Improved ICU Stay and Mortality Prediction via Feature Engineering of Vital Sign Data

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GitHub Link: https://github.com/juliatompkins/surgical_critical_event_prediction

Exectutive Summary

The operating room is a data-rich environment in which analytical frameworks offer great potential for improving health outcomes and reducing costs through improved decision-making. Both patients and surgeons must make decisions about whether to proceed with a surgery, which involves weighing risks against potential benefits. Additionally, as patients recover, hospitals must allocate resources to these patients in proportion to the intensity of their recovery process. Thus, our workflow aims to address these challenges through two prediction tasks. First, we will predict the likelihood of mortality for a patient during/following their surgery, which will help doctors and patients determine if a surgery is worth doing. Second, we will predict the number of days a patient will spend recovering in the ICU, which will help hospitals determine the volume of supplies they are likely to require over a given window. The unique contribution of our project will be the integration between clinical patient information features and biosignal (time series) features in our workflow. This project uses the **vitaldb** dataset, which contains clinical and biosignal data from 6,388 non-cardiac surgical patients across 10 different operating rooms in Seoul National University Hospital, Seoul, Republic of Korea.

Data Preprocessing

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy import stats
import scipy.signal as signal
import seaborn as sns
from scipy.spatial import distance
from statsmodels.tsa.seasonal import STL
import neurokit2 as nk
```

Reading in data

First, we read in data from the **vitaldb** dataset, which is an open source Python dataset. We load in patient information (not time series) and tracks, which is a list of waveform objects for each patient.

In [2]:

```
df_info = pd.read_csv("https://api.vitaldb.net/cases")
df_ids = pd.read_csv("https://api.vitaldb.net/trks")
```

We select the non-waveform variables we want to use for our analysis. In addition to the unique identifier `subjectid` , we chose age, height, weight, sex, operation start and end time, and surgical approach as our features. For our target variable, we have two options, and we are still deciding which one we want to use.

Option 1, `death_inhosp` , is a boolean variable representing whether the patient died in the hospital. This is a particularly consequential target variable, but there is a major class imbalance here, with less than 1% of patients dying in the hospital.

Option 2, `icu_days`, is the number of days a patient spends in the ICU (intensive care unit) after surgery. There is less of a class imbalance here, but ICU stays are not solely determined by adverse events during surgery and also are not necessarily always correlated with adverse outcomes.

This dataset is incredibly large, and we already know that death from a surgery is incredibly unlikely. One idea we have to reduce the class imbalance is to take some subset of the data representing only high-risk surgeries or high-risk patients.

In [3]:
```
info = df_info[['subjectid', 'age', 'height', 'weight', 'sex', 'opstart', 'opend', 'approa
info.head()
```

Out[3]:

	subjectid	age	height	weight	sex	opstart	opend	approach	icu_days	death_inhosp
0	5955	77.0	160.2	67.5	M	1668	10368	Open	0	0
1	2487	54.0	167.3	54.8	M	1721	14621	Open	0	0
2	2861	62.0	169.1	69.7	M	1090	3010	Videoscopic	0	0
3	1903	74.0	160.6	53.0	M	2522	17822	Videoscopic	1	0
4	4416	66.0	171.0	59.7	M	2591	20291	Open	13	0

In [4]:
```
num_death = sum(info['death_inhosp'])
pct_death = sum(info['death_inhosp'])/len(info)
print(f'Class imbalance: there are only {num_death} cases of death in the hospital, accour
```

```
Class imbalance: there are only 57 cases of death in the hospital, accounting for 0.89 of
our instances.
```

Data Cleaning/Initial Statistical Exploration

First, we did some initial data preprocessing. This included changing boolean variables like `sex` and `death_inhosp` from True/False to 0/1, combining OP start and end times into a new variable `OP_time` representing total time in the operating room, and using one-hot encoding on the `approach` feature. We also intridduced a new option for a target variable, `icu`, which is a boolean 0/1 for whether the patient went to the ICU after surgery, as opposed to how many days they spent there.

In [5]:
```
info_new = info[['subjectid']].copy()
info_new['Age'] = info['age']
info_new['Ht'] = info['height']
info_new['Wt'] = info['weight']
info_new.loc[:,'Sex'] = info.loc[:,'sex'].apply(lambda x: 1 if x == 'F' else 0)
info_new['OP_time'] = (info['opend'] - info['opstart'])/60
one_hot_approaches = pd.get_dummies(info['approach'])
info_new = info_new.join(one_hot_approaches)
info_new['icu_days'] = info['icu_days']
info_new['icu'] = (info['icu_days'] >= 1).apply(lambda x: 1 if x == True else 0)
info_new['death_inhosp'] = info['death_inhosp']

info_new.head()
```

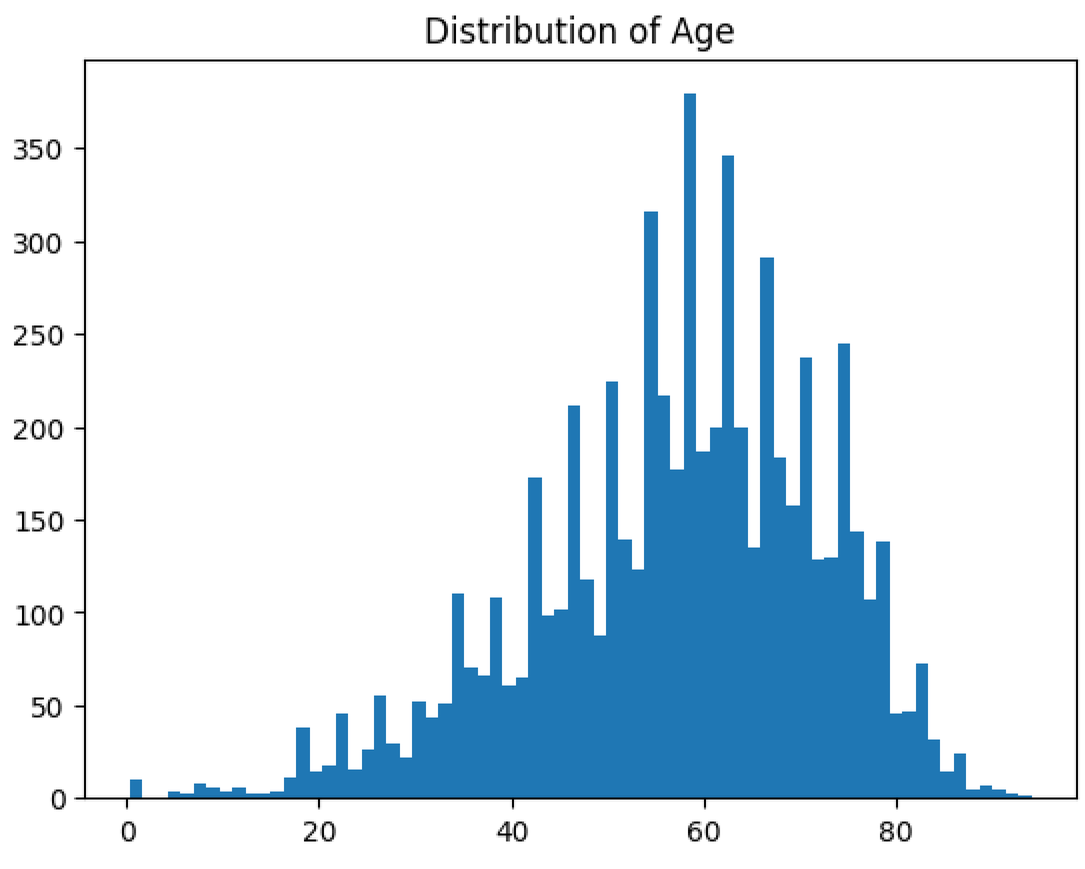
Out[5]:

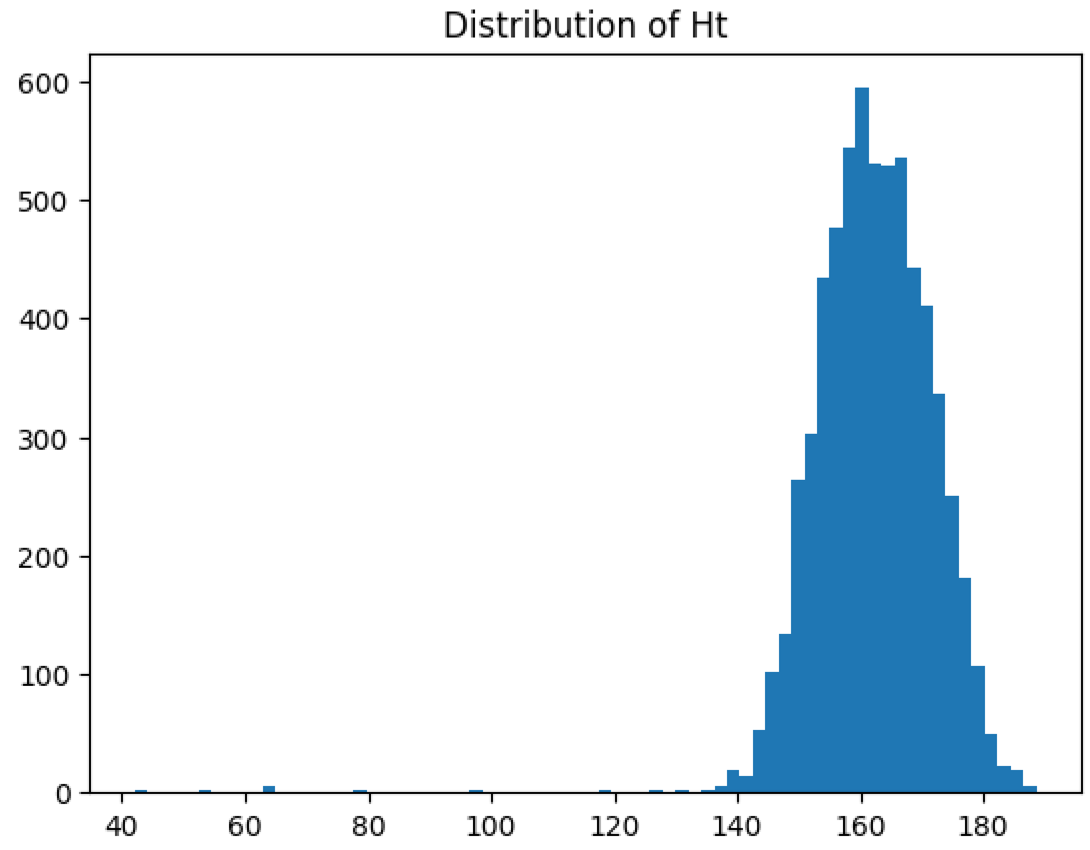
	subjectid	Age	Ht	Wt	Sex	OP_time	Open	Robotic	Videoscopic	icu_days	icu	death_inhosp
0	5955	77.0	160.2	67.5	0	145.0	1	0	0	0	0	0
1	2487	54.0	167.3	54.8	0	215.0	1	0	0	0	0	0
2	2861	62.0	169.1	69.7	0	32.0	0	0	1	0	0	0

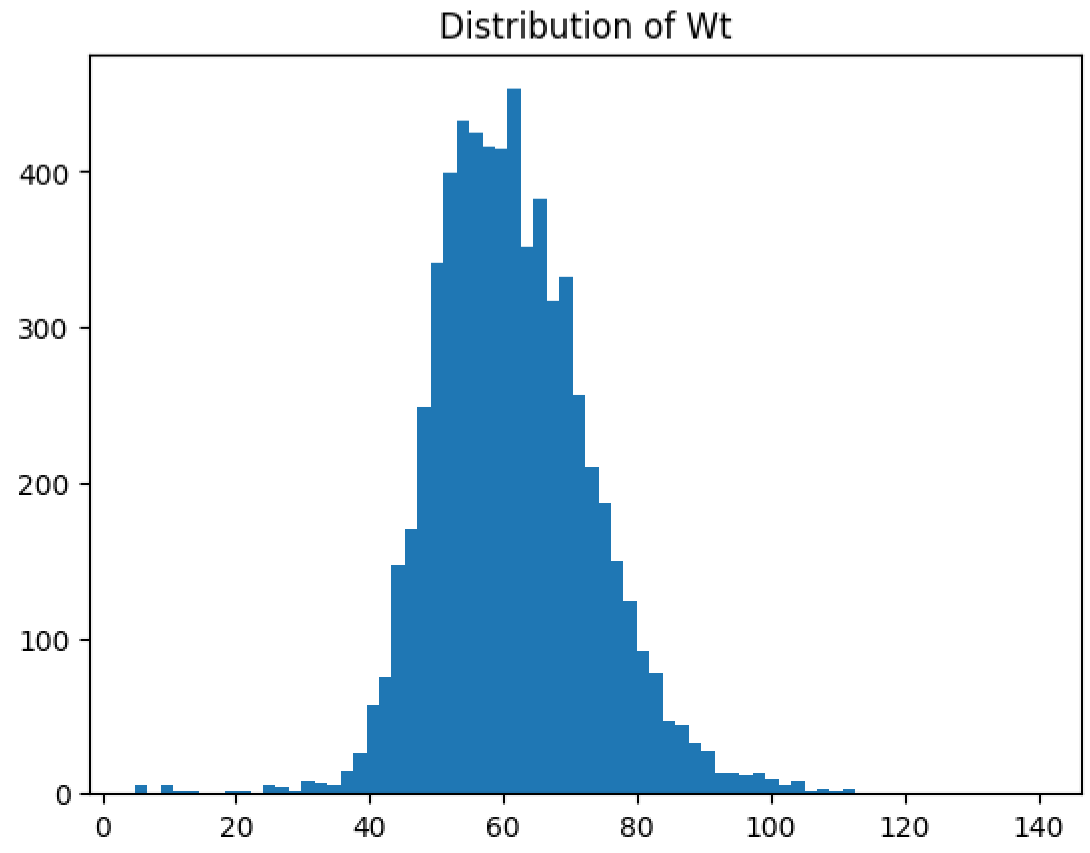
	subjectid	Age	Ht	Wt	Sex	OP_time	Open	Robotic	Videoscopic	icu_days	icu	death_inhosp
3	1903	74.0	160.6	53.0	0	255.0	0	0	1	1	1	0
4	4416	66.0	171.0	59.7	0	295.0	1	0	0	13	1	0

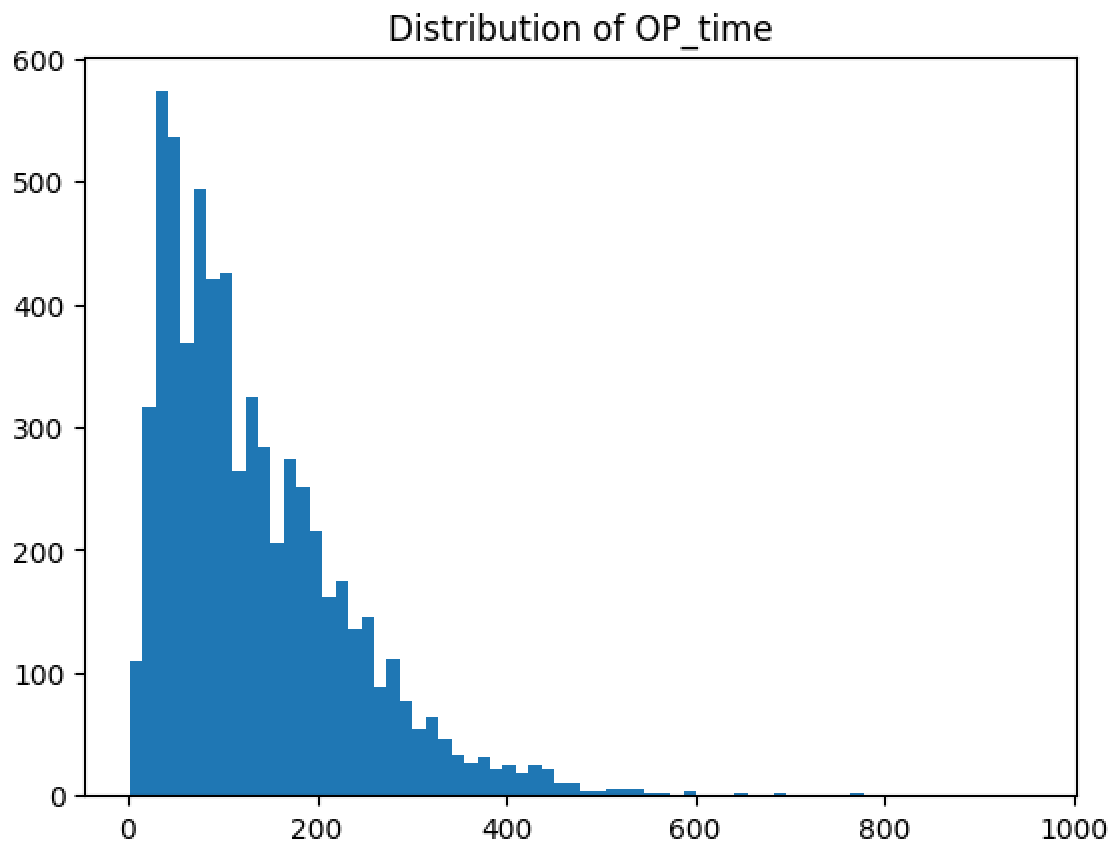
Next, for all of our continuous numerical features, we plotted histograms to visualize the initial distrubution. We found that all of our features were unimodal, and that age, height, and weight were roughly normally distributed. We plotted `icu_days` on a log scale to better visualize the distribution, since the majority of patients spent 0 days in the ICU.

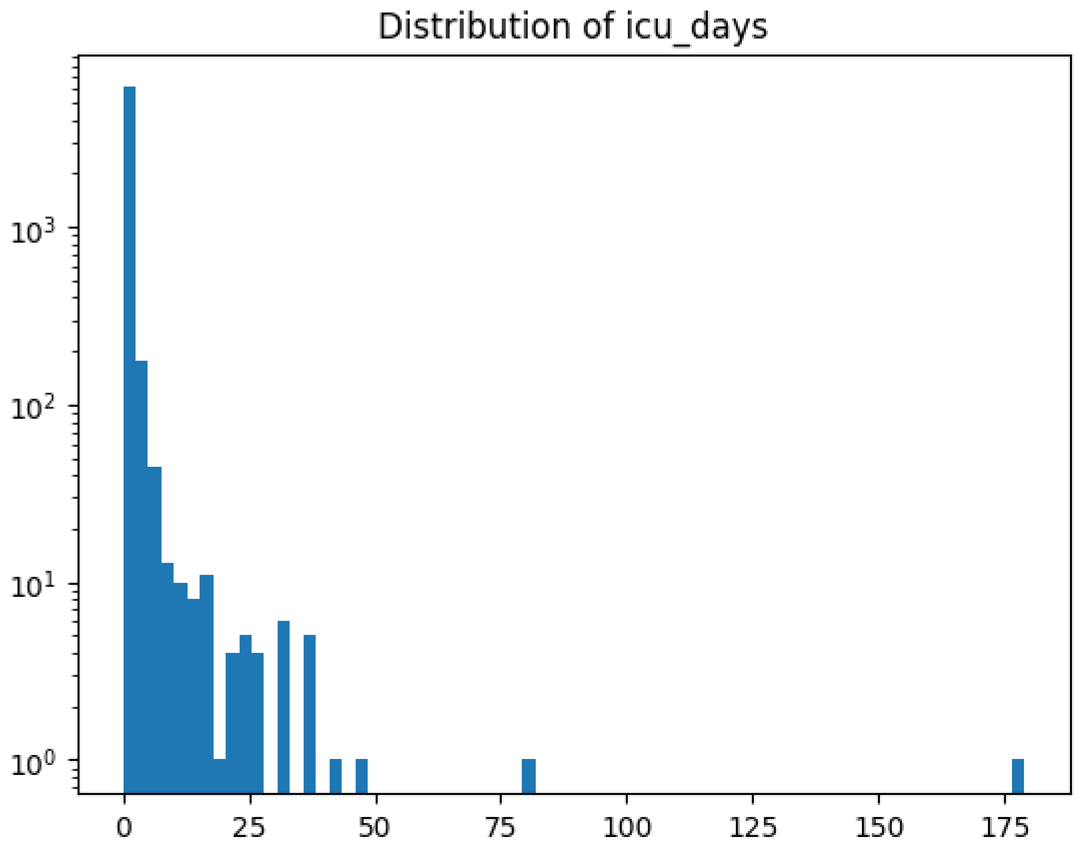
In [6]:
```
for var in ['Age','Ht','Wt','OP_time', 'icu_days']:
    plt.figure()
    var_unique, counts = np.unique(info_new[var], return_counts=True)
    if var == 'icu_days':
        plt.hist(info_new[var], bins = 70)
        plt.title(f'Distribution of {var}')
        plt.yscale('log')
        plt.show()
    else:
        plt.hist(info_new[var], bins = 70)
        plt.title(f'Distribution of {var}')
        plt.show()
```




Distribution of Ht
600
500
400
300
200
100
0
40
60
80
100
120
140
160
180


Distribution of Wt
400
300
200
100
0
0
20
40
60
80
100
120
140





We also plotted some descriptive statistics for all of our variables. For our categorical variables, we printed the mode and class balance, and for our continuous numerical variables, we printed the mean and standard deviation. The class imbalance in our target variables is clear here.

In [7]:
```
for var in ['Age','Ht','Wt','Sex','OP_time', 'Open', 'Robotic', 'Videoscopic', 'icu_days',
    print(f'For variable {var}:')
    if var in ['Sex', 'Open', 'Robotic', 'Videoscopic', 'icu', 'death_inhosp']:
        print(f'mode={stats.mode(info_new[var]).mode[0]}')
        print(f'class balance: {np.sum(info_new[var])} to {len(info_new)-np.sum(info_new[v
    else:
        print(f'mean={np.mean(info_new[var])}')
        print(f'standard deviation={np.std(info_new[var])}\n')
```

