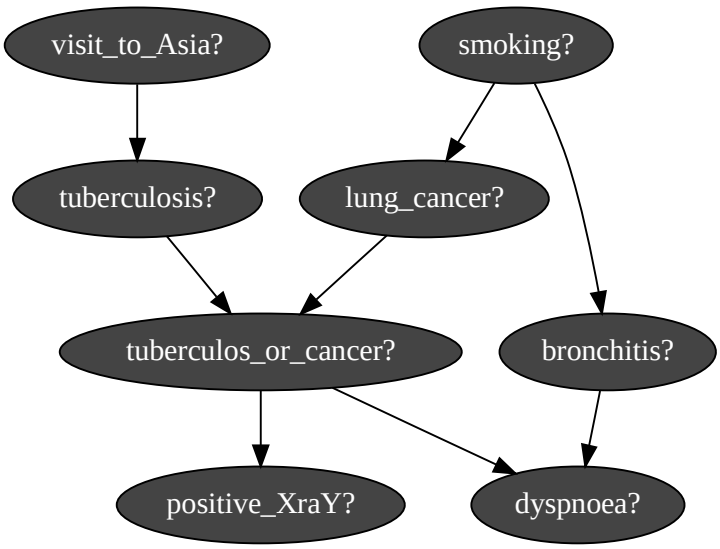
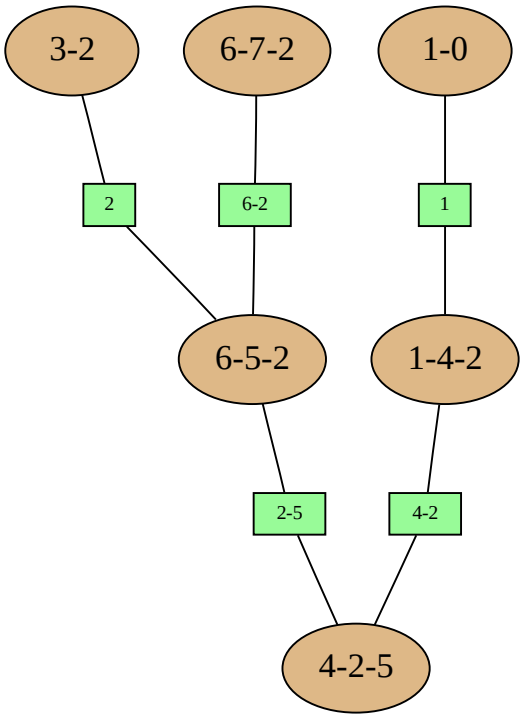
In [59]:
```
import pyAgrum as gum
import gumLib.notebook as gnb
```

In [60]:
```
bn=gum.loadBN("C:/Users/phw/Dropbox/BayesNetRepository/asia.bif")
gnb.showBN(bn)
```



In [61]:
```
gnb.showJunctionTree(bn)
```



In [62]:
```
bn.ids()
```

Out[62]:
```
[0, 1, 2, 3, 4, 5, 6, 7]
```

In [63]:
```
bn.topologicalOrder()
```

Out[63]:
```
[5, 4, 6, 0, 1, 2, 7, 3]
```

In [67]:
```
bn.arcs()
```

Out[67]:
```
[(0, 1), (5, 6), (2, 3), (2, 7), (4, 2), (1, 2), (5, 4), (6, 7)]
```

In [68]:
```
print(bn.variable(6))
print(bn.variable(7))
```

```
bronchitis?<g1,g2>
dyspnoea?<h1,h2>
```

In [69]:
```
print(bn.cpt(7)) # dispnoea
```

```
<dyspnoea?:h1|bronchitis?:g1|tuberculos_or_cancer?:c1> :: 0.9 /<dyspnoea?:h
2|bronchitis?:g1|tuberculos_or_cancer?:c1> :: 0.1 /<dyspnoea?:h1|bronchitis
?:g2|tuberculos_or_cancer?:c1> :: 0.7 /<dyspnoea?:h2|bronchitis?:g2|tubercu
los_or_cancer?:c1> :: 0.3 /<dyspnoea?:h1|bronchitis?:g1|tuberculos_or_cance
r?:c2> :: 0.8 /<dyspnoea?:h2|bronchitis?:g1|tuberculos_or_cancer?:c2> :: 0.
2 /<dyspnoea?:h1|bronchitis?:g2|tuberculos_or_cancer?:c2> :: 0.1 /<dyspnoea
?:h2|bronchitis?:g2|tuberculos_or_cancer?:c2> :: 0.9
```

In [70]:
```
ie=gum.LazyPropagation(bn)
jt=ie.junctionTree()
print(jt)
```

```
list of nodes:
 -- node: 0
    clique:  3  2
 -- node: 1
    clique:  6  7  2
 -- node: 2
    clique:  1  0
 -- node: 3
    clique:  1  4  2
 -- node: 4
    clique:  6  5  2
 -- node: 5
    clique:  4  2  5


list of edges:
1--4  3--5  2--3  4--5  0--4
```

In [71]:
```
jt.ids()
```

Out[71]: [0, 1, 2, 3, 4, 5]

In [72]:
```
jt.edges()
```

Out[72]: [(1, 4), (3, 5), (2, 3), (4, 5), (0, 4)]

In [73]:
```
c3=jt.clique(3)
c1=jt.clique(1)
```

In [74]:
```
c3.intersection(c1)
```

Out[74]: {2}

In [75]:
```
print(bn.variable(2))
```

```
tuberculos_or_cancer?<c1,c2>
```

In [76]:
```
jt.clique(4)
```

Out[76]: {2, 5, 6}

In [77]:
```
bn=gum.loadBN("C:/Users/phw/Dropbox/BayesNetRepository/asia.bif")
target=["dyspnoae?","bronchitis?"]
evs={"smoking?":[1,0]}

def nomPotentiel(jt,c):
    res="Phi"
    for n in jt.clique(c):
        res+=str(n)+"_"
    return res

for c in jt.ids():
    res="Creation du potential : "+nomPotentiel(jt,c)
    print(res)

for c in jt.ids():
    for n in jt.clique(c):
        print("ajout de la variable "+str(n)+" à "+nomPotentiel(jt,c))
```

```
Creation du potential : Phi2_3_
Creation du potential : Phi2_6_7_
Creation du potential : Phi0_1_
Creation du potential : Phi1_2_4_
Creation du potential : Phi2_5_6_
Creation du potential : Phi2_4_5_
ajout de la variable 2 à Phi2_3_
ajout de la variable 3 à Phi2_3_
ajout de la variable 2 à Phi2_6_7_
ajout de la variable 6 à Phi2_6_7_
ajout de la variable 7 à Phi2_6_7_
ajout de la variable 0 à Phi0_1_
ajout de la variable 1 à Phi0_1_
ajout de la variable 1 à Phi1_2_4_
ajout de la variable 2 à Phi1_2_4_
ajout de la variable 4 à Phi1_2_4_
ajout de la variable 2 à Phi2_5_6_
ajout de la variable 5 à Phi2_5_6_
ajout de la variable 6 à Phi2_5_6_
ajout de la variable 2 à Phi2_4_5_
ajout de la variable 4 à Phi2_4_5_
ajout de la variable 5 à Phi2_4_5_
```

In []: