SI-618 Final Project
Live or Die: Predicting Outcome When Horses Colic

MY_UNIQNAME = 'vdall'

Header and Scrap

In [940]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
from scipy import stats
import warnings
warnings.filterwarnings('ignore')

colic_df = pd.read_csv('horse.csv')
```

In [941]:
```
colic_df.sample(5)
```

Out[941]:

	surgery	age	hospital_number	rectal_temp	pulse	respiratory_rate	temp_of_extremities	peripheral_pulse	mucous_membrane	capillary_refill_time	...	packed_cell_volume
93	no	adult	530310	NaN	NaN	NaN	cool	reduced	normal_pink	less_3_sec	...	38.0
59	no	adult	528904	NaN	96.0	NaN	cool	reduced	pale_pink	more_3_sec	...	60.0
248	no	adult	528169	38.2	48.0	NaN	warm	NaN	normal_pink	more_3_sec	...	34.0
45	no	adult	529827	NaN	120.0	NaN	cold	reduced	pale_cyanotic	more_3_sec	...	60.0
133	yes	adult	527524	NaN	100.0	NaN	cool	NaN	pale_cyanotic	more_3_sec	...	59.0

5 rows × 28 columns

In [942]:
```
colic_df.describe()
```

Out[942]:

	hospital_number	rectal_temp	pulse	respiratory_rate	nasogastric_reflux_ph	packed_cell_volume	total_protein	abdomo_protein	lesion_1	lesion_2	lesi
count	2.990000e+02	239.000000	275.000000	241.000000	53.000000	270.000000	266.000000	101.000000	299.000000	299.000000	299.00
mean	1.087733e+06	38.168619	72.000000	30.460581	4.707547	46.307407	24.274436	3.039604	3659.709030	90.528428	7.38
std	1.532032e+06	0.733744	28.646219	17.666102	1.982311	10.436743	27.364194	1.967947	5408.472421	650.637139	127.74
min	5.184760e+05	35.400000	30.000000	8.000000	1.000000	23.000000	3.300000	0.100000	0.000000	0.000000	0.00
25%	5.289040e+05	37.800000	48.000000	18.000000	3.000000	38.000000	6.500000	2.000000	2111.500000	0.000000	0.00
50%	5.303010e+05	38.200000	64.000000	25.000000	5.000000	45.000000	7.500000	2.300000	2322.000000	0.000000	0.00
75%	5.347360e+05	38.500000	88.000000	36.000000	6.500000	52.000000	56.750000	3.900000	3209.000000	0.000000	0.00
max	5.305629e+06	40.800000	184.000000	96.000000	7.500000	75.000000	89.000000	10.100000	41110.000000	7111.000000	2209.00

In [943]:
```
colic_df.dtypes
```

Out[943]:
```
surgery                   object
age                       object
hospital_number            int64
rectal_temp              float64
pulse                    float64
respiratory_rate         float64
temp_of_extremities       object
peripheral_pulse          object
mucous_membrane           object
capillary_refill_time     object
pain                      object
peristalsis               object
abdominal_distention      object
nasogastric_tube          object
nasogastric_reflux        object
nasogastric_reflux_ph    float64
rectal_exam_feces         object
abdomen                   object
packed_cell_volume       float64
total_protein            float64
abdomo_appearance         object
abdomo_protein           float64
outcome                   object
surgical_lesion           object
lesion_1                   int64
lesion_2                   int64
lesion_3                   int64
cp_data                   object
dtype: object
```

In [1105]:
```
scrap_df=colic_df[["abdominal_distention","surgery","outcome"]]
scrap_df.groupby(["abdominal_distention","surgery","outcome"]).size().to_frame(name='count').reset_index()
```

Out[1105]:

	abdominal_distention	surgery	outcome	count
0	moderate	no	died	4
1	moderate	no	euthanized	7
2	moderate	no	lived	4
3	moderate	yes	died	23
4	moderate	yes	euthanized	5
5	moderate	yes	lived	22
6	none	no	died	3
7	none	no	euthanized	3
8	none	no	lived	35
9	none	yes	died	4
10	none	yes	euthanized	4
11	none	yes	lived	26
12	severe	no	died	6
13	severe	no	euthanized	4
14	severe	no	lived	1
15	severe	yes	died	9
16	severe	yes	euthanized	6
17	severe	yes	lived	12
18	slight	no	died	4
19	slight	no	euthanized	2
20	slight	no	lived	28
21	slight	yes	died	10
22	slight	yes	euthanized	2
23	slight	yes	lived	19

In [1119]:
```
scrap2_df=colic_df[["peristalsis","surgery","outcome"]]
scrap2_df.groupby(["peristalsis","surgery","outcome"]).size().to_frame(name='count').reset_index()
```

Out[1119]:

	peristalsis	surgery	outcome	count
0	absent	no	died	9
1	absent	no	euthanized	5
2	absent	no	lived	4
3	absent	yes	died	19
4	absent	yes	euthanized	12
5	absent	yes	lived	24
6	hypermotile	no	died	1
7	hypermotile	no	euthanized	1
8	hypermotile	no	lived	26
9	hypermotile	yes	died	2
10	hypermotile	yes	euthanized	1
11	hypermotile	yes	lived	8
12	hypomotile	no	died	6
13	hypomotile	no	euthanized	6
14	hypomotile	no	lived	37
15	hypomotile	yes	died	25
16	hypomotile	yes	euthanized	9
17	hypomotile	yes	lived	44
18	normal	no	euthanized	1
19	normal	no	lived	4
20	normal	yes	euthanized	2
21	normal	yes	lived	9

Q 1: Surgery is a risky proposition and done as a last resort. Of the horses that underwent surgery, how many recovered? Also, is there a relationship between the horse's age and likelihood it will recover from surgery?

Figure out what percentage of horses recovered from surgery and represent that as a visualization. The same would be done with horses that were considered an adult (over 6 months) or not.

Use Seaborn/Matplotlib

In [944]:
```
q1_df=colic_df[["hospital_number","age","surgery","outcome"]]
q1_df.sample(5)
```

Out[944]:

	hospital_number	age	surgery	outcome
65	534885	adult	yes	lived
22	521681	adult	yes	lived
24	533692	adult	yes	lived
16	5301219	young	yes	died
56	528872	adult	yes	lived

In [945]:
```
print(q1_df["outcome"].value_counts())
print(q1_df["age"].value_counts())
print(q1_df["surgery"].value_counts())
print(q1_df.count())
```

```
lived         178
died           77
euthanized     44
Name: outcome, dtype: int64
adult    275
young     24
Name: age, dtype: int64
yes    180
no     119
Name: surgery, dtype: int64
hospital_number    299
age                299
surgery            299
outcome            299
dtype: int64
```

In [946]:
```
surgery=q1_df.groupby(["surgery","outcome","age"]).size().to_frame(name='count').reset_index()
surgery_filter = surgery[(surgery['surgery'] == 'yes')]
surgery_filter #not used for visualization, just looking at results
```

Out[946]:

	surgery	outcome	age	count
5	yes	died	adult	48
6	yes	died	young	10
7	yes	euthanized	adult	26
8	yes	euthanized	young	1
9	yes	lived	adult	88
10	yes	lived	young	7

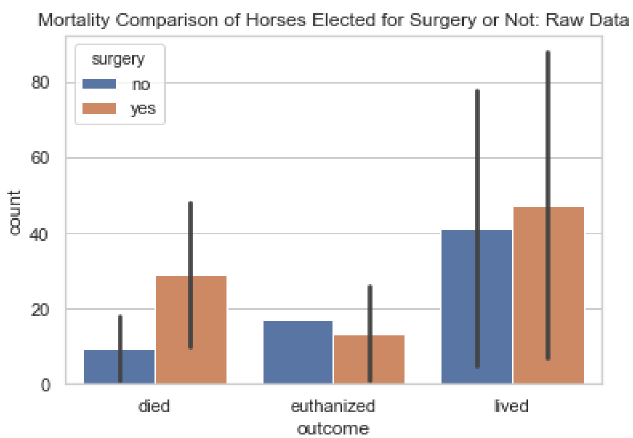
In [947]:
```
surgery
```

Out[947]:

	surgery	outcome	age	count
0	no	died	adult	18
1	no	died	young	1
2	no	euthanized	adult	17
3	no	lived	adult	78
4	no	lived	young	5
5	yes	died	adult	48
6	yes	died	young	10
7	yes	euthanized	adult	26
8	yes	euthanized	young	1
9	yes	lived	adult	88
10	yes	lived	young	7

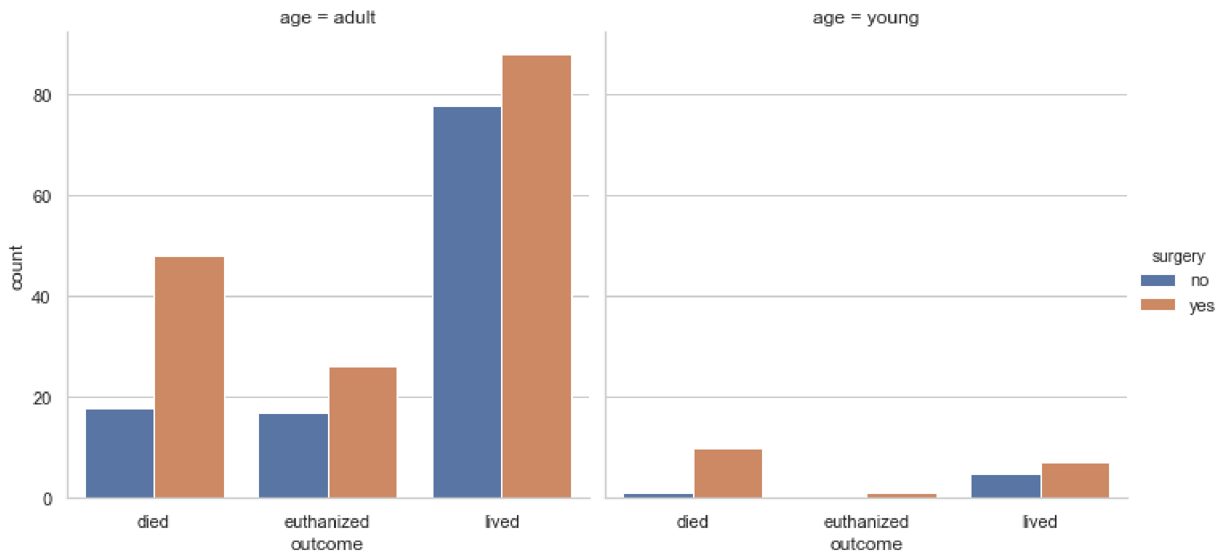
In [948]:
```
sns.barplot(x="outcome",y="count",hue="surgery",data=surgery).set(title="Mortality Comparison of Horses Elected for Surgery or No
t: Raw Data")
```

Out[948]:
```
[Text(0.5, 1.0, 'Mortality Comparison of Horses Elected for Surgery or Not: Raw Data')]
```



In [949]:
```
sns.catplot(x="outcome", y="count",
                hue="surgery", col="age",
                data=surgery, kind="bar")
```

Out[949]: <seaborn.axisgrid.FacetGrid at 0x1c49e45ac8>



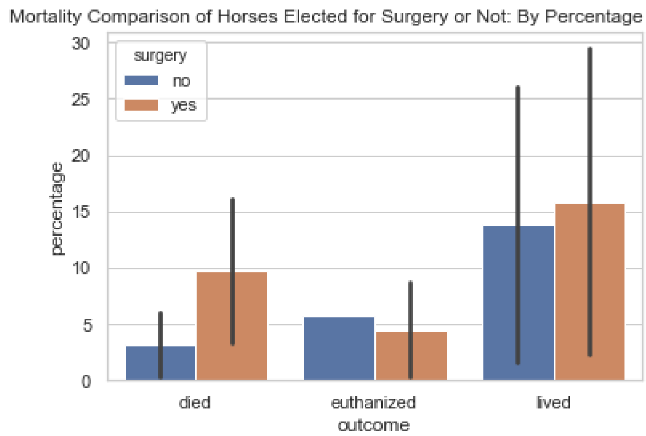
In [950]:
```
surgery_stat=(100*surgery["count"]/surgery["count"].sum()).to_frame(name='percentage')
surgery_stat

merged_s = surgery.merge(surgery_stat, left_index=True, right_index=True)
merged_s
```

Out[950]:

	surgery	outcome	age	count	percentage
0	no	died	adult	18	6.020067
1	no	died	young	1	0.334448
2	no	euthanized	adult	17	5.685619
3	no	lived	adult	78	26.086957
4	no	lived	young	5	1.672241
5	yes	died	adult	48	16.053512
6	yes	died	young	10	3.344482
7	yes	euthanized	adult	26	8.695652
8	yes	euthanized	young	1	0.334448
9	yes	lived	adult	88	29.431438
10	yes	lived	young	7	2.341137

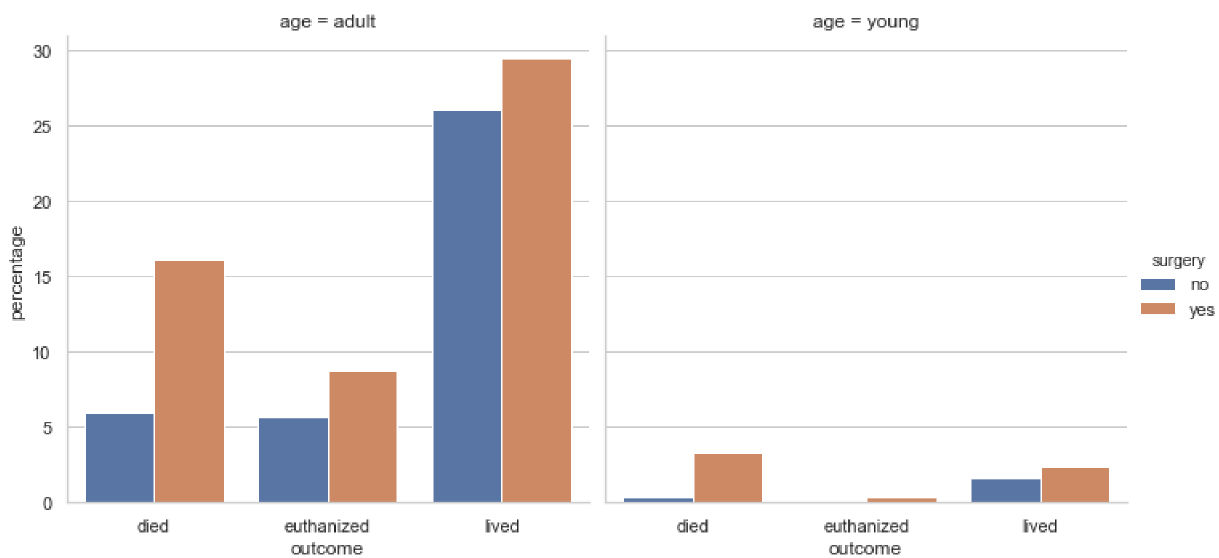
In [951]:
```
sns.barplot(x="outcome",y="percentage",hue="surgery",data=merged_s).set(title="Mortality Comparison of Horses Elected for Surgery or Not: By Percentage of Patients")
```

Out[951]:
```
[Text(0.5, 1.0, 'Mortality Comparison of Horses Elected for Surgery or Not: By Percentage of Patients')]
```



In [952]:
```
sns.catplot(x="outcome", y="percentage",
                hue="surgery", col="age",
                data=merged_s, kind="bar")
```

Out[952]:
```
<seaborn.axisgrid.FacetGrid at 0x1c4a06ca90>
```



Q 2: Veterinarians record numerous vitals when a horse presents with colic. Are certain vital level measurements (e.g. temperature, respiratory rate, pulse, and total protein) predictive of whether or not a horse will recover from colic?

Create a pairplot using the chosen vitals and figure out the variations between the different groups.

Use Seaborn/Matplotlib and ANOVA/Regression

In [1160]:
```
q2_df=colic_df[["rectal_temp","pulse","respiratory_rate","packed_cell_volume","total_protein","abdomo_protein","outcome"]]
q2_df.dropna(0,inplace=True)
q2_df.sample(5)
```

Out[1160]:

	rectal_temp	pulse	respiratory_rate	packed_cell_volume	total_protein	abdomo_protein	outcome
262	37.1	75.0	36.0	48.0	7.4	3.2	died
191	38.2	48.0	18.0	48.0	74.0	2.0	lived
222	37.7	66.0	12.0	31.5	6.2	1.6	lived
64	39.0	64.0	36.0	44.0	7.5	5.0	lived
155	38.6	52.0	20.0	36.0	6.6	5.0	lived

In [1161]:
```
q2_df.mean()
```

Out[1161]:
```
rectal_temp           38.145714
pulse                 76.071429
respiratory_rate      29.600000
packed_cell_volume    47.392857
total_protein         25.898571
abdomo_protein         3.007143
dtype: float64
```

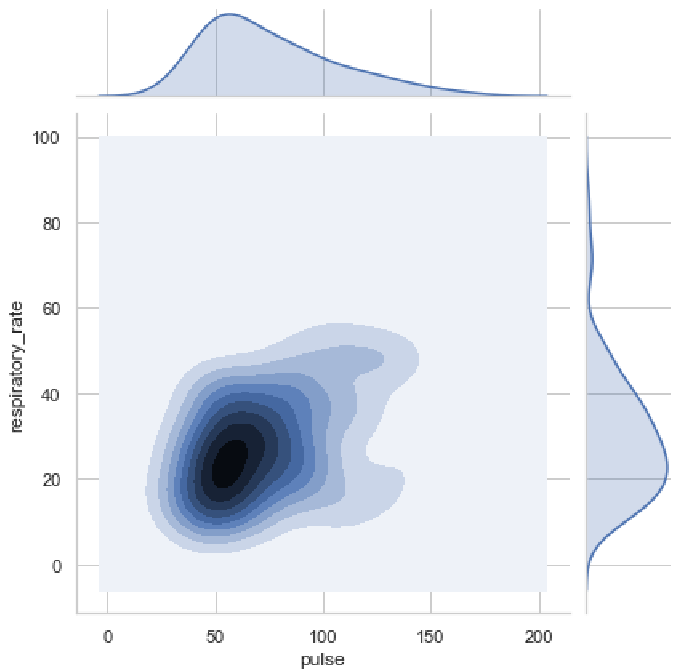
In [955]:
```
sns.pairplot(q2_df, hue="outcome")
```

