“Disease spreading processes through the lens of Multilayer Networks”

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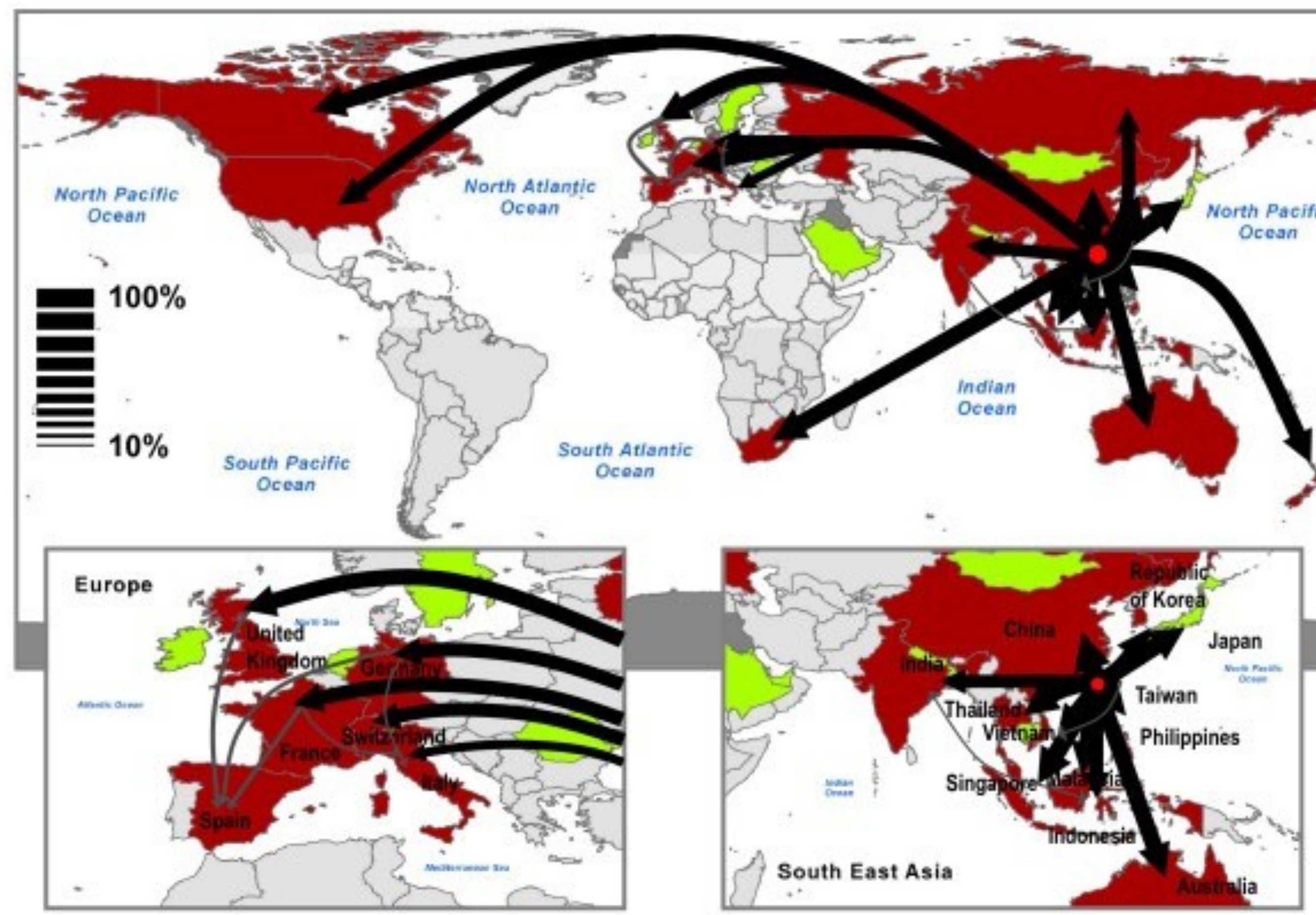
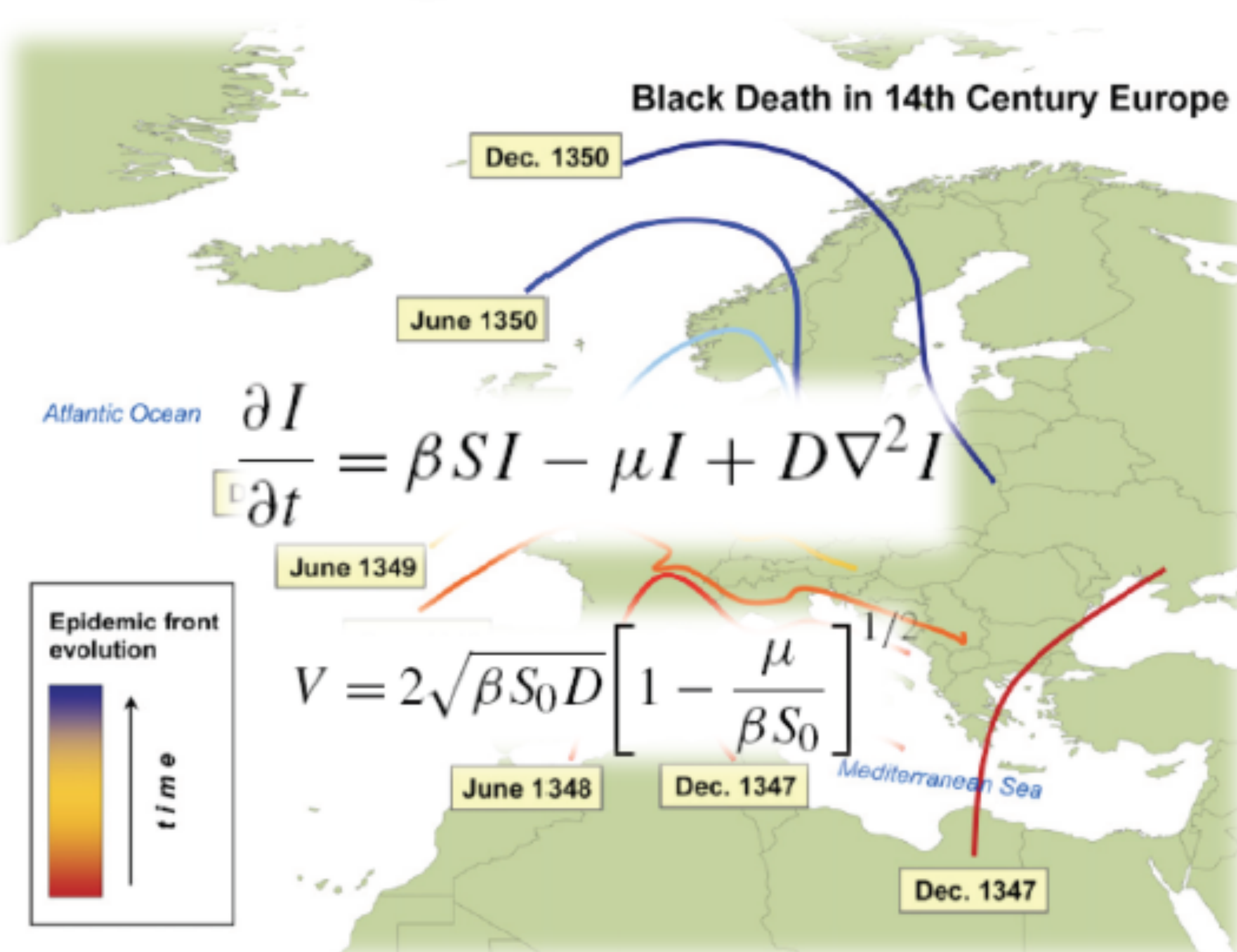
One of the current major threats is a large-scale disease. Can we predict it?



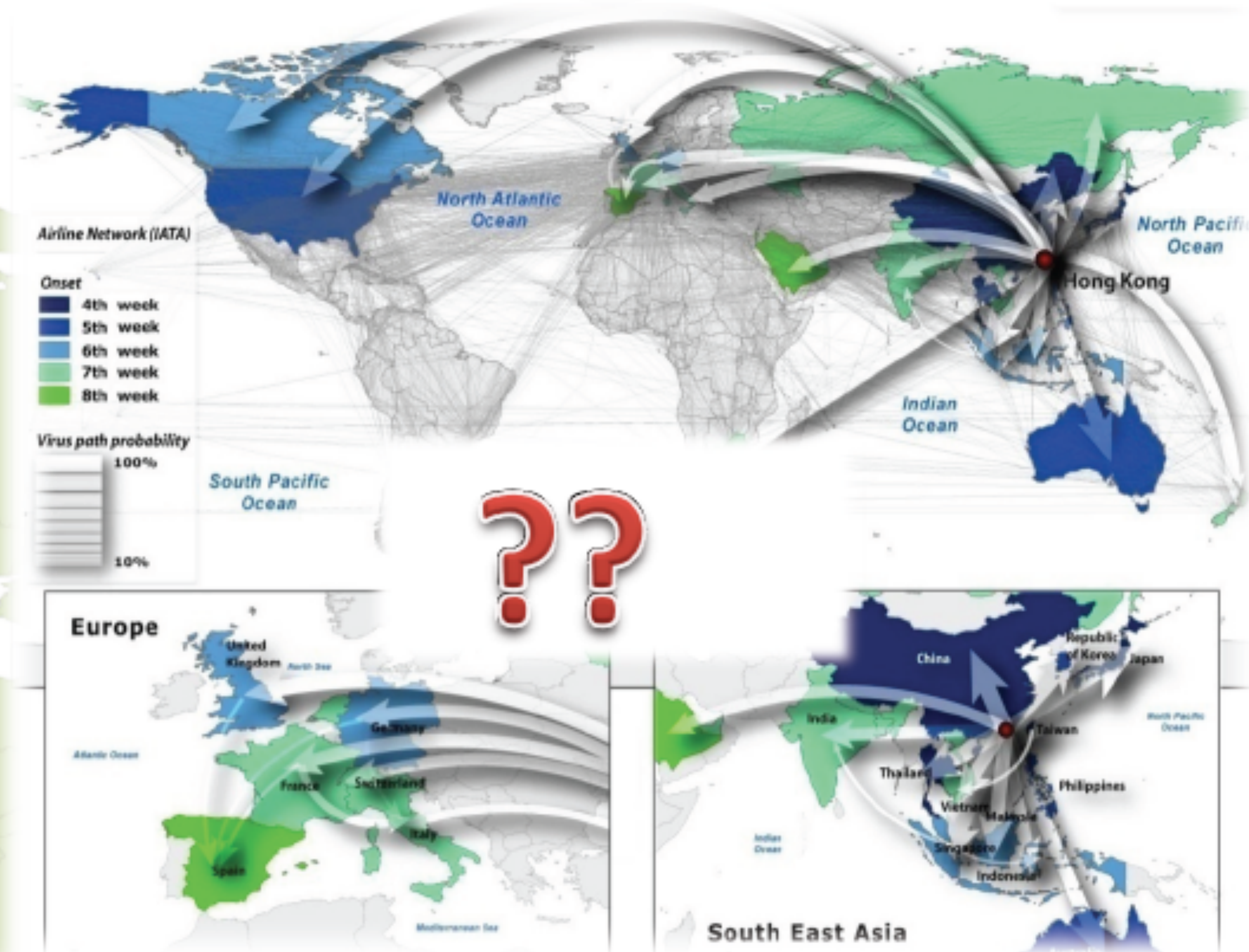
from A. Vespignani

What have changed that makes prediction harder than before?

Black death in1347: a continuous diffusion process

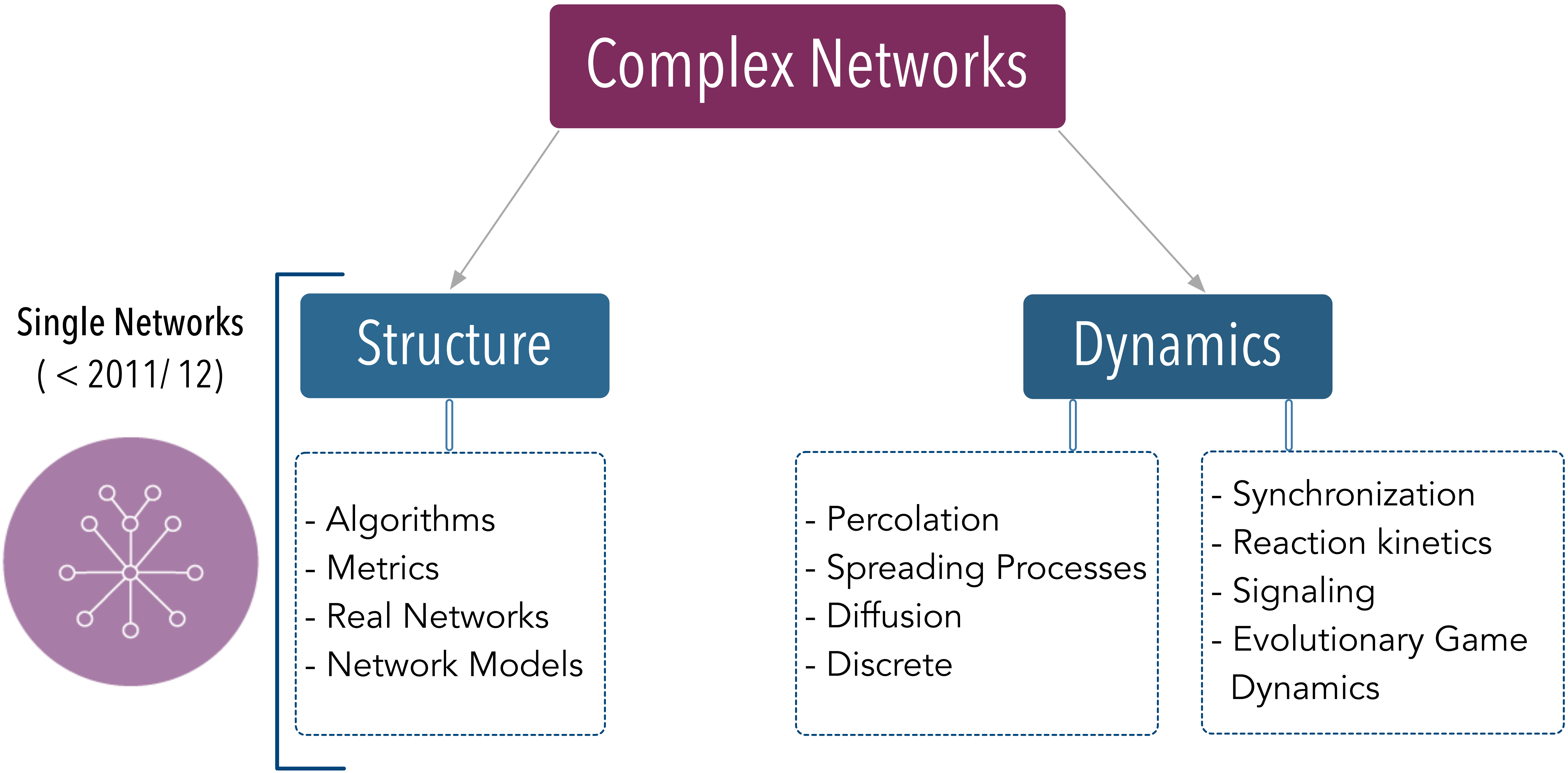


SARS epidemics: a discrete network driven process



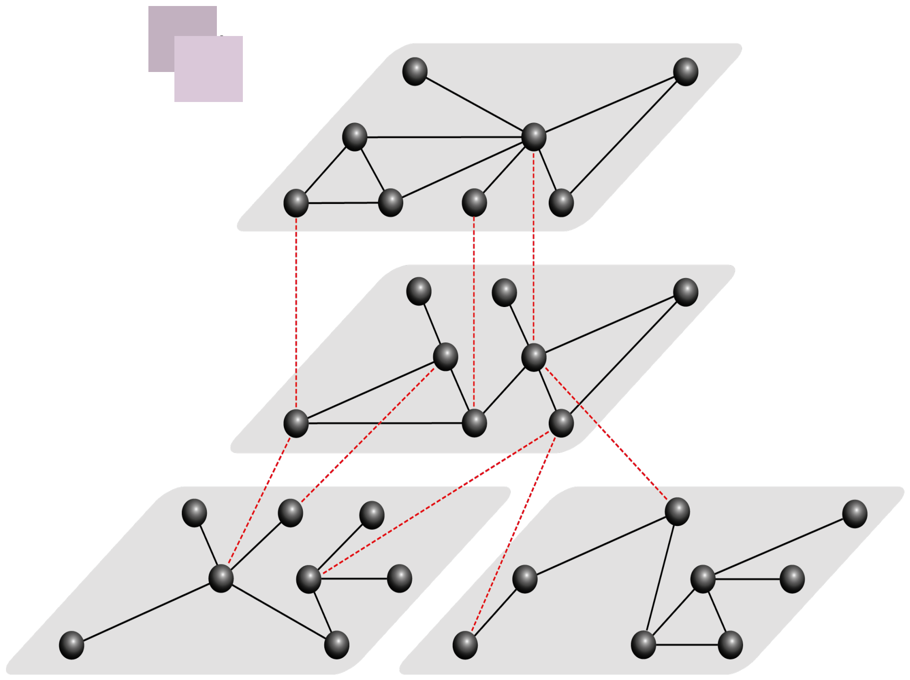
from A. Vespignani

What has changed?


Complex Networks
Single Networks
(< 2011/ 12)
Structure
- Algorithms
- Metrics
- Real Networks
- Network Models
Dynamics
- Percolation
- Spreading Processes
- Diffusion
- Discrete
- Synchronization
- Reaction kinetics
- Signaling
- Evolutionary Game Dynamics

Multilayer Networks

State of the Art (> 2011-2012)



- New Theoretical Framework
- Characterization real networks
- New metrics
- (Simple) Dynamics: Diffusion, Percolation, Spreading

M. Kivela, A. Arenas, M. Barthelemy, J. P. Gleeson, **Y. Moreno**, and M. A. Porter, "**Multilayer Networks", Journal of Complex Networks 2**, 203-271 (2014).

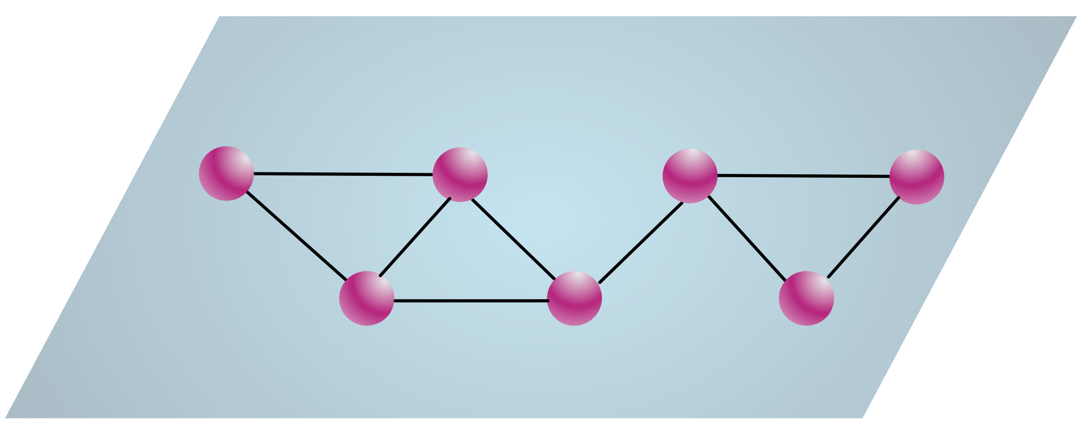
A. Aleta and **Y. Moreno**, "**Multilayer Networks in a Nutshell",** to appear in **Annual Reviews of Condensed Matter Physics**, (2019).

G Bianconi,"**Multilayer Networks"**

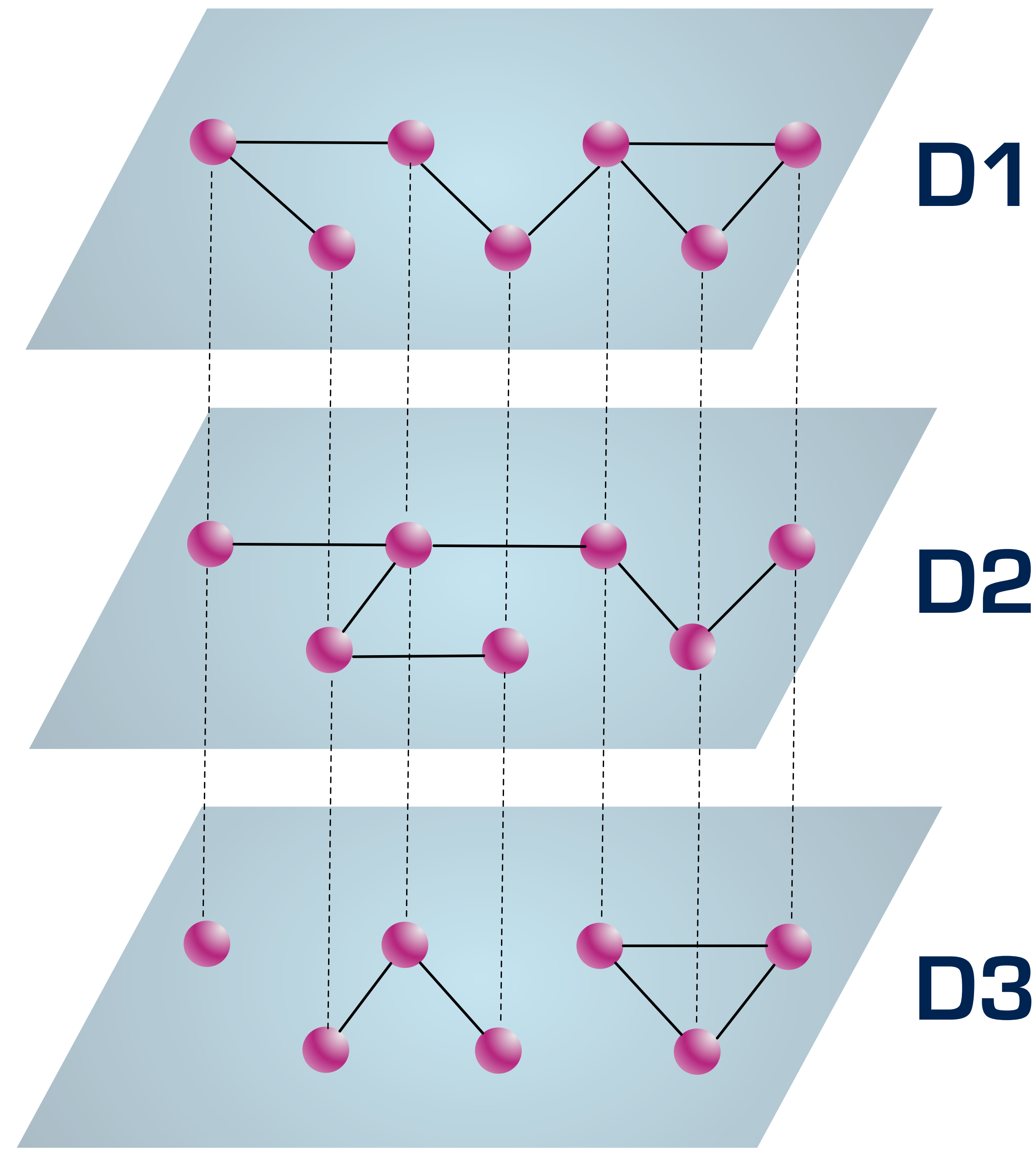
E. Cozzo, G. F. de Arruda, F. A. Rodrigues and **Y. Moreno**,"**Multilayer Networks: basic formalisms and structural properties",** (2018).

Layers account for different networks of contacts

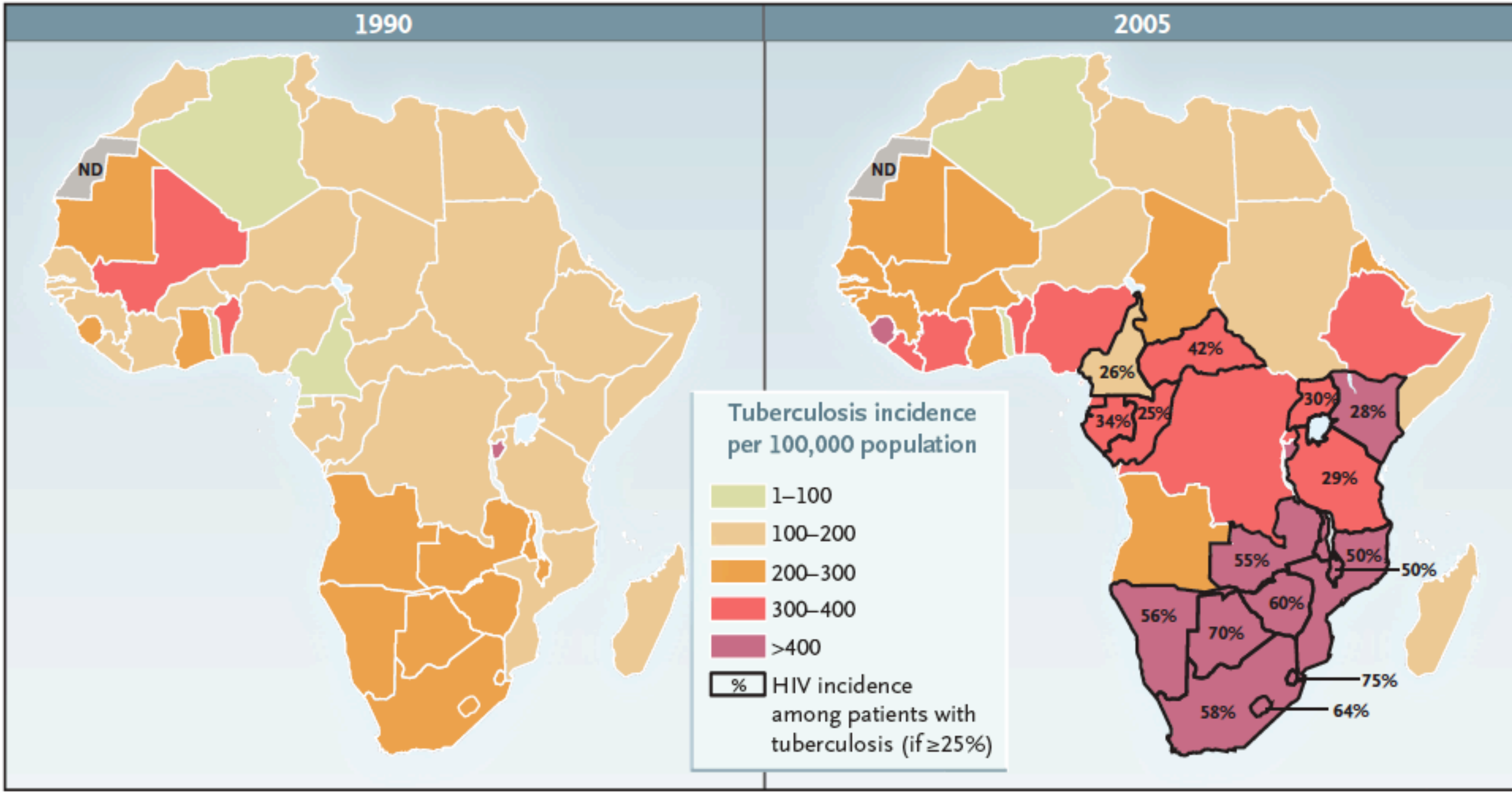
Original, aggregate network



Host Population



Co-occurrence TB-HIV:



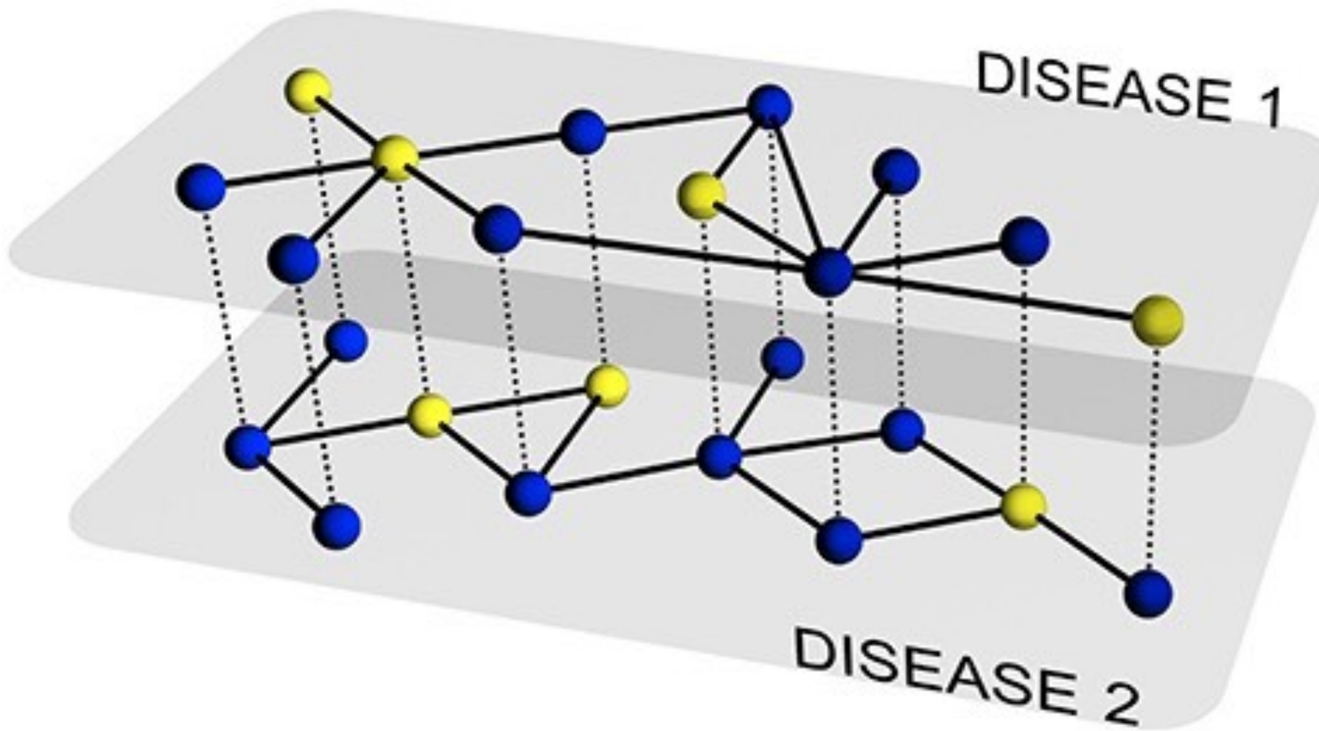
Estimated Incidence of Tuberculosis per 100,000 Population in African Countries in 1990 and 2005.
Data are from the World Health Organization. ND denotes no data.

From "**Tuberculosis in Africa, combating an HIV-driven Crisis**" Chaisson, R.E. & Martinson, N.A., New Eng. J. Med., March 2008.

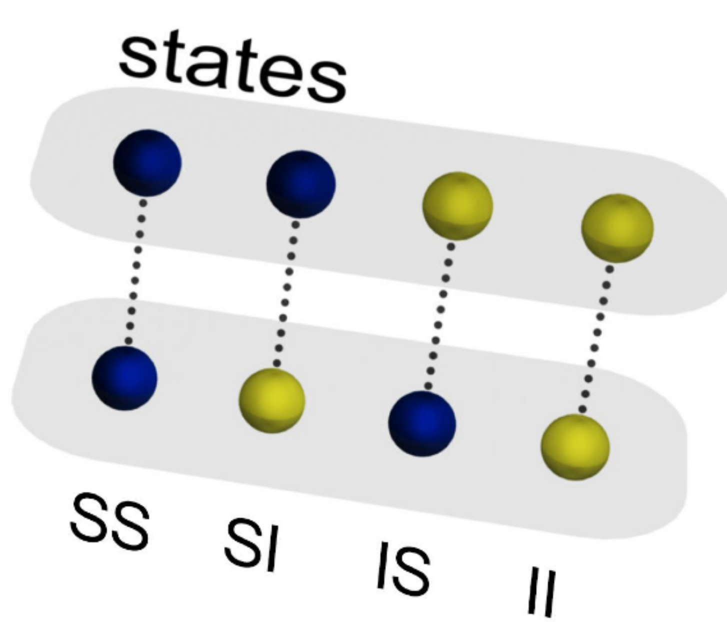
How?

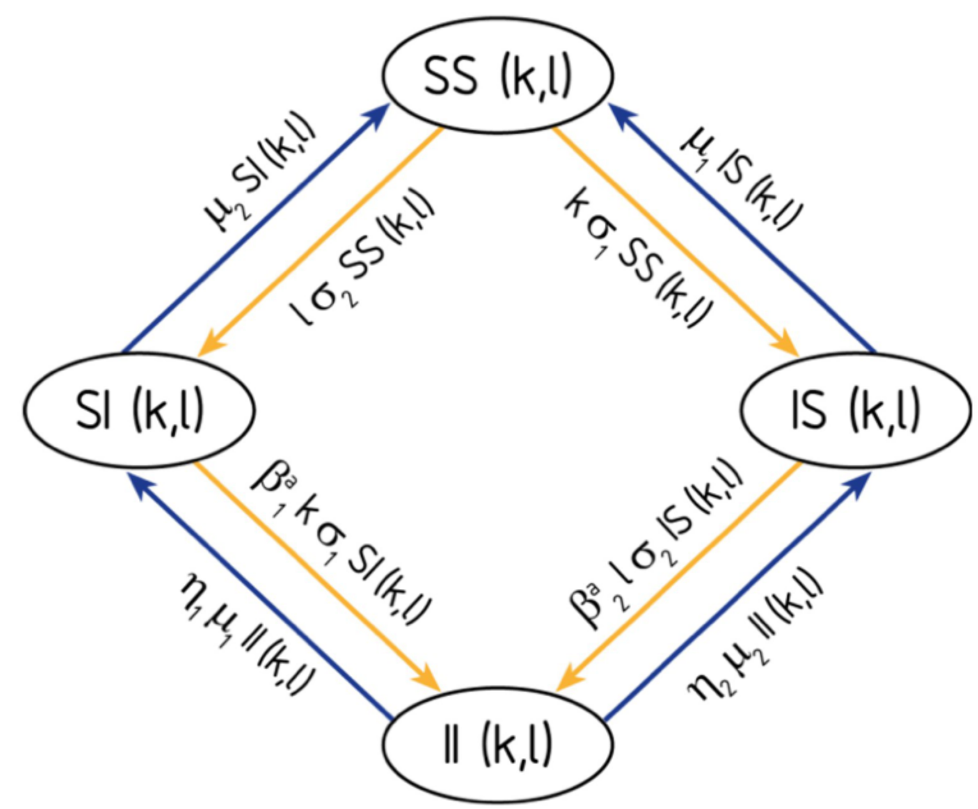
J. Sanz, C.-Y. Xia, S. Meloni, Y.Moreno, **Physical Review X 4, 041005** (2014).

- Two interconnected networks:

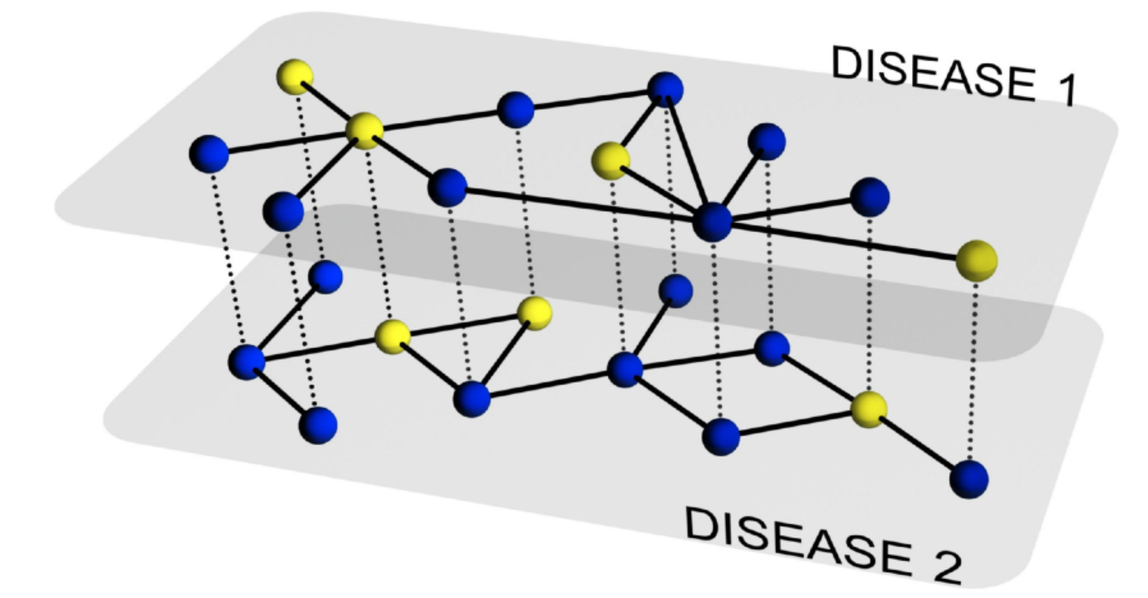


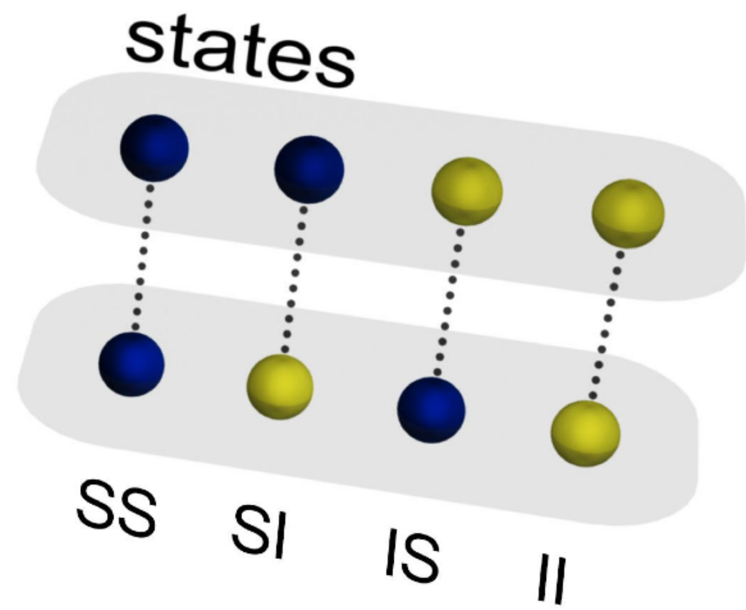
- Two coupled epidemic models:





Two coupled SIS





Interaction

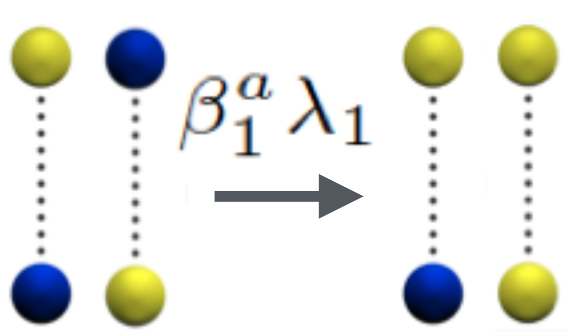
Modified susceptibility

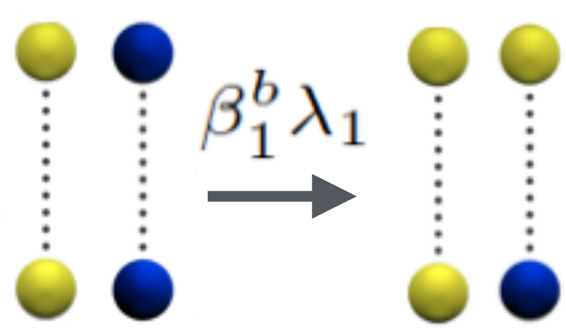
Modified infectivity

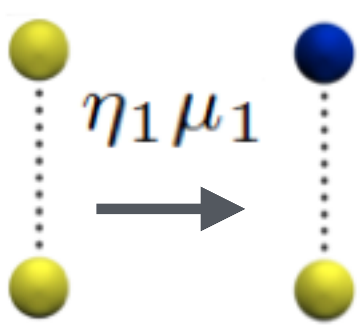
β_1^a

β_1^b

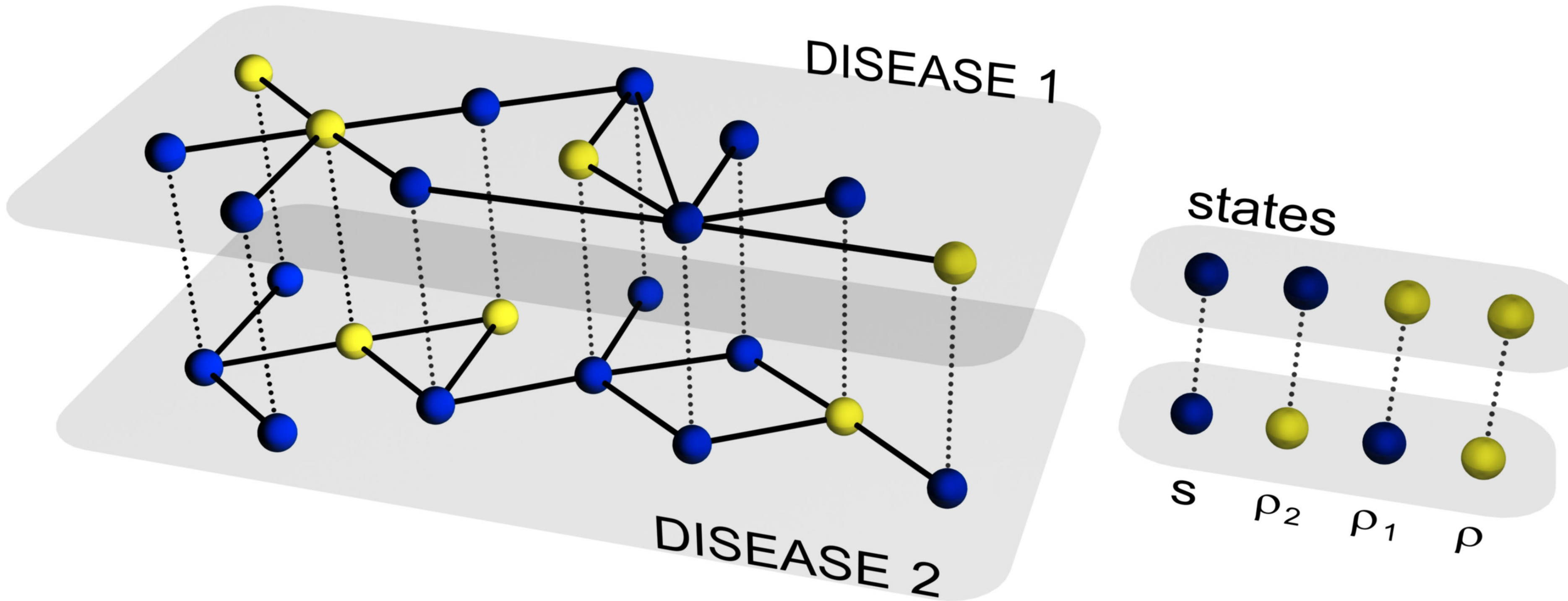
η_1



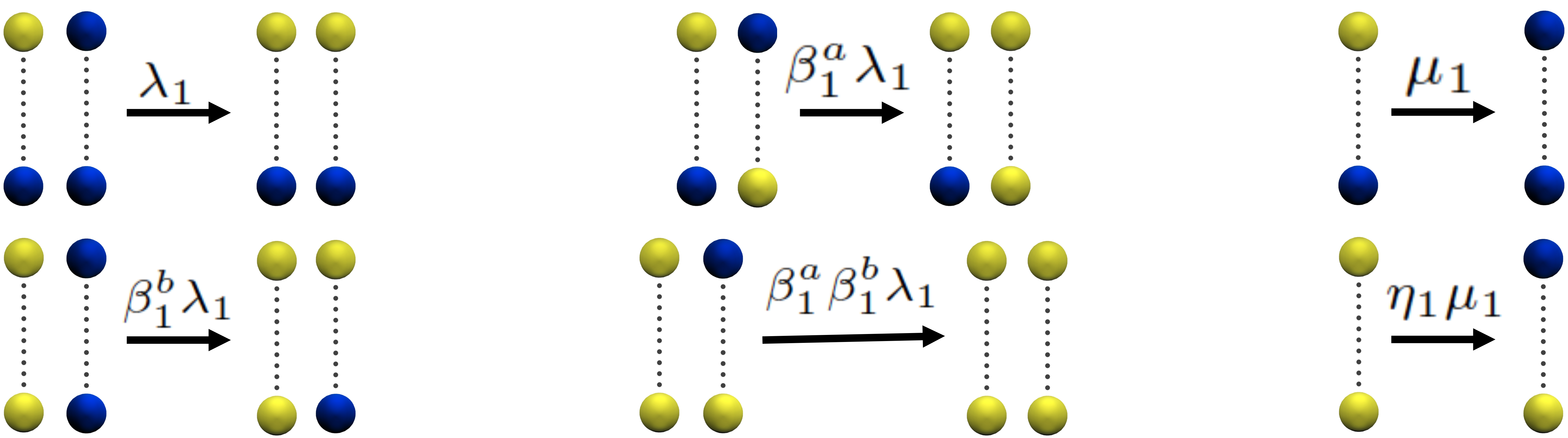




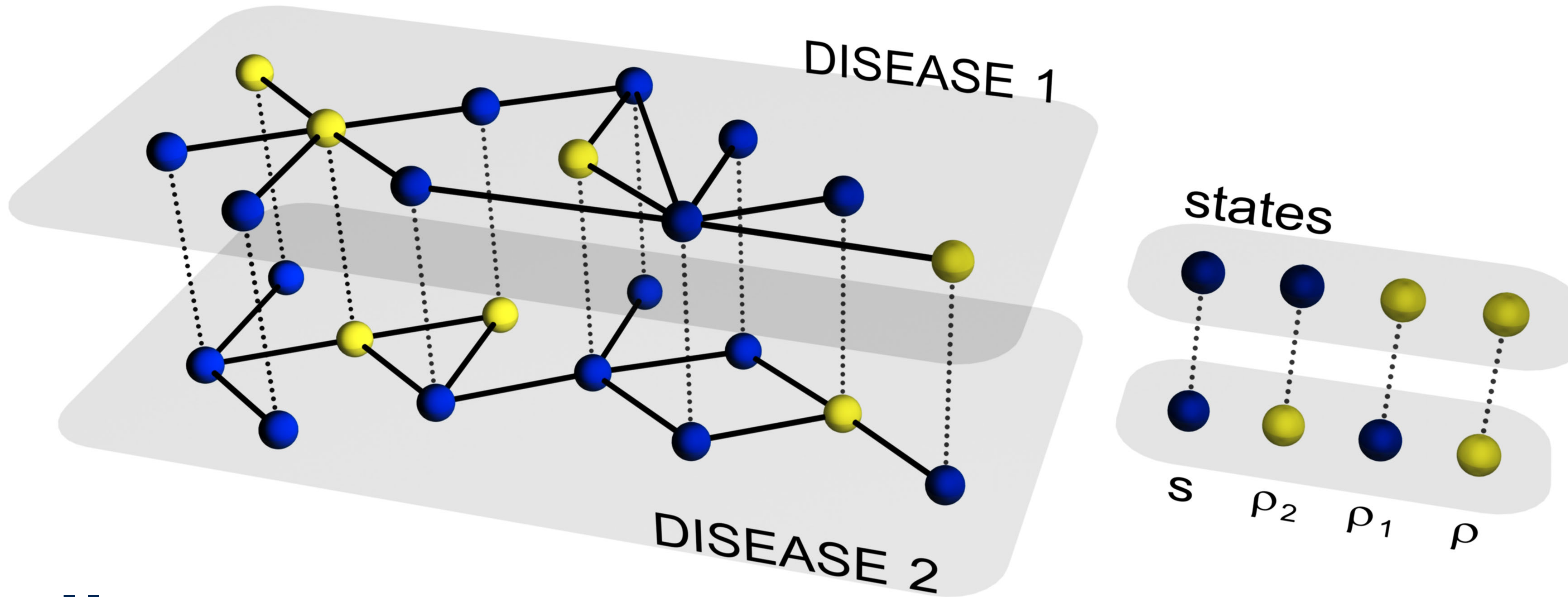
Summing up



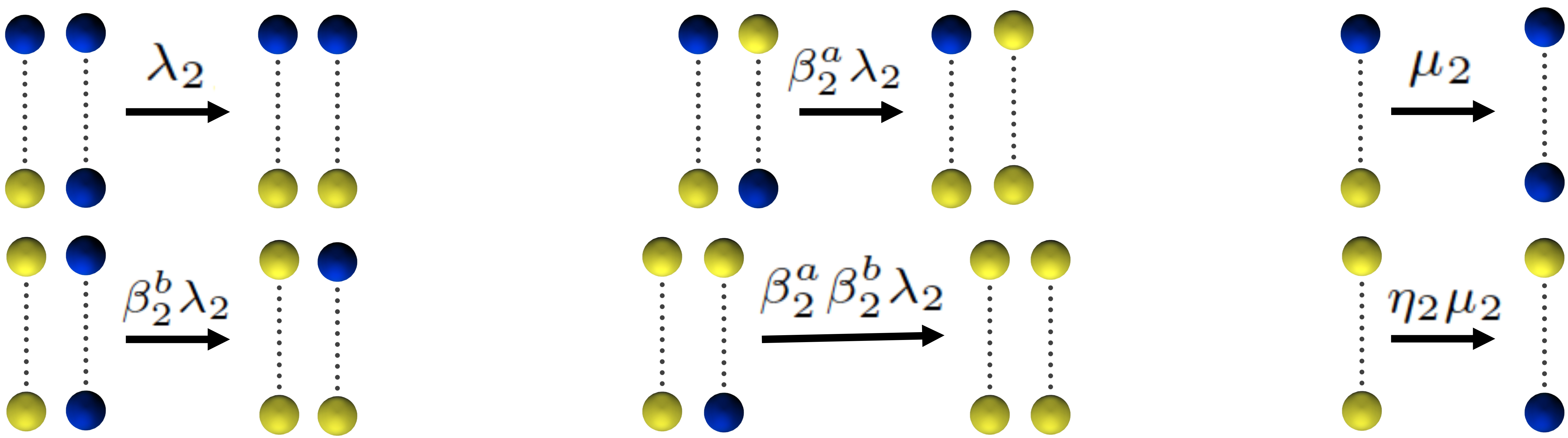
Disease I



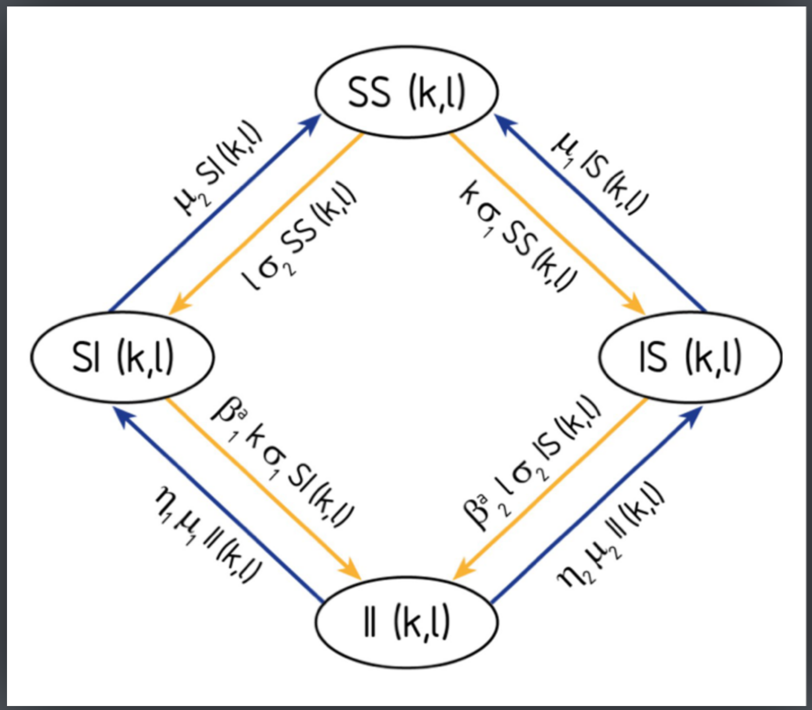
Summing up



Disease II



Heterogenous Mean-field Formulation…



Equations

$$\dot{SS}(k,l) = -(k\sigma_1 + l\sigma_2)SS(k,l) + \mu_1 IS(k,l) + \mu_2 SI(k,l)$$
$$\dot{IS}(k,l) = k\sigma_1 SS(k,l) - l\beta_2^a\sigma_2 IS(k,l) - \mu_1 IS(k,l) + \eta_2\mu_2 II(k,l)$$
$$\dot{SI}(k,l) = l\sigma_2 SS(k,l) - k\beta_1^a\sigma_1 SI(k,l) - \mu_2 SI(k,l) + \eta_1\mu_1 II(k,l)$$
$$\dot{II}(k,l) = k\beta_1^a\sigma_1 SI(k,l) + l\beta_2^a\sigma_2 IS(k,l) - (\eta_1\mu_1 + \eta_2\mu_2)II(k,l)$$

with

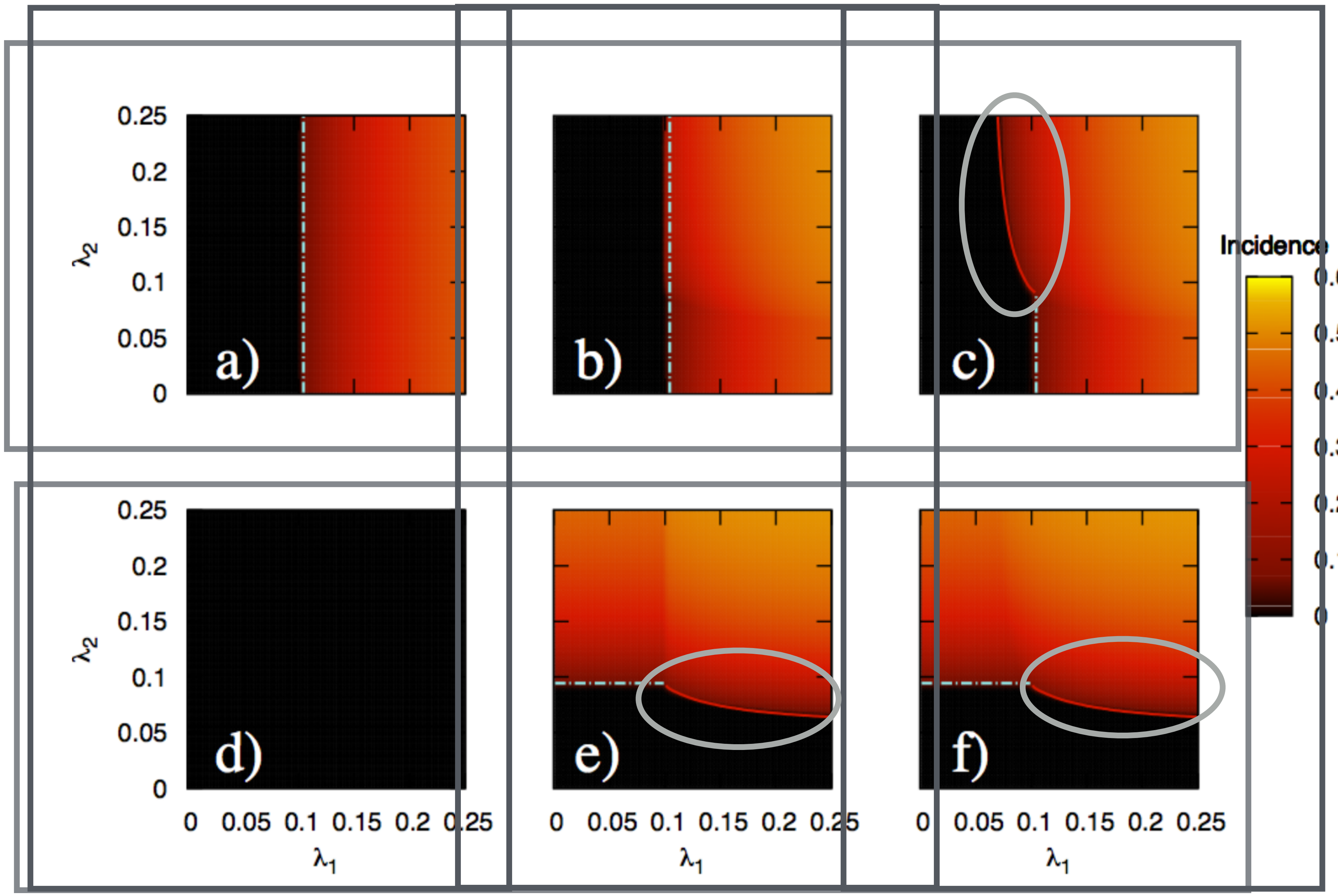
$$\sigma_1 = \lambda_1(\theta_1^{IS} + \beta_1^b\theta_1^{II}) \qquad \sigma_2 = \lambda_2(\theta_2^{SI} + \beta_2^b\theta_2^{II})$$

The Threshold

$$\lambda_1^c(\sigma_2) = \mu_1 \frac{\langle k\rangle}{\sum_{k,l} P(k,l) k^2 \frac{l^2\sigma_2^2\beta_2^a\beta_1^a\beta_1^b + l\sigma_2(\eta_2\mu_2\beta_1^a + \beta_1^b(\beta_1^a\mu_1 + \beta_2^a\mu_2)) + \mu_2(\eta_1\mu_1 + \eta_2\mu_2)}{l^2\sigma_2^2\beta_2^a\eta_1 + l\sigma_2(\eta_1\mu_1 + \eta_2\mu_2 + \beta_2^a\eta_1\mu_2) + \mu_2(\eta_1\mu_1 + \eta_2\mu_2)}}$$

Mutual enhancement: Homogeneous contact patterns

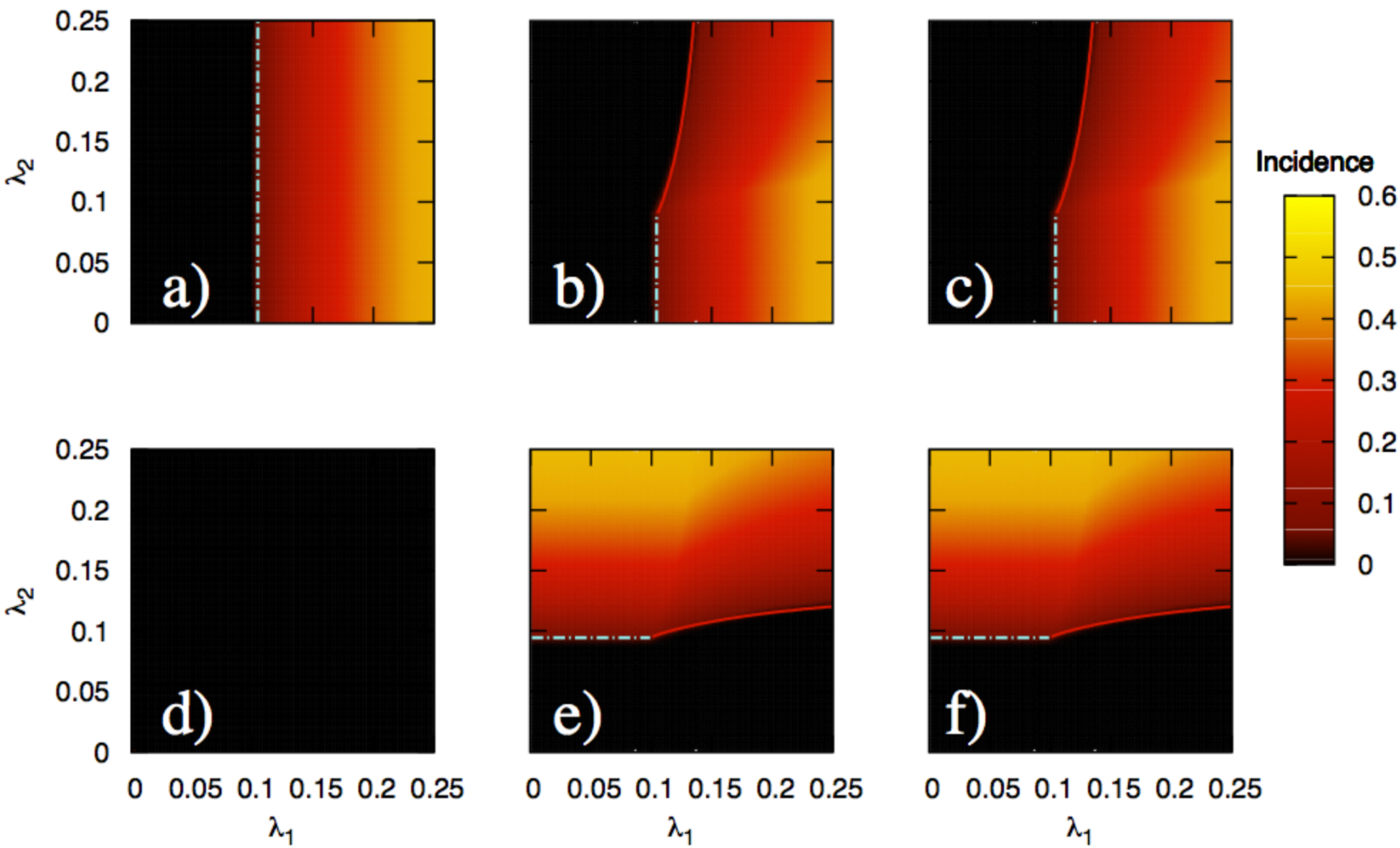
$\beta > 1.0$ $\eta < 1.0$ disease 2



Regions where a disease becomes endemic only after the installation of the other disease on the population

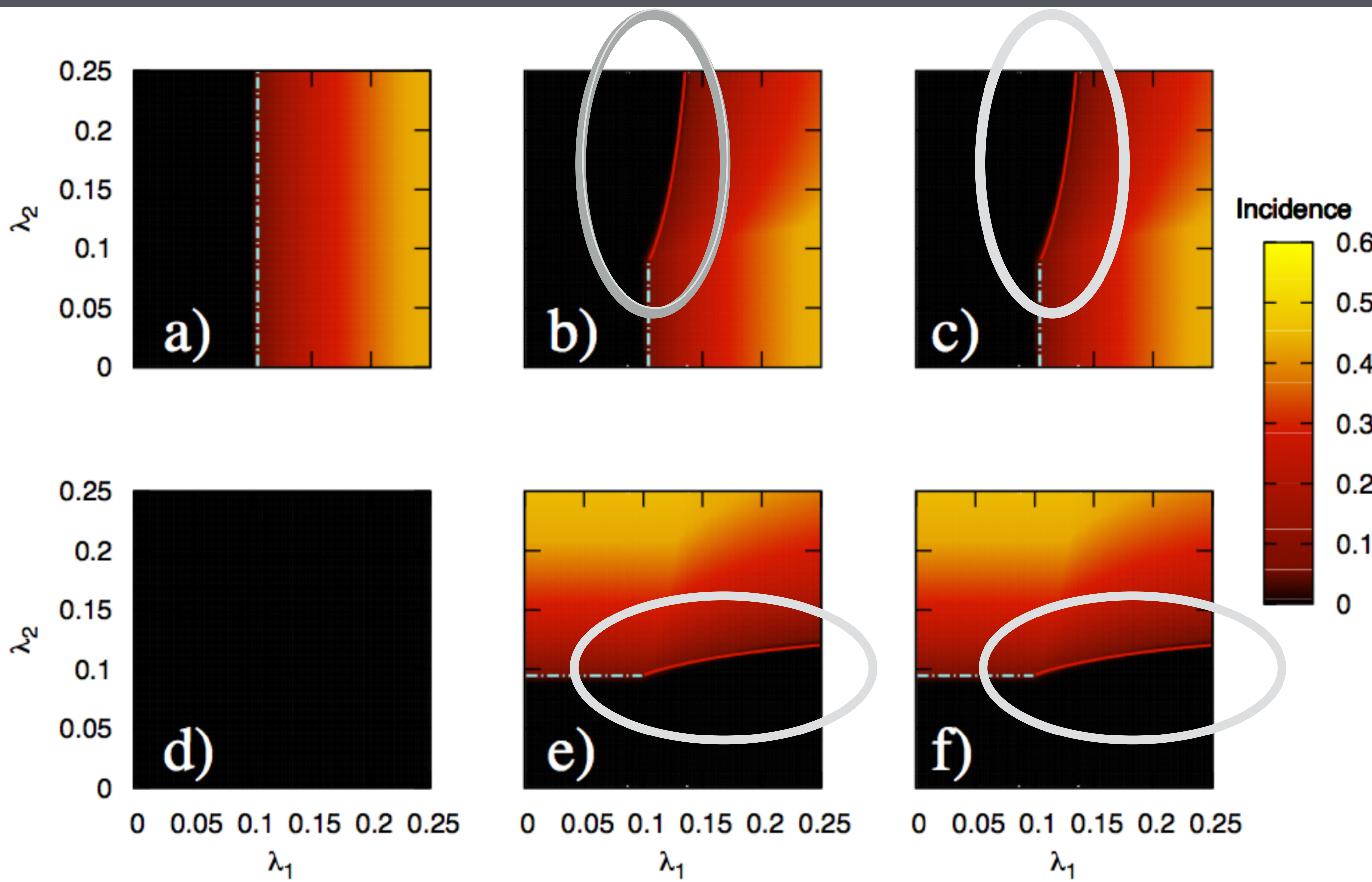
Partial Cross Immunity: Homogeneous contact patterns

$\beta < 1.0 \qquad \eta > 1.0$



Partial Cross Immunity: Homogeneous contact patterns

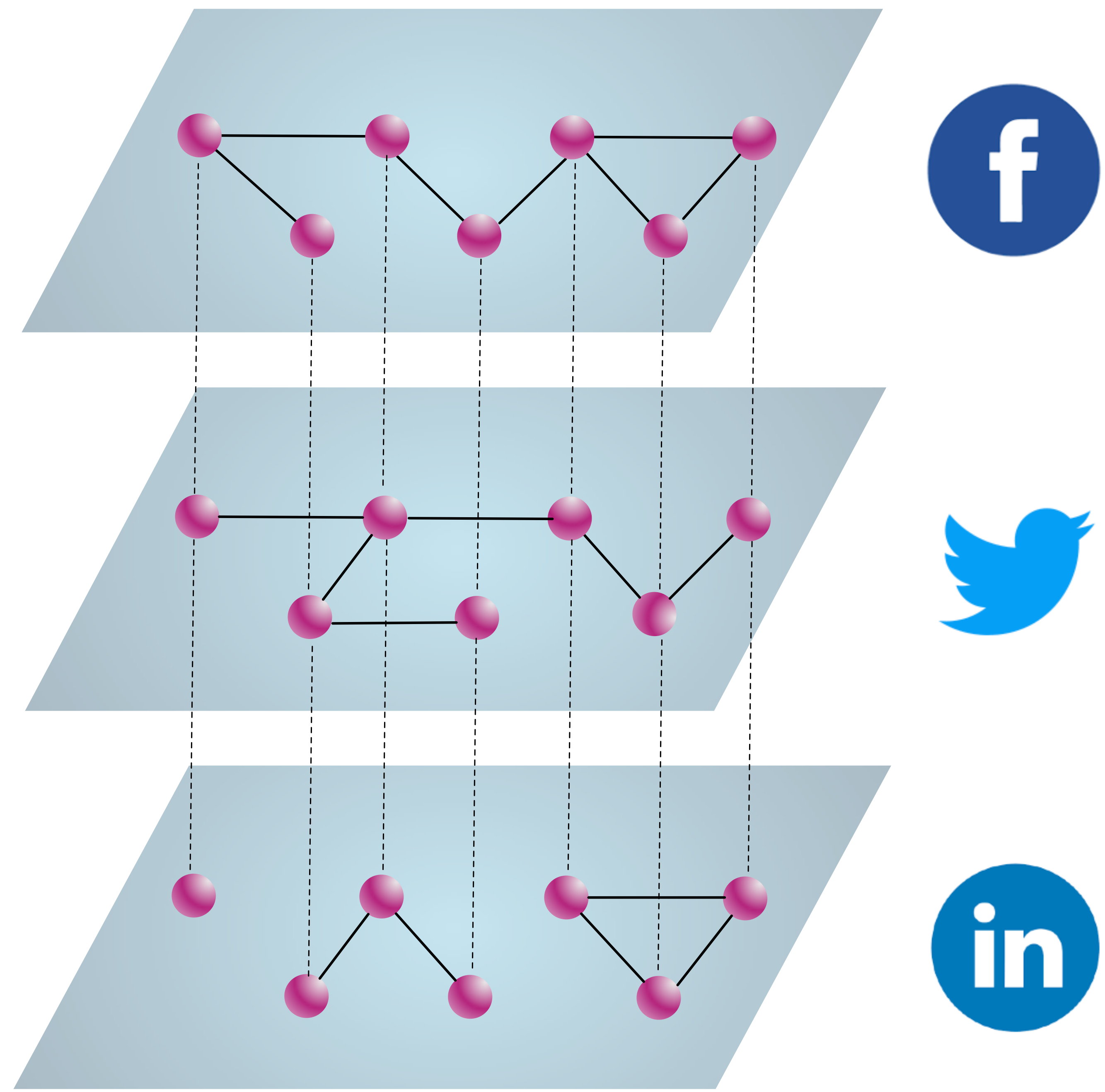
$\beta < 1.0 \qquad \eta > 1.0$



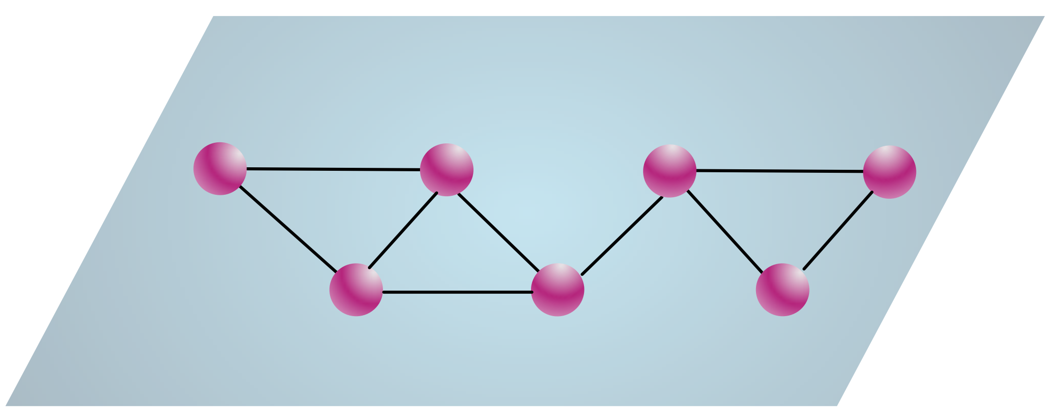
Regions where a disease can be eradicated only after the installation of the conjugate disease on the population

Multilayer Networks: Social Systems

When unfolded, layers appear



Original, aggregate network



Single layer Microscopic Markov Chain

$$p_i(t+1) = (1-q_i(t))(1-p_i(t)) + (1-\mu)p_i(t) + \mu(1-q_i(t))p_i(t)$$

Threshold

$$q_i(t) = \prod_{j=1}^{N}(1-\beta r_{ij} p_j(t))$$

$$r_{ij} = 1 - \left(1 - \frac{a_{ij}}{k_i}\right)^{\lambda_i}$$

Probability of not being infected by any neighbor

$$\left(\frac{\beta}{\mu}\right)_c = \frac{1}{\Lambda_{max}}$$

Contacts Matrix

Contacts per time

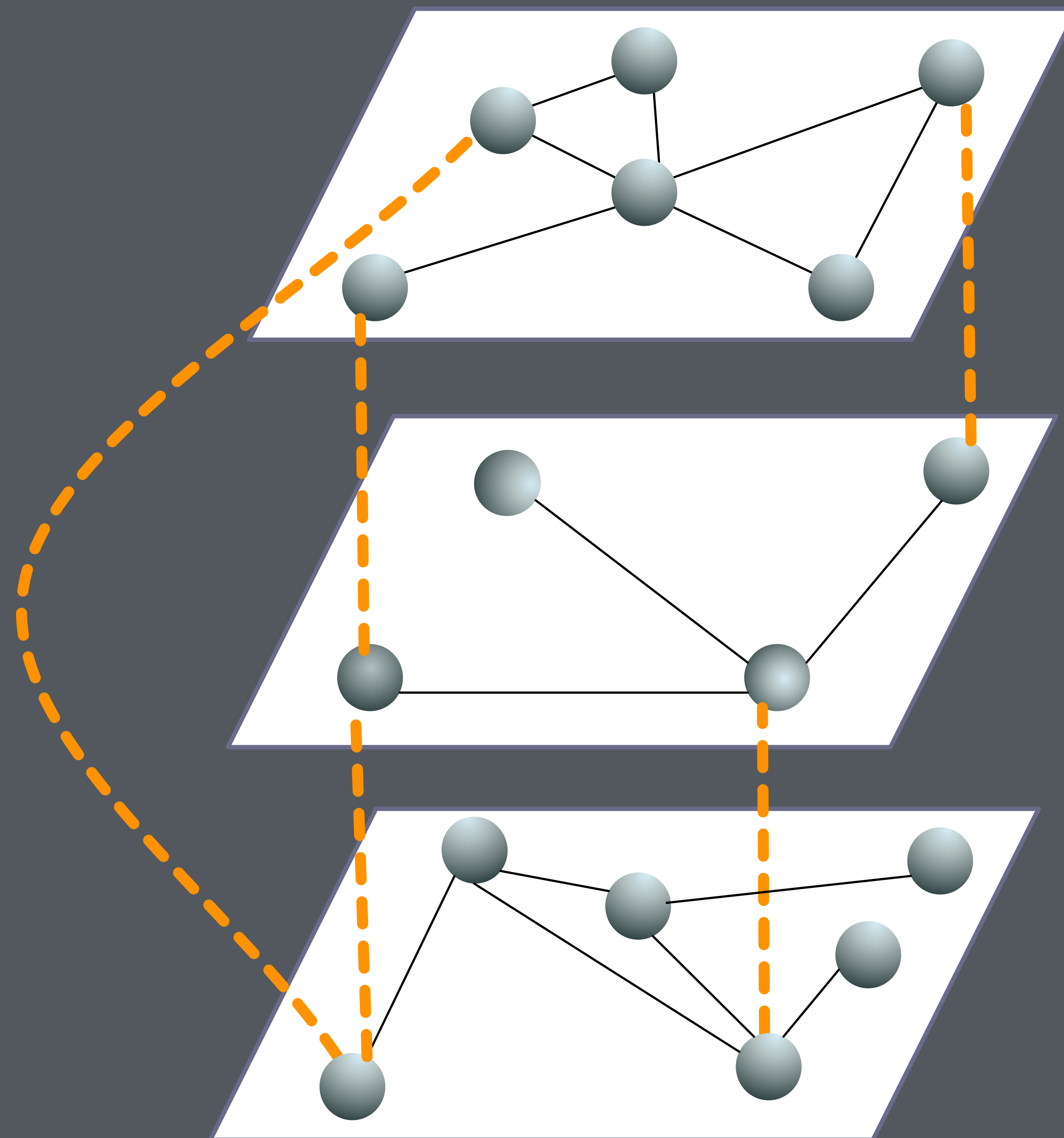
S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

How to represent it

Supra-Adjacency Matrix

$$\bar{A} = \bigoplus_{\alpha} A_{\alpha} + C = A + C$$

$$\bar{A} = \left(\begin{array}{c|c|c} A_1 & C_{1,2} & C_{1,3} \\ \hline C_{2,1} & A_2 & C_{2,3} \\ \hline C_{3,1} & C_{3,2} & A_3 \end{array}\right)$$



A_i Layer adjacency matrix

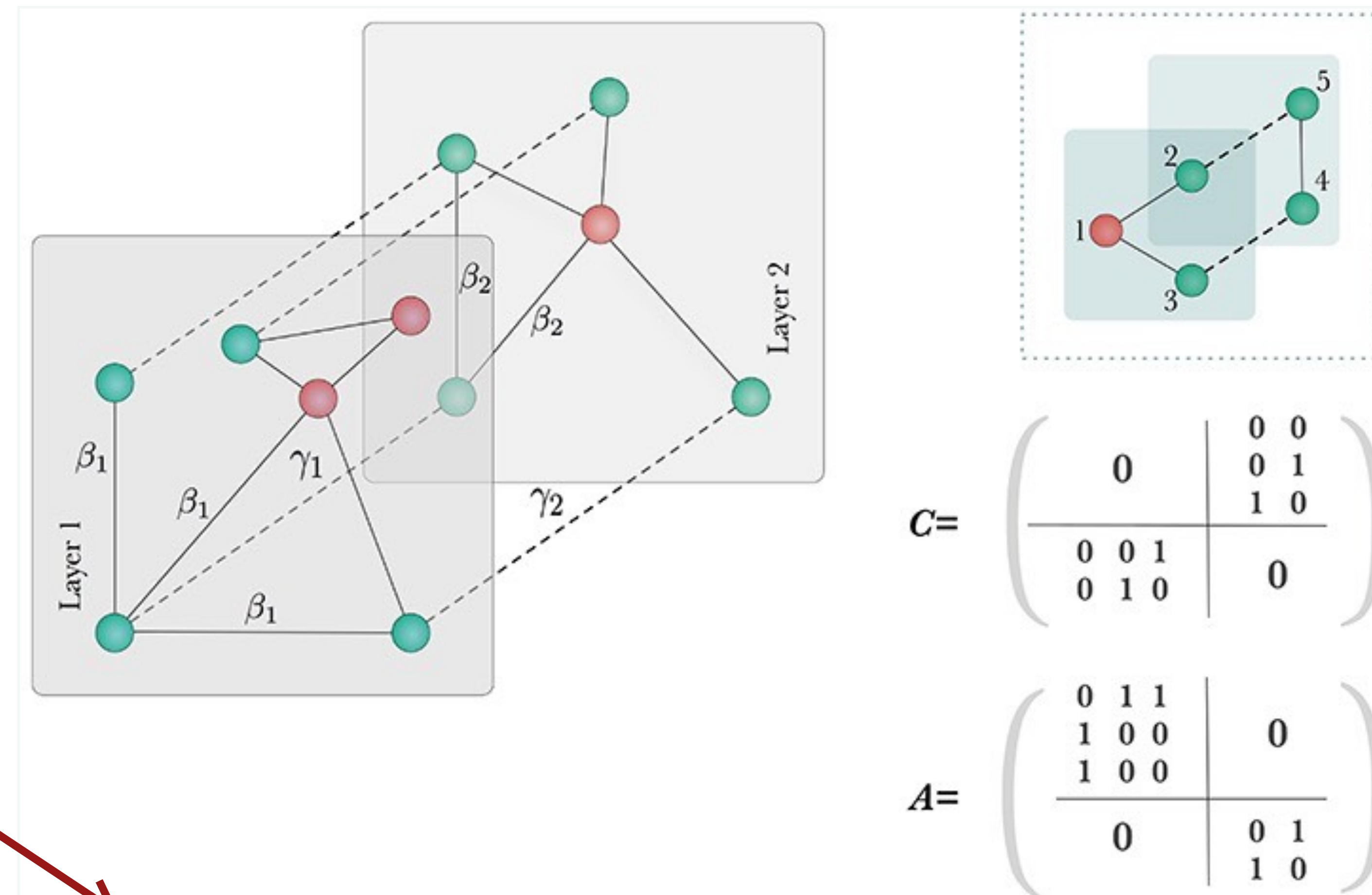
$C_{i,j}$ Coupling matrix

Microscopic Markov Chain on Multiplex

$$\vec{p}(t+1) = (\vec{1} - \vec{p}(t)) * (\vec{1} - \vec{q}(t)) + (\vec{1} - \vec{\mu}) * \vec{p}(t)\vec{\mu} * (\vec{1} - \vec{q}(t)) * \vec{p}(t)$$

Supra-Contacts Matrix

$$\bar{R} = \bigoplus_{\alpha} R_{\alpha} + \left(\frac{\vec{\gamma}}{\beta}\right)^{T} C$$



"self infection" probability

$$(R_{\alpha})_{ij} = 1 - \left(1 - \frac{(A_{\alpha})_{ij}}{k_{\alpha\,i}}\right)^{\lambda_{\alpha\,i}}$$

Cozzo et al. Phys. Rev. E 88, 050801(R) (2013)

Solving it

$$[\bar{R} - \frac{\mu}{\beta} I]p = 0$$

$$\left(\frac{\beta}{\mu}\right)_c = \frac{1}{\bar{\Lambda}_{max}}$$

The largest eigenvalue of $\bar{R}$ sets the critical value but…

What does $\bar{\Lambda}_{max}$ look like?

The largest eigenvalue of $\bar{R}$

Perturbative Analysis

$$\bar{R} = R + \epsilon C$$

$$\bar{\Lambda}_{max} \simeq \Lambda + \epsilon \triangle \Lambda$$

$$\bar{\Lambda}_{max} = \max_{\alpha}\{\Lambda_\alpha\}$$

$$\triangle \Lambda_{max} = \frac{\vec{v}^T C \vec{v}}{\vec{v}^T \vec{v}}$$

If $\Lambda_{1_{max}} >> \Lambda_{\alpha_{max}}$

$$\vec{v} = \begin{pmatrix} \vec{v}_{(1)} \\ 0 \end{pmatrix} \rightarrow \triangle \Lambda = 0$$

At first order:

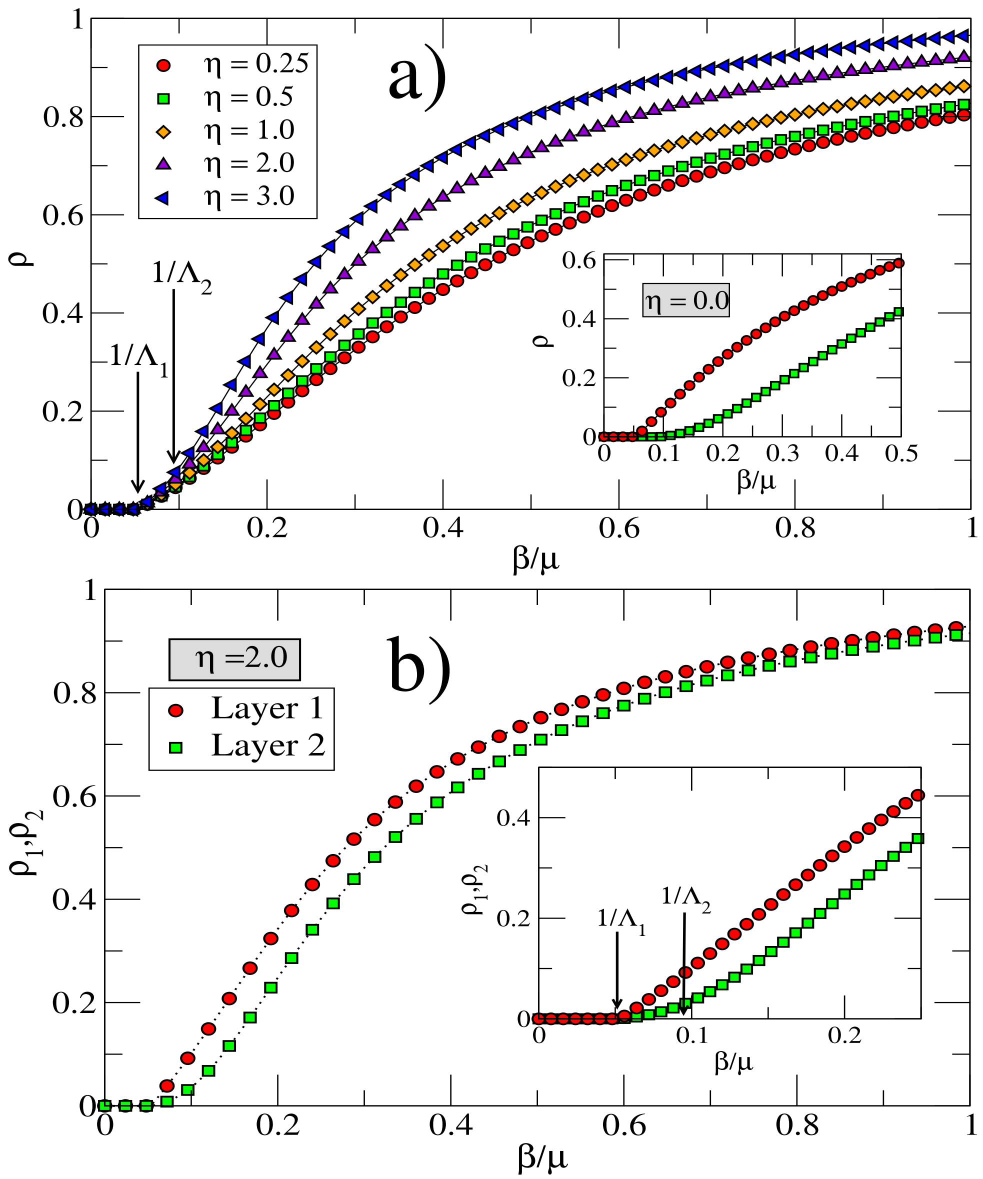
$$\bar{\Lambda}_{max} = \Lambda_{max}$$

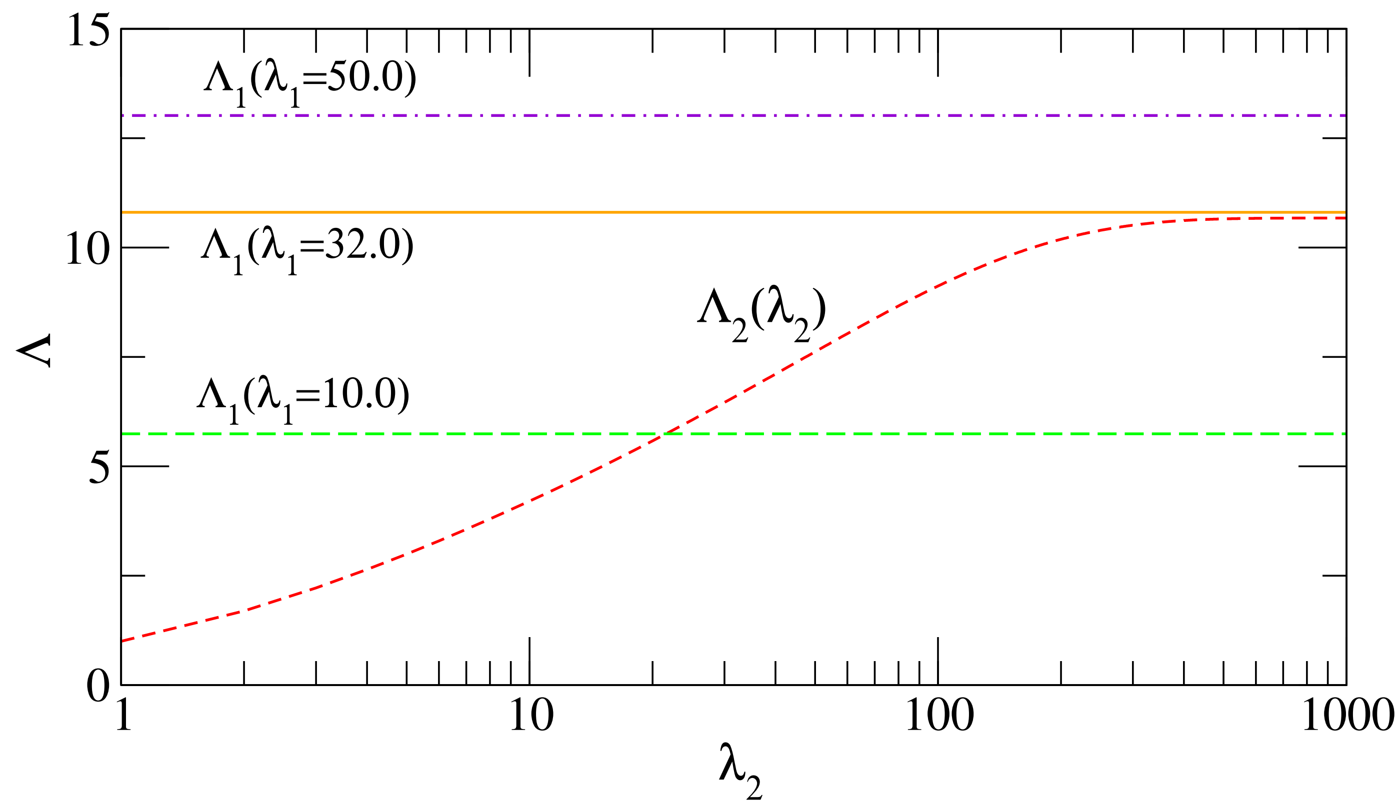
Dominant Layer

The Dominant Layer sets the critical point for the outbreak but…

Dominance depends on both topology and activity

$$(R_\alpha)_{ij} = 1 - \left(1 - \frac{(A_\alpha)_{ij}}{k_{\alpha i}}\right)^{\lambda_{\alpha i}}$$





G. F. de Arruda et al **Physical Review X 7**, 011014 (2017)

Indeed, one can go a bit more abstract:

(continuous) dynamics on a single layer network:

$$\frac{dX_i}{dt} = -\mu X_i + (1 - X_i)\lambda \sum_j A(i,j) X_j$$

(continuous) dynamics on a multilayer network:

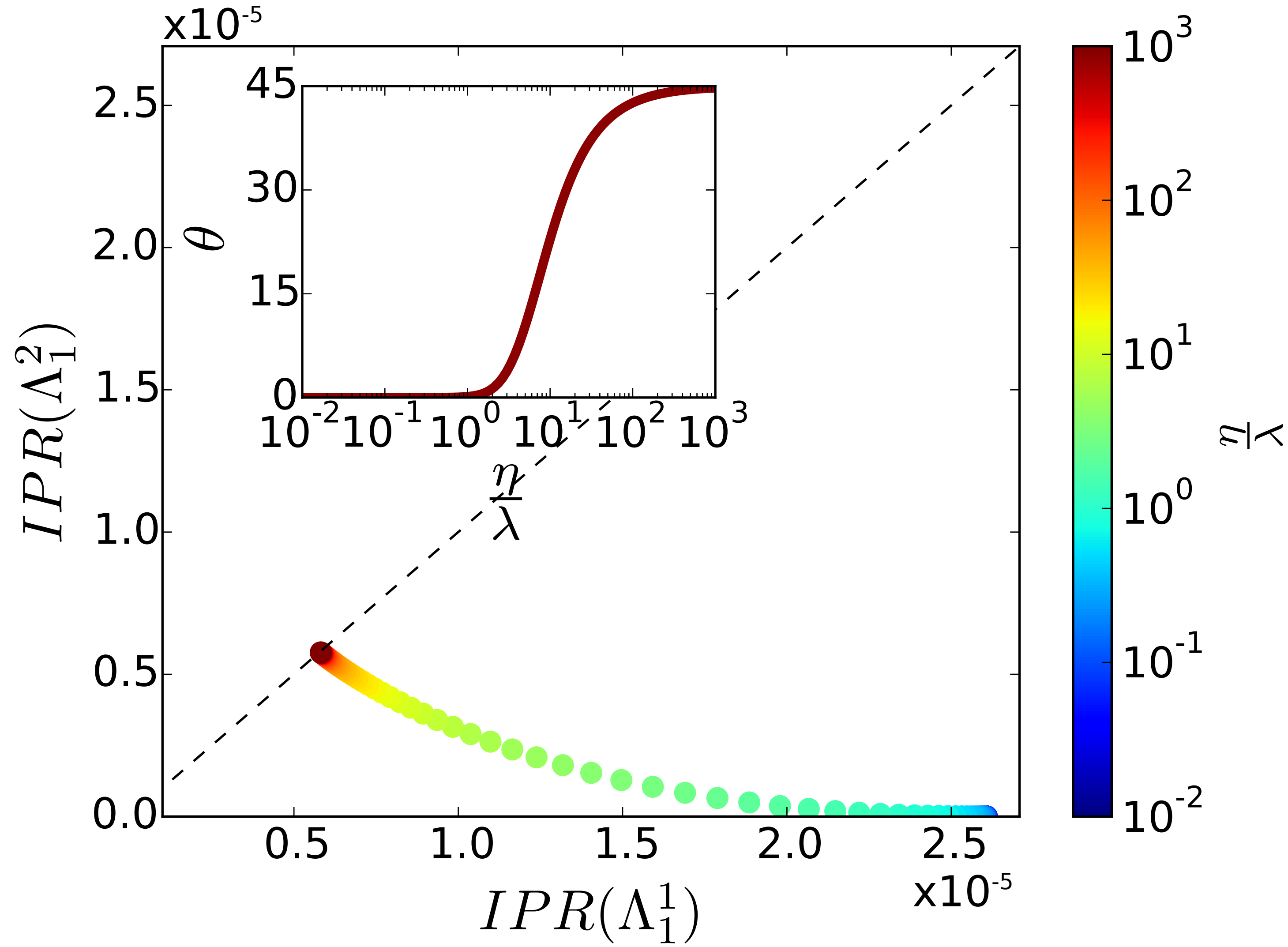
$$\frac{dX_{\beta\tilde{\delta}}}{dt} = -\mu X_{\beta\tilde{\delta}} + (1 - X_{\beta\tilde{\delta}})\lambda \mathcal{R}^{\alpha\tilde{\gamma}}_{\beta\tilde{\delta}}(\lambda,\eta) X_{\alpha\tilde{\gamma}}$$

$$\mathcal{R}^{\alpha\tilde{\gamma}}_{\beta\tilde{\delta}}(\lambda,\eta) = M^{\alpha\tilde{\eta}}_{\beta\tilde{\sigma}} E^{\tilde{\sigma}}_{\tilde{\eta}}(\tilde{\gamma}\tilde{\delta})\delta^{\tilde{\gamma}}_{\tilde{\delta}} + \frac{\eta}{\lambda} M^{\alpha\tilde{\eta}}_{\beta\tilde{\sigma}} E^{\tilde{\sigma}}_{\tilde{\eta}}(\tilde{\gamma}\tilde{\delta})(U^{\tilde{\gamma}}_{\tilde{\delta}} - \delta^{\tilde{\gamma}}_{\tilde{\delta}})$$

intra inter

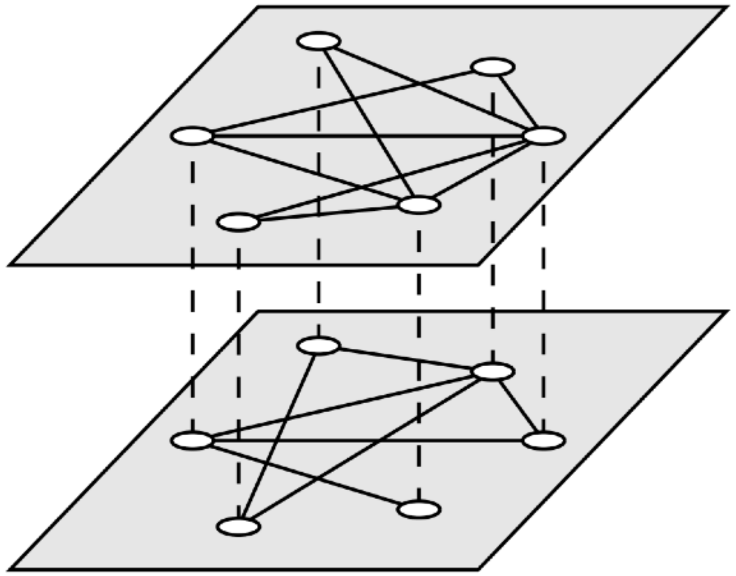
Disease Localization: $\mathrm{IPR}(\Lambda) \equiv (f_{\beta\delta}(\Lambda))^4 U^{\beta\delta}$

In the localized phase, only the entries of the eigentensor associated with the dominant layer are effectively populated, while the entries associated with the other layers are not. In the delocalized phase, all the entries are equally populated.



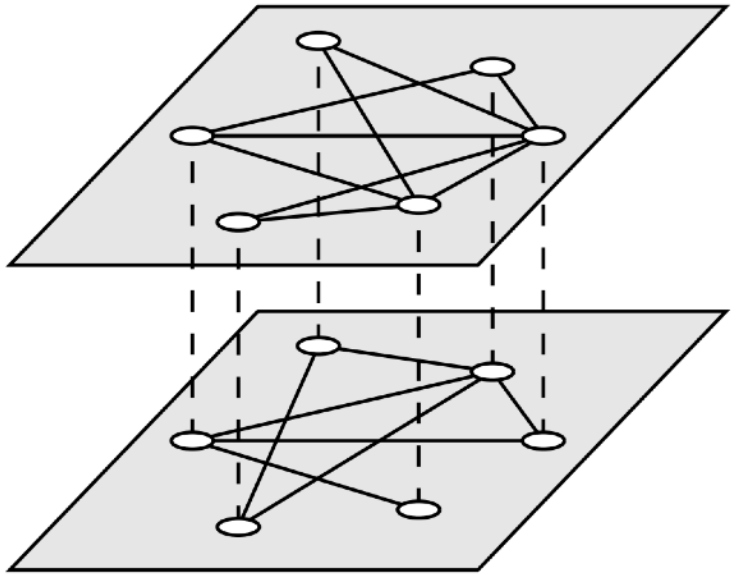
G. F. de Arruda et al **Physical Review X 7**, 011014 (2017)

Diffusion Dynamics on Multiplex



Gómez et al., *Diffusion Dynamics on Multiplex Networks*, Phys. Rev. Lett. **110**, 028701 (2013).

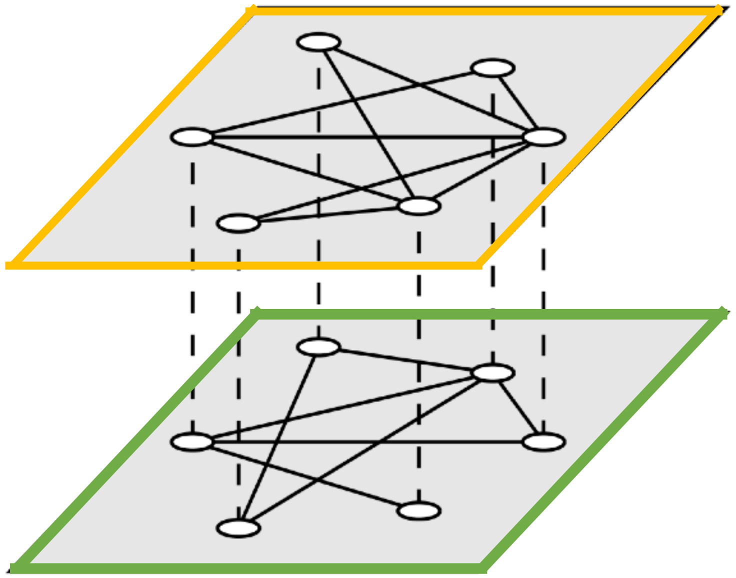
Diffusion Dynamics on Multiplex



$$\mathcal{L} = \begin{pmatrix} D_1 L_1 & 0 \\ 0 & D_2 L_2 \end{pmatrix} + D_x \begin{pmatrix} I & -I \\ -I & I \end{pmatrix}$$

Gómez et al., *Diffusion Dynamics on Multiplex Networks*, Phys. Rev. Lett. **110**, 028701 (2013).

Diffusion Dynamics on Multiplex



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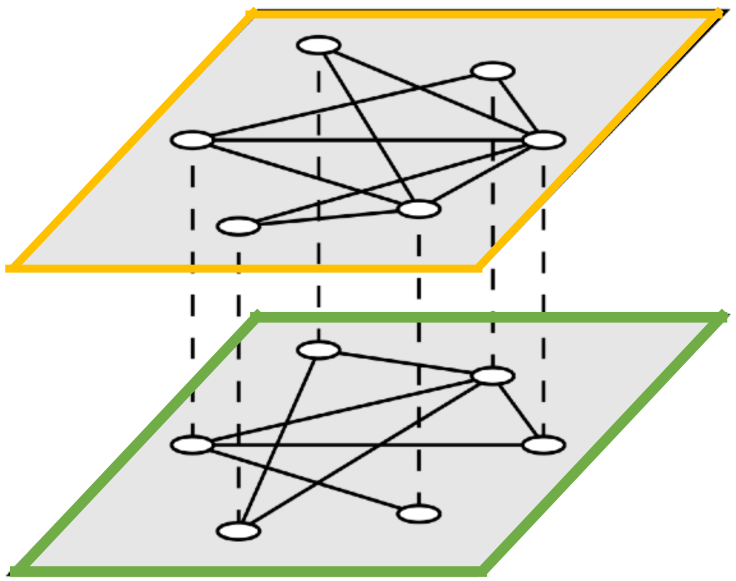
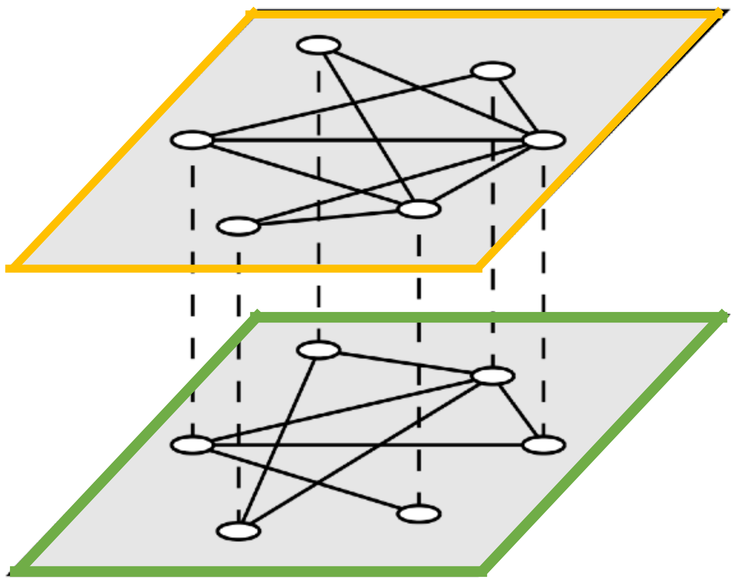


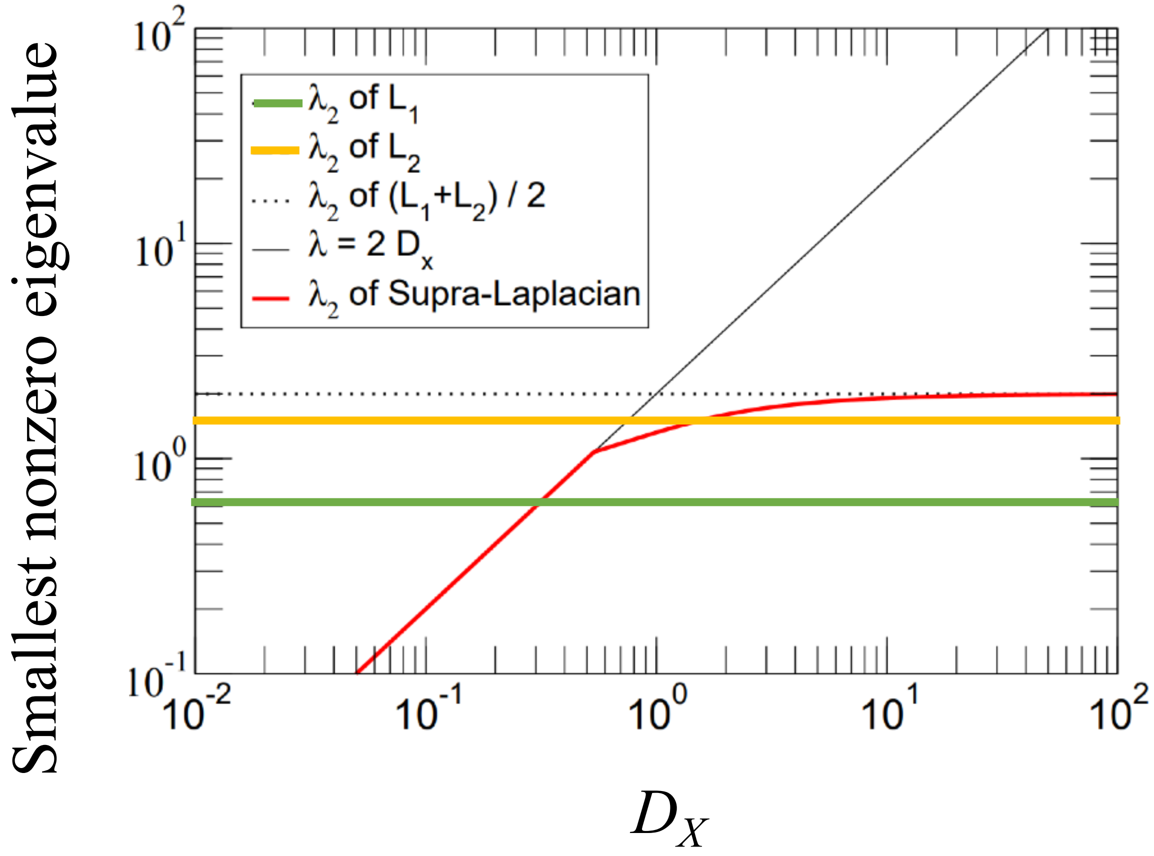
$$\mathcal{L} = \begin{pmatrix} D_1 L_1 & 0 \\ 0 & D_2 L_2 \end{pmatrix} + D_x \begin{pmatrix} I & -I \\ -I & I \end{pmatrix}$$

$$\tau \propto 1 / \text{Smallest nonzero eigenvalue, } \Lambda_2$$

Gómez et al., *Diffusion Dynamics on Multiplex Networks*, Phys. Rev. Lett. **110**, 028701 (2013).

