

Kernel methods in computational biology

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Outline

1. About kernels
2. What you can do with a kernel
3. Kernelizing the proteome
4. Application: comparison of a protein network and expression data

Part 1

Kernels

Definition

- Let \mathcal{X} be a set (e.g., discrete)
- A kernel is a mapping $K : \mathcal{X} \times \mathcal{X} \rightarrow \mathbb{R}$ which is:
 - ★ **symmetric** : $K(x, y) = K(y, x)$,
 - ★ **positive semi-definite**: $\sum_{i,j} a_i a_j K(x_i, x_j) \geq 0$ for all $a_i \in \mathbb{R}$ and $x_i \in \mathcal{X}$

Example

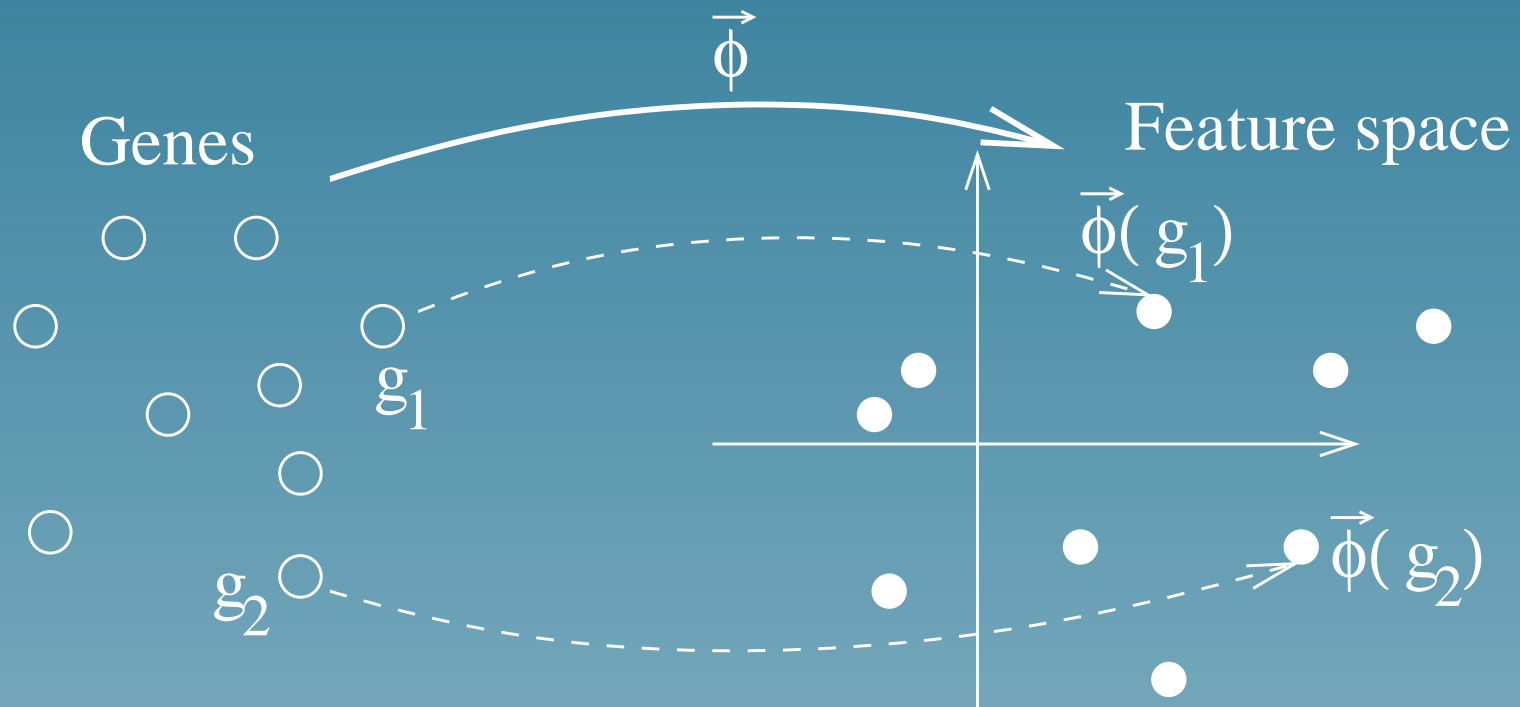
- Suppose $\mathcal{X} = \mathbb{R}^d$. Then the following is a valid kernel:

$$K(\vec{x}, \vec{y}) = \vec{x} \cdot \vec{y}$$

- Indeed:
 - ★ $\vec{x} \cdot \vec{y} = \vec{y} \cdot \vec{x}$
 - ★ $\sum_{i,j} a_i a_j \vec{x}_i \cdot \vec{x}_j = \|\sum_i a_i \vec{x}_i\|^2 \geq 0$

Example: kernel in feature space

$$K(g_i, g_j) \stackrel{def}{=} \vec{\Phi}(g_i) \cdot \vec{\Phi}(g_j)$$



All kernels are inner product

- If $K(.,.)$ is a kernel, then **there exists** a Hilbert space \mathcal{H} and a mapping $\Phi : \mathcal{X} \rightarrow \mathcal{H}$ such that:

$$K(x, y) = \langle \Phi(x), \Phi(y) \rangle_{\mathcal{H}} .$$

- Proof: by diagonalizing the kernel operator
- Second proof: by explicitly constructing such a \mathcal{H}

RKHS

- A **reproducing kernel Hilbert space (RKHS)** is a Hilbert space, subset of $\mathbb{R}^{\mathcal{X}}$, defined as the **completion** of:

$$\text{span} \{K(x, \cdot), s \in \mathcal{X}\}.$$

- The **inner product** between two elements $f = \sum_i a_i K(x_i, \cdot)$ and $g = \sum_i b_i K(x_i, \cdot)$ is defined by:

$$\langle f, g \rangle_{\mathcal{H}} = \sum_{i,j} a_i b_j K(x_i, x_j).$$

RKHS (2)

- Let $\Phi : \mathcal{X} \rightarrow \mathcal{H}$ defined by $\Phi(x) = K(x, \cdot)$. Then:

$$K(x, y) = \langle \Phi(x), \Phi(y) \rangle_{\mathcal{H}} = \langle K(x, \cdot), K(y, \cdot) \rangle_{\mathcal{H}}$$

- For any $x \in \mathcal{X}$ and $f \in \mathcal{H}$, the following holds:

$$\langle f, K(x, \cdot) \rangle_{\mathcal{H}} = f(x).$$

RKHS (3)

- We have seen that a kernel K defines a Hilbert structure on (a subset of) $\mathcal{X}^{\mathbb{R}}$
- **Conversely**: let \mathcal{H} be a Hilbert space, subset of $\mathcal{X}^{\mathbb{R}}$, such that for any $x \in \mathcal{X}$ the evaluation functional $f \in \mathcal{H} \rightarrow f(x)$ be continuous
- **Then there exists a kernel K such that \mathcal{H} be its associated RKHS.**

Representer theorem (Wahba, 1971)

Let \mathcal{H} be a RKHS with kernel K , and $(x_1, \dots, x_N) \in \mathcal{X}^N$. Then the solution of:

$$\min_{f \in \mathcal{H}} \sum_{i=1}^N c(x_i, f(x_i)) + \lambda \|f\|_{\mathcal{H}}^2$$

where $c : \mathcal{X} \times \mathbb{R} \rightarrow \mathbb{R}$, can always be written in the form:

$$f(x) = \sum_{i=1}^n a_i K(x_i, x).$$

Example

For a Gaussian kernel:

$$K(x, y) = \exp\left(-\frac{\|x - y\|^2}{2\sigma^2}\right),$$

the norm in RKHS is:

$$\|f\|_{\mathcal{H}}^2 = \frac{1}{2\pi\sigma^2} \int |\hat{f}(\omega)|^2 \exp\left(\frac{\sigma^2\|\omega\|^2}{2}\right) d\omega.$$

Partie 2

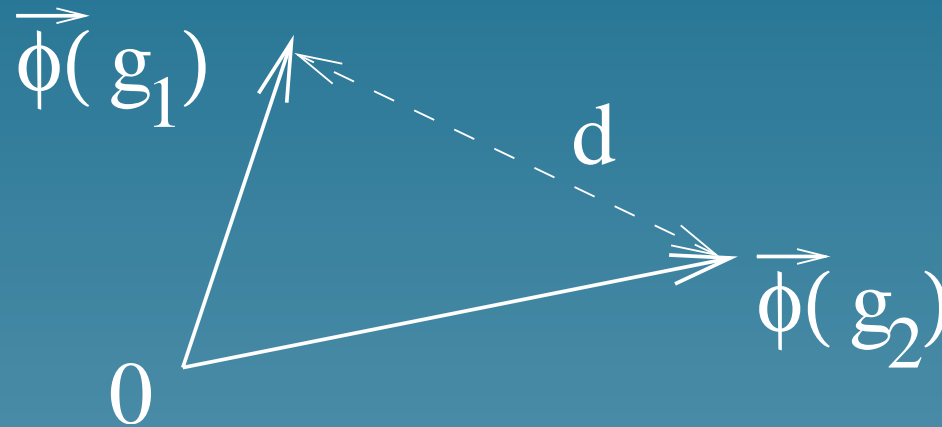
What can you do with a kernel

Overview

Let $K(x, y)$ be a given kernel. Then is it possible to perform various algorithms **implicitly** in the feature space (thanks to the representer theorem), such as:

