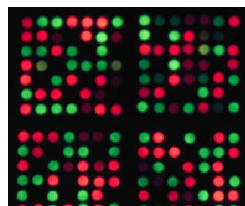
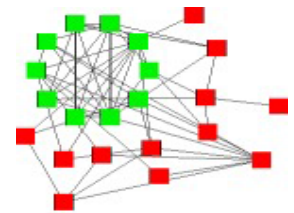
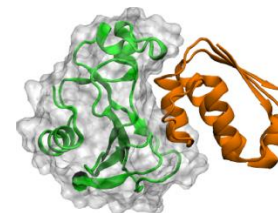
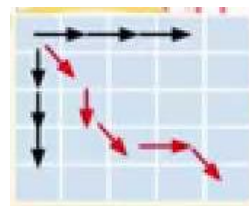


# Приложение на NGS технологията за анализ на взаимодействието патоген - гостоприемник.

Доц. д-р. Румен Димитров



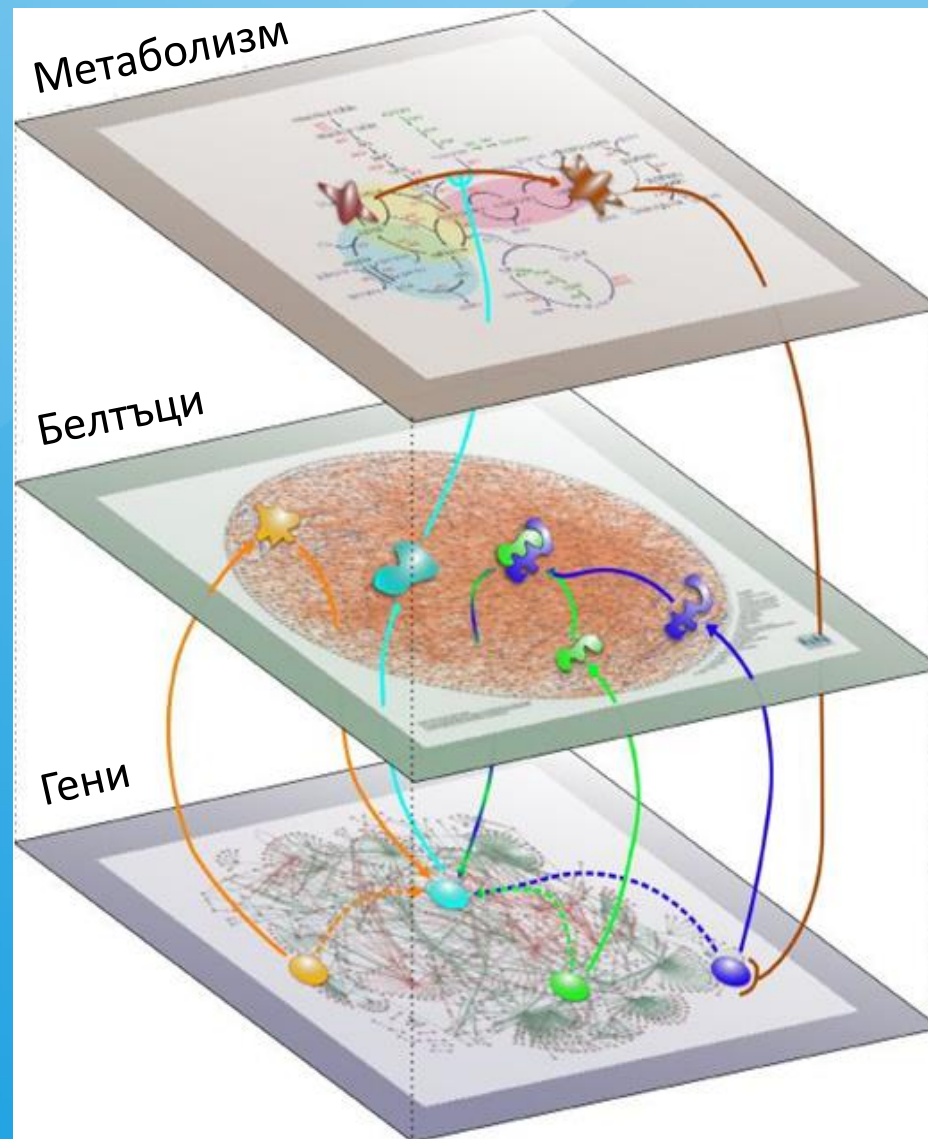
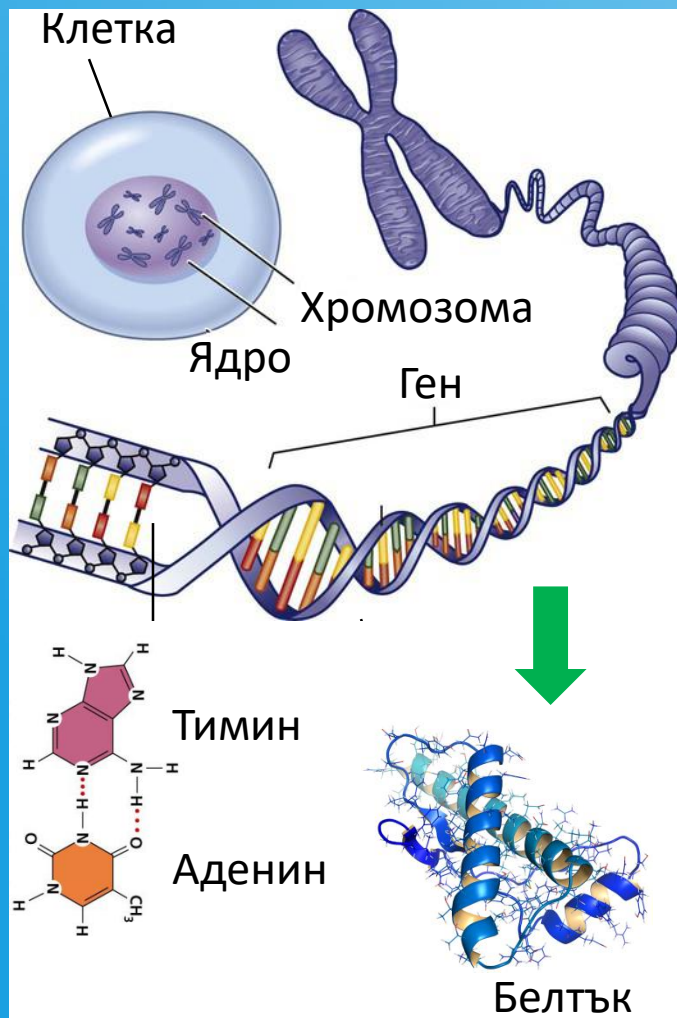
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TCTTGGG



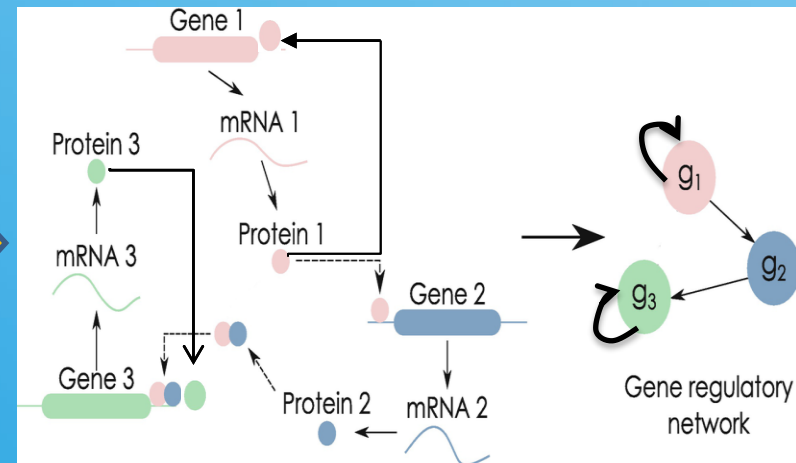
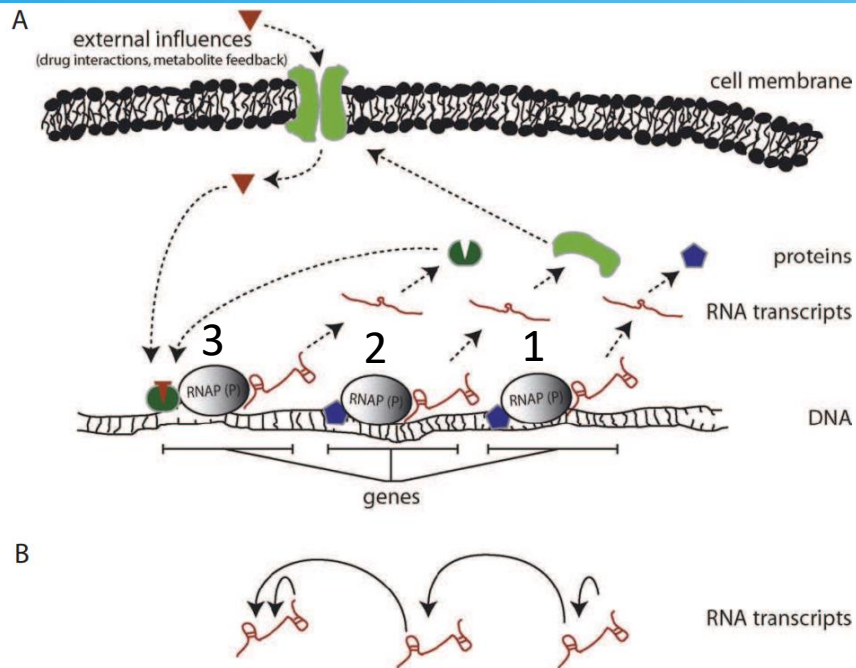
# КРАТКО РЕЗЮМЕ НА ПРЕЗЕНТАЦИЯТА

1. Информационно моделиране на клетъчните функции
2. Генетична регулативна мрежа
3. взаимодействие между патогените и имунната система на гостоприемника - **сигнална регулативна мрежа**
4. **Биологична задача** – популационна генетика на патогена
  - Молекулярна еволюция – **физичен модел**
  - ДНК и РНК секвениране
5. Биологични мрежи – **основни принципи за построяване**
6. Биологични мрежи – **корелационен анализ**

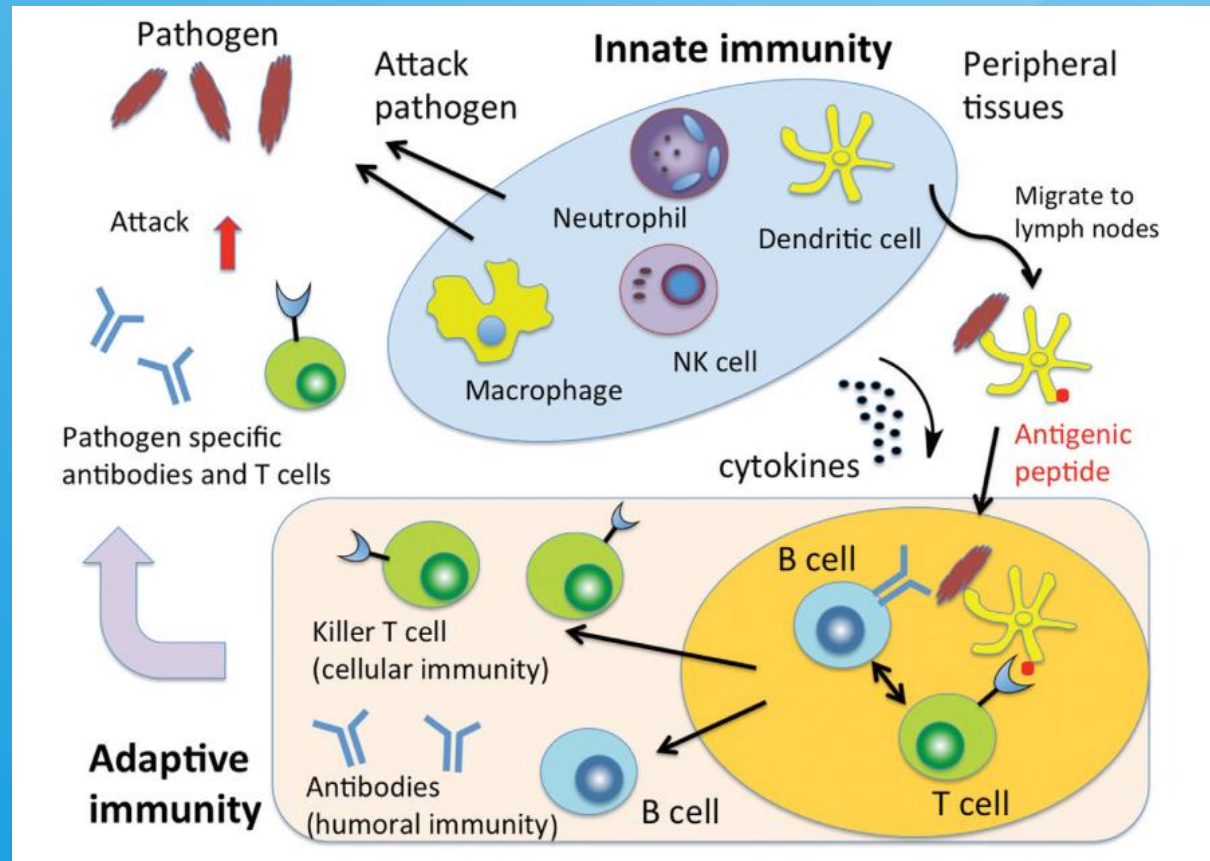
# 1. Информационно моделиране на клетъчните функции



### 3. Информационно моделиране на клетъчните функции-генетична регулативна мрежа



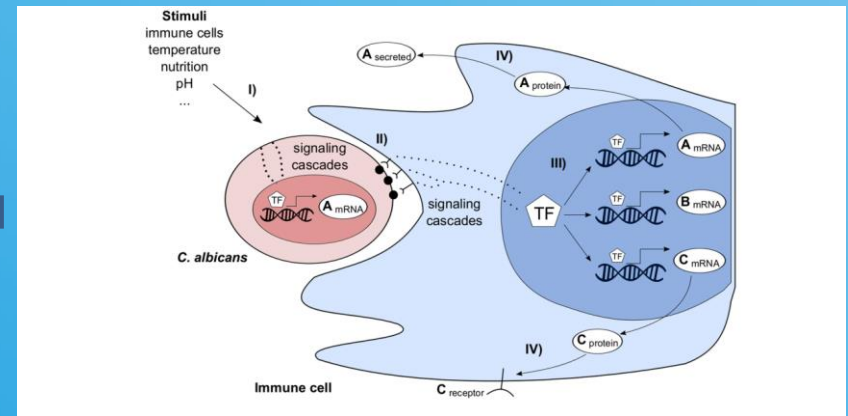
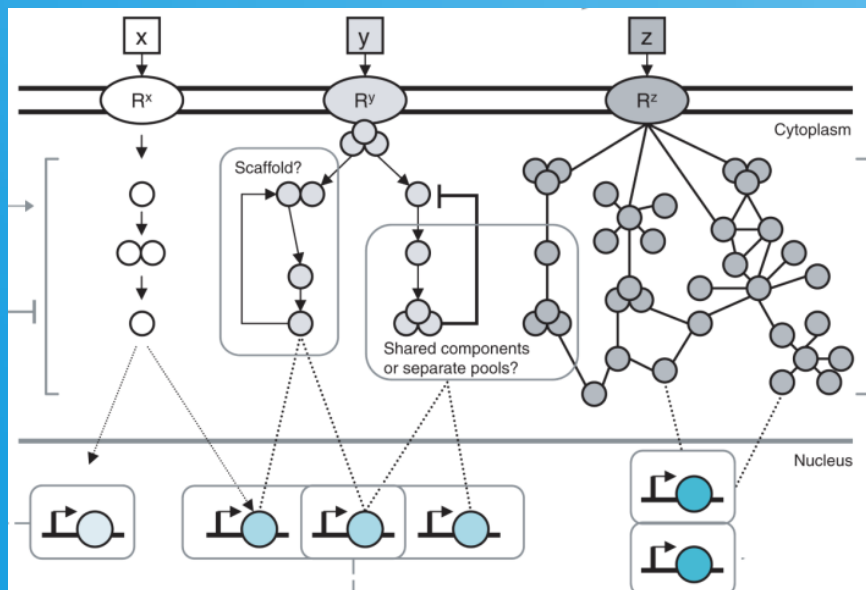
### 3. Биологична задача – взаимодействие между патогените и имунната система на гостоприемника



**Fig. 1** The innate immune system operates largely in peripheral tissues, where it recognizes foreign pathogens. Upon binding of PAMPs to PRRs, the innate immune system is activated and provides a first line of defence against the invader. Subsequently, the adaptive immune system is activated, and with help from the innate immune system, pathogen-specific antibodies and killer T cells are produced (adapted from [11]).

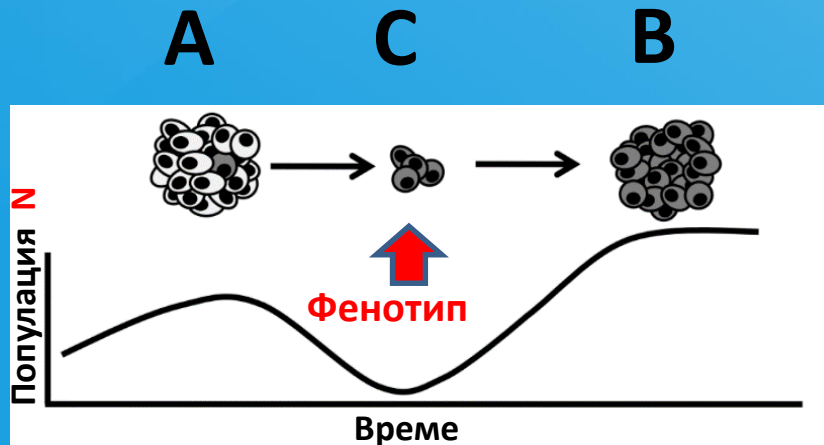
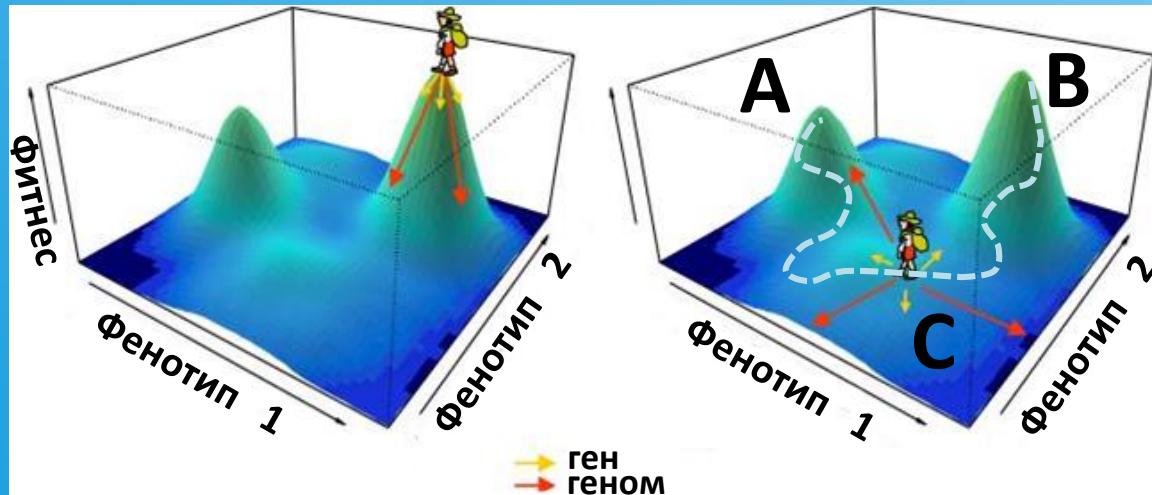


#### 4. Патоген-Гостоприемник -сигнална регулативна мрежа

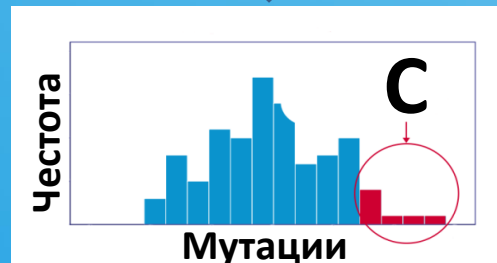
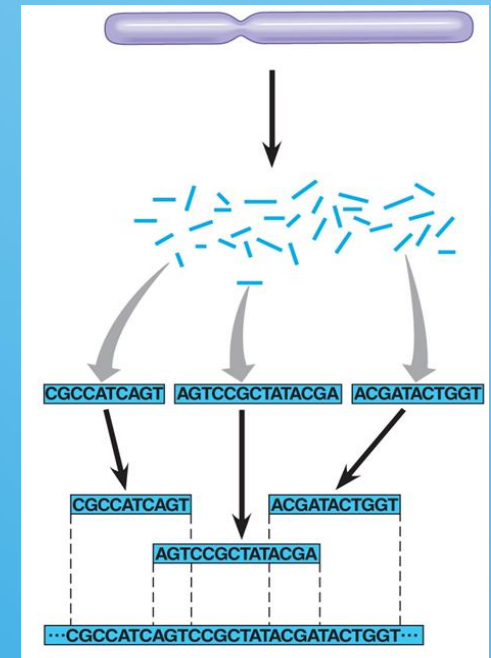


## 4. Биологична задача – популяционна генетика на патогена

преходи между различни клетъчни състояния (стохастичен процес)

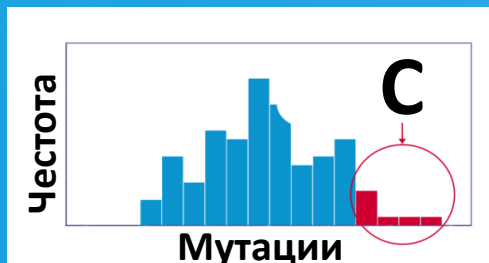
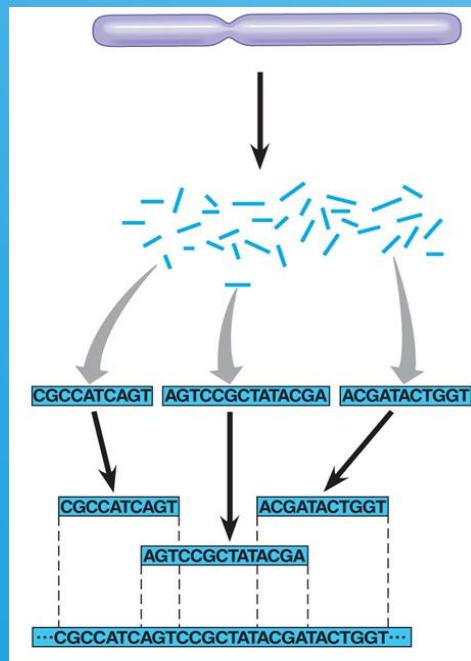


NGS – База от данни



## 2. Основни проблеми в рамките на биологическата задача

### NGS – База от данни



### 1. Геномика:

- подреждане на секвенции и структури;
- асемблиране;
- анотация;
- функционална геномика - секвениране на РНК;
- популационна генетика;
- сравнителна геномика;
- филогенетика.

### 2. Структурна биоинформатика:

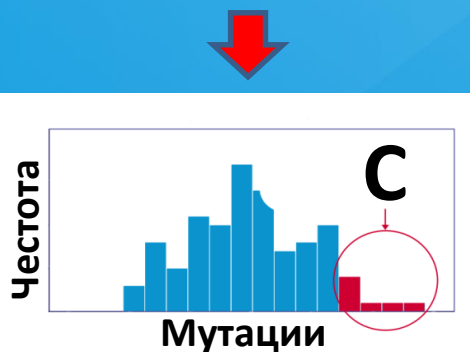
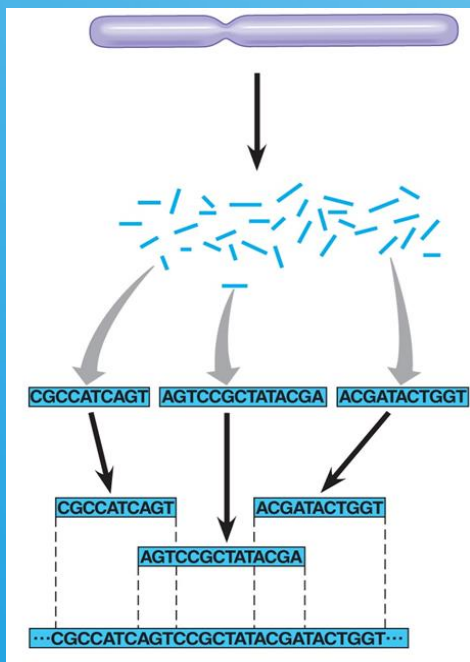
- предсказване на 2D и 3D структурата – хомологично моделиране;
- предсказване на функцията;
- молекулярни машини;
- докинг;
- дизайн на лекарства.

### 3. Мрежова биоинформатика:

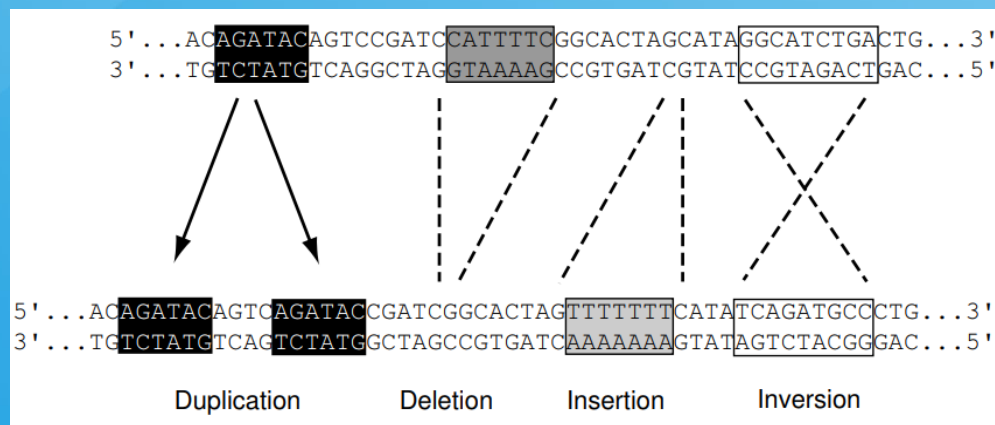
- биологични мрежи.



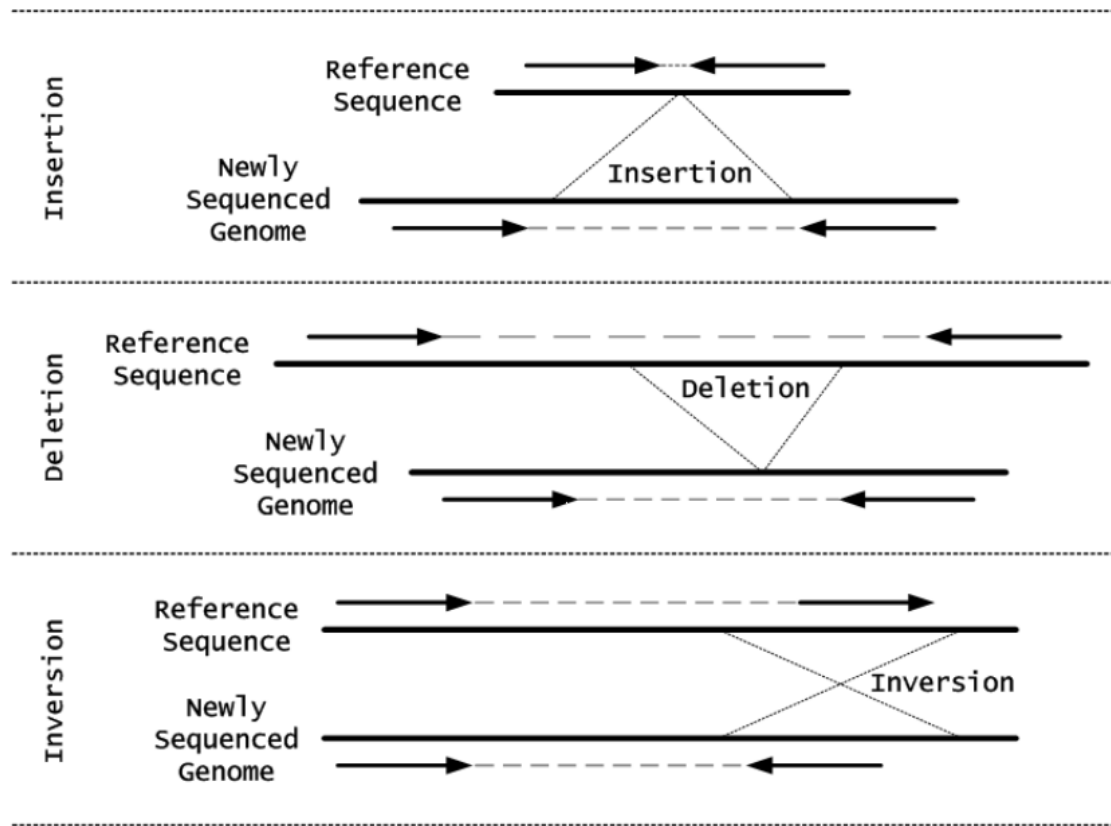
## NGS – База от данни



#### 4. Каква задача решава Асемблирането?

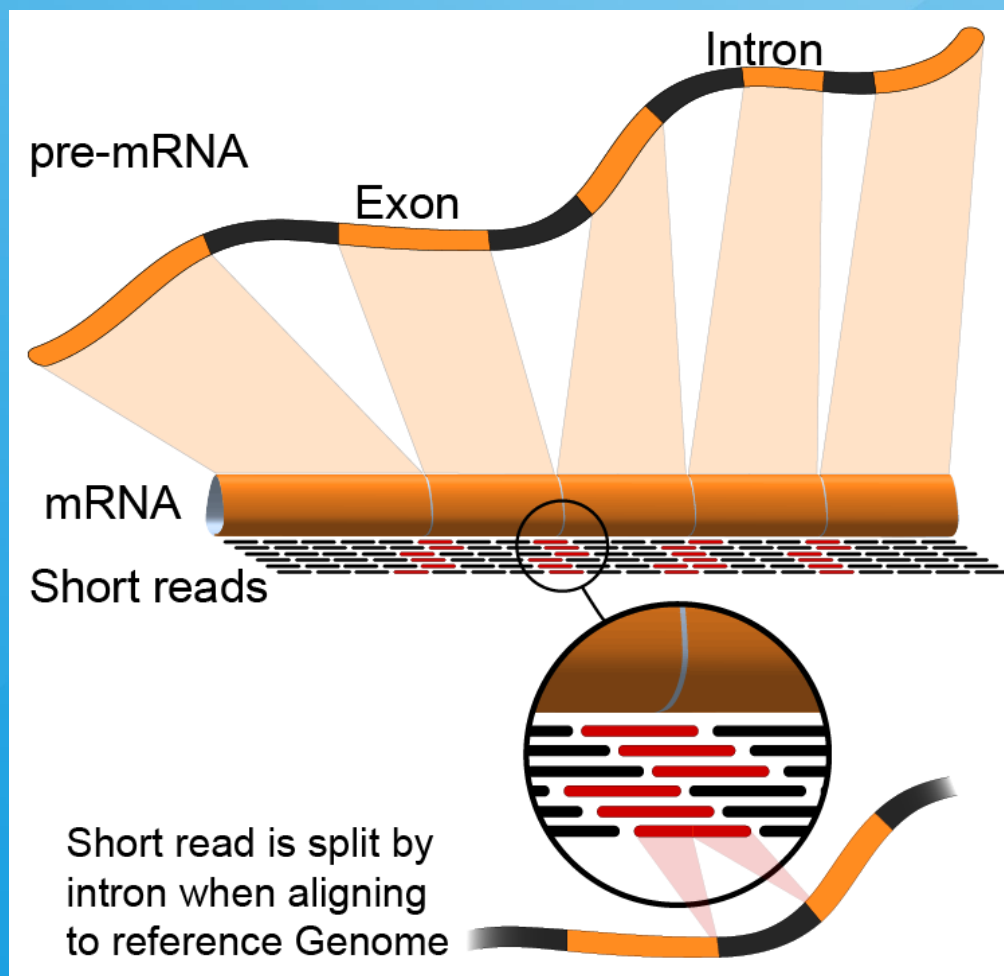


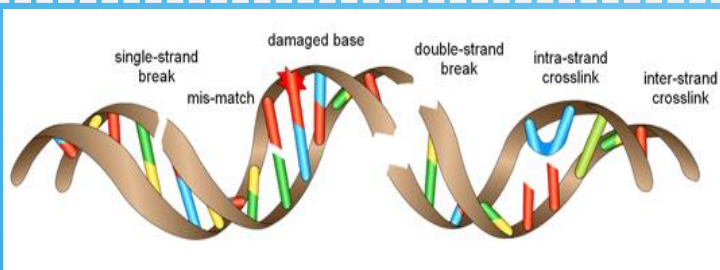
## 4. Каква задача решава Асемблирането?



**Figure 13.3:** Deviations from the expected mate-pair distance indicate possible insertion or deletions. Inversions can be detected if the order of the two mate-pair reads is preserved but one of them changed its orientation.

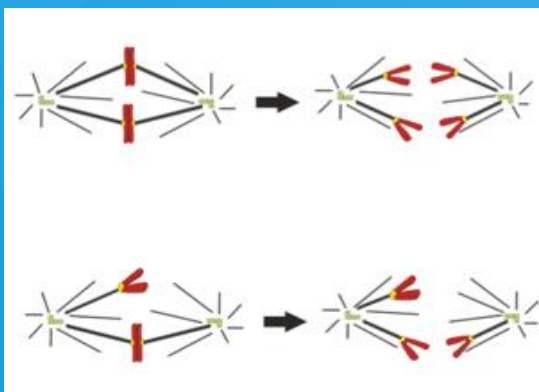
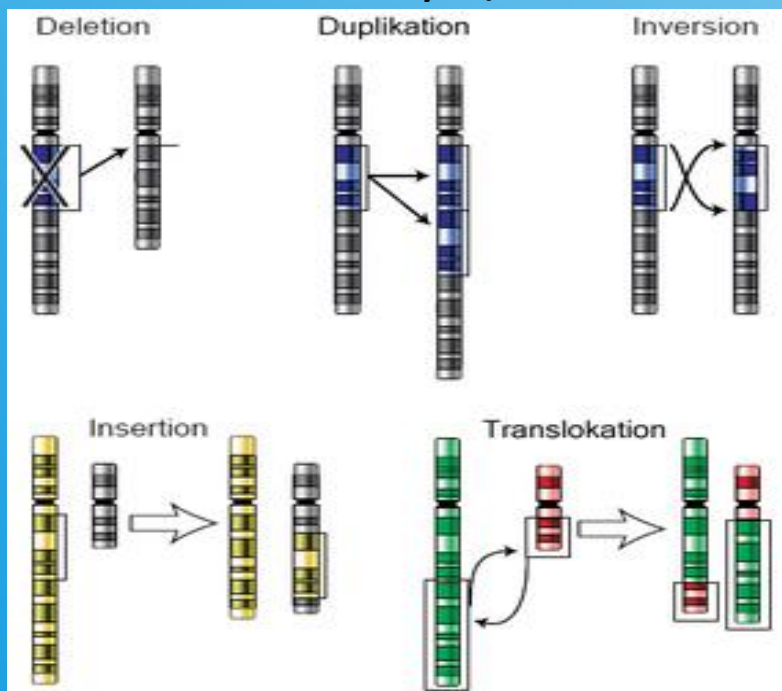
#### 4. Каква задача решава Асемблирането?





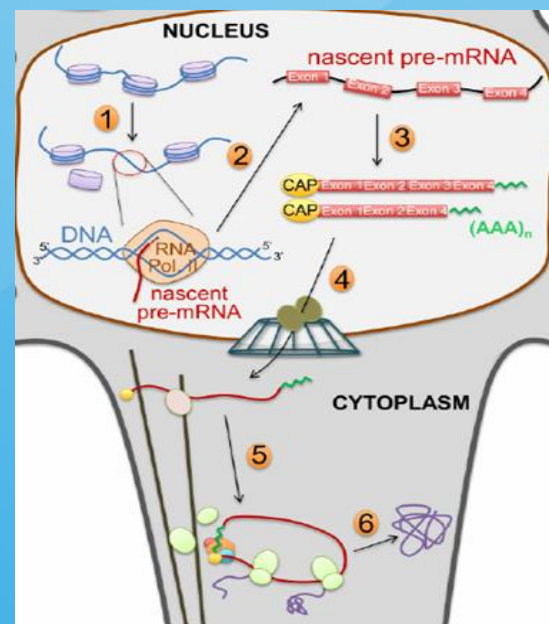
Точкови мутации

Геномни мутации



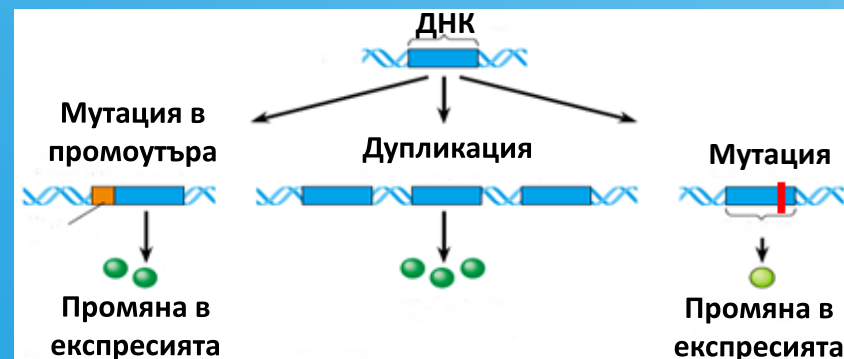
Анеоплоиди

## 2. Молекулярна еволюция – биологичен модел



Клетка

Генетична експресия

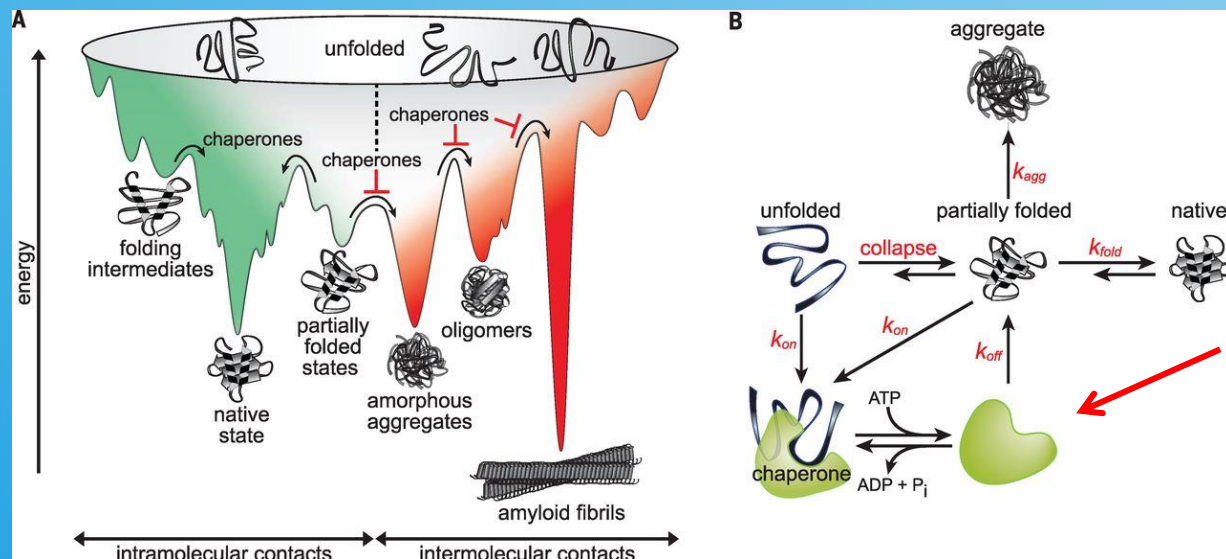


РНК

Белтък

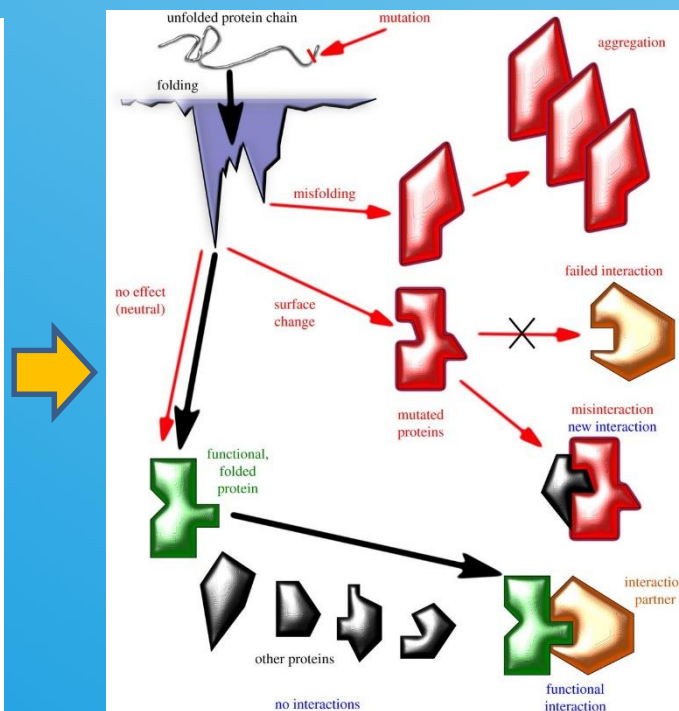
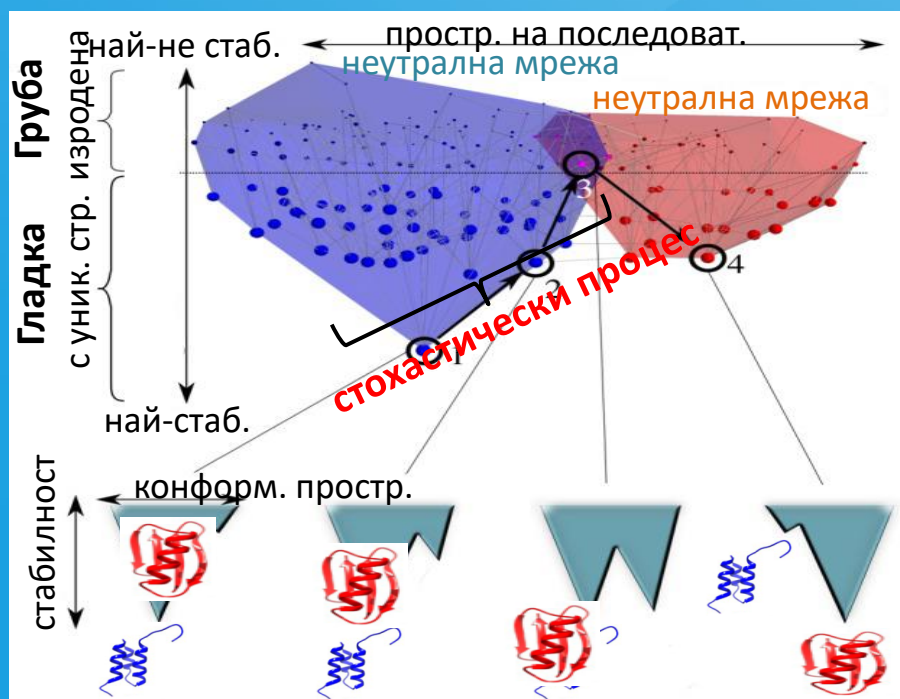
?

## 2. Молекулярна еволюция – биологичен модел



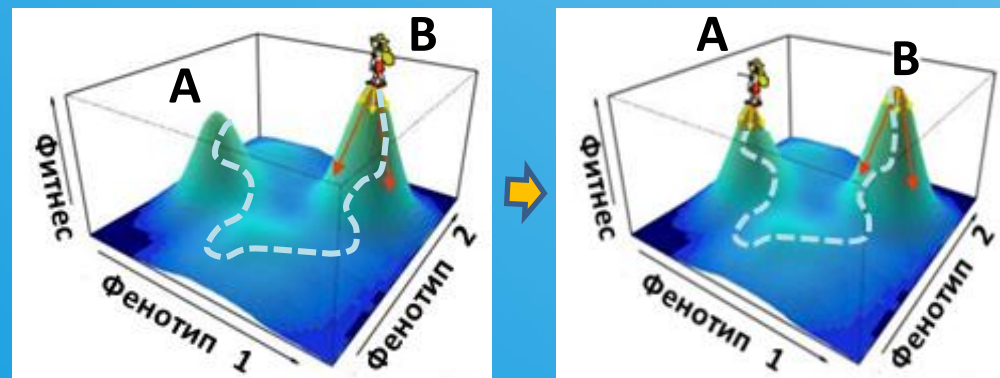
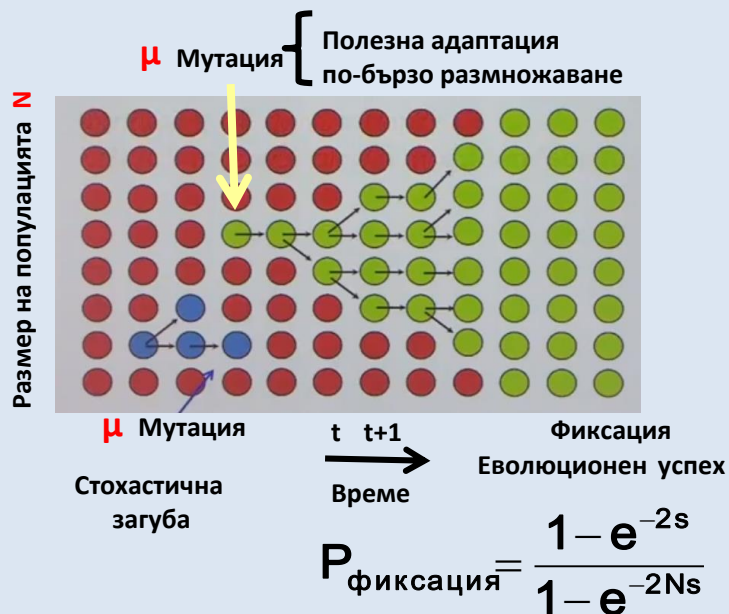
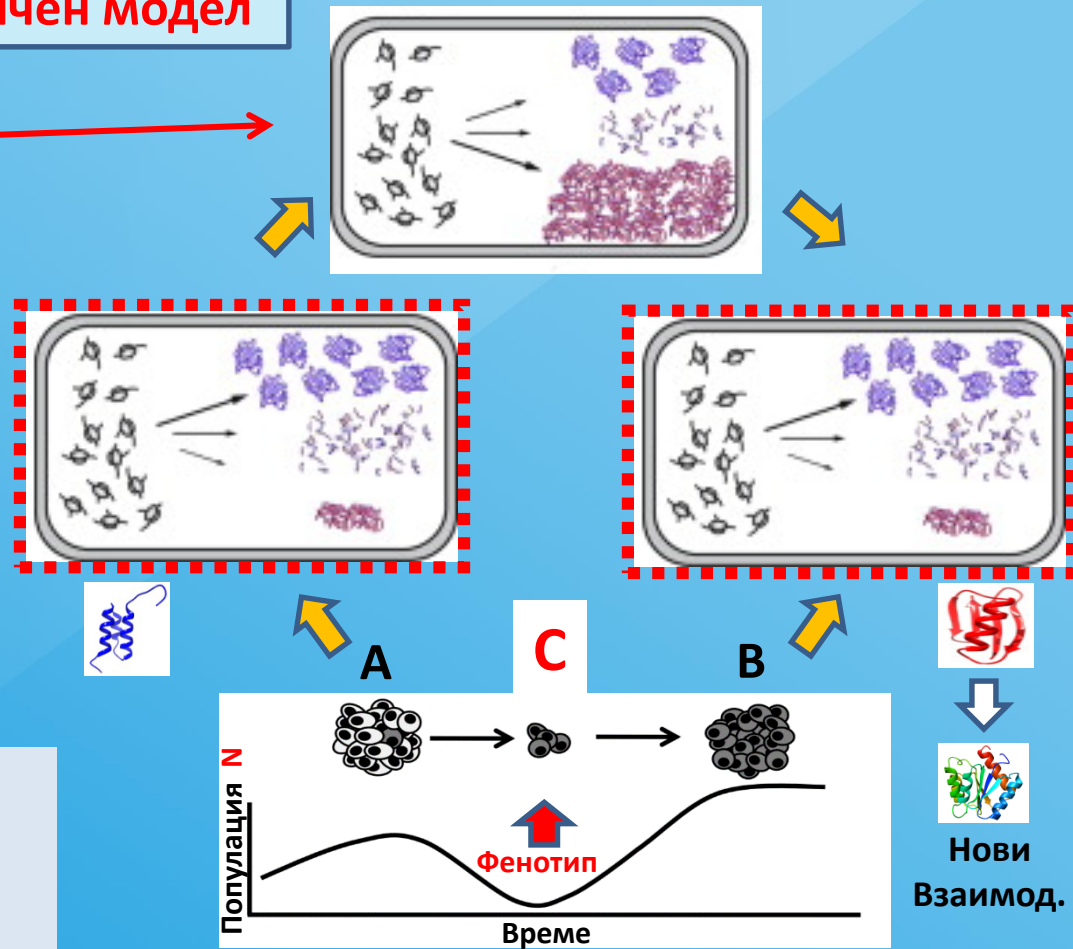
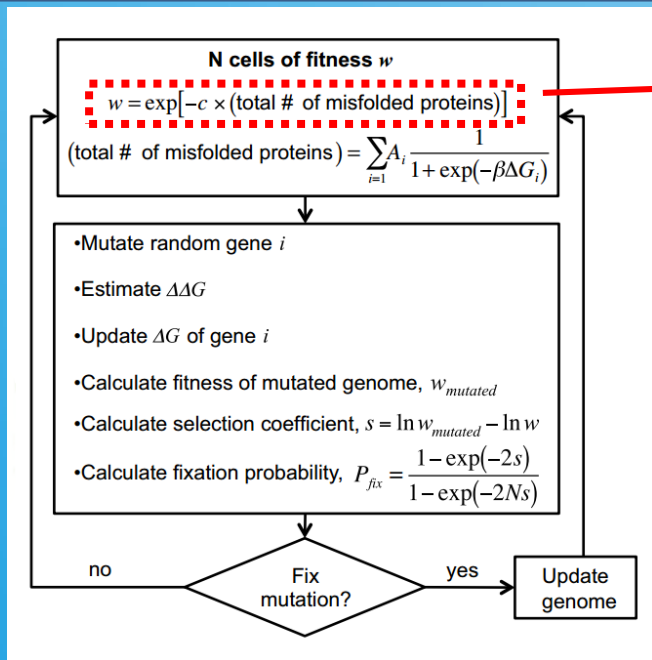
Белтък

Роля на  
Чаперионите в  
молекулярната  
еволюция



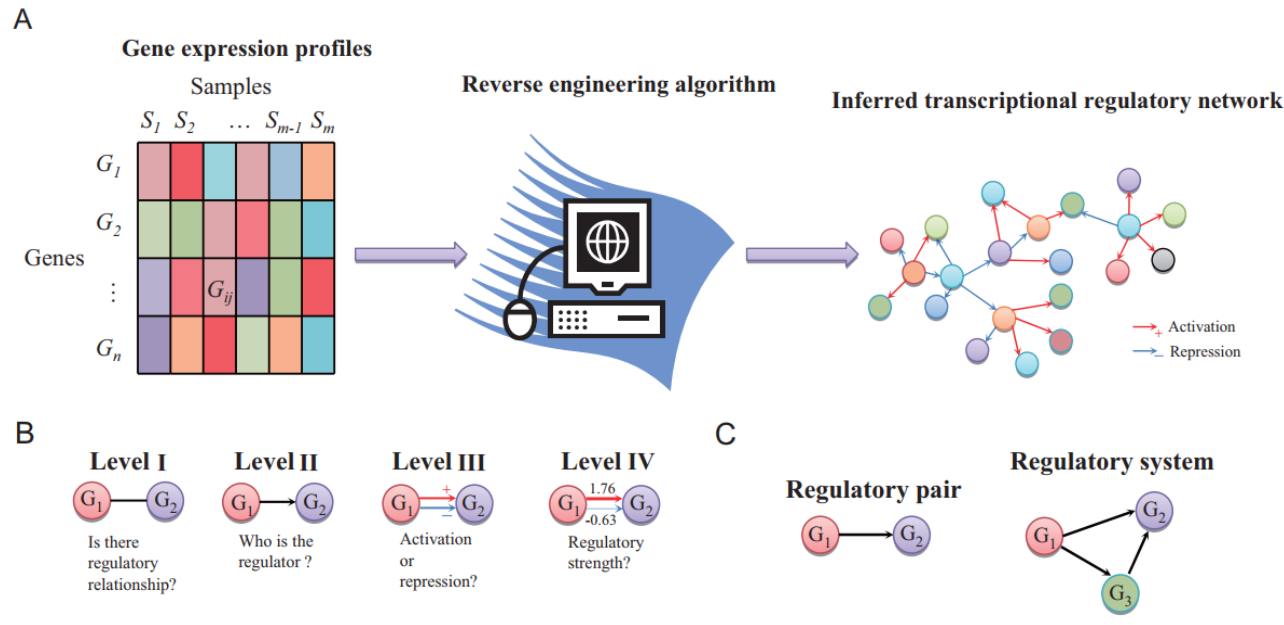


## 2. Молекулярна еволюция – физичен модел



Нови  
Взаимод.

# 5. Биологични мрежи – основни принципи за построяване



$$\mathbf{A} = \begin{pmatrix} a_{11} & \dots & a_{1q} & \dots & a_{1n} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ a_{p1} & \dots & a_{pq} & \dots & a_{pn} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ a_{n1} & \dots & a_{nq} & \dots & a_{nn} \end{pmatrix},$$

$$\mathbf{X} = \begin{pmatrix} x_{11} & \dots & x_{1j} & \dots & x_{1m} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{i1} & \dots & x_{ij} & \dots & x_{im} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{n1} & \dots & x_{nj} & \dots & x_{nm} \end{pmatrix},$$

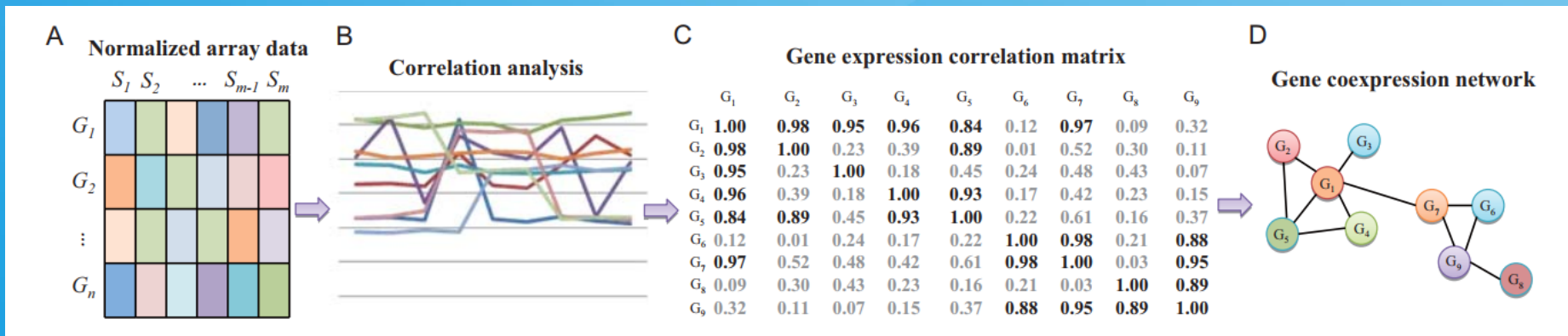
$$a_{12}, a_{21} = \text{or} \neq 0$$

$$a_{12} \neq 0, a_{21} = 0$$

$$a_{12} > 0, a_{21} = 0$$

$$a_{12} < 0, a_{21} = 0$$

## 6. Биологични мрежи – корелационен анализ



**Fig. (2).** The framework of building gene coexpression regulatory network (A) The array data. (B) The correlation analysis of these genes. (C) Pairwise gene correlation matrix. The bold numbers are those over a defined threshold 0.80. (D) The built gene coexpression network.

$$r_{XY} = \frac{\sum_{i=1}^m (X_i - \bar{X})(Y_i - \bar{Y})}{(m-1)S_X S_Y} = \frac{\sum_{i=1}^m (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^m (X_i - \bar{X})^2} \sqrt{\sum_{i=1}^m (Y_i - \bar{Y})^2}},$$

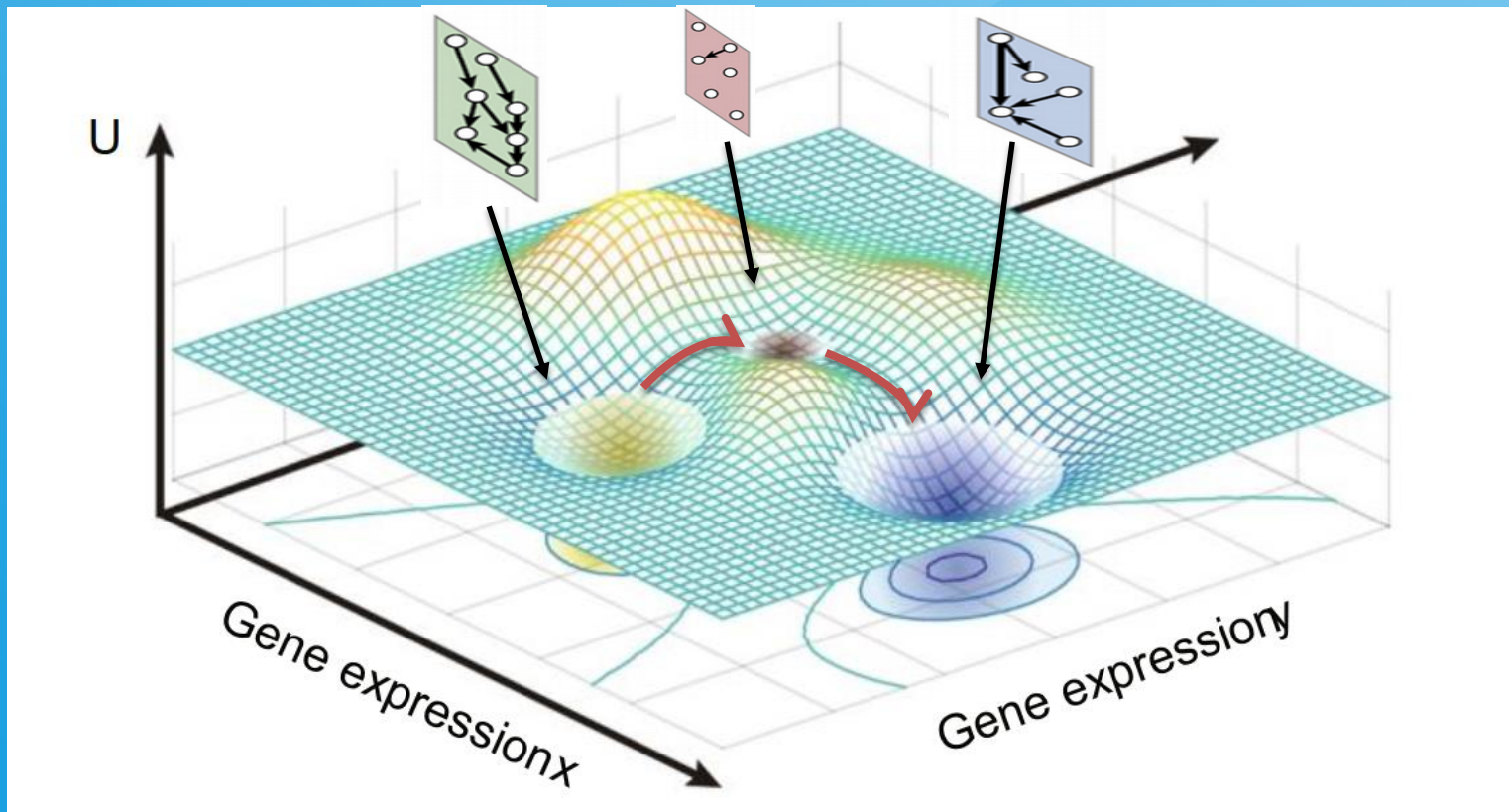
$$\frac{dx}{dt} = \mathbf{f}(\mathbf{x}, \Theta, \mathbf{u}(t), t).$$

$$\frac{d\mathbf{x}}{dt} = A\mathbf{x}$$

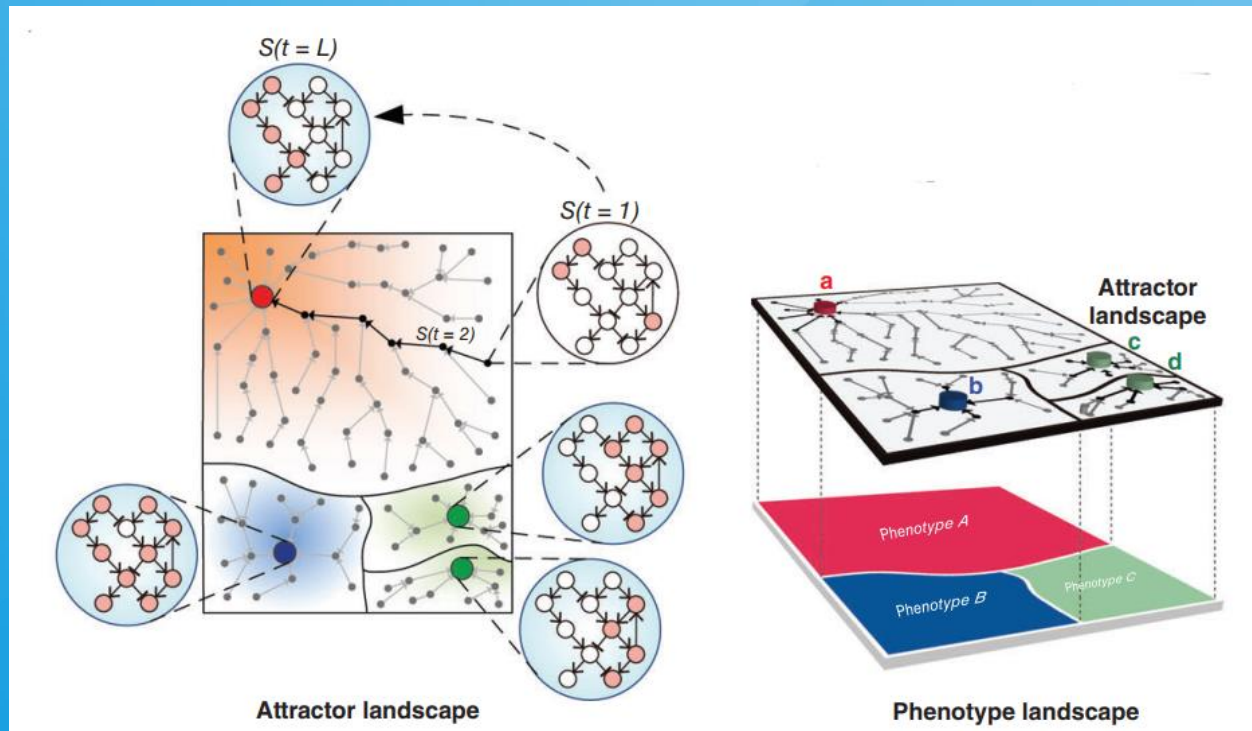
$$P(X_1, \dots, X_G) = P(X_1) \prod_{i=2}^G P(X_i | X_1, \dots, X_{i-1})$$

$$P(X, Y) = P(X|Y)P(Y)$$

## 7. Биологични мрежи – динамични атрактори



## 2. Биологични мрежи – динамични атрактори и фенотипен ландшафт





## 2. Биологични мрежи – динамични атрактори

