Pseudocode of the Simulation Program

Code written by Diego F. Leal (www.diegoleqal.info)
Project: Three Essays on Network Dynamics and Liminality, Ph.D. dissertation
Sociology department, UMass-Amherst

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FIRST PROCEDURE (Populate Model, Initialize Parameters)

- Select and create a number of agents (**N**)
  - where $\mathbf{N} \in [100,\infty)$ and $\{\mathbf{N} : \mathbf{N} \in (\mathbb{Z}^+)\}$
- Select a level of Consolidation (**C**)
  - where $\mathbf{C} \in [0,1]$ and $\{\mathbf{C} : \mathbf{C} \in (\mathbb{R}^+ \cup [0])\}$
- Select a level of Homophily Bias (**H**)
  - where $\mathbf{H} \in [0,1]$ and $\{\mathbf{H} : \mathbf{H} \in (\mathbb{R}^+ \cup [0])\}$
- Select a number of Groups or Communities (**G**)
  - where $2 \leq \mathbf{G} \leq x$ with $\{x : x \in [3,\infty)$ and $x \in \mathbb{Z}^+\}$ and $\{\mathbf{G} : \mathbf{G} \in \mathbb{Z}^+\}$
- Select a number of secondary boundaries (**B**)
  - where $2 \leq \mathbf{B} \leq n$ with $\{n : n \in [3,\infty)$ and $n \in \mathbb{Z}^+\}$ and $\{\mathbf{B} : \mathbf{B} \in \mathbb{Z}^+\}$.
- Select a margin of error for (**F**)
  - where $\mathbf{F} \in [0.01,0.05]$ and $\{\mathbf{F} : \mathbf{F} \in (\mathbb{R}^+ \cup [0])\}$
- Select a mean degree (**Z**)
  - where $\mathbf{Z} \in [4,10]$ and $\{\mathbf{Z} : \mathbf{Z} \in (\mathbb{Z}^+)\}$
- Select a number of iterations (**Q**)
  - where $\mathbf{Q} \in [100,\infty)$ and $\{\mathbf{Q} : \mathbf{Q} \in (\mathbb{Z}^+)\}$
- Select the population mean for the adoption thresholds ($\mathbf{T}_{\mathbf{mean}}$)
  - where $0 \leq \mathbf{T}_{\mathbf{mean}} \leq 1$ where $\{\mathbf{T}_{\mathbf{mean}} : \mathbf{T}_{\mathbf{mean}} \in (\mathbb{R}^+ \cup [0])\}$
- Select the population standard deviation for the adoption thresholds ($\mathbf{T}_{\mathbf{sd}}$)
  - where $0 \leq \mathbf{T}_{\mathbf{sd}} \leq 1$ where $\{\mathbf{T}_{\mathbf{sd}} : \mathbf{T}_{\mathbf{sd}} \in (\mathbb{R}^+ \cup [0])\}$

SECOND PROCEDURE (Consolidation)

- For agent i to agent **N**:
  - Randomly assign agent i to one, and only one, of the possible values of **G** (i.e. group membership).
    - Call this distribution of agents within groups the primary boundary (**PB**)
- Create **B** copies of **PB**
  - Induce a **C** level of correlation between each **B** and **PB** by partially reshuffling the secondary boundaries
    - Stop if the average pair-wise Pearson correlation coefficient between all the boundaries is equal to **C** +/- **F**

THIRD PROCEDURE (Homophily Bias)

- While **Z** has not been reached:
  - Ask a randomly selected agent i to:

- Select a social boundary at random (any of the secondary boundaries or the **PB** can be selected). Call the selected boundary **b**
- Draw a random number **r** from the unit interval (**r** ∈ [0,1] and {**r : r** ∈ ($\mathbb{R}^+$ ∪ [0])}
- If-else **r** ≤ **H**
  - Create an undirected tie with a random alter j that has the same value (i.e. group membership) in **b**
  - Create an undirected tie with a random an alter j that has a different value (i.e. group membership) in **b**

FOURTH PROCEDURE (Diffusion)

- For agent i to agent **N**:
  - Compute agent's i degree ($\mathbf{D_i}$) intercultural capacity for brokerage ($\mathbf{IB_i}$), and betweenness centrality ($\mathbf{BE_i}$)
  - Create a variable A_i to indicate if the agent has adopted the innovation. Initially, no agent is an adopter (i.e. $\mathbf{A_i} = 0$)
  - Calculate similarity to all other agents in the society using the simple matching coefficient (SMC), see equation 3 in the article.
  - Generate a random number ($\mathbf{T_i}$), where $\mathbf{T_i} \sim N\ (\mathbf{T_{mean}}, \mathbf{T_{sd}})$
- Rank-order agents based on $\mathbf{D_i}$, $\mathbf{IB_i}$, and $\mathbf{BE_i}$. There is one unique ranking per measure.
- Select one of three rules to pick the seed agent: IB, degree, betweenness. or random
- Based on the previous step, select the agent with highest $\mathbf{D_i}$ or $\mathbf{IB_i}$ or $\mathbf{BE_i}$ or select an agent at random. Call the selected agent **seed.**
- Ask agent **seed** and all her immediate neighbors to become adopters (i.e. $\mathbf{A_i} = 1$). Call this set the seed neighborhood (**s**)
- Repeat **Q** times:
  - Ask a randomly selected non-adopter (i.e. $\mathbf{A_i} = 0$) agent i to:
    - Randomly select one of her neighbors j
    - Adopt the innovation (i.e. $\mathbf{A_i} = 1$) if j has already adopted the innovation (i.e. $\mathbf{A_j} = 1$) and the similarity to agent j (i.e. SMC_{ij}) is ≥ $\mathbf{T_i}$

FIFTH PROCEDURE (Compute Dependent Variables)

- Compute the following quantities:
  - $\mathbf{A_{overall}} = \frac{\sum_i^{Nns} A_i}{N_{ns}}$
  - $\mathbf{A_{in}} = \frac{\sum_i^{Nns} A_i\, G_{i,seed}}{\sum_i^{Nns} G_{i,seed}}$
  - $\mathbf{A_{out}} = \frac{\sum_i^{Nns} A_i\, |G_{i,seed} - 1)\,|}{\sum_i^{Nns} |G_{i,seed} - 1)\,|}$

Where $\mathbf{N_{ns}}$ is the set of all agents that are not part of the seed neighborhood, and $\mathbf{G_{i,seed}} = 1$ if the i^{th} agent has the same group membership in the primary boundary that the seed agent, 0 otherwise.