```
For variable Age:
mean=57.2964934251722
standard deviation=14.975289087630228

For variable Ht:
mean=162.18883218534754
standard deviation=9.904554043925097

For variable Wt:
mean=61.48492172824045
standard deviation=11.944200387476357

For variable Sex:
mode=0
class balance: 3145 to 3243

For variable OP_time:
mean=135.98546232519305
standard deviation=101.15376625280668

For variable Open:
mode=1
class balance: 3365 to 3023

For variable Robotic:
mode=0
class balance: 269 to 6119

For variable Videoscopic:
mode=0
class balance: 2754 to 3634

For variable icu_days:
mean=0.5527551659361303
standard deviation=3.4120403936109827

For variable icu:
mode=0
class balance: 1204 to 5184

For variable death_inhosp:
mode=0
class balance: 57 to 6331
```

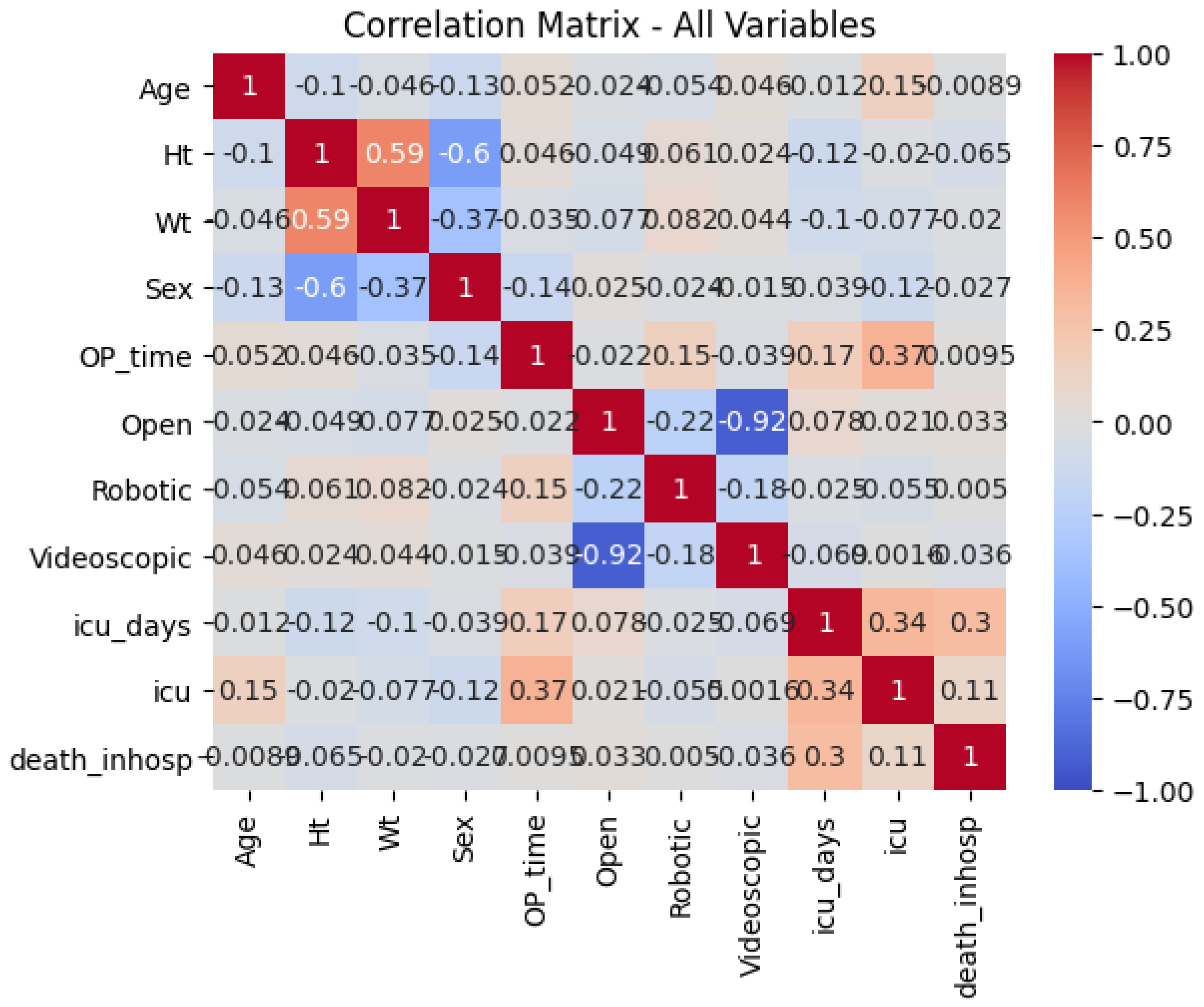
We plotted a correlation matrix of all of the variables to get a sense of the relationships between the variables.

In [8]:

