In [43]:
```
import pandas as pd
from mdl_scorer import MDL_Scorer
from network import network
import matplotlib.pyplot as plt
import numpy as np
from ep import EP
import algo_tools
import random
from IPython.display import Image
from numpy.random import choice
from aep import AEP
```

Learning Bayesian Networks with Evolutionary Programming

0. Introduction

The main issue with Bayesian Networks is that there are too many options of causal relationships. Unless you are an expert on the specific set of data, it is challenging to support your proposed network. Evolutionary programming works to solve this problem to find a simple network that accurately models the data. Throughout this report we will be using a dataset of Diabetes patients.

In [44]:
```
diabetes = pd.read_csv('diabetes.csv')
columns = list(diabetes.columns)
columns[-1] = "Diabetes"
diabetes.columns = columns
scorer = MDL_Scorer(diabetes)
diabetes.describe()
```

Out[44]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Diabetes
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

1. Intro to MDL. It Prefers Simpler Models

Before starting evolutionary programming, we need a way to compare Bayes Nets to each other.
We can consider the probability that a network properly models the data. Intuitively this probability should factor in the complexity of the network as well as how well it models the data. Let's look at the minimum description length (MDL) score.

1.1 MDL Equation

Let

- D = data
- h = hypothesis (the Bayes Net in this case)

- HuffSize(x) = The size of the Huffman encoding of X

The MDL is the maximum probability that this is the correct hypothesis for the data. More formally it is Pr(h|D)

MDL = argmax$_h$ Pr(h|D)

We can then recognize that this probability is a posterior. Thus, let's look at the likelihood and the prior (not normalized).

MDL = argmax$_h$ Likelihood * Prior MDL = argmax$_h$ P(D|h) * P(h)

Next, we can take the $\log_2$ of these probabilities. Through log rules we need to add the terms instead of multiply them. Since we are taking the argmax this will not change the final relative answer

MDL = argmin$_h$ [$\log_2$ P(D|h) + $\log_2$ P(h)]

Let's now multiply the logs by -1. Since we are substracting the logs instead of adding them, we will need to swap the argmax for an argmin. This leads us with

MDL = argmin$_h$ [- $\log_2$ P(D|h) - $\log_2$ P(h)]

Through Information Theory we recognize that -$\log_2$P(.) = Optimal Code Length. Thus,

MDL = argmin$_h$ [length(D|h) + length(h)]

What we see is that the MDL has a term with the length of the network length(h). We also see that we use the term length(D|h). This is the length of the data given the hypothesis. In simpler terms, this is the length of the data encoded with the probability distributions of the network. Specifically, these terms use the Huffman encoding. Thus

MDL = argmin$_h$ [HuffSize(Data using network probabilities) + HuffSize(network)]

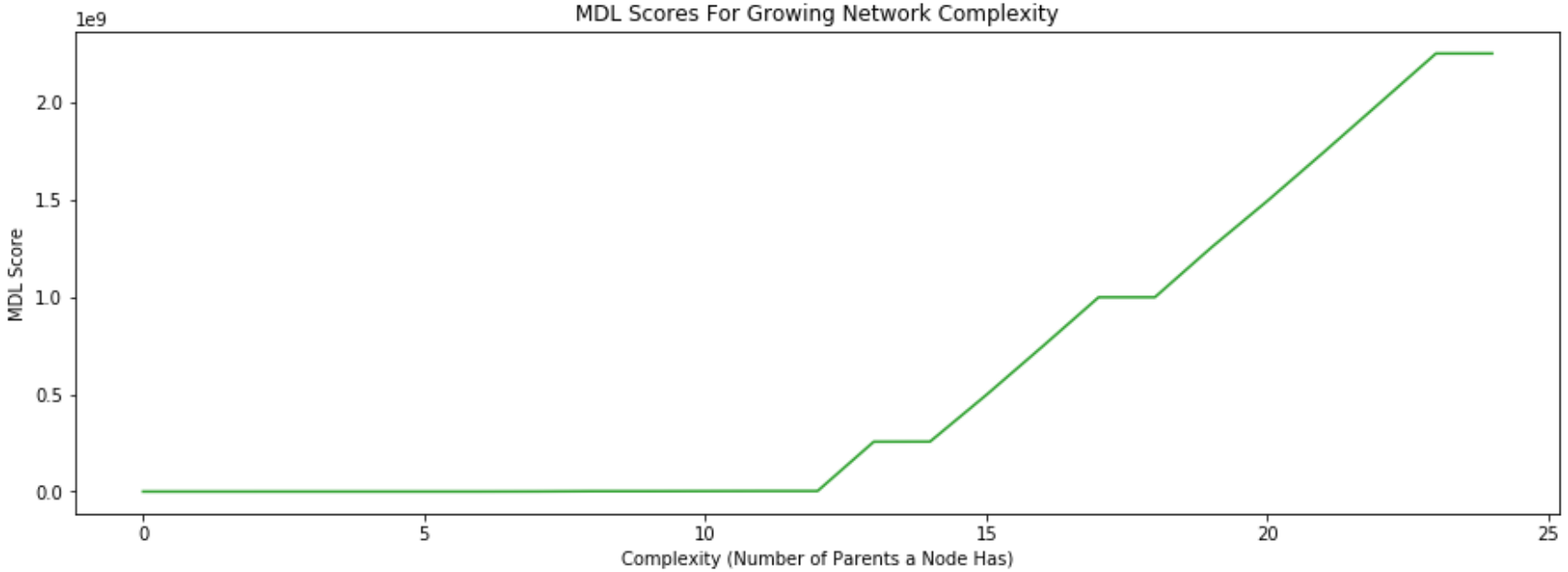
1.2 Simple Networks Lead to Small MDL Scores

First, in the equation derivation we stated that simpler networks have smaller MDL scores. Let's confirm this by running a small experiment. We will simply plot networks in order of increasing complexity and we will plot their corresponding MDL scores

In [45]:

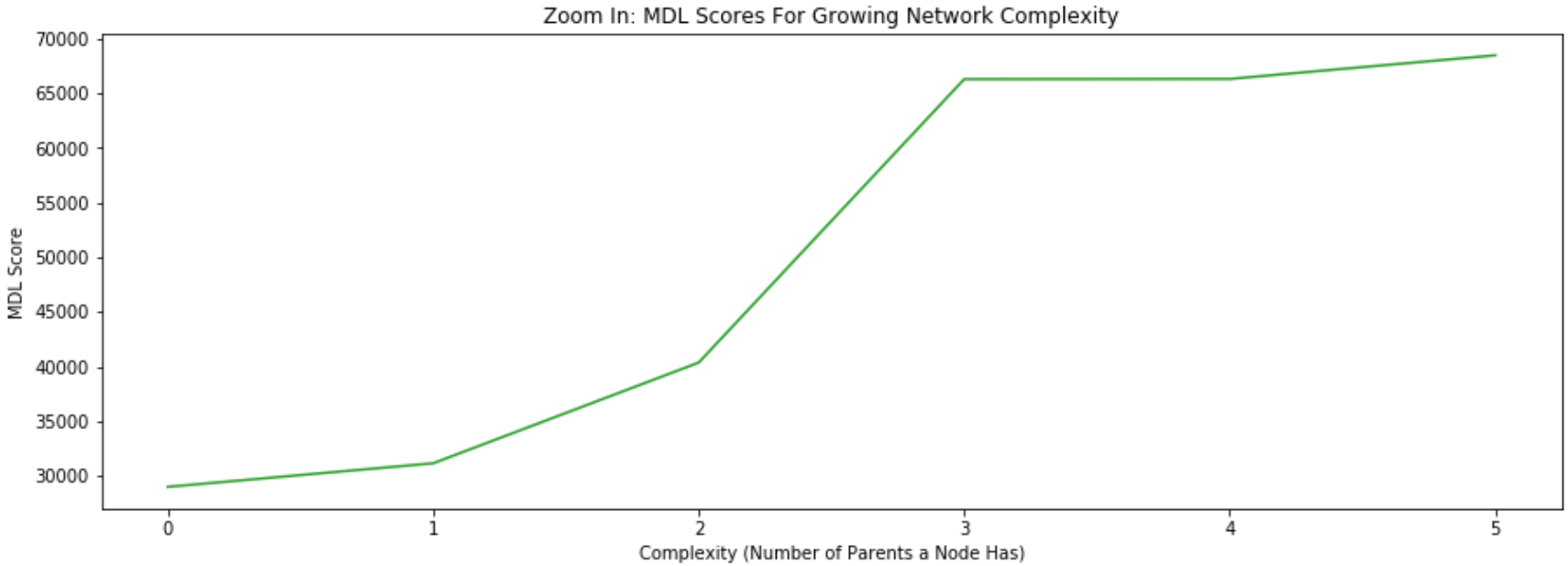
```
def simple_to_complex_example():
    matrix = algo_tools.create_blank_matrix(len(list(diabetes.columns)))
    n = network(matrix, diabetes.columns)
    scores = []
    networks = []

    for i in range(int(len(diabetes.columns))):
        if i % 2 == 0:
            for j in range(int(len(diabetes.columns))):
                if j % 2 == 0:
                    if i != j:
                        matrix[i][j] = 1
                        n = network(matrix, diabetes.columns)
                    networks.append(n)
                    scores.append(scorer.score(n))
    return {'networks': networks, 'scores': scores}

results = simple_to_complex_example()
```