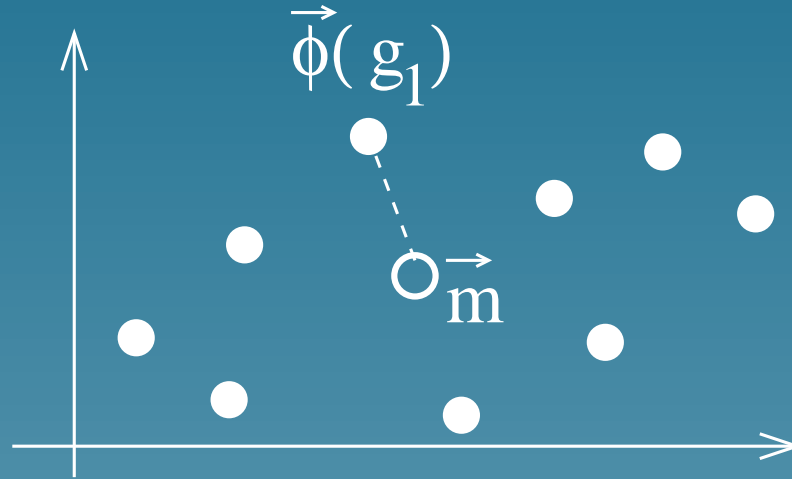
- Compute the distance between points
- Principal component analysis (PCA)
- Canonical correlation analysis (CCA)
- Classification by Support vector machines (SVM)

Compute the distance between objects



$$\begin{aligned}
 d(g_1, g_2)^2 &= \|\vec{\Phi}(g_1) - \vec{\Phi}(g_2)\|^2 \\
 &= \left(\vec{\Phi}(g_1) - \vec{\Phi}(g_2)\right) \cdot \left(\vec{\Phi}(g_1) - \vec{\Phi}(g_2)\right) \\
 &= \vec{\Phi}(g_1) \cdot \vec{\Phi}(g_1) + \vec{\Phi}(g_2) \cdot \vec{\Phi}(g_2) - 2\vec{\Phi}(g_1) \cdot \vec{\Phi}(g_2) \\
 d(g_1, g_2)^2 &= K(g_1, g_1) + K(g_2, g_2) - 2K(g_1, g_2)
 \end{aligned}$$

Distance to the center of mass

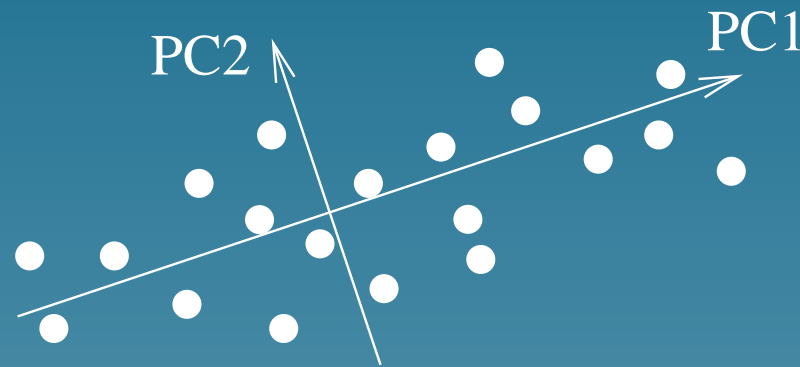


Center of mass: $\vec{m} = \frac{1}{N} \sum_{i=1}^N \vec{\Phi}(g_i)$, hence:

$$\|\vec{\Phi}(g_1) - \vec{m}\|^2 = \vec{\Phi}(g_1) \cdot \vec{\Phi}(g_1) - 2\vec{\Phi}(g_1) \cdot \vec{m} + \vec{m} \cdot \vec{m}$$

$$= K(g_1, g_1) - \frac{2}{N} \sum_{i=1}^N K(g_1, g_i) + \frac{1}{N^2} \sum_{i,j=1}^N K(g_i, g_j)$$

Principal component analysis

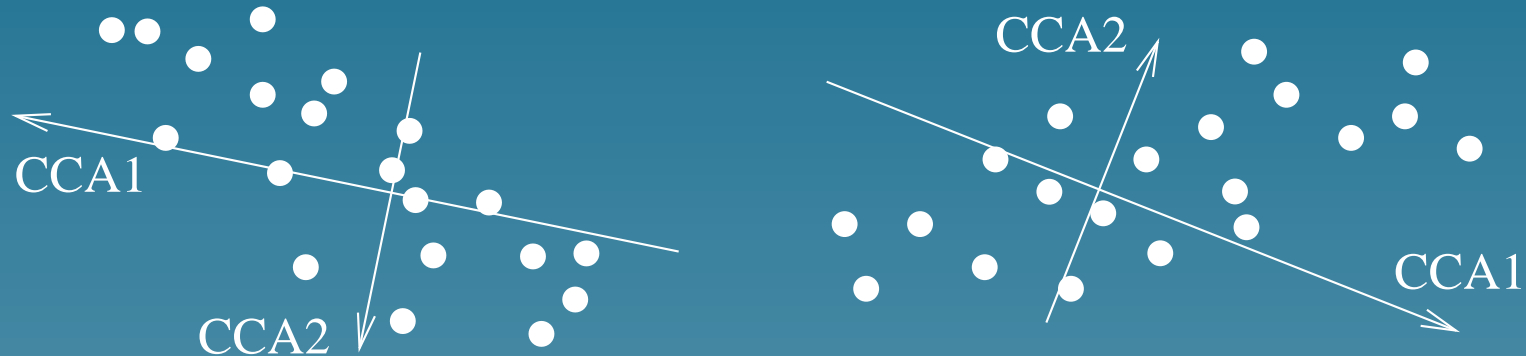


It is equivalent to find the eigenvectors of

$$\begin{aligned} K &= \left(\vec{\Phi}(g_i) \cdot \vec{\Phi}(g_j) \right)_{i,j=1\dots N} \\ &= \left(K(g_i, g_j) \right)_{i,j=1\dots N} \end{aligned}$$

Useful to project the objects on small-dimensional spaces (feature extraction).

Canonical correlation analysis

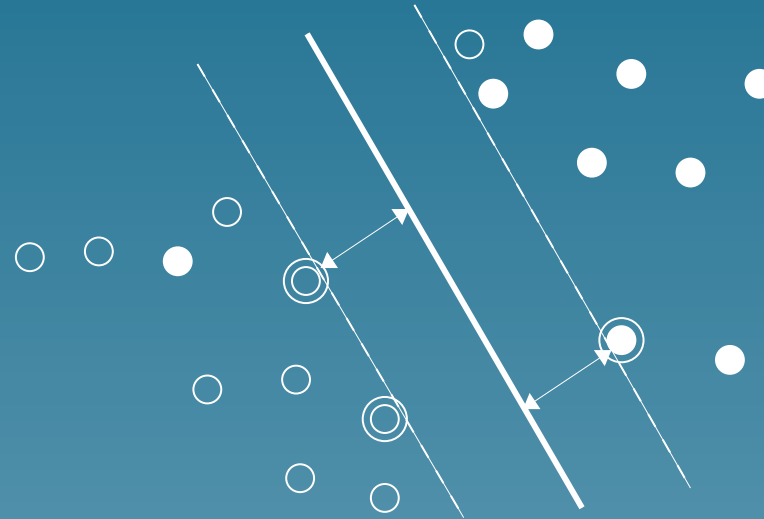


K_1 and K_2 are two kernels for the same objects. CCA can be performed by solving the following generalized eigenvalue problem:

$$\begin{pmatrix} 0 & K_1 K_2 \\ K_2 K_1 & 0 \end{pmatrix} \vec{\xi} = \rho \begin{pmatrix} K_1^2 & 0 \\ 0 & K_2^2 \end{pmatrix} \vec{\xi}$$

Useful to find correlations between different representations of the same objects (ex: genes, ...)

Classification: support vector machines (SVM)



Find a linear boundary with large margin and few errors

$$\begin{cases} \max_{\vec{\alpha}} \sum_{i=1}^n \alpha_i - \frac{1}{2} \sum_{i,j=1}^n \alpha_i \alpha_j y_i y_j K(g_i, g_j) \\ \forall i = 1, \dots, n \quad 0 \leq \alpha_i \leq C \\ \sum_{i=1}^n \alpha_i y_i = 0 \end{cases}$$

Examples: SVM in bioinformatics

- Gene functional classification from microarray: Brown et al. (2000), Pavlidis et al. (2001)
- Tissue classification from microarray: Mukherje et al. (1999), Furey et al. (2000), Guyon et al. (2001)
- Protein family prediction from sequence: Jaakkoola et al. (1998)
- Protein secondary structure prediction: Hua et al. (2001)
- Protein subcellular localization prediction from sequence: Hua et al. (2001)

Summary

- Once a kernel $K(x, y)$ is given, several analysis can be performed implicitly in the feature space
- These methods are considered currently among the most powerful on many real-world problems
- Modularity: each kernel can work with each method

Part 3

Kernelizing the proteome

What is a gene

- a DNA sequence?
- a primary, secondary or 3D structure of a protein?
- an expression profile?
- a node in a regulatory or interaction network?
- a promoter region?
- a phylogenetic profile?
- ...

Kernel for sequences

- spectrum kernel (Eskin et al., 2002)
- Fisher kernel (Jaakkola et al., 1999)
- Pair HMM kernels (Haussler, 1999)
- Very good results for remote homology detection

Kernels for expression profiles

An expression profile is a vector $\vec{\Phi}(x)$:

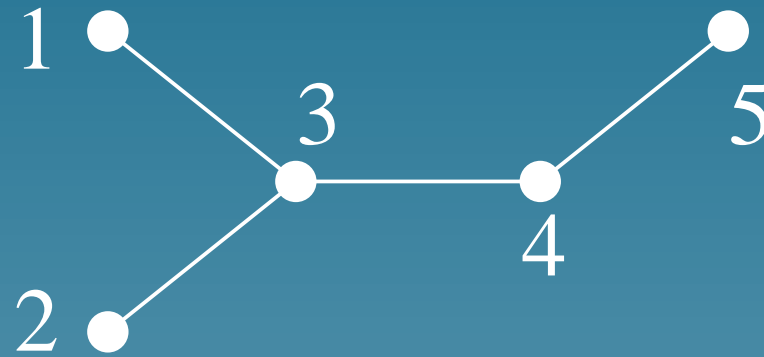
- **Linear kernel:** $K(x, y) = \vec{\Phi}(x) \cdot \vec{\Phi}(y)$.
- **Polynomial kernel:** $K(x, y) = \left(\vec{\Phi}(x) \cdot \vec{\Phi}(y) + 1 \right)^d$.
- **Gaussian kernel:** $K(x, y) = \exp \left(-\frac{\|\vec{\Phi}(x) - \vec{\Phi}(y)\|^2}{2\sigma^2} \right)$.

Diffusion kernel for the nodes of a graph (Kandor, 2001)

- Let G a graph with vertices \mathcal{X} .
- Let $L = A - D$ be the Laplacian matrix of the graph.
- For any $\lambda > 0$, the following is a valid kernel

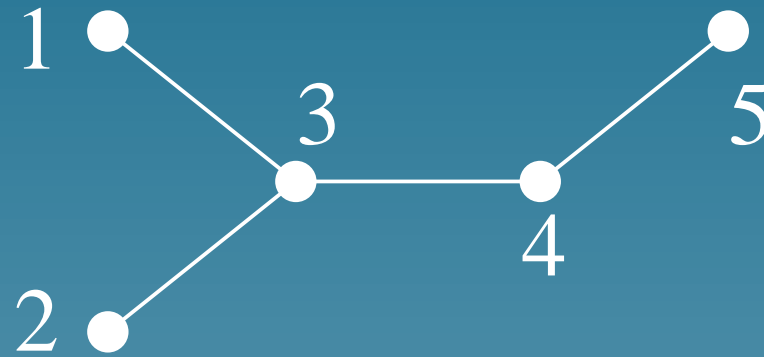
$$K = \exp(-\lambda L)$$

Example (1)



$$L = \begin{pmatrix} -1 & 0 & 1 & 0 & 0 \\ 0 & -1 & 1 & 0 & 0 \\ 1 & 1 & -3 & 1 & 0 \\ 0 & 0 & 1 & -2 & 1 \\ 0 & 0 & 0 & 1 & -1 \end{pmatrix}$$

Example (2)



$$K = \exp(-L) = \begin{pmatrix} 0.49 & 0.12 & 0.23 & 0.10 & 0.03 \\ 0.12 & 0.49 & 0.23 & 0.10 & 0.03 \\ 0.23 & 0.23 & 0.24 & 0.17 & 0.10 \\ 0.10 & 0.10 & 0.17 & 0.31 & 0.30 \\ 0.03 & 0.03 & 0.10 & 0.30 & 0.52 \end{pmatrix}$$

More kernels

- Information diffusion kernels (Lafferty and Lebanon, 2002) for probability densities
- Kernels on finite groups (Kondor)
- Kernels for 3D structures

Operations on kernels

- The space of kernels is a **closed convex cone** (closed under addition, pointwise limit, multiplication by a positive scalar)
- Closed under **product** and **tensor product**
- linear combinations can be optimized by **semi-definite programming (SDP)**
- A kernel is a covariance function which defines a Gaussian process. The information geometry of Gaussian process defines a **natural geometry on kernels**.

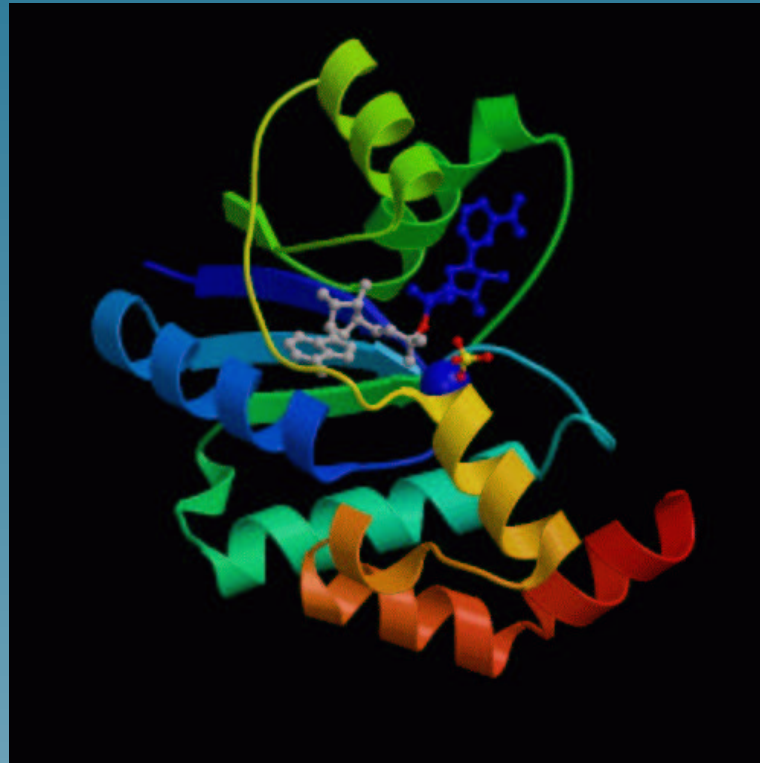
Summary

- Kernels can be built from **a priori knowledge**, or obtained by **various operations** from initial kernels
- A kernel can be thought of as a **measure of similarity**; this can be useful to make new kernels for any given type of data
- **Kernel engineering** and **kernel optimization** is an active field of research currently

Part 4

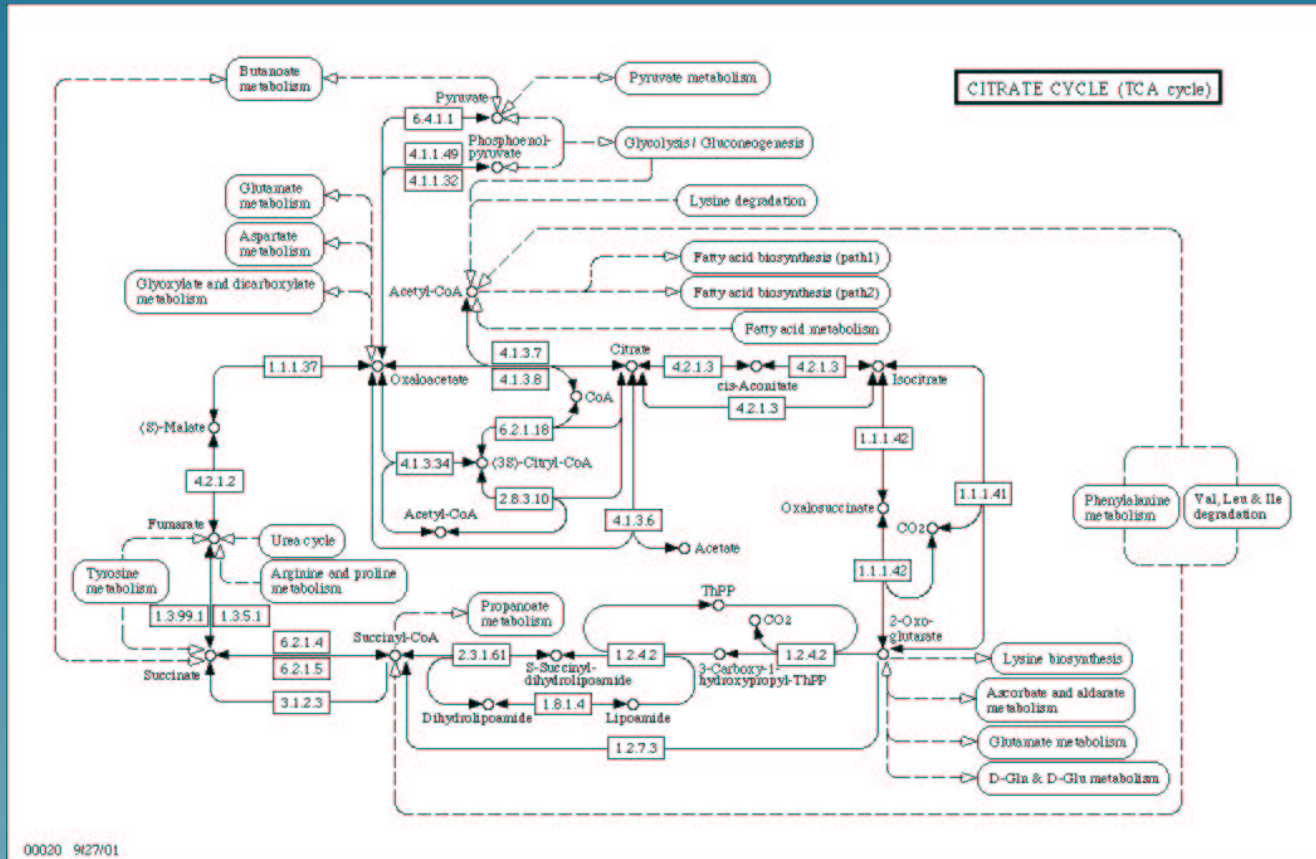
Application: comparing a protein network and expression data

