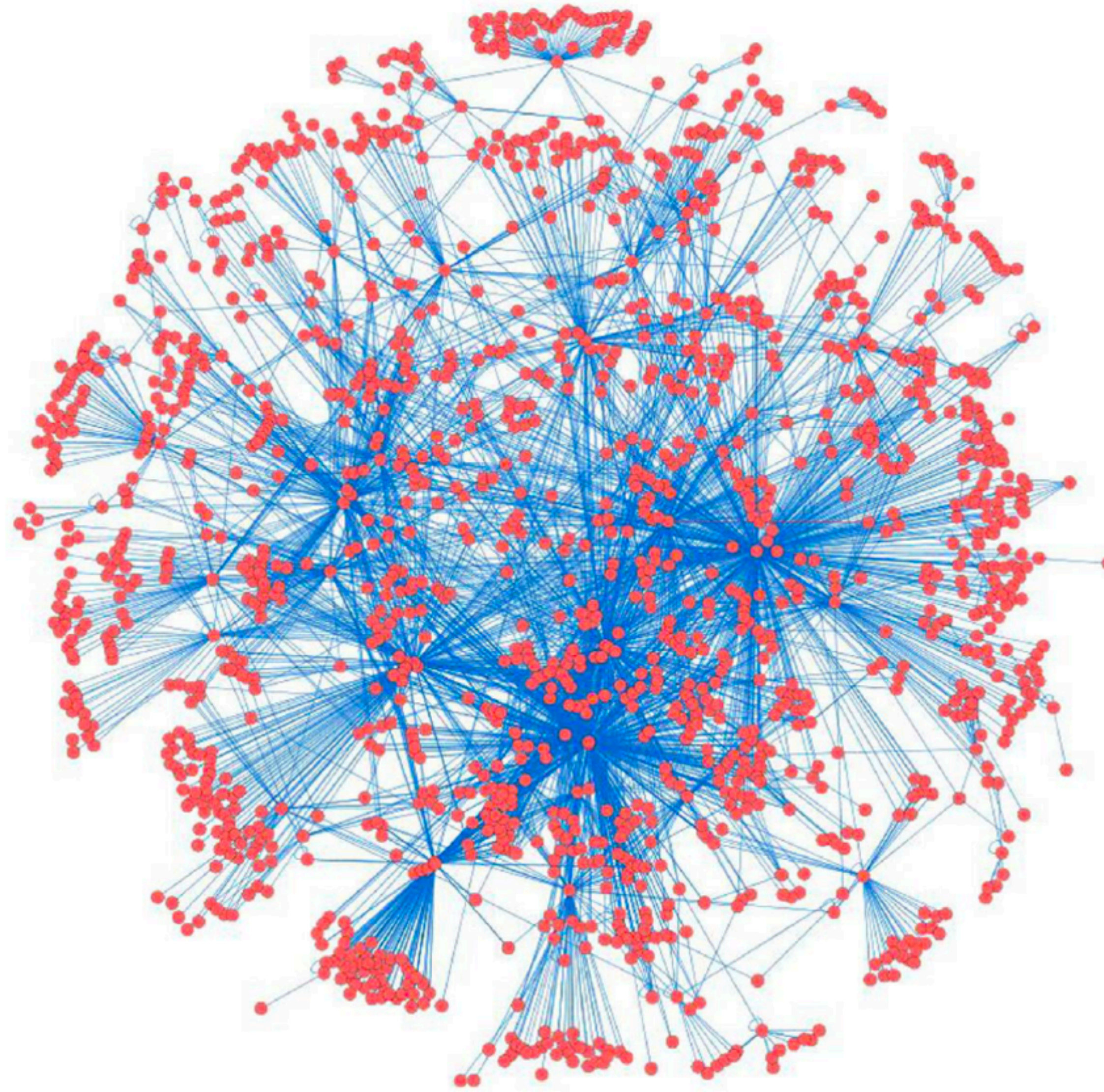


LECTURE 6

REGULATION MOTIFS



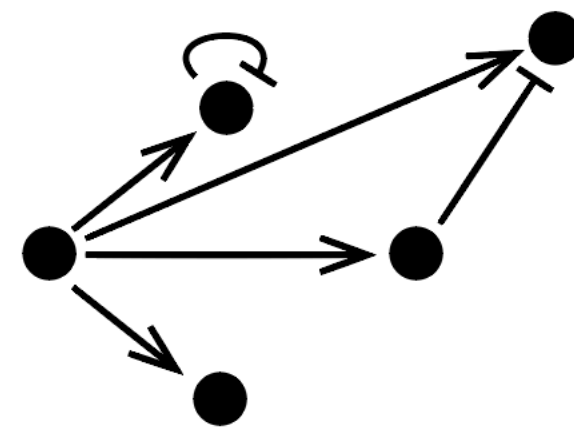
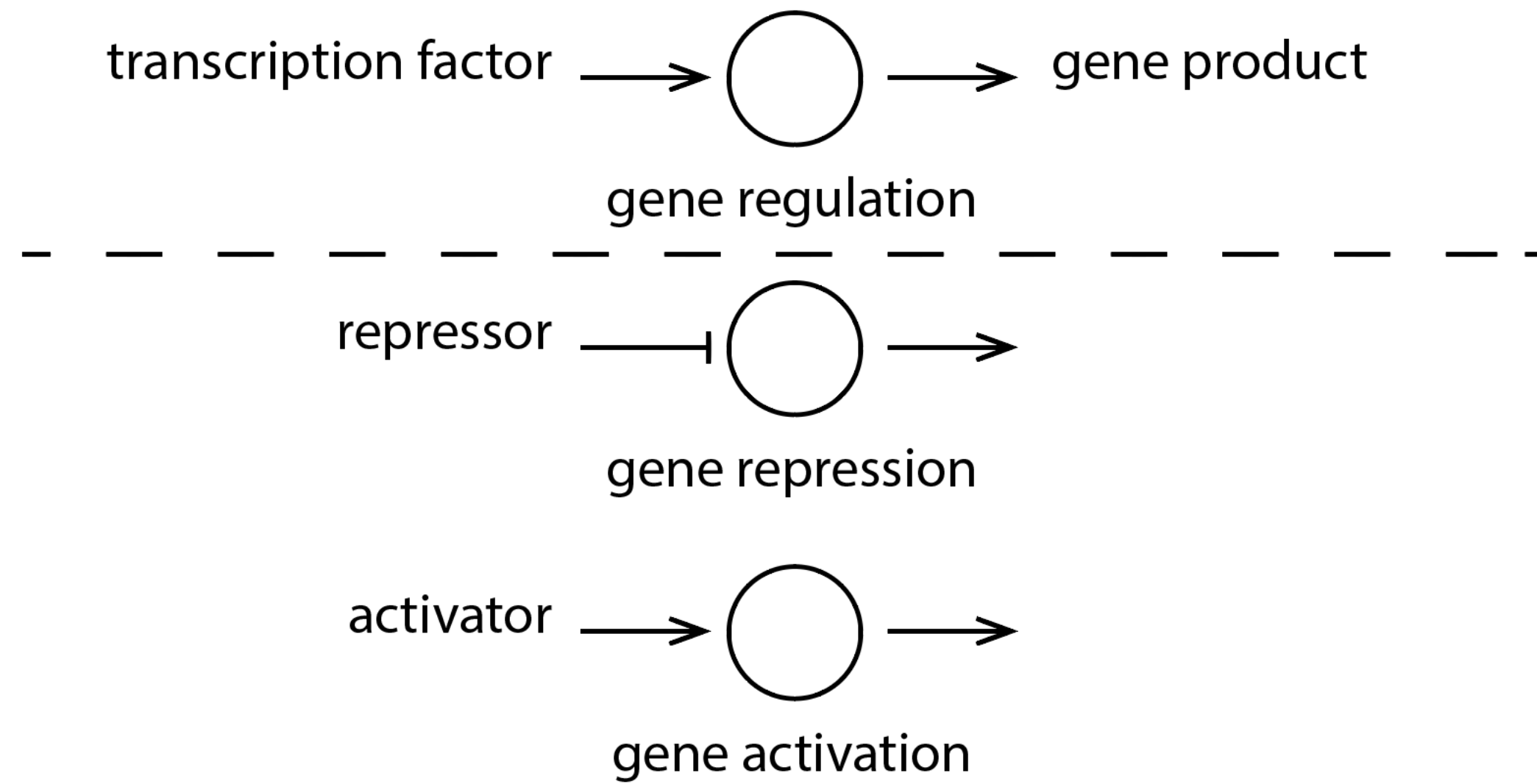
Gene regulation
Time constants of gene regulation
Gene repression
Separation of fast and slow
Dissociation constant
EC50
Hill coefficient
Boolean approximation
Gene activation
Gene regulatory network model
Multidimensional promoters (AND, OR)

E. coli network
5M bp, 4000 genes, 300 TFs (DoFs)
20% network (Shen-Orr 2002)
 $N=420$, $E=520$
Erdos random network, $p = E/N^2$
Motif
Single node motifs

$p_{\text{self}} = 1/N$, $\langle n_{\text{self}} \rangle = \text{var} = E/N$
NAR motif
approximate model
steady state normalization
rise time, $\text{Tr} = K/2/V_{\text{max}}$
comparison with unregulated model
speed up module
robustness module
PAR motif
approximate model
rise time
delay module

EXERCISE
create a random GRN ($N=10, E=10$)
make direction and sign binomially dist
make K_m uniform between 0 and 1
let $V_{\text{max}} = 1$
choose input and output at random
generate ensemble of $1e6$ step resp

BIONUMBERS
(<https://bionumbers.hms.harvard.edu/>)
Transcription rate (20-40nt/sec)
mRNA export time (1-10min)
Translation rate (5-10 codons/sec)
Folding time (10-30min/protein)
Diffusion time yeast (0.5sec)
Diffusion rate in cytoplasm ($8\mu\text{m}^2/\text{sec}$)
Diffusion rate in water ($100\mu\text{m}^2/\text{sec}$)
ER flux yeast (460molecules/sec)
Secretion time (~20min)



transcriptional regulatory network

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ODE model
(gene repression)

Chemical Reaction Network:

gene expression: $G \xrightarrow{k_1} G+P$
 degradation: $P \xrightarrow{k_2} \emptyset$
 repression: $G+I \xrightleftharpoons[k_4]{k_3} G^*$

Full ODE:

$$\begin{aligned} \dot{G} &= k_1 G^* - k_2 G I^n \\ \dot{G}^* &= k_3 G I^n - k_4 G^* \\ \dot{P} &= k_1 G - k_2 P \end{aligned}$$

Mass Conservation:
 $G + G^* = G_T$ (constant)

Reduced ODE:

$$\begin{aligned} \dot{G} &= k_4(G_T - G) - k_3 G I^n \\ &= k_4 G_T - G(k_4 + k_3 I^n) \\ \dot{P} &= k_1 G - k_2 P \end{aligned}$$

Time scale separation:
 Fast dynamics \rightarrow gene regulation \sim sec
 Slow dynamics \rightarrow gene expression \sim 10min

Fully reduced ODE:
 $\frac{\tilde{k}_4}{\epsilon} = k_4, \frac{\tilde{k}_3}{\epsilon} = k_3$

Handwritten notes on the right side of the page:

pseudo eq. $\Rightarrow G = \frac{k_4 G_T}{k_4 + k_3 I^n}$
 $= \frac{G_T}{1 + \left(\frac{I}{\sqrt[n]{\frac{k_4}{k_3}}}\right)^n}$ ← hill coef.
 $= \frac{G_T}{1 + \left(\frac{I}{K_d}\right)^n}$ ← diss. constant

Graph of G vs I showing sigmoidal curves for different n . The y-axis is G and the x-axis is I . The curves start at G_T and approach 0 as I increases. The dissociation constant K_d is marked on the x-axis. The text says "as $n \rightarrow \infty$ more like true logic gate".

ZÁPADOČESKÁ UNIVERZITA V PLZNI

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what is the activation ODE?

how would you model the multi-input gene below?

