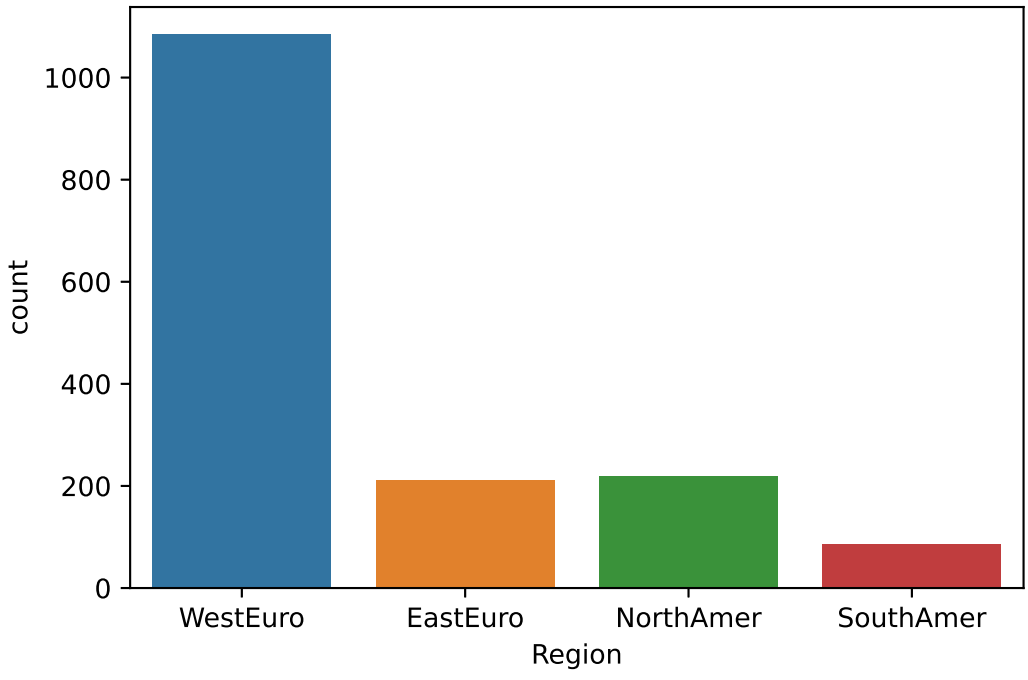
In [278…
```
region = ['RegionAsia',
 'RegionEastEuro',
 'RegionNorthAmer',
 'RegionSouthAmer',
 'RegionWestEuro']
```

In [279…
```
def get_region(data):
    if data['RegionAsia'] == 1:
        return 'Asia'
    elif data['RegionEastEuro'] == 1:
        return 'EastEuro'
    elif data['RegionNorthAmer'] == 1:
        return 'NorthAmer'
    elif data['RegionSouthAmer'] == 1:
        return 'SouthAmer'
    else:
        return 'WestEuro'
```

In [280…
```
data['Region'] = data[region].apply(get_region, axis=1)
```

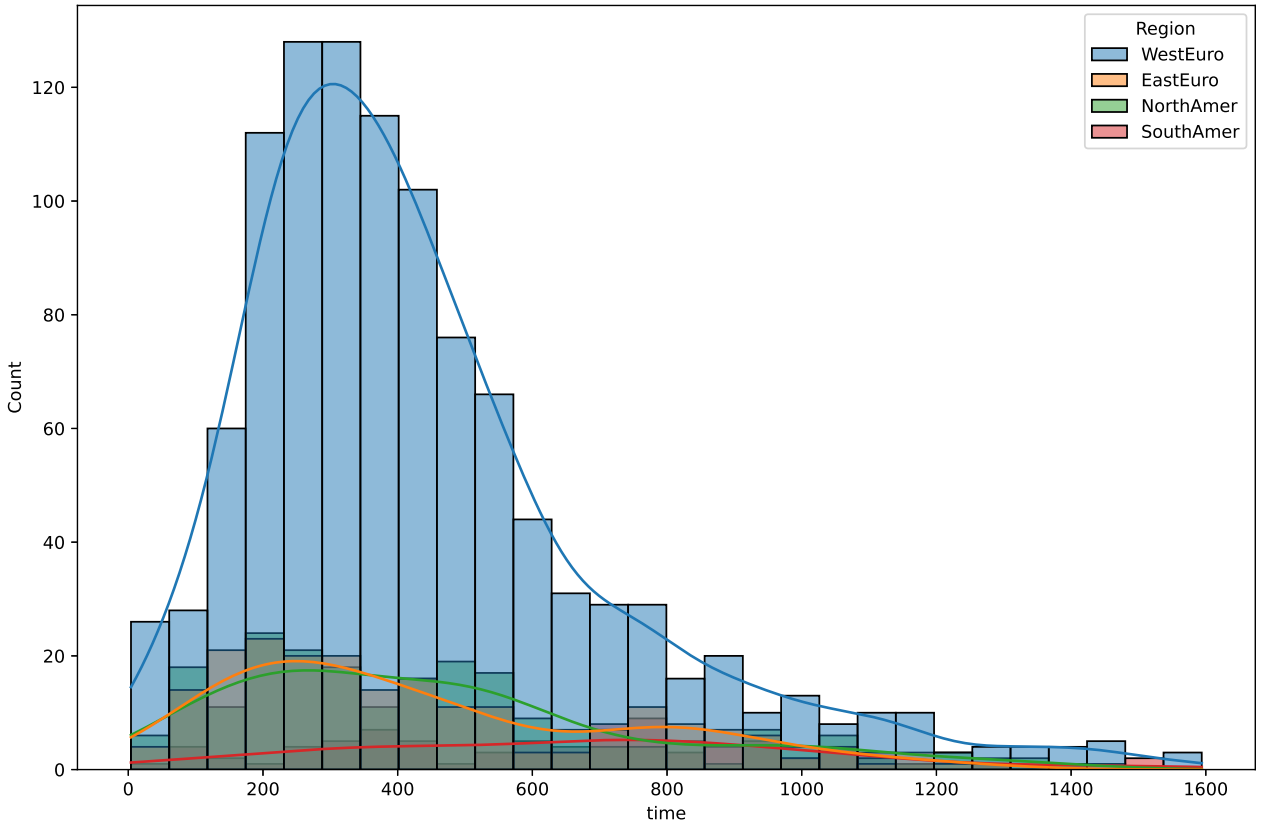
In [281…
```
sns.countplot(x='Region',data=data)
```

