Import Libraries

In [1]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import csv
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_absolute_error, mean_squared_error, r2_score
from sklearn.preprocessing import MinMaxScaler
from sklearn.neighbors import KNeighborsRegressor
from sklearn.linear_model import LinearRegression
from sklearn.svm import SVR
from sklearn.ensemble import RandomForestRegressor
from sklearn.tree import DecisionTreeRegressor
from scipy.stats import pearsonr
from sklearn.ensemble import GradientBoostingRegressor
from sklearn.linear_model import SGDRegressor
from sklearn.metrics import mean_squared_error
import statsmodels.api as sm
from xgboost import XGBRegressor
from sklearn.model_selection import GridSearchCV
```

In [2]:

```
import sys
import os
sys.path.append(os.path.dirname(os.path.dirname(os.getcwd())))
if not os.path.exists("./data"):
    os.makedirs("./data")
if not os.path.exists("./data/model"):
    os.makedirs("./data/model")
if not os.path.exists("./data/preprocessing"):
    os.makedirs("./data/preprocessing")
if not os.path.exists("./data/dataset"):
    os.makedirs("./data/dataset")
```

Reusable Function

In [21]:

```
def boxplot_los_groupby(variable, los_range=(-1, 30), size=(8,4)):
    results = df[[variable, 'los']].groupby(variable).median().reset_index()

    categories = results[variable].values.tolist()

    hist_data = []
    for cat in categories:
        hist_data.append(df['los'].loc[df[variable]==cat].values)

    fig, ax = plt.subplots(figsize=size)
    ax.boxplot(hist_data, 0, '', vert=False)
    ax.set_xlim(los_range)
    ax.set_yticklabels(categories)
    ax.set_xlabel('Length of Stay (days)')
    ax.tick_params(left=False, right=False)
    ax.set_title('Comparison of {} categories'.format(variable))
    plt.tight_layout()
    plt.show()
```

Extract Patients Data from ICUstays

In [3]:

```
icu = pd.read_csv('./mimiciv/2.0/icu/icustays.csv.gz',compression='gzip')
adm = pd.read_csv('./mimiciv/2.0/hosp/admissions.csv.gz',compression='gzip')
patients = pd.read_csv('./mimiciv/2.0/hosp/patients.csv.gz',compression='gzip'
```

In [4]:

```
icu.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 73181 entries, 0 to 73180
Data columns (total 8 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   subject_id      73181 non-null  int64  
 1   hadm_id         73181 non-null  int64  
 2   stay_id         73181 non-null  int64  
 3   first_careunit  73181 non-null  object 
 4   last_careunit   73181 non-null  object 
 5   intime          73181 non-null  object 
 6   outtime         73181 non-null  object 
 7   los             73181 non-null  float64
dtypes: float64(1), int64(3), object(4)
memory usage: 4.5+ MB
```

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

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 431231 entries, 0 to 431230
Data columns (total 16 columns):
 #   Column               Non-Null Count   Dtype 
---  ------               --------------   ----- 
 0   subject_id           431231 non-null  int64 
 1   hadm_id              431231 non-null  int64 
 2   admittime            431231 non-null  object
 3   dischtime            431231 non-null  object
 4   deathtime            8598 non-null    object
 5   admission_type       431231 non-null  object
 6   admit_provider_id    431227 non-null  object
 7   admission_location   431231 non-null  object
 8   discharge_location   312076 non-null  object
 9   insurance            431231 non-null  object
 10  language             431231 non-null  object
 11  marital_status       421998 non-null  object
 12  race                 431231 non-null  object
 13  edregtime            299282 non-null  object
 14  edouttime            299282 non-null  object
 15  hospital_expire_flag 431231 non-null  int64 
dtypes: int64(3), object(13)
memory usage: 52.6+ MB
```

In [6]:
```
#drop unneccessary columns
drop_adm = adm.drop(columns=['admittime','dischtime','deathtime','admission_ty
                             'admit_provider_id','admission_location','dischar
                             'insurance','language','marital_status','race','e
```

In [7]:
```
drop_adm.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 431231 entries, 0 to 431230
Data columns (total 3 columns):
 #   Column               Non-Null Count   Dtype
---  ------               --------------   -----
 0   subject_id           431231 non-null  int64
 1   hadm_id              431231 non-null  int64
 2   hospital_expire_flag 431231 non-null  int64
dtypes: int64(3)
memory usage: 9.9 MB
```

In [8]:
```
#merge icu with filtered admission
df = icu.merge(drop_adm[['hadm_id','hospital_expire_flag']], on='hadm_id', how
```

In [9]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 73181 entries, 0 to 73180
Data columns (total 9 columns):
 #   Column               Non-Null Count  Dtype  
---  ------               --------------  -----  
 0   subject_id           73181 non-null  int64  
 1   hadm_id              73181 non-null  int64  
 2   stay_id              73181 non-null  int64  
 3   first_careunit       73181 non-null  object 
 4   last_careunit        73181 non-null  object 
 5   intime               73181 non-null  object 
 6   outtime              73181 non-null  object 
 7   los                  73181 non-null  float64
 8   hospital_expire_flag  73181 non-null  int64  
dtypes: float64(1), int64(4), object(4)
memory usage: 5.6+ MB
```

In [10]:
```
df.head()
```

Out[10]:

	subject_id	hadm_id	stay_id	first_careunit	last_careunit	intime	outtime	los
0	10000032	29079034	39553978	Medical Intensive Care Unit (MICU)	Medical Intensive Care Unit (MICU)	2180-07-23 14:00:00	2180-07-23 23:50:47	0.410266
1	10000980	26913865	39765666	Medical Intensive Care Unit (MICU)	Medical Intensive Care Unit (MICU)	2189-06-27 08:42:00	2189-06-27 20:38:27	0.497535
2	10001217	24597018	37067082	Surgical Intensive Care Unit (SICU)	Surgical Intensive Care Unit (SICU)	2157-11-20 19:18:02	2157-11-21 22:08:00	1.118032
3	10001217	27703517	34592300	Surgical Intensive Care Unit (SICU)	Surgical Intensive Care Unit (SICU)	2157-12-19 15:42:24	2157-12-20 14:27:41	0.948113
4	10001725	25563031	31205490	Medical/Surgical Intensive Care Unit (MICU/SICU)	Medical/Surgical Intensive Care Unit (MICU/SICU)	2110-04-11 15:52:22	2110-04-12 23:59:56	1.338588

In [11]:
```
#Filter the 'icu' DataFrame to include only patients with at least 5 hours of
filtered_icu = icu[icu['los'] > 5/24]
```

In [12]:
```
#Merge the 'patients' and filtered 'icu' DataFrames based on the 'subject_id'
filtered_pats = patients.merge(filtered_icu[['subject_id',
                                             'intime', 'los']],on='subject_id'
```

In [13]:
```
filtered_pats.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 72390 entries, 0 to 72389
Data columns (total 8 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   subject_id         72390 non-null  int64  
 1   gender             72390 non-null  object 
 2   anchor_age         72390 non-null  int64  
 3   anchor_year        72390 non-null  int64  
 4   anchor_year_group  72390 non-null  object 
 5   dod                27908 non-null  object 
 6   intime             72390 non-null  object 
 7   los                72390 non-null  float64
dtypes: float64(1), int64(3), object(4)
memory usage: 5.0+ MB
```

In [14]:
```
# Filter out anyone whose age is less than or equal to 17 at the time of ICU ac
filtered_pats = filtered_pats[filtered_pats['anchor_age'] > 17]
```

In [15]:
```
filtered_pats.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 72390 entries, 0 to 72389
Data columns (total 8 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   subject_id         72390 non-null  int64  
 1   gender             72390 non-null  object 
 2   anchor_age         72390 non-null  int64  
 3   anchor_year        72390 non-null  int64  
 4   anchor_year_group  72390 non-null  object 
 5   dod                27908 non-null  object 
 6   intime             72390 non-null  object 
 7   los                72390 non-null  float64
dtypes: float64(1), int64(3), object(4)
memory usage: 5.0+ MB
```

In [16]:
```
df = df.merge(filtered_pats[['subject_id','gender','anchor_age']], on='subject_
```

In [18]:

```
df.info()
```

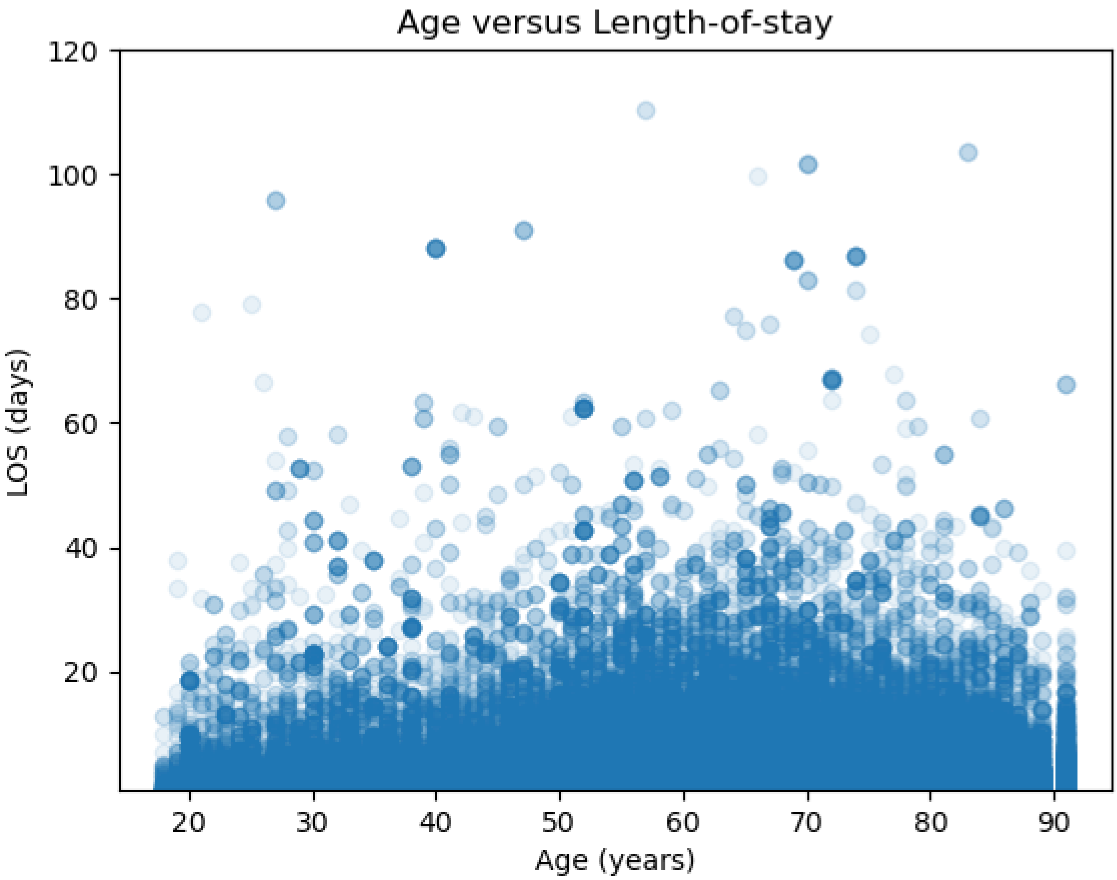
```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 170453 entries, 0 to 170452
Data columns (total 11 columns):
 #   Column                Non-Null Count   Dtype  
---  ------                --------------   -----  
 0   subject_id            170453 non-null  int64  
 1   hadm_id               170453 non-null  int64  
 2   stay_id               170453 non-null  int64  
 3   first_careunit        170453 non-null  object 
 4   last_careunit         170453 non-null  object 
 5   intime                170453 non-null  object 
 6   outtime               170453 non-null  object 
 7   los                   170453 non-null  float64
 8   hospital_expire_flag  170453 non-null  int64  
 9   gender                170453 non-null  object 
 10  anchor_age            170453 non-null  int64  
dtypes: float64(1), int64(5), object(5)
memory usage: 15.6+ MB
```

In [17]:

```
#save icu cohort csv file
df.to_csv('./data/preprocessing/icu_cohort.csv.gz', index=False)
```

```
In [19]: #plot for patients age vs los
         plt.scatter(df['anchor_age'], df['los'], alpha=0.1)
         plt.ylabel('LOS (days)')
         plt.xlabel('Age (years)')
         plt.title('Age versus Length-of-stay')
         plt.ylim(1, 120)
```

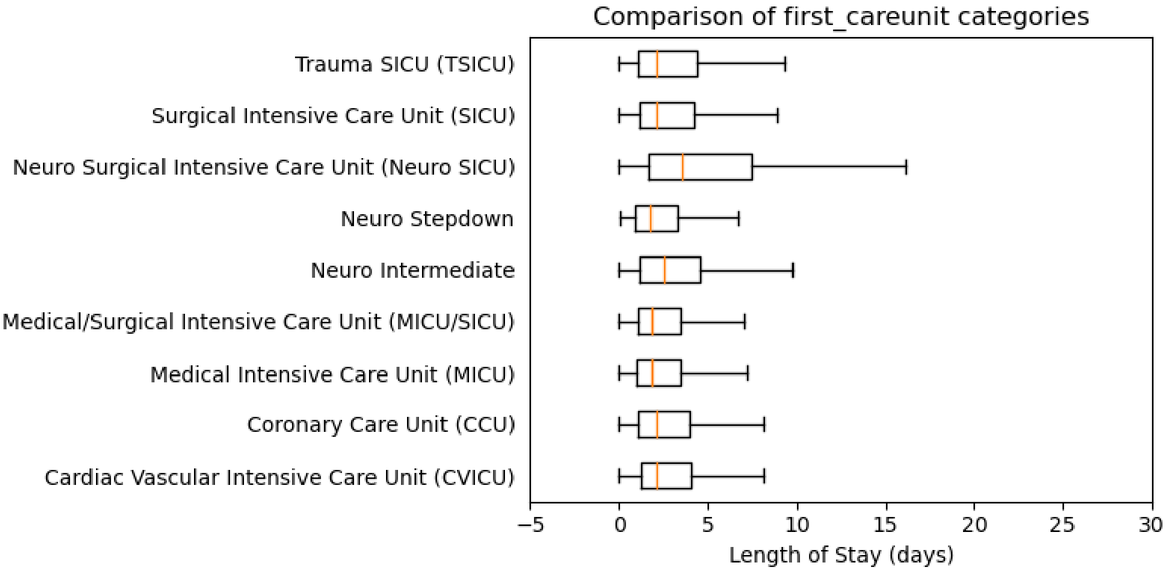
```
Out[19]: (1.0, 120.0)
```



Scatter Plot Observation

- The average LOS for patients in their 60s is around 10 days, but there are some patients in this age group who have an LOS of less than 5 days or more than 20 days.
- The median LOS is around 10 days.
- There are a few outliers (Higher than average LOS) in the data.

```
In [22]: boxplot_los_groupby('first_careunit',los_range=(-5,30))
```



Labs Stay

extracting the itemids for all the labevents that occur within the time bounds for our cohort

```
In [3]: icu_cohort = pd.read_csv('./data/preprocessing/icu_cohort.csv.gz',compression=
```

```
In [4]: labitems = pd.read_csv('./mimiciv/2.0/hosp/d_labitems.csv.gz',compression='gzi
```

```
In [27]: labitems.head()
```

Out[27]:

	itemid	label	fluid	category
0	50801	Alveolar-arterial Gradient	Blood	Blood Gas
1	50802	Base Excess	Blood	Blood Gas
2	50803	Calculated Bicarbonate, Whole Blood	Blood	Blood Gas
3	50804	Calculated Total CO2	Blood	Blood Gas
4	50805	Carboxyhemoglobin	Blood	Blood Gas

```
In [28]: category_counts = labitems.groupby('category')['itemid'].count()

         print(category_counts)
```

```
category
Blood Gas       64
Chemistry      777
Hematology     781
Name: itemid, dtype: int64
```

In [29]:

```
file_path = './mimiciv/2.0/hosp/labevents.csv.gz'

chunk_size = 100000
chunks = []

for chunk in pd.read_csv(file_path, chunksize=chunk_size):
    merge_chunk = chunk.merge(icu_cohort[['stay_id', 'hadm_id', 'intime', 'los

    # Filter only numerical data
    merge_chunk = merge_chunk[merge_chunk['valuenum'].notnull()]

    # Convert the 'charttime' and 'intime' columns to pandas DateTime objects
    merge_chunk['charttime'] = pd.to_datetime(merge_chunk['charttime'])
    merge_chunk['intime'] = pd.to_datetime(merge_chunk['intime'])

    # Calculate the time difference between 'charttime' and 'intime' in days
    # we want to extract measurements between admission and the end of the pat
    merge_chunk['time_diff_days'] = (merge_chunk['charttime'] - merge_chunk['i

    # Filter the rows in 'merge_chunk'
    merge_chunk = merge_chunk[(merge_chunk['time_diff_days'] >= -1) & (merge_c

    chunks.append(merge_chunk)

labsstay = pd.concat(chunks, ignore_index=True)
```

```
C:\Users\User\AppData\Local\Temp\ipykernel_7652\1204666657.py:6: DtypeWarni
ng: Columns (5) have mixed types. Specify dtype option on import or set low
_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_7652\1204666657.py:6: DtypeWarni
ng: Columns (5) have mixed types. Specify dtype option on import or set low
_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_7652\1204666657.py:6: DtypeWarni
ng: Columns (5) have mixed types. Specify dtype option on import or set low
_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_7652\1204666657.py:6: DtypeWarni
ng: Columns (5) have mixed types. Specify dtype option on import or set low
_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_7652\1204666657.py:6: DtypeWarni
ng: Columns (5) have mixed types. Specify dtype option on import or set low
_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
```

In [30]:

```
labsstay.shape
```

Out[30]:

```
(38372040, 20)
```

Common Labs

Average Observation Per Stay

getting the average number of times each itemid appears in an icustay

In [31]:

```
labsstay_counts = labsstay['stay_id'].value_counts().reset_index()
labsstay_counts.columns = ['stay_id', 'labsstay_count']
labsstay_counts
```

Out[31]:

	stay_id	labsstay_count
0	36479755	63765
1	36671290	51252
2	31469106	48580
3	38199253	46222
4	34814635	46143
...	...	...
72093	36400520	1
72094	38046396	1
72095	32169536	1
72096	38886407	1
72097	39302677	1

72098 rows × 2 columns

In [32]:

```
labsstay_counts.shape
```

Out[32]:

```
(72098, 2)
```

In [33]:
```
ICU_counts = icu_cohort['stay_id'].value_counts().reset_index()
ICU_counts.columns = ['stay_id', 'ICU_count']
ICU_counts
```

Out[33]:

	stay_id	ICU_count
0	31073147	37
1	34456715	37
2	32346798	37
3	35383104	37
4	34115393	37
...	...	...
72991	39824196	1
72992	33302469	1
72993	32622345	1
72994	33199830	1
72995	36195440	1

72996 rows × 2 columns

In [34]:
```
ICU_counts.shape
```

Out[34]:
```
(72996, 2)
```

In [35]:
```
#keep stayid where labsstay count > icu count
merged_counts = ICU_counts.merge(labsstay_counts, on='stay_id', how='outer').f
filtered_stayid = merged_counts[(merged_counts['labsstay_count']) > merged_cou
filtered_stayid
```

Out[35]:

	stay_id	ICU_count	labsstay_count
0	31073147	37	2701.0
1	34456715	37	370.0
2	32346798	37	111.0
3	35383104	37	2183.0
4	34115393	37	3663.0
...	...	...	...
72991	39824196	1	487.0
72992	33302469	1	621.0
72993	32622345	1	55.0
72994	33199830	1	24.0
72995	36195440	1	92.0

72042 rows × 3 columns

In [36]:
```
filtered_stayid.shape
```

Out[36]:
```
(72042, 3)
```

In [37]:
```
#Filter labsstays to only have these stay_ids
filtered_stayid_list = filtered_stayid['stay_id'].tolist()
```

In [38]:
```
chunk_size = 100000
num_chunks = len(labsstay) // chunk_size + 1

chunks = []

# Process the DataFrame in chunks
for i in range(num_chunks):
    start_idx = i * chunk_size
    end_idx = (i + 1) * chunk_size

    # Select the current chunk based on start and end indices
    chunk = labsstay.iloc[start_idx:end_idx]

    # Filter the chunk using 'filtered_stayid_list'
    filtered_chunk = chunk[chunk['stay_id'].isin(filtered_stayid_list)]

    # Append the processed chunk to the list
    chunks.append(filtered_chunk)

# After processing all chunks, concatenate them into a final DataFrame
filtered_labsstay = pd.concat(chunks, ignore_index=True)
```

In [39]:
```
filtered_labsstay.shape
```

Out[39]:
```
(38371885, 20)
```

In [40]:
```
# Group by 'itemid' and 'stay_id' and calculate the observation count for each
obs_per_stay = filtered_labsstay.groupby(['itemid', 'stay_id']).size().reset_i
obs_per_stay.head()
```

Out[40]:

	itemid	stay_id	count
0	50801	30004627	1
1	50801	30005362	1
2	50801	30007565	2
3	50801	30010930	1
4	50801	30011071	7

In [41]:

```python
min_count = obs_per_stay['count'].min()
max_count = obs_per_stay['count'].max()
avg_count = obs_per_stay['count'].mean()

print(f"Minimum Count: {min_count}")
print(f"Maximum Count: {max_count}")
print(f"Average Count: {avg_count}")
```

```
Minimum Count: 1
Maximum Count: 2340
Average Count: 11.43886010517153
```

In [42]:

```python
# Group by 'itemid' and calculate the average count for each 'itemid'
avg_obs_per_itemid = obs_per_stay.groupby('itemid')['count'].mean().reset_inde
avg_obs_per_itemid.head()
```

Out[42]:

	itemid	avg_obs
0	50801	3.885140
1	50802	20.290459
2	50803	3.004698
3	50804	20.291189
4	50805	2.327273

In [43]:

```python
min_count = avg_obs_per_itemid['avg_obs'].min()
max_count = avg_obs_per_itemid['avg_obs'].max()
avg_count = avg_obs_per_itemid['avg_obs'].mean()

print(f"Minimum Count: {min_count}")
print(f"Maximum Count: {max_count}")
print(f"Average Count: {avg_count}")
```

```
Minimum Count: 1.0
Maximum Count: 21.194129476701896
Average Count: 4.071320464236379
```

In [44]:

