Master equation for the degree distribution of a Duplication and Divergence network

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MTC
Modelos Teóricos e Computacionias

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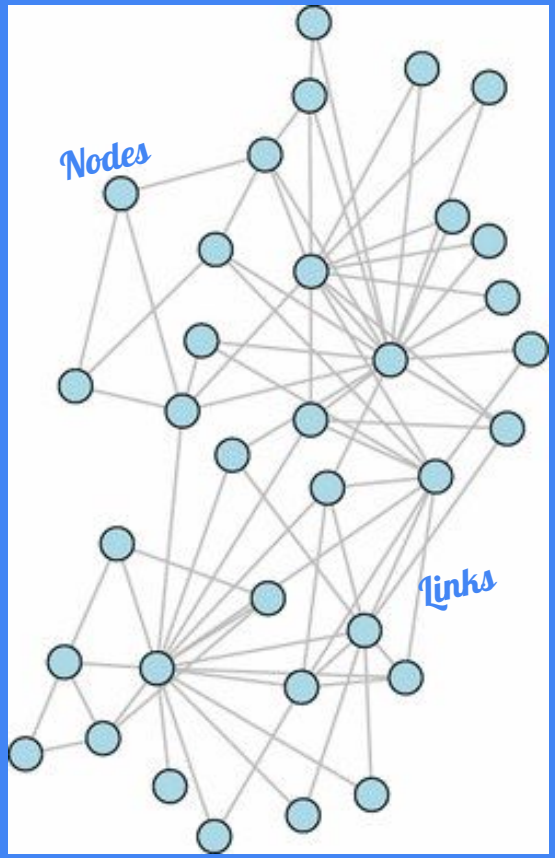
LabCel

Networks

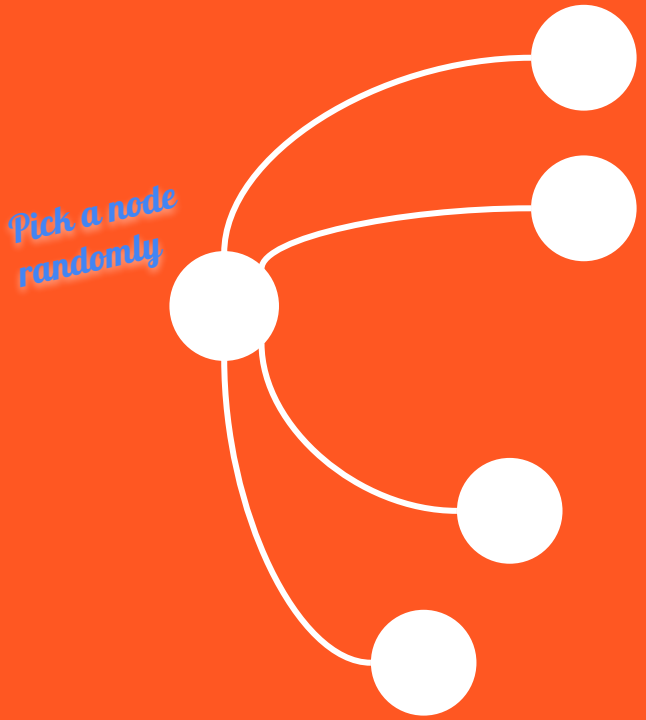
A set of **nodes** and a set of **links** among them.

Social networks, author citations, flights connections, metabolic models, protein–protein interactions

Network dynamics - the growth of a network



Duplication and divergence networks



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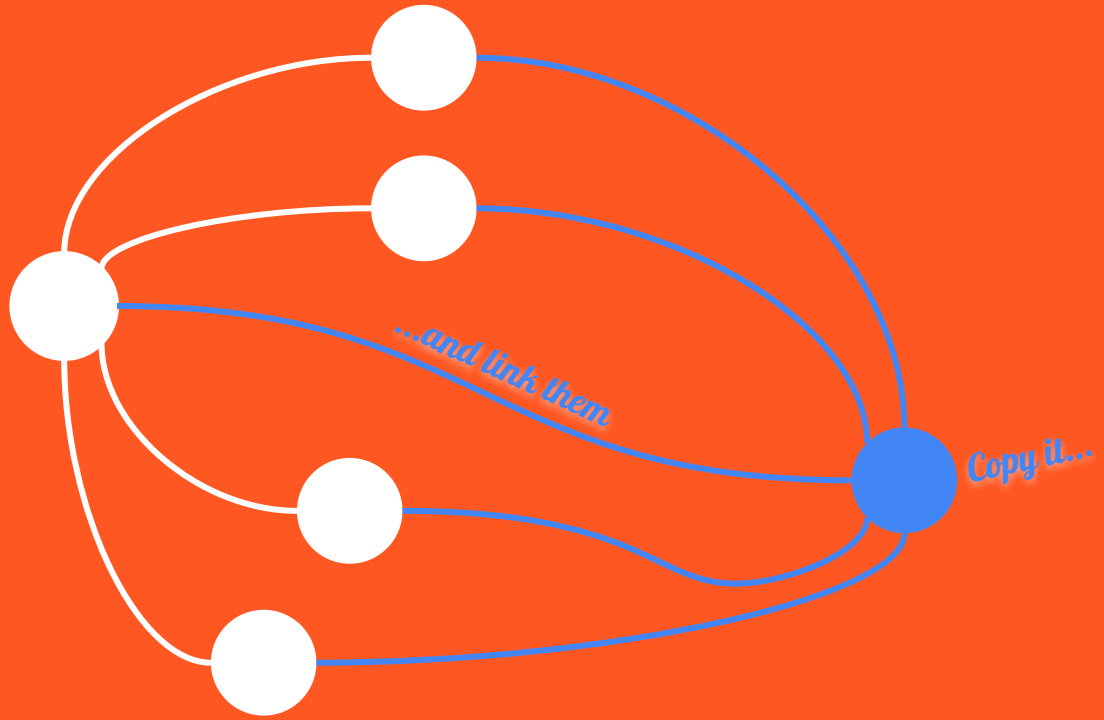
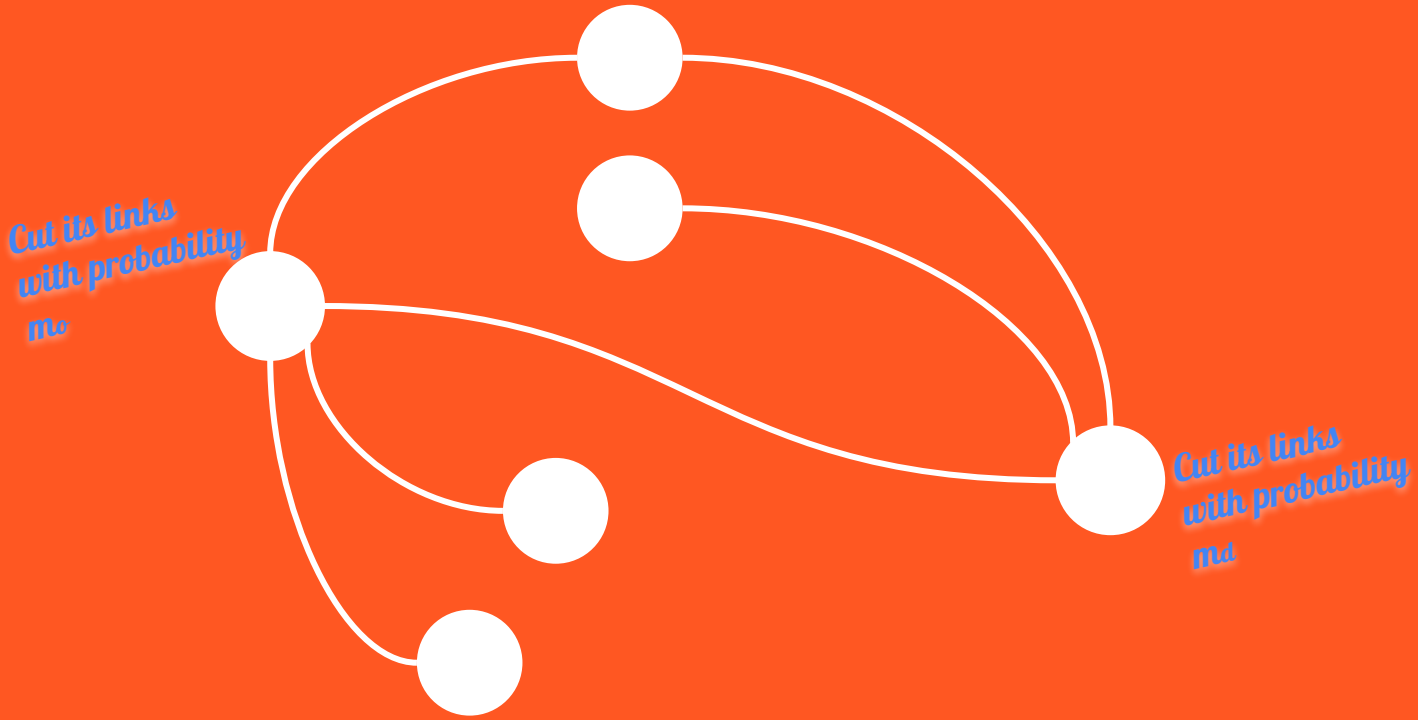
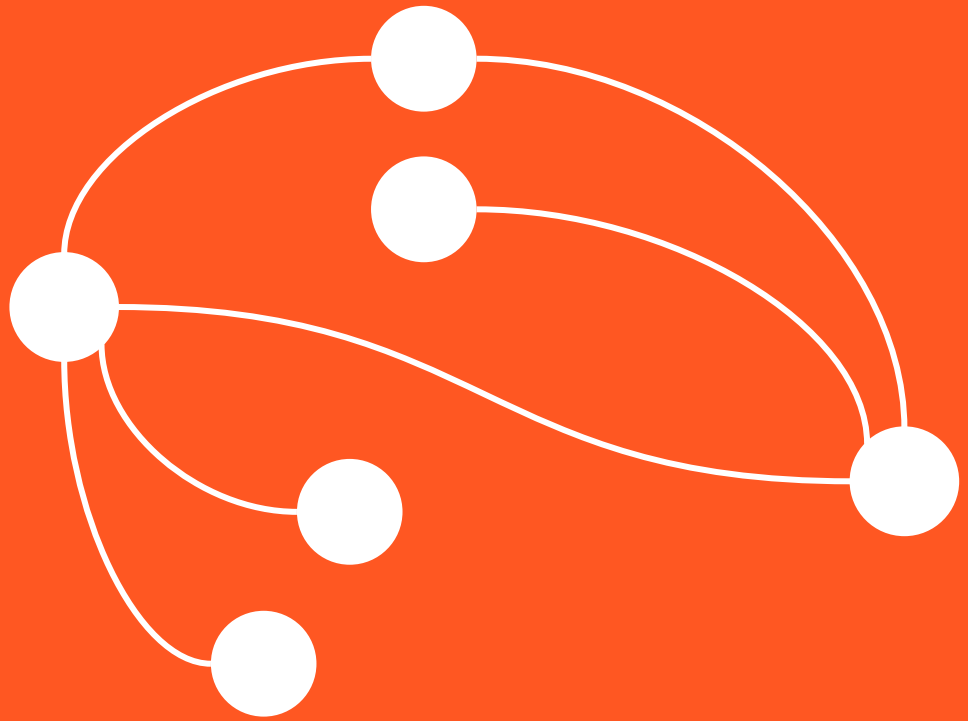


Duplication and divergence networks



Duplication and divergence networks

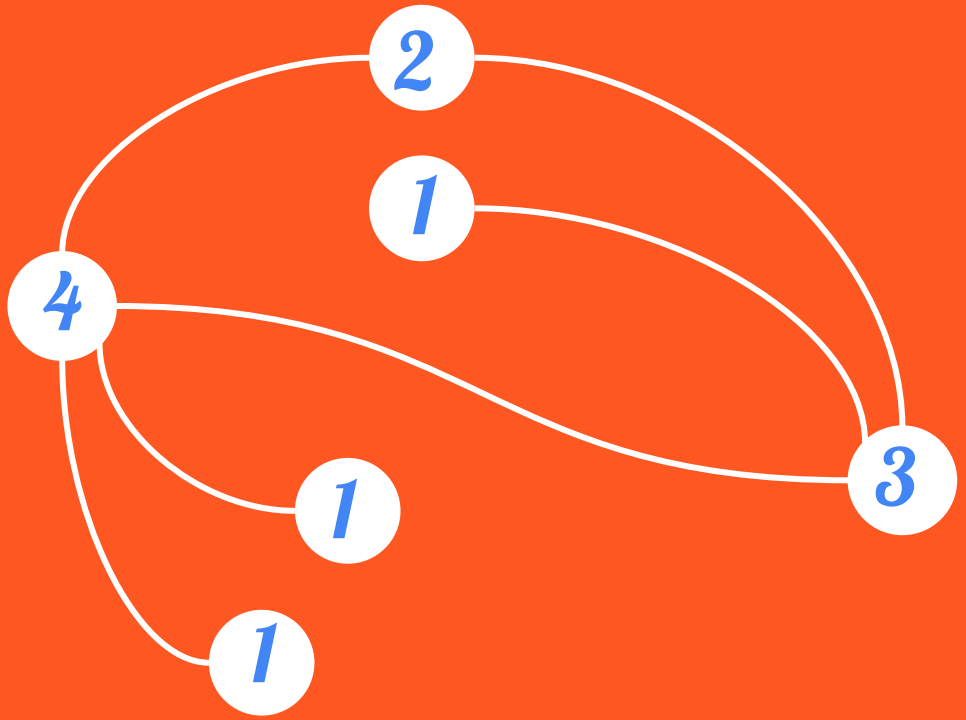


Total mutation

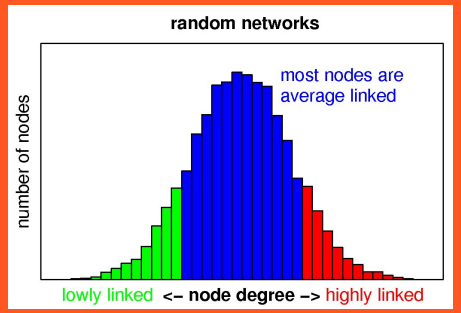
$$M = m_o + m_d$$

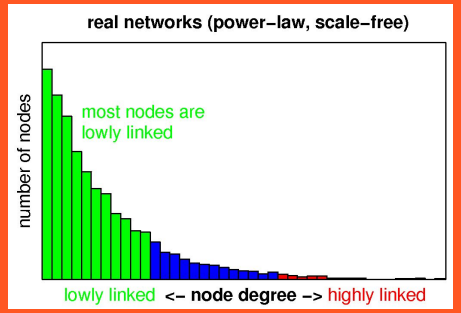
This model of network dynamics applied to protein–protein interaction networks allows **all proteins to evolve from a common ancestor** through **gene copies** (represented by duplications) and **mutations** (divergence). Therefore, *it would mimic the entire history of a genome evolution*

Node degree



Degree distribution





Analytical results

Mean degree as a function of total number of nodes:

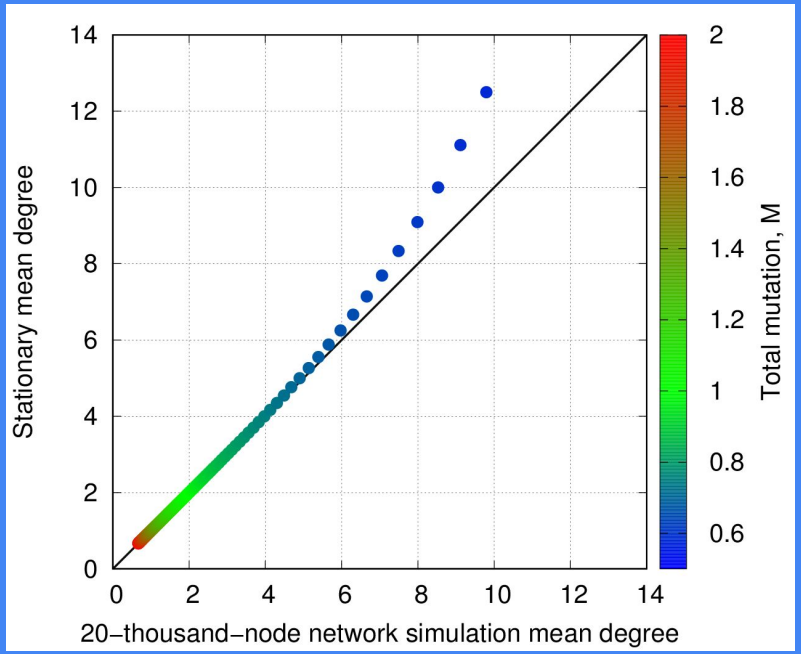
$$\bar{k}(t) = \begin{cases} c(t+1)^{1-2M} + \frac{2}{2M-1} & \text{for } M \neq 0.5; \\ 2\log(t+1) + c & \text{for } M = 0.5\,, \end{cases}$$

Asymptotic behaviour:

$M > 0.5$: The mean degree converges to $\dfrac{2}{2M-1}$

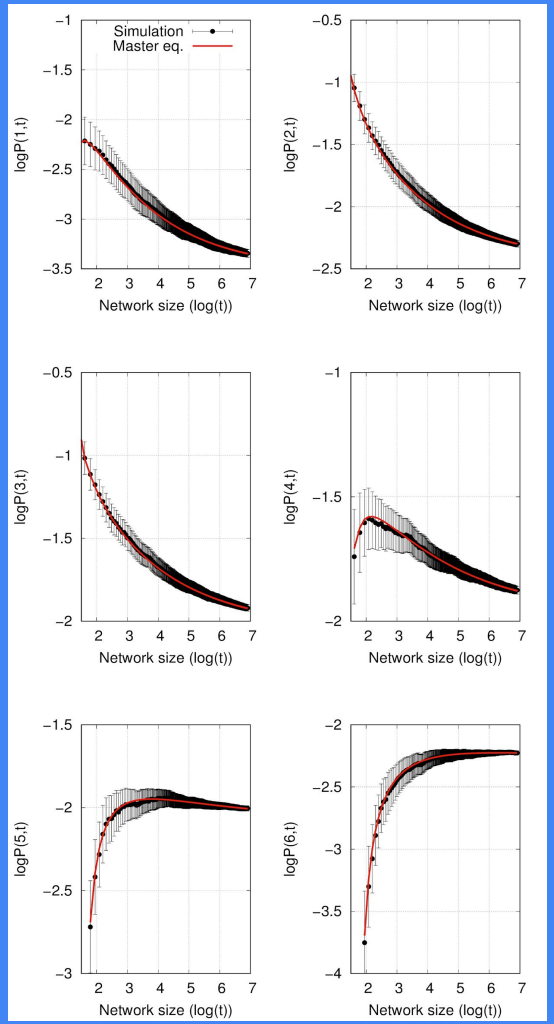
$M < 0.5$: The mean degree diverges as t^{1-2M}.

Scatter plot comparing stationary analytical solution with simulated networks

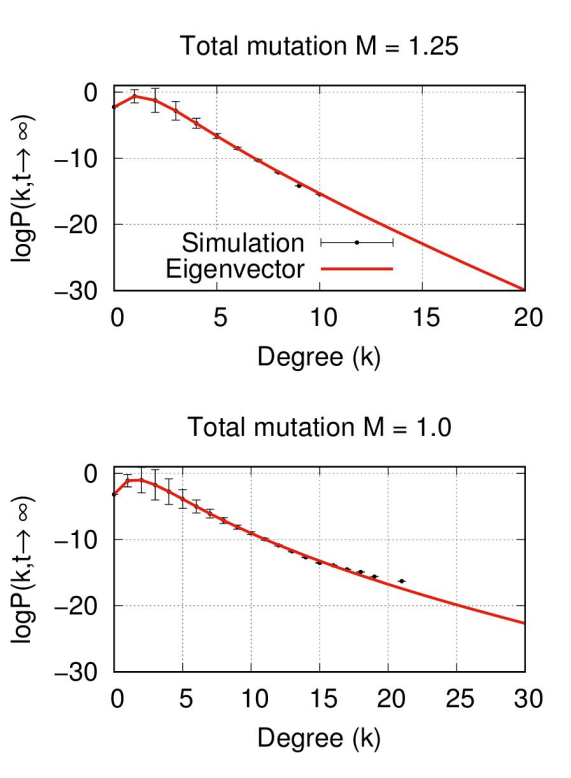


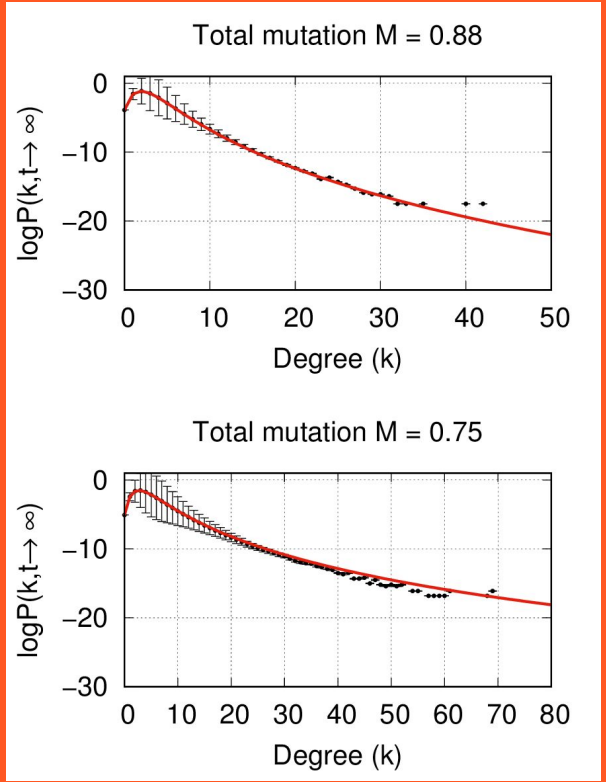
Master equation

$$
\begin{aligned}
N(k,t+1) &= N(k,t) \\
&- \frac{N(k,t)}{t} \\
&+ \sum_{i=k-1}^{t-1} P_o(i \to k) \frac{N(i,t)}{t} \\
&+ \sum_{i=k-1}^{t-1} P_d(i \to k) \frac{N(i,t)}{t} \\
&+ \frac{(k-1)N(k-1,t)}{t}(1-m_o)(1-m_d) \\
&+ \frac{(k+1)N(k+1,t)}{t} m_o m_d \\
&- \frac{kN(k,t)}{t}[(1-m_o)(1-m_d) + m_o m_d]
\end{aligned}
$$



Asymptotic distribution

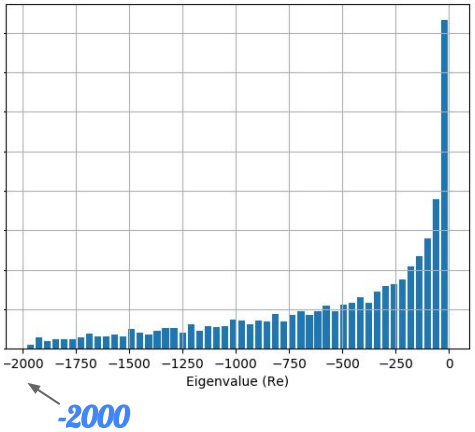




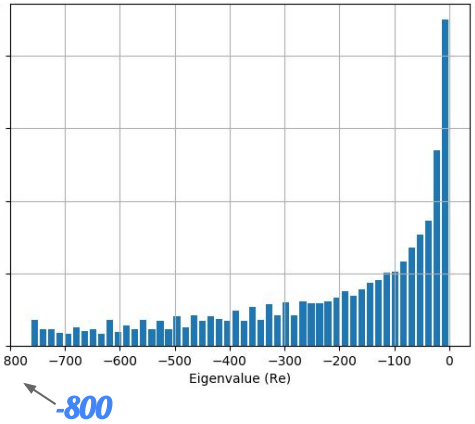
Symmetries of parameters

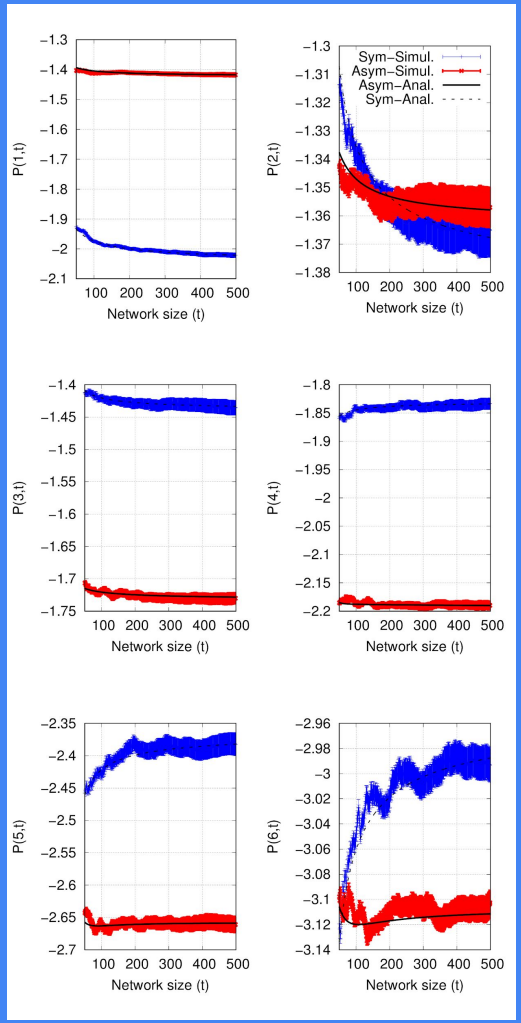
$$M = m_o + m_d$$

$m_o = m_d = 0.4$



$m_o = 0.79$ & $m_d = 0.01$





Conclusions

- We calculate the mean degree as function of network size
  - We separate stationary regimes in this dynamics
- We derived an analytical master equation
- We observe the effects of changing the mutation parameters

Future: Fitting real biological networks with our model!

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Thank you!