Out[281… <AxesSubplot:xlabel='Region', ylabel='count'>



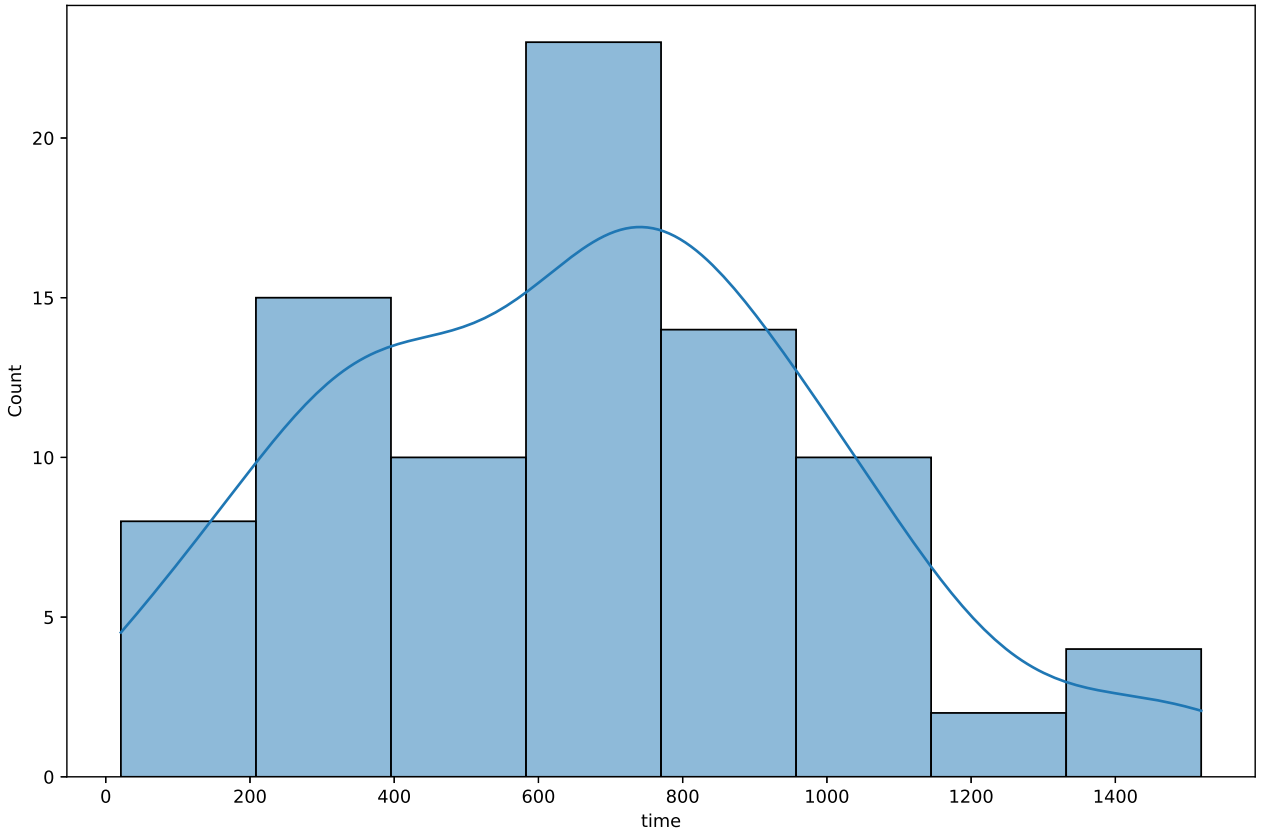
In [289…
```
plt.figure(figsize=(12,8))
sns.histplot(x='time',data=data, hue='Region', kde=True)
```