```python
# Filter the results based on the condition 'avg(count) > 10'
# we want the features to have more than 10 values entered for the average pat
avg_obs_per_stay = avg_obs_per_itemid[avg_obs_per_itemid['avg_obs'] > 10]
avg_obs_per_stay.head()
```

Out[44]:

	itemid	avg_obs
1	50802	20.290459
3	50804	20.291189
6	50808	15.252943
7	50809	12.308465
10	50813	12.994940

In [45]:
```
avg_obs_per_stay.shape
```

Out[45]:
```
(44, 2)
```

In [46]:
```
# Merge 'labsstay' with 'd_labitems' on 'itemid'
#only keep the 44 itemid
chunk_size = 100000
num_chunks = len(filtered_labsstay) // chunk_size + 1

chunks = []

# Process the DataFrame in chunks
for i in range(num_chunks):
    start_idx = i * chunk_size
    end_idx = (i + 1) * chunk_size

    # Select the current chunk based on start and end indices
    chunk = filtered_labsstay.iloc[start_idx:end_idx]

    # Merge the current chunk with 'labitems' on 'itemid'
    merged_chunk = chunk.merge(labitems[['itemid', 'label']], on='itemid', how
    # Merge the result with 'avg_obs_per_stay' on 'itemid'
    merged_chunk = merged_chunk.merge(avg_obs_per_stay[['avg_obs','itemid']], 

    # Append the merged chunk to the list
    chunks.append(merged_chunk)

# After processing all chunks, concatenate them into a final DataFrame
df = pd.concat(chunks, ignore_index=True)
```

In [47]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 32503253 entries, 0 to 32503252
Data columns (total 22 columns):
 #   Column             Dtype
---  ------             -----
 0   labevent_id        int64
 1   subject_id         int64
 2   hadm_id            float64
 3   specimen_id        int64
 4   itemid             int64
 5   order_provider_id  object
 6   charttime          datetime64[ns]
 7   storetime          object
 8   value              object
 9   valuenum           float64
 10  valueuom           object
 11  ref_range_lower    float64
 12  ref_range_upper    float64
 13  flag               object
 14  priority           object
 15  comments           object
 16  stay_id            int64
 17  intime             datetime64[ns]
 18  los                float64
 19  time_diff_days     float64
 20  label              object
 21  avg_obs            float64
dtypes: datetime64[ns](2), float64(7), int64(5), object(8)
memory usage: 5.3+ GB
```

In [48]:
```
# Group by 'label' and 'avg_obs', and then calculate the count of distinct 'st
commonlabs = df.groupby(['label', 'avg_obs']).agg(count=('stay_id', 'nunique')
commonlabs.shape
```

Out[48]:
```
(44, 3)
```

In [49]:

```
commonlabs
```

Out[49]:

	label	avg_obs	count
0	Amikacin	17.421053	76
1	Anion Gap	15.790314	71426
2	Base Excess	20.290459	44891
3	Bicarbonate	15.844876	71446
4	Calcium, Total	14.961132	68977
5	Calculated Total CO2	20.291189	44885
6	Chloride	16.497069	71475
7	Creatinine	15.829617	71480
8	Cyclosporin	14.471111	225
9	Free Calcium	15.252943	33213
10	Glucose	12.308465	24382
11	Glucose	15.615444	71381
12	H	19.829110	24741
13	Hematocrit	15.779609	71373
14	Hemoglobin	14.255044	71266
15	Heparin	18.980545	257
16	I	19.828981	24740
17	INR(PT)	10.830669	63798
18	L	19.829022	24740
19	Lactate	12.994940	46636
20	MCH	13.976786	71251
21	MCHC	13.980155	71252
22	MCV	13.977545	71254
23	Magnesium	15.514601	70338
24	Oxygen Saturation	13.402124	23734
25	PT	10.832409	63798
26	PTT	11.948269	63405
27	Phenobarbital	10.683706	313
28	Phosphate	15.047005	68992
29	Platelet Count	14.266822	71276
30	Potassium	16.777214	71481
31	Potassium, Whole Blood	11.162885	26092
32	RDW	13.971461	71236
33	RDW-SD	15.542799	30702
34	Rapamycin	11.573427	143
35	Red Blood Cells	13.977349	71256

	label	avg_obs	count
36	Sodium	16.693580	71477
37	Temperature	10.859185	19863
38	Urea Nitrogen	15.791723	71472
39	White Blood Cells	14.000000	71266
40	pCO2	20.290555	44883
41	pH	21.194129	46742
42	pO2	20.298839	44887
43	tacroFK	19.620936	1261

In [50]:
```
commonlabs.to_csv('./data/preprocessing/commonlabs.csv.gz', index=False)
```

In [51]:
```
del commonlabs
```

Labs Patients

extract the most common lab tests and the corresponding counts of how many patients have values for those labs

In [6]:
```
commonlabs = pd.read_csv('./data/preprocessing/commonlabs.csv.gz',compression=
```

In [7]:

```
file_path = './mimiciv/2.0/hosp/labevents.csv.gz'

chunk_size = 100000
chunks = []

for chunk in pd.read_csv(file_path, chunksize=chunk_size):

    merged_chunk = pd.merge(chunk,labitems, on = 'itemid', how='inner')
    #merged_chunk = pd.merge(merged_chunk, commonlabs,  on='label', how='inner
    merged_chunk = pd.merge(merged_chunk, icu_cohort, on=['hadm_id','subject_i

    chunks.append(merged_chunk)

df = pd.concat(chunks, ignore_index=True)
```

```
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_15052\2847547336.py:6: DtypeWarn
ing: Columns (5) have mixed types. Specify dtype option on import or set lo
w_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_15052\2847547336.py:6: DtypeWarn
ing: Columns (5) have mixed types. Specify dtype option on import or set lo
w_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_15052\2847547336.py:6: DtypeWarn
ing: Columns (5) have mixed types. Specify dtype option on import or set lo
w_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_15052\2847547336.py:6: DtypeWarn
ing: Columns (5) have mixed types. Specify dtype option on import or set lo
w_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
C:\Users\User\AppData\Local\Temp\ipykernel_15052\2847547336.py:6: DtypeWarn
ing: Columns (5) have mixed types. Specify dtype option on import or set lo
w_memory=False.
  for chunk in pd.read_csv(file_path, chunksize=chunk_size):
```

In [8]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 102039133 entries, 0 to 102039132
Data columns (total 28 columns):
 #   Column               Dtype  
---  ------               -----  
 0   labevent_id          int64  
 1   subject_id           int64  
 2   hadm_id              float64
 3   specimen_id          int64  
 4   itemid               int64  
 5   order_provider_id    object 
 6   charttime            object 
 7   storetime            object 
 8   value                object 
 9   valuenum             float64
 10  valueuom             object 
 11  ref_range_lower      float64
 12  ref_range_upper      float64
 13  flag                 object 
 14  priority             object 
 15  comments             object 
 16  label                object 
 17  fluid                object 
 18  category             object 
 19  stay_id              int64  
 20  first_careunit       object 
 21  last_careunit        object 
 22  intime               object 
 23  outtime              object 
 24  los                  float64
 25  hospital_expire_flag  int64  
 26  gender               object 
 27  anchor_age           int64  
dtypes: float64(5), int64(7), object(16)
memory usage: 21.3+ GB
```

In [9]:
```
df.head()
```

Out[9]:

	labevent_id	subject_id	hadm_id	specimen_id	itemid	order_provider_id	charttime	storetir
0	406	10000032	29079034.0	43001398	51237	NaN	2180-07-24 06:35:00	2180-(08:10:
1	460	10000032	29079034.0	87246904	51237	NaN	2180-07-25 04:45:00	2180-(07:07:
2	407	10000032	29079034.0	43001398	51274	NaN	2180-07-24 06:35:00	2180-(08:10:
3	461	10000032	29079034.0	87246904	51274	NaN	2180-07-25 04:45:00	2180-(07:07:
4	409	10000032	29079034.0	74547069	50861	NaN	2180-07-24 06:35:00	2180-(08:11:

5 rows × 28 columns

In [10]:
```
df.shape
```

Out[10]:
```
(102039133, 28)
```

In [11]:
```
#keep only the 44 common labs
labels = commonlabs['label'].tolist()
chunk_size = 100000
num_chunks = len(df) // chunk_size + 1

chunks = []

# Process the DataFrame in chunks
for i in range(num_chunks):
    start_idx = i * chunk_size
    end_idx = (i + 1) * chunk_size

    chunk = df.iloc[start_idx:end_idx]

    filtered_chunk = chunk.merge(pd.DataFrame({'label': labels}), on='label', 

    chunks.append(filtered_chunk)

filtered_df = pd.concat(chunks, ignore_index=True)
```

In [12]:
```
del df
```

In [13]:
```
filtered_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 83646249 entries, 0 to 83646248
Data columns (total 28 columns):
 #   Column               Dtype  
---  ------               -----  
 0   labevent_id          int64  
 1   subject_id           int64  
 2   hadm_id              float64
 3   specimen_id          int64  
 4   itemid               int64  
 5   order_provider_id    object 
 6   charttime            object 
 7   storetime            object 
 8   value                object 
 9   valuenum             float64
 10  valueuom             object 
 11  ref_range_lower      float64
 12  ref_range_upper      float64
 13  flag                 object 
 14  priority             object 
 15  comments             object 
 16  label                object 
 17  fluid                object 
 18  category             object 
 19  stay_id              int64  
 20  first_careunit       object 
 21  last_careunit        object 
 22  intime               object 
 23  outtime              object 
 24  los                  float64
 25  hospital_expire_flag  int64  
 26  gender               object 
 27  anchor_age           int64  
dtypes: float64(5), int64(7), object(16)
memory usage: 17.4+ GB
```

In [14]:
```
filtered_df.shape
```

Out[14]:
```
(83646249, 28)
```

In [15]:
```
import math
```

In [16]:
```
filtered_df['charttime'] = pd.to_datetime(filtered_df['charttime'])
```

In [17]:
```
filtered_df['intime'] = pd.to_datetime(filtered_df['intime'])
```

In [18]:
```
# we want to extract measurements between admission and the end of the patients
filtered_df['labresultoffset_min'] = ((filtered_df['charttime'] - filtered_df[
```

In [19]:

```
# we want to extract measurements between admission and the end of the patients
filtered_df['labresultoffset_sec'] = (filtered_df['charttime'] - filtered_df['
```

In [20]:

```
filtered_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 83646249 entries, 0 to 83646248
Data columns (total 30 columns):
 #   Column               Dtype         
---  ------               -----         
 0   labevent_id          int64         
 1   subject_id           int64         
 2   hadm_id              float64       
 3   specimen_id          int64         
 4   itemid               int64         
 5   order_provider_id    object        
 6   charttime            datetime64[ns]
 7   storetime            object        
 8   value                object        
 9   valuenum             float64       
 10  valueuom             object        
 11  ref_range_lower      float64       
 12  ref_range_upper      float64       
 13  flag                 object        
 14  priority             object        
 15  comments             object        
 16  label                object        
 17  fluid                object        
 18  category             object        
 19  stay_id              int64         
 20  first_careunit       object        
 21  last_careunit        object        
 22  intime               datetime64[ns]
 23  outtime              object        
 24  los                  float64       
 25  hospital_expire_flag int64         
 26  gender               object        
 27  anchor_age           int64         
 28  labresultoffset_min  int64         
 29  labresultoffset_sec  float64       
dtypes: datetime64[ns](2), float64(6), int64(8), object(14)
memory usage: 18.7+ GB
```

In [21]:

