

Exploratory data analysis for microarrays

Adrian Alexa



Computational Biology and Applied Algorithmics
Max Planck Institute for Informatics
D-66123 Saarbrücken

MAX-PLANCK-GESellschaft

slides by Jörg Rahmenführer

NGFN - Courses in Practical DNA Microarray Analysis
Berlin, February 28, 2006



MAX-PLANCK-GESellschaft

Classification tasks for microarrays

- **Classification of SAMPLES**
Generate gene expression profiles that can
 - (i) discriminate between different **known** cell types or conditions, e.g. between tumor and normal tissue,
 - (ii) identify different and previously **unknown** cell types or conditions, e.g. new subclasses of an existing class of tumors.
- **Classification of GENES**
 - (i) Assign an unknown cDNA sequence to one of a set of **known** gene classes.
 - (ii) Partition a set of genes into new (**unknown**) functional classes on the basis of their expression patterns across a number of samples.

Overview

- **Exploratory data analysis: Unsupervised learning**
- **Example: Time series**
- **Distance measures: Object (dis-)similarities**
- **Cluster algorithms: Grouping of data**
- **Other exploratory methods for microarray data**



MAX-PLANCK-GESellschaft

Classification

Seminal microarray analysis paper (Golub et al.)

Molecular classification of cancer: **class discovery** and **class prediction** by gene expression monitoring, *Science* 1999, 86:531-537, see <http://www.genome.wi.mit.edu/MPR>

Cancer classification	Class discovery	Class prediction
Machine learning	Unsupervised learning	Supervised learning
Statistics	Cluster analysis	Discriminant analysis



MESSAGE 1

Discriminant analysis: CLASSES KNOWN

Cluster analysis: CLASSES NOT KNOWN

Goal in cluster analysis:

Grouping a collection of objects into subsets or “clusters”, such that those within each cluster are more closely related to one another than objects assigned to different clusters.



Classification



- Difference between **discriminant analysis** (supervised learning) and **cluster analysis** (unsupervised learning) is important:
- If the class labels are **known**, many different **supervised learning** methods are available. They can be used for prediction of the outcome of future objects.
- If the class labels are **unknown**, **unsupervised learning** methods have to be used. For those, it is **difficult to ascertain the validity of inferences** drawn from the output.

Cluster analysis

Goal in cluster analysis:

Grouping a collection of objects into subsets or “clusters”, such that those within each cluster are more closely related to one another than objects assigned to different clusters.

Two ingredients are needed to group objects:

Distance measure

A notion of distance or similarity of two objects: **When are two objects close to each other?**

Cluster algorithm

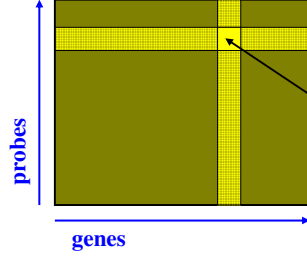
A procedure to minimize distances of objects within groups and/or maximize distances between groups.



Cluster analysis

- Clustering columns: **grouping similar samples**
- Clustering rows: **grouping genes with similar trajectories**

The gene expression matrix



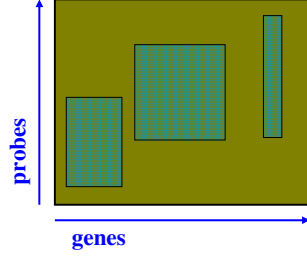
L_{ij} : expression level of gene i in probe j



Cluster analysis: Bi-Clustering

- Clustering columns: **grouping similar samples**
- Clustering rows: **grouping genes with similar trajectories**
- **Bi-clustering**: Group genes that have similar partial trajectories in a subset of the samples

The gene expression matrix



Literature

Tanay, A., Sharan, R., and Shamir, R. (2002): **Discovering Statistically Significant Biclusters in Gene Expression Data**, *Bioinformatics* 18, Suppl.1, 136-144.



Time series example

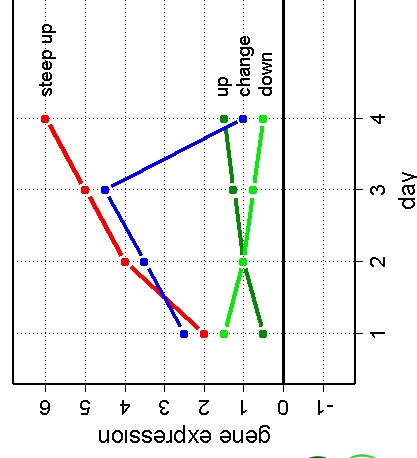
Biology

Measurements of gene expression on 4 (consecutive) days.

Statistics

Every gene is coded by a vector of length 4.

- **steep up**: $x_1 = (2, 4, 5, 6)$
- **up**: $x_2 = (2/4, 4/4, 5/4, 6/4)$
- **down**: $x_3 = (6/4, 4/4, 3/4, 2/4)$
- **change**: $x_4 = (2.5, 3.5, 4.5, 1)$



Distance measures - Time series example

Euclidean distance

The distance between two vectors is the square root of the sum of the squared differences over all coordinates.

$$d_E(x_1, x_2) = \sqrt{(2-2/4)^2 + (4-4/4)^2 + (5-5/4)^2 + (6-6/4)^2} = 3\sqrt{3/4} \approx 2.598$$

- **steep up**: $x_1 = (2, 4, 5, 6)$
- **up**: $x_2 = (2/4, 4/4, 5/4, 6/4)$





Distance measures - Time series example

MAX PLANCK GESELLSCHAFT

Euclidean distance

The distance between two vectors is the square root of the sum of the squared differences over all coordinates.

$$d_E(x_1, x_2) = \sqrt{(2-2/4)^2 + (4-4/4)^2 + (5-5/4)^2 + (6-6/4)^2} = 3\sqrt{3/4} \approx 2.598$$

- **steep up:** $x_1 = (2, 4, 5, 6)$
- **up:** $x_2 = (2/4, 4/4, 5/4, 6/4)$
- **down:** $x_3 = (6/4, 4/4, 3/4, 2/4)$
- **change:** $x_4 = (2.5, 3.5, 4.5, 1)$

0	2.60	2.75	2.25
2.60	0	1.23	2.14
2.75	1.23	0	2.15
2.25	2.14	2.15	0

Matrix of pairwise distances



Distance measures - Time series example

MAX PLANCK GESELLSCHAFT

Manhattan distance

The distance between two vectors is the sum of the absolute (unsquared) differences over all coordinates.

$$d_M(x_1, x_2) = |2-2/4| + |4-4/4| + |5-5/4| + |6-6/4| = 51/4 = 12.75$$

- **steep up:** $x_1 = (2, 4, 5, 6)$
- **up:** $x_2 = (2/4, 4/4, 5/4, 6/4)$



Distance measures - Time series example

MAX PLANCK GESELLSCHAFT

Manhattan distance

The distance between two vectors is the sum of the absolute (unsquared) differences over all coordinates.

$$d_M(x_1, x_2) = |2-2/4| + |4-4/4| + |5-5/4| + |6-6/4| = 51/4 = 12.75$$

- **steep up:** $x_1 = (2, 4, 5, 6)$
- **up:** $x_2 = (2/4, 4/4, 5/4, 6/4)$
- **down:** $x_3 = (6/4, 4/4, 3/4, 2/4)$
- **change:** $x_4 = (2.5, 3.5, 4.5, 1)$

0	12.75	13.25	6.50
12.75	0	2.50	8.25
13.25	2.50	0	7.75
6.50	8.25	7.75	0

Matrix of pairwise distances



Distance measures - Time series example

MAX PLANCK GESELLSCHAFT

Correlation distance

Distance between two vectors is $1-\rho$, where ρ is the Pearson correlation of the two vectors.

$$d_C(x_1, x_2) = 1 - \frac{(2-\frac{17}{4})(\frac{2}{4}-\frac{17}{16}) + (4-\frac{17}{4})(\frac{4}{4}-\frac{17}{16}) + (5-\frac{17}{4})(\frac{5}{4}-\frac{17}{16}) + (6-\frac{17}{4})(\frac{6}{4}-\frac{17}{16})}{\sqrt{(2-\frac{17}{4})^2 + (4-\frac{17}{4})^2 + (5-\frac{17}{4})^2 + (6-\frac{17}{4})^2} \sqrt{(\frac{2}{4}-\frac{17}{16})^2 + (\frac{4}{4}-\frac{17}{16})^2 + (\frac{5}{4}-\frac{17}{16})^2 + (\frac{6}{4}-\frac{17}{16})^2}}$$

