

Homework - Case Study 6

July 3, 2017

Network homophily occurs when nodes that share an edge share a characteristic more often than nodes that do not share an edge. In this case study, we will investigate homophily of several characteristics of individuals connected in social networks in rural India.

```
In [109]: import pandas as pd
```

`individual_characteristics.dta` contains several characteristics for each individual in the dataset such as age, religion, and caste. Use the pandas library to read in and store these characteristics as a dataframe called `df`

```
In [110]: data_filepath = 'https://s3.amazonaws.com/assets.datacamp.com/production/individual_characteristics.dta'
df = pd.read_stata(data_filepath + "individual_characteristics.dta")
```

Store separate datasets for individuals belonging to Villages 1 and 2 as `df1` and `df2`, respectively.

```
In [111]: df1 = df[df.village == 1]
df2 = df[df.village == 2]
```

```
# Enter code here!
df1.head()
```

```
Out[111]:
```

	village	adjmatrix_key	pid	hhid	resp_id	resp_gend	\
0	1	5	100201	1002	1	1	
1	1	6	100202	1002	2	2	
2	1	23	100601	1006	1	1	
3	1	24	100602	1006	2	2	
4	1	27	100701	1007	1	1	

		resp_status	age	religion	caste	...	\
0		Head of Household	38	HINDUISM	OBC	...	
1	Spouse of	Head of Household	27	HINDUISM	OBC	...	
2		Head of Household	29	HINDUISM	OBC	...	
3	Spouse of	Head of Household	24	HINDUISM	OBC	...	
4		Head of Household	58	HINDUISM	OBC	...	

```
privategovt work_outside work_outside_freq shgparticipate shg_no
```

0	PRIVATE BUSINESS	Yes	0	No	NaN
1		NaN	NaN	No	NaN
2	OTHER LAND	No	NaN	No	NaN
3	PRIVATE BUSINESS	No	NaN	Yes	1
4	OTHER LAND	No	NaN	No	NaN

	savings	savings_no	electioncard	rationcard	rationcard_colour
0	No	NaN	Yes	Yes	GREEN
1	No	NaN	Yes	Yes	GREEN
2	No	NaN	Yes	Yes	GREEN
3	Yes	1.0	Yes	No	
4	No	NaN	Yes	Yes	GREEN

[5 rows x 48 columns]

In this dataset, each individual has a personal ID, or PID, stored in `key_vilno_1.csv` and `key_vilno_2.csv` for villages 1 and 2, respectively. Use `pd.read_csv` to read in and store `key_vilno_1.csv` and `key_vilno_2.csv` as `pid1` and `pid2` respectively.

```
In [112]: pid1 = pd.read_csv(data_filepath + "key_vilno_1.csv", dtype=int, header =
        pid2 = pd.read_csv(data_filepath + "key_vilno_2.csv", dtype=int, header =
```

```
In [113]: type(pid1)
```

```
Out[113]: pandas.core.frame.DataFrame
```

```
In [114]: sex1      = dict(zip(df1.pid, df1.resp_gend))
        caste1     = dict(zip(df1.pid, df1.caste))
        religion1  = dict(zip(df1.pid, df1.religion))

        # Continue for df2 as well.
        sex2       = dict(zip(df2.pid, df2.resp_gend))
        caste2     = dict(zip(df2.pid, df2.caste))
        religion2  = dict(zip(df2.pid, df2.religion))
```

