Pseudo-Code for the Agent-Based Model *Liminality and the Diffusion of Innovations among Adolescents* by Diego F. Leal (www.diegoleal.info)

FIRST PROCEDURE/LOOP (Populate Model)

- Extract Add Health friendship nomination network data (e.g. Sunshine High data) and nodes' attributes data (race, ethnicity, income, age, grade, gender).
- Symmetrize the network using the weak rule.
- Create as many agents as there are in the school under analysis. Denote the number of agents as n.
- Bestow each agent with the attributes (sex, race, grade, income, and ethnicity) of the student it represents.
- Create a variable for each agent, A_i, that signals adoption (A_i = 1 adopted; A_i =0 did not adopt)

SECOND PROCEDURE/LOOP (Model Diffusion)

- For agent i to agent n, where n is the number of agents in a given school (e.g. Sunshine High)
    - Make agent i the seed agent, that is, the seed innovator (A_i = 1)
    - Make i's group of friends adopt the innovation. Call this set of agents the seed neighborhood (S_i)
    - Repeat N times (N ∈ [1,n]):
        - In random order, and with no replacement, ask each agent/alter outside S_i to:
            - Adopt the innovation if a given user-defined proportion, T, of her friends have adopted the innovation (T ∈ [0,1])
    - Retrieve the number of agents infected by agent i. Call this quantity M_{i_raw}
    - Calculate the proportion of the population infected by agent i (M_{i_raw}/n). Call this quantity the *spreading capacity* of agent i (CAP_i).

THIRD PROCEDURE/LOOP (Calculate Centrality Measures & Average Spreading Capacity)

- Calculate the following centrality scores for each ego:
    - Degree (deg_i); Betweenness ($betw_i$); Closeness ($close_i$); interracial brokerage (IB_i); egonetwork diversity ($diver_i$); Eigenvector centrality ($eigen_i$); Local clustering coefficient ($clust_i$)
- Consider a user-defined proportion p of the most efficient spreaders (p ∈ [0,1])
- Define the set $\Upsilon_{CAP}(p)$ as the portion p of agents with the highest spreading capacity (CAP_i)
- Compute the average proportion of alters infected for each ego included in $\Upsilon_{CAP}(p)$. Call this quantity $AVG_{CAP}(p)$
- Define the set $\Upsilon_{centrality\_measure}(p)$ as the portion p of agents with the highest score in a given centrality measure. For instance, the set $\Upsilon_{degree}(p)$ is the portion p of agents with the highest degree centrality.
- Compute the average proportion of alters infected for each ego included in $\Upsilon_{centrality\_measure}(p)$. Call this quantity $AVG_{CAP\_centrality\_measure}(p)$

FOURTH PROCEDURE/LOOP (Compute Imprecision Function)

- To assess the merit of using a given centrality measure to identify efficient spreaders, one needs to compare the sets $AVG_{CAP}(p)$ and $AVG_{CAP\_centrality\_measure}(p)$. In order to do so, Follow Kitsak et al. (2010) by computing an *imprecision function* based on these two quantities:

$$IM_{centrality\_measure}(p) = 1 - [AVG_{CAP\_centrality\_measure}(p)/AVG_{CAP}(p)]$$

    - Note: A value of IM close to 0 represents a very precise decision process because the nodes chosen under the centrality measure under analysis (e.g. degree centrality) are those who, indeed, individually contribute most to the diffusion process.