- **steep up:** $x_1 = (2, 4, 5, 6)$
- **up:** $x_2 = (2/4, 4/4, 5/4, 6/4)$

Distance measures - Time series example

Correlation distance

Distance between two vectors is $1-\rho$, where ρ is the Pearson correlation of the two vectors.

$$d_C(x_1, x_2) = 1 - \frac{(2-\frac{17}{4})(\frac{2}{4}-\frac{17}{16}) + (4-\frac{17}{4})(\frac{4}{4}-\frac{17}{16}) + (5-\frac{17}{4})(\frac{4}{4}-\frac{17}{16}) + (6-\frac{17}{4})(\frac{4}{4}-\frac{17}{16})}{\sqrt{(2-\frac{17}{4})^2 + (4-\frac{17}{4})^2 + (5-\frac{17}{4})^2 + (6-\frac{17}{4})^2} \sqrt{(\frac{2}{4}-\frac{17}{16})^2 + (\frac{4}{4}-\frac{17}{16})^2 + (\frac{4}{4}-\frac{17}{16})^2 + (\frac{4}{4}-\frac{17}{16})^2}}$$

- **steep up:** $x_1 = (2, 4, 5, 6)$
- **up:** $x_2 = (2/4, 4/4, 5/4, 6/4)$
- **down:** $x_3 = (6/4, 4/4, 3/4, 2/4)$
- **change:** $x_4 = (2.5, 3.5, 4.5, 1)$

0	0	2	1.18
0	0	2	1.18
2	2	0	0.82
1.18	1.18	0.82	0

Matrix of pairwise distances

Distance measures - Time series example

Summary

- **Euclidean distance measures average difference across coordinates.**
- **Manhattan distance measures average difference across coordinates, in a robust way.**
- **Correlation distance measures difference with respect to trends.**

Distance measures - Time series example

	Euclidean				Manhattan				Correlation			
0	2.60	2.75	2.25	0	12.75	13.25	6.50	0	0	2	1.18	
2.60	0	1.23	2.14	12.75	0	2.50	8.25	0	0	2	1.18	
2.75	1.23	0	2.15	13.25	2.50	0	7.75	2	2	0	0.82	
2.25	2.14	2.15	0	6.50	8.25	7.75	0	1.18	1.18	0.82	0	

		steep up	up	steep up	down	change
steep up	0	0	0	9	9	0
up	9	9	0	0	0	0
down	10	10	10	4	1	10
change	8	4	5	7	6	5

Comparison:
All distances are normalized to the interval [0,10] and then rounded.

Distance measures - standardization

Standardization

- Data points are **normalized with respect to mean and variance**:
Apply transformation $x \mapsto \frac{x-\hat{\mu}}{\hat{\sigma}}$, where $\hat{\mu}$ is an estimator of the mean (usually average across coordinates) and $\hat{\sigma}$ is an estimator of the variation (usually empirical standard deviation).
- After standardization, Euclidean distance and Correlation distance are **equivalent(!)**:
 $d_E(x_1, x_2)^2 = 2nd_C(x_1, x_2)$
- Standardization makes sense, if you are **not interested in the magnitude of the effects**, but in the effect itself. Results can be misleading for noisy data.



MESSAGE 2

Appropriate choice of distance measure depends on your intention!

Dissimilarities that do not depend on a metric can be used!



There are three different types of cluster algorithms:

combinatorial algorithms, *mixture modeling* and *mode seeking*

Most popular cluster algorithms:

- **Hierarchical clustering**
- **K-means**
- **PAM (Partitioning around medoids)**
- **SOM's (Self-Organizing Maps)**
- K-means and SOM's take original data directly as input: **the attributes are assumed to live into an Euclidean space.**
- Hierarchical cluster algorithms and PAM allow the choice of a **dissimilarity matrix \mathbf{d}** , that assigns to each pair of objects x_i and x_j a value $d(x_i, x_j)$ as their distance.



- **Hierarchical clustering** was the first algorithm used in microarray research to cluster genes (Eisen et al. (1998)).

1. First, each object is assigned to its own cluster.
2. **Iteratively:**
 - **the two most similar clusters are joined**, representing a new node of the clustering tree. The node is computed as **"average" of all objects of the joined clusters.**
 - the similarity matrix is updated with this **new node replacing the two joined clusters.**
3. Step 2 is repeated until only one single cluster remains.