```
cor_mat = info_new[['Age','Ht','Wt','Sex','OP_time', 'Open', 'Robotic', 'Videoscopic', 'ic
sns.heatmap(cor_mat,cmap='coolwarm',vmin=-1.0,vmax=1.0,annot=True)
plt.title('Correlation Matrix - All Variables')
```

Out[8]:

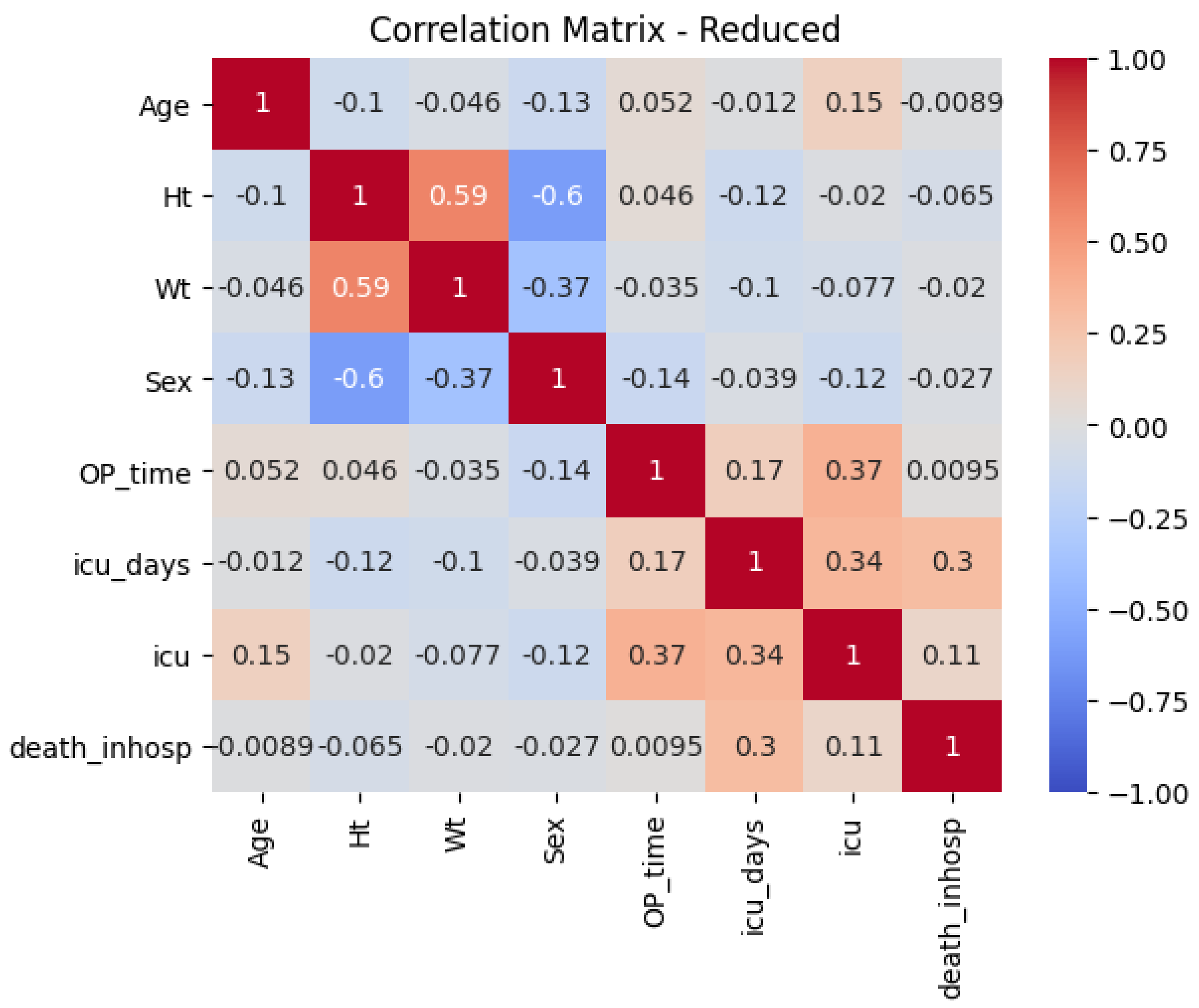
```
Text(0.5, 1.0, 'Correlation Matrix - All Variables')
```



We removed `Open`, `Robotic`, and `Videoscopic` from our correlation matrix because they really only correlated with each other. We may add them back in later, but this also made for a more comprehensible visualization.

In [9]:
```
# Remove variables with low correlations
cor_mat = info_new[['Age','Ht','Wt','Sex','OP_time', 'icu_days', 'icu', 'death_inhosp']].c
sns.heatmap(cor_mat,cmap='coolwarm',vmin=-1.0,vmax=1.0,annot=True)
plt.title('Correlation Matrix - Reduced')
```

Out[9]:
```
Text(0.5, 1.0, 'Correlation Matrix - Reduced')
```



	Age	Ht	Wt	Sex	OP_time	icu_days	icu	death_inhosp
Age	1	-0.1	-0.046	-0.13	0.052	-0.012	0.15	-0.0089
Ht	-0.1	1	0.59	-0.6	0.046	-0.12	-0.02	-0.065
Wt	-0.046	0.59	1	-0.37	-0.035	-0.1	-0.077	-0.02
Sex	-0.13	-0.6	-0.37	1	-0.14	-0.039	-0.12	-0.027
OP_time	0.052	0.046	-0.035	-0.14	1	0.17	0.37	0.0095
icu_days	-0.012	-0.12	-0.1	-0.039	0.17	1	0.34	0.3
icu	0.15	-0.02	-0.077	-0.12	0.37	0.34	1	0.11
death_inhosp	-0.0089	-0.065	-0.02	-0.027	0.0095	0.3	0.11	1

Outlier Detection

Next, we moved on to the outlier detection step. We used the Mahalanobis distance method for outlier detection. We felt it was valid to use this method because all of our individual distributions were unimodal, so we assumed our overall data to be unimodal. We know that the Mahalanobis distance method works poorly on multimodal data, but is a good metric for unimodal data. We are also conscious that our data is high-dimensional, so if we add more features, we will need to consider if the Mahalanobis distance metric is still valid.

In [10]:
```
num_data = info_new[['Age','Ht','Wt','Sex','OP_time']]
mu = list(np.mean(num_data))
iv = np.linalg.inv(num_data.cov())
```

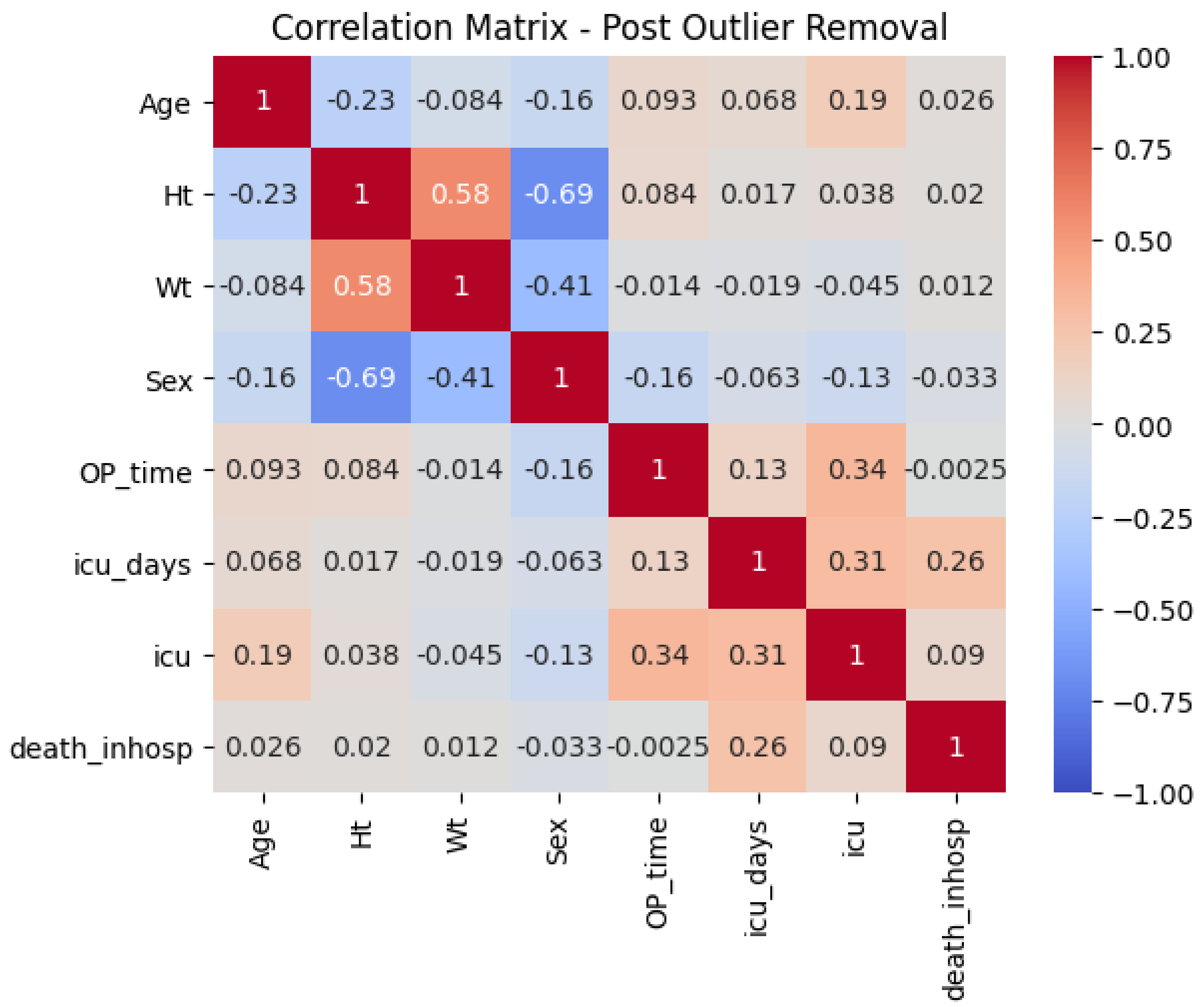
In [11]:
```
info_new['Mahalanobis'] = num_data.apply(lambda x: distance.mahalanobis(x,mu,iv),axis=1)
```

In [12]:
```
# Remove data points with top 5% mahalanobis distance
thresh = np.quantile(list(info_new['Mahalanobis']),0.95)
data = info_new[info_new['Mahalanobis'] < thresh]
print(f'We removed {len(info_new[info_new["Mahalanobis"] >= thresh])} outliers, leaving {l
```

```
We removed 320 outliers, leaving 6068 points remaining
```

In [13]:
```
# evaluate change in correlation between height and age
cor_mat_new = data[['Age','Ht','Wt','Sex','OP_time', 'icu_days', 'icu', 'death_inhosp']].c
sns.heatmap(cor_mat_new,cmap='coolwarm',vmin=-1.0,vmax=1.0,annot=True)
plt.title('Correlation Matrix - Post Outlier Removal')
```

