Fully coupled systems with activator-inhibitor states linked within homophilic dynamically evolving networks

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Vision:
We live in a digital world. Across all aspects of our society, modern advances in ICT and their explosive take up and adaptation are producing new spaces within which individuals can work, rest, and play; and new ways to observe and understand human behaviour. Where the innovations resonate with the users this disrupts and changes entire sectors, our social norms and our own aspirations. Forever.

Mission:
To be the originator of modelling concepts, methods and applications delivering high impact and value to public and commercial exploiters within the digital society and data rich R&D sectors. To be the partner of choice for public, commercial and academic innovators and exploiters.
• How does networking lead to instability?
  – Emergence of structure: non uniform states
  – Applications to norms, attitudes, behaviour...

• What happens when the states affect the dynamic networking (Homophily)?
• For small and large populations?
• For deterministic and stochastic systems?

• Will increased communication lead to more social instabilities?
“New lamps for old”
Consider an evolving social network: \( N \) vertices = individuals. The attitude of the \( i \)th individual: state variables, \( \mathbf{x}_i(t) : \mathbb{R} \rightarrow \mathbb{R}^m \). Let \( \mathbf{X}(t) = \{\mathbf{x}_1(t)^T, \ldots, \mathbf{x}_N(t)^T\} \) (an \( N \times m \) matrix).

Assume individuals are connected by an evolving network with adjacency matrix \( A(t) \) (symmetric, zero diagonal, binary).

Each edge evolves independently – though each is conditionally dependent the current network (can be correlated!).

The edge independence assumption implies that rather than specify a full probability distribution for future evolution, say

\[
P_{\delta t}(A(t + \delta t)|A(t)),
\]

it is enough to specify its expected value \( E(A(t+\delta t)|A(t)) \) (a matrix containing all edge probabilities, from which edges may be generated independently).

Their equivalence is trivial, since

\[
E(A(t + \delta t)|A(t)) = \sum_B B P_{\delta t}(B|A(t)),
\]

and

\[
P_{\delta t}(B|A(t)) = \prod_{i_1=1,i_2=i_1+1}^{N-1,N} (W)_{i_1,i_2}^{(B)_{i_1,i_2}} \cdot (1 - (W)_{i_1,i_2})^{1-(B)_{i_1,i_2}},
\]

where \( W = E(A(t + \delta t)|A(t)) \).
Thus our model for the stochastic network evolution is specified by writing

\[
E(A(t + \delta t)|A(t)) = A(t) + \delta t \mathcal{F}(A(t), \mathbf{X}(t)),
\]

valid as \( \delta t \to 0 \). Here the real valued matrix value function \( \mathcal{F} \) is symmetric; it has a zero diagonal (all elements of right hand side in \([0,1]\)).

We should have

\[
\mathcal{F}(A(t), \mathbf{X}(t)) = -A(t) \circ \{Death rates\} + (1 - A(t)) \circ \{Birth rates\}.
\]

Example.

\[
\mathcal{F}(A(t), \mathbf{X}(t)) = -A(t) \circ (1 - \Phi(\mathbf{X}(t)).\omega + (1 - A(t)) \circ \Phi(\mathbf{X}(t)).\delta.
\]

Here \( \Phi(\mathbf{X}(t))_{i,j} \in [0, 1] \) is a monotonically DECREASING function of

\[
||x_j(t) - x_i(t)||.
\]

For instance \( \Phi(\mathbf{X}(t))_{i,j} \sim 1 \) for \( ||x_j(t) - x_i(t)|| < \epsilon \), and = 0 otherwise.
Activator-Inhibitor Processes

- In **psychology**, large literature on individuals having a tensioned equilibrium between activating processes and inhibiting processes.
  - Gray’s (1987) introduction of a *model* for behavior activation and behavior inhibition led to a very large amount of research.
  - The *Dual Control Model*, summarized by Bancroft et al (2009), proposes that individuals’ sexual responses involve an interaction between sexual excitatory and sexual inhibitory processes.
  - It is now generally accepted that most brain functions are at a balance between activator and inhibitory processes.

- In **applied mathematics**, Activator-Inhibitor systems are hugely important: a uniform equilibrium across a population of individual units becomes destabilized by “passive” coupling.
  - Such **Turing instabilities** naturally break the uniform symmetry, resulting in localized subsets of increased activation and increased inhibition: *patterns*.
  - Occurs when the coupling between the individuals’ is stronger for the inhibitor variables than for the activator variables.
  - Such instabilities may seem counter intuitive at first sight since individuals are seeking pairwise alignment of individually stable systems.
Turing instability

\[ \dot{x}_i = f(x_i) + \sum_{j=1}^{N} A_{ij} D(x_j - x_i) \]

Suppose \( f(x^*) = 0 \) so there is a uniform equilibrium \( x_i = x^* \), for \( i = 1, \ldots, N \),

If \( A \) is constant, let \( \lambda_j > 0 \) \( (j = 1, \ldots, N) \) be eigenvalues of \( A \)'s Laplacian.

Then the equilibrium is STABLE iff

\[ df(x^*) - \lambda_j D \]

is a Stability Matrix, for each \( j = 1, \ldots, N \).

Think of

\[ df(x^*) - \lambda D \]

as a function of \( \lambda \).

There is a window of instability: \( (\lambda_{\text{min}}, \lambda_{\text{max}}) \), depending on \( D \) etc. Associated non constant equilibria bifurcate (pitchforks) as any eigenvalue move in and out of this window,

Typically, for instabilities, the diffusion of the inhibitor species must be greater than than of the activator(s).
Fully Coupled - Deterministic

Identical Activator – Inhibiter dynamics

Diffusion driven (Turing) instability

Homophily term


\[ \dot{x}_i(t) = f(x_i(t)) + \sum_{j=1}^{N} A_{ij}(t) D(x_j(t) - x_i(t)) \quad i = 1, \ldots, N \]

\[ \dot{A}_{ij}(t) = \mu A_{ij}(t) (1 - A_{ij}(t)) (\epsilon - \phi(x_j(t) - x_i(t))) \quad i, j = 1, \ldots, N \]
N=2 and Schnackenberg Dynamics

\[
x_1'[t] = p + D_1 a[s][t] (-x_1[t] + x_2[t]) - x_1[t] y_1[t]^2
\]
\[
y_1'[t] = q - y_1[t] + x_1[t] y_1[t]^2 + D_2 a[s][t] (-y_1[t] + y_2[t])
\]
\[
x_2'[t] = p - D_1 a[s][t] (-x_1[t] + x_2[t]) - x_2[t] y_2[t]^2
\]
\[
y_2'[t] = q - y_2[t] + x_2[t] y_2[t]^2 - D_2 a[s][t] (-y_1[t] + y_2[t])
\]
\[
a[s]'[t] = 10000 (1 - a[s][t]) a[s][t] (\text{epsilon} - (-x_1[t] + x_2[t])^2)
\]

\[p = 1.25\]
\[q = 0.01\]
\[D_1 = 1\]
\[D_2 = 0.01\]
\[\text{epsilon} = 10.^-6\]
\[\text{mu} = 10^4\]
$x_1(t)$ inhibitor variable
$x_1(t)$ and $x_2(t)$
$a(t)$ coupling strength
$a$ versus $(x_1 - x_2)$ and $(x_1 + x_2)/2$
$a$ versus $(x1-x2)$ and $(y1-y2)$
Fully Coupled – Stochastic

Identical Activator – Inhibitor dynamics

Diffusion driven (Turing) instability

Homophilly terms

\[ \dot{x}_i(t) = f(x_i(t)) + \sum_{j=1}^{N} A_{ij}(t)D(x_j(t) - x_i(t)) \quad i = 1, \ldots, N \]

Let \( \mathbf{1} \) denote the \( N \times N \) adjacency matrix for the clique (all 1’s except for zeros on the diagonal).

Let \( \Phi(\mathbf{X}) \) denote the real, symmetric \( N \times N \) matrix with \((i, j)\)th term given by \( \phi(x_j - x_i) \).

Let \( \circ \) denote the element-wise multiplication of matrices.

\[
E(A(t + \delta t) | A(t)) = A(t) + \delta t \cdot \mu.( -A(t) \circ (1 - \Phi(\mathbf{X}(t)).\omega + (1 - A(t)) \circ \Phi(\mathbf{X}(t)).\delta) )
\]
Inhibition variables

N=40, Extremes (top 10 and bottom 10)

\[ p = 2; \]
\[ q = 1; \]
\[ D1 = 2.5; \]
\[ D2 = 0.005; \]
\[ \Delta = 0.01; \]
\[ \epsilon = 10^{-4}; \]
\[ \delta = 0.8; \]
\[ \omega = 0.8; \]
2 D projection of evolving network
N=40, Clique projection and next principal projection

\[ \begin{align*}
  p &= 2; \\
  q &= 1; \\
  D_1 &= 2.5; \\
  D_2 &= 0.005; \\
  \Delta &= 0.01 \\
  \epsilon &= 10^{-4}; \\
  \delta &= 0.8; \\
  \omega &= 0.8;
\end{align*} \]
Next steps...

• Analysis of large and small deterministic systems
• Analysis of stochastic systems
• Nonlinear network dynamics: triad closure, stratification, and beyond...

• New applications to new behavioral phenomena
  – Centre for Applied Behavioural Sciences at UoR
  – Consortium for Exploratory Research in Security
  – Other government: MOD, HMRC,...
  – Commerce: Ad/Media, Telco, Energy, Security and beyond

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