Pseudocode of the Simulation Program

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

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 ($\mathbf{r} \in [0,1]$ and $\{\mathbf{r} : \mathbf{r} \in (\mathbb{R}^+ \cup [0])\}$
- If-else $\mathbf{r} \leq \mathbf{H}$
  - 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 ($\mathbf{D_i}$) and intercultural capacity for brokerage ($\mathbf{IB_i}$)
  - 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 $\mathbf{D_i}$ and $\mathbf{IB_i}$
- Select one of three rules to pick the seed agent: IB, degree, or random
- Based on the previous step, select the agent with highest $\mathbf{D_i}$ or $\mathbf{IB_i}$ 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 $\geq \mathbf{T_i}$

FIFTH PROCEDURE (Compute Dependent Variables)

- Compute the following quantities:
- $\mathbf{A_{overall}} = \dfrac{\sum_i^{Nns} A_i}{N_{ns}}$

- $\mathbf{A_{in}} = \dfrac{\sum_i^{Nns} A_i\, G_{i,seed}}{\sum_i^{Nns} G_{i,seed}}$

- $\mathbf{A_{out}} = \dfrac{\sum_i^{Nns} A_i\, |G_{i,seed} - 1)\,|}{\sum_i^{Nns} |G_{i,seed} - 1)\,|}$

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 ith agent has the same group membership in the primary boundary that the seed agent, and 0 otherwise.