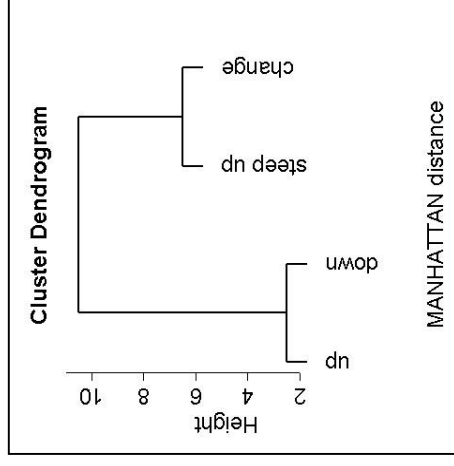
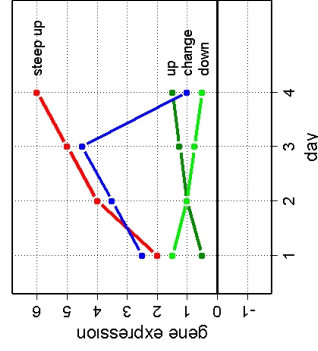
- **Calculation of distance $d(G, H)$** between two clusters **G** and **H** is based on object dissimilarity between the objects from the two clusters:
 - o Single linkage uses the **smallest distance**: $d_s(G, H) = \min_{i \in G, j \in H} d_{ij}$
 - o Complete linkage uses the **largest distance**: $d_c(G, H) = \max_{i \in G, j \in H} d_{ij}$
 - o Average linkage uses the **average distance**: $d_A(G, H) = \frac{1}{N_G N_H} \sum_{i \in G} \sum_{j \in H} d_{ij}$
- Instead of agglomerative clustering, sometimes **divisive clustering** is used: **Iteratively, best possible splits are calculated.**

Hierarchical cluster algorithms

- **Visualization** of hierarchical clustering through **dendrogram**:
 - Clusters that are joined are combined by a line.
 - Height of line is the **"average"** distance between clusters.
 - Cluster with smaller variation is plotted on left side.
- The procedure provides a **hierarchy of clusterings**, with the number of clusters ranging from 1 to the number of objects.
- **BUT**:
 - Parameters for distance matrix: $n(n-1)/2$
 - Parameters for dendrogram: $n-1$.
 - **Hierarchical clustering does not show the full picture!**

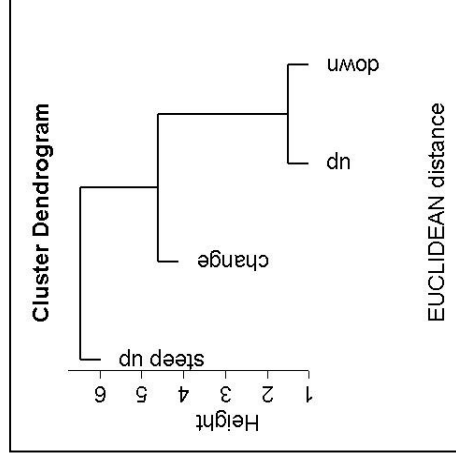
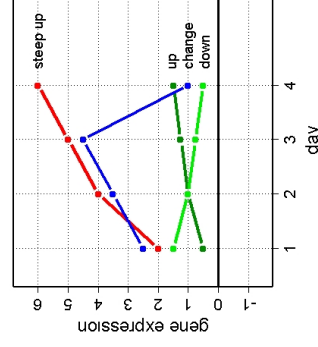
Time series example

- **Manhattan distance**
Similar values are clustered together (robust)



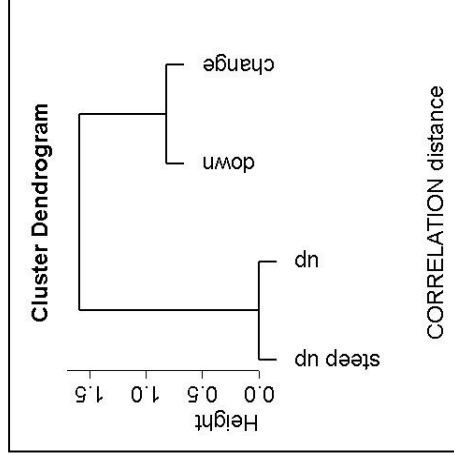
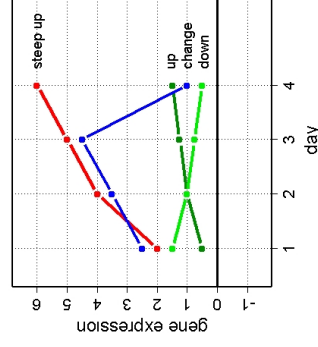
Time series example