Out[289… <AxesSubplot:xlabel='time', ylabel='Count'>



In [307…
```
plt.figure(figsize=(12,8))
sns.histplot(x='time',data=data[data['Region'] == 'SouthAmer'], kde=True)
```

Out[307… <AxesSubplot:xlabel='time', ylabel='Count'>



In [294…
```
data.corr()[region].loc[['time','death']]
```

Out[294…

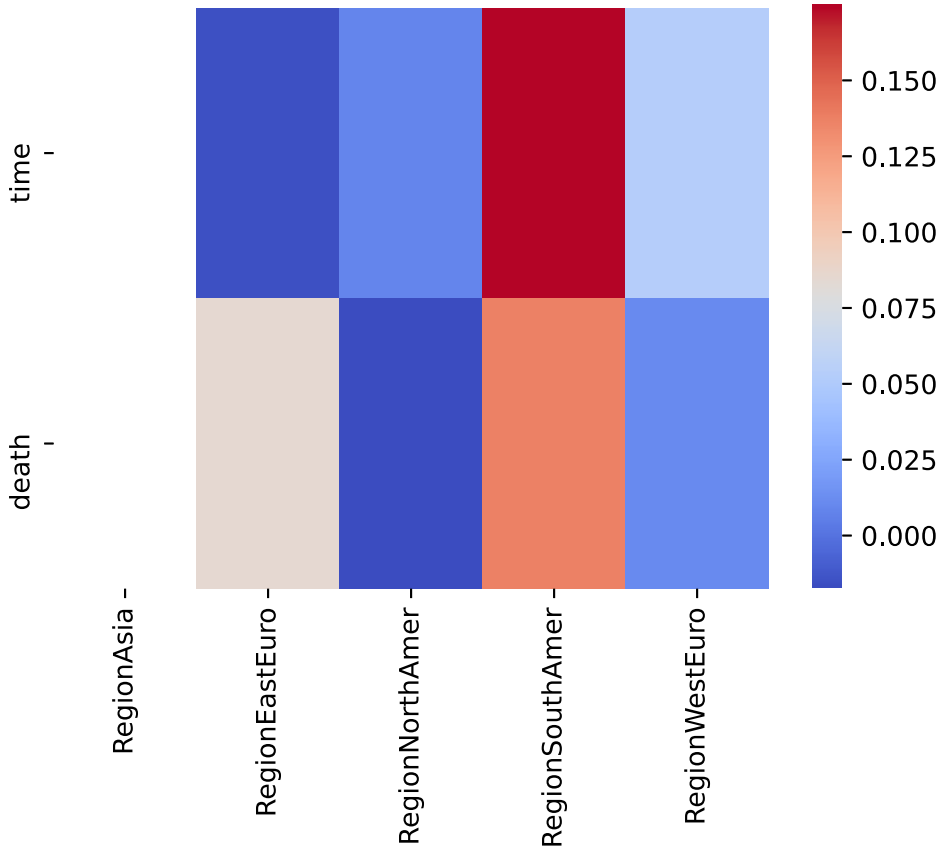
	RegionAsia	RegionEastEuro	RegionNorthAmer	RegionSouthAmer	RegionWestEuro
time	NaN	-0.015503	0.008615	0.173898	0.052483
death	NaN	0.084620	-0.017527	0.137065	0.010665

In [296…
```
data[region].sum()
```

Out[296…
```
RegionAsia           0
RegionEastEuro     211
RegionNorthAmer    219
RegionSouthAmer     86
RegionWestEuro     459
dtype: int64
```

In [301…
```
sns.heatmap(data.corr()[region].loc[['time','death']],cmap='coolwarm')
```

Out[301…
```
<AxesSubplot:>
```



In [306…

```
data.corr()['time'].sort_values(ascending=False)
```

Out[306…

```
time                1.000000
CORTICOSTEROID      0.205400
RegionSouthAmer     0.173898
TBILI               0.160275
HB                  0.149179
                      ...
NEUperLEU          -0.134277
LDH                -0.141076
ALP                -0.152988
TESTO              -0.207605
RegionAsia               NaN
Name: time, Length: 103, dtype: float64
```

In [ ]: