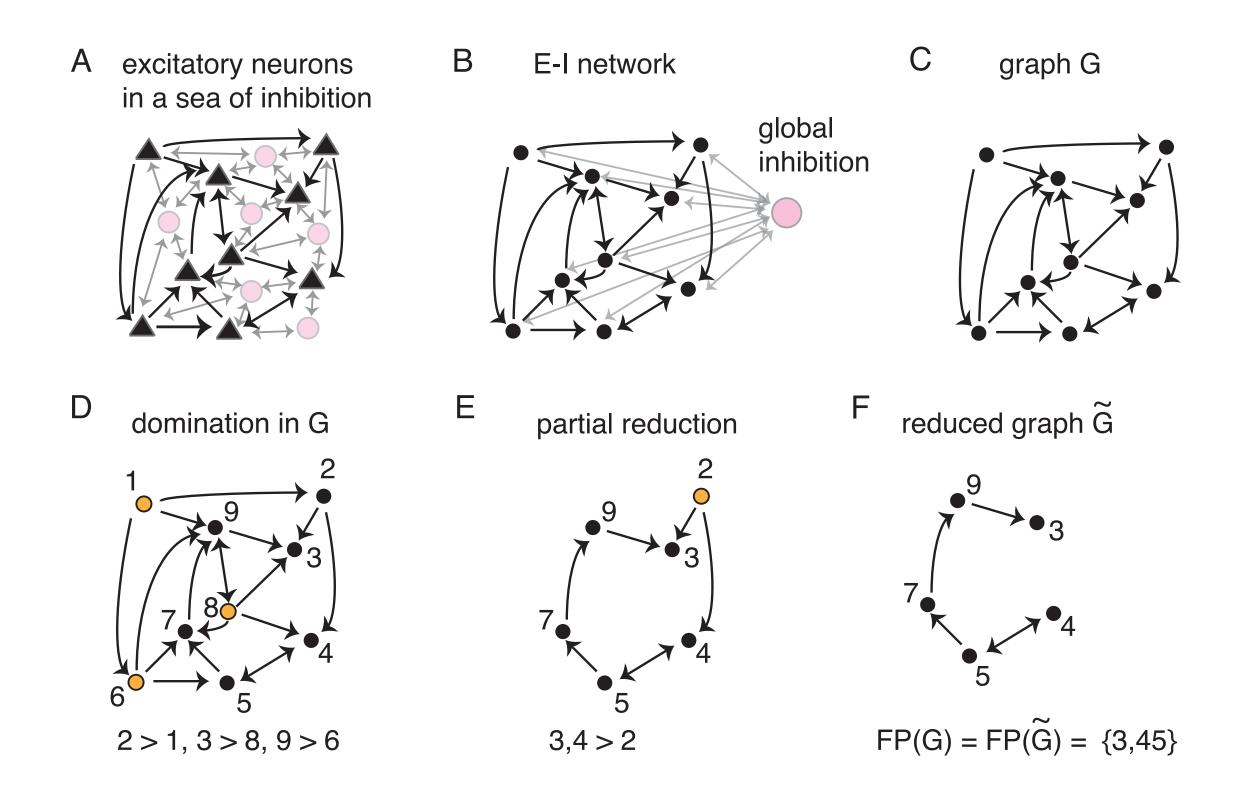
Domination and reduction for E-I TLNs built from graphs



Carina Curto, Brown University

Janelia workshop: Analysis and Modeling of Connectomes

June 3, 2025

Motivating questions and ideas:

- 1. How does connectivity shape dynamics?
- 2. The relationship between connectivity and neural activity depends on the dynamical system you associate to the connectome.
- 3. By studying neuroscience-inspired (nonlinear!) dynamical systems on graphs, we can generate hypotheses about the dynamic meaning/role of various network motifs.



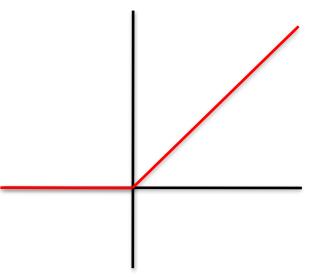
TLNs — nonlinear recurrent network models

Threshold-linear network dynamics:

$$\frac{dx_i}{dt} = -x_i + \left[\sum_{j=1}^n W_{ij}x_j + b_i\right]_{+}$$

W is an $n \times n$ matrix

$$b \in \mathbb{R}^n$$



The TLN is defined by (W, b)

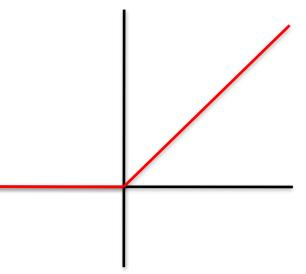
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Basic Question: Given (W,b), what are the network dynamics?

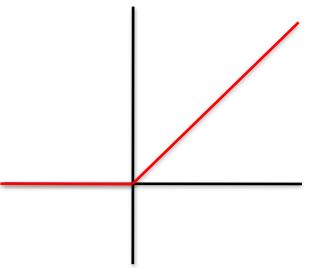
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Linear network dynamics:

$$\frac{dx}{dt} = Ax + b$$

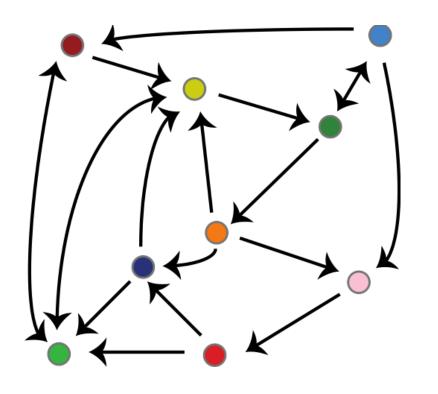
 $A \text{ is an } n \times n \text{ matrix}$ $b \in \mathbb{R}^n$

Long-term behavior is easy to infer from eigenvalues, eigenvectors—linear algebra tells us everything.

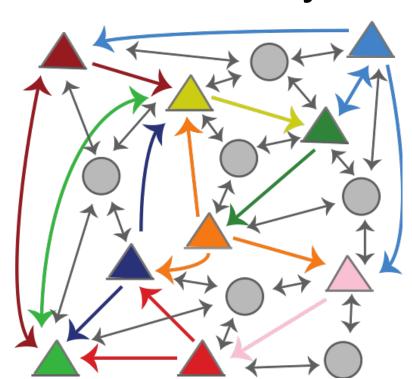
Basic Question: Given (W,b), what are the network dynamics?

The most special case: Combinatorial Threshold-Linear Networks (CTLNs)

graph G



Idea: network of excitatory and inhibitory cells



Graph G determines the matrix W

$$W_{ij} = \begin{cases} 0 & \text{if } i = j \\ -1 + \varepsilon & \text{if } i \leftarrow j \text{ in } G \\ -1 - \delta & \text{if } i \not\leftarrow j \text{ in } G \end{cases}$$

parameter constraints:
$$\delta > 0 \quad \theta > 0 \quad 0 < \varepsilon < \frac{\delta}{\delta + 1}$$

TLN dynamics:

$$\frac{dx_i}{dt} = -x_i + \left[\sum_{j=1}^n W_{ij}x_j + \theta\right]_+$$

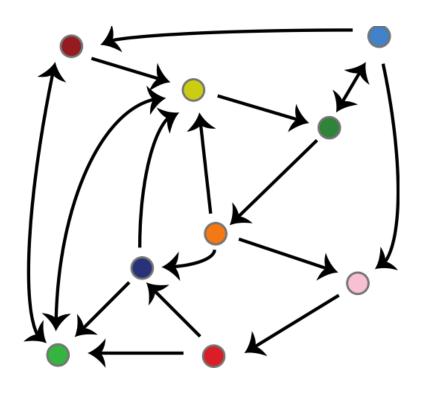
The graph encodes the pattern of weak and strong inhibition

Think: generalized WTA networks

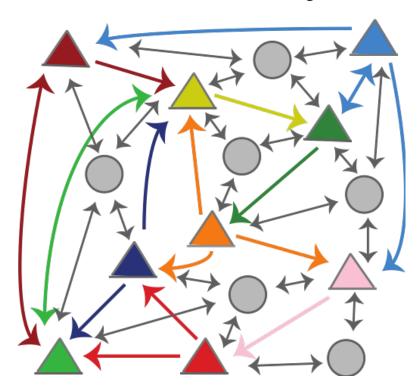
For fixed parameters, only the graph changes isolates the role of connectivity

Less special: generalized Combinatorial Threshold-Linear Networks (gCTLNs)

graph G



Idea: network of excitatory and inhibitory cells



TLN dynamics:

$$\frac{dx_i}{dt} = -x_i + \left[\sum_{j=1}^n W_{ij}x_j + \theta\right]_+$$

The gCTLN is defined by a graph G and two vectors of parameters: ε,δ

$$W_{ij} = \left\{ egin{array}{ll} -1 + arepsilon_j & ext{if } j
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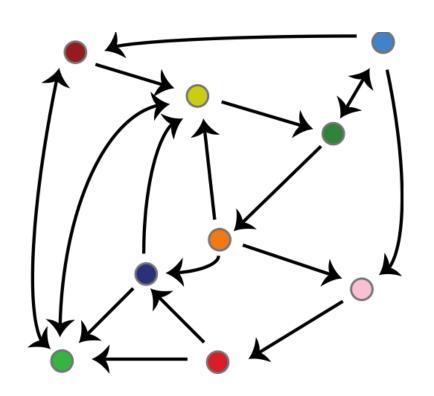
The graph encodes the pattern of weak and strong inhibition

$$b_i = \theta > 0$$
 for all neurons

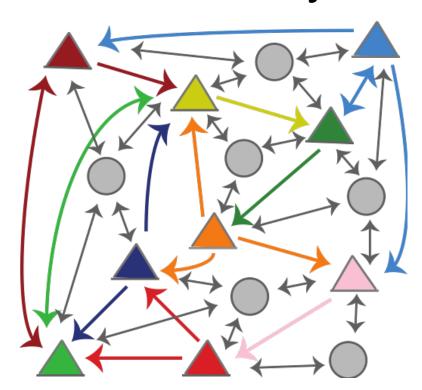
(default is uniform across neurons, constant in time)

Less special: generalized Combinatorial Threshold-Linear Networks (gCTLNs)

graph G



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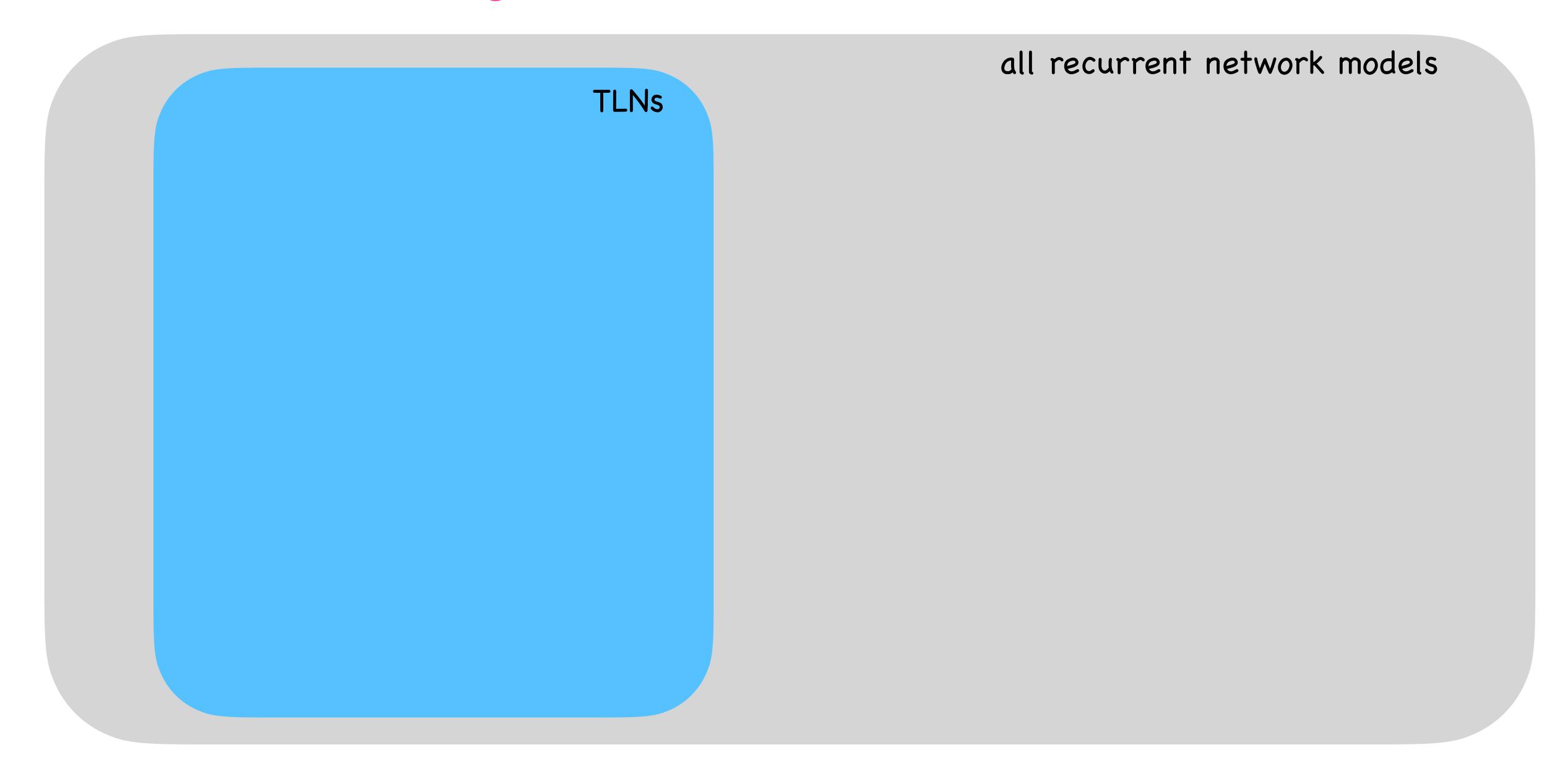
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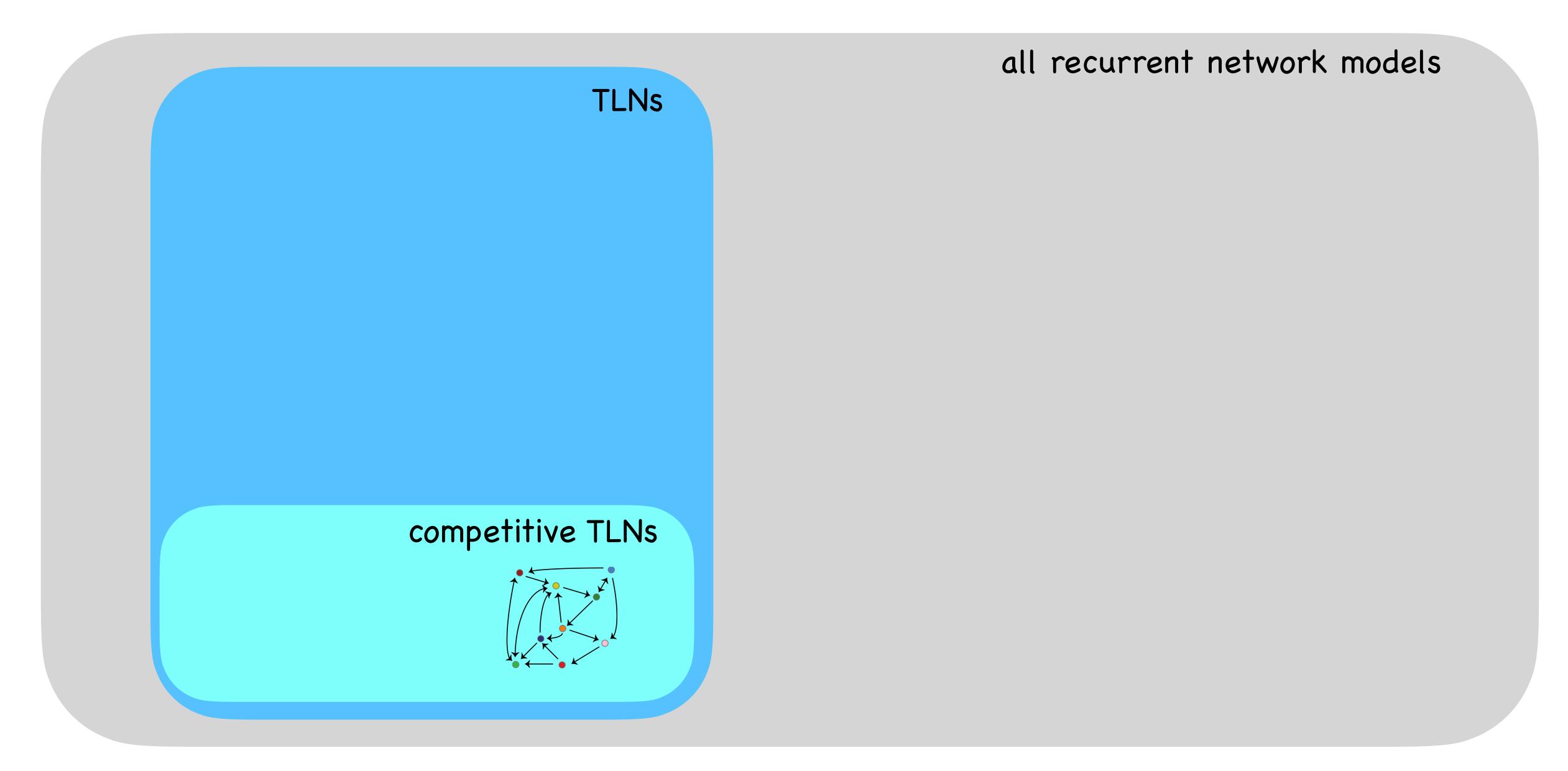
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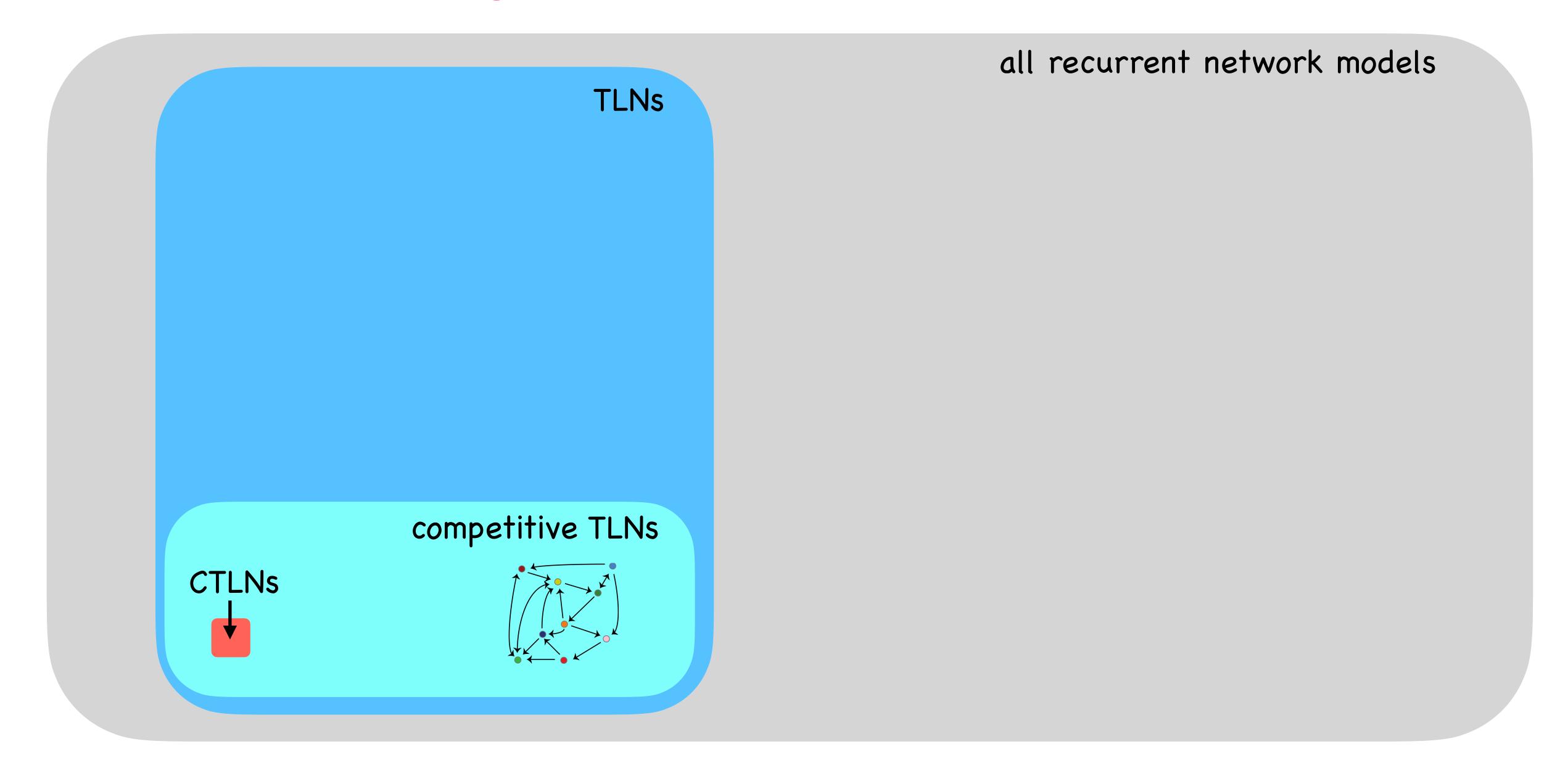
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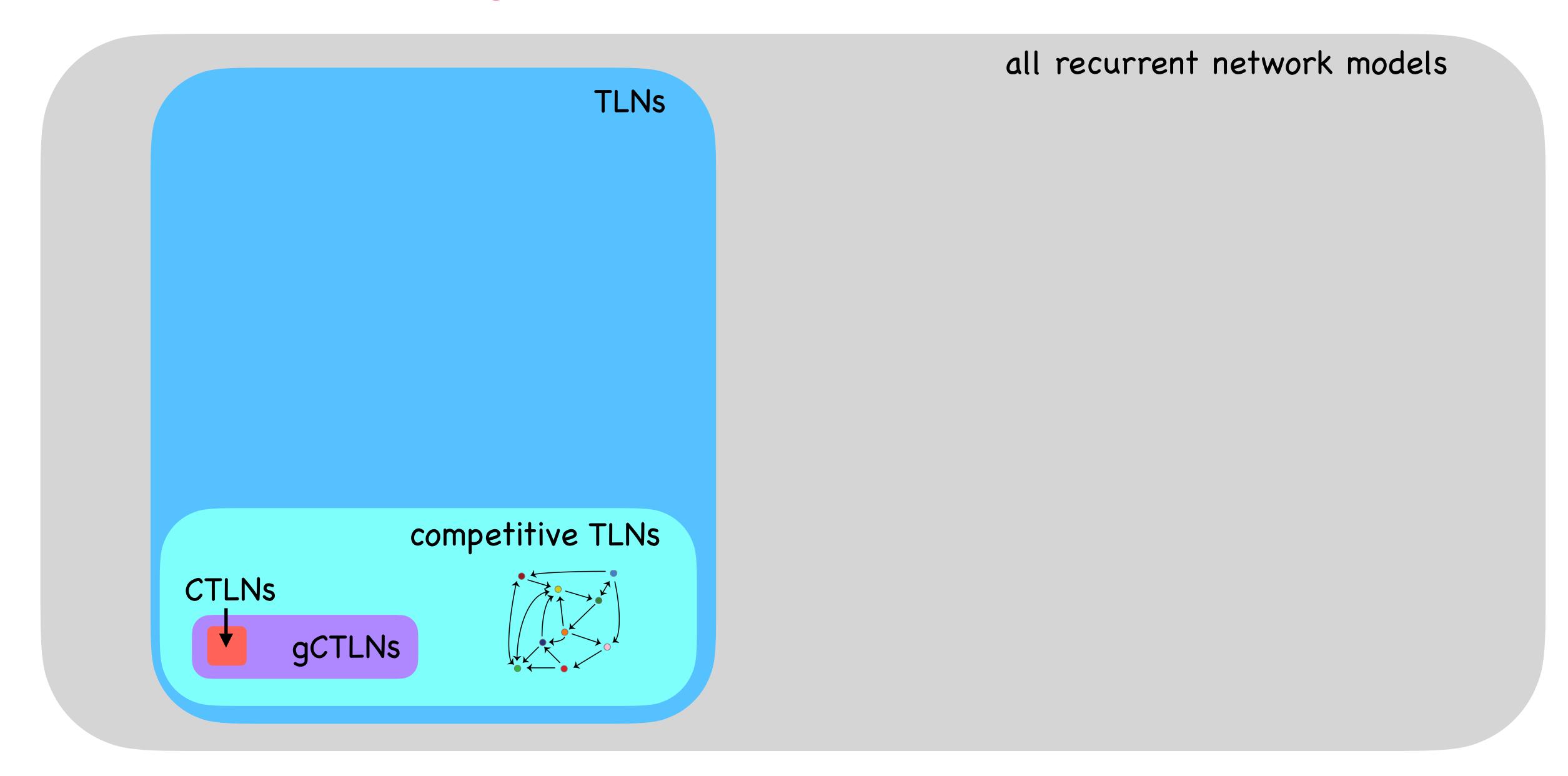


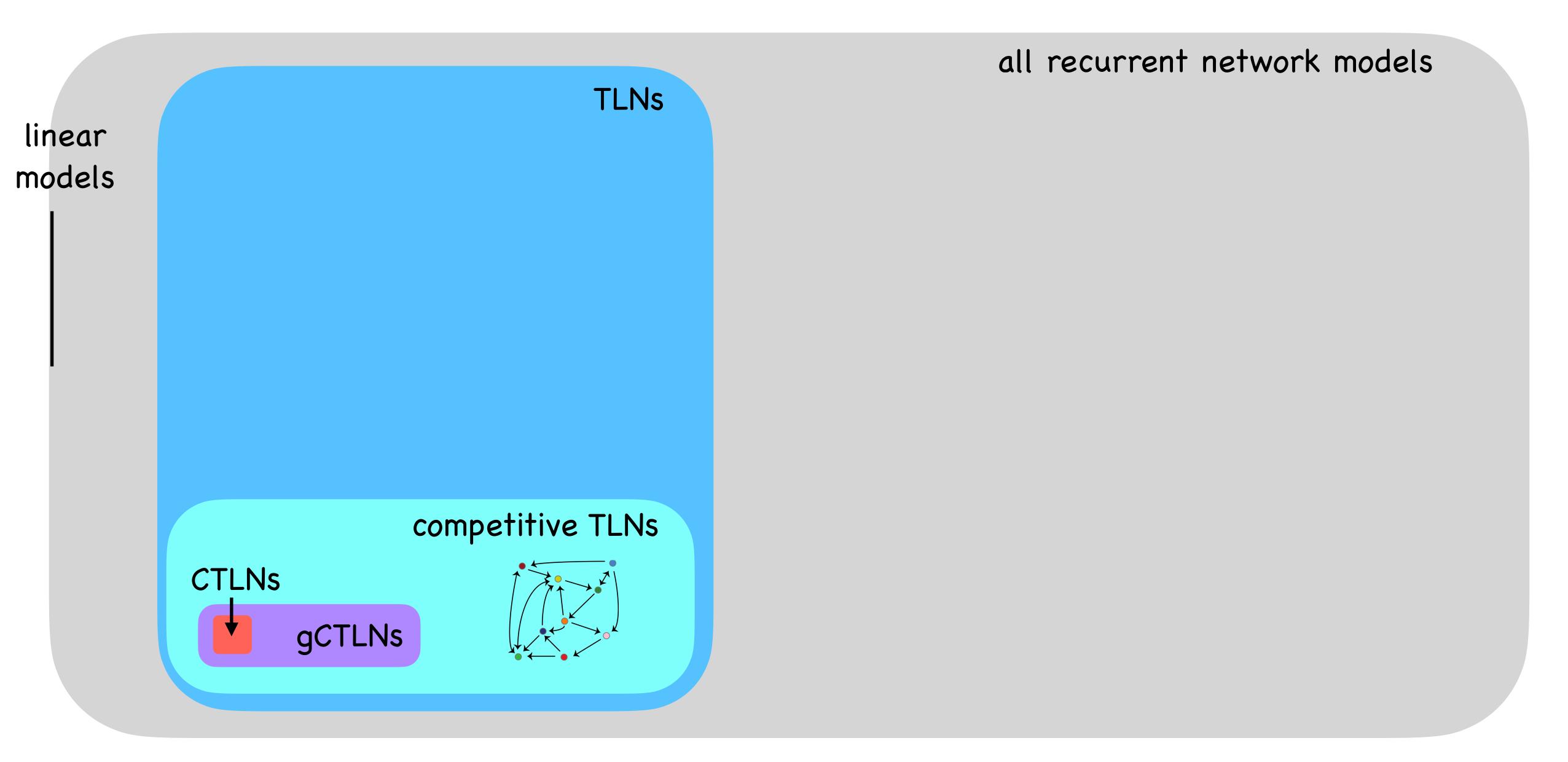
Special case: if the parameters ε_j, δ_j are the same for all neurons, we have a CTLN.



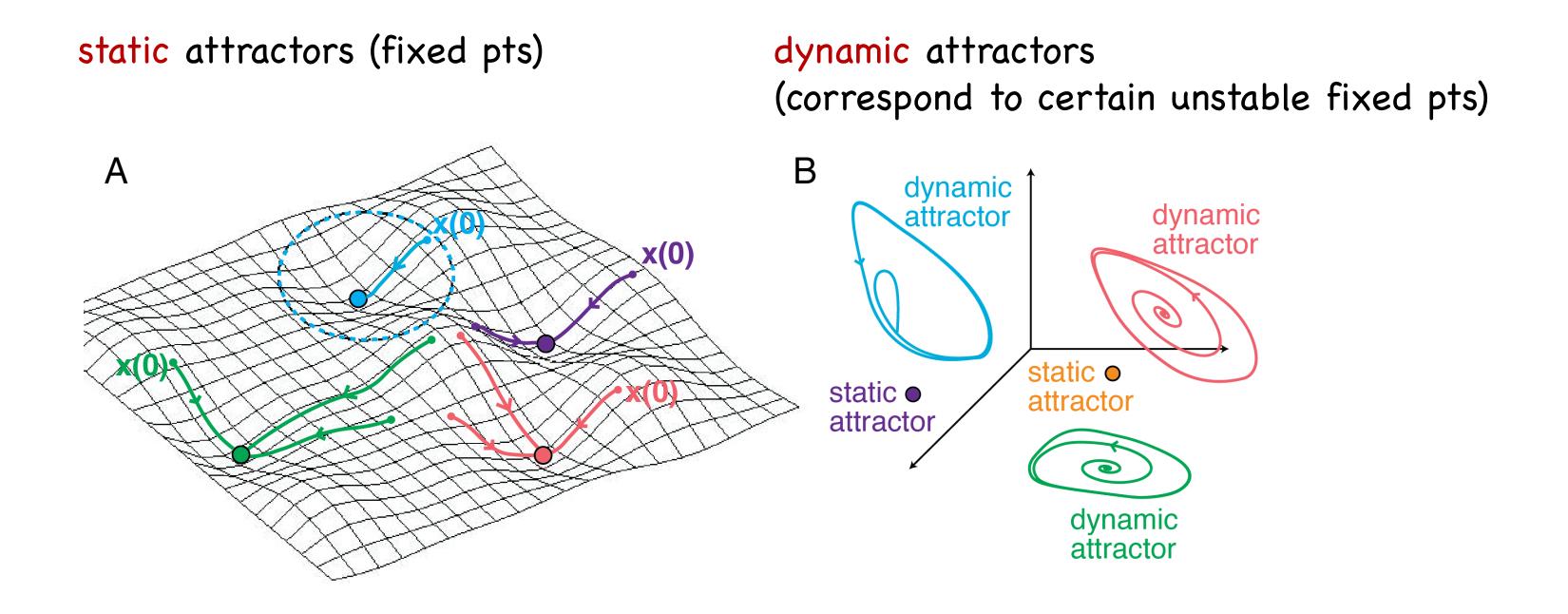






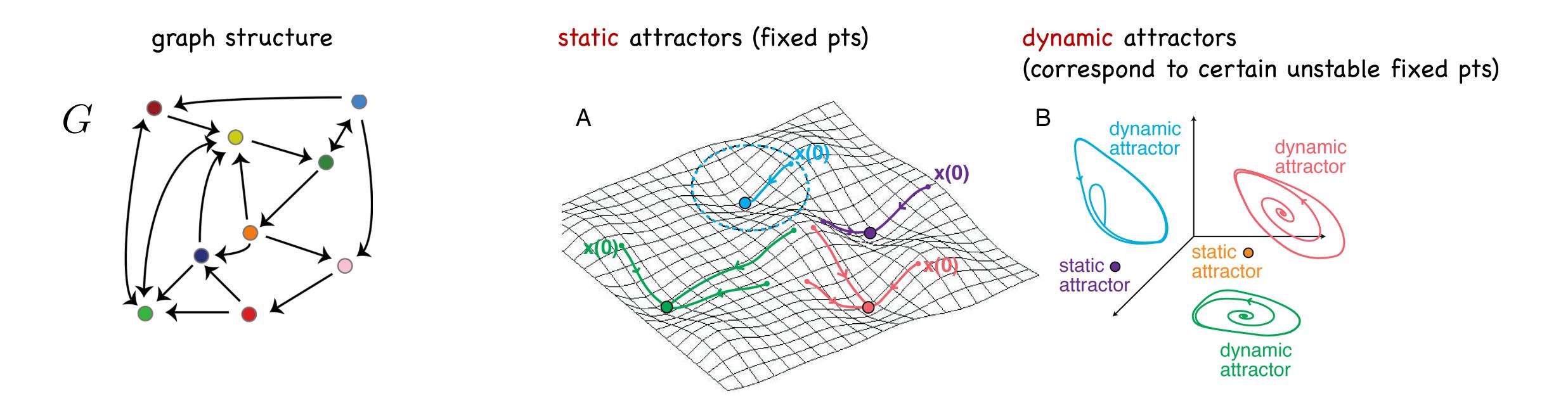


1. Display rich nonlinear dynamics: multistability, limit cycles, chaos...

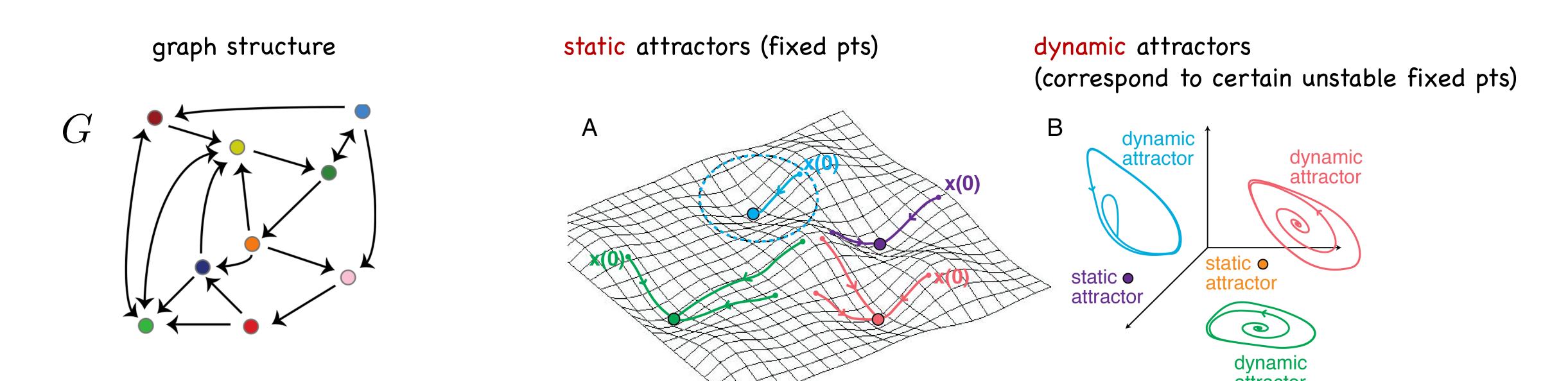


Curto & Morrison, 2023 (review paper): Graph rules for recurrent neural network dynamics

- 1. Display rich nonlinear dynamics: multistability, limit cycles, chaos...
- 2. Mathematically tractable: we can prove theorems directly connecting graph structure to dynamics.



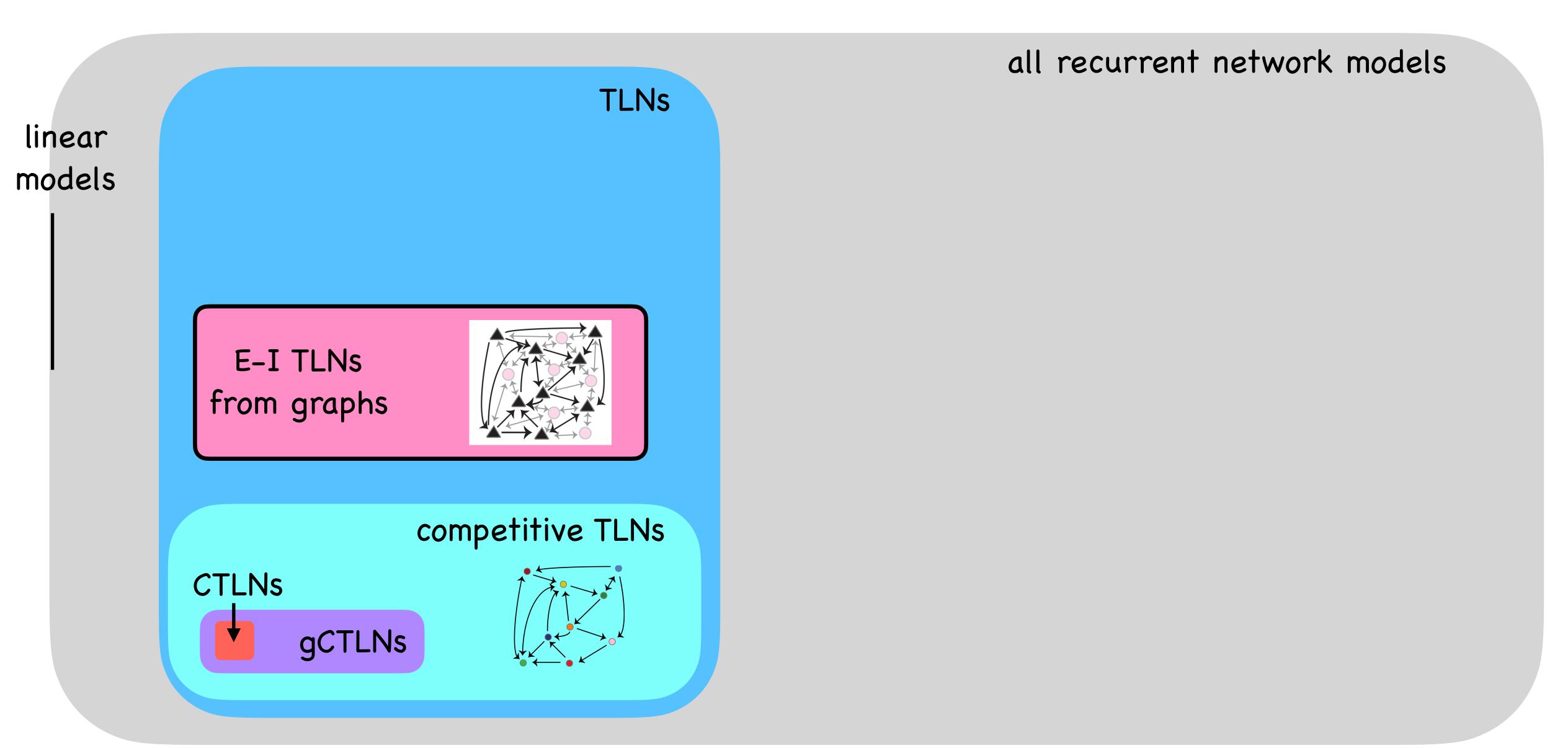
- 1. Display rich nonlinear dynamics: multistability, limit cycles, chaos...
- 2. Mathematically tractable: we can prove theorems directly connecting graph structure to dynamics.
- 3. Both stable and unstable fixed points play a critical role in shaping the dynamics (the vector field).



$$FP(G) = FP(G, \varepsilon, \delta) = \{ \text{ fixed points (stable and unstable) } \}$$

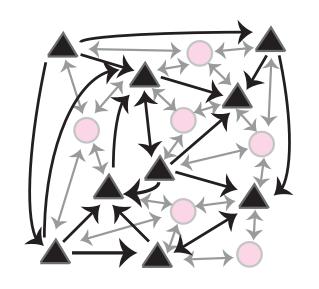
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TLNs, CTLNs, and gCTLNs ... and E-I TLNs from graphs



E-I TLNs from graphs

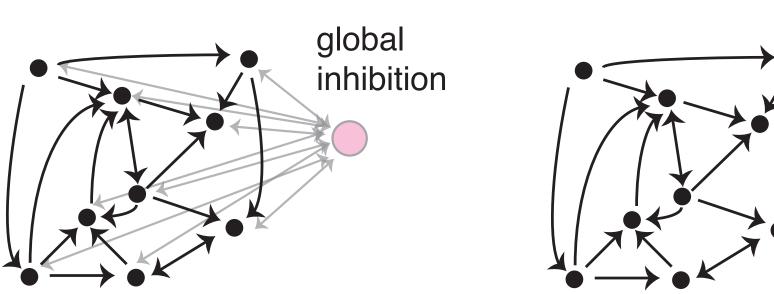
excitatory neurons in a sea of inhibition



E-I network

С

graph G



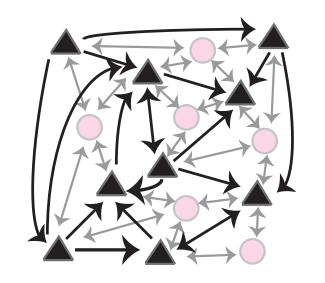
$$\frac{dx_i}{dt} = -x_i + \left[\sum_{j=1}^n W_{ij}x_j + W_{iI}(x_I - W_{Ii}x_i) + b_i\right]_+, i = 1, \dots, n,$$

$$\frac{dx_I}{dt} = \frac{1}{\tau_I} \left(-x_I + \left[\sum_{j=1}^n W_{Ij} x_j + b_I \right]_+ \right).$$

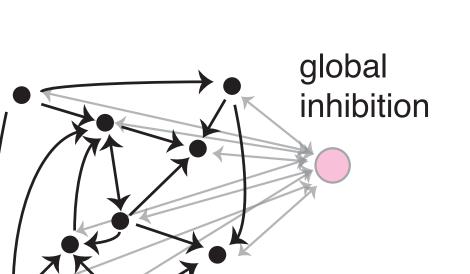
$$W_{ij} = \begin{cases} a_j & \text{if } j \to i \text{ in } G, \\ 0 & \text{if } j \not\to i \text{ in } G, \\ 0 & \text{if } i = j, \end{cases} \quad \text{and} \quad \begin{aligned} W_{Ij} &= c_j, \\ W_{iI} &= -1, \\ W_{II} &= 0. \end{aligned}$$

E-I TLNs from graphs

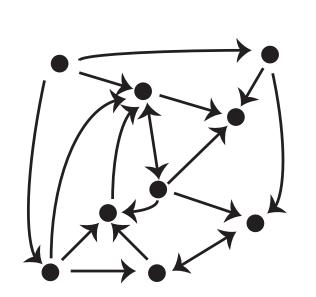
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E-I network



graph G

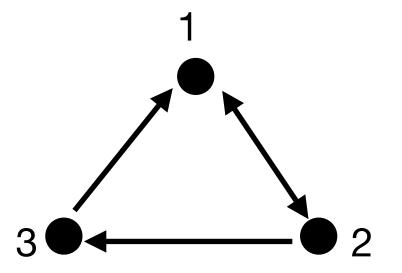


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Example G:



W for E-I TLN

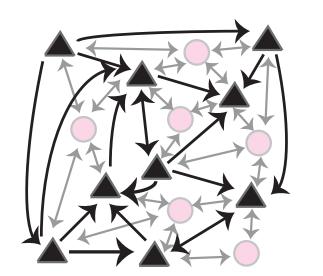
$$W = \left(egin{array}{cccc} 0 & a_2 & a_3 & -1 \ a_1 & 0 & 0 & -1 \ 0 & a_2 & 0 & -1 \ c_1 & c_2 & c_3 & 0 \end{array}
ight)$$

W for gCTLN

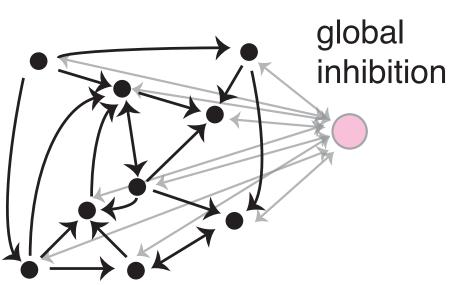
$$W = \begin{pmatrix} 0 & -1 + \varepsilon_2 & -1 + \varepsilon_3 \\ -1 + \varepsilon_1 & 0 & -1 - \delta_3 \\ -1 - \delta_1 & -1 + \varepsilon_2 & 0 \end{pmatrix}$$

There is a mapping from E-I TLNs to gCTLNs that preserves fixed points

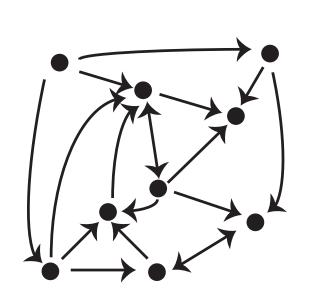
excitatory neurons in a sea of inhibition



E-I network



graph G



$$\frac{dx_i}{dt} = -x_i + \left[\sum_{j=1}^n W_{ij}x_j + \underbrace{W_{iI}(x_I - W_{Ii}x_i)}_{+} + b_i\right]_+, i = 1, \dots, n,$$

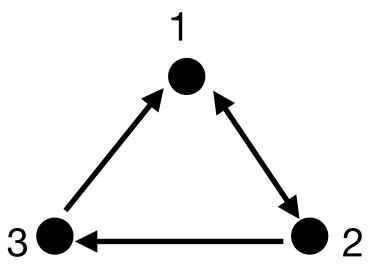
$$\frac{dx_I}{dt} = \frac{1}{\tau_I} \left(-x_I + \left[\sum_{j=1}^n W_{Ij} x_j + b_I \right]_+ \right).$$

Parameter mapping to get the same fixed points:

$$\varepsilon_j = 1 + a_j - c_j,$$

$$\delta_j = c_j - 1.$$

Example G:



W for E-I TLN

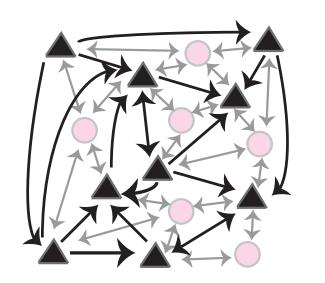
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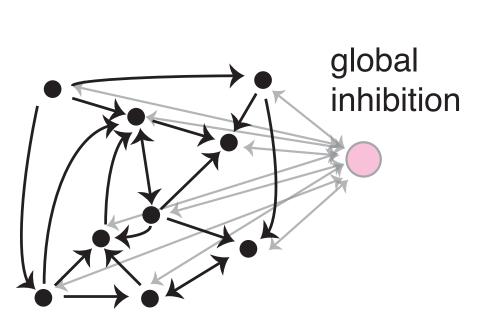
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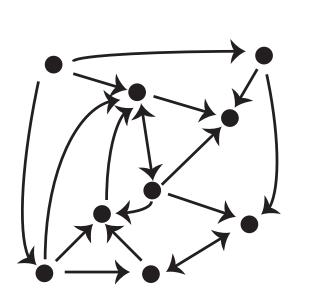
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E-I network



graph G



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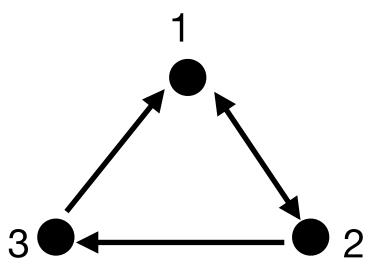
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The mapping says nothing about the timescale of inhibition!

Example G:

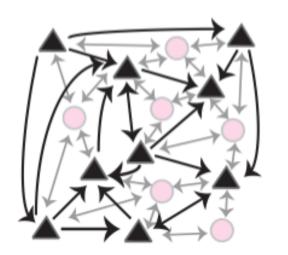


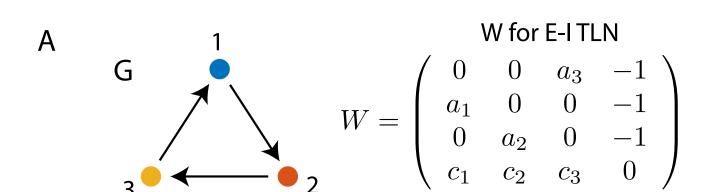
W for E-I TLN

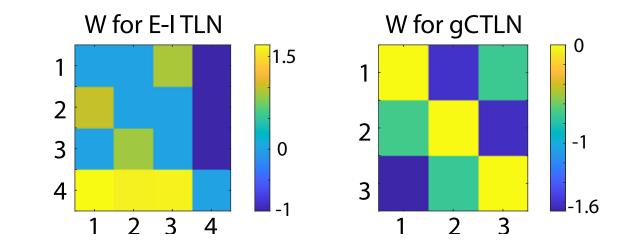
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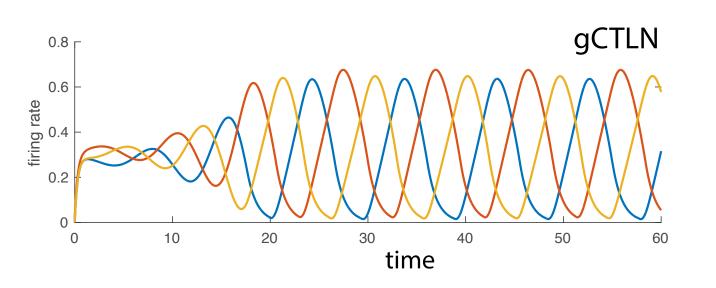
W for gCTLN

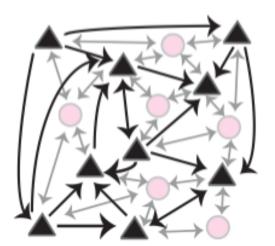
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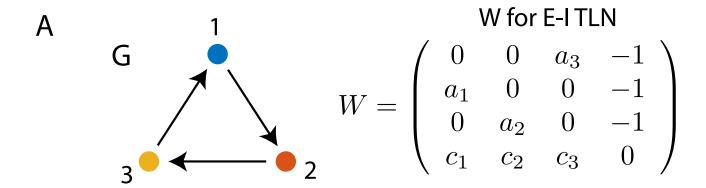


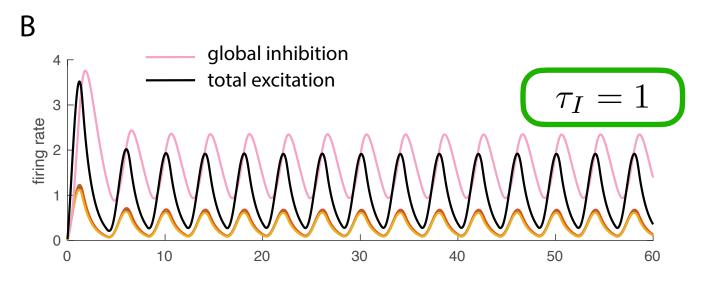


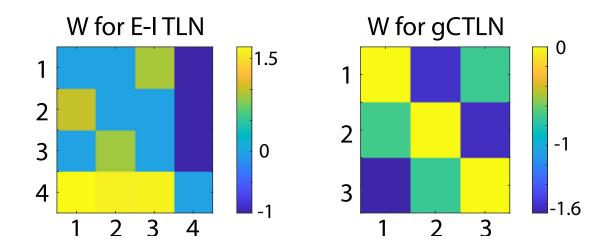


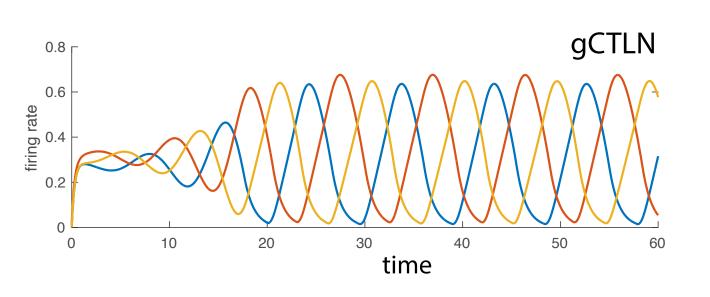


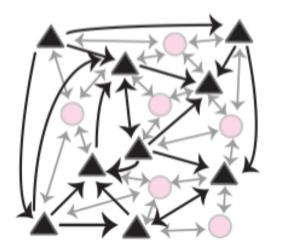


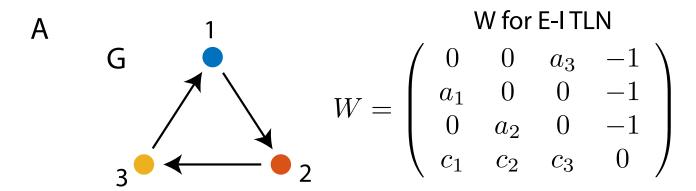


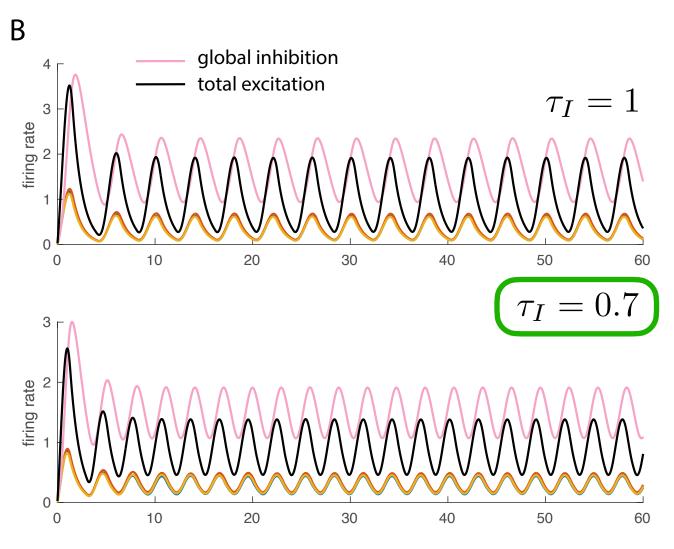


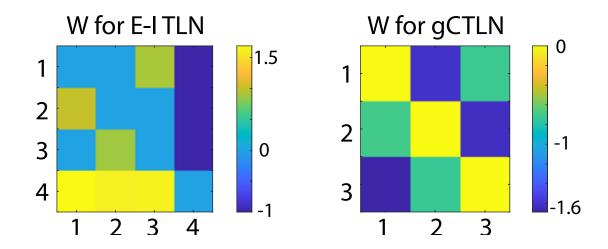


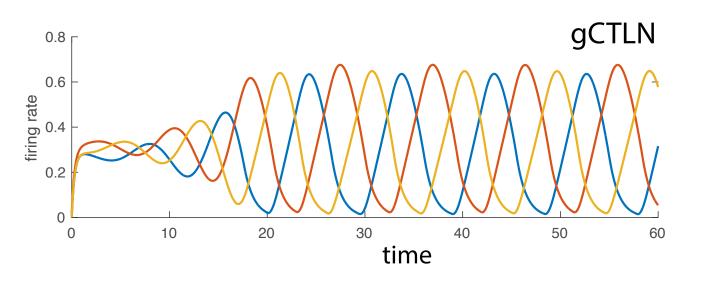


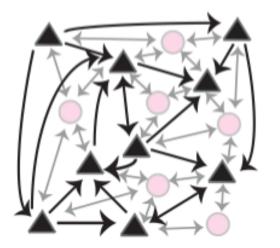


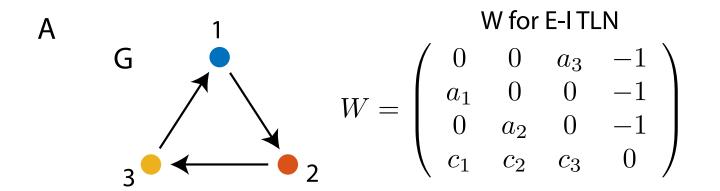


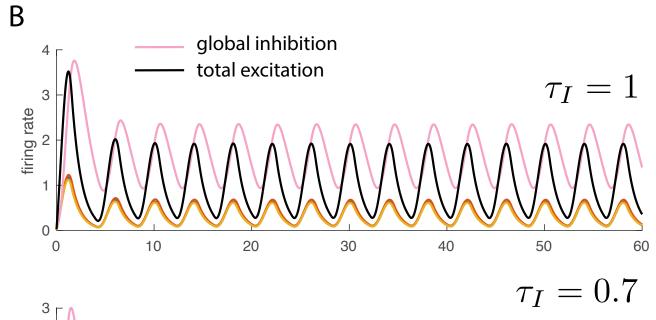


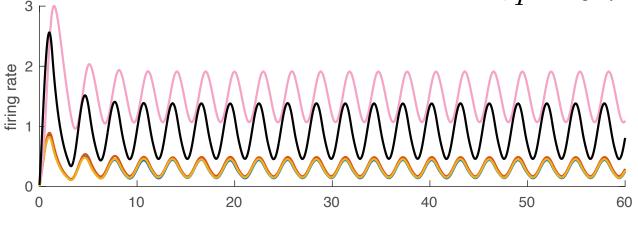


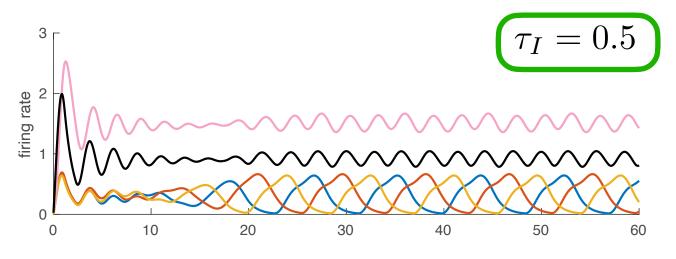


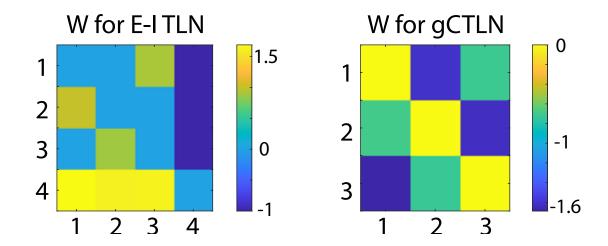


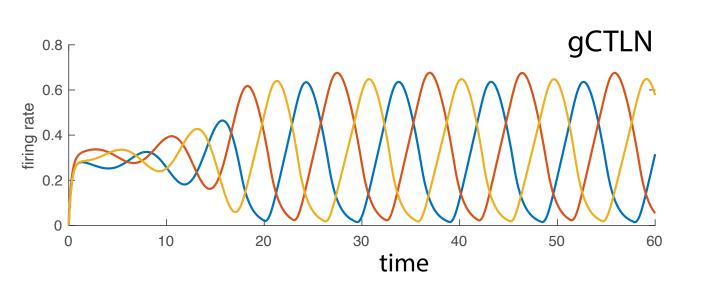


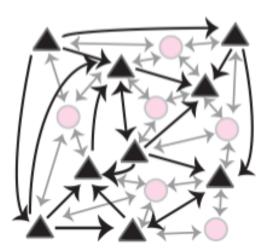


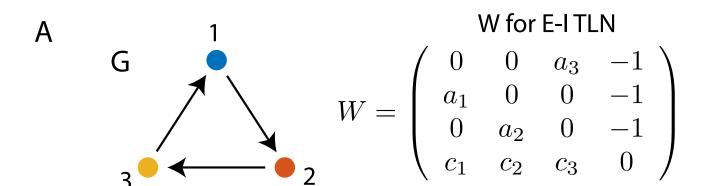


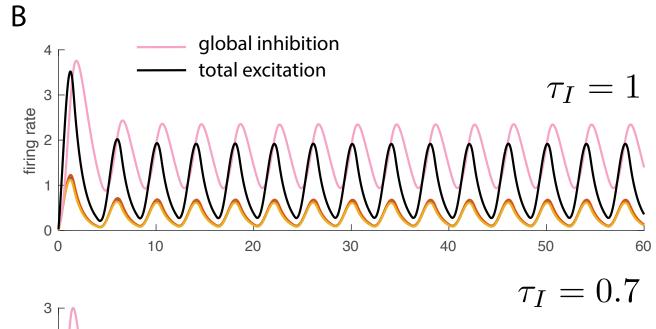


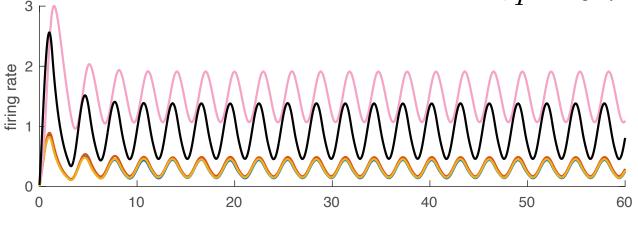


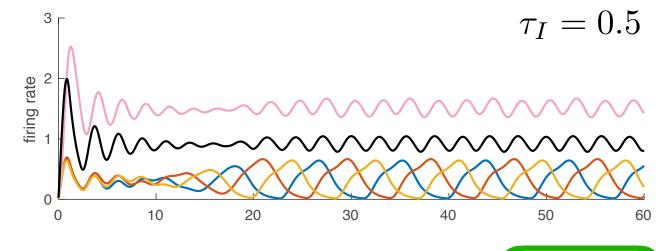


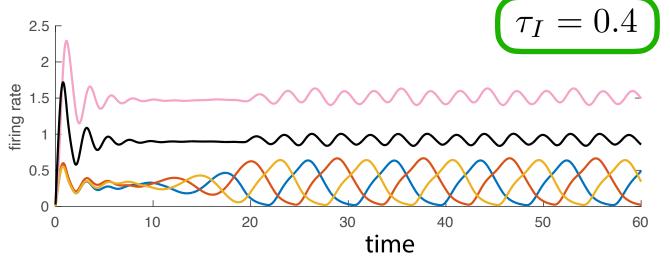


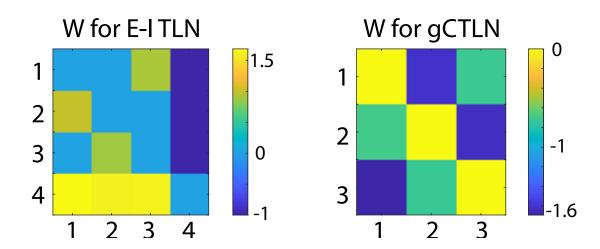


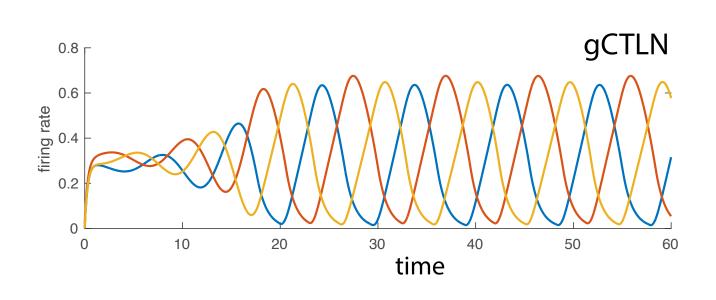


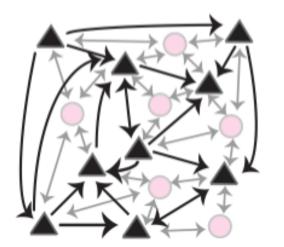


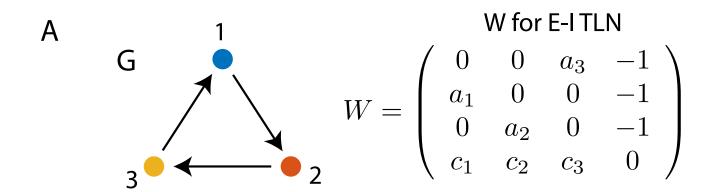


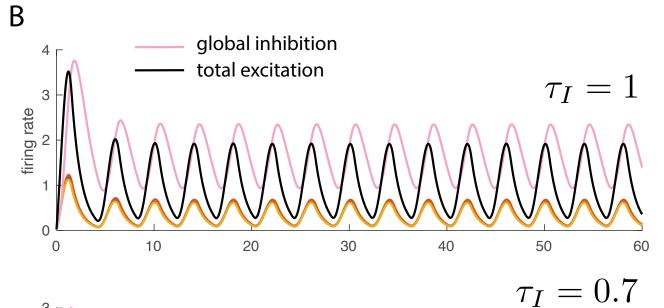


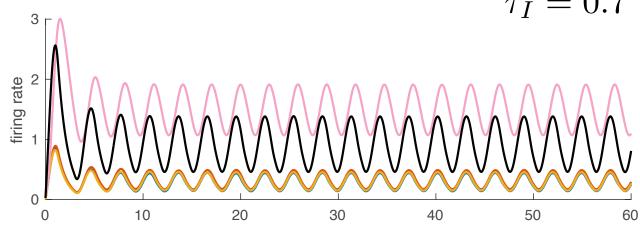


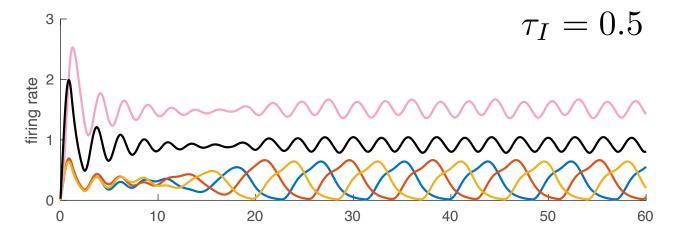


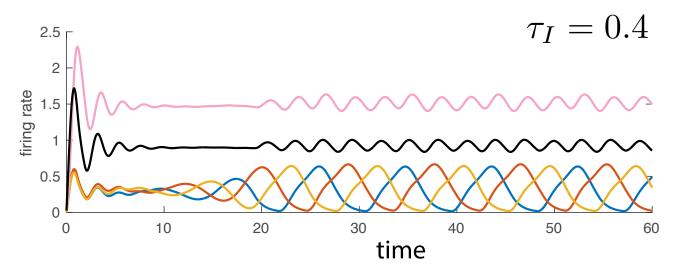


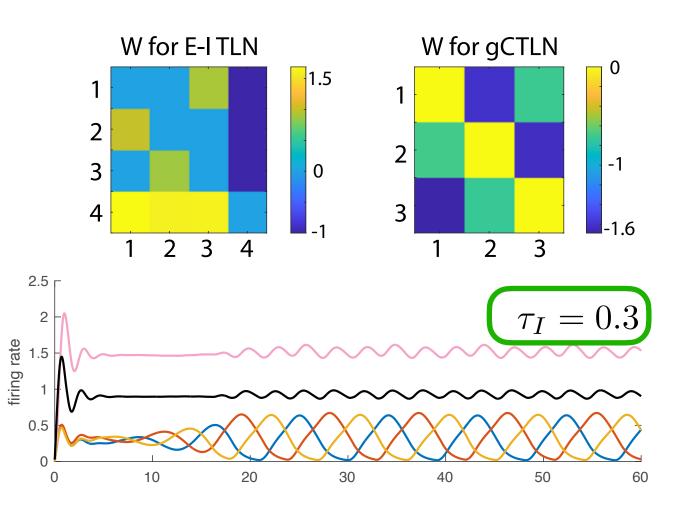


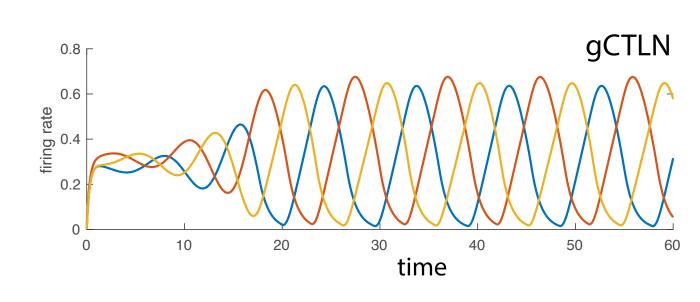


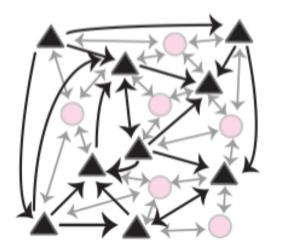


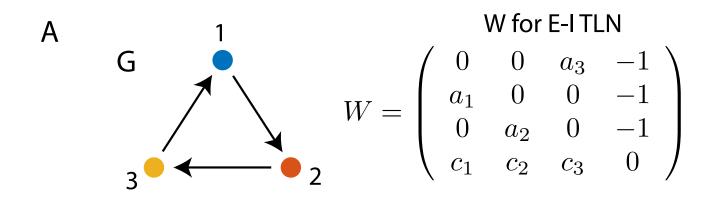


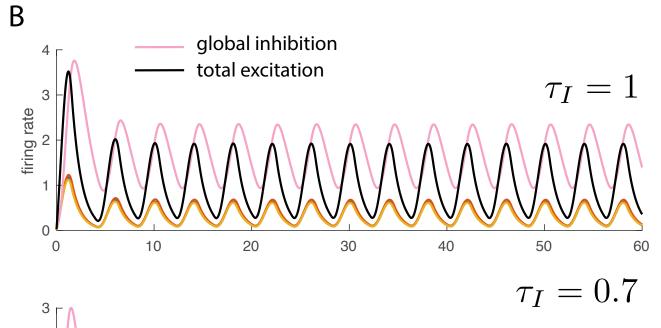


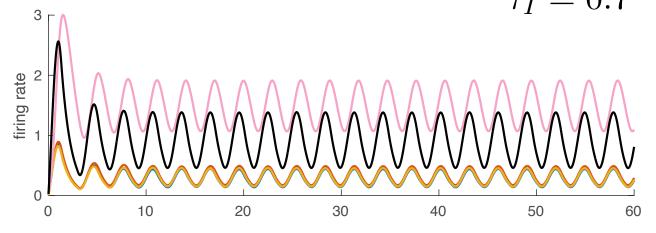


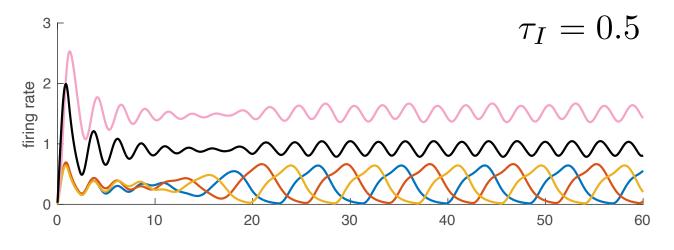


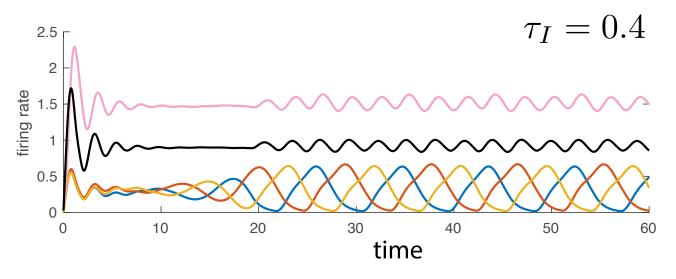


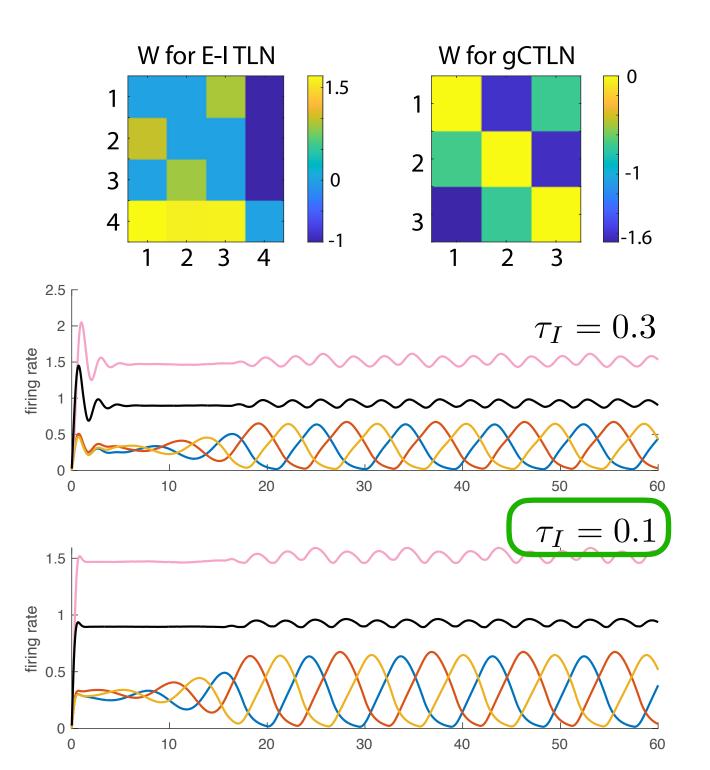


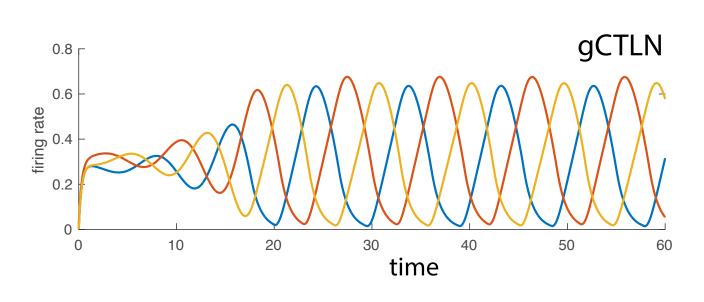


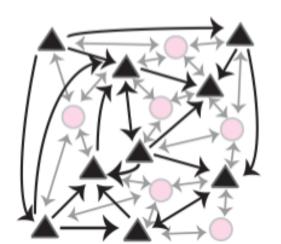


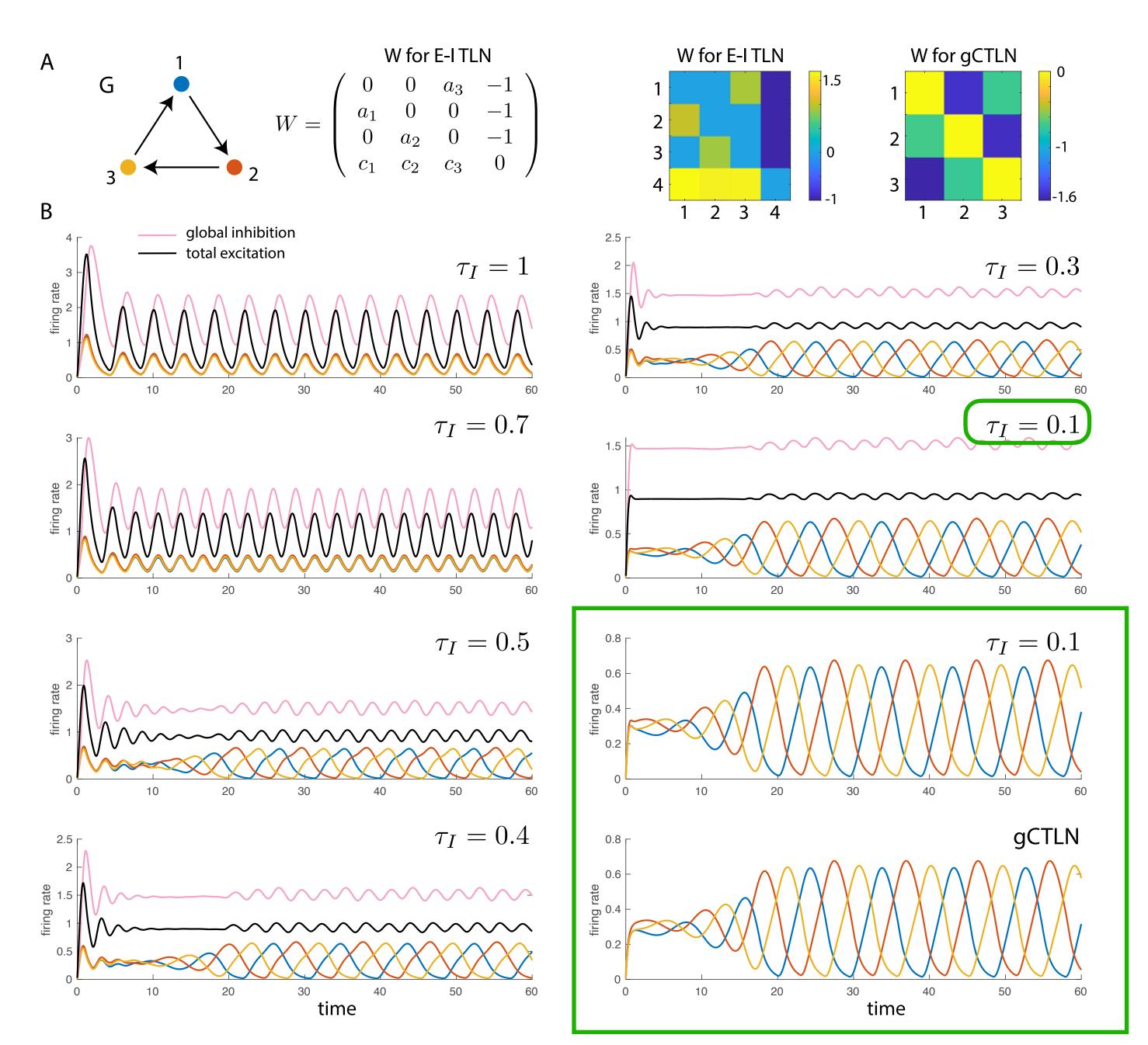


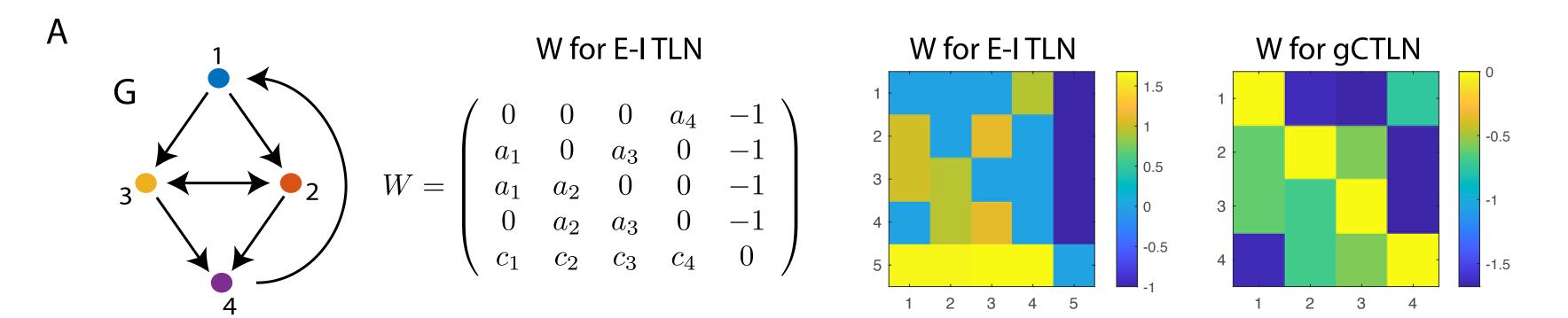


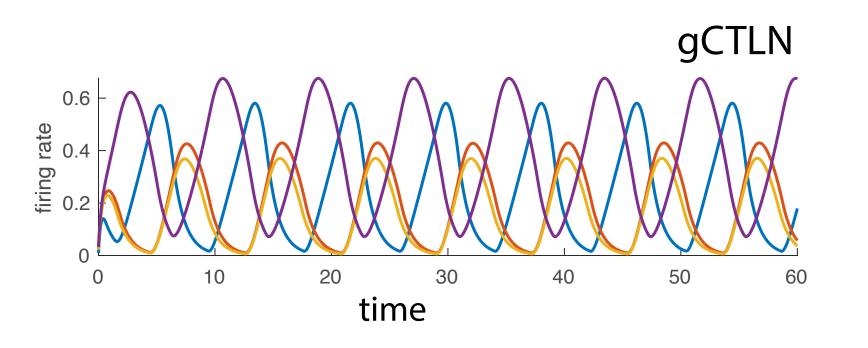


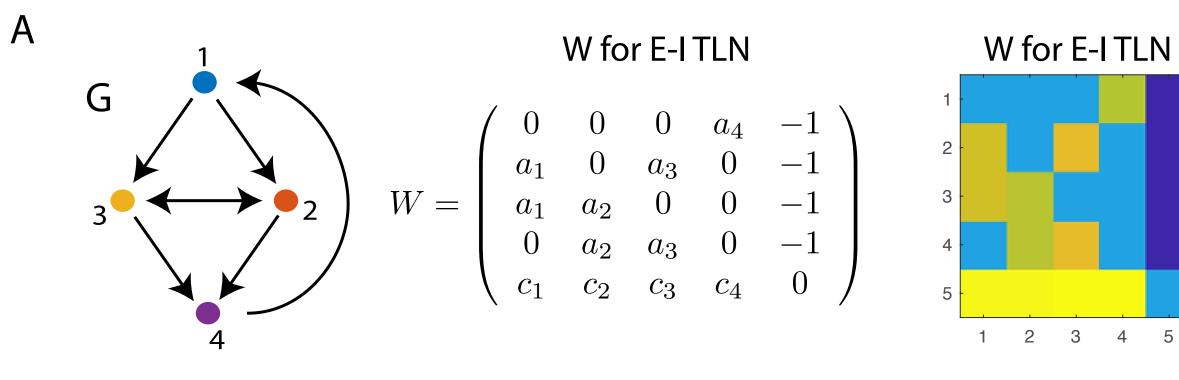


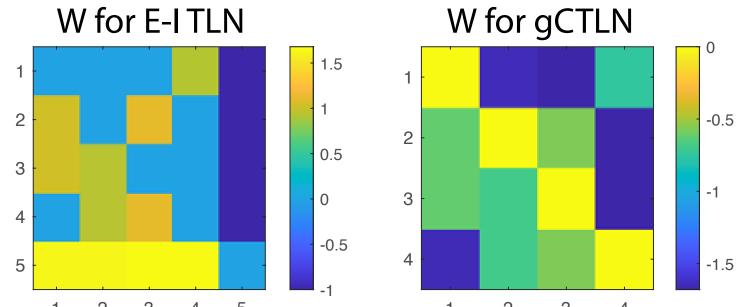


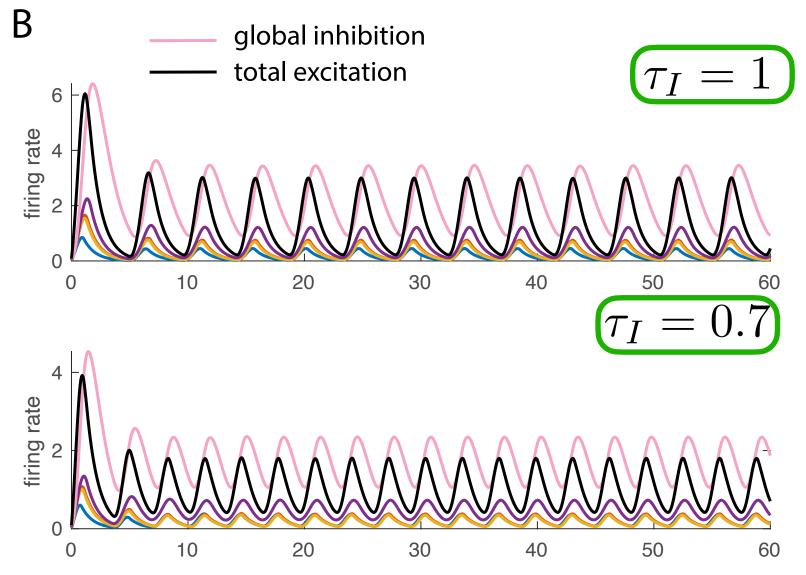


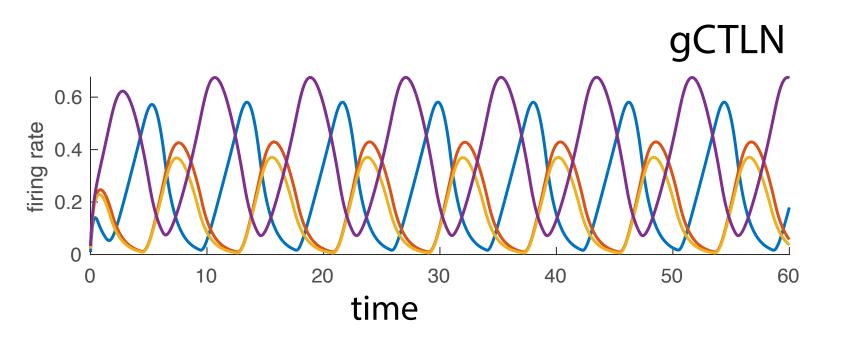


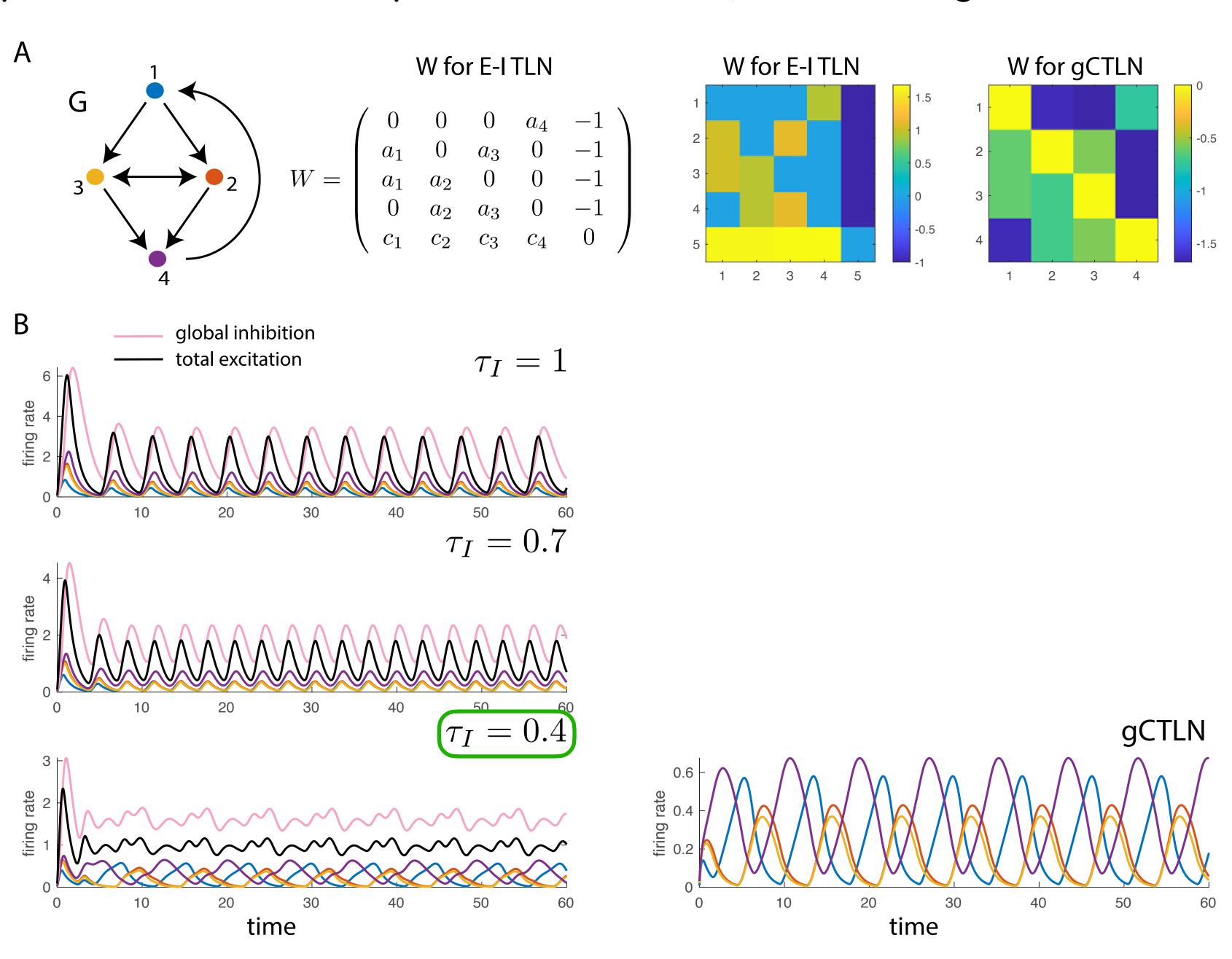


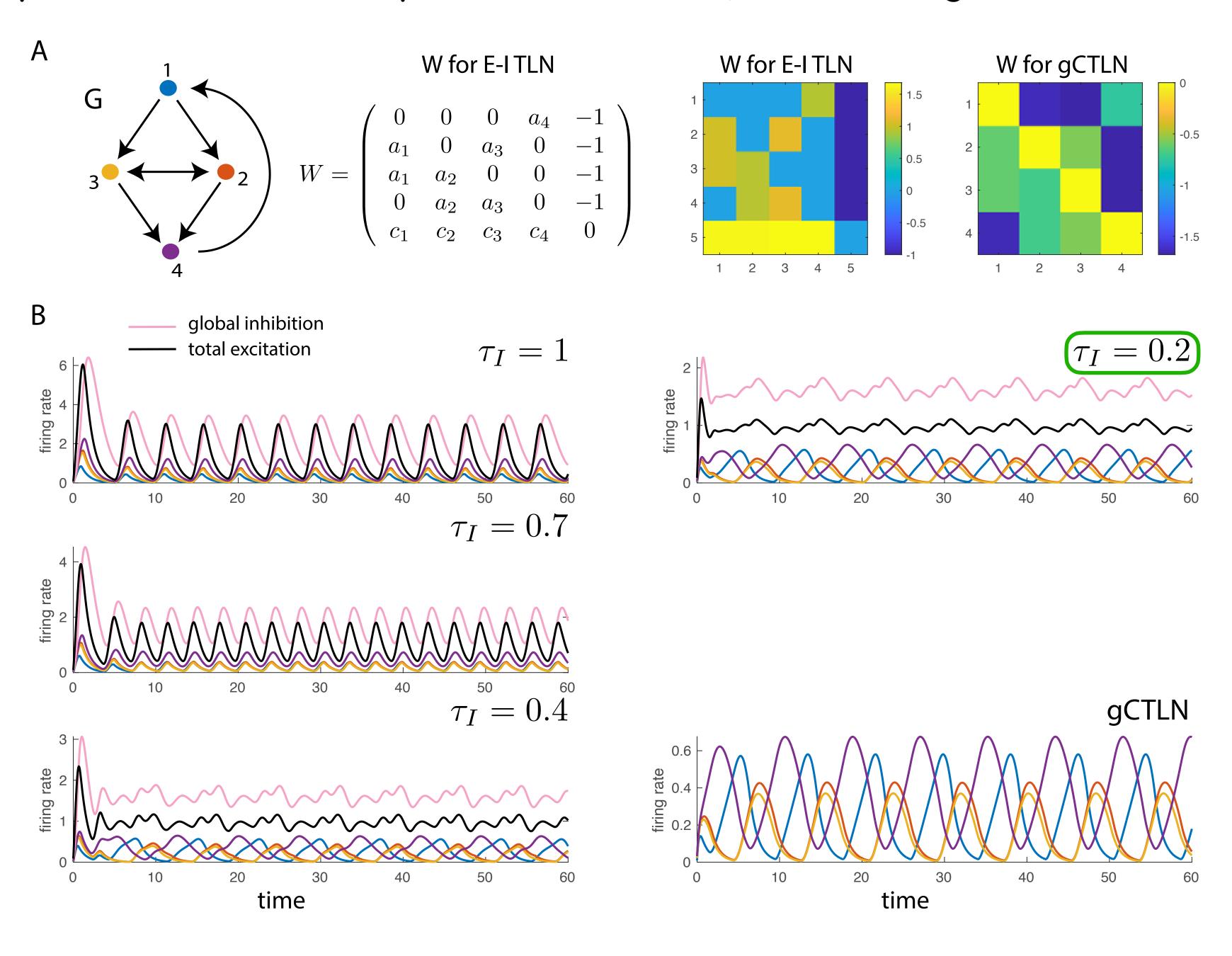


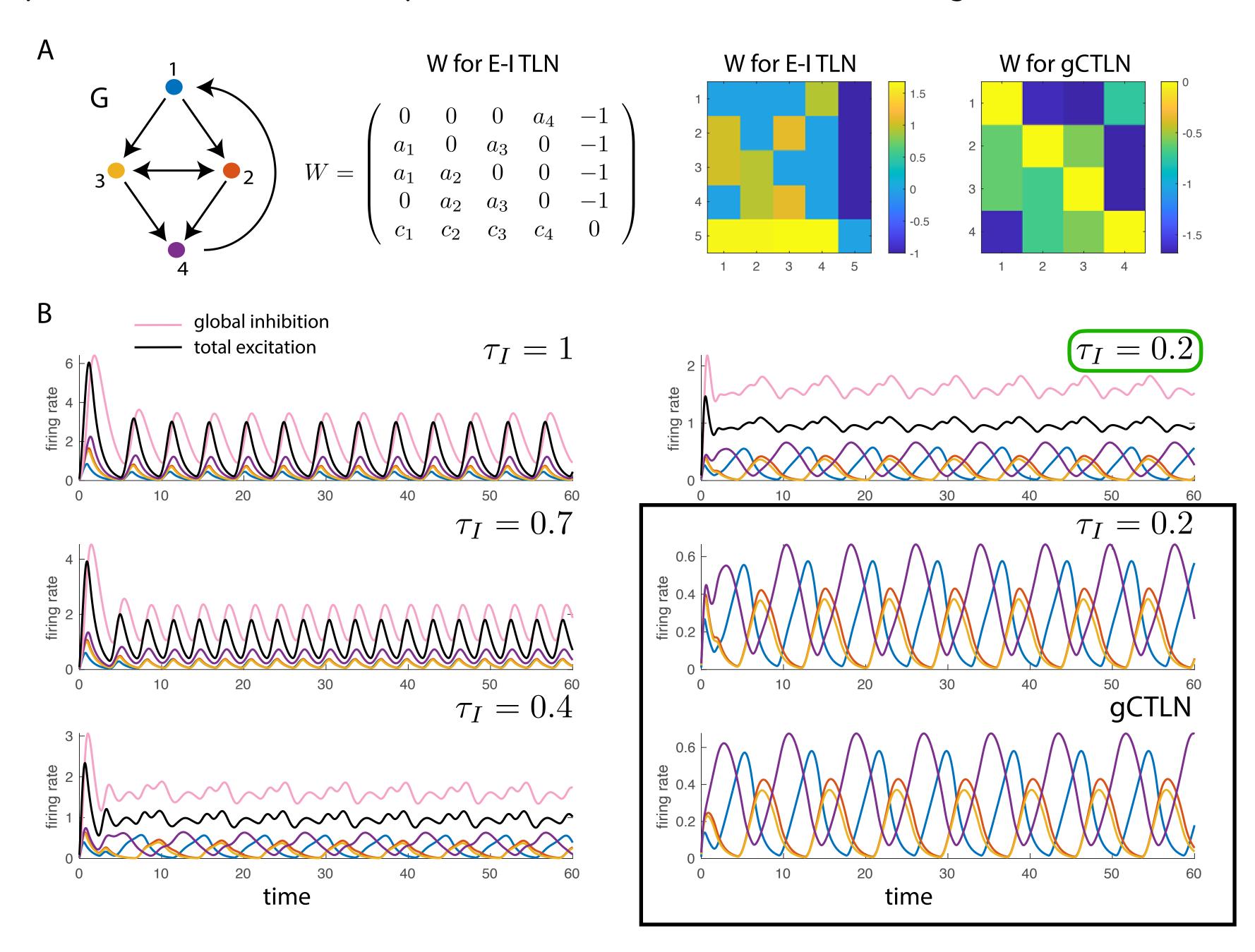




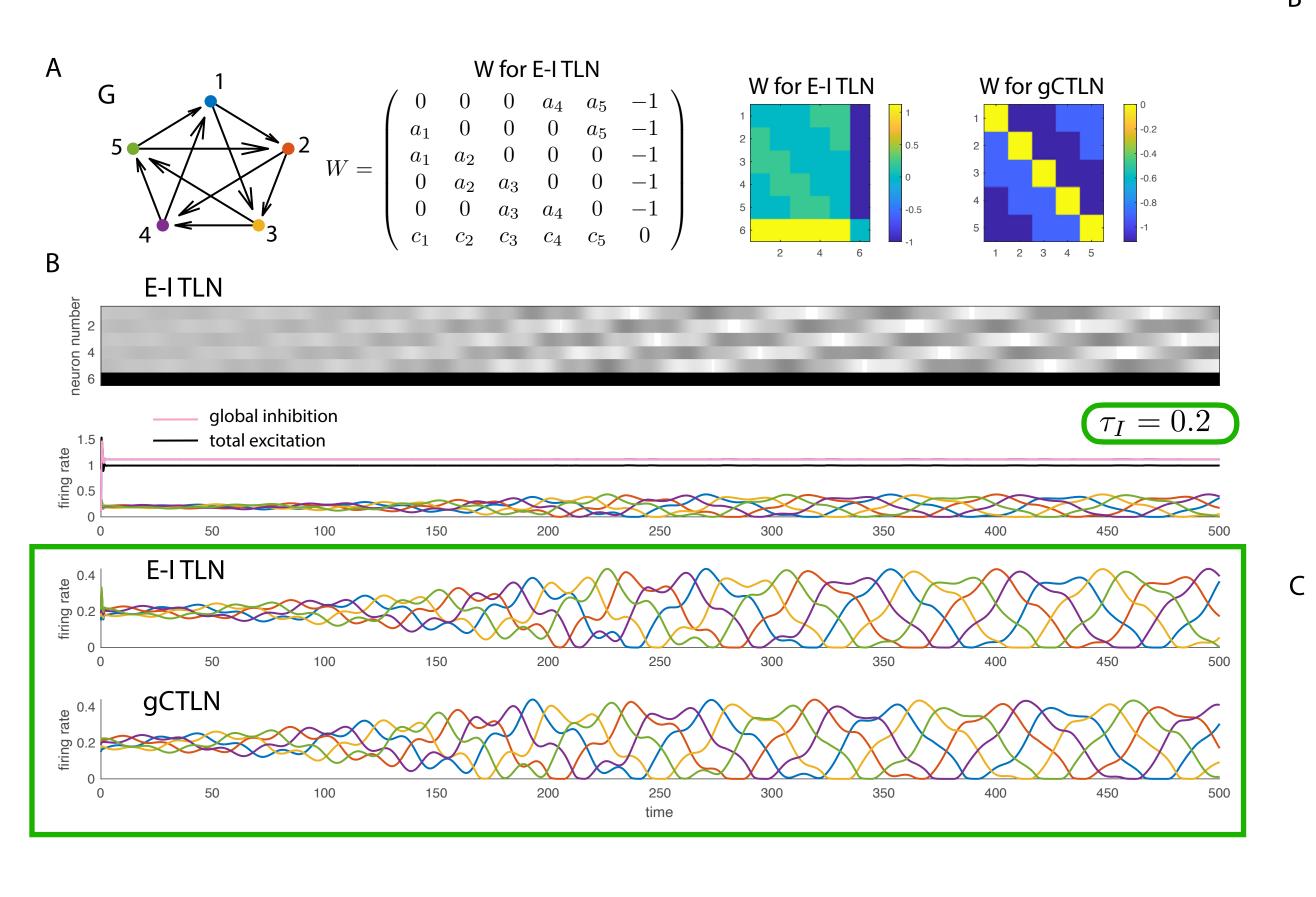


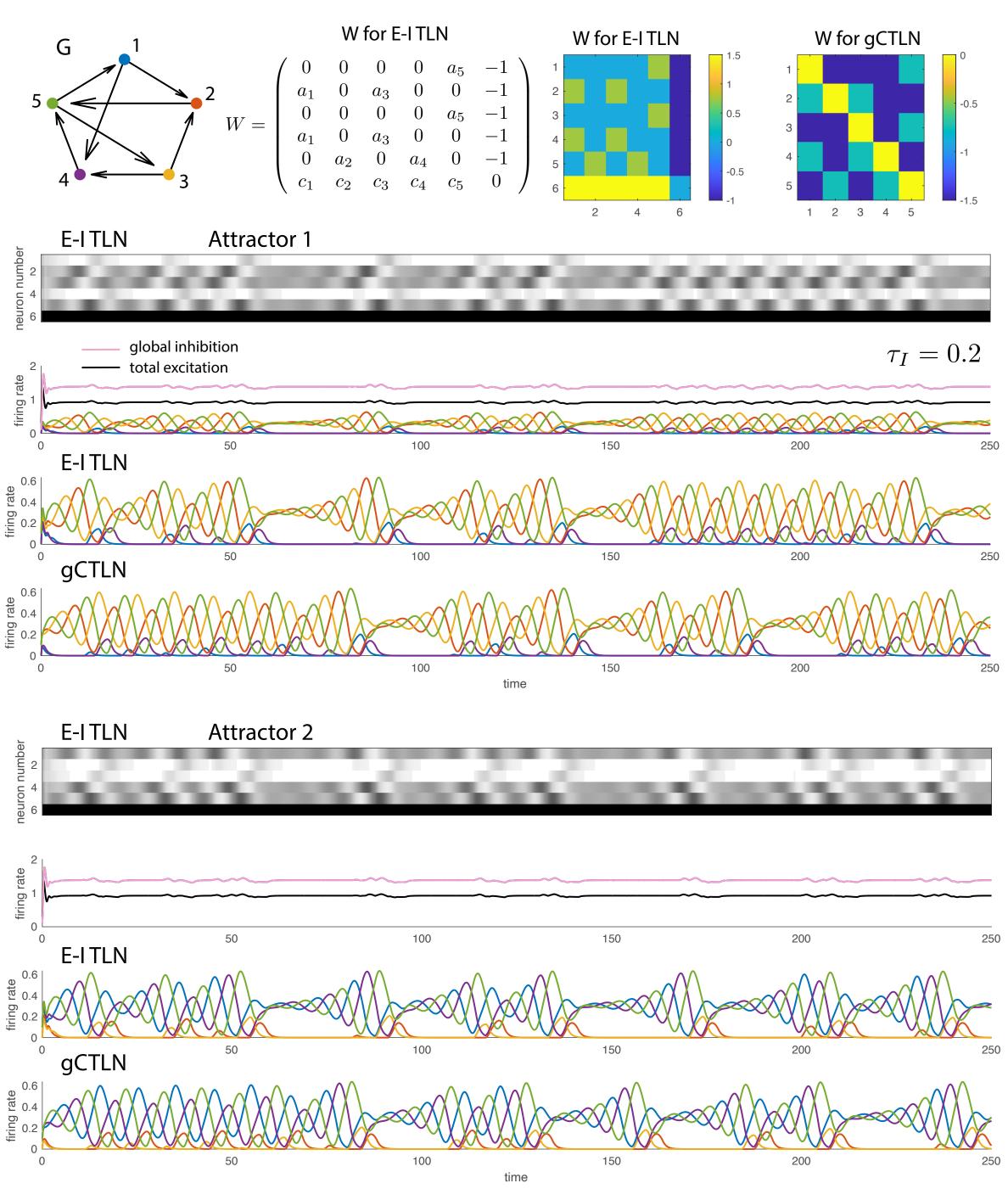




