

# Local and “Personalised” Modeling and Knowledge Discovery in Bioinformatics: The Evolving Neuro-Fuzzy Approach

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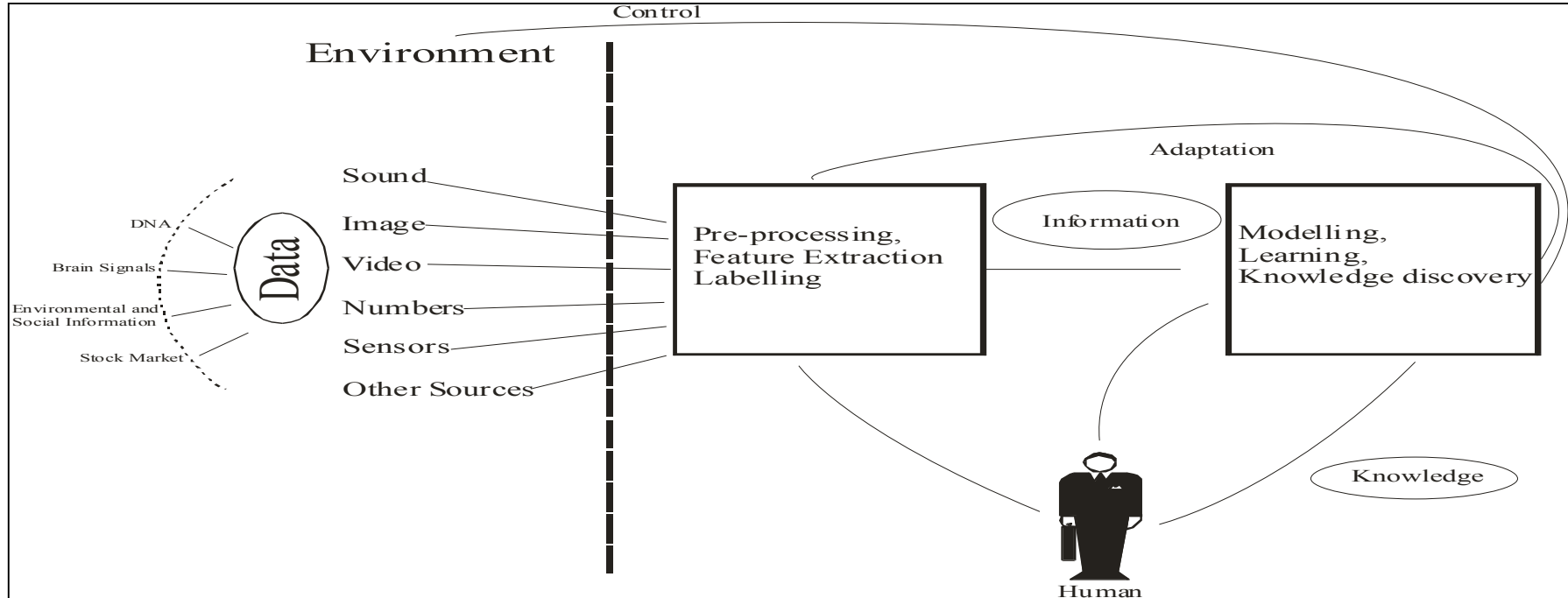
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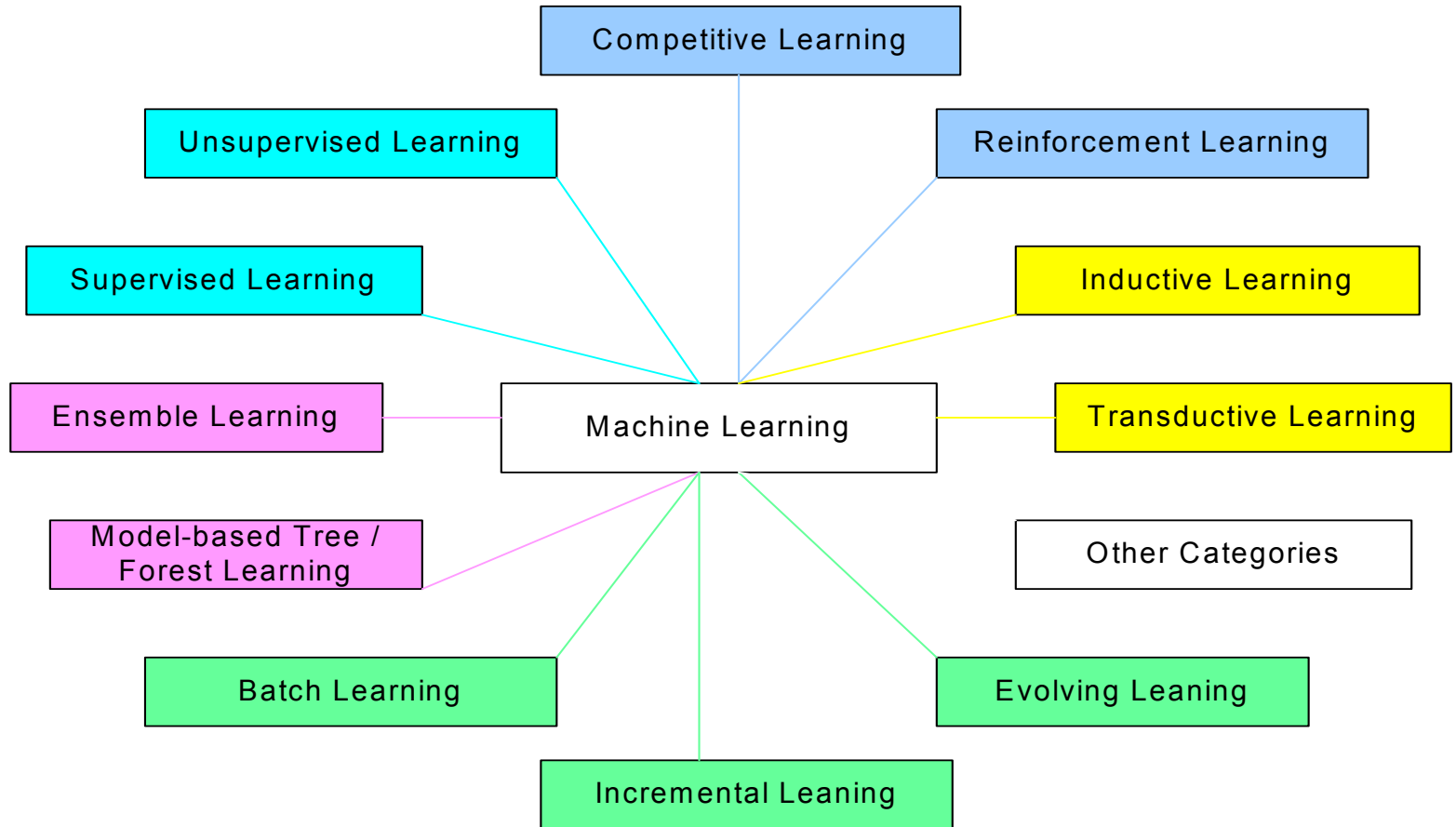
and Pacific Edge Biotechnology Ltd ([www.peblnz.com](http://www.peblnz.com))

# 1. Global, local and personalised modelling: Problem definition



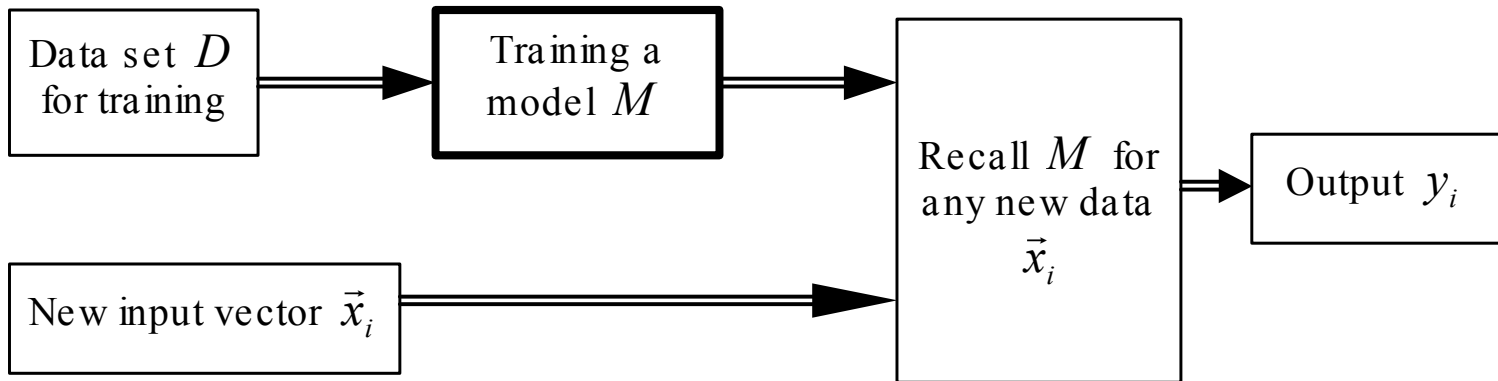
- Adaptive modelling of complex dynamic processes
- Incremental learning and improvement
- Extracting relationship rules, knowledge
- Facilitating discoveries across disciplines – Bioinformatics, Neuroinformatics, Health informatics, Industrial Informatics, Business, Environment

# Machine learning algorithms



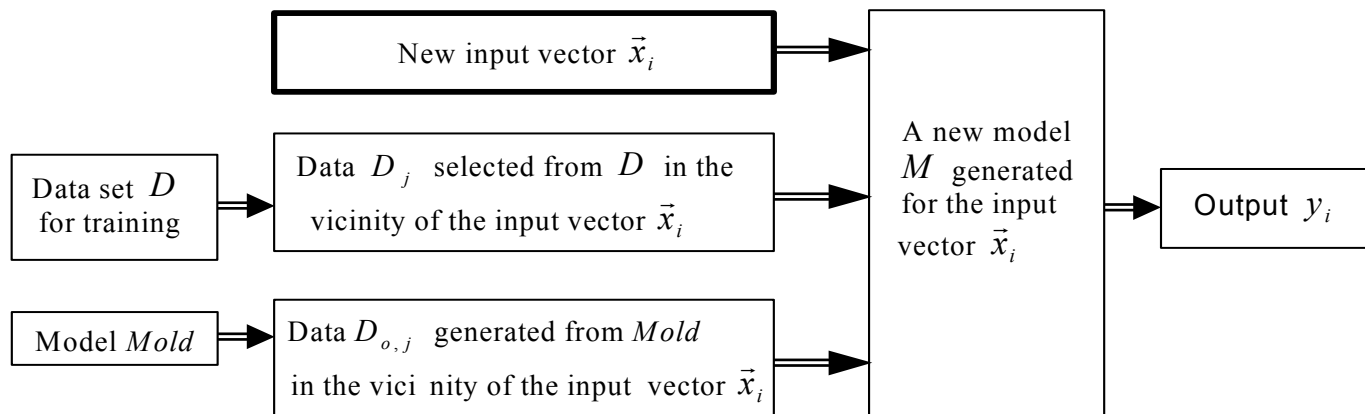
## Inductive learning framework

- Inductive Learning extrapolates from a given set of examples so that we can make accurate predictions about future examples.
- Given a **training set** of positive and negative examples of a concept, construct a description that will accurately classify whether future examples are positive or negative. That is, learn some good estimate of function  $f$  given a training set  $\{(\mathbf{x}_1, \mathbf{y}_1), (\mathbf{x}_2, \mathbf{y}_2), \dots, (\mathbf{x}_n, \mathbf{y}_n)\}$  where each  $\mathbf{y}_i$  is either + (positive) or - (negative).



## Transductive learning framework

- Transductive learning is concerned with the estimation of a function in a single point of the space only. For every new input vector  $x_i$ , a new model  $M_i$  is dynamically created from these samples to approximate the function in the locality of point  $x_i$
- Compared with inductive learning, transductive learning specially takes both labeled data and unlabeled data into account.
- Neuro-fuzzy method for transductive learning (TWNFI, IEEE TrFS,2004)



# Global Models - Statistical Methods

- Linear Discriminant Analysis (LDA)

- Find a linear subspace that maximises class separability among the feature vector projections in the data space.