```
Out[955]: <seaborn.axisgrid.PairGrid at 0x1c491d2b00>
```


rectal_temp
pulse
respiratory_rate
packed_cell_volume
total_protein
abdomo_protein
outcome
euthanized
died
lived

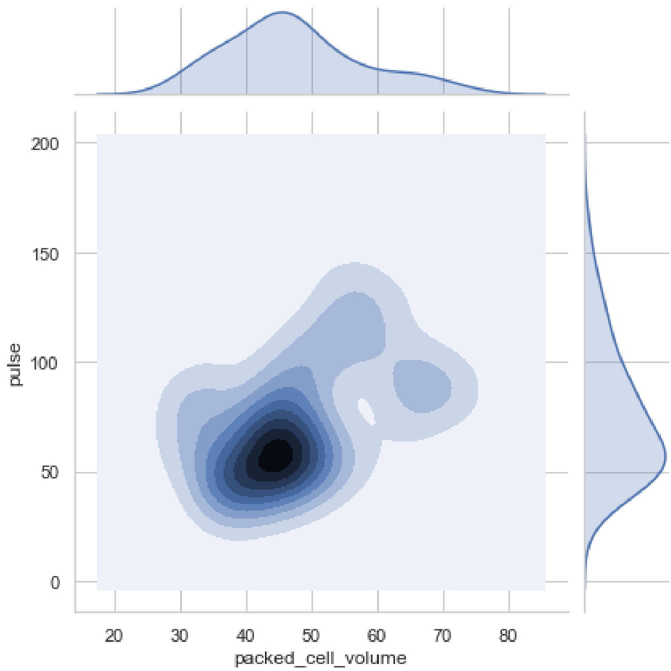
In [1157]:
```
sns.jointplot("pulse","respiratory_rate", data=q2_df, kind='kde') #normal rr is 8-10 p/min
```

Out[1157]: <seaborn.axisgrid.JointGrid at 0x1c52ef6080>

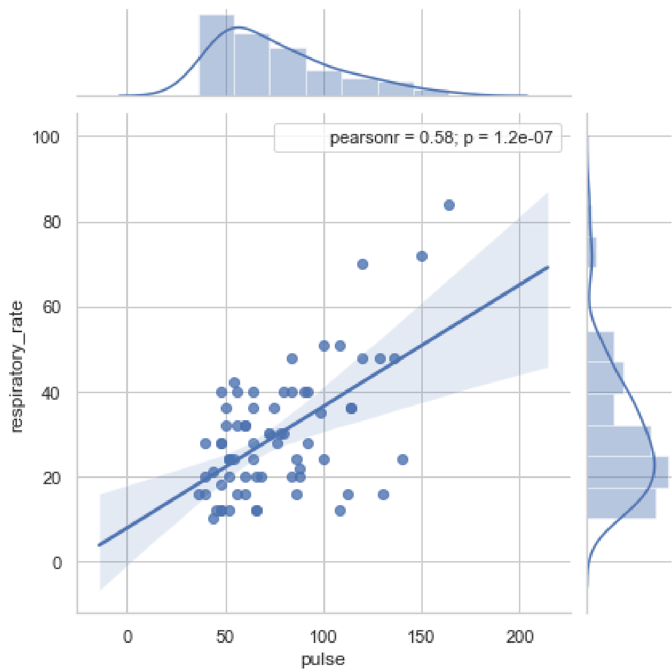


In [1155]:
```
sns.jointplot("packed_cell_volume","pulse", data=q2_df, kind='kde')#normal pcv is between 30-50; pulse 28-44 bpm
```

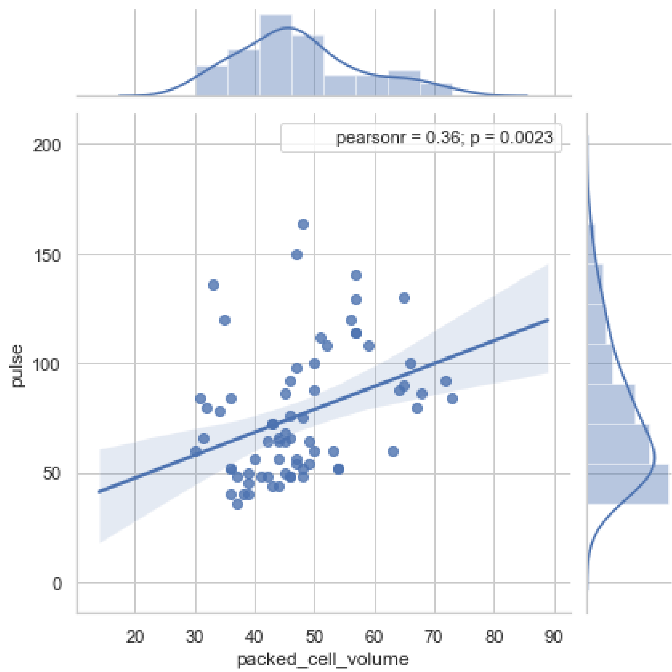
Out[1155]: <seaborn.axisgrid.JointGrid at 0x1c5286abe0>



In [958]:
```
g = sns.JointGrid(data=q2_df,x='pulse',y='respiratory_rate')
g = g.plot(sns.regplot, sns.distplot)
g = g.annotate(stats.pearsonr)
```



In [1154]:
```
g = sns.JointGrid(data=q2_df,x='packed_cell_volume',y='pulse')
g = g.plot(sns.regplot, sns.distplot)
g = g.annotate(stats.pearsonr)
```



In [1158]:
```
import statsmodels.api as sm
import statsmodels.formula.api as smf
```

In [1162]:
```
x={'lived':1,'died':2,'euthanized':3}
q2_df['outcome']=q2_df['outcome'].map(x)
new_q2=q2_df
new_q2.sample(5)
```

Out[1162]:

	rectal_temp	pulse	respiratory_rate	packed_cell_volume	total_protein	abdomo_protein	outcome
257	37.5	52.0	12.0	36.0	61.0	1.0	1
171	38.5	129.0	48.0	57.0	66.0	2.0	1
111	38.3	40.0	16.0	38.0	58.0	2.0	1
3	39.1	164.0	84.0	48.0	7.2	5.3	2
14	38.2	76.0	28.0	46.0	81.0	2.0	1

In [1163]:

```
new_q2['isalive'] = np.where(new_q2['outcome']==1,'alive','dead')
new_q2.sample(5)
```

Out[1163]:

	rectal_temp	pulse	respiratory_rate	packed_cell_volume	total_protein	abdomo_protein	outcome	isalive
224	38.4	54.0	24.0	49.0	7.2	8.0	1	alive
220	38.5	92.0	40.0	46.0	67.0	2.0	1	alive
49	37.2	84.0	48.0	73.0	5.5	4.1	2	dead
99	39.6	108.0	51.0	59.0	8.0	2.6	1	alive
33	38.2	64.0	28.0	49.0	8.6	6.6	1	alive

In [1164]:

```
new_q2.mean()
```

Out[1164]:

```
rectal_temp           38.145714
pulse                 76.071429
respiratory_rate      29.600000
packed_cell_volume    47.392857
total_protein         25.898571
abdomo_protein         3.007143
outcome                1.714286
dtype: float64
```

In [1166]:
```
anova_q1 = smf.ols('pulse ~ C(isalive)', data=new_q2).fit()
anova_q1.summary()
```

Out[1166]:

OLS Regression Results

Dep. Variable:	pulse	**R-squared:**	0.121
Model:	OLS	**Adj. R-squared:**	0.109
Method:	Least Squares	**F-statistic:**	9.399
Date:	Tue, 21 Apr 2020	**Prob (F-statistic):**	0.00311
Time:	06:32:34	**Log-Likelihood:**	-331.98
No. Observations:	70	**AIC:**	668.0
Df Residuals:	68	**BIC:**	672.5
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P>|t|**	**[0.025**	**0.975]**
Intercept	66.3243	4.630	14.323	0.000	57.084	75.564
C(isalive)[T.dead]	20.6757	6.744	3.066	0.003	7.218	34.133

Omnibus:	11.662	**Durbin-Watson:**	1.593
Prob(Omnibus):	0.003	**Jarque-Bera (JB):**	11.932
Skew:	0.942	**Prob(JB):**	0.00256
Kurtosis:	3.737	**Cond. No.**	2.56

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [1167]:
```
aov_table = sm.stats.anova_lm(anova_q1, typ=2)
print(aov_table)
```

