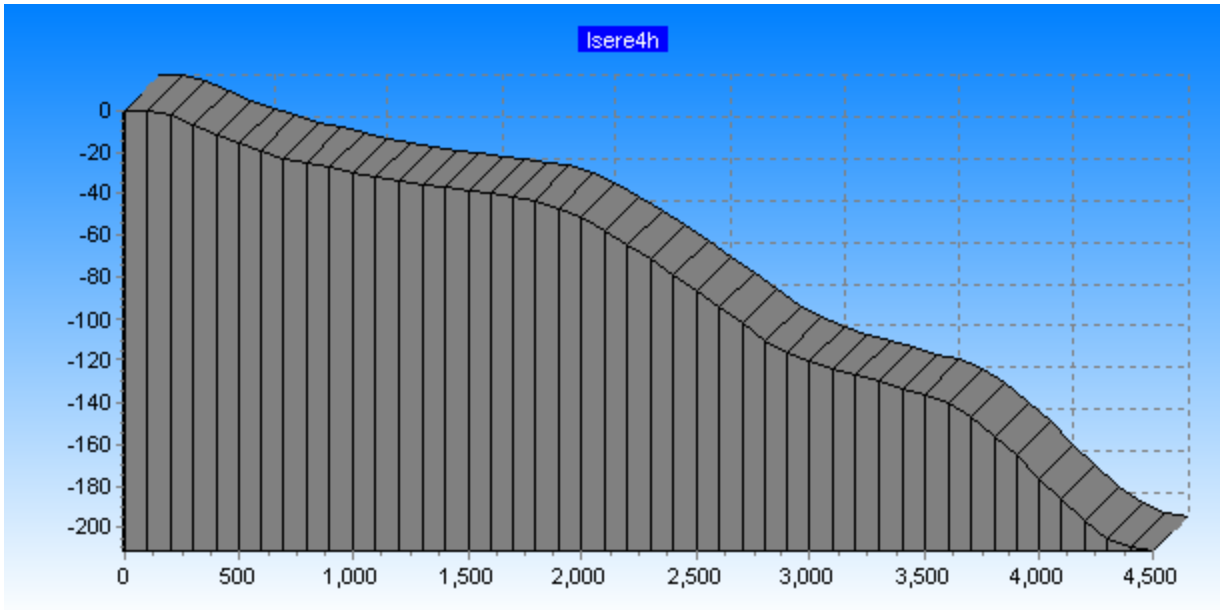
Optimization of brake utilization for heavy-duty trucks

General reference:
www.me.chalmers.se/~mwahde/AdaptiveSystems/Publications/LingmanWahdeAVEC2002.pdf

Problem description:



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Brake systems

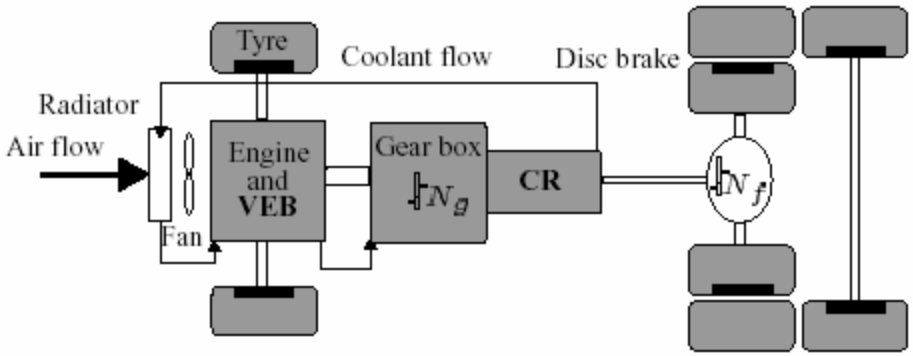

Fig. 1. Volvo retardation system

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Brake systems

- Downhill cruising: select a set speed and maintain it.
- Requires gear changes and activation of pedal brakes (**foundation brakes**) and **auxiliary brakes** (e.g. engine brake and compact retarder).
- Problem: too much usage of the foundation brakes => overheating => fading => no braking force => accident.
- Overheating of disc brakes: fading
- Overheating of auxiliary brakes: cooling system saturation

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Possible solutions

- Use a lower set speed

  Problem: Slower transportation, road congestion etc.

- Use auxiliary brakes to save brake pads and discs

  Problem: high drive tyre wear, leading to high maintenance cost.

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Problem

To find an optimal strategy for brake blending (usage of different brakes), taking into account constraints, such as brake temperature, speed, engine speed etc.

The problem was studied using a simplified vehicle model.

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Equations of motion

Longitudinal motion equation:

$$m\dot{v} = F_{\text{drive}} - F_{\text{air}} - F_{\text{roll}} - F_{\text{grade}} - \\ -F_{\text{aux}} - F_{\text{found}}$$

F_{drive} is assumed to be zero for downhill cruising.

(+ equations for brake dynamics, air resistance etc.), see

www.me.chalmers.se/~mwahde/AdaptiveSystems/Publications/LingmanWahdeAVEC2002.pdf

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Wear dynamics: (needed e.g. for studying costs aspects of various strategies)

$$\dot{S}_{\text{pad}} = q_{\text{in}} S_0 e^{c T_1^{k_0}}$$

$$\dot{S}_{\text{tyre}} = v(a + b\tau_{\text{tyre}}^2 + c\tau_{\text{tyre}}^4 + d\tau_{tyre}^6)$$

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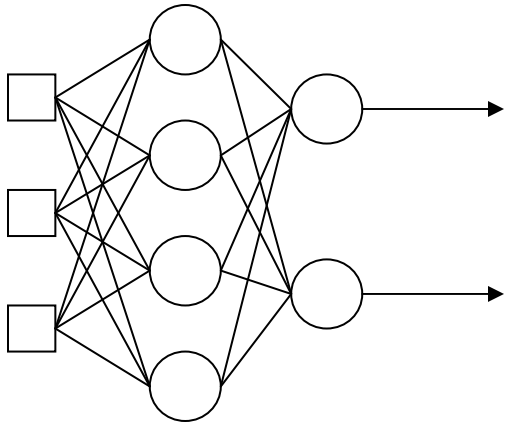
Method

- Brake blending represented by feedforward neural networks



- Network size: 5-7-4, sigmoid slope = 1.

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Method

- Inputs: vehicle speed (v), current road slope (α), disc brake temperature (T_1), coolant temperature ($T_{coolant}$), engine speed (v_E).

- Outputs: (1) total retardation force request, (2) gear choice (inc, dec, unchanged), (3) fraction of braking force taken from foundation brakes, (4) split of auxiliary braking force from VEB (engine brakes) and CR (compact retarder).

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Method

- Constraints:

  $T_1 < 500$ C, $v > 5$ m/s, $v < 25$ m/s, $v_E < 2300$ rpm,
  $v_E > 600$ rpm, time < 200s

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Optimization method

- Feedforward network, *but* no input-output pairs (for every instant)
- Use a genetic algorithm instead.
- Only parametric optimization was used.
- The (minimum) numer of neurons in the middle layer was determined using trial-and-error.
- Typical parameters: population size = 100, number of generations = 1,000

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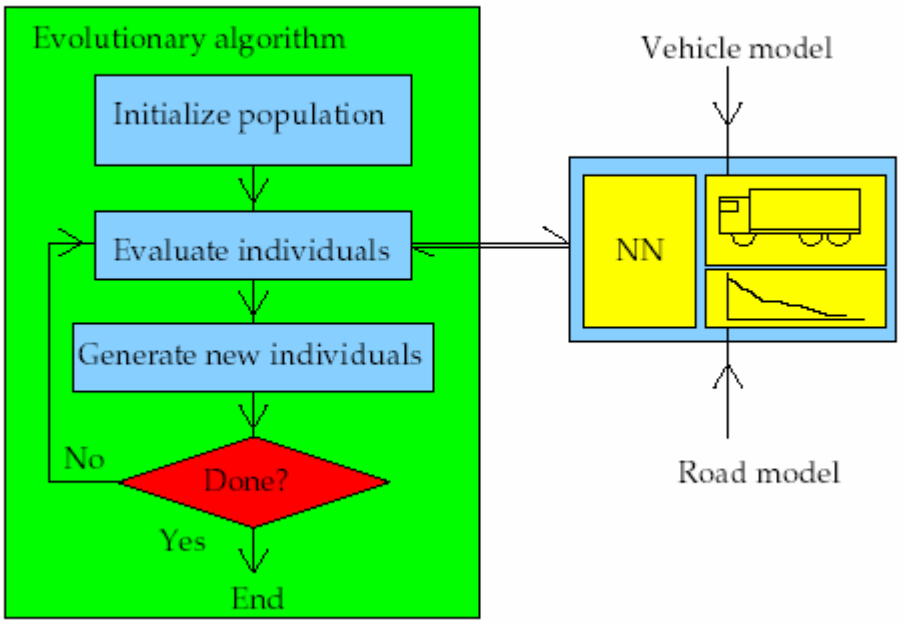
Optimization method

- **Fitness measure:**

  The distance travelled in a given maximum time (evaluation terminated if constraints were broken).



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Road profiles

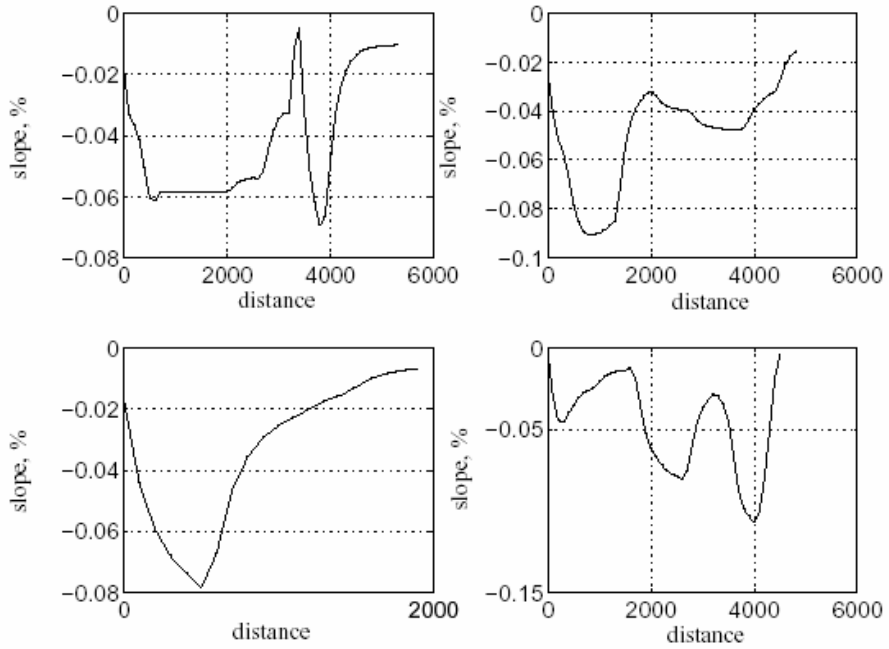

Fig. 5. Example of measured road profiles used. French alps, Isère1-4

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Theoretical limitations

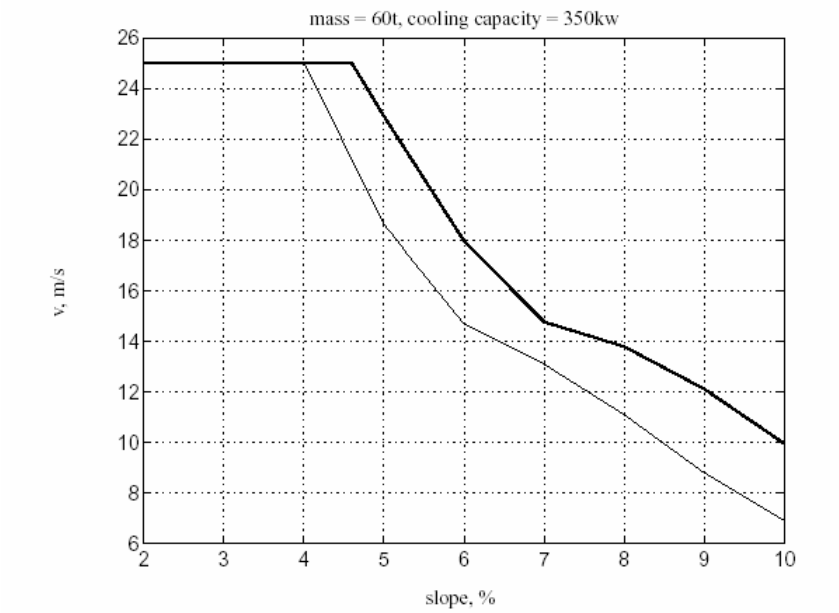

Fig. 4. Maximum stationary speed for different slopes. Thin solid line: using only auxiliary brakes. Thick solid line: optimal blending

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Results

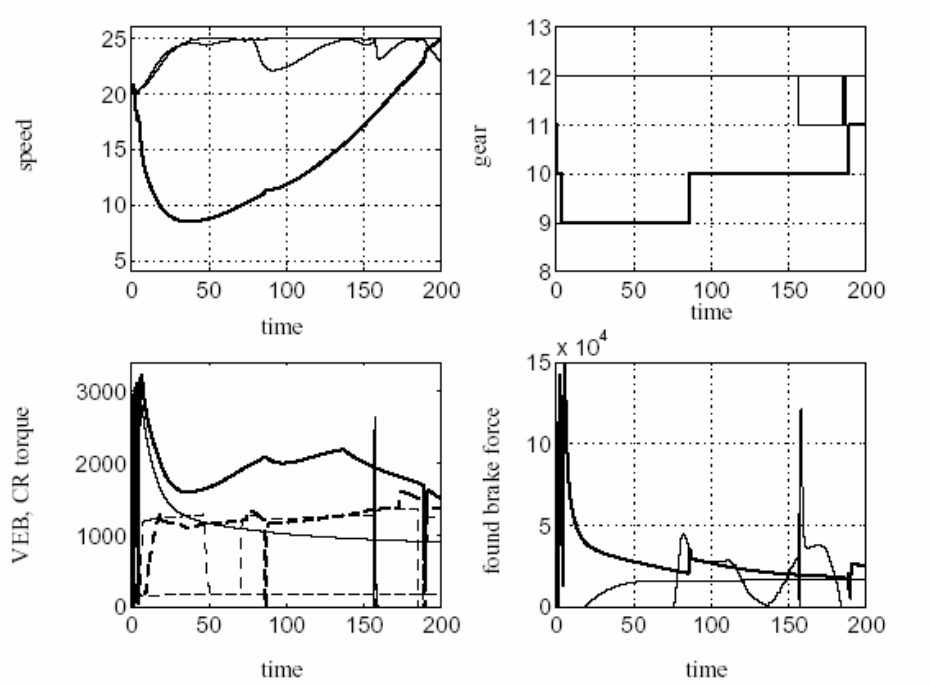

Fig. 3. Optimal blending for high mean speed on 3 roads. Thick solid line: 10% constant slope, Medium solid line: Isère 4 road, Thin solid line: 5% constant slope

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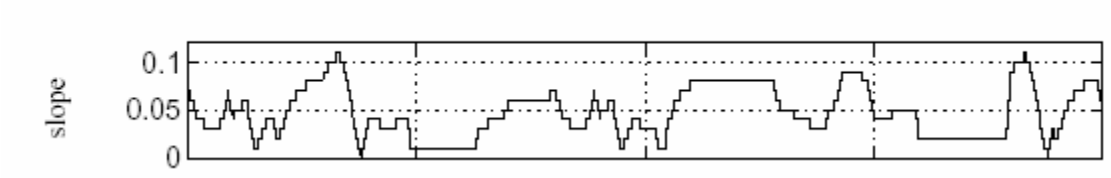
Problem: Adaptation to specific conditions in the training roads

Solution: Construct a long, artificial road, containing as many relevant aspects as possible (using parts from the French alps (Isère), and Kassel hills in Germany).



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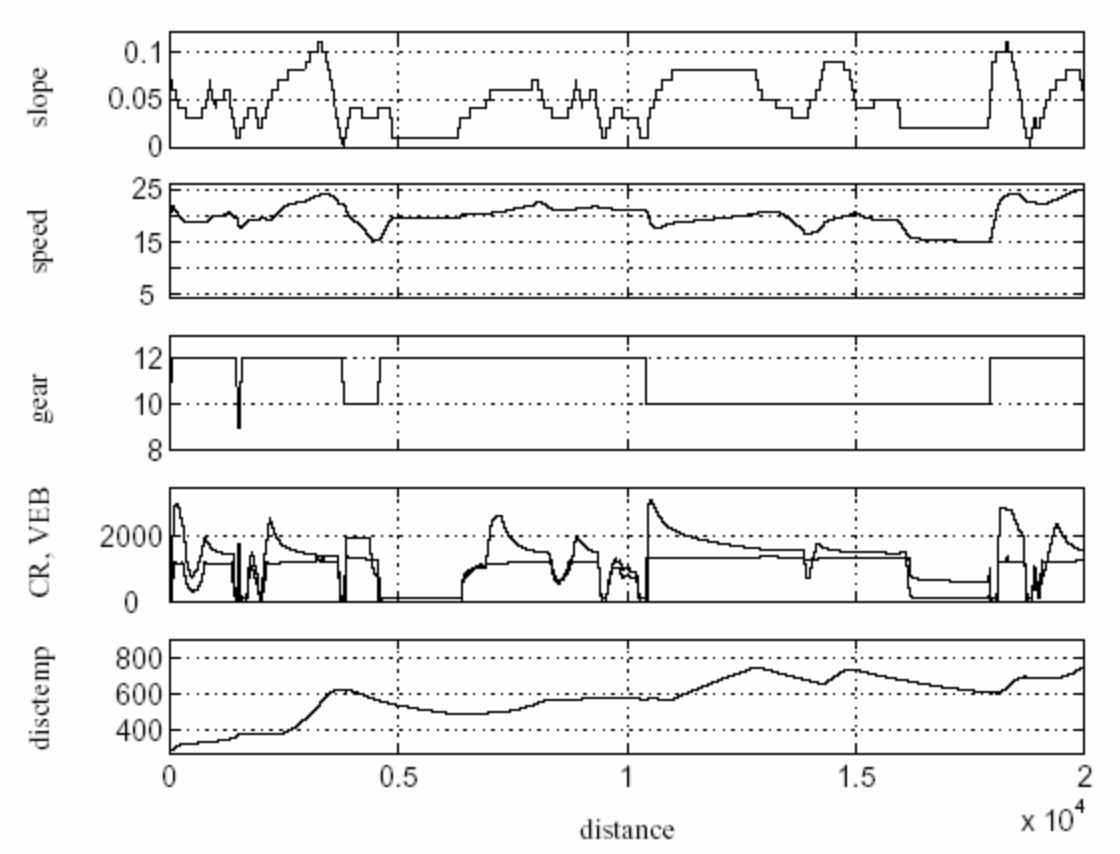
Results



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Generalization measures

- Two measures were defined:

$$G = \frac{1}{N_r} \sum_{i=1}^{N_r} \frac{d_i}{L_i}; V = \frac{1}{N_r v_{max}} \sum_{i=1}^{N_r} \bar{v}_i$$

- 14 different test roads were defined, i.e. N_r (the number of test roads) was set to 14.

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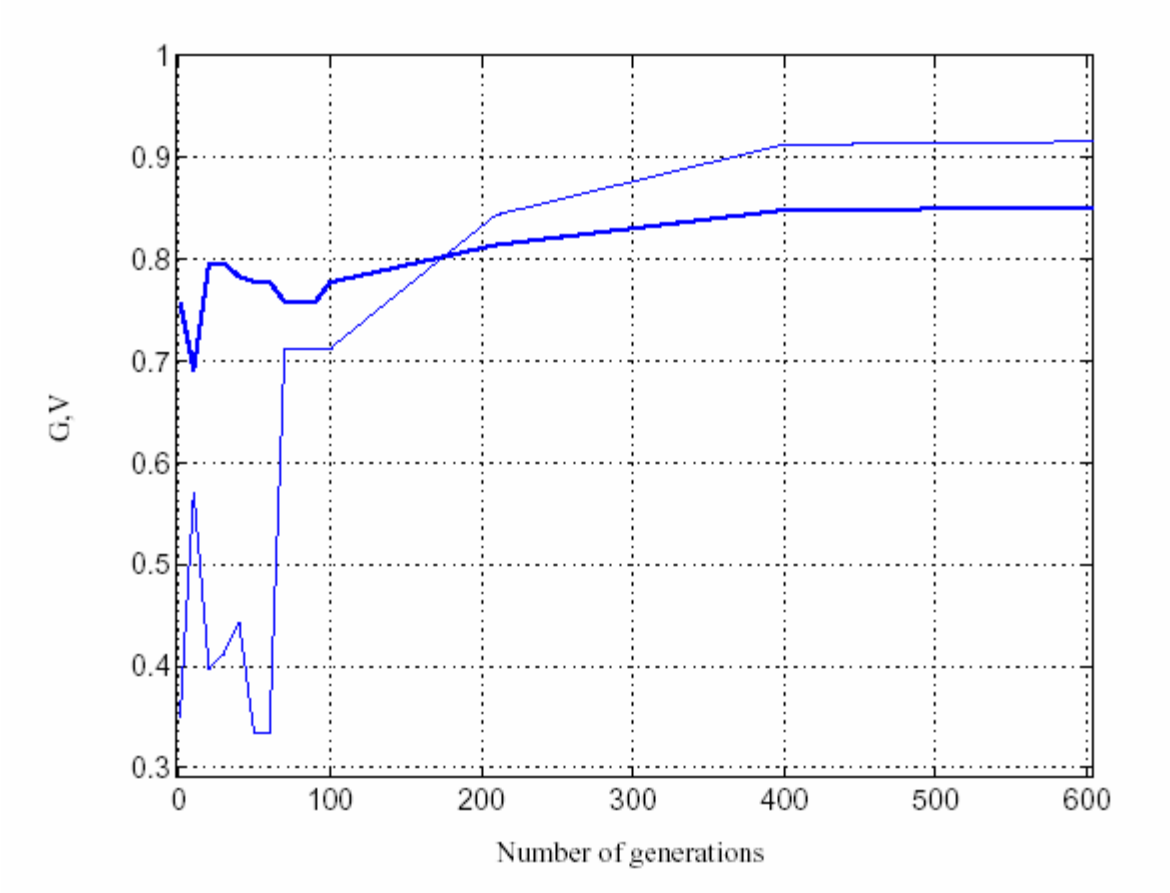
Generalization results



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Reverse engineering of genetic regulatory networks

- General reference:
  www.me.chalmers.se/~mwahde/AdaptiveSystems/Publications/WahdeHertzJCB2001.pdf

- With microarrays, it is possible to measure the activity (expression levels) of thousands of genes simultaneously.

- Genes interact with each other, forming genetic regulatory networks.

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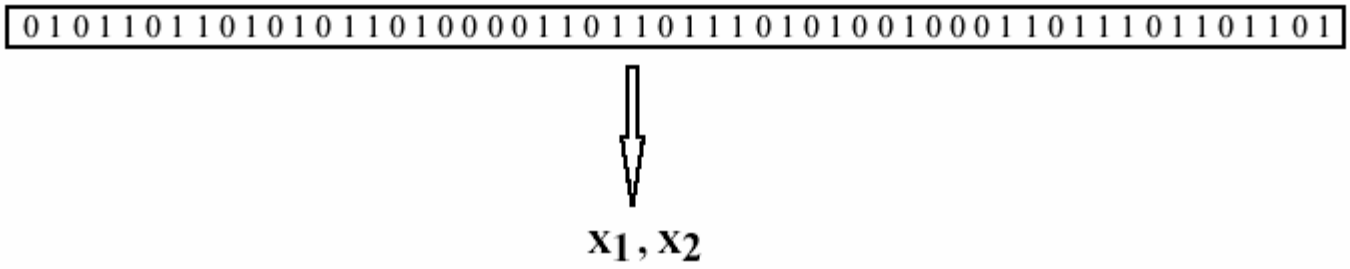
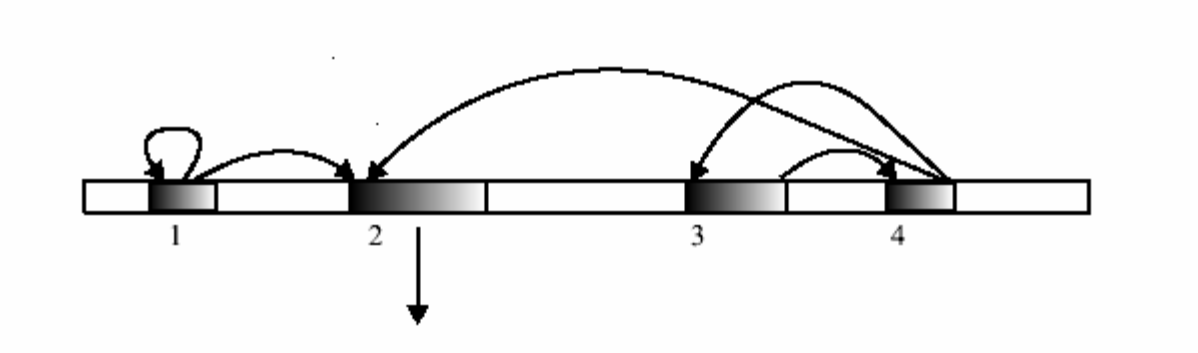
GA



Biology (simplified representation)



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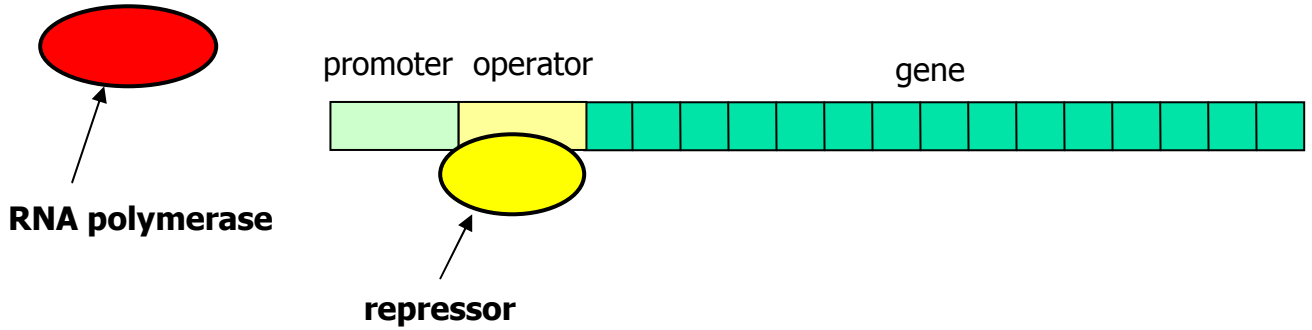
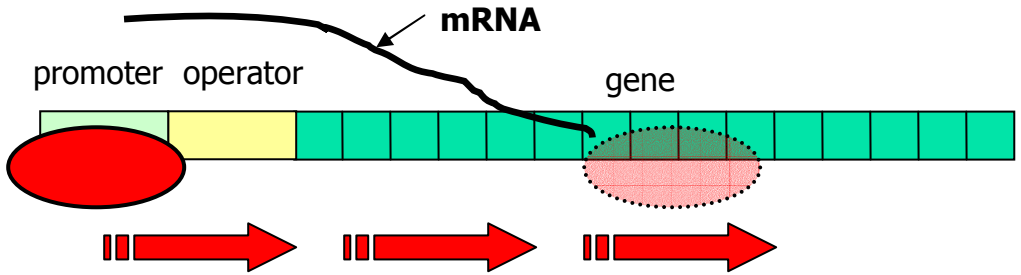
Regulatory genes: (transcription factors) genes that regulate the expression of other genes.

Example of gene regulation:

Repressor protein (= the product of some other (regulatory) gene) bound to operator site: transcription is prevented



Repressor *not* bound to operator: the RNA polymerase can reach the promoter and proceed with transcription:



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Problem

- *Given time series measurements of the activation (expression) levels of various genes, determine the interactions between the genes.*

- If a model of the network dynamics is available, this problem can be reduced to the problem of finding the appropriate model parameters

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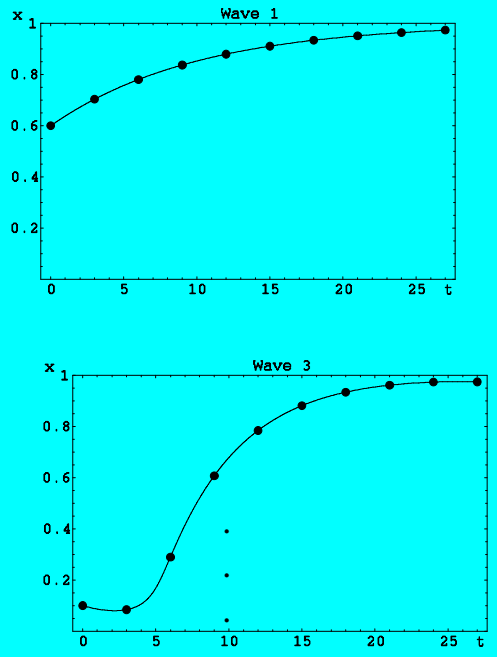
Problem



$$\Rightarrow \quad \tau_i, w_{ij}, b_i$$

This is a so called *inverse problem*.

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Coarse-grained modeling of genetic regulatory networks

Simplifications in **coarse-grained modeling**:

- Usually, only mRNA levels are taken into account. Levels of proteins and other molecules (metabolites, ions etc.) are not included in the models.
- Sometimes, the model variables are not expression levels of *individual* genes (due to lack of data). Instead, genes are grouped together (forming *waves*).
- The interactions are modeled in a highly simplified way (e.g. additive models).

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Model

$$\tau_i \frac{dx_i}{dt} + x_i = g(b_i + \sum_j w_{ij} x_j)$$

- x_i denotes the expression level of unit i.
- The model is formally equivalent to a continuous-time recurrent neural network.
- The squashing function allows more complex interactions than in a linear network.
- See also
  www.me.chalmers.se/~mwahde/AdaptiveSystems/Publications/WahdeHertzBioSystems2000.pdf

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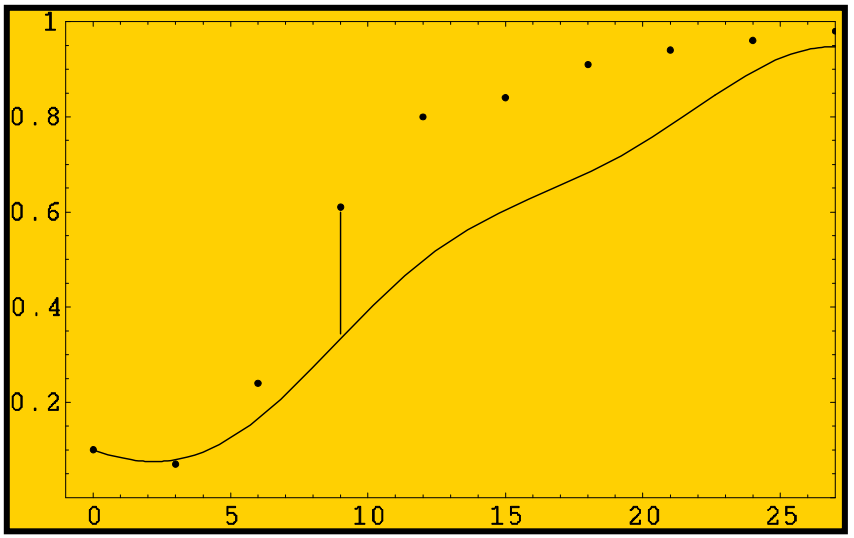
- Fitness measure

$$f = \frac{1}{1 + \frac{1}{K}\sum_k \delta_k^2}$$

δ measures the difference between the measured data and the output from the model.



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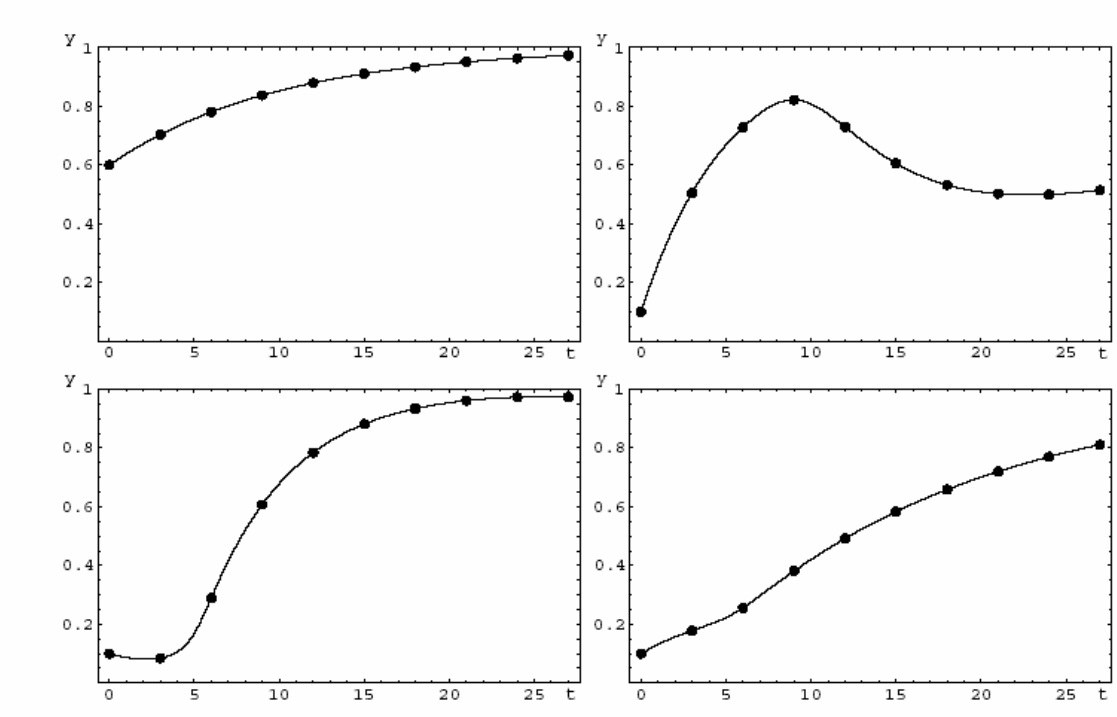

$$\tau_i \dot{y}_i(t) + y_i(t) = \sigma\left(b_i + \sum_{j=1}^{n} w_{ij} y_j(t)\right),$$

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Results

- Artificial sample network with N=4.
- ++ = strongly positive weight, -- = strongly negative weight etc.
- Different time series correspond to different initial conditions.

	w_{ij}				τ_i
1 time series (P=1):	0	0	0	0	11
	++	−−	0	0	7.5
	0	0	0	0	9.1
	0	0	0	−−	16
5 time series (P=5):	++	−−	0	0	11
	++	−−	0	0	6.3
	0	−−	++	+	6.3
	0	0	++	−−	5.8
Actual network:	++	−−	0	0	10
	++	−−	0	0	5
	0	−	++	0	5
	0	0	+	−−	5

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- Real data set: rat spinal cord and hippocampus development (Wen et al.):

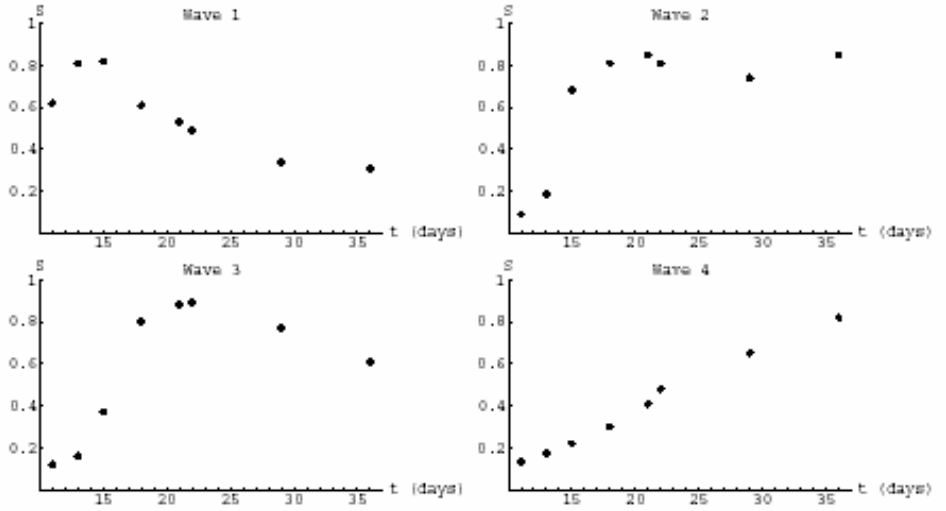
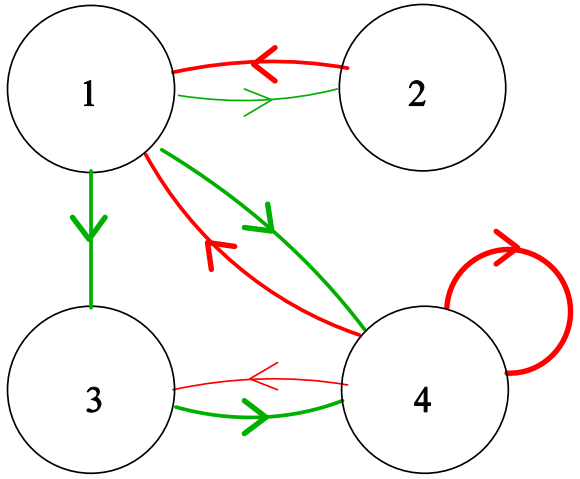


Figure 2: Waves of expression for the spinal cord data.

- Nodes represent groups (clusters) of genes.

- Excitatory connections are shown in green, inhibitory connections in red.



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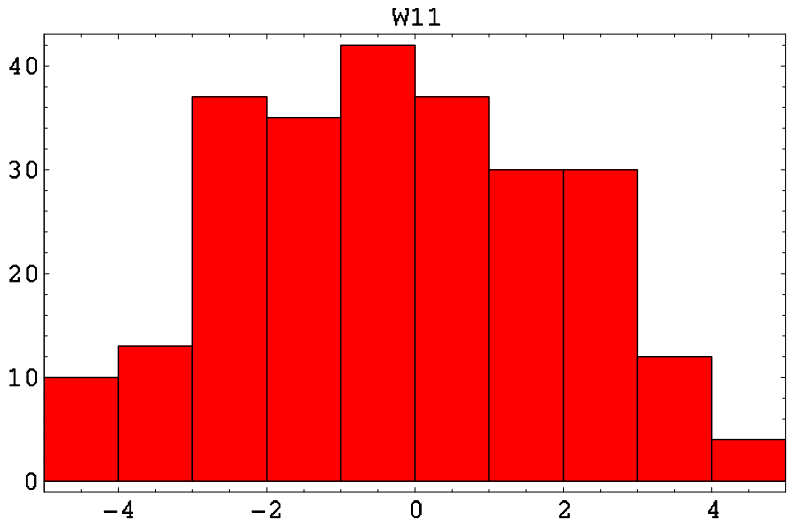
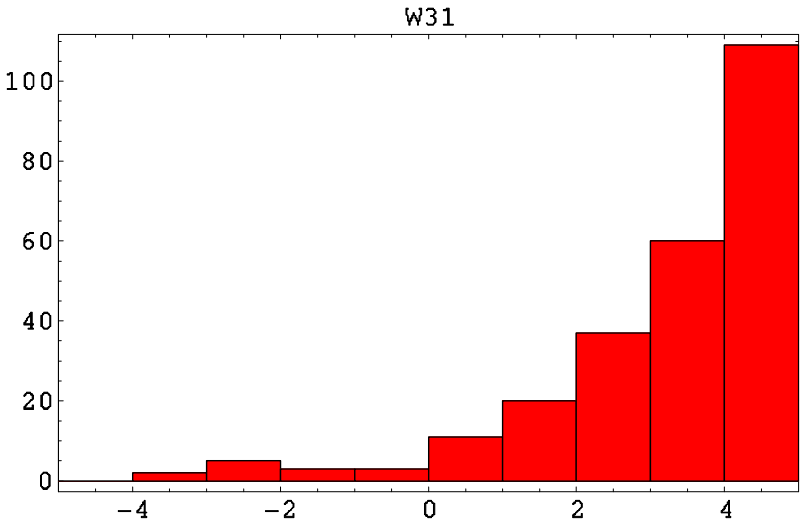
- There is a degree of uncertainty in the weights obtained. Thus, the GA is applied many times (~100), so that histograms of the weight distributions can be found:





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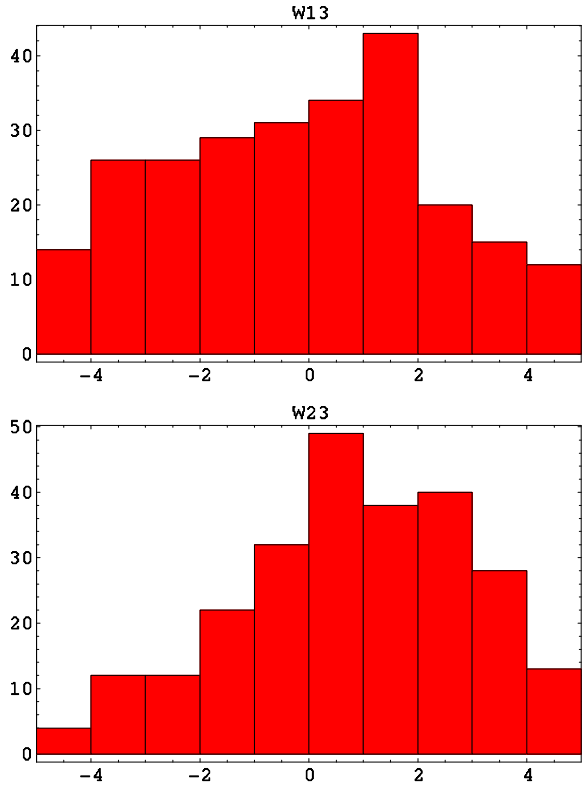
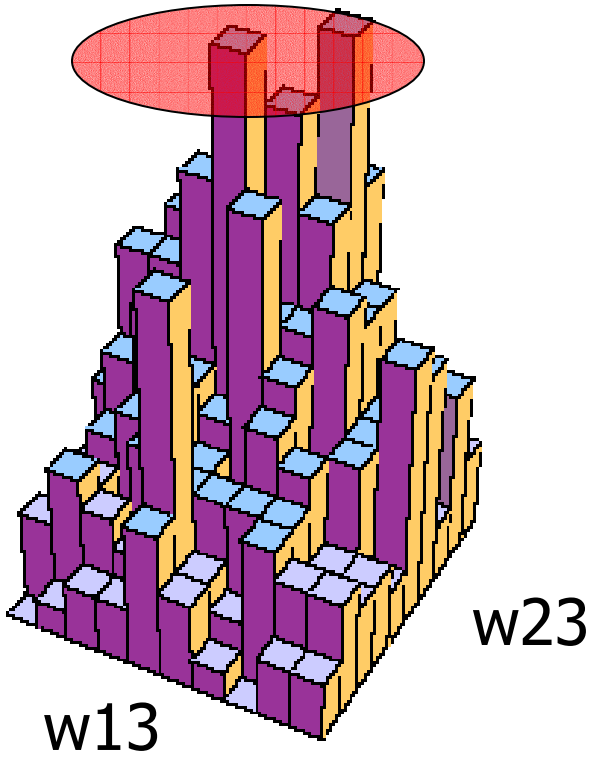
For badly determined weights, examine higher-order histograms:





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Data classification

General reference:

www.me.chalmers.se/~mwahde/AdaptiveSystems/Publications/
WahdeSzallasi2006_Preprint.pdf

Problem formulation: *Determine a combination of features that can accurately assign a given sample to the correct class.*

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Binary classification: Two classes defined: I and II.

Typical data set:

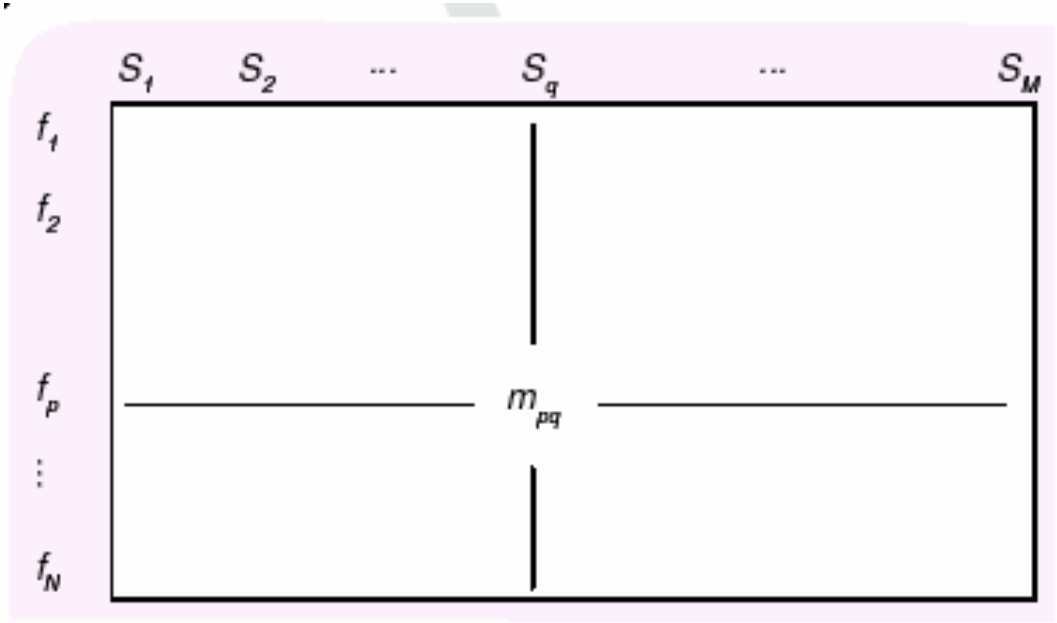

Figure 1. A gene expression data matrix, containing N rows and M columns. Each column represents a sample, and each row represents the expression level of a gene across the samples.

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Typical applications:

- Credit risk applications

Should a given person be given a loan?

Typical features: salary, marital status, wealth, previous behavior, criminal record

- Medical applications

What features are indicative of a given disease (e.g. diabetes, cancer)

Typical features: age, weight, smoking habits, genetic factors (or even gene expression data, if available).

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Methods:

Linear discriminant analysis, principal component analysis, neural networks, various clustering methods etc. etc.

Common problem: overfitting!

Possible solution: Try to find classifiers using a minimal number of features.

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Classifier structure:

$$h(g_{i_1}, g_{i_2}, \ldots, g_{i_n}) > 0,$$

$$h(g_{i_1}, g_{i_2}, \ldots, g_{i_n}) \approx \beta + \sum_{j=1}^{n} \alpha_j g_{i_j} + O(g_{i_j}^2).$$

$$\beta + \sum_{j=1}^{n} \alpha_j g_{i_j} > 0,$$

Linear, single-threshold classifier

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Determine features (and classifier structure) using an EA

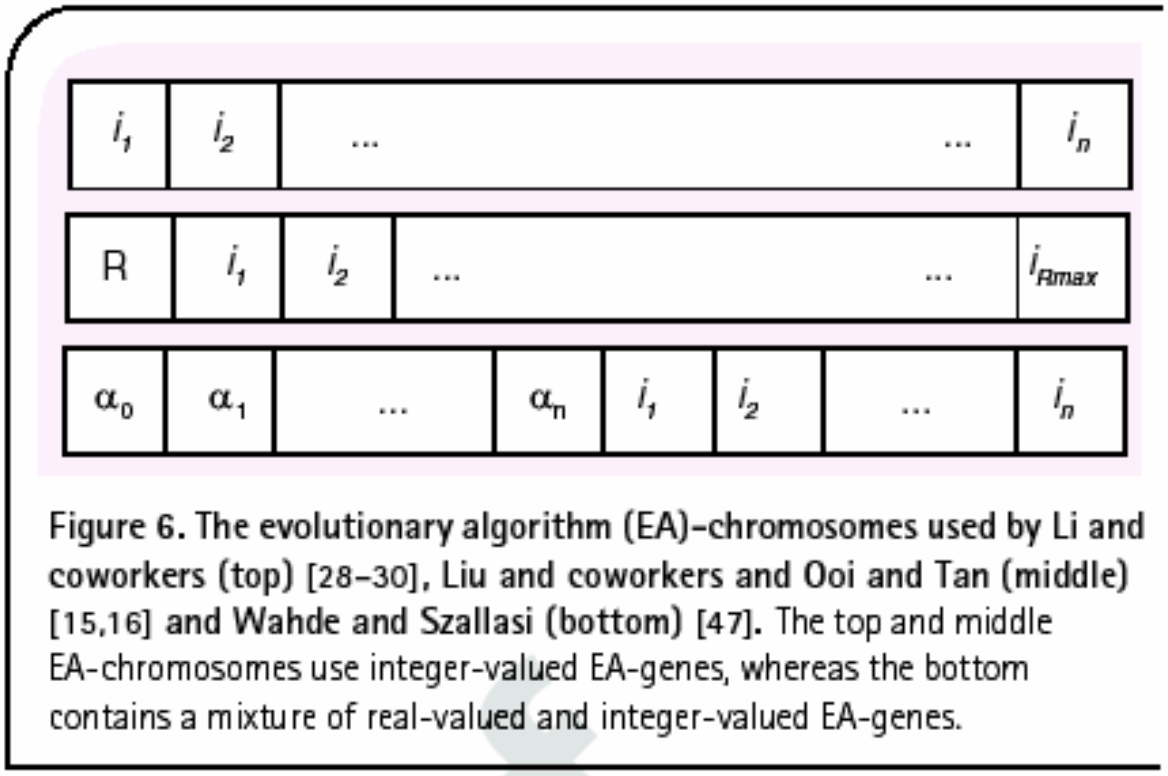

Figure 6. The evolutionary algorithm (EA)–chromosomes used by Li and coworkers (top) [28–30], Liu and coworkers and Ooi and Tan (middle) [15,16] and Wahde and Szallasi (bottom) [47]. The top and middle EA-chromosomes use integer-valued EA-genes, whereas the bottom contains a mixture of real-valued and integer-valued EA-genes.

Application:

Prediction of breast-cancer survival

Class I: Survival > 5 years
Class II: Survival < 5 years

Data set: 97 samples, 5,277 features (gene expression data)

Training set: 78 samples
Validation set: 19 samples

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First step: Consider the ability of *single* genes to classify the data set:

Gene ID	# correct
4730	61
50	61
62	60
1	60

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Second step: Evolve multi-gene classifiers:

Fitness measures:

$$f_1(M_c) = \frac{M_c}{M},$$

$$f_2(M_c, \overline{d}_c) = \frac{M_c}{M} + \epsilon_1 \overline{d}_c,$$

Average distance to separating hyperplane

$$f_3(M_c, M_{c,r}, \overline{d_{c,r}}) = \frac{M_c}{M} - \epsilon_2 \left(M_{c,r} - \epsilon_3 \overline{d_{c,r}}\right),$$

Samples near the separating hyperplane

Average distance to separating hyperplane of those samples

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Results:

n	M_c^T	% correct	n	M_c^T	% correct
2	68	87.2%	6	74	94.9%
3	71	91.0%	7	76	97.4%
4	74	94.9%	≥ 8	≤ 76	97.4%
5	74	94.9%			

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Results:

n	Classifier	Result
2	$-0.5090g_{1} + 0.8607g_{689} > 0.0779$	87.2%
3	$-0.5248g_{13} - 0.6366g_{1278} + 0.5651g_{3353} > -0.0129$	91.0%
3	$-0.4355g_{1} + 0.8270g_{689} - 0.3555g_{4148} > 0.0894$	91.0%
3	$-0.4283g_{1} + 0.6286g_{61} - 0.6492g_{5247} > 0.1275$	91.0%
4	$-0.3153g_{1} - 0.3381g_{2} + 0.6517g_{689} - 0.6013g_{4723} > 0.0873$	94.9%
5	$-0.2960g_{13} - 0.4546g_{42} - 0.4900g_{46} + 0.4584g_{62} - 0.5054g_{4401} > 0.1189$	94.9%
6	$-0.4688g_{1} + 0.5259g_{50} + 0.4569g_{62} - 0.4816g_{391} - 0.2346g_{819} - 0.0890g_{5247} > 0.2693$	94.9%
6	$-0.3023g_{1} + 0.5954g_{50} + 0.5171g_{62} - 0.2137g_{391} - 0.2811g_{879} - 0.4026g_{1917} > 0.2693$	94.9%
6	$-0.3215g_{1} + 0.5133g_{61} + 0.6458g_{689} - 0.3627g_{4148} - 0.0823g_{4574} - 0.2788g_{5247} > 0.1309$	94.9%
6	$-0.5243g_{1} - 0.4239g_{8} + 0.5188g_{689} + 0.3226g_{1305} + 0.0191g_{2509} + 0.4145g_{5120} > 0.0619$	94.9%
7	$-0.3504g_{1} - 0.1534g_{13} - 0.1107g_{47} + 0.5495g_{61} + 0.5200g_{689} + 0.0959g_{1989} - 0.5097g_{5247} > 0.1007$	97.4%

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Results:

M_c^{T}	$M_{c,0.02}^{\mathrm{T}}$	$\overline{d}_c^{T}$	M_c^{V}	$M_{c,0.02}^{\mathrm{V}}$	$\overline{d}_c^{V}$
71	6	0.1629	13	4	0.1563
71	6	0.2208	13	1	0.2018
71	4	0.2724	15	1	0.2884
74	7	0.1986	14	3	0.1507
74	6	0.2430	13	2	0.2641
74	5	0.3264	12	2	0.2340
74	3	0.2527	13	1	0.2091
74	4	0.2361	16	2	0.2011
74	4	0.2931	13	3	0.2686
76	5	0.2611	17	0	0.2249

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