```
# Keep only the rows where 'labresultoffset_sec' is between -1 and 'los' and n
chunk_size = 100000
num_chunks = len(filtered_df) // chunk_size + 1

chunks = []

for i in range(num_chunks):
    start_idx = i * chunk_size
    end_idx = (i + 1) * chunk_size

    chunk = filtered_df.iloc[start_idx:end_idx]
    filtered_chunk = chunk[(chunk['labresultoffset_sec'] >= -1) & (chunk['labr

    chunks.append(filtered_chunk)

lab = pd.concat(chunks, ignore_index=True)
```

```
In [22]: lab.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 34200597 entries, 0 to 34200596
Data columns (total 30 columns):
 #   Column                Dtype         
---  ------                -----         
 0   labevent_id           int64         
 1   subject_id            int64         
 2   hadm_id               float64       
 3   specimen_id           int64         
 4   itemid                int64         
 5   order_provider_id     object        
 6   charttime             datetime64[ns]
 7   storetime             object        
 8   value                 object        
 9   valuenum              float64       
 10  valueuom              object        
 11  ref_range_lower       float64       
 12  ref_range_upper       float64       
 13  flag                  object        
 14  priority              object        
 15  comments              object        
 16  label                 object        
 17  fluid                 object        
 18  category              object        
 19  stay_id               int64         
 20  first_careunit        object        
 21  last_careunit         object        
 22  intime                datetime64[ns]
 23  outtime               object        
 24  los                   float64       
 25  hospital_expire_flag  int64         
 26  gender                object        
 27  anchor_age            int64         
 28  labresultoffset_min   int64         
 29  labresultoffset_sec   float64       
dtypes: datetime64[ns](2), float64(6), int64(8), object(14)
memory usage: 7.6+ GB
```

```
In [26]: lab.to_csv('./data/preprocessing/lab.csv.gz', index=False)
```

Chart Stay

extract the most common chartevents and the corresponding counts of how many patients have values for those chartevents

In [5]:

```
#extracting the itemids for all the chartevents that occur within the time boun
chartevent_path = r"./mimiciv/2.0/icu/chartevents.csv.gz"
icucohort_path = r"./data/preprocessing/icu_cohort.csv.gz"

chunk_size = 100000

icucohort_df = pd.read_csv(icucohort_path)
chartevent_iter = pd.read_csv(chartevent_path, chunksize=chunk_size)

merged_chunks = []

# Iterate over the chunks and merge them with 'icucohort_df'
for chartevent_chunk in chartevent_iter:
    # Filter only numerical data from chartevent_chunk
    chartevent_chunk = chartevent_chunk[chartevent_chunk['valuenum'].notnull()
    chartevent_chunk.drop(columns=['caregiver_id','warning','storetime'], inpla

    # Merge chartevent_chunk with icucohort_df on 'stay_id'
    merged_chunk = pd.merge(chartevent_chunk, icucohort_df[['stay_id', 'intime
    merged_chunks.append(merged_chunk)

    #convert intime and chartime to datetime
    merged_chunk['charttime'] = pd.to_datetime(merged_chunk['charttime'])
    merged_chunk['intime'] = pd.to_datetime(merged_chunk['intime'])

    #extract measurements between admission and the end of the patients' stay
    merged_chunk['time_difference_days'] = (merged_chunk['charttime'] - merged_

    # Filter the data where the time difference is between -1 and 'los'
    merged_chunk = merged_chunk[(merged_chunk['time_difference_days'] >= -1) &

    merged_chunk.drop(columns=['time_difference_days'], inplace=True)

# Concatenate the merged chunks into a single DataFrame
chartstay = pd.concat(merged_chunks)

# Save the merged DataFrame to a CSV file
chartstay.to_csv("./data/preprocessing/chartstay.csv.gz", index=False)
```

```
s/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://p
andas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-vi
ew-versus-a-copy)
  merged_chunk.drop(columns=['time_difference_days'], inplace=True)
C:\Users\User\AppData\Local\Temp\ipykernel_18476\163717513.py:32: SettingWi
thCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-doc
s/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://p
andas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-vi
ew-versus-a-copy)
  merged_chunk.drop(columns=['time_difference_days'], inplace=True)
C:\Users\User\AppData\Local\Temp\ipykernel_18476\163717513.py:32: SettingWi
thCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-doc
s/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://p
andas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-vi
```

In [6]:

```
chartstay.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 295056465 entries, 0 to 21355
Data columns (total 11 columns):
 #   Column                Dtype         
---  ------                -----         
 0   subject_id            int64         
 1   hadm_id               int64         
 2   stay_id               int64         
 3   charttime             datetime64[ns]
 4   itemid                int64         
 5   value                 object        
 6   valuenum              float64       
 7   valueuom              object        
 8   intime                datetime64[ns]
 9   los                   float64       
 10  time_difference_days  float64       
dtypes: datetime64[ns](2), float64(3), int64(4), object(2)
memory usage: 26.4+ GB
```

In [7]:

```
chartstay.shape
```

Out[7]:

```
(295056465, 11)
```

In [11]:

```
#getting the average number of times each itemid appears in an icustay
columns_needed = ['itemid', 'stay_id']

chunksize = 100000
data_chunks = pd.read_csv("./data/preprocessing/chartstay.csv.gz", usecols=col

obs_per_stay = pd.DataFrame()

for chunk in data_chunks:
    # calculate counts per stay_id for each itemid
    obs_per_stay_chunk = chunk.groupby(['itemid', 'stay_id']).size().reset_ind

    # Concatenate the results of each chunk to the main DataFrame
    obs_per_stay = pd.concat([obs_per_stay, obs_per_stay_chunk])

# Calculate the average number of observations per stay for each itemid
avg_obs_per_stay = obs_per_stay.groupby('itemid')['count'].mean().reset_index(

avg_obs_per_stay.describe()
```

Out[11]:

```
              itemid     avg_obs
count     939.000000  939.000000
mean   226524.889244   48.714249
std      2366.602913  104.407604
min    220045.000000    1.000000
25%    224900.500000    5.082748
50%    226998.000000   14.450213
75%    228233.500000   43.906732
max    229882.000000  976.492958
```

In [12]:
```
avg_obs_per_stay
```

Out[12]:

	itemid	avg_obs
0	220045	208.922726
1	220046	20.095912
2	220047	20.104746
3	220050	172.164118
4	220051	172.098523
...	...	...
934	229865	2.037221
935	229872	9.250000
936	229880	39.590476
937	229881	65.483871
938	229882	28.722222

939 rows × 2 columns

In [13]:
```
avg_obs_per_stay.shape
```

Out[13]:
```
(939, 2)
```

In [14]:
```
# Filter the results to keep only those with an average count greater than 49
avg_obs_per_stay = avg_obs_per_stay[avg_obs_per_stay['avg_obs'] > 49]
```

In [15]:
```
avg_obs_per_stay.shape
```

Out[15]:
```
(199, 2)
```

Common Charts

extract the most common chartevents and the corresponding counts of how many patients have values for those chartevents

In [7]:
```
d_items = pd.read_csv('./mimiciv/2.0/icu/d_items.csv.gz',compression='gzip')
```

In [8]:
```
d_items.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4014 entries, 0 to 4013
Data columns (total 9 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   itemid           4014 non-null   int64  
 1   label            4014 non-null   object 
 2   abbreviation     4014 non-null   object 
 3   linksto          4014 non-null   object 
 4   category         4014 non-null   object 
 5   unitname         1592 non-null   object 
 6   param_type       4014 non-null   object 
 7   lownormalvalue   19 non-null     float64
 8   highnormalvalue  22 non-null     float64
dtypes: float64(2), int64(1), object(6)
memory usage: 282.4+ KB
```

In [9]:
```
d_items.head()
```

Out[9]:

	itemid	label	abbreviation	linksto	category	unitname	param_type	lownormalval
0	220001	Problem List	Problem List	chartevents	General	NaN	Text	N
1	220003	ICU Admission date	ICU Admission date	datetimeevents	ADT	NaN	Date and time	N
2	220045	Heart Rate	HR	chartevents	Routine Vital Signs	bpm	Numeric	N
3	220046	Heart rate Alarm - High	HR Alarm - High	chartevents	Alarms	bpm	Numeric	N
4	220047	Heart Rate Alarm - Low	HR Alarm - Low	chartevents	Alarms	bpm	Numeric	N

In [16]:

```
columns_needed = ['itemid', 'stay_id']

chunksize = 100000
data_chunks = pd.read_csv("./data/preprocessing/chartstay.csv.gz", usecols=col
                          chunksize=chunksize)

result = pd.DataFrame()

for chunk in data_chunks:
    merged_data = chunk.merge(d_items, on='itemid', how='inner')
    merged_data = merged_data.merge(avg_obs_per_stay, on='itemid', how='inner'

    result = pd.concat([result, merged_data])
```

In [17]:

```
result.to_csv("./data/preprocessing/merge_ditems_chart_avgobs.csv.gz", index=F
```

In [7]:

```
result = pd.read_csv('./data/preprocessing/merge_ditems_chart_avgobs.csv.gz')
```

In [8]:

```
grouped_result = result.groupby(['label', 'avg_obs'])['stay_id'].nunique().res
```

In [9]:

```
# Calculate the threshold for the minimum number of stay_ids required
threshold = len(icu_cohort['stay_id'].unique()) * 0.25
threshold
```

Out[9]:

```
18249.0
```

In [10]:

```
# Filter the results to keep only rows where count is greater than the thresho
filtered_result = grouped_result[grouped_result['count'] > threshold]
```

In [11]:

```
# Sort the filtered results by count in descending order
ld_commonchart = filtered_result.sort_values(by='count', ascending=False)
```

In [12]:
```
ld_commonchart
```

Out[12]:

	label	avg_obs	count
75	Heart Rate	208.922726	72978
164	Respiratory Rate	207.225807	72907
108	O2 saturation pulseoxymetry	204.530713	72902
62	GCS - Eye Opening	49.738155	72572
64	GCS - Verbal Response	49.641869	72561
63	GCS - Motor Response	49.530978	72551
106	Non Invasive Blood Pressure mean	139.544098	72067
107	Non Invasive Blood Pressure systolic	139.534886	72061
105	Non Invasive Blood Pressure diastolic	139.505182	72058
186	Temperature Fahrenheit	50.333491	71800
92	Inspired O2 Fraction	54.795313	36455
7	Activity / Mobility (JH-HLM)	85.090176	31219
16	Arterial Blood Pressure mean	171.522424	27785
15	Arterial Blood Pressure diastolic	172.098523	27574
17	Arterial Blood Pressure systolic	172.164118	27566
109	Orientation	166.041201	23261

In [13]:
```
ld_commonchart.shape
```

Out[13]:
```
(16, 3)
```

In [14]:
```
ld_commonchart.to_csv("./data/preprocessing/ld_commonchart.csv.gz", index=Fals
```

Chartevents Processed

Keep features from the most common chart features

In [8]:
```
ld_commonchart= pd.read_csv('./data/preprocessing/ld_commonchart.csv.gz')
```

In [11]:

```
def calculate_chartoffset(charttime, intime):
    return (charttime - intime).total_seconds() // 60

columns_needed = ['stay_id', 'charttime', 'itemid', 'valuenum']

chunksize = 10000
data_chunks = pd.read_csv("./mimiciv/2.0/icu/chartevents.csv.gz", usecols=colu

ld = pd.DataFrame()

for chunk in data_chunks:

    # Join chunk with d_items on itemid
    merged_data = chunk.merge(d_items, on='itemid', how='inner')

    # Join merged_data with ld_commonchart on label
    merged_data = merged_data.merge(ld_commonchart, on='label', how='inner')