```
                  sum_sq    df         F    PR(>F)
C(isalive)   7456.534749   1.0  9.399091  0.003113
Residual    53946.108108  68.0       NaN       NaN
```

In [1168]:
```
anova_q2 = smf.ols('respiratory_rate ~ C(isalive)', data=new_q2).fit()
anova_q2.summary()
```

Out[1168]:

OLS Regression Results

Dep. Variable:	respiratory_rate	**R-squared:**	0.003
Model:	OLS	**Adj. R-squared:**	-0.012
Method:	Least Squares	**F-statistic:**	0.1947
Date:	Tue, 21 Apr 2020	**Prob (F-statistic):**	0.660
Time:	06:32:43	**Log-Likelihood:**	-286.74
No. Observations:	70	**AIC:**	577.5
Df Residuals:	68	**BIC:**	582.0
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P>|t|**	**[0.025**	**0.975]**
Intercept	28.8649	2.426	11.897	0.000	24.023	33.706
C(isalive)[T.dead]	1.5594	3.534	0.441	0.660	-5.492	8.611

Omnibus:	23.749	**Durbin-Watson:**	2.403
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	36.030
Skew:	1.328	**Prob(JB):**	1.50e-08
Kurtosis:	5.303	**Cond. No.**	2.56

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [1169]:
```
aov_table = sm.stats.anova_lm(anova_q2, typ=2)
print(aov_table)
```

```
                 sum_sq    df         F    PR(>F)
C(isalive)     42.41507   1.0  0.194743  0.660398
Residual    14810.38493  68.0       NaN       NaN
```

In [1170]:
```
anova_q3 = smf.ols('packed_cell_volume ~ C(isalive)', data=new_q2).fit()
anova_q3.summary()
```

Out[1170]:

OLS Regression Results

Dep. Variable:	packed_cell_volume	**R-squared:**	0.218
Model:	OLS	**Adj. R-squared:**	0.207
Method:	Least Squares	**F-statistic:**	18.99
Date:	Tue, 21 Apr 2020	**Prob (F-statistic):**	4.55e-05
Time:	06:33:06	**Log-Likelihood:**	-253.07
No. Observations:	70	**AIC:**	510.1
Df Residuals:	68	**BIC:**	514.6
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P>|t|**	**[0.025**	**0.975]**
Intercept	42.9054	1.500	28.606	0.000	39.912	45.898
C(isalive)[T.dead]	9.5188	2.184	4.358	0.000	5.160	13.878

Omnibus:	0.028	**Durbin-Watson:**	1.793
Prob(Omnibus):	0.986	**Jarque-Bera (JB):**	0.037
Skew:	0.016	**Prob(JB):**	0.982
Kurtosis:	2.892	**Cond. No.**	2.56

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [1171]:
```
aov_table = sm.stats.anova_lm(anova_q3, typ=2)
print(aov_table)
```

```
                 sum_sq    df         F    PR(>F)
C(isalive)  1580.466904   1.0  18.98801  0.000046
Residual    5659.979525  68.0       NaN       NaN
```

In [1172]:
```
anova_q4 = smf.ols('total_protein ~ C(isalive)', data=new_q2).fit()
anova_q4.summary()
```

Out[1172]:

OLS Regression Results

Dep. Variable:	total_protein	**R-squared:**	0.000
Model:	OLS	**Adj. R-squared:**	-0.014
Method:	Least Squares	**F-statistic:**	0.01918
Date:	Tue, 21 Apr 2020	**Prob (F-statistic):**	0.890
Time:	06:33:20	**Log-Likelihood:**	-331.79
No. Observations:	70	**AIC:**	667.6
Df Residuals:	68	**BIC:**	672.1
Df Model:	1		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	25.4595	4.618	5.513	0.000	16.245	34.674
C(isalive)[T.dead]	0.9314	6.726	0.138	0.890	-12.489	14.352

Omnibus:	18.194	**Durbin-Watson:**	2.250
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	11.967
Skew:	0.871	**Prob(JB):**	0.00252
Kurtosis:	1.967	**Cond. No.**	2.56

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [1173]:
```
aov_table = sm.stats.anova_lm(anova_q4, typ=2)
print(aov_table)
```