In [47]:
```
x = list(range(len(results['scores'])))
y = results['scores']

fig, axs = plt.subplots(figsize=(15,5))
plt.plot(x, y, color="tab:green")
plt.ylabel('MDL Score')
plt.xlabel('Complexity (Number of Parents a Node Has)')
plt.title("MDL Scores For Growing Network Complexity")
plt.show()
```



What we notice is that this does indeed fit our theory that simpler networks do have smaller MDL scores. Notice that the first 10 networks have such small scores compared to the last few networks. Let's zoom in on these first few networks

In [48]:
```
x = list(range(len(results['scores'][:6])))
y = results['scores'][:6]

fig, axs = plt.subplots(figsize=(15,5))
plt.plot(x, y, color="tab:green")
plt.ylabel('MDL Score')
plt.xlabel('Complexity (Number of Parents a Node Has)')
plt.title("Zoom In: MDL Scores For Growing Network Complexity")
plt.show()
```



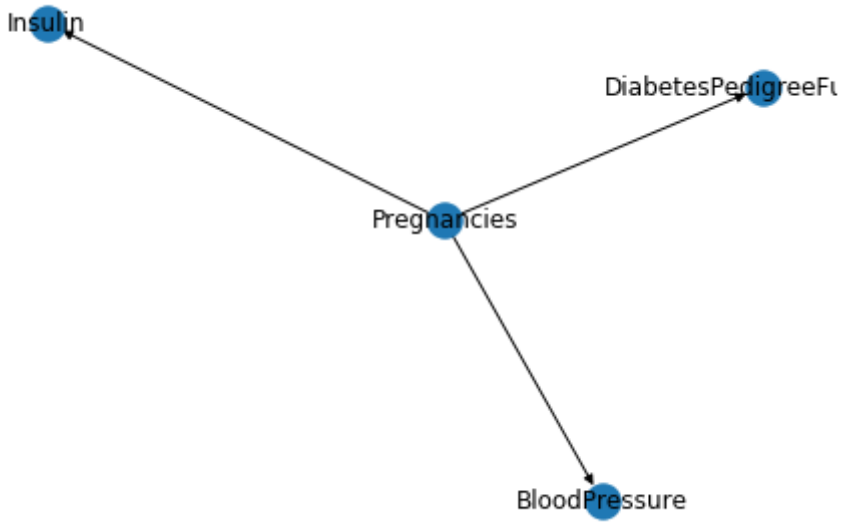
From the zoomed out view, it almost looked as if there was no change at all. This zoomed in view gives us a reality check that there is actually an increase in MDL score. Secondly, we notice that first network (which has no edgese) does have an MDL score. This shows us

that even the simplest of network has a score and that MDL scores do not calibrate to 0. This is just something to take note of moving forward

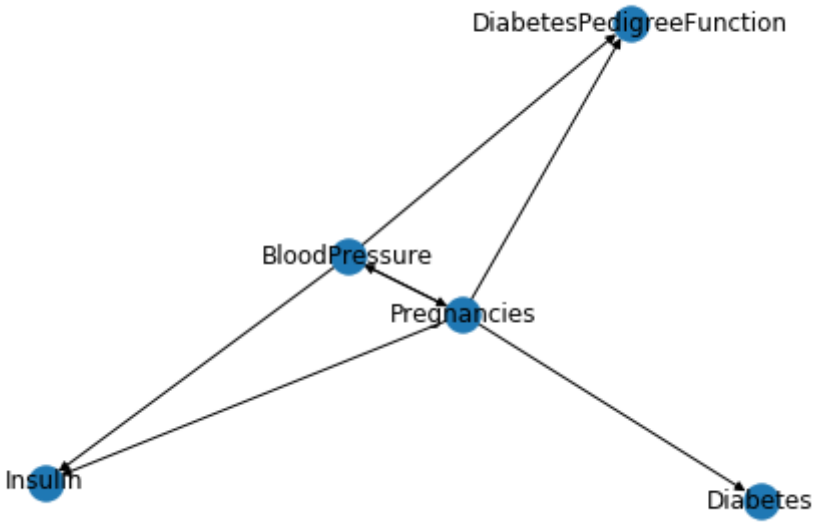
Next, let's actually take a look at the networks to confirm that they have increasing complexity.

In [24]:
```
print("Simple Structure")
results['networks'][3].draw()

print("Medium Structure")
results['networks'][8].draw()

print("Complex Structure")
results['networks'][20].draw()
```

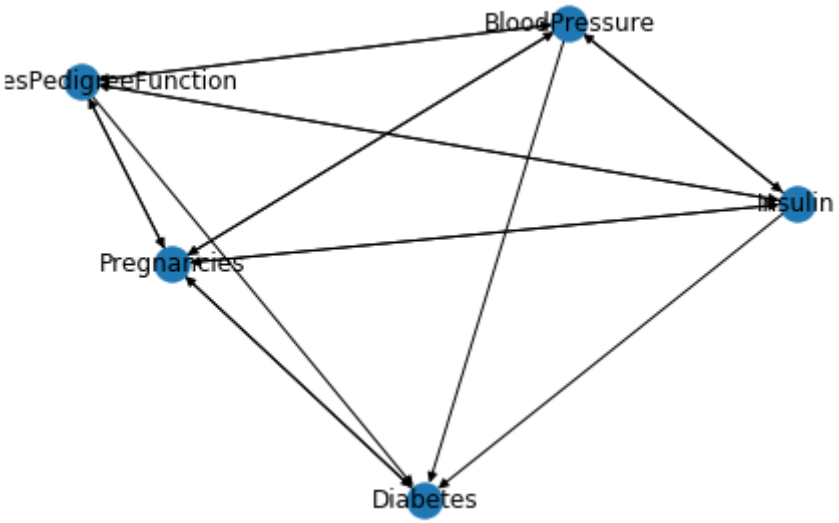
```
Simple Structure
```




```
Medium Structure
```



Complex Structure



Out of these three networks, the simplest network in this example, each node had only one parent. This lead to the smallest MDL score of the three. As the networks increased from simpler to medium to complex structures, the MDL scores increased as well

1.3 MDL Prefers To Fit the Data

In the derivation of the MDL equation we stated two factors of MDL. These were the complexity of the network and how well the network fits the data. In section 1.2 we analyzed the former of these terms. In this section we will analyze the latter. That is, do networks that fit the data have better (lower) MDL scores?

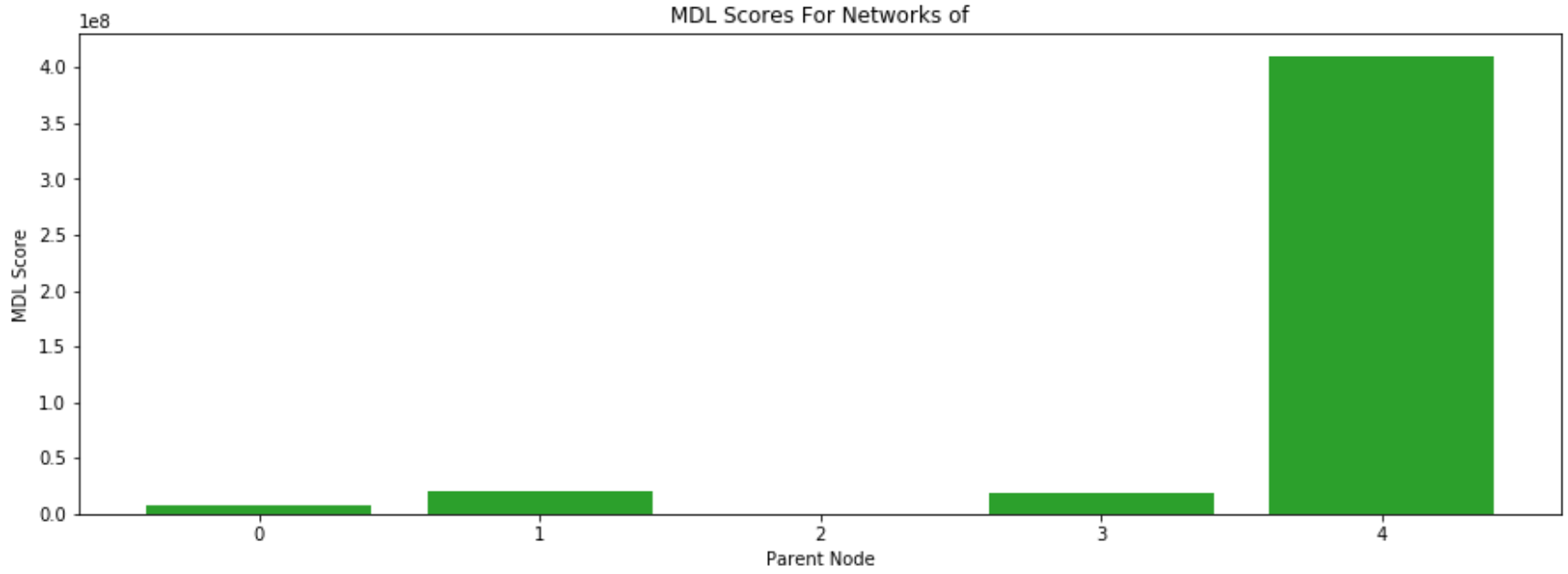
In [3]:
```python
def find_new_edge(matrix, last_node1, last_node2):
    node1 = last_node1
    node2 = last_node2

    if bool(random.getrandbits(1)):
        while matrix[node1][node2] == 1 or node1 == node2:
            if bool(random.getrandbits(1)):
                node1 = (node1 + 1) % len(matrix)
            else:
                node1 = (node1 - 1) % len(matrix)
    else:
        while matrix[node1][node2] == 1 or node1 == node2:
            if bool(random.getrandbits(1)):
                node2 = (node2 + 1) % len(matrix)
            else:
                node2 = (node2 - 1) % len(matrix)

    matrix[node1][node2] = 1
    return matrix, node1, node2
```

In [12]:
```
def same_sized_networks_example(num_edges):
    # create a population with equal number of edges
    width = len(list(diabetes.columns))
    array_model = np.zeros(width ** 2)
    matrix = array_model.reshape((width, width))

    pop_size = 5

    population = []
    scores = []
    for i in range(pop_size):
        print(i)
        new_matrix = matrix.copy()
        last_node1 = 0
        last_node2 = 0
        for j in range(num_edges):
            new_matrix, last_node1, last_node2 = find_new_edge(new_matrix, last_node1, last_node2)
        print("created", i)
        n = network(new_matrix, diabetes.columns)
        population.append(n)
        scores.append(scorer.score(n))

    return {'networks': population, 'scores': scores}

results2 = same_sized_networks_example(5)
```

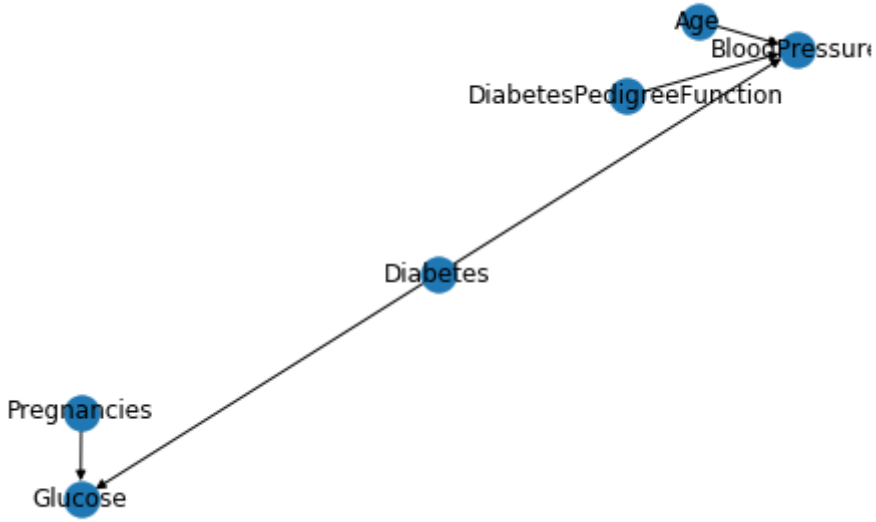
```
0
created 0
1
created 1
2
created 2
3
created 3
4
created 4
```

We will start answering this questoin with an experiment. We want to keep the complexity of the network constant while changing how a network models the data. To keep the complexity constant we will require each network to have 5 edges. We can then see which combinations of edges will lead to lower or higher MDL scores.

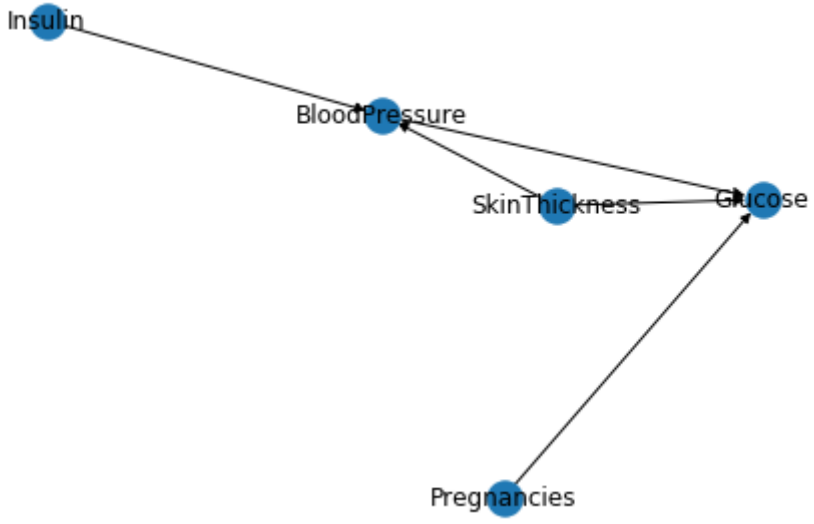
In [14]:
```
x = list(range(len(results2['scores'])))
y = results2['scores']

fig, axs = plt.subplots(figsize=(15,5))
plt.bar(x, y, color="tab:green")
plt.ylabel('MDL Score')
plt.xlabel('Parent Node')
plt.title("MDL Scores For Networks of 5 edges")
plt.show()

i = 0
for n in results2['networks']:
    print("Network", i)
    n.draw()
    i += 1
```



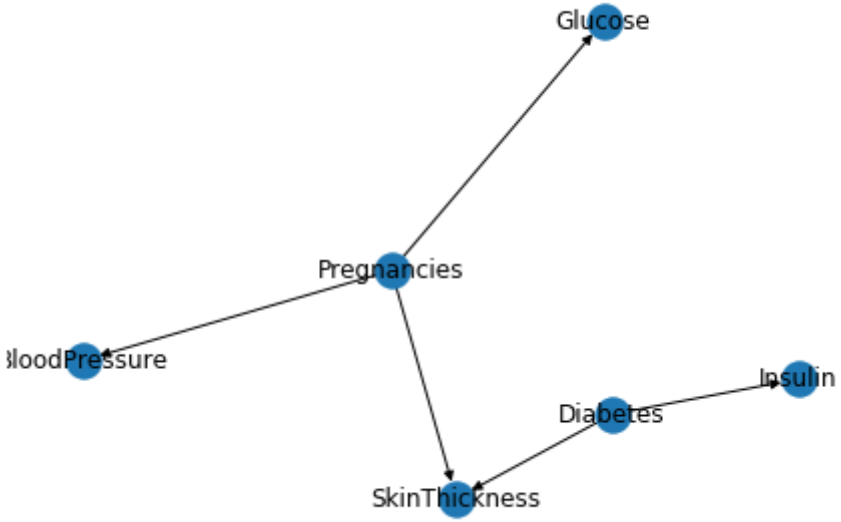

```
Network 0
```



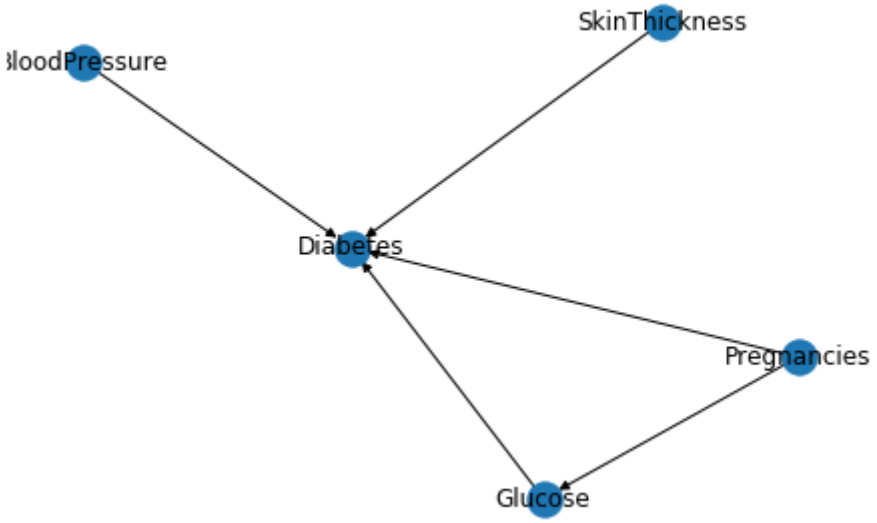
Network 1



Network 2

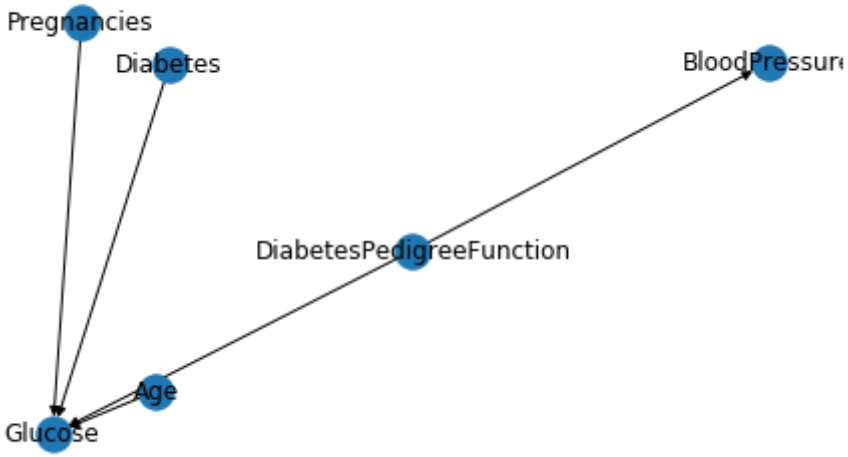


Network 3



Network 4

Network 4



From this small sample of networks, we can see that Network 4 has a significantly higher MDL score than the rest. This suggests that Network 4 models the data significantly worse than the other networks. While Networks 0 through 3 at least look like an attempt at finding relationships in the data, Network 4 falsely suggests that everything else has a direct relationship to Glucose (with the acception of Blood Pressure). Intuitively, someone would have a much easier time disporoving Network 4 rather than disproving Networks 0 through 3. Thus, this experiment gave us a macro view to show us that MDL prefers networks that model the data accurately. However, we can verify this at the micro level in the next section

2. MDL Score Agrees With Intuition

Perhaps, it will help us gain a better understanding of MDL if we looked at a micro level. Instead of considering the whole network let's just focus on one node. Particularly, let's look at pregnancies because they are easy for intuition purposes.