    # Join merged_data with ld_labels on stay_id
    merged_data = merged_data.merge(icu_cohort[['stay_id', 'intime','los']], o

    # Convert 'charttime' & 'intime' column to datetime type
    merged_data['charttime'] = pd.to_datetime(merged_data['charttime'])
    merged_data['intime'] = pd.to_datetime(merged_data['intime'])

    # Calculate chartoffset using the calculate_chartoffset function
    merged_data['chartoffset'] = merged_data.apply(lambda row: calculate_chart

    # Filter data based on the time interval and non-null valuenum
    filtered_data = merged_data[(merged_data['chartoffset'] >= -60) & (merged_
                                & merged_data['valuenum'].notnull()]

    # Concatenate the processed chunk to the ld DataFrame
    ld = pd.concat([ld, filtered_data])
```

In [13]:

```
ld.to_csv("./data/preprocessing/ld.csv.gz", index=False)
#ld = pd.read_csv('./data/preprocessing/ld.csv.gz')
```

In [15]:
```
ld.head()
```

Out[15]:

	stay_id	charttime	itemid	valuenum	label	abbreviation	linksto	category	unitnam
0	39553978	2180-07-23 21:01:00	220179	82.0	Non Invasive Blood Pressure systolic	NBPs	chartevents	Routine Vital Signs	mmH
1	39553978	2180-07-23 22:00:00	220179	85.0	Non Invasive Blood Pressure systolic	NBPs	chartevents	Routine Vital Signs	mmH
2	39553978	2180-07-23 19:00:00	220179	93.0	Non Invasive Blood Pressure systolic	NBPs	chartevents	Routine Vital Signs	mmH
3	39553978	2180-07-23 20:00:00	220179	90.0	Non Invasive Blood Pressure systolic	NBPs	chartevents	Routine Vital Signs	mmH
4	39553978	2180-07-23 14:11:00	220179	84.0	Non Invasive Blood Pressure systolic	NBPs	chartevents	Routine Vital Signs	mmH

Combine Data

In [5]:
```
def process_mimiciv(input_file, output_file, columns_to_include):
    # Read the entire CSV file
    data = pd.read_csv(input_file)

    # Calculate the average valuenum for each distinct stay_id and itemid comb
    avg_valuenum = data.groupby(['stay_id', 'label'])['valuenum'].mean().reset_

    # Pivot the data to create distinct itemid columns
    pivoted_data = avg_valuenum.pivot(index='stay_id', columns='label',
                                      values='valuenum').reset_index()

    # Replace NaN values with 0 in every column
    pivoted_data = pivoted_data.fillna(0)

    # Select the specified columns to include in the final processed data
    final_data = pivoted_data.merge(data[columns_to_include].drop_duplicates()
                                    how='inner')

    # Save the processed data to a CSV file
    final_data.to_csv(output_file, index=False)
```

In [6]:
```
columns_to_include = ['stay_id', 'los']
process_mimiciv("./data/preprocessing/ld.csv.gz", "./data/preprocessing/proces
                columns_to_include)
```

In [7]:
```
processed_chart= pd.read_csv('./data/preprocessing/processed_chart.csv.gz')
```

In [8]:
```
processed_chart.head()
```

Out[8]:

	stay_id	Activity / Mobility (JH-HLM)	Arterial Blood Pressure diastolic	Arterial Blood Pressure mean	Arterial Blood Pressure systolic	GCS - Eye Opening	GCS - Motor Response	GCS - Verbal Response	Heart F
0	30000153	0.0	66.935484	90.300000	137.387097	3.541667	5.875000	3.458333	104.804
1	30000213	3.5	0.000000	0.000000	0.000000	3.818182	5.818182	3.636364	82.736
2	30000484	0.0	0.000000	0.000000	0.000000	3.866667	4.933333	3.066667	91.881
3	30000646	0.0	0.000000	0.000000	0.000000	4.000000	6.000000	5.000000	94.046
4	30001148	0.0	58.833333	73.541667	108.291667	3.285714	5.285714	3.857143	74.592

In [9]:
```
processed_chart.shape
```

Out[9]:
```
(72980, 18)
```

In [10]:
```
columns_to_include = ['stay_id', 'los','gender','anchor_age']
process_mimiciv("./data/preprocessing/lab.csv.gz", "./data/preprocessing/proce
```

```
C:\Users\User\AppData\Local\Temp\ipykernel_1424\2272975284.py:3: DtypeWarnin
g: Columns (5) have mixed types. Specify dtype option on import or set low_me
mory=False.
  data = pd.read_csv(input_file)
```

In [11]:
```
processed_lab= pd.read_csv('./data/preprocessing/processed_lab.csv.gz')
```

In [12]:
```
processed_lab.head()
```

Out[12]:

	stay_id	Amikacin	Anion Gap	Base Excess	Bicarbonate	Calcium, Total	Calculated Total CO2	Chloride	Cre
0	30000153	0.0	12.000000	-3.333333	21.000000	7.700000	22.666667	115.000000	1.0
1	30000213	0.0	15.666667	0.500000	23.333333	8.333333	27.000000	100.666667	3.6
2	30000484	0.0	10.000000	1.000000	27.666667	8.133333	33.000000	105.000000	1.2
3	30000646	0.0	12.000000	-1.000000	22.125000	7.625000	21.000000	109.500000	0.7
4	30001148	0.0	10.500000	2.444444	27.666667	0.000000	28.111111	106.666667	0.7

5 rows × 47 columns

In [13]:
```
processed_lab.shape
```

Out[13]:
```
(72043, 47)
```

In [14]:
```
processed_data = processed_lab.merge(processed_chart, on=['stay_id','los'], ho
```

In [15]:
```
processed_data.head()
```

Out[15]:

	stay_id	Amikacin	Anion Gap	Base Excess	Bicarbonate	Calcium, Total	Calculated Total CO2	Chloride	Cre
0	30000153	0.0	12.000000	-3.333333	21.000000	7.700000	22.666667	115.000000	1.
1	30000213	0.0	15.666667	0.500000	23.333333	8.333333	27.000000	100.666667	3.
2	30000484	0.0	10.000000	1.000000	27.666667	8.133333	33.000000	105.000000	1.
3	30000646	0.0	12.000000	-1.000000	22.125000	7.625000	21.000000	109.500000	0.
4	30001148	0.0	10.500000	2.444444	27.666667	0.000000	28.111111	106.666667	0.

5 rows × 63 columns

In [16]:
```
processed_data.shape
```

Out[16]:
```
(72030, 63)
```

In [17]:
```
processed_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 72030 entries, 0 to 72029
Data columns (total 63 columns):
 #   Column                                 Non-Null Count  Dtype  
---  ------                                 --------------  -----  
 0   stay_id                                72030 non-null  int64  
 1   Amikacin                               72030 non-null  float64
 2   Anion Gap                              72030 non-null  float64
 3   Base Excess                            72030 non-null  float64
 4   Bicarbonate                            72030 non-null  float64
 5   Calcium, Total                         72030 non-null  float64
 6   Calculated Total CO2                   72030 non-null  float64
 7   Chloride                               72030 non-null  float64
 8   Creatinine                             72030 non-null  float64
 9   Cyclosporin                            72030 non-null  float64
 10  Free Calcium                           72030 non-null  float64
 11  Glucose                                72030 non-null  float64
 12  H                                      72030 non-null  float64
 13  Hematocrit                             72030 non-null  float64
 14  Hemoglobin                             72030 non-null  float64
 15  Heparin                                72030 non-null  float64
 16  I                                      72030 non-null  float64
 17  INR(PT)                                72030 non-null  float64
 18  L                                      72030 non-null  float64
 19  Lactate                                72030 non-null  float64
 20  MCH                                    72030 non-null  float64
 21  MCHC                                   72030 non-null  float64
 22  MCV                                    72030 non-null  float64
 23  Magnesium                              72030 non-null  float64
 24  Oxygen Saturation                      72030 non-null  float64
 25  PT                                     72030 non-null  float64
 26  PTT                                    72030 non-null  float64
 27  Phenobarbital                          72030 non-null  float64
 28  Phosphate                              72030 non-null  float64
 29  Platelet Count                         72030 non-null  float64
 30  Potassium                              72030 non-null  float64
 31  Potassium, Whole Blood                 72030 non-null  float64
 32  RDW                                    72030 non-null  float64
 33  RDW-SD                                 72030 non-null  float64
 34  Rapamycin                              72030 non-null  float64
 35  Red Blood Cells                        72030 non-null  float64
 36  Sodium                                 72030 non-null  float64
 37  Temperature                            72030 non-null  float64
 38  Urea Nitrogen                          72030 non-null  float64
 39  White Blood Cells                      72030 non-null  float64
 40  pCO2                                   72030 non-null  float64
 41  pH                                     72030 non-null  float64
 42  pO2                                    72030 non-null  float64
 43  tacroFK                                72030 non-null  float64
 44  los                                    72030 non-null  float64
 45  gender                                 72030 non-null  object 
 46  anchor_age                             72030 non-null  int64  
 47  Activity / Mobility (JH-HLM)           72030 non-null  float64
 48  Arterial Blood Pressure diastolic      72030 non-null  float64
 49  Arterial Blood Pressure mean           72030 non-null  float64
 50  Arterial Blood Pressure systolic       72030 non-null  float64
 51  GCS - Eye Opening                      72030 non-null  float64
 52  GCS - Motor Response                   72030 non-null  float64
 53  GCS - Verbal Response                  72030 non-null  float64
 54  Heart Rate                             72030 non-null  float64
 55  Inspired O2 Fraction                   72030 non-null  float64
 56  Non Invasive Blood Pressure diastolic  72030 non-null  float64
 57  Non Invasive Blood Pressure mean       72030 non-null  float64
 58  Non Invasive Blood Pressure systolic   72030 non-null  float64
 59  O2 saturation pulseoxymetry            72030 non-null  float64
 60  Orientation                            72030 non-null  float64
 61  Respiratory Rate                       72030 non-null  float64
 62  Temperature Fahrenheit                 72030 non-null  float64
dtypes: float64(60), int64(2), object(1)
memory usage: 35.2+ MB
```

In [19]:
```
processed_data.to_csv('./data/preprocessing/processed_data.csv.gz', index=Fals
```

In [20]:
```
# remove some binary and less useful variables from the original set
los=processed_data.drop(columns=['stay_id','Orientation', 'Temperature','Base 
                                 'Amikacin','Cyclosporin'])
```

In [21]:
```
los.tail()
```

Out[21]:

	Anion Gap	Bicarbonate	Calcium, Total	Calculated Total CO2	Chloride	Creatinine	Free Calcium	Glucose
72025	13.500000	23.500000	8.80	22.666667	108.500000	1.65	1.1200	184.00000C
72026	16.000000	24.000000	8.60	0.000000	103.000000	2.20	1.1100	116.00000C
72027	11.500000	26.000000	8.80	27.166667	105.666667	0.70	1.1275	114.444444
72028	11.333333	24.333333	8.50	0.000000	103.666667	0.90	0.0000	106.00000C
72029	15.400000	23.400000	8.88	0.000000	104.400000	1.00	0.0000	112.00000C

5 rows × 57 columns

In [22]:

