Markov Chain Mixing Times And Applications

Ivona Bezáková

(Rochester Institute of Technology)

Nayantara Bhatnagar

(University of Delaware)

Simons Institute for the Theory of Computing
Counting Complexity and Phase Transitions Bootcamp

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Introduction to Markov Chains

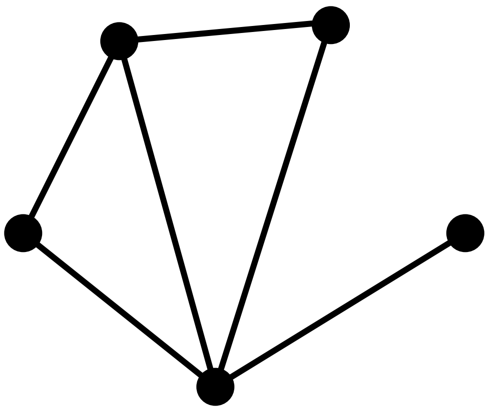
A (discrete) **Markov chain** is a random process that

- has a set of states Ω
- in one step moves from the current state to a random "neighboring" state
- the distribution for the move does not depend on previously visited states

Example:

A random walk on a graph

1. Start at a vertex
2. Randomly choose a neighbor and move there
3. Repeat step 2.



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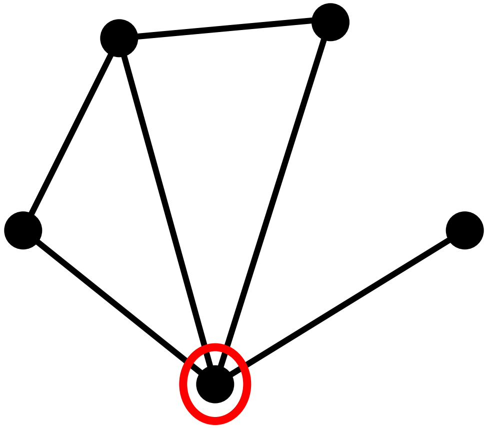

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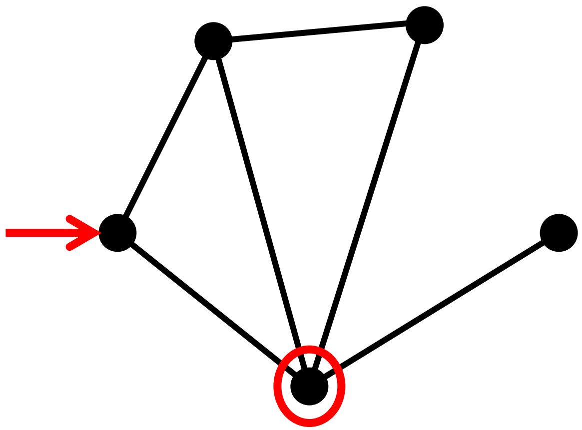

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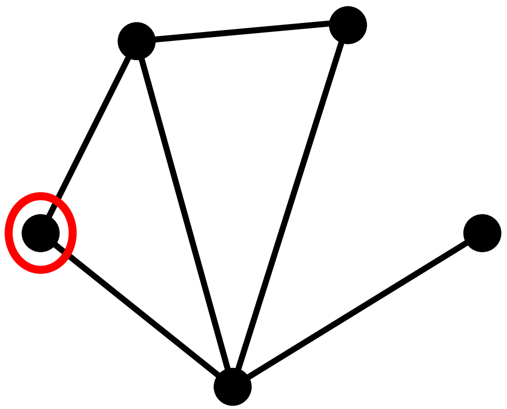

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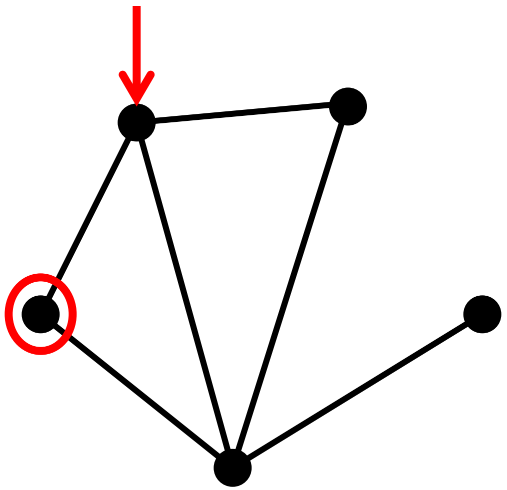

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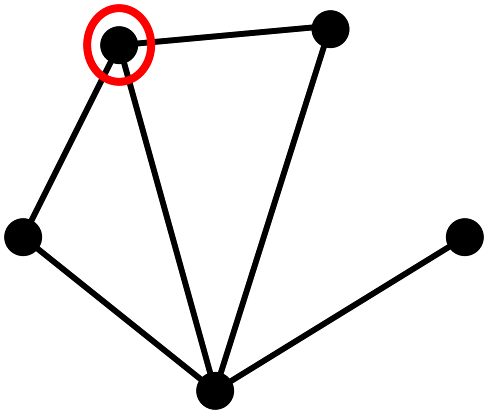

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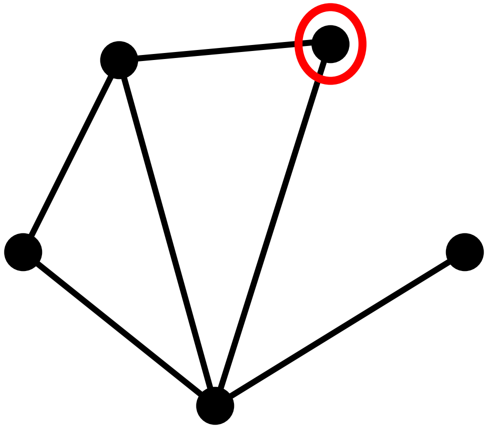

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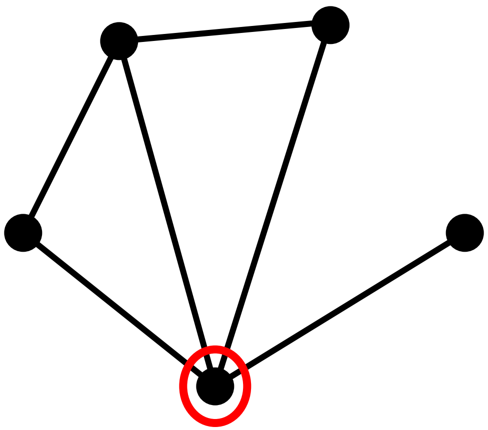

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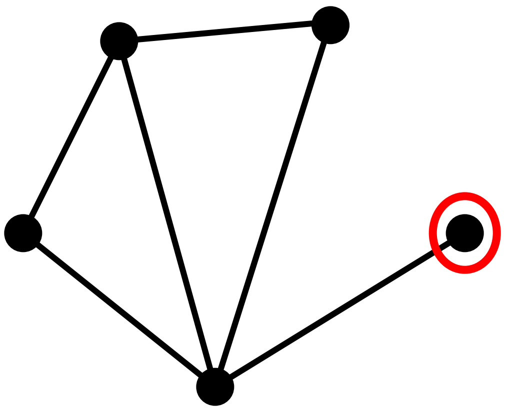

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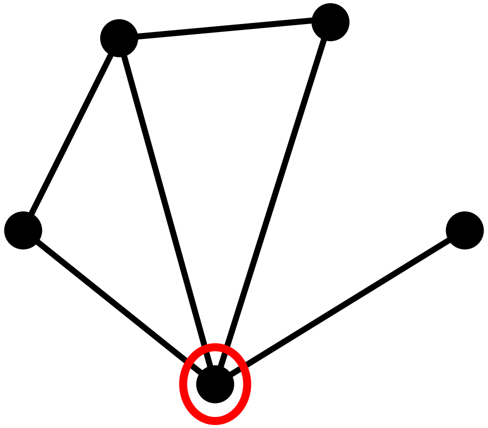

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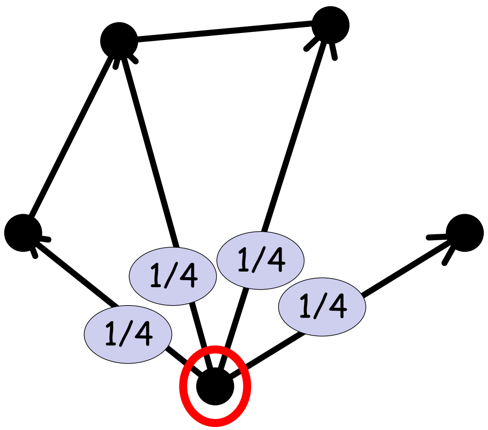

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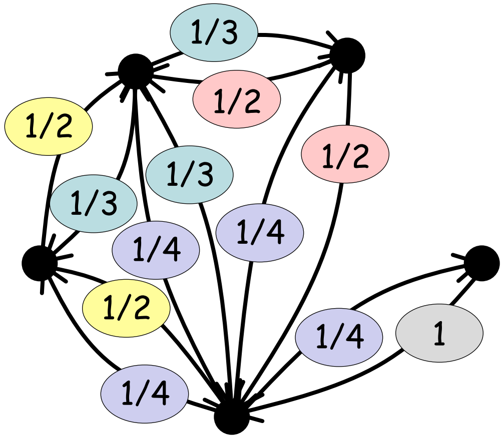

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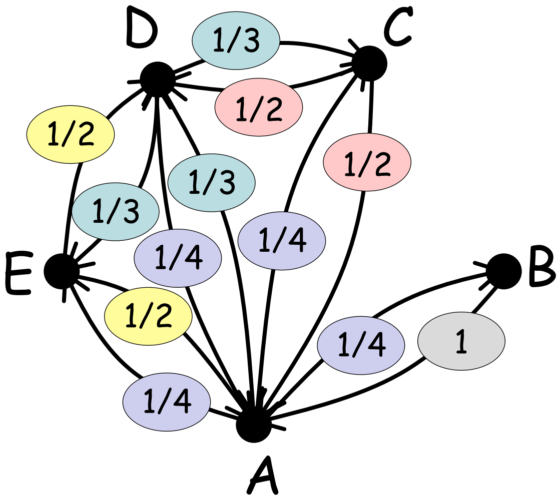
Example:

Transition matrix for this MC:

	A	B	C	D	E
A	0	1/4	1/4	1/4	1/4
B	1	0	0	0	0
C	1/2	0	0	1/2	0
D	1/3	0	1/3	0	1/3
E	1/2	0	0	1/2	0



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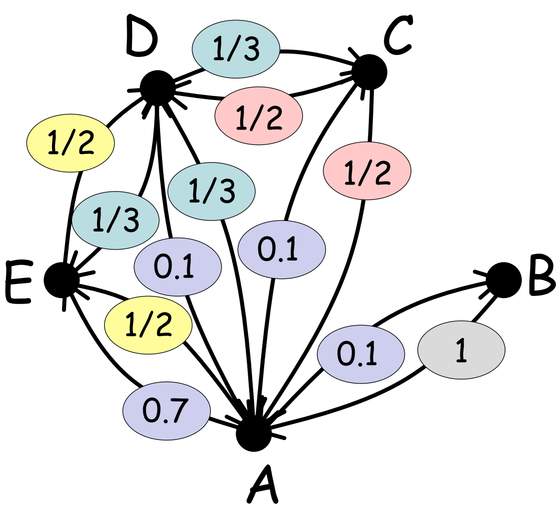
Example:

Transition matrix for another MC:

	A	B	C	D	E
A	0	0.1	0.1	0.1	0.7
B	1	0	0	0	0
C	1/2	0	0	1/2	0
D	1/3	0	1/3	0	1/3
E	1/2	0	0	1/2	0



Introduction to Markov Chains

Def: A (discrete) **Markov chain** M is a pair (Ω, P) where P is an $|\Omega| x |\Omega|$ matrix where each of its rows is a distribution. Ω is the state space and P is the transition matrix.

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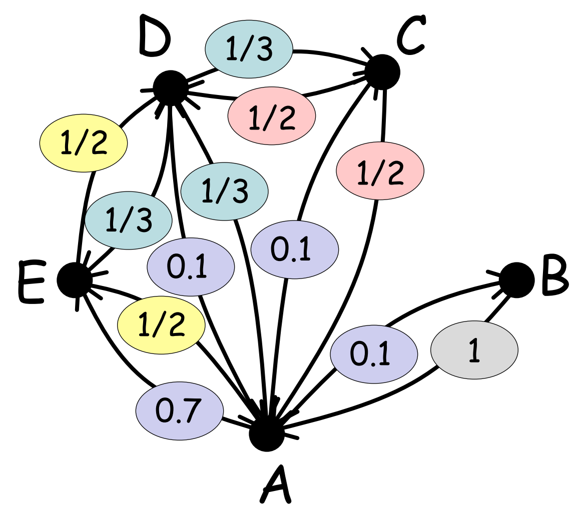

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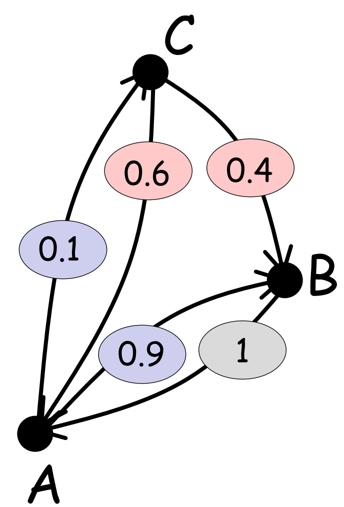
Def: A (discrete) **Markov chain** M is a pair (Ω, P) where P is an $|\Omega| \times |\Omega|$ matrix where each of its rows is a distribution. Ω is the state space and P is the transition matrix.

A distribution π on Ω is stationary if $\pi P = \pi$.

Example:

A simple MC:

	A	B	C
A	0	0.9	0.1
B	1	0	0
C	0.6	0.4	0



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Example:

A simple MC:

P=

	A	B	C
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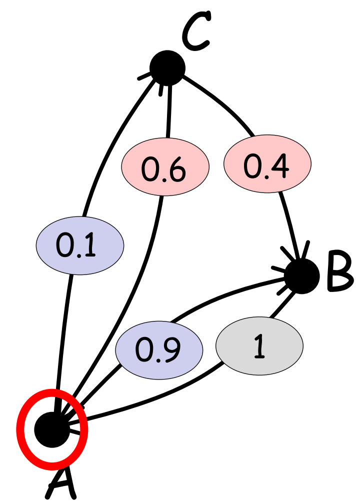
Start in A:

- start distribution: $\sigma = (1,0,0)$



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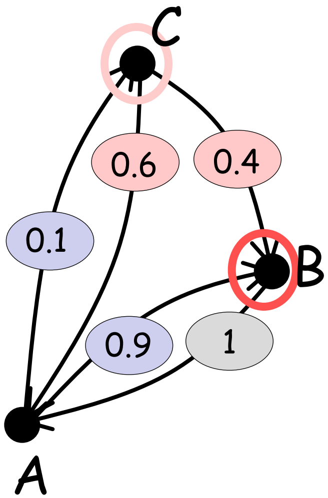
- after one step: $\sigma P = (0,0.9,0.1)$



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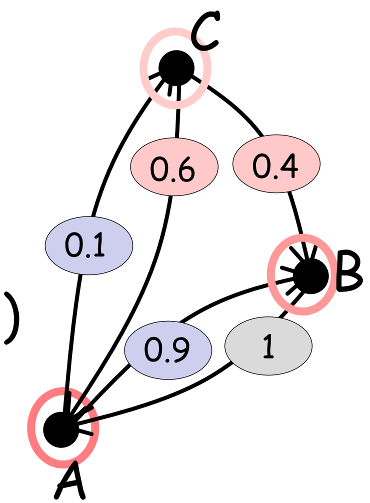
Start in A:

- start distribution: $\sigma = (1,0,0)$
- after one step: $\sigma P = (0,0.9,0.1)$
- after t steps: σP^t



Introduction to Markov Chains

<u>Def:</u> A Markov chain M=(Ω,P) is

• <u>irreducible</u> if there is a path in the transition graph from every state to every other state

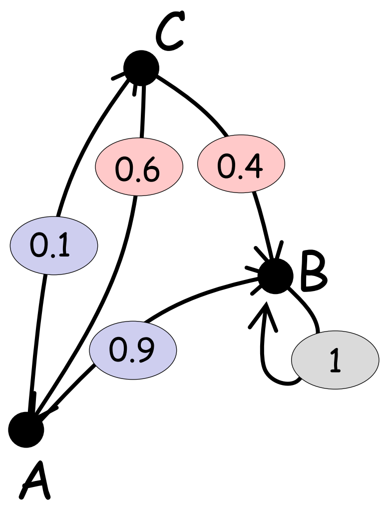
• <u>aperiodic</u> if for each state s, the gcd of all walk lengths from s to s is 1

<u>Example:</u>

Another simple MC (not irreducible):

P=

	A	B	C
A	0	0.9	0.1
B	0	1	0
C	0.6	0.4	0



Introduction to Markov Chains

Def: A Markov chain $M=(\Omega,P)$ is

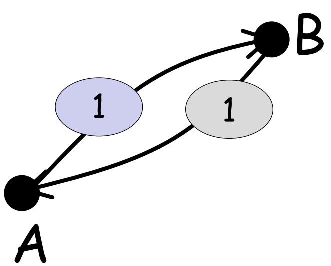
- irreducible if there is a path in the transition graph from every state to every other state
- aperiodic if for each state s, the gcd of all walk lengths from s to s is 1

Example:

Even simpler MC (not aperiodic):

P=

	A	B
A	0	1
B	1	0



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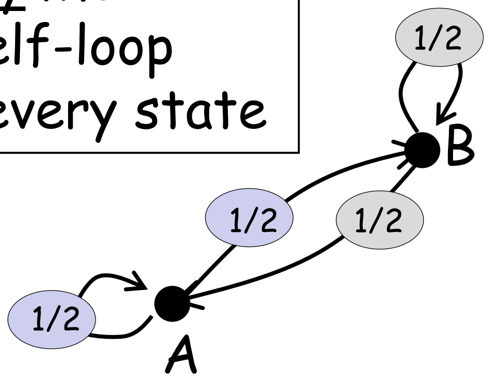
Example:

Even simpler MC (now aperiodic):

Lazy MC:
a self-loop
at every state

$$P = \begin{array}{c|cc} & A & B \\ A & 1/2 & 1/2 \\ B & 1/2 & 1/2 \end{array}$$



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Def: A Markov chain $M=(\Omega,P)$ is

- irreducible if there is a path in the transition graph from every state to every other state
- aperiodic if for each state s, the gcd of all walk lengths from s to s is 1
- ergodic if both irreducible and aperiodic

Thm: An ergodic MC has a unique stationary distribution.

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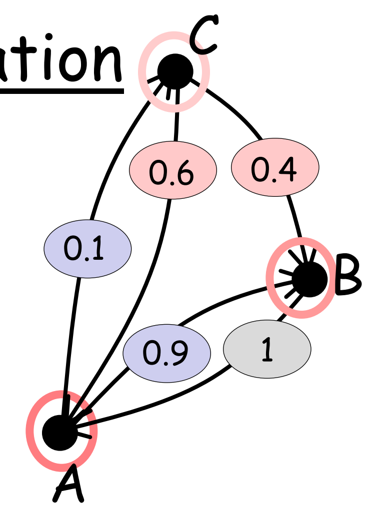
Def: For ϵ>0, mixing time is # steps needed to get ϵ-close to the stationary distribution π. Formally:

For a start state x, let σ_x be the corresponding starting distribution. Then

$t_{mix}(\epsilon)$ = minimum t such that for every x, $||\sigma_x P^t - \pi||_{tv} < \epsilon$

where, for two distributions μ,ν, their total variation distance is

$$||\mu - \nu||_{tv} = \frac{1}{2} \sum_{x \in \Omega} |\mu(x) - \nu(x)|$$



Example:

$||(1,0,0) - (0,0.9,0.1)||_{tv} = \frac{1}{2}(1+0.9+0.1) = 1$

$||(0.5,0.4,0.1) - (0.6,0.4,0)||_{tv} = \frac{1}{2}(0.1+0.1) = 0.1$

Introduction to Markov Chains

Thm: An ergodic MC has a unique stationary distribution.

$\pi P = \pi$

Observations:

- Eigenvalue: 1, with eigenvector π
- All eigenvalues, in absolute value, ≤ 1
- Mixing time depends on the spectral gap (difference between 1 and the 2nd largest eigenvalue in absolute value)

Thm: For an ergodic MC, let $1 = \lambda_1 > \lambda_2 \geq \ldots \geq \lambda_{min}$ be the eigenvalues and $\pi_{min} = \min_x \pi(x)$. Then

$$t_{mix}(\varepsilon) \leq \frac{1}{1 - \max\{|\lambda_2|, |\lambda_{\min}|\}} \log\left(\frac{1}{\varepsilon \pi_{\min}}\right)$$

$$t_{mix}(\varepsilon) \geq \frac{|\lambda_2|}{1 - \max\{|\lambda_2|, |\lambda_{\min}|\}} \log\left(\frac{1}{2\varepsilon}\right)$$

Exponential State Space

A MC on Colorings:

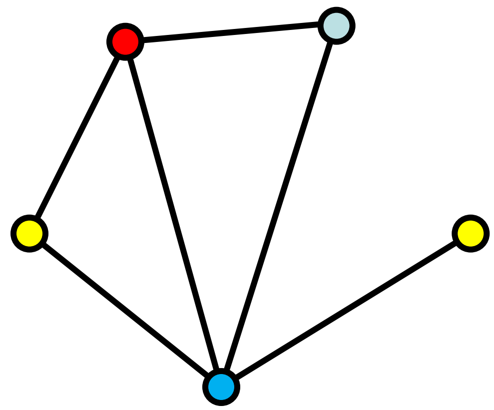
Given is a graph G and a set [q]. A coloring assigns to each vertex a color from [q], so that adjacent vertices have different colors. Let Ω be the set of all colorings.

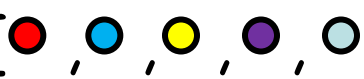
MC on Ω:

1. Choose a random vertex v and a random color c.
2. If no neighbor of v is colored by c, recolor v by c, otherwise, do nothing.

Example:

G:



[q] = {  }

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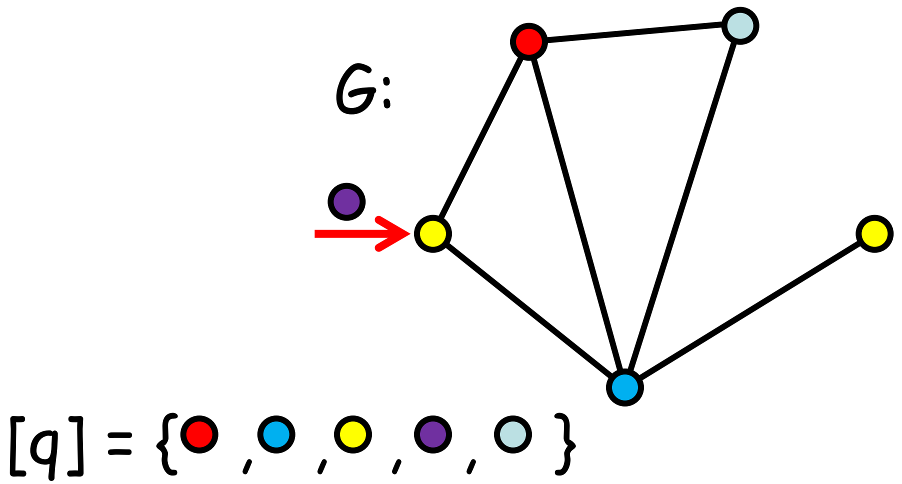

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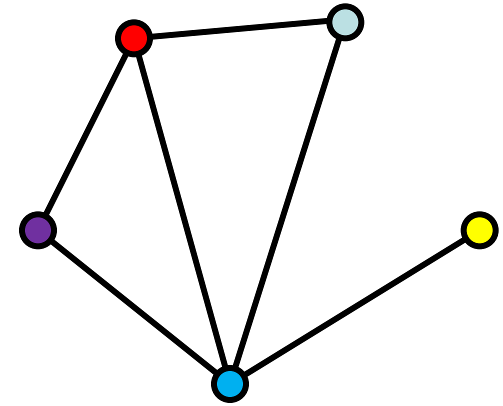
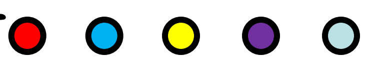


[q] = {  }

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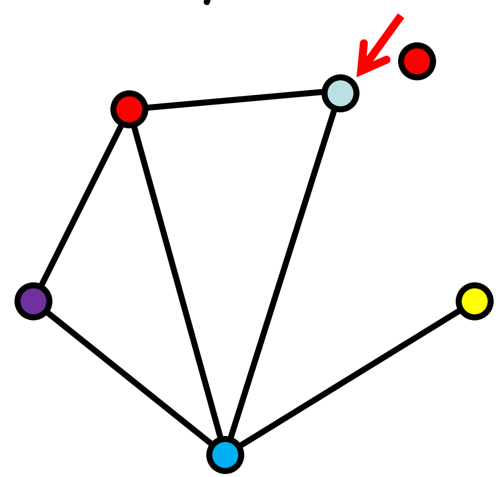
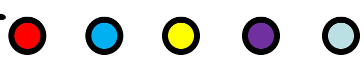


$[q] = \{$  $\}$

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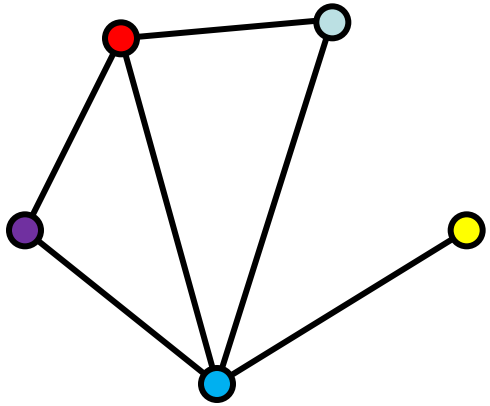
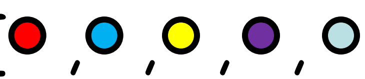


$[q] = \{$  $\}$

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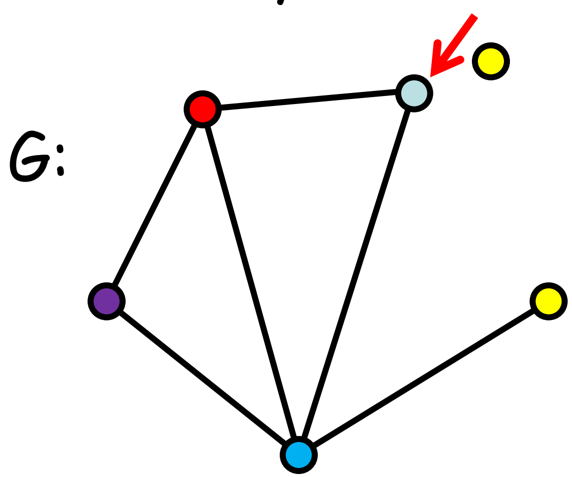

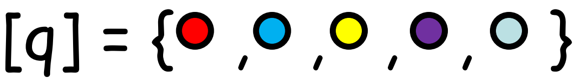

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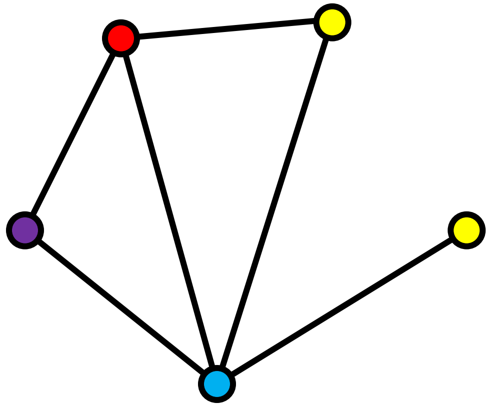
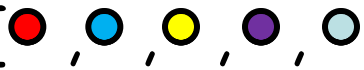


[q] = {  }

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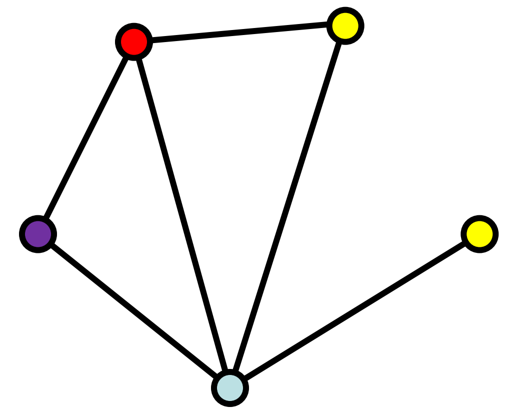
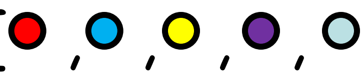


[q] = {  }

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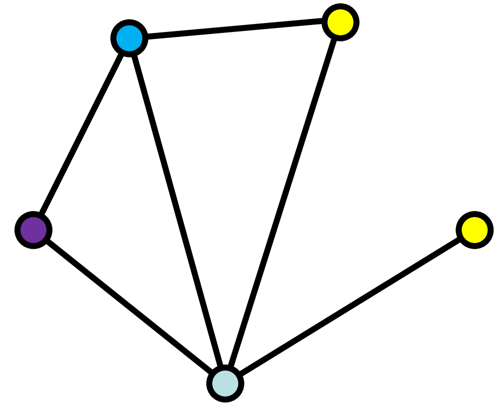
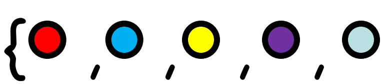


[q] = {  }

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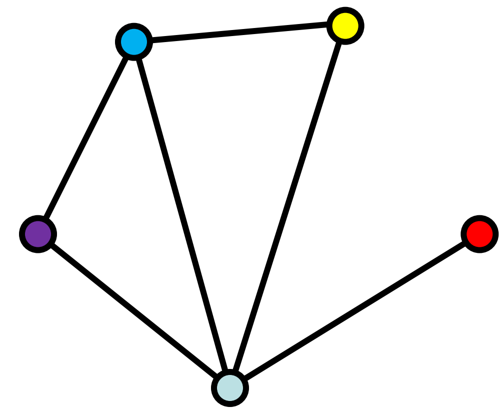
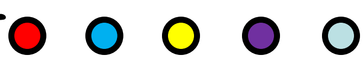


[q] = {  }

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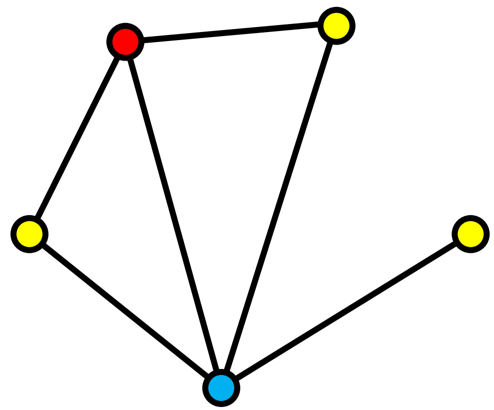

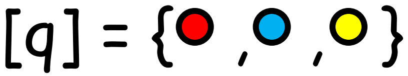

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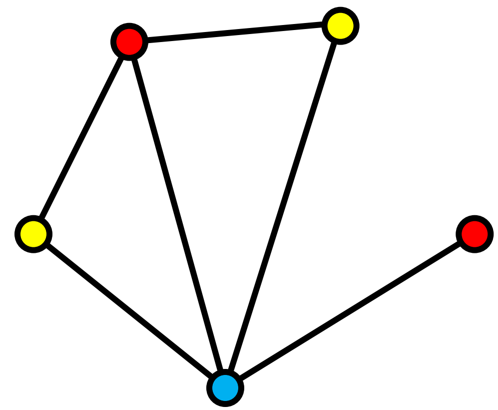

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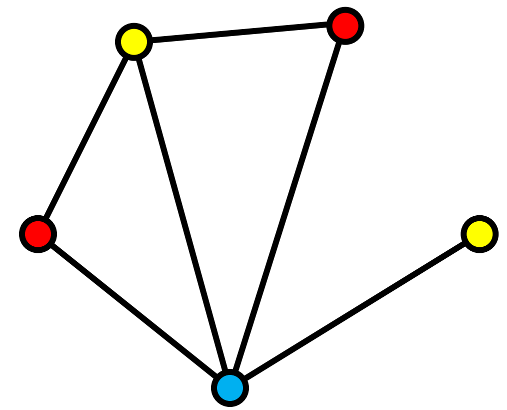

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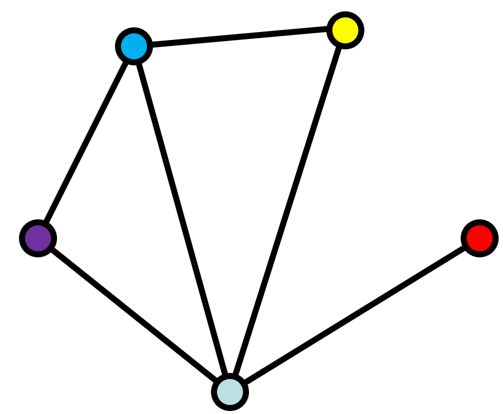
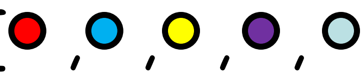