In [28]:
```
1 scorer.local_score('Pregnancies', [])
```

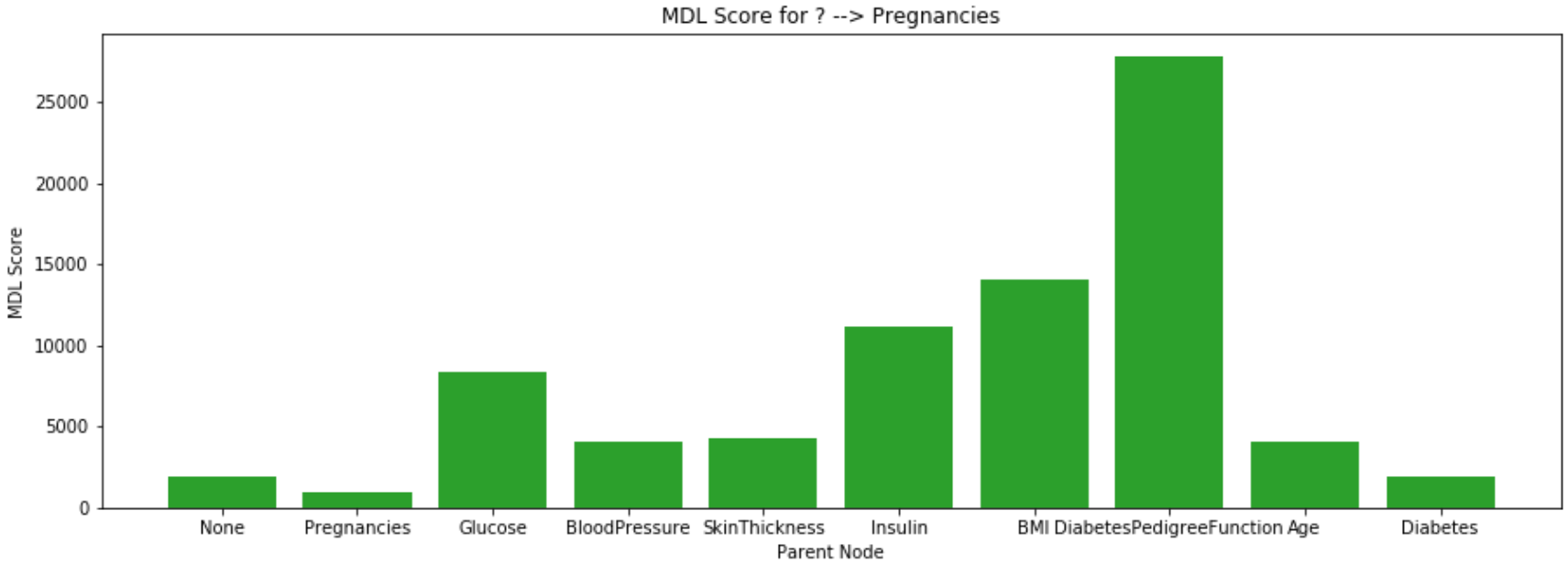
Out[28]: 1906.773475884517

With no parents, the Pregnancies node has an MDL score of 1906. This is the baseline for this node. The question is, how do other parents cause a change in this score?

We should be able to intuitively recognize that Age is a cause of Pregnancies. Thus, we would expect that the network `Age --> Pregnancies` should have a lower MDL relative to any other network `?--> Age`

In [31]:

```
def which_parent(data, child_name): # add none to this
    scorer = MDL_Scorer(data)
    parents = []
    scores = []


    # No parents
    parents.append("None")
    scores.append(scorer.local_score(child_name, []))

    # Do the actual one
    df_2 = data.copy()
    df_2['Duplicated'] = data[child_name]
    scorer_2 = MDL_Scorer(df_2)
    parents.append(child_name)
    scores.append(scorer_2.local_score(child_name, ['Duplicated']))

    for i in range(len(list(data.columns))):
        node = list(data.columns)[i]
        if node != child_name:
            parents.append(node)
            scores.append(scorer.local_score(child_name, [node]))

    x = list(range(len(parents)))
    y = scores

    fig, axs = plt.subplots(figsize=(15,5))
    plt.bar(x, y, color="tab:green")
    axs.set_xticklabels(parents)
    plt.ylabel('MDL Score')
    plt.xlabel('Parent Node')
    plt.xticks(x)
    plt.title("MDL Score for ? --> " + child_name)
    plt.show()

which_parent(diabetes, 'Pregnancies')
```



We see here that pregnancies has the lowest MDL score. This intuitively makes sense as pregnancies should be the best node to describe pregnancies. Ruling this out, we see that Age is one of the four best choices for a parent of pregnancies.
There are $\binom{9}{0} + \binom{9}{1} + \ldots + \binom{9}{9}$ possible combinations of parents to choose from. And this is just for one node. Thus, you cannot search the entire state space! This is where evolutionary programming comes into play. This will help us minimize the search space.

In total there are $2^{(9*9)} = 2 * 10^{24}$ possible networks. It is not feasible to search through every single network to find the one with the global minimal MDL score. Thus, we will need a different approach. This is where Evolutionary Programming comes into play.

3. Evolutionary Programming Using MDL

3.1 Pseudocode for Evolutionary Programming

What is evolutiionary programming? Essentially the basics are to...

1. Start with an initial population which is created randomly
2. Create a mutation on each of the individuals in the population. Mutations can be to either create an edge or to delete an edge. Mutated networks are called "offspring" while the networks that the offspring came from are called "parents".
3. Sort each network (offspring and parents) by their MDL score.

4. Cut the population in half such that the new population has the half with the lower MDL scores.
5. Repeat this process for a specified number of iterations. Each iteration is called a "generation"

Pseudocode for this process is below. My actual implementation for this can be found at `ep.py`

```
population = initial population

while current_generation < max_generation:
    offspring = mutate each network in the population
    population = population + offspring
    sort population based on MDL score

    population = the half of the population with the lowest MDL score
    current_generation++
```

3.2 Using Diabetes Sample

Let's run an experiment on the diabetes dataset* using evolutionary programming. What insights can we gaini by comparing the generations of the network to their MDL score?
* Note that the program took a lot of time (10+ hours) to run on the dataset. Thus, I created a smaller sample of only 15 rows. While this is not optimal, it will be addressed later on. Additionally, there are still insights to learn even if the resulting network was not reliable

In [49]:
```
small_diabetes = diabetes.sample(n=15, random_state=1)
```

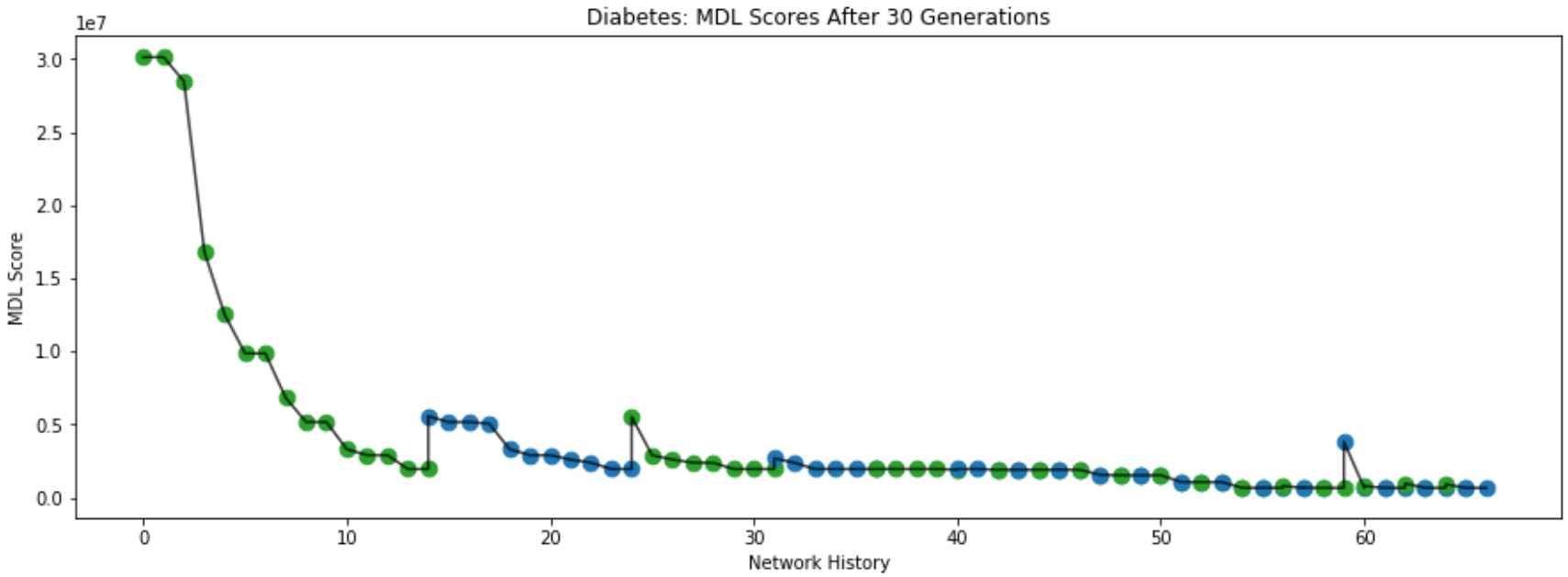
In [14]:
```
diabetes_results = EP(p_init=10, Gen_total=30, dataframe=small_diabetes, verbose=0)
```