```
Out[13]: Text(0.5, 1.0, 'Correlation Matrix - Post Outlier Removal')
```

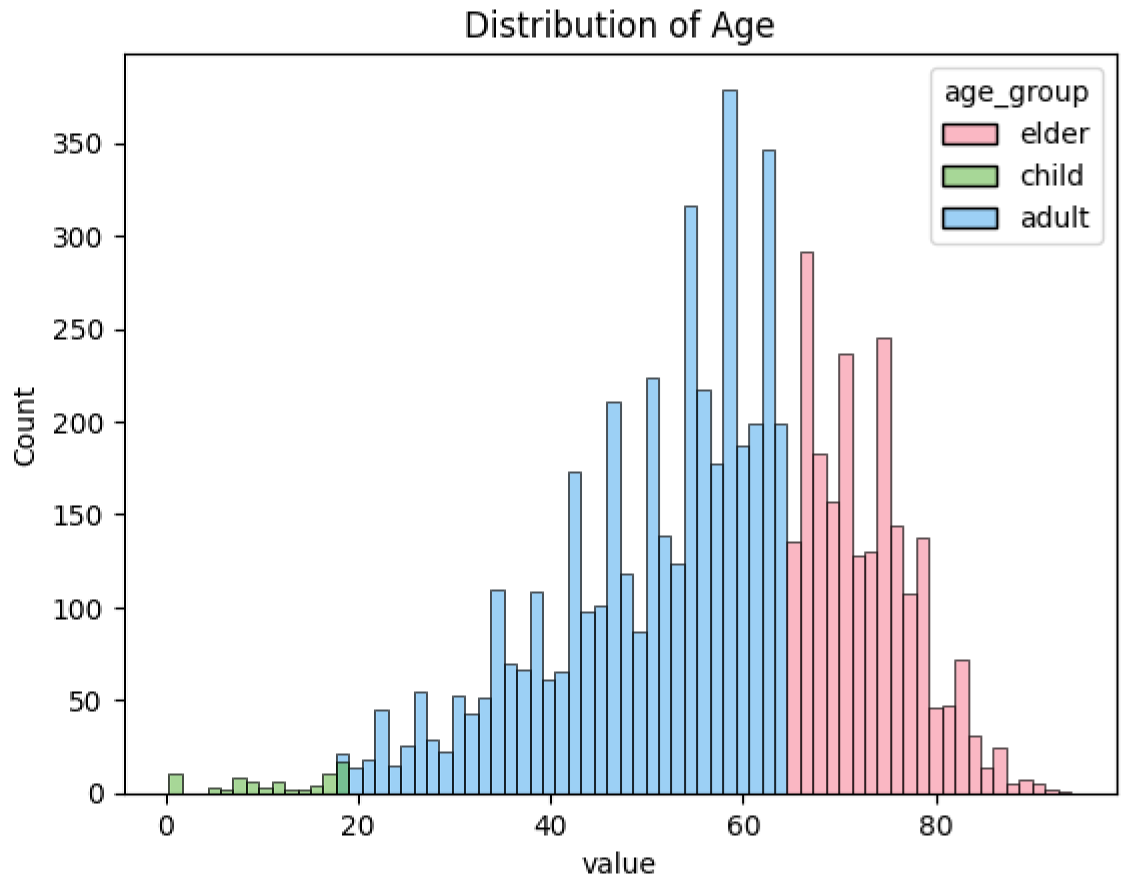


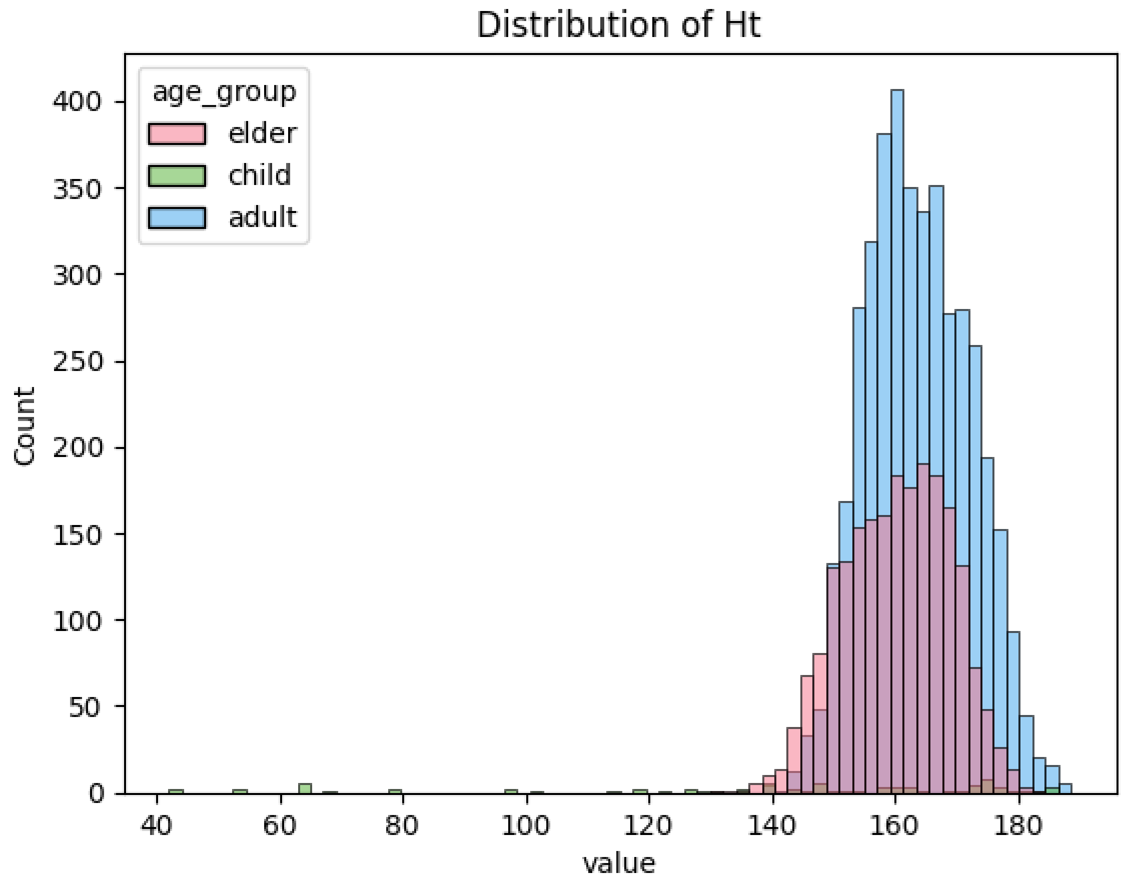
	Age	Ht	Wt	Sex	OP_time	icu_days	icu	death_inhosp
Age	1	-0.23	-0.084	-0.16	0.093	0.068	0.19	0.026
Ht	-0.23	1	0.58	-0.69	0.084	0.017	0.038	0.02
Wt	-0.084	0.58	1	-0.41	-0.014	-0.019	-0.045	0.012
Sex	-0.16	-0.69	-0.41	1	-0.16	-0.063	-0.13	-0.033
OP_time	0.093	0.084	-0.014	-0.16	1	0.13	0.34	-0.0025
icu_days	0.068	0.017	-0.019	-0.063	0.13	1	0.31	0.26
icu	0.19	0.038	-0.045	-0.13	0.34	0.31	1	0.09
death_inhosp	0.026	0.02	0.012	-0.033	-0.0025	0.26	0.09	1

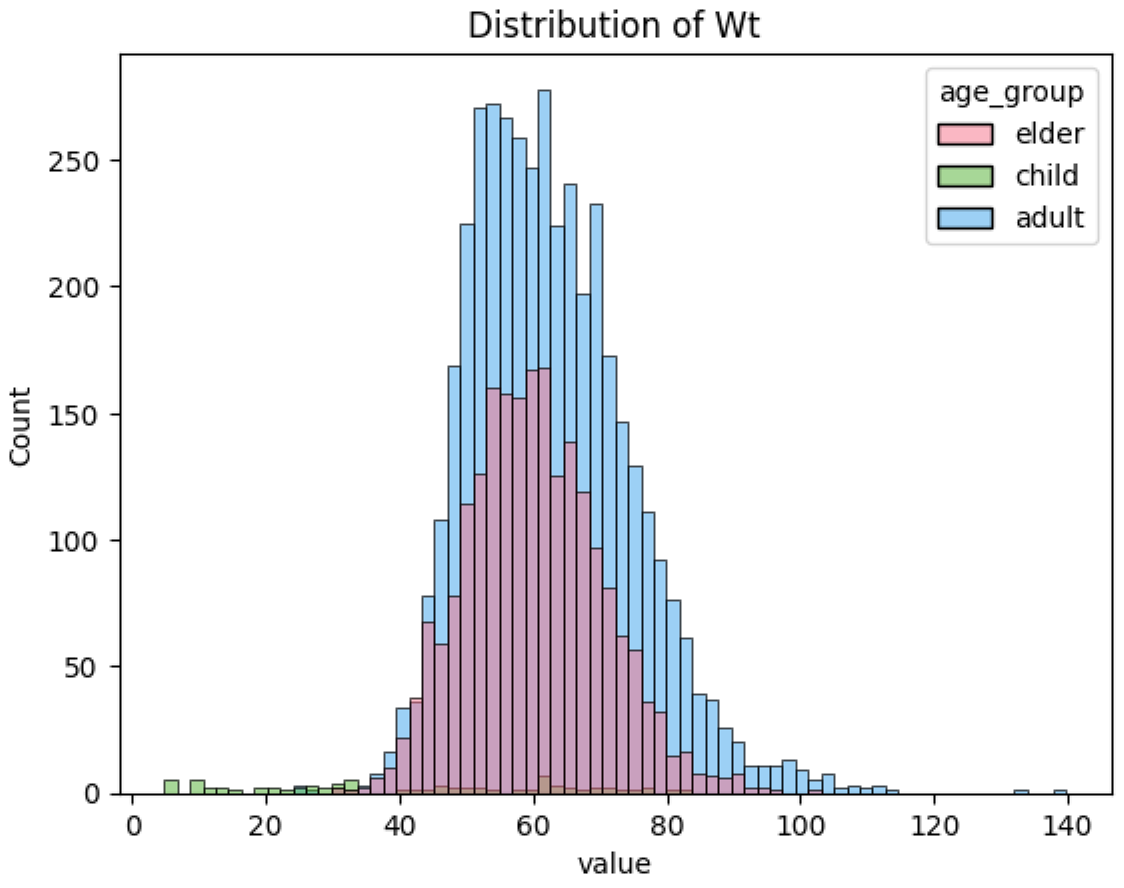
Age Stratification

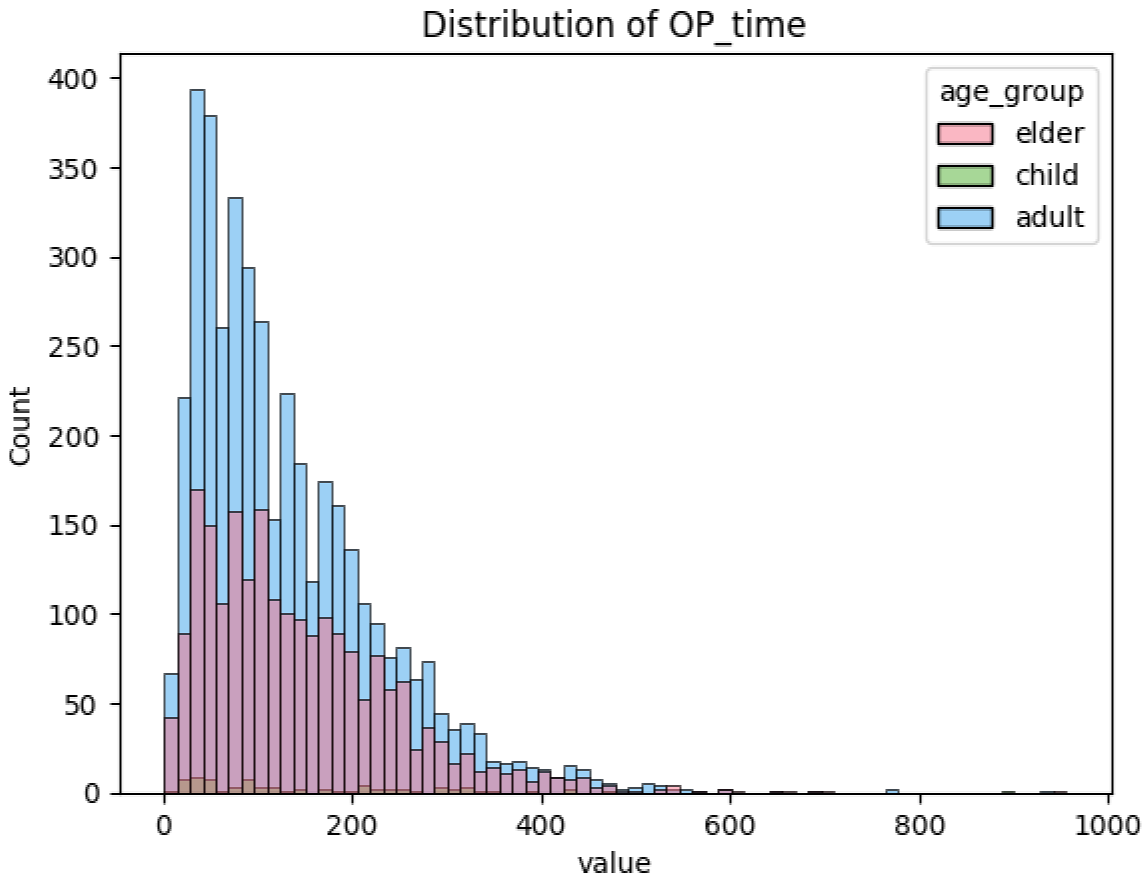
Because of potential for different physical characteristics, we realized that there is probably a need to treat people from different age groups differently when performing outlier detection methods. To do this, we introduced three age classes: children (18 and under), adult (19-64), and elderly (65 and older). We redid everything from the previous section, but stratified by age.

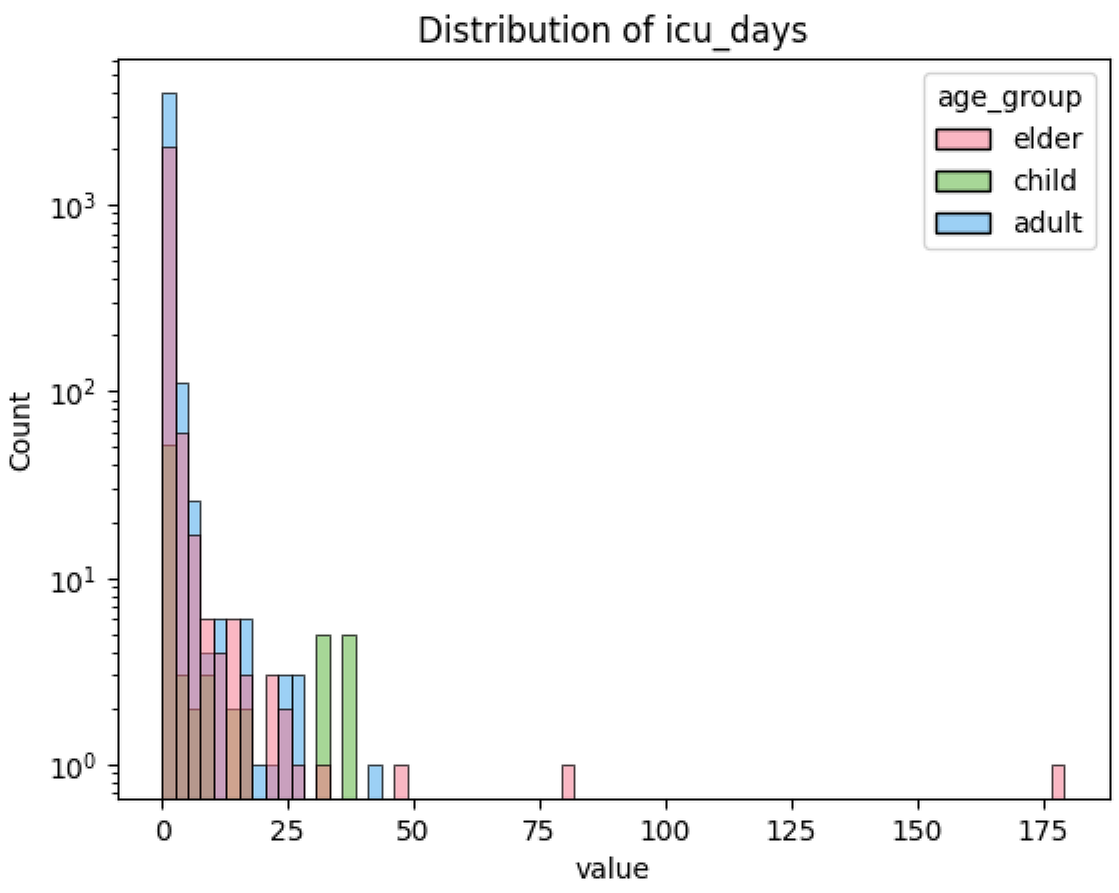
```
In [14]:
info_new['age_group'] = info_new['Age'].apply(lambda x: 'child' if x < 19 else ('elder' if

for var in ['Age','Ht','Wt','OP_time', 'icu_days']:
    to_plot = info_new.melt(id_vars='age_group', value_vars=var, var_name='variable', valu
    to_plot['age_group'] = pd.Categorical(to_plot['age_group'], categories=reversed(sorted
    palette = sns.color_palette("husl", n_colors=len(to_plot['age_group'].unique()))

    plt.figure()
    sns.histplot(data=to_plot, x='value', hue='age_group', multiple='layer', bins=70, alph
    plt.title(f'Distribution of {var}')
    if var == 'icu_days':
        plt.yscale('log')
    plt.show()
```


Distribution of Age
age_group
elder
child
adult
Count
value
0
50
100
150
200
250
300
350
0
20
40
60
80


Distribution of Ht
age_group
elder
child
adult
Count
value
0
50
100
150
200
250
300
350
400
40
60
80
100
120
140
160
180


Distribution of Wt
age_group
elder
child
adult
Count
value
0
50
100
150
200
250
0
20
40
60
80
100
120
140


Distribution of OP_time
age_group
elder
child
adult
Count
value
0
50
100
150
200
250
300
350
400
0
200
400
600
800
1000



In [15]:

```
for var in ['Age','Ht','Wt','Sex','OP_time', 'Open', 'Robotic', 'Videoscopic', 'icu_days',
    print(f'\nFor variable {var}:')
    for g in ['child','adult','elder']:
        print(f'In class {g},')
        if var in ['Sex', 'Open', 'Robotic', 'Videoscopic', 'icu', 'death_inhosp']:
            print(f'mode={stats.mode(info_new[info_new["age_group"]==g][var]).mode[0]}')
            print(f'class balance: {np.sum(info_new[info_new["age_group"]==g][var])} to {
        else:
            print(f'mean={np.mean(info_new[info_new["age_group"]==g][var])}')
            print(f'standard deviation={np.std(info_new[info_new["age_group"]==g][var])}\
```

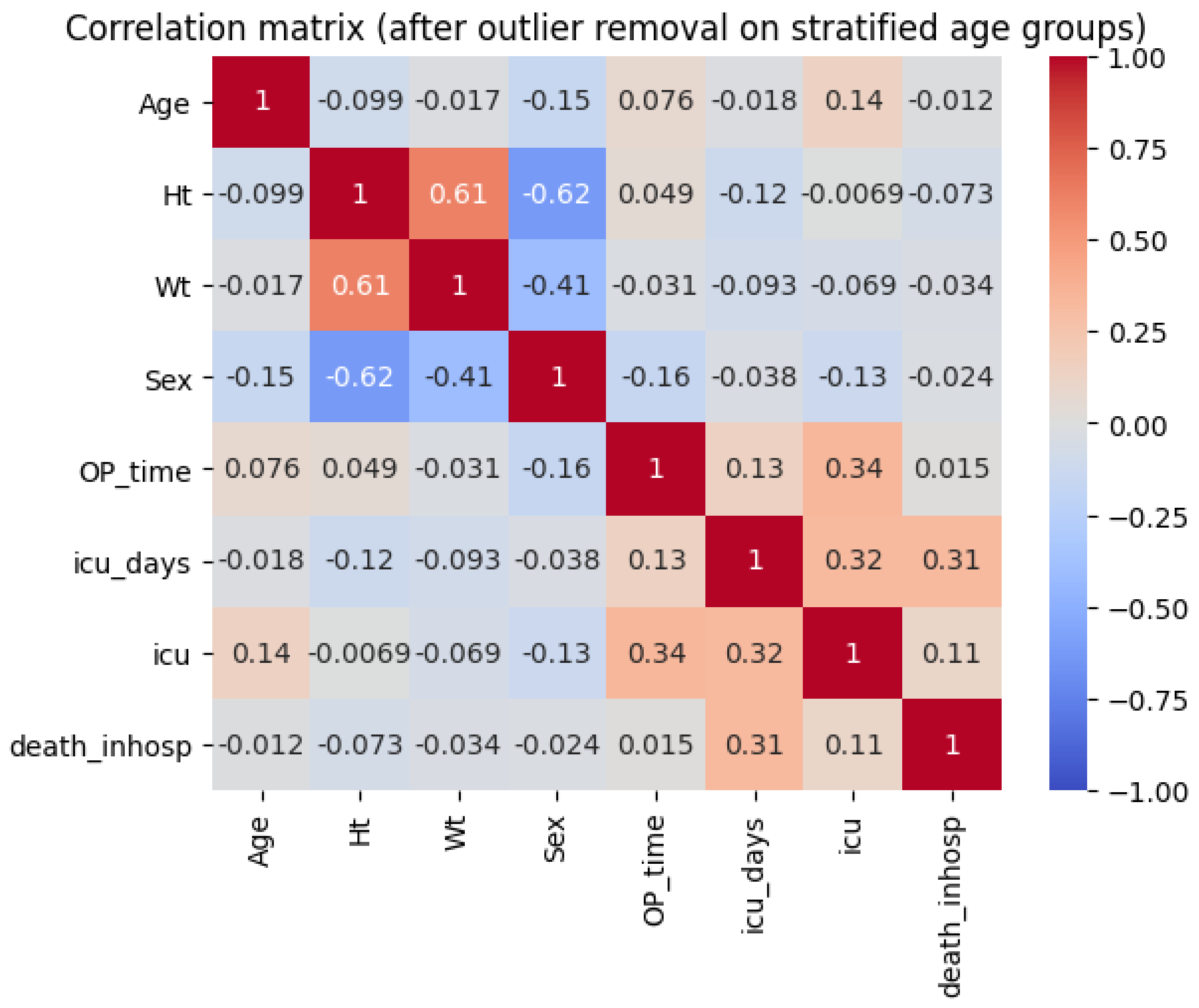
```
For variable Age:
In class child,
mean=11.675675675675675
standard deviation=6.0248093120168615

In class adult,
mean=50.184153661464585
standard deviation=10.888893800440728

In class elder,
mean=72.6519311307585
standard deviation=5.484172602364935


For variable Ht:
In class child,
mean=138.98918918918918
standard deviation=40.214057537966866

In class adult,
mean=163.63847779111646
standard deviation=8.383937382770833

In class elder,
mean=160.17812936249422
standard deviation=8.54638486809783


For variable Wt:
In class child,
mean=40.935810810810814
standard deviation=23.001716328837627

In class adult,
mean=62.55960864345739
standard deviation=12.106093865585805

In class elder,
mean=60.10966030711959
standard deviation=10.15585202779337


For variable Sex:
In class child,
mode=0
class balance: 36 to 38

In class adult,
mode=1
class balance: 2241 to 1924

In class elder,
mode=0
class balance: 868 to 1281


For variable OP_time:
In class child,
mean=161.4536036036036
standard deviation=148.34567339778695

In class adult,
mean=131.35488595438179
standard deviation=98.59816191804548

In class elder,
mean=144.0830463781604
standard deviation=103.37579812668092


For variable Open:
In class child,
mode=1
class balance: 58 to 16

In class adult,
mode=1
class balance: 2179 to 1986

In class elder,
mode=1
class balance: 1128 to 1021


For variable Robotic:
In class child,
mode=0
class balance: 2 to 72

In class adult,
mode=0
class balance: 200 to 3965

In class elder,
mode=0
class balance: 67 to 2082


For variable Videoscopic:
In class child,
mode=0
class balance: 14 to 60

In class adult,
mode=0
class balance: 1786 to 2379

In class elder,
mode=0
class balance: 954 to 1195


For variable icu_days:
In class child,
mean=6.45945945945946
standard deviation=11.994581196781915

In class adult,
mean=0.3575030012004802
standard deviation=1.679955841128645

In class elder,
mean=0.7277803629595161
standard deviation=4.782945870657876


For variable icu:
In class child,
mode=0
class balance: 34 to 40

In class adult,
mode=0
class balance: 586 to 3579

In class elder,
mode=0
class balance: 584 to 1565


For variable death_inhosp:
In class child,
mode=0
class balance: 5 to 69

In class adult,
mode=0
class balance: 28 to 4137

In class elder,
mode=0
class balance: 24 to 2125
```

This time, when we removed outliers, we counted how many were removed from each class. The numbers seemed representative of the class balance, which is good.

In [16]:
```
data = pd.DataFrame()

for c in ['child','adult','elder']:
    small_data = info_new[info_new['age_group']==c].copy()
    num_data = small_data[['Age','Ht','Wt','Sex','OP_time']]
    mu = list(np.mean(num_data))
    iv = np.linalg.inv(num_data.cov())
    small_data['Mahalanobis'] = num_data.apply(lambda x: distance.mahalanobis(x,mu,iv),axi
    thresh = np.quantile(list(small_data['Mahalanobis']),0.95)
    print(f'removing {len(small_data[small_data["Mahalanobis"] >= thresh])} outliers from
    data = pd.concat([data, small_data[small_data['Mahalanobis'] < thresh]], ignore_index=
```

```
removing 4 outliers from child class
removing 209 outliers from adult class
removing 108 outliers from elder class
```

In [17]:
```
cor_mat_new = data[['Age','Ht','Wt','Sex','OP_time', 'icu_days', 'icu', 'death_inhosp']].c
sns.heatmap(cor_mat_new,cmap='coolwarm',vmin=-1.0,vmax=1.0,annot=True)
plt.title('Correlation matrix (after outlier removal on stratified age groups)')
plt.show()
```

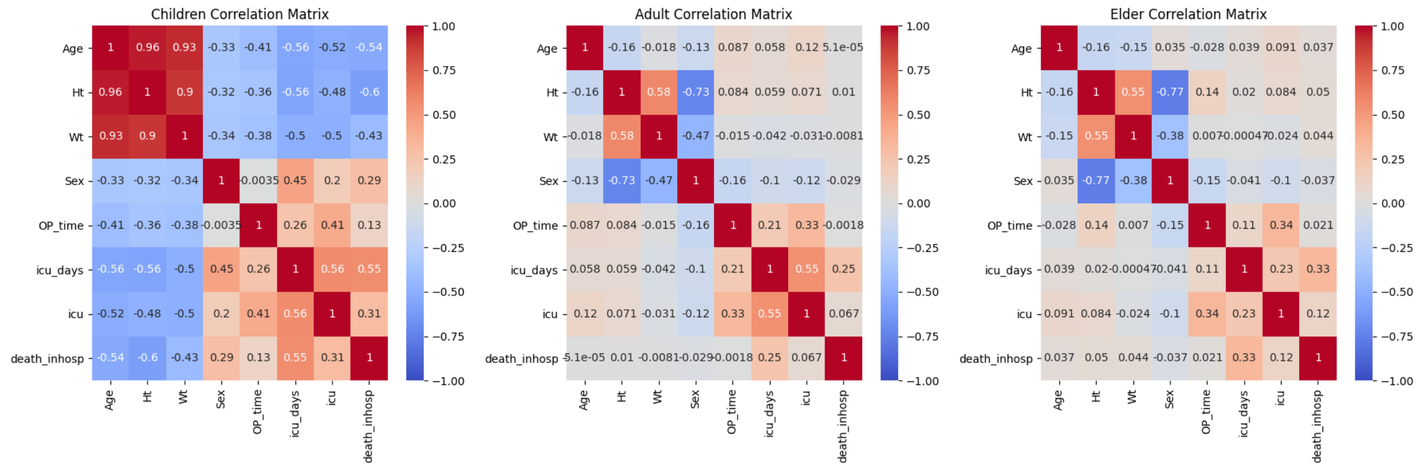


	Age	Ht	Wt	Sex	OP_time	icu_days	icu	death_inhosp
Age	1	-0.099	-0.017	-0.15	0.076	-0.018	0.14	-0.012
Ht	-0.099	1	0.61	-0.62	0.049	-0.12	-0.0069	-0.073
Wt	-0.017	0.61	1	-0.41	-0.031	-0.093	-0.069	-0.034
Sex	-0.15	-0.62	-0.41	1	-0.16	-0.038	-0.13	-0.024
OP_time	0.076	0.049	-0.031	-0.16	1	0.13	0.34	0.015
icu_days	-0.018	-0.12	-0.093	-0.038	0.13	1	0.32	0.31
icu	0.14	-0.0069	-0.069	-0.13	0.34	0.32	1	0.11
death_inhosp	-0.012	-0.073	-0.034	-0.024	0.015	0.31	0.11	1

We wanted to explore what relationships were present between our variables according to each class, particularly noting some of the differences in children. We expected age, hwight, and weight to be more correlated in children, but we found it interesting that every feature was more correlated in children. We expect that this is because of the inherent risks associated with surgery for infants.

In [18]:
```
cor_mat_children = data[data['age_group'] == 'child'][['Age','Ht','Wt','Sex','OP_time', 'i
```

```
cor_mat_adults = data[data['age_group'] == 'adult'][['Age','Ht','Wt','Sex','OP_time', 'icu
cor_mat_elders = data[data['age_group'] == 'elder'][['Age','Ht','Wt','Sex','OP_time', 'icu

fig, axs = plt.subplots(1, 3, figsize=(18, 6))

sns.heatmap(cor_mat_children, ax=axs[0], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)
sns.heatmap(cor_mat_adults, ax=axs[1], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)
sns.heatmap(cor_mat_elders, ax=axs[2], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)

axs[0].set_title('Children Correlation Matrix')
axs[1].set_title('Adult Correlation Matrix')
axs[2].set_title('Elder Correlation Matrix')

plt.tight_layout()
plt.show()
```



Time Series Outlier Detection (SNUADC ECG)

Next, we wanted to move forward into looking at waveform data. The tracks data from **vitaldb** contained many different measurements from many different devices for many different patients. To simplify things, we decided to focus on one measurement from one device: the ECG reading from the SNUADC device. Still, there were waveforms for 6355 patients just on this measurement and this device.

In [19]:
```
ecg_info = df_ids[df_ids['tname'] == 'SNUADC/ECG_II']
ecg_info
```

Out[19]:

	caseid	tname	tid
41	1	SNUADC/ECG_II	8c9161aaae8cb578e2aa7b60f44234d98d2b3344
122	2	SNUADC/ECG_II	62204d727b2e31e42f9602c054c7d9e598b2db05
198	3	SNUADC/ECG_II	2012a9532285255e1051e9be389d69e2778373ba
279	4	SNUADC/ECG_II	be29325ee538657798f5c804bf72596fb3fd47ea
366	5	SNUADC/ECG_II	3431cd35ca4bc15b6de13e4c49b2db56e6bc5a37
...	...	...	...
486118	6384	SNUADC/ECG_II	38fda47c2e06534015012c131657edd66e36f4d2
486191	6385	SNUADC/ECG_II	0e030d618ae6101448128542f7b2964e66ad6272
486266	6386	SNUADC/ECG_II	7f4f673135fff8b4474dcbd852c774aad89e3c0d
486342	6387	SNUADC/ECG_II	66401ffc5c1ef2d8904e021f55c2d745e2bd5936
486420	6388	SNUADC/ECG_II	cedfc6b4610363ed0ac5a4ac4a23e007bda34fe6

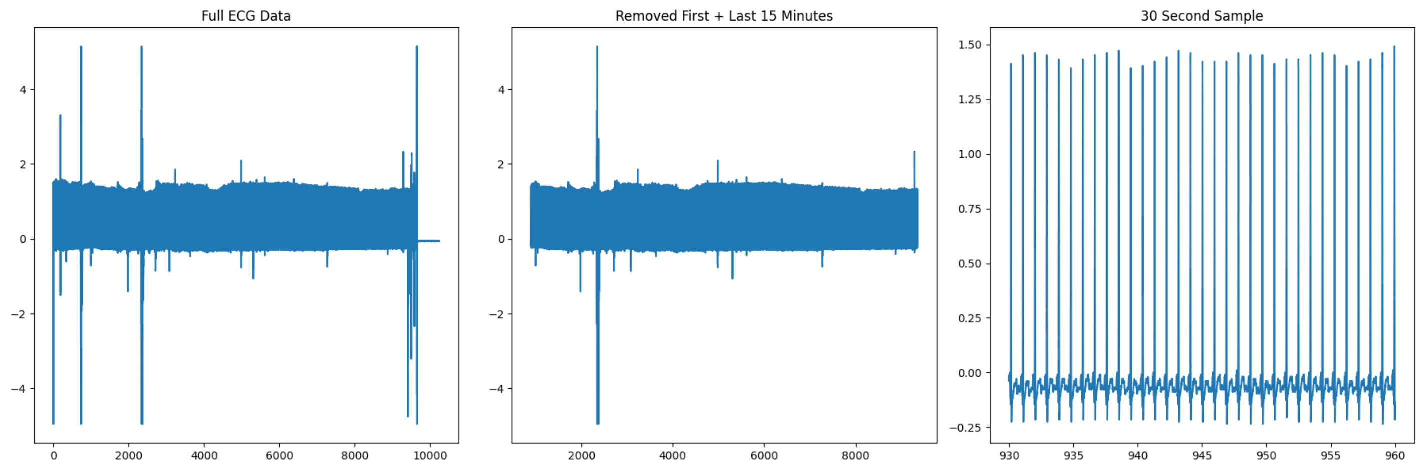
6355 rows × 3 columns

In [20]:
```
def get_data_for(tid):
    data = pd.read_csv(f"https://api.vitaldb.net/{tid}")
    arr = np.array(data['SNUADC/ECG_II'])
    time_array = np.linspace(0, np.array(data['Time'])[-1], len(data))
    return time_array, arr
```

We started by just looking at one patient to speed up calculations and better understand the waveform data and what we were trying to accomplish. After initially looking at a plot of the waveform, we found that the beginning and end showed unusual behavior. Because of this, we decided to clip off the first and last 15 minutes of each surgery so that we could exclusively focus on the central portion. We also made an even smaller section, which was 15,000 data points (or about 30 seconds), which we used in intermediate steps when visualizing specific beats was helpful.

In [21]:
```
ecg_time, ecg_data = get_data_for("cedfc6b4610363ed0ac5a4ac4a23e007bda34fe6")
fs = 500
valid_data = ecg_data[(ecg_time > 900) & (ecg_time < ecg_time[-1]-900)]
valid_time = ecg_time[(ecg_time > 900) & (ecg_time < ecg_time[-1]-900)]
small_time = valid_time[15000:30000]
small_data = valid_data[15000:30000]
```

In [22]:
```
fig, axs = plt.subplots(1, 3, figsize=(18, 6))

axs[0].plot(ecg_time,ecg_data)
axs[0].set_title('Full ECG Data')
axs[1].plot(valid_time,valid_data)
axs[1].set_title('Removed First + Last 15 Minutes')
axs[2].plot(small_time,small_data)
axs[2].set_title('30 Second Sample')

plt.tight_layout()
plt.show()
```

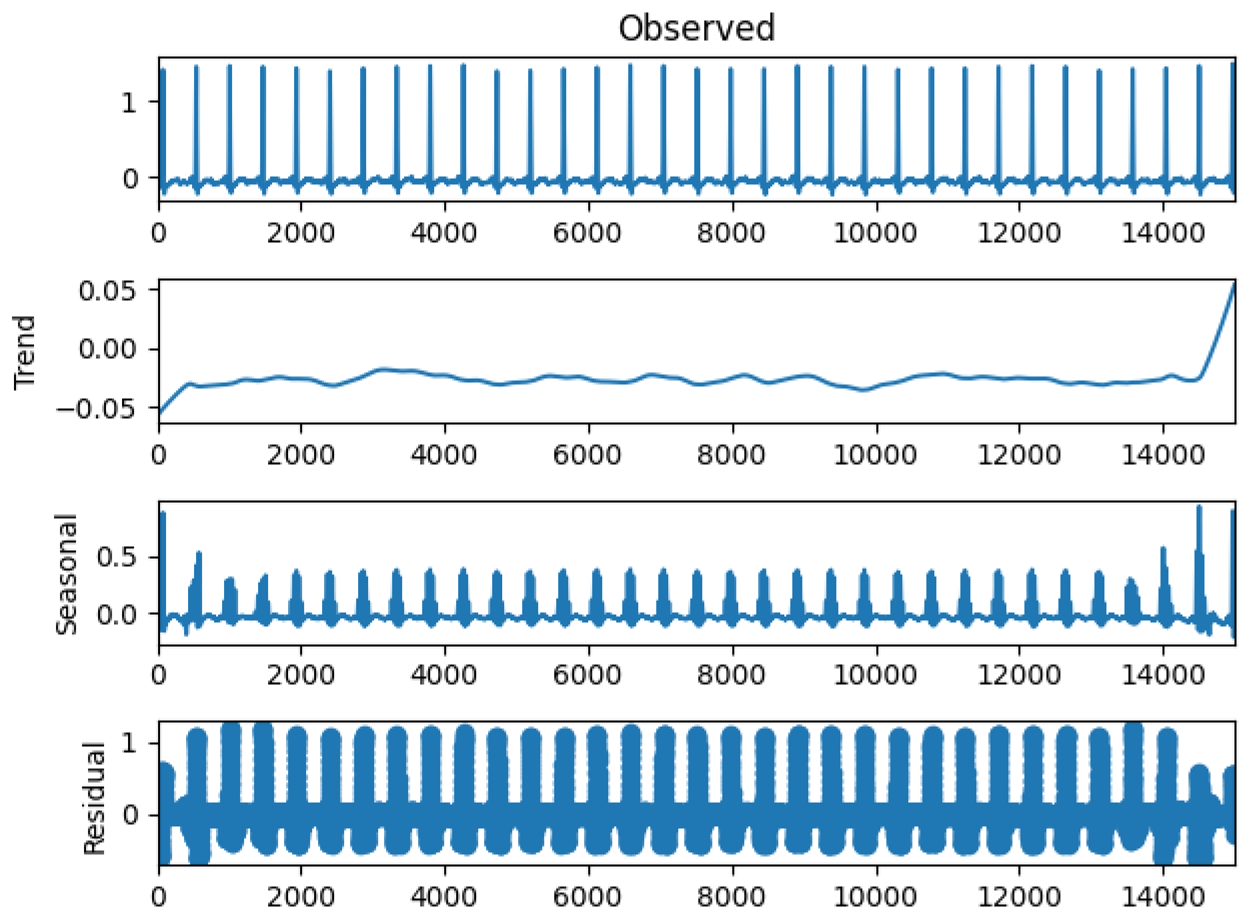


Option 1: STL

First, we tried using trend, seasonal, and residual decomposition to analyze these waveforms, which was the method we discussed in class. We found that even on only 30 seconds of data, and only for one patient, this was quite slow, and it also did not seem to work as we wanted it to. We expected a constant trend and a seasonality matching the original waveform, but what we found was that the residual was also capturing much of the periodic behavior of the waveform. After some research, we found that STL decomposition is not recommended for ECG data because it is actually made up of a composition of multiple waveforms.

In [23]:
```
periodicity = int(np.round(1 / (valid_time[1] - valid_time[0])))
stl = STL(small_data, period = periodicity)
ts_decomposed = stl.fit()
```

In [24]:
```
ts_decomposed.plot()
plt.show()
```

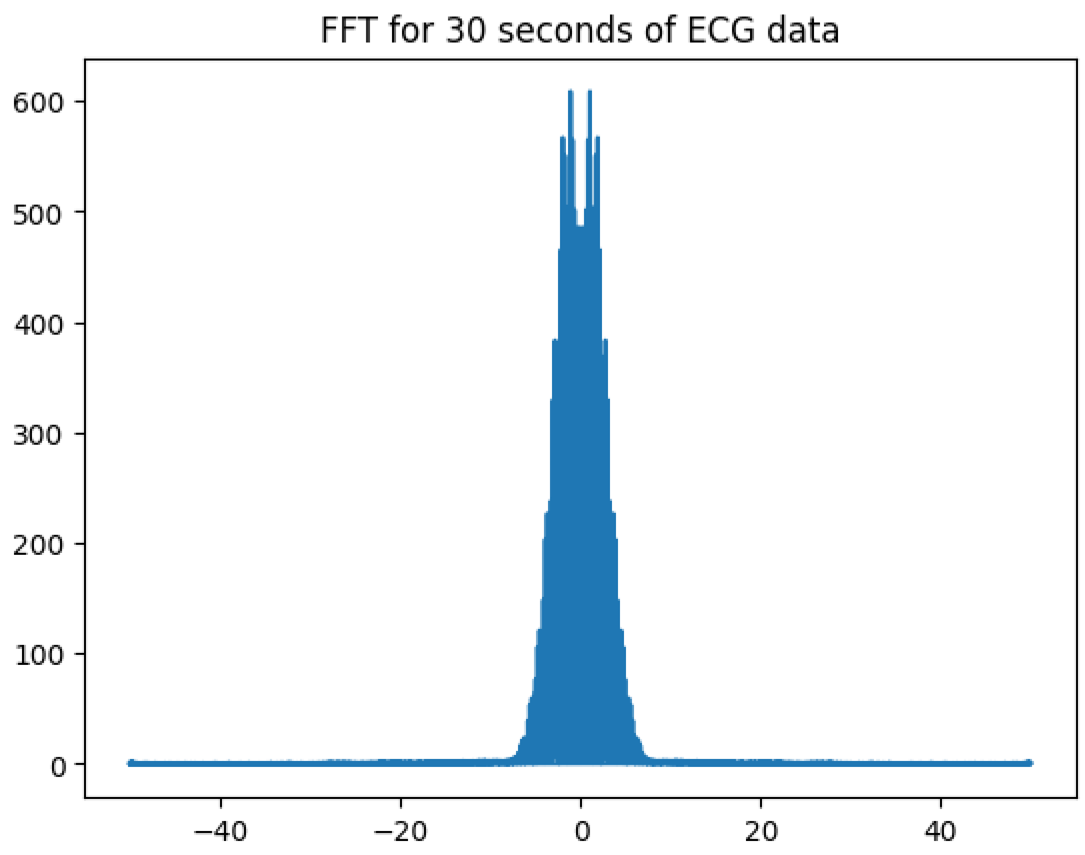


Option 2: FFT

After learning that ECG data is made up of multiple waveforms, we thought of using some sort of Fourier decomposition. Ultimately, however, we did not end up spending much time on this method.

In [25]:
```
fft_signal = np.fft.fft(small_data)
freqs = np.fft.fftfreq(len(small_data), 0.01)
plt.plot(freqs, np.abs(fft_signal))
plt.title('FFT for 30 seconds of ECG data')
```

Out[25]:
```
Text(0.5, 1.0, 'FFT for 30 seconds of ECG data')
```



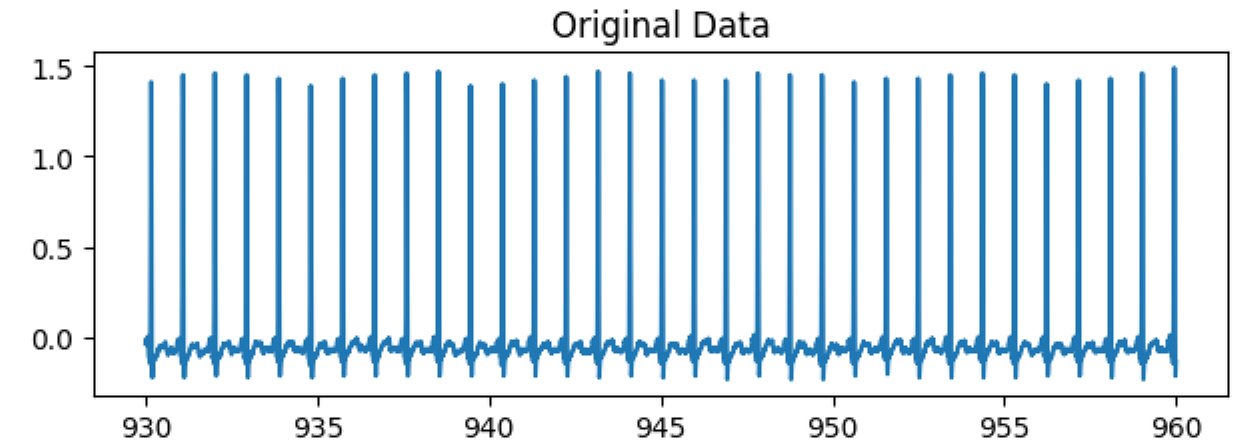
Option 3: RR Intervals

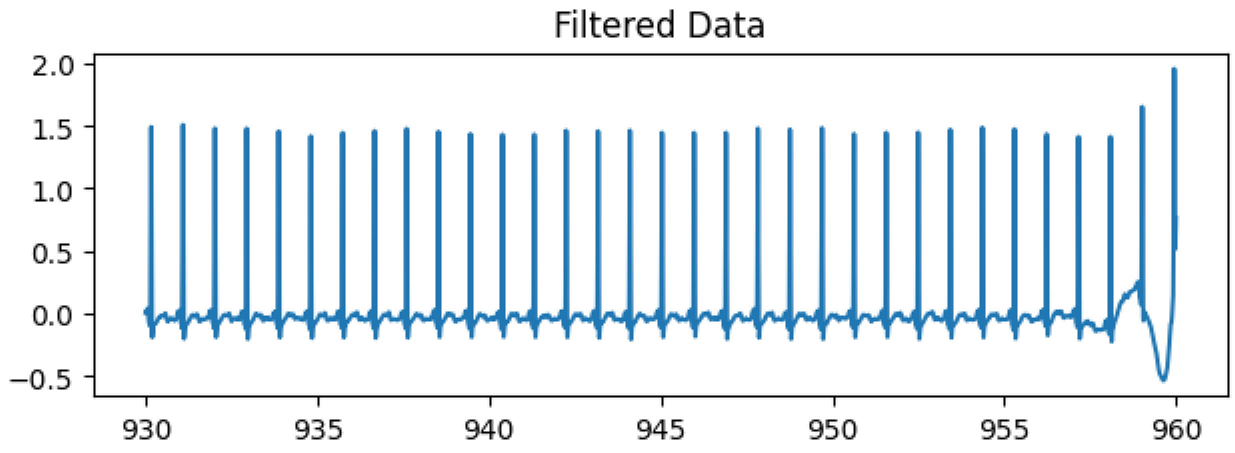
The last method we explored for analyzing our waveforms was looking at the RR intervals (https://imotions.com/blog/learning/best-practice/heart-rate-variability/). The waveform from ECG data is made up of three parts, known as the QRS complex. The RR interval is the time between two R peaks. There is a lot more interesting stuff to explore in this article, but for now, we just focused on finding RR intervals and doing some basic measures on them.

First, we applied a band-pass filter to our data to smooth it a bit before diving in.

In [26]:

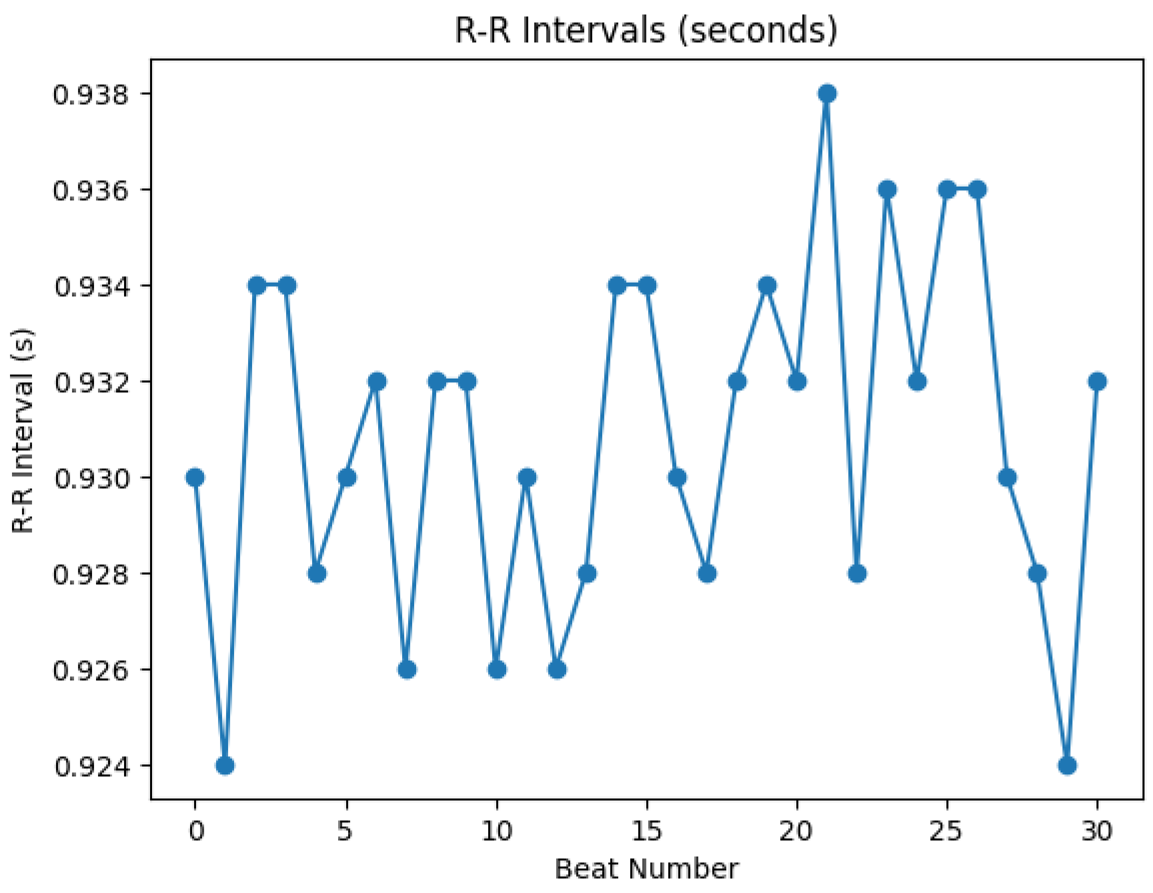
```
lowcut = 0.5
highcut = 40.0
order = 4
nyquist = 0.5 * fs
low = lowcut / nyquist
high = highcut / nyquist
b, a = signal.butter(order, [low,high], btype='band')
filtered = signal.filtfilt(b,a,small_data)

