**Lab 3 - ALAAM (****Autologistic Actor Attribute Model)**

***CompSci 396-0: Social Networking Analysis* *Win 2022***

Student Name: Jiaqi Guo NetID: JGR9647

* **Responses to Question**
  + **Part II: Hypotheses**

**Contagion effect not presented:**

**Hypothesis 1:** Those who use alcohol regularly, are more likely to smoke regularly.

**Hypothesis 2:** Those who are reported as friends more, are more likely to smoke regularly.

**Hypothesis 3:** Those who report more friends, are more likely to smoke regularly.

**Hypothesis 4:** Those who have more reciprocal friends, are less likely to smoke regularly.

**Hypothesis 5:** Those who are reported as friends by many people, are less likely to smoke regularly.

**Contagion effect presented:**

**Hypothesis 6:** There is a positive contagion effect for smoking behavior.  
**Hypothesis 7:** Those who exercise regularly, are more likely to smoke regularly.

**Hypothesis 8:** Those who use alcohol regularly, are more likely to smoke regularly.

**Hypothesis 9:** Those who report more friends, are more likely to smoke regularly.

* + **Model A: Non-contagion Model**

1. **(2 points) Build the first ALAAM model by using “BayesALAAM” function taking smoking behavior as the dependent variable. Include all the covariates you built in previous section. Also set “contagion = 'none'” to have a non-contagion model. Set the number of iterations to 1,000. Call this model res.0. Include the final table that you get after running the model in your report.**

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1. **(5 points) You will notice in the output that the simple contagion effect is reported as zero because it hasn't been estimated. From the table you got in (A.1) you see the effective sample sizes (ESS). What those numbers mean to you? What are good values for ESS in general?**

From the graph above, it is clear that individual gender can influence the choice of whom an employee seeks advice from. A few typical nodes are Node 40 and node 31, and most of the nodes pointing to them are **homogenous**, which meet our expectations in **hypothesis 3**.

1. **(7 points) Plot the MCMC output in trace plots and include them in your report. What those plots tell you? (i.e. How those plots supposed to be? Are they as supposed to?)**

Although the specific information about the number of connections cannot be accurately obtained from the image, we can still observe that the connection density near nodes with higher in-degree centrality is also higher (low transparency), which means that these nodes receive more information through ESM. This phenomenon matches our expectations on **Hypotheses 4**.

1. **(14 points) Now increase the number of iterations to 10,000 and run the model again and include the table in your report. Again, plot the MCMC output in trace plots and include them in your report. Compare the model that you ran in part (A.1) with this model in terms of ESS and MCMC plots. Is the model with more iterations improved?**

From the graph above, it is clear that individual gender can influence the choice of whom an employee seeks advice from. A few typical nodes are Node 40 and node 31, and most of the nodes pointing to them are **homogenous**, which meet our expectations in **hypothesis 3**.

1. **(5 points) Using “write.res.table” function, summarize the results of the model with 10,000 iterations and include the table in your report. Using the table decide on the Hypotheses 1 to 5. Note that for each hypothesis you should say if the hypothesis is supported or not and why is that. (Hint: look at the sign of the mean. Also note that if 0 is included in the interval [the last two columns], the parameter test is not significant.)**

From the graph above, it is clear that individual gender can influence the choice of whom an employee seeks advice from. A few typical nodes are Node 40 and node 31, and most of the nodes pointing to them are **homogenous**, which meet our expectations in **hypothesis 3**.

* + **Model B:** **Simple Social Contagion Model**

1. **(2 points) Build the simple social contagion ALAAM model by using “BayesALAAM” function taking smoking behavior as the dependent variable. Include Sport, alcohol and outdegree from the list of covariates you built in previously. Also set “contagion = 'simple'” or just simply not include that (simple contagion is the default of the function). By doing so, you have a simple contagion model. Set the number of iterations to 1,000. Call this model res.1. Include the final table that you get after running the model in your report.**
2. **(7 points) Plot the MCMC output in trace plots and include them in your report. What those plots tell you? (i.e. How those plots supposed to be? Are they as supposed to?)**
3. **(2 points) Improve the model with taking the theta estimates from the model as inputs to another model. It is possible by setting Propsigma to thetas in BayesALAAM function. Using this trick build a model as in B.1 but set the Propsigma. Also increase the iterations to 5,000. Call the model res.2 and run the model again and include the table in your report**
4. **(7 points) Plot the MCMC output in trace plots for the improved model and include them in your report. How those changed as compared to the ones in B.2?**
5. **(21 points) Using “write.res.table” function, summarize the results of the model res.2 and include the table in your report. Using the table decide on the Hypotheses 6 to 9. Note that for each hypothesis you should say if the hypothesis is supported or not and why is that. (Hint: look at the sign of the mean. Also note that if 0 is included in the interval [the last two columns], the parameter test is not significant.)**
   * **Part V:** **Goodness-of-fit test**
6. **(10 points) Based on the posterior draws in res.0 model with 10,000 iterations (Thetas of the model), draw outcomes for goodness-of-fit for model 1 and put the last table in your report. Interpret the gof results. (Hint: higher p-values mean better fit).**