- Popular separability criterion is ratio of between-class scatter and within-class scatter
- LDA seeks directions efficient for discrimination

- Regression analysis



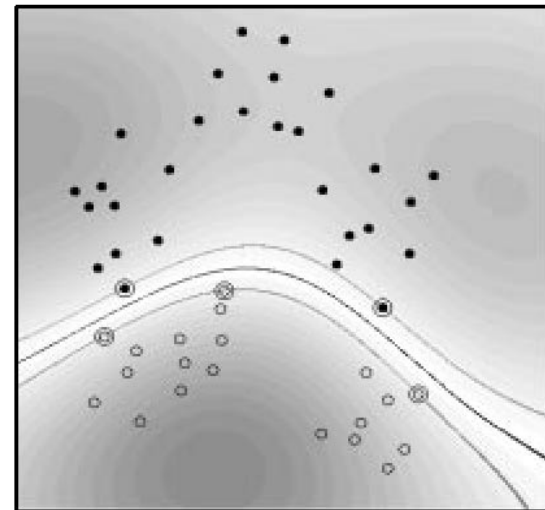
# Support Vector Machines

- The idea of support vector machine is to map the training data into higher dimensional feature space via kernel computation, and constructing a separating hyperplane with maximum margin there.
- The type of the kernel function defines the type of the model: global, or local.
- These kernel functions could be:
  - Polynomial functions

- Radial basis:  $K(x_i, x_j) = (x_i \cdot x_j + 1)^d$

- Line:  $K(x_i, x_j) = \exp\left(\frac{\|x_i - x_j\|^2}{2\sigma^2}\right)$

$$K(x_i, x_j) = x_i \cdot x_j$$



Example of a SVM hyperplane

# NeuCom: A software environment for data analysis, modeling and knowledge discovery

Data analyses, model creation, and knowledge discovery

Feature extraction (statistical, PCA, clustering, SNR, ...)

Model creation, model validation for classification, prediction, optimisation, control

Rule extraction

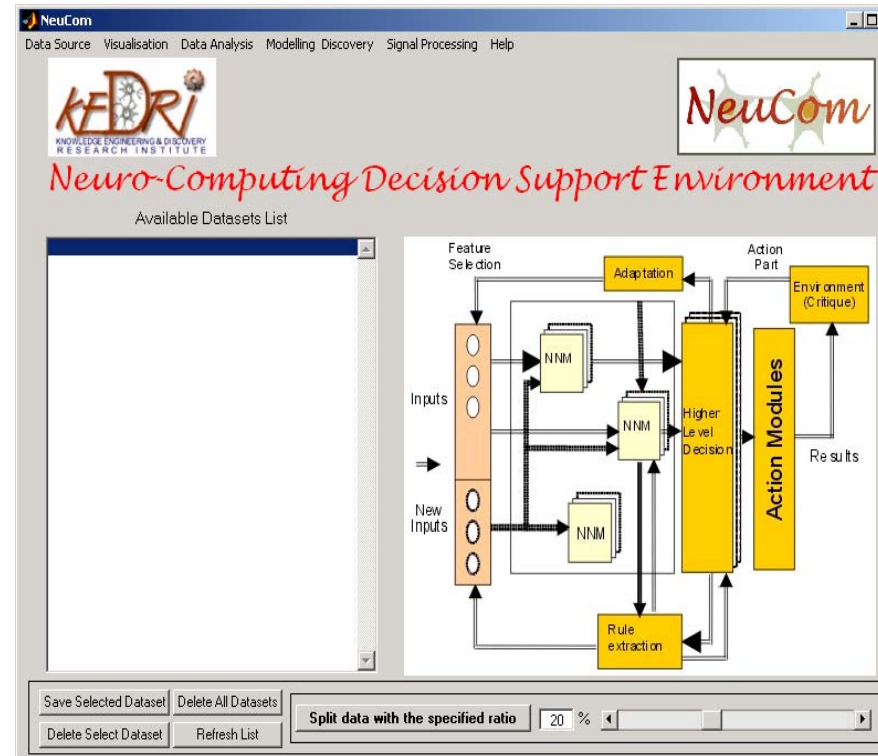
Module and data integration

Case study data and problems

Free student version, limited

Full version (unlimited) – license available for approx. 1,600Euro

[www.theneucom.com](http://www.theneucom.com)

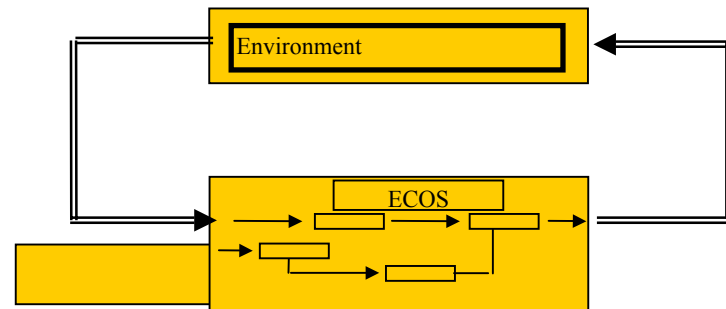




## 2. Local Learning in ECOS

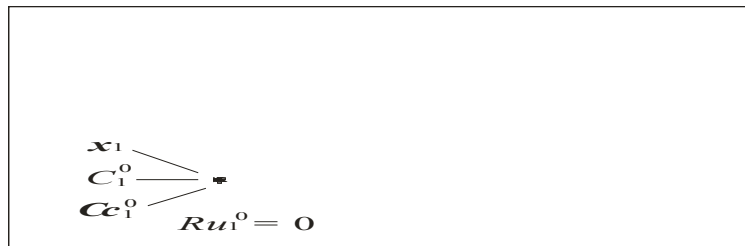
- Creating multiple local models in the problem space, all of them covering the whole space through inductive learning.
- Examples:
  - Local regressions
  - ECOS - modular connectionist-based systems that evolve their structure and functionality in a continuous, self-organised, on-line, adaptive, interactive way from incoming information; they can process both data and knowledge in a supervised and/or unsupervised way.
- N. Kasabov, *Evolving connectionist systems – methods and applications in bio-informatics, brain study and intelligent machine*, Springer Verlag, 2002

*‘Throw the “chemicals” and let the system grow’ Prof. Walter Freeman, UC at Berkeley.*

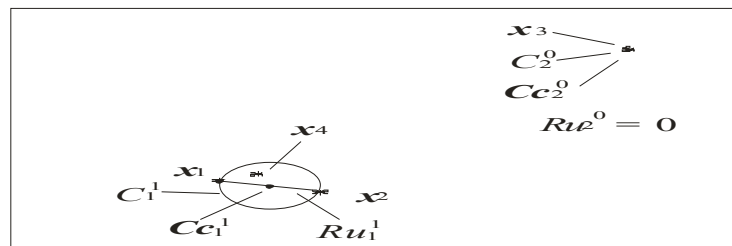


# Local learning based on clustering of input (or input-output) vectors and learning local models

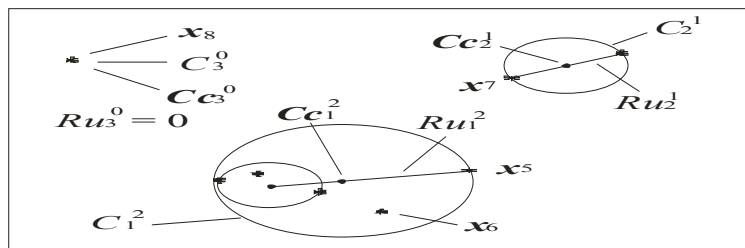
(a)



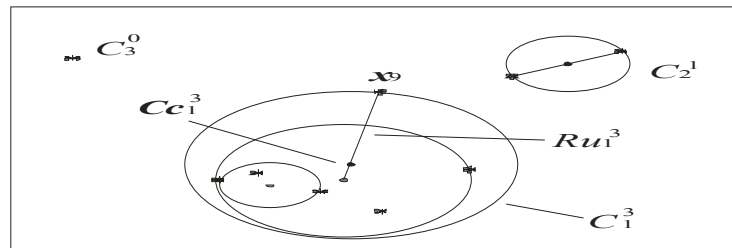
(b)



(c)



(d)



\*  $x_i$ : sample

•  $Ce_j^k$ : cluster centre



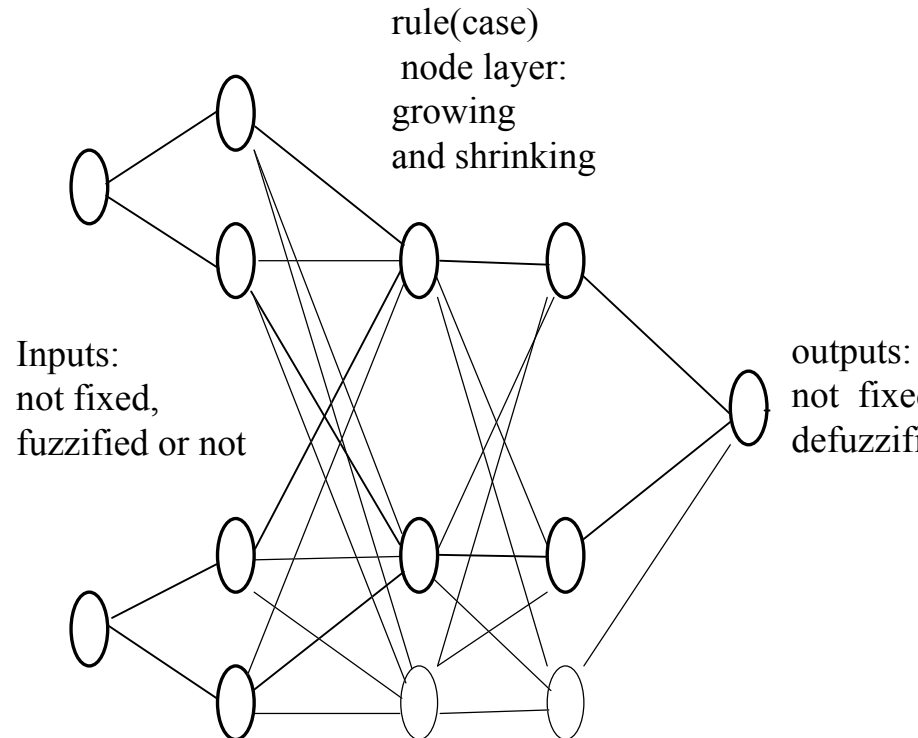
$C_j^k$ : cluster

$Ru_j^k$ : cluster radius

*An evolving clustering process using ECM with consecutive examples  $x_1$  to  $x_9$  in a 2D space (Kasabov and Song, DENFIS, IEEE Tr FS, 2002)*

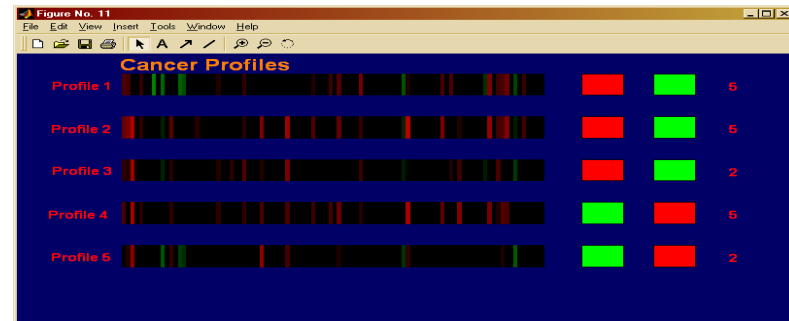
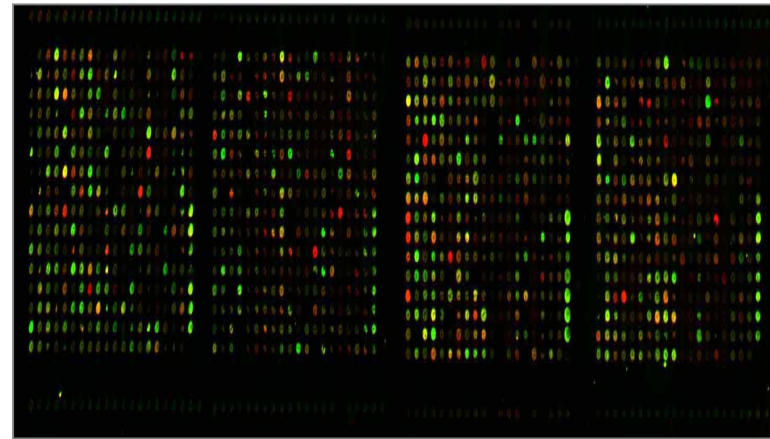
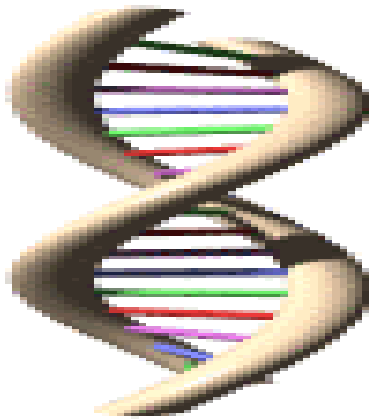
# Evolving Fuzzy Neural Network (EFuNN)

- Learning is based on clustering in the input space and a function estimation for this cluster
- Prototype rules represent the clusters and the functions associated with them
- Different types of rules: e.g. – Zadeh-Mamdani, or Takagi-Sugeno
- The system grows and shrinks in a continuous way
- Feed-forward and feedback connections (not shown)
- Fuzzy concepts may be used
- Not limited in number and types of inputs, outputs, nodes, connections
- On-line/off line training
- *ECF – evolving classifier function – a partial case of EFuNN – no output MF*
- N. Kasabov, IEEE Tr SMC, 2001,



# Gene Expression Data Analysis, Modelling and Profiling

- Problems:
  - large data bases;
  - data always being added and modified;
  - different sources of information
- Local models are suitable – each cluster is represented as a [rule = profile]
- Applications for markers and drug discoveries
- PEBL  
([www.peblnz.com](http://www.peblnz.com))



# SIFTWARE – A software systems for gene expression data analysis, modelling and profiling

(License available from PEBL, [www.peblnz.com](http://www.peblnz.com))

Case example: DLBCL outcome prediction, data from: M. Ship et al, Nature Medicine, vol.8, n.1, January 2002, 68-74

**Siftware**  
Data Source Visualisation Data Analysis Modelling Discovery Help

**KEDRI**  
KNOWLEDGE ENGINEERING & DISCOVERY  
RESEARCH INSTITUTE

## Gene Expression Profiling Siftware Environment

Available Datasets List

- genedata\_100var.txt
- genedata\_40var.txt
- genedata\_30var.txt

Available Labels List

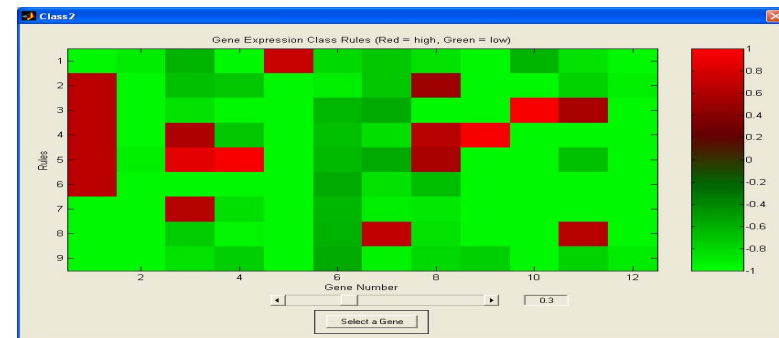
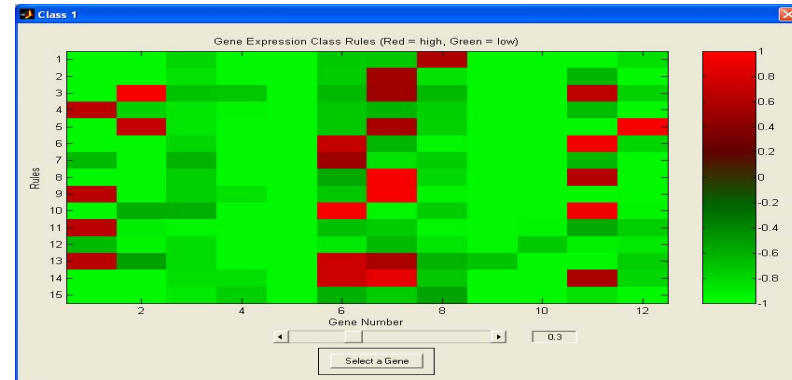
- geneLabels100.mat
- geneLabels40.mat

Save Selected Dataset Delete All Datasets

Delete Selected Dataset Refresh List

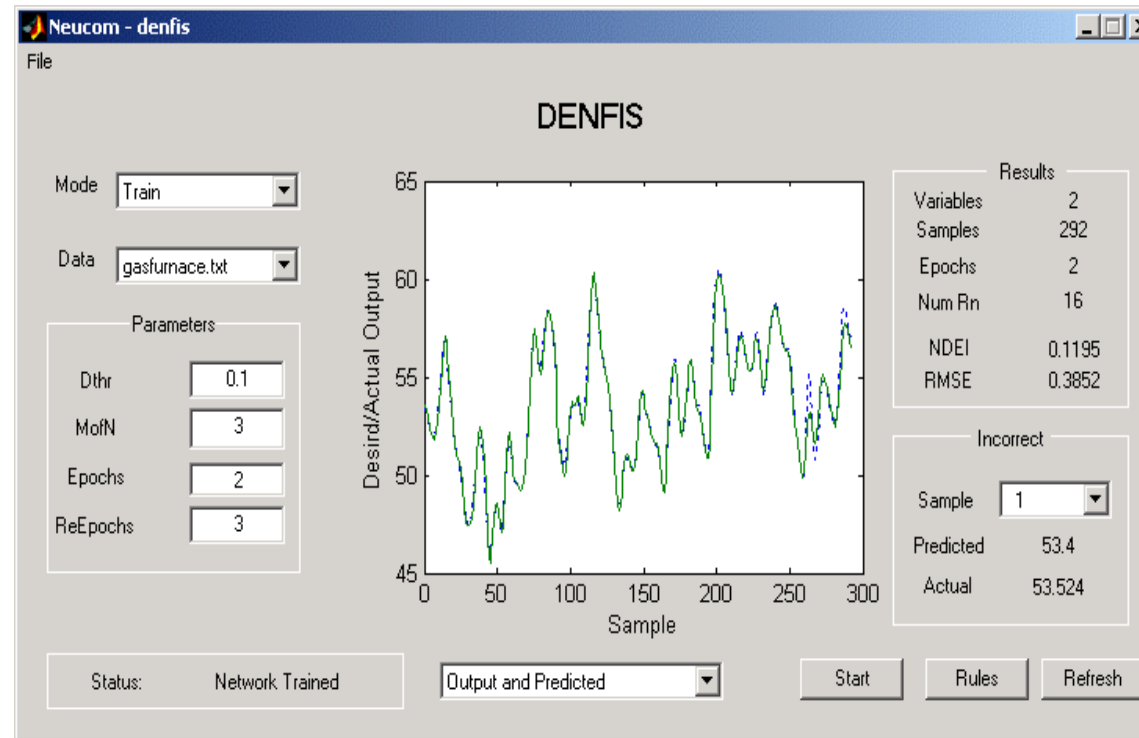
Split data with the specified ratio 20 %

Diagram illustrating the workflow: DNA → Neural Network → Gene Expression Profiling (Heatmap).



# Dynamic Evolving Neuro-Fuzzy Systems (DENFIS)

- Modeling, prediction and knowledge discovery from dynamic time series
- Cluster –based local modelling where each cluster evolves a model (a function) of the same type
- Kasabov, N., and Song, Q., DENFIS: Dynamic Evolving Neural-Fuzzy Inference System and its Application for Time Series Prediction, IEEE Transactions on Fuzzy Systems, 2002, April



# Local, incremental learning of cluster-based fuzzy rules in DENFIS

- Input vector:  $\mathbf{x} = [x_1, x_2, \dots, x_q]$
- Result of inference:

$$y = \frac{\sum_{i=1,m} [\omega_i f_i(x_1, x_2, \dots, x_q)]}{\sum_{i=1,m} \omega_i}$$

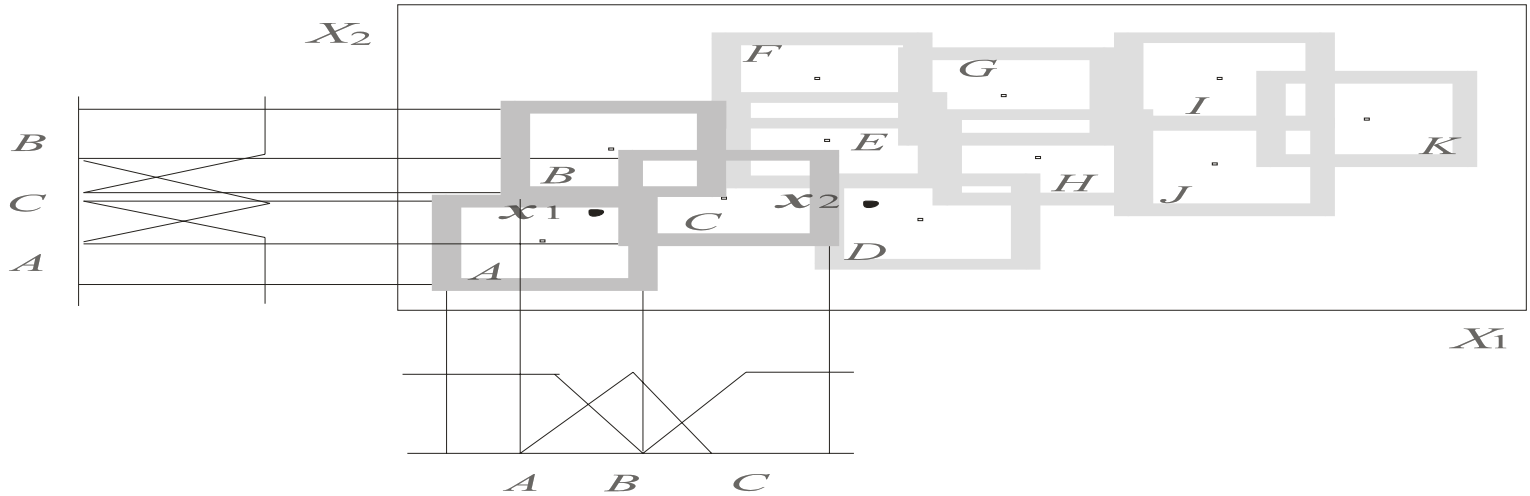
- A partial case is using linear regression functions:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_q x_q.$$

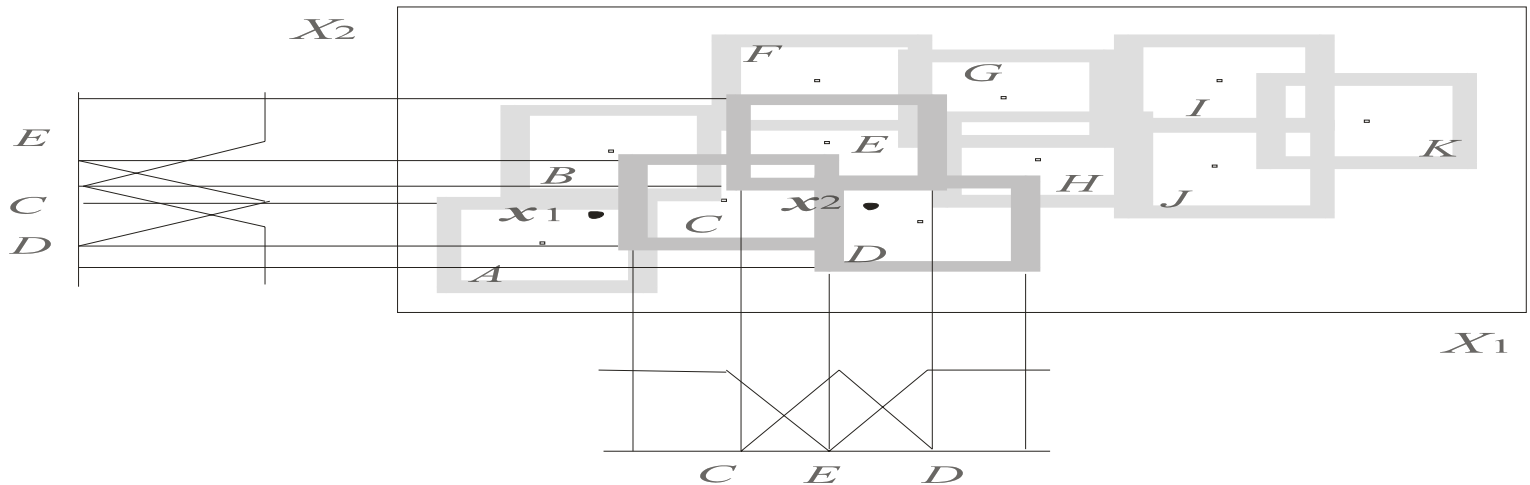
- Fuzzy rules: IF  $\mathbf{x}$  is in cluster  $C_j$  THEN  $y_j = f_j(\mathbf{x})$
- Incremental learning of the function coefficients through least square error

# Learning and Inference in DENFIS

(a) Fuzzy rule group 1 for a DENFIS



(b) Fuzzy rule group 2 for a DENFIS





## The case study on GFR prediction for renal medical decision support

A real data set from a medical institution is used here for experimental analysis. The data set has 447 samples, collected at hospitals in New Zealand and Australia. Each of the records includes six variables (inputs): age, gender, serum creatinine, serum albumin, race and blood urea nitrogen concentrations, and one output - the glomerular filtration rate value (GFR). All experimental results reported here are based on 10-cross validation experiments with the same model and parameters and the results are averaged. In each experiment 70% of the whole data set is randomly selected as training data and another 30% as testing data.