```
                  sum_sq    df        F    PR(>F)
C(isalive)     15.133395   1.0  0.01918  0.89026
Residual    53652.016462  68.0      NaN      NaN
```

Q 3: Some of the vitals taken, like pain, temperature of extremities, and characteristics of the abdomen, are more on the subjective side. How do these ratings correlate to whether a horse will require surgery or not?

Create a contingency table to explore the relationship between the different categories of measurement. Further representations can be made using heatmaps.

Use Seaborn/Matplotlib and Contingency Table/Chi-squared

In [972]:
```
from scipy.stats import chi2_contingency
q3_df=colic_df[['hospital_number','surgery','pain','temp_of_extremities','peristalsis','abdominal_distention']]
q3_df.sample(10)
#variables with subjective criteria
```

Out[972]:

	hospital_number	surgery	pain	temp_of_extremities	peristalsis	abdominal_distention
174	527929	yes	NaN	NaN	NaN	NaN
152	528804	no	alert	cool	hypomotile	slight
200	528641	yes	severe_pain	normal	absent	moderate
237	528702	no	mild_pain	cool	hypomotile	slight
86	529388	yes	extreme_pain	cool	absent	moderate
47	529821	no	alert	normal	hypermotile	none
241	530354	yes	extreme_pain	normal	hypomotile	moderate
259	534933	no	severe_pain	NaN	hypomotile	slight
270	534626	yes	extreme_pain	cool	absent	none
46	529888	yes	extreme_pain	cool	absent	severe

Abdominal Distention

In [1096]:
```
ab=pd.crosstab(q3_df.abdominal_distention,q3_df.surgery,margins=False)
ab.drop(ab[-1:].index,inplace=True)
ab
```

Out[1096]:

surgery	no	yes
abdominal_distention		
moderate	15	50
none	41	34
severe	11	27

In [1097]:
```
chi2, p, dof, ex_ab = chi2_contingency(ab)
print("chi2 = ", chi2)
print("p-val = ", p)
print("degree of freedom = ",dof)
```

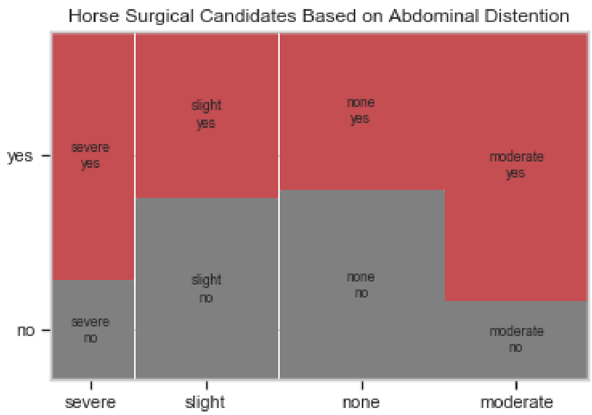
```
chi2 =  16.359548778339036
p-val =  0.0002802651638528373
degree of freedom =  2
```

In [1098]:
```
pd.DataFrame(ex_ab)
```

Out[1098]:

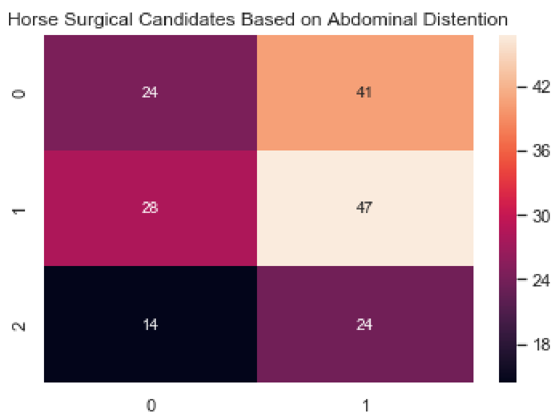
	0	1
0	24.466292	40.533708
1	28.230337	46.769663
2	14.303371	23.696629

In [1099]:
```
from statsmodels.graphics.mosaicplot import mosaic
props = lambda key: {'color': 'r' if 'yes' in key else 'gray'}
ab_vis = mosaic(q3_df, ['abdominal_distention','surgery'],title='Horse Surgical Candidates Based on Abdominal Distention',propert
ies=props)
```



In [1101]:
```
sns.heatmap(ex_ab,annot=True).set(title="Horse Surgical Candidates Based on Abdominal Distention")
```

Out[1101]:
```
[Text(0.5, 1, 'Horse Surgical Candidates Based on Abdominal Distention')]
```



Peristalsis

In [1114]:
```
peristalsis=pd.crosstab(q3_df.peristalsis,q3_df.surgery,margins=False)
peristalsis
```

Out[1114]:

surgery	no	yes
peristalsis		
absent	18	55
hypermotile	28	11
hypomotile	49	78
normal	5	11

In [1115]:
```
chi2, p, dof, ex_peri = chi2_contingency(peristalsis)
print("chi2 = ", chi2)
print("p-val = ", p)
print("degree of freedom = ",dof)
```

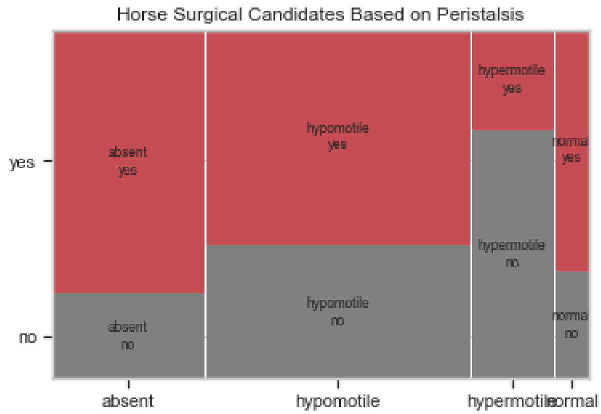
```
chi2 =  24.30360054000535
p-val =  2.158706853482651e-05
degree of freedom =  3
```

In [1116]:
```
pd.DataFrame(ex_peri)
```

Out[1116]:

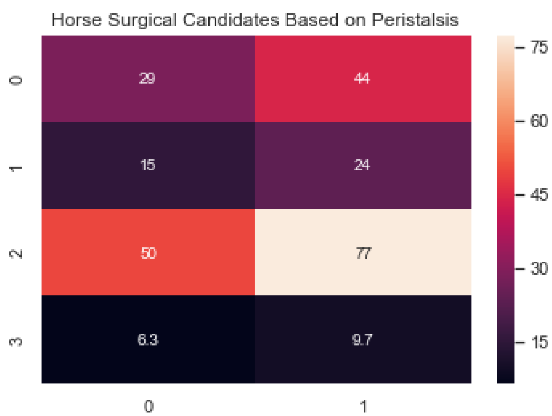
	0	1
0	28.627451	44.372549
1	15.294118	23.705882
2	49.803922	77.196078
3	6.274510	9.725490

In [1117]:
```
props = lambda key: {'color': 'r' if 'yes' in key else 'gray'}
peri_vis = mosaic(q3_df, ['peristalsis','surgery'],title='Horse Surgical Candidates Based on Peristalsis',properties=props)
```



In [1118]:
```
sns.heatmap(ex_peri,annot=True).set(title='Horse Surgical Candidates Based on Peristalsis')
```

Out[1118]: [Text(0.5, 1, 'Horse Surgical Candidates Based on Peristalsis')]



Pain

In [1120]:
```
pain = pd.crosstab(q3_df.pain,q3_df.surgery,margins=False)
#pain.drop(pain[-1:].index,inplace=True)
pain
```

Out[1120]:

surgery	no	yes
pain		
alert	29	9
depressed	25	34
extreme_pain	9	33
mild_pain	28	39
severe_pain	10	28

In [1121]:
```
chi2, p, dof, ex_pain = chi2_contingency(pain)
print("chi2 = ", chi2)
print("p-val = ", p)
print("degree of freedom = ",dof)
```