```
los.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 72030 entries, 0 to 72029
Data columns (total 57 columns):
 #   Column                                 Non-Null Count  Dtype  
---  ------                                 --------------  -----  
 0   Anion Gap                              72030 non-null  float64
 1   Bicarbonate                            72030 non-null  float64
 2   Calcium, Total                         72030 non-null  float64
 3   Calculated Total CO2                   72030 non-null  float64
 4   Chloride                               72030 non-null  float64
 5   Creatinine                             72030 non-null  float64
 6   Free Calcium                           72030 non-null  float64
 7   Glucose                                72030 non-null  float64
 8   H                                      72030 non-null  float64
 9   Hematocrit                             72030 non-null  float64
 10  Hemoglobin                             72030 non-null  float64
 11  Heparin                                72030 non-null  float64
 12  I                                      72030 non-null  float64
 13  INR(PT)                                72030 non-null  float64
 14  L                                      72030 non-null  float64
 15  Lactate                                72030 non-null  float64
 16  MCH                                    72030 non-null  float64
 17  MCHC                                   72030 non-null  float64
 18  MCV                                    72030 non-null  float64
 19  Magnesium                              72030 non-null  float64
 20  Oxygen Saturation                      72030 non-null  float64
 21  PT                                     72030 non-null  float64
 22  PTT                                    72030 non-null  float64
 23  Phenobarbital                          72030 non-null  float64
 24  Phosphate                              72030 non-null  float64
 25  Platelet Count                         72030 non-null  float64
 26  Potassium                              72030 non-null  float64
 27  Potassium, Whole Blood                 72030 non-null  float64
 28  RDW                                    72030 non-null  float64
 29  RDW-SD                                 72030 non-null  float64
 30  Rapamycin                              72030 non-null  float64
 31  Red Blood Cells                        72030 non-null  float64
 32  Sodium                                 72030 non-null  float64
 33  Urea Nitrogen                          72030 non-null  float64
 34  White Blood Cells                      72030 non-null  float64
 35  pCO2                                   72030 non-null  float64
 36  pH                                     72030 non-null  float64
 37  pO2                                    72030 non-null  float64
 38  tacroFK                                72030 non-null  float64
 39  los                                    72030 non-null  float64
 40  gender                                 72030 non-null  object 
 41  anchor_age                             72030 non-null  int64  
 42  Activity / Mobility (JH-HLM)           72030 non-null  float64
 43  Arterial Blood Pressure diastolic      72030 non-null  float64
 44  Arterial Blood Pressure mean           72030 non-null  float64
 45  Arterial Blood Pressure systolic       72030 non-null  float64
 46  GCS - Eye Opening                      72030 non-null  float64
 47  GCS - Motor Response                   72030 non-null  float64
 48  GCS - Verbal Response                  72030 non-null  float64
 49  Heart Rate                             72030 non-null  float64
 50  Inspired O2 Fraction                   72030 non-null  float64
 51  Non Invasive Blood Pressure diastolic  72030 non-null  float64
 52  Non Invasive Blood Pressure mean       72030 non-null  float64
 53  Non Invasive Blood Pressure systolic   72030 non-null  float64
 54  O2 saturation pulseoxymetry            72030 non-null  float64
 55  Respiratory Rate                       72030 non-null  float64
 56  Temperature Fahrenheit                 72030 non-null  float64
dtypes: float64(55), int64(1), object(1)
memory usage: 31.9+ MB
```

In [23]:

```
los['gender'].replace({'M': 0, 'F':1}, inplace=True)
```

In [24]:

```
los.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 72030 entries, 0 to 72029
Data columns (total 57 columns):
 #   Column                                 Non-Null Count  Dtype  
---  ------                                 --------------  -----  
 0   Anion Gap                              72030 non-null  float64
 1   Bicarbonate                            72030 non-null  float64
 2   Calcium, Total                         72030 non-null  float64
 3   Calculated Total CO2                   72030 non-null  float64
 4   Chloride                               72030 non-null  float64
 5   Creatinine                             72030 non-null  float64
 6   Free Calcium                           72030 non-null  float64
 7   Glucose                                72030 non-null  float64
 8   H                                      72030 non-null  float64
 9   Hematocrit                             72030 non-null  float64
 10  Hemoglobin                             72030 non-null  float64
 11  Heparin                                72030 non-null  float64
 12  I                                      72030 non-null  float64
 13  INR(PT)                                72030 non-null  float64
 14  L                                      72030 non-null  float64
 15  Lactate                                72030 non-null  float64
 16  MCH                                    72030 non-null  float64
 17  MCHC                                   72030 non-null  float64
 18  MCV                                    72030 non-null  float64
 19  Magnesium                              72030 non-null  float64
 20  Oxygen Saturation                      72030 non-null  float64
 21  PT                                     72030 non-null  float64
 22  PTT                                    72030 non-null  float64
 23  Phenobarbital                          72030 non-null  float64
 24  Phosphate                              72030 non-null  float64
 25  Platelet Count                         72030 non-null  float64
 26  Potassium                              72030 non-null  float64
 27  Potassium, Whole Blood                 72030 non-null  float64
 28  RDW                                    72030 non-null  float64
 29  RDW-SD                                 72030 non-null  float64
 30  Rapamycin                              72030 non-null  float64
 31  Red Blood Cells                        72030 non-null  float64
 32  Sodium                                 72030 non-null  float64
 33  Urea Nitrogen                          72030 non-null  float64
 34  White Blood Cells                      72030 non-null  float64
 35  pCO2                                   72030 non-null  float64
 36  pH                                     72030 non-null  float64
 37  pO2                                    72030 non-null  float64
 38  tacroFK                                72030 non-null  float64
 39  los                                    72030 non-null  float64
 40  gender                                 72030 non-null  int64  
 41  anchor_age                             72030 non-null  int64  
 42  Activity / Mobility (JH-HLM)           72030 non-null  float64
 43  Arterial Blood Pressure diastolic      72030 non-null  float64
 44  Arterial Blood Pressure mean           72030 non-null  float64
 45  Arterial Blood Pressure systolic       72030 non-null  float64
 46  GCS - Eye Opening                      72030 non-null  float64
 47  GCS - Motor Response                   72030 non-null  float64
 48  GCS - Verbal Response                  72030 non-null  float64
 49  Heart Rate                             72030 non-null  float64
 50  Inspired O2 Fraction                   72030 non-null  float64
 51  Non Invasive Blood Pressure diastolic  72030 non-null  float64
 52  Non Invasive Blood Pressure mean       72030 non-null  float64
 53  Non Invasive Blood Pressure systolic   72030 non-null  float64
 54  O2 saturation pulseoxymetry            72030 non-null  float64
 55  Respiratory Rate                       72030 non-null  float64
 56  Temperature Fahrenheit                 72030 non-null  float64
dtypes: float64(55), int64(2)
memory usage: 31.9 MB
```

In [28]:

```
los.to_csv('./data/dataset/los.csv.gz', index=False)
```

Length-of-Stay Prediction Model

In [3]:

```
df = pd.read_csv('./data/dataset/los.csv.gz')
```

In [4]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 72030 entries, 0 to 72029
Data columns (total 57 columns):
 #   Column                                 Non-Null Count  Dtype  
---  ------                                 --------------  -----  
 0   Anion Gap                              72030 non-null  float64
 1   Bicarbonate                            72030 non-null  float64
 2   Calcium, Total                         72030 non-null  float64
 3   Calculated Total CO2                   72030 non-null  float64
 4   Chloride                               72030 non-null  float64
 5   Creatinine                             72030 non-null  float64
 6   Free Calcium                           72030 non-null  float64
 7   Glucose                                72030 non-null  float64
 8   H                                      72030 non-null  float64
 9   Hematocrit                             72030 non-null  float64
 10  Hemoglobin                             72030 non-null  float64
 11  Heparin                                72030 non-null  float64
 12  I                                      72030 non-null  float64
 13  INR(PT)                                72030 non-null  float64
 14  L                                      72030 non-null  float64
 15  Lactate                                72030 non-null  float64
 16  MCH                                    72030 non-null  float64
 17  MCHC                                   72030 non-null  float64
 18  MCV                                    72030 non-null  float64
 19  Magnesium                              72030 non-null  float64
 20  Oxygen Saturation                      72030 non-null  float64
 21  PT                                     72030 non-null  float64
 22  PTT                                    72030 non-null  float64
 23  Phenobarbital                          72030 non-null  float64
 24  Phosphate                              72030 non-null  float64
 25  Platelet Count                         72030 non-null  float64
 26  Potassium                              72030 non-null  float64
 27  Potassium, Whole Blood                 72030 non-null  float64
 28  RDW                                    72030 non-null  float64
 29  RDW-SD                                 72030 non-null  float64
 30  Rapamycin                              72030 non-null  float64
 31  Red Blood Cells                        72030 non-null  float64
 32  Sodium                                 72030 non-null  float64
 33  Urea Nitrogen                          72030 non-null  float64
 34  White Blood Cells                      72030 non-null  float64
 35  pCO2                                   72030 non-null  float64
 36  pH                                     72030 non-null  float64
 37  pO2                                    72030 non-null  float64
 38  tacroFK                                72030 non-null  float64
 39  los                                    72030 non-null  float64
 40  gender                                 72030 non-null  int64  
 41  anchor_age                             72030 non-null  int64  
 42  Activity / Mobility (JH-HLM)           72030 non-null  float64
 43  Arterial Blood Pressure diastolic      72030 non-null  float64
 44  Arterial Blood Pressure mean           72030 non-null  float64
 45  Arterial Blood Pressure systolic       72030 non-null  float64
 46  GCS - Eye Opening                      72030 non-null  float64
 47  GCS - Motor Response                   72030 non-null  float64
 48  GCS - Verbal Response                  72030 non-null  float64
 49  Heart Rate                             72030 non-null  float64
 50  Inspired O2 Fraction                   72030 non-null  float64
 51  Non Invasive Blood Pressure diastolic  72030 non-null  float64
 52  Non Invasive Blood Pressure mean       72030 non-null  float64
 53  Non Invasive Blood Pressure systolic   72030 non-null  float64
 54  O2 saturation pulseoxymetry            72030 non-null  float64
 55  Respiratory Rate                       72030 non-null  float64
 56  Temperature Fahrenheit                 72030 non-null  float64
dtypes: float64(55), int64(2)
memory usage: 31.3 MB
```

In [5]:

```
# Target Variable (Length-of-Stay)
LOS = df['los'].values
# Prediction Features
features = df.drop(columns=['los'])
```

In [6]:

```
actual_mean_los = np.mean(LOS)
actual_median_los = np.median(LOS)
print(f"actual mean LOS = {actual_mean_los}\nactual median los = {actual_media
```

```
actual mean LOS = 3.493232738352332
actual median los = 1.9532812499999999
```

In [7]:

```
# Split into train 80% and test 20%
X_train, X_test, y_train, y_test = train_test_split(features,
                                                    LOS,
                                                    test_size = .20,
                                                    random_state = 0)

# Show the results of the split
print("Training set has {} samples.".format(X_train.shape[0]))
print("Testing set has {} samples.".format(X_test.shape[0]))
```

```
Training set has 57624 samples.
Testing set has 14406 samples.
```

In [19]:

```
from sklearn.model_selection import cross_val_score
# Regression models for comparison
models = [GradientBoostingRegressor(random_state=0),
    KNeighborsRegressor(),
    RandomForestRegressor(random_state=0),
    XGBRegressor(random_state=0)]

mae = {}
mse = {}
rmse = {}
r2 = {}

for model in models:
    # Instantiate and fit Regressor Model
    reg_model = model
    reg_model.fit(X_train, y_train)

    # Make predictions with model
    y_test_preds = reg_model.predict(X_test)

    # Grab model name and store results associated with model
    name = str(model).split("(")[0]

    # Evaluation metrics
    mae[name] = mean_absolute_error(y_test, y_test_preds)
    mse[name] = mean_squared_error(y_test, y_test_preds)
    rmse[name] = mean_squared_error(y_test, y_test_preds, squared=False)
    r2[name] = r2_score(y_test, y_test_preds)

    print('{} done.'.format(name))
```

```
GradientBoostingRegressor done.
KNeighborsRegressor done.
RandomForestRegressor done.
XGBRegressor done.
```