# Local, adaptive GFR Renal Function Evaluation System based on DENFIS: GFR-DENFIS

(Marshal, Song, Ma, McDonell and Kasabov, Kidney International, May 2005)

**GFR-ECOS DEMO, Nov. 2003, KEDRI, AUT, NZ**

File Function Help

## GFR-ECOS: Evolving Medical Decision Support System

1. Age    2. Sex    3. Screat    4. Surea    5. Race    6. Salb    ECOS    MDRD    CurrentVec    InputVector       

InputVectorPattern    Input PCA Space (1st & 2nd principal components)    Fuzzy Rule 12 Info

1 2 3 4 5 6  
RnPattern

RnPattern

RnPattern

RnPattern

RnPattern

Circle: Fuzzy Rule Node    Triangle: Input    Label

1. Age    2. Sex    3. Screat    4. Surea    5. Race    6. Salb

RuleNodePattern

Fuzzy Rule 12

If    Age is about 21.3  
    &Sex is Female  
    &Screat is about 0.25  
    &Surea is about 15.4  
    &Race is White  
    &Salb is about 43

Then GFR = 0.372  
    x Age<sup>(-0.0791)</sup>  
    x 2<sup>(0.0656)</sup>  
    x Screat<sup>(-0.438)</sup>  
    x Surea<sup>(-0.277)</sup>  
    x 1  
    x Salb<sup>(0.0194)</sup>

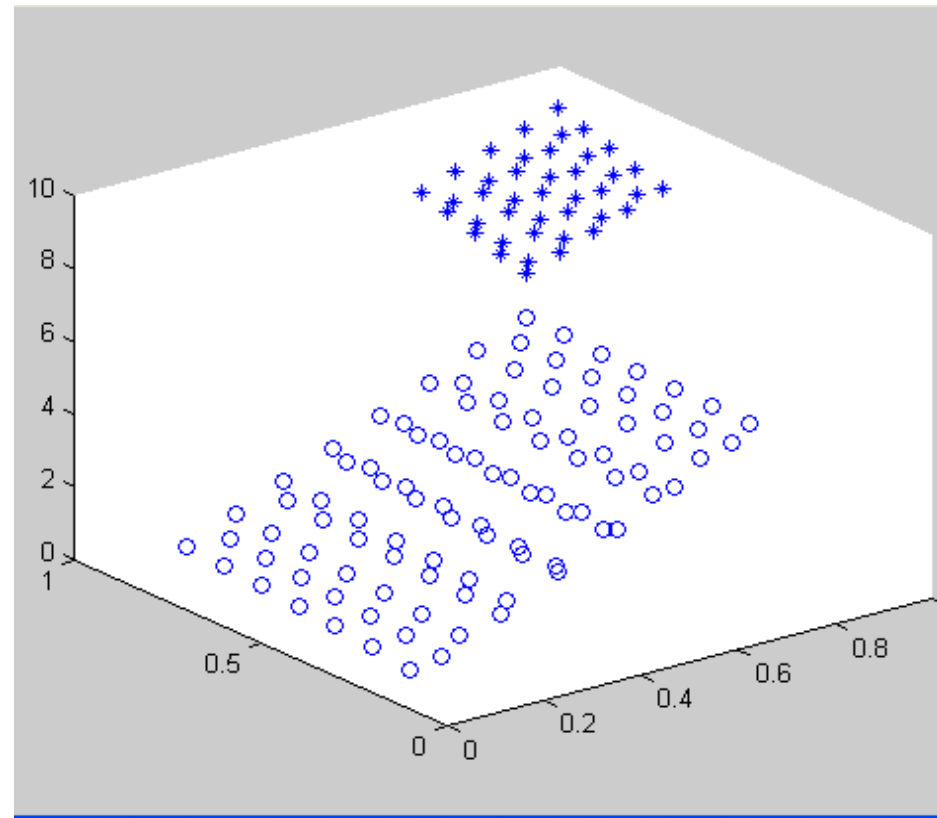
ECOS System: ExtRRes1.mat    NumSystemRules: 21    NumEngineRules: 4    12

### 3. Data and model integration through local learning and modelling

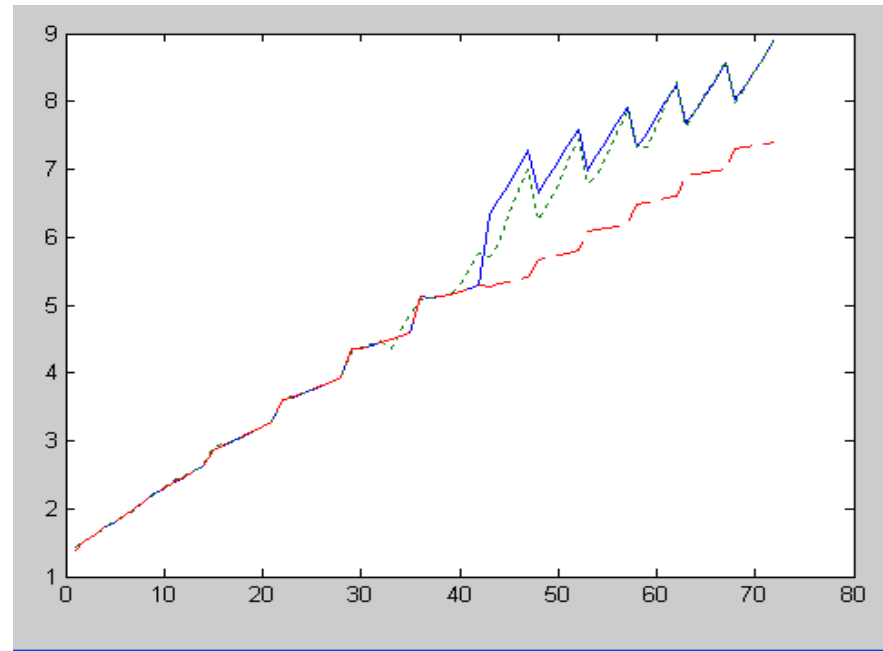
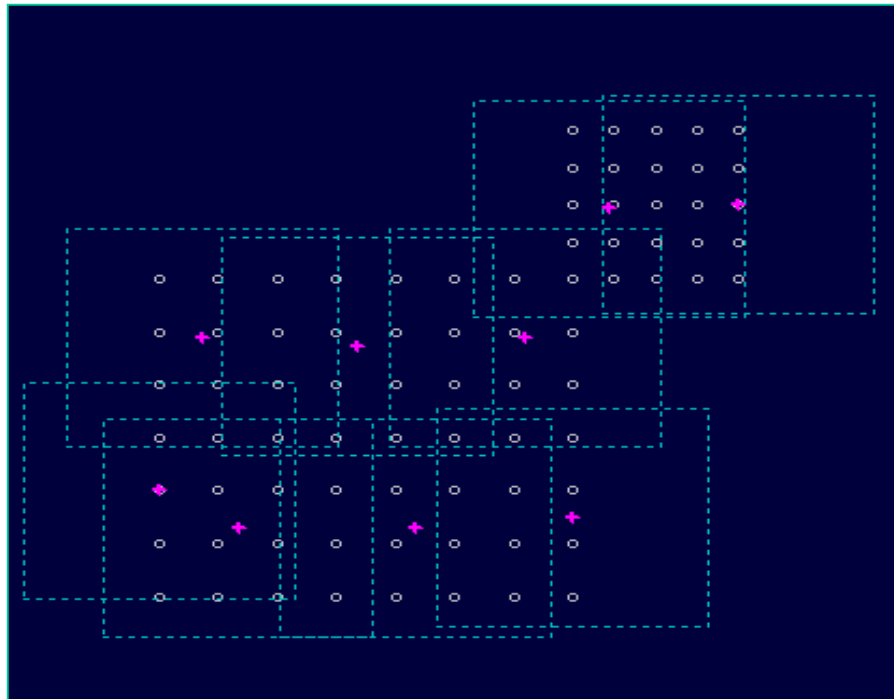
A case study of a model  $M$  (formula) and a data set  $D$  of new data integration through an ECOS.

- **Model  $M$ :** A 3D plot of data  $D_0$  (data samples denoted as “o”) generated from a model  $M$  (formula)  $y = 5.1x_1 + 0.345x_1^2 - 0.83x_1 \log_{10} x_2 + 0.45x_2 + 0.57 \exp(x_2^{0.2})$  in the sub-space of the problem space defined by  $x_1$  and  $x_2$  both having values between 0 and 0.7, and

- New data  $D$  (samples denoted as “\*”) defined by  $x_1$  and  $x_2$  having values between 0.7 and 1;



After integration through incremental learning in ECOS, the system performs better on the new data



# Prototype rules extracted from DENFIS and EFuNN after model and data integration

## Takagi-Sugeno fuzzy rules (DENFIS):

- Rule 1: IF  $x_1$  is (-0.05, 0.05, 0.14) and  $x_2$  is (0.15,0.25,0.35) THEN  $y = 0.01 + 0.7x_1 + 0.12x_2$
- Rule 2: IF  $x_1$  is (0.02, 0.11, 0.21) and  $x_2$  is (0.45,0.55, 0.65) THEN  $y = 0.03 + 0.67x_1 + 0.09x_2$
- Rule 3: IF  $x_1$  is (0.07, 0.17, 0.27) and  $x_2$  is (0.08,0.18,0.28) THEN  $y = 0.01 + 0.71x_1 + 0.11x_2$
- Rule 4: IF  $x_1$  is (0.26, 0.36, 0.46) and  $x_2$  is (0.44,0.53,0.63) THEN  $y = 0.03 + 0.68x_1 + 0.07x_2$
- Rule 5: IF  $x_1$  is (0.35, 0.45, 0.55) and  $x_2$  is (0.08,0.18,0.28) THEN  $y = 0.02 + 0.73x_1 + 0.06x_2$
- Rule 6: IF  $x_1$  is (0.52, 0.62, 0.72) and  $x_2$  is (0.45,0.55,0.65) THEN  $y = -0.21 + 0.95x_1 + 0.28x_2$
- Rule 7: IF  $x_1$  is (0.60, 0.69,0.79) and  $x_2$  is (0.10,0.20,0.30) THEN  $y = 0.01 + 0.75x_1 + 0.03x_2$

## New rules:

- Rule 8: IF  $x_1$  is (0.65,0.75,0.85) and  $x_2$  is (0.70,0.80,0.90) THEN  $y = -0.22 + 0.75x_1 + 0.51x_2$
- Rule 9: IF  $x_1$  is (0.86,0.95,1.05) and  $x_2$  is (0.71,0.81,0.91) THEN  $y = 0.03 + 0.59x_1 + 0.37x_2$

## Zhade-Mamdani fuzzy rules (ECF, EFuNN):

Rule 1: IF  $x_1$  is (Low 0.8) and  $x_2$  is (Low 0.8) THEN  $y$  is (Low 0.8), radius  $R_1=0.24$ ;  $N_{1ex}=6$

Rule 2: IF  $x_1$  is (Low 0.8) and  $x_2$  is (Medium 0.7) THEN  $y$  is (Small 0.7),  $R_2=0.26$ ,  $N_{2ex}=9$

Rule 3: IF  $x_1$  is (Medium 0.7) and  $x_2$  is (Medium 0.6) THEN  $y$  is (Medium 0.6),  $R_3=0.17$ ,  $N_{3ex}=17$

Rule 4: IF  $x_1$  is (Medium 0.9) and  $x_2$  is (Medium 0.7) THEN  $y$  is (Medium 0.9),  $R_4=0.08$ ,  $N_{4ex}=10$

Rule 5: IF  $x_1$  is (Medium 0.8) and  $x_2$  is (Low 0.6) THEN  $y$  is (Medium 0.9),  $R_5=0.1$ ,  $N_{5ex}=11$