Diffusion Dynamics on Multiplex





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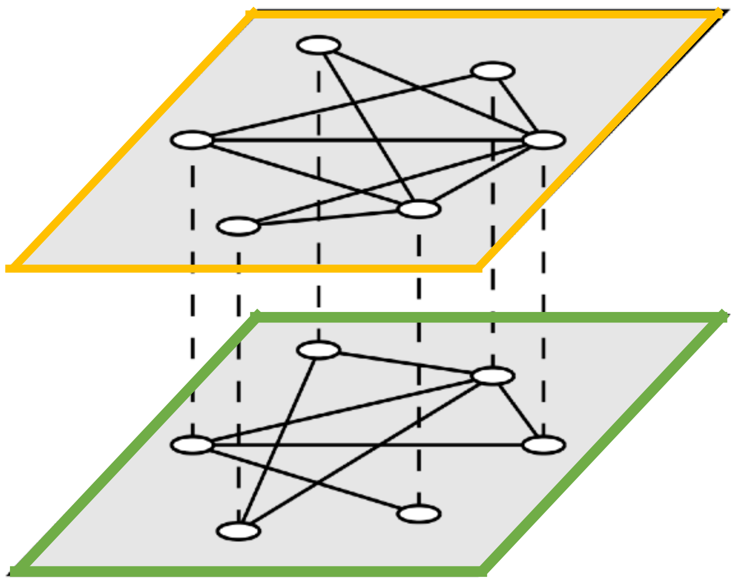
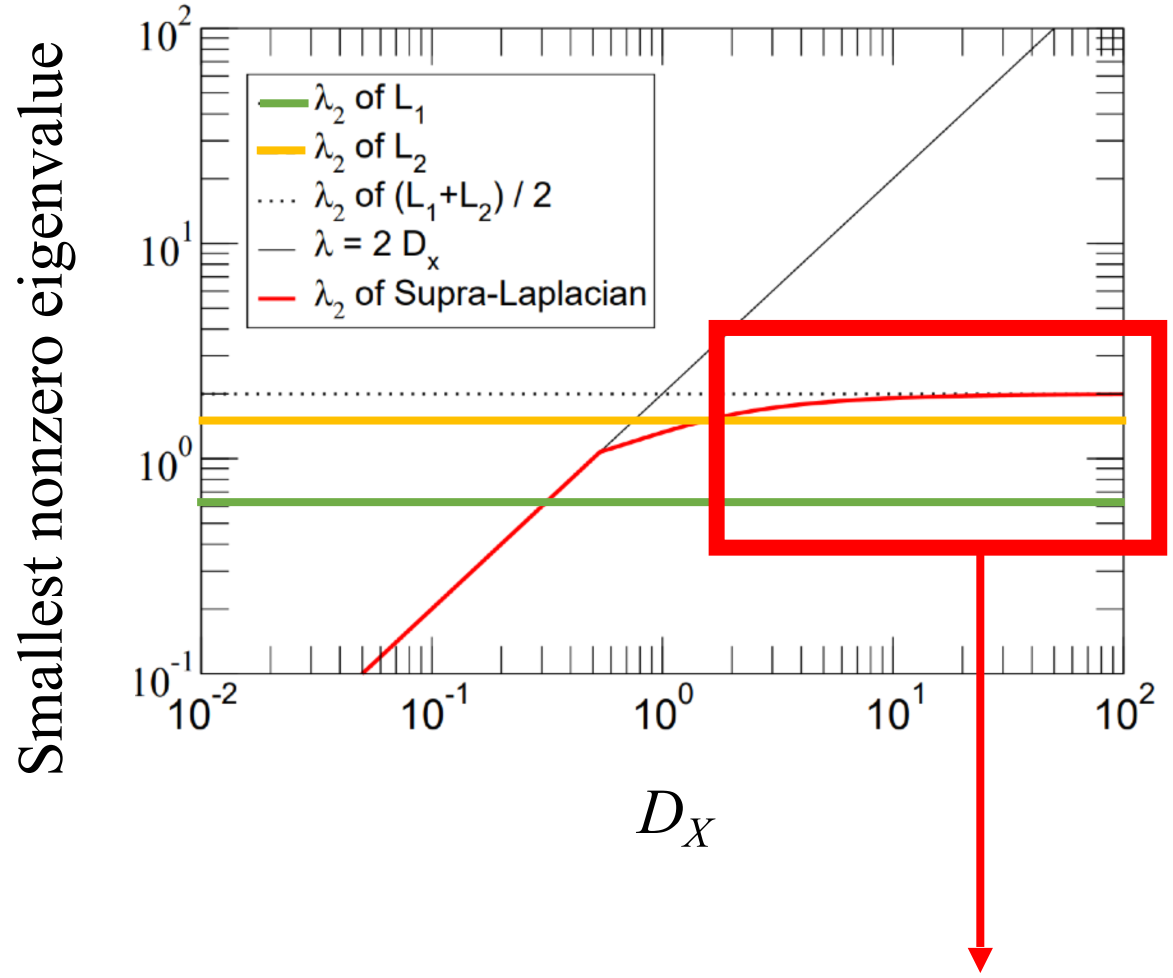
Diffusion Dynamics on Multiplex





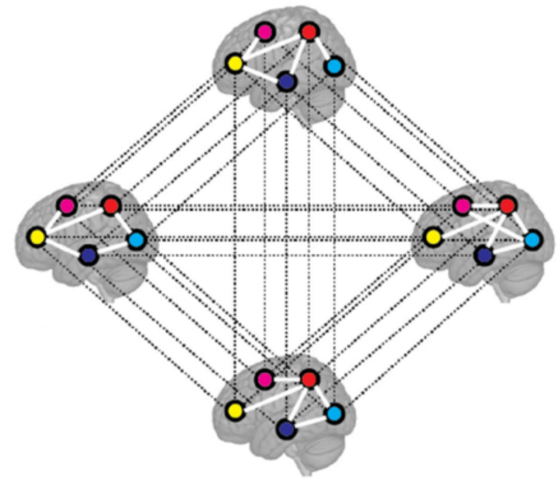
$$\mathcal{L} = \begin{pmatrix} D_1 L_1 & 0 \\ 0 & D_2 L_2 \end{pmatrix} + D_x \begin{pmatrix} I & -I \\ -I & I \end{pmatrix}$$

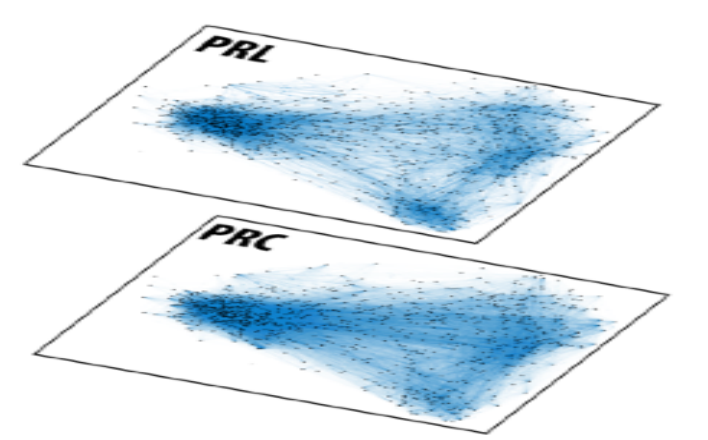
$\tau \propto 1 /$ Smallest nonzero eigenvalue, Λ_2

Gómez et al., *Diffusion Dynamics on Multiplex Networks*, Phys. Rev. Lett. **110**, 028701 (2013).

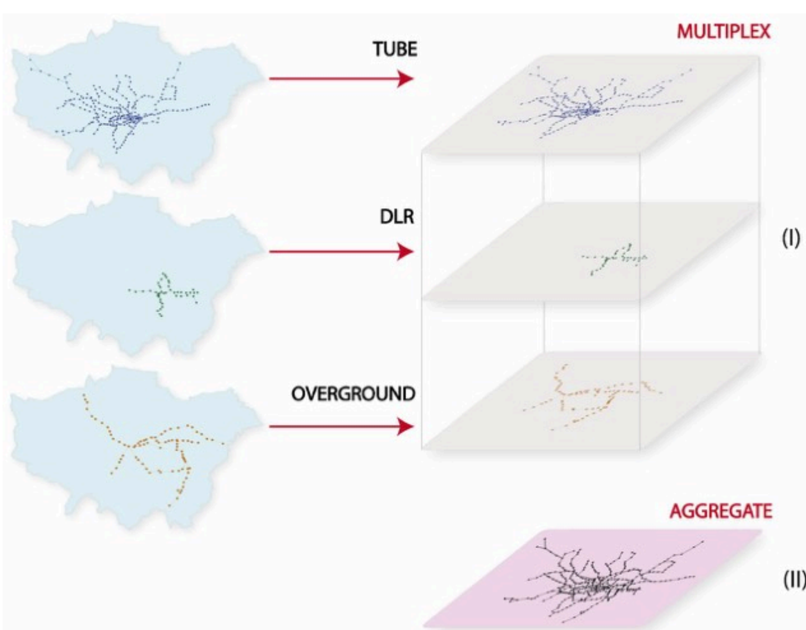
Multiplex Networks

Cardillo et al., 2013 (*Sci. Rep.*)

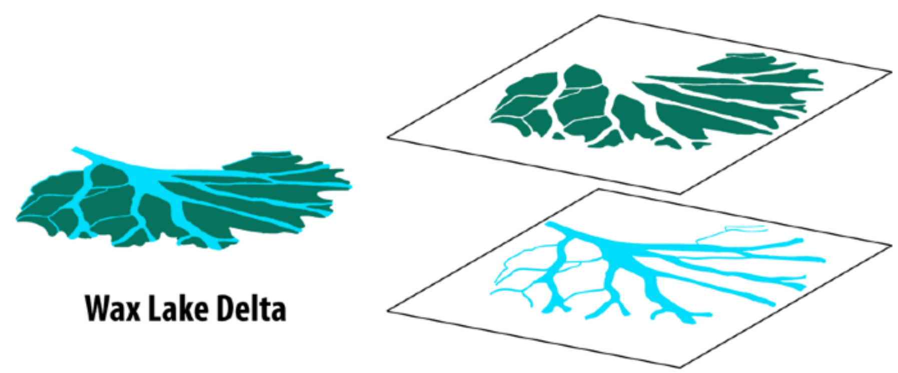




De Domenico et al., 2016 (*Front. Neurosci*)

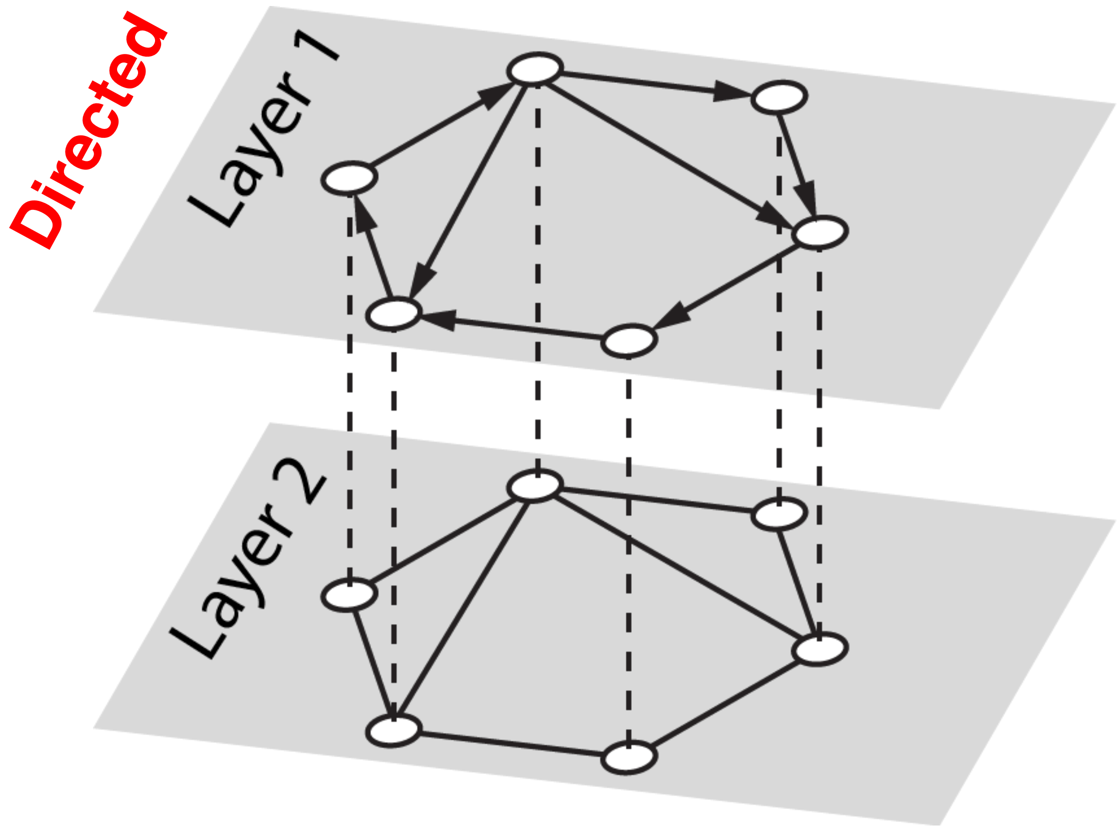


De Domenico et al., 2014 (*PNAS*)



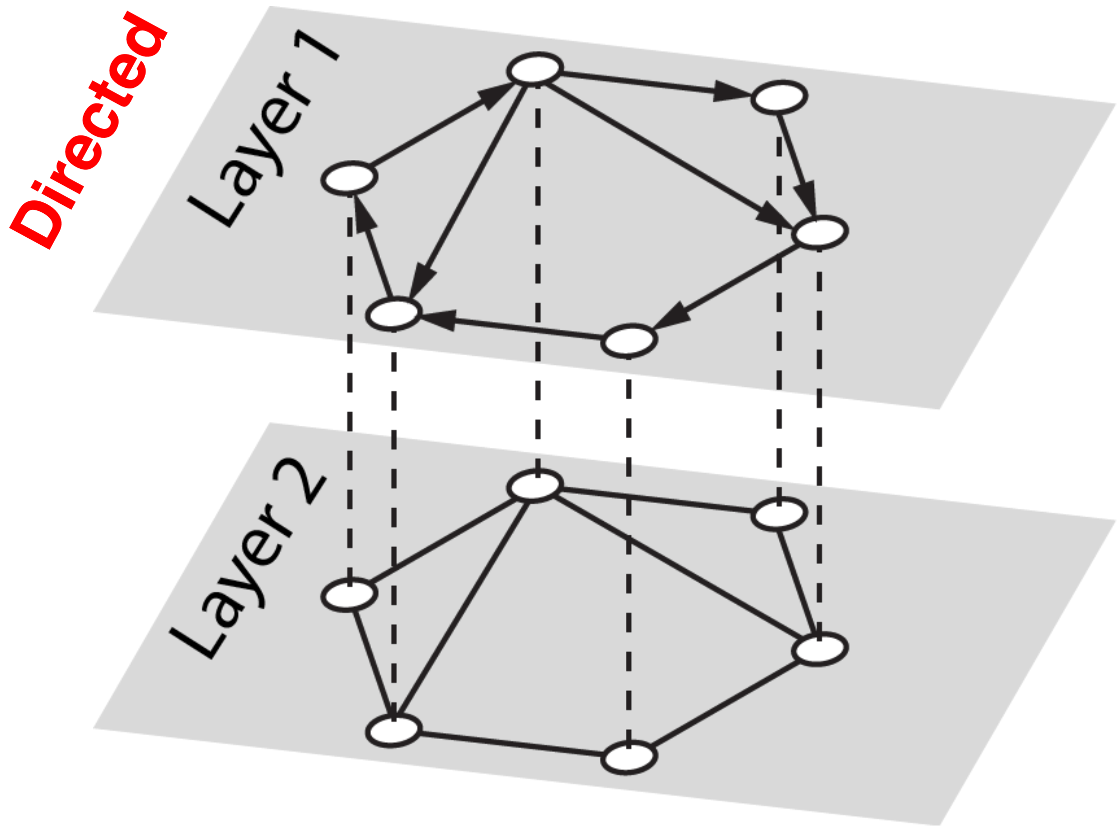
Tejedor et al., 2018 (*Geophys. Res. Lett.*)

Diffusion Dynamics on Directed Multiplex



A. Tejedor, A. Longjas, E. Foufoula-Georgiou, T. T. Georgiou, and Y. Moreno (2018)
Diffusion Dynamics and Optimal Coupling in Multiplex Networks with Directed Layers. Phys. Rev. X 8, 031071

Diffusion Dynamics on Directed Multiplex



$$\mathcal{L} = \begin{pmatrix} D_1 L_1 & 0 \\ 0 & D_2 L_2 \end{pmatrix} + D_x \begin{pmatrix} I & -I \\ -I & I \end{pmatrix}$$

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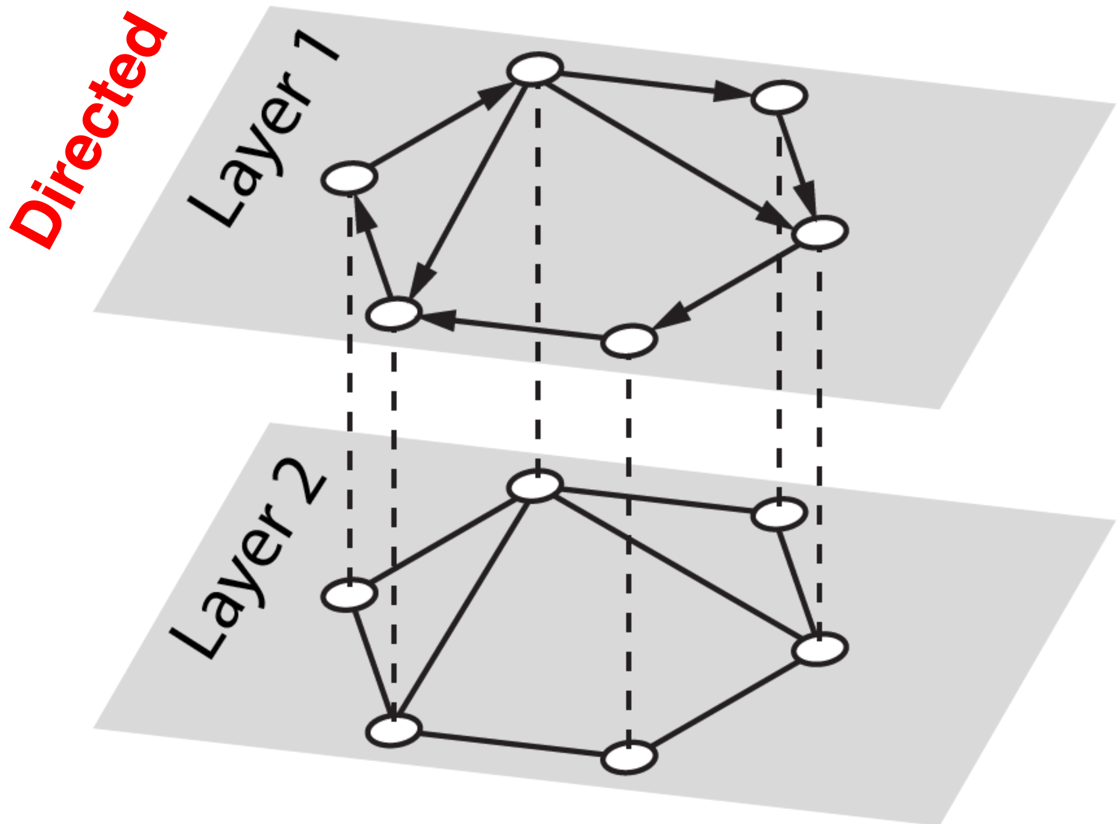

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$\tau \propto 1 \big/$ Smallest nonzero eigenvalue, $\mathrm{Re}(\Lambda_2)$

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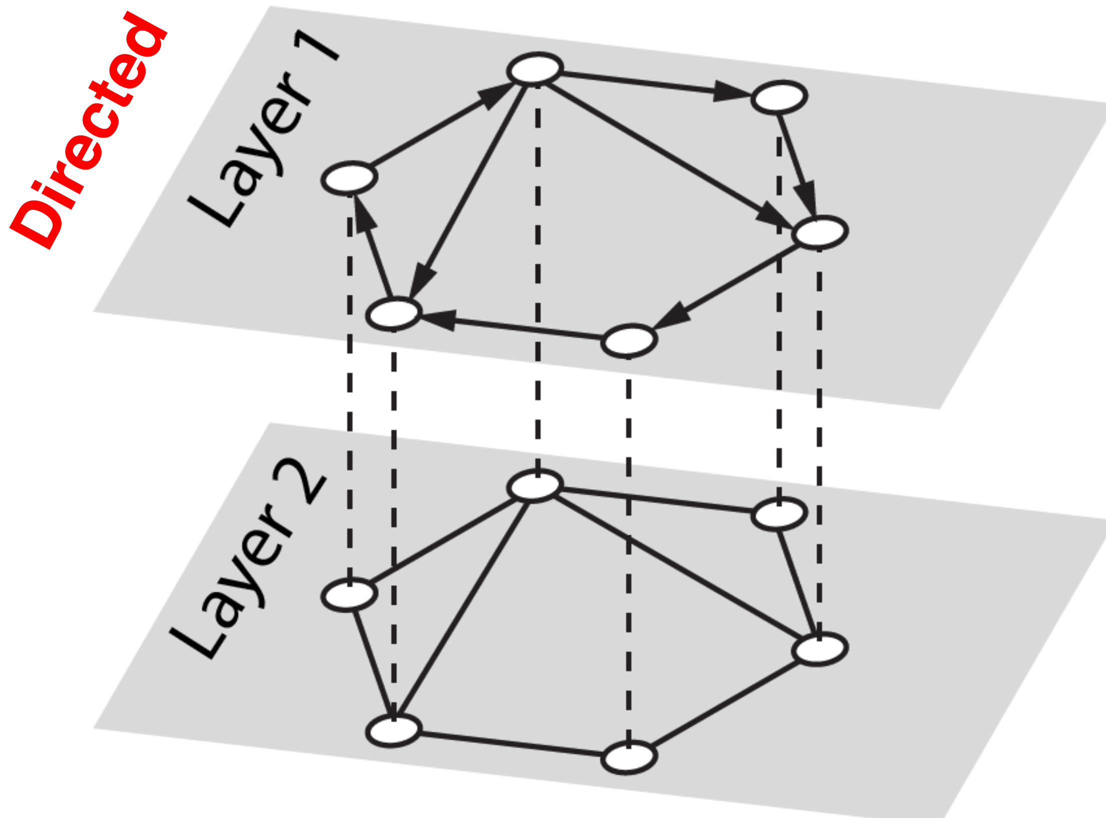

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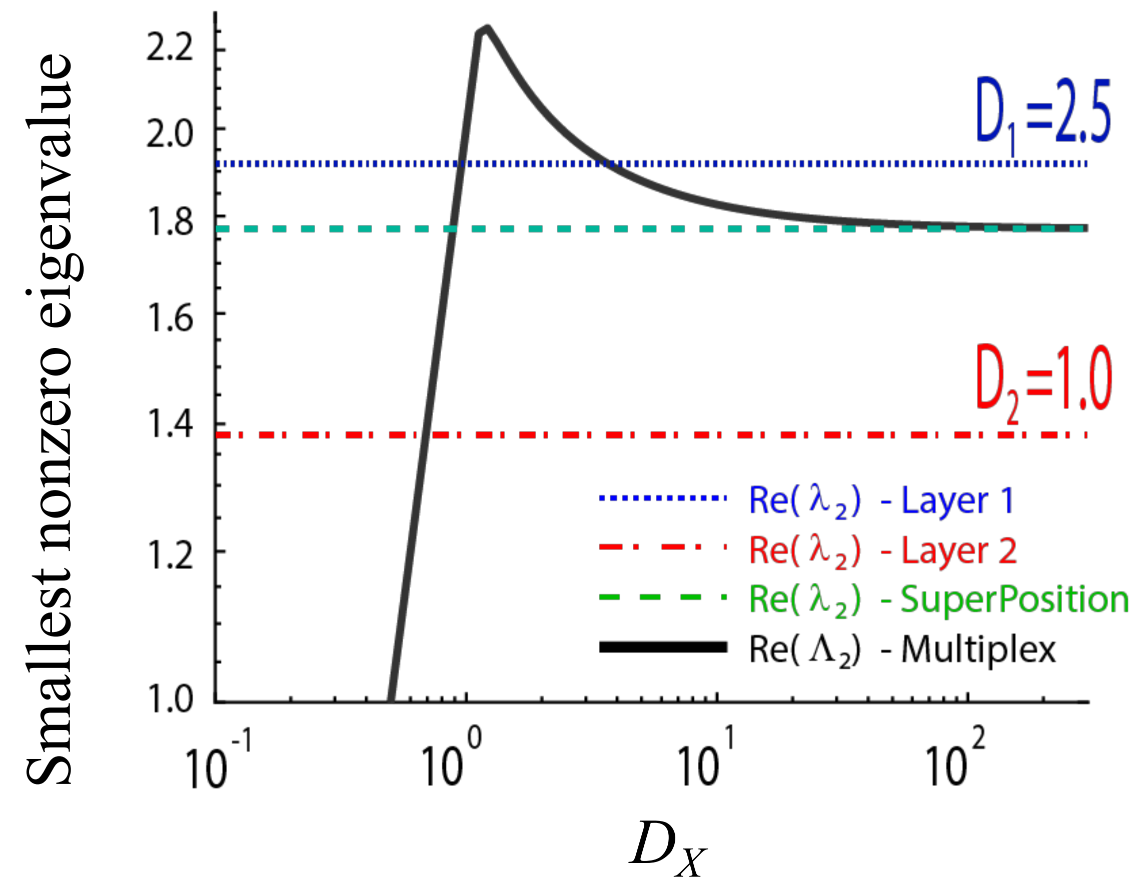

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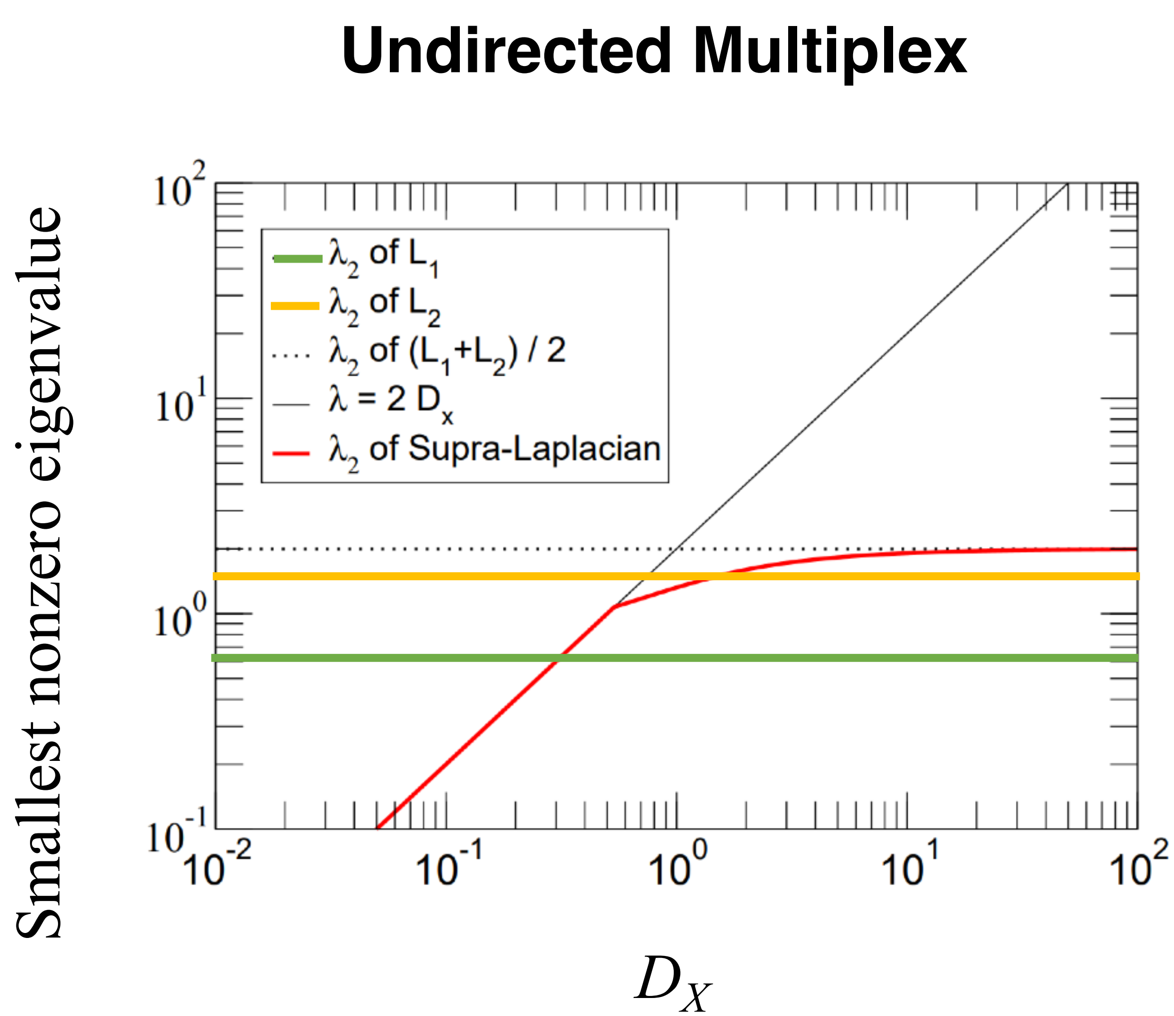

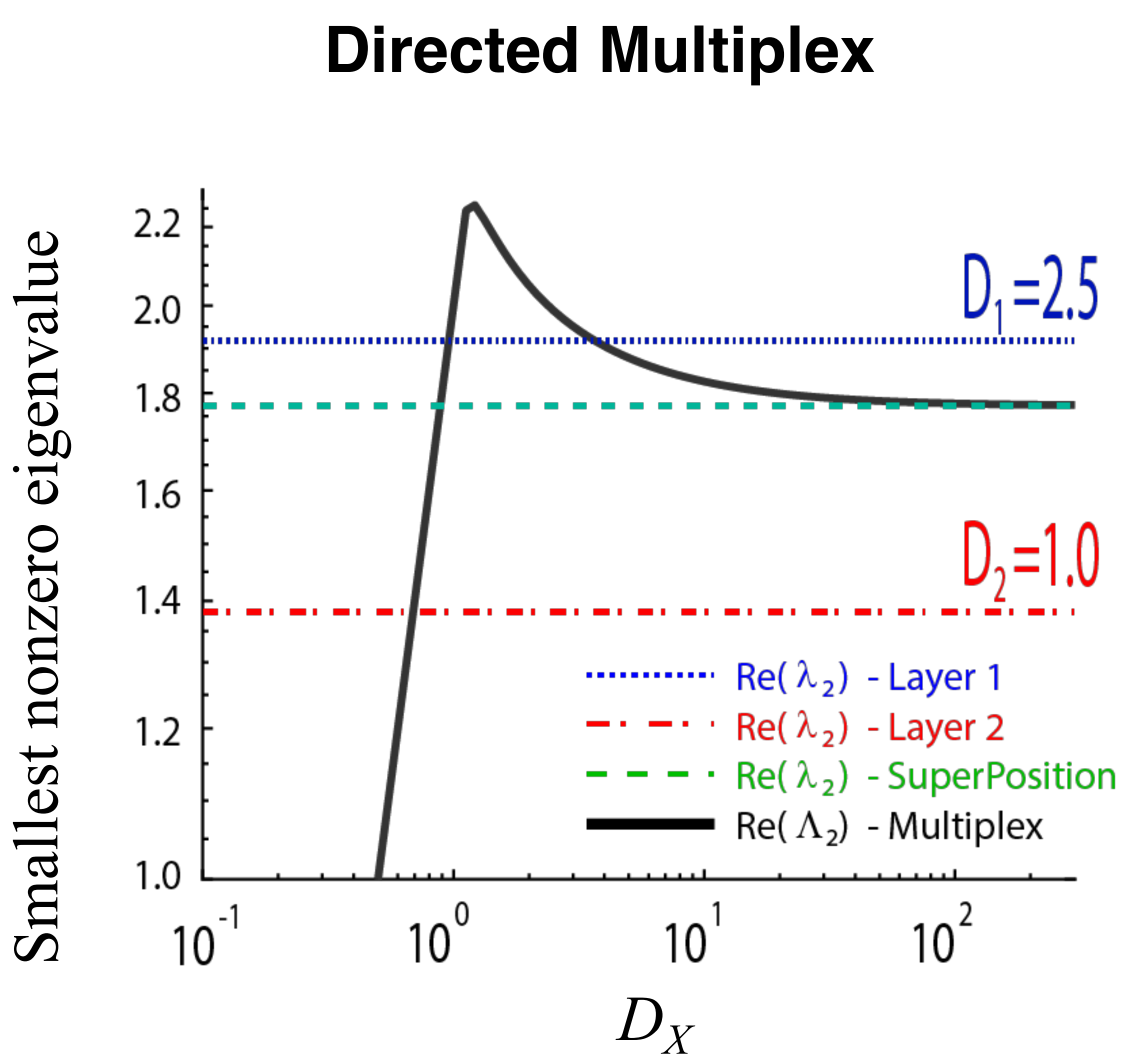

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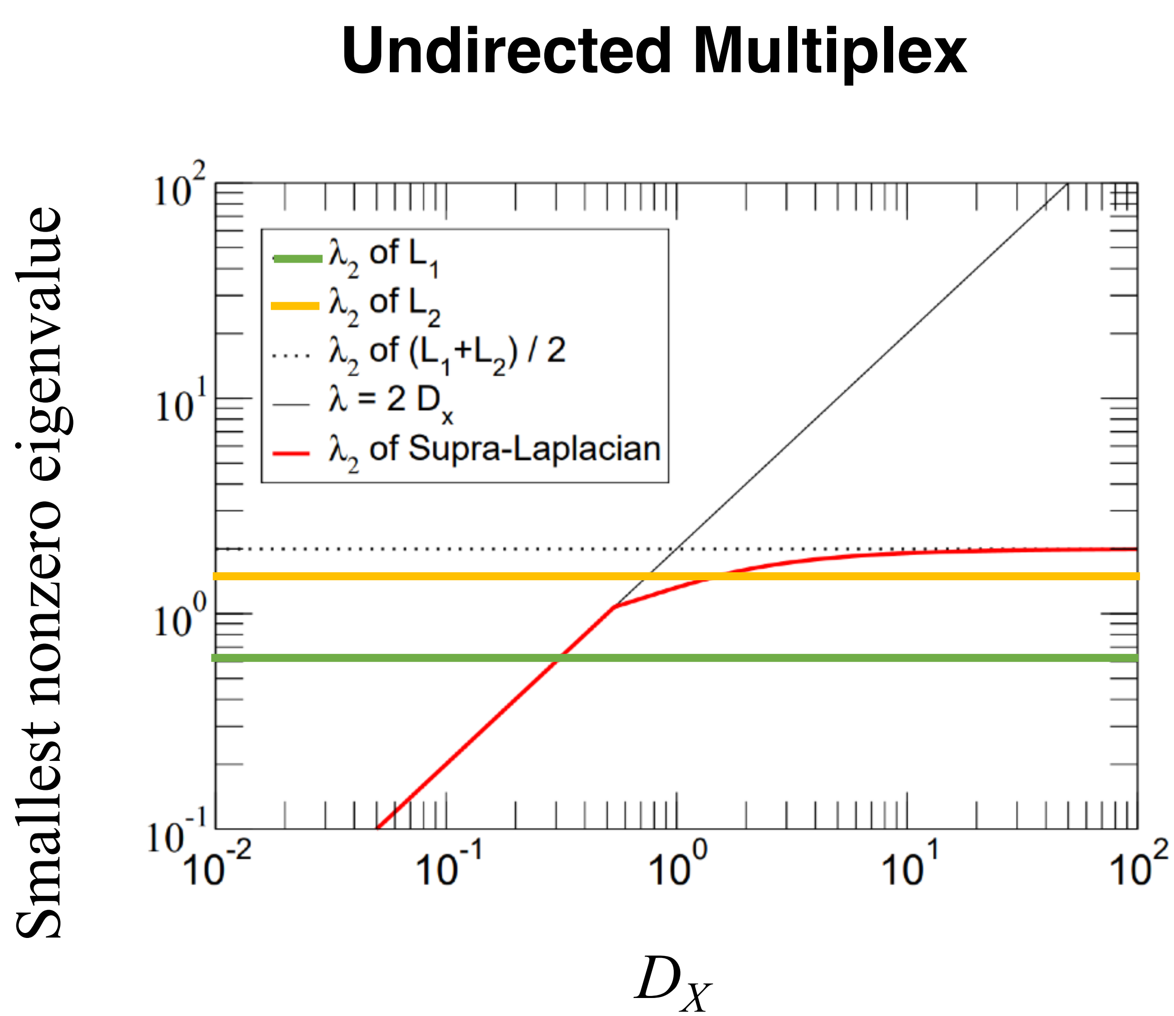

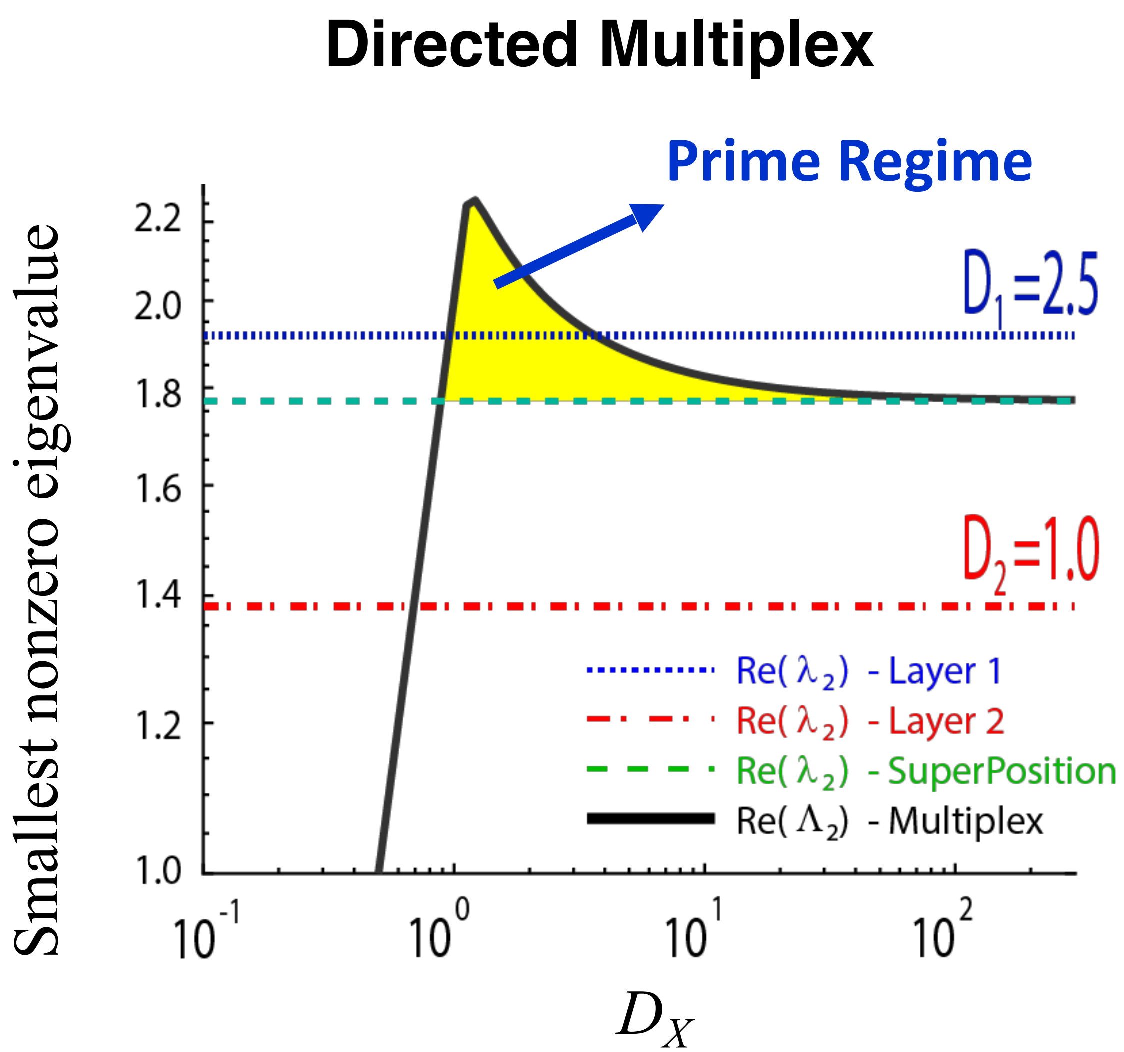

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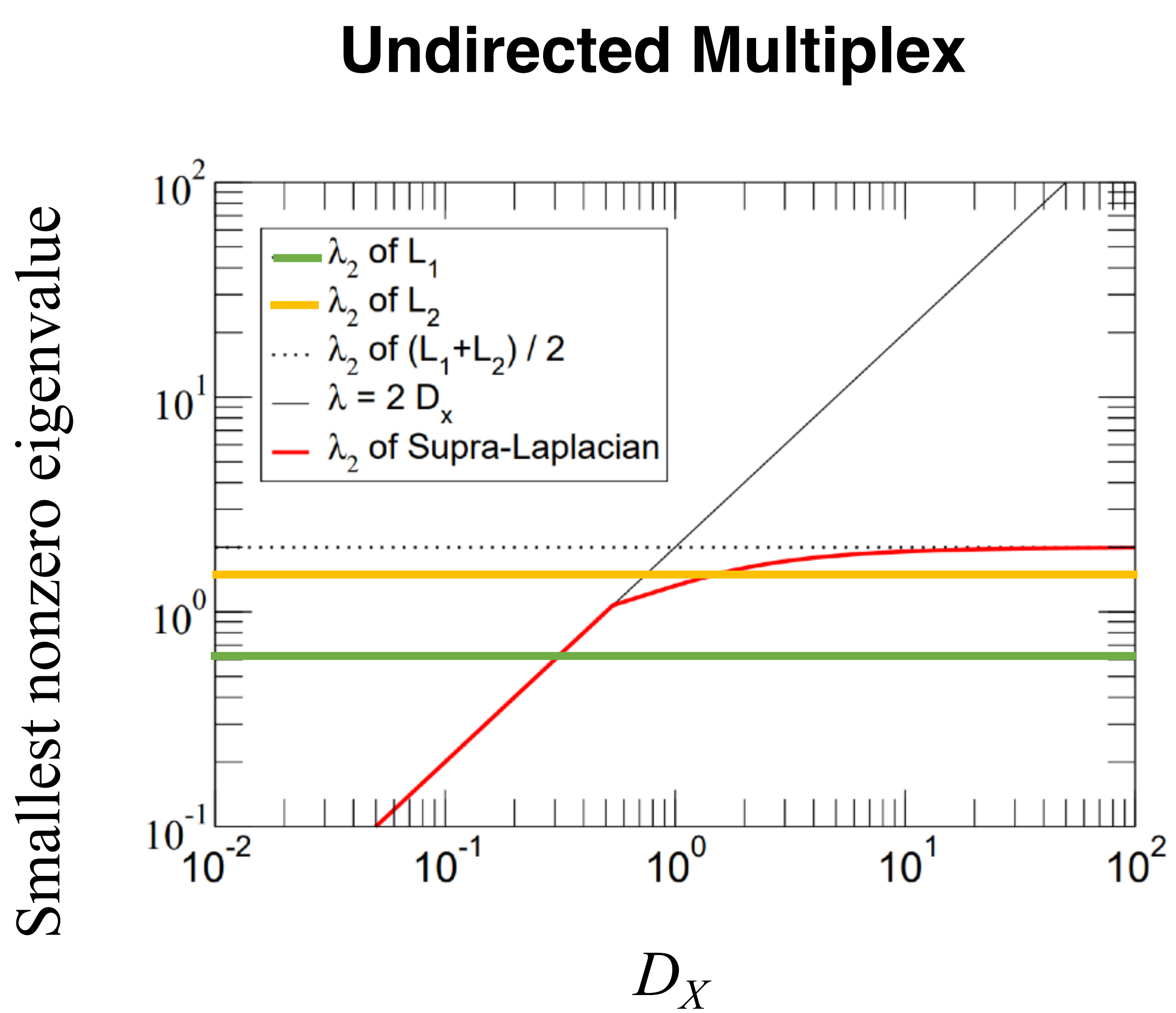

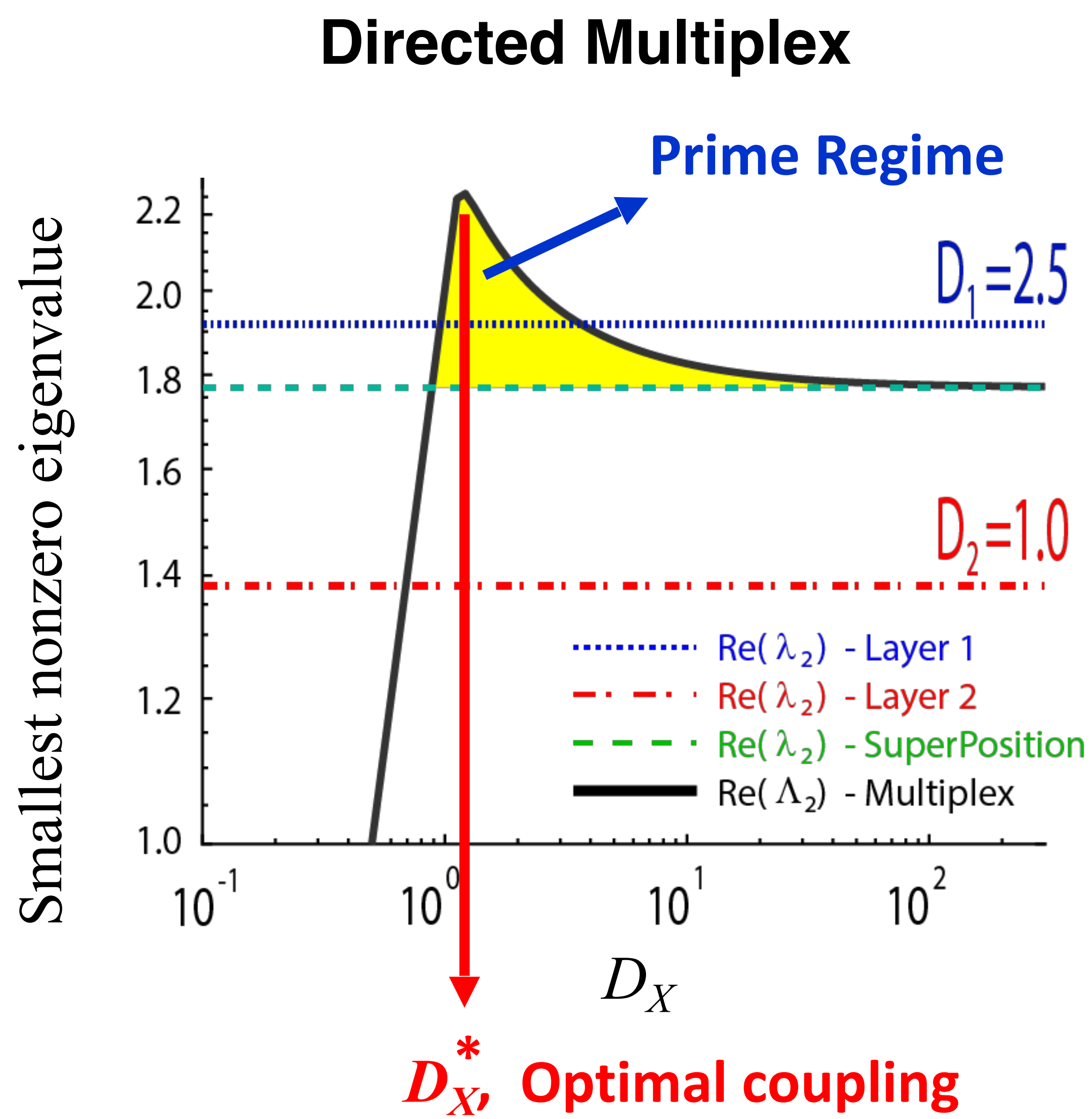

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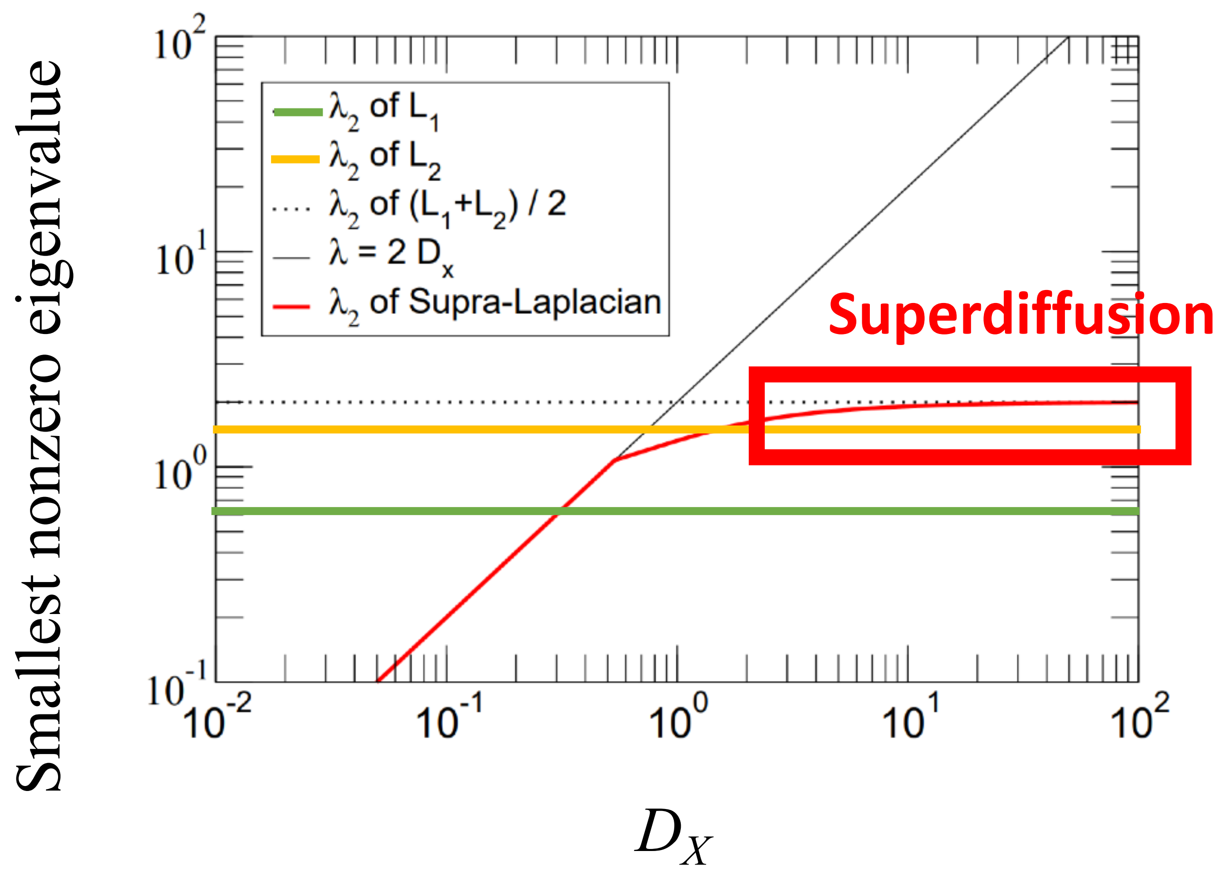
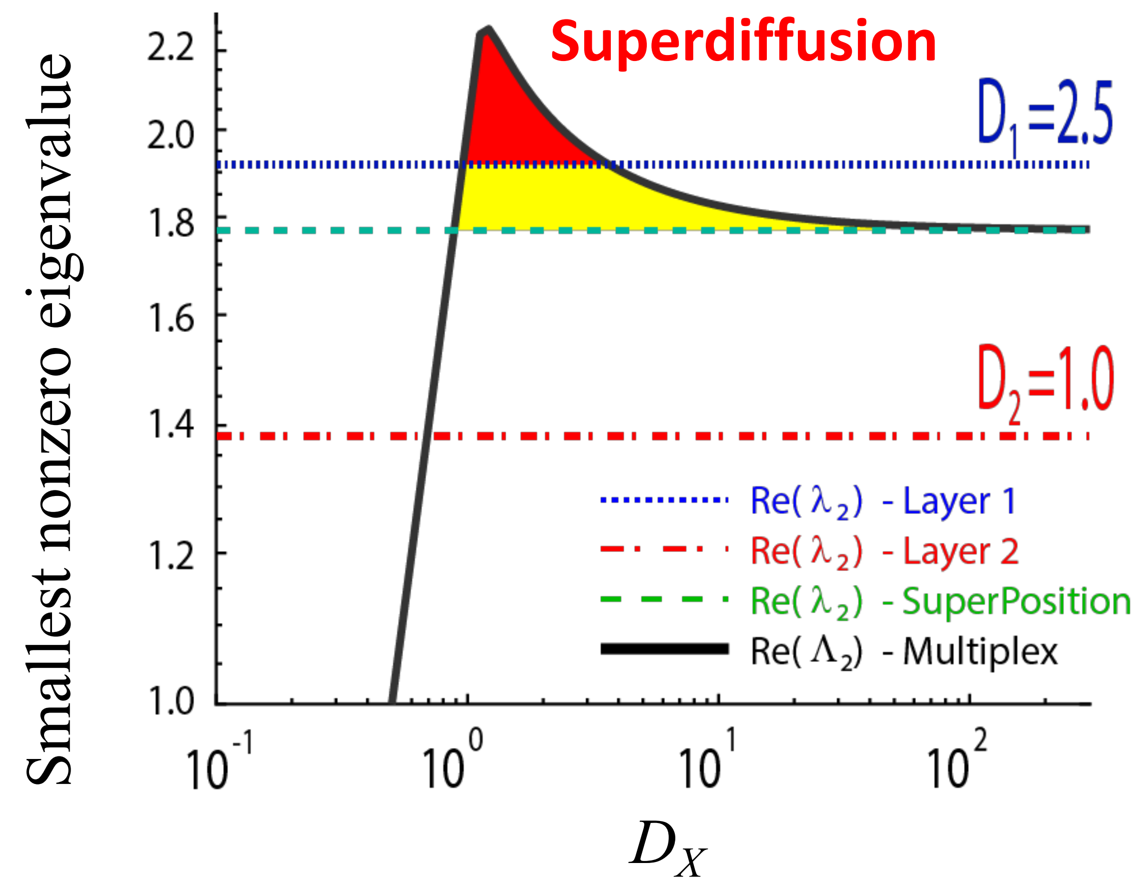
Diffusion Dynamics on Directed Multiplex

Undirected Multiplex



Directed Multiplex



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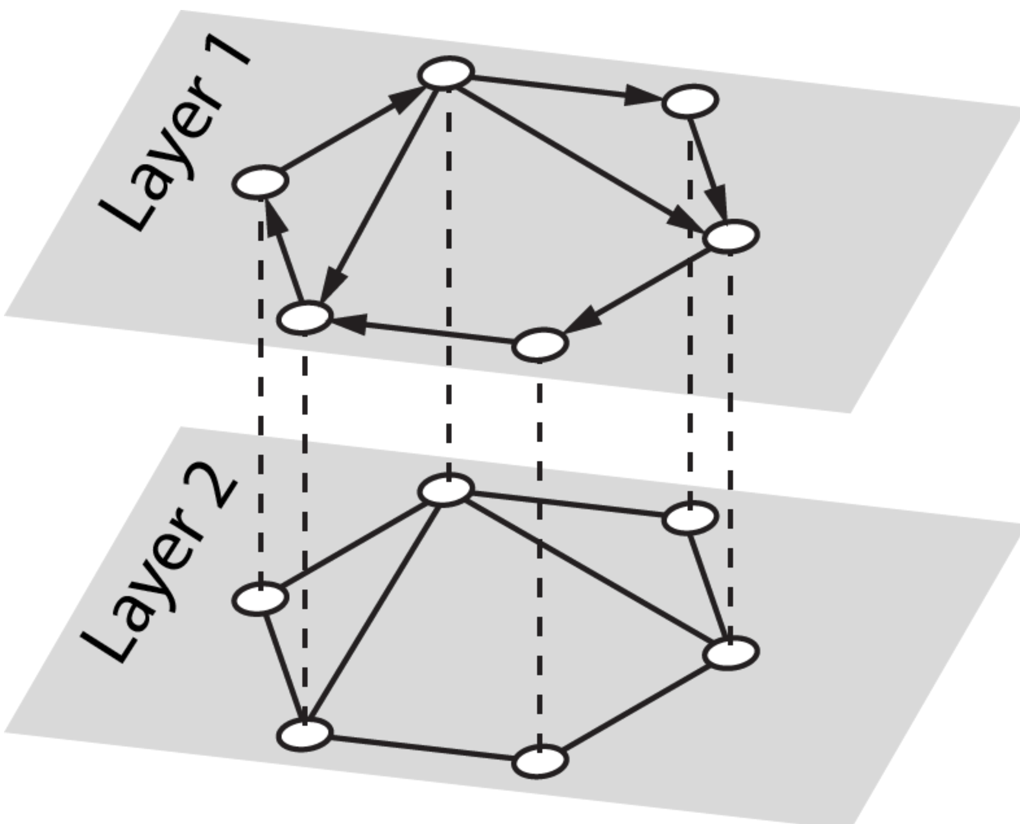

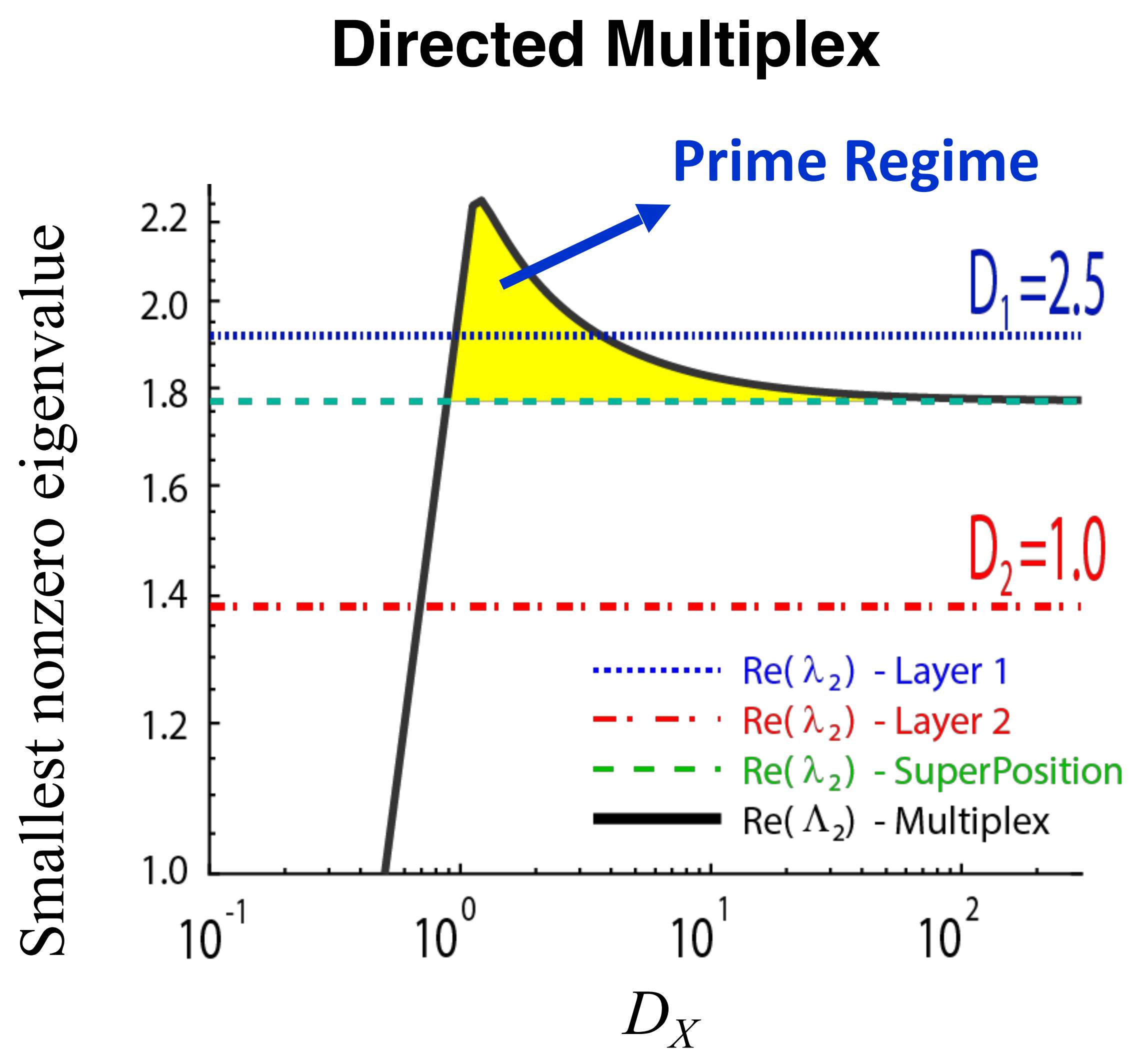

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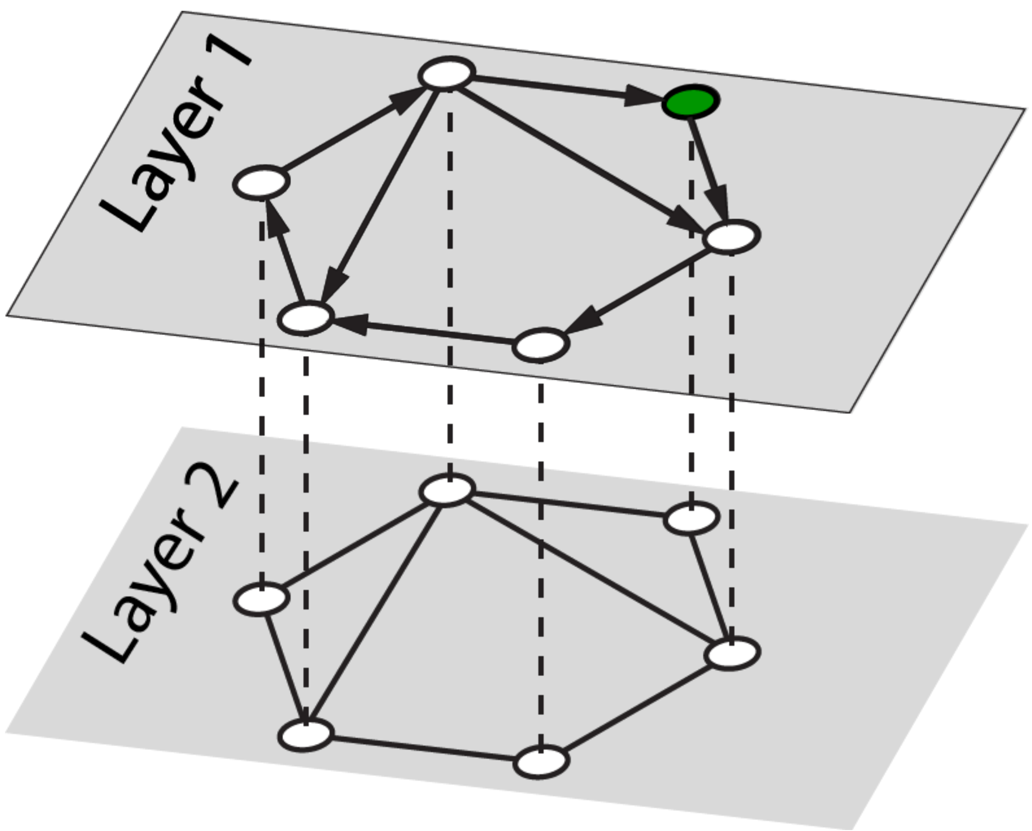

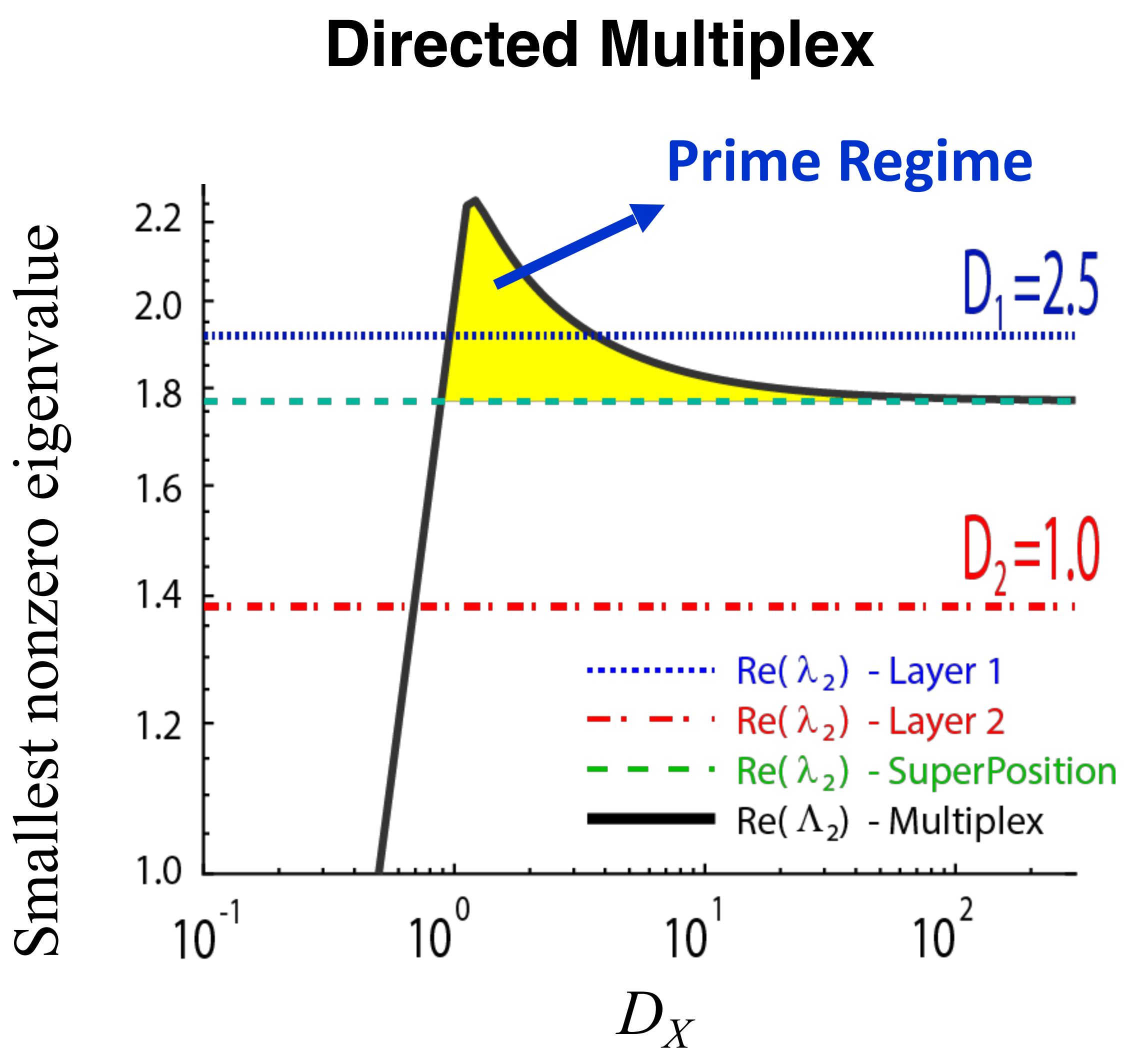

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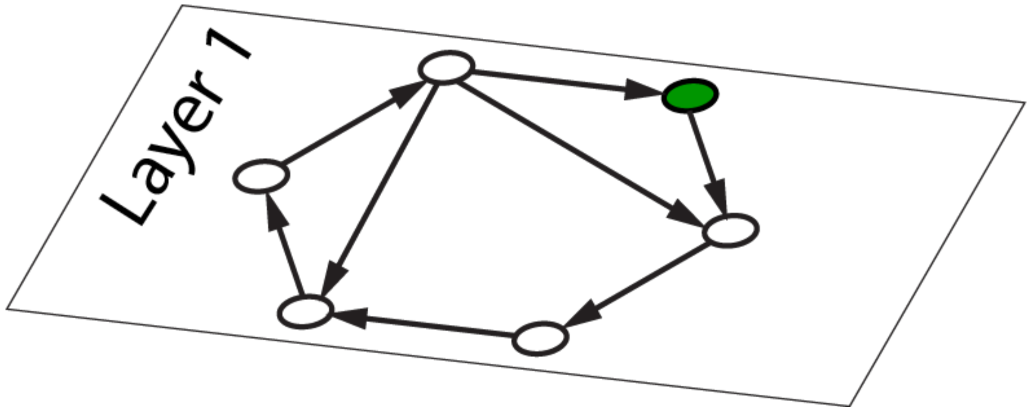
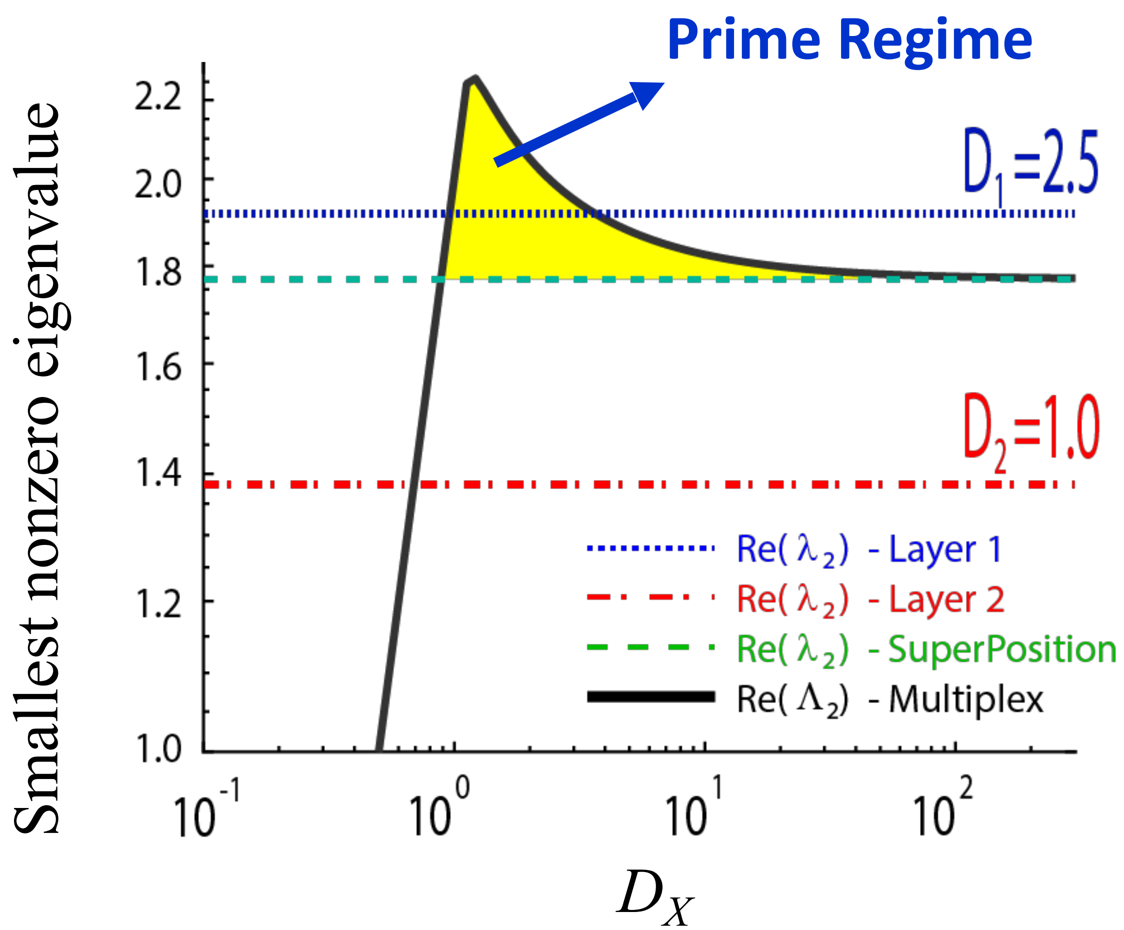


Directed Multiplex



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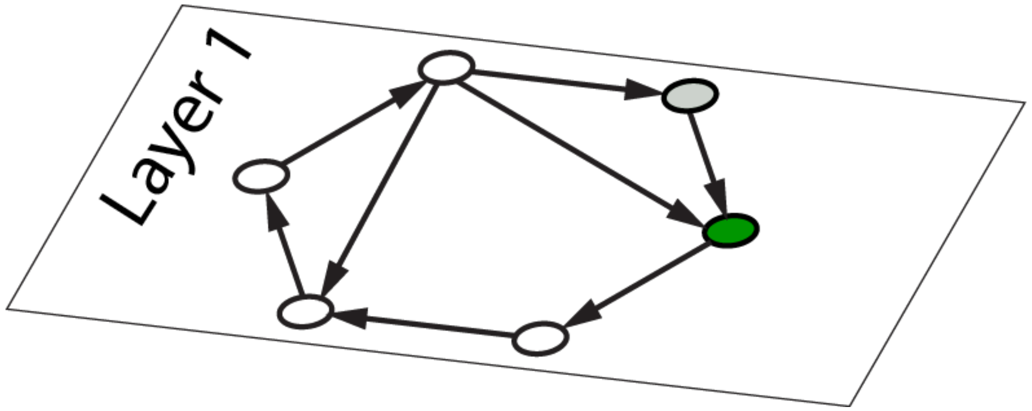

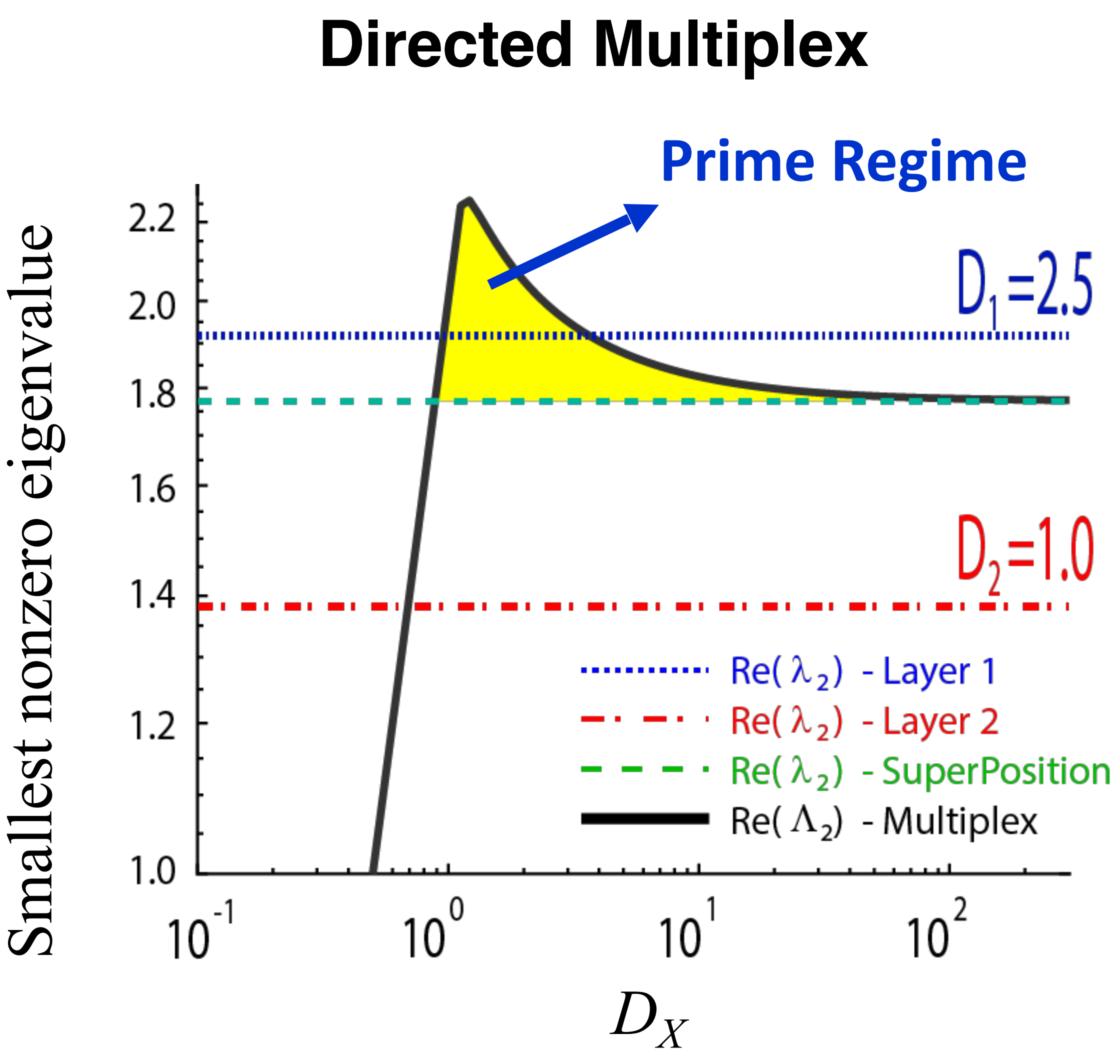

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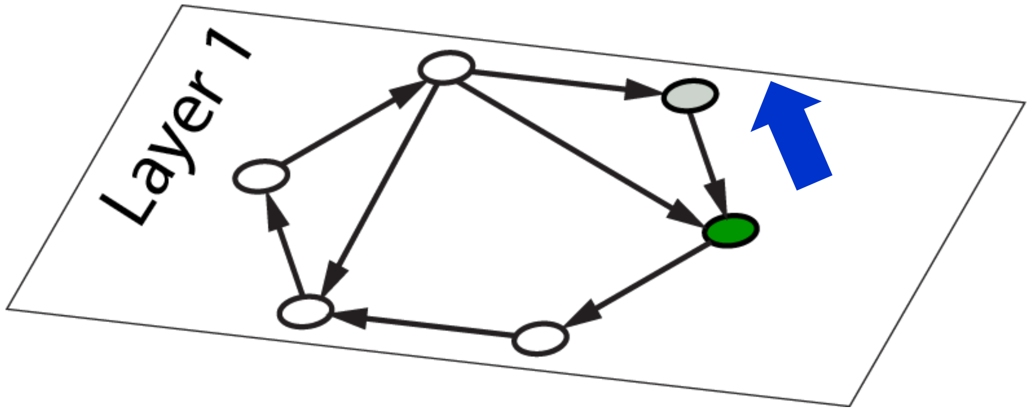

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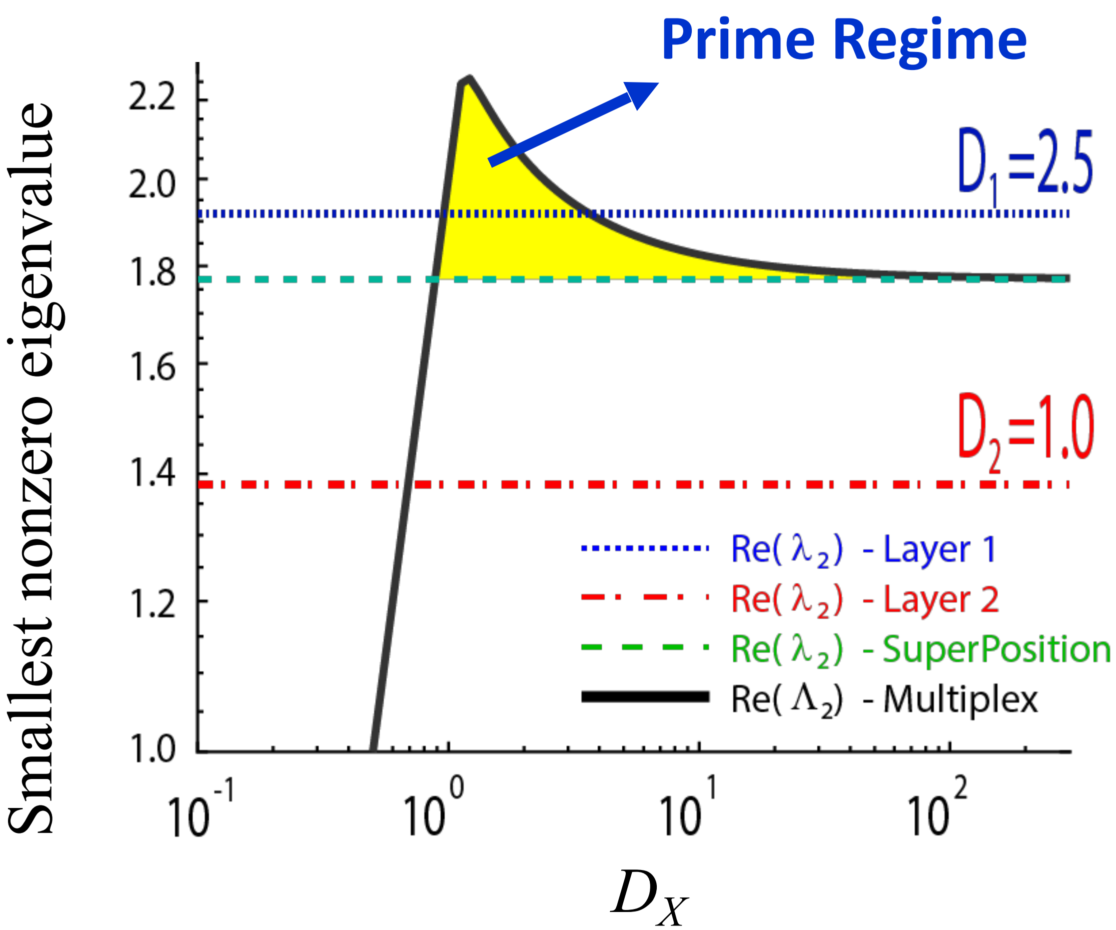

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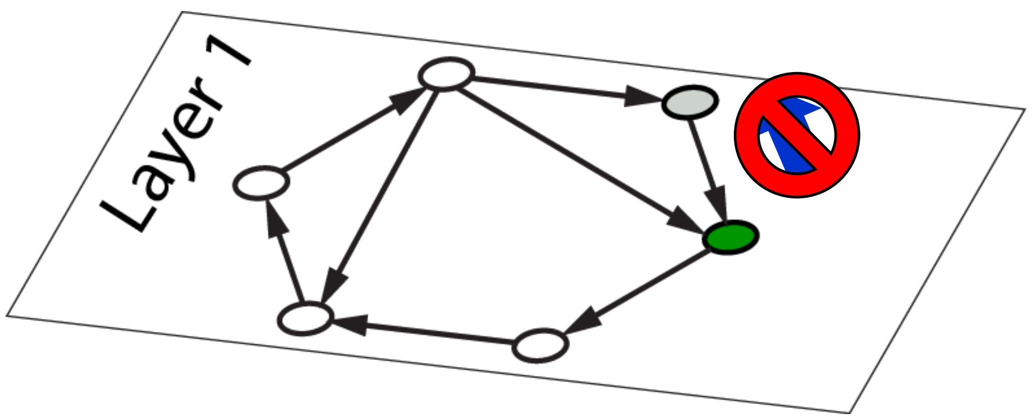

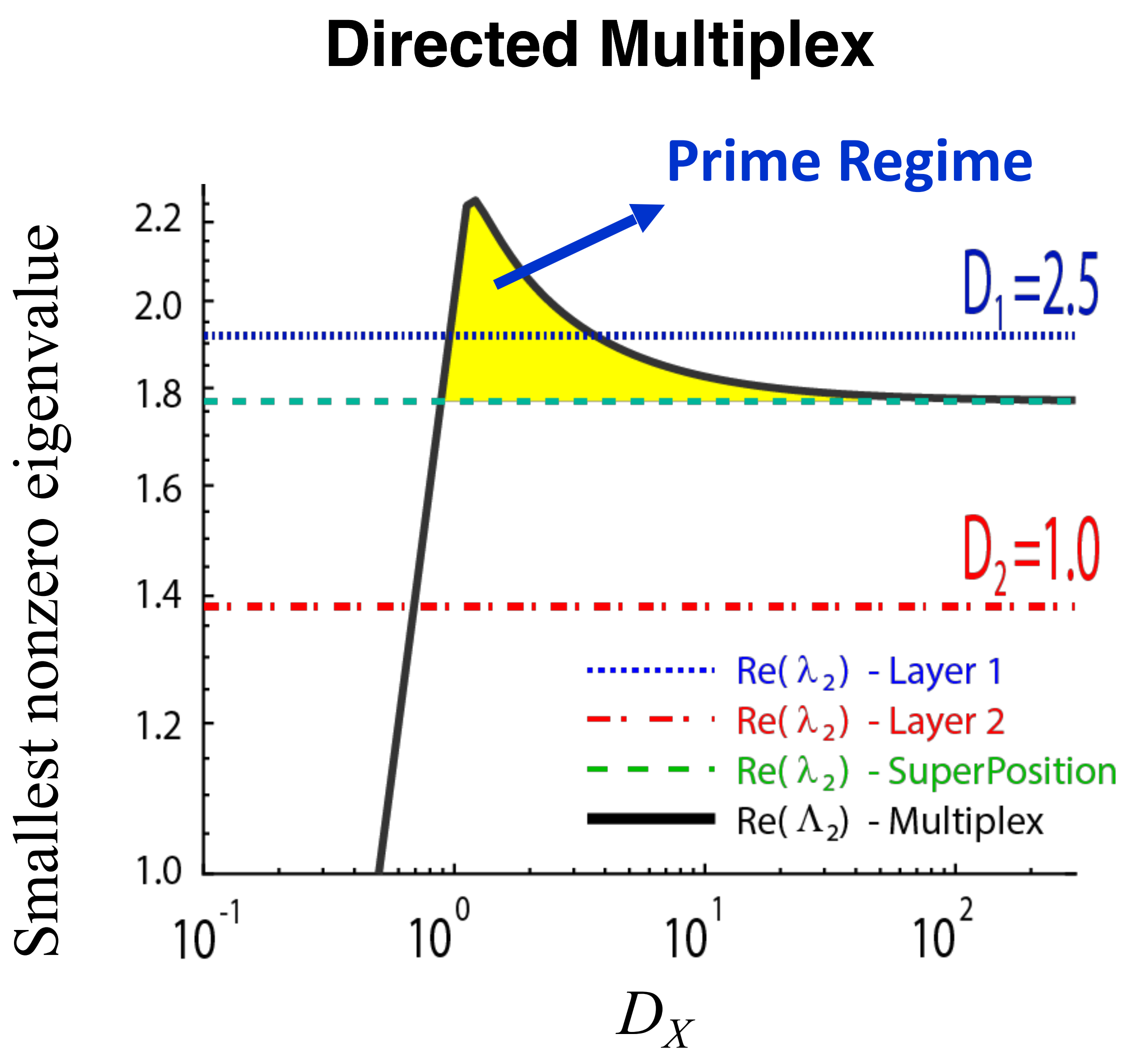

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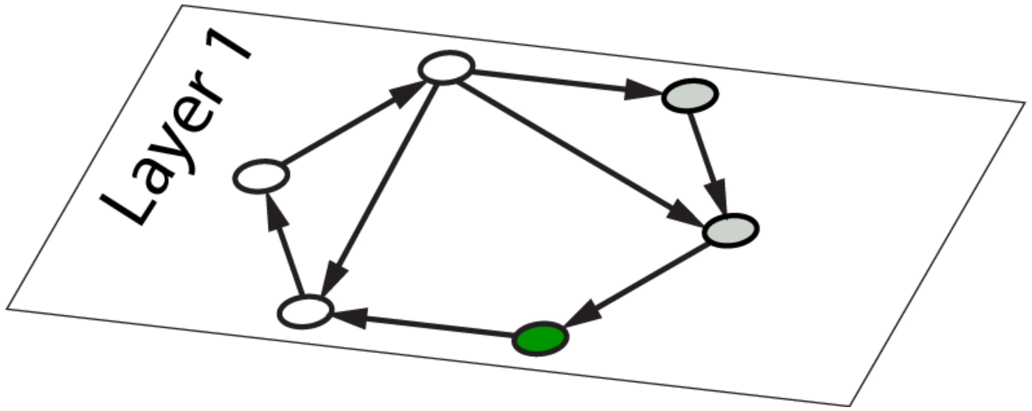

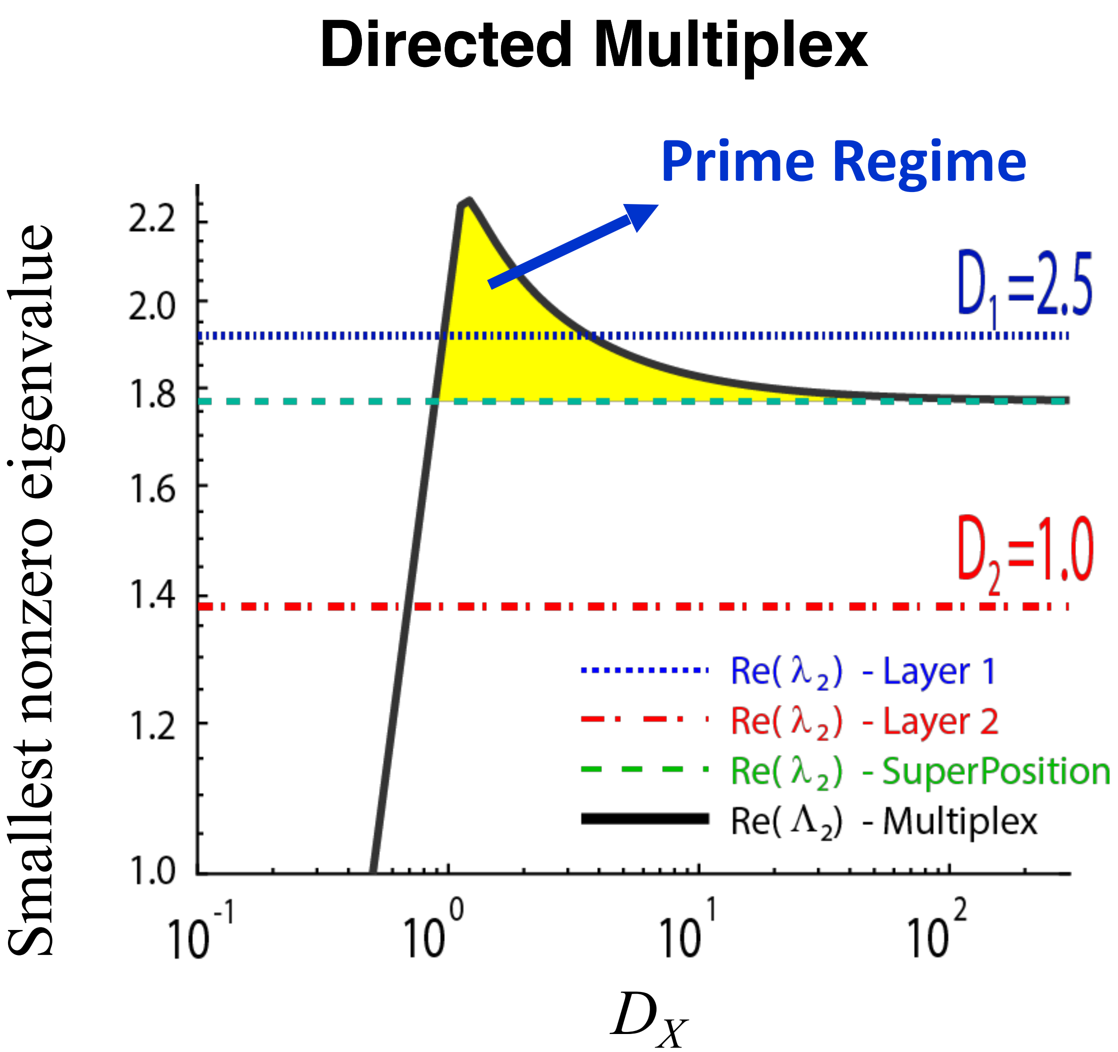

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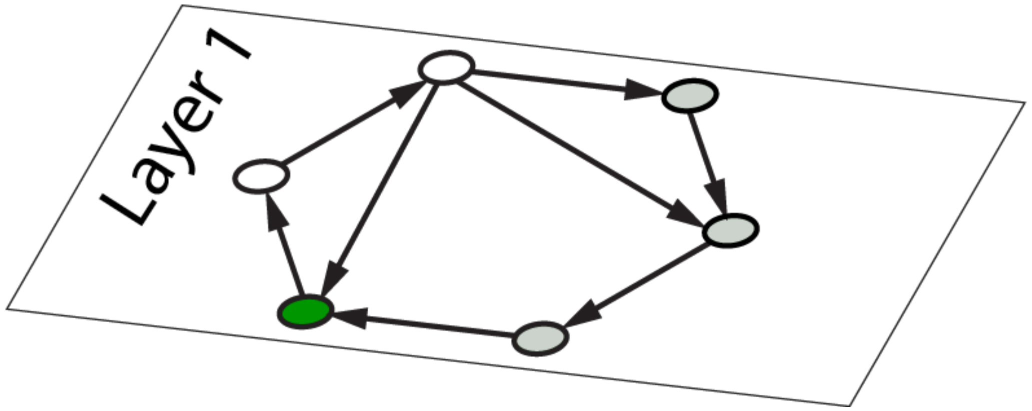

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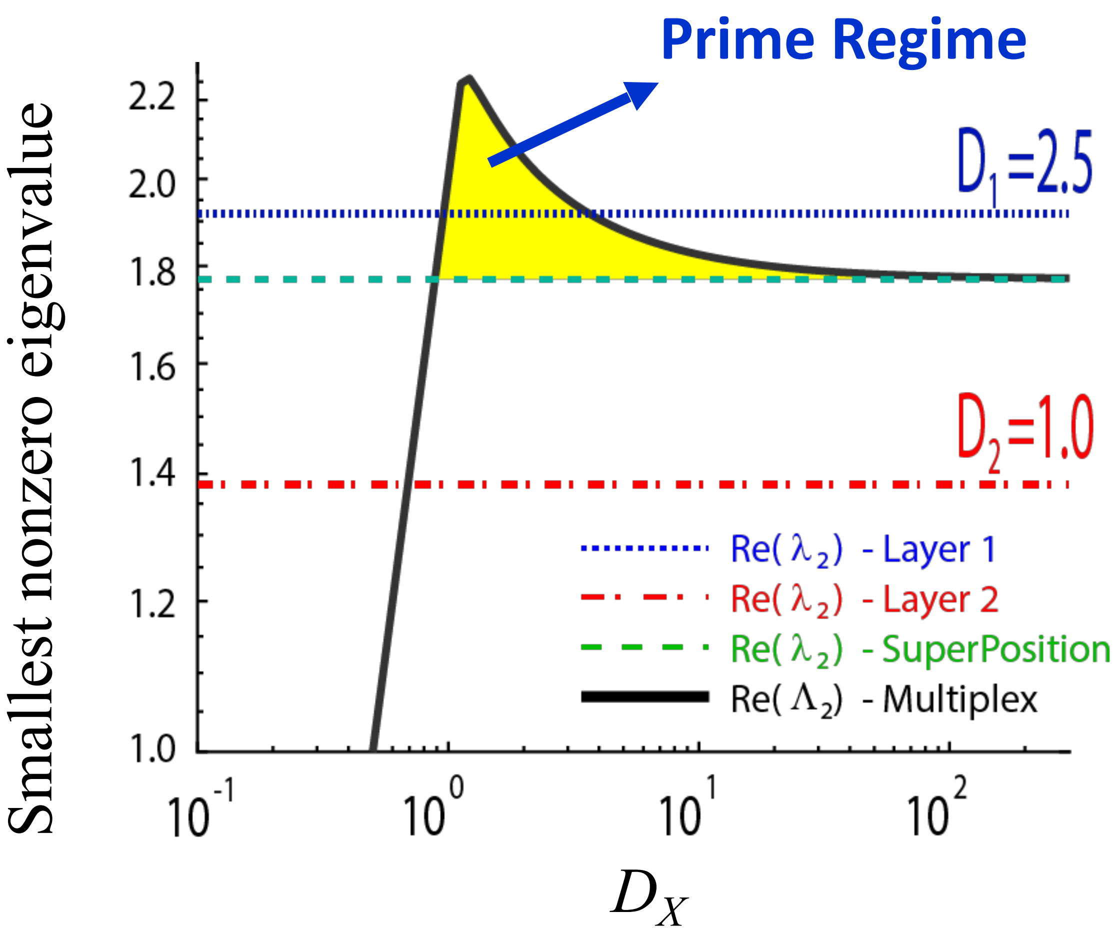

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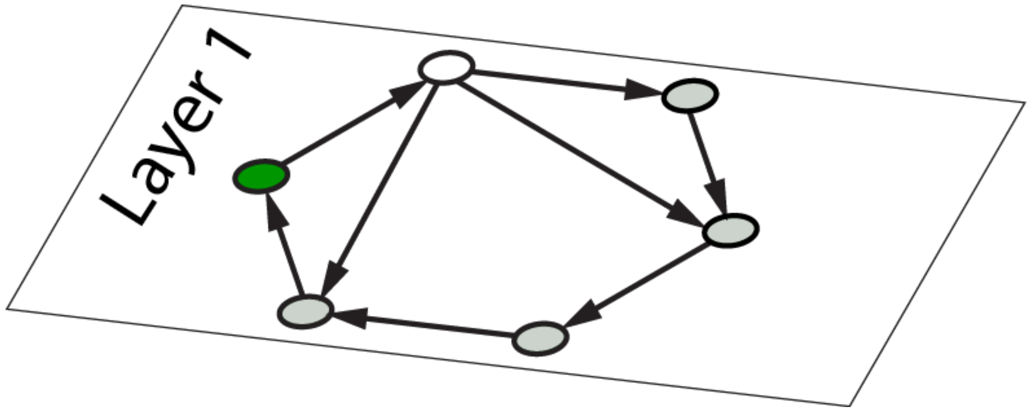

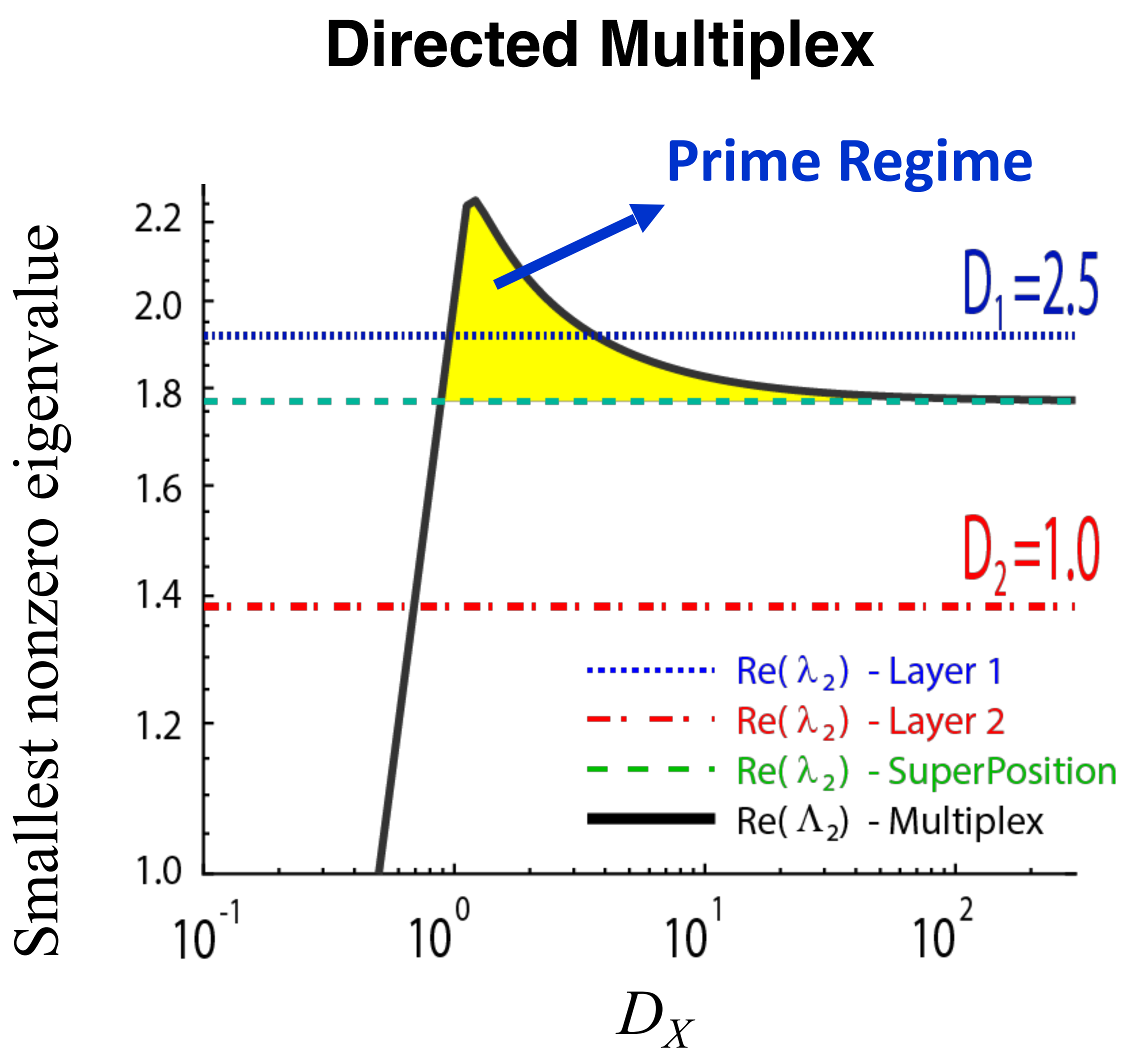

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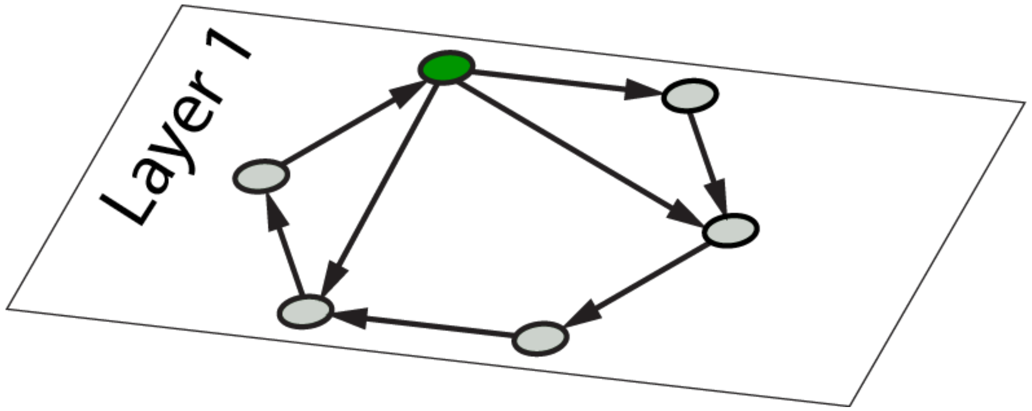

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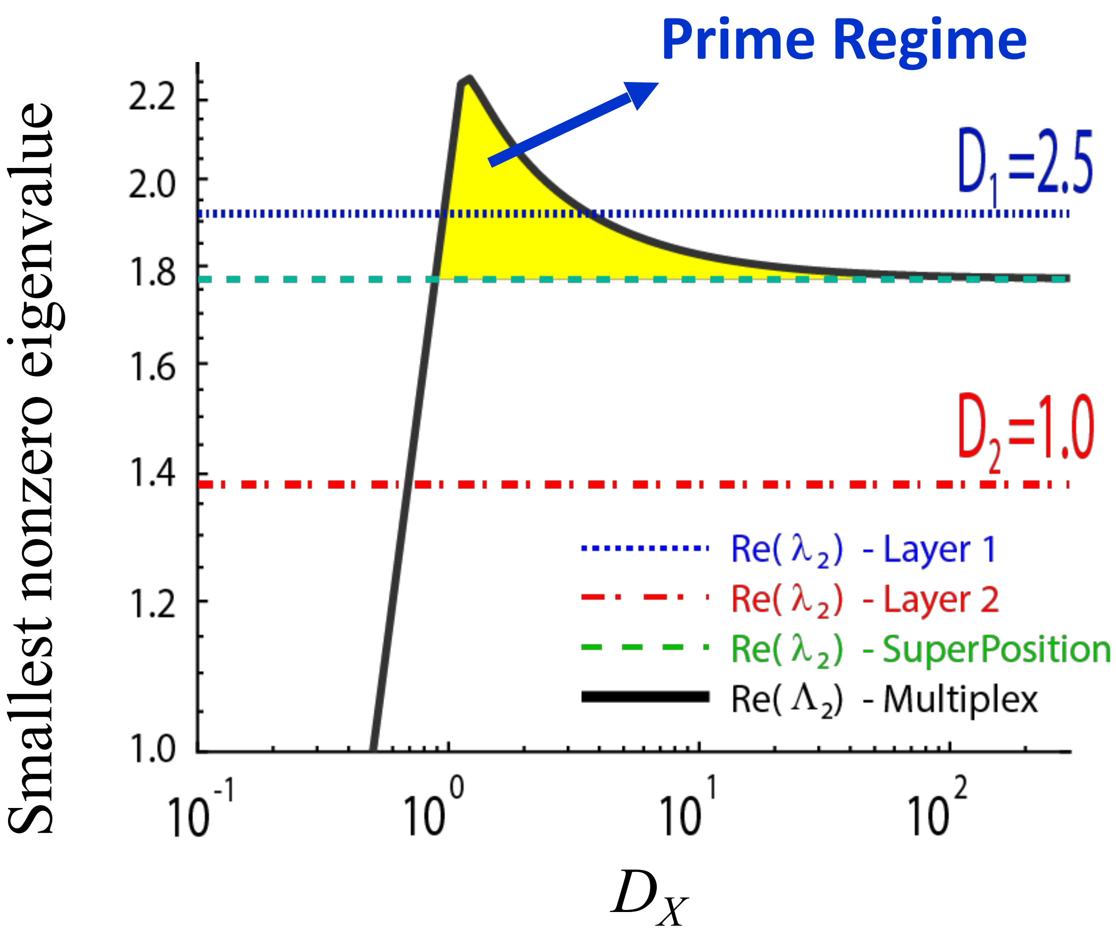

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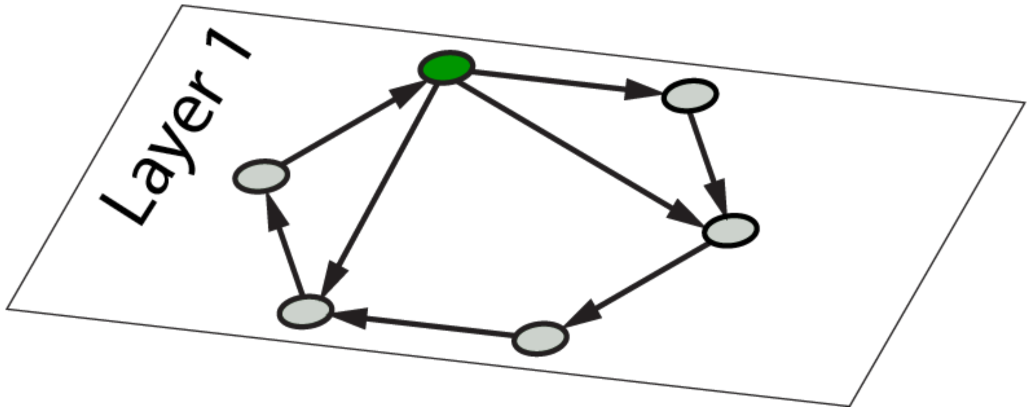

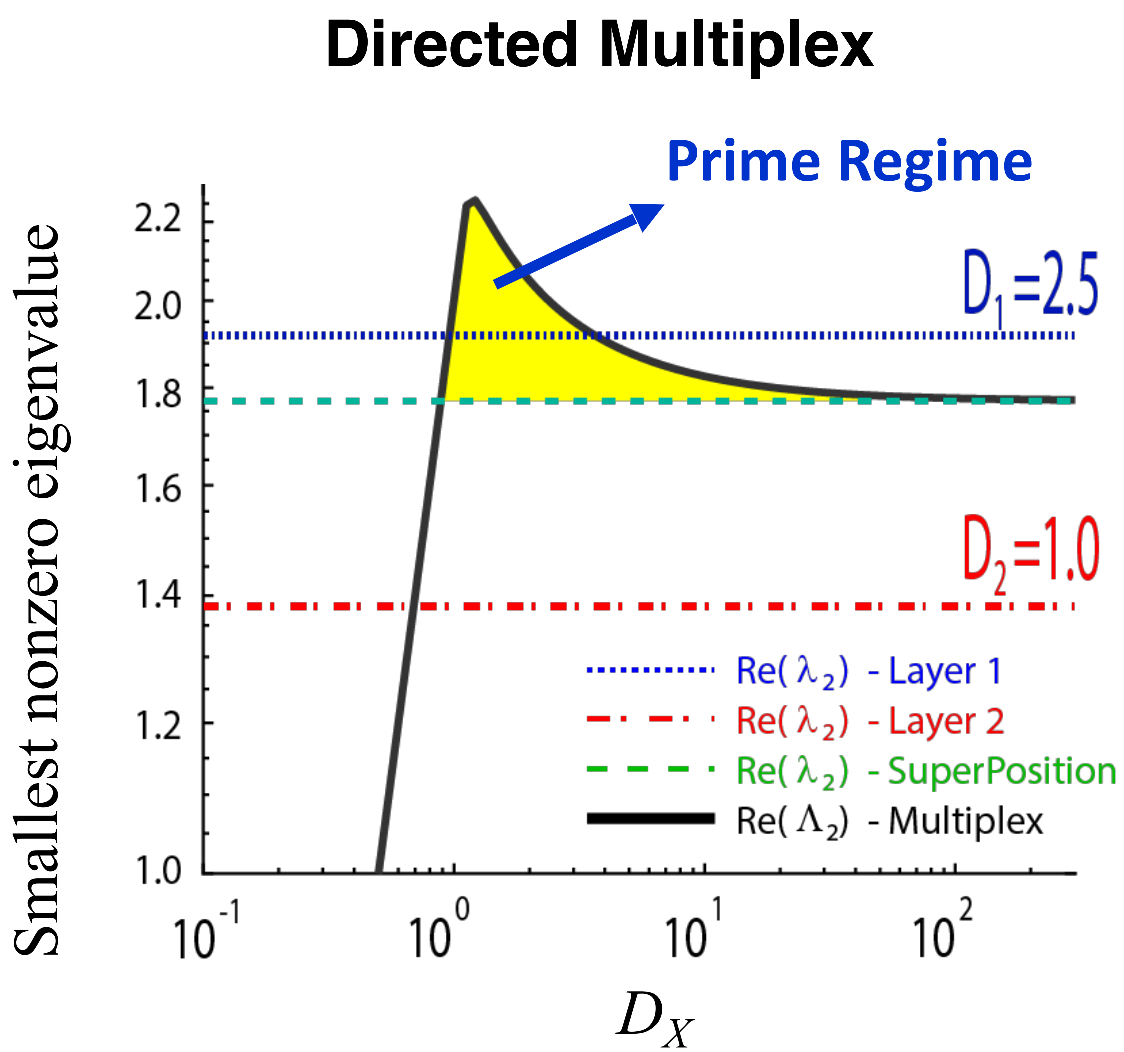

Faster Node Exploration

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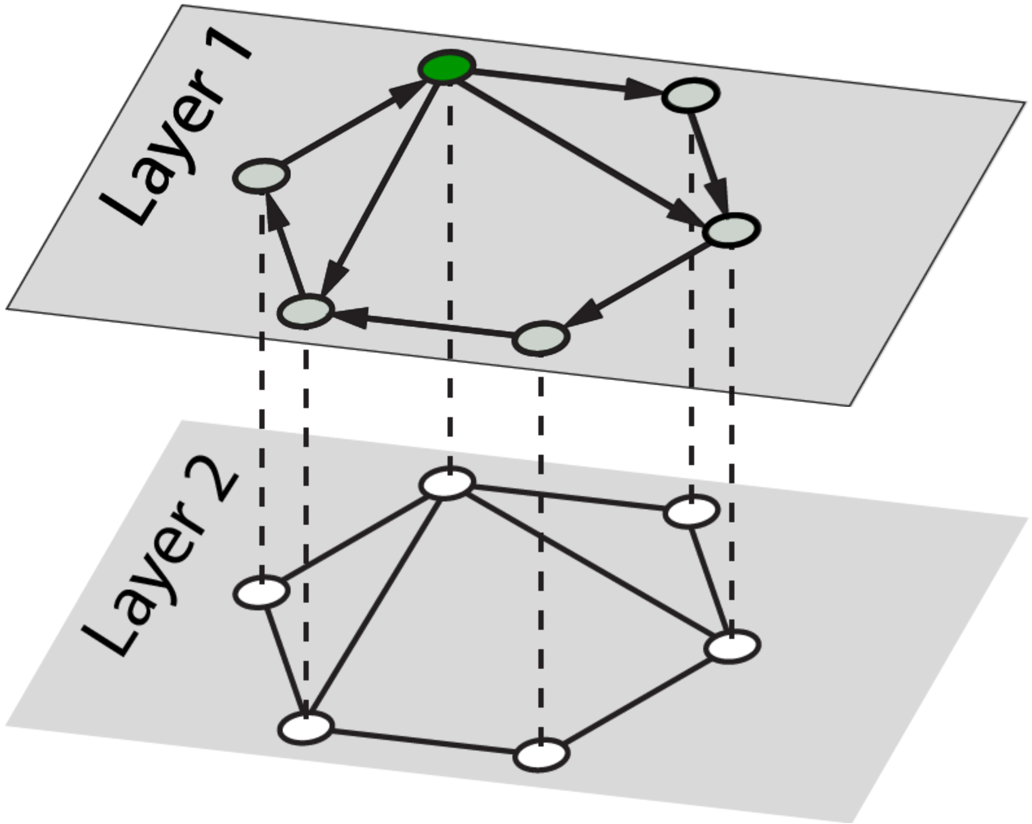

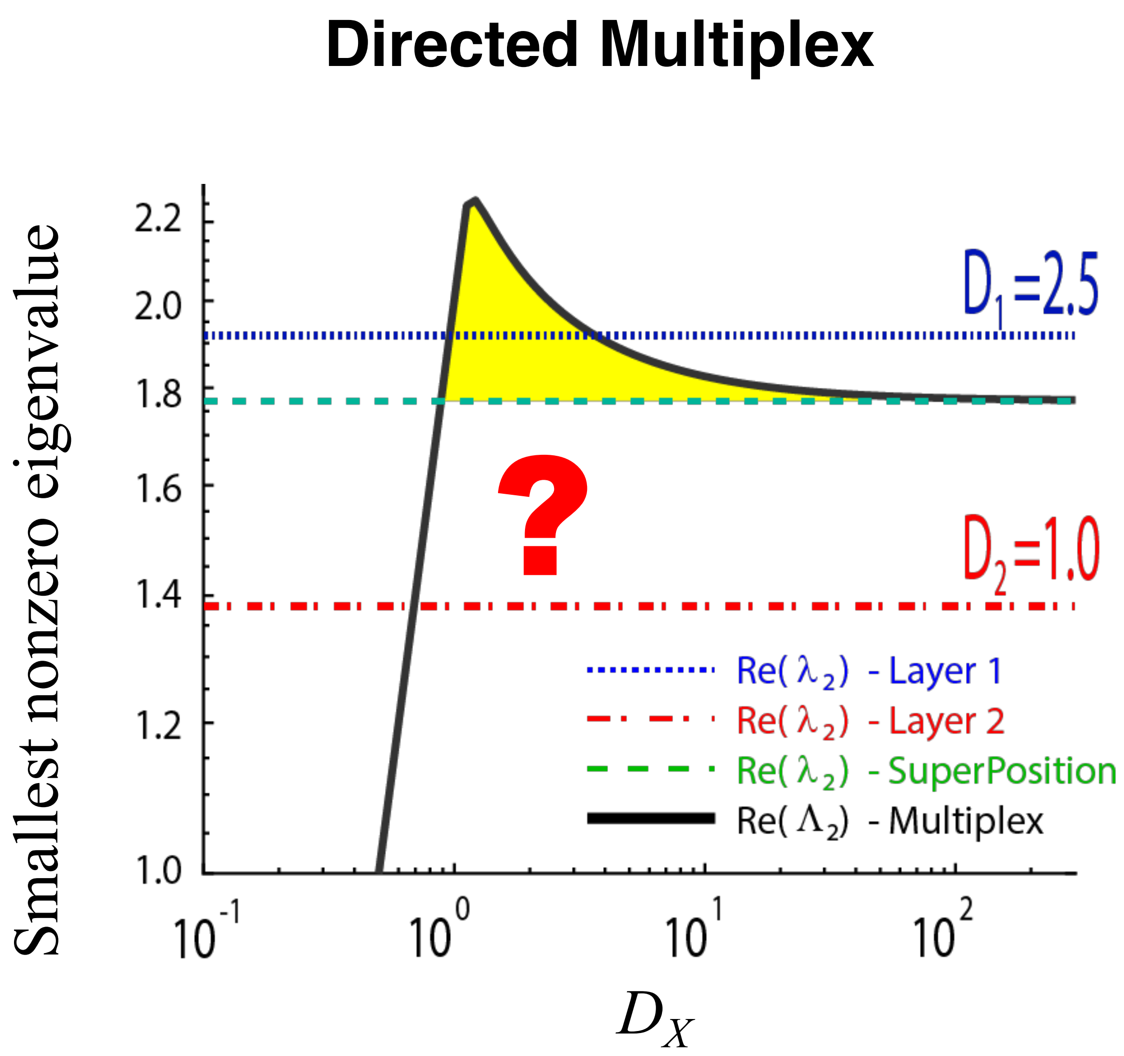

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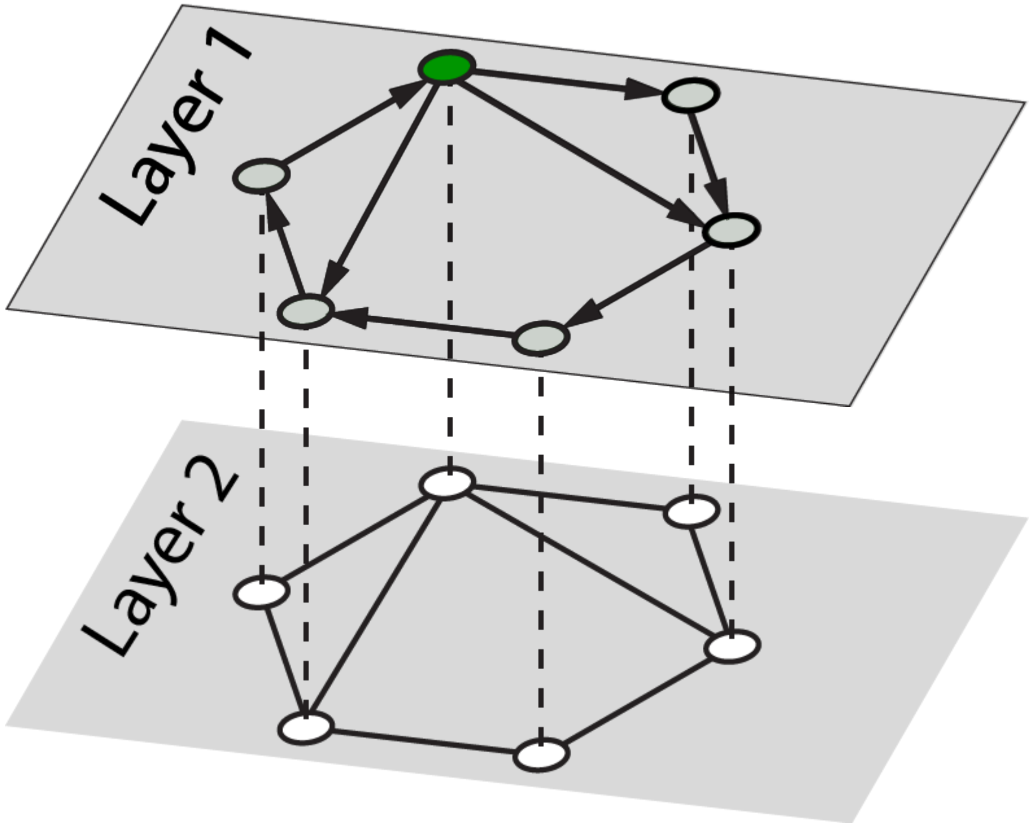

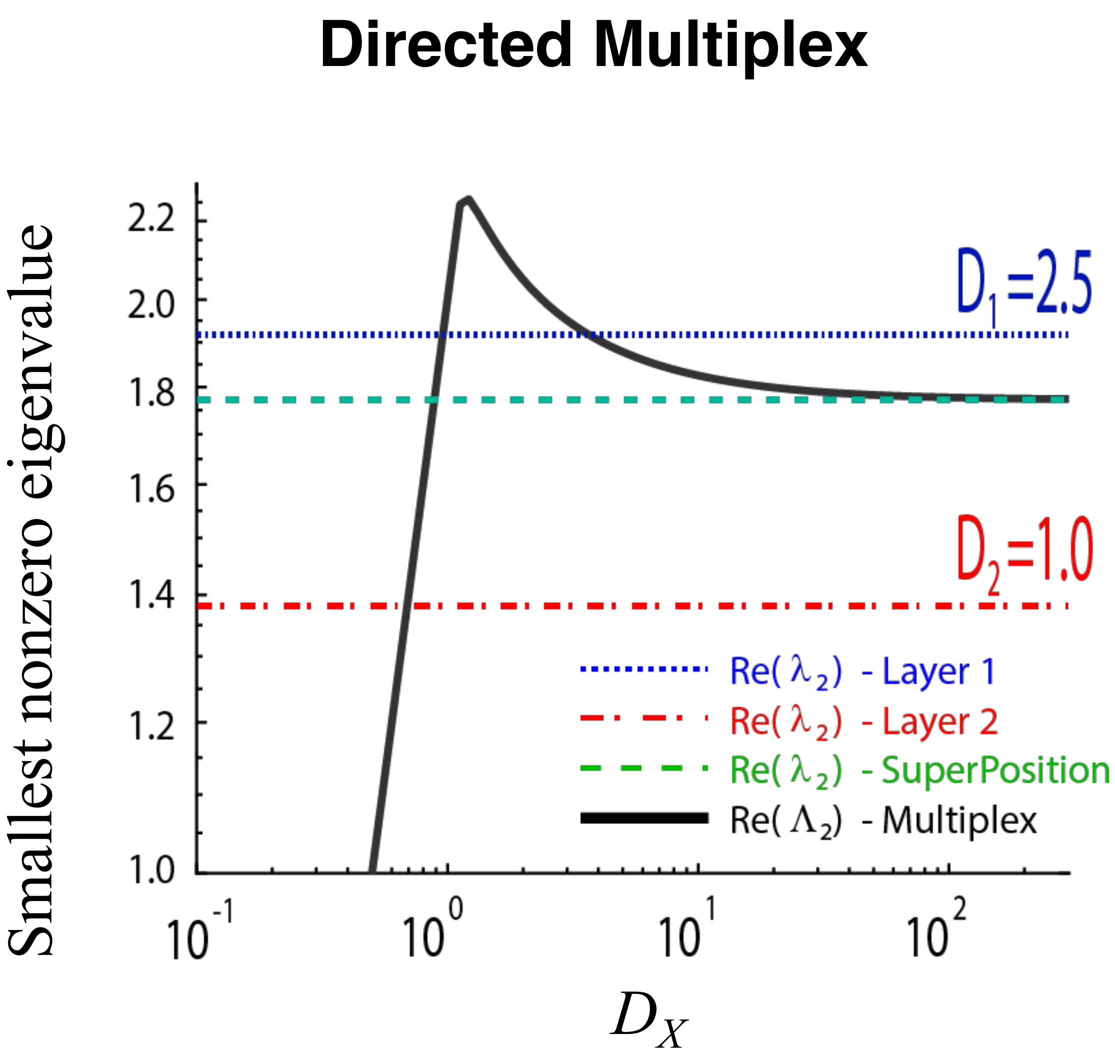

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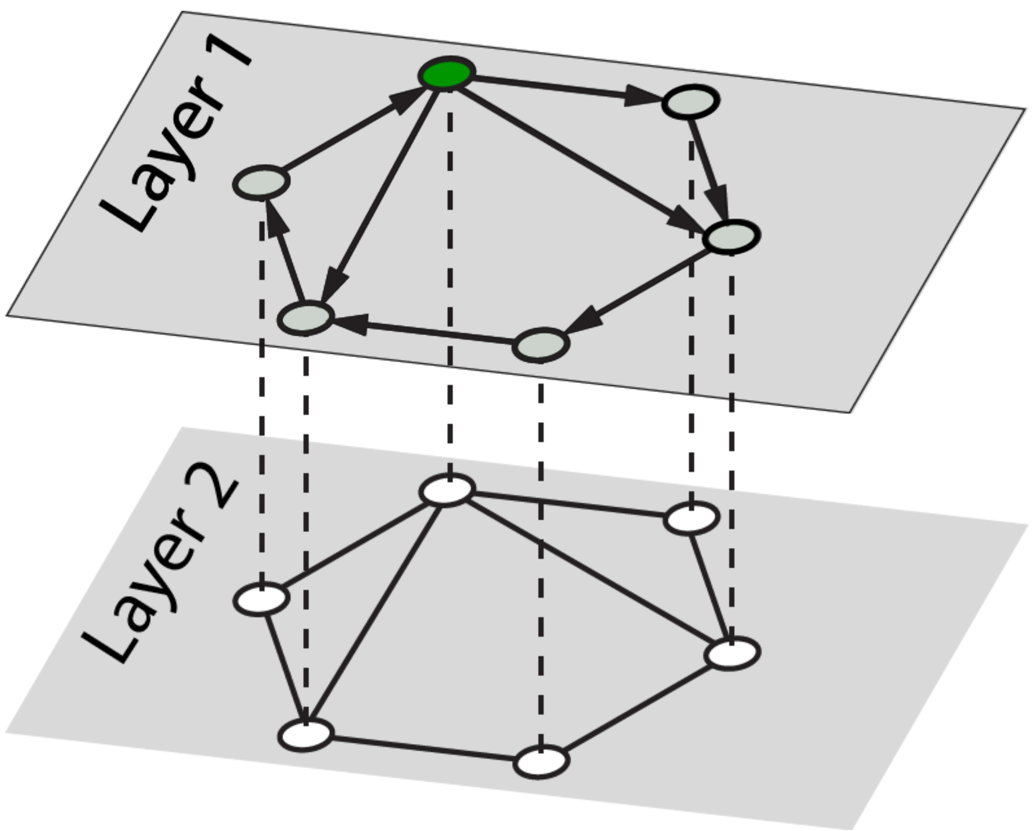

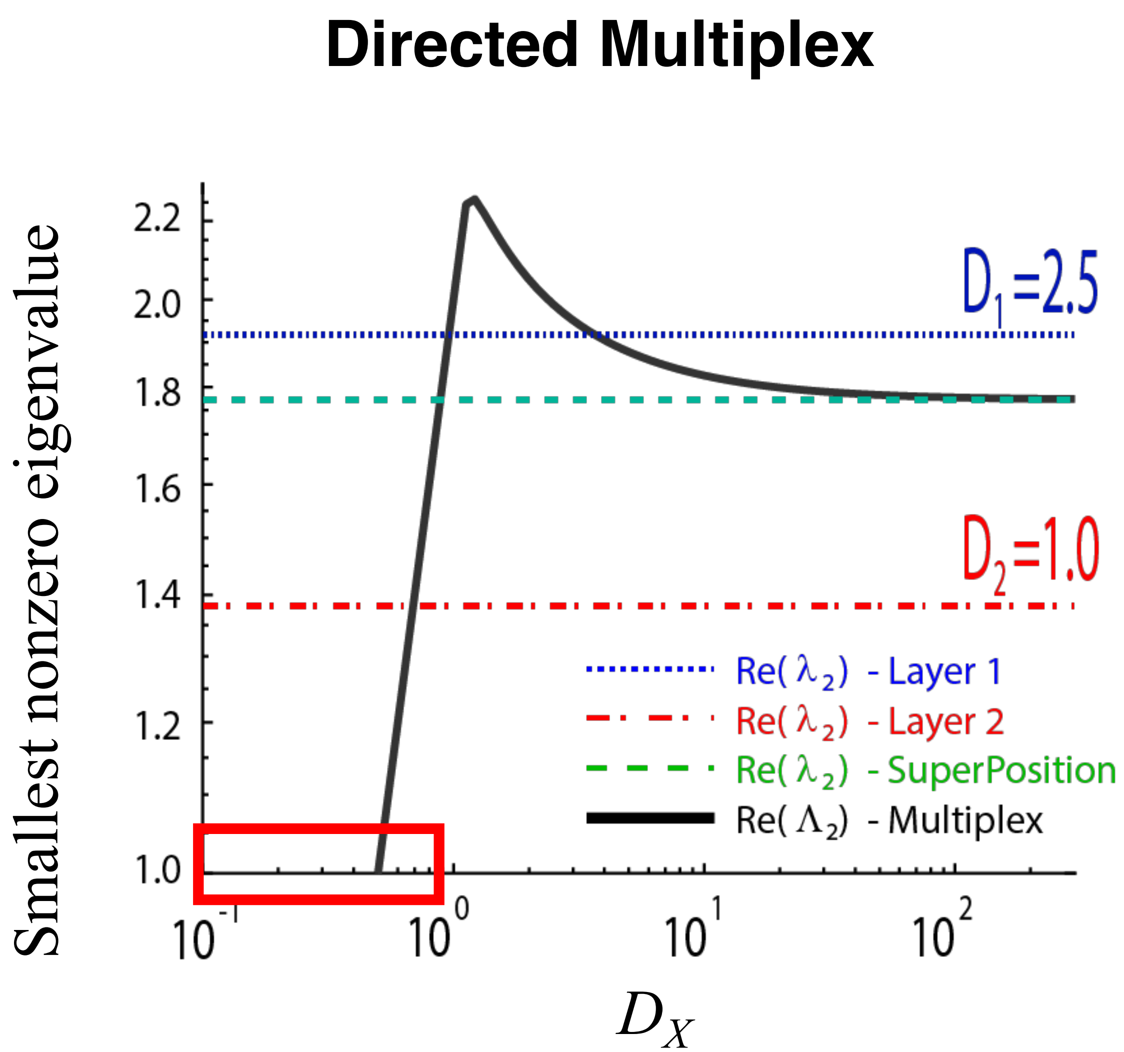

Small D_X

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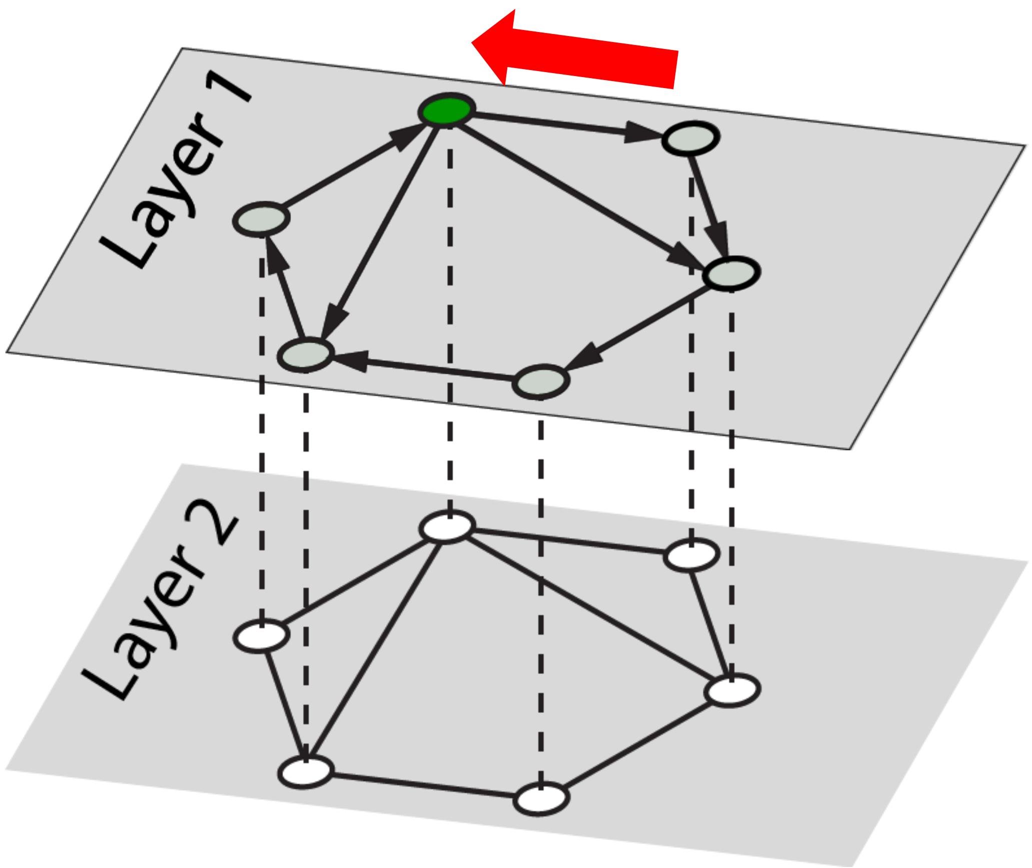

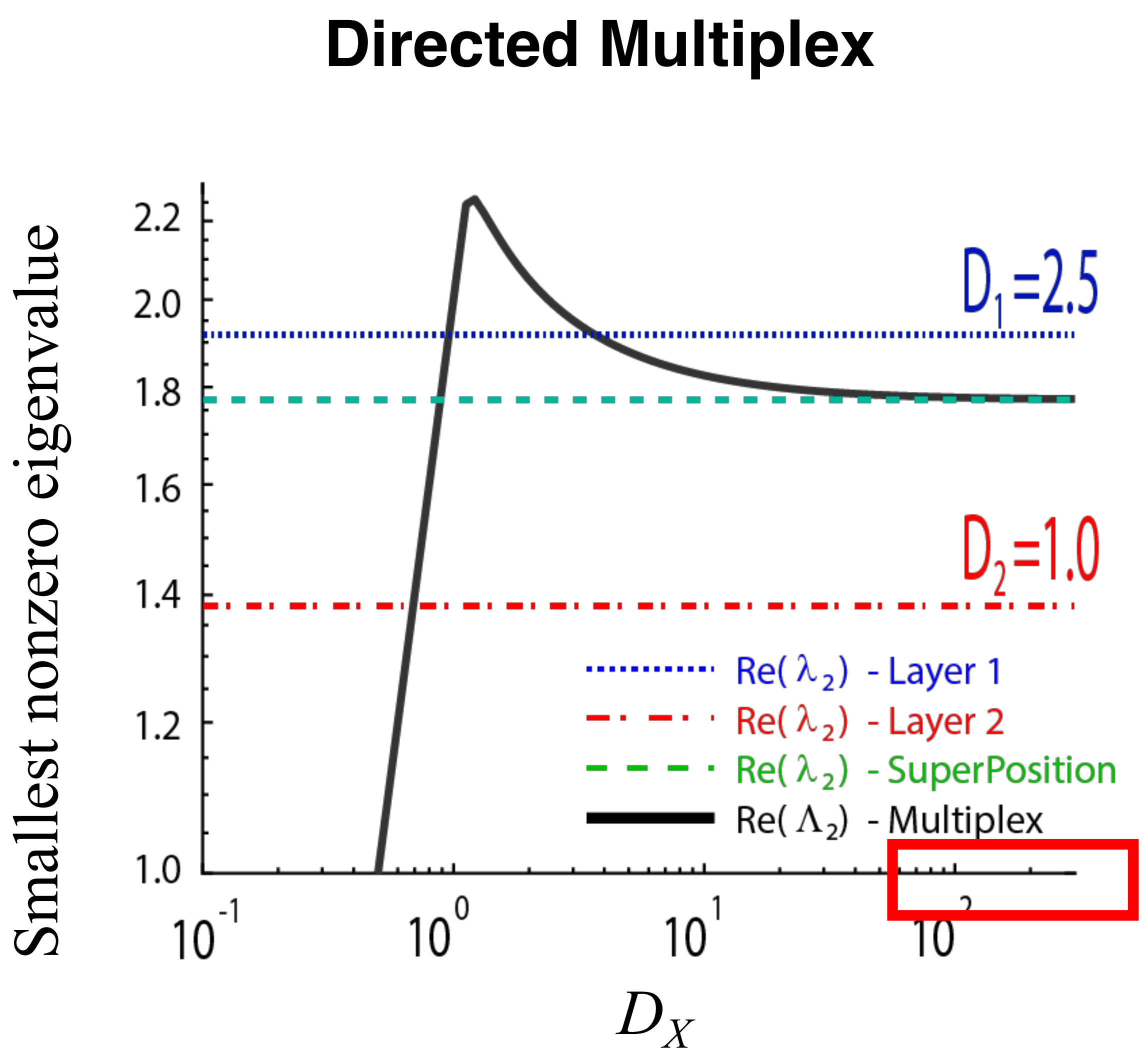

Large D_X

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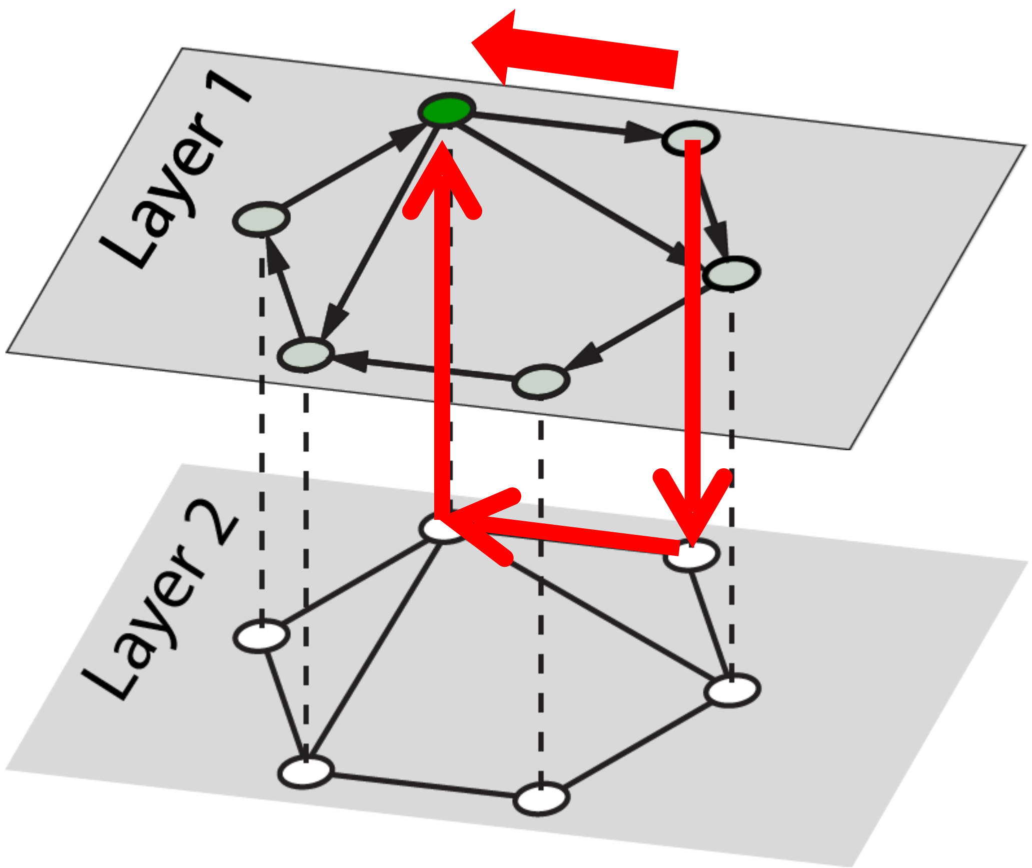

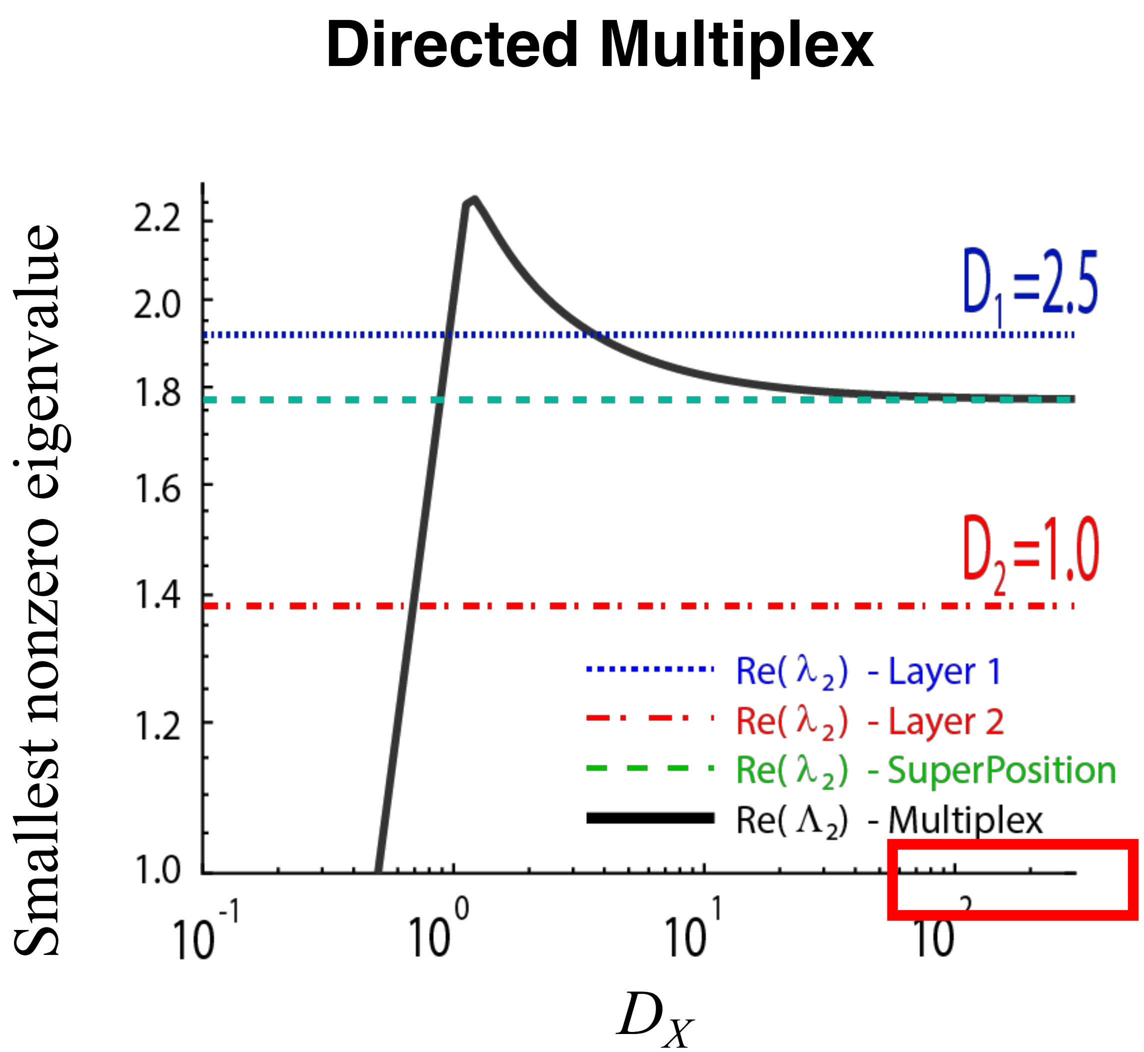

Large D_X

~~Faster Node Exploration~~

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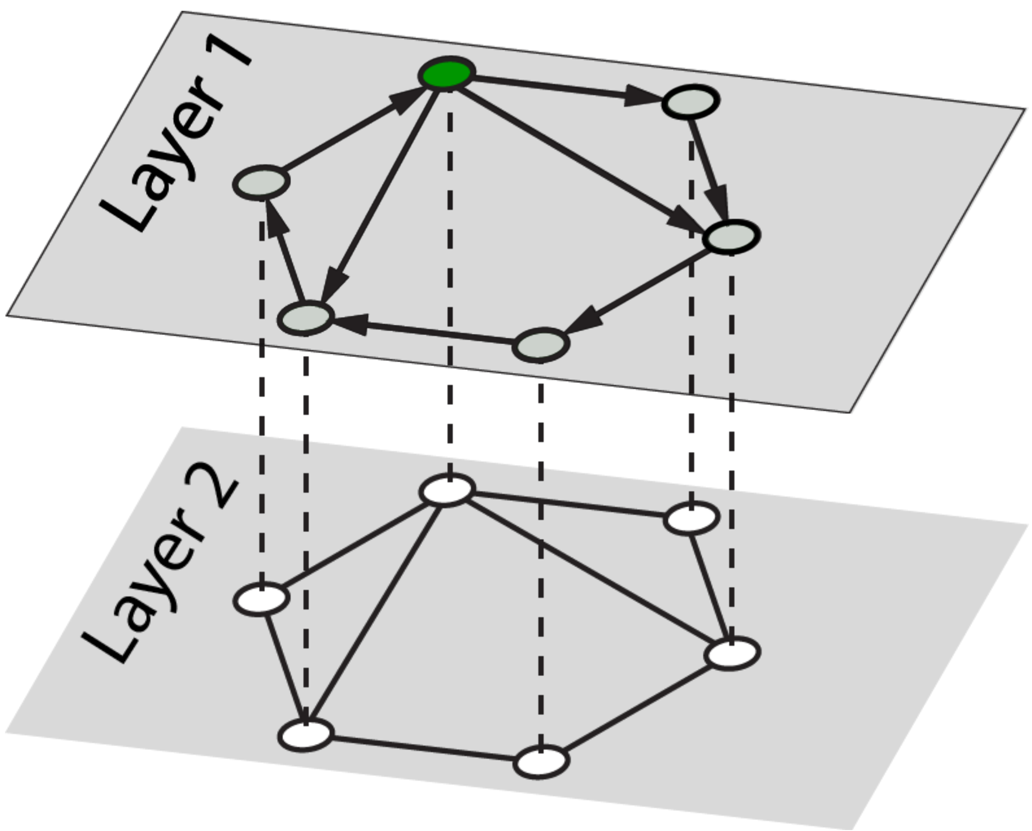

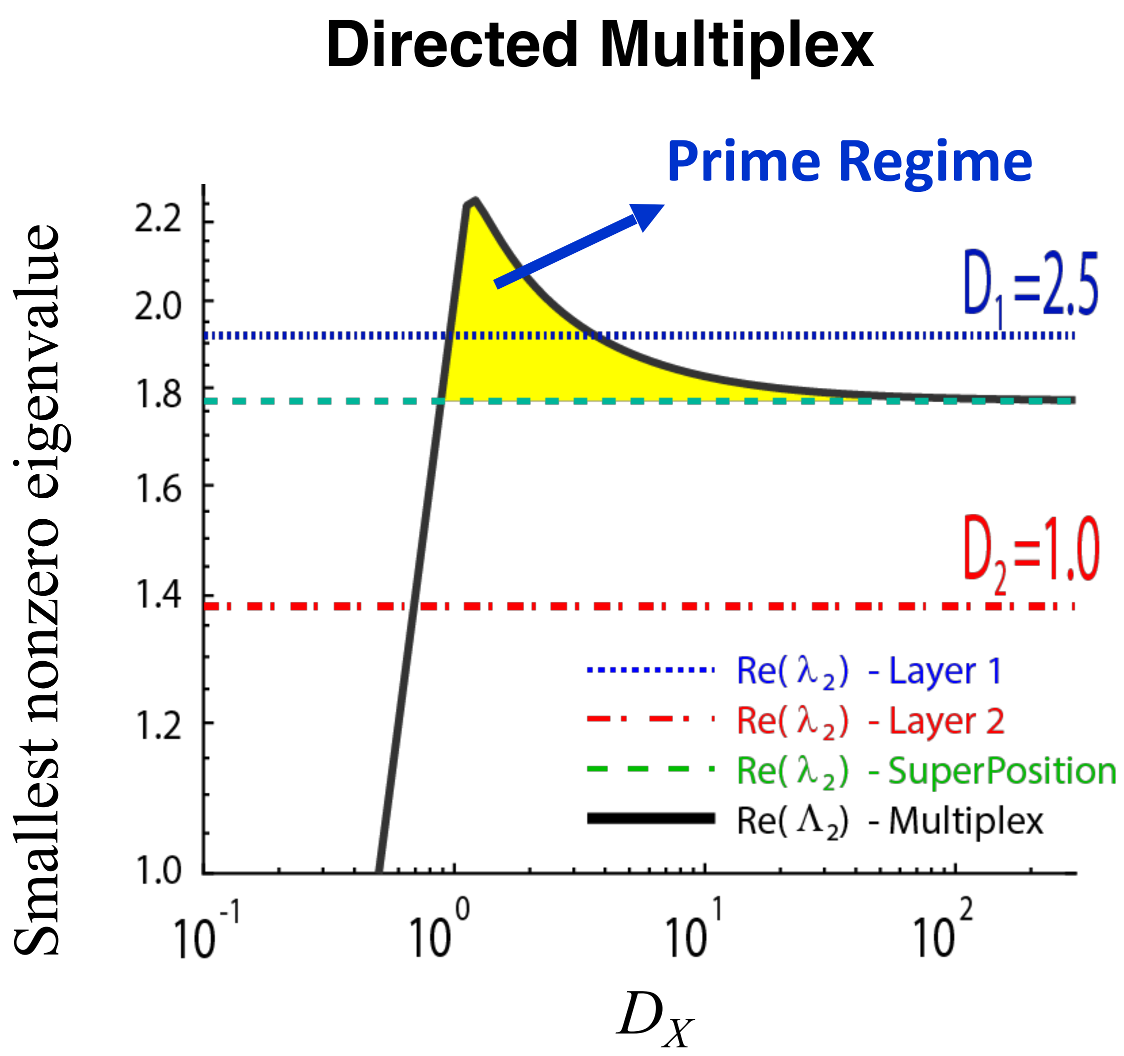

Faster Node Exploration + COUPLING SWEET SPOT

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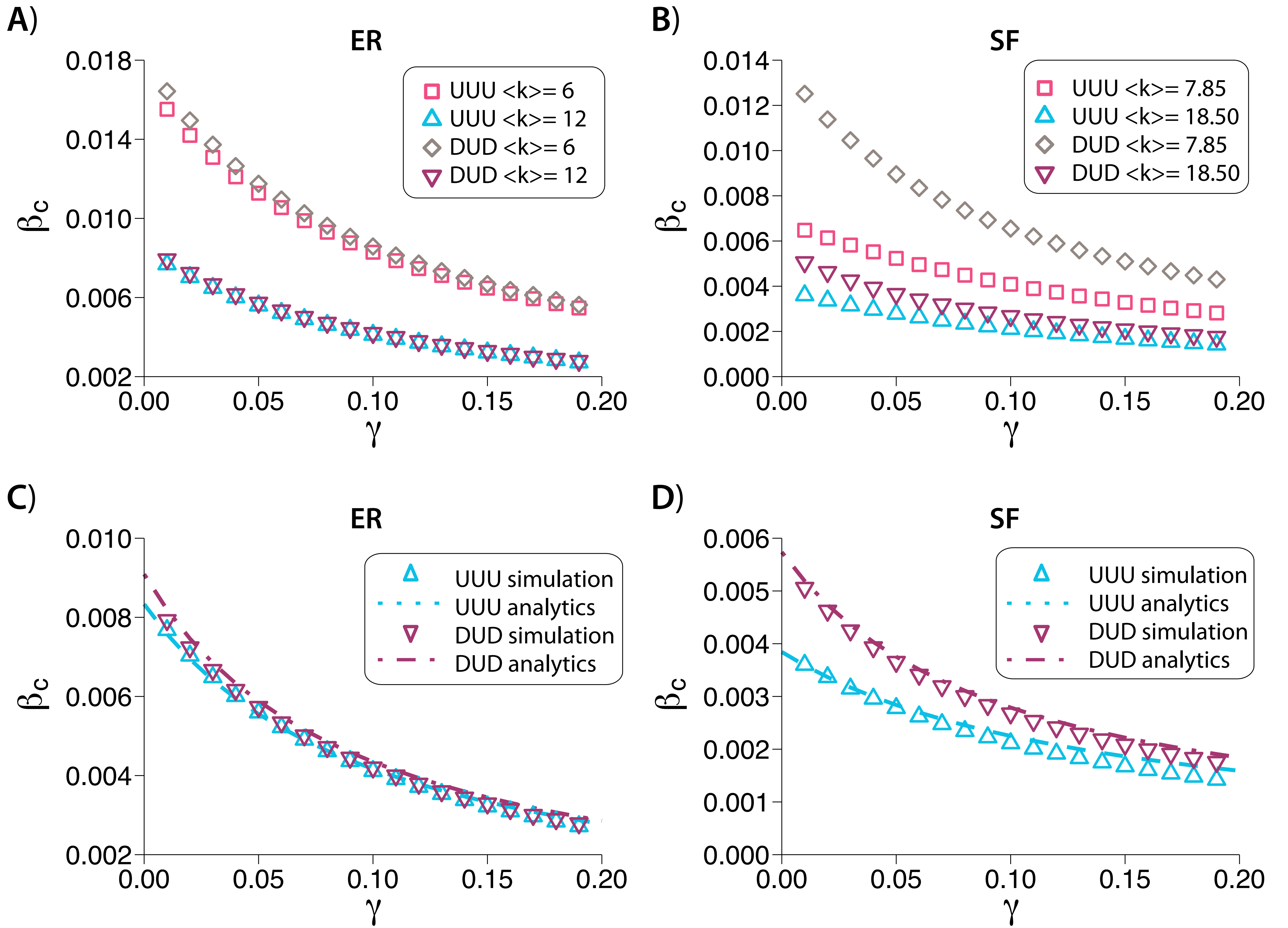
Disease Spreading in Directed Multilayer Networks



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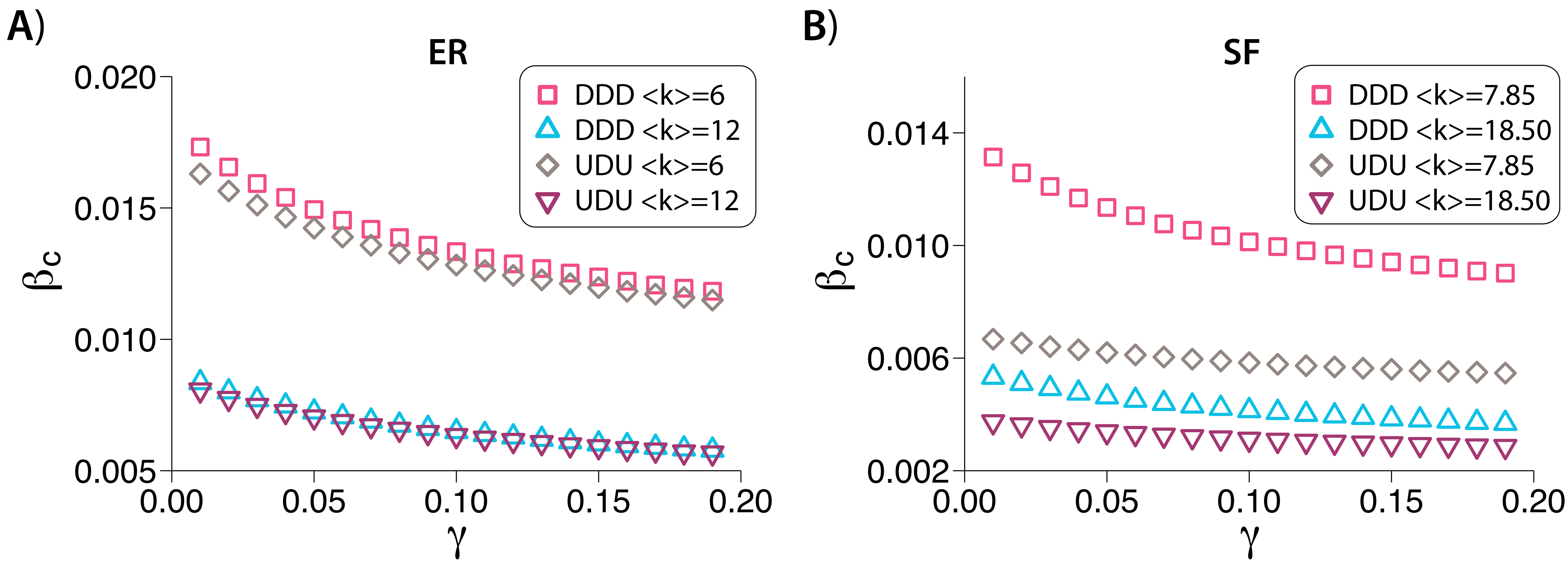


Disease Spreading in Directed Multilayer Networks

$$T_c = \frac{1 - T_{uv}}{\langle k \rangle + 1 - T_{uv}} \qquad \text{(ER-UUU)}$$

$$T_c = \frac{1 - T_{uv}}{\langle k \rangle} \qquad \text{(ER-DUD)}$$

$$T_c = \frac{2}{\langle k \rangle (2 + m + \sqrt{m(m+8)})} \qquad \text{(ER-DDD)}$$

$$T_c = \frac{2(1 + \langle k \rangle) + m' - \sqrt{m'(4 + 8\langle k \rangle + m')}}{2((1 + \langle k \rangle)^2 - m'\langle k \rangle)} \qquad \text{(ER-UDU)}$$

Disease Spreading in Directed Multilayer Networks

$$T_c = \frac{\langle k \rangle (1 - T_{uv})}{\langle k^2 \rangle (1 - T_{uv}) + \langle k \rangle^2 T_{uv}} \qquad \text{(SF-UUU)}$$

for the UUU configuration,

$$T_c = \frac{1 - T_{uv}}{\langle k \rangle} \qquad \text{(SF-DUD)}$$

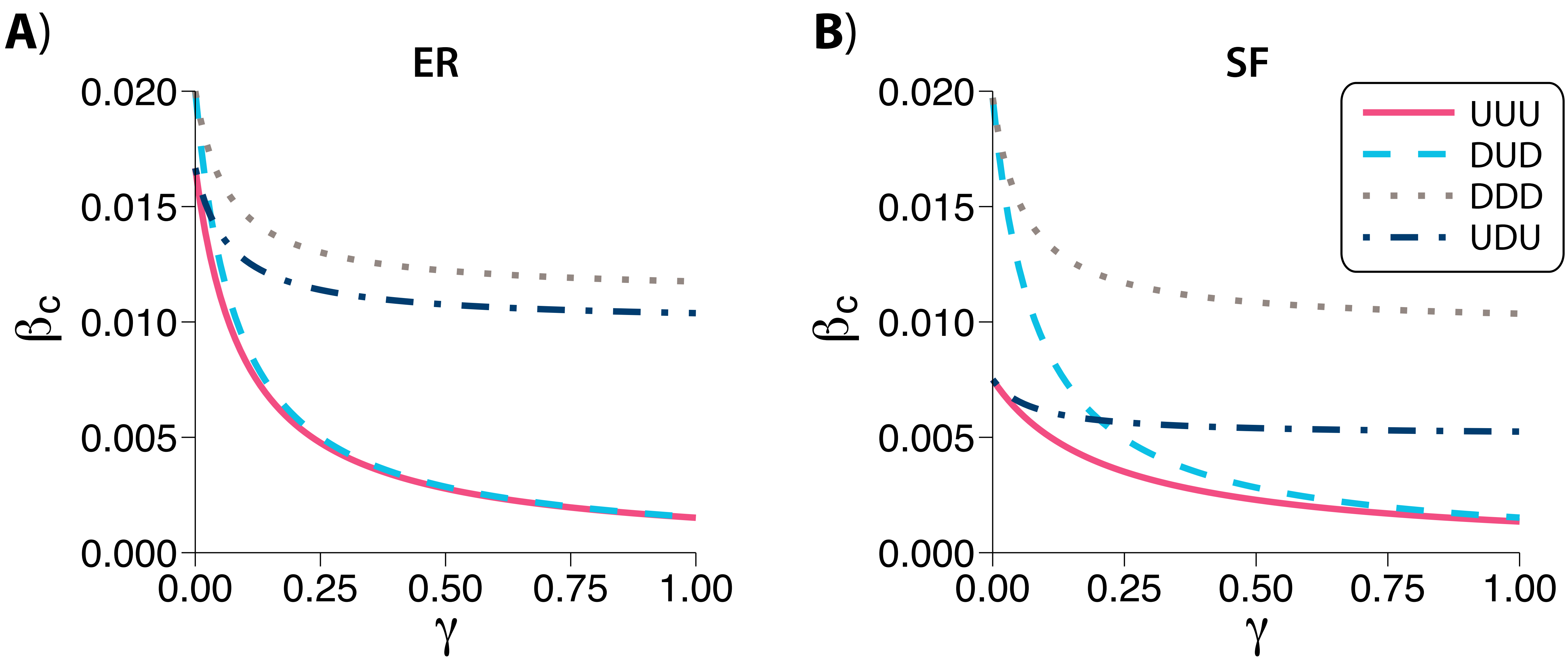
for the DUD configuration,

$$T_c = \frac{2}{\langle k \rangle (2 + m + \sqrt{m(m+8)})} \qquad \text{(SF-DDD)}$$

with $m = p(1-p)T_{uv}^2$ for the DDD configuration and

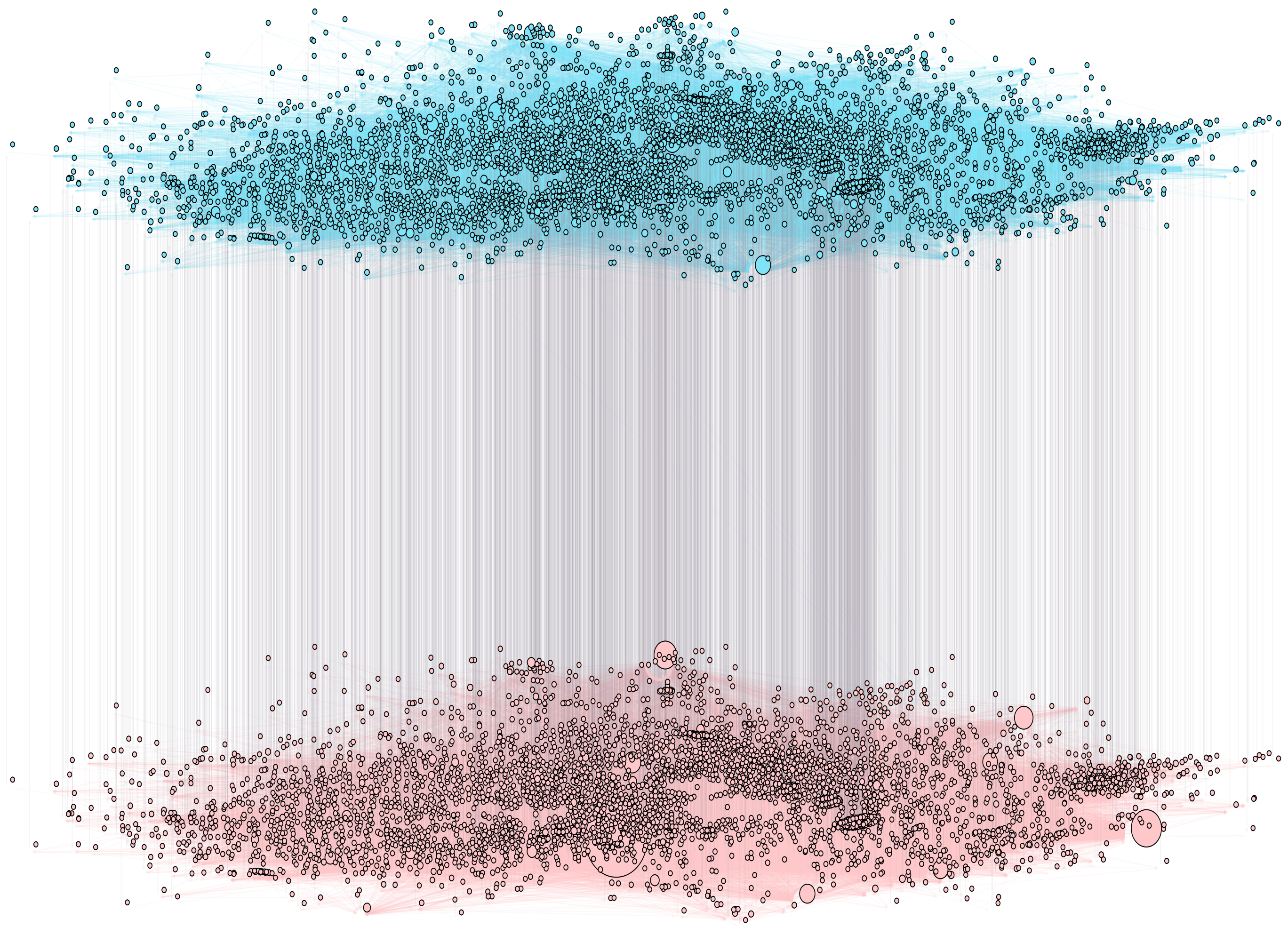
$$T_c = \frac{2\langle k^2 \rangle \langle k \rangle + \langle k \rangle^2 \left(\langle k \rangle m - \sqrt{m(4\langle k^2 \rangle + \langle k \rangle^2 (4 + m))} \right)}{2((\langle k^2 \rangle^2 - \langle k \rangle^4 m)} \qquad \text{(SF-UDU)}$$

Disease Spreading in Directed Multilayer Networks



Disease Spreading in Directed Multilayer Networks

A)



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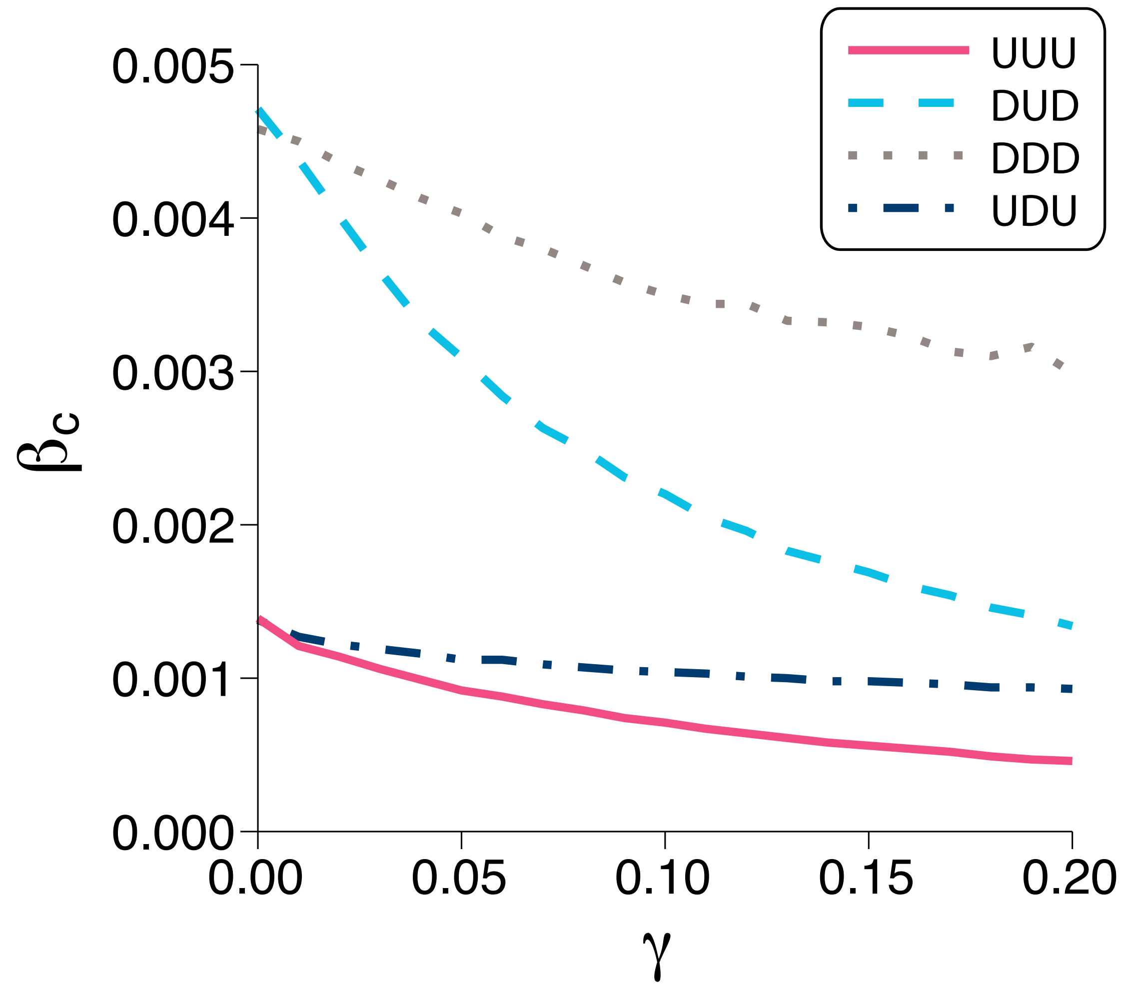

Acknowledgements

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- Joaquín Sanz
- Sandro Meloni
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SEVENTH FRAMEWORK PROGRAMME

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