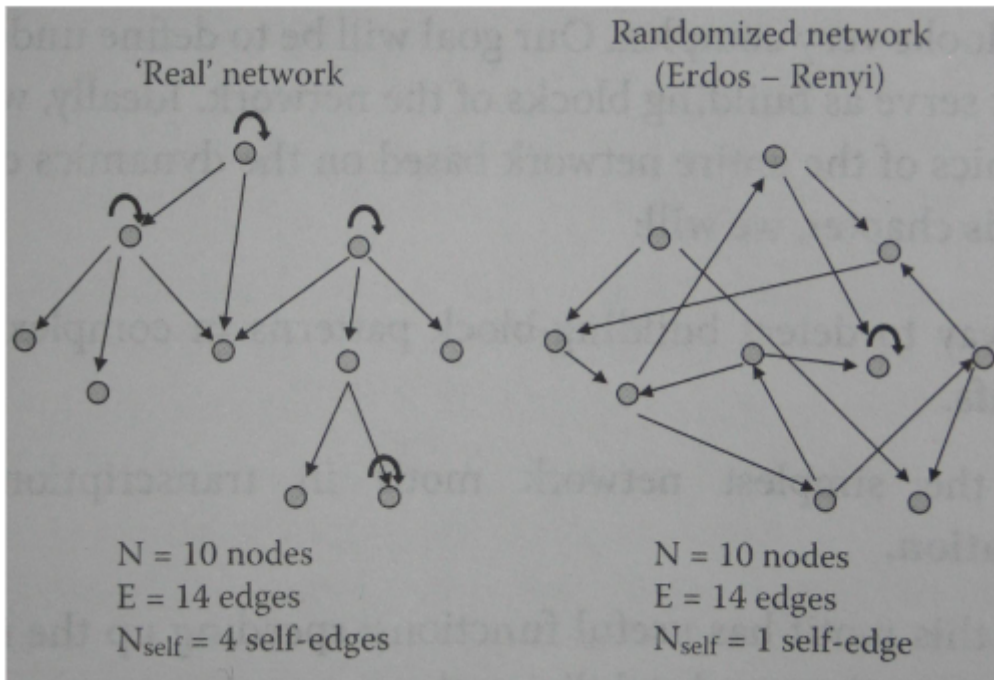
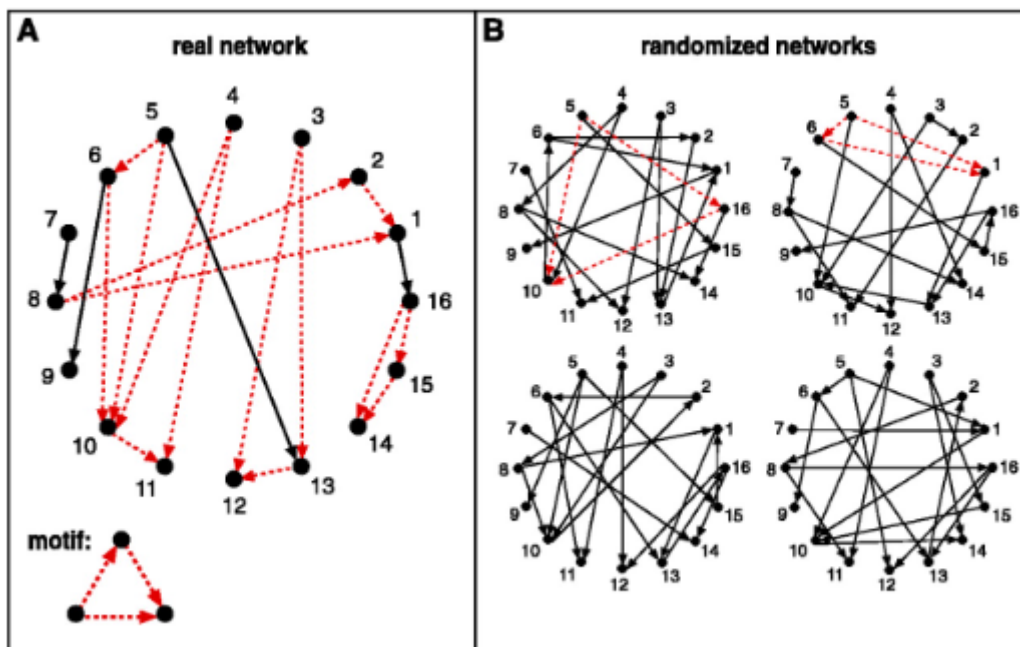


# Hands-on Boolean networks

## Motif Finding and network randomization



Create the real network from the figure using networkx. Create 100 ER random networks with the same parameter. Count the number of self loops for each random net. Using this values create an empirical distribution and calculate mean, SD and the significance for the observed pattern in the real network



Create the real network from the figure using networkx. Create 100 ER random networks with the same parameters. Count the number of motif (trinagles). Using this values create an empirical distribution and

calculate mean, SD and the significance for the observed pattern in the real network

## Introduction to Boolean Models with GINsim

---

Objective:

- To introduce students to Boolean modeling of biological systems using GINsim.
- To familiarize students with the concepts of regulatory networks and their analysis using GINsim.

Pre-requisites:

- Basic knowledge of Boolean algebra.
- Familiarity with biological regulatory networks.

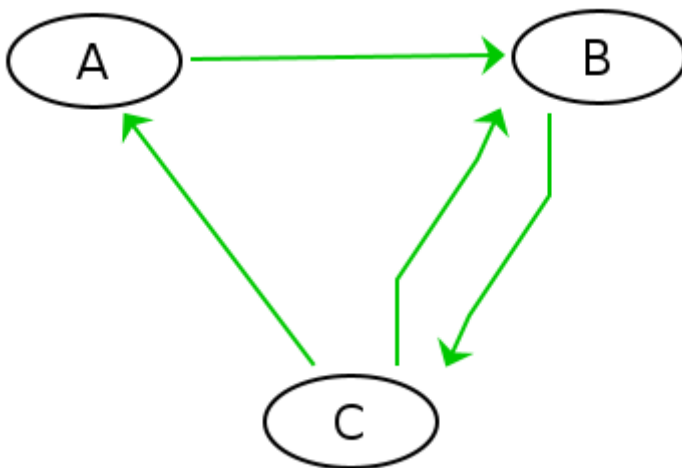
Tools: GINsim (Graphical Network Simulator)

### Installation and Setup

- 1- Download GINsim: <http://ginsim.org/>
- 2- Open the software: `java -jar GINsim-3.0.0b-with-deps.jar`
- 3- Familiarize yourself with the interface.

### Excercise 2.1 - Creating a Simple Regulatory Network

Create a simple regulatory network with 3 nodes (A, B, C) and 3 regulatory interactions.



Define the logical rules for each node as follows:

```
A = C
B = A OR C
C = B
```

For node **A**:

| Modelling Attributes |                          | Style |                     |
|----------------------|--------------------------|-------|---------------------|
| Id                   | A                        | Value | Active Interactions |
| Name                 | A                        | 1     | C                   |
| Input                | <input type="checkbox"/> |       |                     |
| Max                  | 1                        |       |                     |

C [1,max] ; positive

For node **B**:

| Modelling Attributes |                          | Style |                     |
|----------------------|--------------------------|-------|---------------------|
| Id                   | B                        | Value | Active Interactions |
| Name                 | B                        | 1     | A C                 |
| Input                | <input type="checkbox"/> | 1     | C                   |
| Max                  | 1                        | 1     | A                   |

A [1,max] ; positive  
C [1,max] ; positive

For node **C**:

| Modelling Attributes |                          | Style |                     |
|----------------------|--------------------------|-------|---------------------|
| Id                   | C                        | Value | Active Interactions |
| Name                 | C                        | 1     | B                   |
| Input                | <input type="checkbox"/> |       |                     |
| Max                  | 1                        |       |                     |

B [1,max] ; positive

Export the model into boolnet format and check the correctness of the formulation by opening the generated text file using a text editor.

## Exercise 2.2 - Simulating the Network

Perform a series of simulations (synchronous/asynchronous) on the network.

- 1-Identify the stable states (attractors) of the network. How many attractor does de model exhibit?
- 2- Are there differences then using different update schemas?

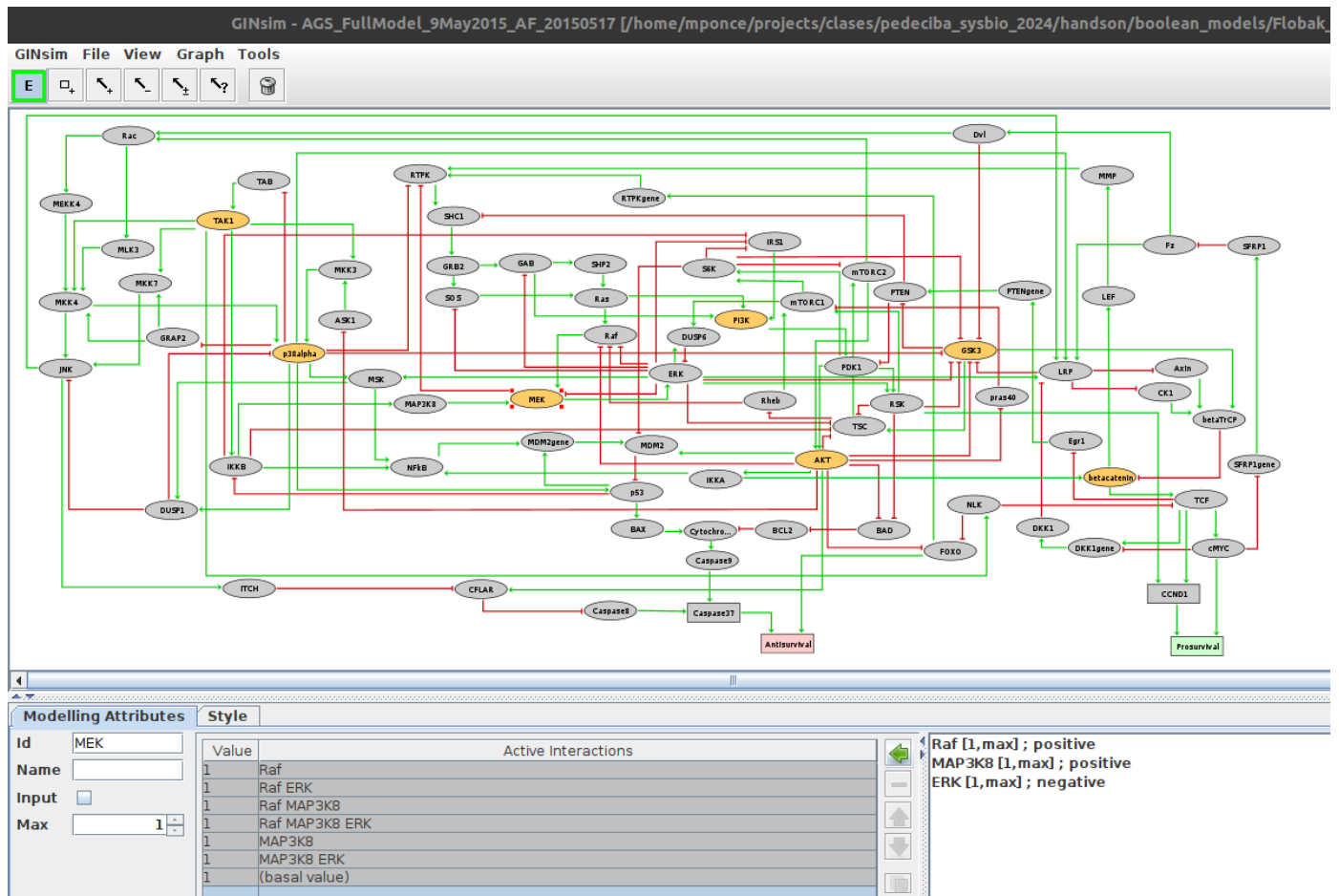
## Exercise 2.3 - Analyzing Attractors

1. Caculate the state transtion graph using:
  1. Synchronous update
  2. Aynchronous update
2. Determine the basins of attraction for each attractor.
3. Introduce perturbations to the network (e.g., ko node). Calculate the state transition graph

## Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling

Load the model from Flobak et al (2015) in GINSim

- <http://ginsim.org/node/194>
- File name: Flobak\_FullModel\_S2\_Dataset.zginml



### Exercise 3.1 - Analyzing Attractors

1. Calculate the stable state for the wild type and single drugs experiments reported in the paper.
2. Measure the fitness of the control (wild type) by taking the difference between prosurvival and antisurvival.
3. Reproduce the synergy experiments from the paper.