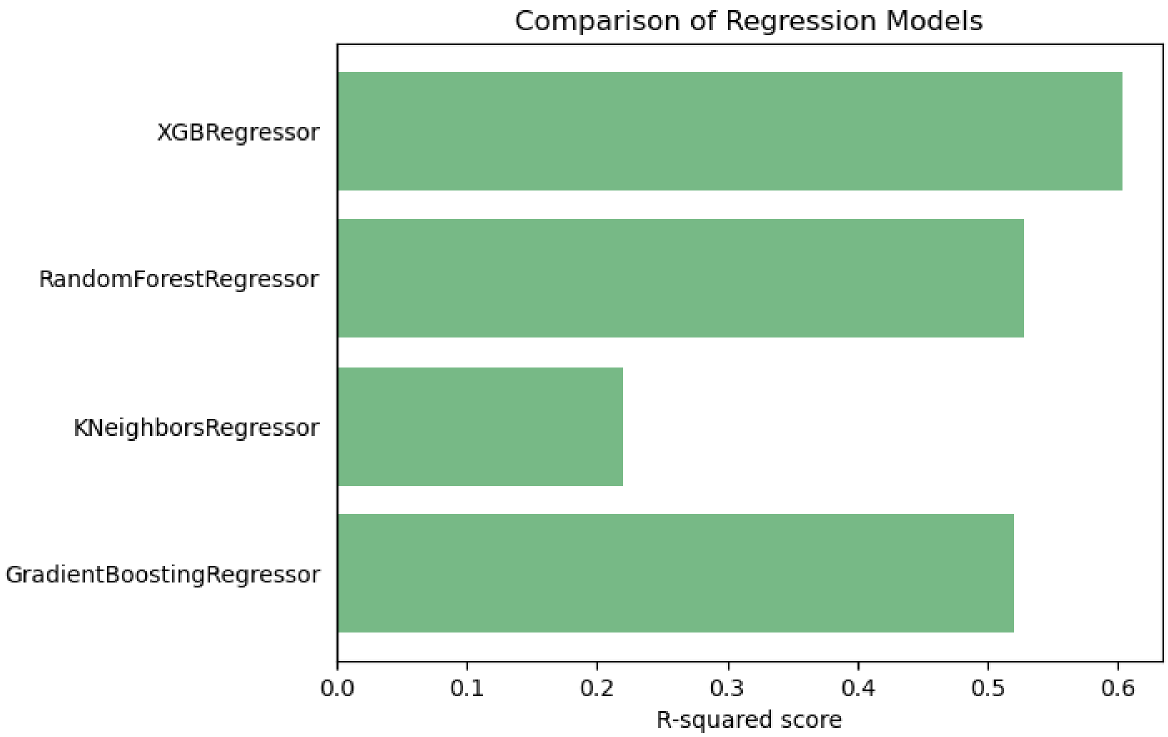
Model Evaluation

In [20]:

```
# R2 score results
fig, ax = plt.subplots()
ind = range(len(r2))
ax.barh(ind, list(r2.values()), align='center',
        color = '#55a868', alpha=0.8)
ax.set_yticks(ind)
ax.set_yticklabels(r2.keys())
ax.set_xlabel('R-squared score')
ax.tick_params(left=False, top=False, right=False)
ax.set_title('Comparison of Regression Models')
#fig.savefig('images/compare_models.png', bbox_inches = 'tight')
```

Out[20]:

```
Text(0.5, 1.0, 'Comparison of Regression Models')
```



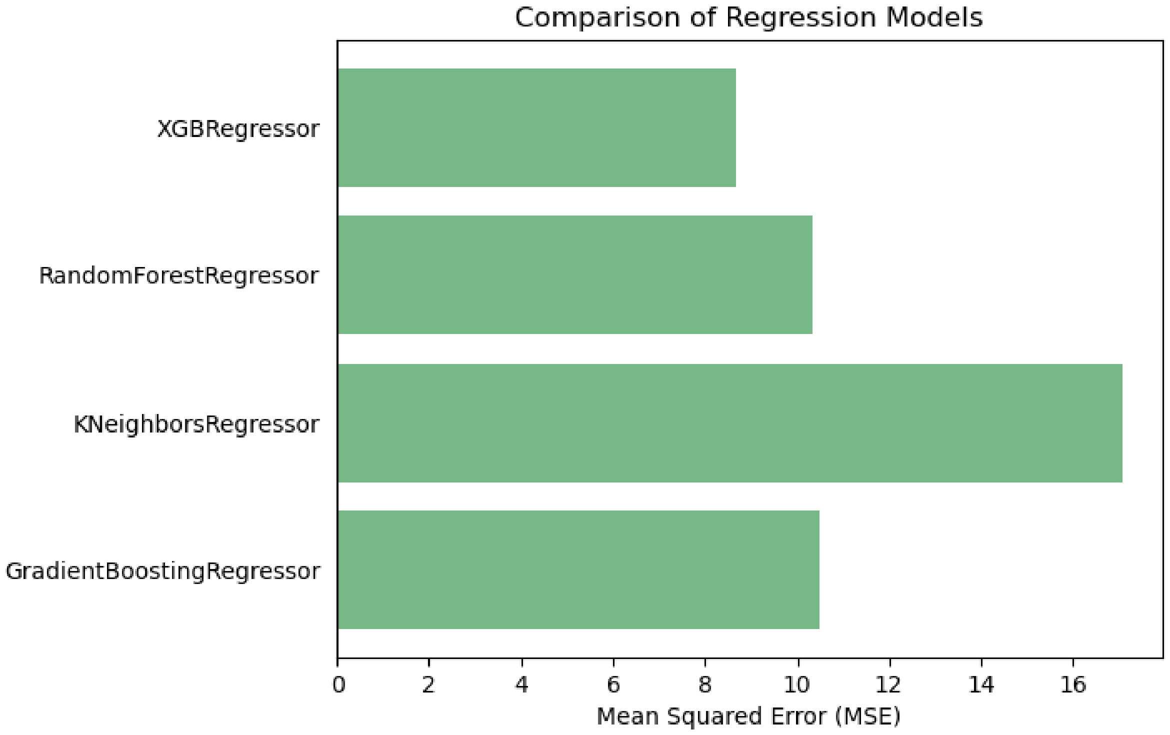
In [21]:

```
#R2 Values
for key, value in r2.items():
    print(f"Key: {key}, Value: {value}")
```

```
Key: GradientBoostingRegressor, Value: 0.520799935008655
Key: KNeighborsRegressor, Value: 0.2196412208098515
Key: RandomForestRegressor, Value: 0.5284204642419412
Key: XGBRegressor, Value: 0.604343214448636
```

In [22]:
```
# mse score results
fig, ax = plt.subplots()
ind = range(len(mse))
ax.barh(ind, list(mse.values()), align='center',
        color = '#55a868', alpha=0.8)
ax.set_yticks(ind)
ax.set_yticklabels(mse.keys())
ax.set_xlabel('Mean Squared Error (MSE)')
ax.tick_params(left=False, top=False, right=False)
ax.set_title('Comparison of Regression Models')
```

Out[22]:
```
Text(0.5, 1.0, 'Comparison of Regression Models')
```

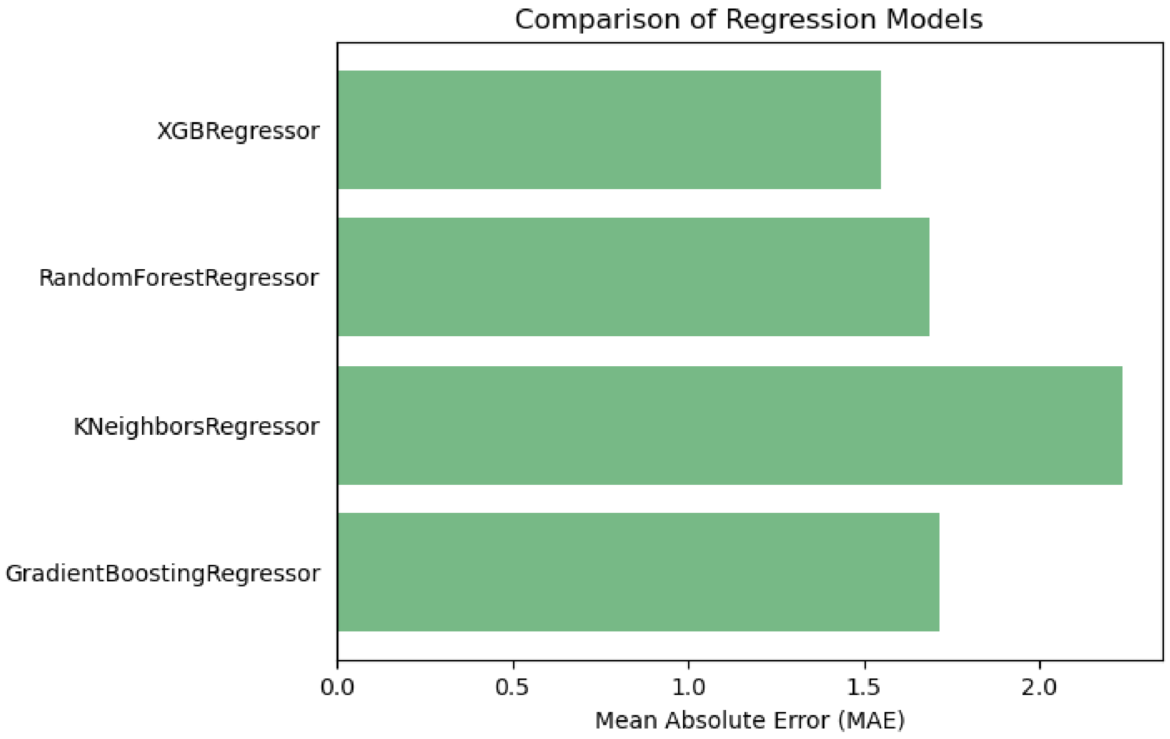


In [23]:
```
#MSE Values
for key, value in mse.items():
    print(f"Key: {key}, Value: {value}")
```

```
Key: GradientBoostingRegressor, Value: 10.493854867362673
Key: KNeighborsRegressor, Value: 17.08883694212695
Key: RandomForestRegressor, Value: 10.326975241025298
Key: XGBRegressor, Value: 8.664366280789716
```

In [24]:
```
# mae score results
fig, ax = plt.subplots()
ind = range(len(mae))
ax.barh(ind, list(mae.values()), align='center',
        color = '#55a868', alpha=0.8)
ax.set_yticks(ind)
ax.set_yticklabels(mae.keys())
ax.set_xlabel('Mean Absolute Error (MAE)')
ax.tick_params(left=False, top=False, right=False)
ax.set_title('Comparison of Regression Models')
```