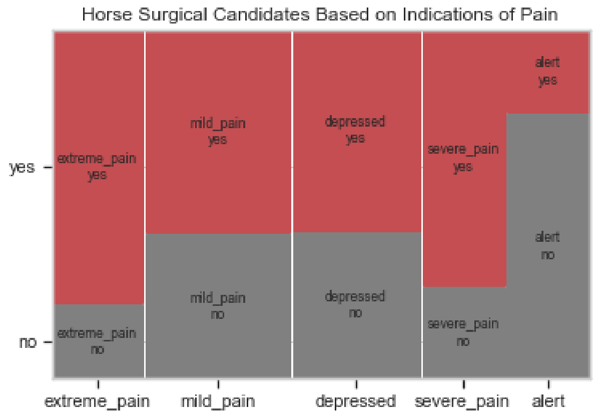
```
chi2 =  29.593077809019498
p-val =  5.922522835804105e-06
degree of freedom =  4
```

In [1122]:
```
pd.DataFrame(ex_pain)
```

Out[1122]:

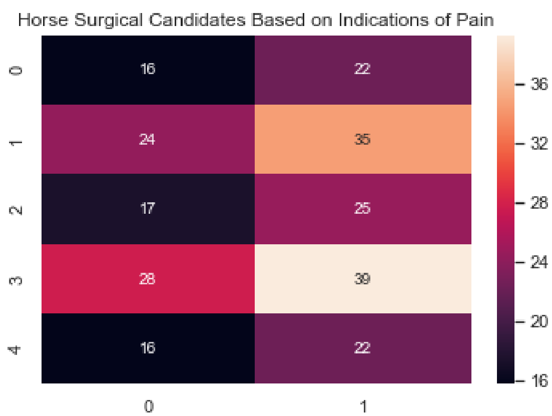
	0	1
0	15.729508	22.270492
1	24.422131	34.577869
2	17.385246	24.614754
3	27.733607	39.266393
4	15.729508	22.270492

In [1123]:
```
props = lambda key: {'color': 'r' if 'yes' in key else 'gray'}
pain_vis = mosaic(q3_df, ['pain','surgery'],title='Horse Surgical Candidates Based on Indications of Pain',properties=props)
```



In [1125]:
```
sns.heatmap(ex_pain,annot=True).set(title="Horse Surgical Candidates Based on Indications of Pain")
```

Out[1125]: [Text(0.5, 1, 'Horse Surgical Candidates Based on Indications of Pain')]



Extremity Temperature

In [1126]:
```
extremity_temp = pd.crosstab(q3_df.temp_of_extremities,q3_df.surgery,margins=False)
extremity_temp
```

Out[1126]:

surgery	no	yes
temp_of_extremities		
cold	7	20
cool	42	66
normal	35	43
warm	19	11

In [1127]:
```
chi2, p, dof, ex_temp = chi2_contingency(extremity_temp)
print("chi2 = ", chi2)
print("p-val = ", p)
print("degree of freedom = ",dof)
```

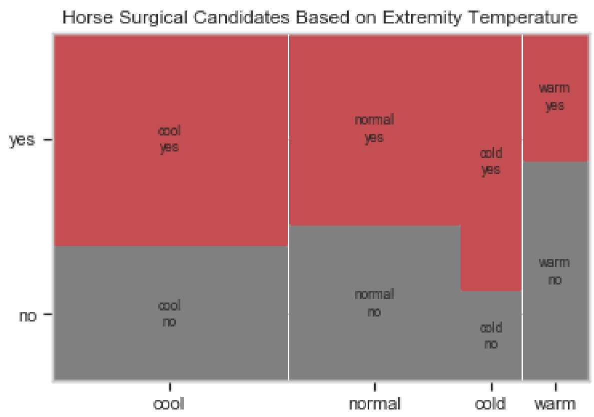
```
chi2 =  9.124231302677906
p-val =  0.02768395988750703
degree of freedom =  3
```

In [1128]:
```
ex_t=pd.DataFrame(ex_temp)
ex_t
```

Out[1128]:

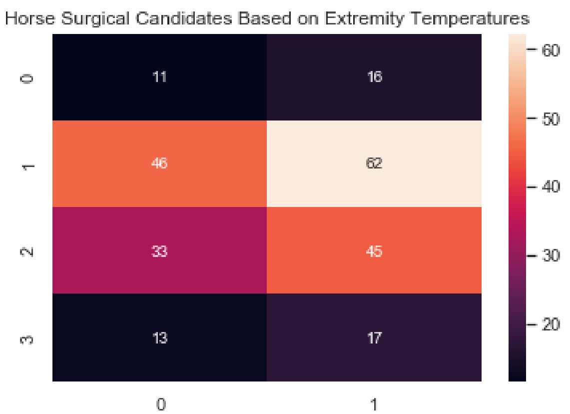
	0	1
0	11.444444	15.555556
1	45.777778	62.222222
2	33.061728	44.938272
3	12.716049	17.283951

In [1129]:
```
props = lambda key: {'color': 'r' if 'yes' in key else 'gray'}
pain_vis = mosaic(q3_df, ['temp_of_extremities','surgery'],title='Horse Surgical Candidates Based on Extremity Temperature',prope
rties=props)
```



In [1131]:
```
sns.heatmap(ex_temp,annot=True).set(title="Horse Surgical Candidates Based on Extremity Temperatures")
```

Out[1131]: [Text(0.5, 1, 'Horse Surgical Candidates Based on Extremity Temperatures')]



Q 4: Using the numerical values provided throughout the dataset, can the implementation of a random forest accurately predict if a horse survives colic?

Train the data and create a random forest to see if there is any predictive value of diagnostics

Use classification

In [1034]:
```
import sklearn as sk
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
import sklearn.ensemble as skens
import sklearn.metrics as skmetric
import sklearn.naive_bayes as sknb
import sklearn.tree as sktree
import sklearn.externals.six as sksix
import IPython.display as ipd
from sklearn.model_selection import cross_val_score
from sklearn import metrics
import os
```

In [1035]:
```
q4_df=colic_df[["rectal_temp","pulse","respiratory_rate","packed_cell_volume","total_protein","abdomo_protein","outcome"]].interp
olate()
```

In [1036]:
```
q4_df.isnull().sum()
```

Out[1036]:
```
rectal_temp           0
pulse                 0
respiratory_rate      0
packed_cell_volume    0
total_protein         0
abdomo_protein        1
outcome               0
dtype: int64
```

In [1037]:
```
fill_q4=q4_df.fillna(0,inplace=True)
```

In [1038]:
```
x=q4_df.loc[:,q4_df.columns!="outcome"]
y=q4_df.loc[:,q4_df.columns=="outcome"]
```

In [1039]:
```
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3,random_state=0)
len(x_train),len(x_test),len(y_train),len(y_test)
```

Out[1039]:
```
(209, 90, 209, 90)
```

In [1040]:
```
rf_model = skens.RandomForestClassifier(n_estimators=10,oob_score=True, criterion='entropy')
rf_model.fit(x_train,y_train)
```

Out[1040]:
```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='entropy',
                       max_depth=None, max_features='auto', max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=10,
                       n_jobs=None, oob_score=True, random_state=None,
                       verbose=0, warm_start=False)
```

In [1041]:
```
predicted_labels=rf_model.predict(x_test)
x_test['predicted_rf_tree']=predicted_labels
```

In [1000]:
```
from sklearn.metrics import accuracy_score
accuracy = accuracy_score(y_test,predicted_labels)
print('Accuracy:{0:.2%}'.format(accuracy))
```