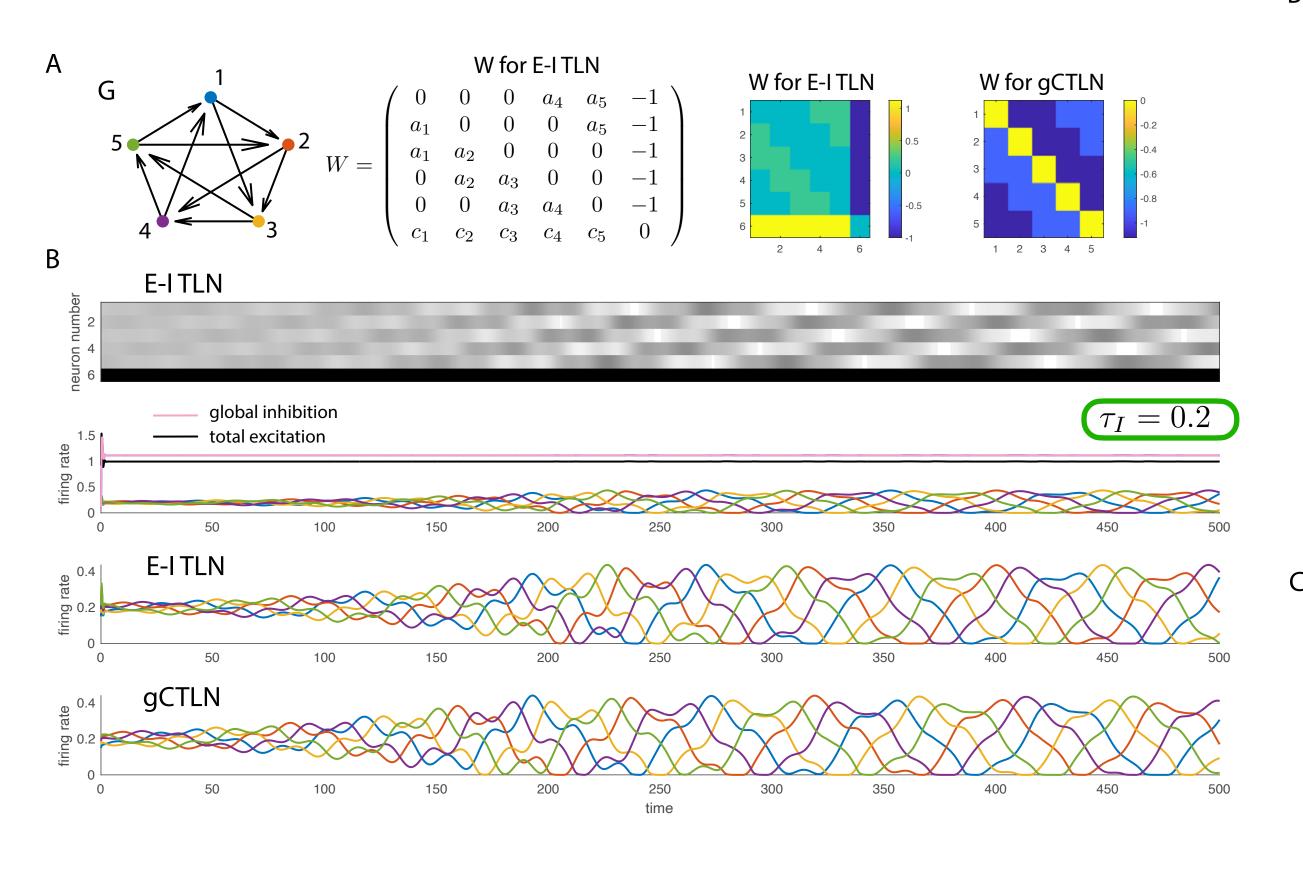


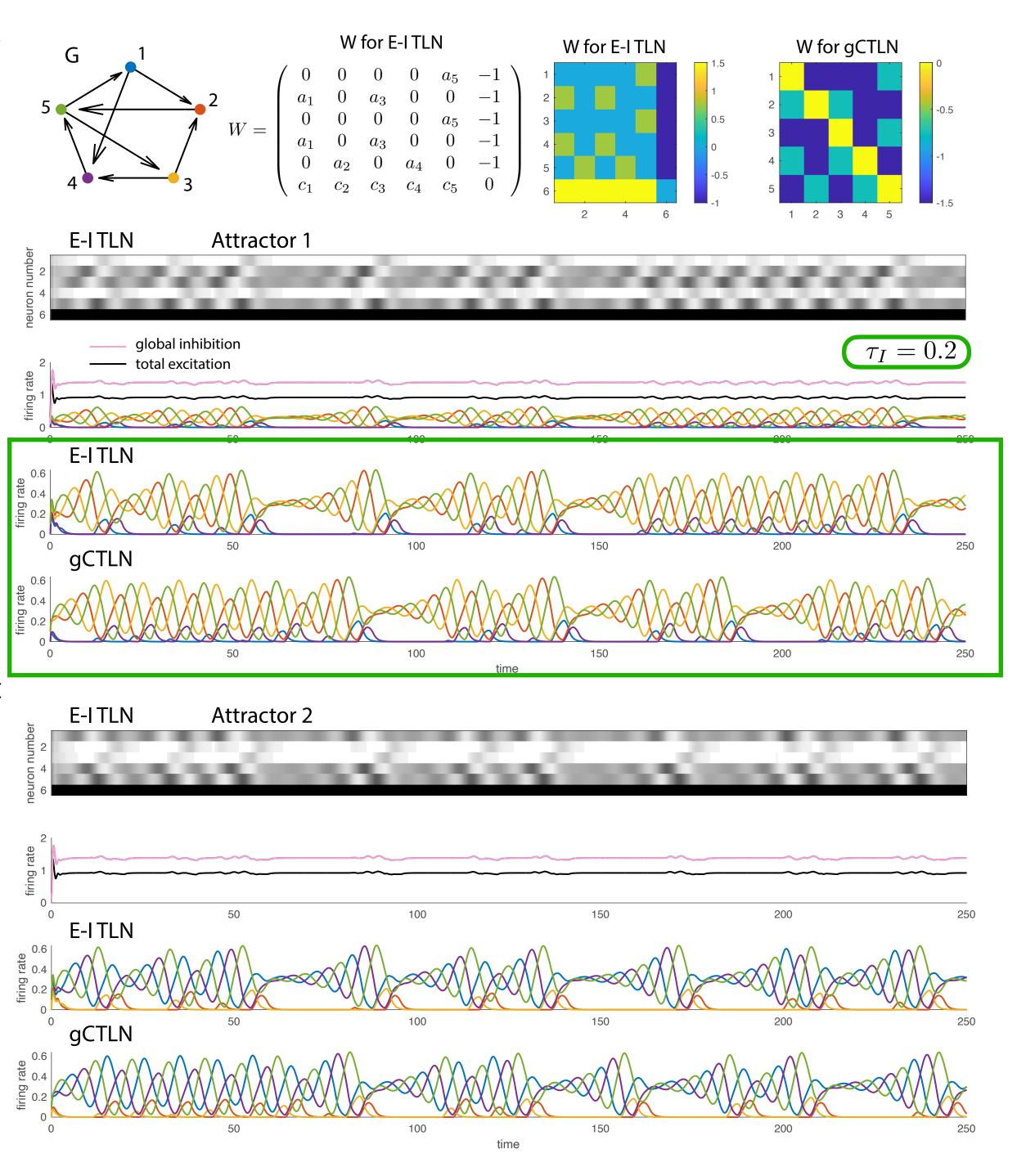
Even "exotic" attractors like Gaudi and baby chaos look the same



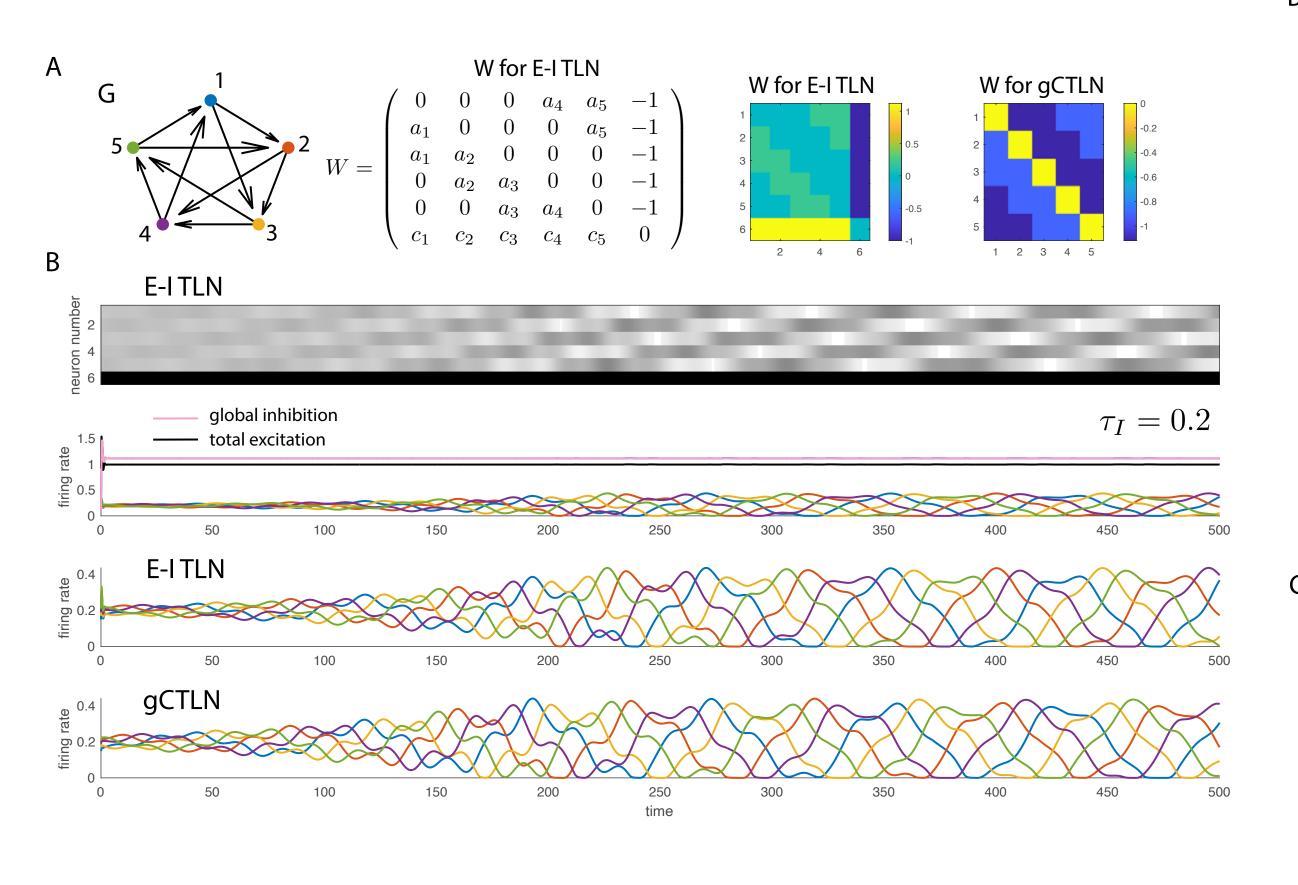


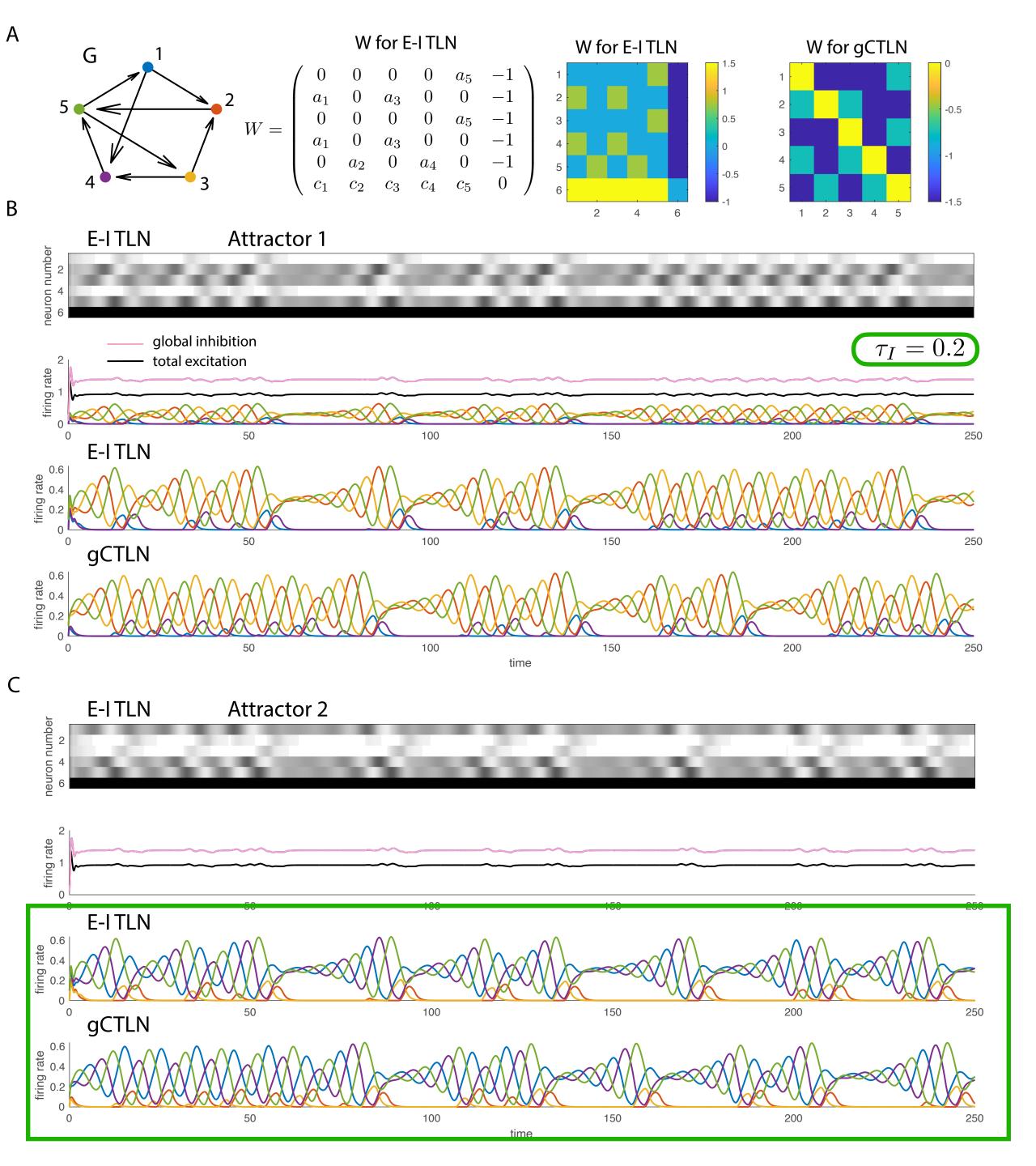
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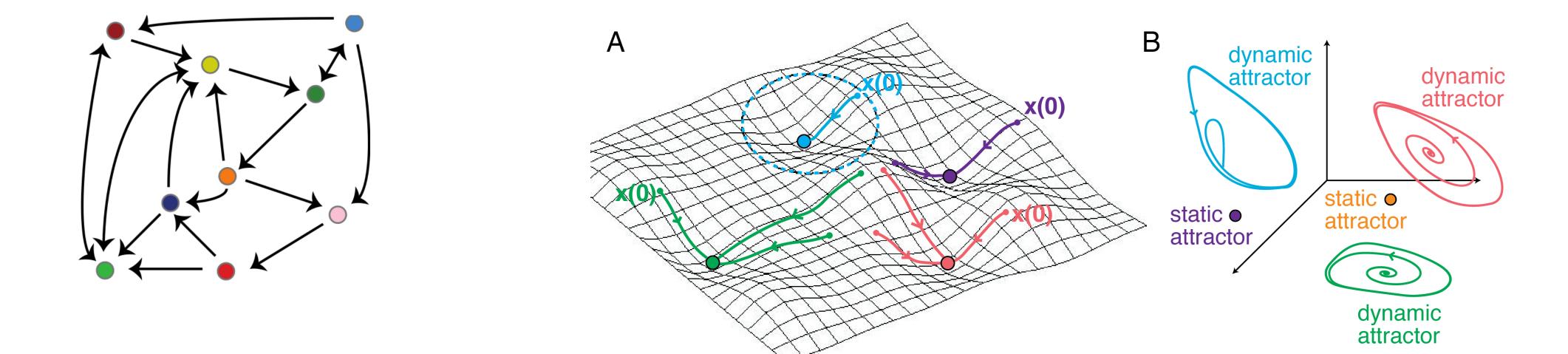
Even "exotic" attractors like Gaudi and baby chaos look the same





We had many mathematical results, called "graph rules" on CTLNs.

Now many of those results also apply to E-I TLNs built from graphs!

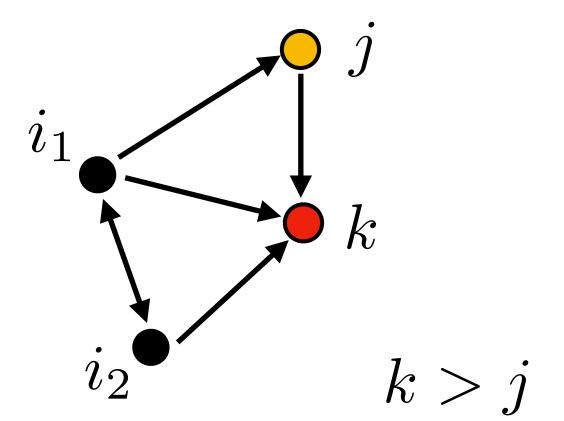


Curto & Morrison, 2023 (review paper): Graph rules for recurrent neural network dynamics

Definition 1.1. Let $j, k \in [n]$ be vertices of G. We say that k graphically dominates j in G if the following two conditions hold:

- (i) For each vertex $i \in [n] \setminus \{j, k\}$, if $i \to j$ then $i \to k$.
- (ii) $j \to k$ and $k \not\to j$.

If there exists a k that graphically dominates j, we say that j is a dominated node (or dominated vertex) of G. If G has no dominated nodes, we say that it is domination free.



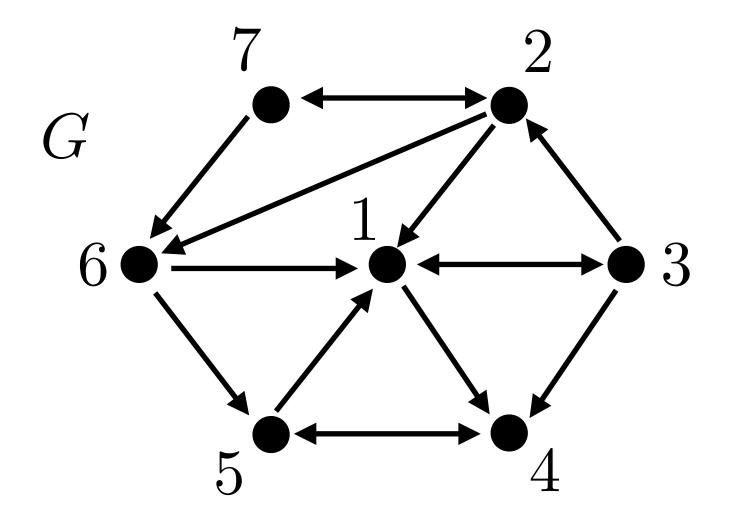
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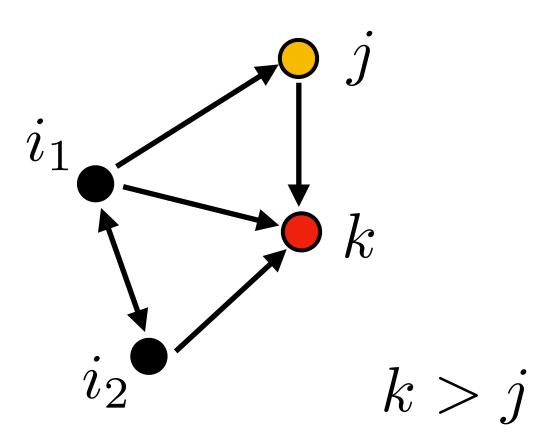
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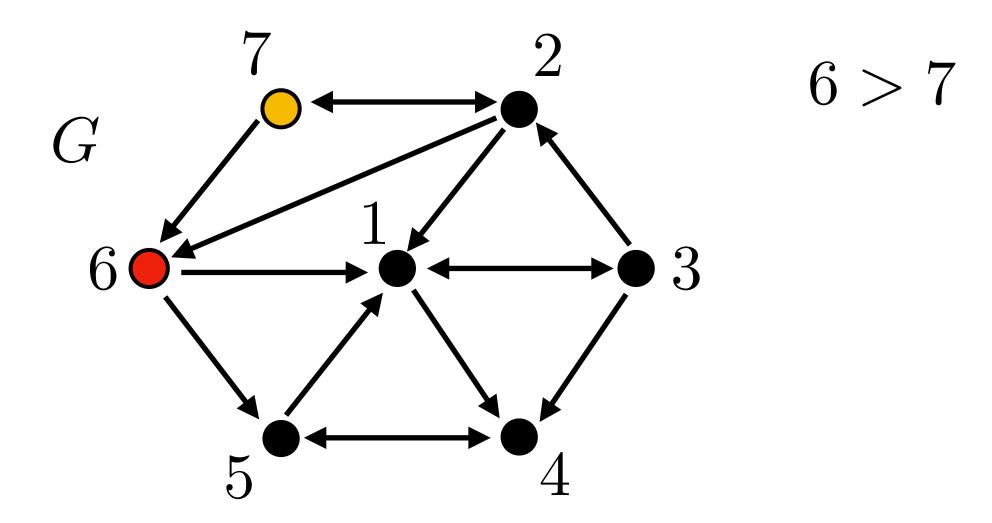
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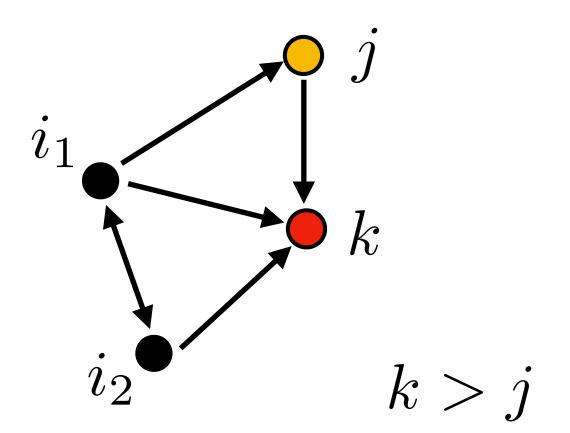
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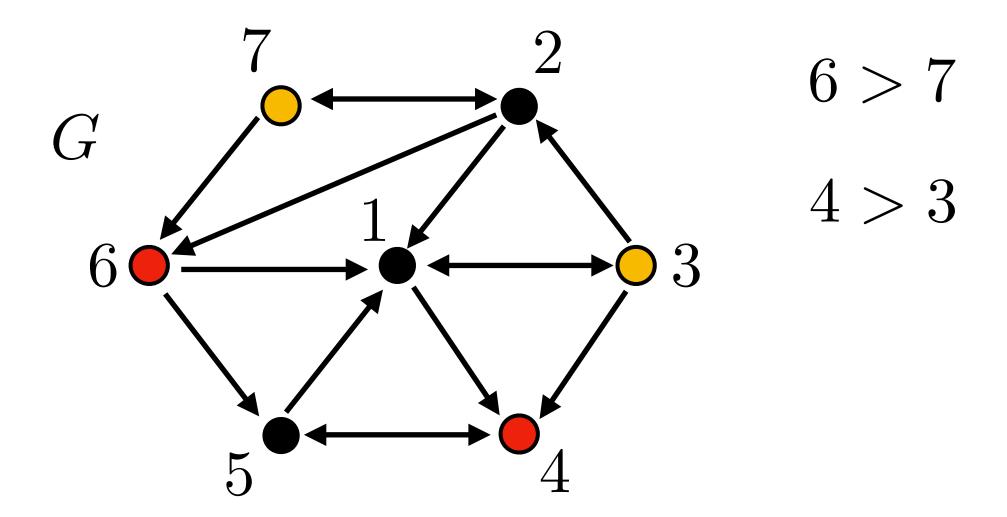
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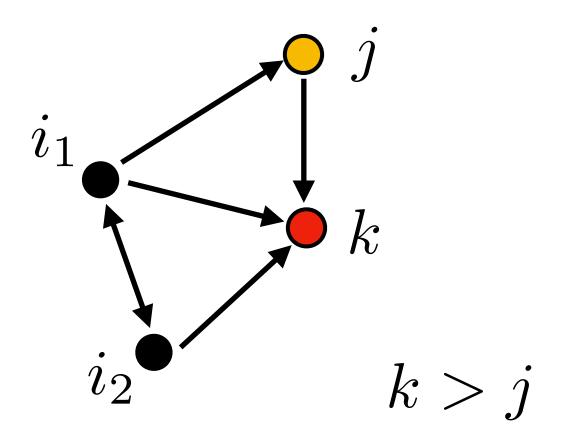
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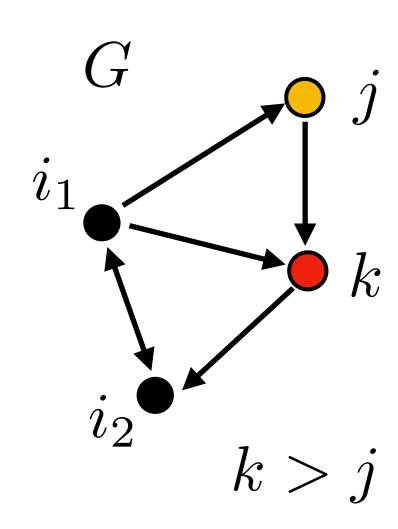
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Theorem 1 (2024)

If j is a dominated node in G, then it drops out!

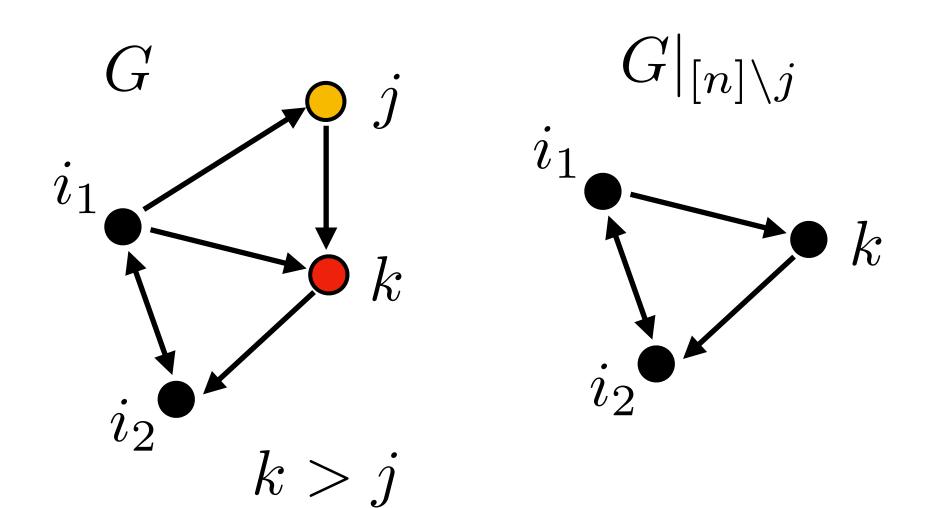
I.e., in any gCTLN, we have:
$$\operatorname{FP}(G) = \operatorname{FP}(G|_{[n] \setminus j})$$



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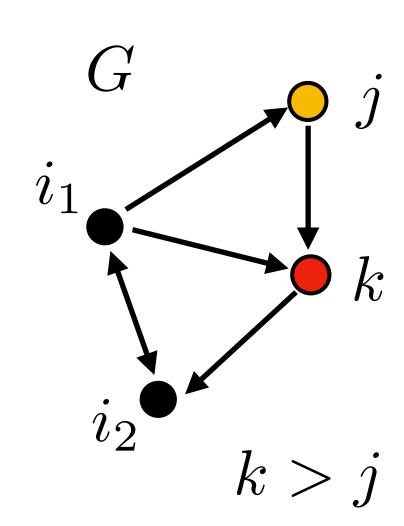
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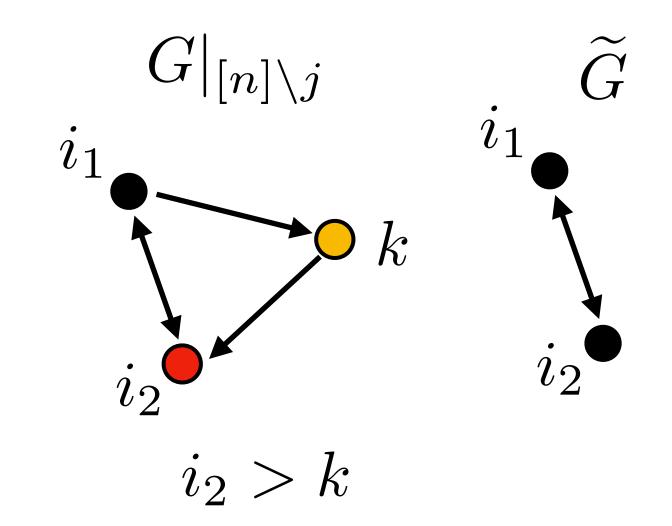
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By iteratively removing dominated nodes, the final reduced graph G-tilde is unique. Moreover, $\operatorname{FP}(G)=\operatorname{FP}(\widetilde{G})$





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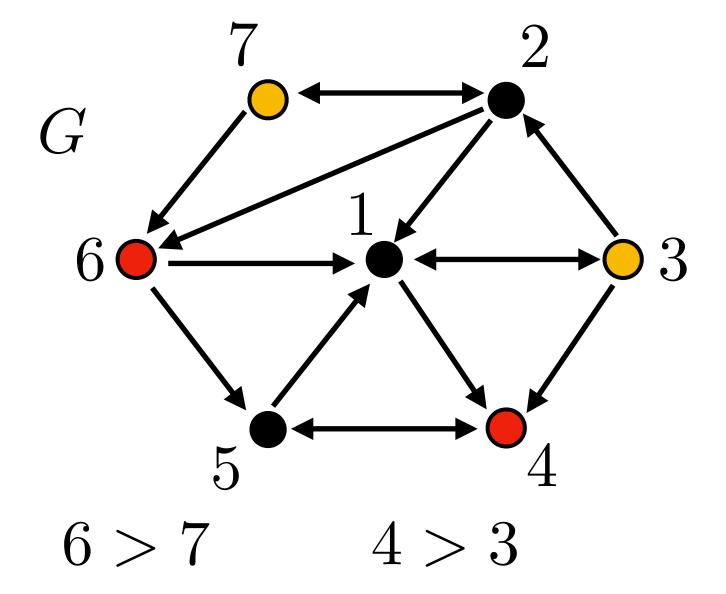
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Theorem 1 (2024)

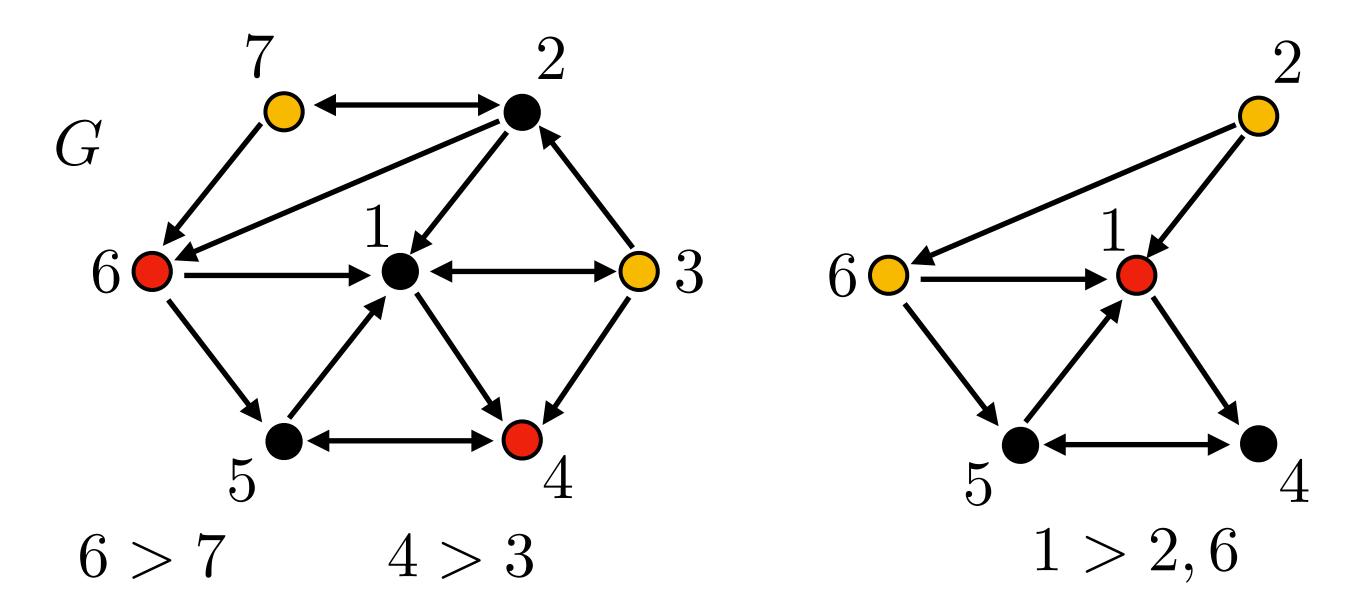
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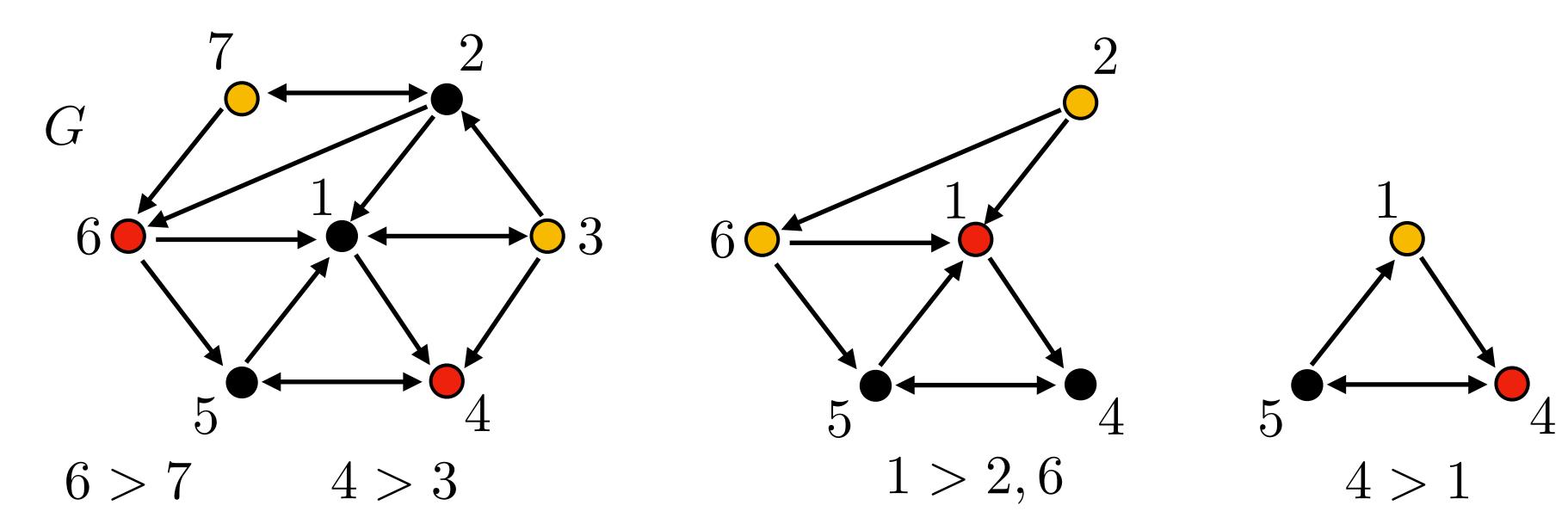
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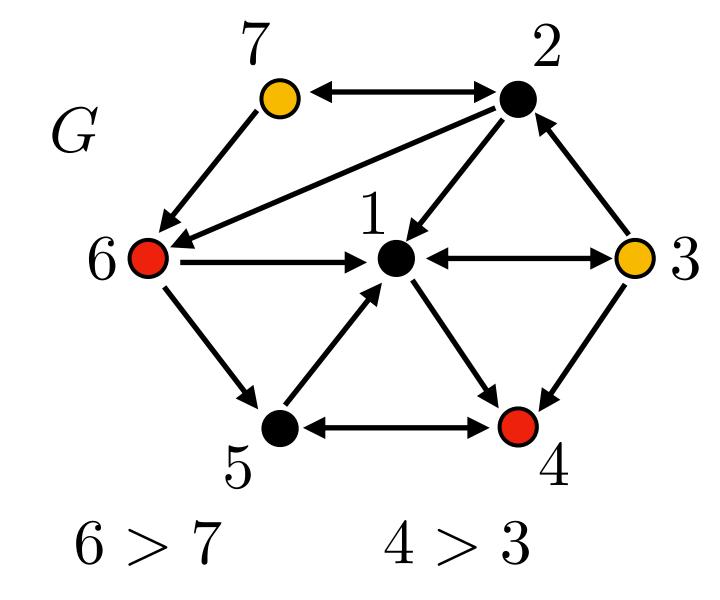
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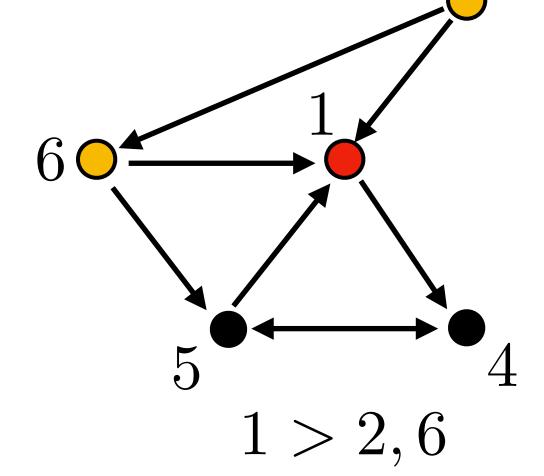
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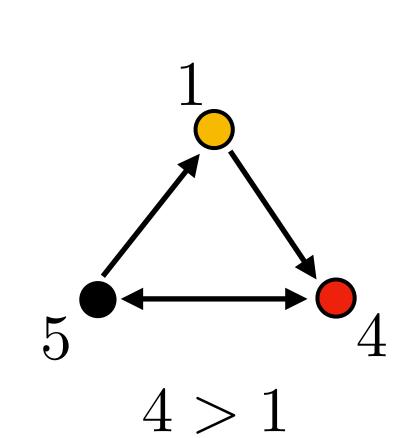
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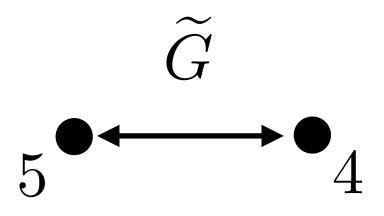


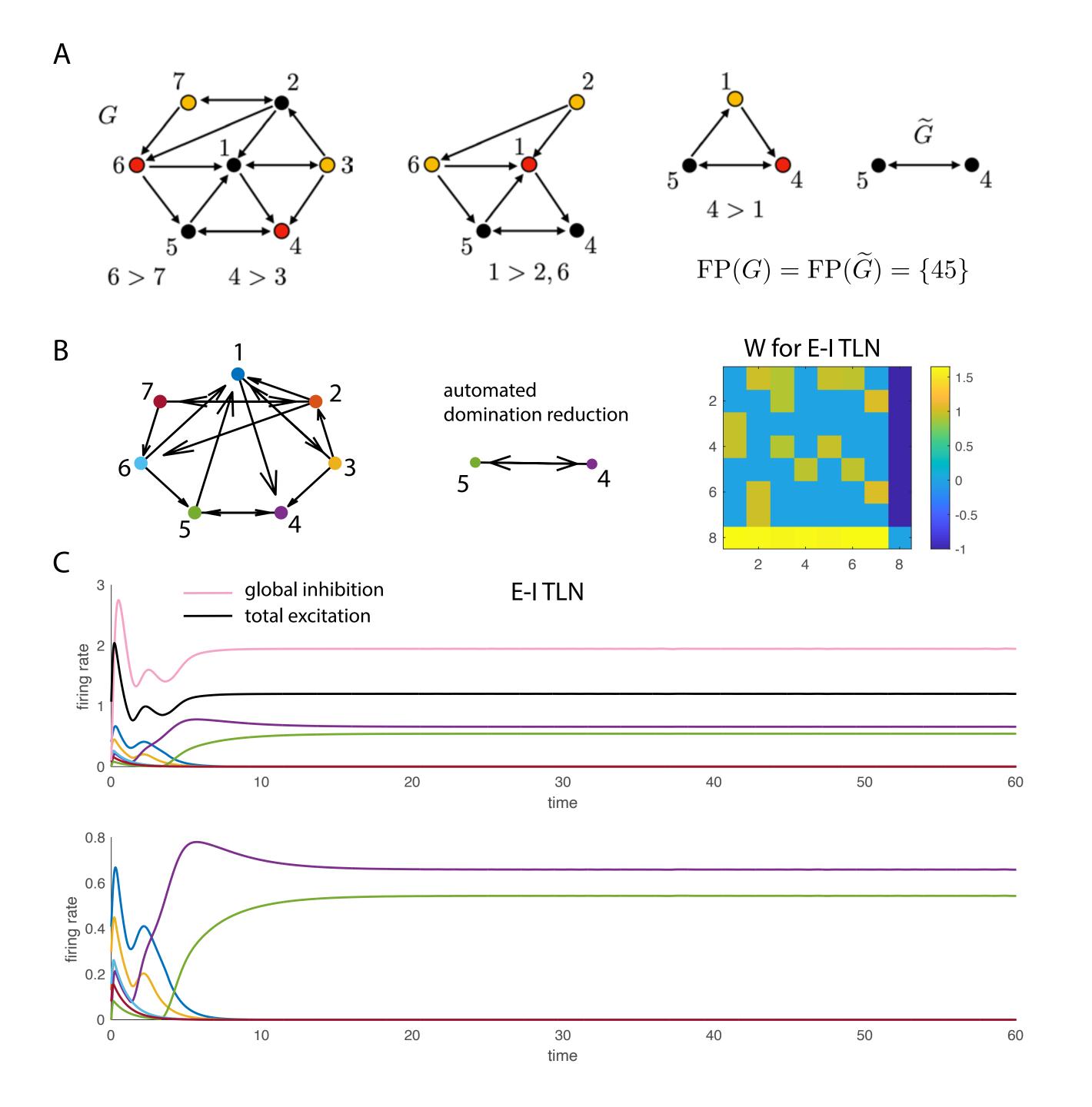


Since E-I TLNs map to gCTLNs with the same fixed points, the domination theorems hold for E-I TLNs, too!