Out[24]:
```
Text(0.5, 1.0, 'Comparison of Regression Models')
```

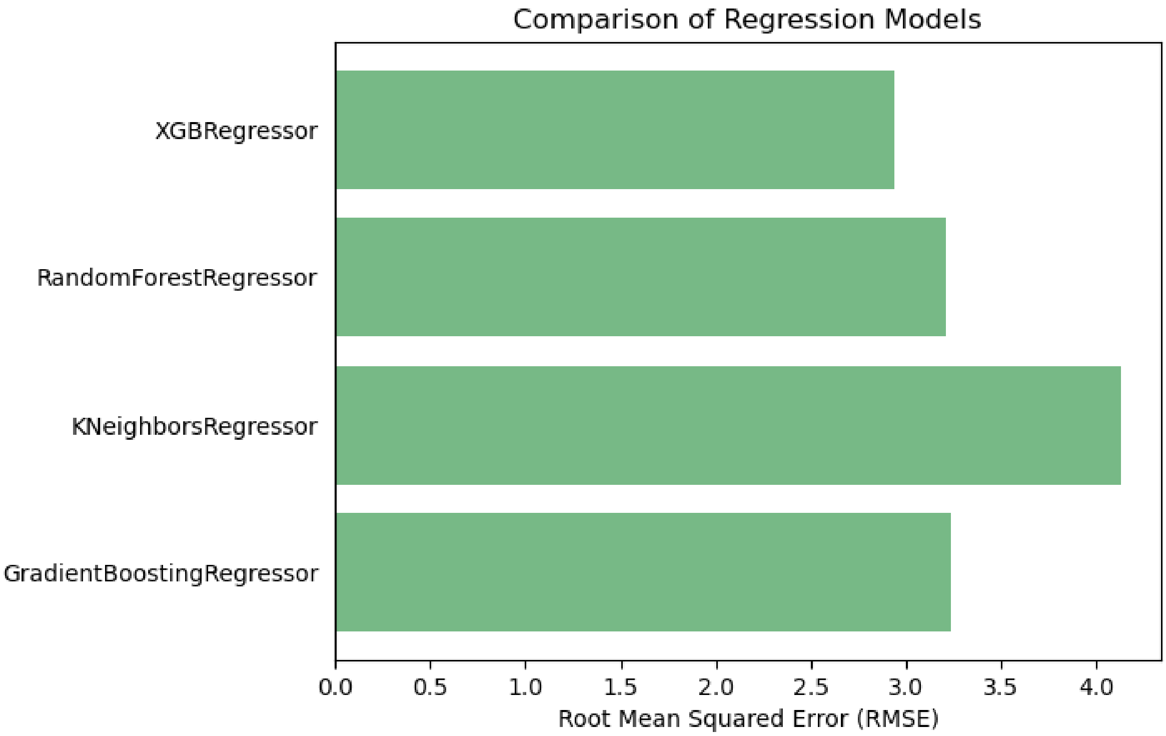


In [25]:
```
#MAE Values
for key, value in mae.items():
    print(f"Key: {key}, Value: {value}")
```

```
Key: GradientBoostingRegressor, Value: 1.7147232102121142
Key: KNeighborsRegressor, Value: 2.238807677870846
Key: RandomForestRegressor, Value: 1.6877608309744911
Key: XGBRegressor, Value: 1.5476066202460712
```

In [26]:
```
# rmse score results
fig, ax = plt.subplots()
ind = range(len(rmse))
ax.barh(ind, list(rmse.values()), align='center',
        color = '#55a868', alpha=0.8)
ax.set_yticks(ind)
ax.set_yticklabels(rmse.keys())
ax.set_xlabel('Root Mean Squared Error (RMSE)')
ax.tick_params(left=False, top=False, right=False)
ax.set_title('Comparison of Regression Models')
```

Out[26]:
```
Text(0.5, 1.0, 'Comparison of Regression Models')
```



In [27]:
```
#RMSE value
for key, value in rmse.items():
    print(f"Key: {key}, Value: {value}")
```

```
Key: GradientBoostingRegressor, Value: 3.2394219958756025
Key: KNeighborsRegressor, Value: 4.133864649710601
Key: RandomForestRegressor, Value: 3.2135611463025406
Key: XGBRegressor, Value: 2.9435295617319213
```

In [15]:

```
# XGBRegressor will be used as the LOS prediction model
reg_model = XGBRegressor(random_state=0)
reg_model.fit(X_train, y_train)
y_test_preds = reg_model.predict(X_test)
r2_not_refined = r2_score(y_test, y_test_preds)
mse_not_refined = mean_squared_error(y_test, y_test_preds)
mae_not_refined = mean_absolute_error(y_test, y_test_preds)
rmse_not_refined = mean_squared_error(y_test, y_test_preds, squared=False)
print(f"R2 score is: {r2_not_refined}")
print(f"MSE score is: {mse_not_refined}")
print(f"MAE score is: {mae_not_refined}")
print(f"RMSE score is: {rmse_not_refined}")
```

```
R2 score is: 0.604343214448636
MSE score is: 8.664366280789716
MAE score is: 1.5476066202460712
RMSE score is: 2.9435295617319213
```

Model Refinement

In [10]:
```
# Split into train 80% and test 20%
X_train, X_test, y_train, y_test = train_test_split(features,
                                                    LOS,
                                                    test_size = .20,
                                                    random_state = 42)

xgb_model = XGBRegressor(objective='reg:squarederror', random_state=42)

# Define the parameter grid for grid search
param_grid = {
    'learning_rate': [0.01, 0.1, 0.2],
    'max_depth': [3, 5, 7],
    'n_estimators': [100, 200, 300],
    'alpha': [0, 0.1, 1],
    'lambda': [0, 0.1, 1]
}

# Initialize GridSearchCV
grid_search = GridSearchCV(estimator=xgb_model, param_grid=param_grid, cv=5, n_

# Perform grid search on the training data
grid_search.fit(X_train, y_train, early_stopping_rounds=10, eval_set=[(X_test,

# Get the best estimator from grid search
best_xgb_model = grid_search.best_estimator_

# Evaluate the best model on the test set
y_pred = best_xgb_model.predict(X_test)

# Calculate evaluation metrics
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)
mae = mean_absolute_error(y_test, y_pred)
rmse = mean_squared_error(y_test, y_pred, squared=False)

# Print the best parameters found
print("Best Parameters:", grid_search.best_params_)
```

```
C:\Users\User\anaconda3\envs\fyp\lib\site-packages\xgboost\sklearn.py:835: Us
erWarning: `early_stopping_rounds` in `fit` method is deprecated for better c
ompatibility with scikit-learn, use `early_stopping_rounds` in constructor or
`set_params` instead.
  warnings.warn(

Best Parameters: {'alpha': 0, 'lambda': 1, 'learning_rate': 0.1, 'max_depth':
7, 'n_estimators': 300}
```

In [13]:

```
#fit the model using the best params
refined_xgb_model = XGBRegressor(reg_alpha=0, reg_lambda=1, learning_rate=0.1,
                                 max_depth=7, n_estimators=300)
# Fit the model to the training data
refined_xgb_model.fit(X_train, y_train)

y_test_preds = refined_xgb_model.predict(X_test)
r2_optimized = r2_score(y_test, y_test_preds)
mse_optimized = mean_squared_error(y_test, y_test_preds)
mae_optimized = mean_absolute_error(y_test, y_test_preds)
rmse_optimized = mean_squared_error(y_test, y_test_preds, squared=False)
print("Optimized R2 score is: {:2f}".format(r2_optimized))
print("Optimized MSE score is: {:2f}".format(mse_optimized))
print("Optimized MAE score is: {:2f}".format(mae_optimized))
print("Optimized RMSE score is: {:2f}".format(rmse_optimized))
```

```
Optimized R2 score is: 0.639121
Optimized MSE score is: 7.902774
Optimized MAE score is: 1.420043
Optimized RMSE score is: 2.811187
```

In [28]:

```
print('Model refinement improved R2 score by {:.4f}'.format(r2_optimized-r2_no
```

```
Model refinement improved R2 score by 0.0348
```

Result

In [29]:

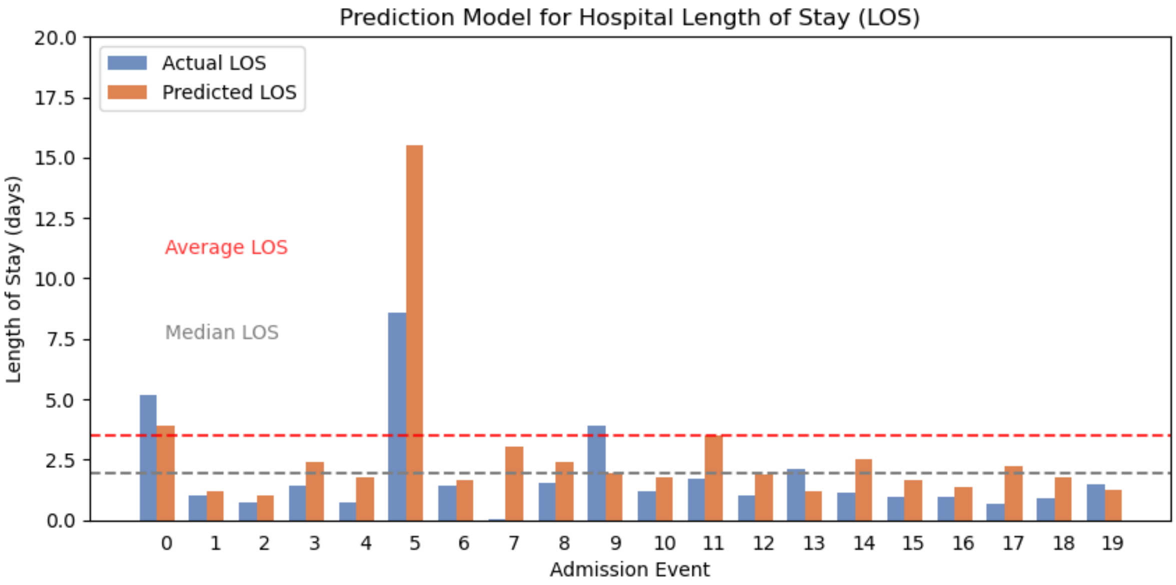
```
LOS_predict = y_test_preds[:20]
LOS_actual = y_test[:20]
```

In [30]:

```
fig, ax = plt.subplots(figsize=(10, 4.5))

ind = np.arange(0,20)
pad = 0.15
width = 0.35
set_actual = ax.bar(pad+ind, LOS_actual, width, color='#4c72b0', alpha=0.8)
set_predict = ax.bar(pad+ind+width, LOS_predict, width, color='#dd8452')

ax.set_ylabel('Length of Stay (days)')
ax.set_xlabel('Admission Event')
ax.set_title('Prediction Model for Hospital Length of Stay (LOS)')
ax.text(0.5, 11, 'Average LOS', fontdict=None, color='red', alpha=0.8)
ax.text(0.5, 7.5, 'Median LOS', fontdict=None, color='gray')
ax.set_xticks(pad + ind + width)
ax.set_ylim(0, 20)
ax.set_xticklabels(list(range(20)))
ax.axhline(y=actual_median_los, xmin=0, xmax=20, ls='--', color='gray')
ax.axhline(y=actual_mean_los, xmin=0, xmax=20, ls='--', color='red', alpha=0.8
ax.legend( (set_actual, set_predict), ('Actual LOS', 'Predicted LOS'),
          loc='upper left')
ax.tick_params(bottom=False, top=False, right=False)
```



In [31]:

```
#save the model
import pickle

filename = './data/model/los_model.sav'
with open(filename, 'wb') as file:
    pickle.dump(refined_xgb_model, file)
```

In [ ]: