IDAPI Coursework 2.

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The results file from the IDAPICoursework02.py code contains the following:

Coursework Two results by Pierre Eugene Valassakis (pev115, 00644379)

```
2. The dependency matrix for the HepatitisC data is:
```

```
0.000 0.045 0.026 0.048 0.034 0.024 0.039 0.086 0.016
0.045 0.000 0.009 0.060 0.069 0.030 0.071 0.083 0.003
0.026 0.009 0.000 0.012 0.007 0.002 0.007 0.005 0.001
0.048 0.060 0.012 0.000 0.539 0.275 0.032 0.032 0.006
0.034 0.069 0.007 0.539 0.000 0.606 0.041 0.051 0.008
0.024\ 0.030\ 0.002\ 0.275\ 0.606\ 0.000\ 0.025\ 0.041\ 0.016
0.039 0.071 0.007 0.032 0.041 0.025 0.000 0.063 0.004
0.086 0.083 0.005 0.032 0.051 0.041 0.063 0.000 0.032
0.016 0.003 0.001 0.006 0.008 0.016 0.004 0.032 0.000
```

3. The dependency list for the HepatitisC data set is:

```
0.606 4.000 5.000
```

- 0.539 3.000 4.000
- 0.275 3.000 5.000
- 0.086 0.000 7.000
- 0.083 1.000 7.000
- 0.071 1.000 6.000
- 0.069 1.000 4.000
- 0.063 6.000 7.000 0.060 1.000 3.000
- 0.051 4.000 7.000
- 0.048 0.000 3.000
- 0.045 0.000 1.000
- 0.041 5.000 7.000
- 0.041 4.000 6.000
- 0.039 0.000 6.000
- 0.034 0.000 4.000
- 0.032 3.000 7.000
- 0.032 7.000 8.000
- 0.032 3.000 6.000 0.030 1.000 5.000
- 0.026 0.000 2.000
- 0.025 5.000 6.000
- 0.024 0.000 5.000
- 0.016 5.000 8.000
- 0.016 0.000 8.000
- 0.012 2.000 3.000
- 0.009 1.000 2.000
- 0.008 4.000 8.000
- 0.007 2.000 4.000
- 0.007 2.000 6.000
- 0.006 3.000 8.000

0.0052.0007.0000.0046.0008.0000.0031.0008.0000.0022.0005.0000.0012.0008.0000.0000.0000.0000.0001.0001.0000.0002.0002.0000.0003.0003.0000.0004.0004.0000.0005.0005.0000.0006.0006.0000.0007.0007.0000.0008.0008.000

4. The spanning tree for the HepatitisC data set is (from 2.4):

4.000 5.000 3.000 4.000

0.000 7.000

1.000 7.000

1.000 6.000

1.000 4.000

7.000 8.000

0.000 2.000

2.3 The network below is the spanning tree for the HepatitisC data set. It is assembled using our Dependency List and joining the nodes in order of dependency (highest first), provided there is no loops that are formed. We furthermore know from the data there are two roots (0 and 1 from the data set - we know roots appear first -), hence we can conclude the causal directions. Overall, we get the following network, which we notice is consistent with our result in question 4:

