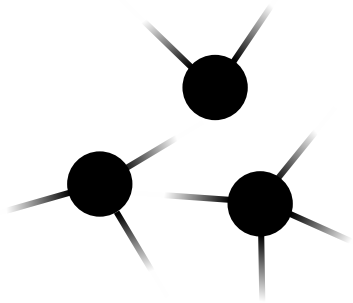






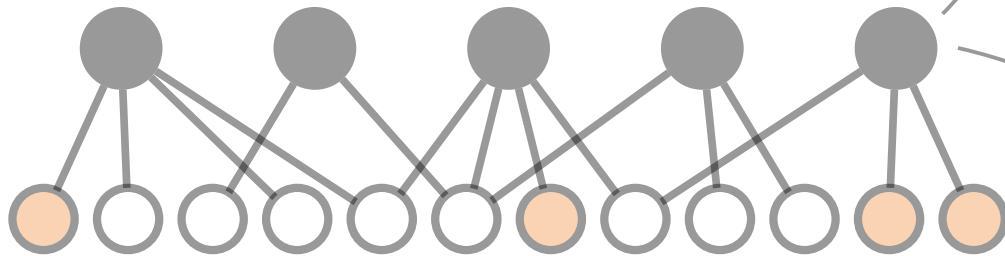
$p_n$

Clique size  
distribution

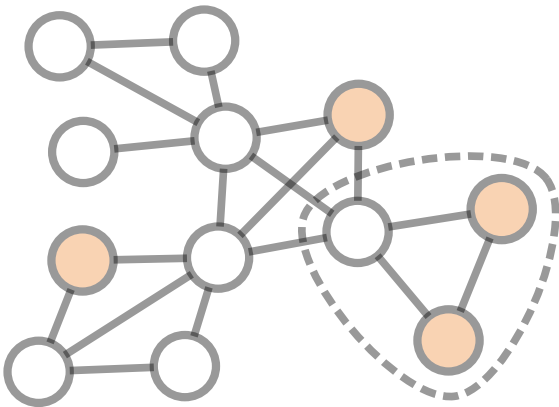


*Cliques*

*Nodes*

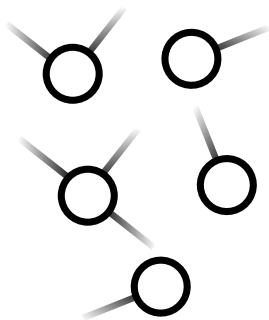


Projection  
on nodes

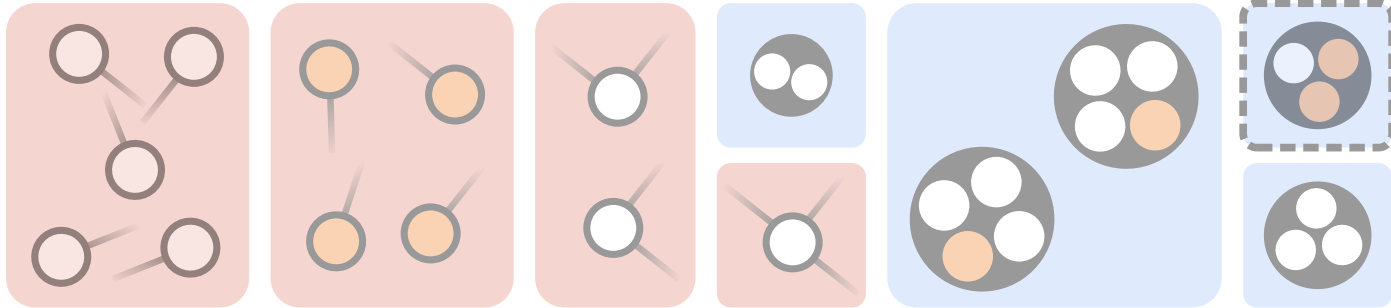


$g_m$

Membership  
distribution

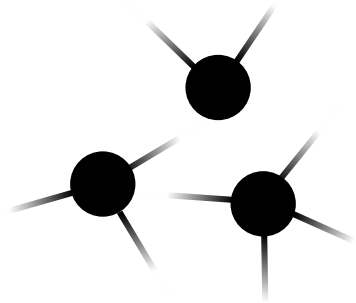


Compartmental formalism



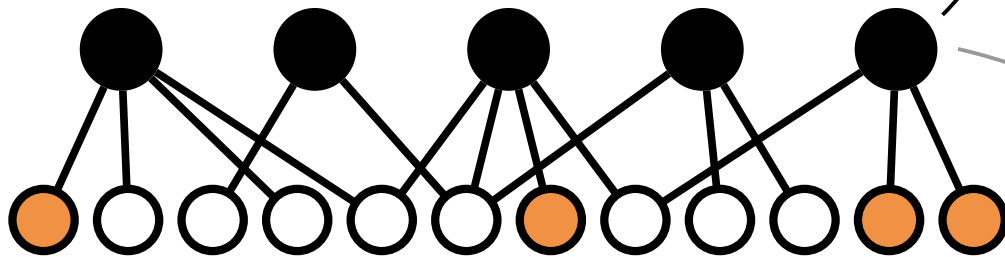
$p_n$

Clique size  
distribution

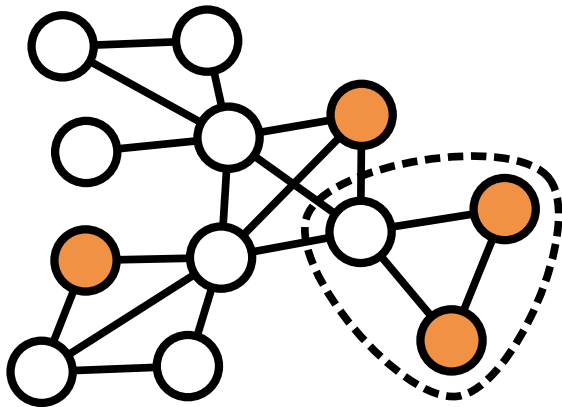


*Cliques*

*Nodes*

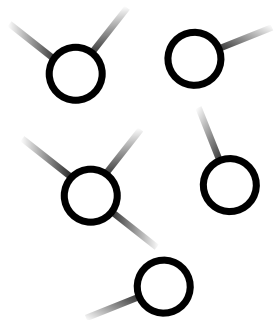


Projection  
on nodes

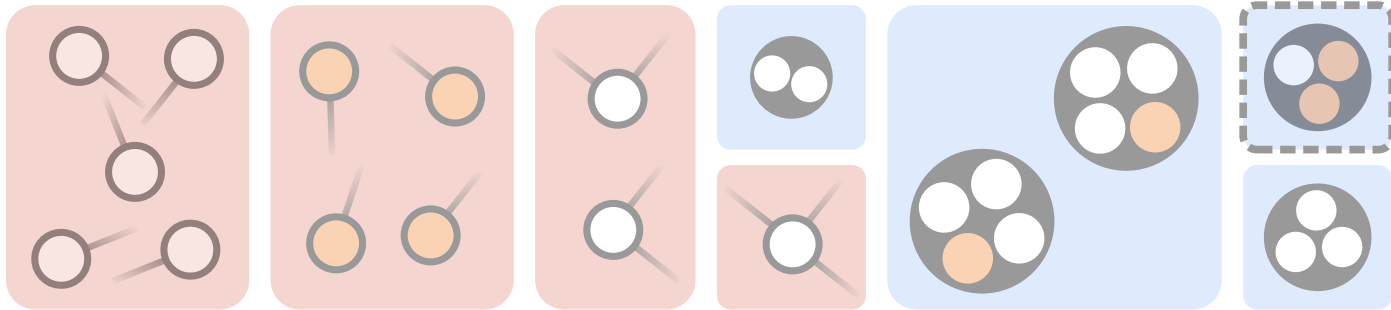


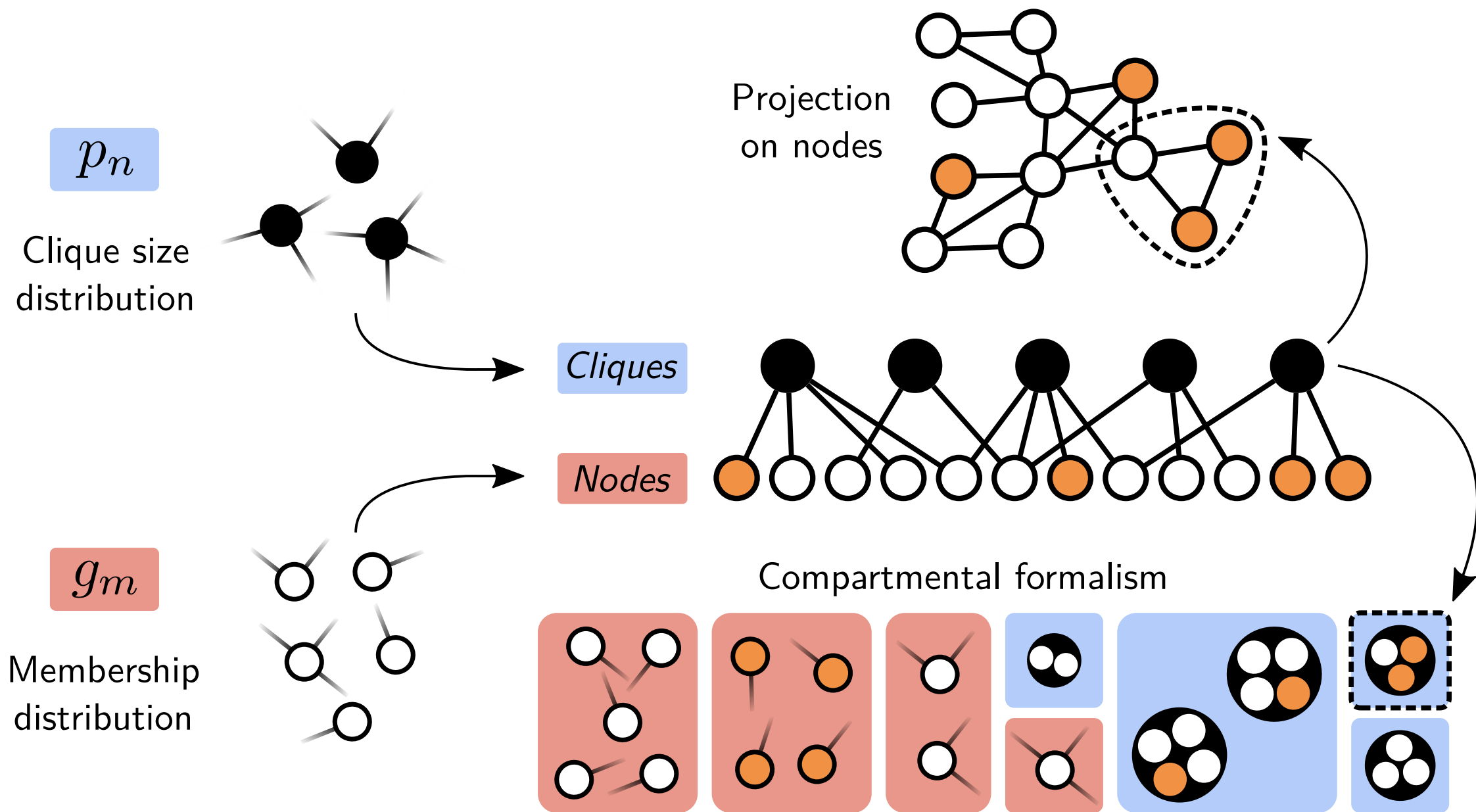
$g_m$

Membership  
distribution



Compartmental formalism





M.E.J. Newman, *Properties of highly clustered networks*, Phys. Rev. E 68, 026121 (2003)

Dynamics at the groups level

$$\begin{aligned}\frac{dG_{n,i}}{dt} = & \mu(i+1)G_{n,i+1} - \mu i G_{n,i} \\ & + (n-i+1)\Theta_{n,i-1,\beta}G_{n,i-1} - (n-i)\Theta_{n,i,\beta}G_{n,i} \\ & + (n-i+1)\rho G_{n,i-1} - (n-i)\rho G_{n,i}\end{aligned}$$

Dynamics at the nodes level

$$\frac{dS_m}{dt} = \mu(g_m - S_m) - m\textcolor{brown}{r}S_m$$

# Mean-field quantities

$$\rho(t) = r(t) \frac{\sum_m m(m-1)S_m}{\sum_m mS_m} ; \quad r(t) = \frac{\sum_{n,i} (n-i)\Theta_{n,i,\beta} G_{n,i}}{\sum_{n,i} (n-i)G_{n,i}}$$



Global prevalence

$$I(t) = \sum_m [g_m - S_m(t)]$$

The model and its mathematical description

$r(t)$  : mean infection rate from a random group to which a random node belongs

$\rho(t)$  : mean infection rate from all *other* groups to which a random node in a random group belongs

$S_m$  : fraction of nodes with membership  $m$  and that are susceptible

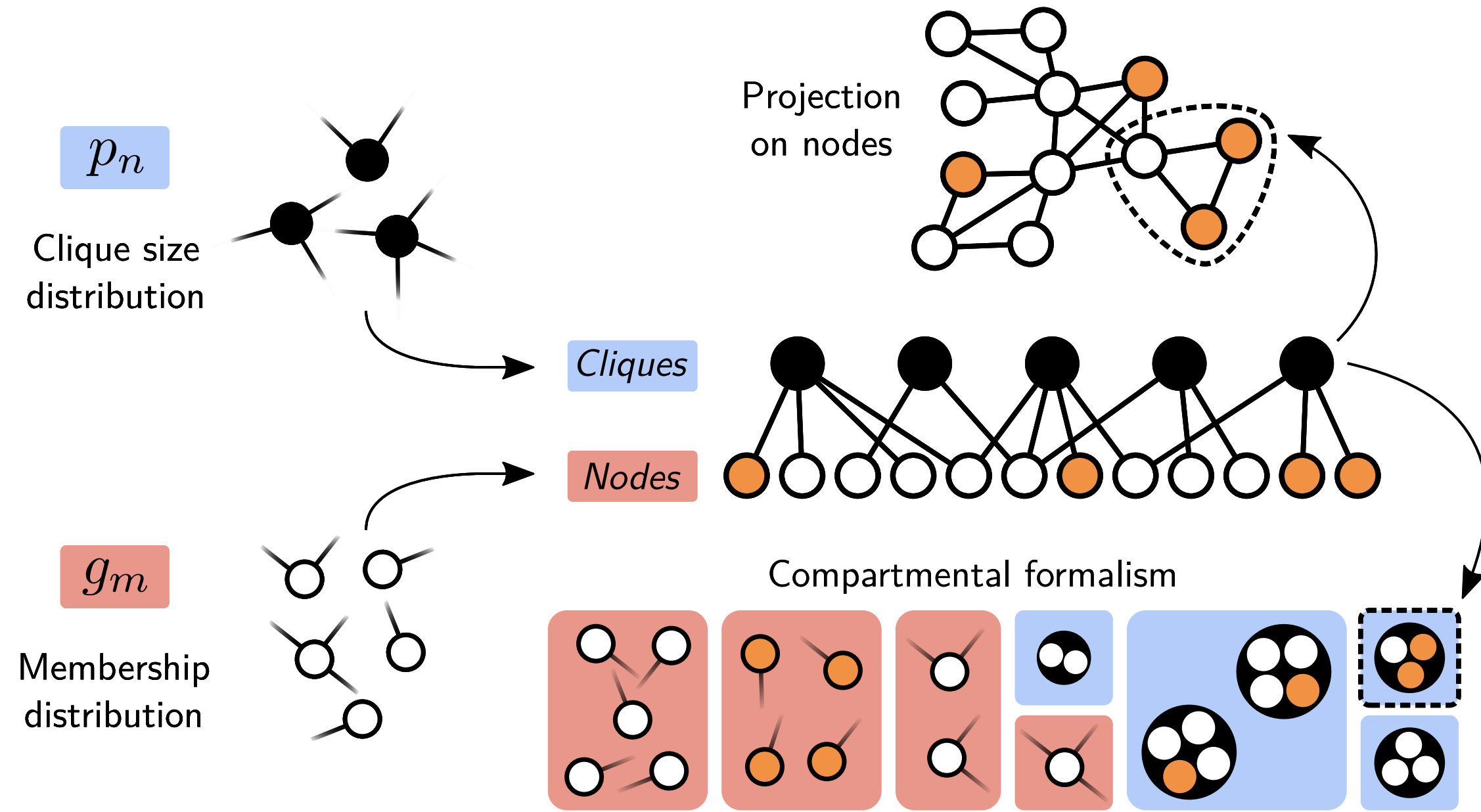
$G_{n,i}$  : fraction of group of size  $n$  and that contain  $i$  infectious nodes

$g_m$  : fraction of nodes with membership  $m$

$p_n$  : fraction of groups of size  $n$

- $\mu$  : recovery rate
- $\beta$  : *weight* associated with transmission
- $\Theta_{n,i,\beta}$  : transmission rate in a group of size  $n$ , with  $i$  infected nodes, and weight  $\beta$

# The model and its mathematical description



$g_m$  : fraction of nodes with membership  $m$

$p_n$  : fraction of groups of size  $n$

$S_m$  : fraction of nodes with membership  $m$  and that are susceptible

$G_{n,i}$  : fraction of group of size  $n$  and that contain  $i$  infectious nodes

$\mu$  : recovery rate

$\beta$  : weight associated with transmission

$\Theta_{n,i,\beta}$  : transmission rate in a group of size  $n$ , with  $i$  infected nodes, and weight  $\beta$

Dynamics at the groups level

$$\begin{aligned} \frac{dG_{n,i}}{dt} = & \mu(i+1)G_{n,i+1} - \mu i G_{n,i} \\ & + (n-i+1)\Theta_{n,i-1,\beta}G_{n,i-1} - (n-i)\Theta_{n,i,\beta}G_{n,i} \\ & + (n-i+1)\rho G_{n,i-1} - (n-i)\rho G_{n,i} \end{aligned}$$

Dynamics at the nodes level

$$\frac{dS_m}{dt} = \mu(g_m - S_m) - m\bar{r}S_m$$

$\bar{r}(t)$  : mean infection rate from a random group to which a random node belongs

$\bar{\rho}(t)$  : mean infection rate from all *other* groups to which a random node in a random group belongs

Mean-field quantities

$$\bar{\rho}(t) = \bar{r}(t) \frac{\sum_m m(m-1)S_m}{\sum_m mS_m} ; \quad \bar{r}(t) = \frac{\sum_{n,i} (n-i)\Theta_{n,i,\beta}G_{n,i}}{\sum_{n,i} (n-i)G_{n,i}}$$

Global prevalence

$$I(t) = \sum_m [g_m - S_m(t)]$$

# The model and its mathematical description

Stationary state

$$S_m^* = \frac{g_m}{1 + mr}$$
$$\mu(i + 1)G_{n,i,\beta}^* = [\mu i + (n - i)(\Theta_{n,i,\beta} + \rho)] G_{n,i,\beta}^* - (n - i + 1)(\Theta_{n,i-1,\beta} + \rho) G_{n,i-1,\beta}^*$$

Epidemic threshold

$$\left. \frac{dF}{d\rho} \right|_{\rho \rightarrow 0} > 1$$

where

$$F(\rho) \equiv r(\rho) \frac{\sum_m m(m - 1) S_m(\rho)}{\sum_m m S_m(\rho)}$$