

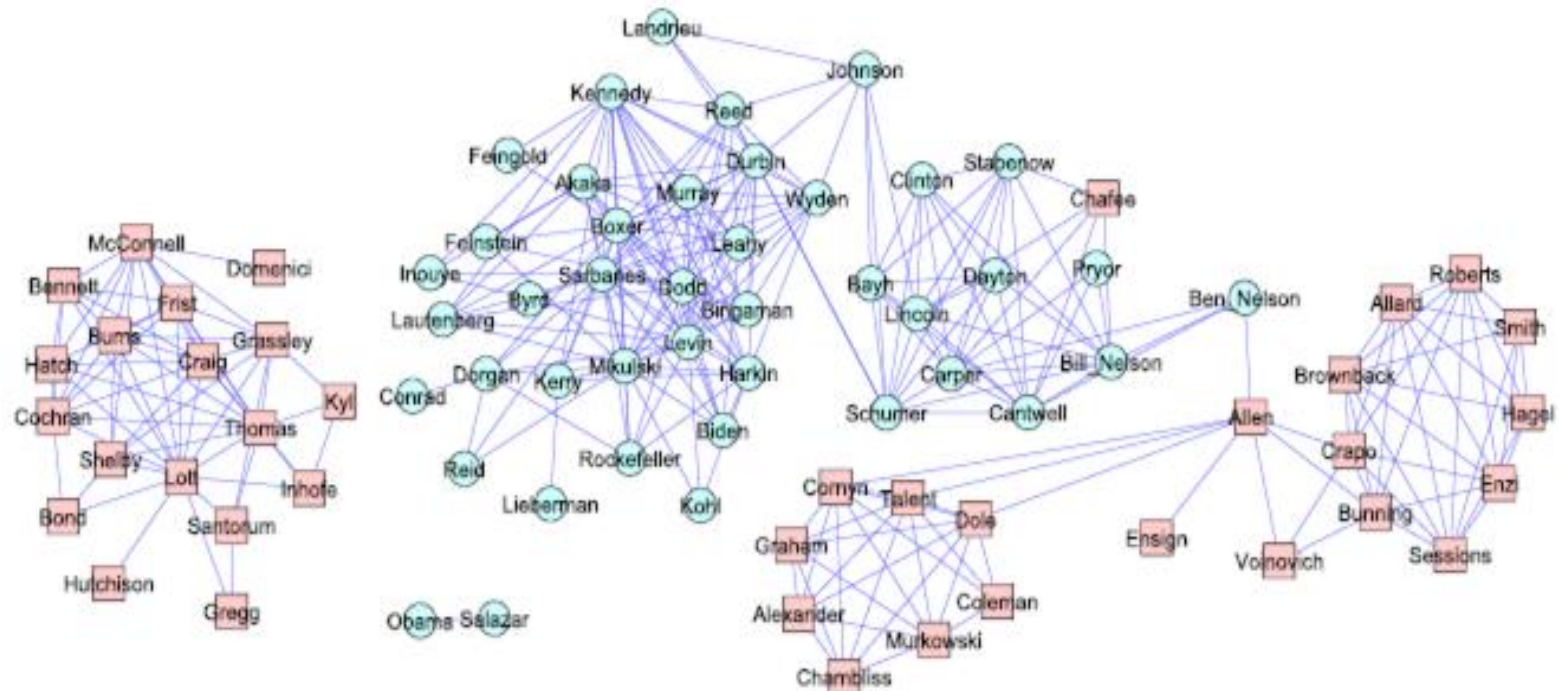
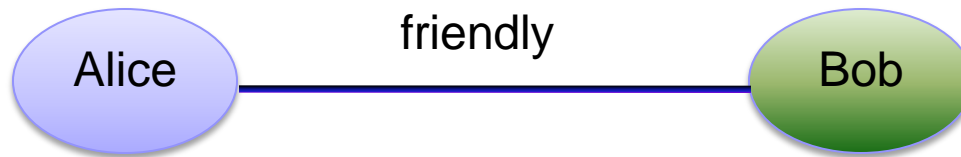
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ROSAEC workshop



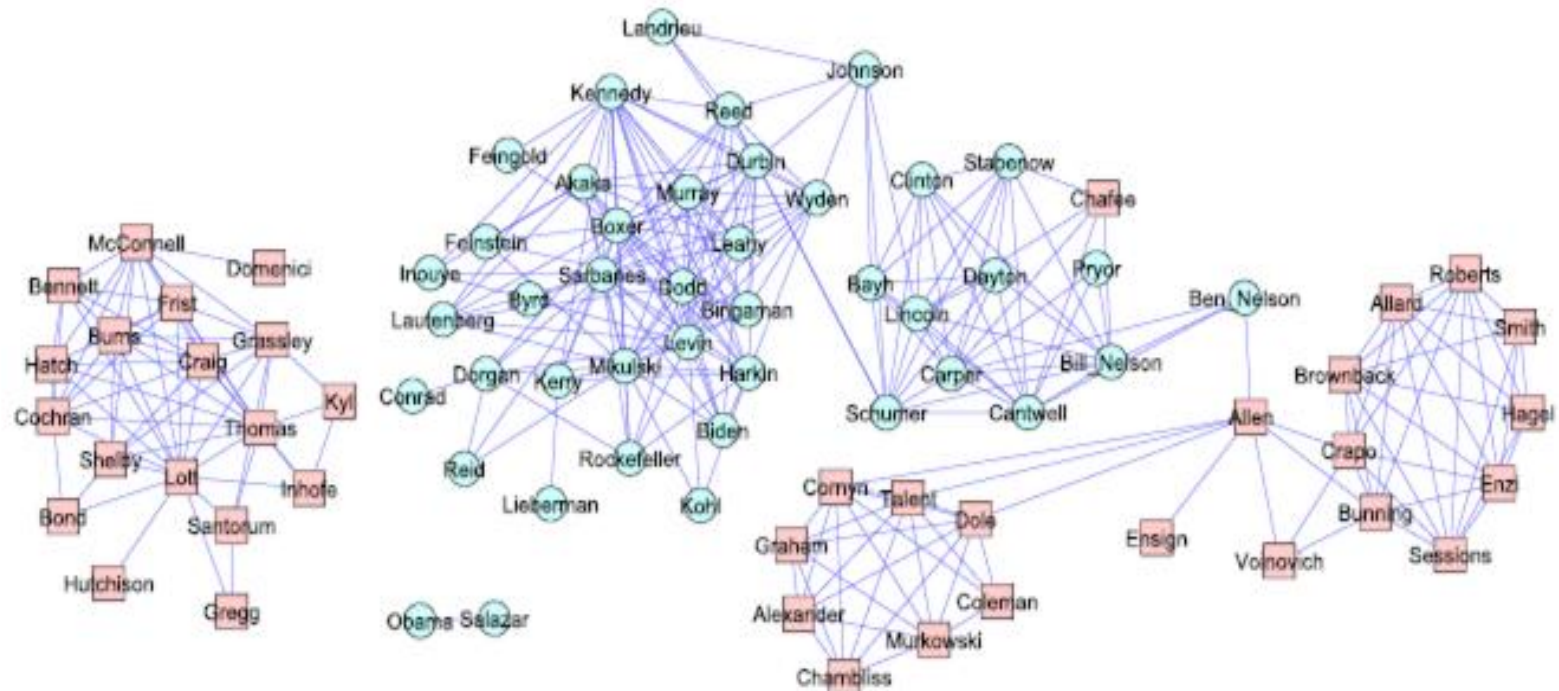
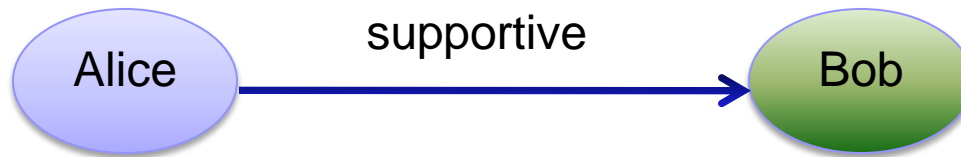
# **Learning Complex Networks, and Its Application to Software Verification**

**Kyomin Jung (KAIST)**

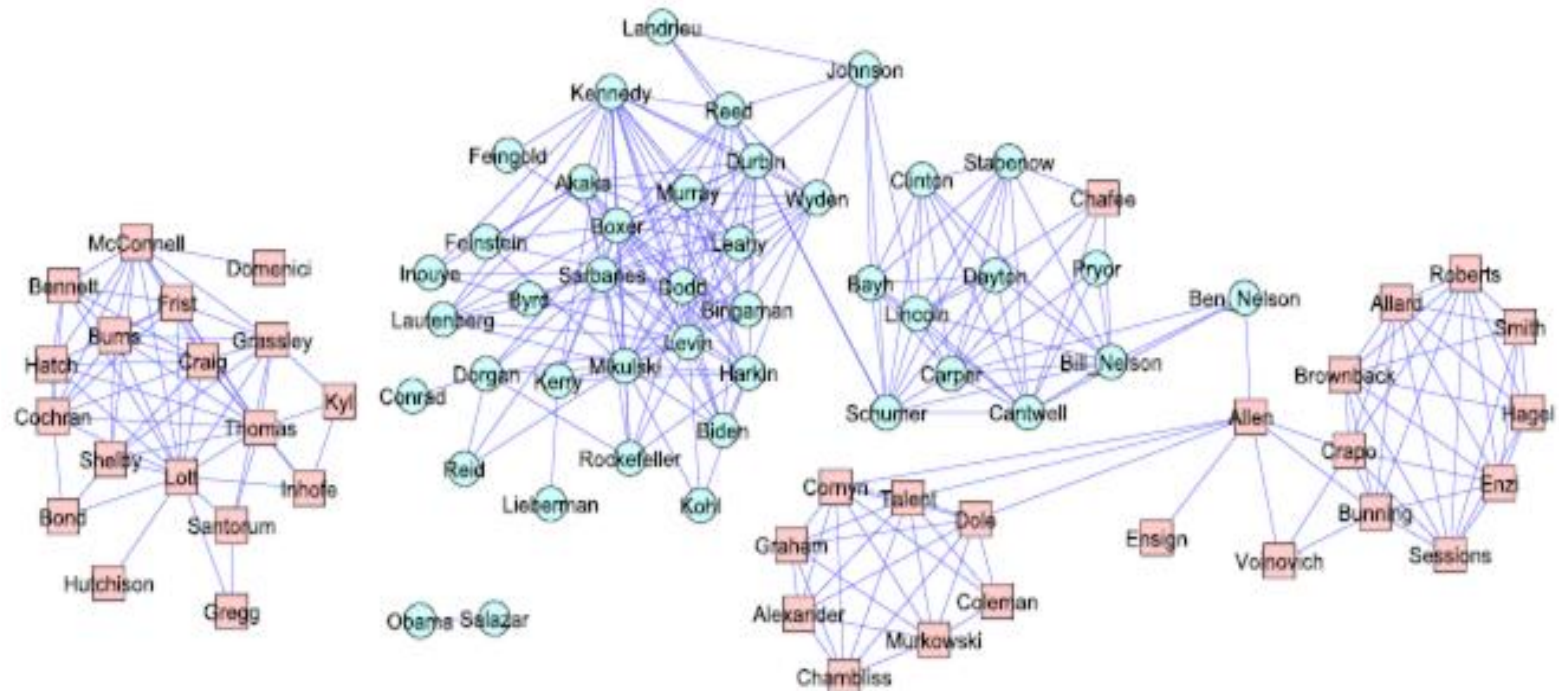
# Complex Network



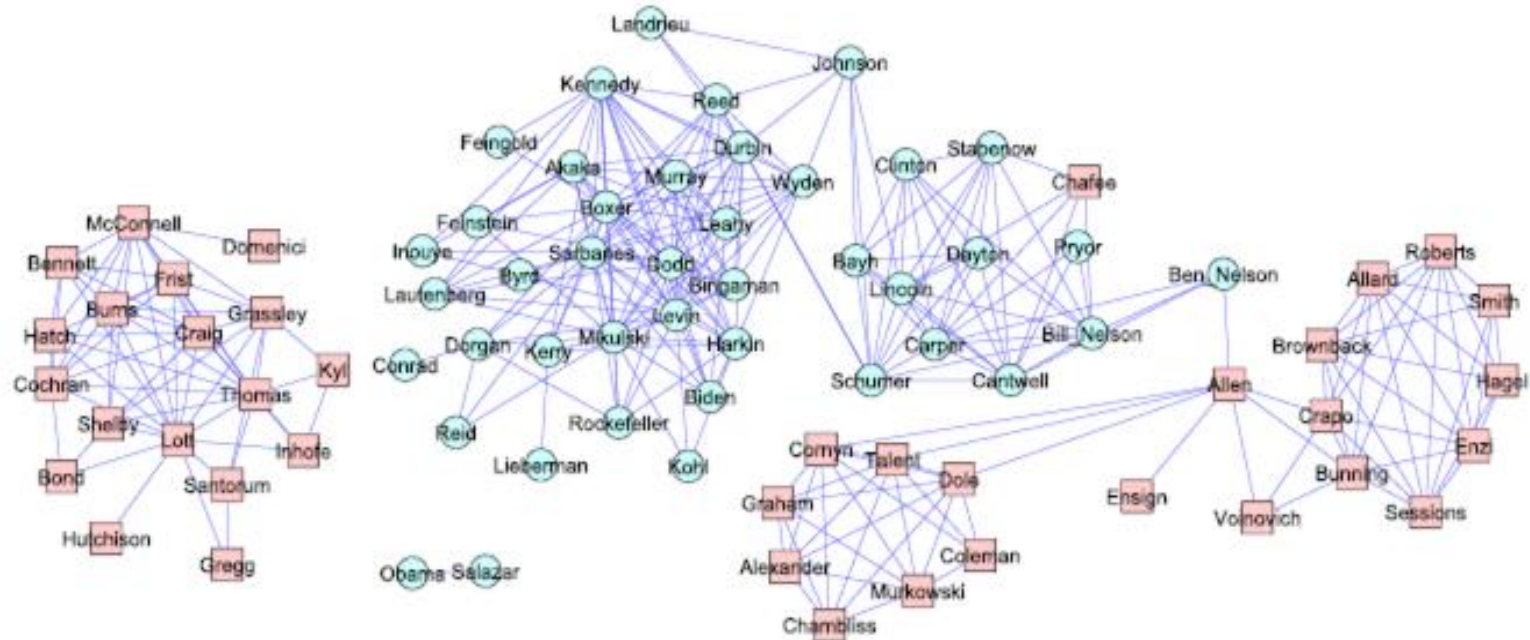
# Complex Network



# Complex Network



- Computational model for a given system
  - Learning the system w.r.t. the model
  - Inference (optimization/computation) based on the model
- The structure of a computer program/software itself can be understood as a complex network

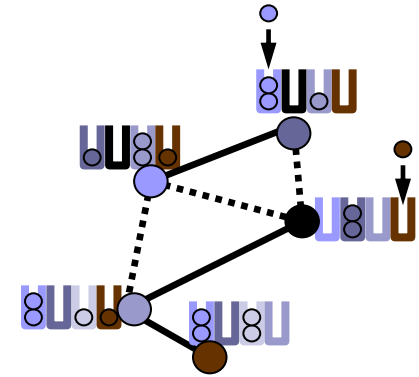


# Outline : Part I



- **Randomized Learning of pseudo-Boolean functions**
- **Has application to Software Verification**
  - **Randomized property testing: test whether a given “program” has an error**
- **Goal : learn the model with less function queries**
- **Our results**
  - We provide an algorithm with **almost optimal number of function queries**
  - We prove **phase transition** of a random fitness model

# Outline : Part II



## ■ Communication networks

- We provide algorithms for learning feasible allocation rate
- Study adversarial networks

## ■ Software Verification

- K-SAT problem



# Part I : Learning Pseudo-Boolean Functions

## ■ Computational models

- To understand and predict properties of complex system

## ■ Example

- Fitness of a species in a given environment
- Widely used for property testing in software verification





# Fitness of gene expression

- Each organism(genotype) is expressed by  $x \in \{0,1\}^n$ .

- Kauffman's model ['89] (a.k.a. NK model)

$$f(x) = \sum_{i=1}^m f_i(x_{i1}, x_{i2} \dots x_{ik})$$

- $f_i \in R$  corresponds to a sub-characteristic of an organism
- Widely used in evolutionary biology and genetic algorithms
  - For evolutions of amino acid sequences (Macken et al '89)
  - Evolutions of protein or RNA sequences (Schuster et al '94)
  - For evaluating encoding schemes and genetic operators (Merz et al '98)

# Learning Pseudo-Boolean function

$$f(x) = \sum_{i=1}^m f_i(x_{i1}, x_{i2} \dots x_{ik})$$

- Our goal is to **learn  $f$  by performing function queries**.
  - function query = checking fitness of one gene expression
- Ex: In genetic engineering, the goal is to understand the species and design a “super organism”
- We provide algorithm to learn  $f$  with  **$O(m \log n)$**  queries

# Relevant Work

## ■ Learning Boolean functions

- KM alg. ['93], Jackson ['97], Bshouty, Jackson, and Tamon ['04]
- Cannot be extended to pseudo-Boolean functions

## ■ Learning Pseudo-Boolean functions

- Kargupta and Park ['01] proposed a deterministic algorithm with  $\theta(n^k)$  queries
- Heckendorn and Wright ['03] proposed a randomized algorithm based on random perturbations, and show that it runs with  $O(mn \log n)$  queries on average case. Choi, Jung, Moon ['08] show the same query complexity for the worst case.

# Theorem (Choi, Jung, Kim)\*

$$f(x) = \sum_{i=1}^m f_i(x_{i1}, x_{i2} \dots x_{ik})$$

- We propose an adaptive, randomized algorithm that learns  $f$  with  $O(m \log n)$  queries with failure probability  $O(\frac{1}{n^{100}})$ .

# Phase Transition of Random Pseudo-Boolean function

$$f(x) = \sum_{i=1}^n f_i(x_i, x_{i2} \dots x_{ik})$$

- To understand average properties of the species, a random fitness model was proposed by Gao and Culberson [’02]
- $f_i$  ‘s are chosen randomly according to a parameter  $z$ 
  - $f_i$  takes maximum value for  $z$  many assignments among  $2^k$  of them
- Problem: Is there a “super organism” ?
- When  $k \leq 2$ , the problem is easy. For  $k=3$ , it is NP-hard.

# Phase Transition of Random Pseudo-Boolean function

$$f(x) = \sum_{i=1}^n f_i(x_i, x_{i2} \dots x_{ik})$$

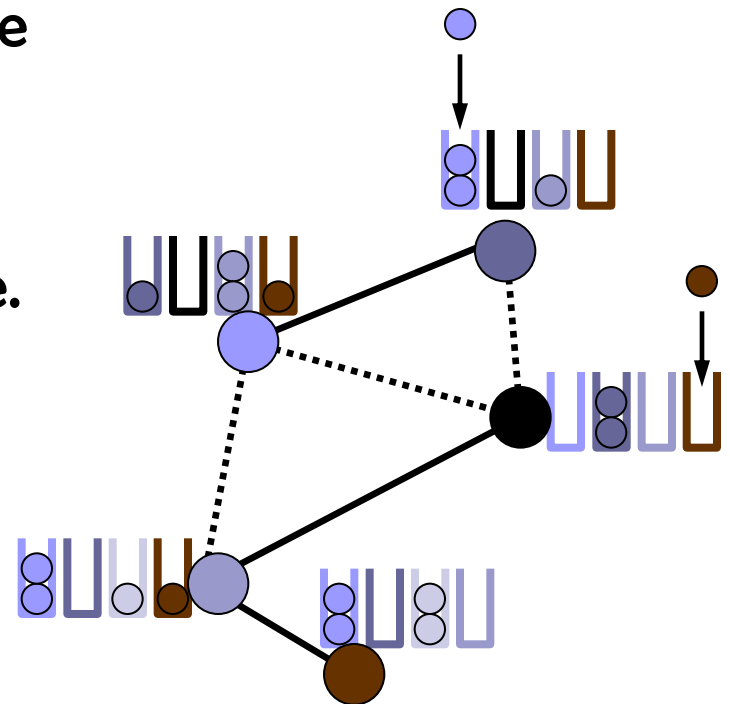
- When  $k=3$ , Gao and Culberson [‘02] proved that when  $z < 5.163$ , “there is no super organism” with high probability.
- Theorem (Choi, Jung, Kim)\*
  - When  $z > 5.163$ , there is a super organism with positive probability.

