## Tarea 4

## Instalación

## Repositorio

https://github.com/hyfi06/pcic-ai241/tree/tarea-4

```
git clone https://github.com/hyfi06/pcic-ai241.git
git checkout tarea-4
```

## Python version

• Python 3.10.6

### Entorno virtual

```
cd Tarea\ 4
python3 -m venv venv
source venv/bin/activate
```

### Instalación de dependencias

```
pip install --upgrade pip
pip install -r requirements.txt
```

# Ejecución

#### Problema de la alarma

Implentación en https://github.com/hyfi06/pcic-ai241/blob/tarea-4/Tarea%204/alarma.py

```
python3 alarma.py
```

### Resultado:

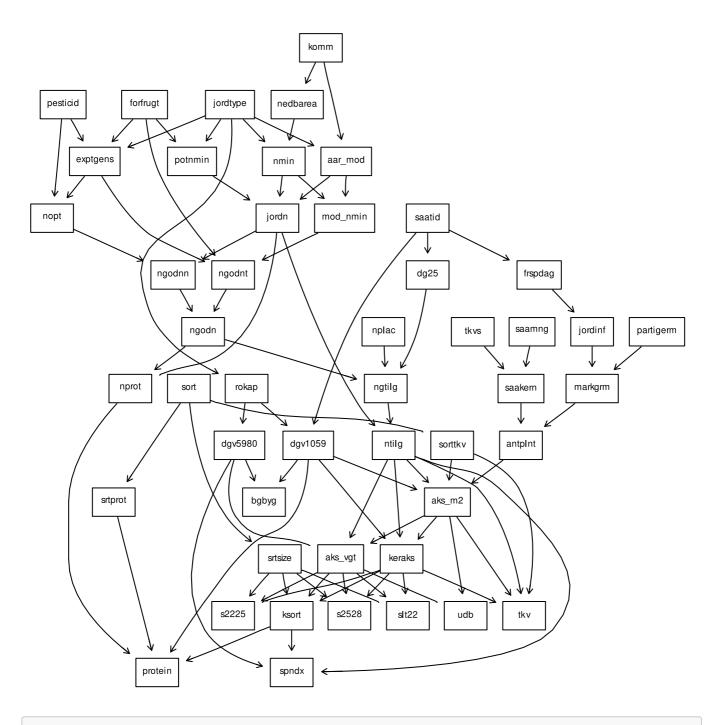
```
P(Burglary | JohnCalls=+j, MaryCalls=+m):
+----+
| B | phi(B) |
+=====+
```

```
| B(-b) | 0.7158 |
+----+
| B(+b) | 0.2842 |
+----+
P(Earthqk | JohnCalls=+j, MaryCalls=+m):
+----+
| E | phi(E) |
+=====+
| E(-e) | 0.8239 |
+----+
| E(+e) | 0.1761 |
+----+
P(JohnCalls | MaryCalls=-m):
+----+
+=====+
| J(-j) | 0.9494 |
+----+
| J(+j) | 0.0506 |
+----+
Están d-separados de "Burglary" al observar "Alarm": {'B': {'E', 'B'}}
```

## Problema Barley

Modelo preliminar para cebada desarrollado en el marco del proyecto: "Producción de cerveza a partir de cebada cervecera danesa cultivada sin el uso de pesticidas" de Kristian Kristensen, Ilse A. Rasmussen y otros.

