

```
!pip install pgmpy --upgrade # Update pgmpy to the latest version. Sometimes 'BayesianModel' moves between versions
from pgmpy.models import DiscreteBayesianNetwork # Use DiscreteBayesianNetwork instead of BayesianNetwork
# %%
cancer_model = DiscreteBayesianNetwork([('Pollution', 'Cancer'), ('Smoker', 'Cancer'), ('Cancer', 'Xray'), ('Cancer', 'Dyspnoea')]) # Replace Bayesi.
```

```
Collecting pgmpy
  Using cached pgmpy-1.0.0-py3-none-any.whl.metadata (9.4 kB)
Requirement already satisfied: networkx in /usr/local/lib/python3.11/dist-packages (from pgmpy) (3.4.2)
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Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (from python-dateutil>=2.8.2->pandas->pgmpy) (1.17.0)
Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.11/dist-packages (from jinja2->torch->pgmpy) (3.0.2)
Using cached pgmpy-1.0.0-py3-none-any.whl (2.0 MB)
Installing collected packages: pgmpy
Successfully installed pgmpy-1.0.0
```

```
print(cancer_model)
```

```
DiscreteBayesianNetwork with 5 nodes and 4 edges
```

```
cancer_model.nodes()
```

```
NodeView(('Pollution', 'Cancer', 'Smoker', 'Xray', 'Dyspnoea'))
```

```
cancer_model.edges()
```

```
OutEdgeView([('Pollution', 'Cancer'), ('Cancer', 'Xray'), ('Cancer', 'Dyspnoea'), ('Smoker', 'Cancer')])
```

```
cancer_model.get_cpds()
#conditional probabilities
```

```
[]
```

```
#creation of cond prob table
```

```
from pgmpy.factors.discrete import TabularCPD #cond probab density
#2 values are passed means 0.9 will be prob when pollution will be high and for low the value is 0.1
cpd_poll = TabularCPD(variable='Pollution',variable_card=2,values=[[0.1],[0.9]])
cpd_smoke = TabularCPD(variable='Smoker',variable_card=2,values=[[0.3],[0.7]])
cpd_cancer=TabularCPD(variable='Cancer',variable_card=2,values=[[0.97,0.95,0.001,0.02],[0.03,0.05,0.999,0.98]],
```

```

        evidence=['Smoker', 'Pollution'],
        evidence_card=[2,2])
cpd_xray=TabularCPD(variable='Xray',variable_card=2,values=[[0.9,0.2],[0.1,0.8]],
        evidence=['Cancer'],
        evidence_card=[2])
cpd_dysp=TabularCPD(variable='Dyspnoea',variable_card=2,values=[[0.65,0.3],[0.35,0.7]],
        evidence=['Cancer'],
        evidence_card=[2])

```

```

cancer_model.add_cpds(cpd_poll,cpd_smoke,cpd_cancer,cpd_xray,cpd_dysp)
cancer_model.check_model()

```

➡ True

```

#cancer_model.is_active_trail('Pollution','Smoker')
!pip install pgmpy --upgrade
from pgmpy.models import DiscreteBayesianNetwork
from pgmpy.inference import CausalInference

```

```

# ... (your existing code for creating and defining cancer_model) ...

```

```

# Create a CausalInference object
infer = CausalInference(cancer_model)

```

```

# Check for d-separation using the is_d_separated method (if available)
# Or, try using other inference methods like query for conditional independence
try:

```

```

    are_d_separated = infer.is_d_separated("Pollution", "Smoker", {}) # Check for is_d_separated method
except AttributeError:
    # If is_d_separated is not available, consider using other inference methods
    # For example, to check for conditional independence:
    # result = infer.query(['Pollution'], evidence={'Smoker': 0}) # Query for Pollution given Smoker=0
    # You can then analyze the result to determine conditional independence
    print("d-separation check not directly supported. Consider using other inference methods.")
    are_d_separated = None # Or handle the case as needed

```

```

# Print the result
print(f"'Pollution' and 'Smoker' are d-separated: {are_d_separated}")

```

➡ Requirement already satisfied: pgmpy in /usr/local/lib/python3.11/dist-packages (1.0.0)