- **Euclidean distance**
Similar values are clustered together



Time series example

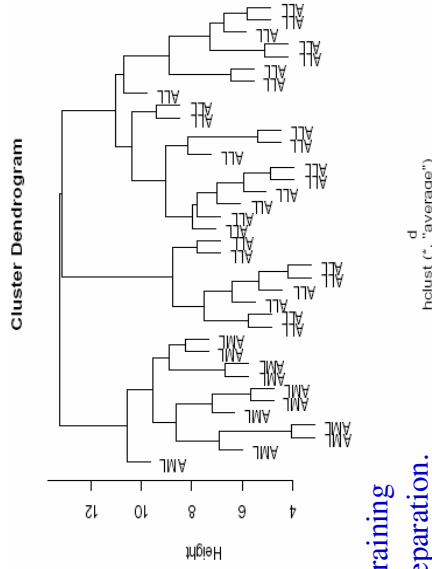
- **Correlation distance**
Similar trends are clustered together



Clustering time series data – literature examples

Golub et al.: Leukemia dataset, <http://www.genome.wi.mit.edu/MPR>

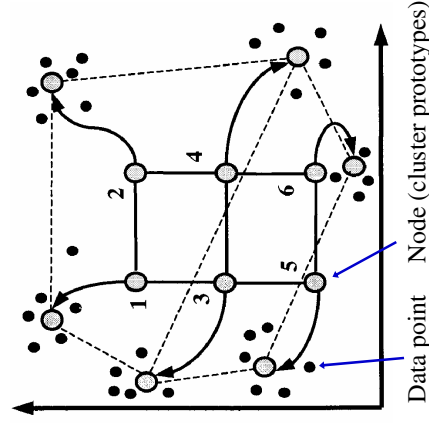
- 3 cancer classes:
 - 25 acute myeloid leukemia (AML),
 - 47 acute lymphoblastic leukemia (ALL), the latter
 - 9 T-cell and 38 B-cell.



Dendrogram for 38 training data shows perfect separation.

Cluster algorithms – Self-Organizing maps

- **SOM's** are similar to **K-means**, but with additional **constraints**.
- Mapping from input space onto one or two-dimensional array of k total nodes.
- Iteration steps (20000-50000):
 - Pick data point P at random
 - Move **all nodes** in direction of P : the closest node the most, the further a node is in network topology, the less
 - Decrease amount of **movement** with iteration steps



Tamayo et al. (1999): First use of SOM's for gene clustering from microarrays

Cluster algorithms – k-means

- **K-means** is a **partitioning algorithm** with a prefixed number k of clusters. It tries to minimize the sum of **within-cluster variances**.
- The a random algorithm chooses sample of k different objects as initial cluster midpoints. Then it alternates between two steps until convergence:
 1. Assign each object to its closest of the k midpoints with respect to **Euclidean distance**.
 2. Calculate k **new midpoints** as the averages of all points assigned to the old midpoints, respectively.
- **K-means** is a randomized algorithm, two runs usually produce different results. Thus, it has to be applied a few times to the same data set and the result with **minimal sum of within-cluster variances** should be chosen.

Cluster algorithms - PAM

- **PAM** (Partitioning around medoids, Kaufman and Rousseeuw (1990)) is a partitioning algorithm, a generalization of **K-means**.
- For an arbitrary dissimilarity matrix d it tries to minimize the sum (over all objects) of distances to the closest of k prototypes.
- Objective function:
$$\sum_{i=1}^n \min_{j=1, \dots, k} d(i, m_j) \quad (d: \text{Manhattan, Correlation, etc.})$$
- **Build phase:** Initial “medoids”.
- **Swap phase:** Repeat until convergence:
 - Consider all pairs of objects (i, j) , where i is a medoid and j not, and make the $i \leftrightarrow j$ swap (if any) which decreases the objective function most.



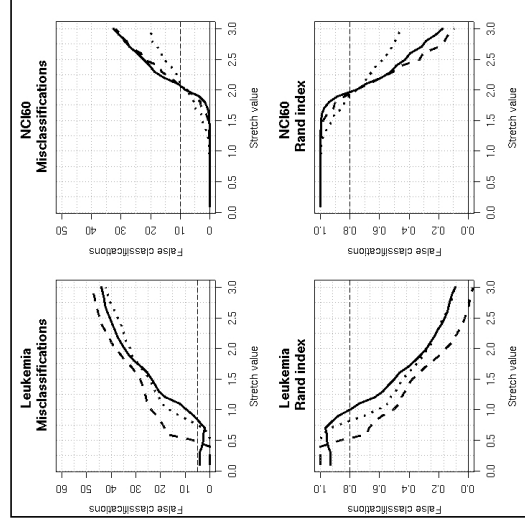
Comparative study

- **Comparative study for tumor classification with microarrays:** Comparison of hierarchical clustering, K-means, PAM and SOM's
- **Data sets:**
 - Golub et al: Leukemia dataset, <http://www.genome.wi.mit.edu/MPR>, 3 cancer classes: 25 acute myeloid leukemia (AML) and 47 acute lymphoblastic leukemia (ALL) (9 T-cell and 38 B-cell), Affymetrix.
 - Ross et al.: NCI60 cancer dataset, <http://genome-www.stanford.edu/nci60>, 9 cancer classes: 9 breast, 6 central nervous system, 7 colon, 8 leukemia, 8 melanoma, 9 lung, 6 ovarian, 2 prostate, 8 renal, cDNA microarray
- **Rahnenführer (2002): Efficient clustering methods for tumor classification with gene expression arrays, Proc. of '26th Ann. Conf. of the Gesellschaft für Klassifikation', Mannheim, July 2002.**



Comparative study - winners

- K-means
- - Hierarchical, Correlation
- PAM, Manhattan



Comparative study – cluster validity

- If true class labels are known, the validity of the clustering can be verified by comparing true class labels and clustering label.

N... table of observations

$$N_{ij} = \frac{n_{ij}}{n_{i.}}$$

n_{11}	n_{12}	...	n_{1l}	$n_{1.}$
n_{21}	n_{22}	...	n_{2l}	$n_{2.}$
\vdots	\vdots	\ddots	\vdots	\vdots
n_{k1}	n_{k2}	...	n_{kl}	$n_{k.}$
$n_{.1}$	$n_{.2}$...	$n_{.l}$	$n_{..}$

Rand index:

Probability of randomly drawing 'consistent' pair of observations

$$Rand = \frac{\sum_{i,j} \binom{n_{ij}}{2} - \left[\sum_i \binom{n_{i.}}{2} \sum_j \binom{n_{.j}}{2} \right] / \binom{n}{2}}{\frac{1}{2} \left[\sum_i \binom{n_{i.}}{2} + \sum_j \binom{n_{.j}}{2} \right] - \left[\sum_i \binom{n_{i.}}{2} \sum_j \binom{n_{.j}}{2} \right] / \binom{n}{2}}$$



Comparative study - results

- **Superiority of k-means with repeated runs**
Similar for discriminant analysis: FLDA best (Dudoit et al., 2001)
- **Superiority of PAM with Manhattan distance for noisy data**
- Differences depend on the specific dataset
- **Preselection of genes**
Various approaches have been **proposed for gene selection**, especially in **supervised learning**.
For clustering samples, a practical proceeding is to choose the **top 100-200 genes with respect to variance (across samples)**. This **decreases noise (!)** and computation time.

MESSAGE 3

Simple cluster algorithms work better in case of little model knowledge!

(But: More sophisticated methods might be more appropriate with more a priori knowledge)

Combinatorial cluster algorithms are approximation algorithms, they converge to local optima!



Recommendations

- Interest in specific genes:**

If you search for genes that are co-regulated with a specific gene of your choice, **DO SO!** Don't use clustering, but generate a list of genes close to your gene with respect to some distance.

- Clustering after feature selection?**

NO! Do not first select genes based on the outcome of some covariable (e.g. tumor type) for your clustering. You will **ALWAYS** find differences w.r.t. this covariable, since this is how you selected the genes!

- Number of clusters**

No general rule how to select the **"correct"** number of clusters.

Adhoc approach is to **try different numbers** and choose cutoff, for which performance of the clustering algorithm breaks down.

The quality of a clustering result depends on the concept of a cluster!



Recommendations – silhouette plot

Heuristic approach for estimation of number of clusters

For each observation i , define **silhouette width** $s(i)$ as follows:

- $a(i)$:= average dissimilarity between i and all other points of its cluster.
- for all *other* clusters C , let

$d(i, C)$:= average dissimilarity of i to all observations of C .

Define $b(i)$:= $\min_C d(i, C)$.

Silhouette width:
$$s(i) := \frac{b(i) - a(i)}{\max\{a(i), b(i)\}}$$

Maximal **average silhouette width** over all observations can be used to select the number of clusters.

Observations with $s(i)$ close to 1 can be considered well-clustered, whereas observations with $s(i)$ close to -1 are misclassified.



Recommendations – silhouette plot

```
x = matrix(morm(10,ncol=2)
row.names(x) = paste("x",1:5,sep=""")
y = matrix(morm(10)+2,ncol=2)
row.names(y) = paste("y",1:5,sep=""")
data = rbind(x,y)

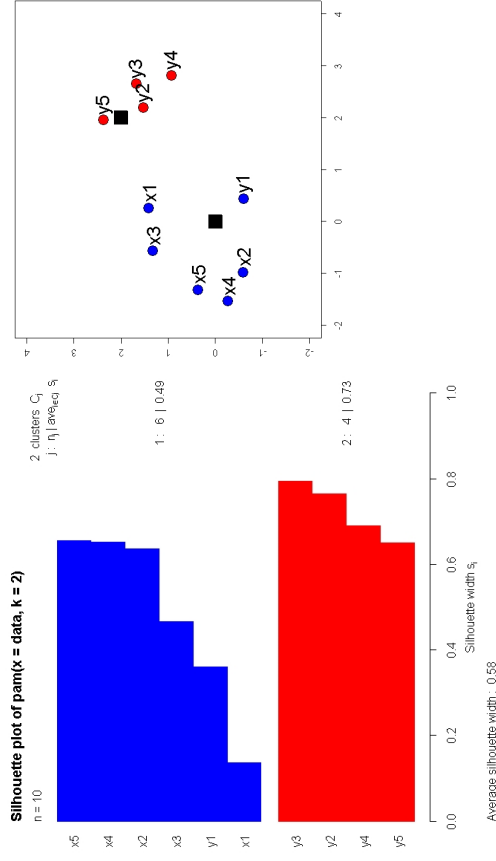
p = pam(data,k=2)
data1 = data[which(p$clusterm==1),]
data2 = data[which(p$clusterm==2),]

plot(0,0,xlim=c(2,4),ylim=c(2,4),xlab="",ylab="",cex.lab=2)
symbols(rbind(c(0,0),c(2,2)),squares=c(0.25,0.25),inches=F,bg="black",add=F)
symbols(data1,circles=rep(0.1,nrow(data1)),inches=F,bg="blue",add=F)
symbols(data2,circles=rep(0.1,nrow(data2)),inches=F,bg="red",add=F)
positions = data
positions[,1] = positions[,1]+0.3
text(positions,rowname$S(data),cex=2)

X11()
color = c(rep("blue",nrow(data1)),rep("red",nrow(data2)))
plot(silhouette(p),col=rev(color),do.col.sort=F)
```



Recommendations – silhouette plot



Adrian Alexa / Jörg Rahnenführer, MPI Informatik

NGFN course, Berlin, February 28, 2006

Literature

- Golub TR, Slonim DK, Tamayo P, Huard C, Gaasenbeek M, Mesirov JP, Coller H, Loh ML, Downing JR, Caligiuri MA, Bloomfield CD, Lander ES. Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science* 1999; 286: 531-37.
- Alizadeh AA, Eisen MB, Davis RE and 28 others. Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 2000; 403: 503-11.
- Jain A, Dubes RC. *Algorithms for Clustering Data*. Englewood Cliffs, New Jersey: Prentice Hall; 1988.
- Azuaje F. Clustering-based approaches to discovering and visualising microarray data patterns. *Brief Bioinformatics* 2003; 4: 31-42.
- Eisen MB, Spellman PT, Brown PO, Botstein D. Cluster analysis and display of genome-wide expression patterns. *PNAS* 1998; 95: 14863-68.
- Tamayo P, Slonim D, Mesirov J, Zhu Q, Kitareewan S, Dmitrovsky E, Lander ES, Golub TR. Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation. *PNAS* 1999; 96: 2907-12.
- Kaufman L, Rousseeuw P. *Finding Groups in Data*. New York: John Wiley and Sons; 1990.
- Ben-Dor A, Shamir R, Yakhini Z. Clustering gene expression patterns. *J. Comput Biol.* 1999; 6: 281-97.

Adrian Alexa / Jörg Rahnenführer, MPI Informatik

NGFN course, Berlin, February 28, 2006

SUMMARY

MESSAGE 1:

Discriminant analysis: CLASSES KNOWN
Cluster analysis: CLASSES NOT KNOWN

MESSAGE 2:

Appropriate choice of distance measure depends on your intention!

MESSAGE 3:

Simple cluster algorithms work better in case of little model knowledge!

Adrian Alexa / Jörg Rahnenführer, MPI Informatik

NGFN course, Berlin, February 28, 2006

Literature

- Cheng Y, Church GM. Biclustering of expression data. *Proc Int Conf Intell Syst Mol Biol.* 2000; 8:93-103.
- Tanay A, Sharan R, Shamir R. Discovering statistically significant biclusters in gene expression data. *Bioinformatics* 2002; Suppl 1: 136-44.
- Hastie T, Tibshirani R, Eisen MB, Alizadeh A, Levy R, Staudt L, Chan WC, Botstein D, Brown P. 'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. *Genome Biol.* 2000; 1(2): RESEARCH0003.
- Yeung KY, Haynor DR, Ruzzo WL. Validating clustering for gene expression data. *Bioinformatics* 2001; 17: 309-18.
- Rahnenführer J. Efficient clustering methods for tumor classification with microarrays. In: *Between Data Science and Applied Data Analysis* (Eds: M. Schader, W. Gaul, M. Vichi), Springer, Proc. 26th Ann. Conf. GfKI 2002; 670-679.
- Dudoit S, Fridlyand J. A prediction-based resampling method to estimate the number of clusters in a dataset. *Genome Biology* 2002; 3:RESEARCH0036.
- Smolkin, M, Ghosh, D. Cluster stability scores for microarray data in cancer studies. *BMC Bioinformatics* 2003, 4:36.

Adrian Alexa / Jörg Rahnenführer, MPI Informatik

NGFN course, Berlin, February 28, 2006

Other exploratory methods

- **PCA: Principal Component Analysis**

Data are projected on lower dimensional space. Iteratively, the direction with largest variance is selected as i -th principal component (orthogonality constraint). Can be used as preprocessing step, but low interpretability.

- **Correspondence Analysis**

Genes and samples are projected into two-dimensional plane to show associations between them.

- **ISIS: A class discovery method**

Search for class distinctions that are characterized by differential expression of just a small set of genes, not by global similarity of the gene expression profile.

Other exploratory methods - CAST

- **CAST (Cluster Affinity Search Technique)**

Ben-Dor A, Shamir R, Yakhini Z (1999): **Clustering gene expression patterns**. *J. Comput Biology* 6: 281-97.

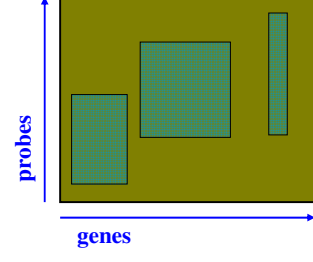
- Input: Similarity matrix and a threshold parameter.
- Iteratively, clusters are generated one at a time. Genes are added to an open cluster, as long as their average similarity (affinity) exceeds the threshold. Then a new cluster is started.
- After termination of the assignment process, objects can still be added or removed from clusters.
- This improves standard hierarchical clustering.

Other exploratory methods - Bi-Clustering

Tanay A, Sharan R, Shamir R (2002): **Discovering Statistically Significant Biclusters in Gene Expression Data**. *Bioinformatics* 18, Suppl.1, 136-144.

- Graph-theoretic algorithm coupled with statistical modeling.
- Genes and samples both represented as nodes of a bipartite graph and connected with weights according to the expression of the respective gene and sample.
- The heaviest subgraph is determined with an algorithm that runs in polynomial time.

The gene
expression matrix



R commands and libraries

- **library(mva)**
 - Hierarchical clustering: *hclust()*
 - Kmeans: *kmeans()*
 - Principal components: *princomp()*
- **library(cluster)**
 - PAM: *pam()*
 - Silhouette information: *silhouette()*
- **ISIS package:** <http://www.molgen.mpg.de/~heydebre>