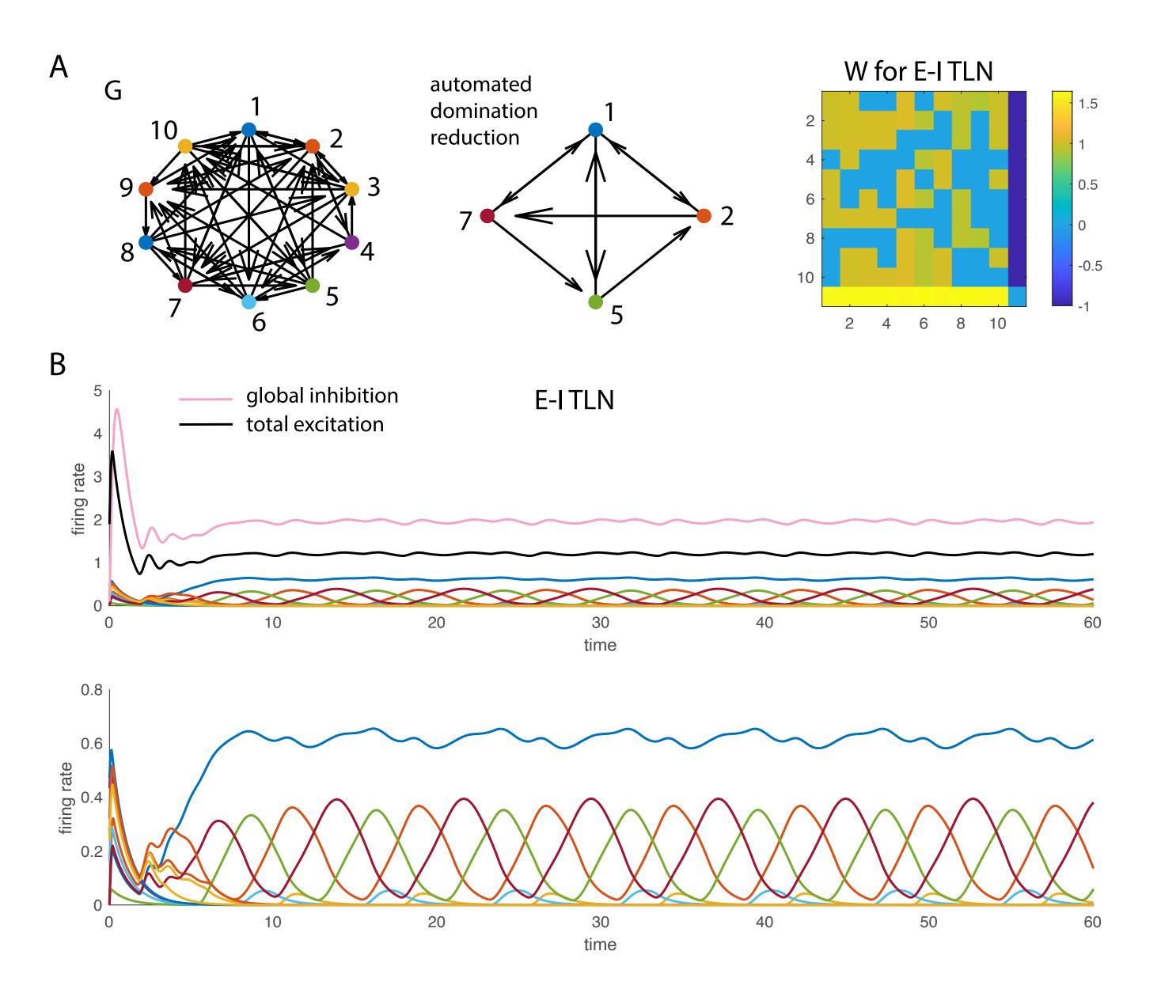
$$FP(G) = \{45\}$$

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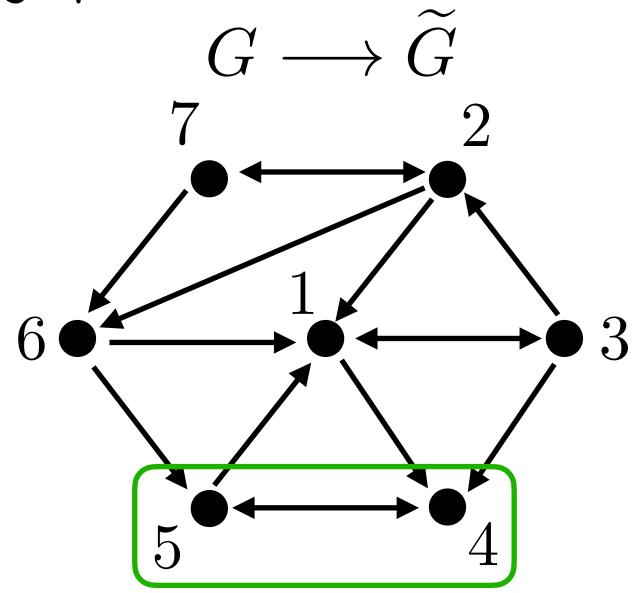


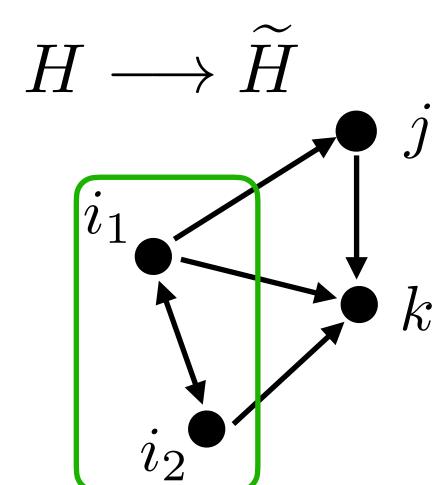
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Can domination be useful for connectome analysis?

Every graph has a unique domination reduction: $G \longrightarrow G$

Two graphs with the same reduction are in the same domination equivalence class.



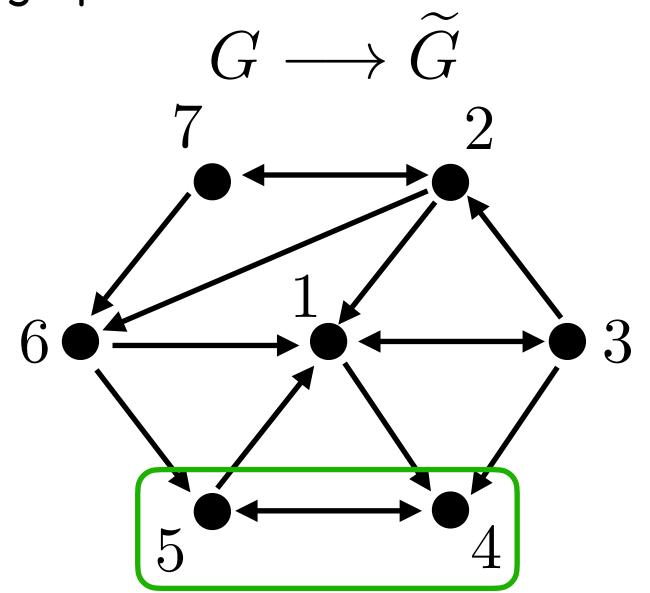


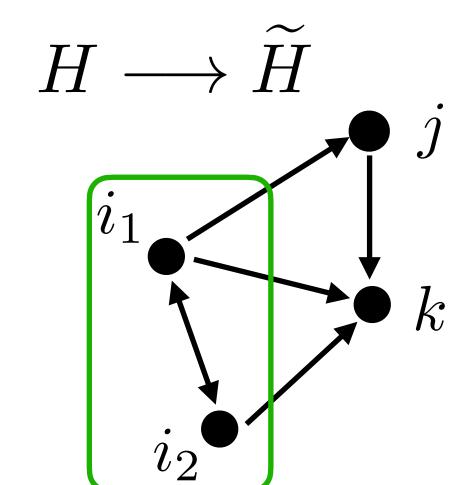
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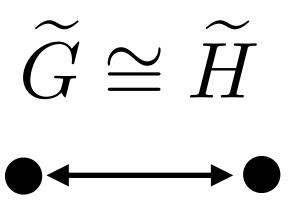
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- 1. Are overrepresented graphical motifs more likely to be reducible or irreducible?
- 2. Which motifs are domination-equivalent?
- 3. What about larger portions of the connectome: do they reduce via domination?

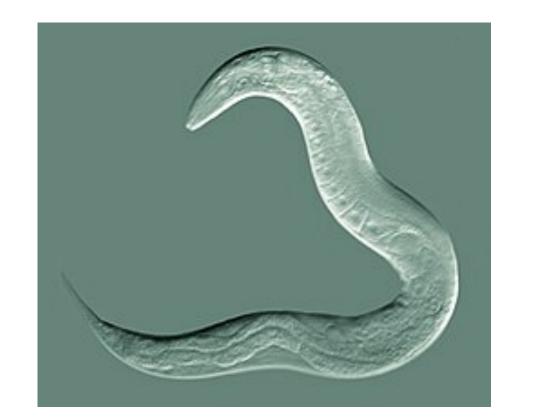
Very preliminary analysis

Graph motifs team at JHU

Jordan Matelsky (also at Penn)

Patricia Rivlin
Michael Robinette
Erik Johnson
Brock Wester

Johns Hopkins University Applied Physics Laboratory, Research & Exploratory Development Department



C. elegans E-E network:

G has143 nodes

reduced G: 104 nodes

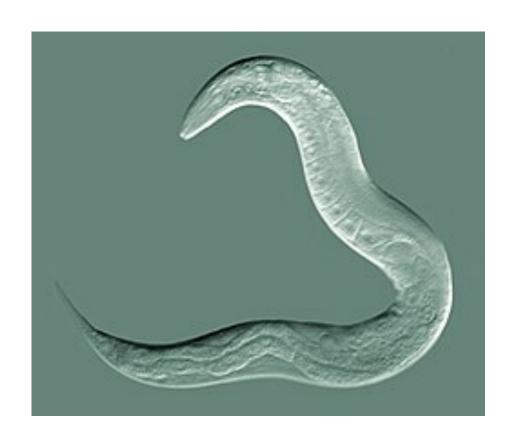


Joaquín Castañeda Castro

We first strip out everything but chemical synapses, then tag neurons by their small-molecule neurotransmitters—acetylcholine/ glutamate as excitatory, GABA as inhibitory—next we grab the induced subgraph of neurons that fire ACh/Glu but no GABA. That's our 'excitatory' network. And yes—it's just a conservative, transmitter-based proxy for valence; real C. elegans synaptic polarity is far messier (receptors, modulators, co-transmission, gap junctions, etc.) All blame goes to Jordan Matelsky, Carina did nothing wrong.

Very preliminary analysis

Is a reduction from 143 -> 104 nodes common or rare in a random graph with matching edge probability?



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Joaquín Castañeda Castro

Very preliminary analysis

Is a reduction from 143 -> 104 nodes common or rare in a random graph with matching edge probability?

1 million E-R random graphs with matching p = 0.054

Distribution of domination reductions:

• 143 nodes: 782,590

• 142 nodes: 189,951

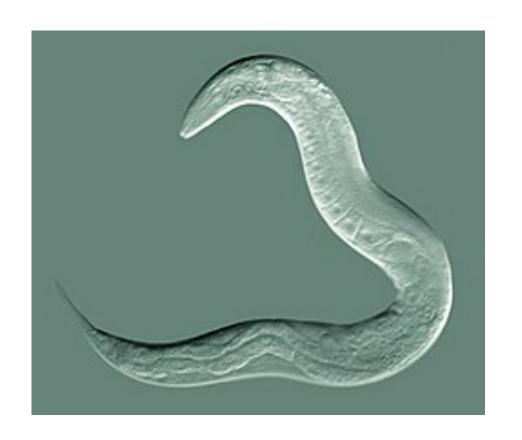
• 141 nodes: 24,951

• 140 nodes: 2,307

• 139 nodes: 185

• 138 nodes: 15

• 137 nodes: 1



C. elegans E-E network:

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VERY RARE!!

C. elegans E-E network reduction:

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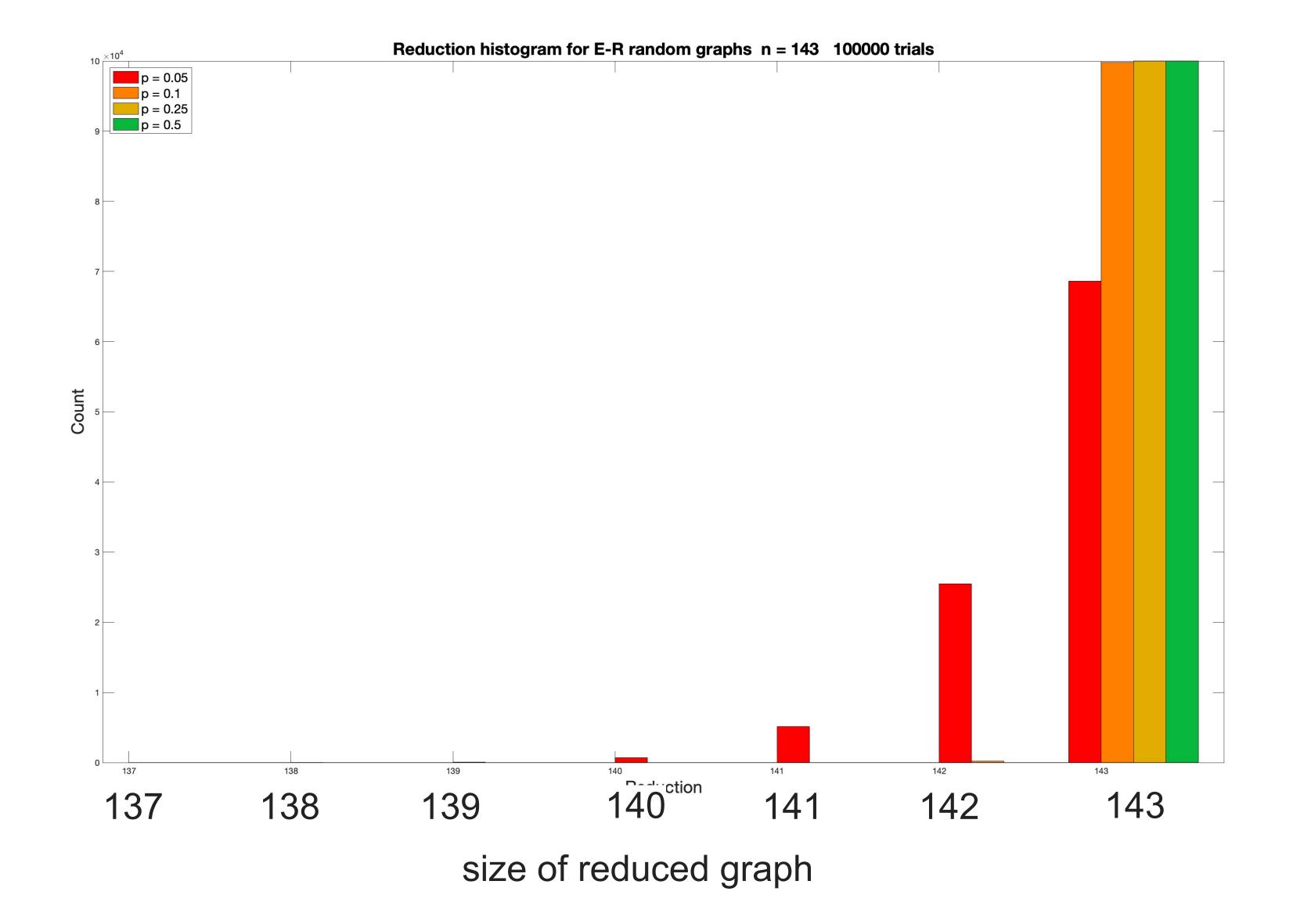
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Reduction sizes of E-R random graphs of size n=143 with p = 0.05, 0.1, 0.25, 0.5



Back to our motivating questions and ideas:

- 1. How does connectivity shape dynamics?
- 2. The relationship between connectivity and neural activity depends on the dynamical system you associate to the connectome.
- 3. By studying neuroscience-inspired (nonlinear!) dynamical systems on graphs, we can generate hypotheses about the dynamic meaning/role of various network motifs.

Domination is a graph property that comes out of the nonlinear dynamics, it is not something that graph theorists or network scientists were already paying attention to.



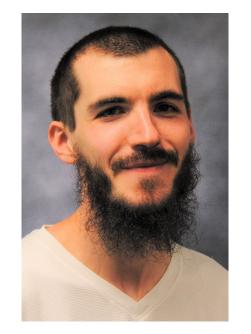
Thank you!

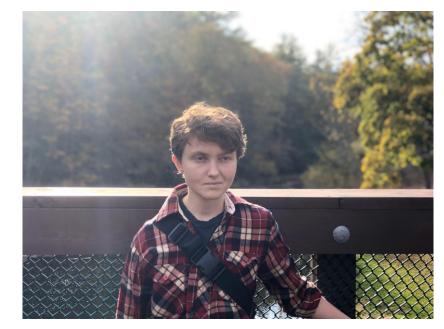






Katie Morrison Caitlyn Parmelee Chris Langdon





Jesse Geneson Caitlin Lienkaemper

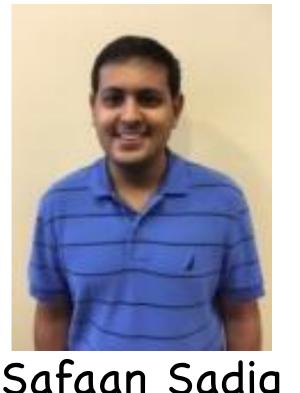
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Zelong Li

Nicole Sanderson Safaan Sadiq



Jency (Yuchen) Jiang grad student:







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