

Heart Disease

CEP

Group Members

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Introduction

Disease:

We work through bayese

Libraries:

- Pandas
- Seaborn
- Urllib
- Pgmpy

Use of Library:

Pandas:

Pandas is used to read out data set from format that is suitable for our model.

Seaborn:

Seaborn is used to visualise our data.

Urllib:

Urllib is used to open urls which help us feed our data set to the model.

Pgmpy:

Pgmpy allows us to work with graphical data.

Graph:

We use the heat graph which help visualise our data.

Data set

- Our dataset is saved in .CSV format. We will be using Python for this task and will use pandas, numpy, seaborn, . This model will help us do our prediction for Heart patients

Program

localhost:8888/notebooks/R%26RP-8.ipynb

jupyter R&RP-8 Last Checkpoint: 24 minutes ago (autosaved) Python 3

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Run

```
In [30]: import pandas as pd
import seaborn as sns
from urllib.request import urlopen
from pgmpy.models import BayesianModel
```

```
In [31]: names = "A,B,C,D,E,F,G,H,I,J,K,L,M,RESULT"
names = names.split(",")
```

```
In [32]: data = pd.read_csv(urlopen("http://bit.do/heart-disease"), names=names)
data.head()
```

Out[32]:

	A	B	C	D	E	F	G	H	I	J	K	L	M	RESULT
0	63.0	1.0	1.0	145.0	233.0	1.0	2.0	150.0	0.0	2.3	3.0	0.0	6.0	0
1	67.0	1.0	4.0	160.0	286.0	0.0	2.0	108.0	1.0	1.5	2.0	3.0	3.0	2
2	67.0	1.0	4.0	120.0	229.0	0.0	2.0	129.0	1.0	2.6	2.0	2.0	7.0	1
3	37.0	1.0	3.0	130.0	250.0	0.0	0.0	187.0	0.0	3.5	3.0	0.0	3.0	0
4	41.0	0.0	2.0	130.0	204.0	0.0	2.0	172.0	0.0	1.4	1.0	0.0	3.0	0

```
In [33]: data.describe()
```

Out[33]:

	A	B	C	D	E	F	G	H	I	J	K	RESULT
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.438944	0.679868	3.158416	131.689769	246.693069	0.148515	0.990099	149.607261	0.326733	1.039604	1.600660	0.937294
std	9.038662	0.467299	0.960126	17.599748	51.776918	0.356198	0.994971	22.875003	0.469794	1.161075	0.616226	1.228536
min	29.000000	0.000000	1.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	1.000000	0.000000
25%	48.000000	0.000000	3.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000
50%	56.000000	1.000000	3.000000	130.000000	241.000000	0.000000	1.000000	153.000000	0.000000	0.800000	2.000000	0.000000

50%	56.000000	1.000000	3.000000	130.000000	241.000000	0.000000	1.000000	153.000000	0.000000	0.800000	2.000000	0.000000
75%	61.000000	1.000000	4.000000	140.000000	275.000000	0.000000	2.000000	166.000000	1.000000	1.600000	2.000000	2.000000
max	77.000000	1.000000	4.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	3.000000	4.000000

```
In [34]: pairwise_correlation = data.corr()
```

```
In [35]: pairwise_correlation
```

```
Out[35]:
```

	A	B	C	D	E	F	G	H	I	J	K	RESULT
A	1.000000	-0.097542	0.104139	0.284946	0.208950	0.118530	0.148868	-0.393806	0.091661	0.203805	0.161770	0.222853
B	-0.097542	1.000000	0.010084	-0.064456	-0.199915	0.047862	0.021647	-0.048663	0.146201	0.102173	0.037533	0.224469
C	0.104139	0.010084	1.000000	-0.036077	0.072319	-0.039975	0.067505	-0.334422	0.384060	0.202277	0.152050	0.407075
D	0.284946	-0.064456	-0.036077	1.000000	0.130120	0.175340	0.146560	-0.045351	0.064762	0.189171	0.117382	0.157754
E	0.208950	-0.199915	0.072319	0.130120	1.000000	0.009841	0.171043	-0.003432	0.061310	0.046564	-0.004062	0.070909
F	0.118530	0.047862	-0.039975	0.175340	0.009841	1.000000	0.069564	-0.007854	0.025665	0.005747	0.059894	0.059186
G	0.148868	0.021647	0.067505	0.146560	0.171043	0.069564	1.000000	-0.083389	0.084867	0.114133	0.133946	0.183696
H	-0.393806	-0.048663	-0.334422	-0.045351	-0.003432	-0.007854	-0.083389	1.000000	-0.378103	-0.343085	-0.385601	-0.415040
I	0.091661	0.146201	0.384060	0.064762	0.061310	0.025665	0.084867	-0.378103	1.000000	0.288223	0.257748	0.397057
J	0.203805	0.102173	0.202277	0.189171	0.046564	0.005747	0.114133	-0.343085	0.288223	1.000000	0.577537	0.504092
K	0.161770	0.037533	0.152050	0.117382	-0.004062	0.059894	0.133946	-0.385601	0.257748	0.577537	1.000000	0.377957
RESULT	0.222853	0.224469	0.407075	0.157754	0.070909	0.059186	0.183696	-0.415040	0.397057	0.504092	0.377957	1.000000

```
In [36]: sns.heatmap(pairwise_correlation, xticklabels='auto', yticklabels='auto')
```

```
Out[36]: <AxesSubplot:>
```





```
In [37]: model = BayesianModel([("A","B"),("B","C"),("C","RESULT")])
model.fit(data)
```

```
In [38]: from pgmpy.inference import VariableElimination
infer = VariableElimination(model)
print(infer.query(variables=["RESULT"],evidence={"A":22}))
```

D:\Anaconda\lib\site-packages\pgmpy\factors\discrete\DiscreteFactor.py:518: UserWarning: Found unknown state name. Trying to switch to using all state names as state numbers

```
warn(
Finding Elimination Order: : 0%|          | 0/2 [00:00<?, ?it/s]
0%|          | 0/2 [00:00<?, ?it/s]
Finding Elimination Order: : 100%|████████| 2/2 [00:00<00:00, 334.39it/s]

Eliminating: B: 100%|████████| 2/2 [00:00<00:00, 401.06it/s]
```

RESULT	phi(RESULT)
RESULT(0)	0.5387
RESULT(1)	0.1824
RESULT(2)	0.1196
RESULT(3)	0.1161
RESULT(4)	0.0433

Output Graph

