A methodology to evaluate the evolution of networks using topological data analysis

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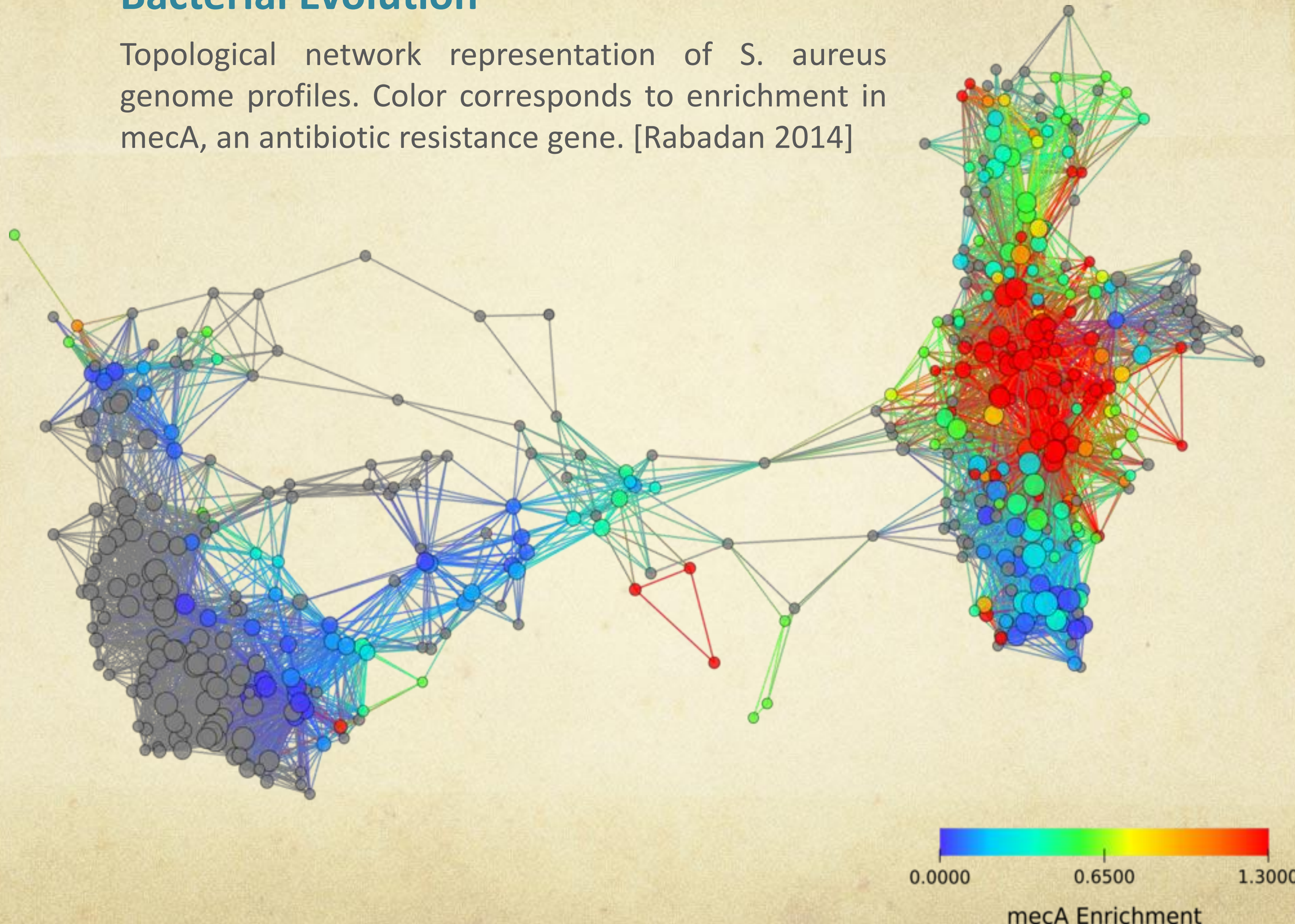
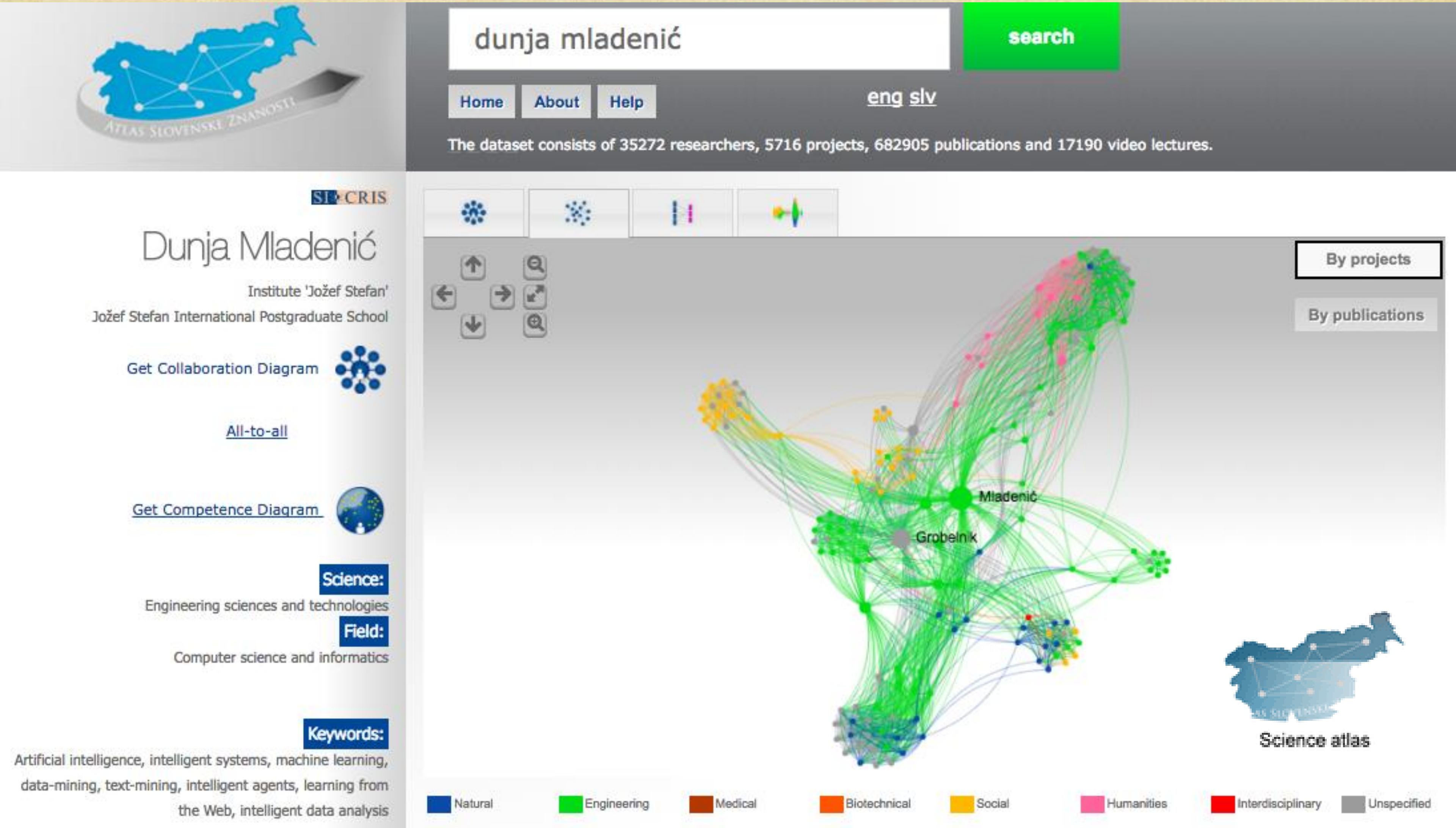
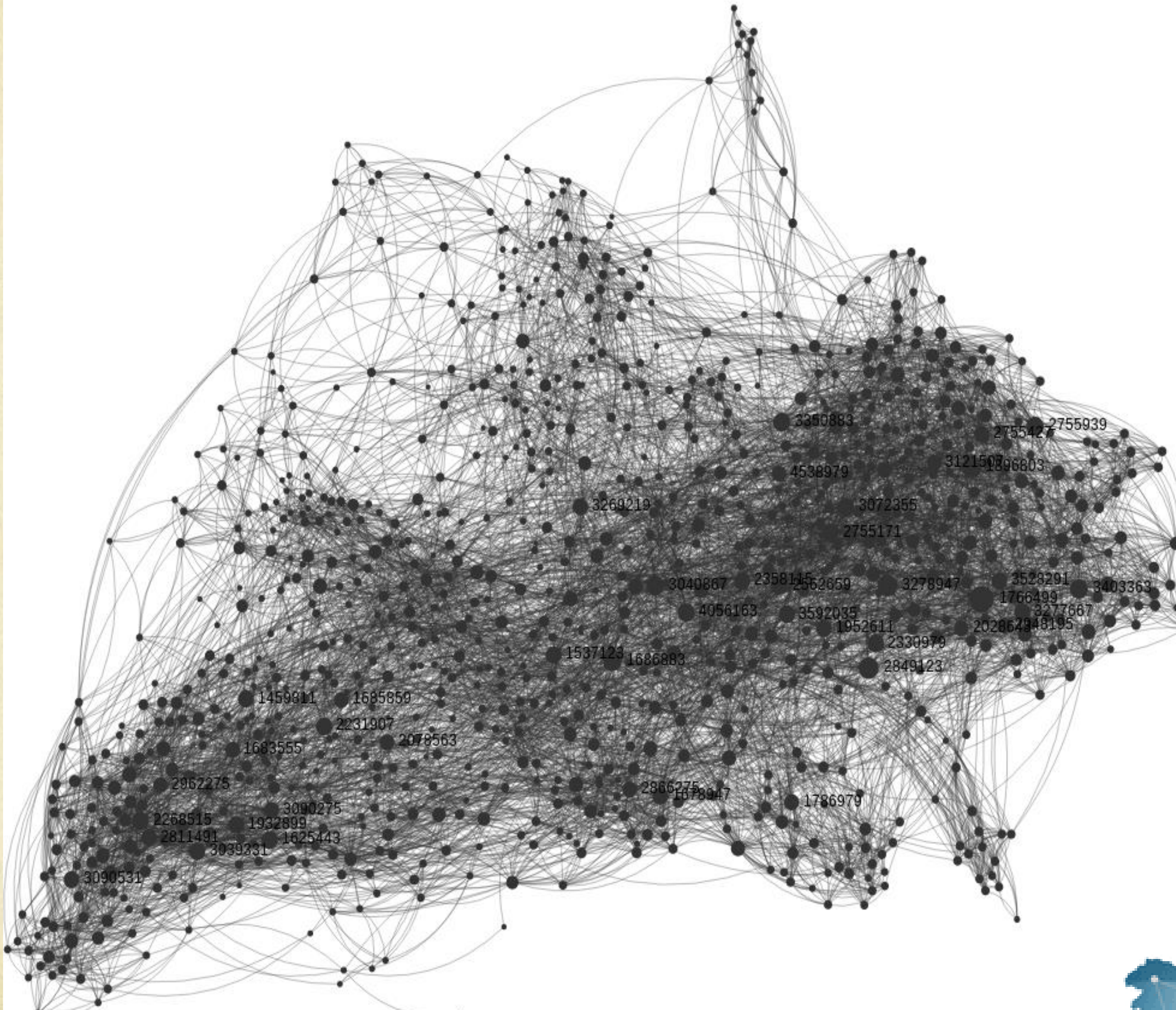
Bacterial Evolution

Topological network representation of S. aureus genome profiles. Color corresponds to enrichment in mecA, an antibiotic resistance gene. [Rabadan 2014]

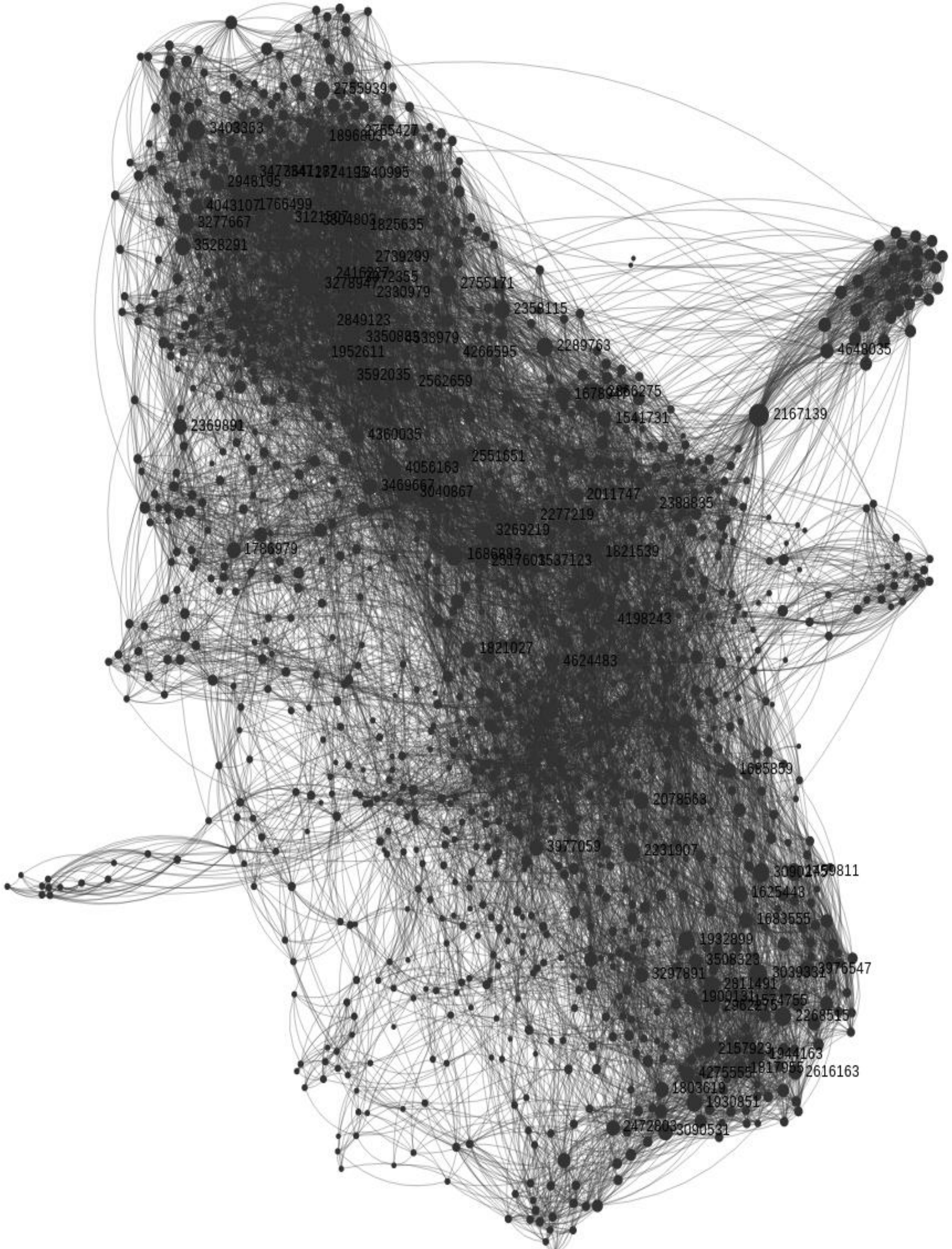




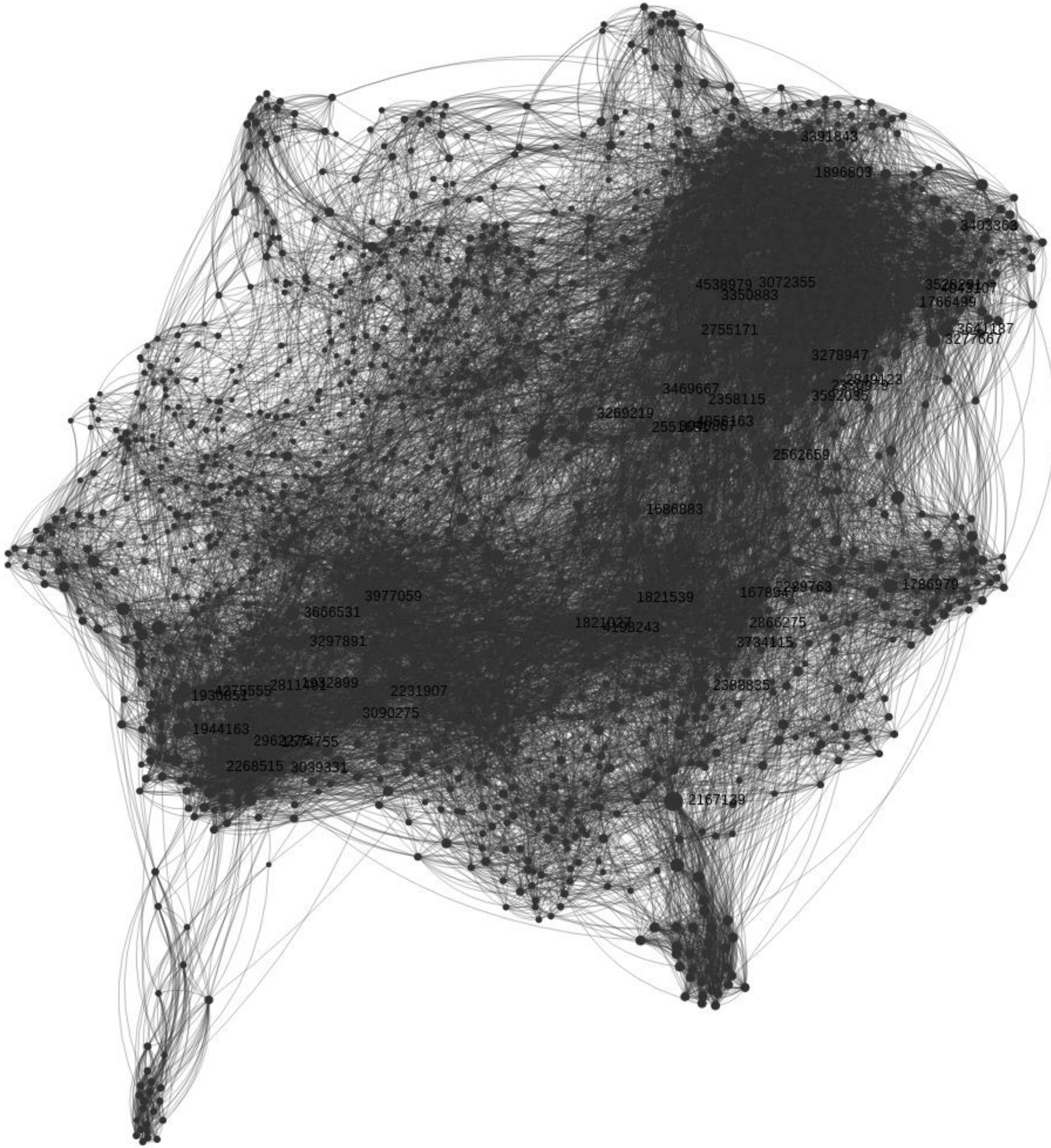
The portal **ScienceAtlas** permits the user to explore scientific collaborations between authors. This is based on the data from the Slovenian Research Agency ARRS, and exhibits a real example of evolving networks: the collaborative research networks of the researchers in the ARRS database.



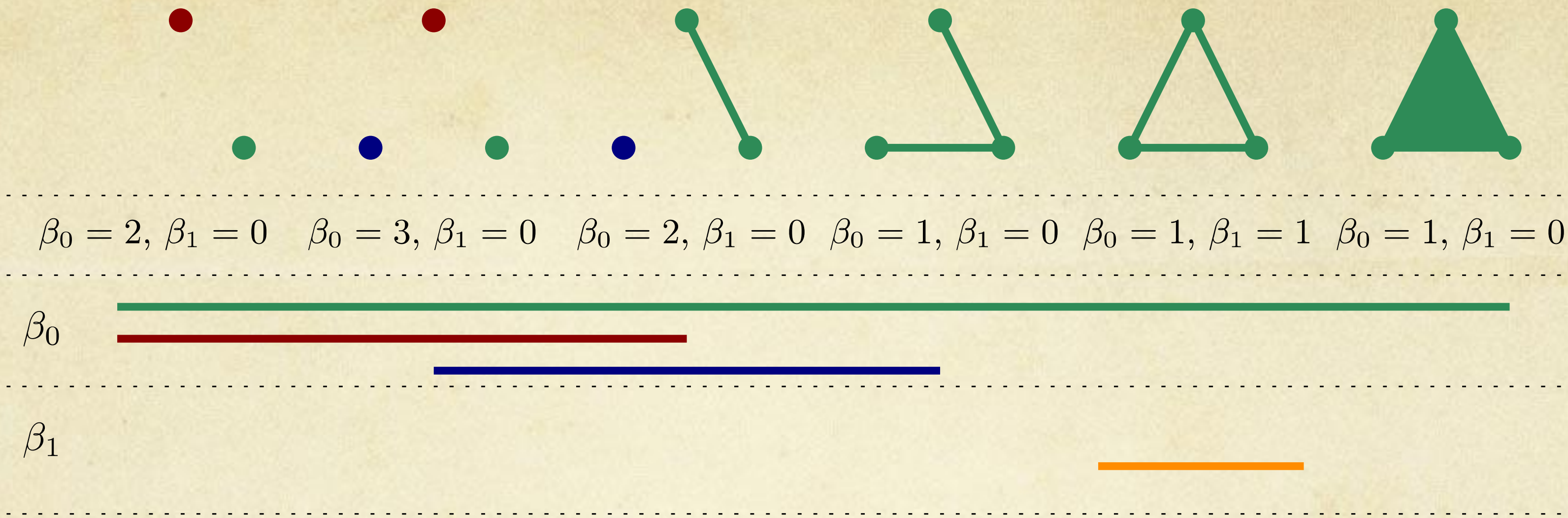
Science atlas



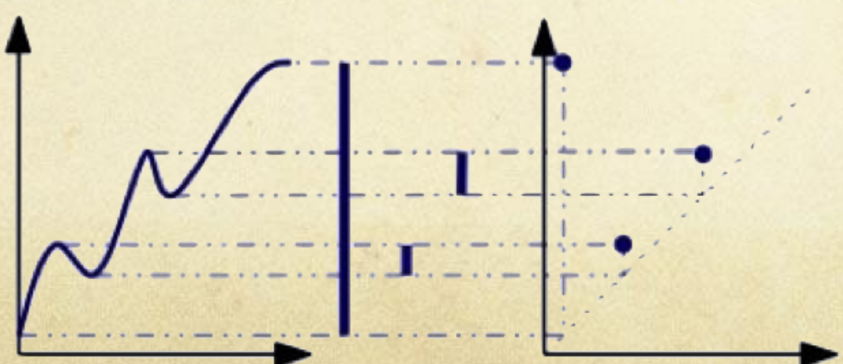
Science atlas

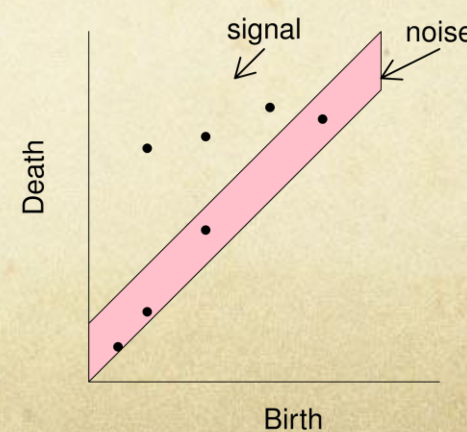


Science atlas

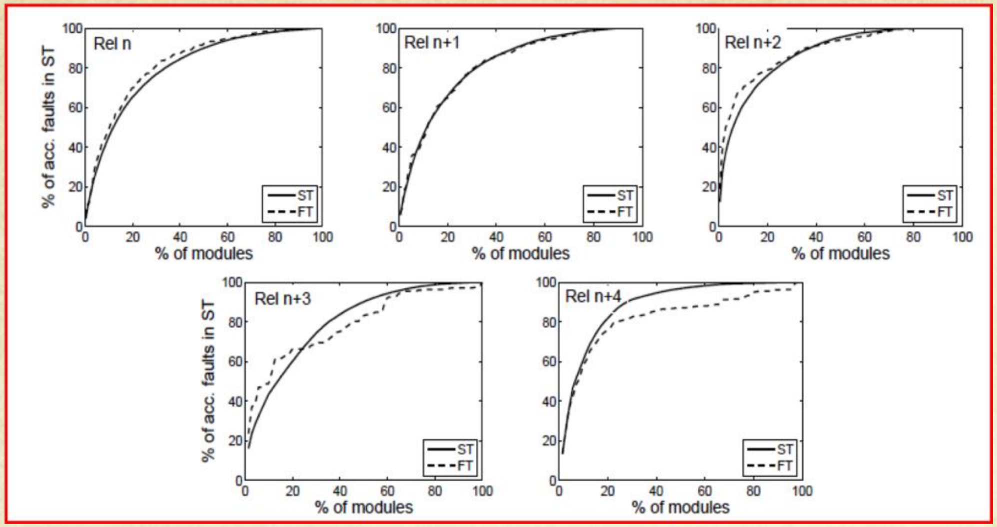


Topological data analysis - **TDA** - is interested in problems relating to **nonlinear systems**, **large scale data** and development of more **accurate models**. Persistent homology permits to consider the homology of the filtered simplicial complex at all times during the filtration. Persistent homology identifies a global structure by inferring **high-dimensional structure from low-dimensional representations** and studying **properties of a (often) continuous space by the analysis of a discrete sample of it.**

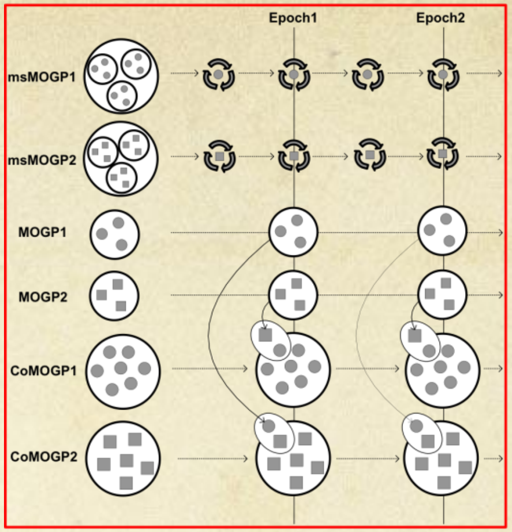




Reliability growth analysis:

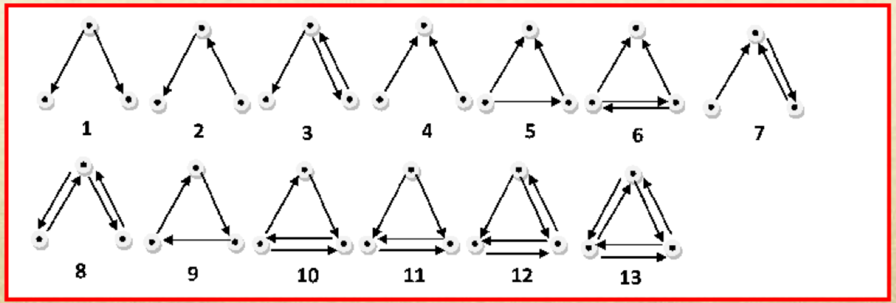


Co-evolutionary MOGP:



Evolving complex software systems - **EVOSOFT** - focus the influence of **abstract software structures** and **local system properties** in **fault distributions**, affecting mission critical system properties, among which availability and reliability and to develop innovative approaches for **smart management of their operation and evolution**. New findings will open opportunities in many fields, especially in **complex systems theory and its applications**, thus interacting with a wide spectrum of sciences, from natural sciences such as biomedicine to social sciences.

System complex structure motifs:



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Hrvatska zaklada za znanost

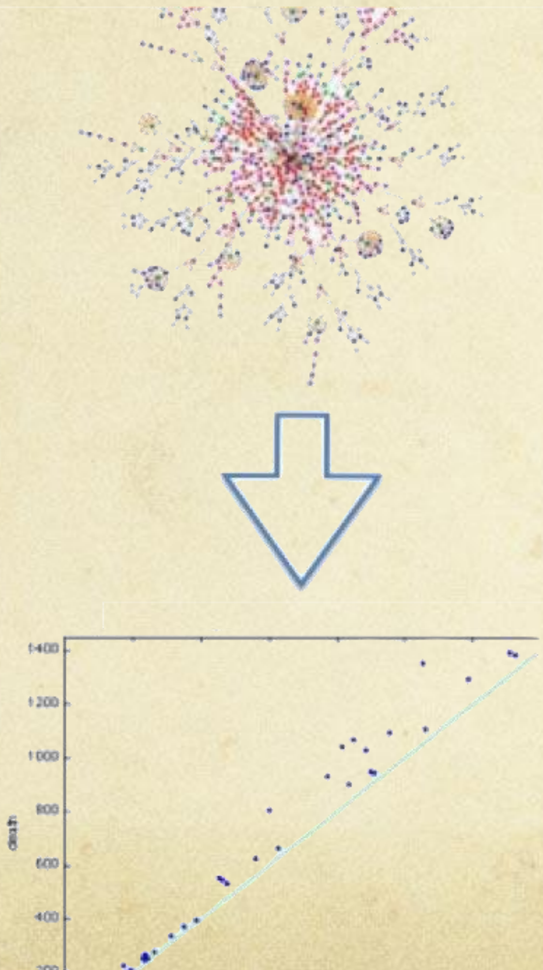
Network Data
Adjacency Matrix

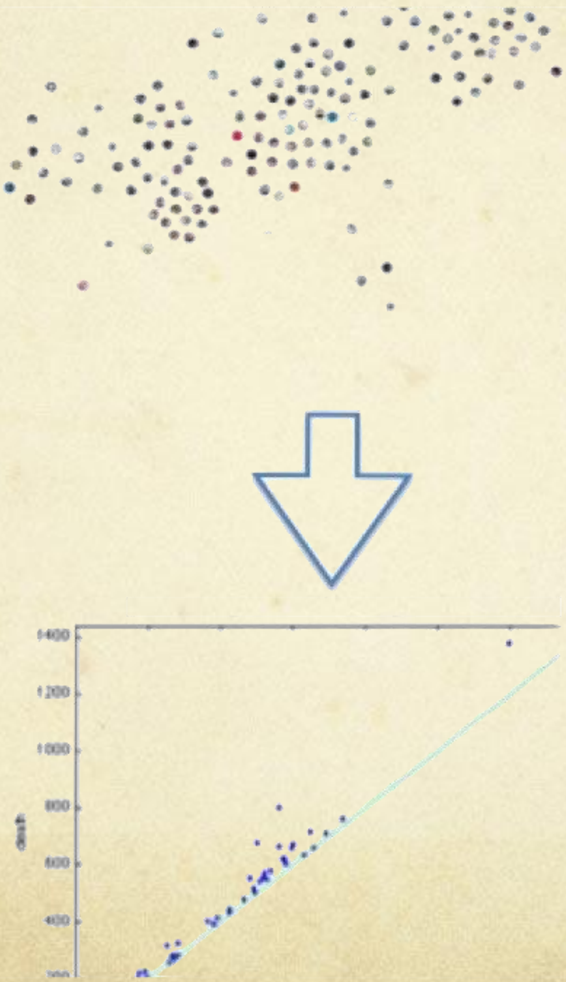
→ Persistent Homology Computation →

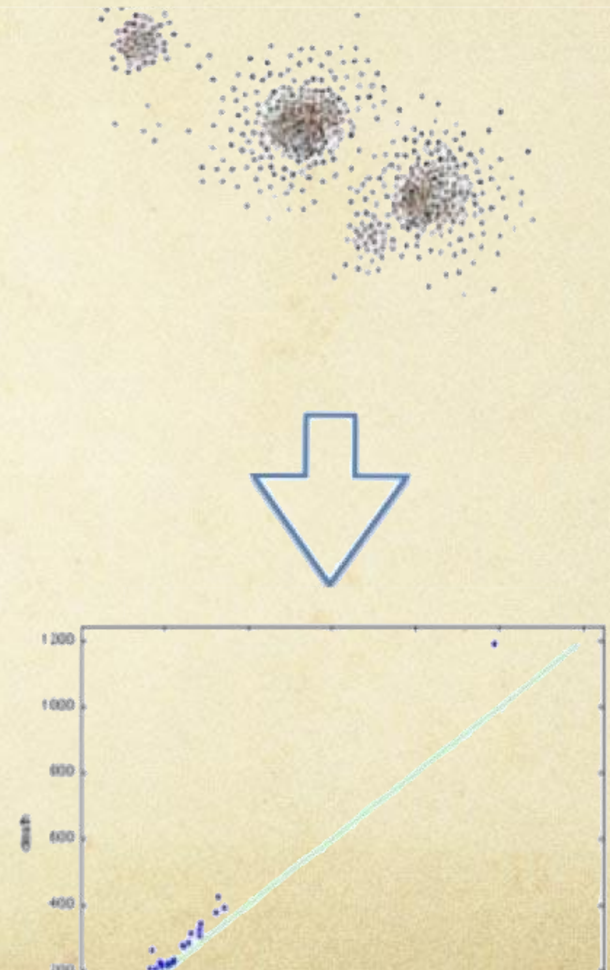
Encoded Topology
Persistence Diagram

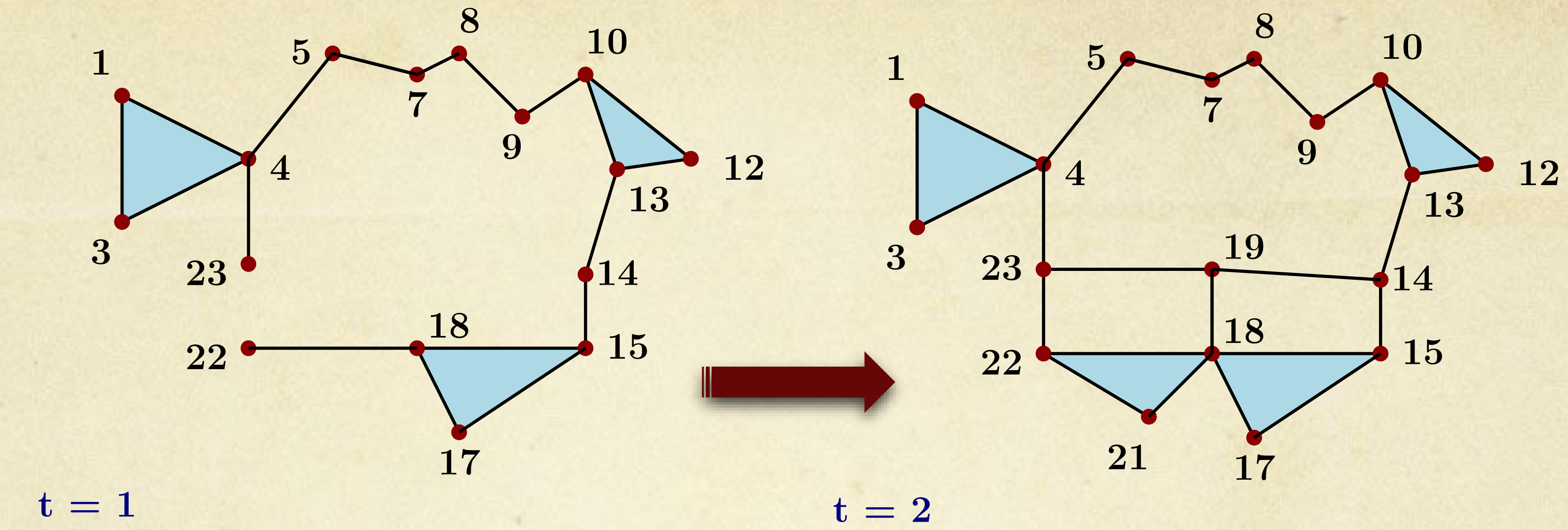
→ Bottleneck Distance Computation →

Absolute Distance
Bottleneck Distance

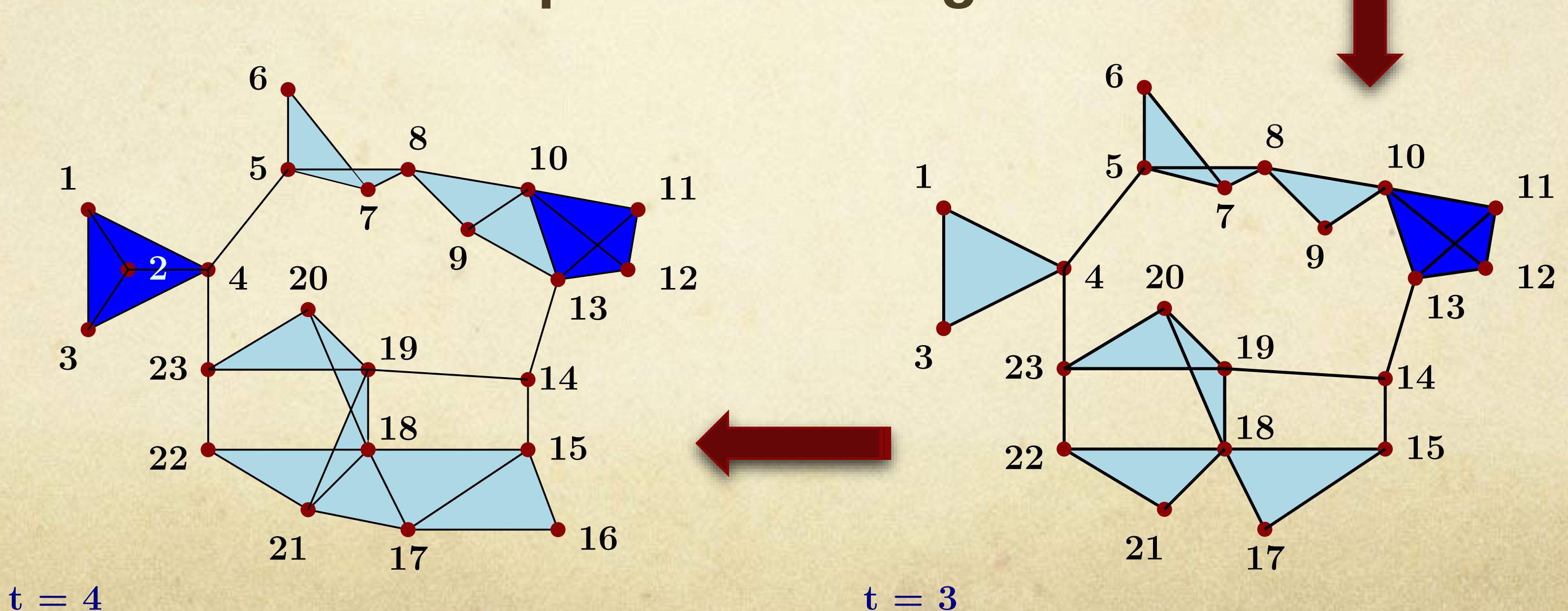


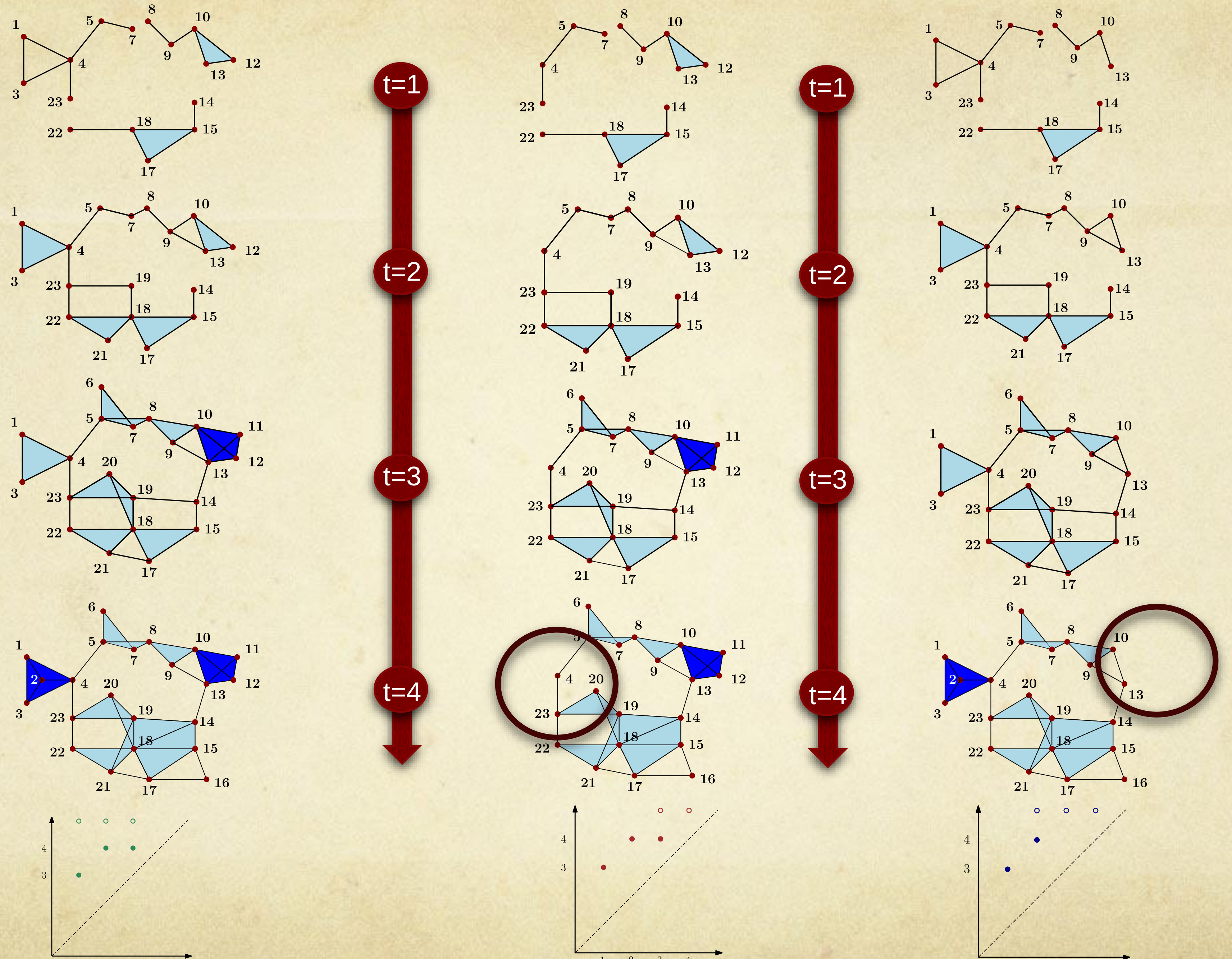






Artificial example of evolving network

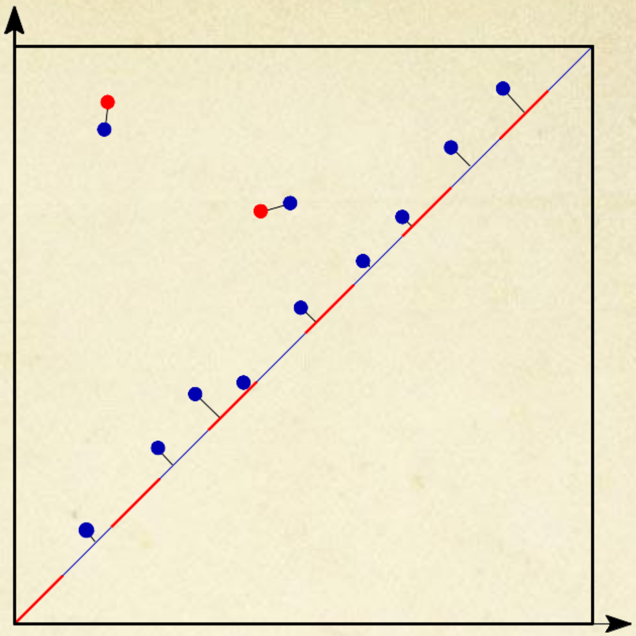




evolvnet A

evolvnet B

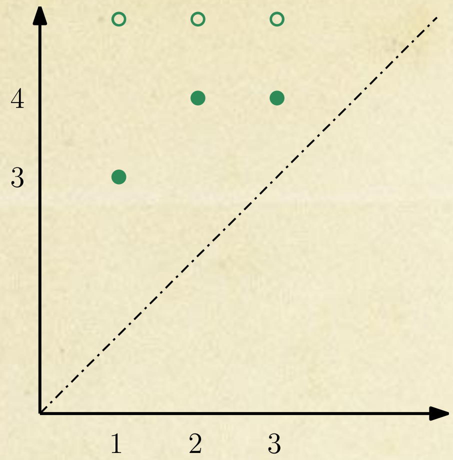
evolvnet C



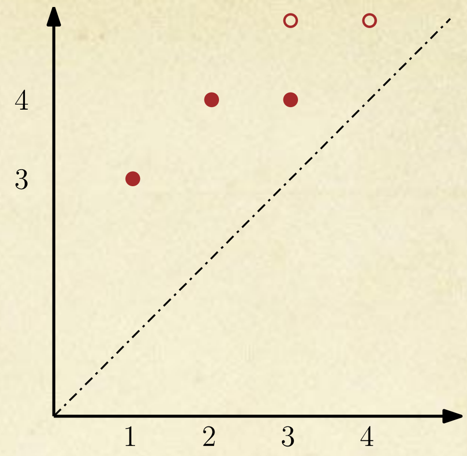
The **bottleneck distance** between X = Dgm(f) and Y = Dgm(g) is defined as

$$d_B(X,Y)=\inf_{\eta} \sup_{x\in X} \|x-\eta(x)\|_\infty$$

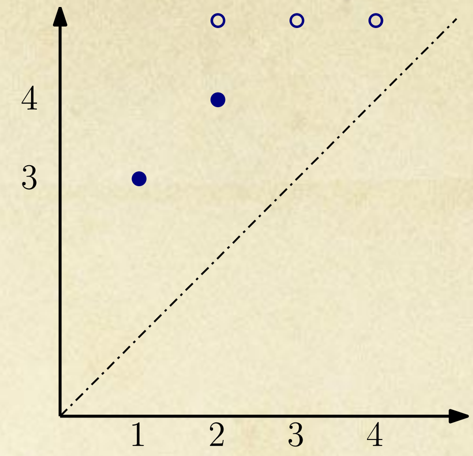
where the infimum is taken over all bijections \eta from X to Y. Each point with multiplicity k in a multiset is interpreted as k individual points, and the bijection is interpreted between the resulting sets.



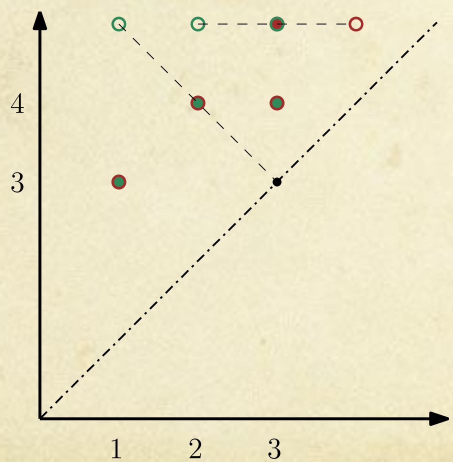
evolvnet A



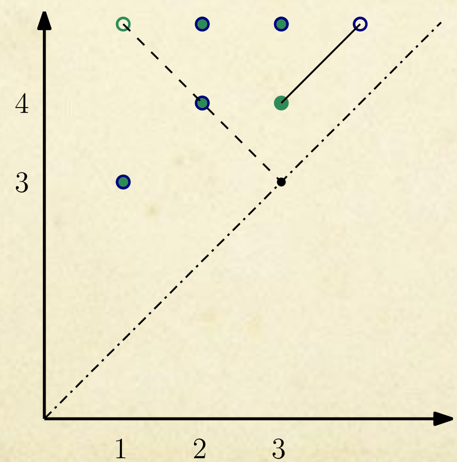
evolvnet B



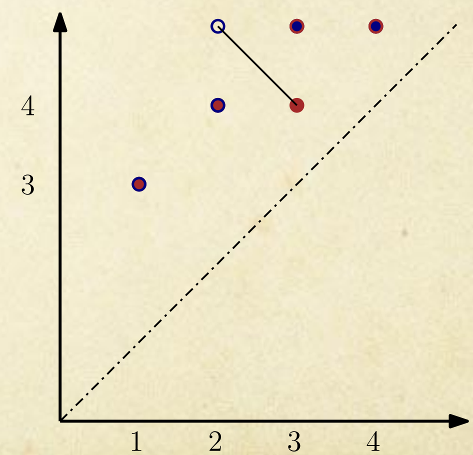
evolvnet C



d(A,B)=0

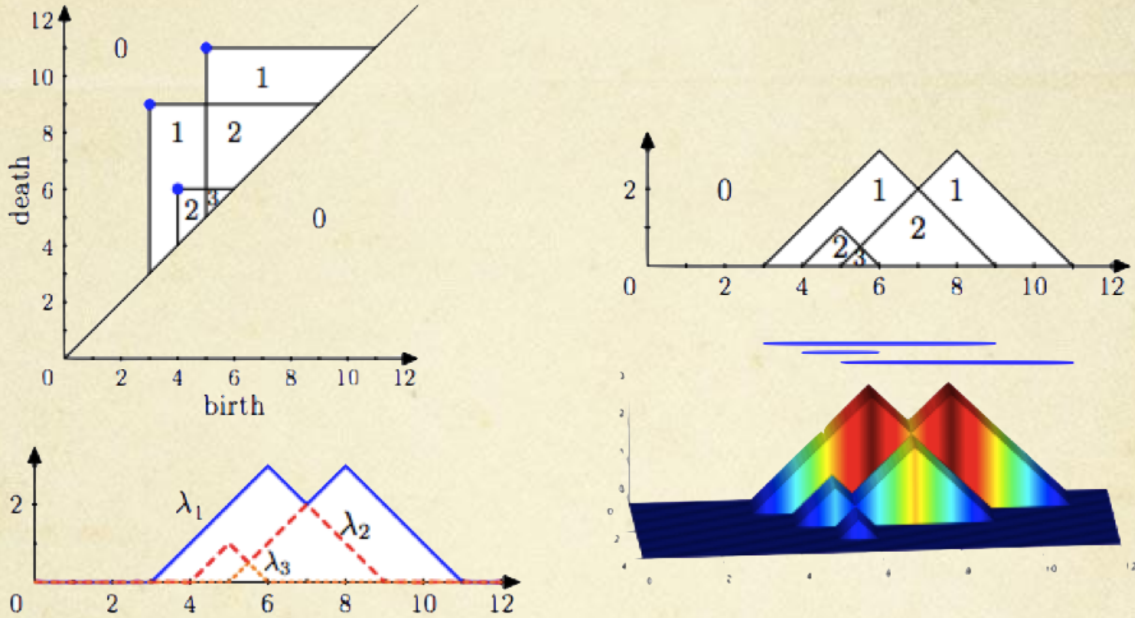


d(A,C)=1



d(B,C)=1

Persistence landscapes are techniques of TDA that permit us to measure the pairwise distance between persistence diagrams at several different levels.

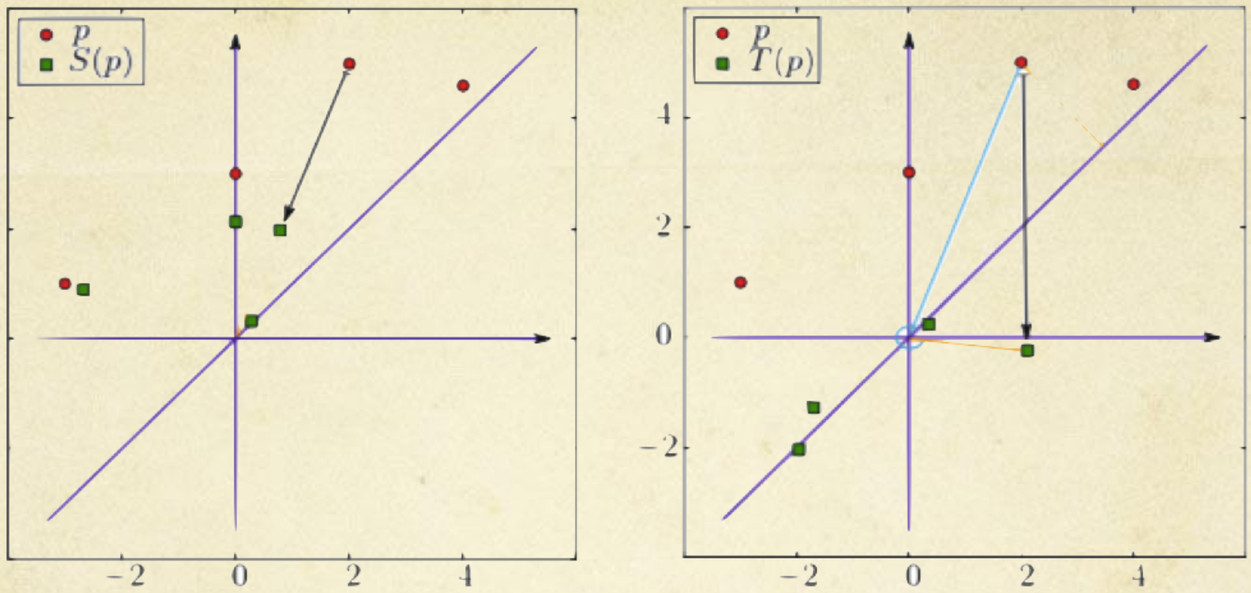


The **persistence landscape** is a function $\lambda : N \times R \to \underline{R}$, where $\underline{R} = [-\infty,\infty]$. Alternatively, it may be thought of as a sequence of functions $\lambda_k : R \to R$, where $\lambda_k(t) = \lambda(k, t)$. Define:

$$\lambda_k(t) = \sup(m \geq 0 \mid \beta^{t-m,t+m} \geq k),$$

with $\lambda : R^2 \to R$ given by:

$$\lambda(m, h) = \beta^{m-h,m+h} \text{ if } h \geq 0 \text{ and } \lambda(m, h) = 0 \text{ otherwise}$$



Given persistence diagram D described by its points $p_1 = (u_1, v_1), \dots , p_s = (u_s, v_s)$ with multiplicities $r_1,\dots,r_s$, the method **complex of vectors** considers complex numbers $z_1=u_1+iv_1,\dots, z_s = u_s+iv_s$ and associates to D the complex polynomial $f_D(t) = \prod_{j=1}^{s}(t - z_j)^{r_j}$ where r_j is the multiplicity of p_j

$p_A=(t-1-3i)(t-2-4i)(t-3-4i)=p_B$ and $p_C=(t-1-3i)(t-2-4i)^2$

Thank You : Hvala : Obrigado

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