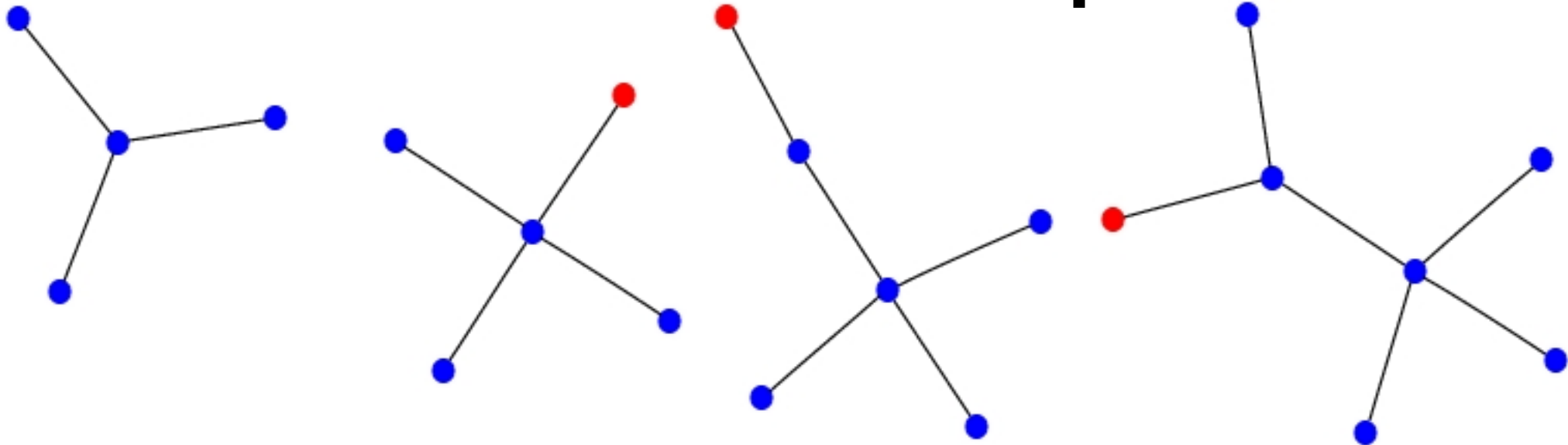


Evolution of co-expression network in Arabidopsis



Moritz Schütte
Max-Planck-Institute
of Molecular Plant Physiology
Potsdam, Germany



International Research Training Group (IRTG)

Genomics and Systems Biology
of Molecular Networks

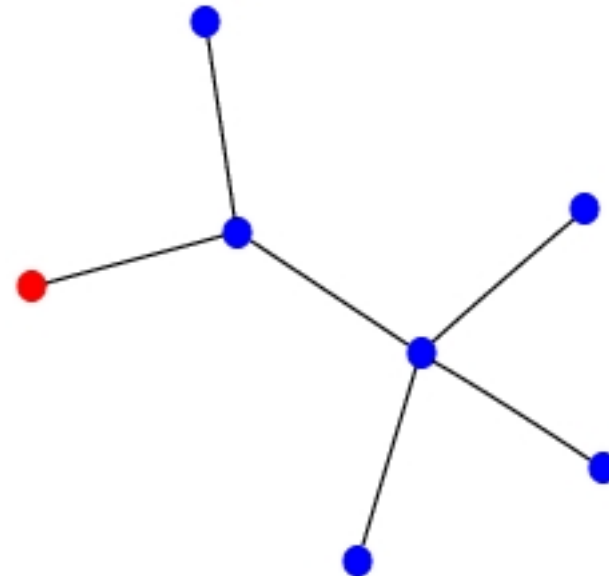
PubMed-GEO microarray data of gene expression

- 357 experiments
- 22810 genes



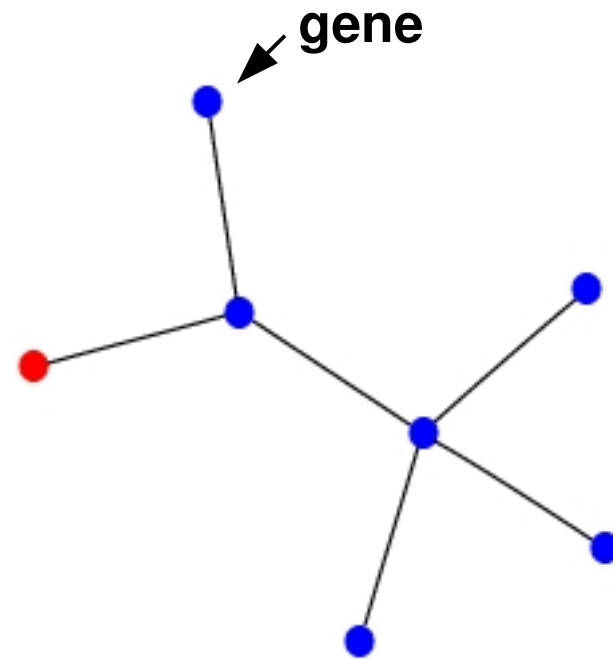
Gene co-expression network with

- 22810 nodes
- 240514 edges



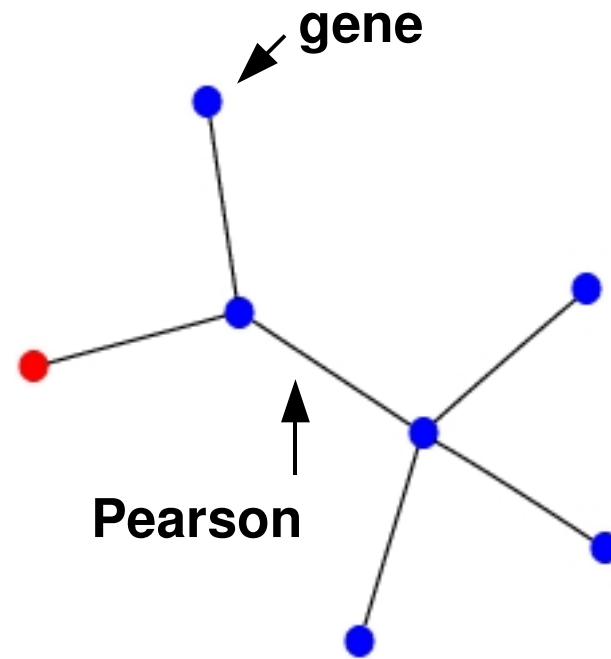
Gene co-expression network

$$k = \begin{pmatrix} \text{exp}_1 \\ \text{exp}_2 \\ \vdots \\ \text{exp}_{357} \end{pmatrix}$$

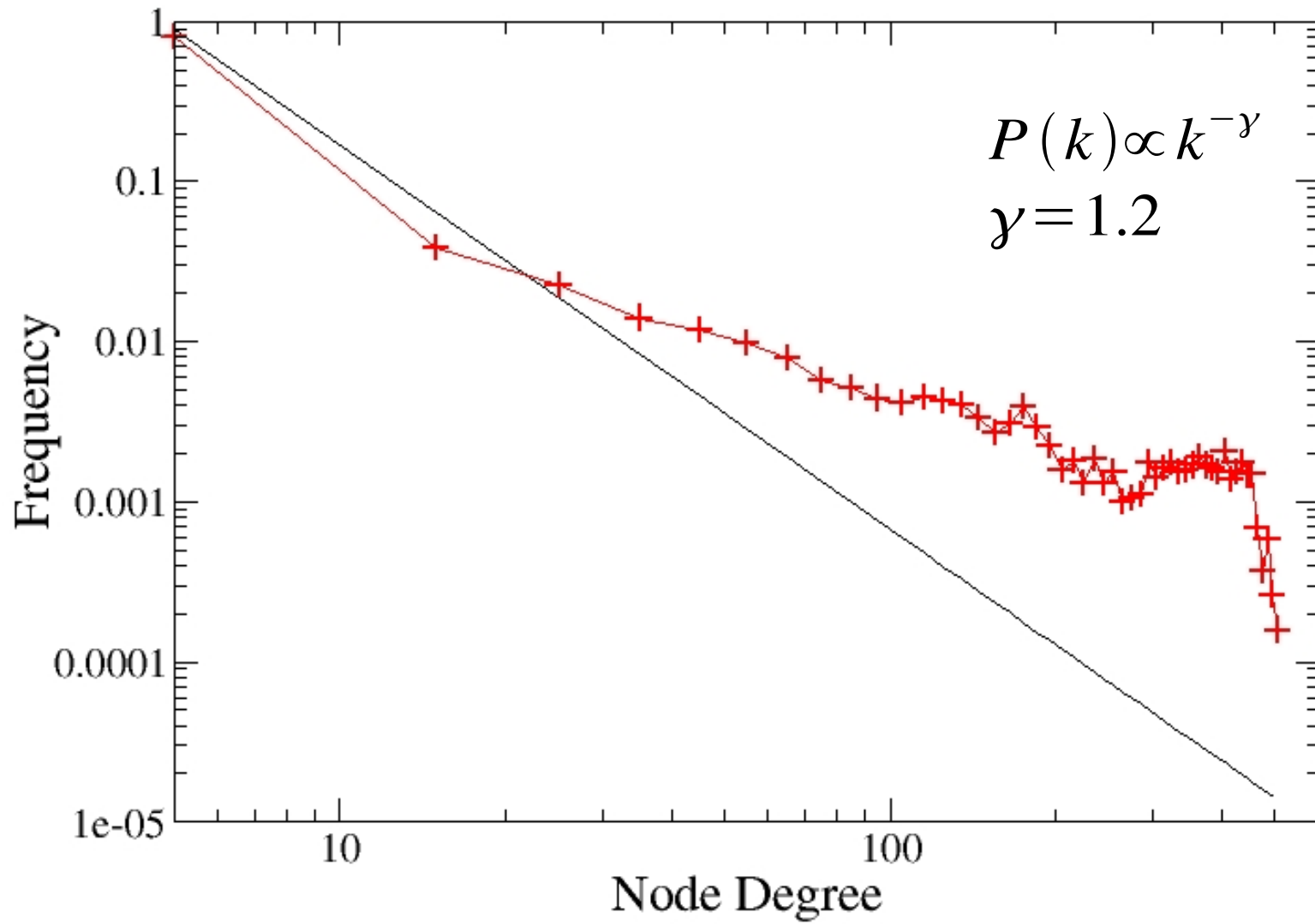


Gene co-expression network

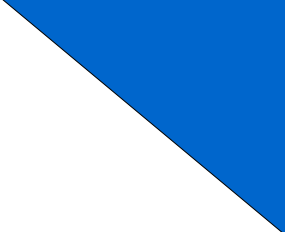
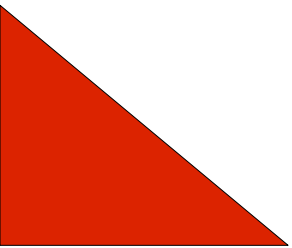
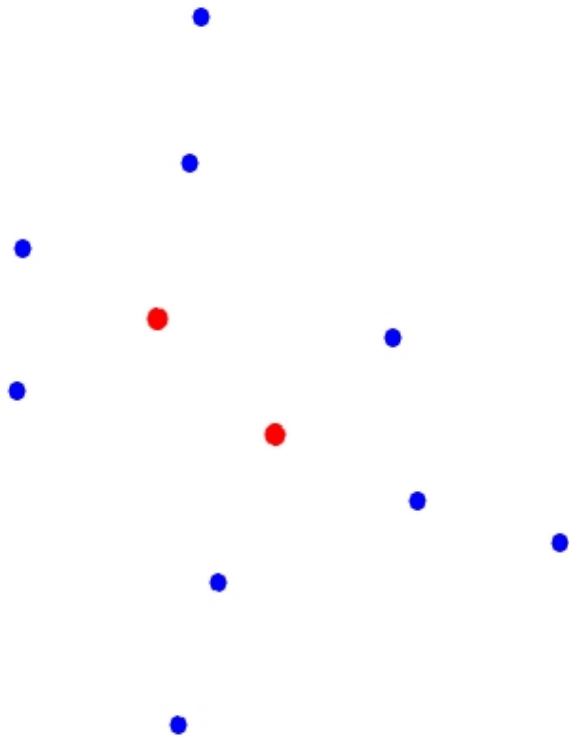
$$k = \begin{pmatrix} \text{exp}_1 \\ \text{exp}_2 \\ \vdots \\ \text{exp}_{357} \end{pmatrix}$$

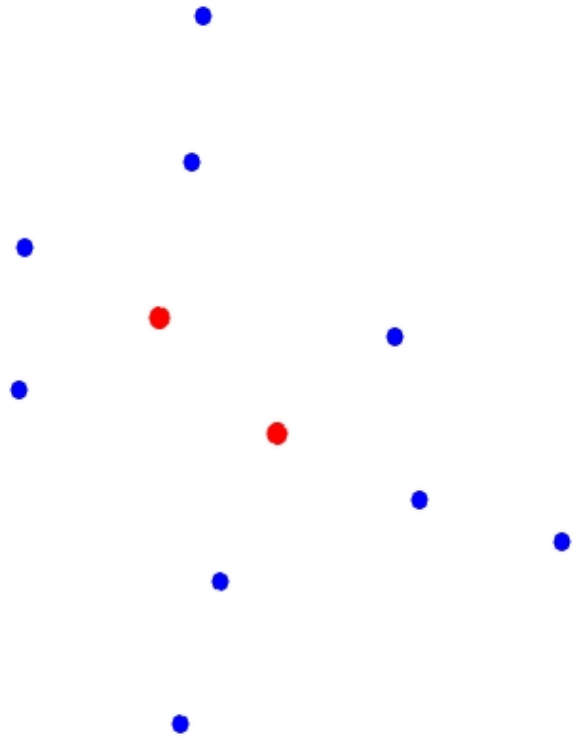


$$r = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_j (y_j - \bar{y})^2}}$$



Protein-protein interaction: $\gamma = 1.5$ Bhan et al. (2002)

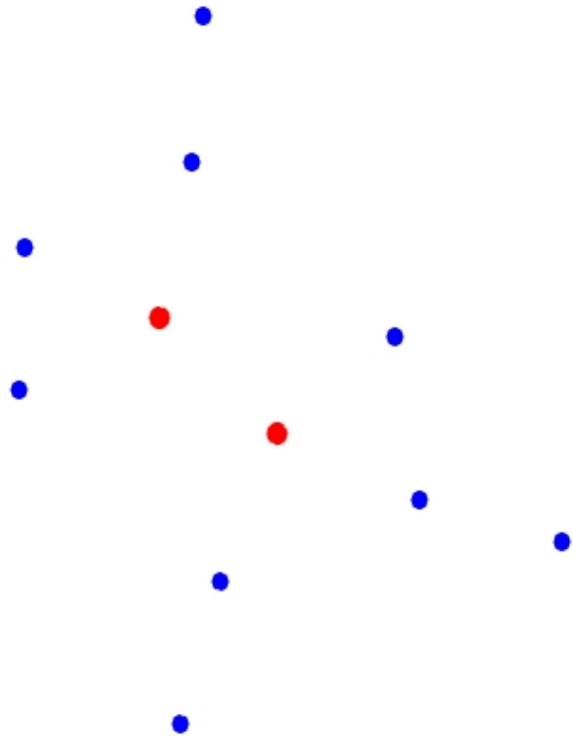




$$\mathbf{k} = \begin{pmatrix} \text{exp}_1 \\ \text{exp}_2 \\ \vdots \\ \text{exp}_D \end{pmatrix}$$

$$k_i \in [-1, 1]$$

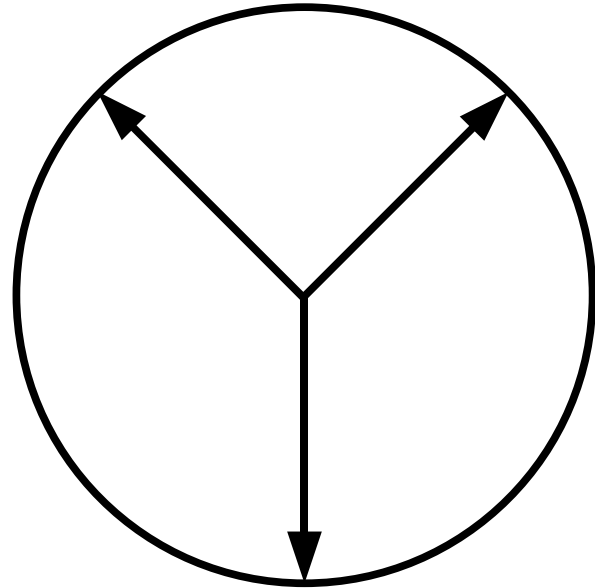
$$|\mathbf{k}| = 1$$

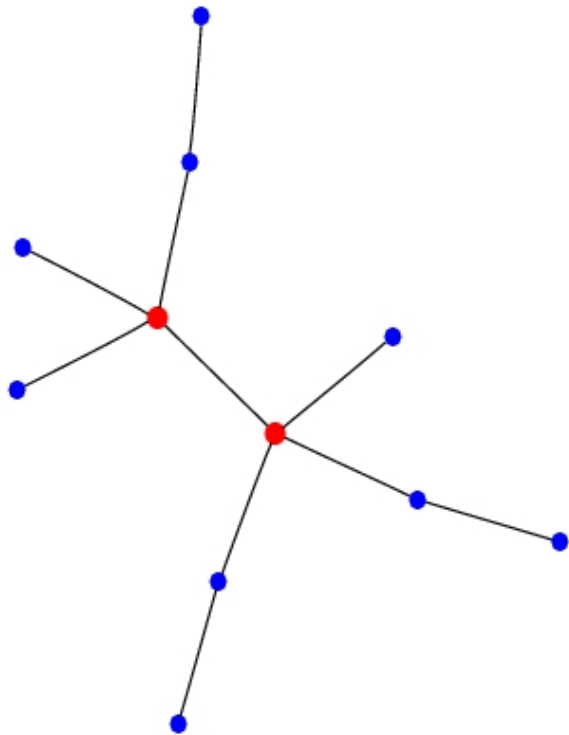


$$\mathbf{k} = \begin{pmatrix} \text{exp}_1 \\ \text{exp}_2 \\ \vdots \\ \text{exp}_D \end{pmatrix}$$

$$k_i \in [-1, 1]$$

$$|\mathbf{k}| = 1$$



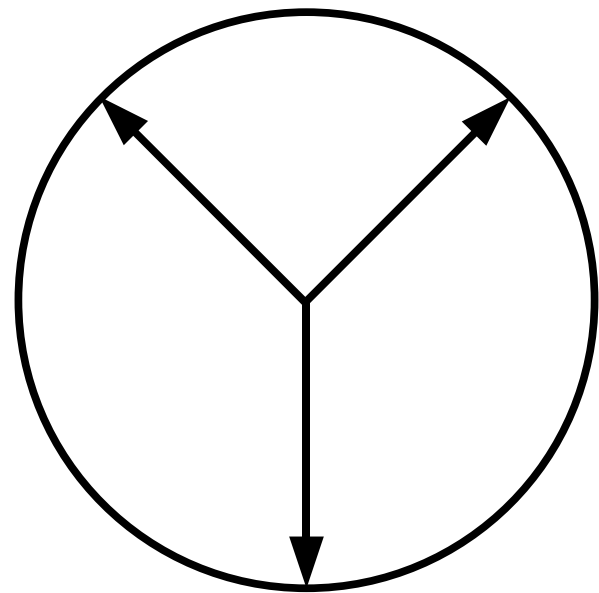


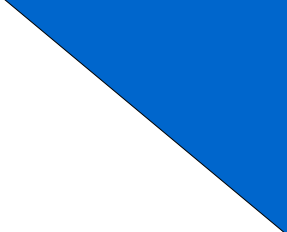
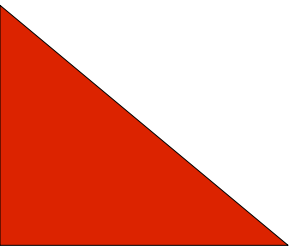
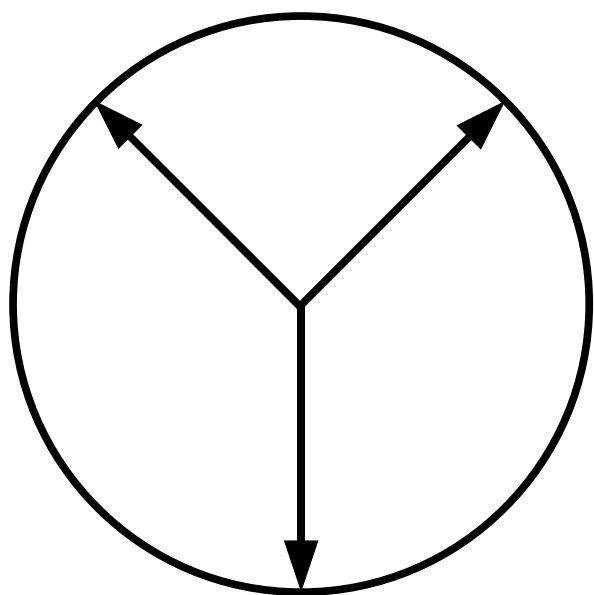
$$\mathbf{k} = \begin{pmatrix} \exp_1 \\ \exp_2 \\ \vdots \\ \exp_D \end{pmatrix}$$

$$k_i \in [-1, 1]$$

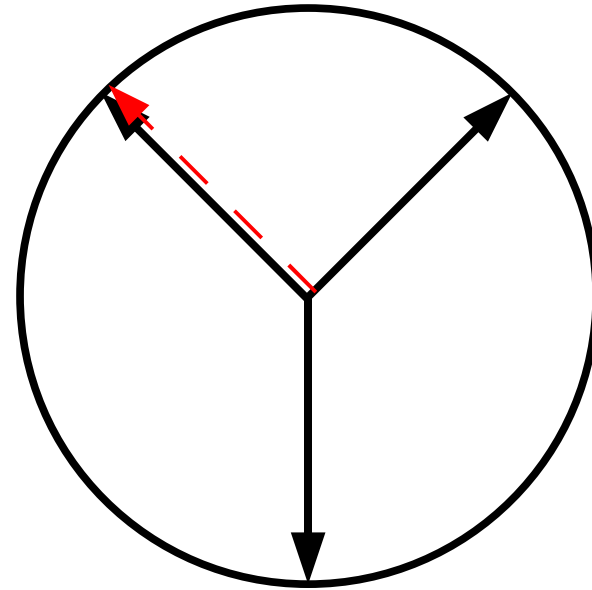
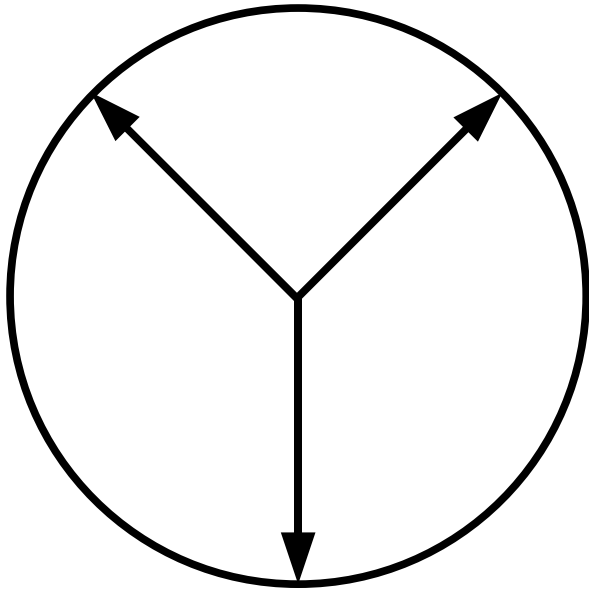
$$|\mathbf{k}| = 1$$

$$r = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_j (y_j - \bar{y})^2}}$$





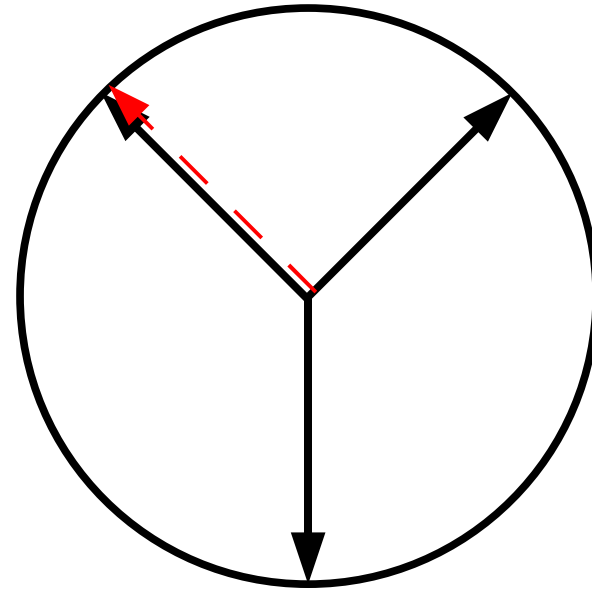
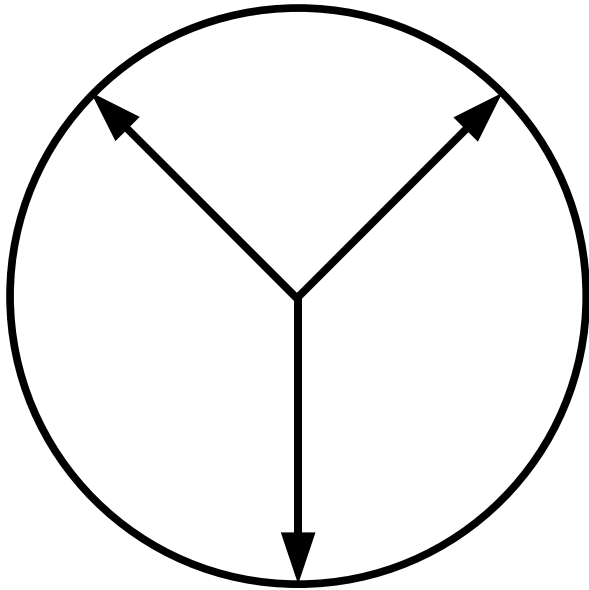
Duplication



90 % of Eukaryote genes

Teichmann & Babu (2004)

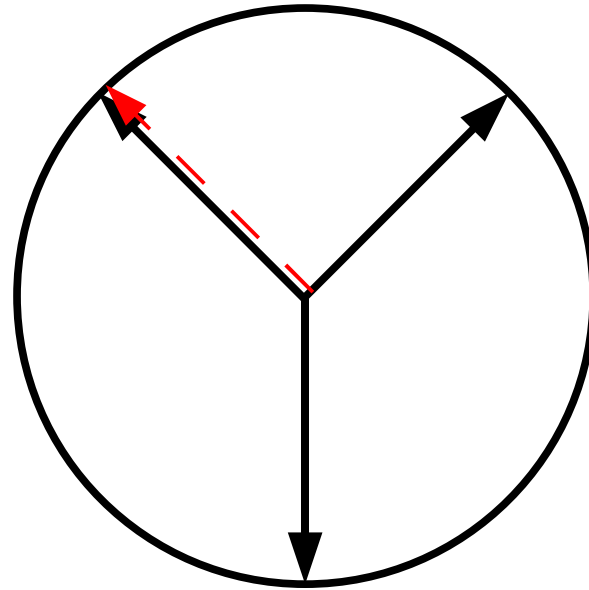
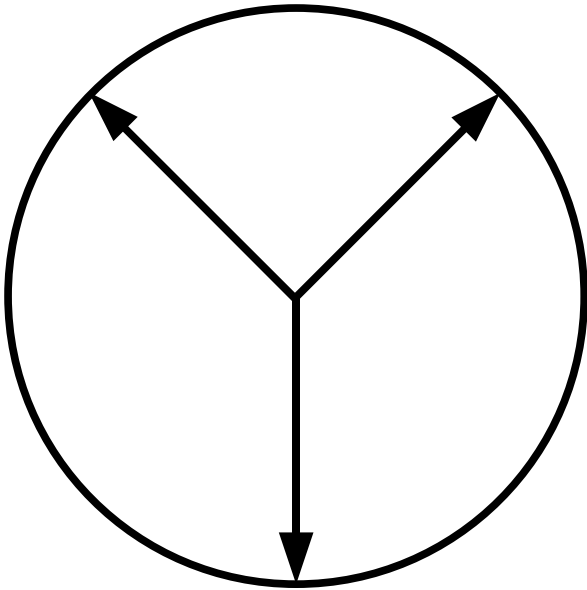
Duplication



Mutation

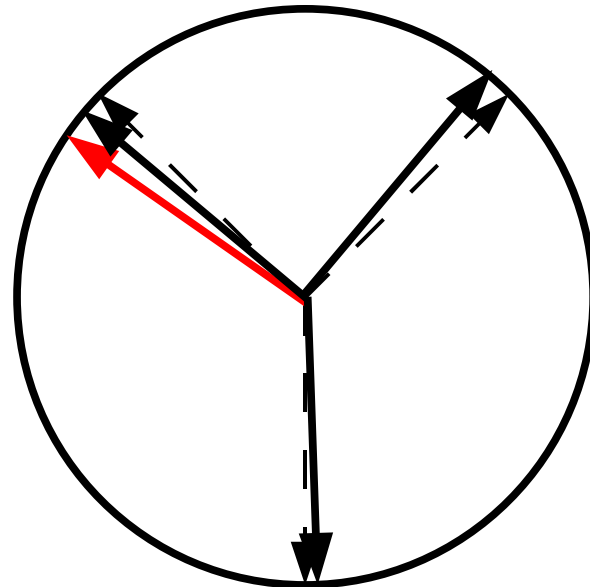
$$\begin{pmatrix} k_1 \\ k_2 \\ \vdots \\ k_D \end{pmatrix} \Rightarrow \begin{pmatrix} k_1 + \xi_1 \\ k_2 + \xi_2 \\ \vdots \\ k_D + \xi_D \end{pmatrix}$$

Duplication

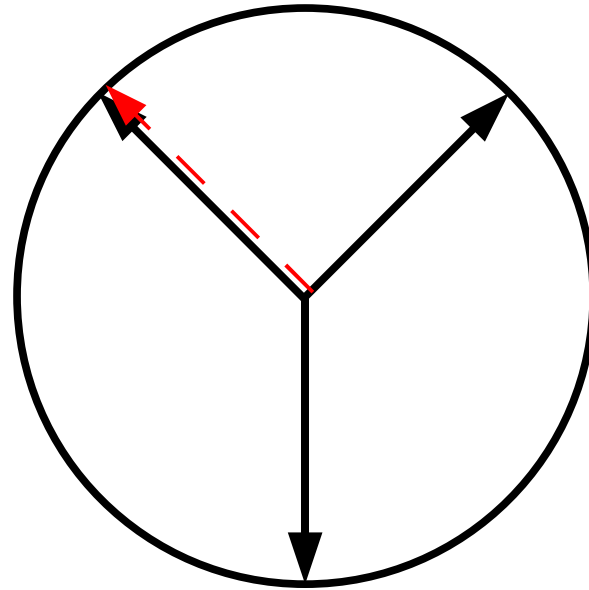
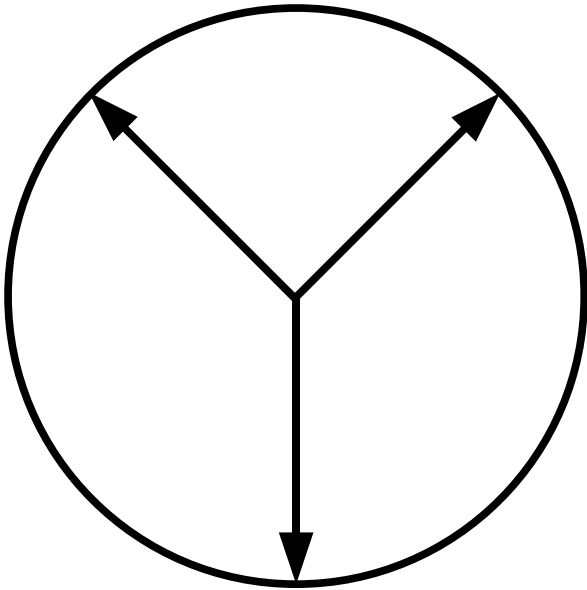


Mutation

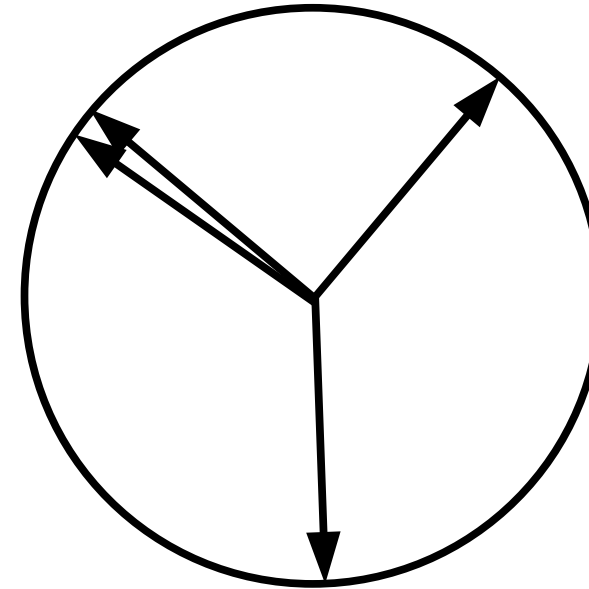
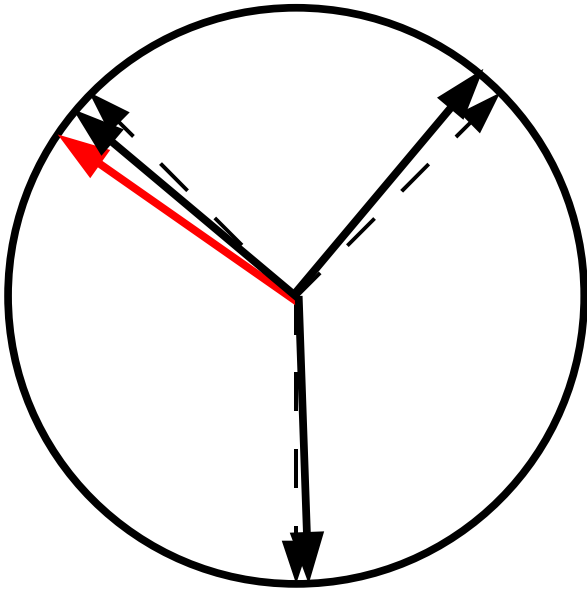
$$\begin{pmatrix} k_1 \\ k_2 \\ \vdots \\ k_D \end{pmatrix} \Rightarrow \begin{pmatrix} k_1 + \xi_1 \\ k_2 + \xi_2 \\ \vdots \\ k_D + \xi_D \end{pmatrix}$$



Duplication

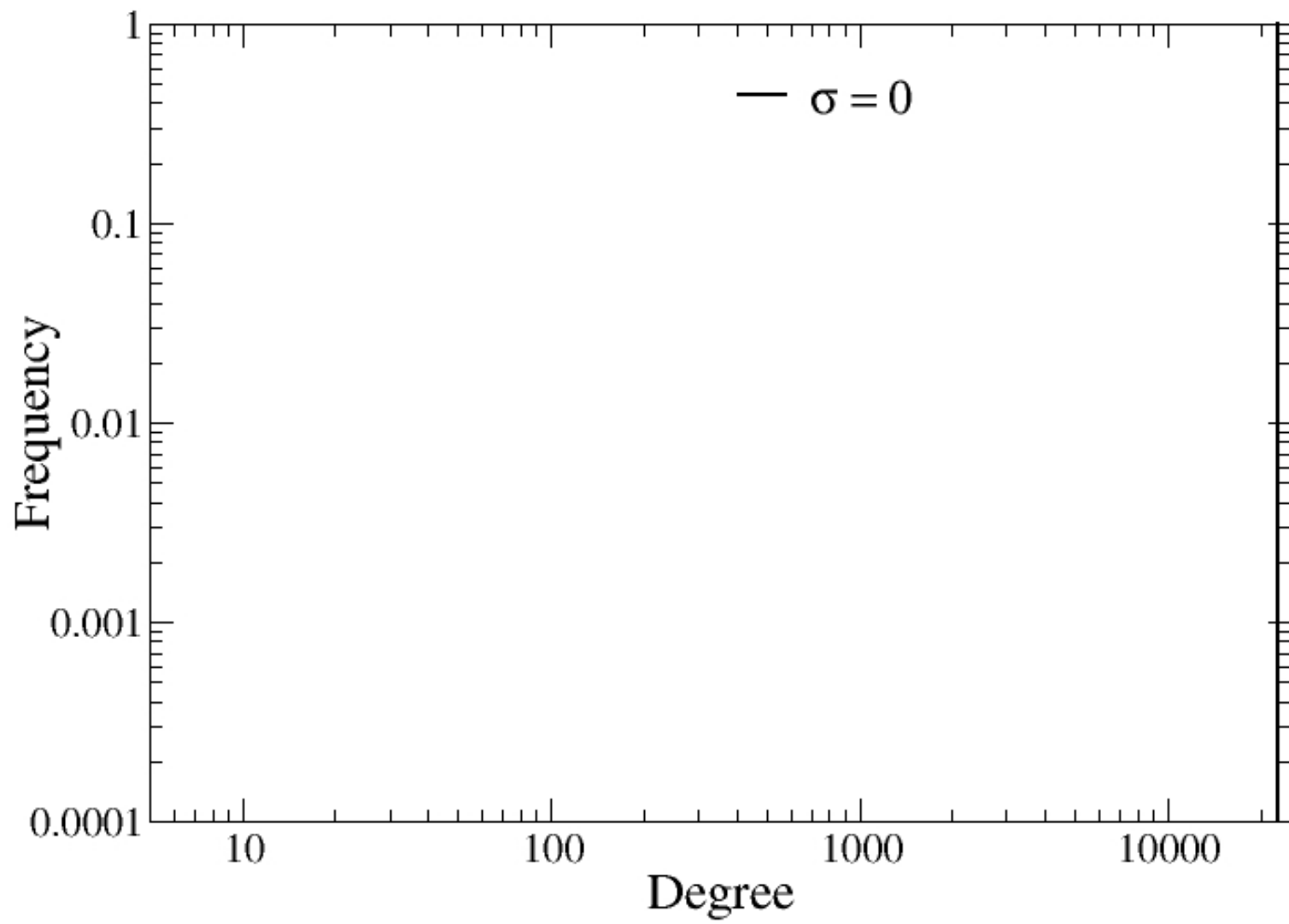


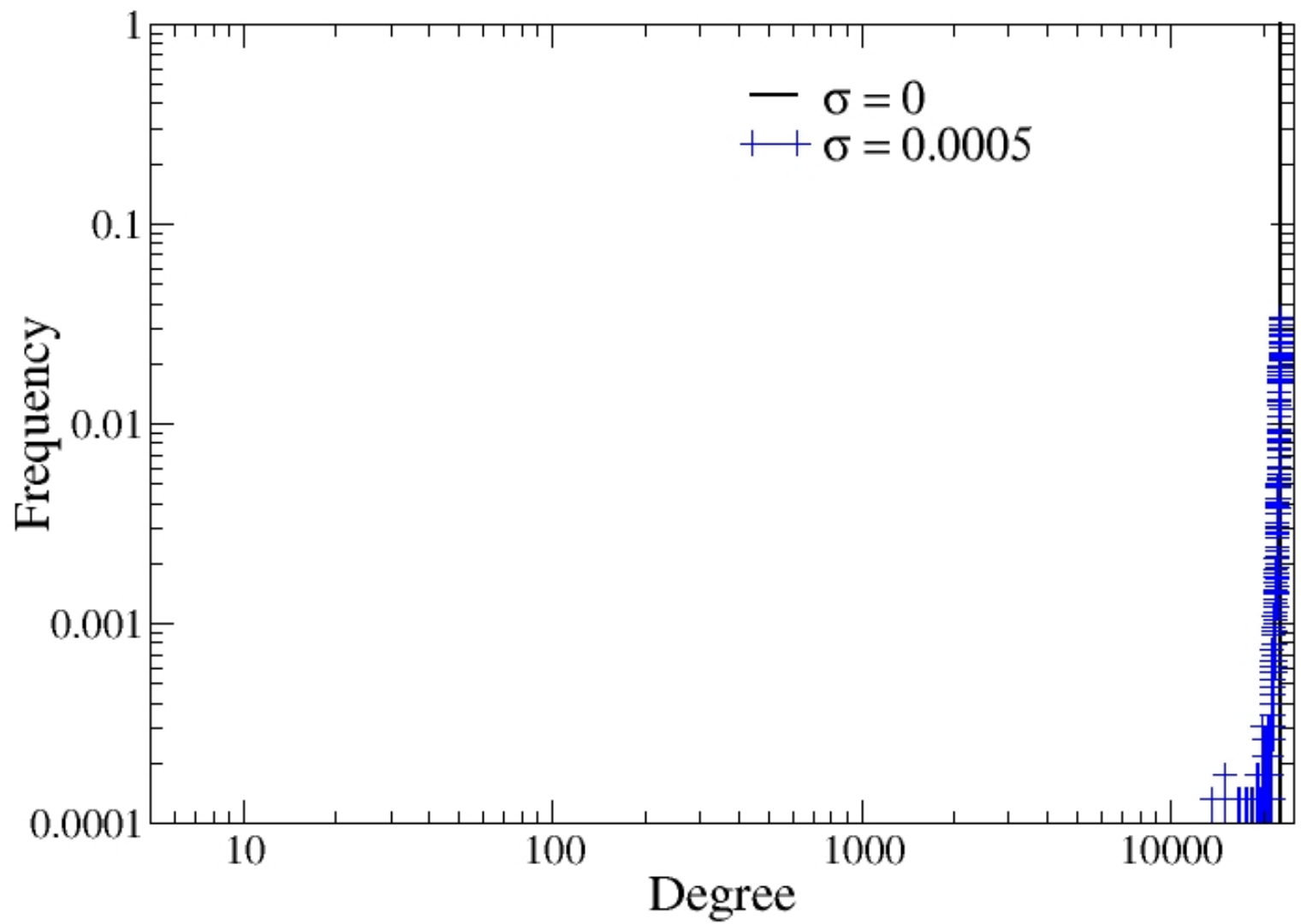
Mutation

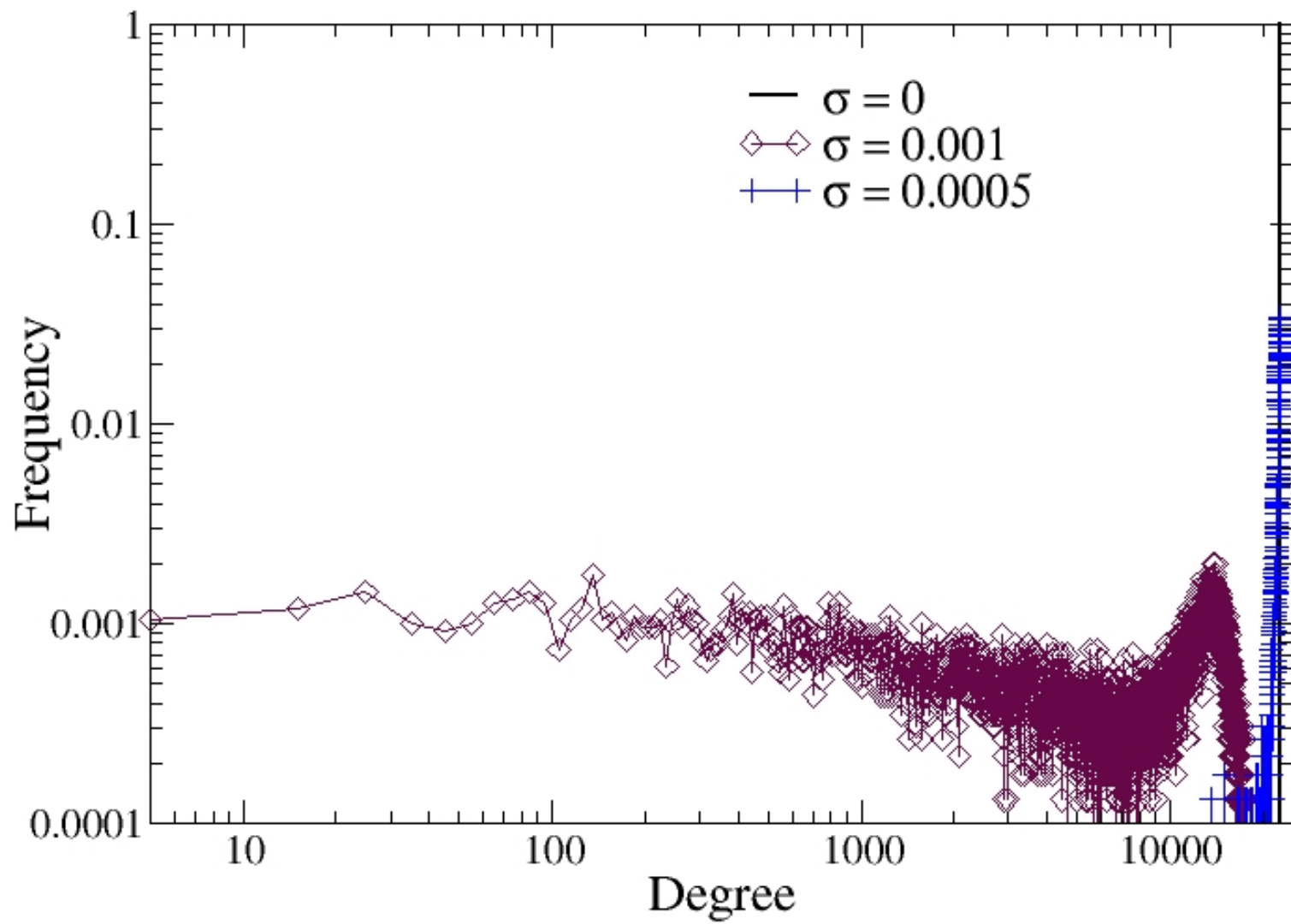


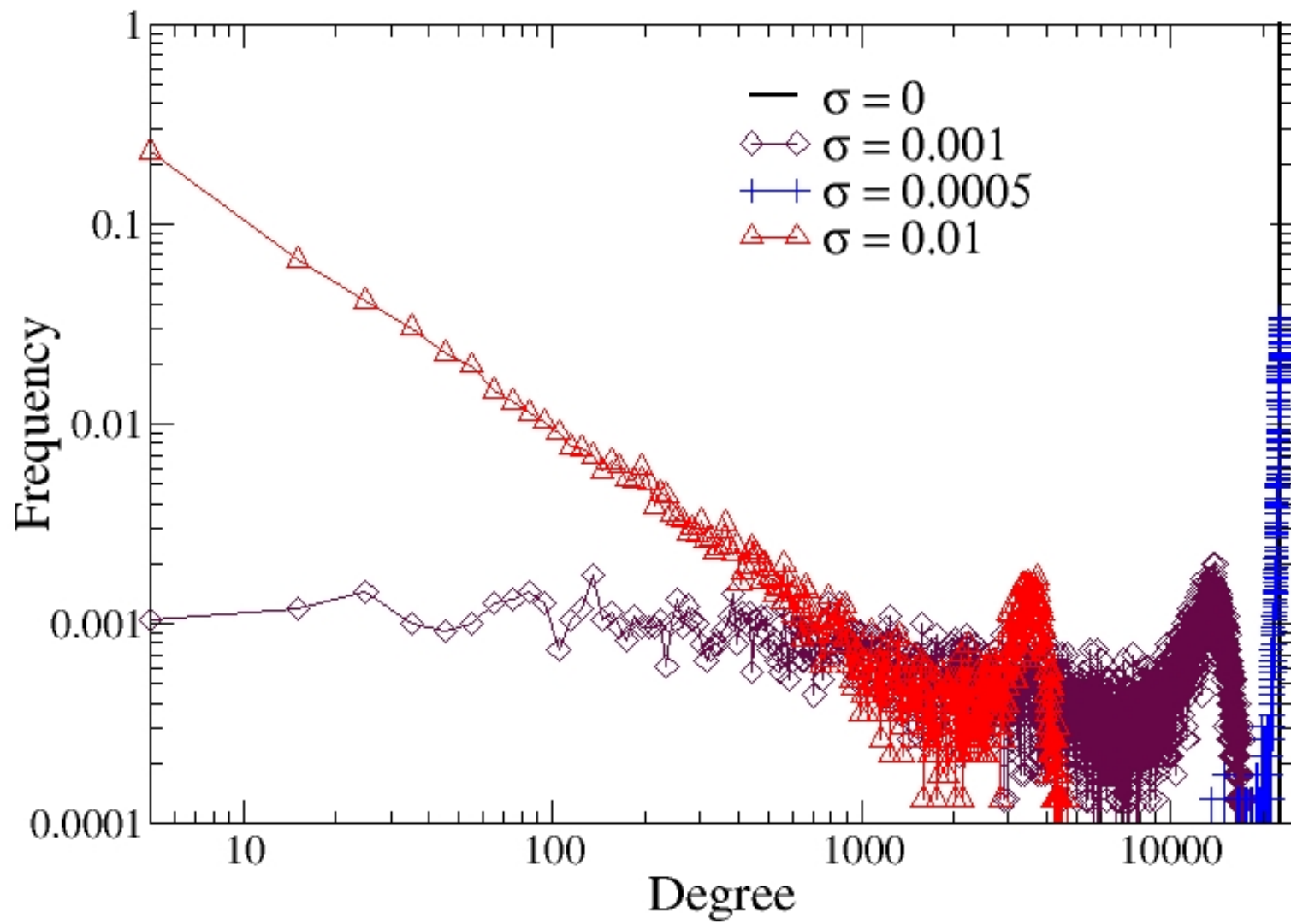
Parameters

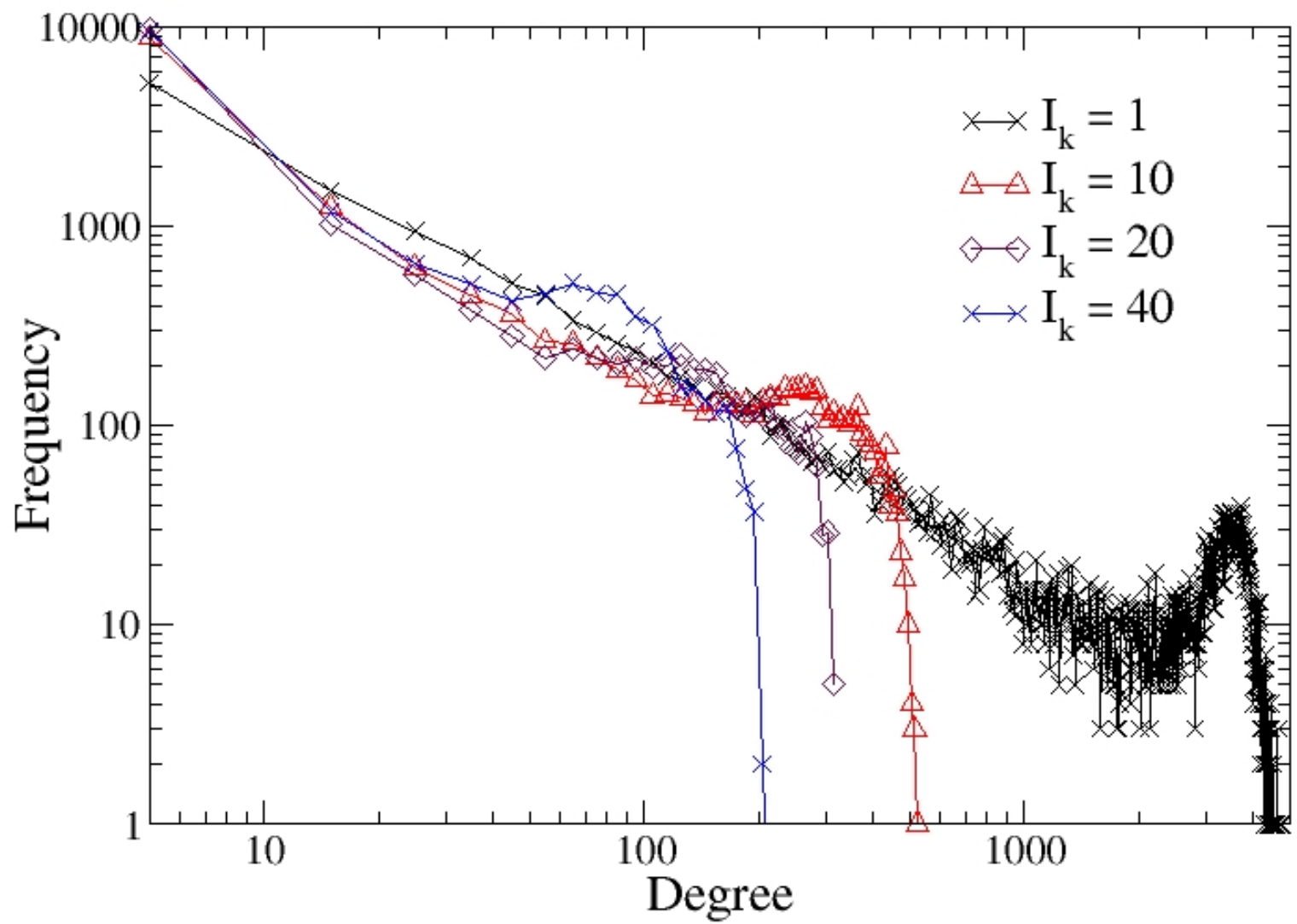
- **Dimension and threshold**
- **Initial nodes, selective pressure**
- **Mutation rate**
- **Genome duplications**

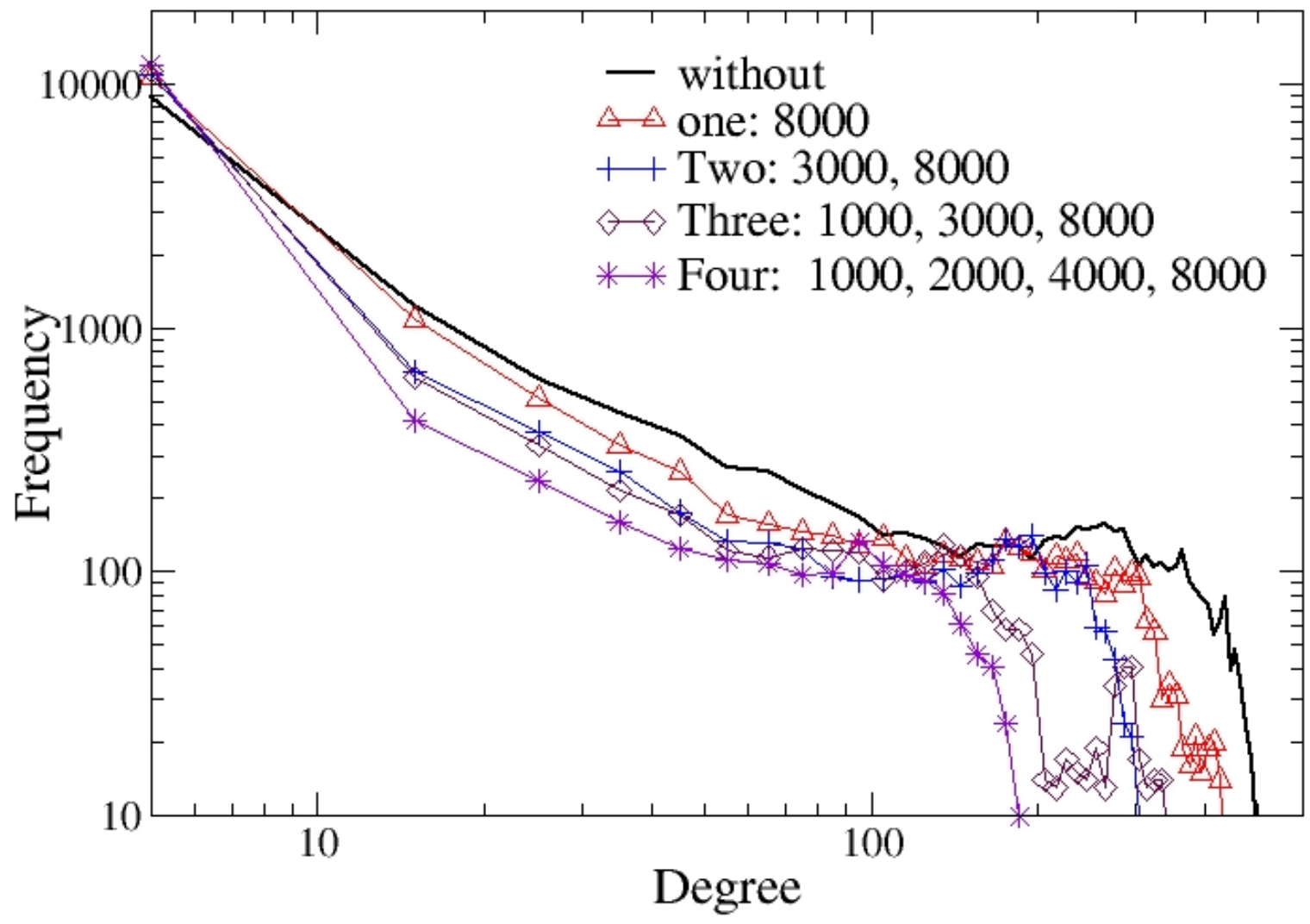


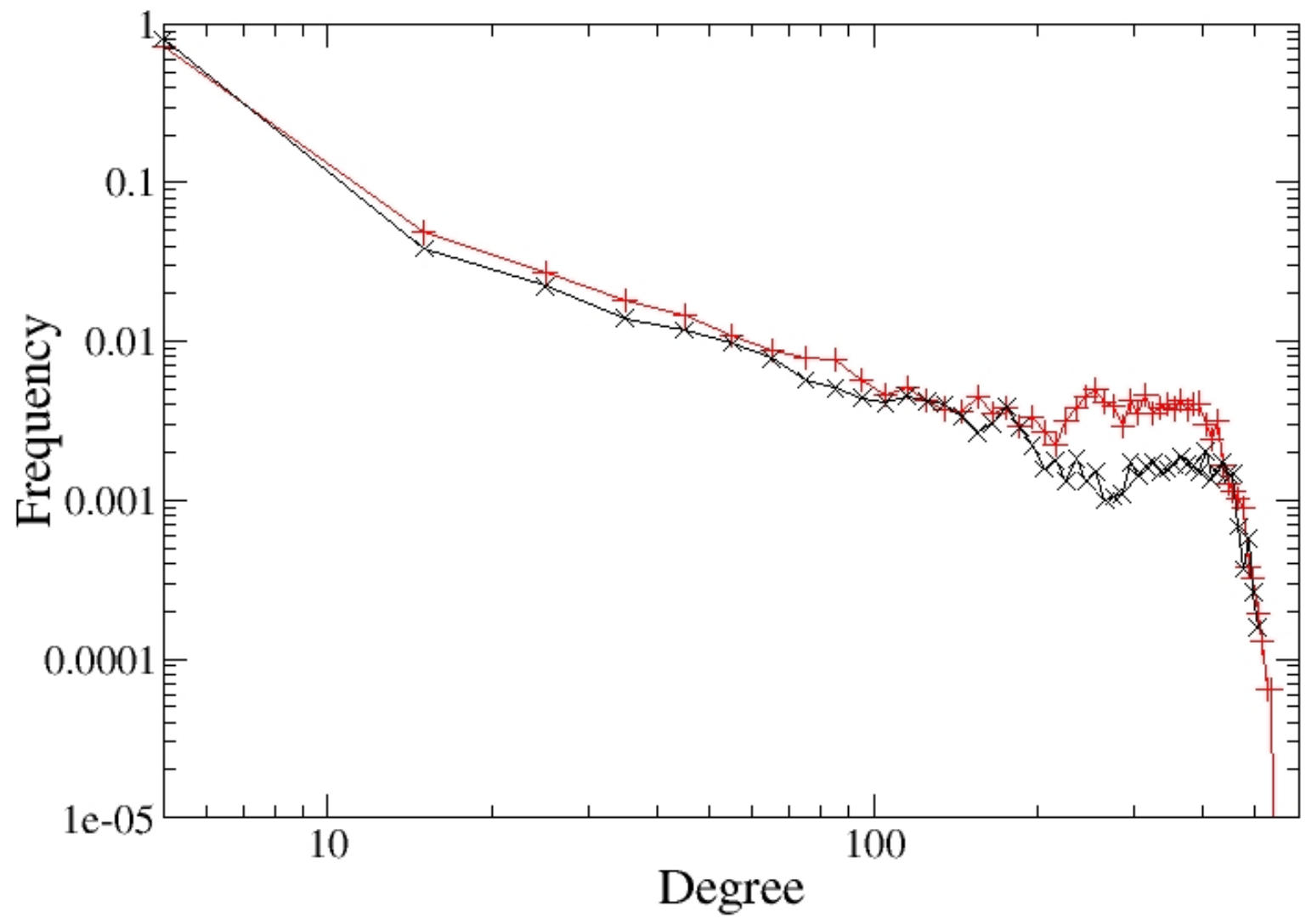












Future goals

- **Gene loss**
- **Genome duplication**
- **Yeast, E.coli ...**



International Research Training Group (IRTG)

**Genomics and Systems Biology
of Molecular Networks**

Future goals

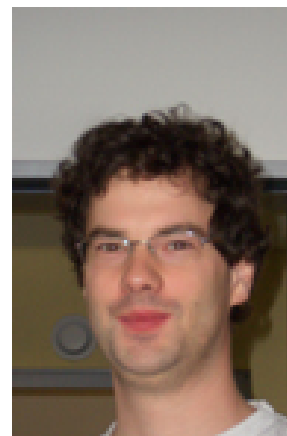
- Gene loss
- Genome duplication
- Yeast, E.coli ...



O. Ebenh h



M. Mutwil



B. Usadel



S. Persson