plt.figure()
plt.subplot(2,1,1)
plt.plot(small_time, small_data)
plt.title('Original Data')
plt.subplot(2,1,2)
plt.plot(small_time, filtered)
plt.title('Filtered Data')
plt.tight_layout()
plt.show()
```





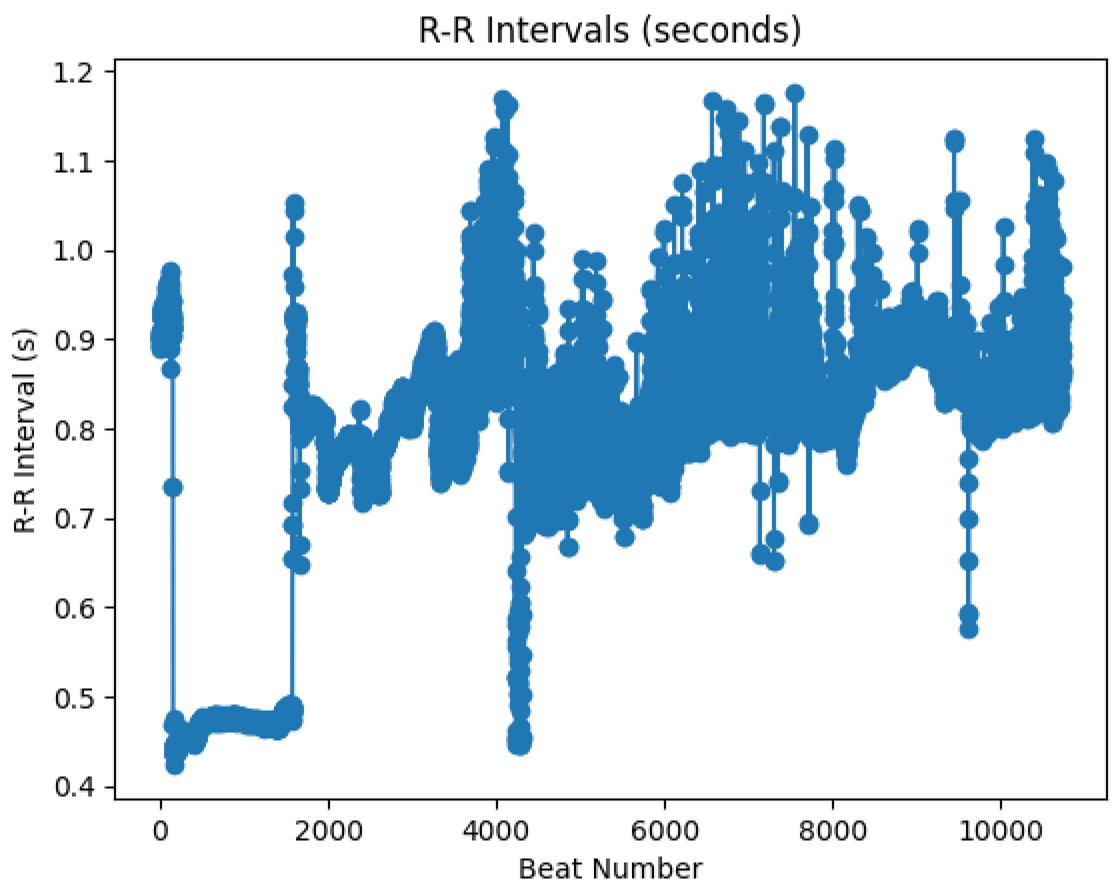
Next, we used the `neurokit2` package to process the waveform and find the RR intervals. We did this first with our 30 second sample and then with our full waveform (minus the first and last 15 minutes).

In [27]:
```
ecg_cleaned = nk.ecg_clean(filtered, sampling_rate=500, method="neurokit")
ecg_signals, ecg_info = nk.ecg_process(ecg_cleaned, sampling_rate=500)
rpeaks = ecg_info['ECG_R_Peaks']
rr_intervals = np.diff(rpeaks) / 500

plt.plot(rr_intervals, marker='o', linestyle='-')
plt.title("R-R Intervals (seconds)")
plt.xlabel("Beat Number")
plt.ylabel("R-R Interval (s)")
plt.show()
```



In [28]:

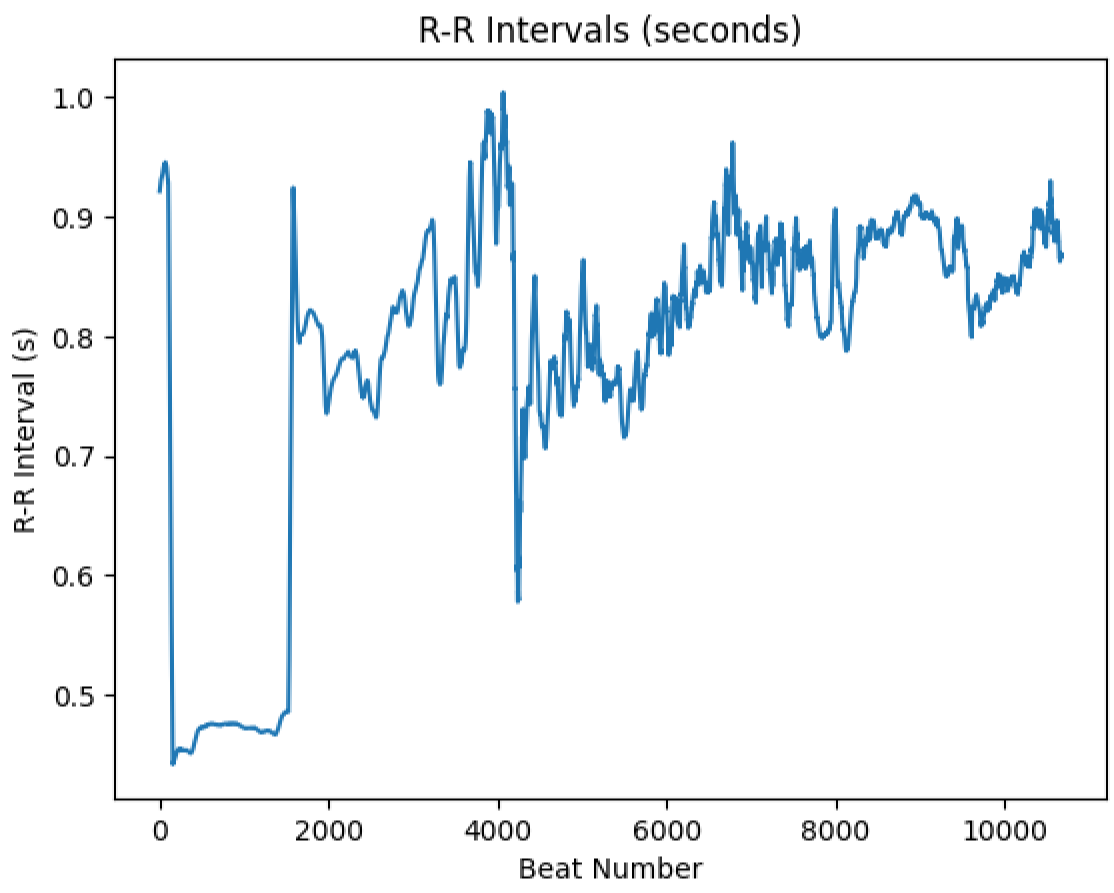
```
filtered = signal.filtfilt(b,a,valid_data)
ecg_cleaned = nk.ecg_clean(filtered, sampling_rate=500, method="neurokit")
ecg_signals, ecg_info = nk.ecg_process(ecg_cleaned, sampling_rate=500)
rpeaks = ecg_info['ECG_R_Peaks']
rr_intervals = np.diff(rpeaks) / 500
plt.plot(rr_intervals, marker='o', linestyle='-')
plt.title("R-R Intervals (seconds)")
plt.xlabel("Beat Number")
plt.ylabel("R-R Interval (s)")
plt.show()
```



Before doing anything with the data, we ran it through a 50-point moving average (0.1 second at our 500 Hz sampling rate) to filter out small blips and focus on more ongoing outliers.

In [29]:

```
ma = np.convolve(rr_intervals, np.ones(50)/50)
plt.plot(ma[50:-50], linestyle='-')
plt.title("R-R Intervals (seconds)")
plt.xlabel("Beat Number")
plt.ylabel("R-R Interval (s)")
plt.show()
```



We want to turn the waveform data into another feature that we can use in our original model. We had two ideas for how to create this feature.

1. Big jumps: find the difference array and set some threshold for a 'big jump', then take the number of big jumps found in the difference array. This represents the number of drastic changes to a patient's heart rate that occurred during the surgery.

2. Deviation from mean: Find the mean of the R-R intervals, then find the percentage of points that fall outside 2 standard deviations of the mean. This can be thought of as the percentage of time that the patient had within an abnormal heart rate zone. We will think about a way to make sure the mean itself is not affected by these outliers.

In [30]:

```
ma_sampled = [ma[15*i] for i in range(int(len(ma)/15))]
diff = np.diff(ma_sampled)
thresh = 0.2
print(f'There are {len(diff[diff>thresh])} big jumps')
print(len(ma))
```

```
There are 3 big jumps
10772
```

In [31]:

```
mu = np.mean(ma)
std = np.std(ma)
print(f'{100*len(ma[(ma>mu+2*std) | (ma<mu-2*std)])/len(ma):0.2f}% of points lie outside t
```