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 Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.11/dist-packages (from jinja2->torch->pgmpy) (3.0.2)
 d-separation check not directly supported. Consider using other inference methods.
 'Pollution' and 'Smoker' are d-separated: None

```
cancer_model.get_cpds()
print(cancer_model.get_cpds('Pollution'))
```

```
↔ +-----+-----+
   | Pollution(0) | 0.1 |
   +-----+-----+
   | Pollution(1) | 0.9 |
   +-----+-----+
```

```
cancer_model.get_cpds()
print(cancer_model.get_cpds('Cancer'))
```

```
↔ +-----+-----+-----+-----+-----+
   | Smoker   | Smoker(0) | Smoker(0) | Smoker(1) | Smoker(1) |
   +-----+-----+-----+-----+-----+
   | Pollution | Pollution(0) | Pollution(1) | Pollution(0) | Pollution(1) |
   +-----+-----+-----+-----+-----+
   | Cancer(0) | 0.97      | 0.95      | 0.001      | 0.02      |
   +-----+-----+-----+-----+-----+
   | Cancer(1) | 0.03      | 0.05      | 0.999      | 0.98      |
   +-----+-----+-----+-----+-----+
```

```
cancer_model.get_cpds()
print(cancer_model.get_cpds('Smoker'))
```

```
↔ +-----+-----+
   | Smoker(0) | 0.3 |
   +-----+-----+
   | Smoker(1) | 0.7 |
   +-----+-----+
```

```
cancer_model.get_cpds()
print(cancer_model.get_cpds('Xray'))
```

```
↔ +-----+-----+-----+
   | Cancer   | Cancer(0) | Cancer(1) |
   +-----+-----+-----+
   | Xray(0)  | 0.9       | 0.2       |
   +-----+-----+-----+
   | Xray(1)  | 0.1       | 0.8       |
   +-----+-----+-----+
```

```
cancer_model.get_cpds()
print(cancer_model.get_cpds('Dyspnoea'))
```

```
↔ +-----+-----+-----+
   | Cancer   | Cancer(0) | Cancer(1) |
   +-----+-----+-----+
   | Dyspnoea(0) | 0.65      | 0.3       |
   +-----+-----+-----+
   | Dyspnoea(1) | 0.35      | 0.7       |
   +-----+-----+-----+
```

#determine local independencies meant which all are independent edges

```
cancer_model.local_independencies('Xray')
```

```
↔ (Xray ⊥ Dyspnoea, Smoker, Pollution | Cancer)
```

```
cancer_model.local_independencies('Pollution')
```

```
↔ (Pollution ⊥ Smoker)
```

```
cancer_model.local_independencies('Smoker')
```

```
↔ (Smoker ⊥ Pollution)
```

```
cancer_model.local_independencies('Dyspnoea')
```

```
↔ (Dyspnoea ⊥ Xray, Smoker, Pollution | Cancer)
```

```
cancer_model.local_independencies('Cancer')
```

```
↔
```

```
cancer_model.get_independencies()
```

```
#taking random 6
```

```
↔ (Dyspnoea ⊥ Smoker | Cancer)
   (Xray ⊥ Smoker | Cancer)
   (Pollution ⊥ Smoker)
   (Dyspnoea ⊥ Xray | Cancer)
   (Pollution ⊥ Xray | Cancer)
   (Pollution ⊥ Dyspnoea | Cancer)
```

#konsa feature kispr dependent hai and which one is better,allows to eliminate the features/variables that are not efficient wrt model
#Inferencing with Bayesian Network

```
from pgmpy.inference import VariableElimination
cancer_infer=VariableElimination(cancer_model)
q=cancer_infer.query(variables=['Cancer'],evidence={'Smoker':1})
print(q)
#if the person is smoker, then the cond prob is this
```

```
↔ +-----+-----+
   | Cancer |   phi(Cancer) |
   +-----+-----+
   | Cancer(0) |      0.0181 |
   +-----+-----+
   | Cancer(1) |      0.9819 |
   +-----+-----+
```

```
q=cancer_infer.query(variables=['Cancer'],evidence={'Smoker': 1,'Pollution':1})
print(q)
```

```
↔ +-----+-----+
   | Cancer |   phi(Cancer) |
   +-----+-----+
   | Cancer(0) |      0.0200 |
   +-----+-----+
   | Cancer(1) |      0.9800 |
   +-----+-----+
```

Start coding or [generate](#) with AI.