\* Appeared in GECCO ‘05 & Artificial Intelligence ‘08



# Part II : Communication Networks

- Routing/scheduling in communication networks with queue
- Main problem
  - Whether the network is **stable**, i.e. queue size is bounded over time



# Our Work on Communication Networks

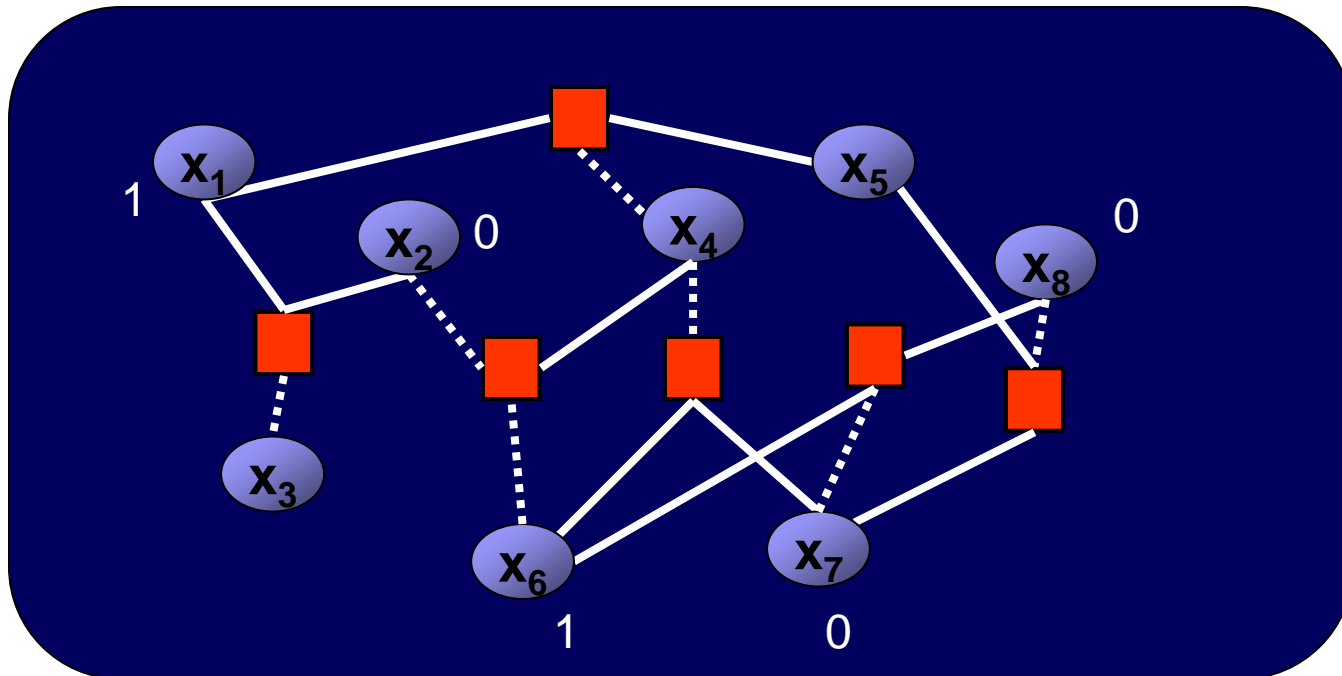
- We design algorithms (Gummadi, Jung, Shah and Sreenivas)\*
  - To learn whether a given **arrival rate vector** makes the network stable or not
  - Utilize structural properties of the network
- Theorem (Andrews, Jung, Stolyar)\*\*
  - Local optimizer, “Max-weight algorithm”, makes the system stable under **adversarial arrival process for dynamic graphs** in the edge interference network.

\* Appeared in INFOCOM '08, INFOCOM '09

\*\* Appeared in STOC '07

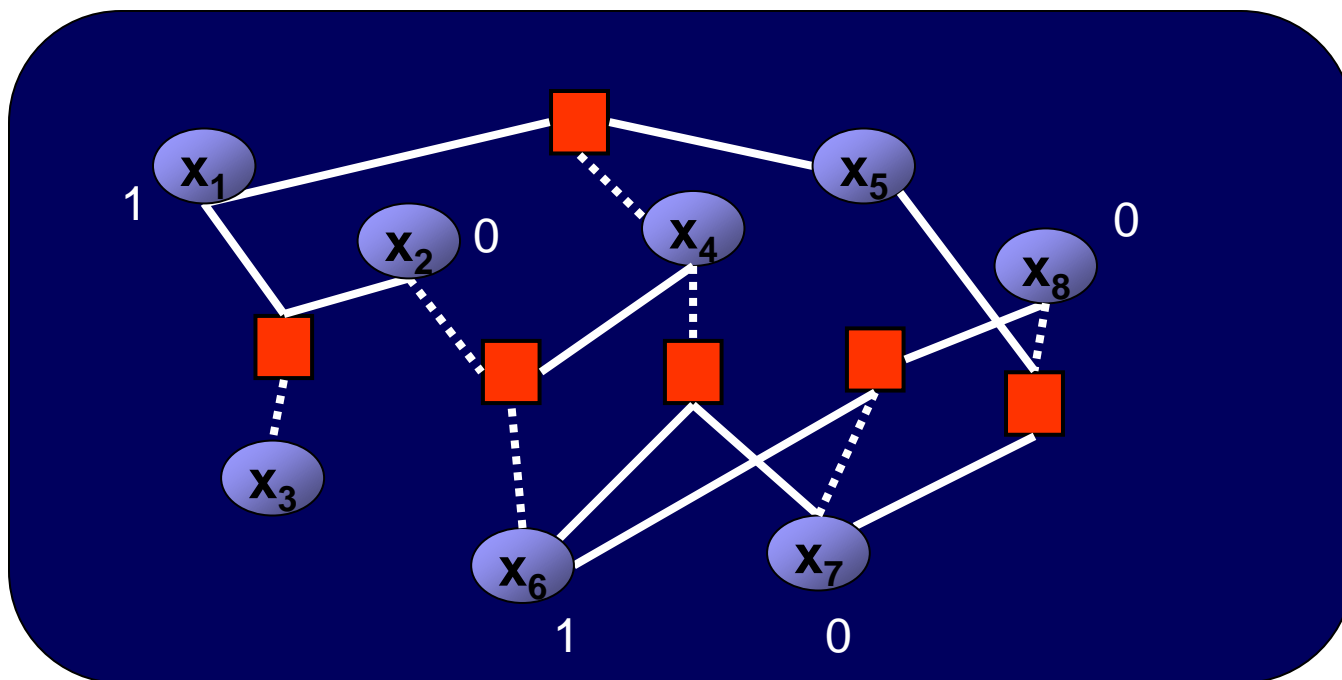
# K-SAT problem

- Variables:  $x_1, x_2, \dots, x_n$  take values {TRUE, FALSE}
- Constraints:  $(x_1 \text{ or } x_2 \text{ or not } x_3)$  ,  $(\text{not } x_2 \text{ or } x_4 \text{ or not } x_6)$ , ...  
 $(x_1 \vee x_2 \vee x_3) \quad \wedge \quad (x_2 \vee x_4 \vee x_6) \wedge \dots$
- Application to Software Verification



# Designing K-SAT solver based on graph structures

- Currently we are working on designing a K-SAT solver based on structural properties of a k-SAT instance.
  - (joint work with Yungbum Jung and Suwon Jang)



Thank you.