[q] = {  }

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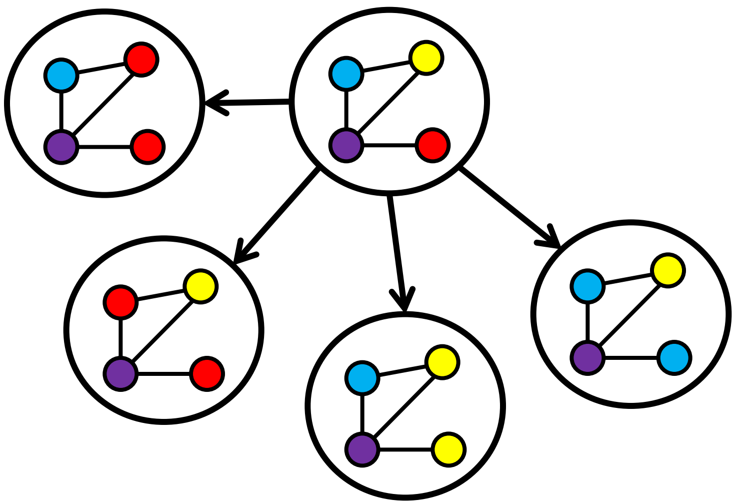
<u>A MC on Colorings:</u>

- ergodic: unique stationary distribution π
- transition probability for neighboring x,y: $P(x,y) = 1/(nq)$



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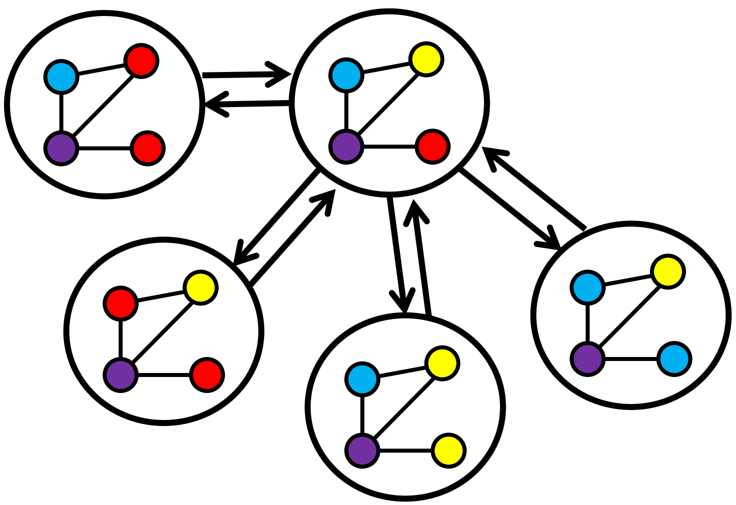

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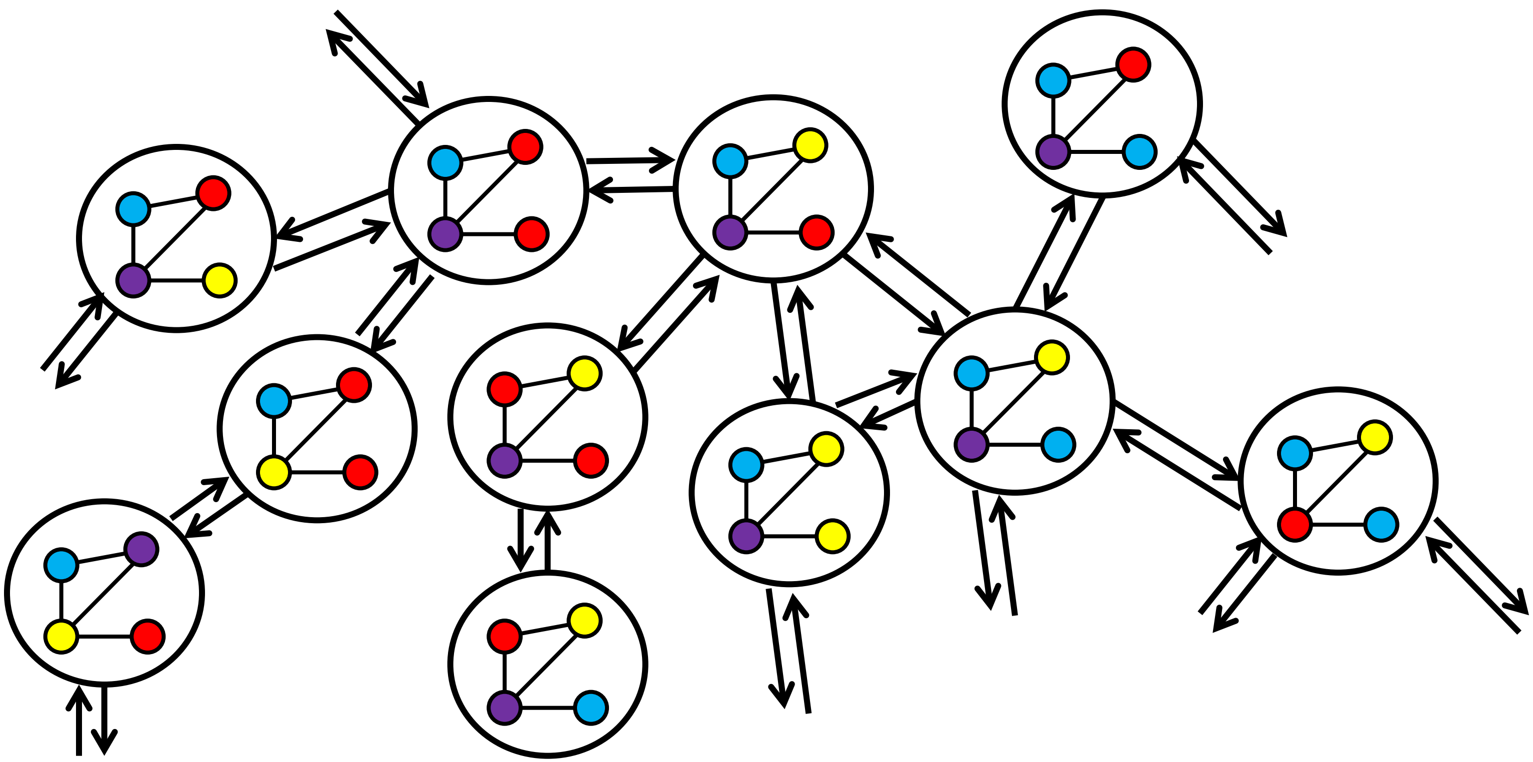

etc...

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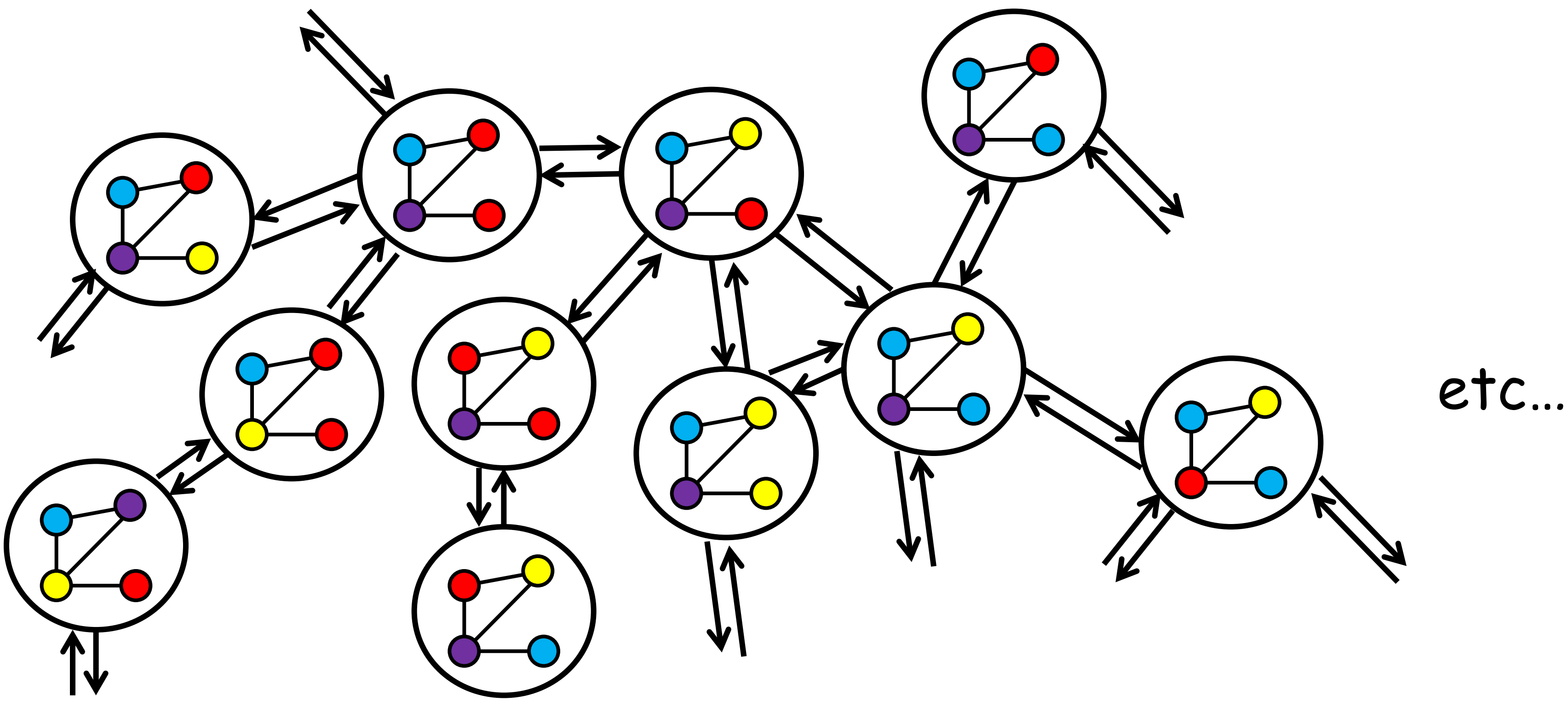

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More generally:

A MC is reversible, if there is a distribution π such that:

$$\pi(x)\, P(x,y) = \pi(y)\, P(y,x)$$

[Also known as detailed balance condition.]

Then, π is stationary.

Designing a Markov Chain

Want: to sample from a target distribution π

How (Metropolis filter):

- start with a symmetric ergodic MC (Ω, P') -> uniform stationary distribution
- modify the probability of a move from x to y as follows:

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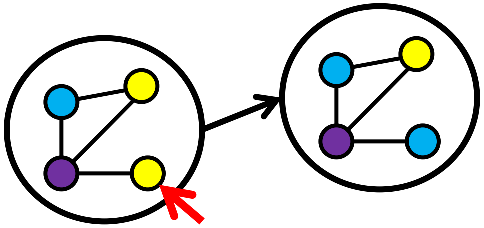

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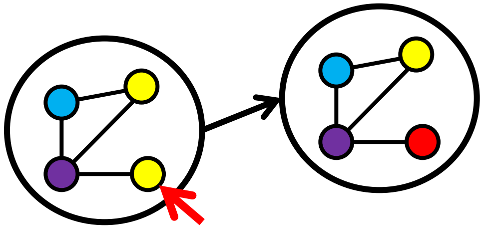

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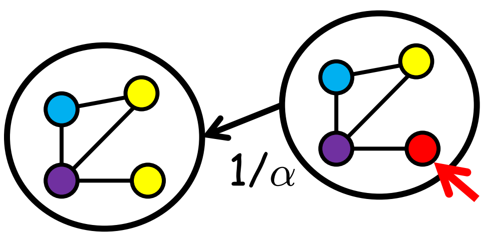

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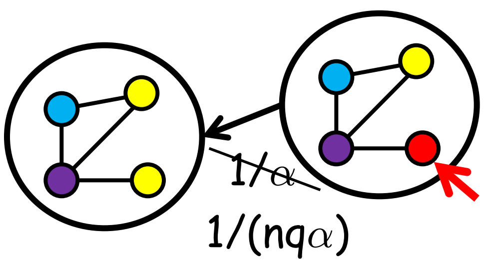
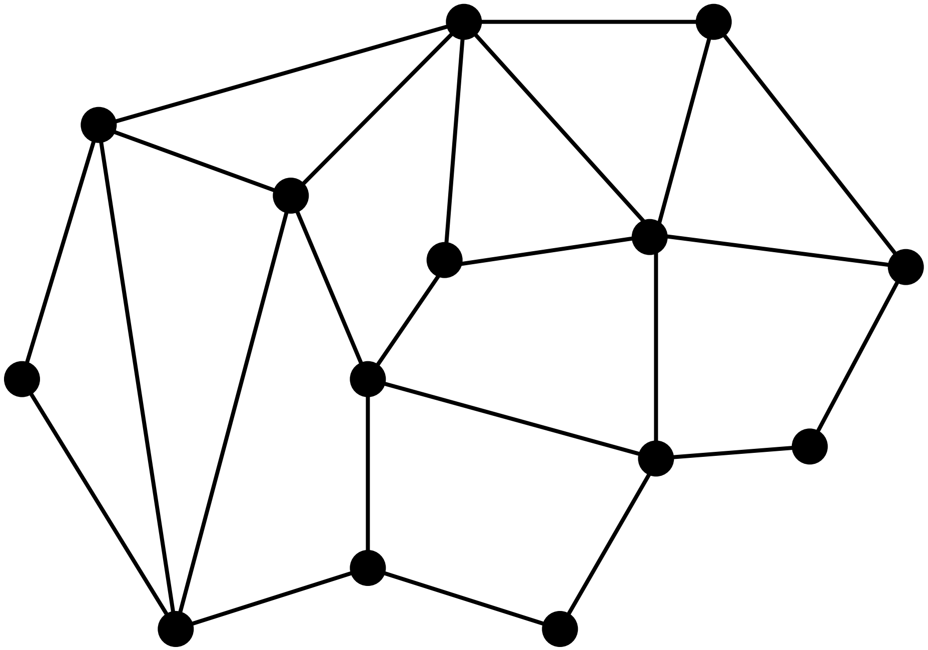


Relation to Counting

Given an undirected graph $G=(V,E)$, a **matching** $M \subseteq E$ is a set of vertex disjoint edges. A matching is **perfect** if $|M|=n/2$, where n = # vertices (and m = # edges).

Example:



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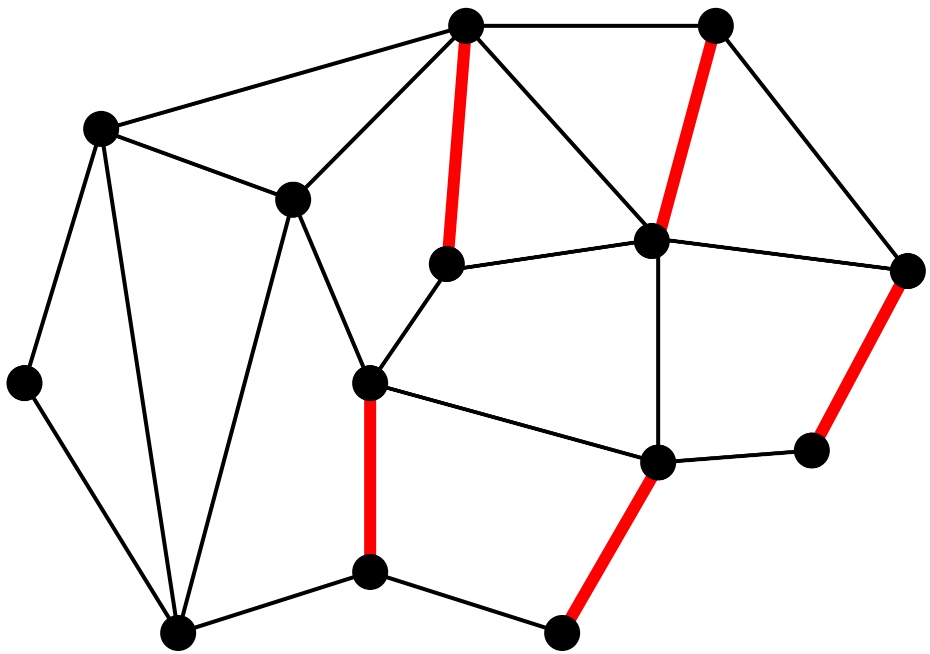
A matching



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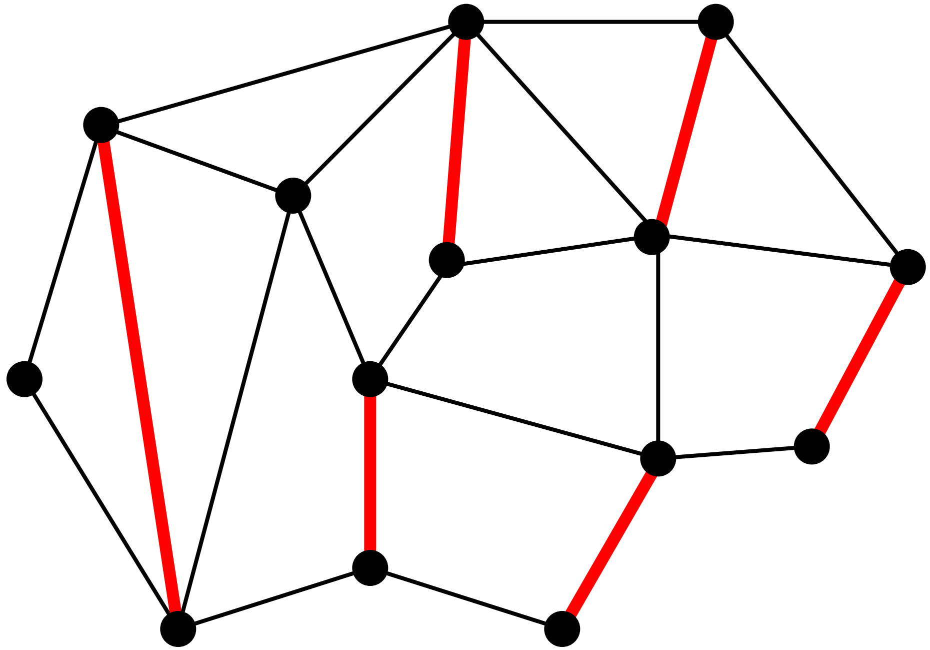

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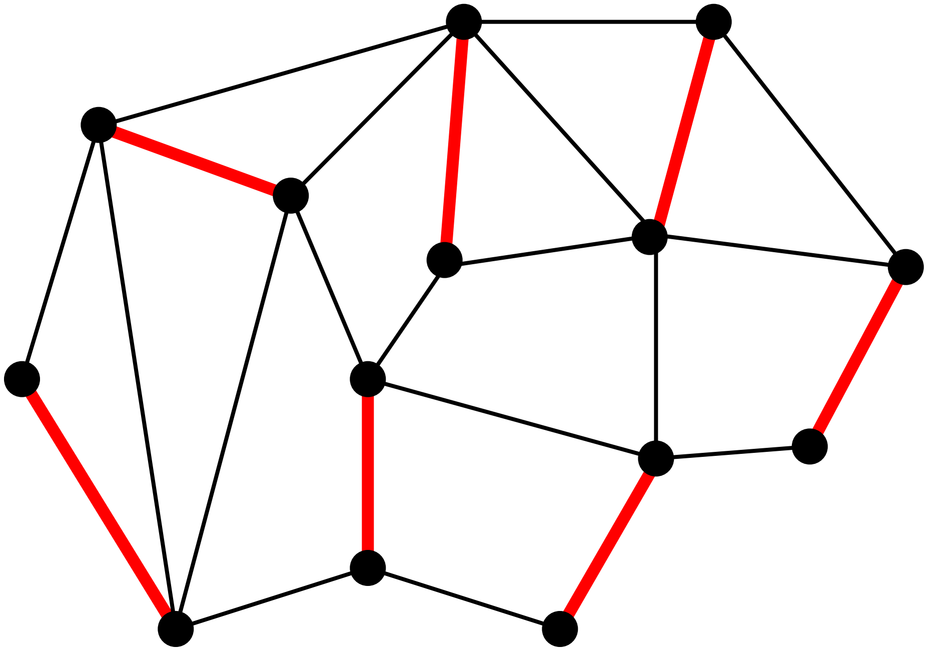

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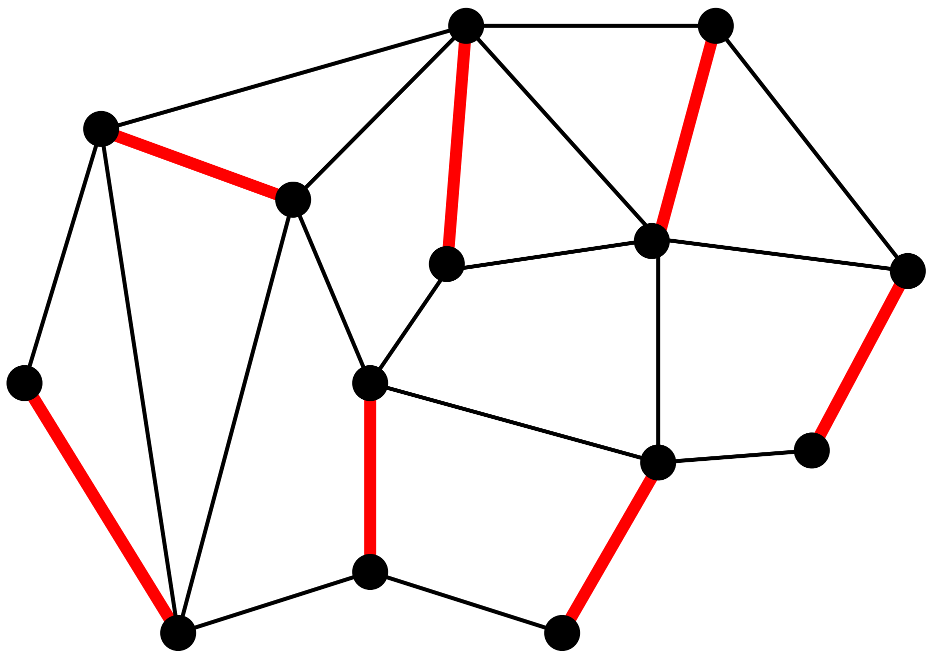
Known:

• Finding a maximum matching can be done in polynomial time [O(m√n) Micali-Vazirani '80]

• Counting perfect matchings is #P-complete [Valiant '79]



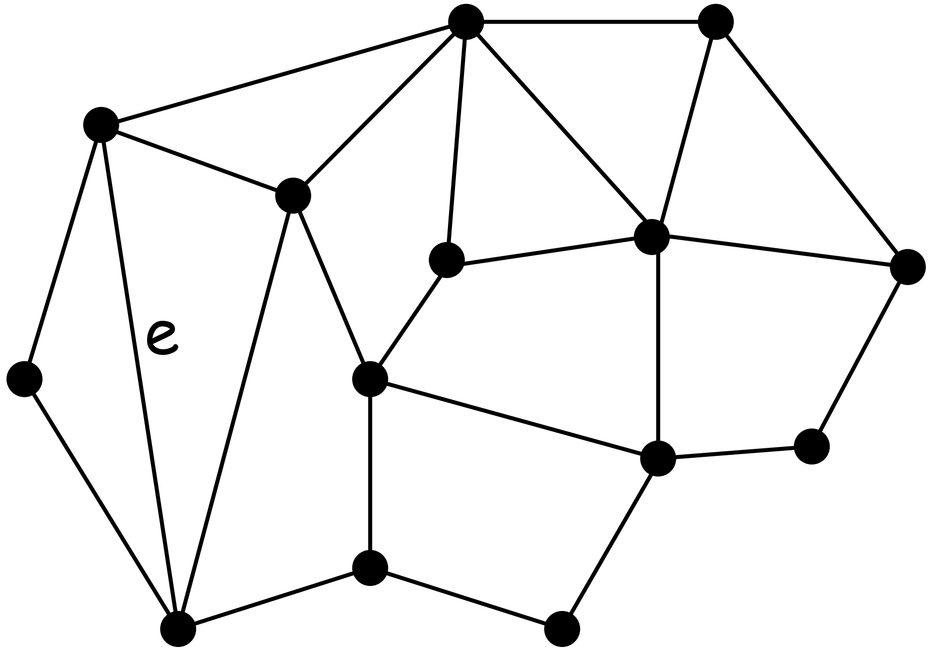
Goal: *Approximate* counting

From Sampling to Counting

Suppose we can sample a uniformly random matching.

Then:

- Let e be an arbitrary edge. Use sampling to determine the fraction of matchings that do not use e.



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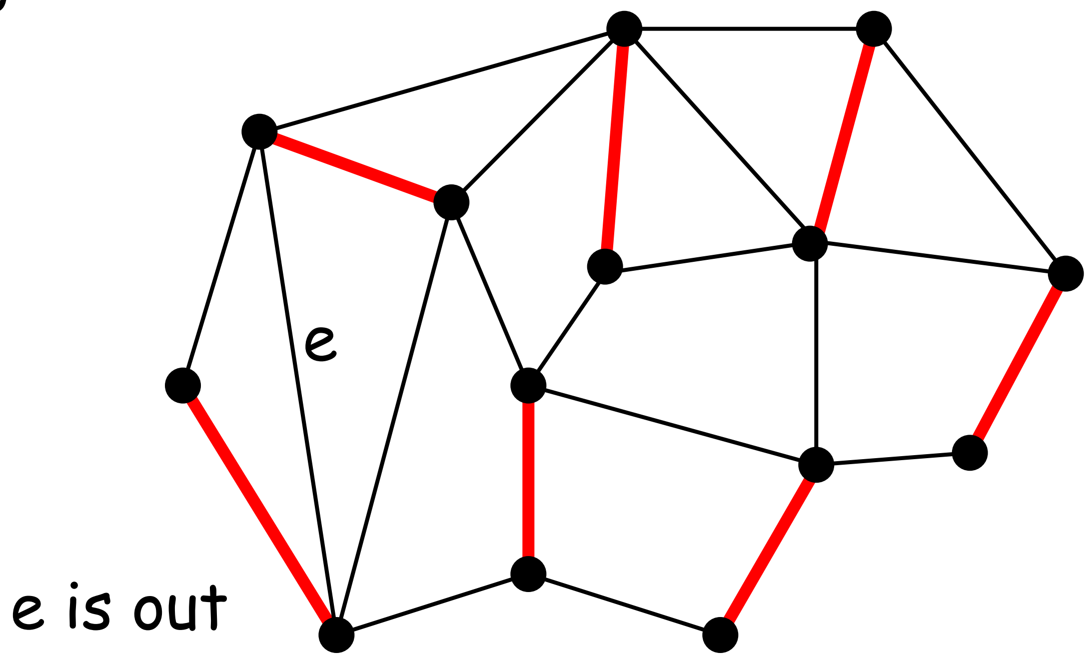

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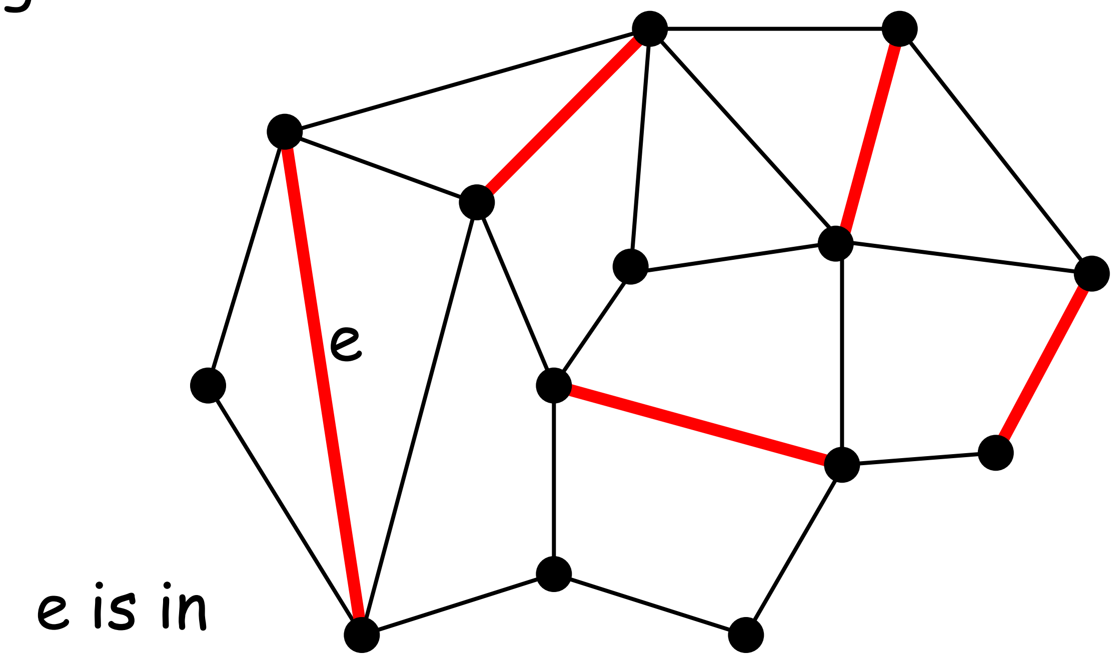

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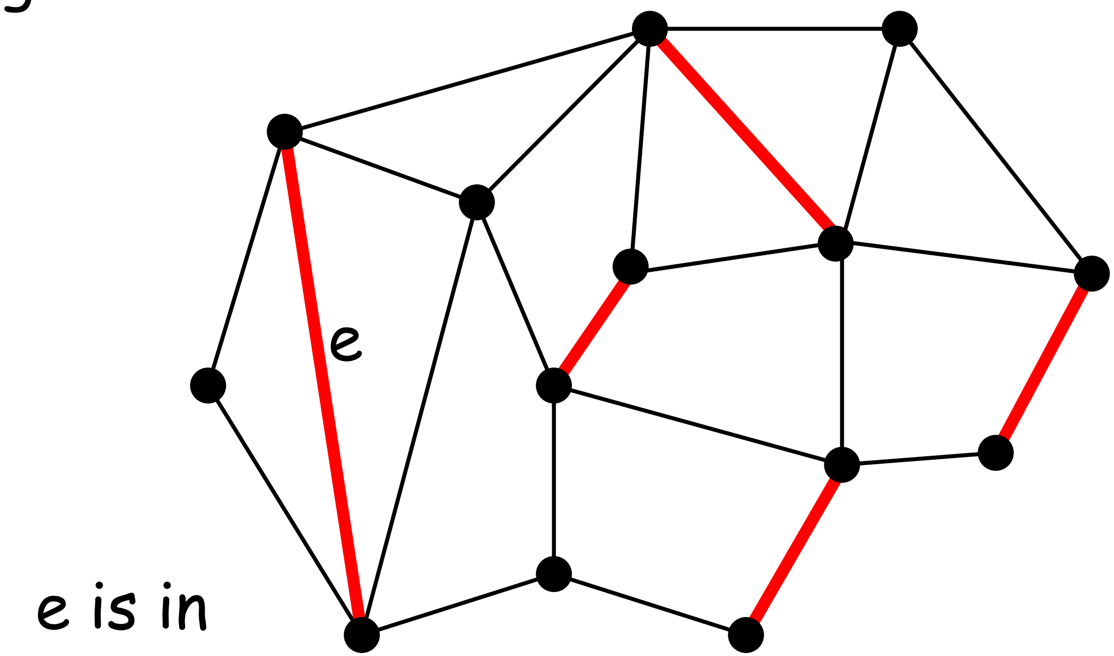

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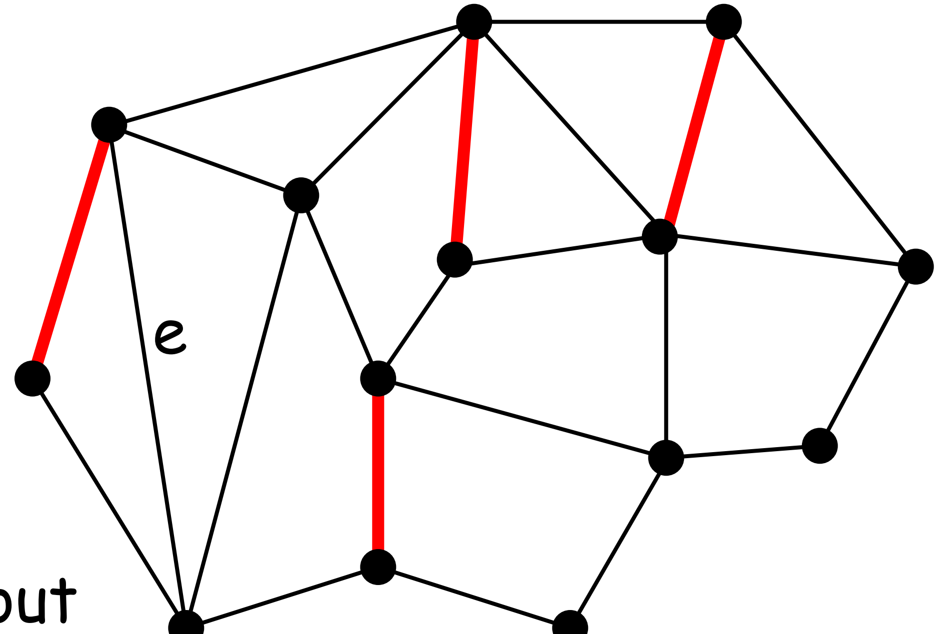


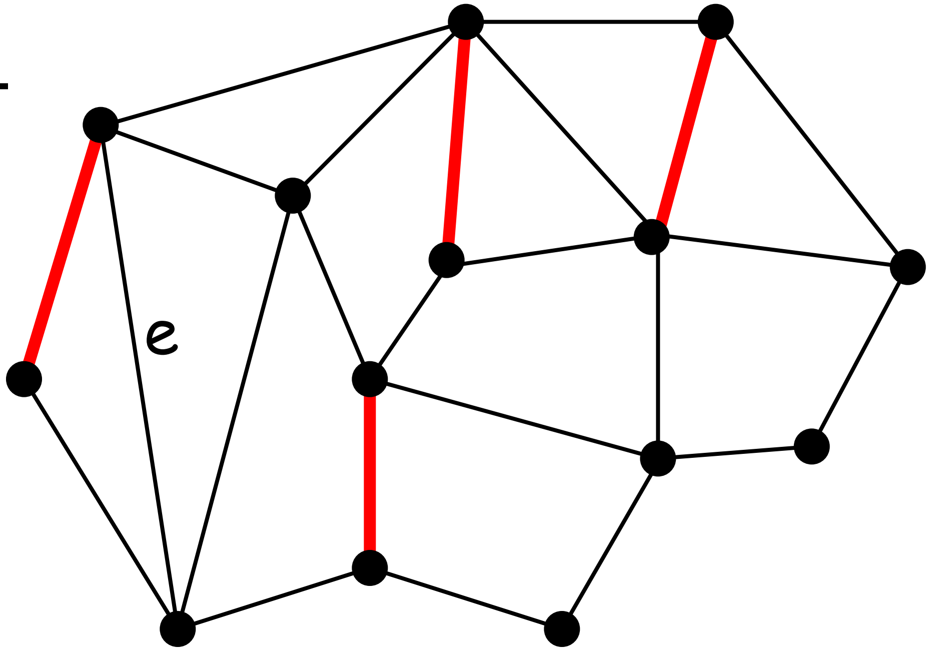
e is out

From Sampling to Counting

Estimator:

Indicator random variable X,
=1 if matching does not contain e and
=0 otherwise

$$E[X] = \frac{\#\text{ matchings without } e}{\#\text{ matchings}}$$



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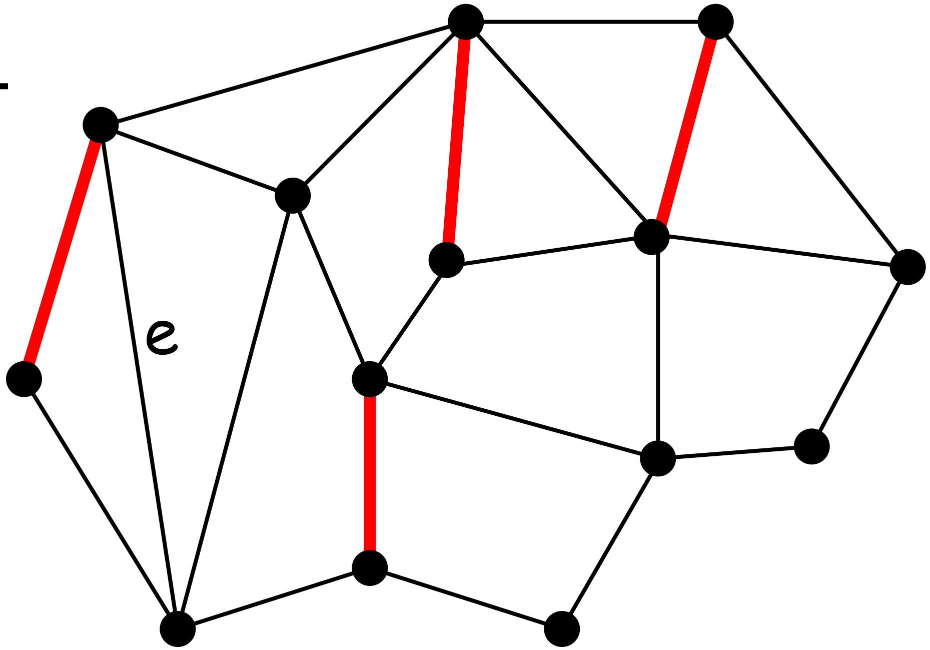
$1/2 \le E[X] \le 1$



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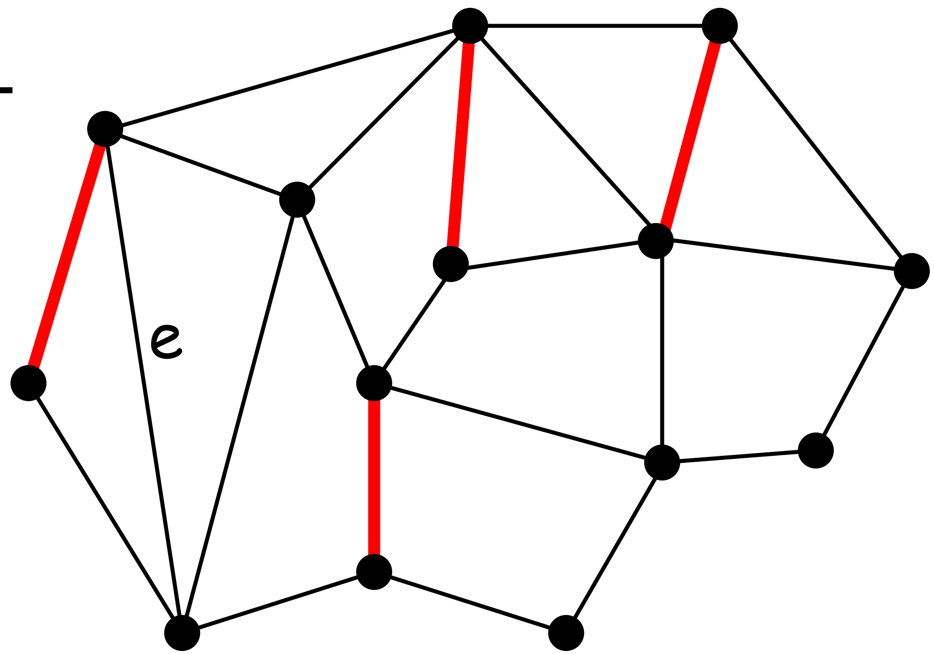

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(For every matching with edge e, we can remove it to get a matching without e.)

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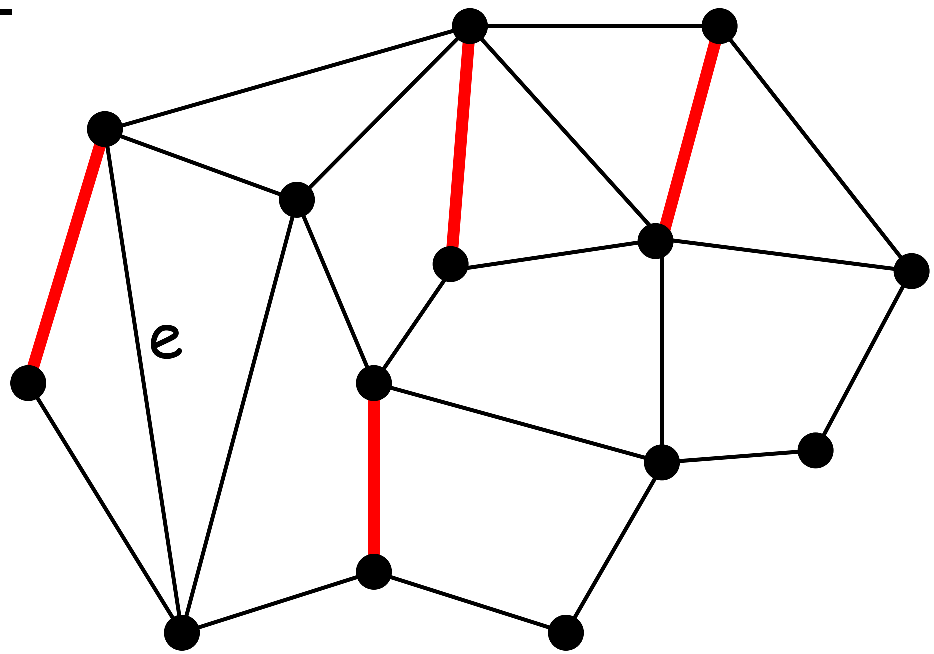

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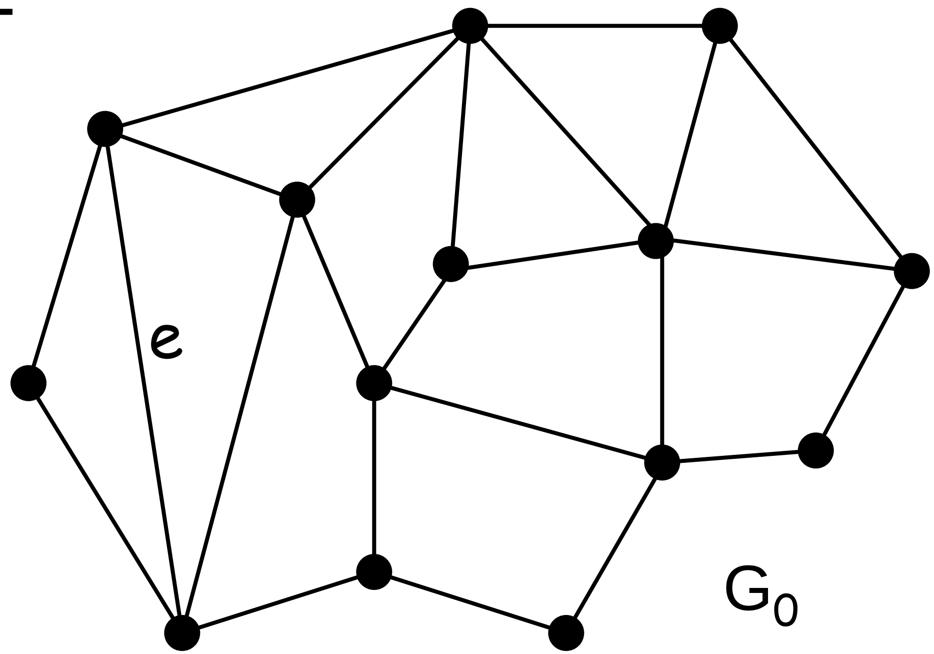

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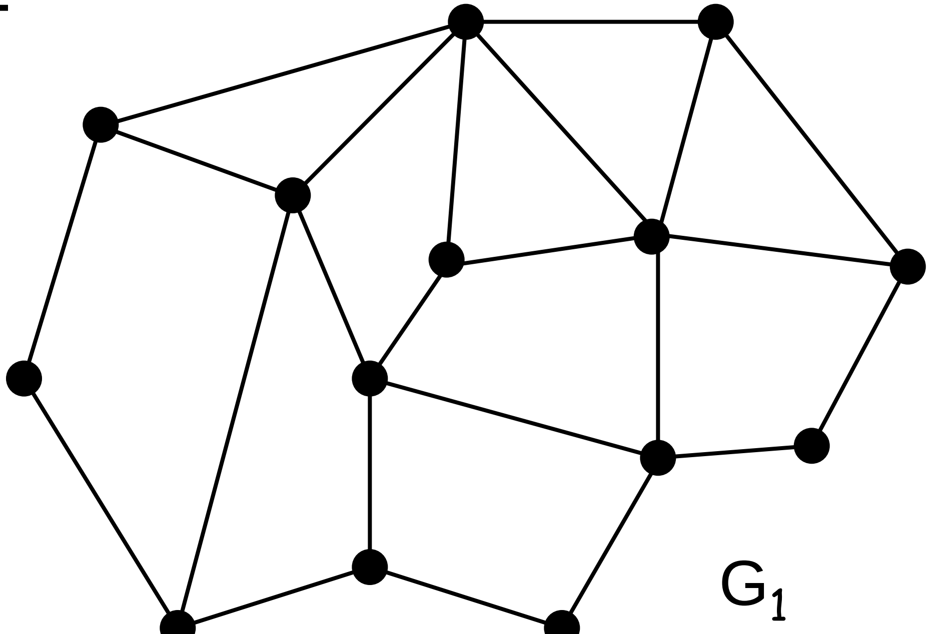

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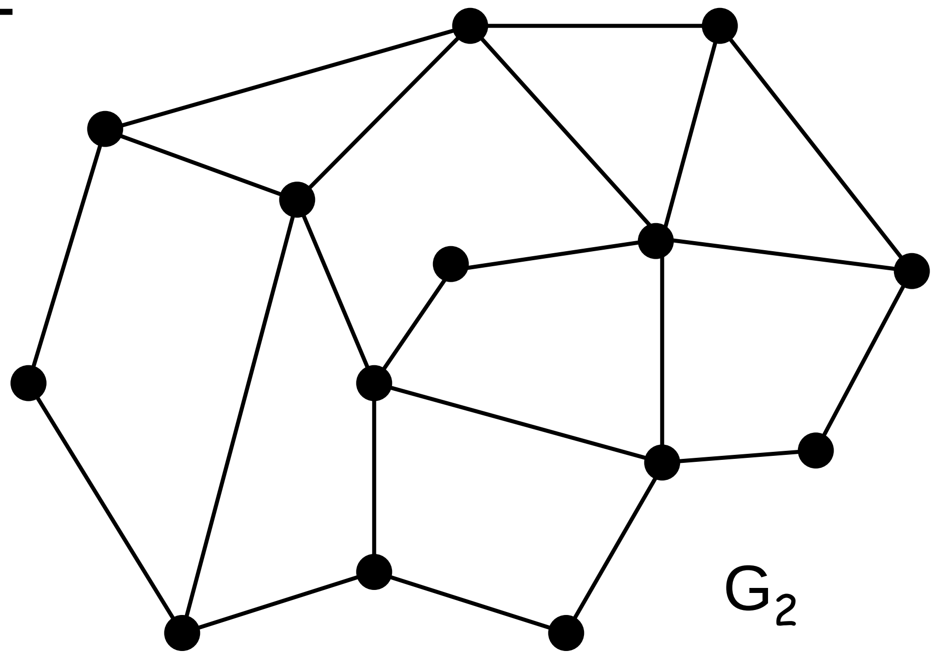

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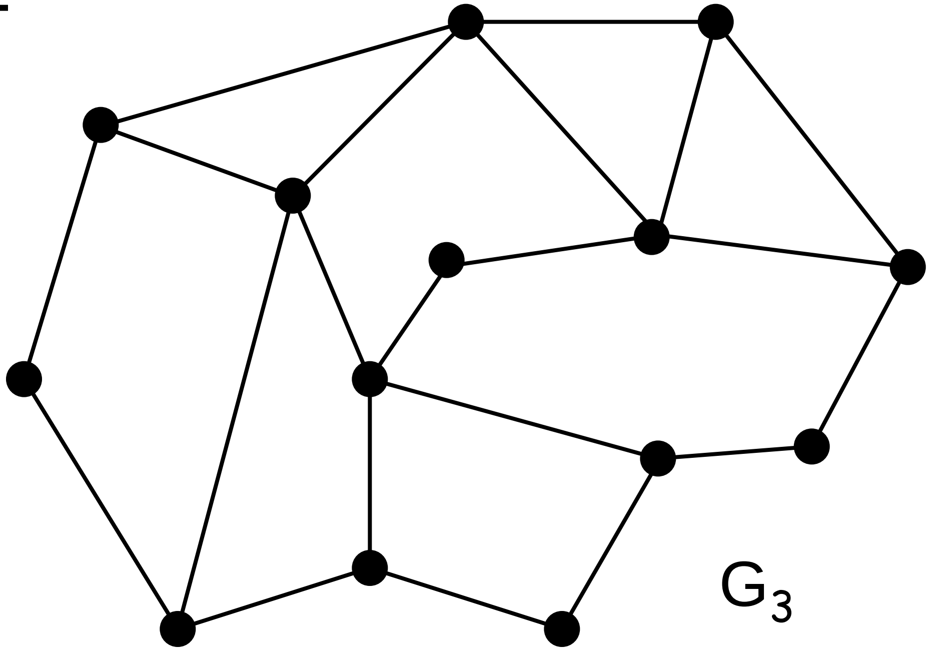
- Let $G_0 = G$ and $G_1 = G\text{-}e$, then:

$$E[X] = \frac{\text{\# matchings in } G_1}{\text{\# matchings in } G_0}$$



From Sampling to Counting

Suppose we can sample a uniformly random matching.

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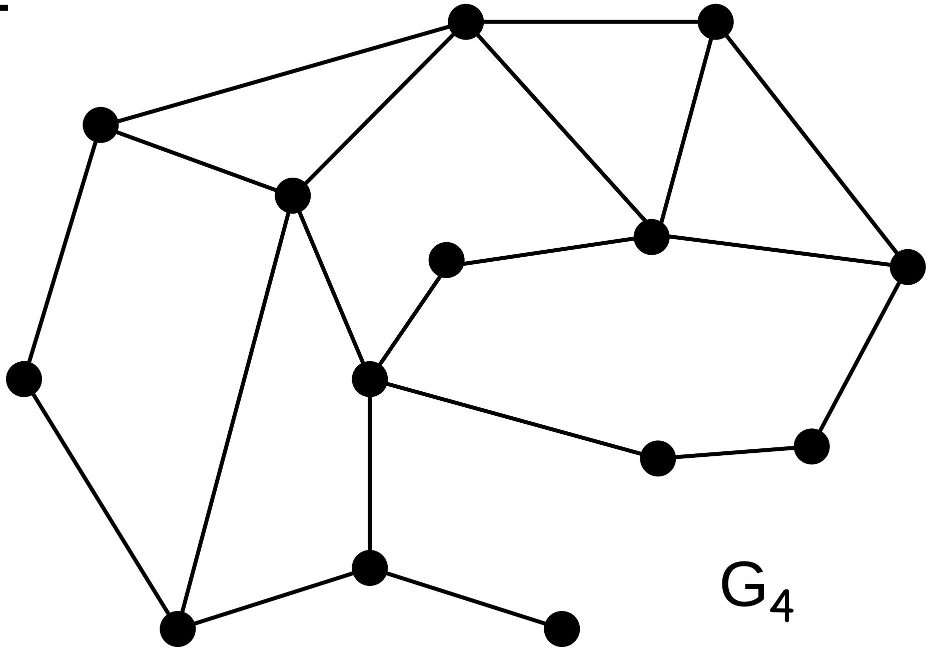

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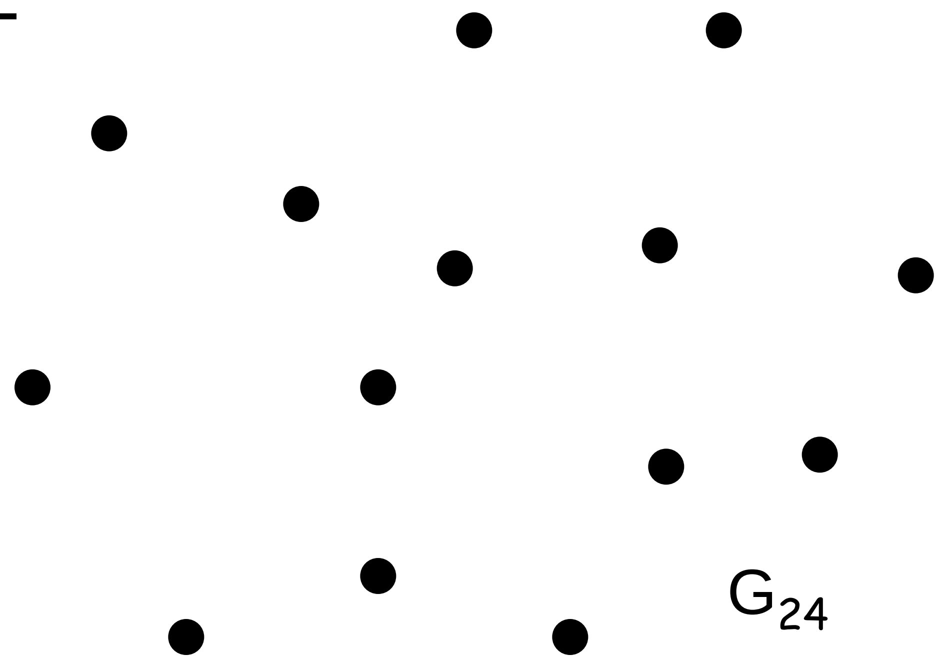

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$$E[X] = \frac{\#\text{ matchings without } e}{\#\text{ matchings}} = \frac{\#\text{ matchings in } G_1}{\#\text{ matchings in } G_0} = \frac{|M(G_1)|}{|M(G_0)|}$$

- Let $e_1,\ldots,e_m$ be the edges of G. Let $G_i = G-\{e_1,\ldots,e_i\}$. Let $M(G)$ be the set of all matchings in G. Estimate: $\frac{|M(G_{i+1})|}{|M(G_i)|}$
- Then:

$$\frac{|M(G_1)|}{|M(G_0)|}\;\frac{|M(G_2)|}{|M(G_1)|}\;\frac{|M(G_3)|}{|M(G_2)|}\cdots\frac{|M(G_m)|}{|M(G_{m-1})|} = \frac{|M(G_m)|}{|M(G_0)|} = \frac{1}{|M(G)|}$$

[**<u>Self-reducibility</u>**]

From Sampling to Counting: Technicalities

Terminology:

- **Almost uniform sampler**: for a tolerance parameter $\delta>0$, it produces a sample from a distribution within variation distance of δ from the uniform distribution

- **Fully polynomial almost uniform sampler (FPAUS)**: runs in time polynomial in input size and log $1/\delta$

- **Randomized approximation scheme**: for a counting problem and error tolerance ϵ, produce an answer within $(1+-\epsilon)$ factor of the count with probability $\geq 3/4$

- **Fully polynomial randomized approximation scheme (FPRAS)**: runs in time polynomial in input size and $1/\epsilon$

From Sampling to Counting: Technicalities

Thm [Jerrum-Valiant-Vazirani '86]:

FPAUS for sampling from all matchings => FPRAS for counting all matchings.

In particular, get an FPRAS with running time

$$O(\ T(n,m,\epsilon/(6m))\ m^2/\epsilon^2\ ),$$

where $T(n,m,\delta)$ is the running time of the FPAUS.

Goal: to design a Markov chain to sample matchings;
better mixing time => better running time of the FPRAS