https://www.bnlearn.com/bnrepository/discrete-medium.html#barley



python3 barley.py

Queries: https://github.com/hyfi06/pcic-ai241/blob/tarea-4/Tarea%204/barley.py

#### Resultado:

```
Nodos:
['jordtype', 'komm', 'nedbarea', 'nmin', 'aar_mod', 'forfrugt', 'potnmin', 'jordn', 'pesticid', 'exptgens', 'mod_nmin', 'ngodnt', 'nopt', 'ngodnn', 'ngodn', 'nprot', 'saatid', 'rokap', 'dgv1059', 'sort', 'srtprot', 'nplac', 'dg25', 'ngtilg', 'ntilg', 'saamng', 'tkvs', 'saakern', 'partigerm', 'frspdag', 'jordinf', 'markgrm', 'antplnt', 'sorttkv', 'aks_m2', 'keraks', 'dgv5980', 'aks_vgt', 'srtsize', 'ksort', 'protein', 'udb', 'spndx', 'tkv', 'slt22', 's2225', 's2528', 'bgbyg']
```

```
Aristas:
[('jordtype', 'nmin'), ('jordtype', 'aar_mod'), ('jordtype', 'potnmin'),
('jordtype', 'exptgens'), ('jordtype', 'rokap'), ('komm', 'nedbarea'),
('komm', 'aar_mod'), ('nedbarea', 'nmin'), ('nmin', 'jordn'), ('nmin',
'mod_nmin'), ('aar_mod', 'jordn'), ('aar_mod', 'mod_nmin'), ('forfrugt',
'potnmin'), ('forfrugt', 'exptgens'), ('forfrugt', 'ngodnt'), ('potnmin',
'jordn'), ('jordn', 'ngodnn'), ('jordn', 'nprot'), ('jordn', 'ntilg'),
('pesticid', 'exptgens'), ('pesticid', 'nopt'), ('exptgens', 'ngodnt'),
('exptgens', 'nopt'), ('mod_nmin', 'ngodnt'), ('ngodnt', 'ngodn'), ('nopt',
'ngodnn'), ('ngodn', 'ngodn', 'nprot'), ('ngodn', 'ngtilg'),
('nprot', 'protein'), ('saatid', 'dgv1059'), ('saatid', 'dg25'), ('saatid',
'frspdag'), ('rokap', 'dgv1059'), ('rokap', 'dgv5980'), ('dgv1059',
'aks_m2'), ('dgv1059', 'keraks'), ('dgv1059', 'protein'), ('dgv1059',
'bgbyg'), ('sort', 'srtprot'), ('sort', 'sorttkv'), ('sort', 'srtsize'),
('srtprot', 'protein'), ('nplac', 'ngtilg'), ('dg25', 'ngtilg'), ('ngtilg',
'ntilg'), ('ntilg', 'aks_m2'), ('ntilg', 'keraks'), ('ntilg', 'aks_vgt'),
('ntilg', 'spndx'), ('ntilg', 'tkv'), ('saamng', 'saakern'), ('tkvs',
'saakern'), ('saakern', 'antplnt'), ('partigerm', 'markgrm'), ('frspdag',
'jordinf'), ('jordinf', 'markgrm'), ('markgrm', 'antplnt'), ('antplnt',
'aks_m2'), ('sorttkv', 'aks_m2'), ('sorttkv', 'tkv'), ('aks_m2', 'keraks'),
('aks_m2', 'aks_vgt'), ('aks_m2', 'udb'), ('aks_m2', 'tkv'), ('keraks',
'ksort'), ('keraks', 'tkv'), ('keraks', 'slt22'), ('keraks', 's2225'),
('keraks', 's2528'), ('dgv5980', 'aks_vgt'), ('dgv5980', 'spndx'),
('dgv5980', 'bgbyg'), ('aks_vgt', 'ksort'), ('aks_vgt', 'udb'), ('aks_vgt',
'slt22'), ('aks_vgt', 's2225'), ('aks_vgt', 's2528'), ('srtsize', 'ksort'),
('srtsize', 'slt22'), ('srtsize', 's2225'), ('srtsize', 's2528'), ('ksort',
'protein'), ('ksort', 'spndx')]
P(keraks| slt22=x0_1, protein=x10_5_11_0)
+----+
| keraks | phi(keraks) |
| keraks(x_13) | 0.0777 |
+----+
| keraks(x13_15) | 0.3962 |
+----+
| keraks(x15_17) | 0.2782 |
+-----
| keraks(x17_19) | 0.1496 |
+----+
| keraks(x19_21) | 0.0980 |
+----+
| keraks(x21_23) |
                     0.0001 |
+----+
| keraks(x_23) |
+----+
P(nprot | aks_m2=x450_550, dgv5980=x15_25)
+----+
| nprot | phi(nprot) |
| nprot(x_40) | 0.0674 |
```

```
| nprot(x40_60) | 0.1881 |
+----+
| nprot(x60_80) | 0.2215 |
+----+
| nprot(x80_100) | 0.2140 |
+-----
| nprot(x100_120) | 0.1527 |
+----+
| nprot(x120_140) | 0.1556 |
+-----
| nprot(x140_160) | 0.0005 |
+----+
| nprot(x_160) | 0.0001 |
+----+
P(protein| spndx=x_7)
+----+
| protein | phi(protein) |
+=====+
+----+
| protein(x9_0_9_5) | 0.0649 |
+----+
| protein(x9_5_10_0) |
+----+
| protein(x10_0_10_5) | 0.1241 |
+----+
| protein(x10_5_11_0) |
                    0.1402 I
+-----
| protein(x11_0_11_5) | 0.1382 |
+----+
| protein(x11_5_12_0) | 0.1194 |
+----+
Están D-separados de 'nprot' al observar 'protein': {'nprot': {'bgbyg',
'nedbarea', 'jordinf', 'keraks', 'ksort', 'potnmin', 'exptgens', 'dgv1059',
'jordtype', 'aks_vgt', 'ngtilg', 'antplnt', 'frspdag', 'sorttkv', 'mod_nmin', 'dgv5980', 'ngodn', 'aar_mod', 'saamng', 'slt22', 'saatid',
'forfrugt', 'jordn', 'nplac', 's2225', 'srtsize', 'sort', 'partigerm',
'spndx', 'rokap', 'nopt', 'ntilg', 'nprot', 'markgrm', 'nmin', 'ngodnn',
'aks_m2', 'pesticid', 'tkv', 's2528', 'dg25', 'srtprot', 'komm', 'udb',
'tkvs', 'saakern', 'ngodnt'}}
```