Rule 6: IF  $x_1$  is (Medium 0.5) and  $x_2$  is (Medium 0.7) THEN  $y$  is (Medium 0.7),  $R_6=0.07$ ,  $N_{6ex}=5$

## New rules:

Rule 7: IF  $x_1$  is (High 0.6) and  $x_2$  is (High 0.7) THEN  $y$  is (High 0.6),  $R_7=0.2$ ,  $N_{7ex}=12$

Rule 8: IF  $x_1$  is (High 0.8) and  $x_2$  is (Medium 0.6) THEN  $y$  is (High 0.6),  $R_8=0.1$ ,  $N_{8ex}=5$

Rule 9: IF  $x_1$  is (High 0.8) and  $x_2$  is (High 0.8) THEN  $y$  is (High 0.8),  $R_9=0.1$ ,  $N_{9ex}=6$

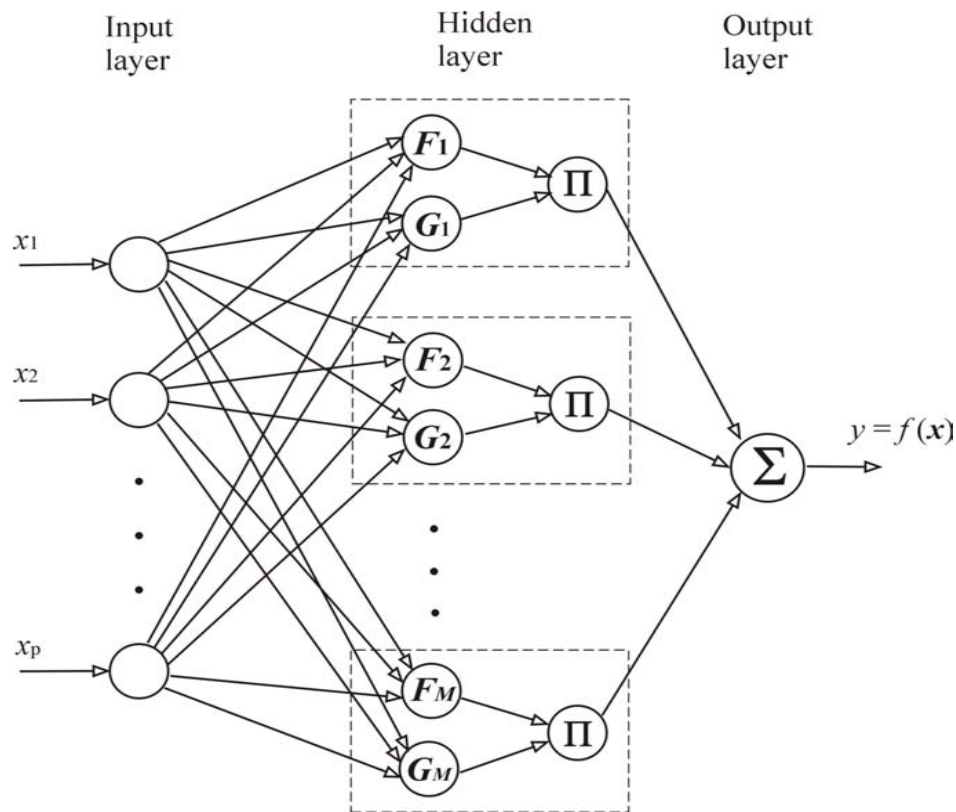
# 4. Integration of regression formulas and kernel methods in a local learning RK-KBNN

(Song, Kasabov, Ma, Marshall, AI in Medicine, December, 2005)

- *Cluster-based local learning, where each cluster has a different shape and a different type of model (function) evolved*
- *A local function  $F$  is selected to approximate data in a local Gaussian kernel*
- $Y(x_i) = G_1(x_i) F_1(x_i) + G_2(x_i) F_2(x_i) + \dots + G_M(x_i) F_M(x_i)$

where:

$$G_l(\mathbf{x}_i) = \alpha_l \prod_{j=1}^P \exp\left[-\frac{(x_{ij} - m_{lj})^2}{2\sigma_{lj}^2}\right]$$

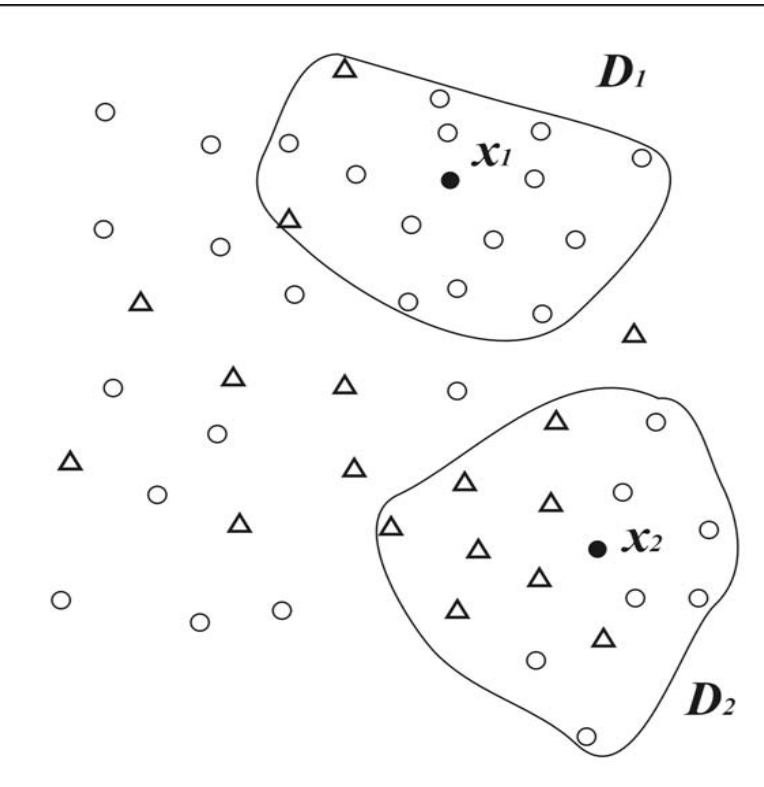


# Global regression formulas versus local RK-KBNN

(A case study on GFR renal function evaluation)

<u>Model</u>	<u>Neurons or rules</u>	<u>RMSE</u>	<u>MAE</u>	<u>Std</u>
Jelliffe71	–	9.13	7.21	12.42
Mawer	–	11.01	8.09	13.34
Jelliffe73	–	7.84	5.90	9.66
Cockcroft-Gault	–	7.97	6.16	10.45
Hull	–	9.50	7.12	12.43
Bjorasson	–	10.29	7.83	12.07
Gates	–	7.49	5.62	9.92
Walser	–	7.36	5.58	10.19
MDRD	–	7.76	5.87	9.27
MLP	12	8.44	5.74	9.06
ANFIS	36	7.43	5.46	8.97
DENFIS	34	7.24	5.27	8.67
RBF	32	7.18	5.39	9.36
<b>Local RK- KBNN</b>	17	6.86	5.07	8.55

## 5. Transductive (“Personalised”) Modelling



- – a new data vector
- – a sample from  $D$
- △ – a sample from  $M$

- A transductive model is created on a sub-set of neighbouring data to each input vector. A new data vector is situated at the centre of such a sub-set (here illustrated with two of them –  $x_1$  and  $x_2$ ), and is surrounded by a fixed number of nearest data samples selected from the training data  $D$  and generated from an existing model  $M$  (*Vapniak*)

- The principle is: “What is good for my neighbors will be good for me”



## Problems of the personalised modelling

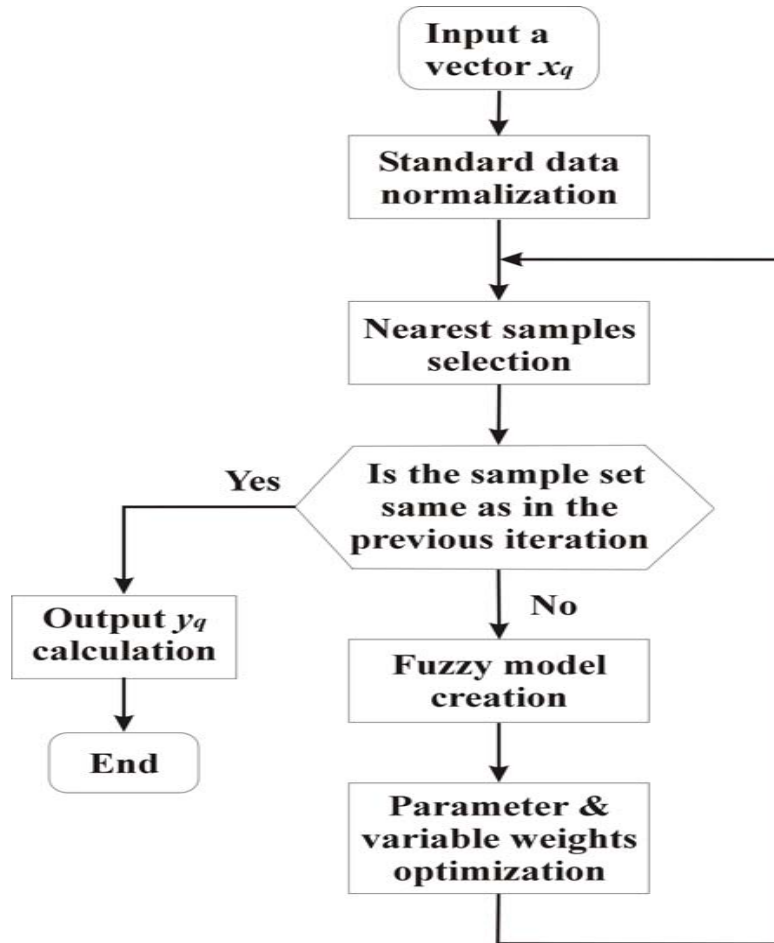
- Defining a correct number of neighbours –  $K$ . Is “the more – the better” principle held here?
- Defining appropriate number of features (variables)
- Defining appropriate “personalised” models, e.g.  $k$ -NN, MLR, MLP, SVM,...
- Defining the distance measure, e.g. Euclidean distance, Hamming distance, Cosine distance, etc.

# Comparative Analysis of Global, Local and Personalised Modelling on the DLBCL Gene Expression Case Study

Model/ InpVar	Induct global MLR	Induct Global SVM	Induct Local ECF	Trans WKNN K=8	Trans WKN K=26 $P_{thr}=0.5$	Trans MLR K=8	Trans MLR k=26	Trans SV M K= 8	Trans SVM k=26	Trans ECF K=8	Trans ECF k=26
1 var: IPI	73 (87,58)	73 (87,58)	46 (0,100)	50 (87,8)	73 (87,56)	50 (87,8)	73 (87,58)	46 (100,0)	73 (87,58)	61 (63,58 )	46 (0,100)
11 var: 11 genes	79 (91,65)	83 (88,78)	86 (88,84)	74 (91,54)	73 (93,47)	66 (66,65)	78 (81,73)	76 (91,58)	78 (91,62)	78 (81,73)	83 (91,73)
12var: IPI+ 11g.	82 (83,81)	86 (90,81)	<b>88</b> <b>(83, 92)</b>	77 (90,62)	76 (100,50)  Pthr=0.4: 77% (73,81)  Pthr=.45, 82% (97,65)	57 (60,54)	79 (80,77)	77 (93,58)	84 (93,73)	75 (83,65)	77 (87,65)

# Transductive Neuro Fuzzy Inference with Weighted Data Normalisation - TWNFI

(Q.Song and N.Kasabov, IEEE Tr FS, December 2005, and Neural Networks, 2005)



After the nearest samples are selected for an input vector  $\mathbf{x}$ , the samples are clustered using ECM.

A fuzzy rule is created/derived for each cluster:

$R_l$ : If  $x_1$  is  $F_{l1}$  and  $x_2$  is  $F_{l2}$  and ...  $x_p$  is  $F_{lp}$ , then  $y$  is  $G_l$ ,

where  $F_{lj}$  and  $G_l$  are fuzzy sets defined by Gaussian type membership functions.

Input variable weights  $w_j$  and fuzzy rule parameters are optimized through the steepest descent algorithm.

$$f(\mathbf{x}_i) = \frac{\sum_{l=1}^M \frac{n_l}{\delta_l^2} \prod_{j=1}^P \alpha_{lj} \exp\left[-\frac{w_j^2(x_{ij} - m_{lj})^2}{2\sigma_{lj}^2}\right]}{\sum_{l=1}^M \frac{1}{\delta_l^2} \prod_{j=1}^P \alpha_{lj} \exp\left[-\frac{w_j^2(x_{ij} - m_{lj})^2}{2\sigma_{lj}^2}\right]}$$

# Comparative analysis of Global, Local and Personalised modelling on the case study of GFR renal function evaluation

Model	Neurons or rules	Testing RMSE	Testing MAE	Weights of input variables					
				Age w1	Sex w2	SCr w3	Surea w4	Race w5	Salb w6
MDRD	—	7.74	5.88	1	1	1	1	1	1
MLP	12	8.44	5.75	1	1	1	1	1	1
ANFIS	36	7.49	5.48	1	1	1	1	1	1
DENFIS	27	7.29	5.29	1	1	1	1	1	1
<b>TNFI</b>	<b>6.8 (average)</b>	<b>7.31</b>	<b>5.30</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>
<b>TWNFI (patent)</b>	<b>6.8 (average)</b>	<b>7.11</b>	<b>5.16</b>	<b>0.89</b>	<b>0.71</b>	<b>1</b>	<b>0.92</b>	<b>0.31</b>	<b>0.56</b>

# A GFR exemplar personalised model of a patient obtained with the use of the TWNFI

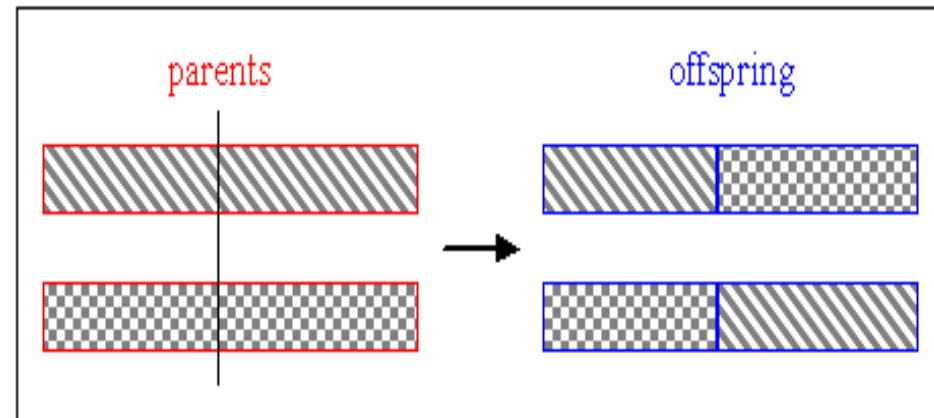
Input variables	Age 58.9	Sex Female	SCr 0.28	Surea 28.4	Face White	Salb 38
Weights of input variables (TWNFI)	0.91	0.73	1	0.82	0.52	0.46
Results	GFR (desired) 18.0		MDRD 14.9		<b>TWRBF 16.6</b>	

## 6. Evolutionary Computation for the Optimisation of Local Models

*Evolutionary computation.*

*Terminology:*

- *Gene*
- *Chromosome*
- *Population*
- *Crossover*
- *Mutation*
- *Fitness function*
- *Selection*

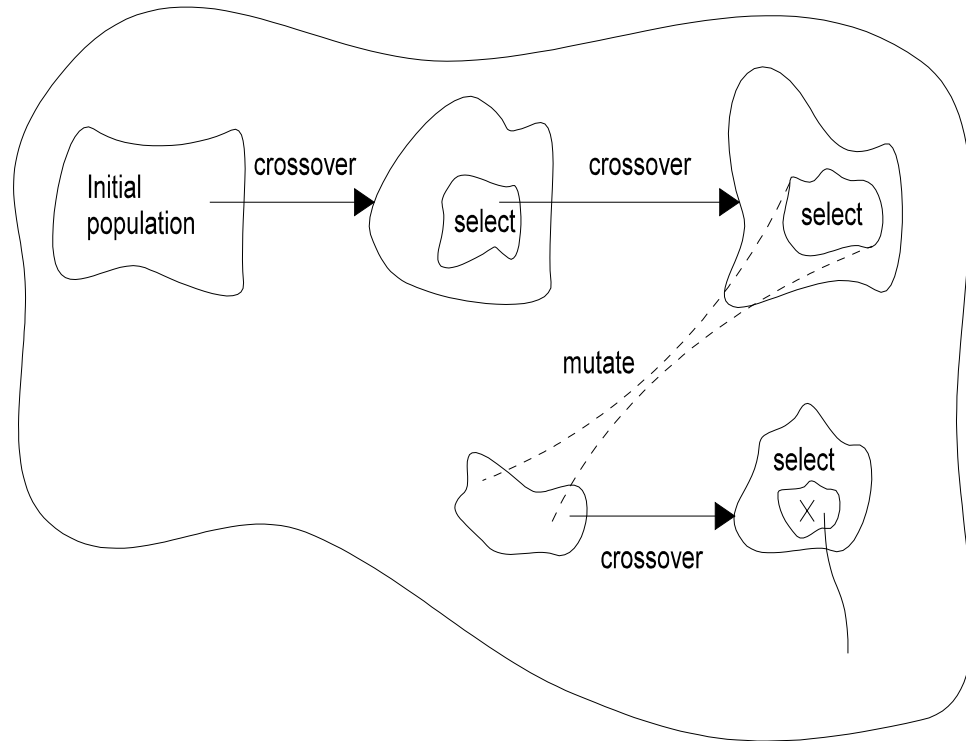


## Genetic Algorithms (GA)

1. Initialize population of possible solutions
2. WHILE a criterion for termination is not reached DO
  - {
  - 2a. Crossover two specimens ("mother and father") and generate new individuals;
  - 2b. Select the most promising ones, according to a fitness function;
  - 2c. Development (if at all);
  - 2d. Possible mutation (rare) }
  - }

# GA

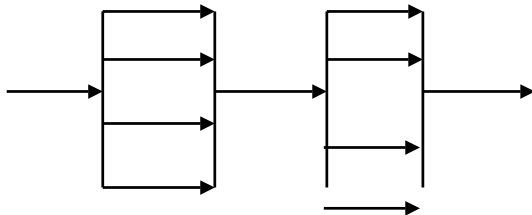
- Many individuals are evolved simultaneously on the same data through a GA method
- A chromosome represents each individual
- Individuals are evaluated and the best one is selected for a further development
- Mutation





# GA feature and parameter optimisation of local ECOS in NeuCom and SIFTWARE

- Optimizing the parameters of the model and the input features
- A chromosome contains as “genes” all model parameters and input features
- Replication of individual ECOS systems and selection of:
  - The best one
  - The best  $m$  averaged, etc



**Data**

Single File: LymphPI11g56s.txt  
% of data for training: 70

Multiple Files: Training Data: LymphPI11g56s.txt  
Testing Data: LymphPI11g56s.txt

**Crossvalidation**

Crossvalidate: 5 Time(s)  
 Split Data Only Once

**Evolve**

Max Field or set as: 0.555  
 Min Field or set as: 0.054  
 m of n or set as: 4  
 Epochs or set as: 7  
 Use GA for Feature Extraction

**GA Parameters**

Generations: 20  
Population: 20  
GA Type: Generational GA  
Crossover Rate =  
Per Gene = 0.02  
Mutation Rate =  
Per Gene = 0.03  
 Maintain Best Solution in Population  
 Allow asexual reproduction  
 Rank based selection  
 Roulette wheel selection  
 Use Fitness Scaling

**Results**

Best Score: 90.622 / 100  
Time Remaining: 0 : 0 : 0  
Remaining Generations: 0  
Individuals: 0  
Genome Length: 28  
Number of Classes: 2  
Number of Features: 9

**Feature Extraction Results**

Status: No Network Loaded

Start

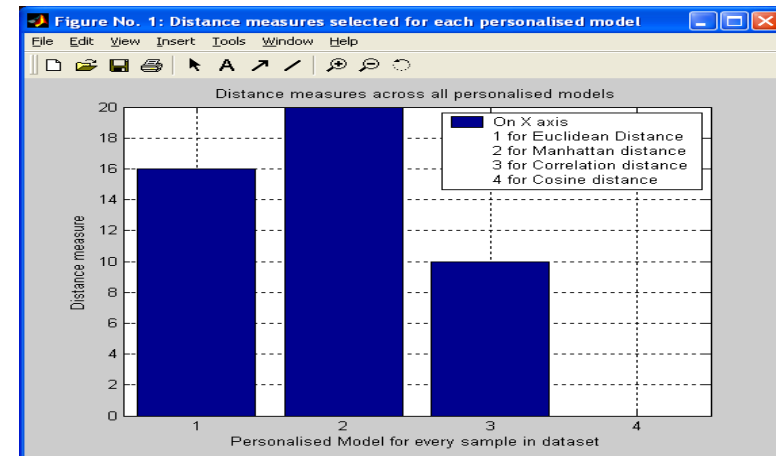
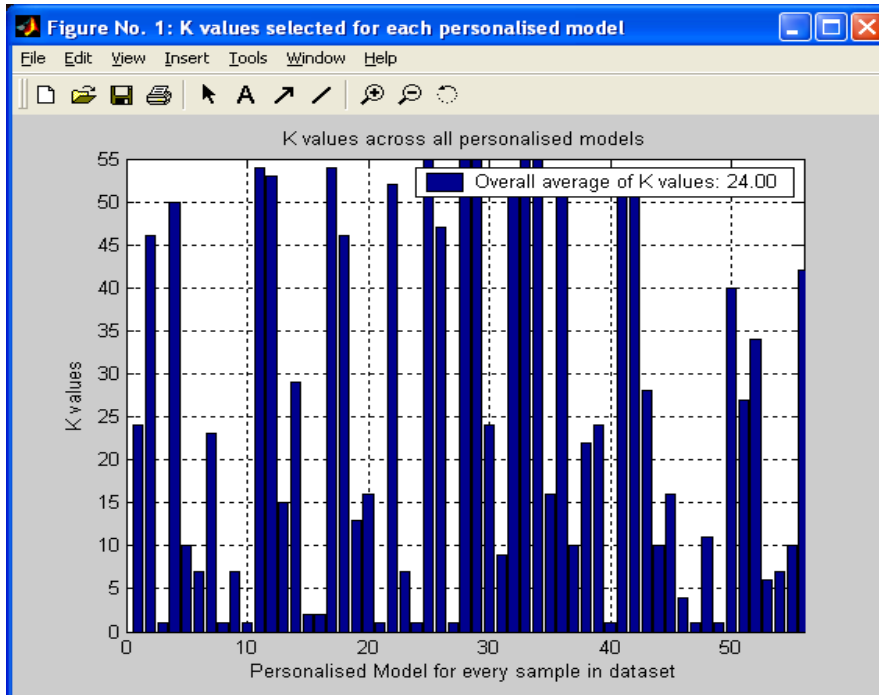
**Score (%) vs Generations**

Generations	Best Score (%)	Average Score (%)
0	75	65
1	85	70
2	85	75
3	85	75
4	85	75
5	85	75
6	85	75
7	85	75
8	85	75
9	85	75
10	85	75
11	85	75
12	85	75
13	85	75
14	85	75
15	85	75
16	85	75
17	85	75
18	85	75
19	85	75
20	85	75

# GA feature and parameter optimisation of personalised models

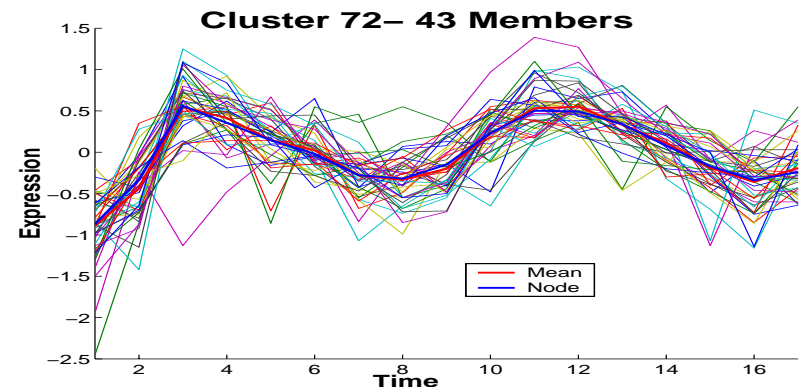
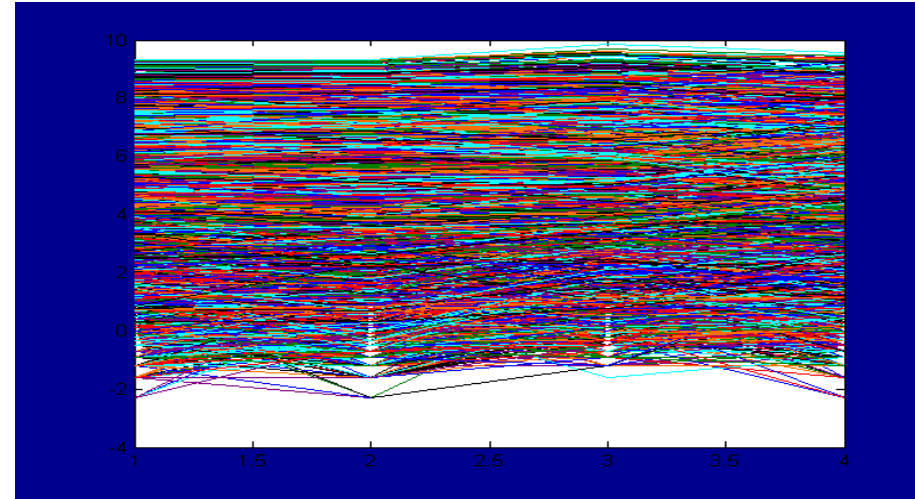
## Optimising the number of neighbours $K$ , the distance measure, and the model type

(N.Mohan and N.Kasabov, IJCNN, IEEE Press, 2005)



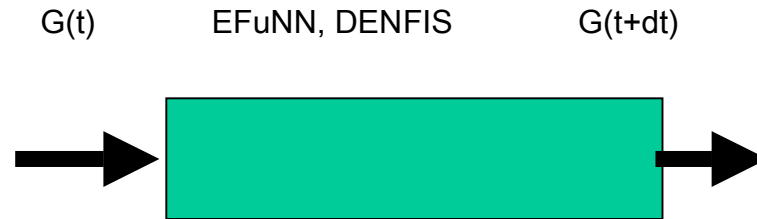
# 7. Gene regulatory network (GRN) modeling and discovery

- Genes that share similar functions usually show similar gene expression profiles and cluster together
- Different clustering techniques:
  - Exact clusters vs fuzzy clusters
  - Pre-defined number of clusters or evolving
  - Batch vs on-line
  - Using different similarity or correlation measure
- Case study:
  - Leukemia cell line U937 (experiments done at the NCI, NIH, Frederick, USA, Dr Dimitrov's lab)
  - Two different clones of the same cell line treated with retinoic Acid
  - 12,680 genes expressed over time points
  - 4 time points (the MINUS clone, the cell died) and
  - 6 time points (PLUS cell line, cancer)



# ECOS for GRN modeling

(Kasabov and Dimitrov, ICONIP 2002, IEEE Press, 2002)



- On-line, incremental learning of GRN
- Adding new inputs/outputs (new genes)
- The rule nodes capture clusters of input genes that are related to the output genes
- Rules can be extracted that explain the relationship between  $G(t)$  and  $G(t+dt)$ , e.g.:
- EFUNN rules:

IF  $g_1(t)$  is High (0.87) and  $g_2(t)$  is Low (0.9)

THEN  $g_1(t+dt)$  is High (0.6) and  $g_4(t+dt)$  is Low

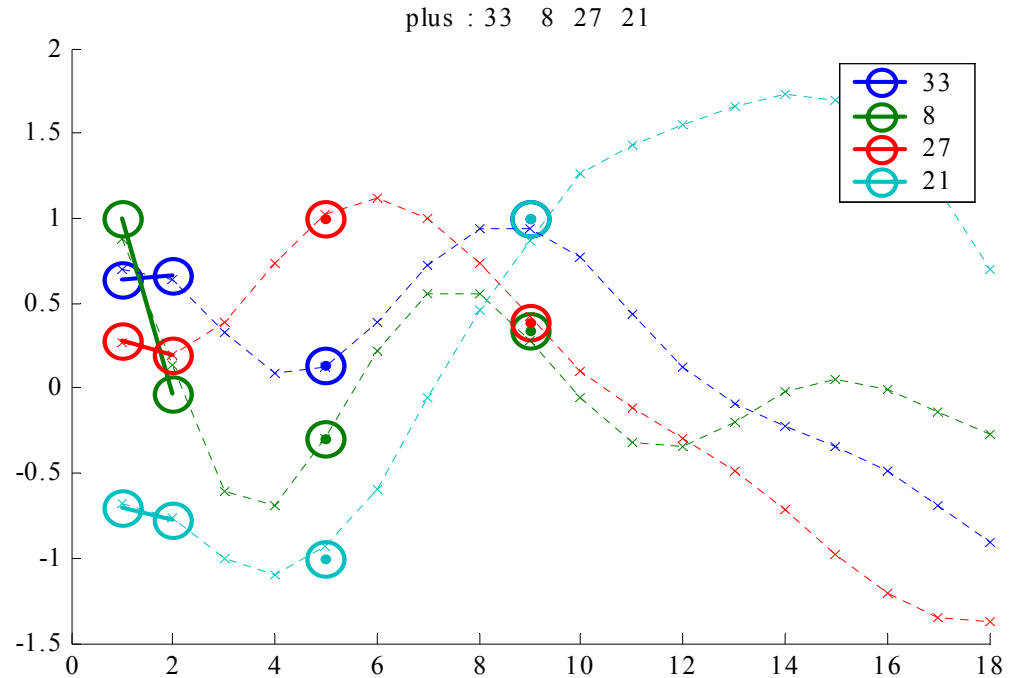
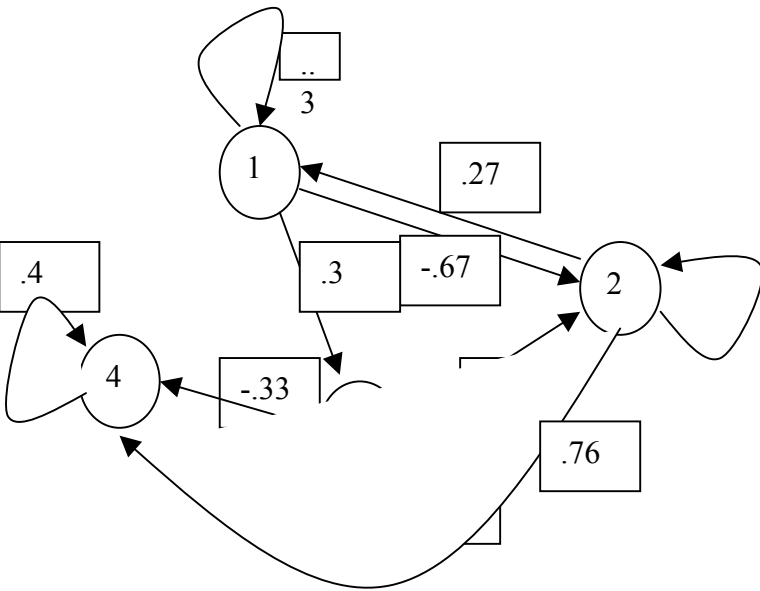
- DENFIS rules:

IF  $g_1(t)$  is ( 0.63 0.70 0.76) and  $g_2(t)$  is ( 0.71 0.77 0.84) and  
 $g_3(t)$  is ( 0.71 0.77 0.84) and  $g_4(t)$  is ( 0.59 0.66 0.72)

THEN  $g_1(t) = 1.84 - 1.26 X_1 - 1.22 X_2 + 0.58 X_3 - 0.03 X_4$

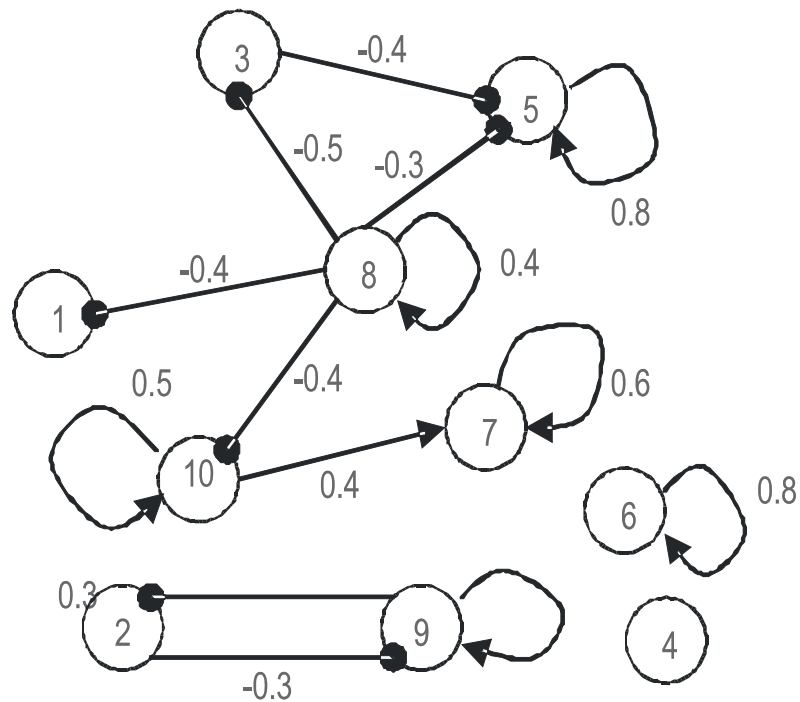
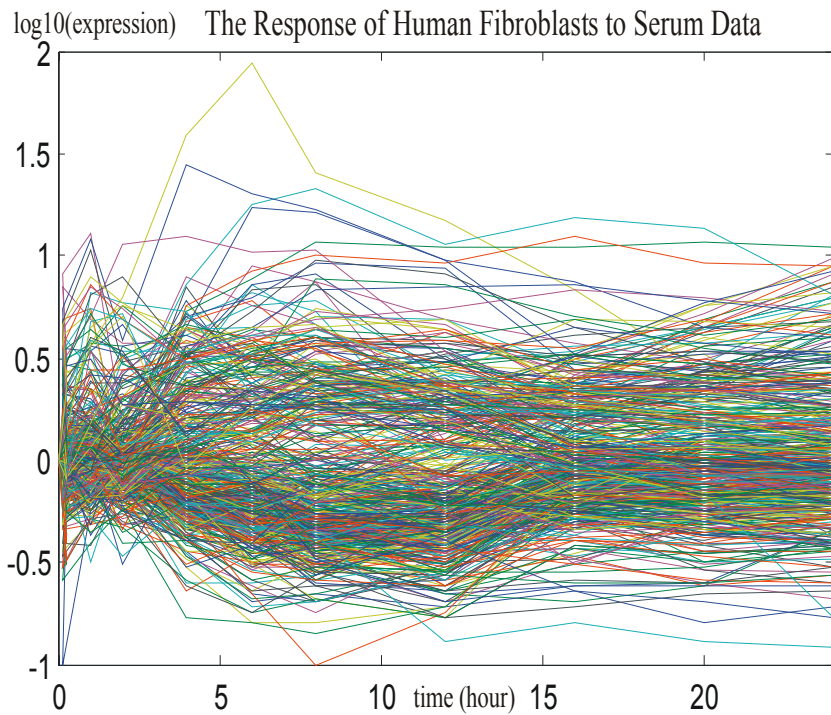
# Using GRN models to predict the expression of genes in a future time

(Zeke Chan, N. Kasabov, I. Sidorov and D. Dimitrov, IEEE Tr CBBI, 2005) .



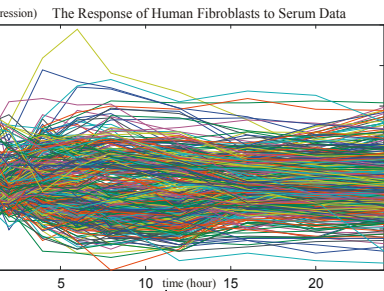
# Example of a GRN derived from gene expression time course data

(Chan, Collins and Kasabov, JBCB, 2005)



# GNetXP methodology and software

(Chan, Collins and Kasabov, JBCB, 2005)

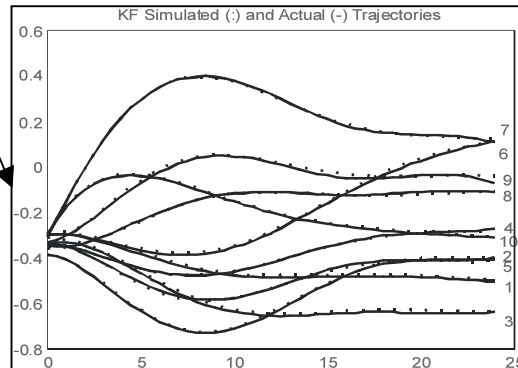


idx	Key Genes in the cluster
1	p57 Kip2
2	CDK1, E2F2, HMG CoA reductase, IPPisomerase, Farnesyl-DFT
3	p27 Kip1; Asparagine synthetase; Squalene epoxidase, Cyp51
4	P18
5	/
6	/
7	HEF1, ATF3 transcription factor
8	Interleukin 18, Interleukin 6, ID2, ID3, Interleukin 8, VEGF, Plasminogen activator inhibitor type 1 and Metallothionein 18; VEGF; Plasminogen activator inhibitor; metalloproteinases type 1
9	CyclinB, Cdc28; metalloproteinases
10	CyclinA, CyclinD1 Cdc2, Madp2, Wee1-like protein kinase, TGFβ and CENP-f; c-FOS, JUNB, MAPK1; Metallothionein 1A, Flap endonuclease; metalloproteinases 1

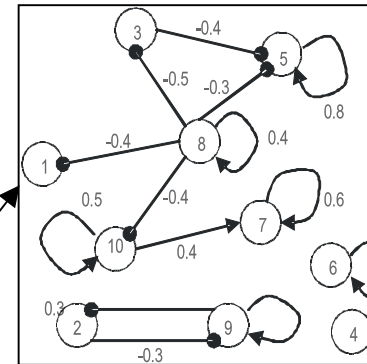
key genes in each cluster

Trajectory

Representative trajectories from the clusters

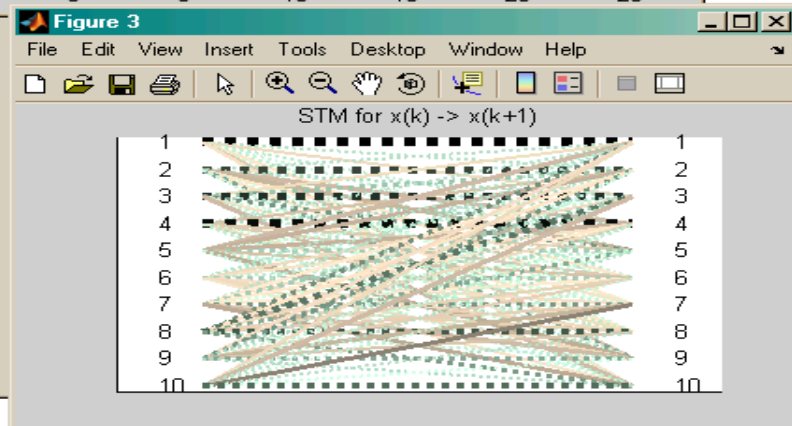
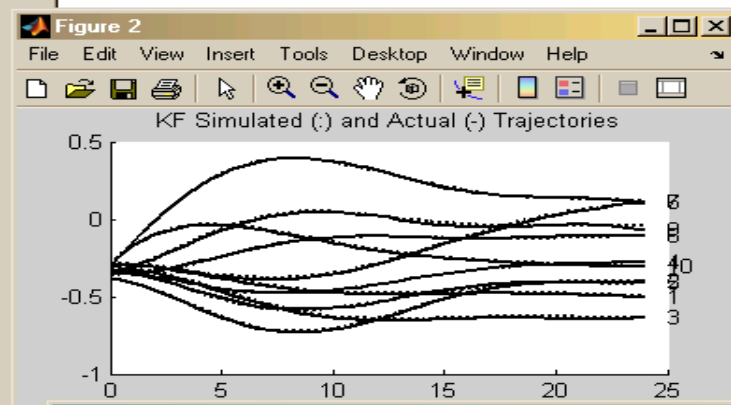
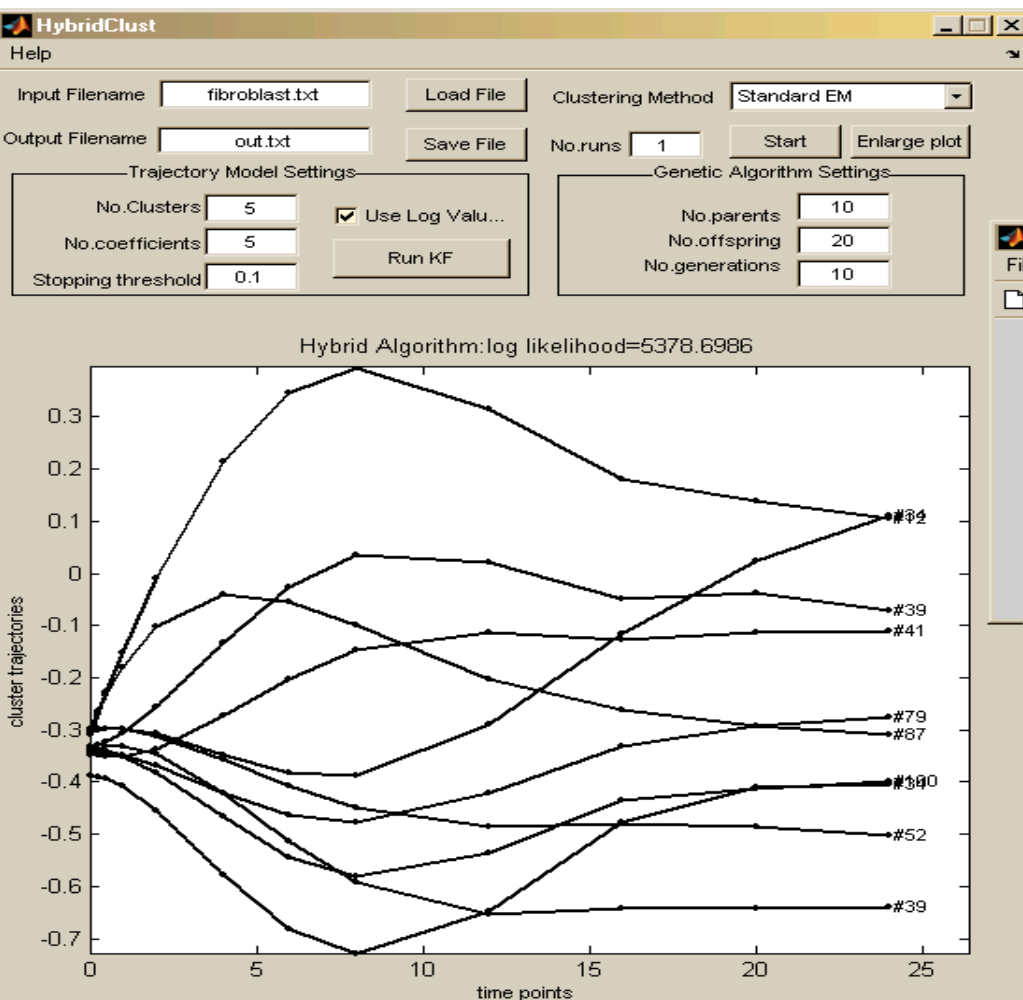


Stage 2: GRN extraction



# The GNetXP software system

(license available from KEDRI, [www.kedri.info](http://www.kedri.info))



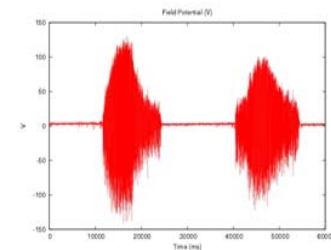
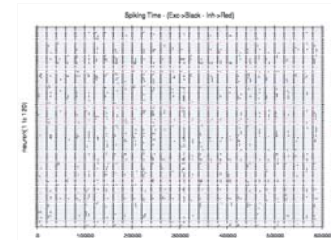
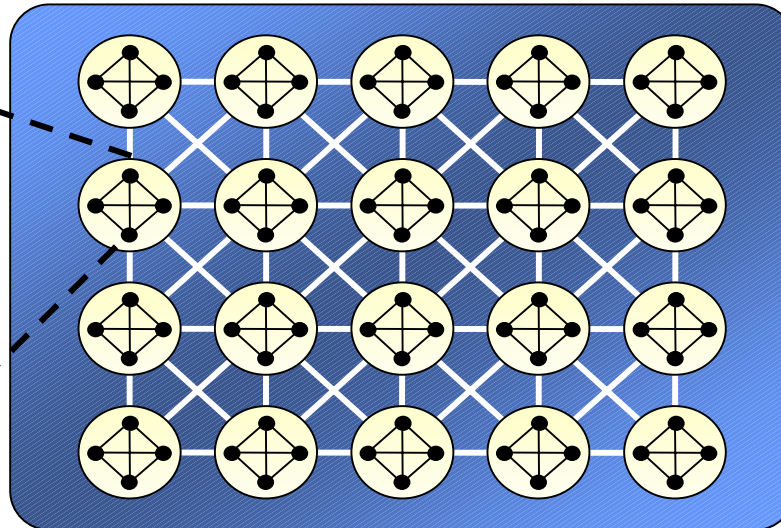
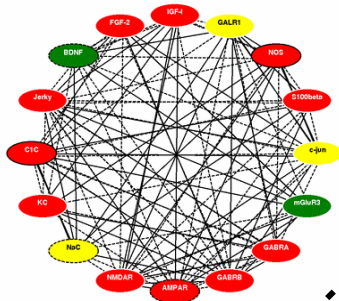


# Computational Neurogenetic Modelling: GRN within neurons as part of a SNN

(L.Benuskova, S.Wysocki, N.Kasabov, IJCNN05 – IEEE Press, 2005, ICANN05- LNCS 3697 Springer, 2005

## CNGM as a SNN

GRN



**SNN Properties**

**Optimization**

**Real Data Analysis**

**Output Analysis**

**Visualization**

**Neuro Genetic Simulator**

**Network (SNN) Parameters**

Simulation Period	1050
Spiking Rate	0.3
Number of Rows	8
Number of Columns	10
Inhibitory Neurons (%)	0.1
Input Weights	0.5

**Excitatory Neurons**

	Fast	Slow
Amplitude	4	1
Time Constant (rise)	1	15
Time Constant (decay)	2	25
Amplitude Weights (Gaussian)	1	
Sigma Weights (Gaussian)	4	
Delay per row/col	1	

**Inhibitory Neurons**

	Fast	Slow
Amplitude	1	3
Time Constant (rise)	28	27.5
Time Constant (decay)	40	25
Amplitude Weights (Gaussian)	1	
Sigma Weights (Gaussian)	4	
Delay per row/col	1	

**GRN Parameters**

**Linking SNN and GRN**

Define which parameter are related to genes and how

**Output Signal Analysis**

Sampling Rate (Hz)	1000
Digital Filter	Frequency (Hz)
	Low 0.1 High 50
Band Relative Intensity Ratio (RIR)	
	RIR Var Frequency (Hz)
delta	0.5 1 0.5 3.5
theta	0.2 1 3.5 7.5
alpha	0.1 1 7.5 12.5
beta1	0.1 1 12.5 18
beta2	0.05 1 18 30
gamma	0.05 1 30 50

Min Max

Signal Amplitude 0 999999

Spiking Rate 0

**Genetic Algorithms Parameters**

Population	10
Mutation (Probability)	0.0001
Noise Amplitude	0.01
Fitness Criteria (1/error)	0.001
Max. N. of Generations	500

**External Data**

File eeg

Sampling Rate

Simulation Period

**Output Graphs**

Choose output

Network.EEG display

Debug eeg.png

## 8. Conclusions and further directions

- Advantages of local and personalised modelling:
  - More accurate
  - Better explanation
  - Different number of variables can be used
- Questions and problems for further research in local and personalised modelling
  - How many neighbouring data points  $D_j$  should be selected in a transductive reasoning (personalised modelling)? That is the problem of choosing  $K$
  - How is “vicinity” measured
  - Choice of distance function
  - Transductive feature selection
  - Speed, when optimisation is needed
- How to combine different models – each of them giving a different perspective, i.e global, local and “personalised”?
- Computational neurogenetic modelling (CNGM)

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- Established March-June 2002.
- Funded by AUT, NERF (FRST), NZ industry.
- Appr. NZ\$ 1mln pa
- 25 research staff and graduate students; 25 associated researchers
- Both fundamental and applied research (theory + practice)
- 95 publications in 2002-05
- 450 publications all together
- Multicultural environment (12 ethnical origins)
- Strong national and international collaboration:
- PEBL ([www.pebl.co.nz](http://www.pebl.co.nz));
- UA – BI, SCOPE project; EEE
- Middlemore hospital
- ViaLactia; FONTERRA
- RIKEN; KIT; Ritsumeikan
- UC Berkeley; NCI, NIH;
- TU Sofia-Plovdiv, BG



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