Genes encode proteins which can catalyse chemical reactions



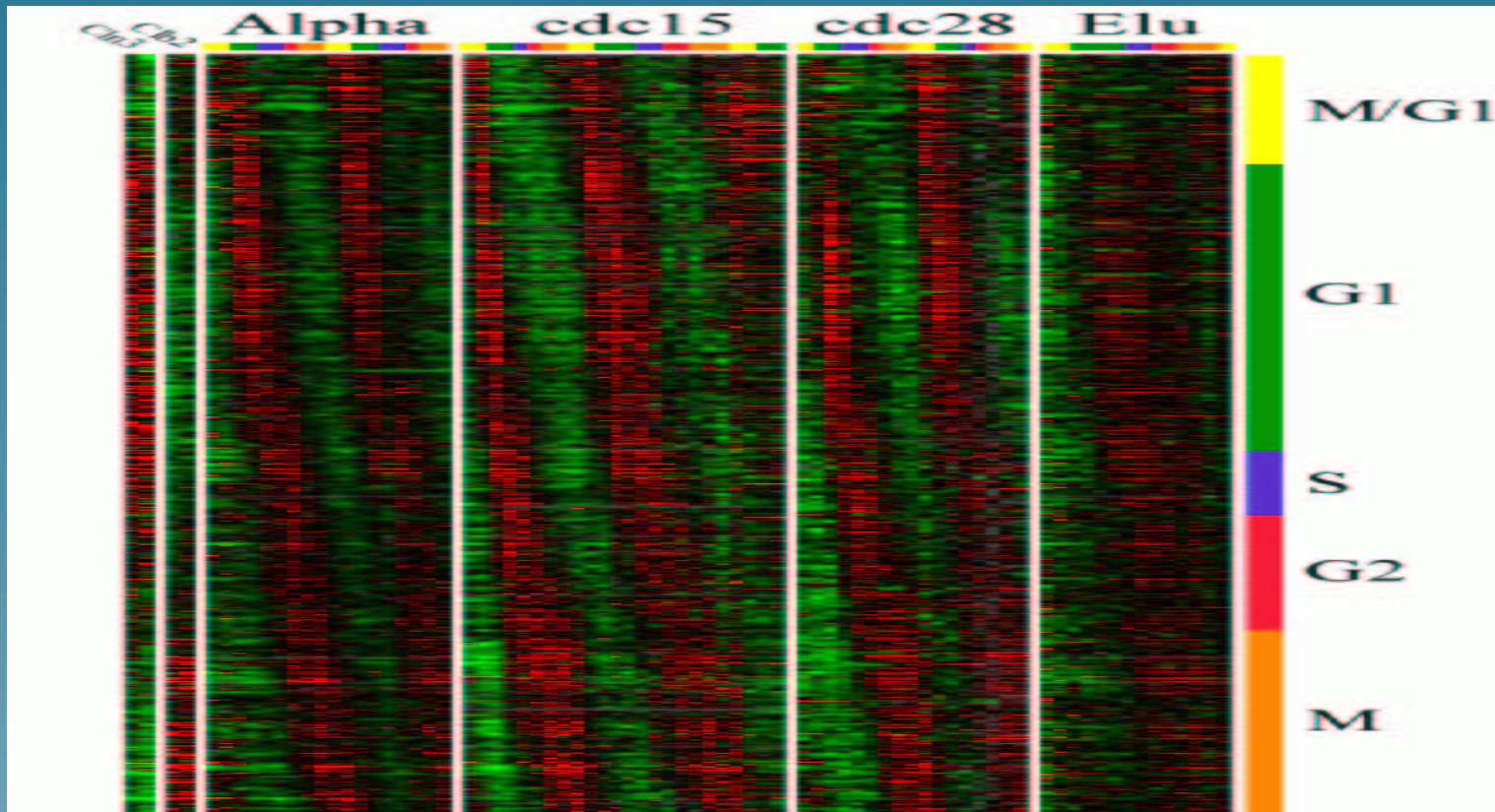
Nicotinamide Mononucleotide Adenylyltransferase With Bound Nad⁺

Chemical reactions are often parts of pathways



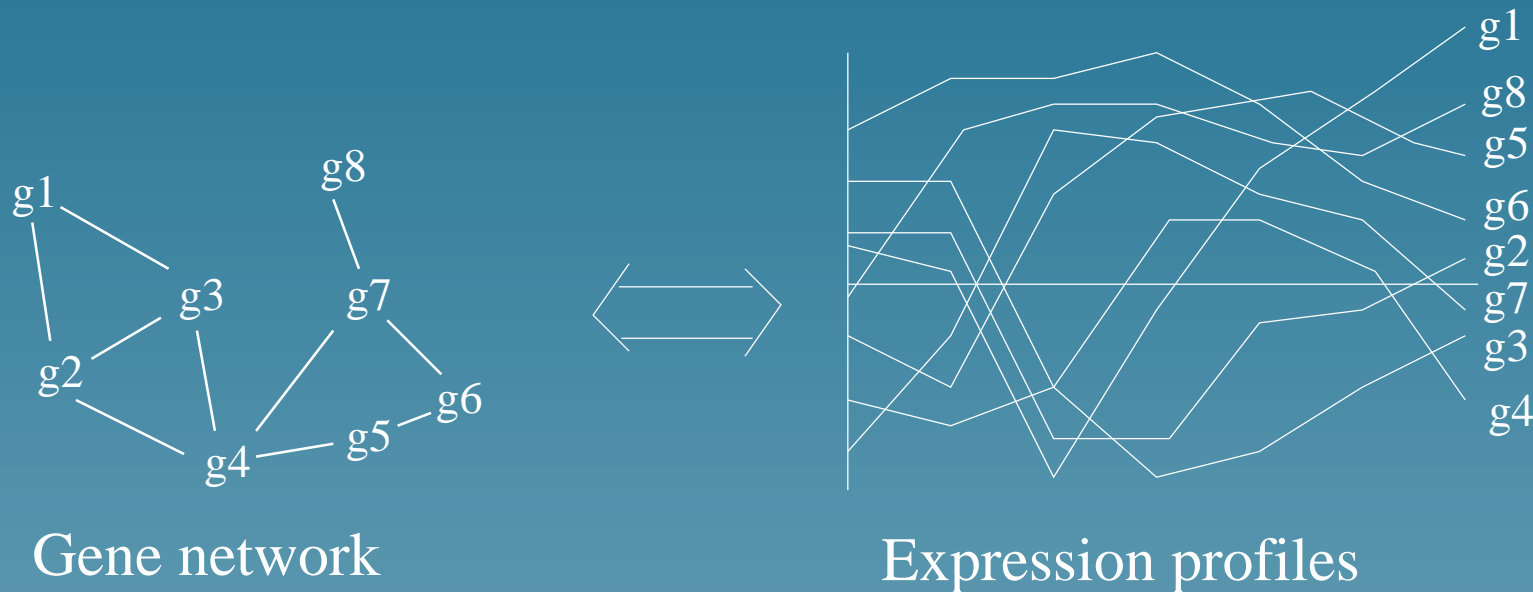
From <http://www.genome.ad.jp/kegg/pathway>

Microarray technology monitors RNA quantity



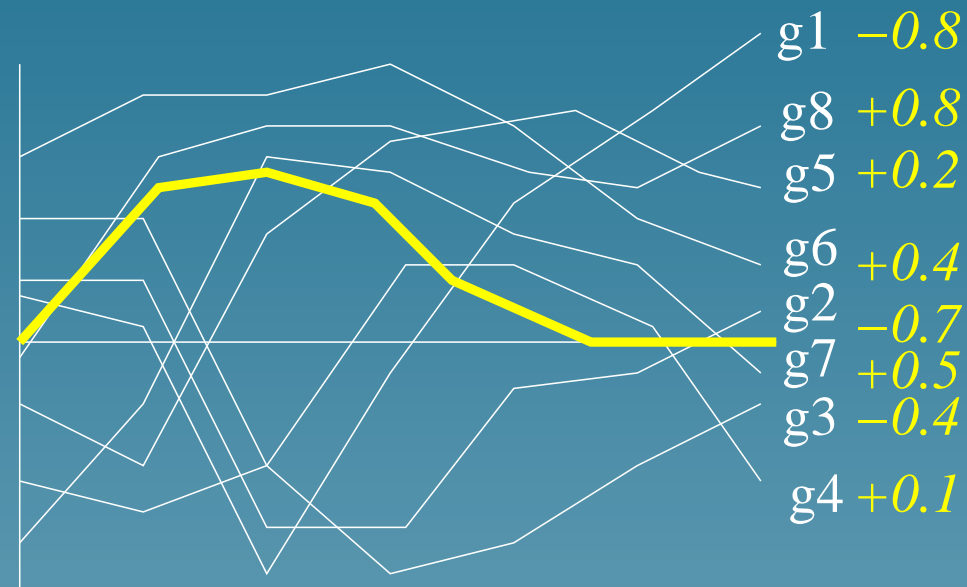
(From Spellman et al., 1998)

Comparing gene expression and protein network



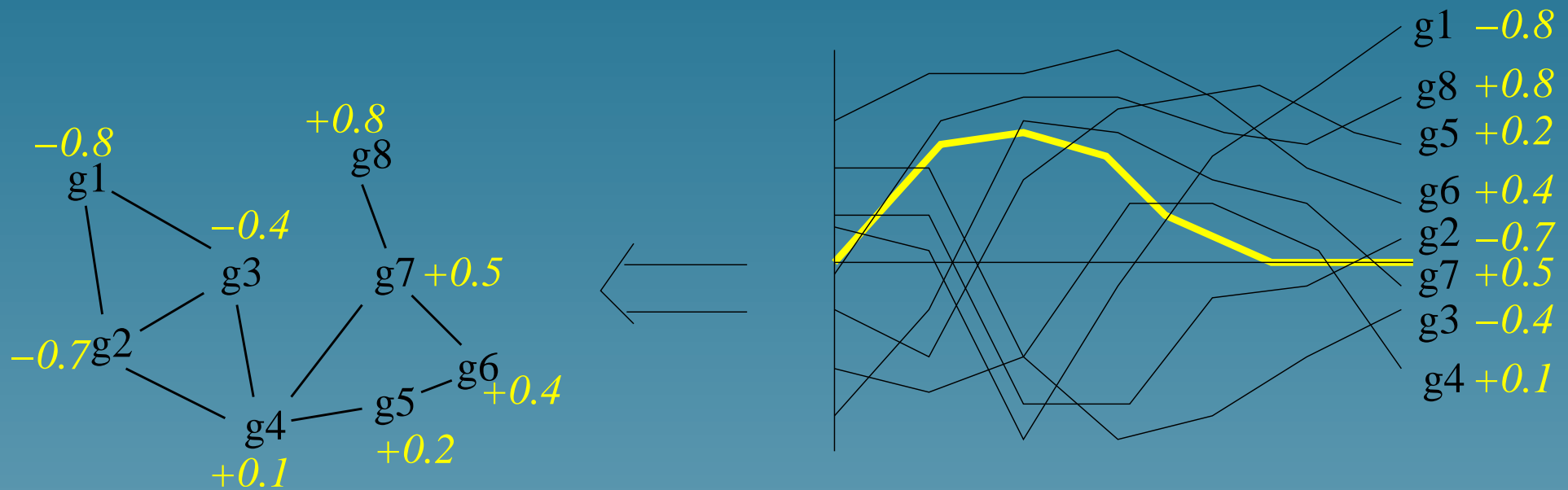
Are there “correlations”?

Pattern of expression



- In yellow: a candidate **pattern** , and the **correlation coefficient** with each gene profile

Pattern smoothness



- The correlation function with **interesting patterns** should vary **smoothly** on the graph

Pattern relevance

- Interesting patterns involve many genes
- The projection of profiles onto an interesting pattern should capture a lot of variations among profiles
- Relevant patterns can be found by PCA

Problem

Find patterns of expression which are **simultaneously**

- smooth
- relevant

Pattern relevance

- Let $e(x)$ the profile of gene x
- Let $K_1(x, y) = e(x).e(y)$ be the **linear kernel**, with RKHS H_1 .
- The norm $\|\cdot\|_{H_1}$ is a relevance functional: the relevance of $f \in H_1$ increases when the following decreases:

$$\frac{\|f\|_{H_1}}{\|f\|_{L_2}}$$

Pattern smoothness

- Let $K_2(x, y)$ be the **diffusion kernel** obtained from the gene network, with RKHS H_2 .
- It can be considered as a discretized version of a Gaussian kernel (solving the heat equation with the graph Laplacian)
- The norm $\|\cdot\|_{H_2}$ is a **smoothness functional**: the smoother a function $f : \mathcal{X} \rightarrow \mathbb{R}$, the larger the function:

$$\frac{\|f\|_{H_1}}{\|f\|_{L_2}}$$

Problem reformulation

Find a linear function f_1 and a function f_2 such that:

- f_1 be relevant : $\|f_1\|_{L^2}/\|f_1\|_{H_1}$ be large
- f_2 be smooth : $\|f_2\|_{L^2}/\|f_2\|_{H_2}$ be large
- f_1 and f_2 be correlated :

$$\frac{f_1 \cdot f_2}{\|f_1\|_{L^2}\|f_2\|_{L^2}}$$

be large

Problem reformulation (2)

The three goals can be combined in the following problem:

$$\max_{f_1, f_2} \frac{f_1 \cdot f_2}{\left(\|f_1\|_{L^2}^2 + \delta \|f_1\|_{H_1}^2 \right)^{\frac{1}{2}} \left(\|f_2\|_{L^2}^2 + \delta \|f_2\|_{H_2}^2 \right)^{\frac{1}{2}}}$$

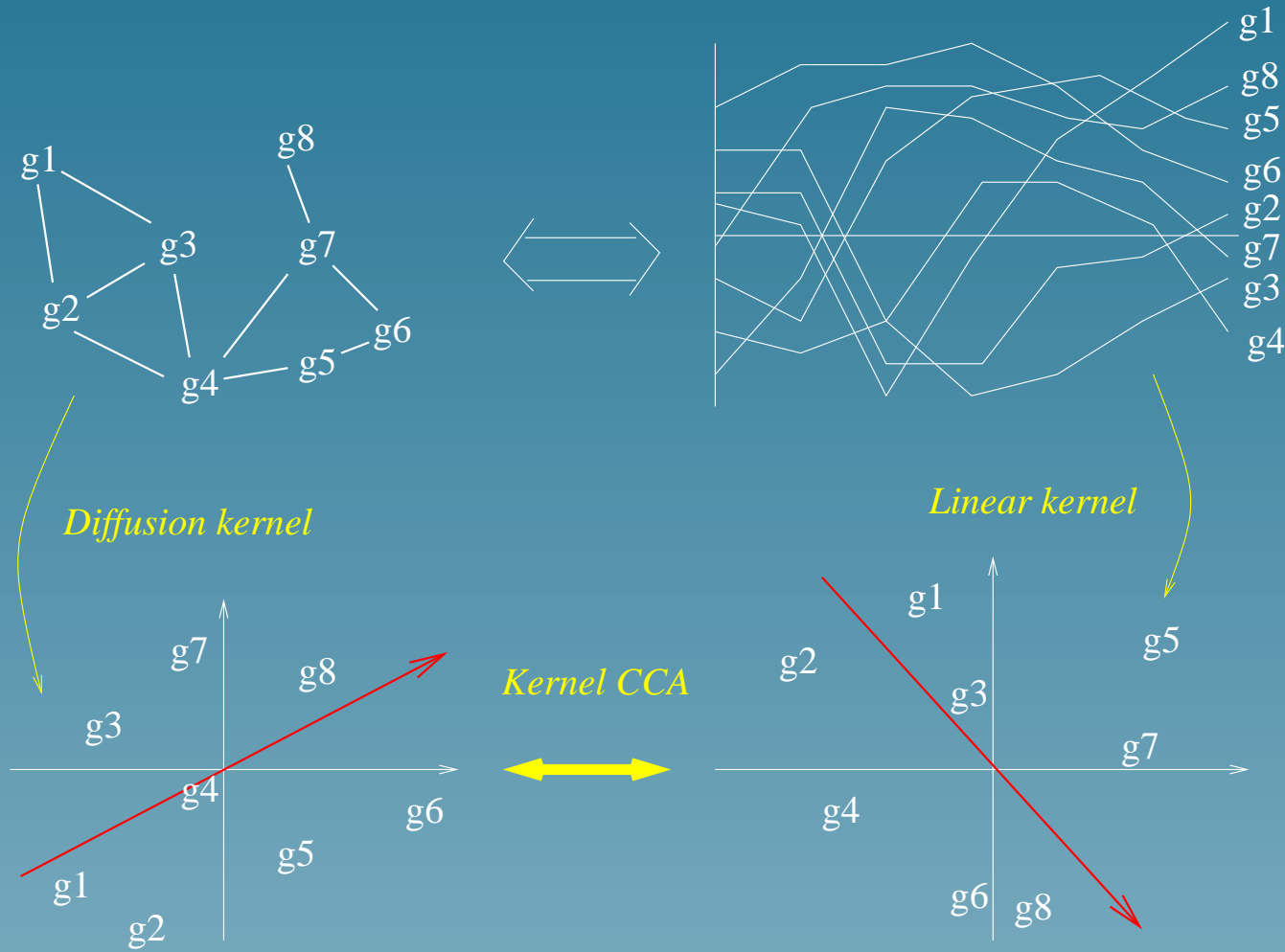
where the parameter δ controls the trade-off between relevance/smoothness on the one hand, correlation on the other hand.

Solving the problem

This formulation is equivalent to a generalized form of CCA (**Kernel-CCA**, Bach and Jordan, 2002), which is equivalent to the following generalized eigenvector problem

$$\begin{pmatrix} 0 & K_1 K_2 \\ K_2 K_1 & 0 \end{pmatrix} \begin{pmatrix} \alpha \\ \beta \end{pmatrix} = \rho \begin{pmatrix} K_1^2 + \delta K_1 & 0 \\ 0 & K_2^2 + \delta K_2 \end{pmatrix} \begin{pmatrix} \alpha \\ \beta \end{pmatrix}$$

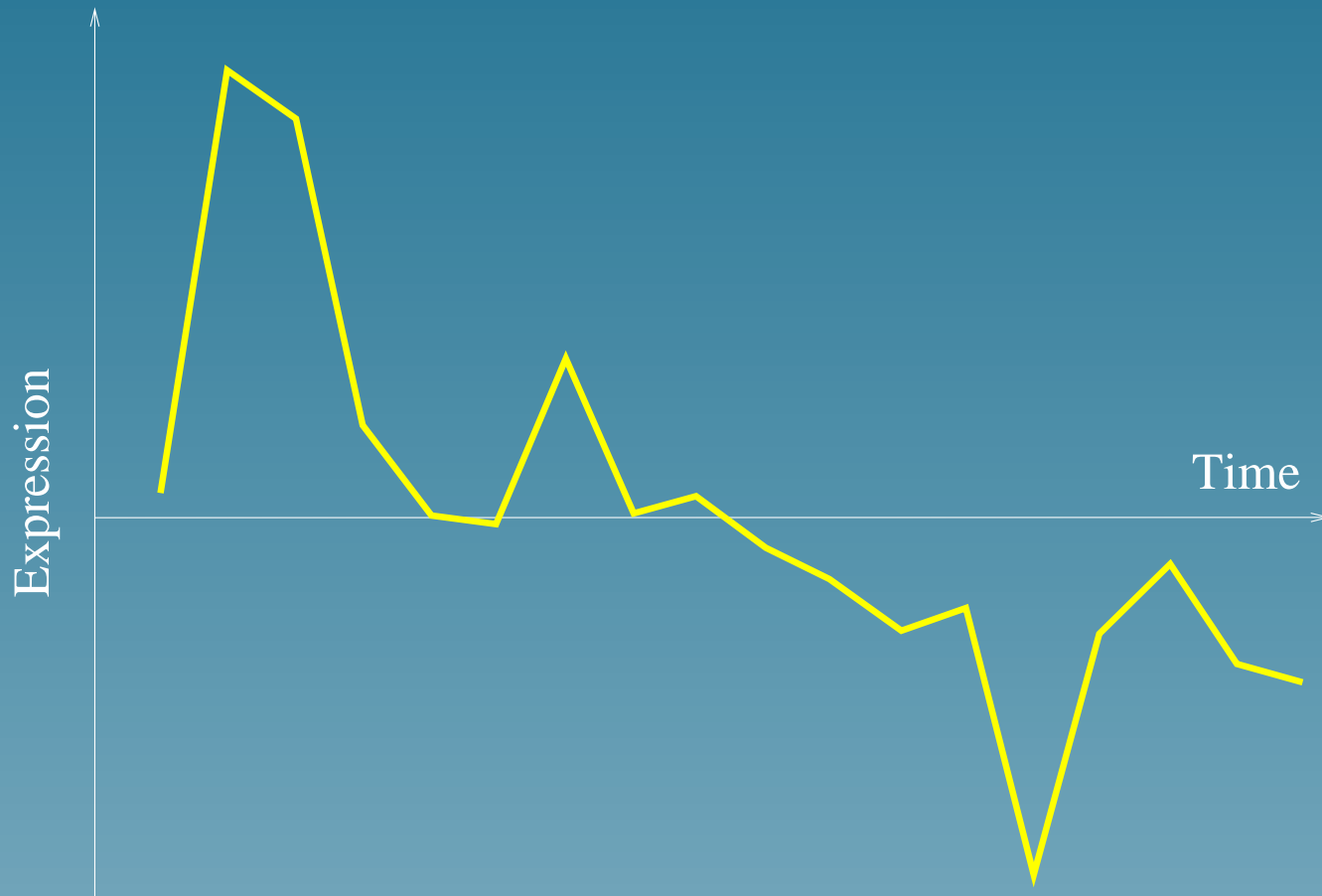
Summary



Data

- **Gene network:** two genes are linked if they catalyze successive reactions in the KEGG database
- **Expression profiles:** 18 time series measures for the 6,000 genes of yeast, during two cell cycles

First pattern of expression

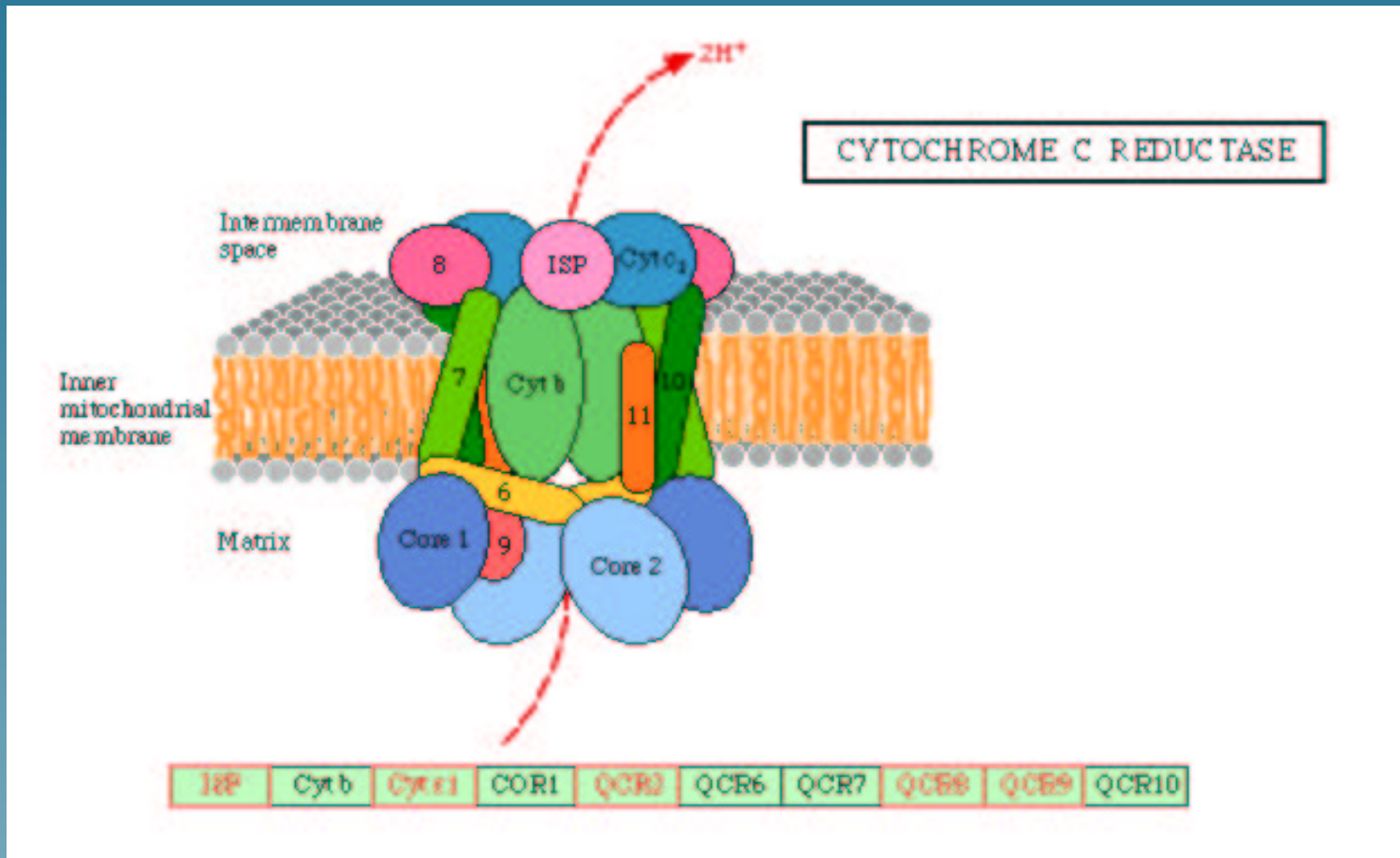


Related metabolic pathways

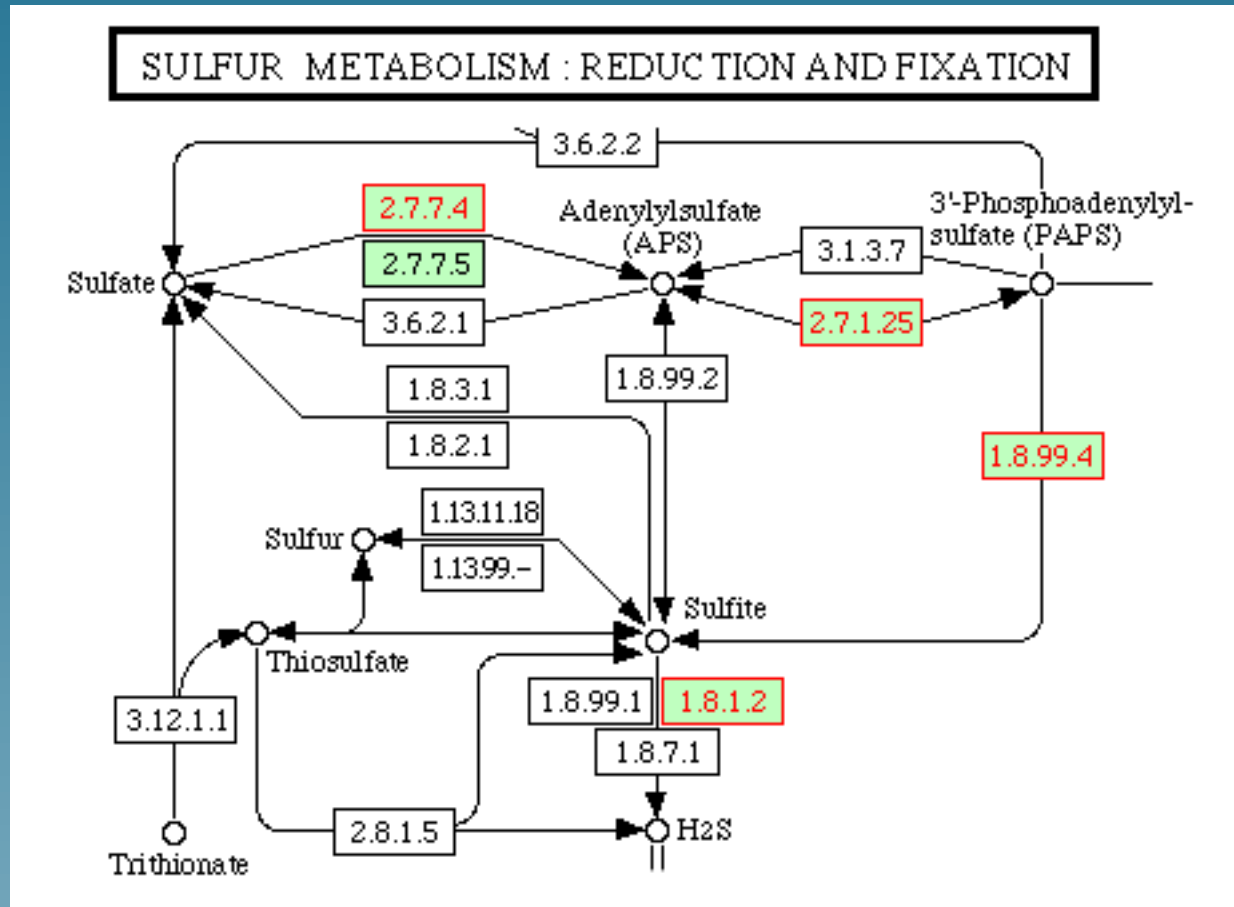
50 genes with highest $s_2 - s_1$ belong to:

- Oxidative phosphorylation (10 genes)
- Citrate cycle (7)
- Purine metabolism (6)
- Glycerolipid metabolism (6)
- Sulfur metabolism (5)
- Selenoaminoacid metabolism (4) , etc...

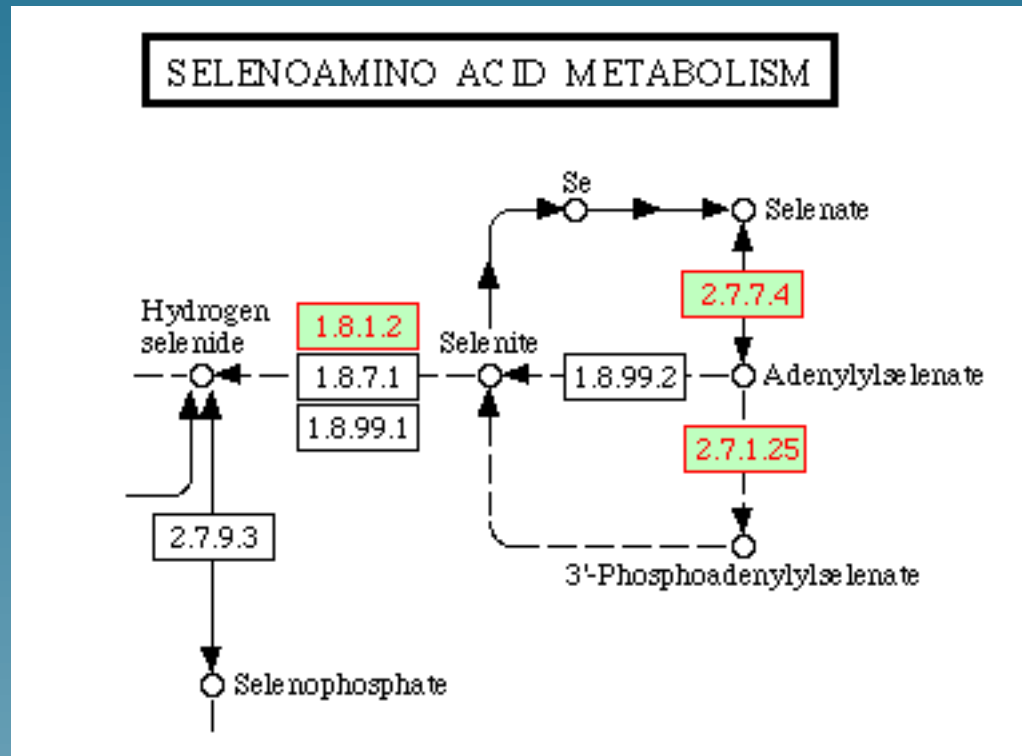
Related genes



Related genes



Related genes



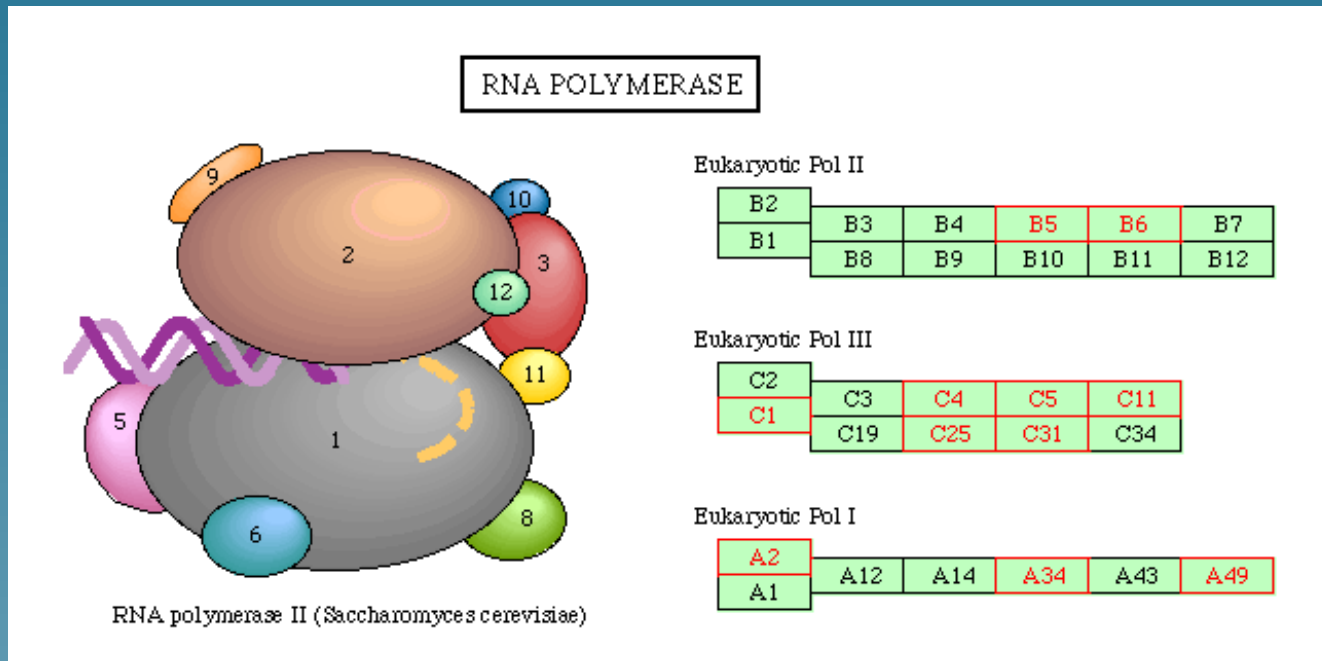
Opposite pattern



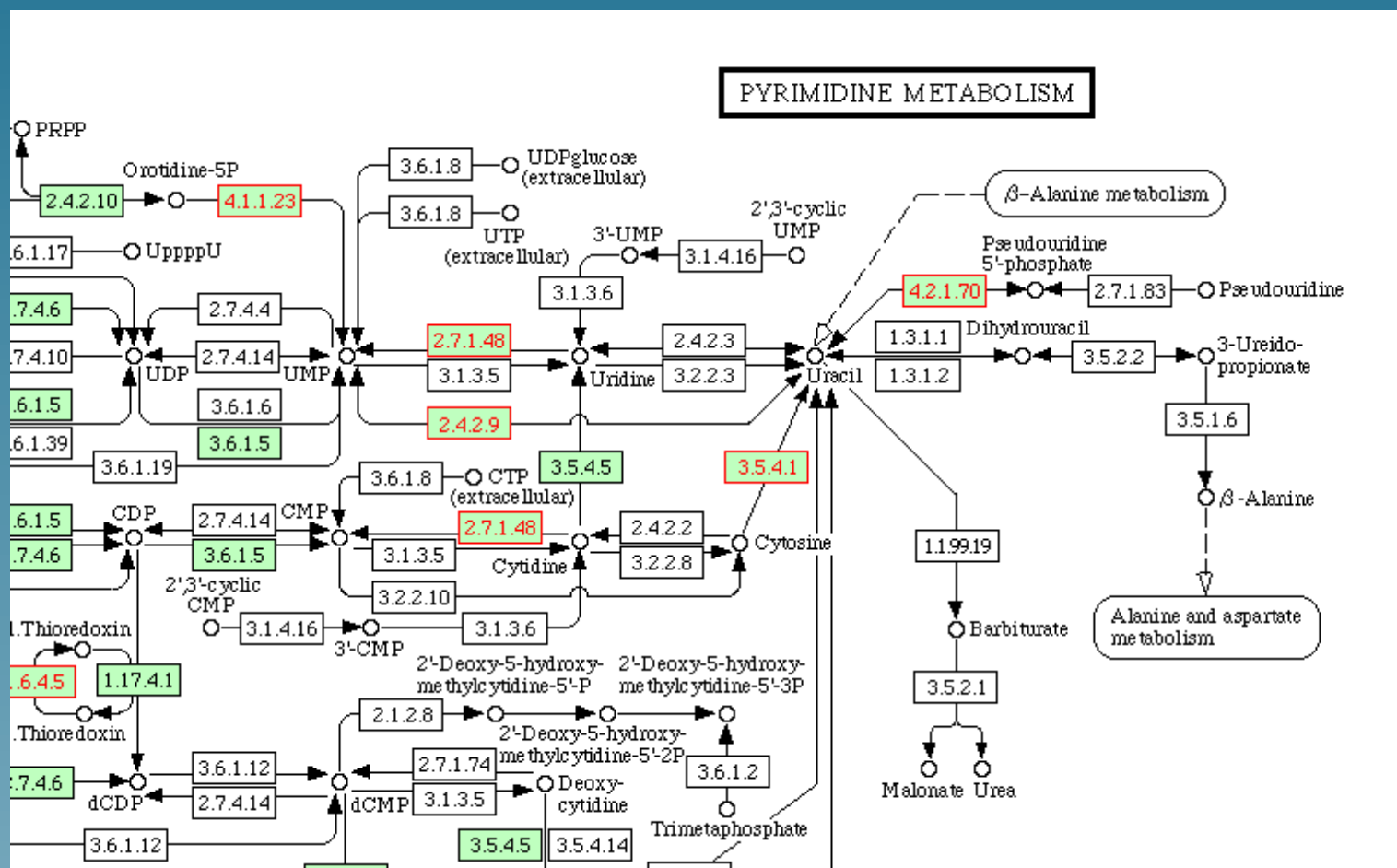
Related genes

- RNA polymerase (11 genes)
- Pyrimidine metabolism (10)
- Aminoacyl-tRNA biosynthesis (7)
- Urea cycle and metabolism of amino groups (3)
- Oxidative phosphorylation (3)
- ATP synthesis(3) , etc...

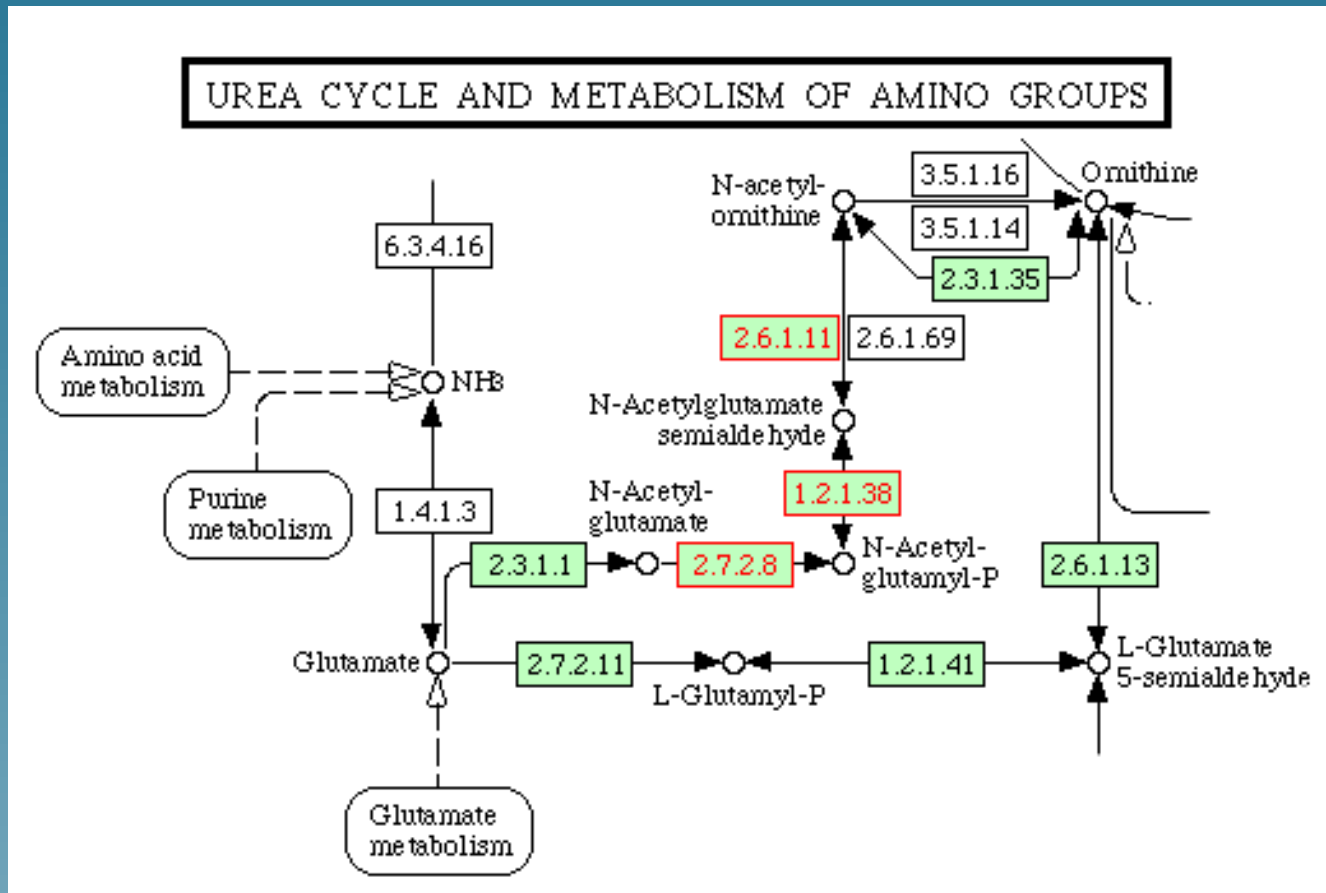
Related genes



Related genes



Related genes



Conclusion

Conclusion

- There is an **urgent need** for formalisms and computational tools to integrate heterogeneous data
- **Kernel methods** offer such a framework.
- Few **conceptual** relationships between genes, but **computational efficiency**.
- Machine learning and kernel methods are currently **boosted by biology**.