In [4]:

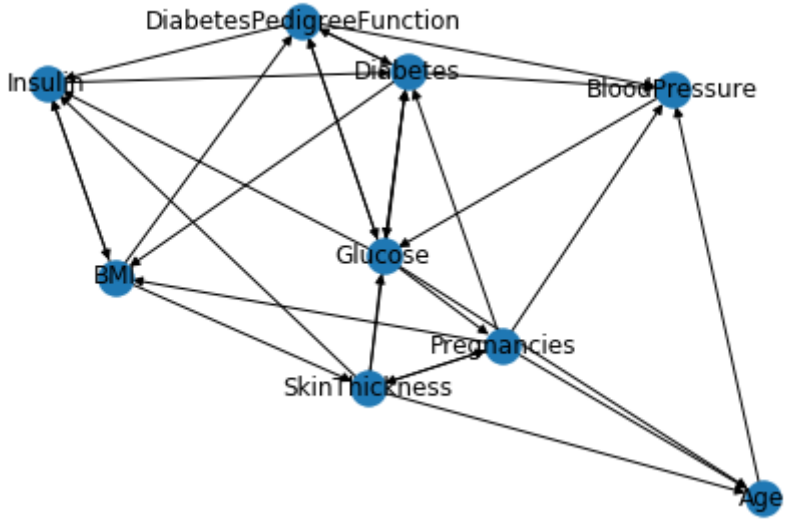
```
def plot_ep_experiment(generations, results3, title):
    Y = list(results3[1].values())
    y_list = []
    x_list = []

    fig, axs = plt.subplots(figsize=(15,5))
    lastx = 0
    for gen in range(len(Y)):
        y = np.flip(Y[gen])
        x = range(lastx, len(y) + lastx)
        y_list += list(y)
        x_list += x
        lastx = x[-1]
        plt.scatter(x, y, color="tab:green" if gen % 2 == 0 else "tab:blue", s=75)

    plt.plot(x_list, y_list, color="black", alpha=.75)

    plt.ylabel('MDL Score')
    plt.xlabel('Network History')
    plt.title(title)
    plt.show()

    gen = generations -1
    print("Most Fit Network: Score", results3[1][gen][-1])
    results3[2][gen][1].draw()
    print(results3[2][gen][1].matrix)
    print("")

    gen = int((generations -1) /2)
    print("Medium Network: Score", results3[1][gen][-1])
    results3[2][gen][1].draw()
    print(results3[2][gen][1].matrix)
    print("")

    gen = 0
    print("Worst Network: Score", results3[1][gen][-1])
    results3[2][gen][1].draw()
    print(results3[2][gen][1].matrix)

```

After plotting the data we see a sharp decline in MDL score. This does suggest that our goal of finding networks with smaller MDL scores.

In [25]:
```
1 plot_ep_experiment(generations=30, results3=diabetes_results, title="Diabetes: MDL Scores After 30 (
```



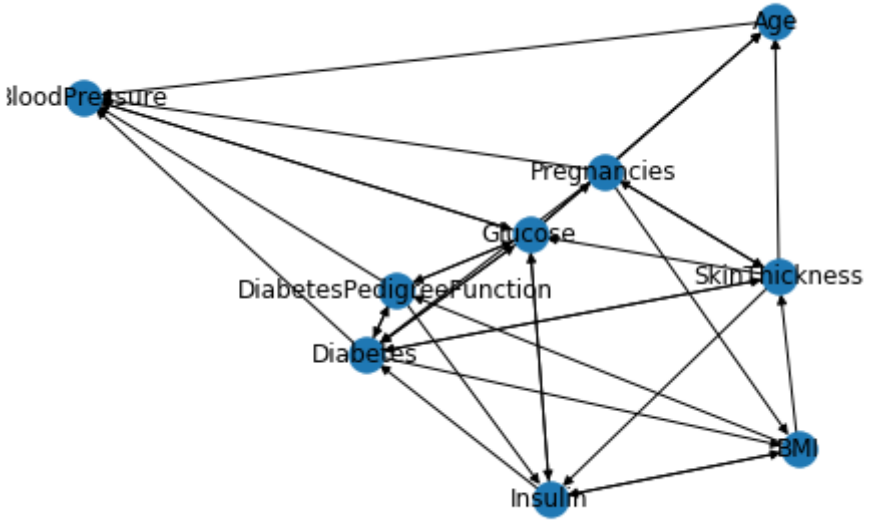

```
Most Fit Network: Score 664445.8755865983
```



0 1 2 3 4 5 6 7 8

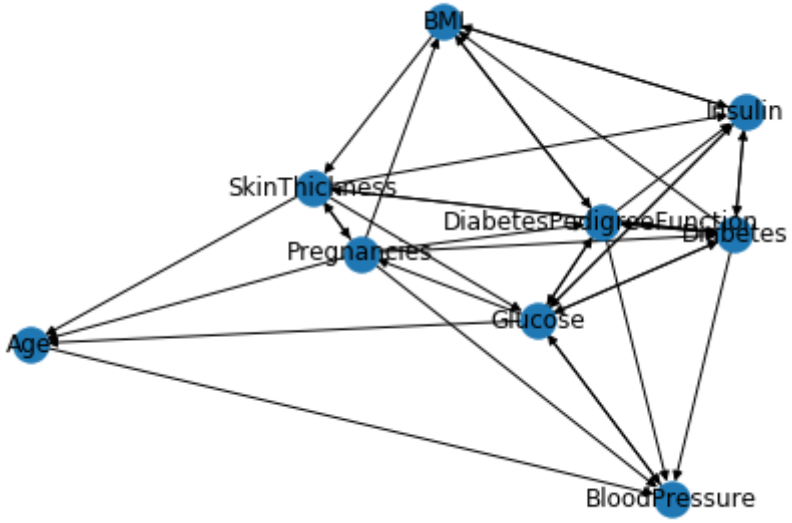
0	0	0	1	1	0	1	0	1	1
1	1	0	0	0	1	0	1	1	1
2	0	1	0	0	0	0	0	0	0
3	1	1	0	0	1	0	0	1	1
4	0	0	0	0	0	1	0	0	1
5	0	0	0	1	1	0	1	0	0
6	0	1	1	0	1	0	0	0	1
7	0	0	1	0	0	0	0	0	0
8	0	1	1	0	0	1	1	0	0

```
Medium Network: Score 1529694.9953407655
```



	0	1	2	3	4	5	6	7	8
0	0	0	1	1	0	1	0	1	1
1	1	0	1	0	1	0	1	1	1
2	0	1	0	0	0	0	0	0	0
3	1	1	0	0	1	0	0	1	1
4	0	1	0	0	0	1	0	0	1
5	0	0	0	1	1	0	1	0	0
6	0	1	1	0	1	0	0	0	1
7	0	0	1	0	0	0	0	0	0
8	0	1	1	1	0	1	1	0	0

```
Worst Network: Score 30116348.996455964
```



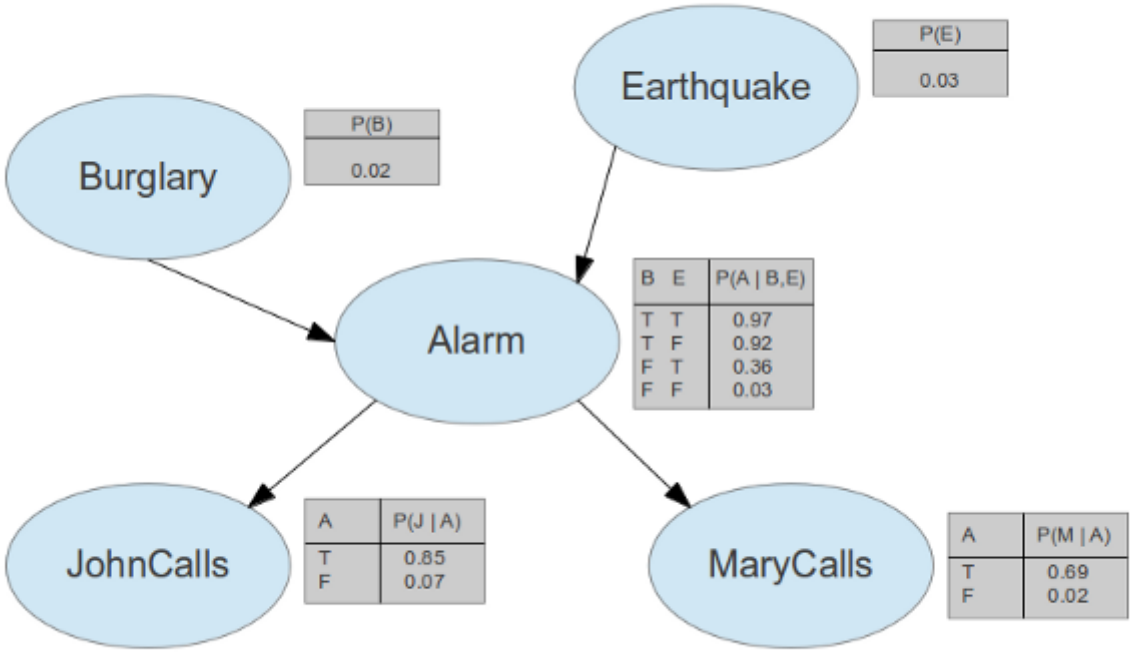
	0	1	2	3	4	5	6	7	8
0	0	0	1	1	0	1	1	1	1
1	1	0	1	0	1	0	1	1	1
2	0	1	0	0	0	0	0	0	0
3	1	1	0	0	1	0	0	1	1
4	0	1	0	0	0	1	0	0	1
5	0	0	0	1	1	0	1	0	0
6	0	1	1	0	1	1	0	0	1
7	0	0	1	0	0	0	0	0	0
8	0	1	1	1	1	1	1	0	0

When visually comparing the most fit network to the medium and worst networks, we see that all three networks still look too complex to interpret. While the diabetes dataset was good for teaching us about the intuition of MDL scores, we should use simpler more understandable data to learn about evolutionary programming

3.2 Alarm Example

In [3]:
```
1 Image("images/example relationships.png")
```

Out[3]:



For the remainder of this report, let's use the classic alarm example to study evolutionary programming. In this example, our alarm can be turned on for one of two reasons. Either there was a burglary or there was an earthquake. In the unlikely case that either of these events happen, our neighbors John and Mary have promised to call us. however, they have different levels of reliability and thus may not actually call.

We are given the probability distributions for each of these events. We can use our knowledge of conditional probability to create a joint probability distribution of the data.

Joint Probability $p(X_1, X - n) = \pi_{i=1}(X_i | Parents(X_i))$

In [32]:

```
# Conditional Probabilities

p_B = {'True': 0.02,
       'False': 0.98}

p_E = {'True': 0.03,
       'False': 0.97}


p_A_given_BE = {'TrueTrueTrue': 0.97,
                'TrueTrueFalse': 0.92,
                'TrueFalseTrue': 0.36,
                'TrueFalseFalse': 0.03,
                'FalseTrueTrue': 0.03,
                'FalseTrueFalse': 0.08,
                'FalseFalseTrue': 0.64,
                'FalseFalseFalse': 0.97}

p_J_given_A = {'TrueTrue': 0.85,
               'TrueFalse': 0.07,
               'FalseTrue': 0.15,
               'FalseFalse': 0.93}

p_M_given_A = {'TrueTrue':0.69,
               "TrueFalse": 0.02,
               "FalseTrue":0.31,
               "FalseFalse": 0.98}
```

In [ ]:
```
def s(*array):
    s_ = ""
    for v in array:
        s_ += str(v)
    return s_

def joint(A, B, E, J, M):
    return p_B[s(B)] * p_E[s(E)] * p_A_given_BE[s(A, B, E)] * p_J_given_A[s(J, A)] * p_M_given_A[s(

joint_probability_dist = {} #A, B, E, J, M

for B in [True, False]:
    for E in [True, False]:
        for A in [True, False]:
            for J in [True, False]:
                for M in [True, False]:
                    string = str(A) + " " + str(B) + " " + str(E) + " " + str(J) + " " + str(M)
                    joint_probability_dist[string] = joint(A, B, E, J, M)
```

We should also perform a quick reality check that the sum of the joint probabilities add up to 1

In [33]:
```
print(sum(list(joint_probability_dist.values())))
```

```
1.0
```

Let's sample from this probability distribution to get data that we can work with. We will have a sample size of 200 rows

In [34]:
```
num_samples = 200

draw = choice(list(joint_probability_dist.keys()), num_samples,
              p=list(joint_probability_dist.values()))

sample = draw
```

In [35]:
```
new_array = []
for row in sample:
    new_array.append(row.split(" "))

alarm = pd.DataFrame(new_array)
alarm.columns = ['Burglary', 'Earthquake', 'Alarm', 'John Calls', 'Mary Calls']
alarm.describe()
```

Out[35]:

	Burglary	Earthquake	Alarm	John Calls	Mary Calls
count	200	200	200	200	200
unique	2	2	2	2	2
top	False	False	False	False	False
freq	186	196	193	178	185

Here is a sample of 10 rows to give us a reality check. We see that each event lines up with their probability distributions

In [42]:
```
alarm.sample(10)
```

Out[42]:

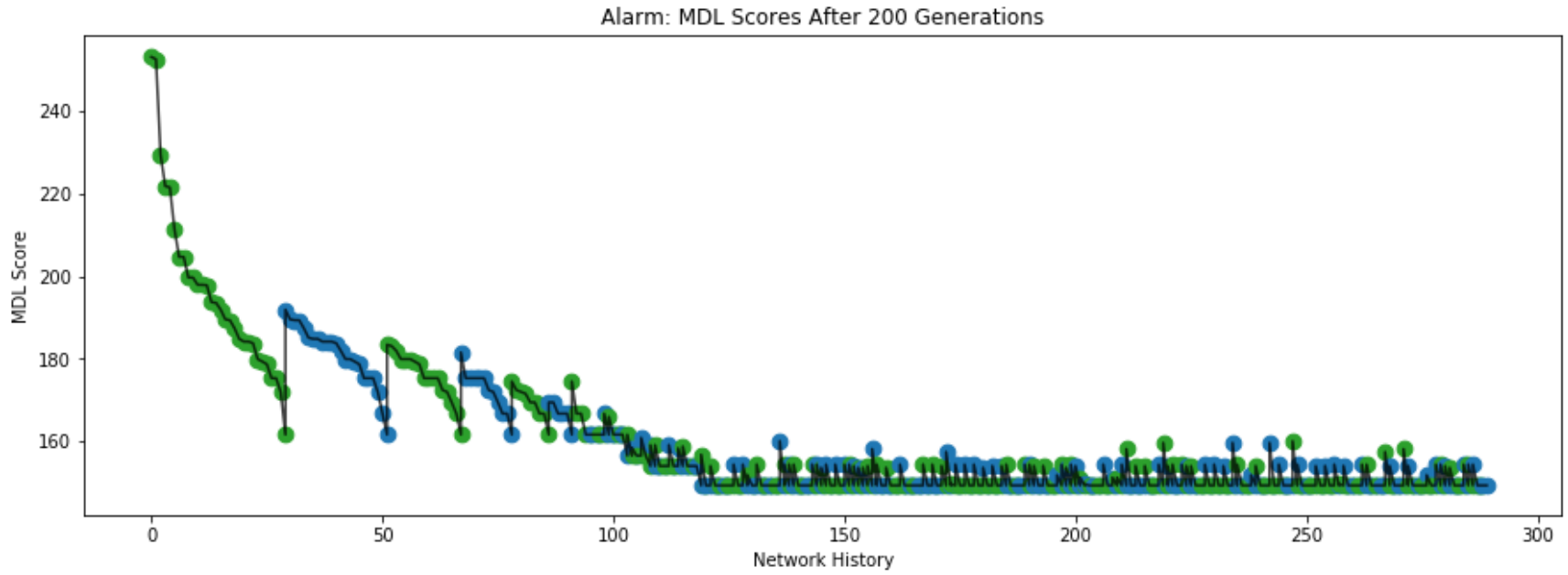
	Burglary	Earthquake	Alarm	John Calls	Mary Calls
51	True	False	False	True	True
146	False	False	False	False	False
62	False	False	False	False	False
52	True	False	True	True	False
188	False	False	False	False	False
159	False	False	False	False	False
57	False	False	False	False	False
119	False	False	False	False	False
97	False	False	False	False	False
20	False	False	False	False	False

In [39]:
```
num_gen = 200
alarm_results = EP(p_init=20, Gen_total=num_gen, dataframe=alarm, verbose=0)
```

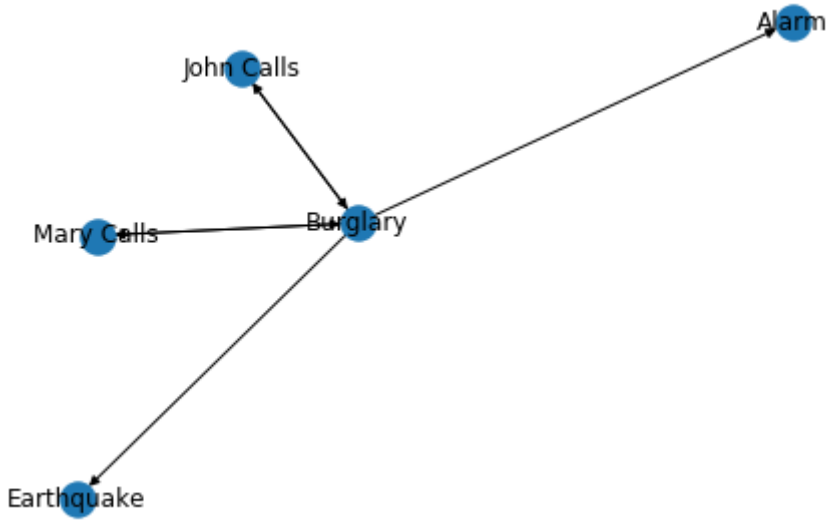
Next, let's run our evolutioniary programming algorithm on the new dataset.

Interestiingly, we see the same behavior as with the diabetes dataset. That is, in both cases, there was a quick decline in MDL scores followed by essentially coasting off at the same scores. This suggests that we are focusing in on a network that describes the data. Now, let's take a look at the actual network visualizations

In [40]:
```
1 plot_ep_experiment(generations=num_gen, results3=alarm_results, title="Alarm: MDL Scores After " + s
```



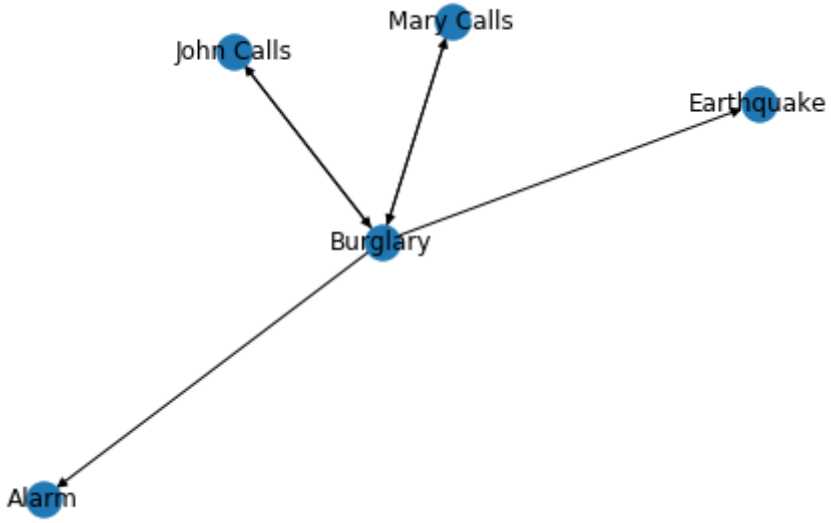

```
Most Fit Network: Score 149.2581755946368
```



0 1 2 3 4

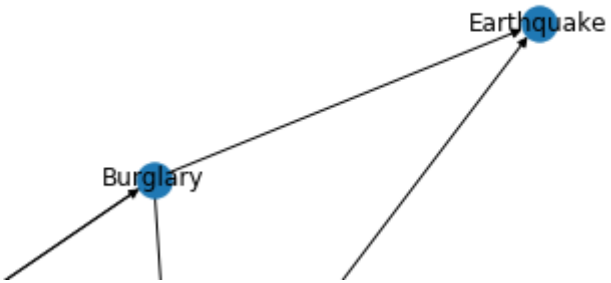
0	0	1	1	1	1
1	0	0	0	0	0
2	0	0	0	0	0
3	1	0	0	0	0
4	1	0	0	0	0

```
Medium Network: Score 149.2581755946368
```



	0	1	2	3	4
0	0	1	1	1	1
1	0	0	0	0	0
2	0	0	0	0	0
3	1	0	0	0	0
4	1	0	0	0	0

```
Worst Network: Score 253.1942536019073
```



	0	1	2	3	4
0	0	1	1	1	0
1	0	0	0	0	0
2	0	1	0	0	0
3	1	0	1	0	0
4	0	0	0	0	0

Interestingly, there is a significant improvement between the worst and the best networks. In the best networks, all the nodes are actually correlated to burglary, except for earthquke. The Burglary --> Earthquake edge is clearly incorrect but this is only one mutation away from a correct network. It is also interesting to notice that the network did correctly recognize that Burglary and the neighbors calling are associated yet it did not correctly recognize that this relationship is truly an indirect relationship rather than direct.

4. Balance Between Diversity and Redundancy

In both evolutionary programming experiments (alarm data and diabetes data) there were some common behaviors. Essentially, the MDL score quickly decreased and then stayed relatively constant. While this may suggest that we are focusing in on the best network there are a few issues. First, the network that we are focusing in on may be good but it is likely not the best network. Secondly, since we are focusing in on one particular network we are performing redundant computations. In fact, we could even be mutating in a loop of similar networks

Rather than focusing in on one network, we should modify our algorithm to prefer diverse networks. We can do this through the following modifications

4.1 Theory: Adaptive Evolutionary Programming

In adaptive evolutionary programming, we will favor diversity yet reduce redundancy. While my specific implementation can be found at `aep.py` The following pseudocode is as follows:

First, the Increasing Routine is meant to favor diversity:

```
Distance(network1, network2):
    Sum of edges (in a matrix representation of a network) that are
    in network_1 but not network_2 or vice versa

Increase Routine:
    if generation_count is under some threshold:
        For each offspring_i:
            If average distance between offspring_i and all other nodes is beyond some threshold
            Then keep offspring_i and its parent_i
```

The increase routine works by finding unique networks (networks that have a high average distance from all other networks). It then favors this network by keeping both it and its parent in the population. We want diversity at the begining of the evolutionary process but not at the end. We can hold this by only running the increase routine if we haven't reached a particular generation yet.

Next, the Decrease routine is meant to decrease redundancy

```
DecreaseRoutine():
    for each pair of mutated individuals and their parents Offspring_i, Offspring_j Parent_i,
Parent_j:
        Select the fitter between Offspring_i and Parent_i
        Select the fitter between Offspring_j and Parent_j


        if the selected pair are both offspring
            if current_population > minimum_population and Distance(Offspring_i, Offspring_j) <
threshold
                Keep the fitter child
```

```
10
11          if Distance between selected pair is 0, current_population > minimum_population,
12              remove one of them
```

In the original algorithm, if the parent and child were both in the top 50% of networks then both would be kept. Yet, with the decrease routine only the child is kept. This reduces redundancy. Furthermore, in the original algoritm it is possible to have identical networks. Thus, we need to perform reduntant computations. In two there are two identical networks then we remove one of them.

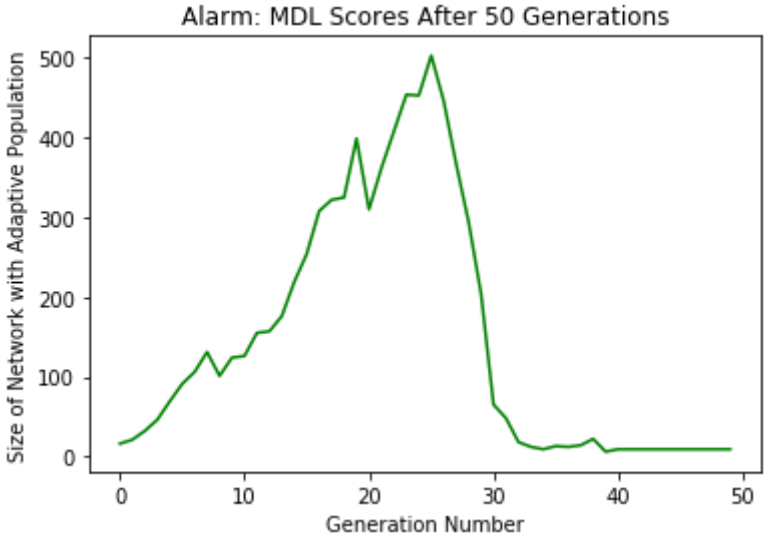
4.2 Analysis

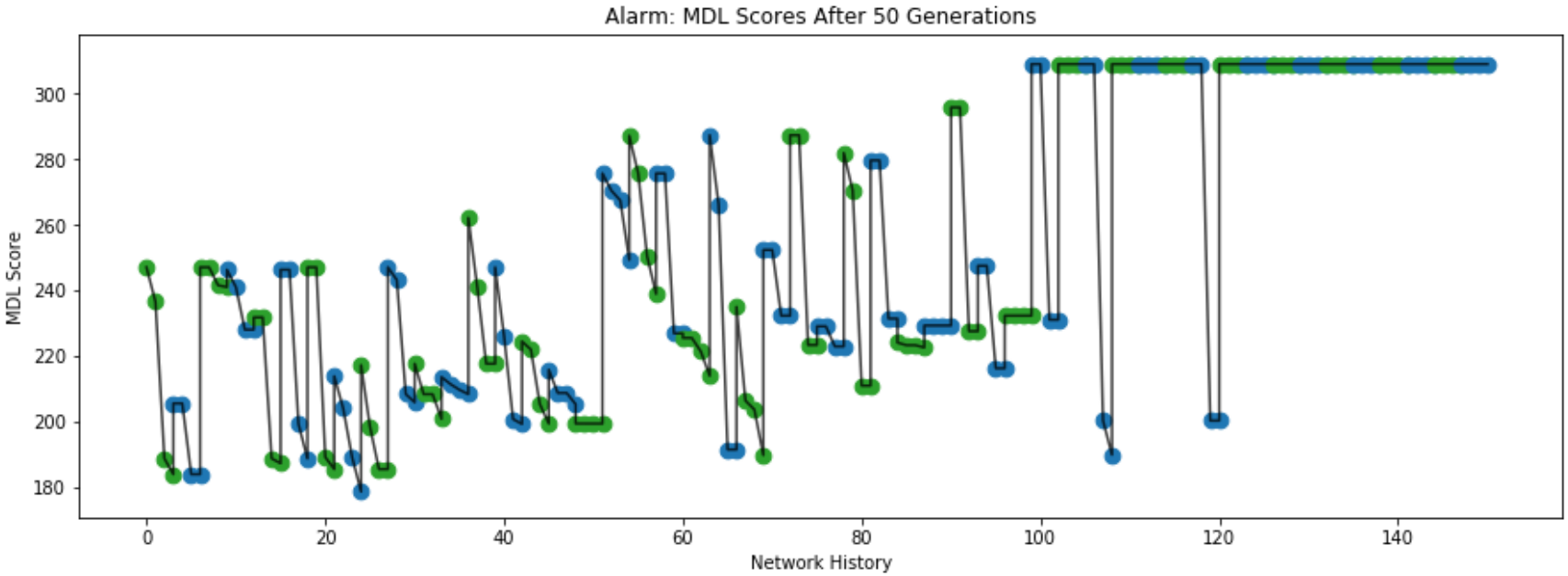
Finally, let's run the alarm data on our adaptive evolutionary programming algorithm and analyze the results

In [24]:
```
# line 97
num_gen= 50
aep_alarm_results = AEP(p_init=10,
                        p_max=30,
                        Gen_total=num_gen,
                        dataframe=alarm,
                        pop_threshold=.9,
                        gen_threshold= int(num_gen/2),
                        distance_theshold=1,
                        verbose=0)
```

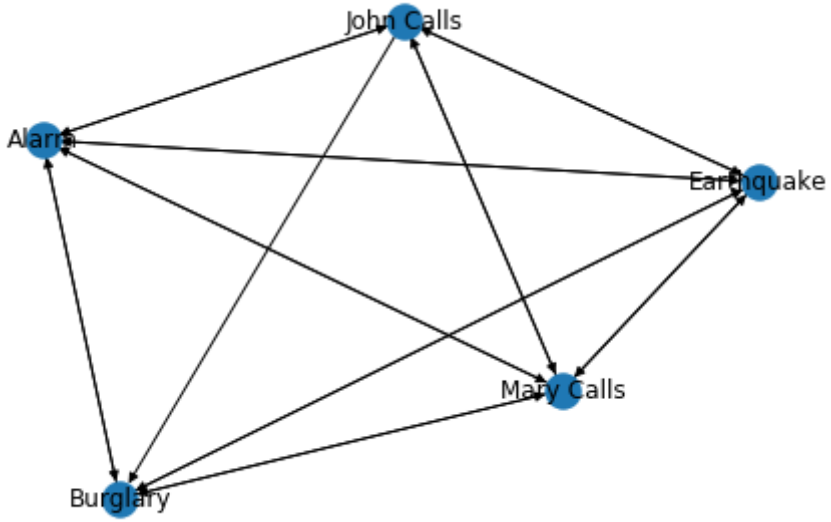
```
     decrease routine
Running Generation 30
     increase routine
     decrease routine
Running Generation 31
     increase routine
     decrease routine
Running Generation 32
     increase routine
     decrease routine
Running Generation 33
     increase routine
     decrease routine
Running Generation 34
     increase routine
     decrease routine
Running Generation 35
     increase routine
     decrease routine
Running Generation 36
```

In [25]:
```
def plot_aep_experiment(generations, results3, title):

x = range(len(aep_alarm_results[3]))
size = aep_alarm_results[3]

plt.plot(x, size, color="green")
plt.xlabel('Generation Number')
plt.ylabel('Size of Network with Adaptive Population')
plt.title(title)
plt.show()


plot_ep_experiment(generations=generations, results3=results3, title=title)

plot_aep_experiment(generations=num_gen, results3=aep_alarm_results, title="Alarm: MDL Scores After " +
```



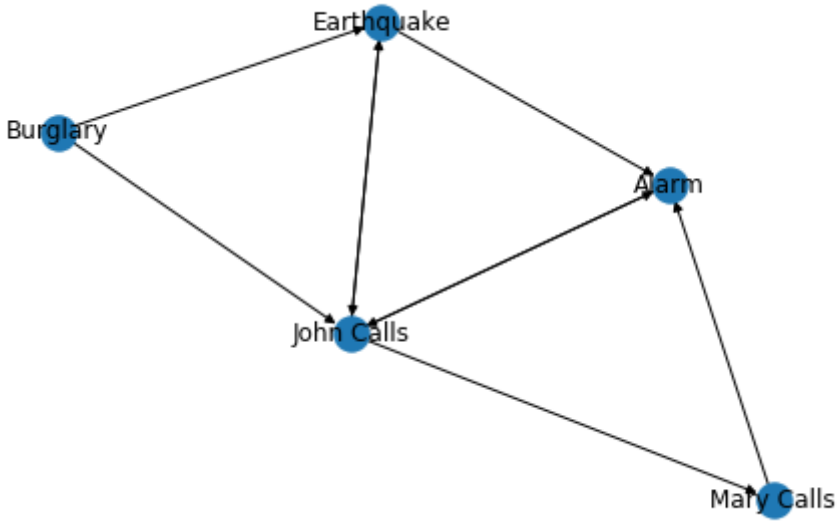



```
Most Fit Network: Score 309.05691664778317
```



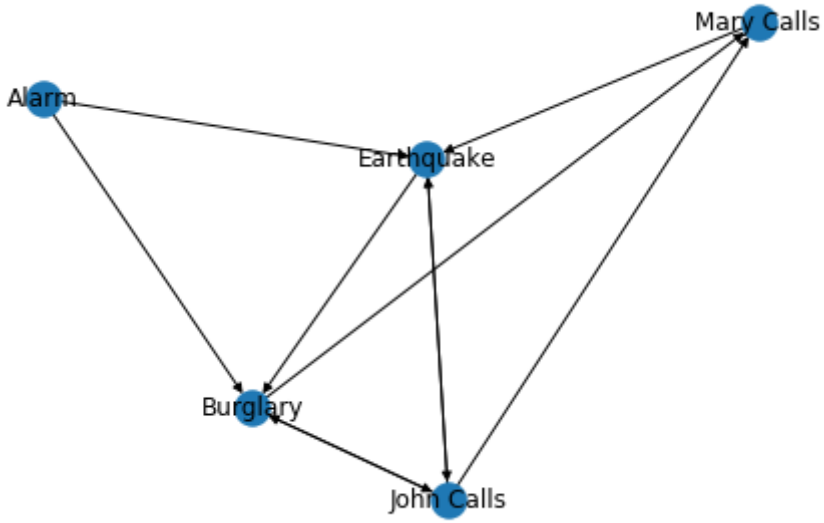
	0	1	2	3	4
0	0	1	1	0	1
1	1	0	1	1	1
2	1	1	0	1	1
3	1	1	1	0	1
4	1	1	1	1	0

```
Medium Network: Score 287.38738767401793
```



	0	1	2	3	4
0	0	1	0	1	0
1	0	0	1	1	0
2	0	0	0	1	0
3	0	1	1	0	1
4	0	0	1	0	0

```
Worst Network: Score 247.14497527826825
```



	0	1	2	3	4
0	0	0	0	1	1
1	1	0	0	1	0
2	1	1	0	0	0
3	1	1	0	0	1
4	0	1	0	0	0

What we see is that the population size did increase until we reached half the generations. Then the population size decreased. This implies that we were increasing the diversity of the population halfway. This was because in the functioni command we specified to only run the increase routine for the first half of the generations. Secondly, after the increase routine is supposed to stop the decrease routine removes any redundancy in the population.

In regards to the MDL scores, we notice much more variablity than before. Given our constraints, this is good as it suggests that the there is a lot of diversity in the network. We also notice that the MDL scores only begin to focus in at a particular score after the halfway point in which the increase routine has stopped running. This further implies that the MDL scores were fluctuating due to the increase routine.

We see that the best network is actually more complex than that of the normal evolutionary programming. While this may seem alarming at first, rest assured that this is actually good. While the network in the original algorithm did point toward a promising design, we agreed that it was too simplistic as it did not recognize any indirect relationships. In contrast, the most fit network of the adaptive evolutionary programming is a complete graph such that all nodes point to each other. This network is closer to our true network from section 3.2. It is actually only a few mutations off from being exactly correct. This suggests that while evolutionary programming is only set to favor lower MDL scores, the modifications in the adaptive evolutionary programming help to favor other factors as well.

5. Conclusion

I have been interested in evolutionary programming for a while and I appreciate the opportunity to use this project to explore my interest. Evolutionary programming with Bayesian networks requires some metric of scoring the networks. One such metric is the minimum descriptive length which takes advantage of information theory to select a simple network that has a high probability of modeling the data. Research in this field looks at the numerious selection techniques for selecting the most probable network. Among these techniques is the standard evolutionary programming which only favors networks with a low MDL score. Furthermore, adaptive evolutionary programming which adapts the size of the population to not only favor low MDL scores but also to favors high diversity and low redundancy. Adaptive evolutionary progamming may find network that is more complex than that of standard evolutionary programming. This suggests that the adaptive technique is putting less of an emphasis on simplicity and more of an emphasis on finding the a more suitable network, even if it is slightly more complex.
Future work could be to implement other evolutionary programming modifications as well as modify the number of generations and the thresholds of the current algorithms.