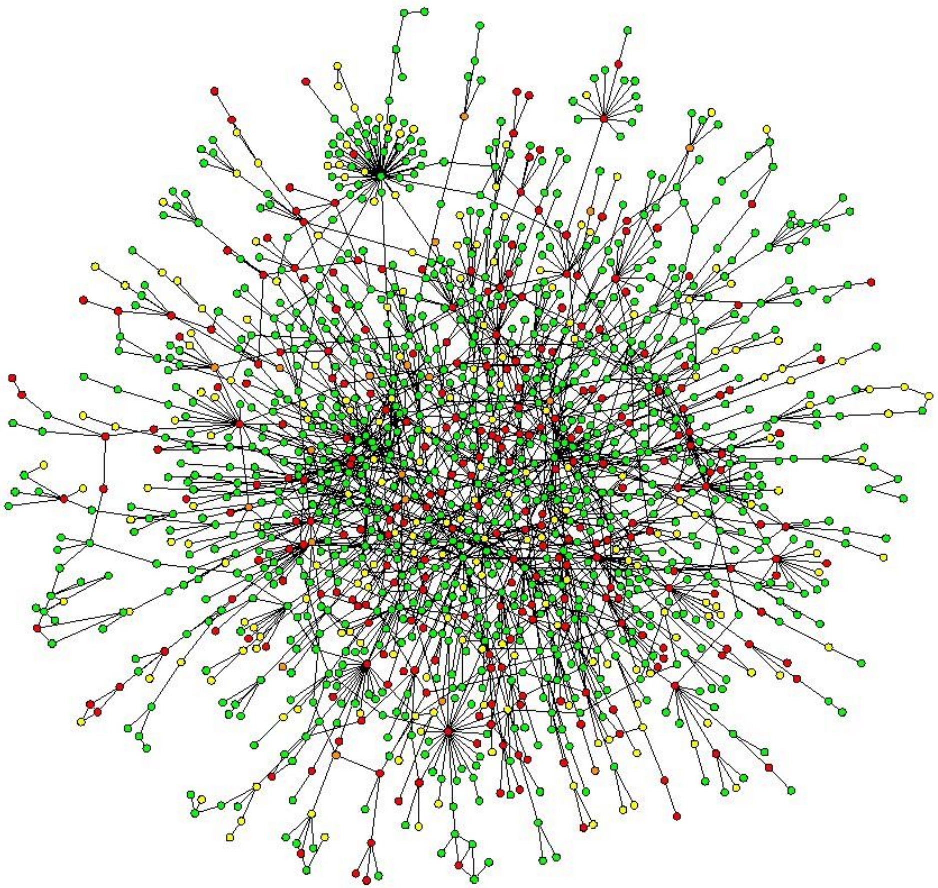
NETADIS
Statistical Physics Approaches to Networks Across Disciplines

MID-TERM REVIEW
Institut Henri Poincaré, Paris
23-24 January 2014

# Approximate inference for stochastic dynamics in large biological networks

Ludovica Bachschmid Romano
Supervisor: Prof. Manfred Opper
Artificial Intelligence group, TU Berlin

The functions of most biological systems arise from complex interactions between the  numerous system's components

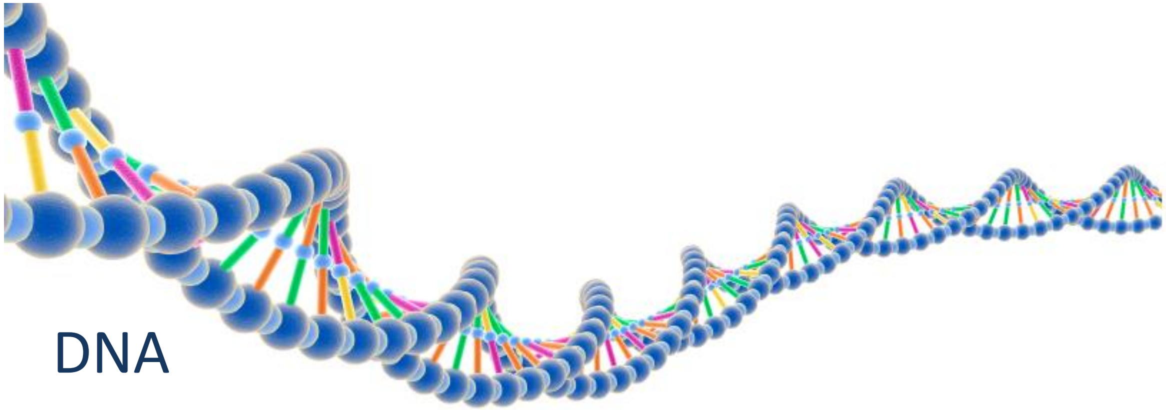


# Gene regulatory network

protein

# Gene regulatory network

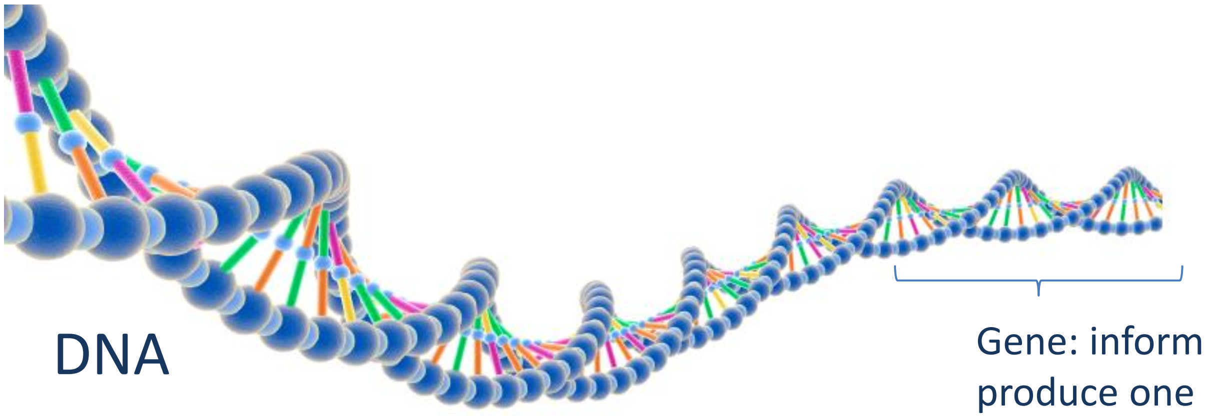
protein



DNA

# Gene regulatory network

protein



DNA

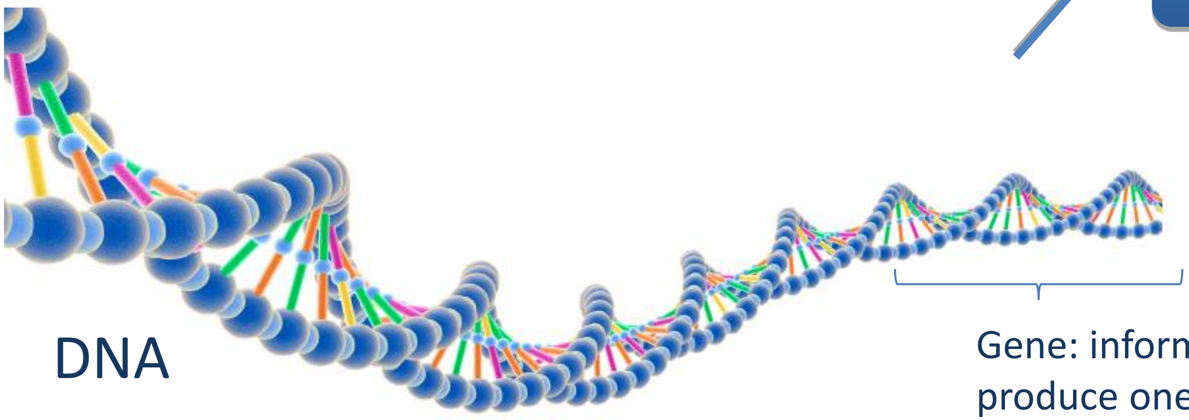
Gene: information needed to produce one kind of proteins

# Gene regulatory network

protein

RNA: copy of the genetic information

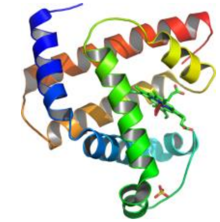
TRANSCRIPTION



DNA

Gene: information needed to produce one kind of proteins

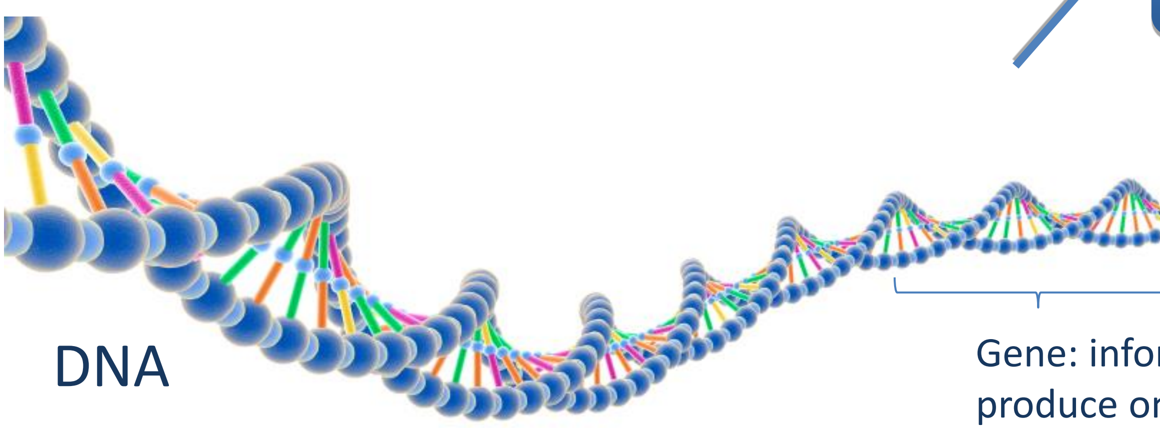
# Gene regulatory network



protein

RNA: copy of the genetic information

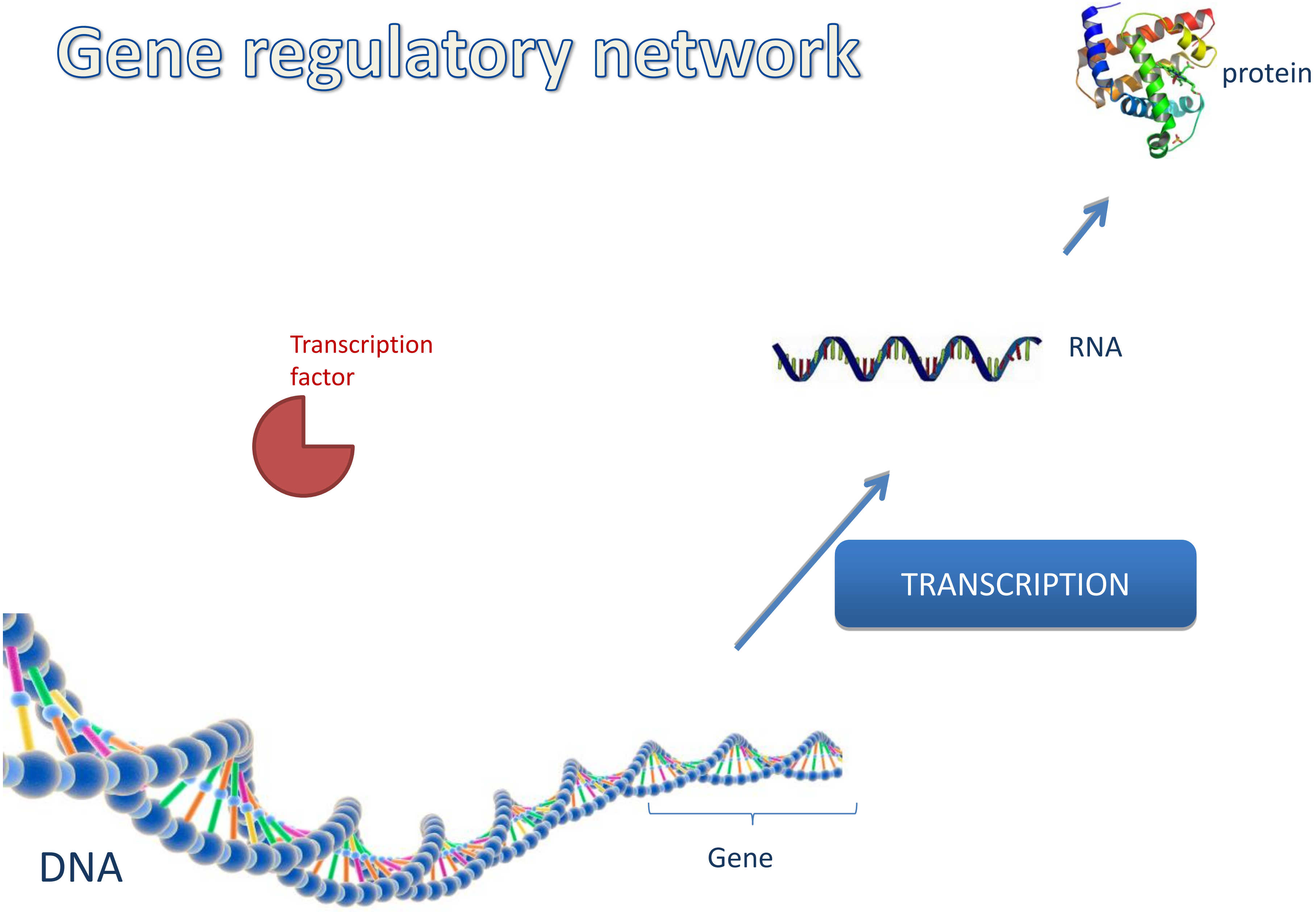
TRANSCRIPTION



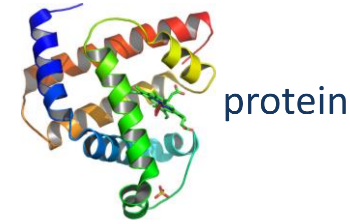
DNA

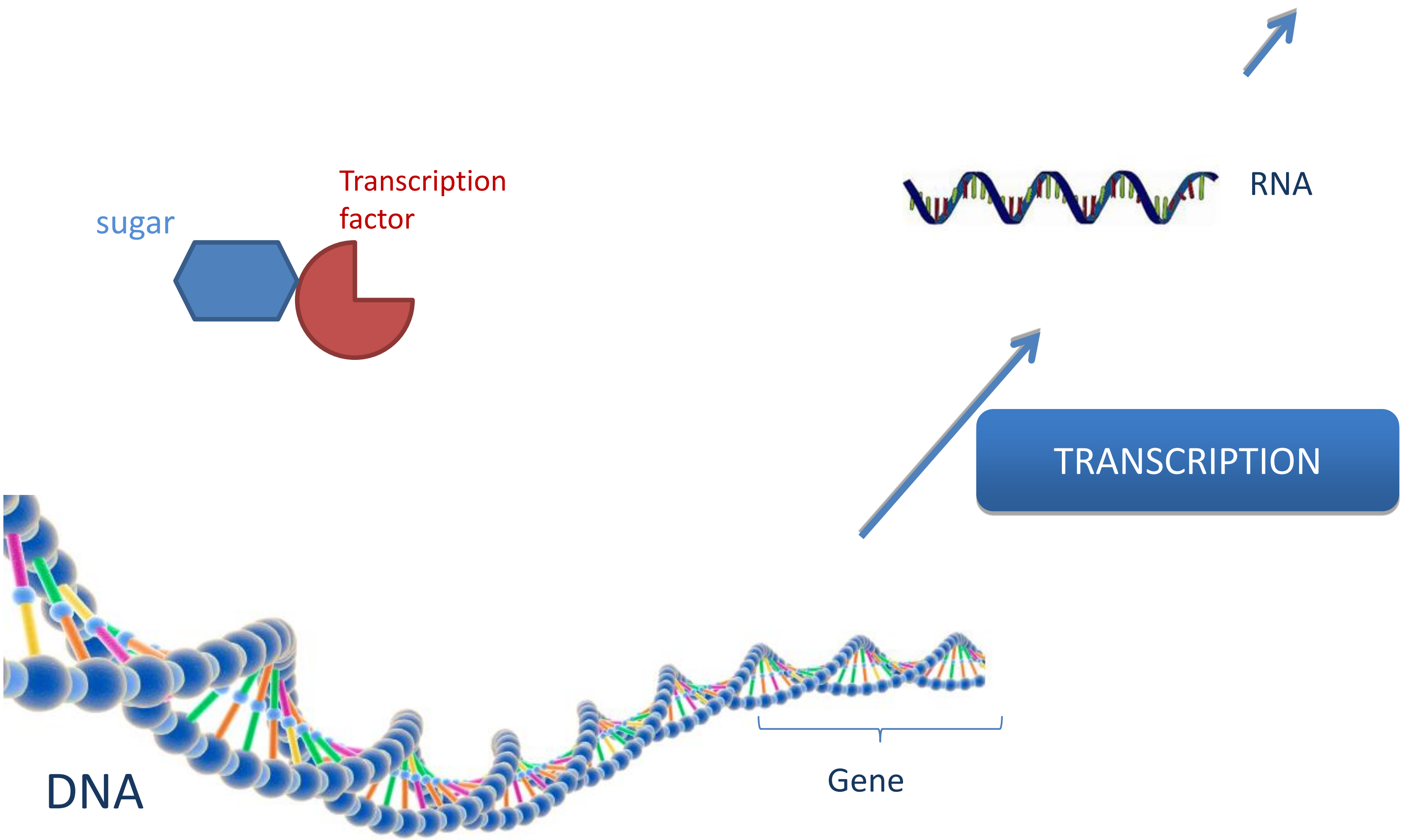
Gene: information needed to produce one kind of proteins

# Gene regulatory network

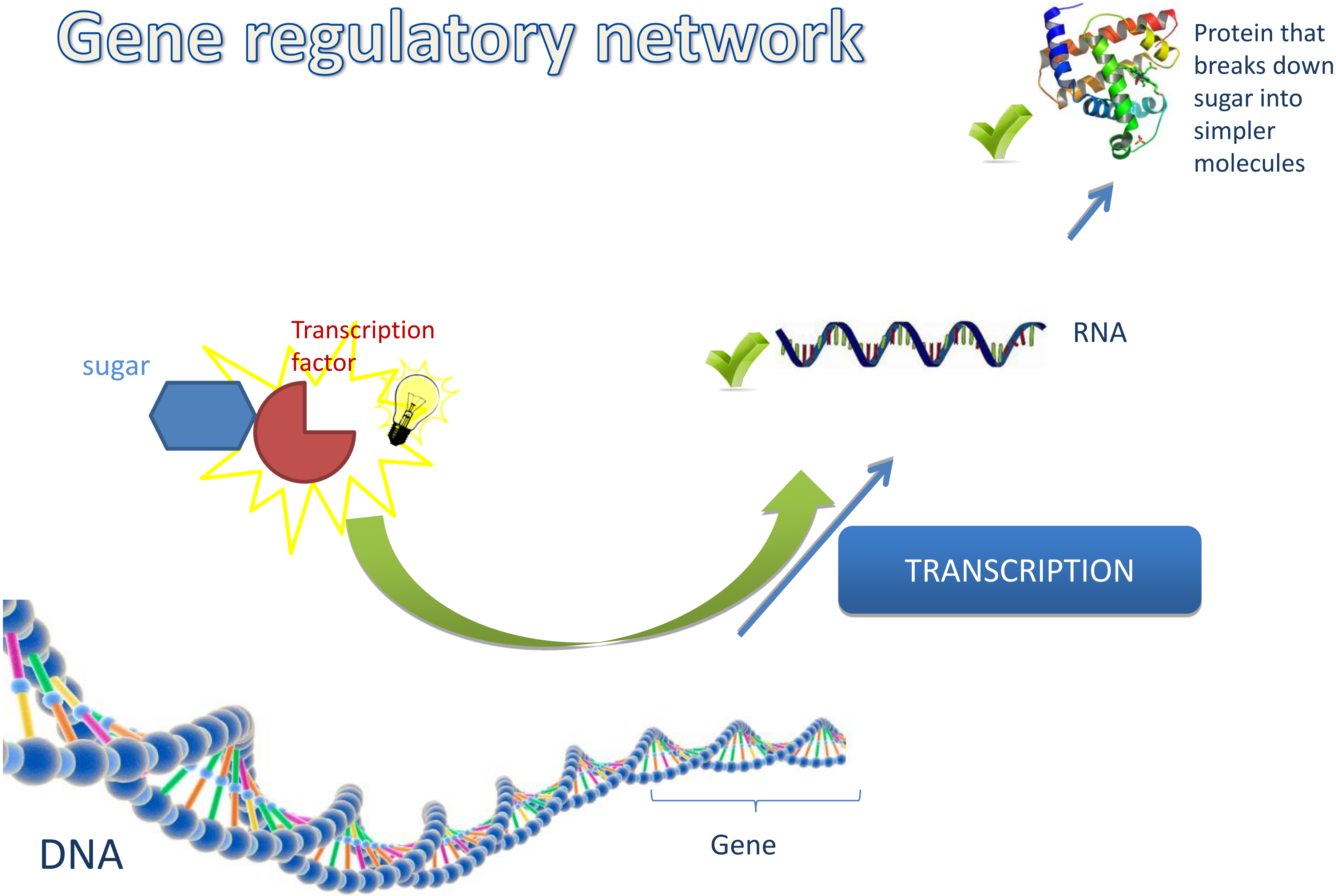


# Gene regulatory network

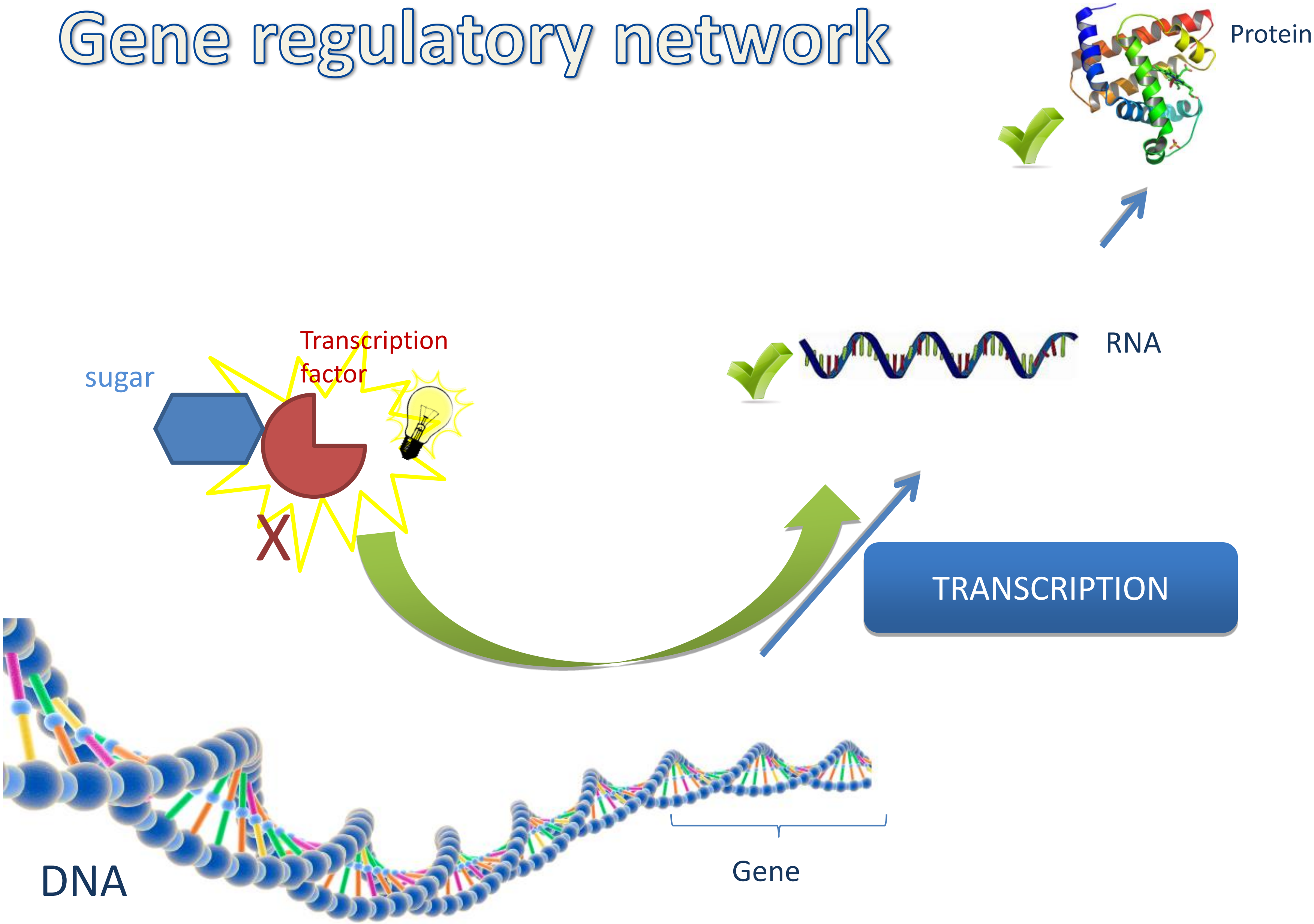


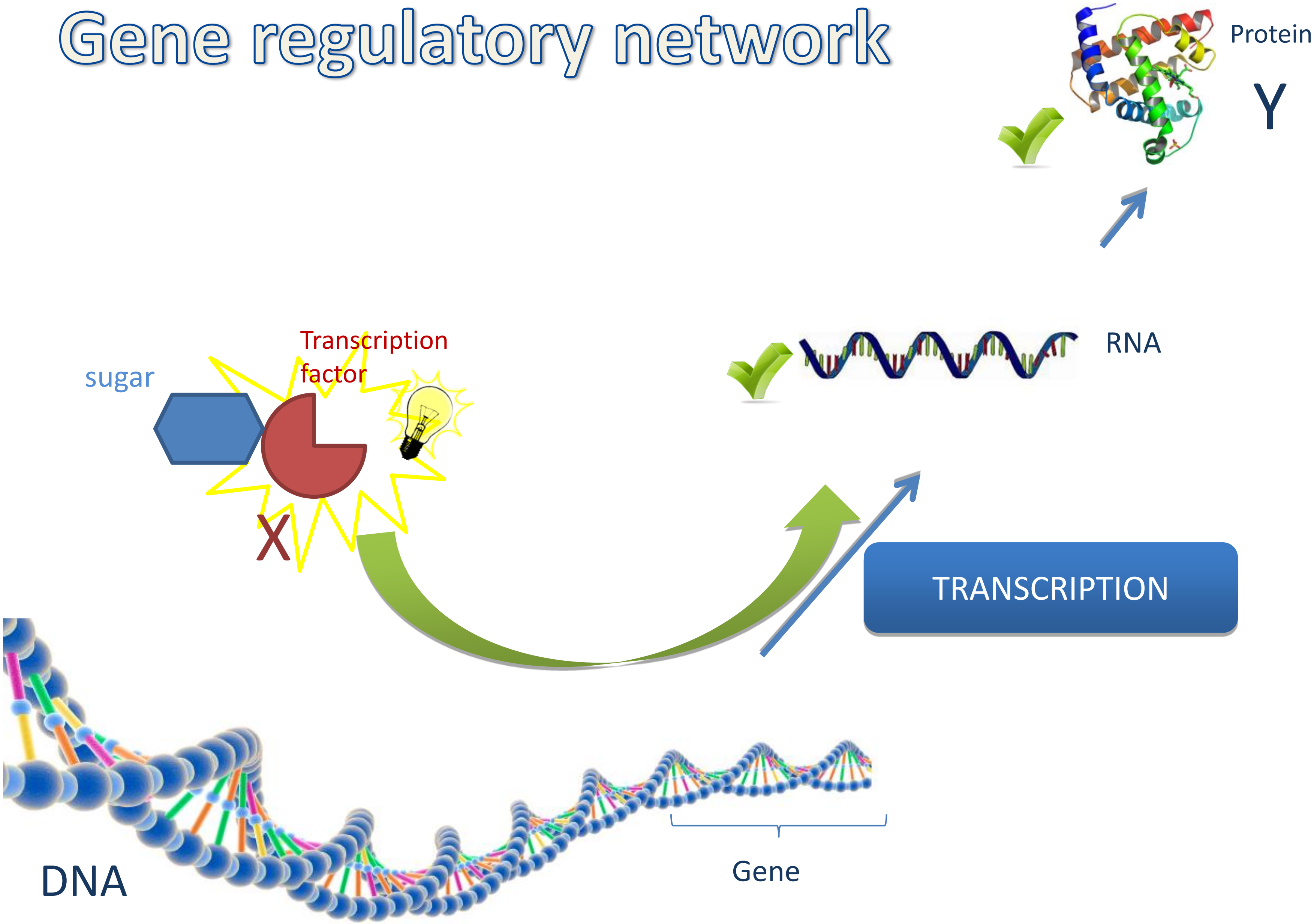
# Gene regulatory network



# Gene regulatory network

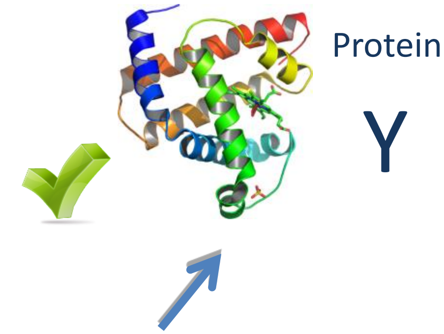


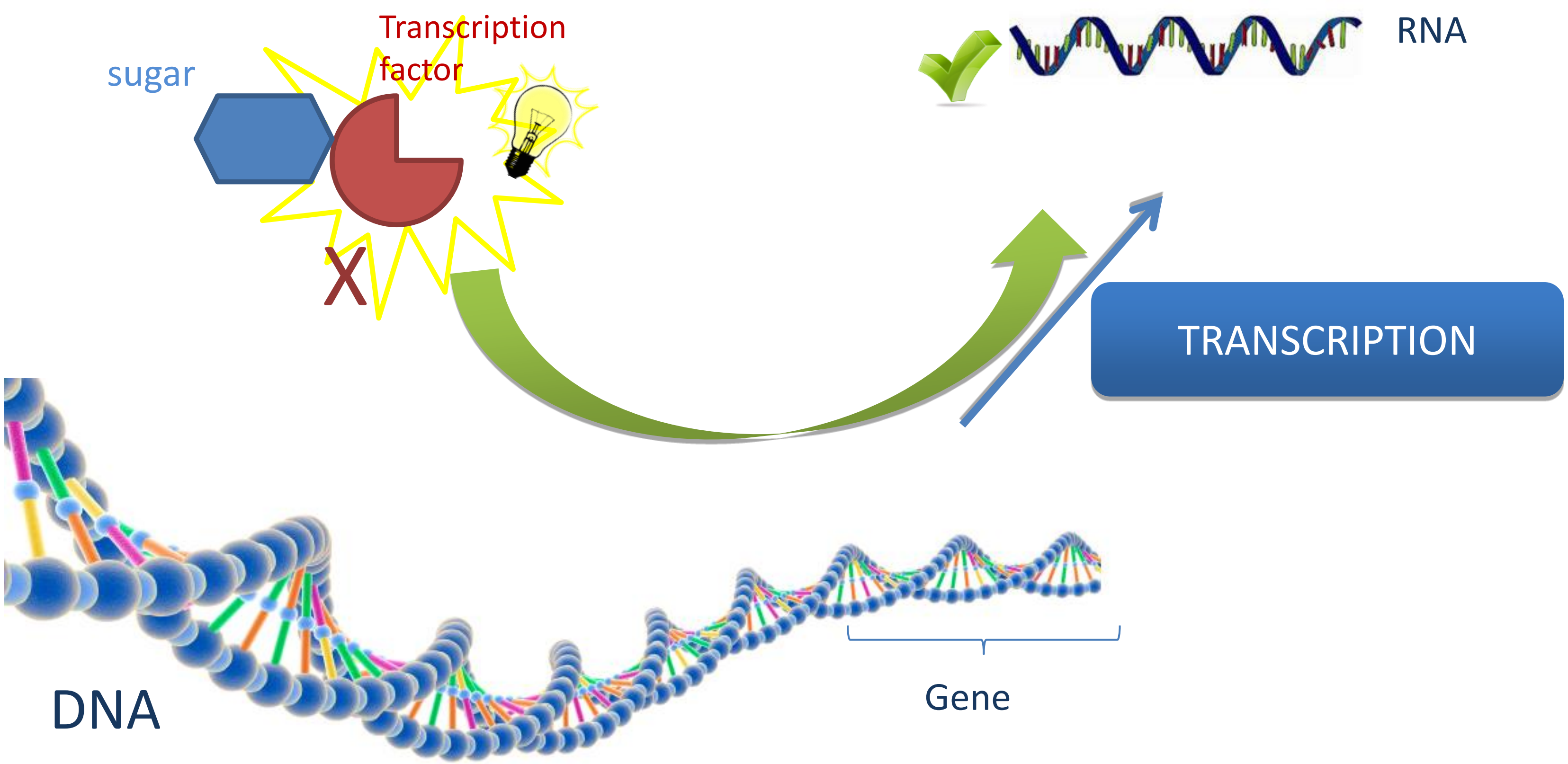
# Gene regulatory network



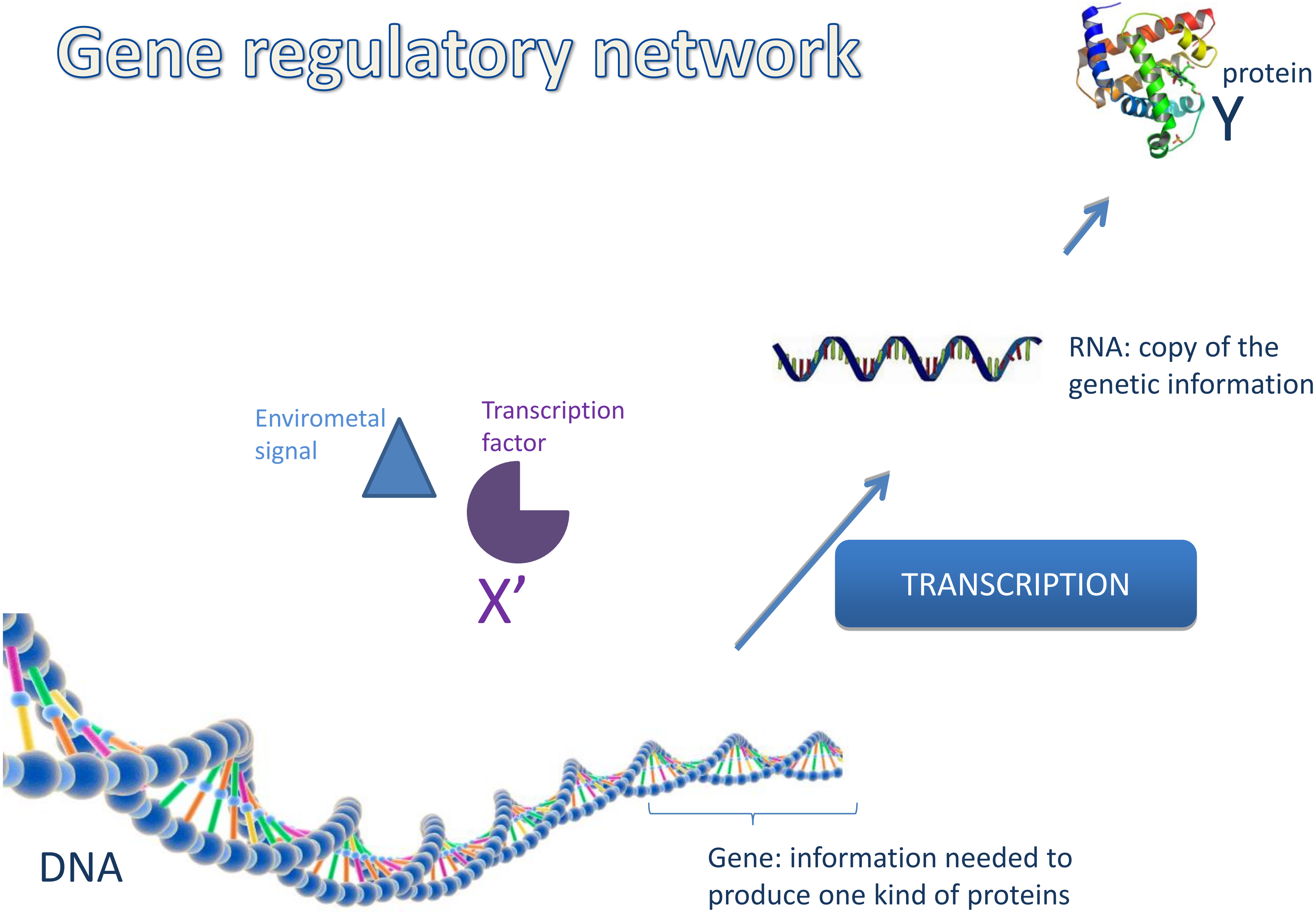
# Gene regulatory network

X increases the production of Y

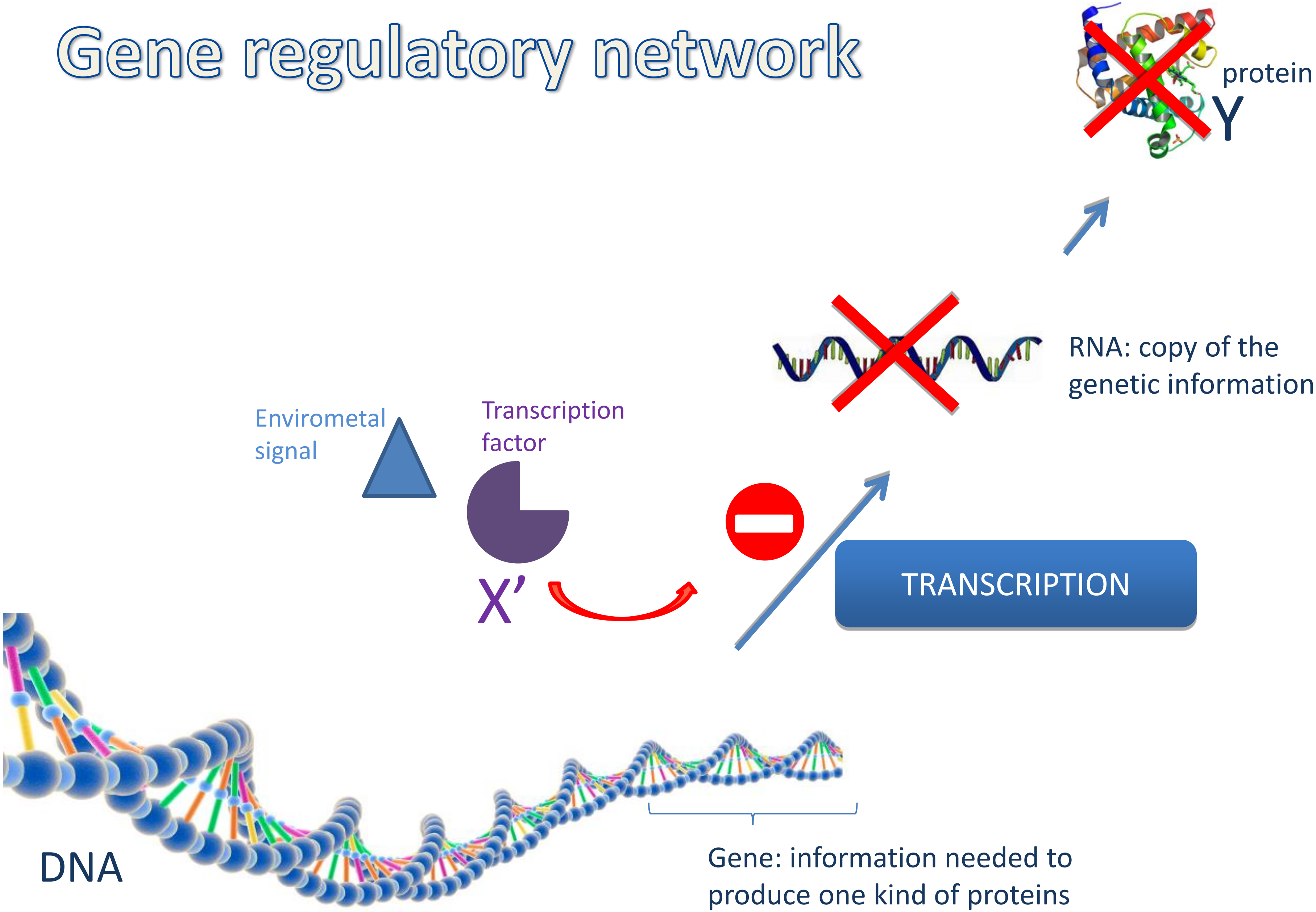


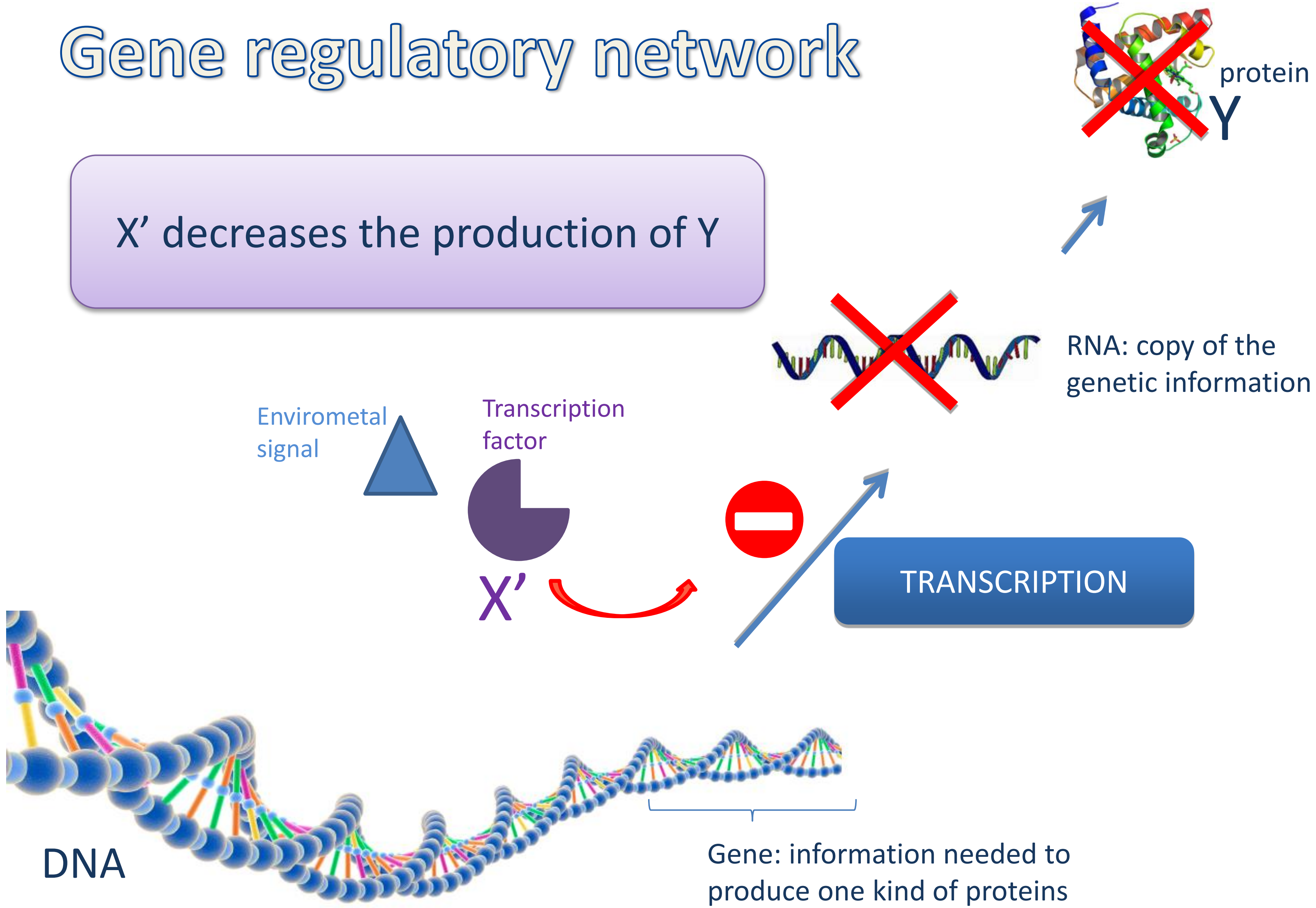
# Gene regulatory network



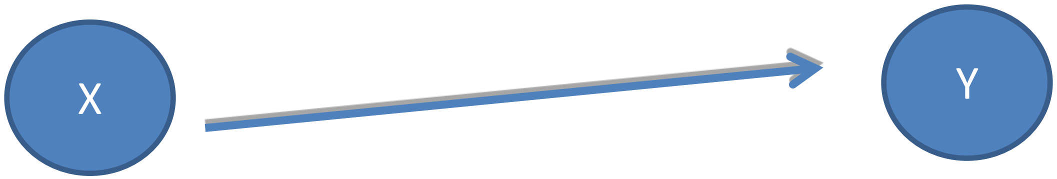
# Gene regulatory network



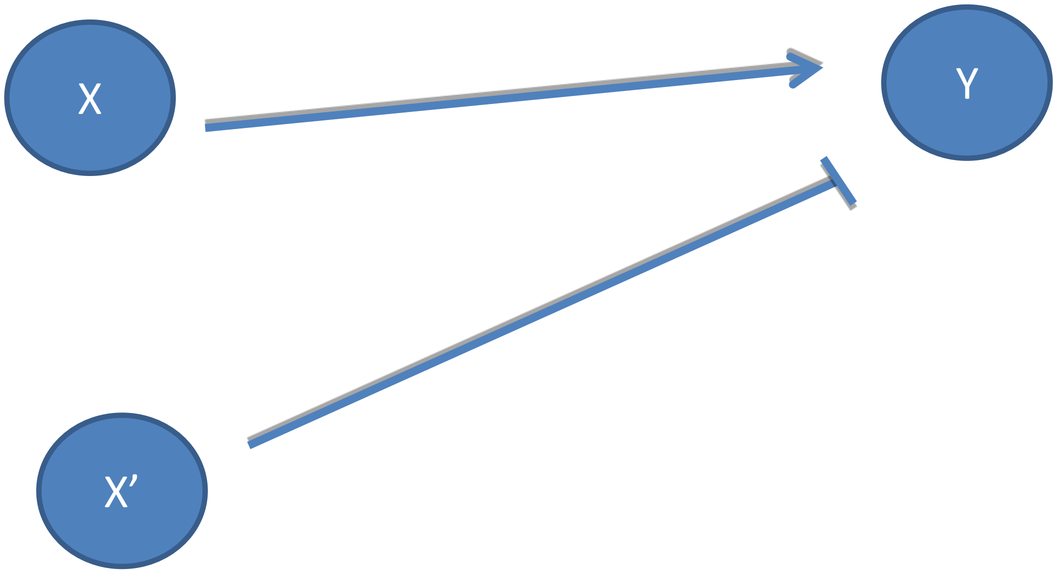
# Gene regulatory network



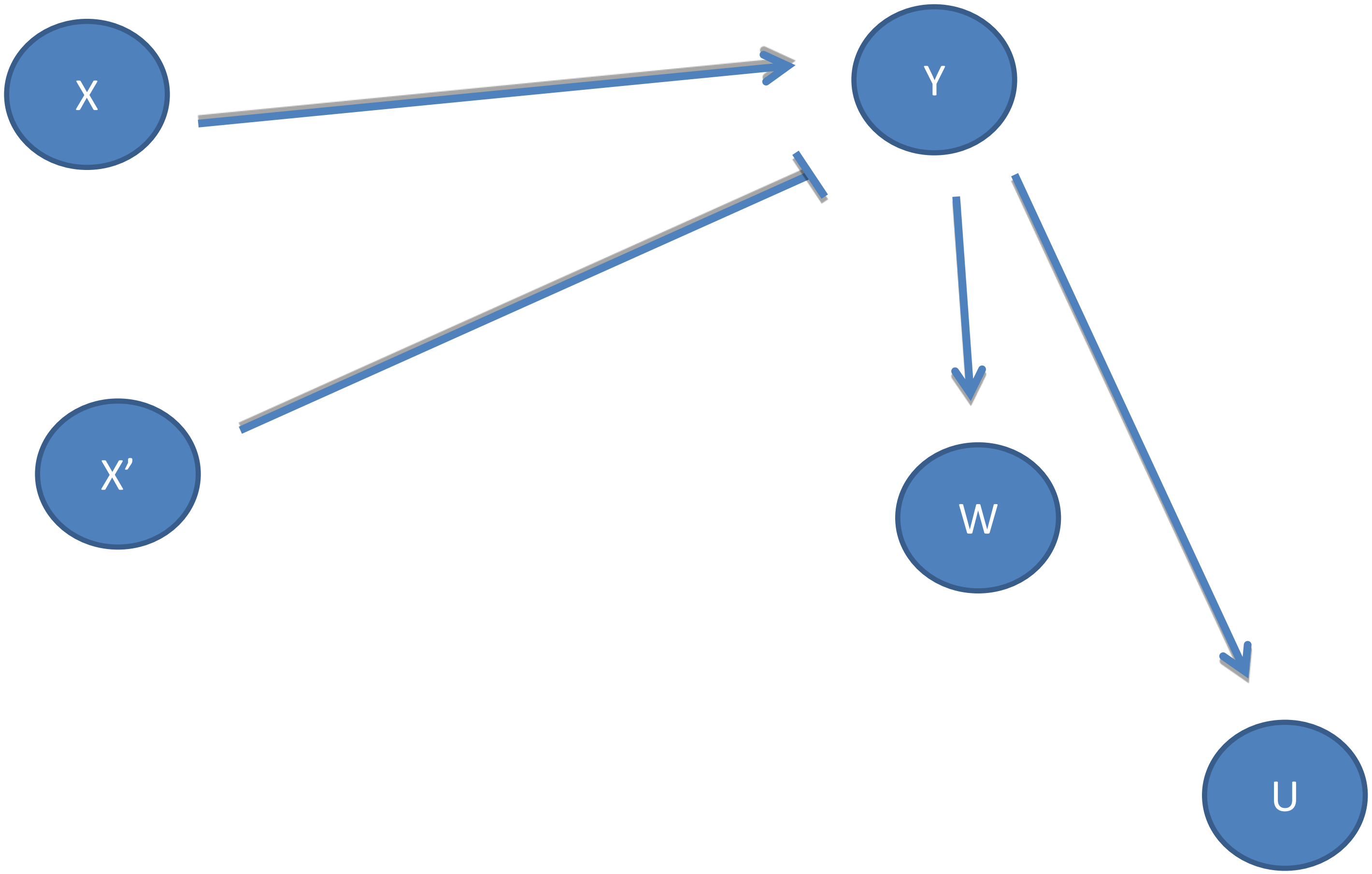
# Gene regulatory network



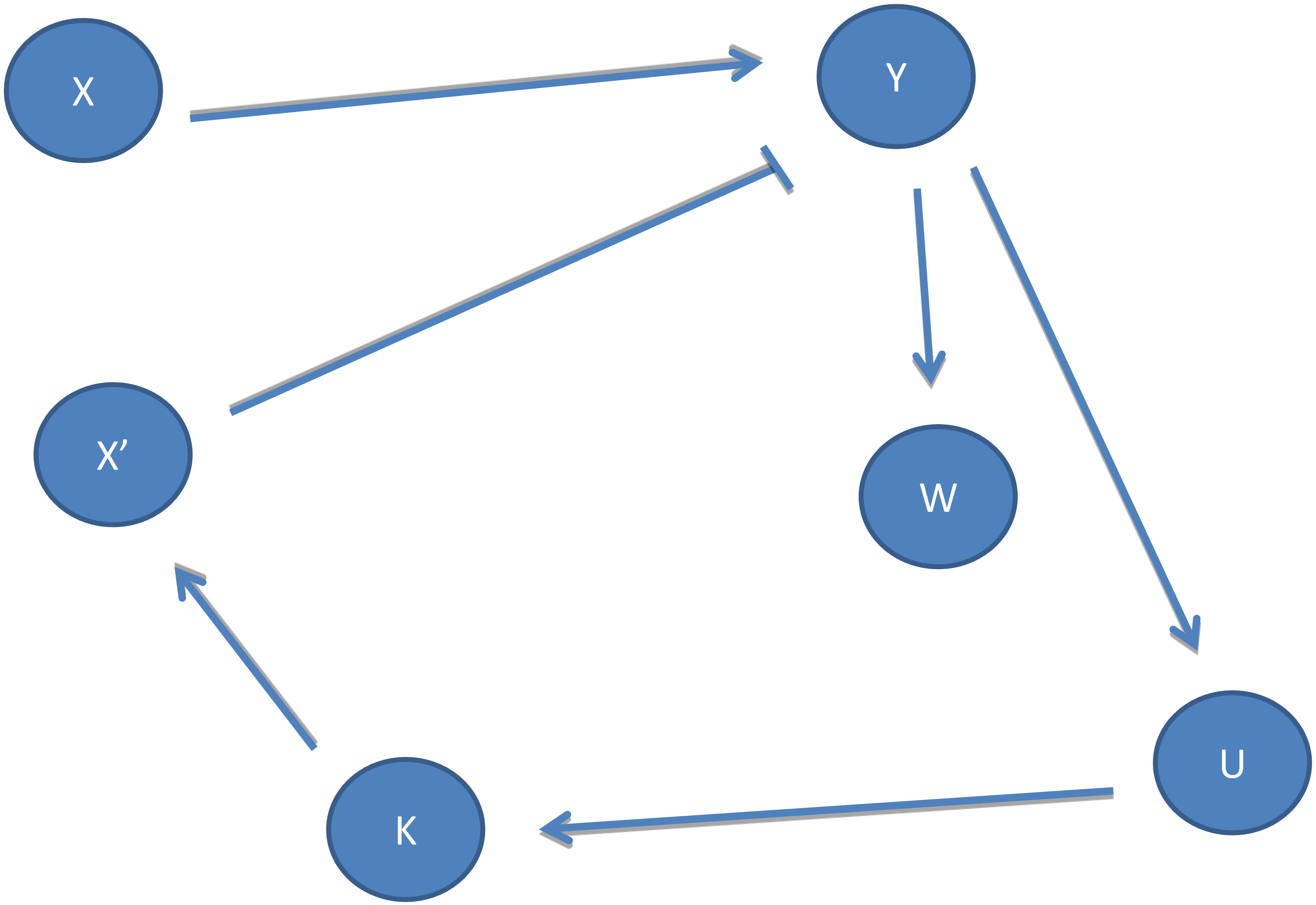
# Gene regulatory network



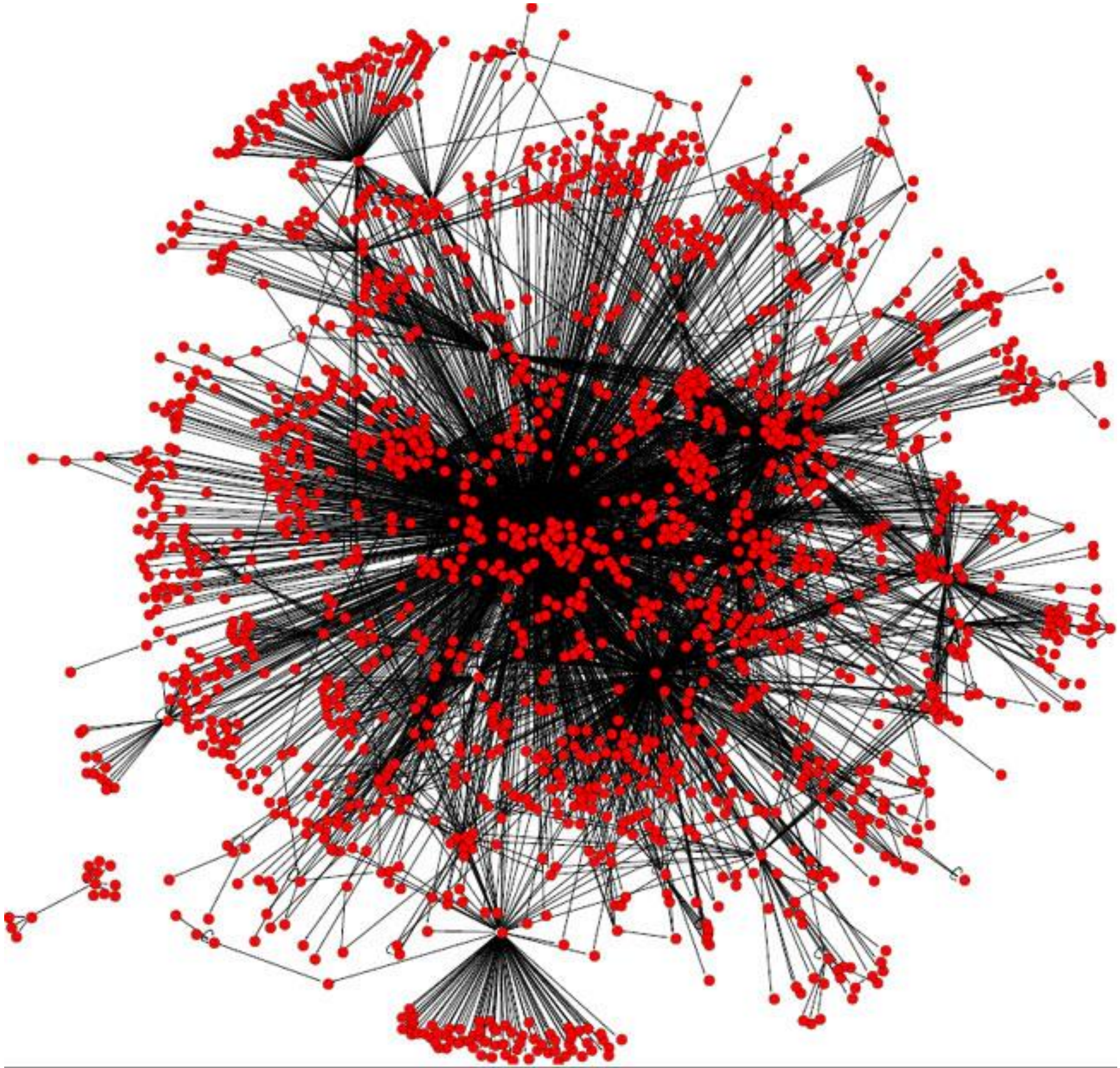
# Gene regulatory network



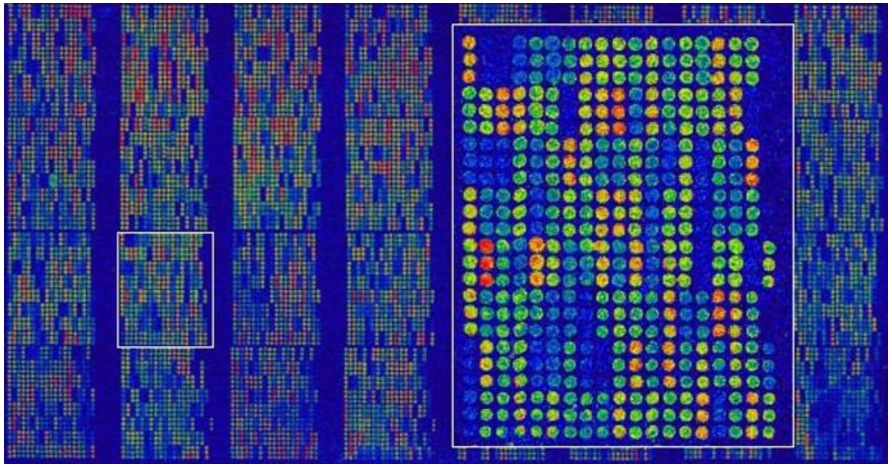
# Gene regulatory network



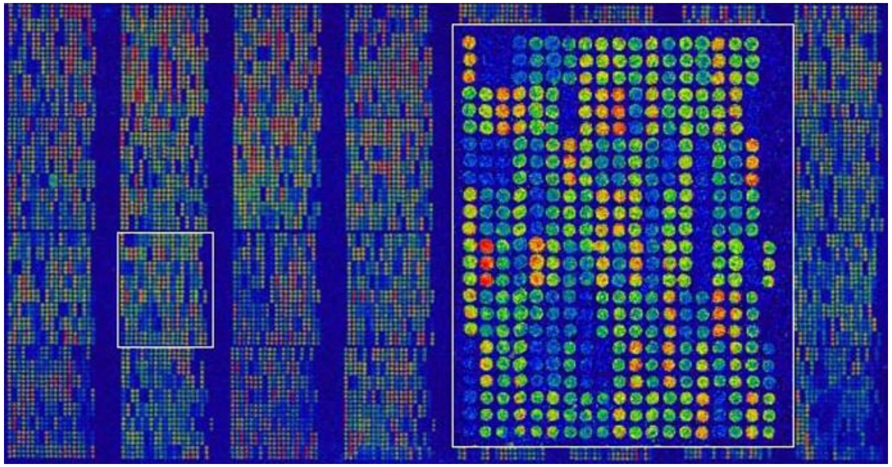
# E. coli regulatory network



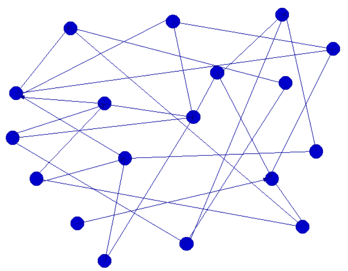
The development of high-throughput data-collection techniques allows for the simultaneous interrogation of the status of cell’s components



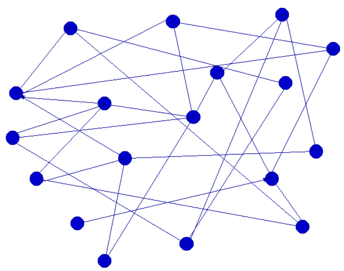
The development of high-throughput data-collection techniques allows for the simultaneous interrogation of the status of cell's components



Big data

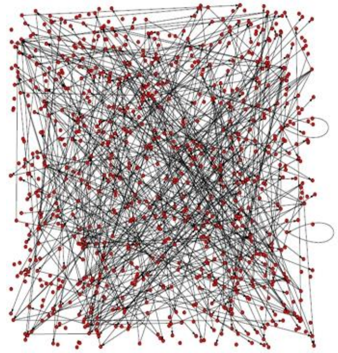


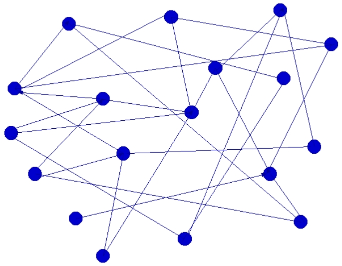
# Challenge: network reconstruction



Challenge: network reconstruction

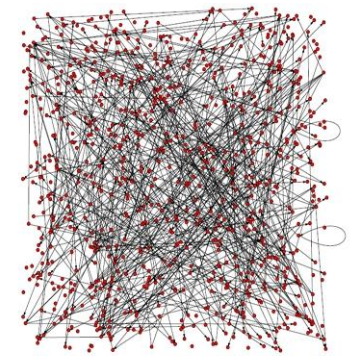
Difficulty: large size (many components) of biological systems





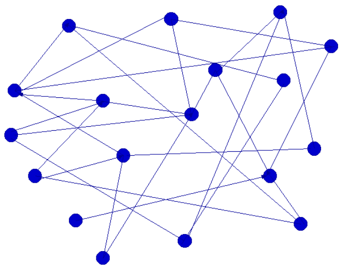
Challenge: network reconstruction

Difficulty: large size (many components) of biological systems



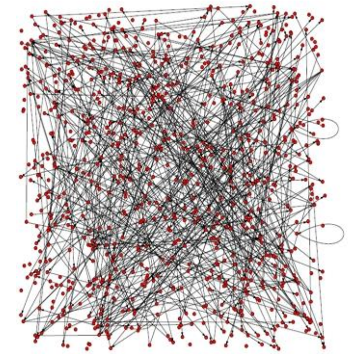
Statistical physics

find approximate methods to solve the problem



Challenge: network reconstruction

Difficulty: large size (many components) of biological systems



Statistical physics

find approximate methods to solve the problem

Most of the current reconstruction techniques do not exploit the temporal information of the data

# GOAL:

Statistical mechanics

# GOAL:

Statistical mechanics

↓

develop new inference techniques that exploit the temporal structure of the data

# GOAL:

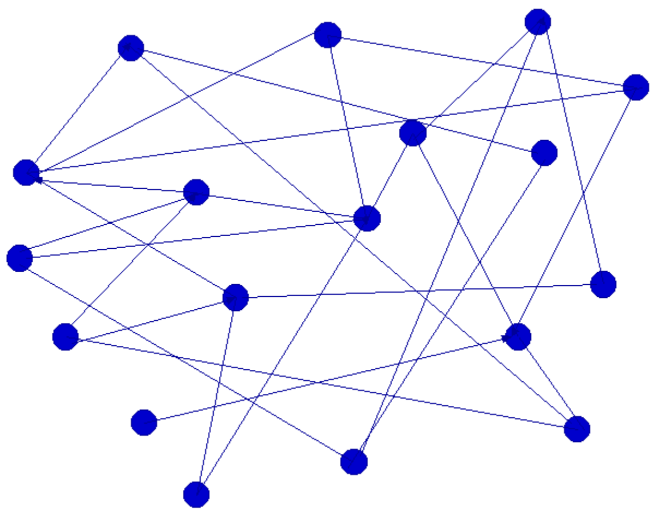
Statistical mechanics

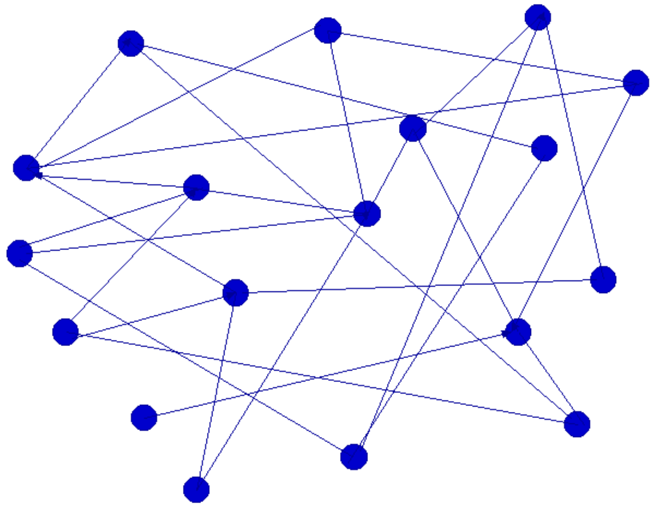
↓

develop new inference techniques that exploit the temporal structure of the data

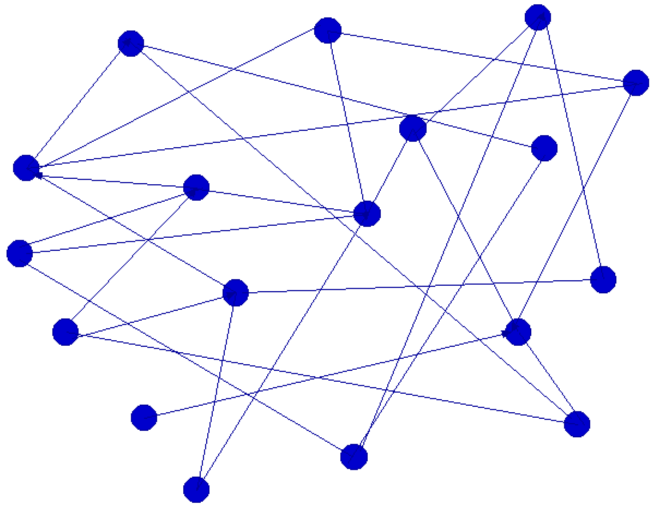
↓

improve the quality of biological network reconstruction



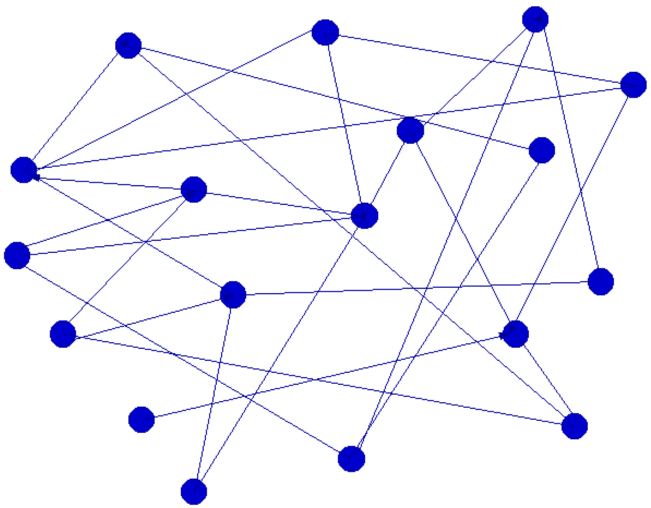


New method to predict the state of the system knowing the value of the links (results agree well with simulations of small systems)



New method to predict the state of the system knowing the value of the links (results agree well with simulations of small systems)

Faster algorithm



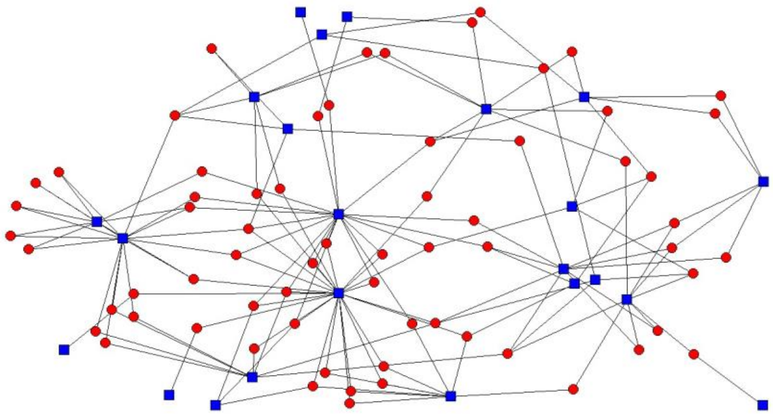
New method to predict the state of the system knowing the value of the links (results agree well with simulations of small systems)

Faster algorithm

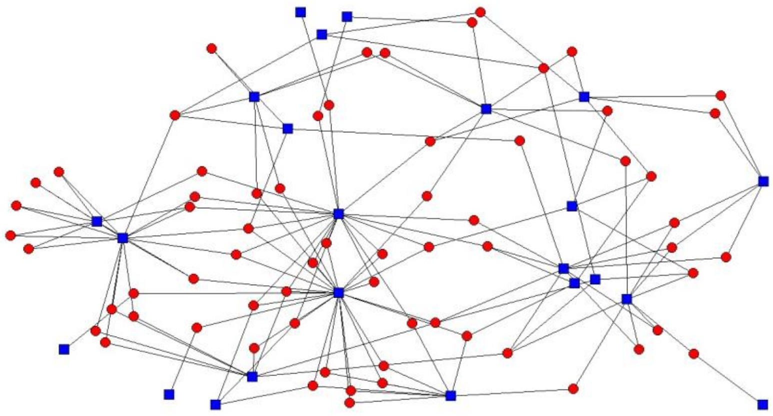
To do:

Inference problem: optimally predict the links

# Hidden nodes

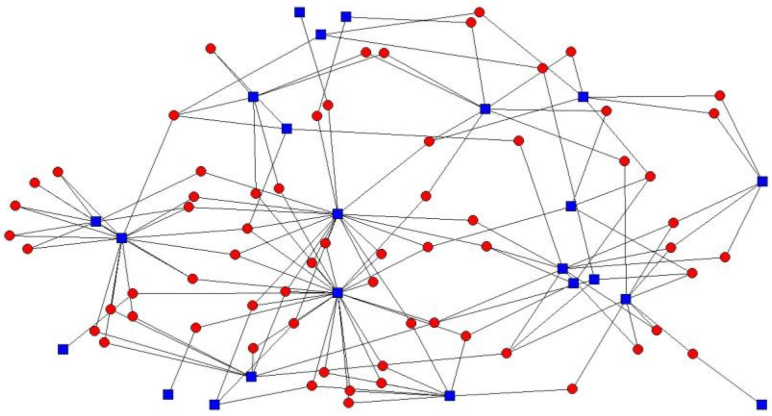


# Hidden nodes



Optimally predict the state of the unobserved variables ( results agree well with simulations of small systems)

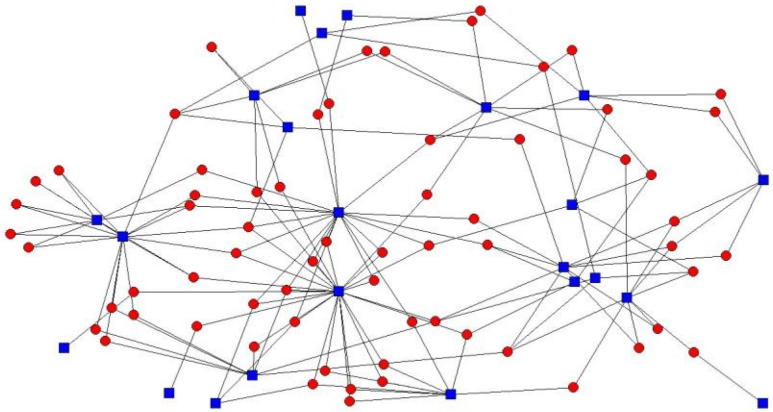
# Hidden nodes



Optimally predict the state of the unobserved variables ( results agree well with simulations of small systems)

Quality of the prediction on the hidden nodes varying the sistem's parameters

# Hidden nodes

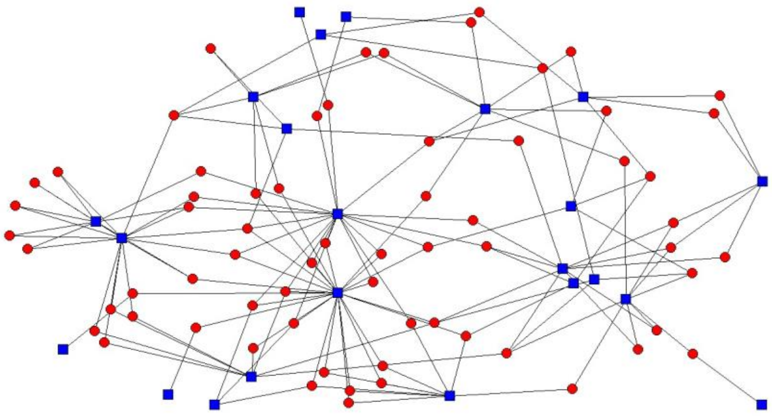


Optimally predict the state of the unobserved variables ( results agree well with simulations of small systems)

Quality of the prediction on the hidden nodes varying the sistem's parameters

Algorithm to infer the links

# Hidden nodes



Optimally predict the state of the unobserved variables ( results agree well with simulations of small systems)

Quality of the prediction on the hidden nodes varying the sistem’s parameters

Algorithm to infer the links

To do:

Study different kinds of networks, continuous variables

- Courses and schools (besides those organized by NETADIS):

TU Berlin:
- Stochastic Systems
- Monte Carlo methods in Artificial Intelligence and Machine Learning
- Probabilistic and Bayesian Modelling in Machine Learning and Artificial Intelligence

Bernstein Center for Computational Neuroscience, Berlin:
Benjamin Lindner´s seminars on "Stochastic Aspects of Neurobiological Problems"

ICTP, Trieste: School on Large Scale Problems in Machine Learning and Workshop on Common Concepts in Machine Learning and Statistical Physics, August 2012.

- Main collaborations: Prof. Sollich’s group and Dr. Roudi group

Thanks for your attention!