Let's consider how much homophily exists in these networks. For a given characteristic, our measure of homophily will be the proportion of edges in the network whose constituent nodes share that characteristic. How much homophily do we expect by chance? If characteristics are distributed completely randomly, the probability that two nodes x and y share characteristic a is the probability both nodes have characteristic a , which is the frequency of a squared. The total probability that nodes x and y share their characteristic is therefore the sum of the frequency of each characteristic in the network. For example, in the dictionary `favorite_colors` provided, the frequency of red and blue is $1/3$ and $2/3$ respectively, so the chance homophily is $(1/3)^2 + (2/3)^2 = 5/9$. Create a function `chance_homophily(chars)` that takes a dictionary with personal IDs as keys and characteristics as values, and computes the chance homophily for that characteristic.

```
In [115]: from collections import Counter
        import numpy as np
```

```

def chance_homophily(chars):
    """
    Computes the chance homophily of a characteristic,
    specific
    """
    #     c = dict(Counter(chars.values()))
    #     result = 0
    #     for v in c.values():
    #         result += (v / sum(c.values()))**2
    #     return result

    # datacamp answer
    chars_counts_dict = Counter(chars.values())
    chars_counts = np.array(list(chars_counts_dict.values()))
    chars_props = chars_counts / sum(chars_counts)
    return sum(chars_props**2)

favorite_colors = {
    "ankit": "red",
    "xiaoyu": "blue",
    "mary": "blue"
}

color_homophily = chance_homophily(favorite_colors)
print(color_homophily)

```

0.55555555555556

```

In [116]: print("Village 1 chance of same sex:", chance_homophily(sex1))
          print("Village 1 chance of same caste:", chance_homophily(caste1))
          print("Village 1 chance of same religion:", chance_homophily(religion1))
          print()
          print("Village 2 chance of same sex:", chance_homophily(sex2))
          print("Village 2 chance of same caste:", chance_homophily(caste2))
          print("Village 2 chance of same religion:", chance_homophily(religion2))

```

Village 1 chance of same sex: 0.502729986168
Village 1 chance of same caste: 0.674148850979
Village 1 chance of same religion: 0.980489698852

Village 2 chance of same sex: 0.500594530321
Village 2 chance of same caste: 0.425368244801
Village 2 chance of same religion: 1.0

Now let's compute the observed homophily in our network. Recall that our measure of homophily is the proportion of edges whose nodes share a characteristic. `homophily(G, chars, IDs)`

takes a network `G`, a dictionary of characteristics `chars`, and node IDs `IDs`. For each node pair, determine whether a tie exists between them, as well as whether they share a characteristic. The total count of these is `num_same_ties` and `num_ties` respectively, and their ratio is the homophily of `chars` in `G`. Complete the function by choosing where to increment `num_same_ties` and `num_ties`.

```
In [122]: def homophily(G, chars, IDs):
    """
    Given a network G, a dict of characteristics chars for node IDs,
    and dict of node IDs for each node in the network,
    find the homophily of the network.
    """
    num_same_ties, num_ties = 0, 0
    for n1 in G.nodes():
        for n2 in G.nodes():
            if n1 > n2: # do not double-count edges!
                if IDs[n1] in chars and IDs[n2] in chars:
                    if G.has_edge(n1, n2):
                        num_ties += 1
                        if chars[IDs[n1]] == chars[IDs[n2]]:
                            num_same_ties += 1
    return (num_same_ties / num_ties)
```

Use your homophily function to compute the observed homophily for sex, caste, and religion in Villages 1 and 2.

```
In [118]: # load networkx graph objects G1 and G2
import networkx as nx

A1 = np.loadtxt("adj_allVillageRelationships_vilno_1.csv", delimiter=",")
A2 = np.loadtxt("adj_allVillageRelationships_vilno_2.csv", delimiter=",")

G1 = nx.to_networkx_graph(A1)
G2 = nx.to_networkx_graph(A2)

In [119]: # convert dataframe to numpy array
array_pid1 = np.array(pid1[0])
array_pid2 = np.array(pid2[0])

In [123]: print("Village 1 observed proportion of same sex:", homophily(G1, sex1, a
print("Village 1 observed proportion of same caste:", homophily(G1, caste
print("Village 1 observed proportion of same religion:", homophily(G1, re
print()
print("Village 2 observed proportion of same sex:", homophily(G2, sex2, a
print("Village 2 observed proportion of same caste:", homophily(G2, caste
print("Village 2 observed proportion of same religion:", homophily(G2, re
```

```
Village 1 observed proportion of same sex: 0.5879345603271984
Village 1 observed proportion of same caste: 0.7944785276073619
Village 1 observed proportion of same religion: 0.99079754601227
```

Village 2 observed proportion of same sex: 0.5622435020519836
Village 2 observed proportion of same caste: 0.826265389876881
Village 2 observed proportion of same religion: 1.0