```
13.33% of points lie outside the normal zone
```

Target Variable Examination

In this section, we look further into the class imbalances.

In [32]:
```
pct_death = 100*info_new['death_inhosp'].sum()/len(info_new)
pct_icu = 100*info_new['icu'].sum()/len(info_new)
med_icu = info_new[info_new['icu']==1]['icu_days'].median()
print(f'{pct_death:.2f}% death in hospital ({info_new["death_inhosp"].sum()} instances),
```

```
0.89% death in hospital (57 instances), 18.85% icu stay (1204 instances), 1.0 day median s
tay for those who went to ICU
```

In [33]:
```
short_icu =  len(info_new[info_new['icu_days']==1])
long_icu = len(info_new[info_new['icu_days']>1])
total_icu = info_new['icu'].sum()
print(f'{short_icu} ({100*short_icu/total_icu:.2f}%) stayed in icu for 1 day , {long_icu}
```

```
815 (67.69%) stayed in icu for 1 day , 389 (32.31%) stayed in icu for more (total 1204)
```

In [34]:
```
pct_icu_death = 100*info_new[info_new['icu']==1]['death_inhosp'].sum()/len(info_new[info_r
print(f'{pct_icu_death:.2f}% of those who had an ICU stay also died in the hospital.')
```

```
2.99% of those who had an ICU stay also died in the hospital.
```

Looking at our data, we have a few options for target variables. Exploring the length of time people are staying in the ICU, we have a total of 1078 individuals who went to the ICU after surgery. This is still a fairly large subset of the data. If we take only these instances and make our target classes 1 day stay vs >1 day stay, the class imbalance becomes about 70/30, which is significantly better than the about 99/1 class imbalance we had using death_inhosp as a target.

In [35]:
```
info_icu = info_new[info_new['icu']==1].copy().drop(columns=['icu','Mahalanobis'])
info_icu['icu_length'] = info_icu['icu_days'].apply(lambda x: 0 if x == 1 else 1)
info_icu = info_icu.drop(columns='icu_days')
info_icu.head()
```

Out[35]:

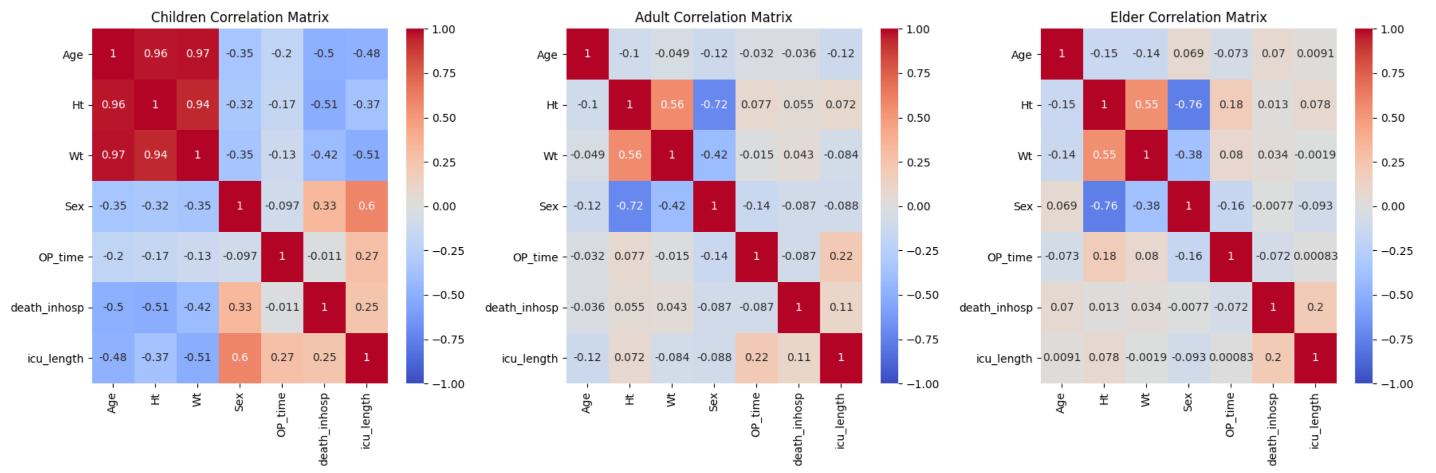
	subjectid	Age	Ht	Wt	Sex	OP_time	Open	Robotic	Videoscopic	death_inhosp	age_group	icu_length
3	1903	74.0	160.6	53.00	0	255.0	0	0	1	0	elder	0
4	4416	66.0	171.0	59.70	0	295.0	1	0	0	0	elder	1
6	5124	52.0	167.7	62.30	1	190.0	0	0	1	0	adult	1
9	2175	72.0	162.5	62.75	0	290.0	0	0	1	0	elder	0
11	491	46.0	169.2	81.40	1	425.0	1	0	0	0	adult	1

Outlier Detection (again)

In [36]:
```
data_icu = pd.DataFrame()

for c in ['child','adult','elder']:
    small_data = info_icu[info_icu['age_group']==c].copy()
    num_data = small_data[['Age','Ht','Wt','Sex','OP_time']]
    mu = list(np.mean(num_data))
    iv = np.linalg.inv(num_data.cov())
    small_data['Mahalanobis'] = num_data.apply(lambda x: distance.mahalanobis(x,mu,iv),axi
    thresh = np.quantile(list(small_data['Mahalanobis']),0.95)
    print(f'removing {len(small_data[small_data["Mahalanobis"] >= thresh])} outliers from
    data_icu = pd.concat([data_icu, small_data[small_data['Mahalanobis'] < thresh]], ignor
```

```
removing 2 outliers from child class
removing 30 outliers from adult class
removing 30 outliers from elder class
```

In [37]:
```
cor_mat_children = data_icu[data_icu['age_group'] == 'child'][['Age','Ht','Wt','Sex','OP_t
cor_mat_adults = data_icu[data_icu['age_group'] == 'adult'][['Age','Ht','Wt','Sex','OP_tir
cor_mat_elders = data_icu[data_icu['age_group'] == 'elder'][['Age','Ht','Wt','Sex','OP_tir

fig, axs = plt.subplots(1, 3, figsize=(18, 6))

sns.heatmap(cor_mat_children, ax=axs[0], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)
sns.heatmap(cor_mat_adults, ax=axs[1], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)
sns.heatmap(cor_mat_elders, ax=axs[2], cmap='coolwarm',vmin=-1.0,vmax=1.0, annot=True)

axs[0].set_title('Children Correlation Matrix')
axs[1].set_title('Adult Correlation Matrix')
axs[2].set_title('Elder Correlation Matrix')

plt.tight_layout()
plt.show()
```



In [38]:
```
print(f'There are {len(data_icu[(data_icu["icu_length"]==1) & (data_icu["age_group"]=="chi
```

```
There are 24 children,  201 adults, and  131 elders in the positive class
```

It's interesting that `op_time` and `icu_length` are correlated so much more heavily in adults than in elders. Some of the high child correlations with various demographic variables and `icu_length` may be due to the small sample size.

In [39]:
```
# so we can use it elsewhere
data_icu.to_csv('data_icu.csv', index=False)
```

Model Updates

For each of our preprocessing steps above, we have created a machine learning morphism.

1. Encode `sex` as a binary variable

$$\mathcal{ML}_1 = (\{M, F\}, \{0,1\}, F(x;\theta) = \begin{cases} 0 & x = M \\ 1 & x = F \end{cases}, P_\Theta(\theta) = 1, L(y, F) = \text{trivial})$$

1. Construct `OP_time`

$$\mathcal{ML}_2 = (\mathbb{R}^2, \mathbb{R}, F(x;\theta) = X[1] - X[0], P_\Theta(\theta) = 1, L(y, F) = \text{trivial})$$

1. One-hot encoding for `approach`

$$\mathcal{ML}_3 = (\{\text{open,robotic,videoscopic}\}, \mathbb{R}^3, F(x;\theta) = \text{injective map}, F : \mathbb{X} \to \mathbb{R}^3, P_\Theta(\theta) = 1, L(y, F) = \text{trivial})$$

1. Construct `icu` as a binary variable

$$\mathcal{ML}_4 = (\mathbb{Z}, \{0,1\}, F(x;\theta) = \begin{cases} 0 & x = 0 \\ 1 & \text{else} \end{cases}, P_\Theta(\theta) = 1, L(y, F) = \text{trivial})$$

1. Mahalanobis distance

$$\mathcal{ML}_5 = (\mathbb{R}^5, \{0,1\}, F(x;\theta) = \sqrt{(x-\mu)^\top \Sigma^{-1}(x-\mu)}, \theta = (\mu, \Sigma), P_\Theta(\theta) = 1, L(y, F) = (y - F(x;\theta))^2)$$

1. Stratification by Age

$$\mathcal{ML}_6 = (\mathbb{R}, \{\text{child,adult,elder}\}, F(x;\theta) = \begin{cases} \text{child} & x < 19 \\ \text{adult} & 18 < x < 65 \\ \text{elder} & \text{else} \end{cases}, P_\Theta(\theta) = 1, L(y, F) = \text{trivial})$$

1. Mahalanobis by age

$$\mathcal{ML}_7 = (\mathbb{R}^5, \{0,1\}, F(x;\theta) = \sqrt{(x-\mu)^\top \Sigma^{-1}(x-\mu)}, \theta = (\mu, \Sigma), P_\Theta(\theta) = 1, L(y, F) = (y - F(x;\theta))^2)$$

, three times, one for each age class

1. Shortening waveform

$$\mathcal{ML}_8 = (\mathbb{X} = \mathbb{R}^{5,124,450}, \mathbb{Y} = \mathbb{R}^{4,224,450}, F(\mathbf{x};\boldsymbol{\theta}) = \begin{cases} x_i & \text{if } 450,000 \le i \le 4,674,450 \\ \mathit{Discard} & \text{else} \end{cases}, P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = \mathit{trivial})$$

1. Bandpass filtering

$$\mathcal{ML}_9 = (\mathbb{X} = \mathbb{R}^{4,224,450}, \mathbb{Y} = \mathbb{R}^{4,224,450}, F(\mathbf{x};\boldsymbol{\theta}) = \mathcal{F}^{-1}(X(w)M(w)), P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = (y - F(x;\theta))^2))$$

where $X(w) = \mathcal{F}(x(t))$ and $M(w) = \begin{cases} 1 & \text{if } 0.5 \le w \le 40 \\ 0 & \text{else} \end{cases}$

1. ECG cleaning and processing

$$\mathcal{ML}_{10} = (\mathbb{X} = \mathbb{R}^{4,224,450}, \mathbb{Y} = \mathbb{R}^{10,724}, F(\mathbf{x};\boldsymbol{\theta}) = \mathit{R.\,Peak.\,Detection}(x(t)), P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = (y - F(x;\theta))^2))$$

1. Differencing (to find R-R intervals)

$$\mathcal{ML}_{11} = (\mathbb{X} = \mathbb{R}^{10,724}, \mathbb{Y} = \mathbb{R}^{10,723}, F_i(\mathbf{x};\boldsymbol{\theta}) = x(i) - x(i-1) \text{ for } i = 2,3,4,\ldots,10,724, P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = \mathit{trivial}$$

1. Moving average

$$\mathcal{ML}_{12} = (\mathbb{X} = \mathbb{R}^{10,723}, \mathbb{Y} = \mathbb{R}^{10,674}, F_i(\mathbf{x};\boldsymbol{\theta}) = \frac{x_i + x_{i+1} + \ldots + x_{i+49}}{50} \text{ for } i = 1,2,\ldots,10,673, P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = (y - F(x;\theta))^2))$$

1. Identifying large jumps

$\mathcal{ML}_{13} = (\mathbb{X} = \mathbb{R}^{10,674}, \mathbb{Y} = \mathbb{R}, F_i(\mathbf{x};\boldsymbol{\theta}) = \sum_{n=1}^{56,321} J_n(x), P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = trivial$ where
$J_n(x) = \begin{cases} 1 & \text{if } x(15n) - x(15(n-1)) > 0.2 \\ 0 & \text{else} \end{cases}$

1. Identifying regions of large deviation from the mean

$$\mathcal{ML}_{14} = (\mathbb{X} = \mathbb{R}^{10,674}, \mathbb{Y} = \mathbb{R}, F_i(\mathbf{x};\boldsymbol{\theta}) = \frac{|\{x|x>\mu_x+2\sigma_x\}\bigcup\{x|x<\mu_x-2\sigma_x\}|}{|x|}, P_\Theta(\boldsymbol{\theta}) = 1, L(\mathbf{y}, F) = trivial$$

1. Overall Morphism

$$\mathcal{ML} = \mathcal{ML}_1 \circ_0 \mathcal{ML}_2 \circ_0 \mathcal{ML}_3 \circ_0 \mathcal{ML}_4 \circ_0 \mathcal{ML}_5 \circ_0 \mathcal{ML}_6 \circ_0 \mathcal{ML}_7 \circ_0 \mathcal{ML}_8 \circ_0 \mathcal{ML}_9 \circ_0 \mathcal{ML}_{10} \circ_0 \mathcal{ML}_{11} \circ_0 \mathcal{ML}_{12} \circ_0 \mathcal{ML}_{13} \circ_0 \mathcal{ML}_{14}$$

We want to start with two simple models: multivariate linear regression, with `icu_days` as a target variable and logistic regression, with `death_inhosp` as a target variable.

For the `death_inhosp` target variable, we then want to explore decision tree based classification methods such as AdaBoost, as these methods are best at handling large class imbalances.

For all of our models, we want to train them twice: once without the waveform data, and once with it. By doing this, we hope to make the point that introducing waveform data into classification models improves accuracy.

Next Steps

We have a few specific areas that we want to look at for our next steps

1. Models

As stated above, we have a few ideas for models, and this will depend how we end up defining our target variable to fix our class imbalance, but we plan to start with a logistic regression model.

1. Feature Engineering

We want to explore more ways, in addition to big jumps and deviation from mean, of creating features from our time series data. We plan to look into the literature and brainstorm using ChatGPT to find additional ways to do this. One problem with the deviation from the mean is that the outliers have an impact on the mean, so we will find methods that work around this problem.