```
Accuracy:61.11%
```

In [1003]:
```
from sklearn.model_selection import GridSearchCV
param_grid={
                'n_estimators':[5,10,15,20,25],
                'max_depth':[2,5,7,9]
}
grid_clf=GridSearchCV(rf_model,param_grid,cv=10)
grid_clf.fit(x_train,y_train)
```

Out[1003]:
```
GridSearchCV(cv=10, error_score='raise-deprecating',
             estimator=RandomForestClassifier(bootstrap=True, class_weight=None,
                                              criterion='entropy',
                                              max_depth=None,
                                              max_features='auto',
                                              max_leaf_nodes=None,
                                              min_impurity_decrease=0.0,
                                              min_impurity_split=None,
                                              min_samples_leaf=1,
                                              min_samples_split=2,
                                              min_weight_fraction_leaf=0.0,
                                              n_estimators=10, n_jobs=None,
                                              oob_score=True, random_state=None,
                                              verbose=0, warm_start=False),
             iid='warn', n_jobs=None,
             param_grid={'max_depth': [2, 5, 7, 9],
                         'n_estimators': [5, 10, 15, 20, 25]},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=False,
             scoring=None, verbose=0)
```

In [1004]:
```
grid_clf.best_estimator_
```

Out[1004]:
```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='entropy',
                       max_depth=5, max_features='auto', max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=25,
                       n_jobs=None, oob_score=True, random_state=None,
                       verbose=0, warm_start=False)
```

In [1005]:
```
grid_clf.best_params_
```

Out[1005]:
```
{'max_depth': 5, 'n_estimators': 25}
```

In [1006]:
```
grid_clf.best_score_
```

Out[1006]:
```
0.7081339712918661
```

In [1007]:
```
pd.DataFrame(grid_clf.cv_results_).sort_values(by='mean_test_score').tail(5)
```

Out[1007]:

	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_max_depth	param_n_estimators	params	split0_test_score	split1_test_score	split2_test_score	sp
1	0.009678	0.001115	0.001976	0.000683	2	10	{'max_depth': 2, 'n_estimators': 10}	0.727273	0.681818	0.681818	
18	0.019881	0.001828	0.002451	0.000448	9	20	{'max_depth': 9, 'n_estimators': 20}	0.727273	0.727273	0.818182	
8	0.019240	0.005396	0.002228	0.000410	5	20	{'max_depth': 5, 'n_estimators': 20}	0.727273	0.681818	0.727273	
12	0.015302	0.001346	0.002214	0.000672	7	15	{'max_depth': 7, 'n_estimators': 15}	0.681818	0.727273	0.818182	
9	0.019361	0.000857	0.002221	0.000092	5	25	{'max_depth': 5, 'n_estimators': 25}	0.681818	0.863636	0.727273	

In [1008]:
```
grid_clf3=GridSearchCV(rf_model,param_grid,cv=5)
grid_clf3.fit(x_train,y_train)
```

Out[1008]:
```
GridSearchCV(cv=5, error_score='raise-deprecating',
             estimator=RandomForestClassifier(bootstrap=True, class_weight=None,
                                              criterion='entropy',
                                              max_depth=None,
                                              max_features='auto',
                                              max_leaf_nodes=None,
                                              min_impurity_decrease=0.0,
                                              min_impurity_split=None,
                                              min_samples_leaf=1,
                                              min_samples_split=2,
                                              min_weight_fraction_leaf=0.0,
                                              n_estimators=10, n_jobs=None,
                                              oob_score=True, random_state=None,
                                              verbose=0, warm_start=False),
             iid='warn', n_jobs=None,
             param_grid={'max_depth': [2, 5, 7, 9],
                         'n_estimators': [5, 10, 15, 20, 25]},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=False,
             scoring=None, verbose=0)
```

In [1009]:
```
grid_clf3.best_estimator_
```

Out[1009]:
```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='entropy',
                       max_depth=9, max_features='auto', max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=25,
                       n_jobs=None, oob_score=True, random_state=None,
                       verbose=0, warm_start=False)
```

In [1010]:
```
grid_clf3.best_score_
```

Out[1010]:
```
0.7081339712918661
```

In [1011]:
```
grid_clf3.best_params_
```

Out[1011]:
```
{'max_depth': 9, 'n_estimators': 25}
```

In [1012]:
```
param_grid2 = {
                 'n_estimators': [4, 8, 16, 24, 28],
                 'max_depth': [2, 5, 7, 9],
             }
grid_clf5=GridSearchCV(rf_model,param_grid2,cv=10)
grid_clf5.fit(x_train,y_train)
```

Out[1012]:
```
GridSearchCV(cv=10, error_score='raise-deprecating',
             estimator=RandomForestClassifier(bootstrap=True, class_weight=None,
                                              criterion='entropy',
                                              max_depth=None,
                                              max_features='auto',
                                              max_leaf_nodes=None,
                                              min_impurity_decrease=0.0,
                                              min_impurity_split=None,
                                              min_samples_leaf=1,
                                              min_samples_split=2,
                                              min_weight_fraction_leaf=0.0,
                                              n_estimators=10, n_jobs=None,
                                              oob_score=True, random_state=None,
                                              verbose=0, warm_start=False),
             iid='warn', n_jobs=None,
             param_grid={'max_depth': [2, 5, 7, 9],
                         'n_estimators': [4, 8, 16, 24, 28]},
             pre_dispatch='2*n_jobs', refit=True, return_train_score=False,
             scoring=None, verbose=0)
```

In [1013]:
```
grid_clf5.best_estimator_
```

Out[1013]:
```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='entropy',
                       max_depth=7, max_features='auto', max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=16,
                       n_jobs=None, oob_score=True, random_state=None,
                       verbose=0, warm_start=False)
```

In [1014]:
```
grid_clf5.best_score_
```

Out[1014]:
```
0.7177033492822966
```

In [1015]:
```
grid_clf5.best_params_
```

Out[1015]:
```
{'max_depth': 7, 'n_estimators': 16}
```

In [1016]:
```
pd.DataFrame(grid_clf5.cv_results_).sort_values(by='mean_test_score').tail(5)
```

Out[1016]:

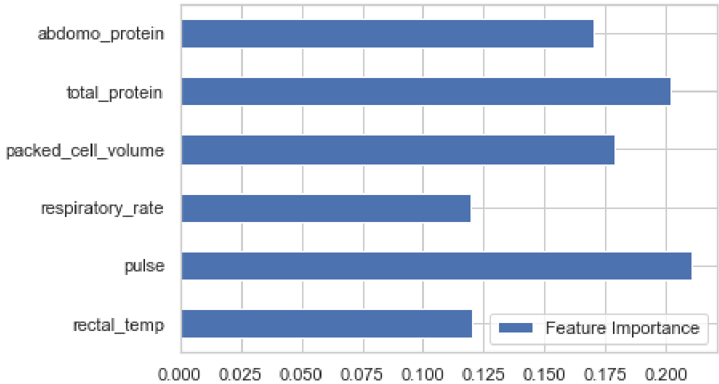
	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_max_depth	param_n_estimators	params	split0_test_score	split1_test_score	split2_test_score	sp
8	0.018007	0.000088	0.002125	0.000060	5	24	{'max_depth': 5, 'n_estimators': 24}	0.727273	0.772727	0.727273	
9	0.020938	0.000363	0.002369	0.000109	5	28	{'max_depth': 5, 'n_estimators': 28}	0.772727	0.818182	0.727273	
19	0.023918	0.002528	0.002675	0.000562	9	28	{'max_depth': 9, 'n_estimators': 28}	0.681818	0.818182	0.818182	
5	0.004943	0.000103	0.001096	0.000079	5	4	{'max_depth': 5, 'n_estimators': 4}	0.772727	0.772727	0.818182	
12	0.013271	0.000131	0.001716	0.000055	7	16	{'max_depth': 7, 'n_estimators': 16}	0.727273	0.818182	0.818182	

In [1018]:
```
feat_importance=rf_model.feature_importances_
feat_importance
```

Out[1018]:
```
array([0.11987981, 0.21008393, 0.11924145, 0.17876866, 0.20190435,
       0.1701218 ])
```

In [1017]:
```
feat_importance = rf_model.feature_importances_
pd.DataFrame({'Feature Importance':feat_importance},
            index=x_train.columns).plot(kind='barh')
```

Out[1017]: `<matplotlib.axes._subplots.AxesSubplot at 0x1c4c72fcf8>`



In [ ]: