

Machine Learning

Unsupervised Methods

Part 2

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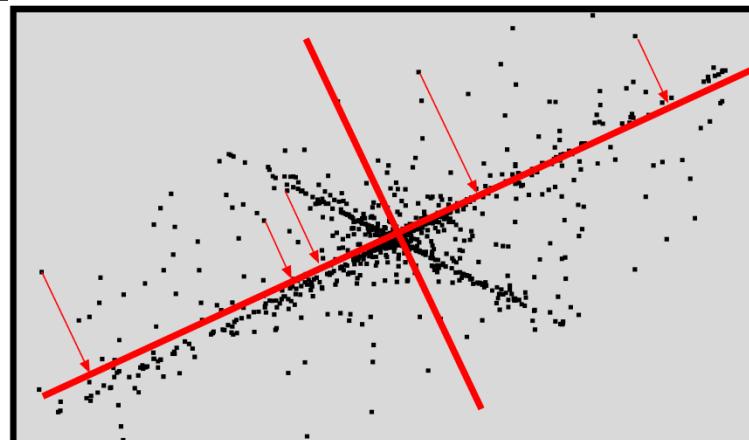
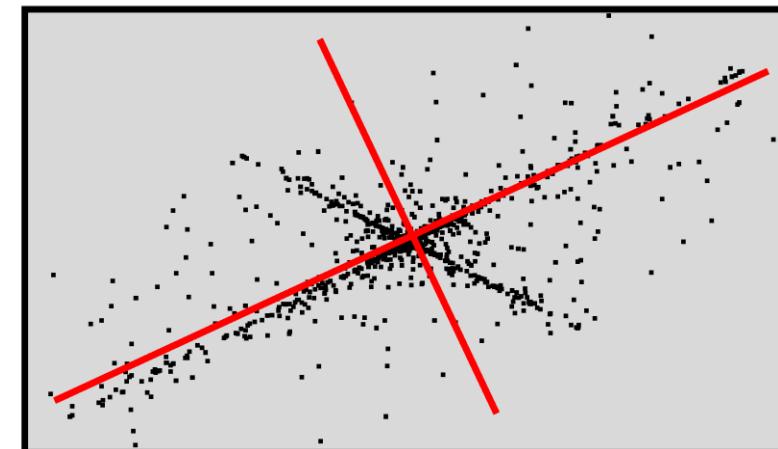
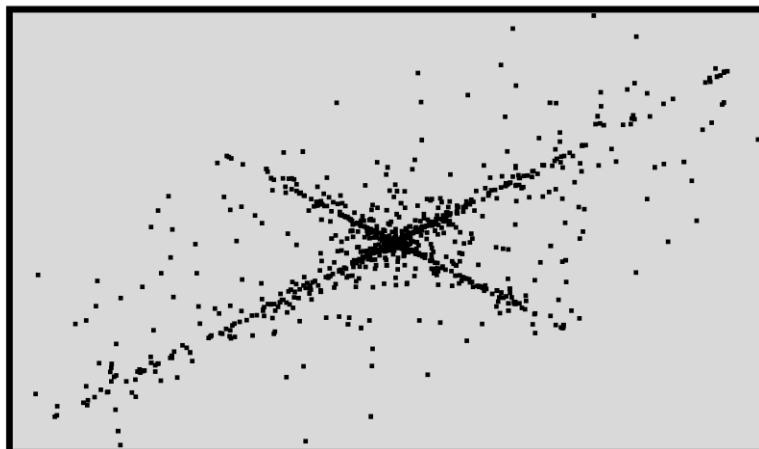
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Principal Component Analysis (PCA), Karhunen-Loéve transform (KTL), Hotelling transform makes a transformation of the coordinate system:

- data has largest variance along the first coordinate
- second largest data variance is along the second coordinate



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summarize multivariate data by PCA via projecting observations onto the first principal components: for visualization the first two

data $\{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}$ summarized by $\mathbf{X} = (\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n)$
data matrix $\mathbf{X} \in \mathbb{R}^{n \times m}$

rows of the data matrix contain the observations
columns contain the features

We assume that the features have zero sample mean
(otherwise, the feature mean must be subtracted)

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sample covariance matrix $C \in \mathbb{R}^{m \times m}$ of features across observations is

$$C_{st} = \frac{1}{n} \sum_{i=1}^n x_{is} x_{it}, \text{ where } x_{is} = (\mathbf{x}_i)_s \text{ and } x_{it} = (\mathbf{x}_i)_t$$

$$\mathbf{C} = \frac{1}{n} \mathbf{X}^T \mathbf{X} = \frac{1}{n} \mathbf{U} \mathbf{D}_m \mathbf{U}^T$$

where $\mathbf{U} \in \mathbb{R}^{m \times m}$ is orthogonal and $\mathbf{D}_m \in \mathbb{R}^{m \times m}$ diagonal

This is the **eigendecomposition** or **spectral decomposition** of \mathbf{C} , which is a symmetric positive definite matrix

diagonal entries of \mathbf{D}_m : **eigenvalues** (positive, sorted decreasingly)
 column vectors $\mathbf{u}_i = [\mathbf{U}]_i$: **eigenvectors (principal components)**

first principal component corresponds to the largest eigenvalue

assume that $n \geq m$ and at least m linear independent observations
 $\rightarrow \mathbf{C}$ has full rank (often ensured by unsupervised feature selection)

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Maximization

singular value decomposition (SVD)

$$\mathbf{X} = \mathbf{V} \mathbf{D} \mathbf{U}^T$$

where $\mathbf{U} \in \mathbb{R}^{m \times m}$ and $\mathbf{V} \in \mathbb{R}^{n \times n}$ are orthogonal, $\mathbf{D} \in \mathbb{R}^{n \times m}$ is diagonal with positive entries, the singular values, sorted decreasingly

Computing $\mathbf{X}^T \mathbf{X}$ we see that $\mathbf{D}_m = \mathbf{D}^T \mathbf{D}$ (the eigenvalues are the singular values squared) and \mathbf{U} is the orthogonal matrix from PCA.

PCA projection: $\mathbf{Y} = \mathbf{X} \mathbf{U} = \mathbf{V} \mathbf{D}$

SVD automatically provides the PCA projections via $\mathbf{V} \mathbf{D}$

For single observations \mathbf{x} the projection is $\mathbf{y} = \mathbf{U}^T \mathbf{x}$

PCA is a matrix decomposition problem: $\mathbf{X} = \mathbf{Y} \mathbf{U}^T$

where \mathbf{U} is orthogonal, $\mathbf{Y}^T \mathbf{Y} = \mathbf{D}_m$ (the \mathbf{y} are orthogonal, decorrelated), and the eigenvalues \mathbf{D}_m are sorted decreasing; for single observations that is $\mathbf{x} = \mathbf{U} \mathbf{y}$

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outer product representation:

$$\mathbf{X} = \sum_{i=1}^m D_{ii} \mathbf{v}_i \mathbf{u}_i^T = \sum_{i=1}^m \mathbf{y}_i \mathbf{u}_i^T$$

\mathbf{u}_i is the i -th orthogonal column vector of \mathbf{U}

\mathbf{v}_i is the i -th orthogonal column vector of \mathbf{V}

$$\mathbf{y}_i = D_{ii} \mathbf{v}_i$$

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Iterative methods for PCA:

current projection is $t = \mathbf{u}^T \mathbf{x}$ then **Oja's rule** is

$$\mathbf{u}^{\text{new}} = \mathbf{u} + \eta (t \mathbf{x} - t^2 \mathbf{u})$$

where η is the learning rate

The eigenvectors of \mathbf{C} are the fixed points of Oja's rule; only the eigenvector with largest eigenvalue is a stable fixed point

$$\begin{aligned} \mathbb{E}_{\mathbf{x}}(\mathbf{u}^{\text{new}}) &= \mathbf{u} + \eta \mathbb{E}_{\mathbf{x}}(\mathbf{x}(\mathbf{x}^T \mathbf{u}) - (\mathbf{u}^T \mathbf{x})(\mathbf{x}^T \mathbf{u}) \mathbf{u}) = \\ &= \mathbf{u} + \eta (\mathbb{E}_{\mathbf{x}}(\mathbf{x} \mathbf{x}^T) \mathbf{u} - (\mathbf{u}^T \mathbb{E}_{\mathbf{x}}(\mathbf{x} \mathbf{x}^T) \mathbf{u}) \mathbf{u}) = \\ &= \mathbf{u} + \eta (\mathbf{C} \mathbf{u} - (\mathbf{u}^T \mathbf{C} \mathbf{u}) \mathbf{u}) \end{aligned}$$

If \mathbf{u} is an eigenvector of \mathbf{C} with eigenvalue λ then

$$\mathbb{E}_{\mathbf{x}}(\mathbf{u}^{\text{new}}) = \mathbf{u} + \eta (\lambda \mathbf{u} - \lambda \mathbf{u}) = \mathbf{u}$$

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The **first principal component** \mathbf{u}_1 is the direction of **maximum variance**:

$$\mathbf{u}_1 = \arg \max_{\|\mathbf{u}\|=1} \sum_{i=1}^n (\mathbf{u}^T \mathbf{x}_i)^2 \quad \sum_{i=1}^n (\mathbf{u}^T \mathbf{x}_i)^2 = \sum_{i=1}^n (\mathbf{u}^T \mathbf{x}_i) (\mathbf{x}_i^T \mathbf{u}) = \mathbf{u}^T \sum_{i=1}^n \mathbf{x}_i \mathbf{x}_i^T \mathbf{u} = n \mathbf{u}^T \mathbf{C} \mathbf{u}$$

$$\mathbf{C} = \sum_{i=1}^m \lambda_i \mathbf{u}_i \mathbf{u}_i^T$$

$$\mathbf{u} = \sum_{i=1}^m a_i \mathbf{u}_i \quad \sum_{i=1}^m a_i^2 = 1$$

This sum is maximal for $a_1 = 1, a_i = 0, i \neq 1$ because $\lambda_1 > \lambda_i > 0$

principal components are the direction of maximal variance orthogonal to all previous components:

$$\mathbf{x}_i^k = \mathbf{x}_i - \sum_{t=1}^{k-1} (\mathbf{u}_t^T \mathbf{x}_i) \mathbf{u}_t \quad \mathbf{u}_k = \arg \max_{\|\mathbf{u}\|=1} \sum_{i=1}^n (\mathbf{u}^T \mathbf{x}_i^k)^2$$

inductively been proved analog to the first principal component
first l components span l -dimensional space of maximal variance

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Is there only one PCA solution? $\mathbf{X} = \mathbf{Y}\mathbf{U}^T$

\mathbf{U} is orthogonal, $\mathbf{Y}^T \mathbf{Y} = \mathbf{D}_m$, \mathbf{D}_m is diagonal with sorted values

PCA is unique up to signs, if the eigenvalues of the covariance matrix are different from each other (proof: see manuscript).

At most one eigenvalue can be zero, which can be removed.

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- first l principal components span l -dim. space of **maximal variance**

$$\sum_{i=1}^l \mathbf{u}_i^T \mathbf{C} \mathbf{u}_i \text{ s.t. } \mathbf{u}_i^T \mathbf{u}_j = \delta_{ij}$$

- **projections onto PCs have zero means:**

$$\frac{1}{n} \sum_{i=1}^n \mathbf{u}_k^T \mathbf{x}_i = \mathbf{u}_k^T \left(\frac{1}{n} \sum_{i=1}^n \mathbf{x}_i \right) = \mathbf{u}_k^T \mathbf{0} = 0$$

- projections onto PCs are mutually **uncorrelated (orthogonal)**:

$$\begin{aligned} \frac{1}{n} \sum_{i=1}^n (\mathbf{u}_t^T \mathbf{x}_i) (\mathbf{u}_s^T \mathbf{x}_i) &= \frac{1}{n} \sum_{i=1}^n (\mathbf{u}_t^T \mathbf{x}_i) (\mathbf{x}_i^T \mathbf{u}_s) \\ &= \frac{1}{n} \sum_{i=1}^n \mathbf{u}_t^T (\mathbf{x}_i \mathbf{x}_i^T) \mathbf{u}_s \\ &= \mathbf{u}_t^T \left(\frac{1}{n} \sum_{i=1}^n \mathbf{x}_i \mathbf{x}_i^T \right) \mathbf{u}_s \\ &= \mathbf{u}_t^T \mathbf{C} \mathbf{u}_s = \lambda_s \mathbf{u}_t^T \mathbf{u}_s = 0 \end{aligned}$$

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- the **sample variance** of the k -th projection is equal to the k -th **eigenvalue** of the sample covariance matrix:

$$\frac{1}{n} \sum_{i=1}^n (\mathbf{u}_k^T \mathbf{x}_i)^2 = \frac{1}{n} \sum_{i=1}^n \mathbf{u}_k^T (\mathbf{x}_i \mathbf{x}_i^T) \mathbf{u}_k = \mathbf{u}_k^T \left(\frac{1}{n} \sum_{i=1}^n \mathbf{x}_i \mathbf{x}_i^T \right) \mathbf{u}_k = \mathbf{u}_k^T \mathbf{C} \mathbf{u}_k = \lambda_k \mathbf{u}_k^T \mathbf{u}_k = \lambda_k$$

- PCs** are ranked **decreasingly** according to their eigenvalues

- The first l PCs **minimize the mean-squared error**: $\hat{\mathbf{x}} = \sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T \mathbf{x}$

$$\begin{aligned}
E(\|\mathbf{x} - \hat{\mathbf{x}}\|^2) &= E(\mathbf{x}^T \mathbf{x} - 2 \mathbf{x}^T \hat{\mathbf{x}} + \hat{\mathbf{x}}^T \hat{\mathbf{x}}) \\
&= E\left(\text{Tr}(\mathbf{x} \mathbf{x}^T) - 2 \text{Tr}\left(\sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T \mathbf{x} \mathbf{x}^T\right) + \text{Tr}\left(\sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T \mathbf{x} \mathbf{x}^T\right)\right) \\
&= \text{Tr}\left(E(\mathbf{x} \mathbf{x}^T) - 2 \sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T E(\mathbf{x} \mathbf{x}^T) + \sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T E(\mathbf{x} \mathbf{x}^T)\right) = \text{Tr}\left(\mathbf{C} - \sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T \mathbf{C}\right) \\
&= \text{Tr}\left(\mathbf{C} - \sum_{k=1}^l \mathbf{u}_k \mathbf{u}_k^T \sum_{k=1}^m \lambda_k \mathbf{u}_k \mathbf{u}_k^T\right) = \text{Tr}\left(\sum_{k=1}^m \lambda_k \mathbf{u}_k \mathbf{u}_k^T - \sum_{k=1}^l \lambda_k \mathbf{u}_k \mathbf{u}_k^T\right) \\
&= \text{Tr}\left(\sum_{k=l+1}^m \lambda_k \mathbf{u}_k \mathbf{u}_k^T\right) = \sum_{k=l+1}^m \lambda_k \text{Tr}(\mathbf{u}_k \mathbf{u}_k^T) = \sum_{k=l+1}^m \lambda_k \text{Tr}(\mathbf{u}_k^T \mathbf{u}_k) = \sum_{k=l+1}^m \lambda_k
\end{aligned}$$

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Example 1: Anderson's or Fisher's Iris data set

Multivariate data set introduced by Sir Ronald Fisher (1936). Iris is a genus of 260-300 species of flowering plants with showy flowers. The three species of the data set are Iris setosa (Beachhead Iris), Iris versicolor (Larger Blue Flag, Harlequin Blueflag), and Iris virginica (Virginia Iris).

Edgar Anderson collected the data to quantify the morphologic variation of Iris flowers of three related species.

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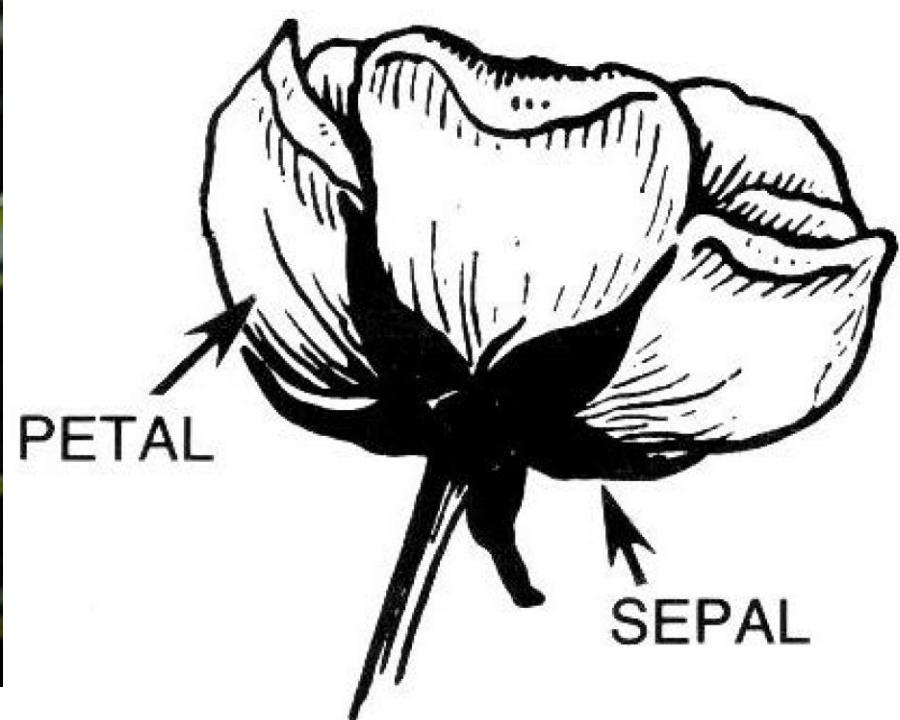
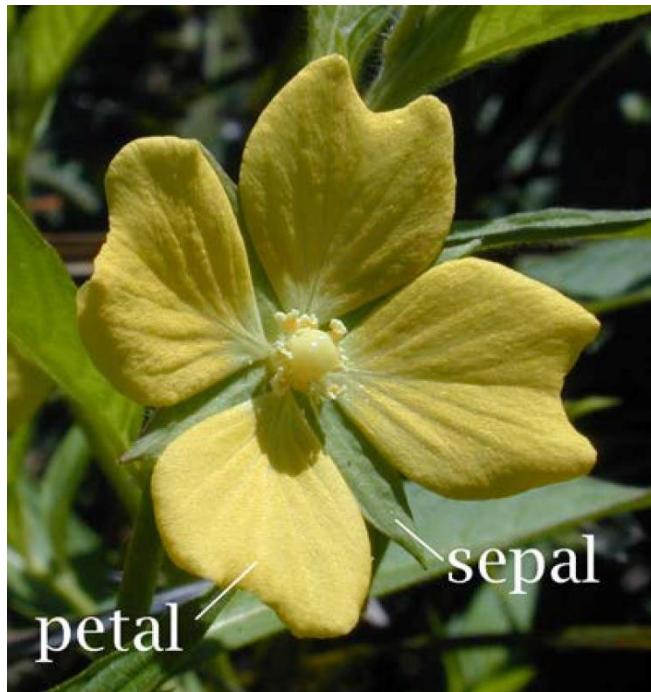
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Maximization

Four features: the length and the width of the sepals and petals (cm)
For each of the three species 50 flowers are measured

No.	Sepal		Petal		Species
	Length	Width	Length	Width	
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
51	7.0	3.2	4.7	1.4	versicolor
52	6.4	3.2	4.5	1.5	versicolor
53	6.9	3.1	4.9	1.5	versicolor
54	5.5	2.3	4.0	1.3	versicolor
55	6.5	2.8	4.6	1.5	versicolor
101	6.3	3.3	6.0	2.5	virginica
102	5.8	2.7	5.1	1.9	virginica
103	7.1	3.0	5.9	2.1	virginica
104	6.3	2.9	5.6	1.8	virginica
105	6.5	3.0	5.8	2.2	virginica

Table 1: Part of the iris data set with features sepal length, sepal width, petal length, and petal width.

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Iris Data Set

Importance of components:

	Comp. 1	Comp. 2	Comp. 3	Comp. 4
Standard deviation	2.0494032	0.49097143	0.27872586	0.153870700
Proportion of Variance	0.9246187	0.05306648	0.01710261	0.005212184
Cumulative Proportion	0.9246187	0.97768521	0.99478782	1.000000000

the first principal component explains 92% of the variance in the data
→ features are correlated which is captured by PC1

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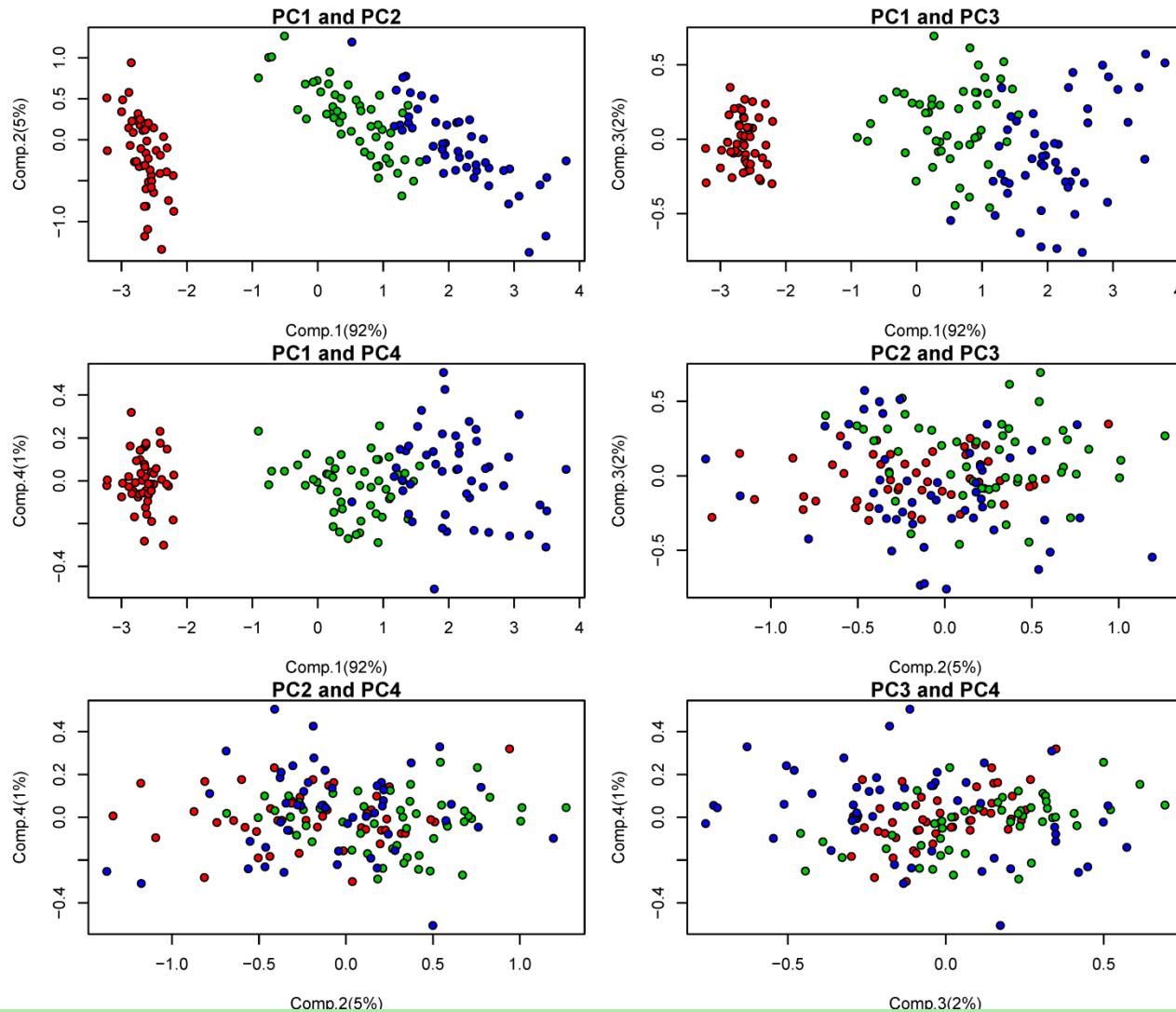
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Only PC1 helps to separate the iris species:



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Multiple Tissue Data Set

- gene expression values microarray
- human and mouse
- 102 samples
- 5,565 genes
- different tissue types
 - breast (Br)
 - prostate (Pr)
 - lung (Lu)
 - colon (Co)

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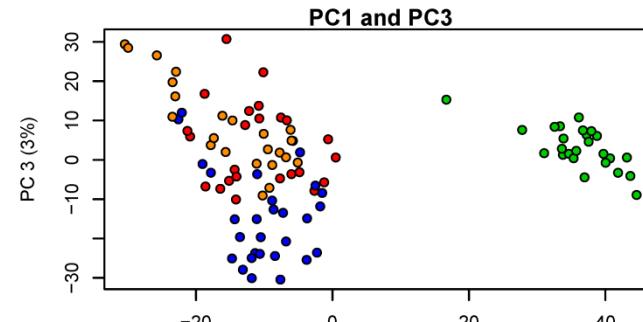
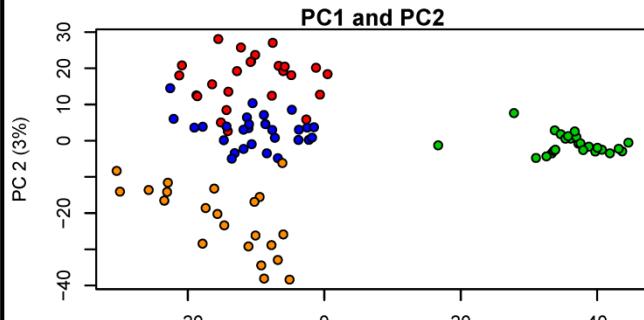
4.8 ICA vs. PCA

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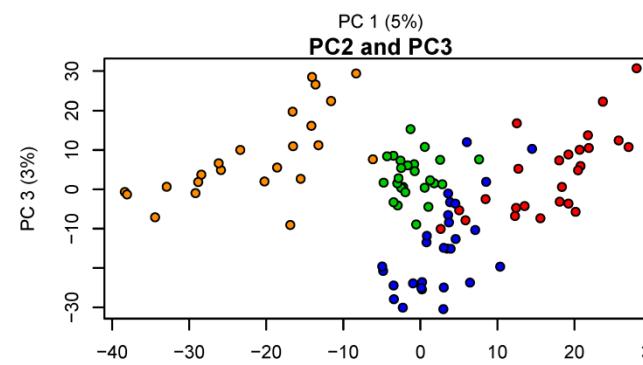
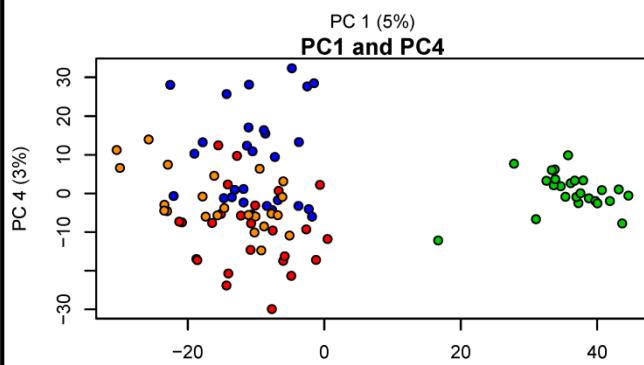
Examples

4.10 Real World ICA Examples

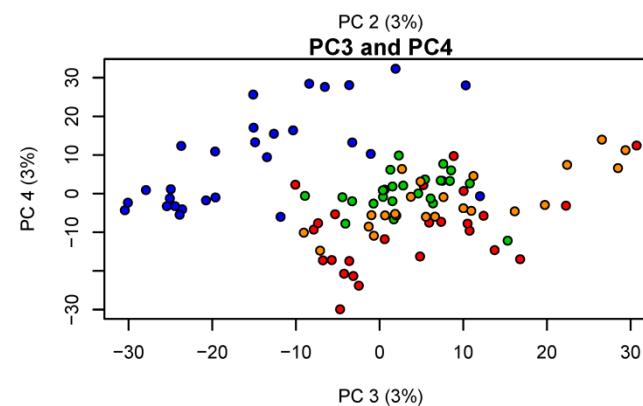
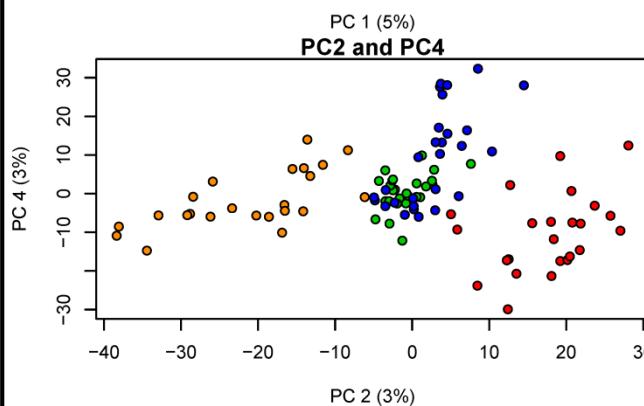
4.11 Kurtosis Maximization



PC1 separates the prostate samples (green) from the rest.



PC2 separates the colon samples (orange) but also breast samples (red).



PC3 separates some lung samples (blue).

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variance filtering before PCA is justified for microarray data

XMultiF1: 101 features

XMultiF2: 13 features

XMultiF3: 5 features

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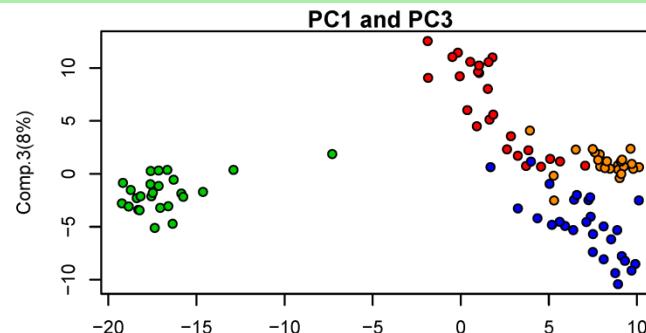
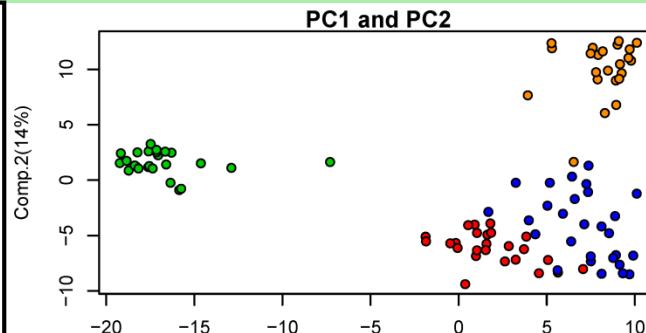
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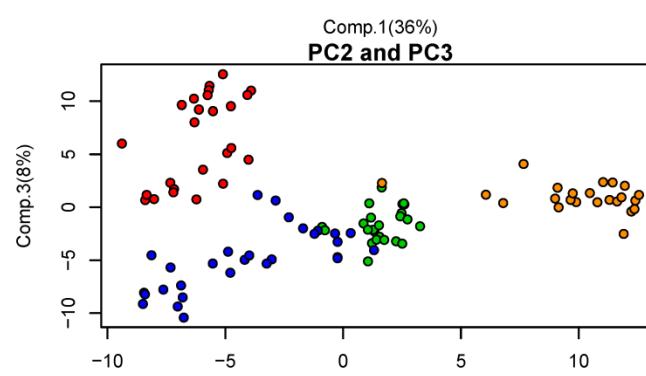
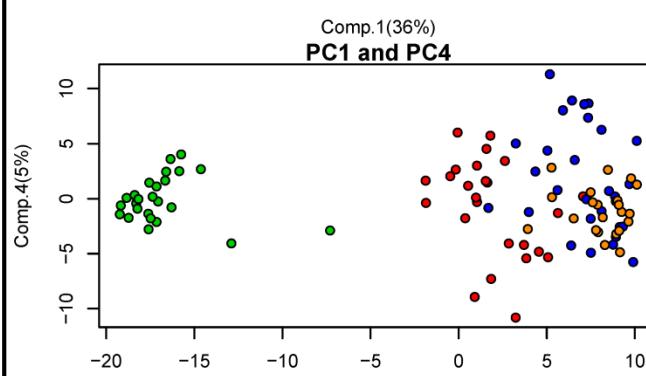
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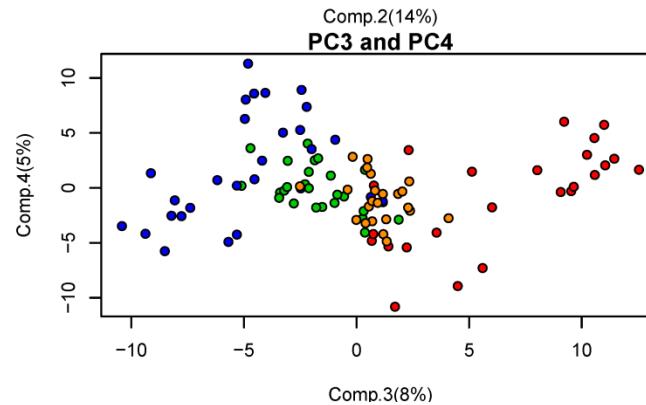
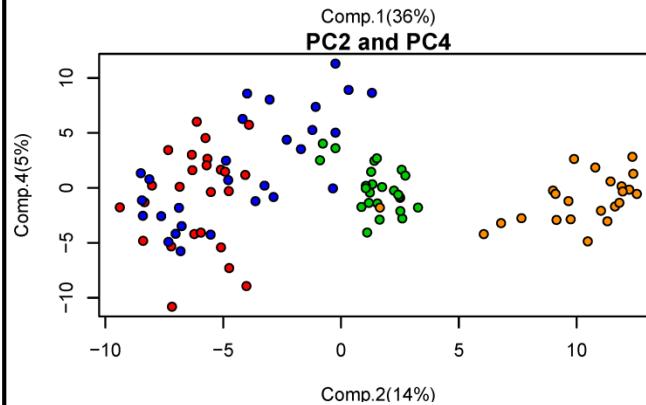
101 genes with the highest variance

PC1 separates the prostate samples (green)



PC2 separates the colon samp. (orange)

PC3 separates the breast samples (red) and lung samp. (blue)



PCA on filtered genes performs better than PCA on all genes for tissue separat.

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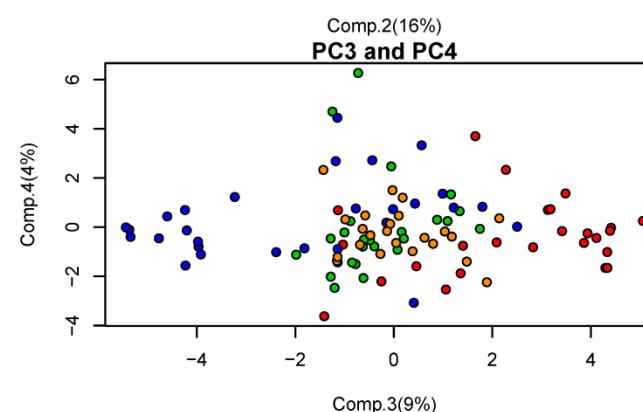
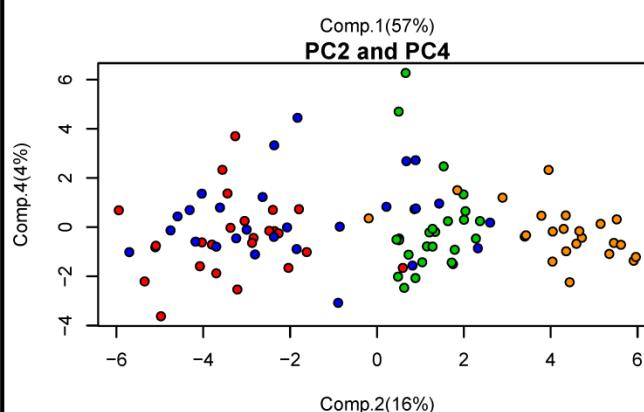
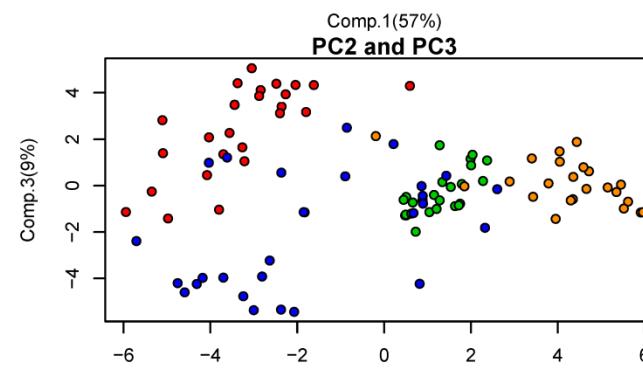
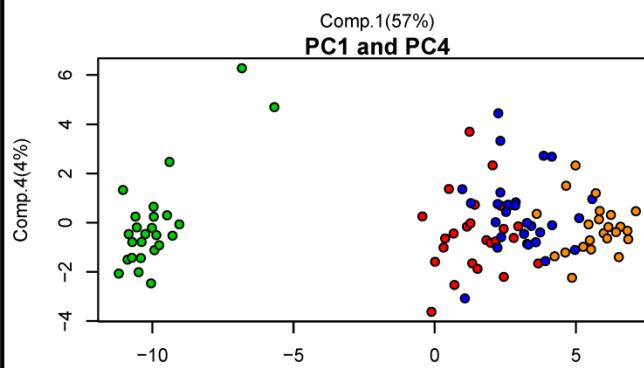
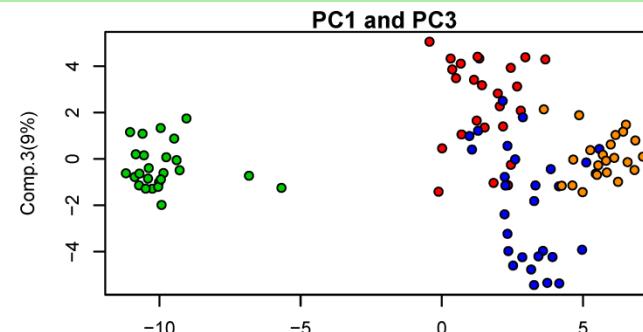
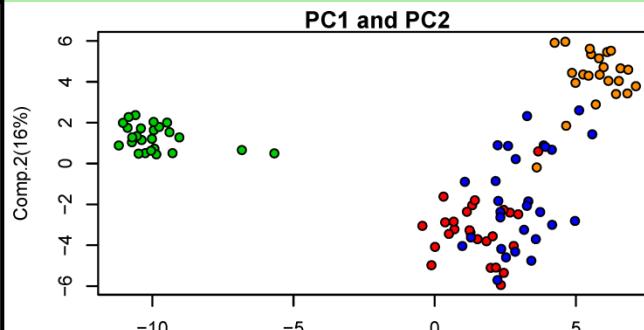
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13 genes with largest variance

PC1 separates the prostate samples (green)

PC2 separates the colon samples (orange)

PC3 separates the breast (red) and lung (blue) samples

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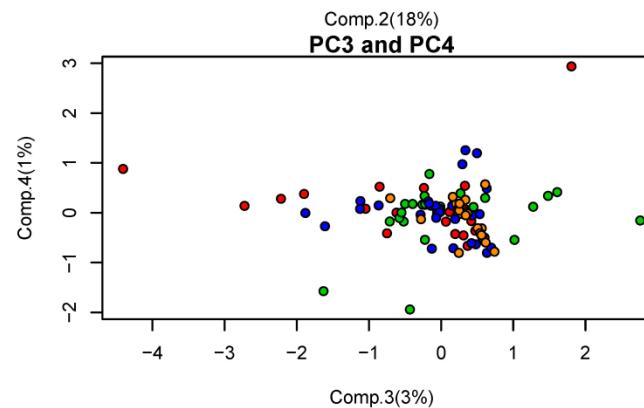
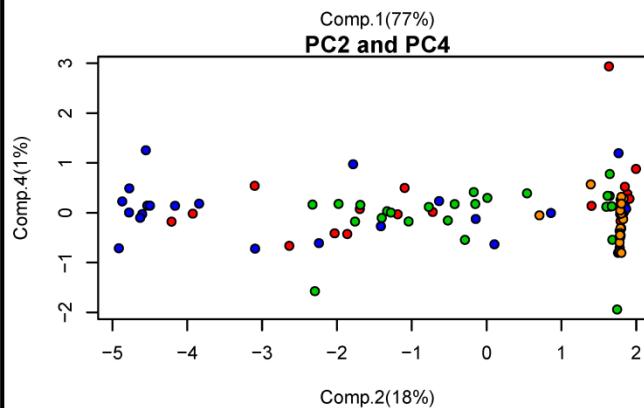
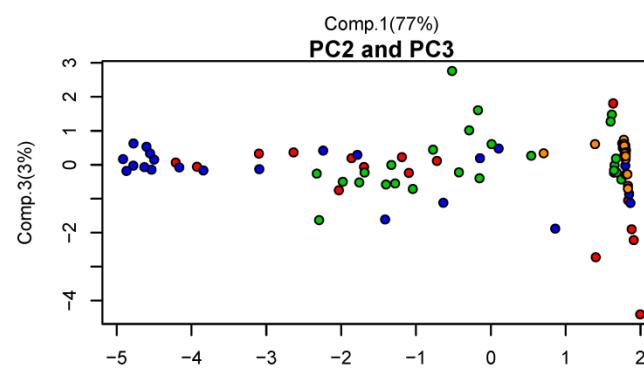
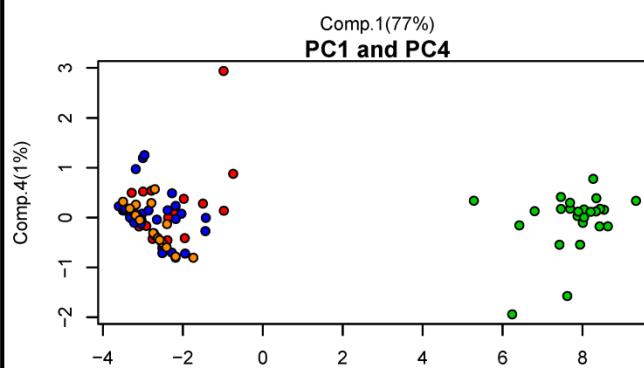
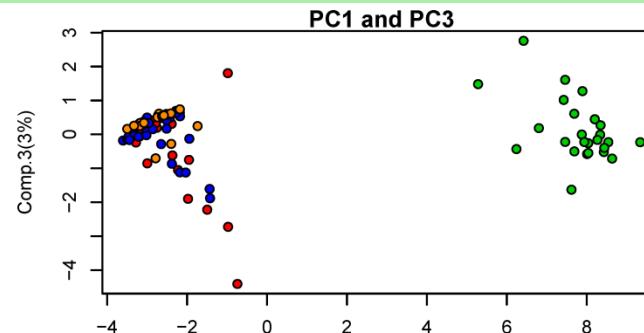
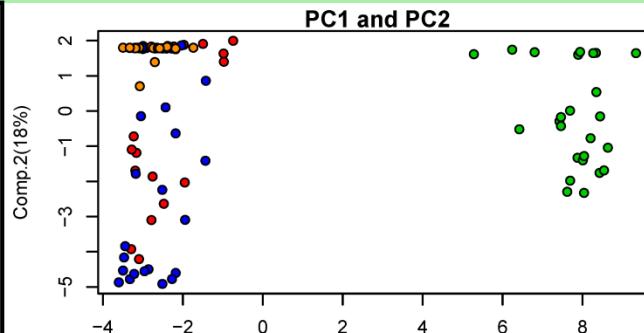
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5 genes with largest variance

Still PC1 separates the prostate samples (green)

However other tissues are difficult to separate

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4 out of 5 genes are highly correlated:

	ACPP	KLK2	KRT5	MSMB	TRGC2
ACPP	1.000000000	0.97567890	-0.004106762	0.90707887	0.947433227
KLK2	0.975678903	1.000000000	-0.029900946	0.89265825	0.951841913
KRT5	-0.004106762	-0.02990095	1.000000000	-0.05565599	0.008877815
MSMB	0.907078869	0.89265825	-0.055655985	1.00000000	0.870922667
TRGC2	0.947433227	0.95184191	0.008877815	0.87092267	1.000000000

GeneCards database:

- ACPP “is synthesized under androgen regulation and is secreted by the epithelial cells of the prostate gland”
- KLK2 “is primarily expressed in prostatic tissue and is responsible for cleaving pro-prostate-specific antigen into its enzymatically active form” (KLK3 is the PSA gene)
- MSMB “is synthesized by the epithelial cells of the prostate gland and secreted into the seminal plasma”

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genes which are not correlated to each other → clustering & prototype

Correlation of XMutiF4

	ABP1	ACPP	AKR1C1	ALDH1A3	ANXA8	APOD
ABP1	1.00000000	-0.1947766	-0.04224634	-0.21577195	-0.2618053	-0.3791812658
ACPP	-0.19477662	1.0000000	-0.22929893	0.88190657	-0.2978638	0.4964638048
AKR1C1	-0.04224634	-0.2292989	1.00000000	-0.07536066	0.4697886	-0.1793466620
ALDH1A3	-0.21577195	0.8819066	-0.07536066	1.00000000	-0.1727669	0.4113925823
ANXA8	-0.26180526	-0.2978638	0.46978864	-0.17276688	1.0000000	-0.1863923785
APOD	-0.37918127	0.4964638	-0.17934666	0.41139258	-0.1863924	1.0000000000

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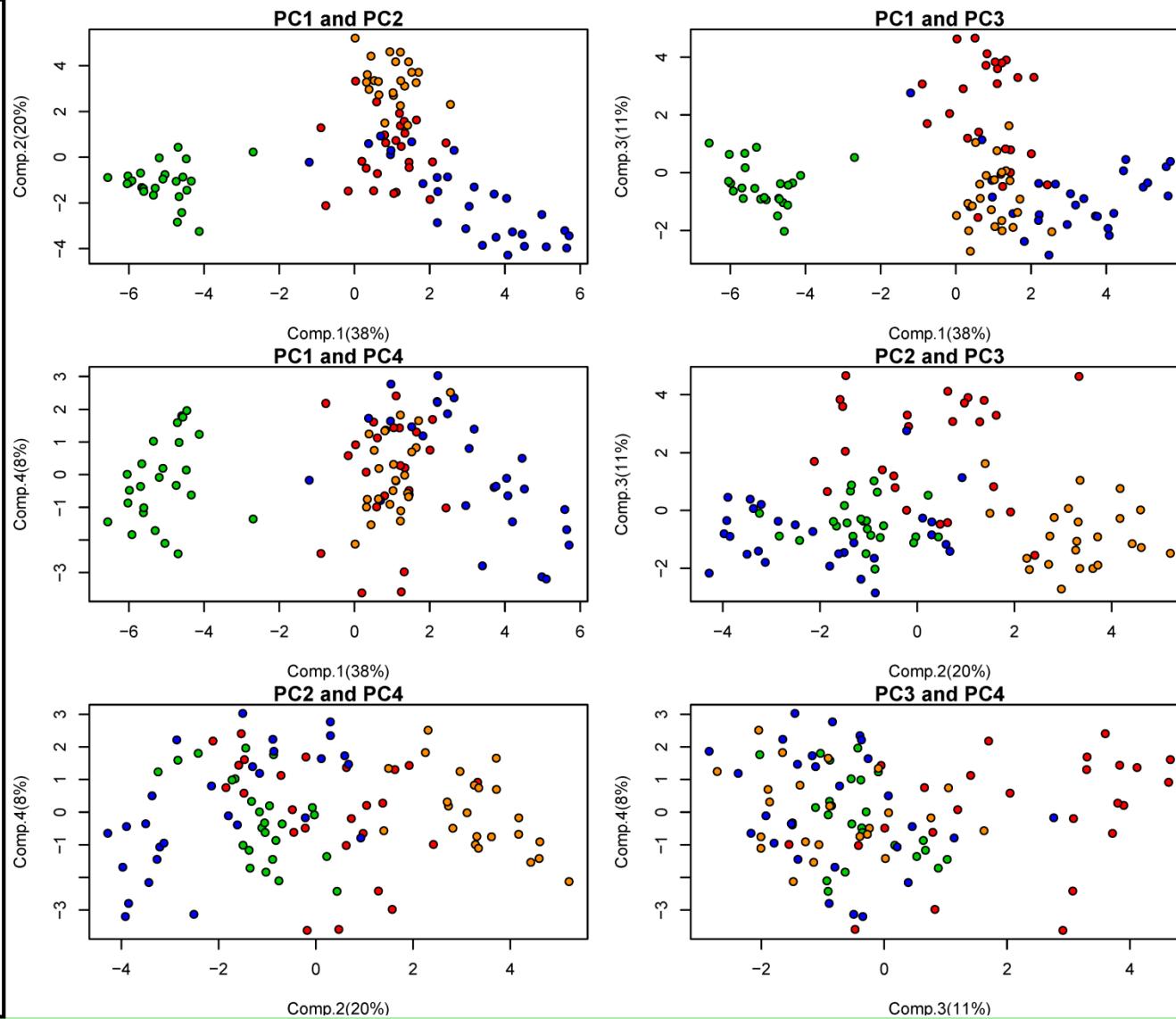
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10 uncorrelated genes

tissues are not as well separated as with maximal variance

→ highly variable genes missed

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hierarchical clustering and variance maximization within one cluster:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----

682	126	1631	742	347	797	196	104	44	35	5	8	12	5	12	14	5	71
-----	-----	------	-----	-----	-----	-----	-----	----	----	---	---	----	---	----	----	---	----

19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----

22	8	16	32	48	72	2	93	22	22	56	9	54	7	4	2	16	26
----	---	----	----	----	----	---	----	----	----	----	---	----	---	---	---	----	----

37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----

3	8	42	1	9	1	7	14	1	2	8	3	2	20	3	2	9	7
---	---	----	---	---	---	---	----	---	---	---	---	---	----	---	---	---	---

55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----

3	2	1	5	2	2	1	1	1	3	9	3	3	3	3	1	2	3
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----

1	1	1	1	2	2	1	3	1	2	1	1	2	1	2	2	1	1
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

91	92																
----	----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

1	1																
---	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

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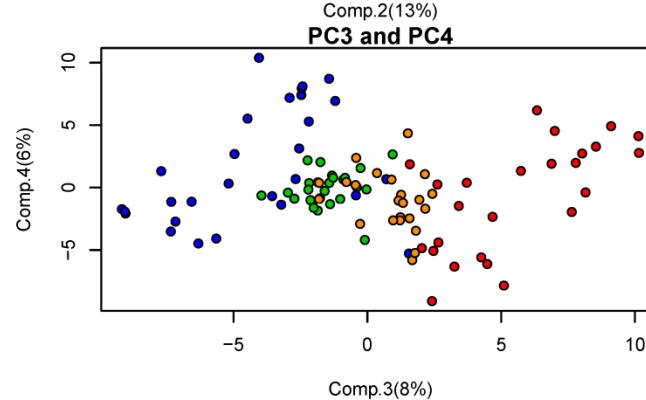
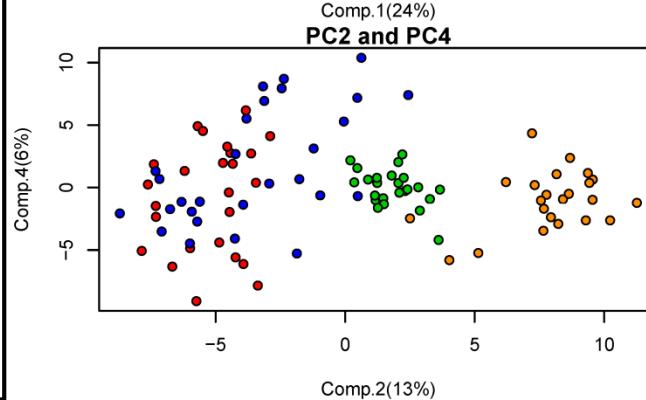
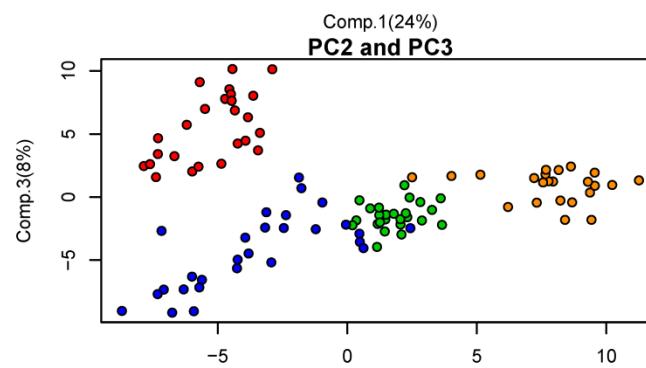
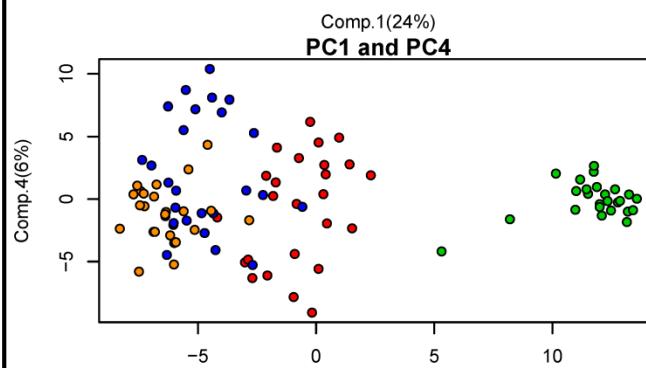
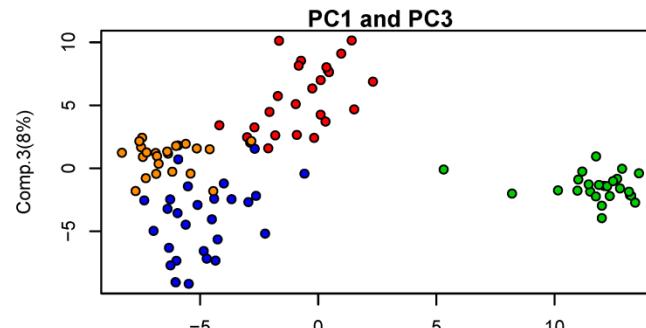
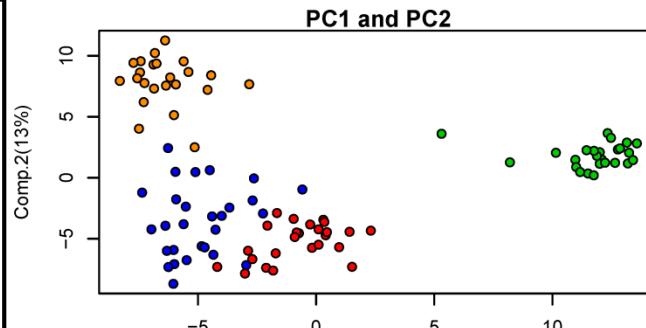
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92 genes uncorrelated but maximal variance

very similar to variance based feature selection

PC3 separates breast (red) from lung (blue) samp.

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Correlation as distance measure for clustering

Genes 2964 and 4663 are constant!

First remove these genes

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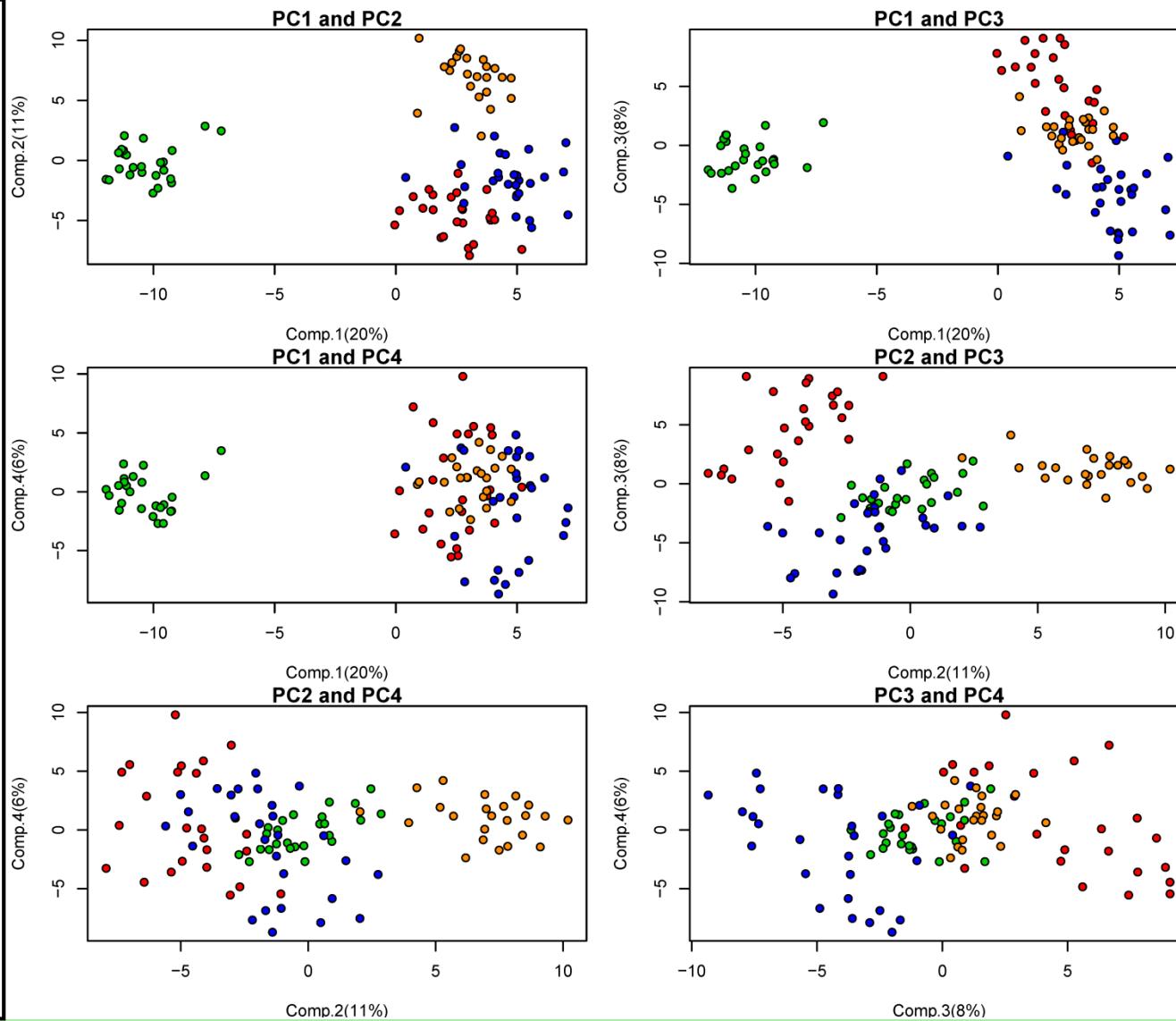
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clustering with correlation coefficient.
95 clusters: gene with maximal variance

very similar to variance based feature selection

PC3 separates breast (red) from lung (blue) samp.

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Kernel Principal Component Analysis or **kernel PCA** (KPCA) extends PCA to nonlinear projections using kernel techniques

linear operations of PCA are performed in a reproducing kernel Hilbert space to which the vectors are non-linearly mapped

$$\mathbf{x} \mapsto \Phi(\mathbf{x})$$

Assume data is centered in the feature space:

$$\sum_{i=1}^n \Phi(\mathbf{x}_i) = \mathbf{0}$$
 covariance matrix in feature space is given by

$$\mathbf{C} = \frac{1}{n} \sum_{i=1}^n \Phi(\mathbf{x}_i) \Phi^T(\mathbf{x}_i)$$

gram matrix:

$$\mathbf{K} : K_{ij} = \Phi^T(\mathbf{x}_j) \Phi(\mathbf{x}_i)$$

We search for

$$\mathbf{C} \mathbf{w} = \lambda \mathbf{w}$$

Problem: we only have

$$K_{ij} = k(\mathbf{x}_i, \mathbf{x}_j) = \Phi^T(\mathbf{x}_j) \Phi(\mathbf{x}_i)$$

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Principal components can be only in directions, where the data has variance (PCA maximizes the variance).

We restrict the **solutions to the span** of $\{\Phi(\mathbf{x}_1), \dots, \Phi(\mathbf{x}_n)\}$

$$\forall 1 \leq s \leq n : (\lambda \mathbf{w})^T \Phi(\mathbf{x}_s) = \lambda \mathbf{w}^T \Phi(\mathbf{x}_s) = \\ (\mathbf{C} \mathbf{w})^T \Phi(\mathbf{x}_s) = \mathbf{w}^T \mathbf{C} \Phi(\mathbf{x}_s)$$

$$\mathbf{C} \mathbf{w} = \lambda \mathbf{w}$$

The solutions of these equations are unique in the span of the mapped data vectors and correspond to eigenvectors of \mathbf{C} in the span.

$$\mathbf{w} = \sum_{i=1}^n \alpha_i \Phi(\mathbf{x}_i) \quad \text{Inserting this equation gives}$$

$$\lambda \sum_{i=1}^n \alpha_i \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}_s) = \\ \frac{1}{n} \left(\sum_{i=1}^n \alpha_i \sum_{j=1}^n \Phi^T(\mathbf{x}_i) (\Phi(\mathbf{x}_j) \Phi^T(\mathbf{x}_j)) \right) \Phi(\mathbf{x}_s)$$

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Gram matrix \mathbf{K} with $K_{ij} = \Phi^T(\mathbf{x}_j)\Phi(\mathbf{x}_i)$

We obtain from the last equation: $n \lambda \mathbf{K} \boldsymbol{\alpha} = \mathbf{K}^2 \boldsymbol{\alpha}$

solve the eigenvalue problem $n \lambda \boldsymbol{\alpha} = \mathbf{K} \boldsymbol{\alpha}$

The eigenvectors have to have length 1:

$$1 = \mathbf{w}^T \mathbf{w} = \sum_{ij=(1,1)}^{(n,n)} \alpha_i \alpha_j \Phi^T(\mathbf{x}_j)\Phi(\mathbf{x}_i) =$$

$$\sum_{ij=(1,1)}^{(n,n)} \alpha_i \alpha_j K_{ij} = \boldsymbol{\alpha}^T \mathbf{K} \boldsymbol{\alpha} = n \lambda \boldsymbol{\alpha}^T \boldsymbol{\alpha}$$

$$n \lambda \|\boldsymbol{\alpha}\|^2 = 1$$

$$\|\boldsymbol{\alpha}\| = \frac{1}{\sqrt{n \lambda}}$$

$$\alpha_i^{\text{new}} = \frac{\alpha_i}{\|\boldsymbol{\alpha}\| \sqrt{n \lambda}}$$

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The projection onto the eigenvectors can be computed as

$$\mathbf{w}^T \Phi(\mathbf{x}) = \sum_{i=1}^n \alpha_i \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}) = \sum_{i=1}^n \alpha_i k(\mathbf{x}_i, \mathbf{x})$$

data centering in feature space:

$$\begin{aligned} & \left(\Phi(\mathbf{x}_i) - \frac{1}{n} \sum_{t=1}^n \Phi(\mathbf{x}_t) \right)^T \left(\Phi(\mathbf{x}_j) - \frac{1}{n} \sum_{t=1}^n \Phi(\mathbf{x}_t) \right) = \\ & \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}_j) - \frac{1}{n} \sum_{t=1}^n \Phi^T(\mathbf{x}_t) \Phi(\mathbf{x}_j) - \frac{1}{n} \sum_{t=1}^n \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}_t) + \\ & \frac{1}{n^2} \sum_{(s,t)=(1,1)}^{(n,n)} \Phi^T(\mathbf{x}_s) \Phi(\mathbf{x}_t) \end{aligned}$$

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$$\frac{1}{n} \sum_{t=1}^n \Phi^T(\mathbf{x}_t) \Phi(\mathbf{x}_i) = \left[\frac{1}{n} \mathbf{K} \mathbf{1} \right]_i$$

$$\frac{1}{n} \sum_{t=1}^n \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}_t) = \left[\frac{1}{n} \mathbf{1}^T \mathbf{K} \right]_i$$

$$\frac{1}{n^2} \sum_{(s,t)=(1,1)}^{(n,n)} \Phi^T(\mathbf{x}_s) \Phi(\mathbf{x}_t) = \frac{1}{n^2} \mathbf{1}^T \mathbf{K} \mathbf{1}$$

centered kernel matrix:

$$\mathbf{K} - \frac{1}{n} \mathbf{K} \mathbf{1} \mathbf{1}^T - \frac{1}{n} \mathbf{1} \mathbf{1}^T \mathbf{K} + \frac{1}{n^2} (\mathbf{1}^T \mathbf{K} \mathbf{1}) \mathbf{1} \mathbf{1}^T$$

new data point:

$$\mathbf{k}(\mathbf{x}, \cdot) = (k(\mathbf{x}, \mathbf{x}_1), \dots, k(\mathbf{x}, \mathbf{x}_l))^T$$

$$\mathbf{k}(\mathbf{x}, \cdot) - \frac{1}{n} \mathbf{K} \mathbf{1} - \frac{1}{n} \mathbf{1}^T \mathbf{k}(\mathbf{x}, \cdot) \mathbf{1} + \frac{1}{n^2} (\mathbf{1}^T \mathbf{K} \mathbf{1}) \mathbf{1}$$

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Given: gram matrix \mathbf{K} with $K_{ij} = k(\mathbf{x}_i, \mathbf{x}_j)$

Centering

center the Gram matrix $\mathbf{K} - \frac{1}{n} \mathbf{K} \mathbf{1} \mathbf{1}^T - \frac{1}{n} \mathbf{1} \mathbf{1}^T \mathbf{K} + \frac{1}{n^2} (\mathbf{1}^T \mathbf{K} \mathbf{1}) \mathbf{1} \mathbf{1}^T$

Eigenvalues

compute eigenvectors $\boldsymbol{\alpha}$ and eigenvalues λ of the Gram matrix \mathbf{K}

Normalization

normalize eigenvectors $\boldsymbol{\alpha}^{new} = \frac{\boldsymbol{\alpha}_i}{\|\boldsymbol{\alpha}\| \sqrt{n} \lambda}$

Projection of a new vector

project a new vector \mathbf{x} onto eigenvectors by center and project it

$$\mathbf{k}(\mathbf{x}, \cdot) = \frac{1}{n} \mathbf{K} \mathbf{1} - \frac{1}{n} \mathbf{1}^T \mathbf{k}(\mathbf{x}, \cdot) \mathbf{1} + \frac{1}{n^2} (\mathbf{1}^T \mathbf{K} \mathbf{1}) \mathbf{1}$$

$$\mathbf{w}^T \Phi(\mathbf{x}) = \sum_{i=1}^n \alpha_i \Phi^T(\mathbf{x}_i) \Phi(\mathbf{x}) = \sum_{i=1}^n \alpha_i k(\mathbf{x}_i, \mathbf{x})$$

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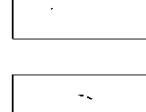
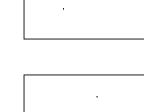
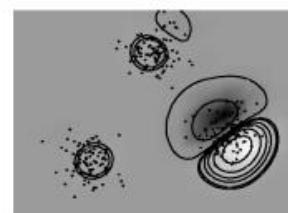
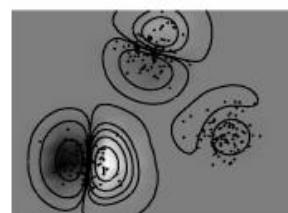
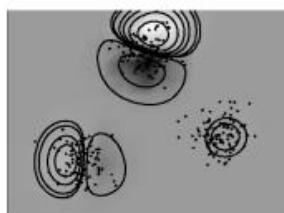
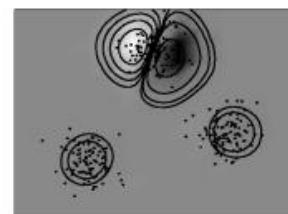
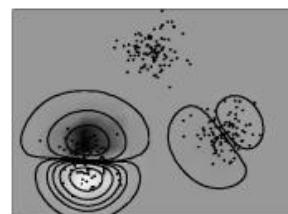
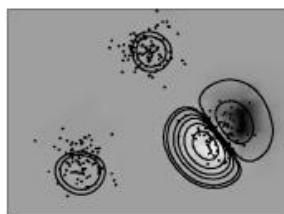
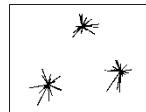
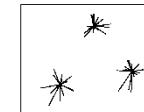
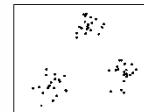
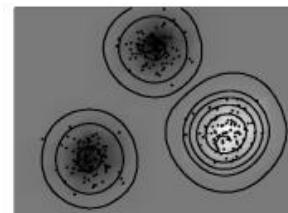
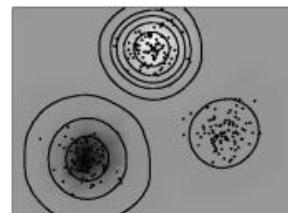
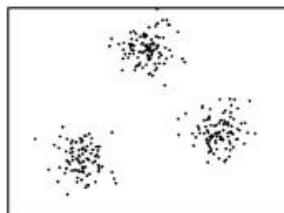
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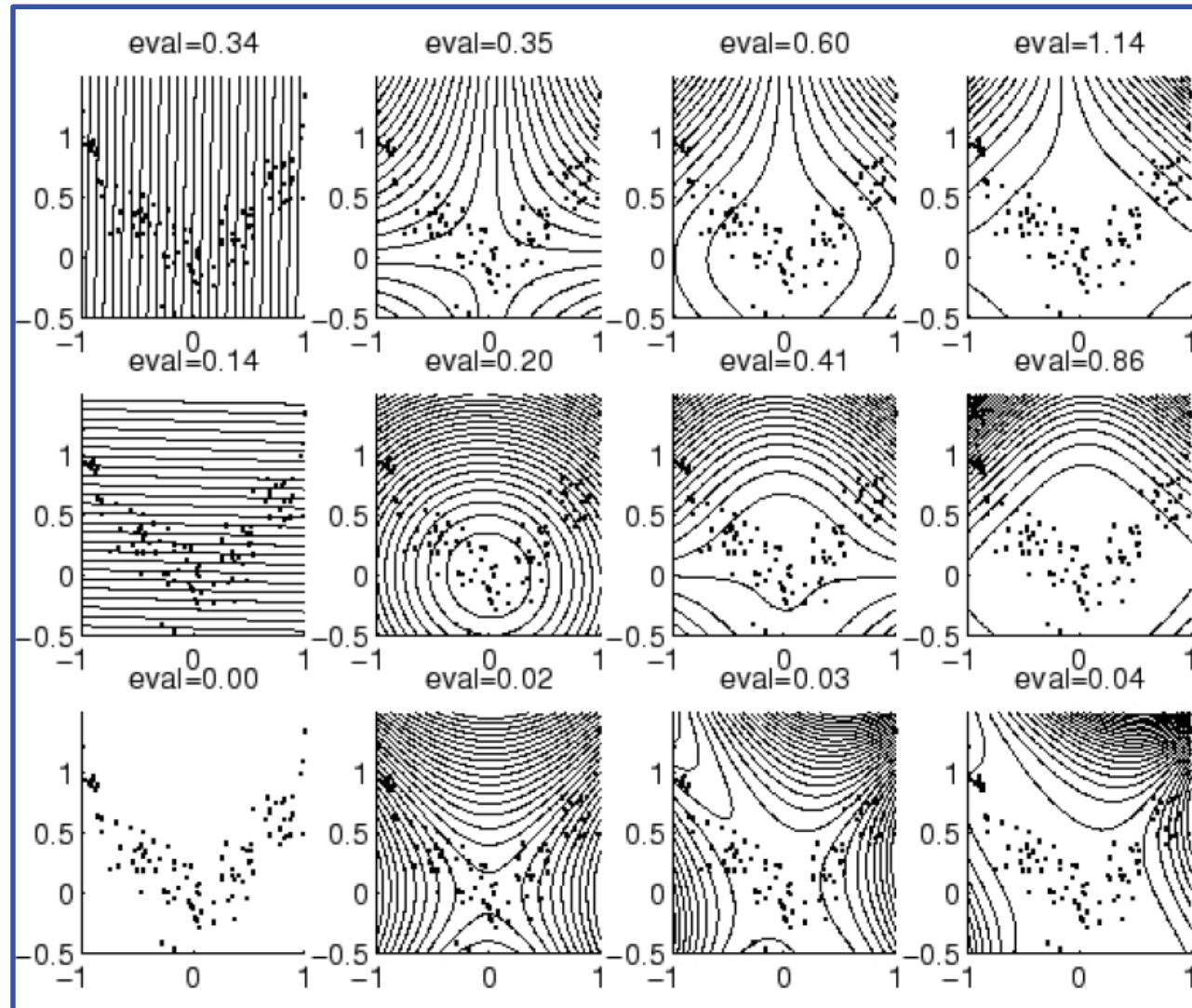
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Independent component analysis (ICA): statistically independent components

ICA differs from PCA:

- ICA does not maximize the variance,
- ICA does not enforce orthogonal projection or demixing matrices,
- ICA aims at statistically independent components,
- ICA components are not ranked.

Generative: $\mathbf{x} = \mathbf{U} \mathbf{y}$ independent sources:

Descriptive: $\mathbf{y} = \mathbf{W} \mathbf{x}$ $p(\mathbf{y}) = \prod_{j=1}^l p(y_j) \quad l \leq m$
 $\mathbf{W} = \mathbf{U}^{-1}$

matrix decomposition: $\mathbf{X} = \mathbf{Y} \mathbf{U}^T$

$\mathbf{Y}^T \mathbf{Y} = \mathbf{D}_m \rightarrow$ decorrelated but even statistically independent

\mathbf{U} is not required to be orthogonal

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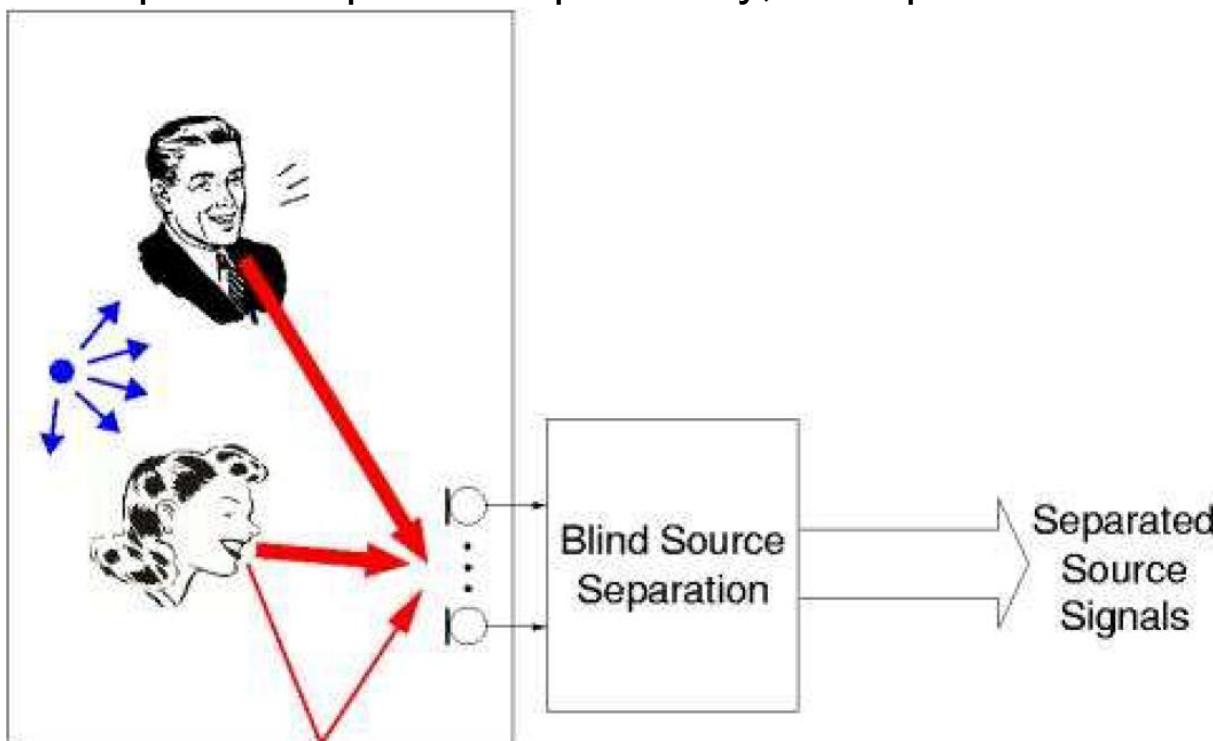
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The outer product representation is $\mathbf{X} = \sum_{j=1}^l \mathbf{y}_j \mathbf{u}_j^T$

\mathbf{u}_j j -th column vector of \mathbf{U}

\mathbf{y}_j j -th column vector of \mathbf{Y}

two speakers speak independently; microphones record acoustic signals



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Original:



Mixtures:



Demixed by ICA:



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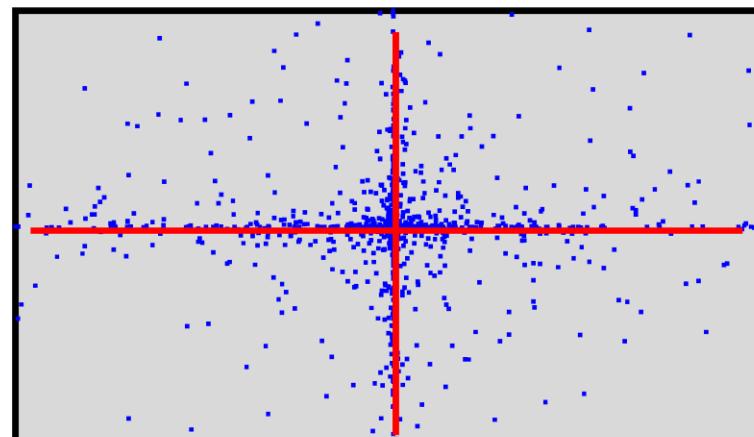
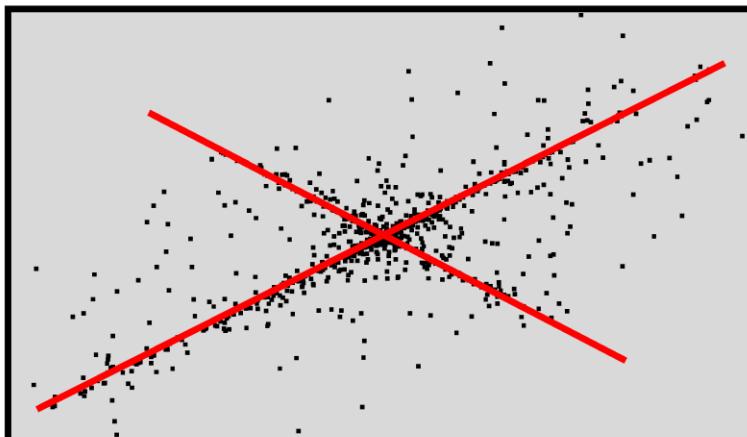
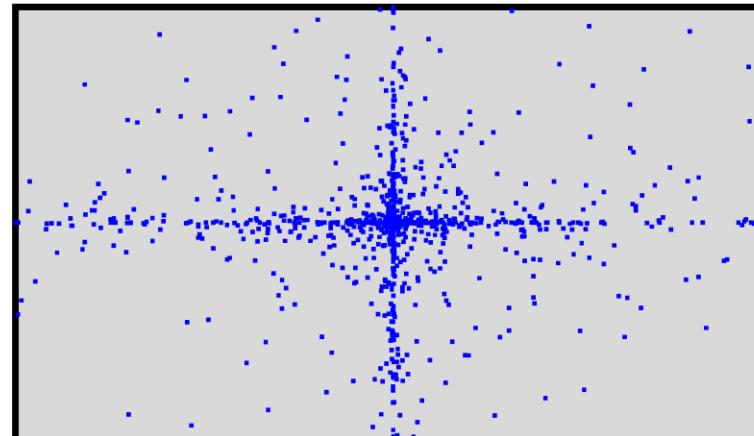
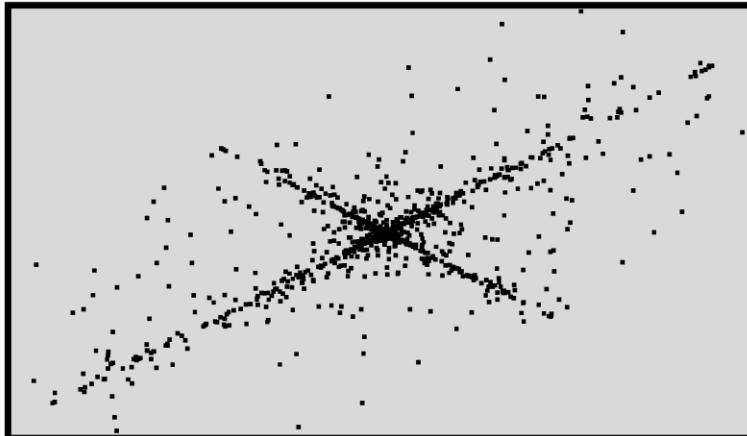
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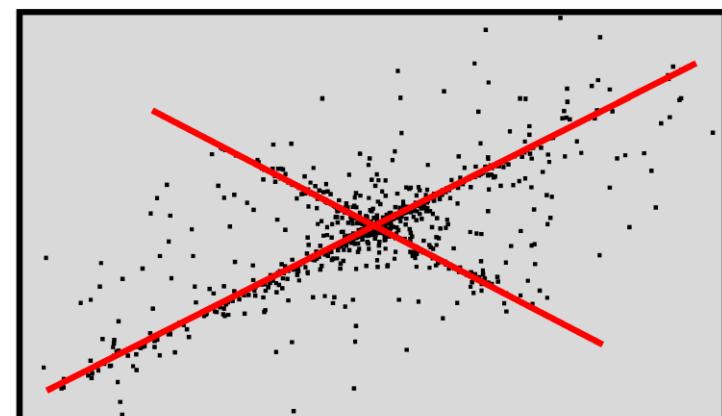
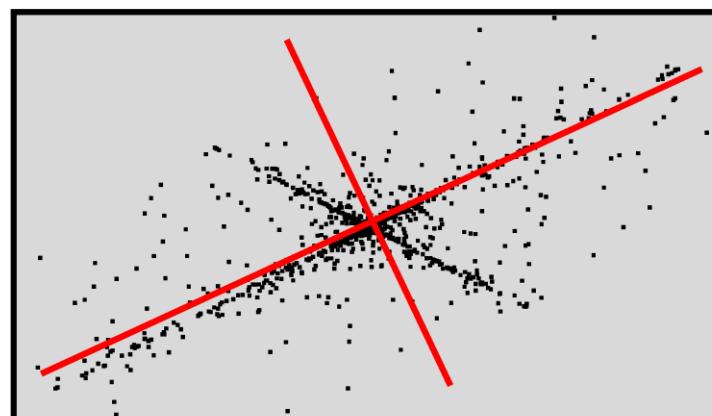
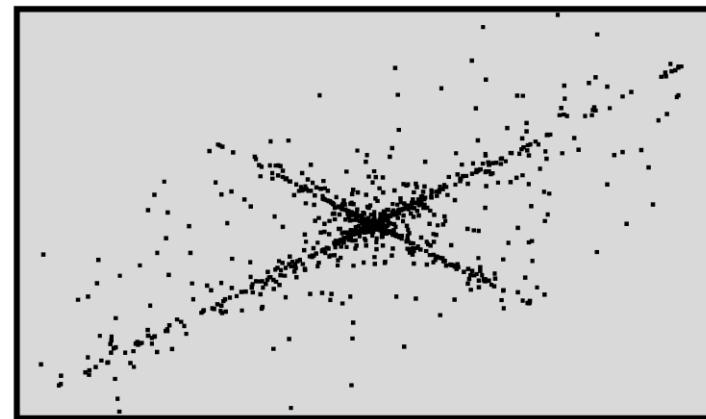
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ICA solution is not unique: $\mathbf{x} = \mathbf{U} \mathbf{P}^{-1} \mathbf{P} \mathbf{y}$

another solution \mathbf{Y}' we have $\mathbf{Y}' = \mathbf{P} \mathbf{Y}$
with $\mathbf{Y}'^T \mathbf{Y}' = \mathbf{D}'_m$

Theorem 1 (Darmois' theorem (1953))

Define the two random variables x_1 and x_2 as

$$x_1 = \sum_{j=1}^m a_j y_j \quad \text{and} \quad x_2 = \sum_{j=1}^m b_j y_j$$

where y_i are independent random variables. Then if x_1 and x_2 are independent, all variables y_j for which $a_j b_j \neq 0$ are Gaussian.

if two variables are independent from each other and they are a weighted sum of independent variables, then they are constructed by mutually different variables.

The exception in the theorem are Gaussian distributions.

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$$\mathbf{Y}' = \mathbf{P} \mathbf{Y}$$

\mathbf{P} cannot mix the statistically independent components of \mathbf{y}

$\Rightarrow \mathbf{P}$ is a product of a permutation and a scaling matrix

The ICA solution is for non-Gaussian sources unique up to permutation and scaling

ICA assumptions:

- non-Gaussian sources
- $l \leq m$ at least as many observations as sources
- \mathbf{U} has full rank l

Let $l = m$ and $\mathbf{U}^{-1} \in \mathbb{R}^{m \times m}$ exists \rightarrow generative framework

generative framework: assumptions on the densities $p(y_i)$

approximated by super-Gaussians or unimodal distributions

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objective for measuring independence

$$p(y_i \mid y_1, \dots, y_{i-1}, y_{i+1}, \dots, y_l) = p(y_i)$$

more than pairwise independence

Two criteria for independence:

- mutual information between components
- non-Gaussianity of components

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Mutual information: entropy of a factorial code is larger than the entropy of the joint distribution

$$I(y_1, \dots, y_l) = \sum_{j=1}^l H(y_j) - H(\mathbf{y})$$

where H denotes the entropy $H(\mathbf{a}) = - \int p(\mathbf{a}) \ln p(\mathbf{a}) d\mathbf{a}$

$$\mathbf{y} = \mathbf{W} \mathbf{x}$$

$$I(y_1, \dots, y_m) = \sum_{j=1}^m H(y_j) - H(\mathbf{x}) - \ln |\mathbf{W}|$$

where $|\mathbf{W}|$ is the absolute value of the determinant

$$p(\mathbf{y}) = \frac{p(\mathbf{x})}{|\mathbf{W}|}$$

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Non-Gaussianity

$$\text{Negentropy: } J(\mathbf{y}) = H(\mathbf{y}_{\text{gauss}}) - H(\mathbf{y})$$

where $\mathbf{y}_{\text{gauss}}$ is a Gaussian random vector with the same covariance matrix as \mathbf{y}

maximizing the negentropy \rightarrow minimizes mutual information

Gaussian: distribution with max. entropy given mean and variance
 \rightarrow negentropy is closely related to entropy maximization

estimation of the negentropy is difficult

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non-Gaussianity is measured by other parameters, e.g.
fourth cumulant (the **kurtosis** $E(x^4) / E(x^2)^2$)

$$\kappa_1 = E(x) = 0$$

$$\kappa_2 = E(x^2)$$

$$\kappa_3 = E(x^3)$$

$$\kappa_4 = E(x^4) - 3(E(x^2))^2$$

Gaussians:

$$\kappa_3 = \kappa_4 = 0$$

positive kurtosis: super-Gaussians (smaller tails than Gaussians)
negative kurtosis: sub-Gaussians (larger tails than Gaussians)

For x_1 and x_2 independent: $\kappa_4(x_1 + x_2) = \kappa_4(x_1) + \kappa_4(x_2)$

$$\kappa_4(\alpha x) = \alpha^4 \kappa_4(x)$$

For super-Gaussians the kurtosis should be maximized because mixtures have a smaller kurtosis than the original sources.

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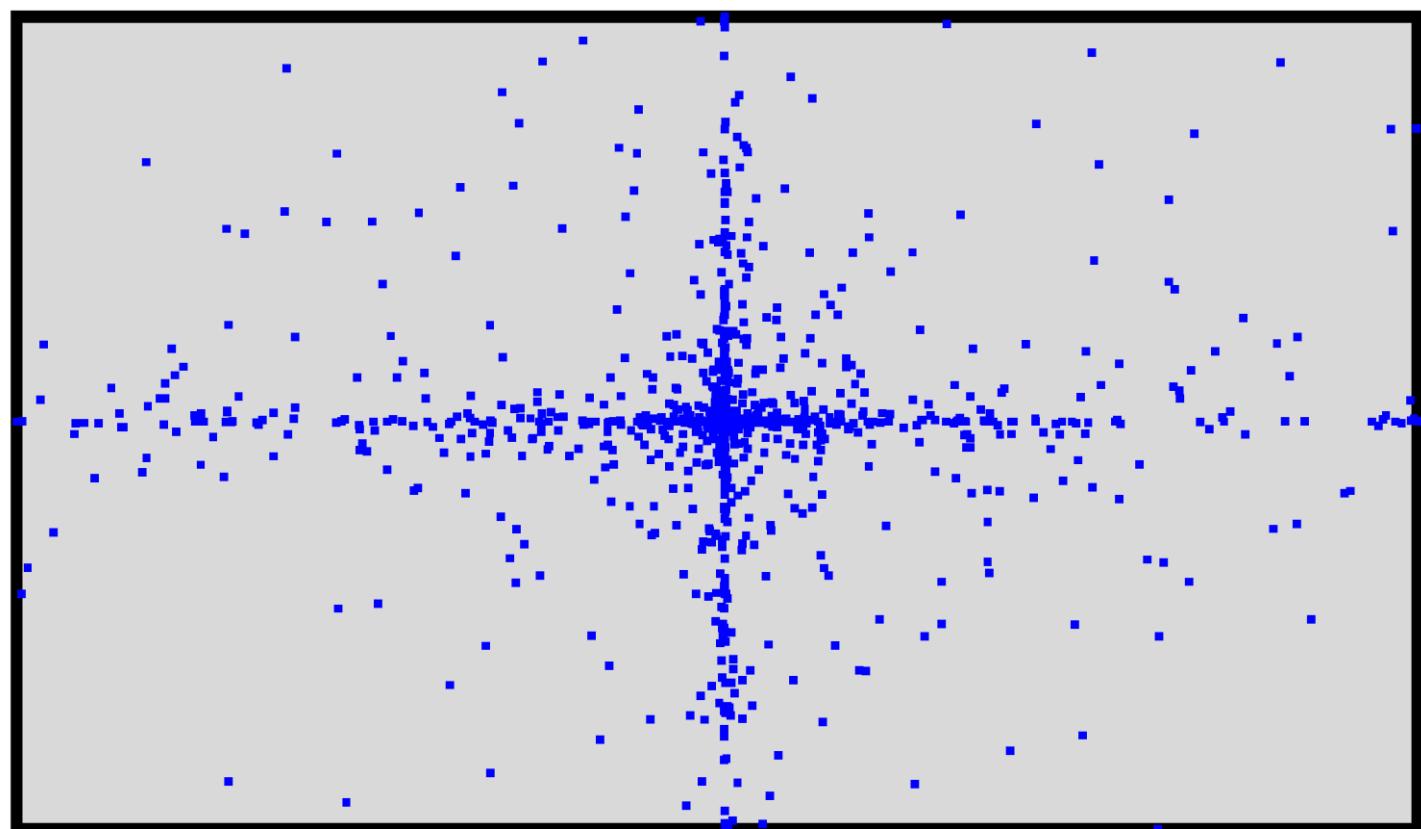
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maximizing the kurtosis = maximizing the sparseness

Sparseness: variable rarely deviates from zero; it deviates the values are relatively large compared to Gaussian with the same variance.
→ sparseness does not mean small variance



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kurtosis: fourth moments → not robust; affected by outliers

contrast functions: measure independence of the variables:

- kurtosis: $\kappa_4(y)$
- $\frac{1}{12} \kappa_3^2(y) + \frac{1}{48} \kappa_4^2(y)$, where the variable y is normalized to zero mean and unit variance
- $|E_y(G(y)) - E_\nu(G(\nu))|^p$, where ν is a standardized Gaussian, $p=1,2$, and y is normalized to zero mean and unit variance. Here G can be the kurtosis for which $G(\nu)=0$ would hold. Other choices for G are $G(x) = \log \cosh(ax)$ and $G(x) = \exp(-ax^2/2)$ with $a \geq 1$

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Maximization

whitening and rotation

independence measured by non-Gaussianity, e.g. FastICA

whitened or sphered data: $\mathbf{Y}^T \mathbf{Y} = \mathbf{I}$ $\mathbf{x} = \mathbf{y} \mathbf{U}^T$ $\mathbf{y} = \mathbf{x} \mathbf{U}^{-T}$

first step in ICA: sphere data because ICA is not unique up to scaling

$$\mathbf{I} = \mathbf{C}^{-1/2} \underbrace{\frac{1}{n} \mathbf{X}^T \mathbf{X}}_{\mathbf{C}} \mathbf{C}^{-1/2} = \frac{1}{n} \mathbf{C}^{-1/2} \mathbf{U} \mathbf{Y}^T \mathbf{Y} \mathbf{U}^T \mathbf{C}^{-1/2} = \frac{1}{n} \mathbf{C}^{-1/2} \mathbf{U} \mathbf{U}^T \mathbf{C}^{-1/2}$$

$\hat{\mathbf{U}} = \frac{1}{\sqrt{n}} \mathbf{C}^{-1/2} \mathbf{U}$ \leftarrow is orthogonal $\mathbf{C}^{-1/2}$ is symmetric $\hat{\mathbf{U}}^T$ is orthogonal

$$\mathbf{Y} = \frac{\sqrt{n}}{\sqrt{n}} \mathbf{X} \mathbf{C}^{-1/2} \mathbf{C}^{1/2} \mathbf{U}^{-T} = \frac{1}{\sqrt{n}} \mathbf{X} \mathbf{C}^{-1/2} \hat{\mathbf{U}}^{-T} = \frac{1}{\sqrt{n}} \mathbf{X} \mathbf{C}^{-1/2} \hat{\mathbf{U}}$$

First whitening $\mathbf{X} \mathbf{C}^{-1/2}$ then determine orthogonal $\hat{\mathbf{U}}$ (rotation)

Objective of rotation is super-Gaussian (kurtosis) or sparseness

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INFOMAX minimizes the mutual information between components

the entropy $H(\mathbf{g}(\mathbf{y}))$ is maximized, where $\mathbf{g}(\mathbf{y}) = (g(y_1), g(y_2), \dots, g(y_l))$

$$\mathbf{y} = \mathbf{W} \mathbf{x}$$

Maximal entropy: $I(g(y_1), \dots, g(y_l)) = \sum_{j=1}^l H(g(y_j)) - H(\mathbf{g}(\mathbf{y})) = 0$

and the components $(g(y_1), \dots, g(y_l))$ are statistically independent

common choice: $g(y_i) = \tanh(y_i)$

$$p(\mathbf{g}(\mathbf{y})) = p(\mathbf{x}) \left| \frac{\partial \mathbf{g}(\mathbf{y})}{\partial \mathbf{y}} \frac{\partial \mathbf{y}}{\partial \mathbf{x}} \right|^{-1} = p(\mathbf{x}) \left| \frac{\partial \mathbf{g}(\mathbf{y})}{\partial \mathbf{y}} \mathbf{W} \right|^{-1}$$

$$\left| \frac{\partial \mathbf{g}(\mathbf{y})}{\partial \mathbf{y}} \mathbf{W} \right| = \left| \prod_{j=1}^l g'(y_j) \right| |\mathbf{W}|$$

generative framework: $g'(y_i) = p(y_i)$

g represents a (transformed) probability function

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Entropy: $H(\mathbf{g}(\mathbf{y})) = \text{E}(-\ln p(\mathbf{g}(\mathbf{y}))) = H(\mathbf{x}) + \text{E}\left(\sum_{j=1}^l |\ln g'(y_j)|\right) + \ln |\mathbf{W}|$

$$\mathbf{y}_i = \mathbf{W} \mathbf{x}_i \approx H(\mathbf{x}) + \frac{1}{n} \sum_{i=1}^n \sum_{j=1}^l |\ln g'(y_{ij})| + \ln |\mathbf{W}|$$

tanh:

$$g(y_j) = \tanh(y_j) \text{ gives } \frac{\partial}{\partial \mathbf{w}_j} \ln g'(y_j) = \frac{g''(y_j)}{g'(y_j)} \mathbf{x}^T = -2 g(y_j) \mathbf{x}^T$$

sigmoid:

$$g(y_j) = \frac{1}{1 + e^{-y_j}} \text{ gives } \frac{\partial}{\partial \mathbf{w}_j} \ln g'(y_j) = (1 - 2 g(y_j)) \mathbf{x}^T$$

$$\frac{\partial}{\partial \mathbf{W}} \ln |\mathbf{W}| = (\mathbf{W}^T)^{-1}$$

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tanh:

$$\frac{\partial}{\partial \mathbf{W}} H(\mathbf{g}(\mathbf{y})) = (\mathbf{W}^T)^{-1} - 2 \mathbf{g}(\mathbf{y}) \mathbf{x}^T$$

sigmoid:

$$\frac{\partial}{\partial \mathbf{W}} H(\mathbf{g}(\mathbf{y})) = (\mathbf{W}^T)^{-1} + (1 - 2 \mathbf{g}(\mathbf{y})) \mathbf{x}^T$$

Update rules:

tanh:

$$\Delta \mathbf{W} \propto (\mathbf{W}^T)^{-1} - 2 \mathbf{g}(\mathbf{y}) \mathbf{x}^T$$

sigmoid:

$$\Delta \mathbf{W} \propto (\mathbf{W}^T)^{-1} + (1 - 2 \mathbf{g}(\mathbf{y})) \mathbf{x}^T$$

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Natural Gradient multiplied with $W^T W$

tanh:

$$\Delta W \propto (I - 2 g(y) y^T) W$$

sigmoid:

$$\Delta W \propto (I + (1 - 2 g(y)) y^T) W$$

INFOMAX is equivalent to a generative approach using maximum likelihood

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EASI Equivariant Adaptive Separation via Independence (EASI)

Update rule:

$$\Delta \mathbf{W} \propto (\mathbf{I} - \mathbf{y} \mathbf{y}^T - \mathbf{g}(\mathbf{y}) \mathbf{y}^T + \mathbf{y} \mathbf{g}^T(\mathbf{y})) \mathbf{W}$$

nonlinear functions g are the same contrast functions as for INFOMAX

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FastICA: probably the most popular ICA algorithm

- whitening and rotation algorithm
- FastICA is a fixed point algorithm (like Oja's rule for PCA)
- kurtosis maximization but extended to other contrast functions

$$\mathbf{w}^{\text{new}} = \mathbb{E}(\mathbf{x} g(\mathbf{w}^T \mathbf{x})) - \mathbb{E}(g'(\mathbf{w}^T \mathbf{x})) \mathbf{w}$$

contrast function: g with derivative g'

FastICA has been extended to extract multiple components

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ICA extensions:

- generative approach
- sub-Gaussian distributions with specific assumptions
- non-linear extensions which are often not unique
- overcomplete basis more sources than observations $l > m$
- fewer sources than observations $l < m$

ICA vs. PCA:

independent component analysis	principal component analysis
causes of the data	geometrical abstractions
statistical independent	decorrelated (orthogonal)
explain super-Gaussians	explain all variance
scale invariant	not scale invariant
unique up to scale and permutation	unique
assume super-Gauss	no assumptions
no ranking	ranked by eigenvalues

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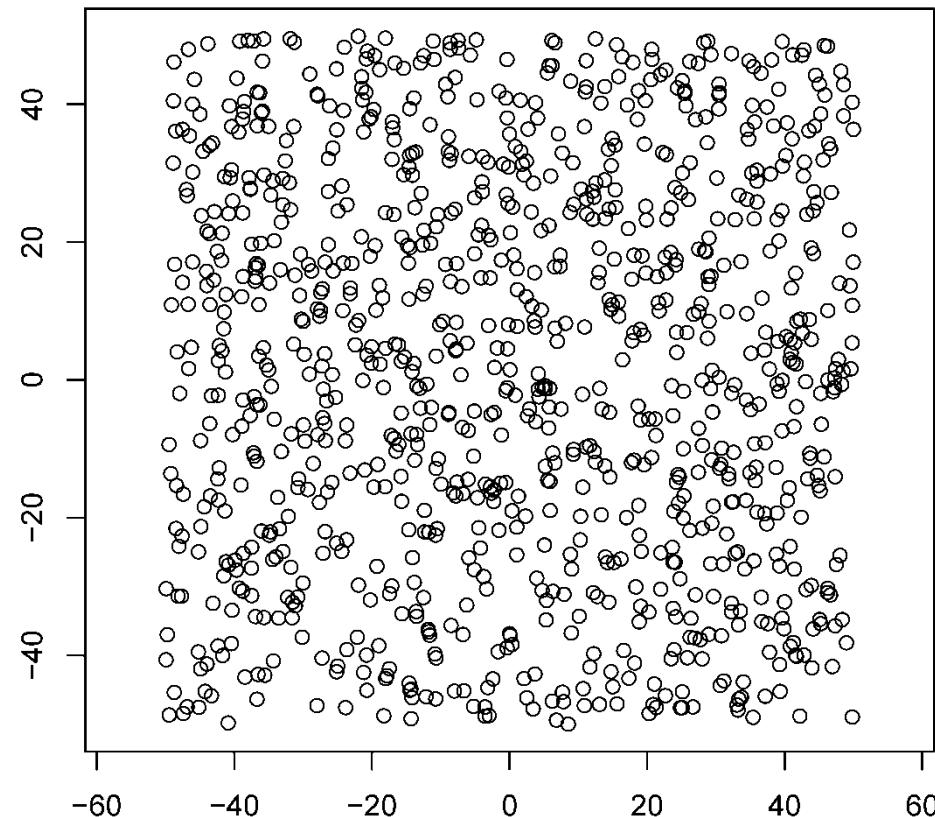
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whitening and rotation for artificial data

1,000 data points drawn from uniform distributions:



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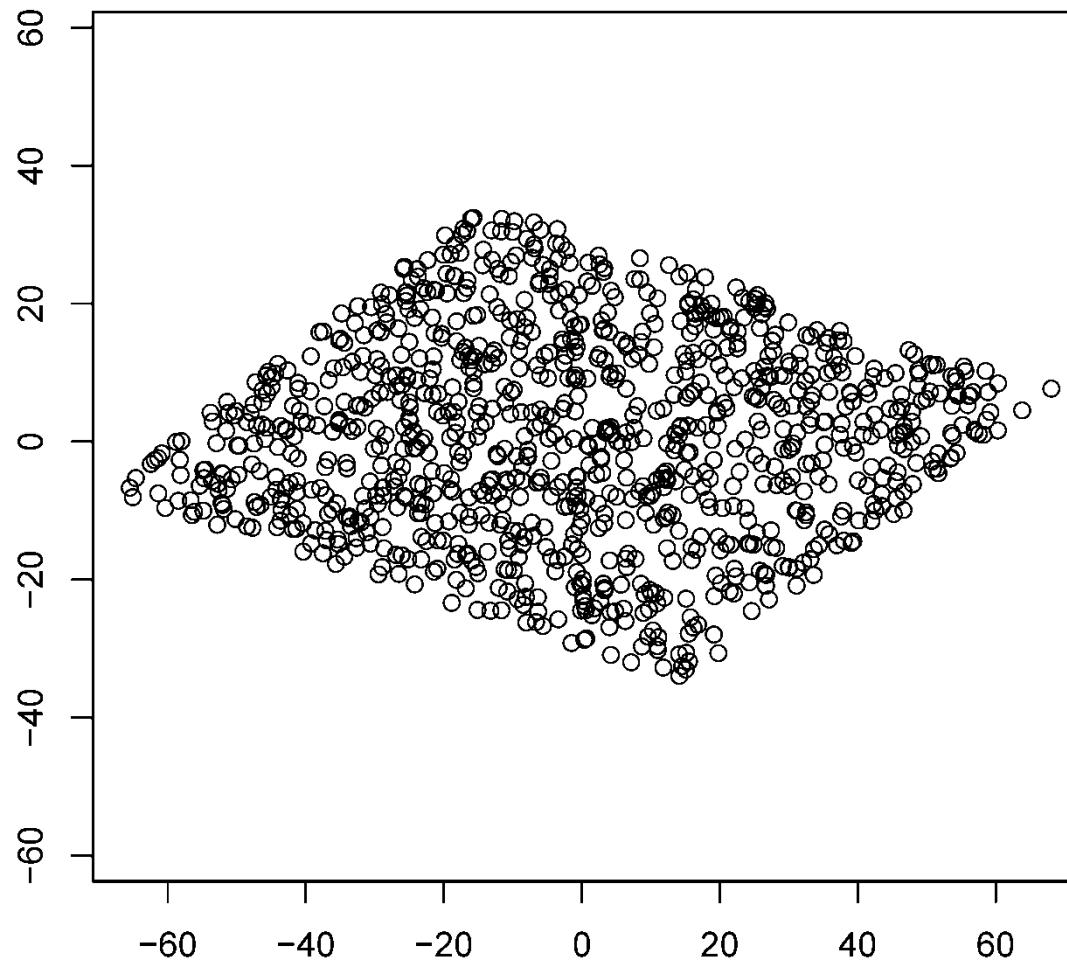
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Mixing gives dependent components: observations



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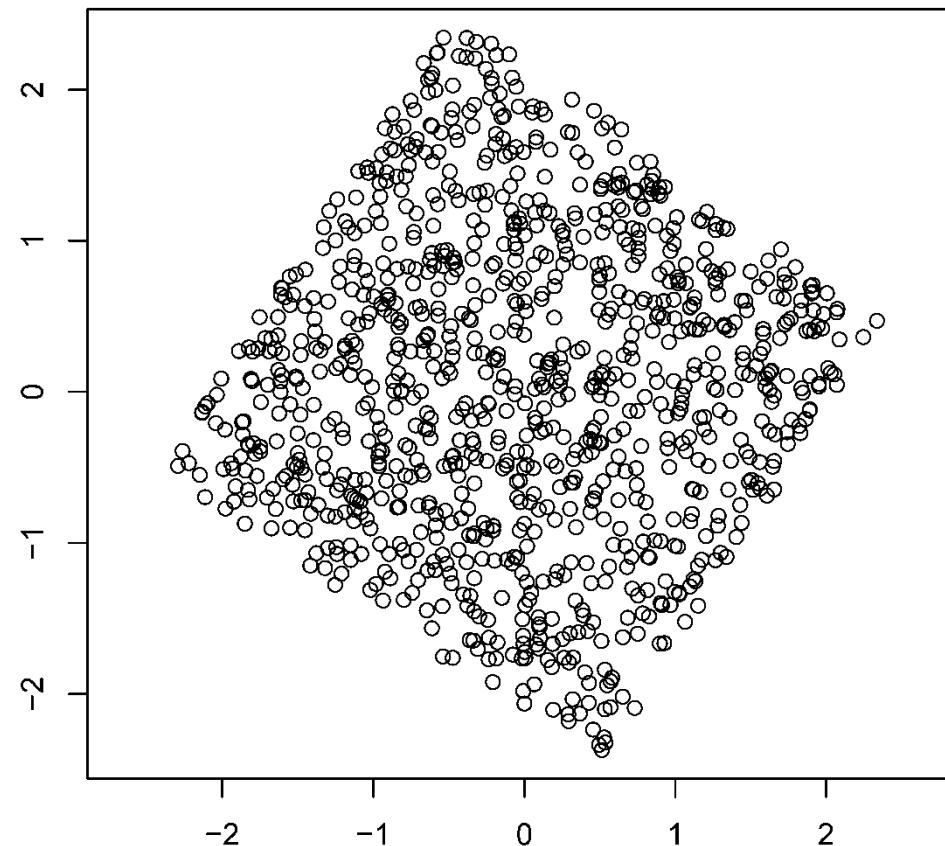
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Whitening of the mixed data:



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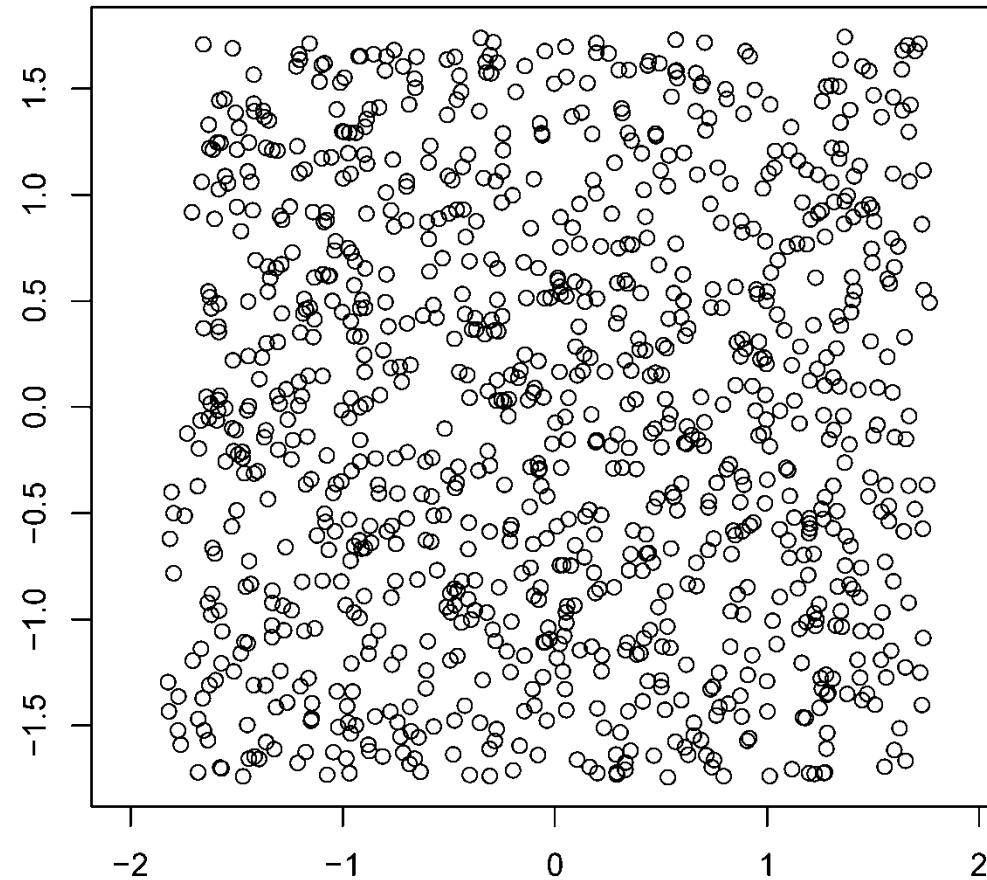
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Rotation of the whitened data:



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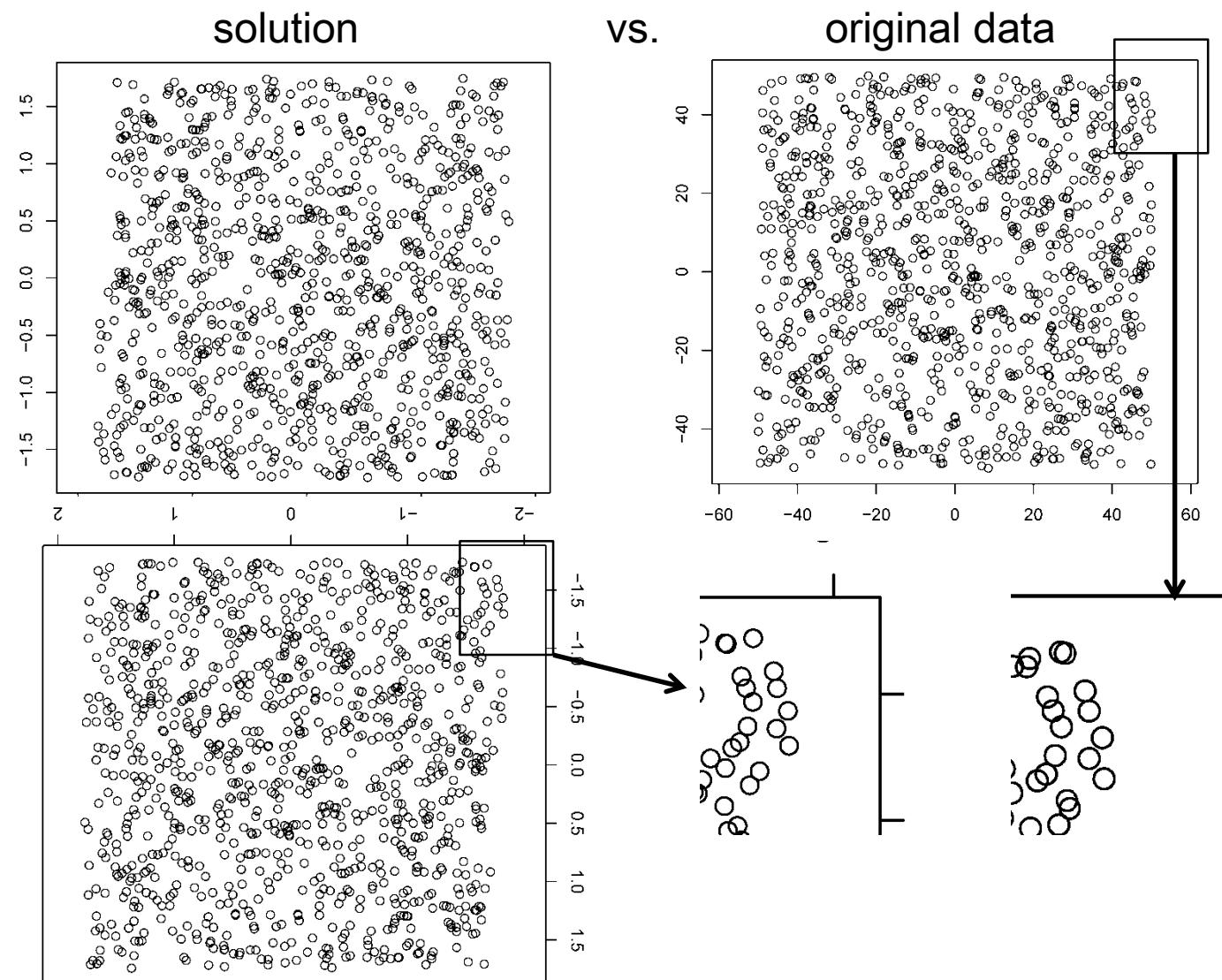
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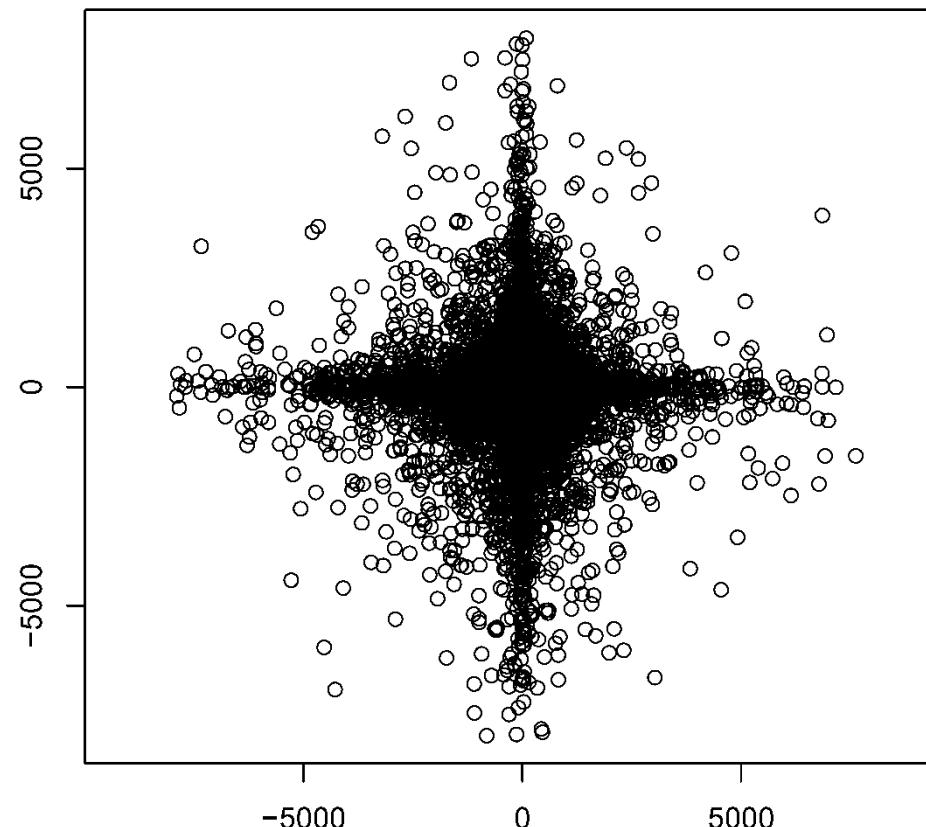
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Toy example with super-Gaussians:



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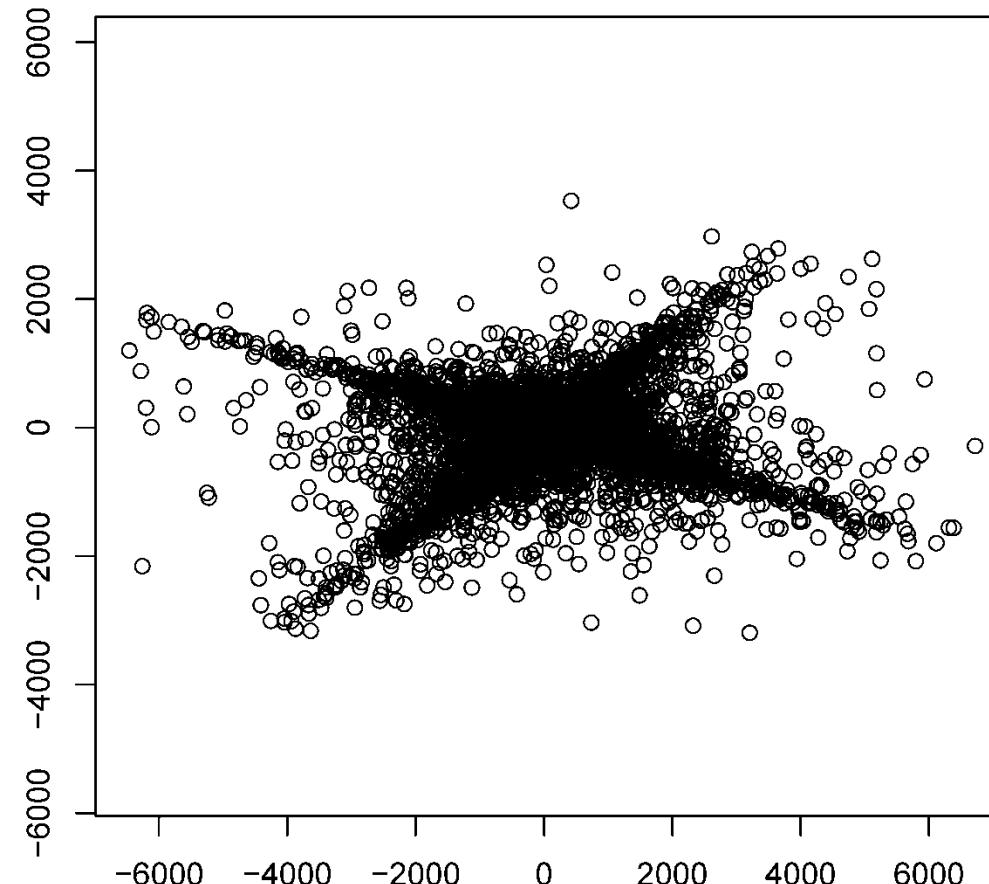
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Mixing:



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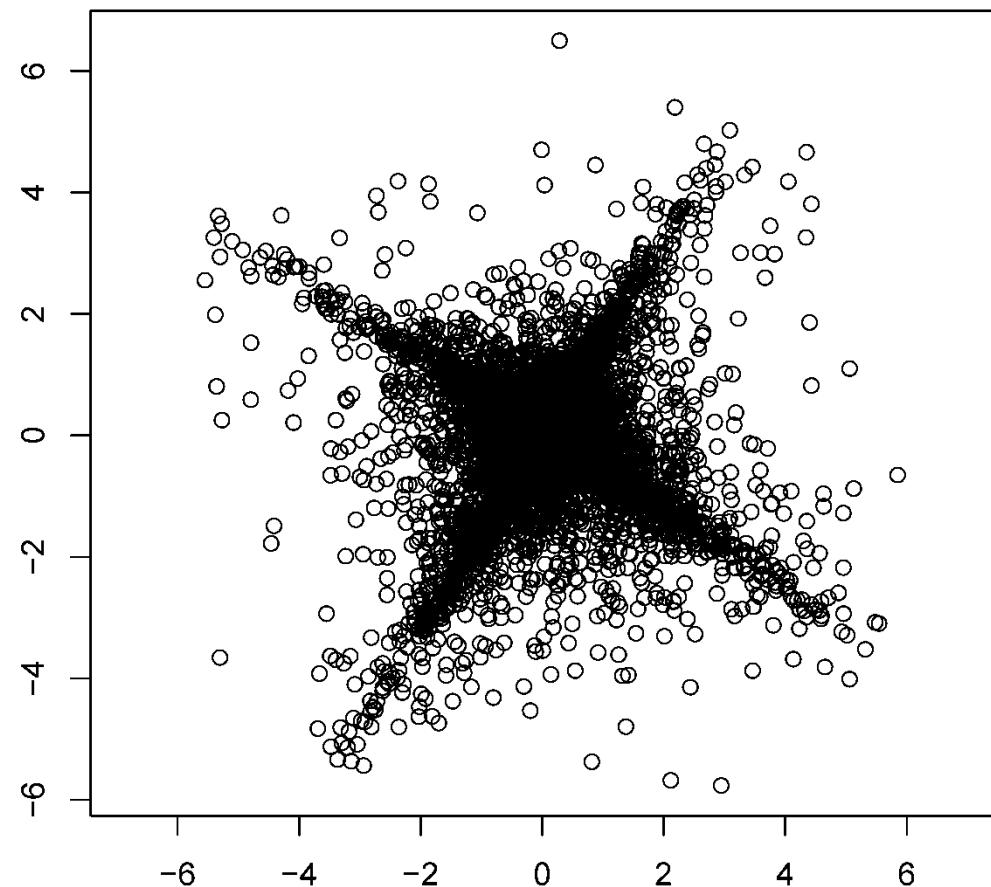
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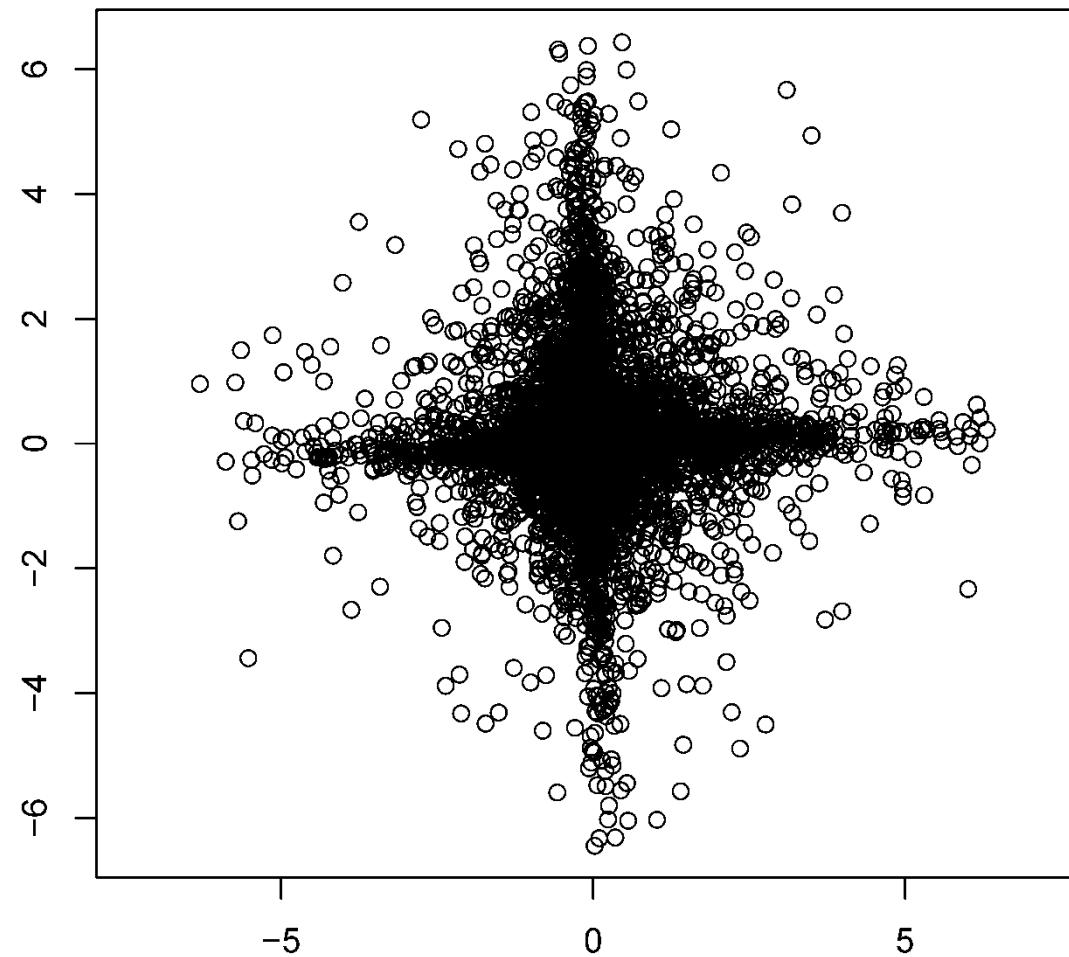
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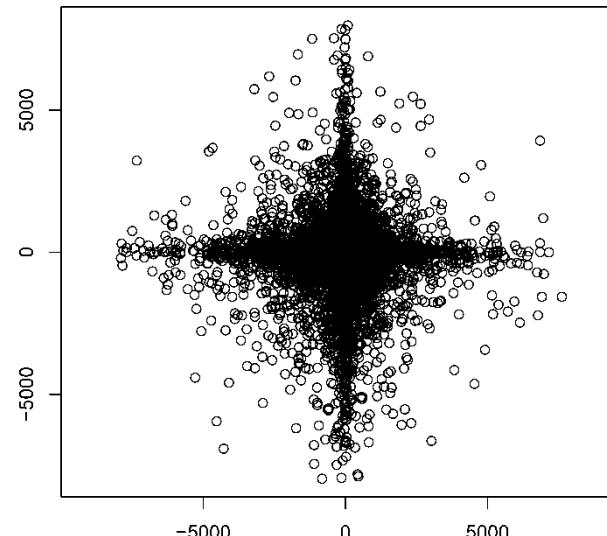
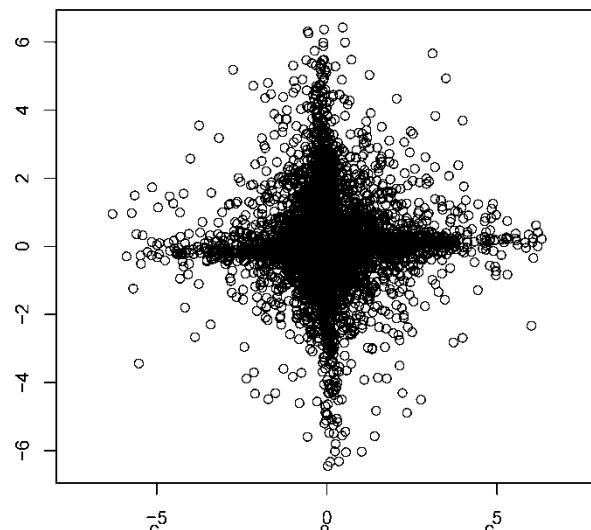
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solution

vs.

original data



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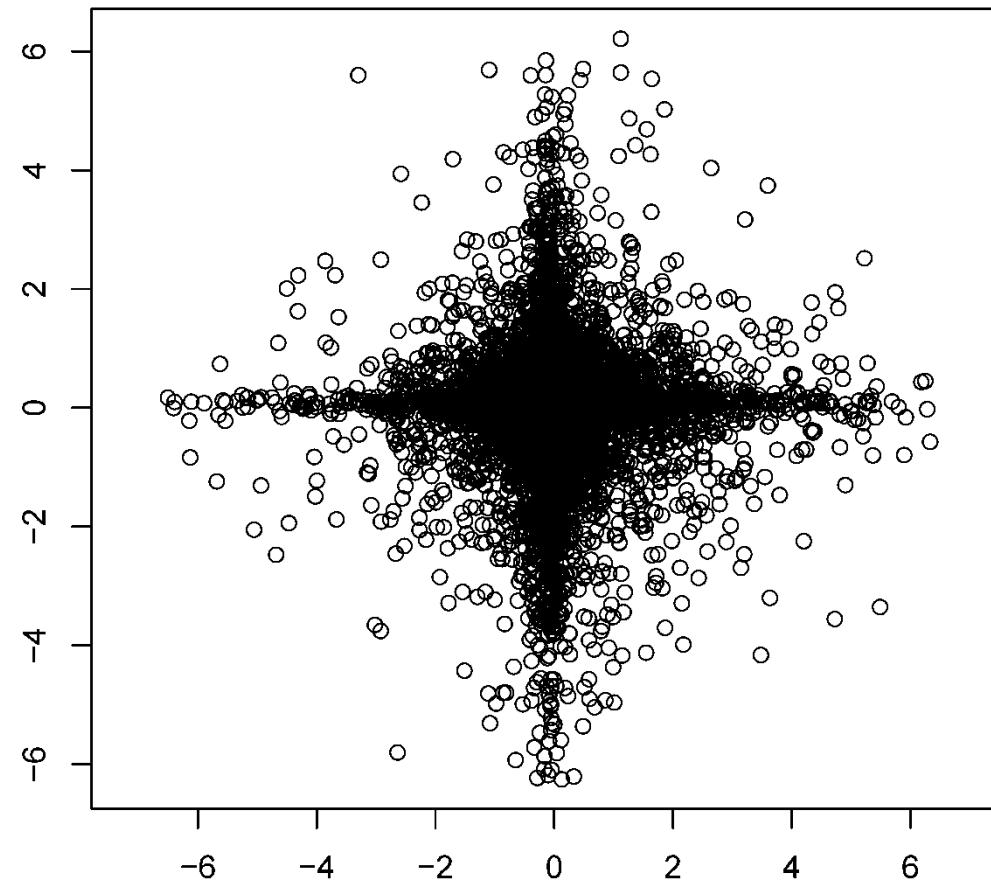
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fastICA:



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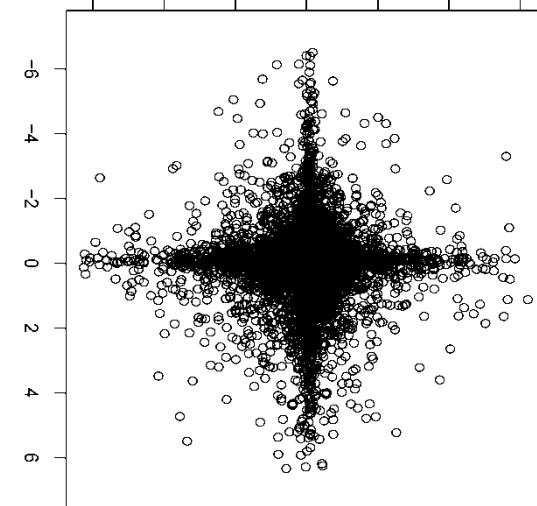
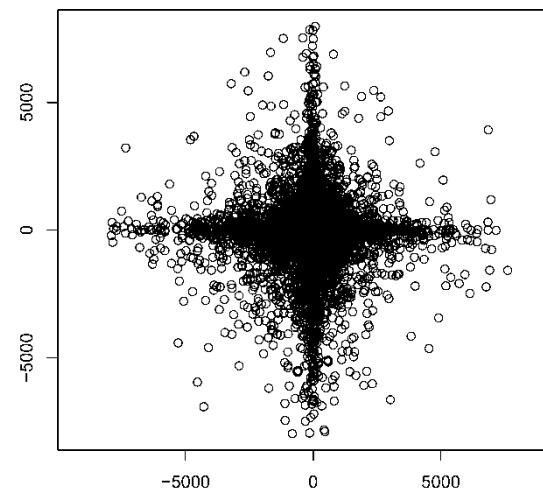
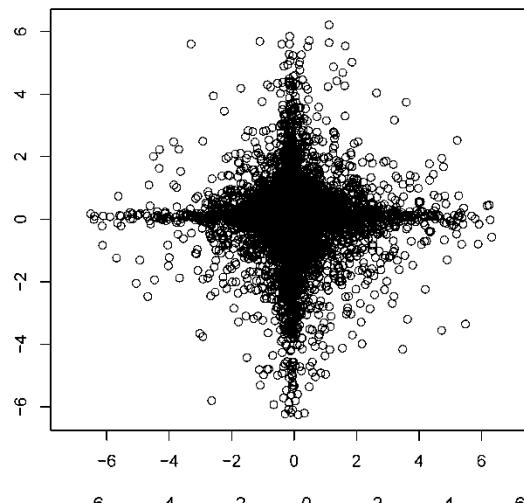
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fastICA solution

vs.

original data



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Iris Data

ICs ordered according to their impact on the observations given by the mixing matrix

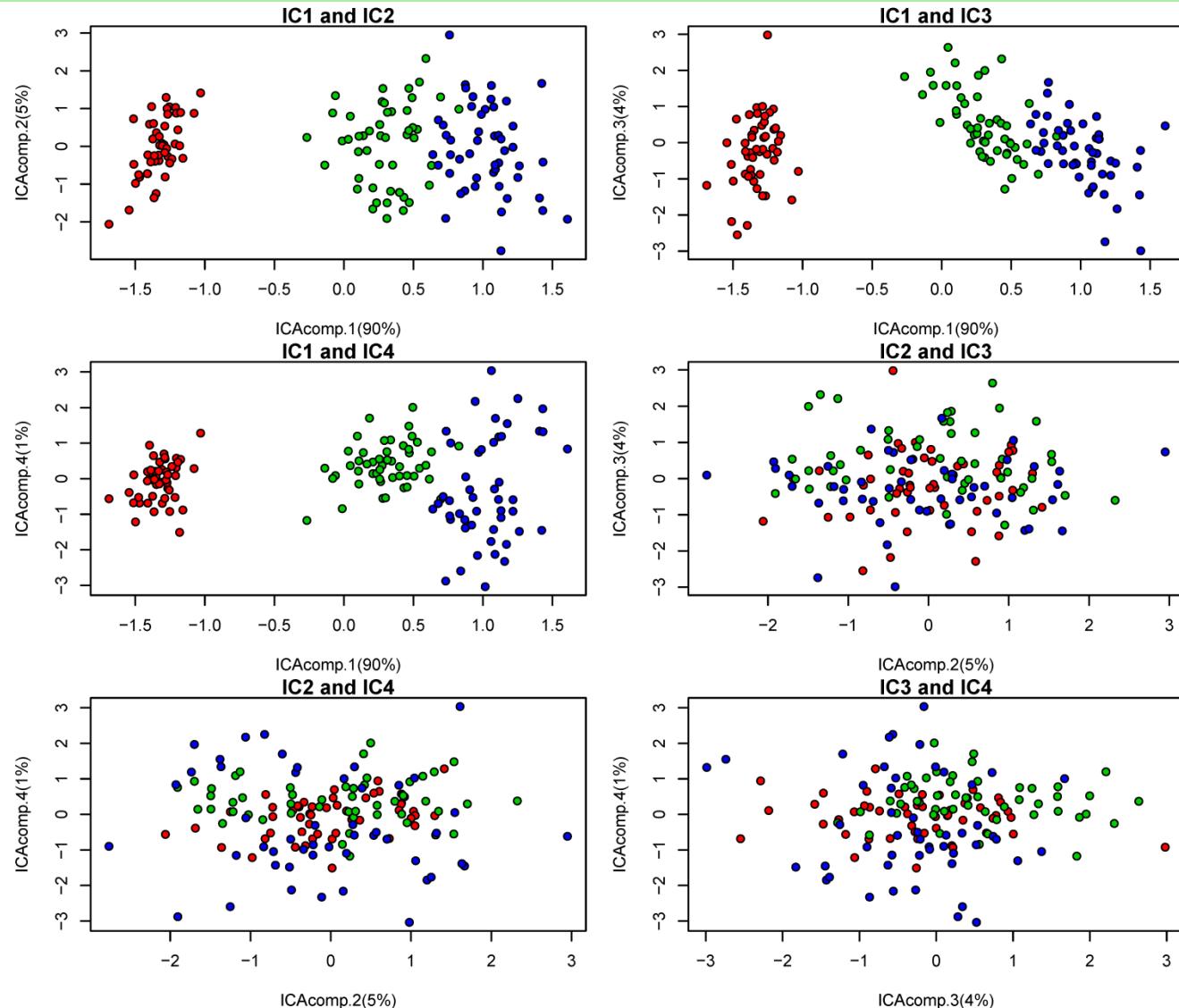
First independent component explains 90% of the variance in the data

Probably IC1 expresses the size of the blossom

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Multiple Tissues Data

- IC1 separates the prostate samples (green) and the breast samples (red) from the colon samples (orange) and the lung samples (blue). Thus, IC1 separates internal organ tissues (colon and lung) from secretory or reproductive organ samples.
- IC2 separates the prostate samples and the lung samples from the breast samples and the colon samples.
- IC3 separates the prostate samples and the colon samples from the breast samples and the lung samples.

All combinations of the first 3 ICs lead to nice separations except for breast samples and lung samples for which some samples cannot be clearly assigned to one of these two classes.

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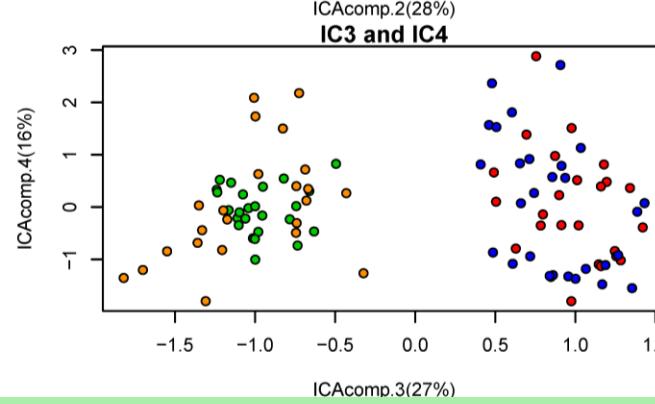
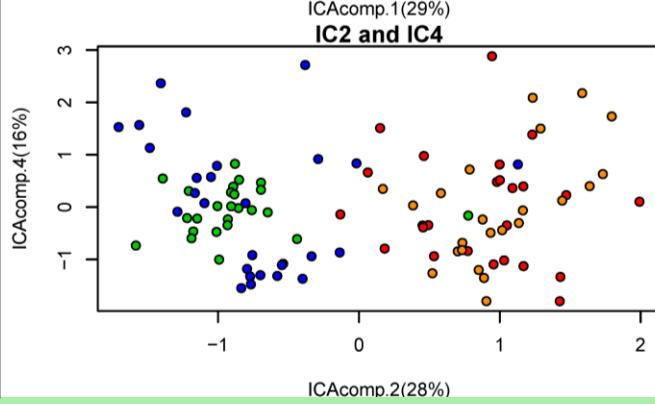
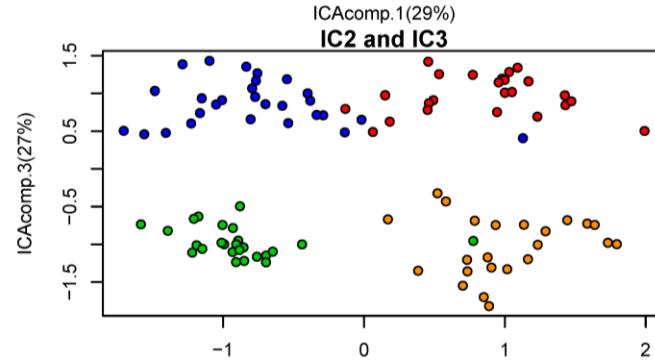
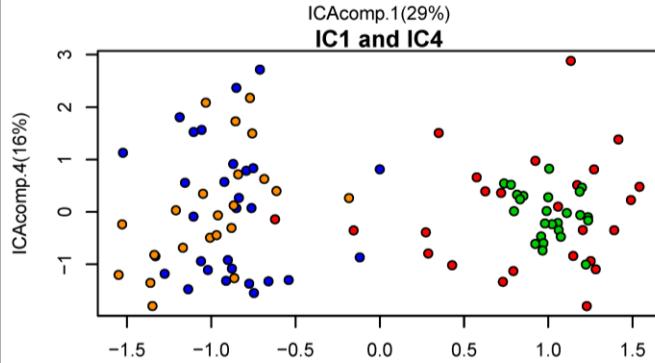
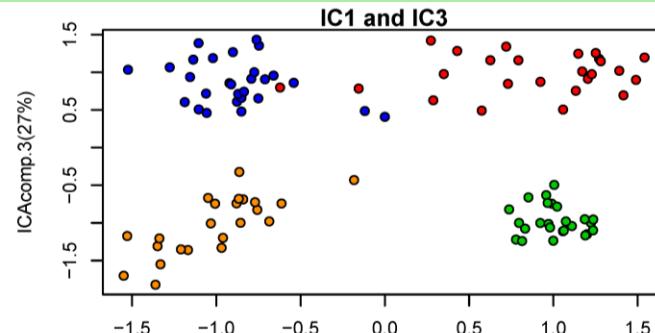
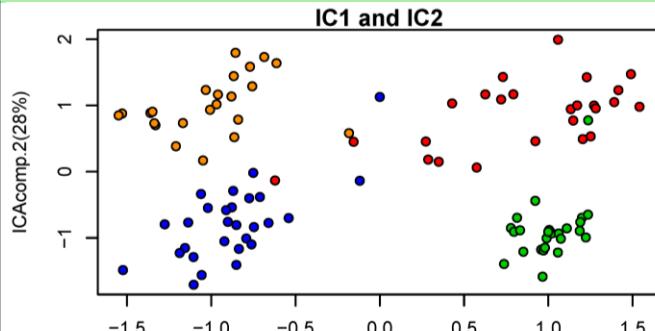
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IC1: prostate (green) and breast (red) vs. colon (orange) and lung (blue)

IC2: prostate and lung vs. breast and colon

IC3: prostate and the colon vs. breast and lung

first 3 ICs lead to nice separations

breast and lung cannot be clearly separated

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genes are correlated to IC1:

"SERPINA7" "LAMB3" "AR" "CCNG2" "KLF5" "CCL20"
"SLC39A14" "ATP1B1" "GSTP1" "LAD1"

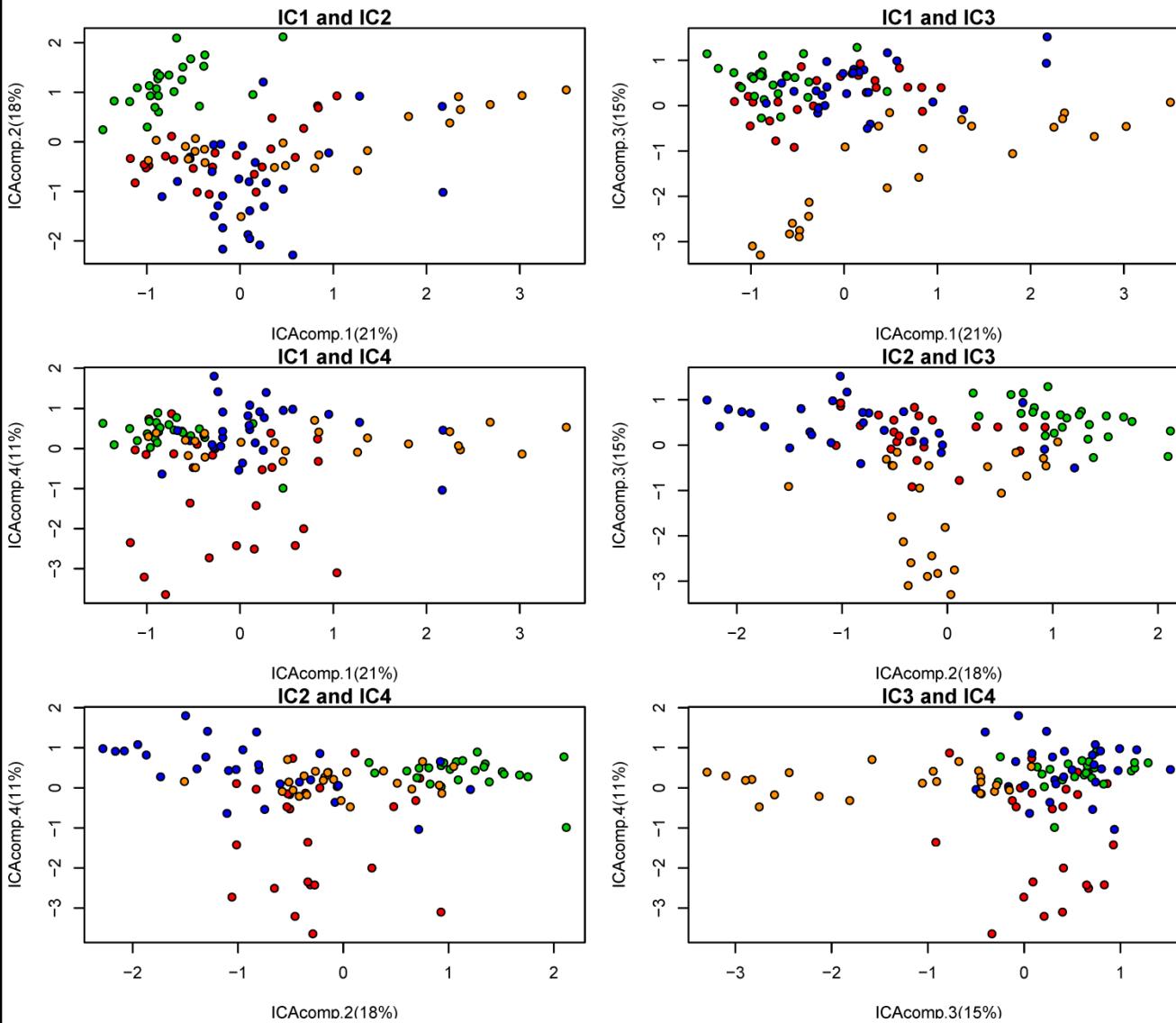
androgen receptor (AR) 3rd most related gene to IC1 which separates prostate and breast samples:

- growth / differentiation of prostate gland is regulated by androgens
- androgens play a role in normal breast physiology

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ICA with 8 components

Separation worse than with 4 comp.

prostate (green) is separated by IC1 and IC2

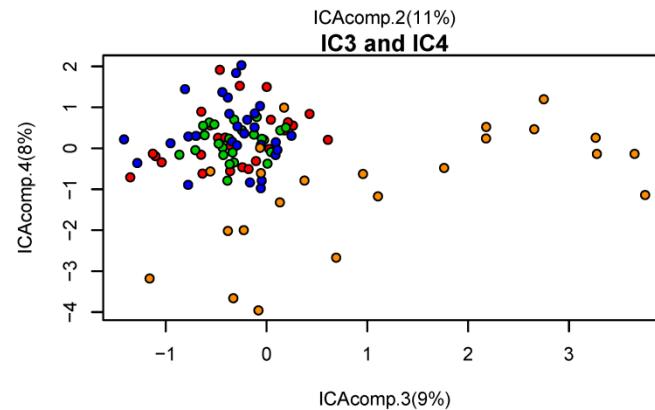
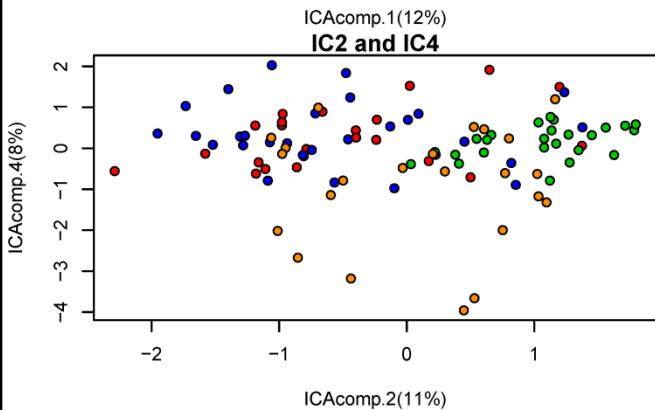
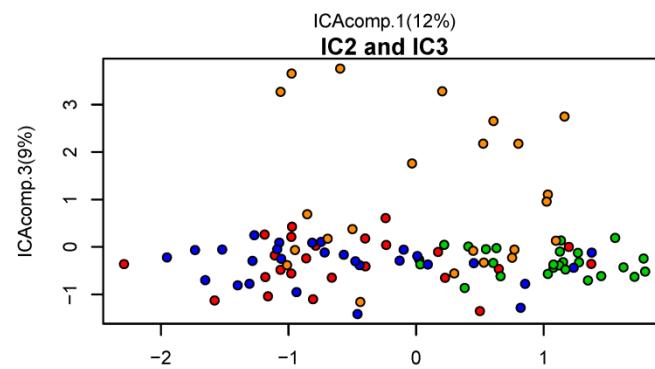
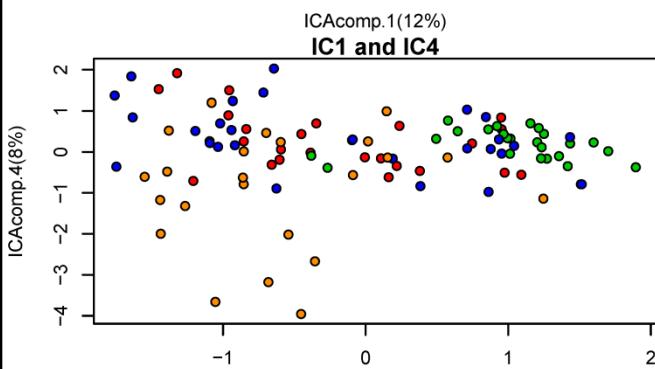
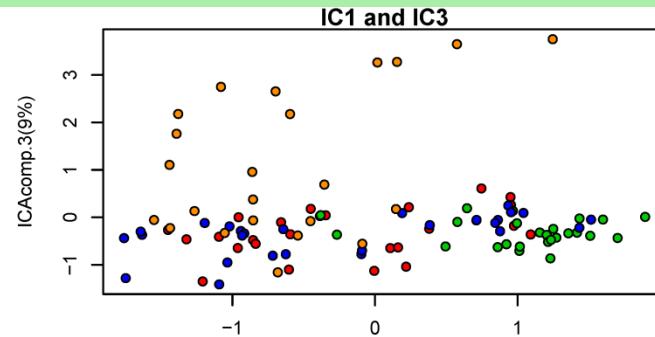
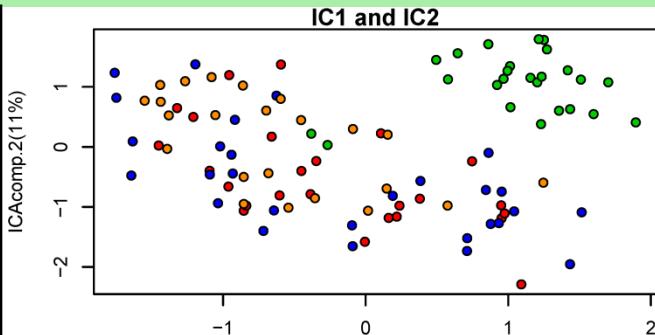
IC3 separates some colon sam. (orange)

ICs focus on smaller subgroups

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ICA with 20 components

result is very similar to 8 components

prostate (green) are separated by IC1 and IC2

IC3 and IC4 separate some colon (orange)

Again smaller subgroups found

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y_1 and y_2 are assumed to be independent from each other and to be super Gaussian.

We show that a linear combination of these signal recovers one of both signals by maximizing the kurtosis.

We assume that y_1 and y_2 are zero centered, symmetric (not skewed), and independent of each other.

We obtain following moments and the reconstruction

$$E(y_1) = 0 ,$$

$$E(y_2) = 0 ,$$

$$E(y_1^2) = v_1 ,$$

$$E(y_2^2) = v_2 ,$$

$$E(y_1 y_2) = 0 ,$$

$$E(y_1^3) = 0 ,$$

$$E(y_2^3) = 0 ,$$

$$E(y_1 y_2^2) = 0 ,$$

$$E(y_2 y_1^2) = 0 ,$$

$$E(y_1^4) = m_1 ,$$

$$E(y_2^4) = m_2 ,$$

$$E(y_1 y_2^3) = 0 ,$$

$$E(y_2 y_1^3) = 0 ,$$

$$E(y_1^2 y_2^2) = v_1 v_2$$

$$y = a y_1 + b y_2$$

If y_1 and y_2 are super-Gaussian (have heavy tails) then the maximal kurtosis of y is obtained for $a=0$ or $b=0$ that is y is proportional to one y_i

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For y we have the moments and the kurtosis:

$$E(y) = 0,$$

$$E(y^2) = a^2 v_1 + b^2 v_2,$$

$$E(y^3) = 0,$$

$$E(y^4) = a^4 m_1 + 6 a^2 b^2 v_1 v_2 + b^4 m_2$$

$$k = \frac{a^4 m_1 + 6 a^2 b^2 v_1 v_2 + b^4 m_2}{(a^2 v_1 + b^2 v_2)^2}$$

The derivatives of the kurtosis with respect to a and b are:

$$\frac{\partial k}{\partial a} = \frac{4ab^2 (a^2 (m_1 - 3v_1^2) v_2 - b^2 v_1 (m_2 - 3v_2^2))}{(a^2 v_1 + b^2 v_2)^3}$$

$$\frac{\partial k}{\partial b} = \frac{4a^2 b (-a^2 (m_1 - 3v_1^2) v_2 + b^2 v_1 (m_2 - 3v_2^2))}{(a^2 v_1 + b^2 v_2)^3}$$

The solution is:

$$a = 0 \quad \text{or}$$

$$b = 0 \quad \text{or}$$

$$a^2 v_2 (m_1 - 3v_1^2) = b^2 v_1 (m_2 - 3v_2^2)$$

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The second order derivatives are:

$$\frac{\partial^2 k}{\partial a^2} = \frac{1}{(a^2 v_1 + b^2 v_2)^4} 4b^2 (-3a^4 v_1 (m_1 - 3v_1^2) v_2 + b^4 v_1 v_2 (-m_2 + 3v_2^2) + a^2 b^2 (5m_2 v_1^2 + 3(m_1 - 8v_1^2) v_2^2))$$

$$\frac{\partial^2 k}{\partial a^2} = \frac{1}{(a^2 v_1 + b^2 v_2)^4} 4a^2 (a^4 v_1 (-m_1 + 3v_1^2) v_2 + 3b^4 v_1 v_2 (-m_2 + 3v_2^2) + a^2 b^2 (3m_2 v_1^2 + (5m_1 - 24v_1^2) v_2^2))$$

$$\frac{\partial^2 k}{\partial a \partial b} = \frac{1}{(a^2 v_1 + b^2 v_2)^4} 8ab (a^4 v_1 (m_1 - 3v_1^2) v_2 + b^4 v_1 v_2 (m_2 - 3v_2^2) - 2a^2 b^2 (m_2 v_1^2 + (m_1 - 6v_1^2) v_2^2))$$

$$\frac{\partial^2 k}{\partial a^2}(a, 0) = 0$$

$$\frac{\partial^2 k}{\partial a^2}(0, b) = \frac{4v_1 (-m_2 + 3v_2^2)}{b^2 v_2^3} \quad \text{Smaller zero!}$$

$$\frac{\partial^2 k}{\partial b^2}(0, b) = 0$$

$$\frac{\partial^2 k}{\partial b^2}(a, 0) = \frac{4(-m_1 + 3v_1^2) v_2}{a^2 v_1^3} \quad \text{Smaller zero!}$$

$$\frac{\partial^2 k}{\partial a \partial b}(0, b) = 0$$

$$\frac{\partial^2 k}{\partial a \partial b}(a, 0) = 0$$

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For the last root of the derivatives we get

$$\hat{a} = b \sqrt{\frac{v_1(m_2 - 3v_2^2)}{v_2(m_1 - 3v_1^2)}}$$

$$\frac{\partial^2 k}{\partial a^2}(\hat{a}, b) = \frac{\partial^2 k}{\partial b^2}(\hat{a}, b) = \frac{8v_1 (m_1 - 3v_1^2)^3 v_2^3 (m_2 - 3v_2^2)}{b^2 (m_2 v_1^2 + (m_1 - 6v_1^2) v_2^2)^3} =$$

$$\frac{8v_1 (m_1 - 3v_1^2)^3 v_2^3 (m_2 - 3v_2^2)}{b^2 (v_1^2 (m_2 - 3v_2^2) + v_2^2 (m_1 - 3v_1^2))^3}$$

Larger zero!

$$\frac{\partial^2 k}{\partial a \partial b}(\hat{a}, b) = - \frac{8 (m_1 - 3v_1^2)^4 v_2^4 \left(\frac{v_1(m_2 - 3v_2^2)}{(m_1 - 3v_1^2)v_2} \right)^{3/2}}{b^2 (m_2 v_1^2 + (m_1 - 6v_1^2) v_2^2)^3} =$$

$$- \left(\frac{(m_1 - 3v_1^2) v_2}{v_1 (m_2 - 3v_2^2)} \right)^{1/2} \frac{\partial^2 k}{\partial a^2}(\hat{a}, b)$$

Smaller zero!

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The eigenvalues of the Hessian are proportional to

$$e_1 \propto 1 - \left(\frac{(m_1 - 3v_1^2) v_2}{v_1 (m_2 - 3v_2^2)} \right)^{1/2}$$

$$e_2 \propto 1 + \left(\frac{(m_1 - 3v_1^2) v_2}{v_1 (m_2 - 3v_2^2)} \right)^{1/2}$$

It is impossible that both eigenvalues are negative as required by a maximum. Therefore the maxima are either $a = 0$ or $b = 0$ for which the Hessian is negative semidefinite.

If the kurtosis $k_2 > k_1$ then $a = 0$

If the kurtosis $k_1 > k_2$ then $b = 0$

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Factor analysis describes the variability of observations in terms of unobserved latent variables, called **factors**, and noise

- factors explain correlation between the variables
- remaining variance is explained by Gaussian noise

factor analysis is a generative approach and models both the noise of the observations and their correlation

assumptions on the distribution of factors and noise

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centered data: $\{x\} = \{x_1, \dots, x_n\}$

$$x = \underbrace{Uy}_{\text{signal}} + \underbrace{\epsilon}_{\text{noise}} \quad \text{where } y \sim \mathcal{N}(0, I) \quad \text{and} \quad \epsilon \sim \mathcal{N}(0, \Psi)$$

- Observations ----- $x \in \mathbb{R}^m$
 - Noise ----- $\epsilon \in \mathbb{R}^m$
 - Factors ----- $y \in \mathbb{R}^l$
 - Factor loading matrix ----- $U \in \mathbb{R}^{m \times l}$
 - Diagonal noise covariance matrix ----- $\Psi \in \mathbb{R}^{m \times m}$
- } parameters

$$x | y \sim \mathcal{N}(Uy, \Psi)$$

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matrix decomposition: $\mathbf{X} = \mathbf{Y} \mathbf{U}^T + \boldsymbol{\Upsilon}$

model assumptions:

$$\frac{1}{n} \mathbf{Y}^T \mathbf{Y} = \mathbf{I}$$

$$\mathbf{Y}^T \boldsymbol{\Upsilon} = \mathbf{0}$$

$$\frac{1}{n} \boldsymbol{\Upsilon}^T \boldsymbol{\Upsilon} = \boldsymbol{\Psi}$$

we obtain:

$$\begin{aligned} \frac{1}{n} \mathbf{X}^T \mathbf{X} &= \frac{1}{n} (\mathbf{Y} \mathbf{U}^T + \boldsymbol{\Upsilon})^T (\mathbf{Y} \mathbf{U}^T + \boldsymbol{\Upsilon}) \\ &= \mathbf{U} \left(\frac{1}{n} \mathbf{Y}^T \mathbf{Y} \right) \mathbf{U}^T + \frac{1}{n} \mathbf{U} \mathbf{Y}^T \boldsymbol{\Upsilon} + \frac{1}{n} \boldsymbol{\Upsilon}^T \mathbf{Y} \mathbf{U}^T + \frac{1}{n} \boldsymbol{\Upsilon}^T \boldsymbol{\Upsilon} \\ &= \mathbf{U} \mathbf{U}^T + \boldsymbol{\Psi} \end{aligned}$$

factor analysis is actually a decomposition of the covariance matrix

$$\mathbf{C} = \frac{1}{n} \mathbf{X}^T \mathbf{X}$$

into an expression of the two parameter matrices.

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fewer factors than features: $m \geq l$

diagonal Ψ : noise of the components are independent

correlations between observations can only be explained by factors

decomposition of the covariance matrix: $\frac{1}{n} \mathbf{X}^T \mathbf{X} = \mathbf{U} \mathbf{U}^T + \Psi$

parameter estimation → maximum likelihood: expectation-maximization

both parameters explain the variance in the observations:

\mathbf{U} explains the dependent part

Ψ explains the independent part

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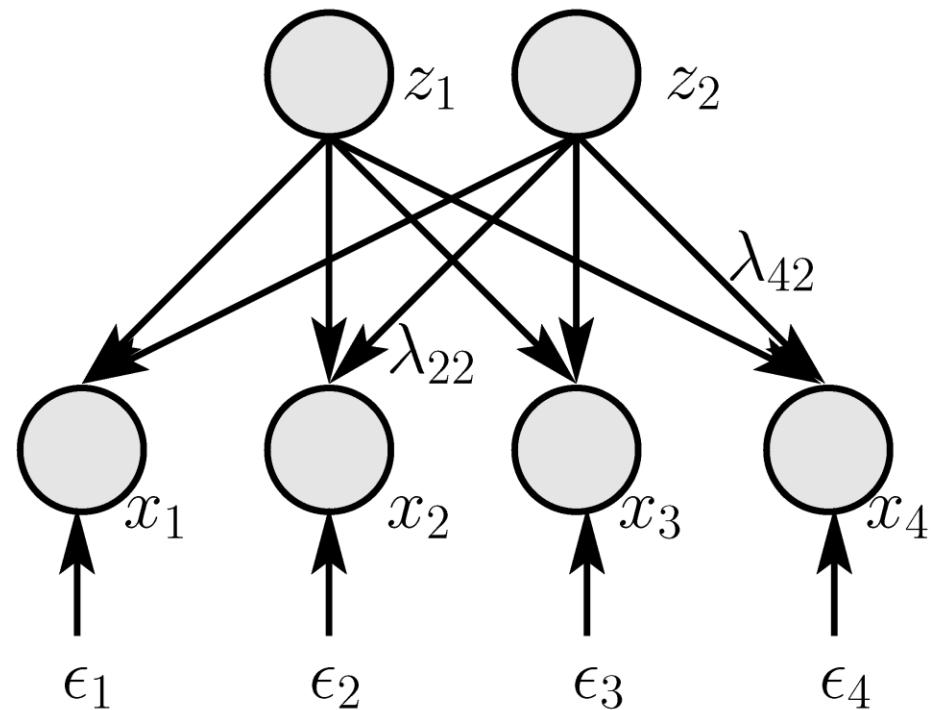
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factor z

loading matrix Λ

observations x

noise ϵ



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Estimation of factors: “projection of the data onto the factors”

regression setting: $\mathbf{Y} = \mathbf{X} \mathbf{A}$ where \mathbf{A} is parameter
least squares solution: $\hat{\mathbf{A}} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}$

model assumptions and empirical approximations:

$$\mathbf{U} \mathbf{U}^T + \boldsymbol{\Psi} = \text{Var}(\mathbf{x}) \approx \frac{1}{n} \mathbf{X}^T \mathbf{X}$$

$$\mathbf{U} = \text{Cov}(\mathbf{x}, \mathbf{y}) \approx \frac{1}{n} \mathbf{X}^T \mathbf{Y}$$

estimation for \mathbf{A} :

$$\hat{\mathbf{A}} = \mathbb{E} \left((\mathbf{X}^T \mathbf{X})^{-1} \right) \mathbb{E} (\mathbf{X}^T \mathbf{Y})$$

$$\hat{\mathbf{A}} = (\mathbf{U} \mathbf{U}^T + \boldsymbol{\Psi})^{-1} \mathbf{U}$$

$$\mathbf{Y} = \mathbf{X} (\mathbf{U} \mathbf{U}^T + \boldsymbol{\Psi})^{-1} \mathbf{U}$$

matrix inversion lemma:

$$\mathbf{Y} = \mathbf{X} \boldsymbol{\Psi}^{-1} \mathbf{U} (\mathbf{I} + \mathbf{U} \boldsymbol{\Psi}^{-1} \mathbf{U}^T)^{-1}$$

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outer product representation for l factors: $\mathbf{X} = \sum_{j=1}^l \mathbf{u}_j \mathbf{y}_j^T + \boldsymbol{\Upsilon}$

\mathbf{u}_j : j -th column vector of \mathbf{U}

\mathbf{y}_j : j -th row vector of \mathbf{Y}

communality c_j of an observation variable x_j (j -th component of \mathbf{x}):

$$c_j = \frac{\text{Var}(x_j) - \text{Var}(\epsilon_j)}{\text{Var}(x_j)} = \frac{\sum_{k=1}^l \lambda_{jk}^2}{\Psi_{jj} + \sum_{k=1}^l \lambda_{jk}^2}$$

proportion in x_j explained by the factors

Here each factor y_t contributes: $\frac{\lambda_{jt}^2}{\Psi_{jj} + \sum_{k=1}^l \lambda_{jk}^2}$

Like with PCA, the projection onto l factors maximizes the variance in the data which can be explained by l factors.

However factor analysis considers only the signal variance (not noise)

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factor projections are orthogonal to each other: $\frac{1}{n} \mathbf{Y}^T \mathbf{Y} = \mathbf{I}$

factors are not unique up to orthogonal transformations (rotations):

$$\mathbf{YU}^T = \mathbf{YV} \mathbf{V}^T \mathbf{U}^T = \mathbf{Y}' \mathbf{U}'^T \quad \text{with orthogonal } \mathbf{V}$$

projections rotated to make the factors more interpretable or to find simpler structures:

- **Varimax rotation**: maximizes the squared loadings of a factor on all the variables; each factor has either large or small loadings of any particular variable; each variable is assigned to a factor.
- **Quartimax rotation**: minimizes the number of factors needed to explain each variable; each factor explains many variables; in most cases not interpretable.
- **Equimax rotation**: compromise between Varimax and Quartimax.

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$$x | z \sim \mathcal{N}(\Lambda z, \Psi)$$

z is given \rightarrow only noise distribution

First and second moment of the data (factor and noise):

$$E(x) = E(\Lambda z + \epsilon) = \Lambda E(z) + E(\epsilon) = \mathbf{0},$$

$$E(x x^T) = E((\Lambda z + \epsilon)(\Lambda z + \epsilon)^T) =$$

$$\Lambda E(z z^T) \Lambda^T + \Lambda E(z) E(\epsilon^T) + E(z) E(\epsilon) \Lambda^T + E(\epsilon \epsilon^T) =$$

$$\Lambda \Lambda^T + \Psi$$

Distribution of the data:

$$x \sim \mathcal{N}(\mathbf{0}, \Lambda \Lambda^T + \Psi)$$

observations are Gaussian distributed

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log-likelihood:

$$\log \prod_{i=1}^l (2\pi)^{-d/2} |\Lambda \Lambda^T + \Psi|^{-1/2}$$
$$\exp \left(-\frac{1}{2} \left((\mathbf{x}^i)^T (\Lambda \Lambda^T + \Psi)^{-1} \mathbf{x}^i \right) \right)$$

maximize the likelihood is difficult: no closed form

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EM-algorithm: hidden states are the factors

$$Q_i(z^i) = p(z^i | \mathbf{x}^i; \boldsymbol{\Lambda}^{\text{old}}, \boldsymbol{\Psi}^{\text{old}})$$

“old” is skipped in the following

$$z^i | \mathbf{x}^i \sim \mathcal{N}(\boldsymbol{\mu}_{z^i|\mathbf{x}^i}, \boldsymbol{\Sigma}_{z^i|\mathbf{x}^i})$$

$$\boldsymbol{\mu}_{z^i|\mathbf{x}^i} = (\mathbf{x}^i)^T (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \boldsymbol{\Lambda}$$

$$\boldsymbol{\Sigma}_{z^i|\mathbf{x}^i} = \mathbf{I} - \boldsymbol{\Lambda}^T (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \boldsymbol{\Lambda}$$

we used

$$\mathbf{v} \sim \mathcal{N}(\boldsymbol{\mu}_v, \boldsymbol{\Sigma}_{vv}), \mathbf{u} \sim \mathcal{N}(\boldsymbol{\mu}_u, \boldsymbol{\Sigma}_{uu}),$$

$$\boldsymbol{\Sigma}_{uv} = \text{Covar}(\mathbf{u}, \mathbf{v}) \text{ and } \boldsymbol{\Sigma}_{vu} = \text{Covar}(\mathbf{v}, \mathbf{u}):$$

$$\mathbf{v} | \mathbf{u} \sim \mathcal{N}(\boldsymbol{\mu}_v + \boldsymbol{\Sigma}_{vu} \boldsymbol{\Sigma}_{uu}^{-1} (\mathbf{u} - \boldsymbol{\mu}_u), \boldsymbol{\Sigma}_{vv} + \boldsymbol{\Sigma}_{vu} \boldsymbol{\Sigma}_{uu}^{-1} \boldsymbol{\Sigma}_{uv})$$

and

$$\mathbb{E}(z\mathbf{x}) = \boldsymbol{\Lambda} \mathbb{E}(z z^T) = \boldsymbol{\Lambda}$$

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$$Q_i(\mathbf{z}^i) = (2\pi)^{-d/2} |\Sigma_{\mathbf{z}^i|\mathbf{x}^i}|^{-1/2} \exp\left(-\frac{1}{2} (\mathbf{z}^i - \boldsymbol{\mu}_{\mathbf{z}^i|\mathbf{x}^i})^T \Sigma_{\mathbf{z}^i|\mathbf{x}^i}^{-1} (\mathbf{z}^i - \boldsymbol{\mu}_{\mathbf{z}^i|\mathbf{x}^i})\right)$$

lower bound for the likelihood:

$$\log(p(\mathbf{x}^i | \boldsymbol{\Lambda}, \boldsymbol{\Psi})) = \log\left(\int_{\mathbb{R}^p} \frac{Q_i(\mathbf{z}^i) p(\mathbf{x}^i, \mathbf{z}^i | \boldsymbol{\Lambda}, \boldsymbol{\Psi})}{Q_i(\mathbf{z}^i)} d\mathbf{z}^i\right) \geq \int_{\mathbb{R}^p} Q_i(\mathbf{z}^i) \log\left(\frac{p(\mathbf{x}^i, \mathbf{z}^i | \boldsymbol{\Lambda}, \boldsymbol{\Psi})}{Q_i(\mathbf{z}^i)}\right) d\mathbf{z}^i$$

expectation

$$\mathbb{E}_{\mathbf{z}^i|\mathbf{x}^i}(f(\mathbf{z}^i)) = \int_{\mathbb{R}^p} Q_i(\mathbf{z}^i) f(\mathbf{z}^i) d\mathbf{z}^i$$

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M-step maximizes $\log \mathcal{L} = \frac{d}{2} l \log (2\pi) - \frac{l}{2} \log |\Psi| - \frac{1}{2} \sum_{i=1}^l \mathbb{E}_{z^i|x^i} \left((x^i - \Lambda z^i)^T \Psi^{-1} (x^i - \Lambda z^i) \right)$

optimality criteria

$$\frac{1}{l} \nabla_{\Lambda} \log \mathcal{L} = \frac{1}{l} \sum_{i=1}^l \Psi^{-1} \Lambda \mathbb{E}_{z^i|x^i} (z^i (z^i)^T) -$$

$$\frac{1}{l} \sum_{i=1}^l \Psi^{-1} x^i \mathbb{E}_{z^i|x^i} (z^i) = \mathbf{0}$$

and

$$\nabla_{\Psi} \log \mathcal{L} = -\frac{l}{2} \Psi^{-1} +$$

$$\frac{1}{2} \sum_{i=1}^l \mathbb{E}_{z^i|x^i} \left(\Psi^{-1} (x^i - \Lambda z^i) (x^i - \Lambda z^i)^T \Psi^{-1} \right) = \mathbf{0}$$

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Solving above equations gives:

$$\boldsymbol{\Lambda}^{\text{new}} = \left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \right) \left(\frac{1}{l} \sum_{i=1}^l \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i (\mathbf{z}^i)^T) \right)^{-1}$$

and

$$\boldsymbol{\Psi}^{\text{new}} =$$

$$\text{diag} \left(\frac{1}{l} \sum_{i=1}^l \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} \left((\mathbf{x}^i - \boldsymbol{\Lambda}^{\text{new}} \mathbf{z}^i) (\mathbf{x}^i - \boldsymbol{\Lambda}^{\text{new}} \mathbf{z}^i)^T \right) \right) =$$

$$\text{diag} \left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i (\mathbf{x}^i)^T - \frac{1}{l} \sum_{i=1}^l \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \mathbf{x}^i (\boldsymbol{\Lambda}^{\text{new}})^T - \right.$$

$$\left. \frac{1}{l} \sum_{i=1}^l \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \boldsymbol{\Lambda}^{\text{new}} (\mathbf{x}^i)^T + \right.$$

$$\left. \frac{1}{l} \sum_{i=1}^l \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i (\mathbf{z}^i)^T) \boldsymbol{\Lambda}^{\text{new}} (\boldsymbol{\Lambda}^{\text{new}})^T \right)$$

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Loading matrix update gives

$$\Lambda^{\text{new}} \left(\frac{1}{l} \sum_{i=1}^l E_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i (\mathbf{z}^i)^T) \right) = \left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i E_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \right)$$

which can be inserted into the update of the noise covariance

→ one term $\frac{1}{l} \sum_{i=1}^l E_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \Lambda^{\text{new}} (\mathbf{x}^i)^T$ cancels

$$\Psi^{\text{new}} = \frac{1}{l} \text{diag} \left(\sum_{i=1}^l \mathbf{x}^i (\mathbf{x}^i)^T - \sum_{i=1}^l E_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) \mathbf{x}^i (\Lambda^{\text{new}})^T \right)$$

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EM updates:

E-step:

$$E_{\mathbf{z}^i|\mathbf{x}^i}(\mathbf{z}^i) = \boldsymbol{\mu}_{\mathbf{z}^i|\mathbf{x}^i}$$

$$E_{\mathbf{z}^i|\mathbf{x}^i}(\mathbf{z}^i (\mathbf{z}^i)^T) = \boldsymbol{\mu}_{\mathbf{z}^i|\mathbf{x}^i} \boldsymbol{\mu}_{\mathbf{z}^i|\mathbf{x}^i}^T + \boldsymbol{\Sigma}_{\mathbf{z}^i|\mathbf{x}^i}$$

M-step:

$$\boldsymbol{\Lambda}^{\text{new}} =$$

$$\left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i E_{\mathbf{z}^i|\mathbf{x}^i}(\mathbf{z}^i) \right) \left(\frac{1}{l} \sum_{i=1}^l E_{\mathbf{z}^i|\mathbf{x}^i}(\mathbf{z}^i (\mathbf{z}^i)^T) \right)^{-1}$$

$$\boldsymbol{\Psi}^{\text{new}} =$$

$$\frac{1}{l} \text{diag} \left(\sum_{i=1}^l \mathbf{x}^i (\mathbf{x}^i)^T - \sum_{i=1}^l E_{\mathbf{z}^i|\mathbf{x}^i}(\mathbf{z}^i) \mathbf{x}^i (\boldsymbol{\Lambda}^{\text{new}})^T \right)$$

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Speed Ups:

matrix inversion lemma: $d > p$ (compute in p -dimensional space)

$$(\Lambda \Lambda^T + \Psi)^{-1} = \Psi^{-1} - \Psi^{-1} \Lambda (\mathbf{I} + \Lambda^T \Psi^{-1} \Lambda)^{-1} \Lambda^T \Psi^{-1}$$

Ψ^{-1} can be evaluated very efficiently → diagonal matrix

covariance C only once computed:

$$\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i \mathbb{E}_{\mathbf{z}^i | \mathbf{x}^i} (\mathbf{z}^i) =$$

$$\left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i (\mathbf{x}^i)^T \right) (\Lambda \Lambda^T + \Psi)^{-1} \Lambda =$$

$$C (\Lambda \Lambda^T + \Psi)^{-1} \Lambda =$$

$$C \left(\Psi^{-1} \Lambda - \Psi^{-1} \Lambda (\mathbf{I} + \Lambda^T \Psi^{-1} \Lambda)^{-1} \Lambda^T \Psi^{-1} \Lambda \right) =$$

$$C \left(\mathbf{A} - \mathbf{A} (\mathbf{I} + \mathbf{B})^{-1} \mathbf{B} \right)$$

$$\mathbf{A} = \Psi^{-1} \Lambda$$

$$\mathbf{B} = \Lambda^T \Psi^{-1} \Lambda = \Lambda^T \mathbf{A}$$

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$$\frac{1}{l} \sum_{i=1}^l \Sigma_{\mathbf{z}^i | \mathbf{x}^i} = \mathbf{I} - \boldsymbol{\Lambda}^T (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \boldsymbol{\Lambda}$$

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$$\frac{1}{l} \sum_{i=1}^l \boldsymbol{\mu}_{\mathbf{z}^i | \mathbf{x}^i} \boldsymbol{\mu}_{\mathbf{z}^i | \mathbf{x}^i}^T =$$

$$\boldsymbol{\Lambda}^T (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \left(\frac{1}{l} \sum_{i=1}^l \mathbf{x}^i (\mathbf{x}^i)^T \right) (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \boldsymbol{\Lambda} =$$

$$\boldsymbol{\Lambda}^T (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \mathbf{C} (\boldsymbol{\Lambda} \boldsymbol{\Lambda}^T + \boldsymbol{\Psi})^{-1} \boldsymbol{\Lambda} =$$

$$(\mathbf{A} - \mathbf{A}(\mathbf{I} + \mathbf{B})^{-1} \mathbf{B})^T \mathbf{C} (\mathbf{A} - \mathbf{A}(\mathbf{I} + \mathbf{B})^{-1} \mathbf{B})$$

sums $\sum_{i=1}^l$ are removed and the matrix \mathbf{C} can be computed once at the beginning of the iterative procedure

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MAP factor analysis

$$p(\Lambda, \Psi \mid \{x\}) \propto p(\{x\} \mid \Lambda, \Psi) p(\Lambda)$$

posterior $p(\Lambda, \Psi \mid \{x\})$

likelihood $p(\{x\} \mid \Lambda, \Psi)$

prior $p(\Lambda)$

log-posterior

$$\log(p(\Lambda, \Psi \mid \{x\})) = \log(p(\{x\} \mid \Lambda, \Psi)) + \log(p(\Lambda))$$

example for the prior: rectified Gaussian $\mathcal{N}_{\text{rect}}(\mu_\Lambda, \sigma_\Lambda)$

→ only positive factor loading values

$$y_j \sim \mathcal{N}(\mu_\Lambda, \sigma_\Lambda)$$

$$\lambda_j = \max\{y_j, 0\}$$

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factor analysis	principal component analysis
causes of the data	geometrical abstractions
explain common variances	explain all variance
variance shared	first l with max. variance
scale invariant	not scale invariant
additive noise (variance lost)	no noise
solution not unique	solution unique
model assumptions	no assumptions
solution depends on l	first l unique
projection uses noise	no noise
no ranking	ranked by eigenvalues

Factor Analysis



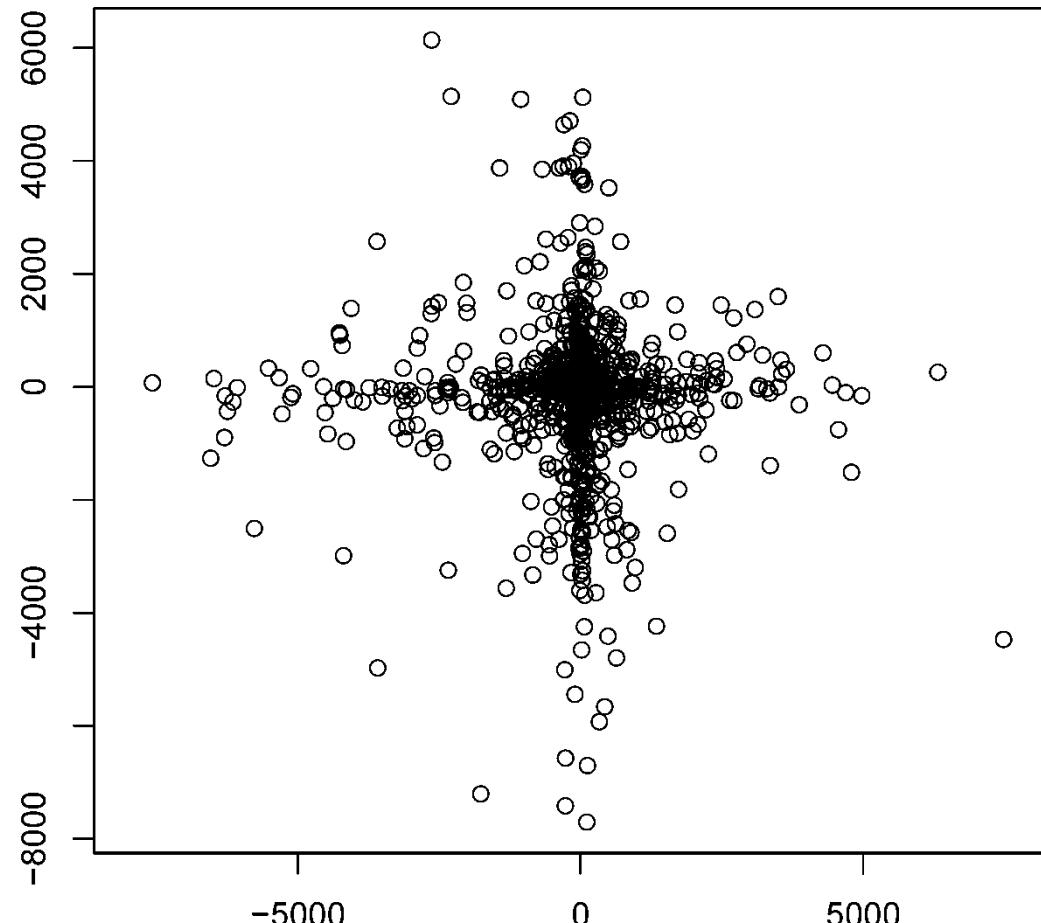
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factor analysis	independent component analysis
additive noise	no noise
solution not unique	unique up to scale & permutation
assumption: Gauss	assumption: super-Gauss
projection averaged over noise	no noise
solution depends on l	does not depend on l

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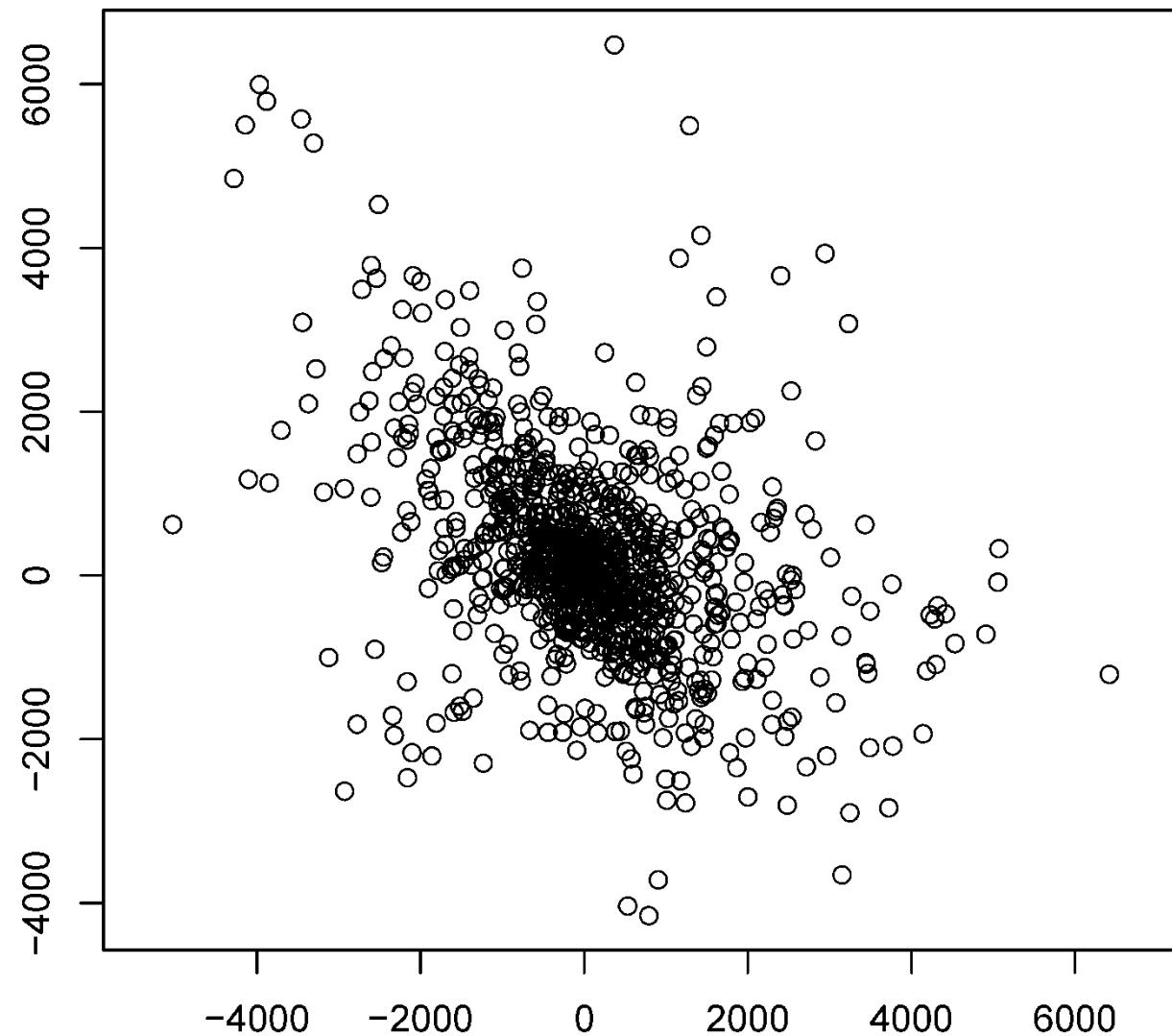
50-dimensional data set with linearly mixed super-Gaussians



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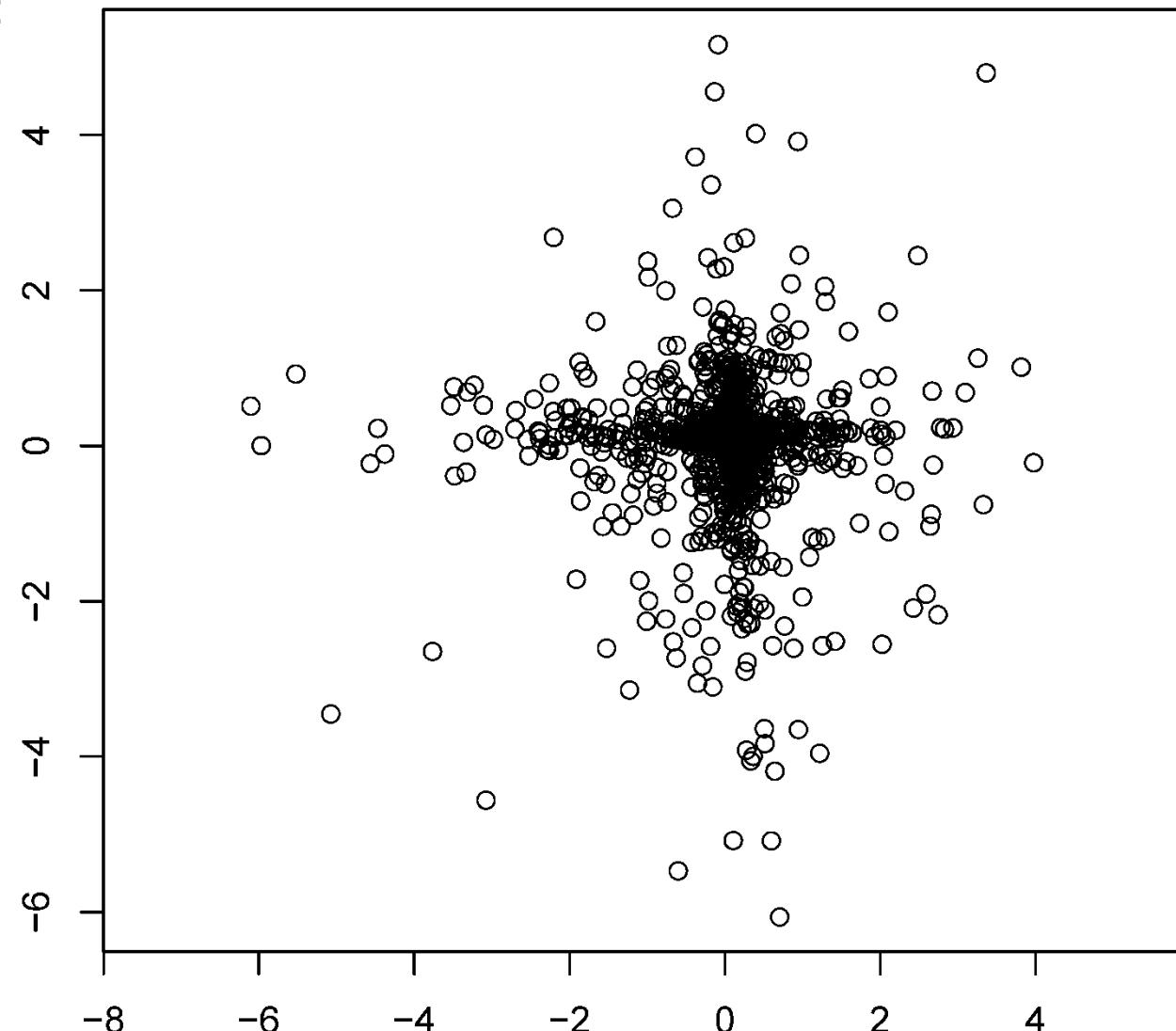
Mixing:



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fastICA:



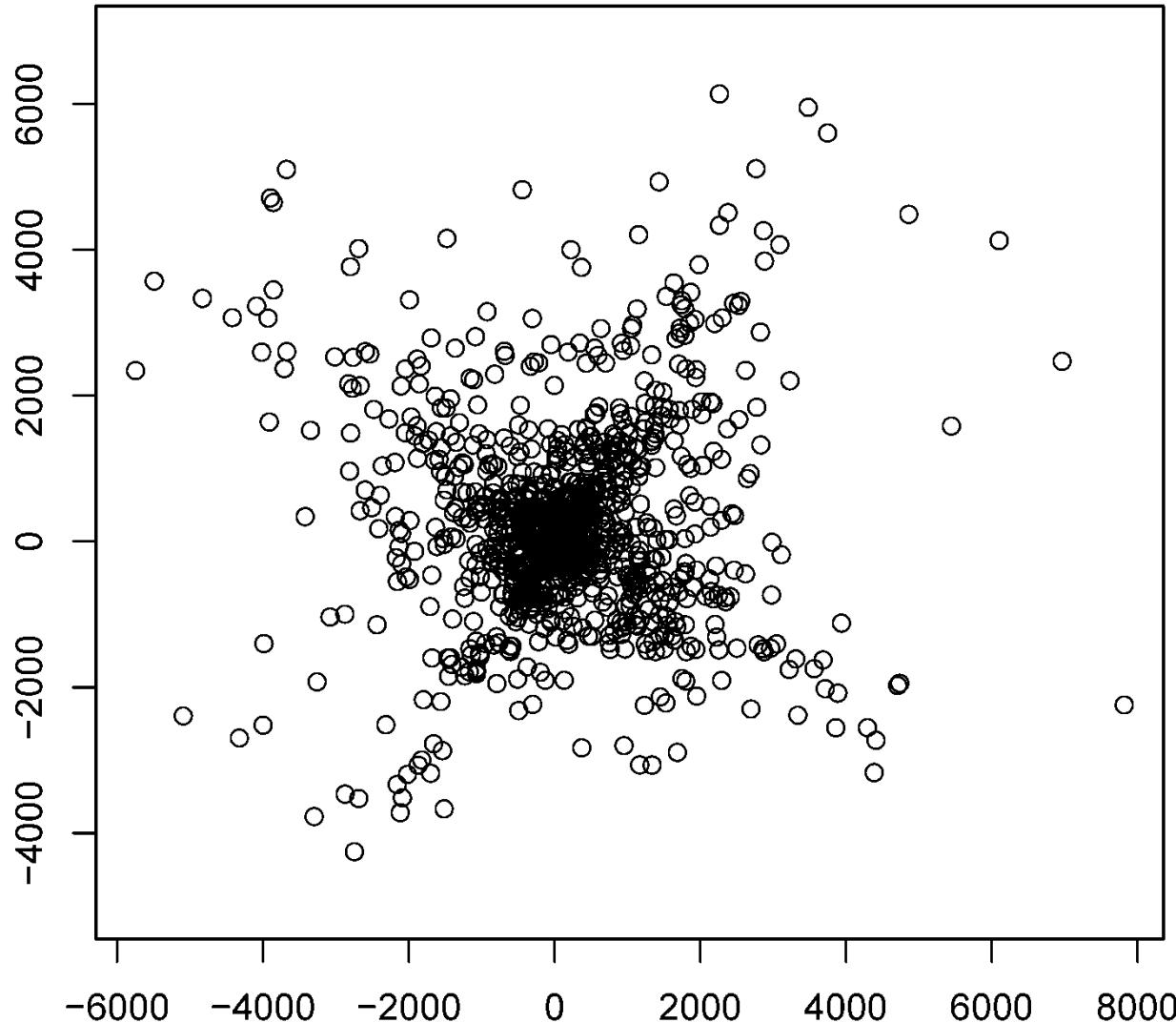
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factor analysis:

demixing is worse than with ICA

factor analysis assumes normally distributed factors while ICA super-Gaussians
 \rightarrow ICA better suited

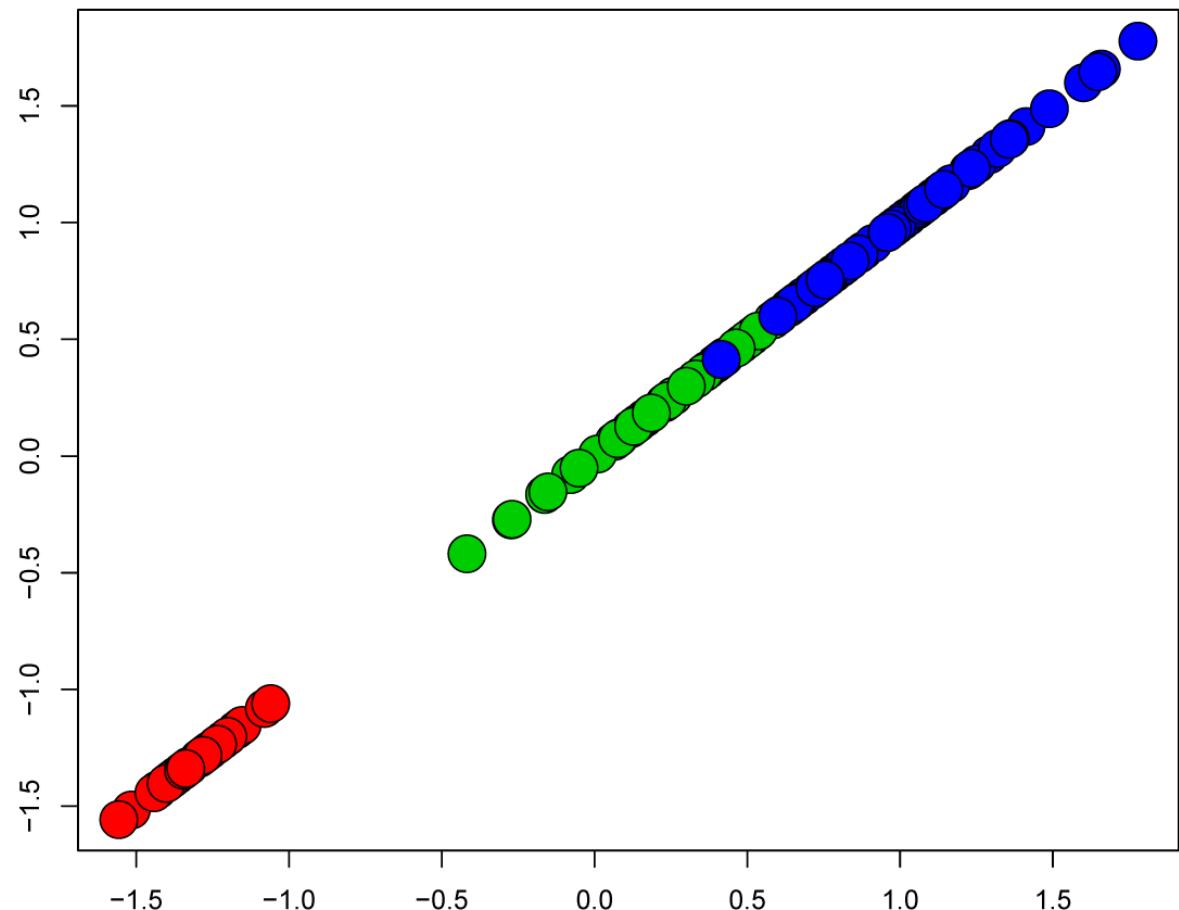


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Iris Data Set only one factor:

Factor Analysis on the Iris Data



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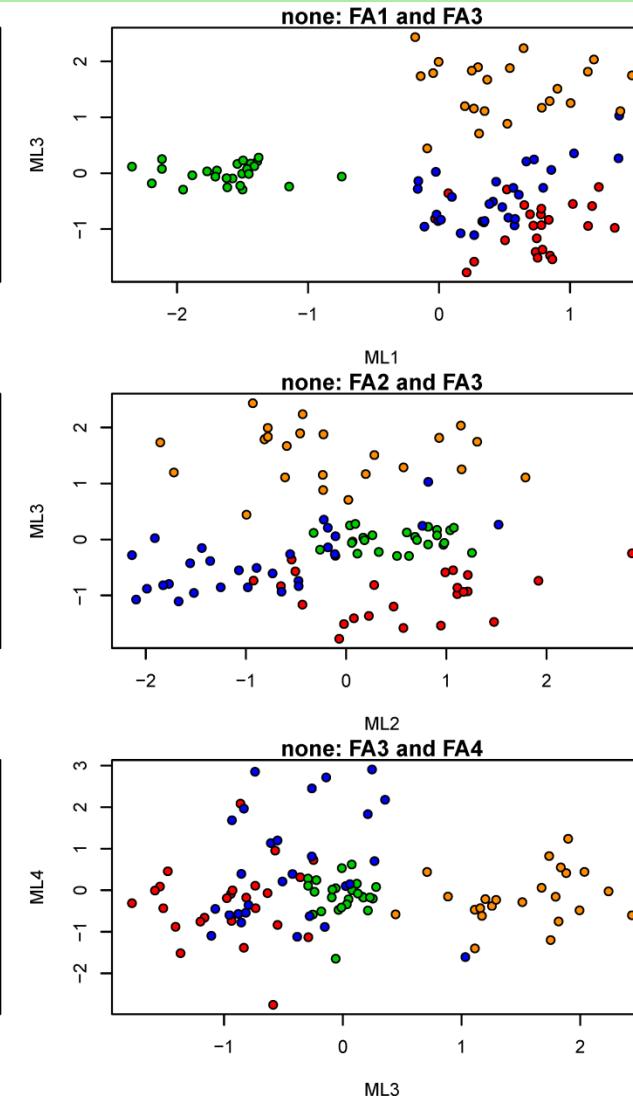
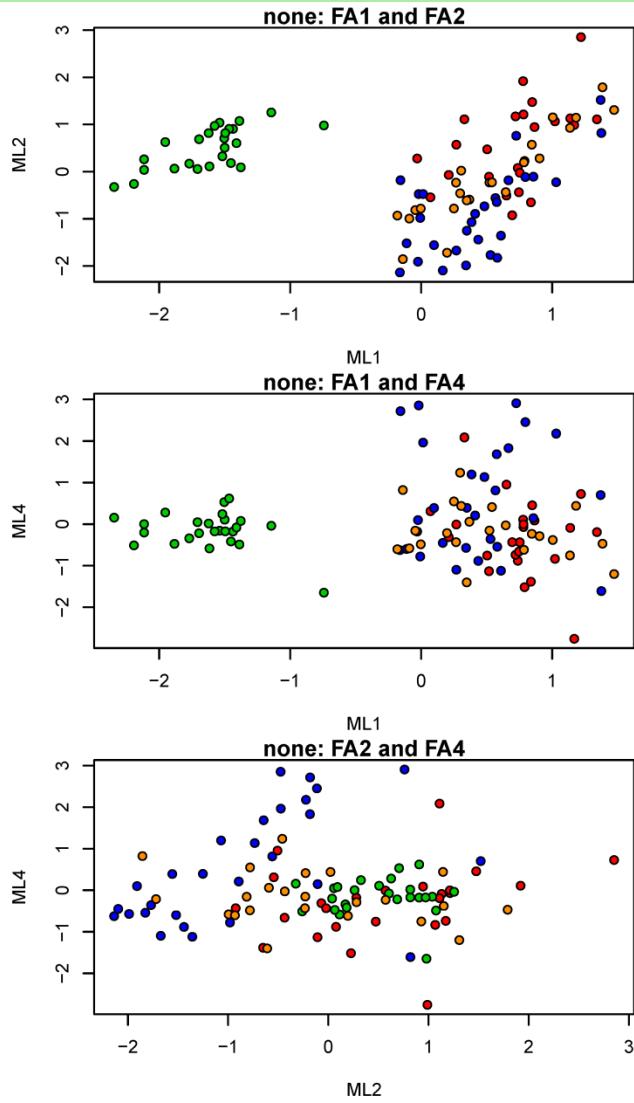
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Multiple Tissue Data Set: 4 factors

n features with largest variance ensure a full rank covariance matrix.

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FA without rotation

FA1 separates prostate (green)

FA2 separates breast (red) from lung (blue) → not very good

FA3 separates colon (orange)

FA4 separates part of lung (blue)

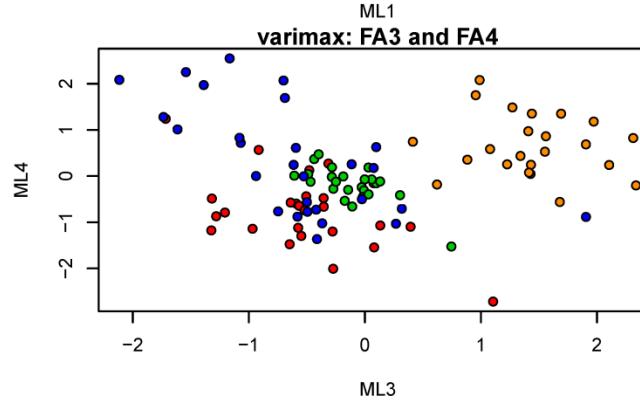
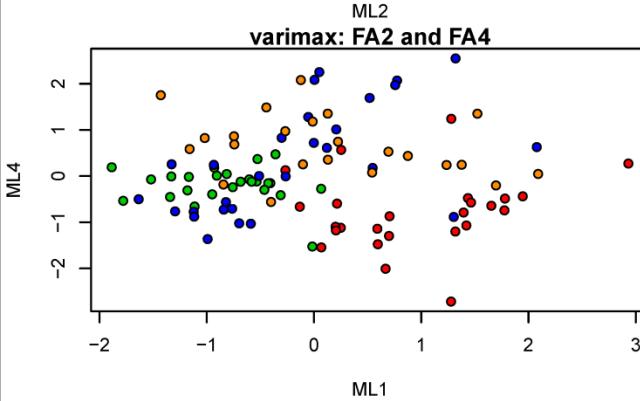
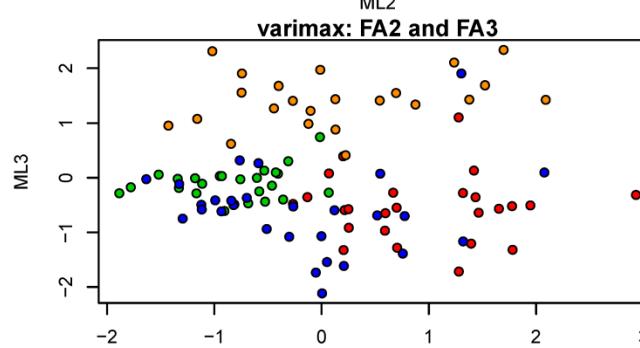
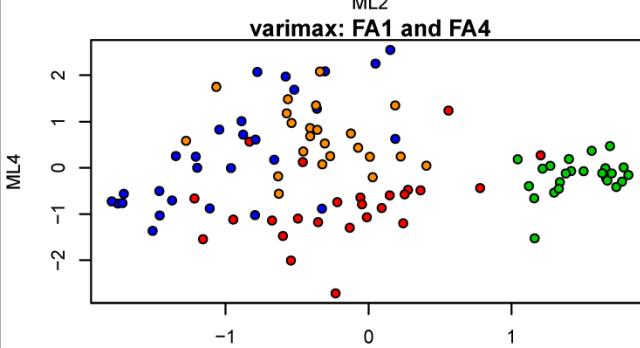
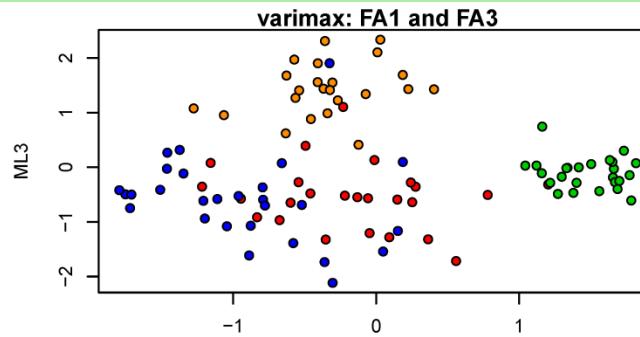
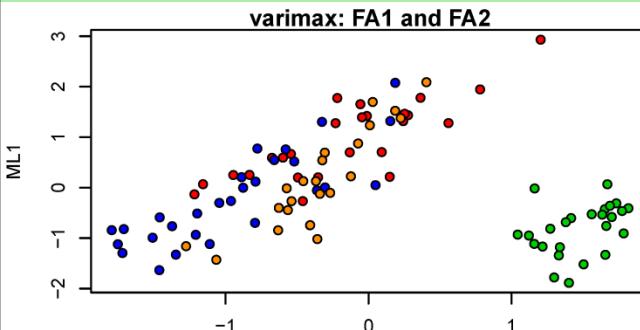
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FA with varimax rotation

separation is slightly worse than without rotations

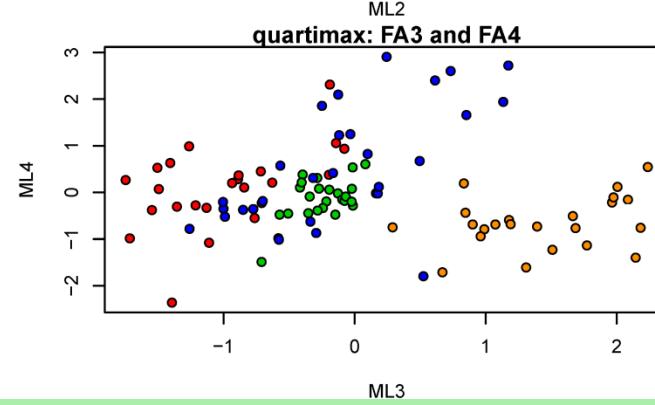
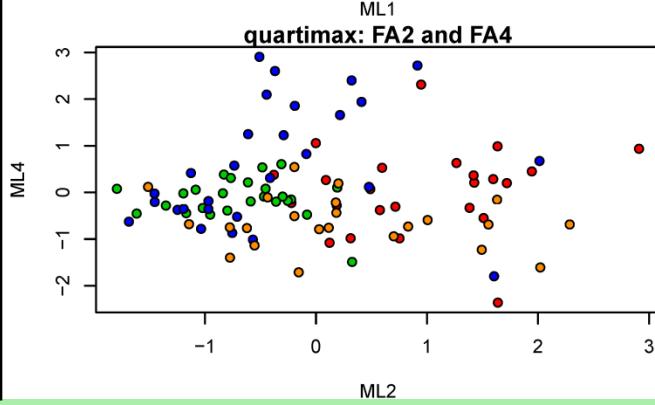
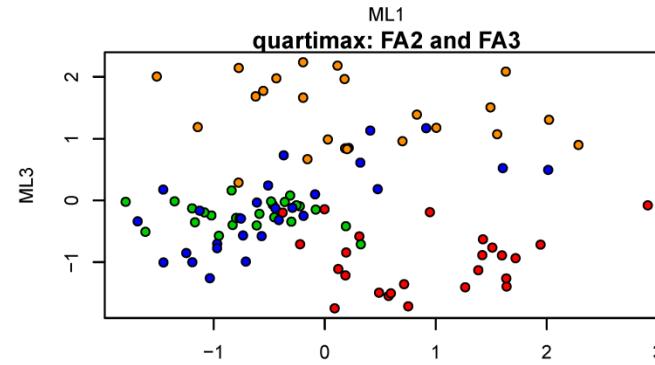
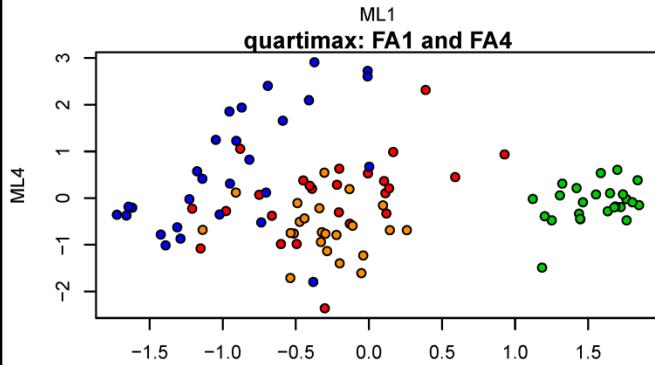
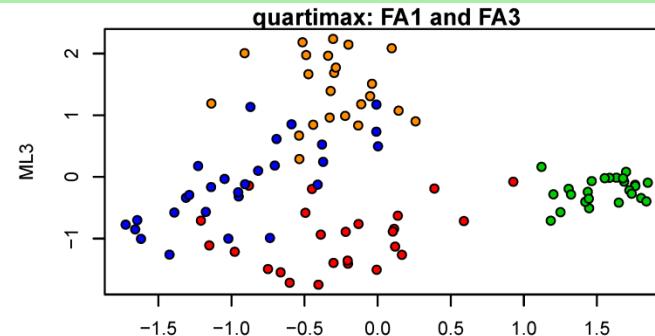
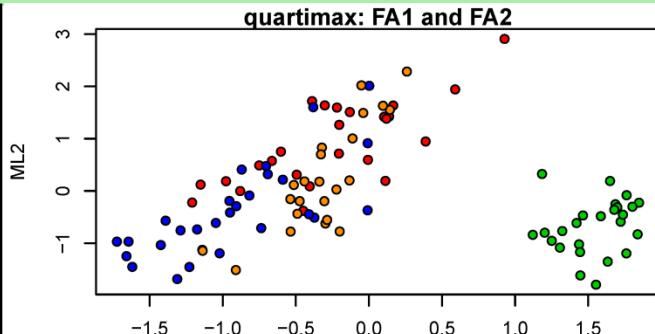
Factor Analysis

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FA with quartimax rotation

result is similar to varimax rotation

separation is slightly worse than without rotations

Scaling and Projection Methods



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projection of the data to a low-dimensional space (“scaling”)

- visualize the data
- represent the data in a low-dimensional space for further processing:
 - model selection using low-complex model classes
 - low-dimensional representation can capture only the main structures
 - noise and outliers are not represented

Projection Pursuit



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Projection pursuit:

least Gaussian (“interesting”) projections of the data

how to define non-Gaussianity?

covariance and mean given: Gaussian distribution maximizes the entropy

Objective: minimize $H(t)$ for $t = \mathbf{w}^T \mathbf{x}$

t is normalized to zero mean and unit variance

This is difficult to optimize

→ finding unimodal super-Gaussians

→ finding multimodal distributions

Other criteria are given for ICA: kurtosis and different contrast functions which measure non-Gaussianity

Multidimensional Scaling

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Multidimensional Scaling (MDS):

projection to a low-dimensional space while **keeping the distances between data points**

$$\mathbf{y}_i = f(\mathbf{x}_i; \mathbf{w})$$

$$\delta_{ij} = \|\mathbf{x}_i - \mathbf{x}_j\|$$

$$d_{ij} = \|\mathbf{y}_i - \mathbf{y}_j\| \quad \text{goal: } d = \delta$$

$$R_1(d, \delta) = \frac{\sum_{i < j} (d_{ij} - \delta_{ij})^2}{\sum_{i < j} \delta_{ij}^2} \propto \sum_{i < j} (d_{ij} - \delta_{ij})^2$$

$$R_2(d, \delta) = \sum_{i < j} \left(\frac{d_{ij} - \delta_{ij}}{\delta_{ij}} \right)^2$$

$$R_3(d, \delta) = \frac{1}{\sum_{i < j} \delta_{ij}} \sum_{i < j} \frac{(d_{ij} - \delta_{ij})^2}{\delta_{ij}} \propto \sum_{i < j} \frac{(d_{ij} - \delta_{ij})^2}{\delta_{ij}}$$

“Kruskal's measure”
 penalizes large errors

fractional (relative)
 errors

“Sammon mapping”
 compromise

\propto means factors constant in the parameters w

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derivatives used in gradient based methods:

$$\frac{\partial}{\partial \mathbf{y}_k} R_1(d, \delta) = \frac{2}{\sum_{i < j} \delta_{ij}^2} \sum_{j \neq k} (d_{kj} - \delta_{kj}) \frac{\mathbf{y}_k - \mathbf{y}_j}{d_{kj}}$$

$$\frac{\partial}{\partial \mathbf{y}_k} R_2(d, \delta) = 2 \sum_{j \neq k} \frac{d_{kj} - \delta_{kj}}{\delta_{kj}^2} \frac{\mathbf{y}_k - \mathbf{y}_j}{d_{kj}}$$

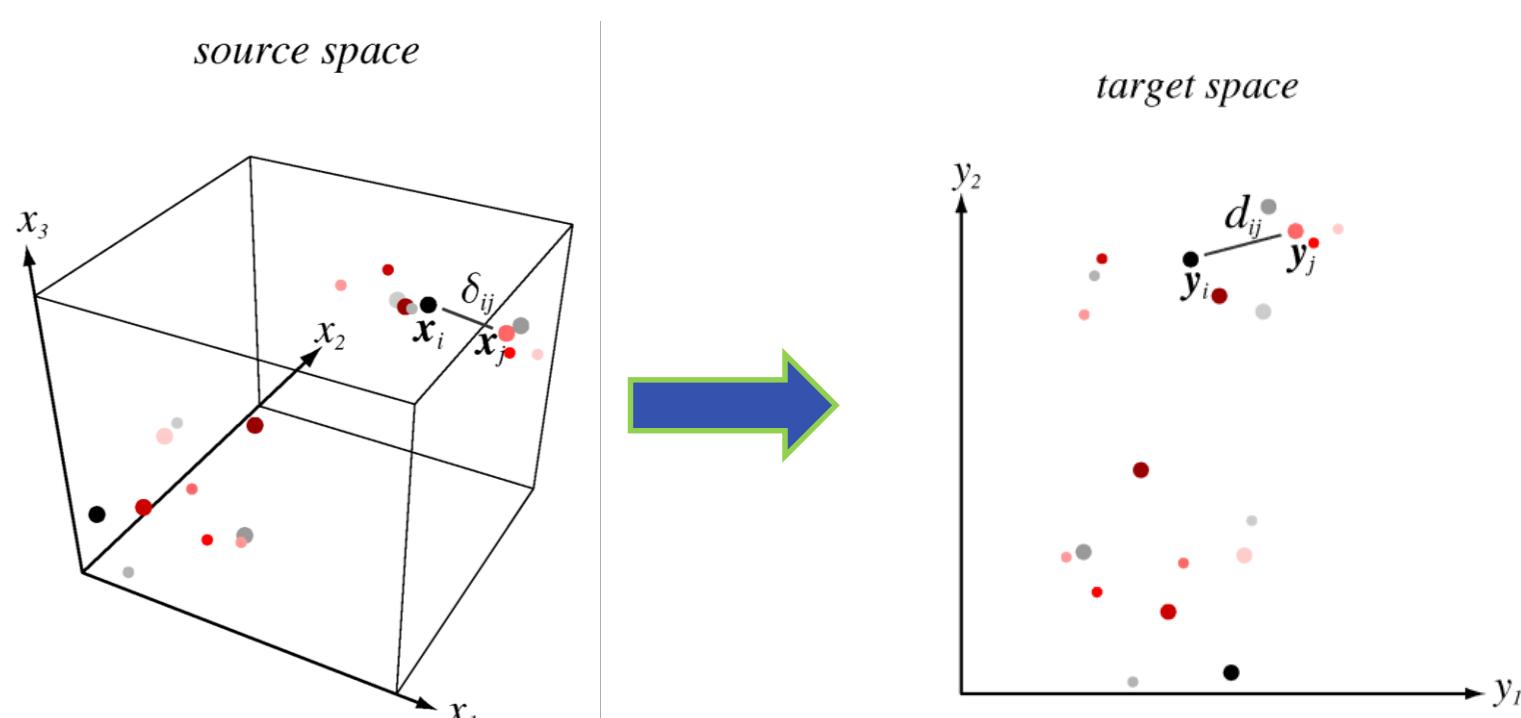
$$\frac{\partial}{\partial \mathbf{y}_k} R_3(d, \delta) = \frac{2}{\sum_{i < j} \delta_{ij}} \sum_{j \neq k} \frac{d_{kj} - \delta_{kj}}{\delta_{kj}} \frac{\mathbf{y}_k - \mathbf{y}_j}{d_{kj}}$$

R viewed as potential function \rightarrow derivatives are forces

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example from Duda, 2001, multidimensional scaling from a 3-dimensional space to a 2-dimensional space (right).



Multidimensional Scaling



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metric MDS or principal coordinates analysis:

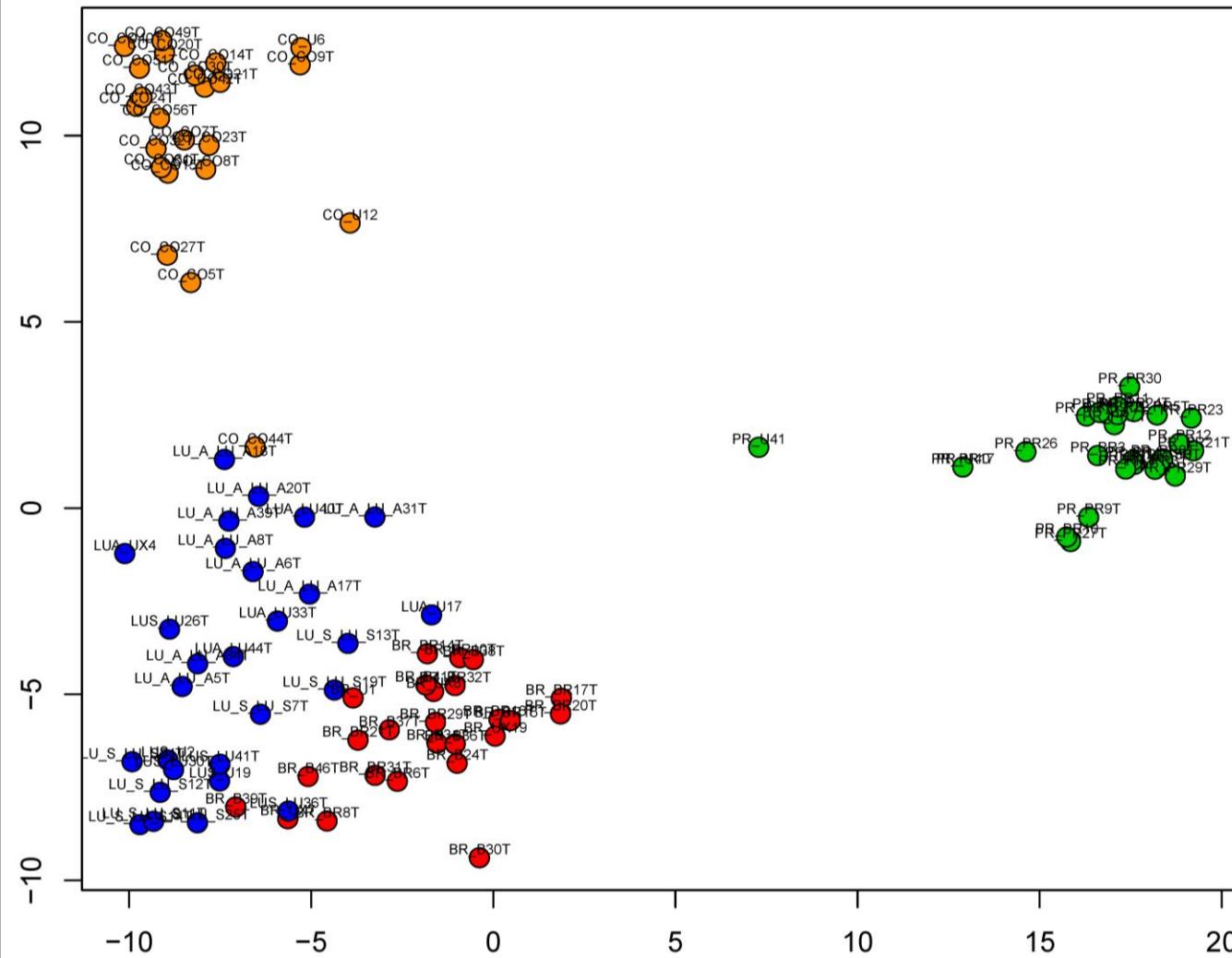
Euclidean distance → coordinates (embedding)

metric multidimensional scaling
is applied to
the multiple tissue data set

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Metric MDS 101 features



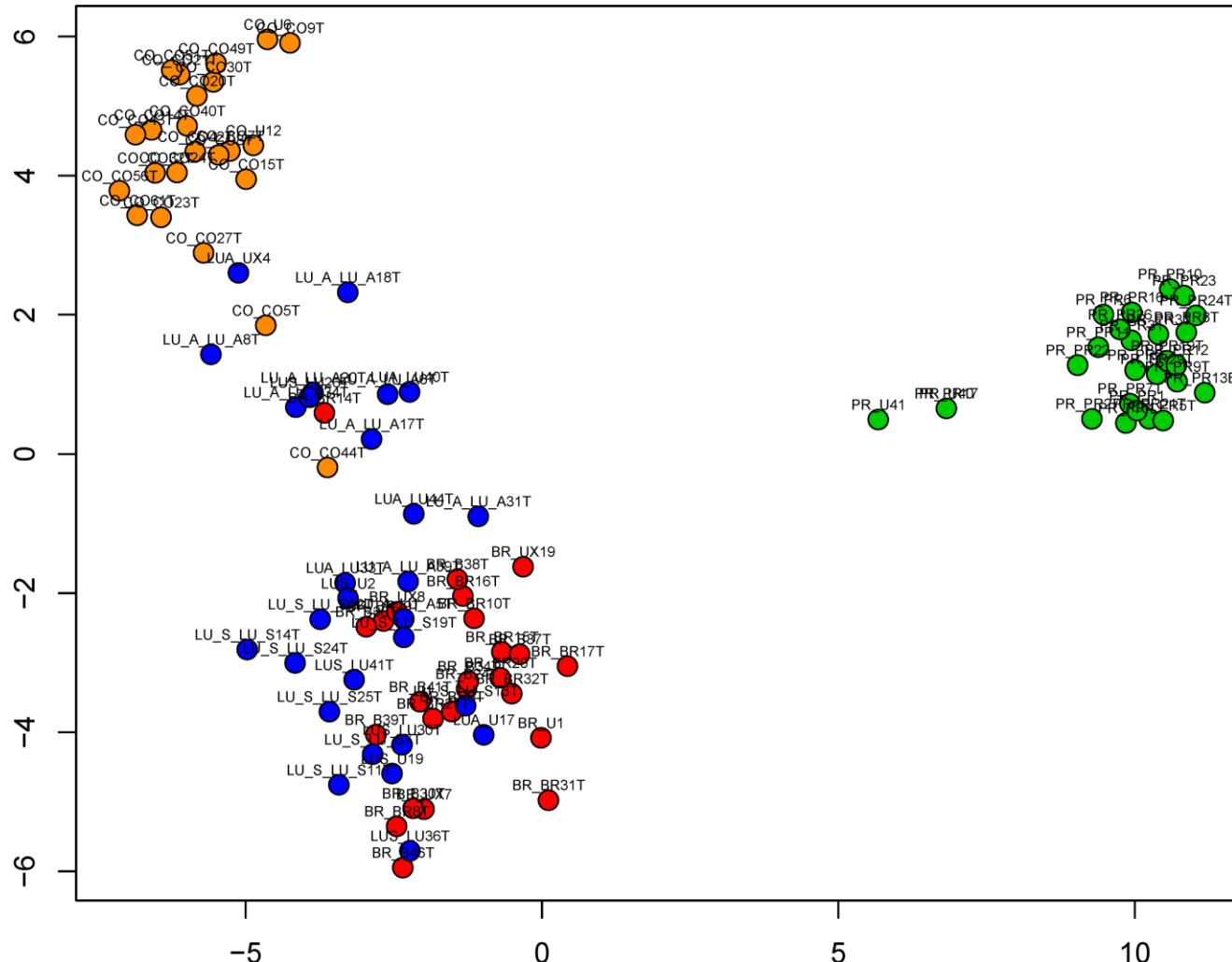
MDS for multiple tissues

the 101 features with largest variance are selected

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Metric MDS 13 features



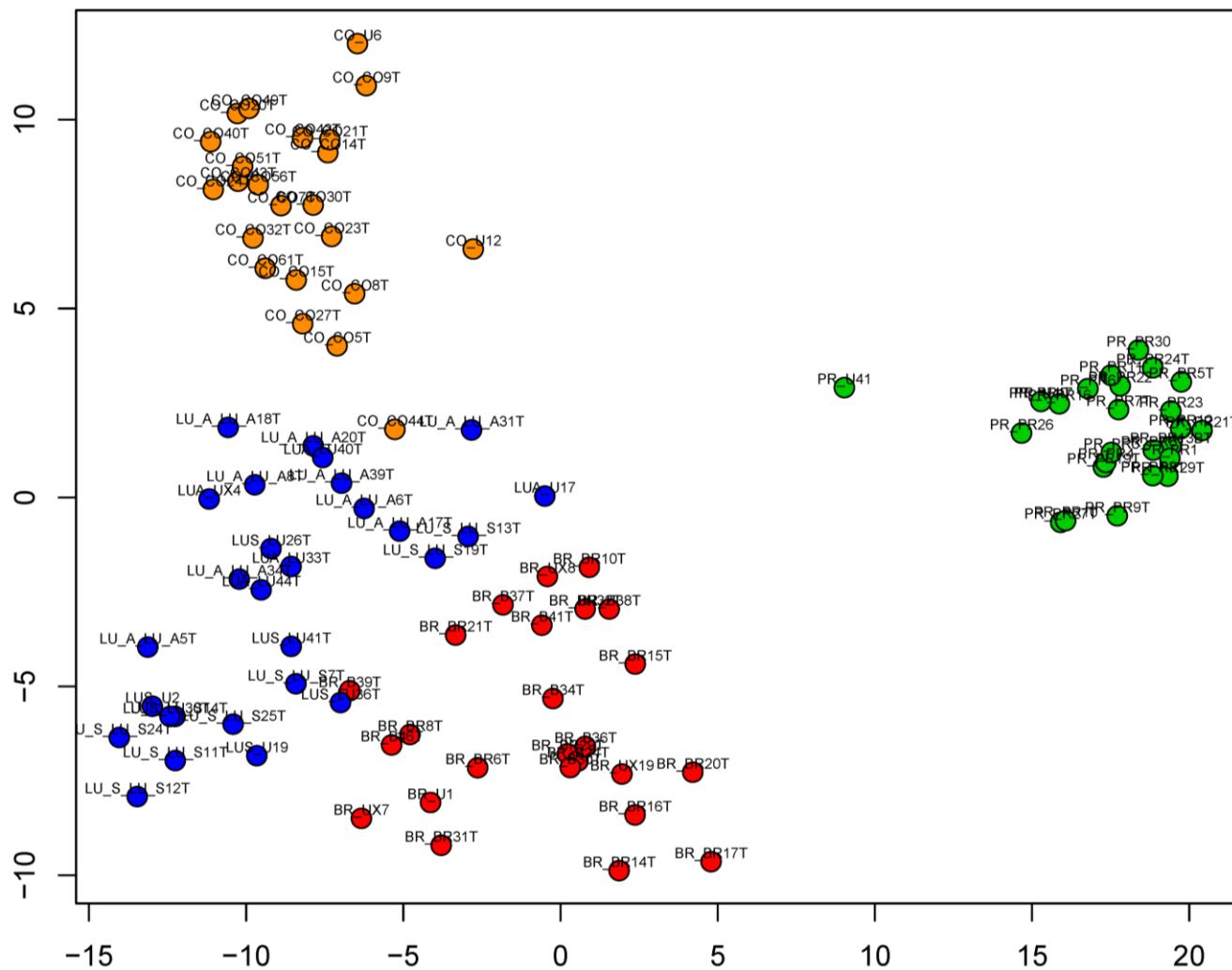
MDS for multiple tissues

the 13 features with largest variance are selected

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Kruskal's MDS 101 features



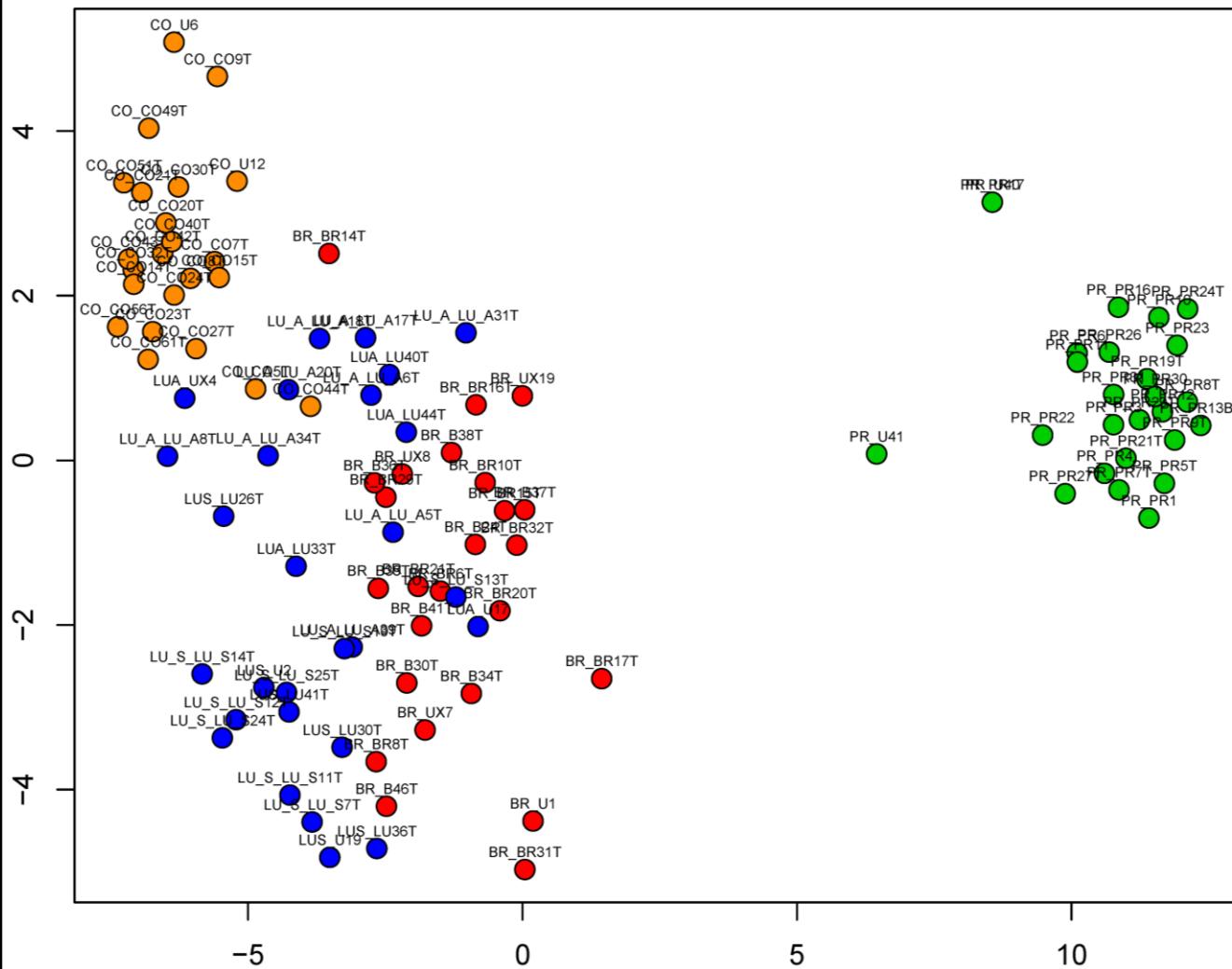
Multiple tissues:
Kruskal's non-metric multidimensional scaling

101 features with the largest variance

Multidimensional Scaling

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Kruskal's MDS 13 features



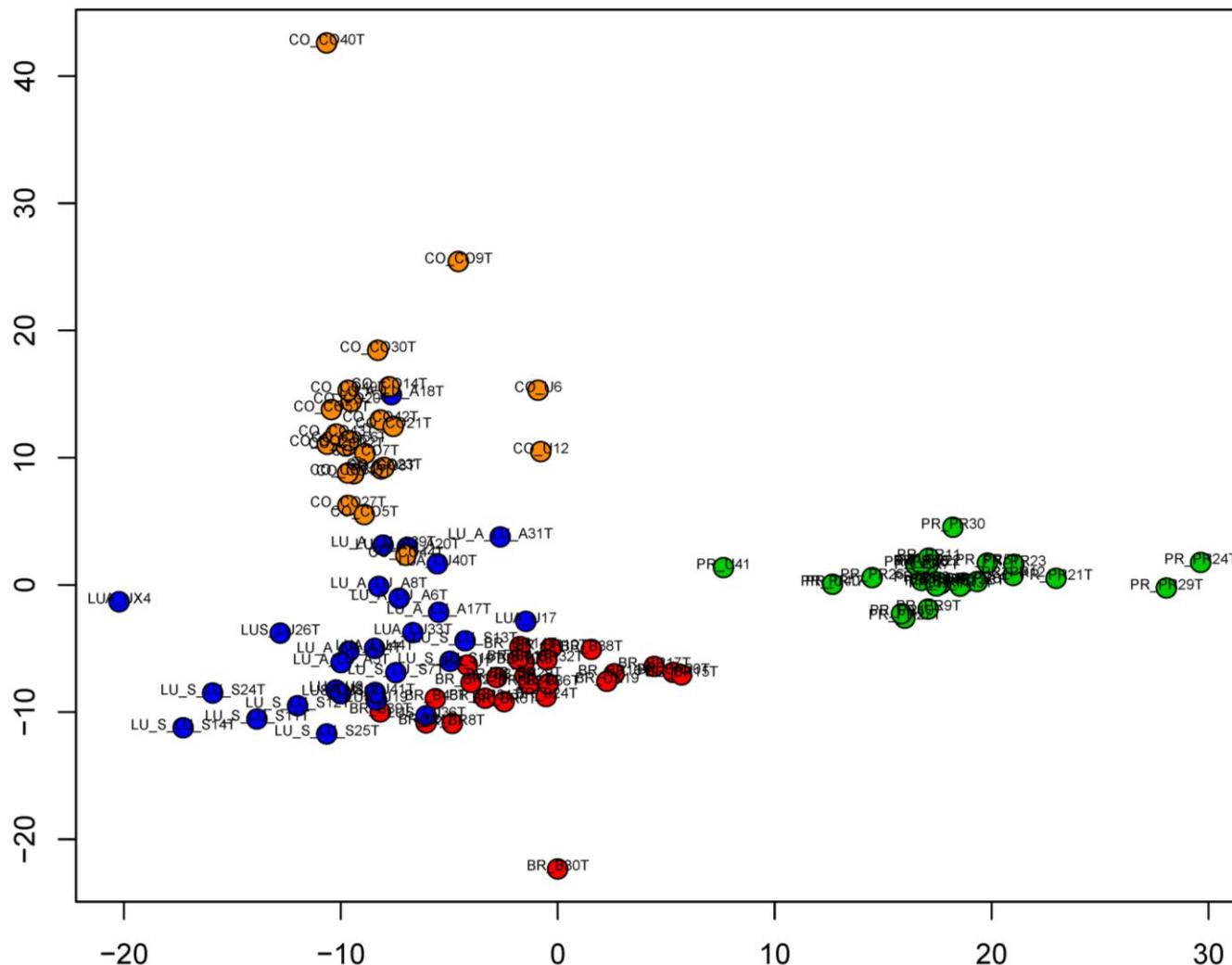
Multiple tissues:
Kruskal's non-metric multidimensional scaling

13 features with the largest variance

Multidimensional Scaling

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Sammon Mapping 101 features



Multiple tissues:
Sammon's non-linear mapping

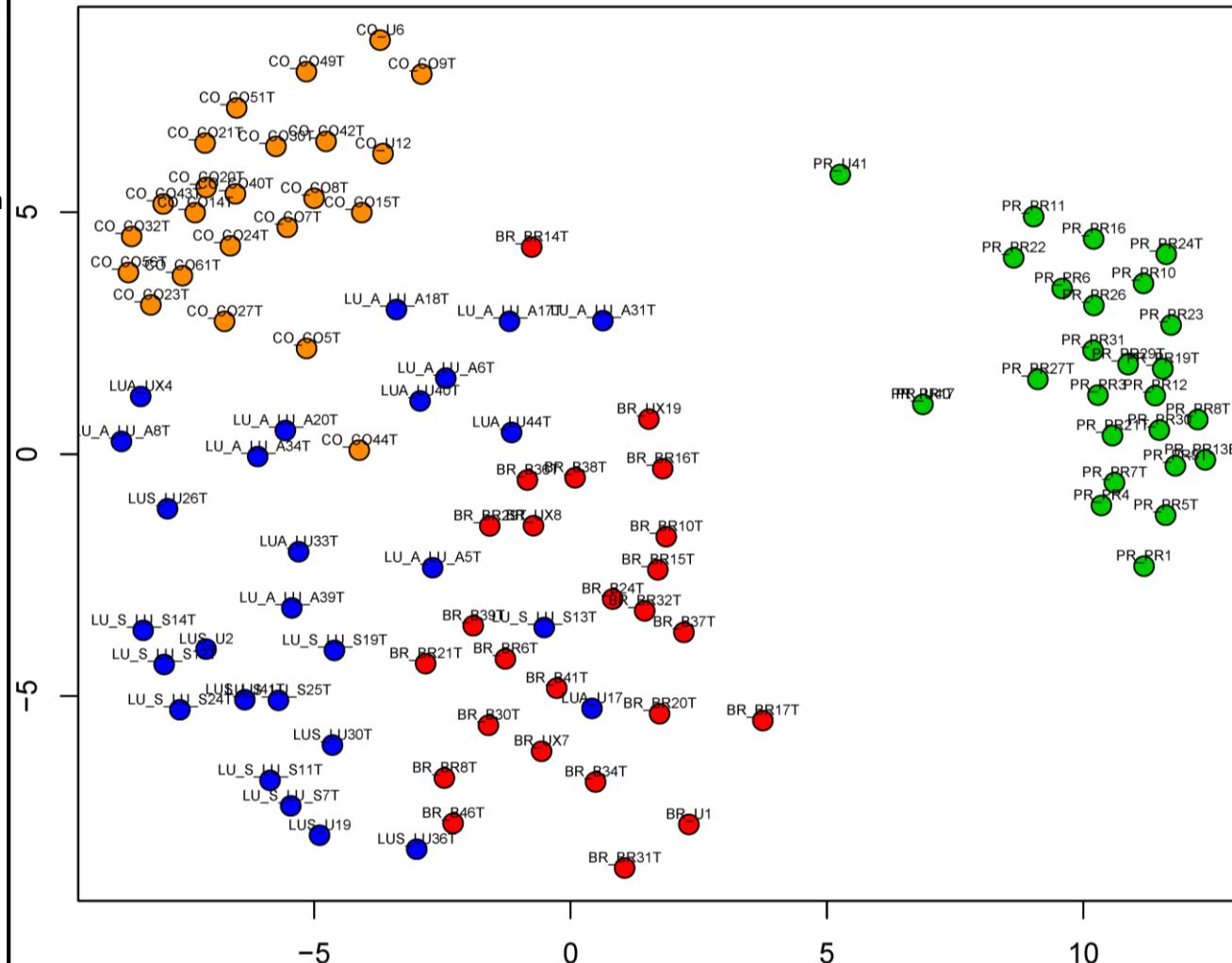
101 features with the largest variance

worse than metric or Kruskal's measure

Multidimensional Scaling

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Sammon Mapping 13 features



Multiple tissues:
Sammon's non-linear mapping

13 features
with the
largest
variance

clusters
are more
spread out

Non-negative Matrix Factorization



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Non-negative matrix factorization (NMF)

is a matrix factorization method where **all matrix entries** are assumed to be **positive**

the non-negativity constraints make the representation of the observations **purely additive**: a **parts-based representation**, where parts are added to the observation but not subtracted (e.g. images)

$$\mathbf{X} \in \mathbb{R}^{n \times m} \quad \mathbf{Y} \in \mathbb{R}^{n \times l} \quad \mathbf{U} \in \mathbb{R}^{m \times l}$$

$$0 \leq X_{ij} \quad 0 \leq Y_{ik} = [\mathbf{y}_k]_i \quad 0 \leq U_{jk} = [\mathbf{u}_k]_j$$

$$\mathbf{X} = \mathbf{Y} \mathbf{U}^T = \sum_{k=1}^l \mathbf{y}_k \mathbf{u}_k^T$$

Non-negative Matrix Factorization

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Objective 1: Kullback-Leibler divergence (positive matrices)

$$D(\mathbf{A} \parallel \mathbf{B}) = \sum_{ij} \left(A_{ij} \log \frac{A_{ij}}{B_{ij}} + A_{ij} - B_{ij} \right) \quad \text{for } \sum_{ij} A_{ij} = \sum_{ij} B_{ij} = 1$$

minimize the Kullback-Leibler divergence $D(\mathbf{X} \parallel \mathbf{Y} \mathbf{U}^T)$ by gradient descent gives:

$$Y_{ik} = Y_{ik} \frac{\sum_{j=1}^m U_{jk} X_{ij} / (\mathbf{Y} \mathbf{U}^T)_{ij}}{\sum_{j=1}^m U_{jk}}$$

$$U_{jk} = U_{jk} \frac{\sum_{i=1}^n Y_{ik} X_{ij} / (\mathbf{Y} \mathbf{U}^T)_{ij}}{\sum_{i=1}^n Y_{ik}}$$

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Objective 2: Euclidean distance (Frobenius norm):

$$\|\mathbf{X} - \mathbf{Y} \mathbf{U}^T\|_F^2 \quad \|\mathbf{A} - \mathbf{B}\|_F^2 = \sum_{ij} (A_{ij} - B_{ij})^2$$

$$Y_{ik} = Y_{ik} \frac{(\mathbf{X} \mathbf{U})_{ik}}{(\mathbf{Y} \mathbf{U}^T \mathbf{U})_{ik}}$$

multiply $\mathbf{X} = \mathbf{Y} \mathbf{U}^T$
from right by \mathbf{U}

$$U_{jk} = U_{jk} \frac{(\mathbf{Y}^T \mathbf{X})_{kj}}{(\mathbf{Y}^T \mathbf{Y} \mathbf{U}^T)_{kj}}$$

multiply $\mathbf{X} = \mathbf{Y} \mathbf{U}^T$
from left by \mathbf{Y}^T

For a fixed point, the left and the right hand side have to be equal

NFM has been extended to sparse NFM (both decomposition matrices); sparse $\mathbf{Y} \rightarrow$ few parts are present

spares $\mathbf{U} \rightarrow$ few measurements indicate part

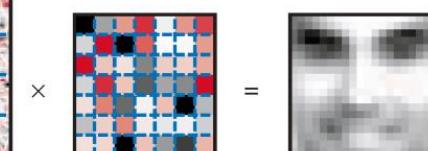
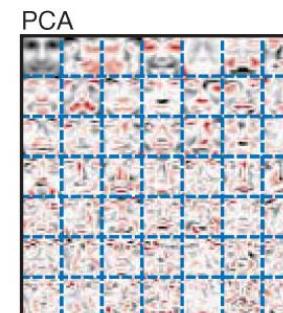
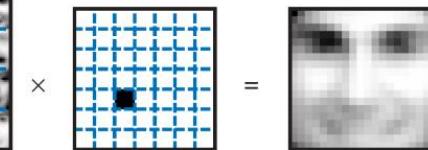
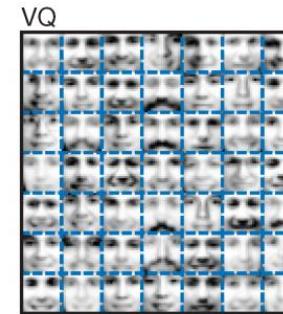
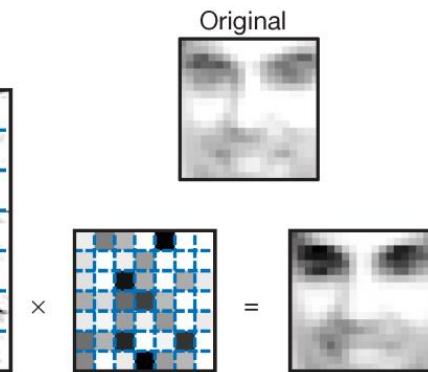
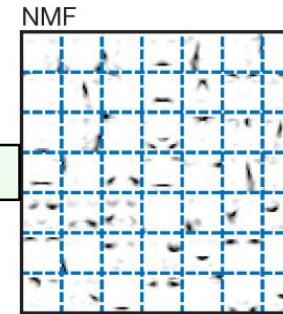
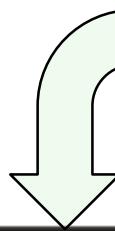
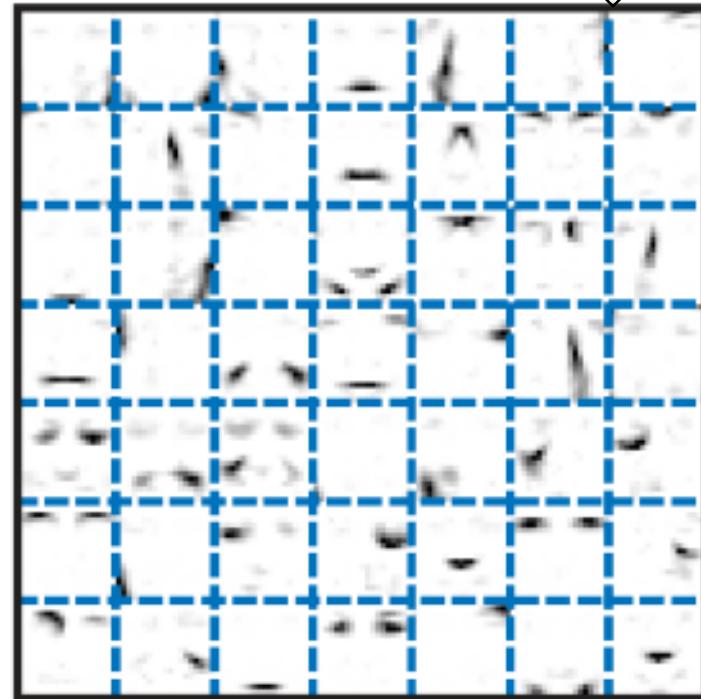
For example gene expression: part = pathway, few genes in pathway and few pathways are active in a sample

Non-negative Matrix Factorization

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parts-based representations
of faces

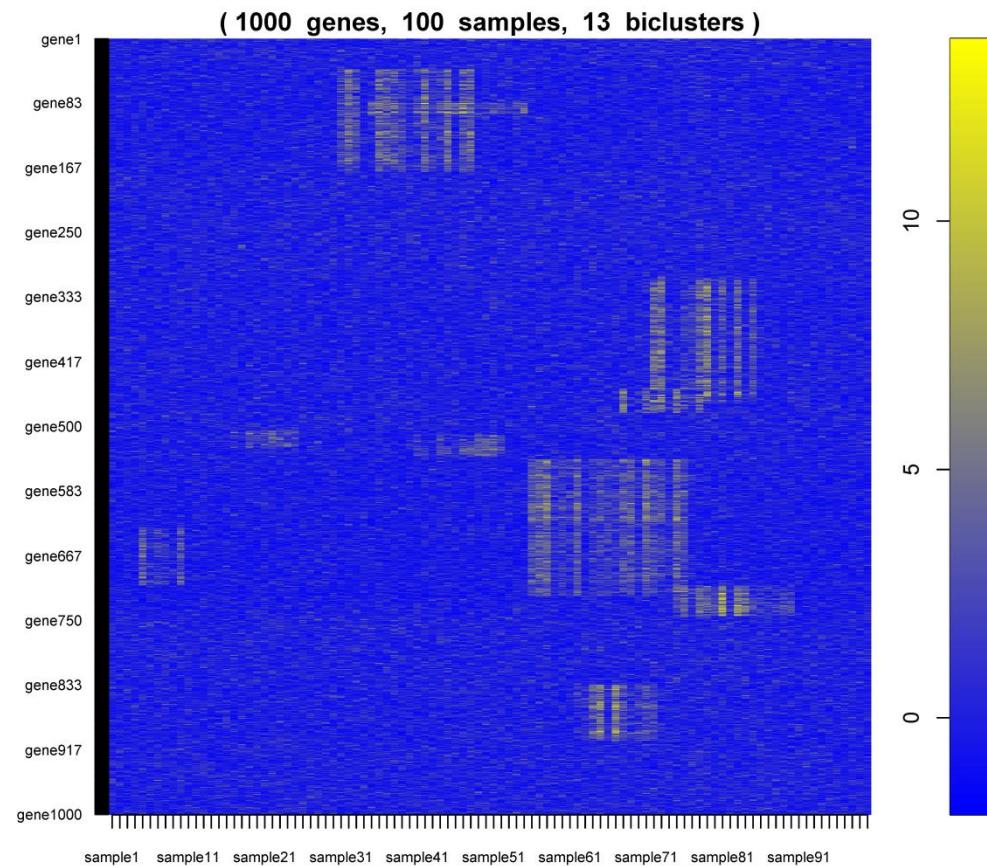
vector quantization (VQ)
and PCA learn
holistic representations



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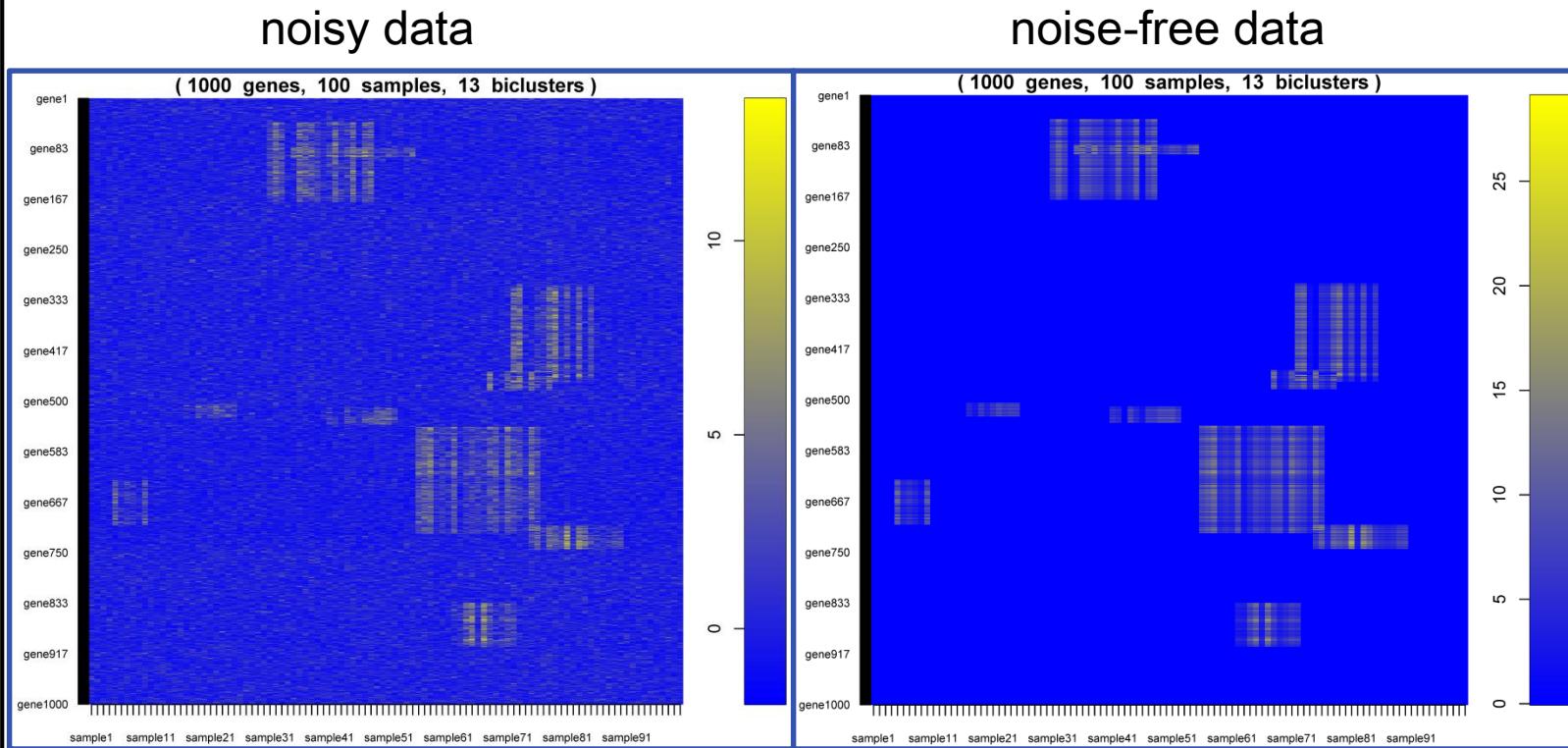
positive toy data generated by FABIA biclustering package



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The data contains blocks of patterns. For visualization purposes only, the blocks are constructed by adjacent row or column elements (blocks are the parts).

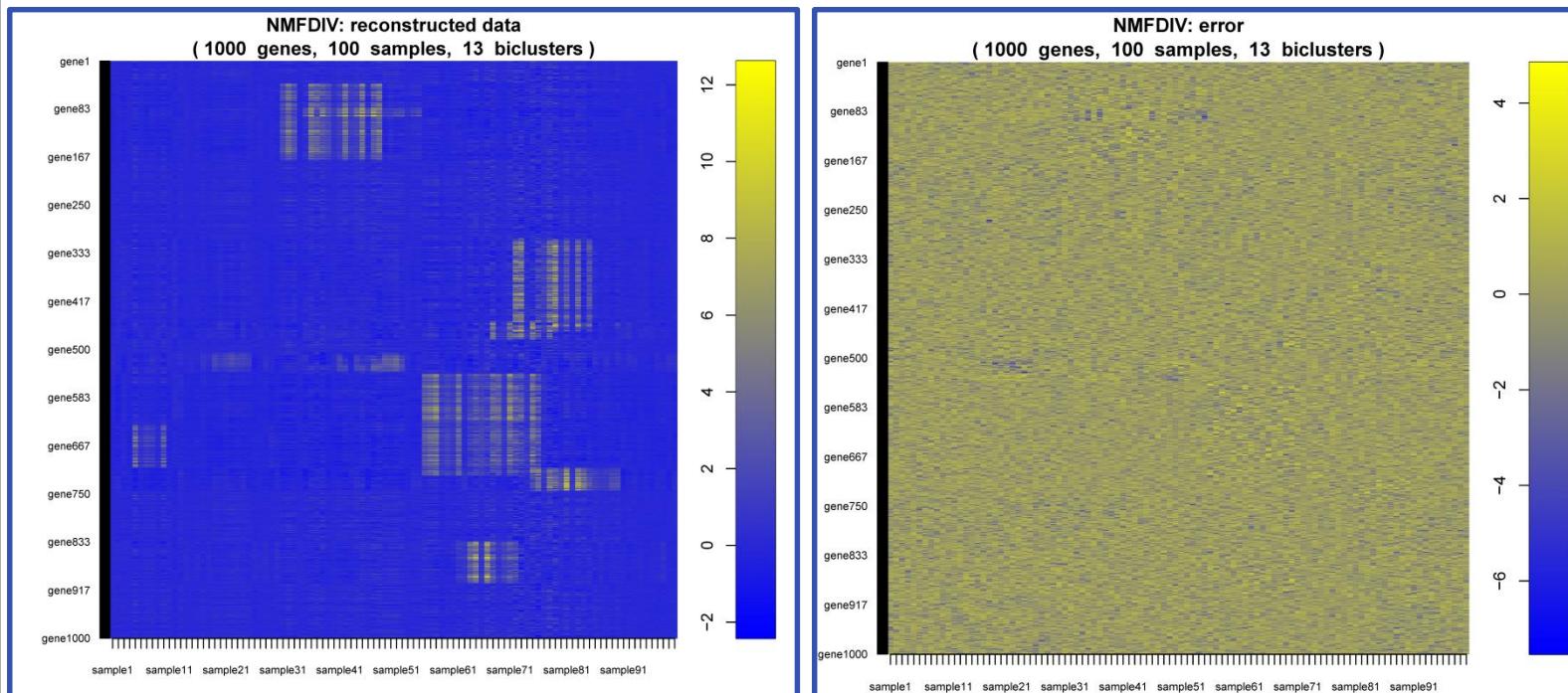


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NMF Kullback-Leibler divergence using the fabia package



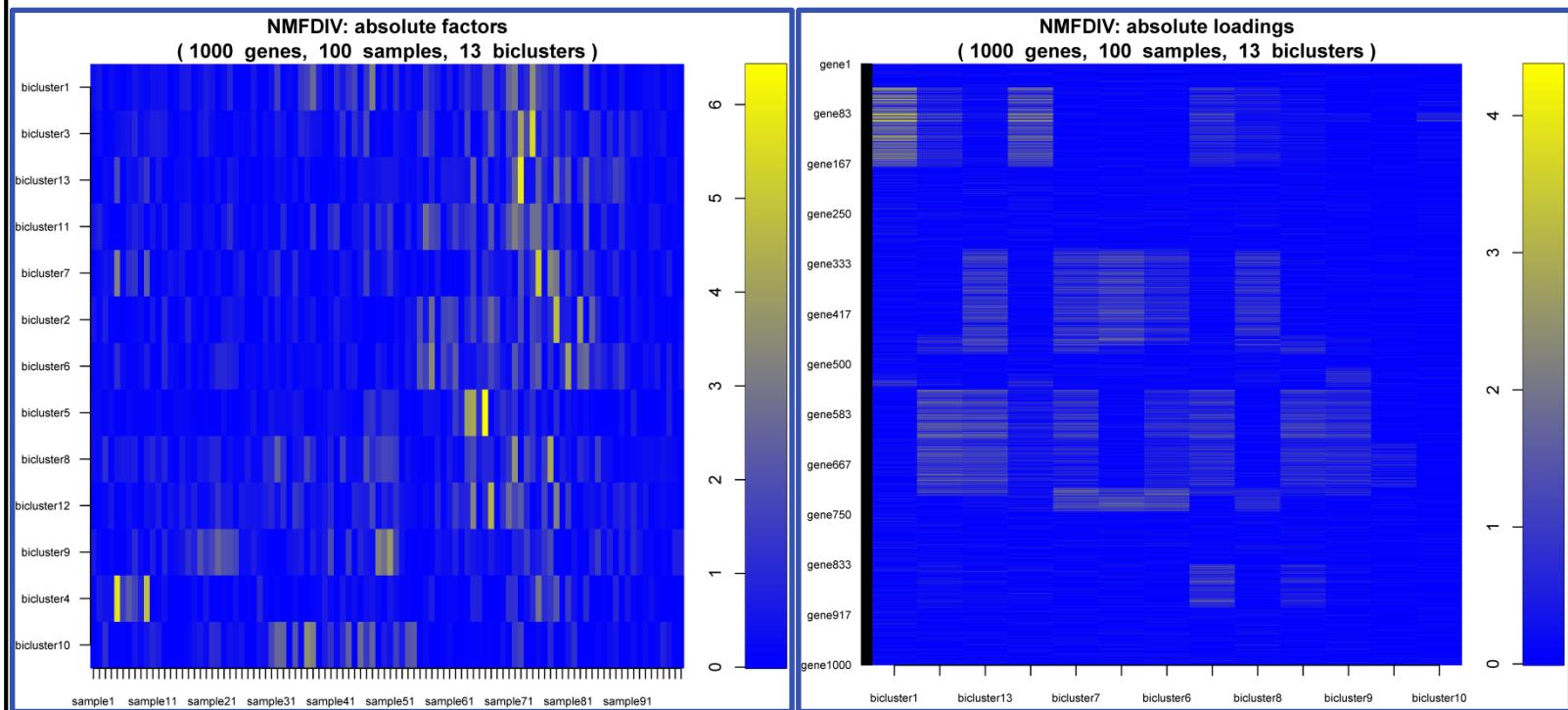
Non-negative Matrix Factorization

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NMF Kullback-Leibler divergence

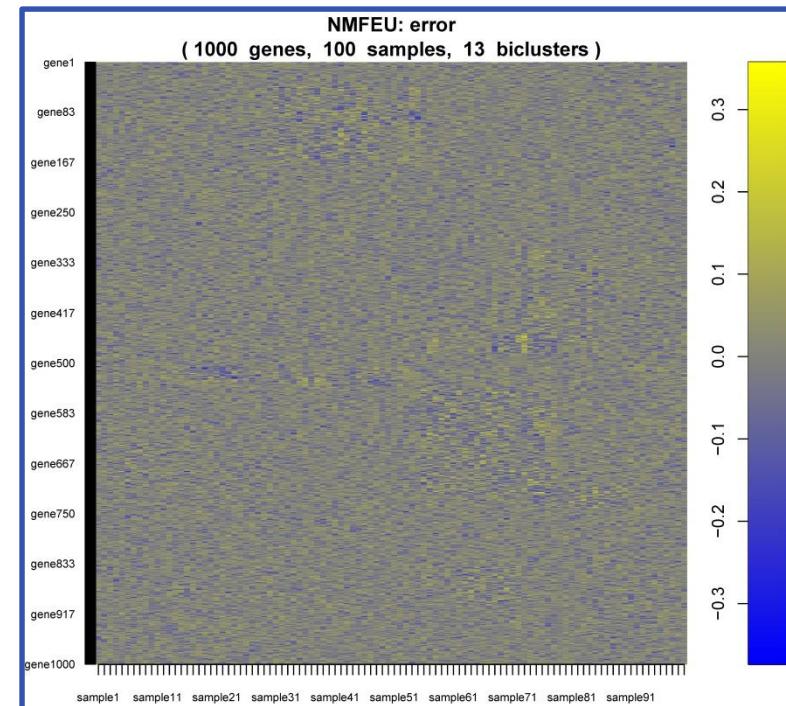
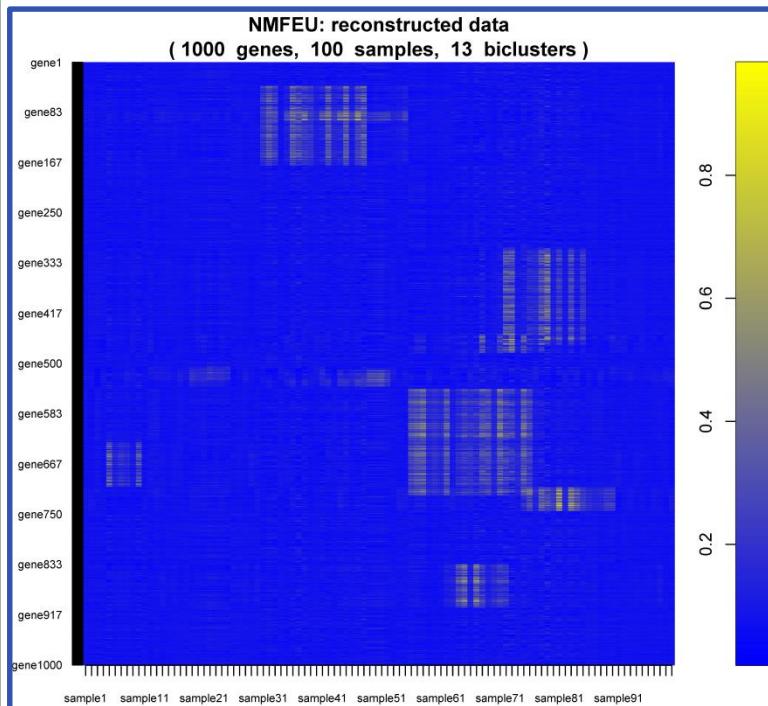


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NMF Euclidean distance: fabia package

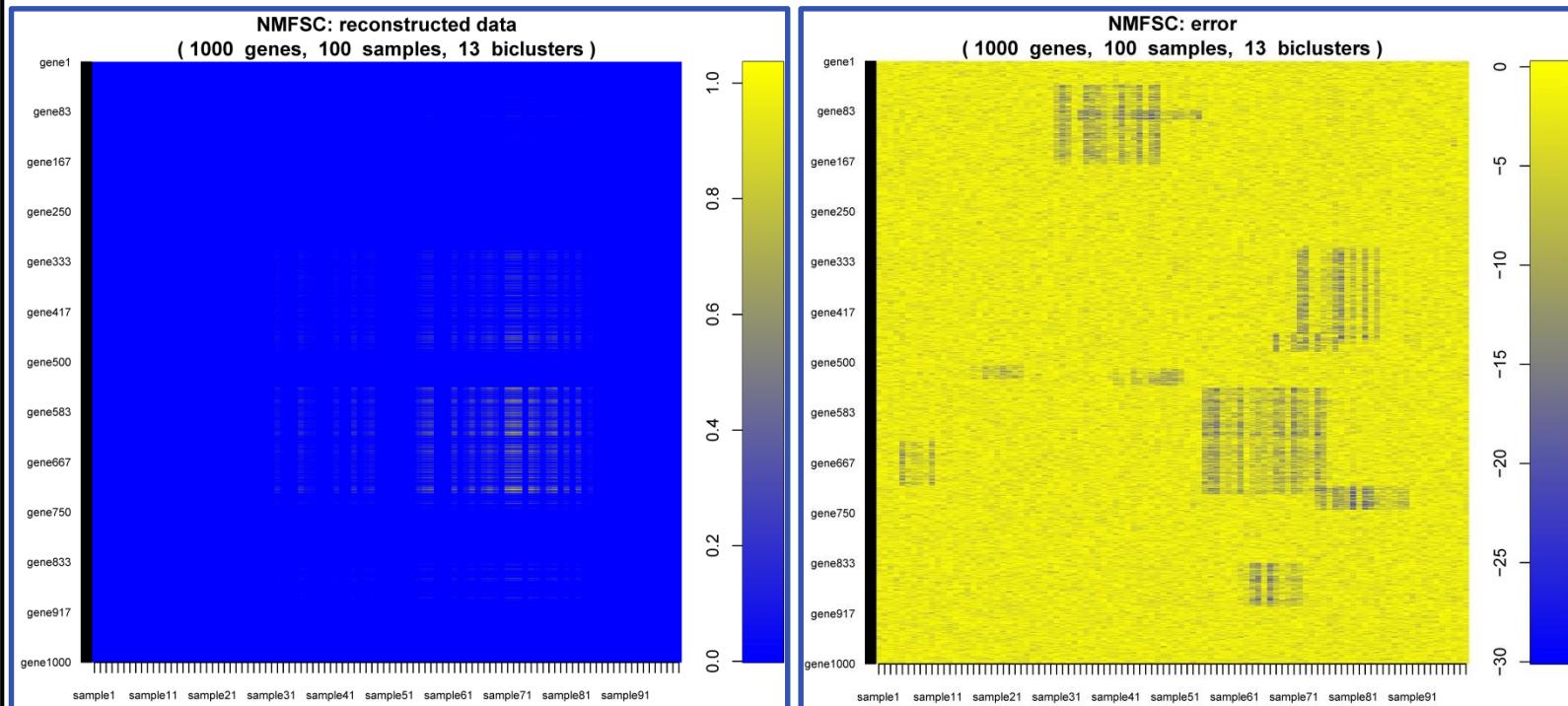


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NMF with sparseness constraints using the fabia package

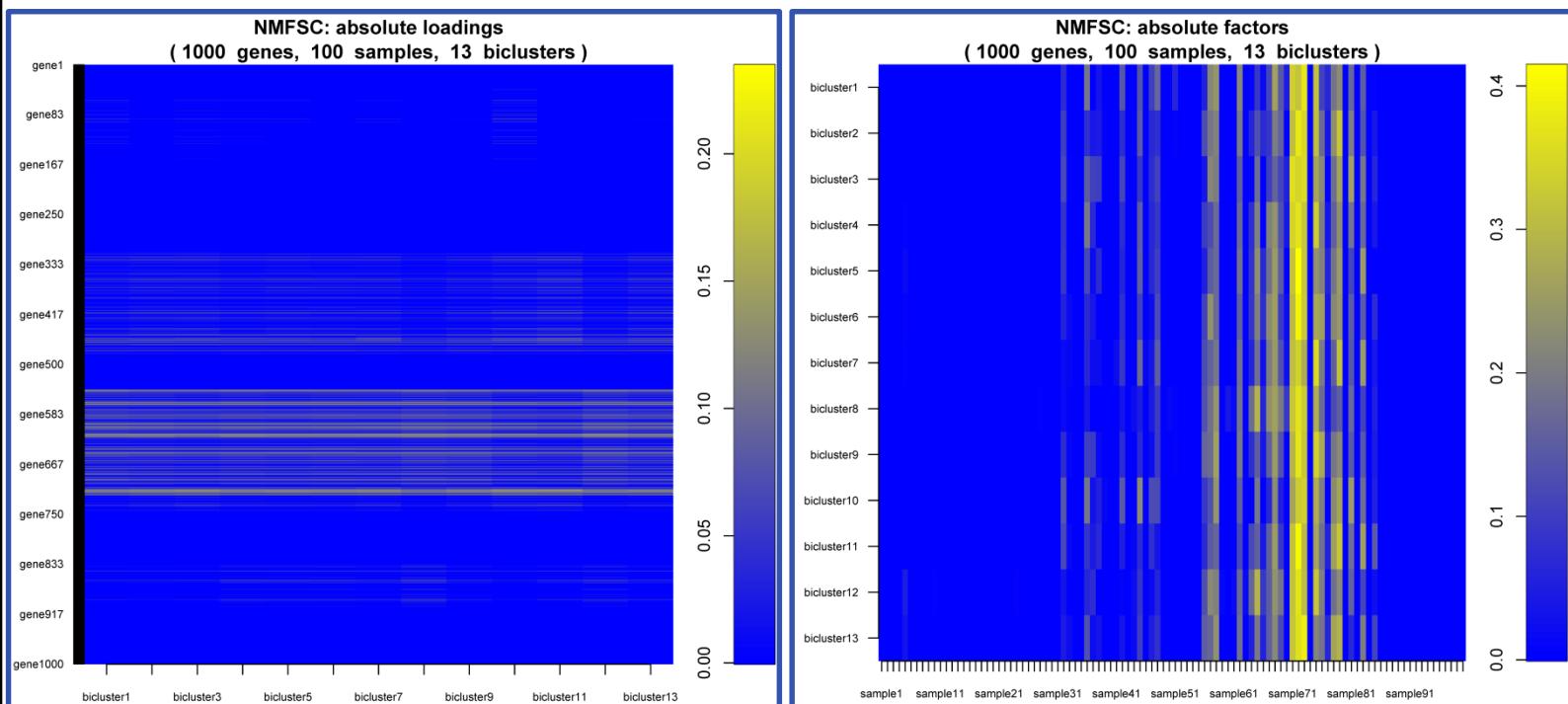


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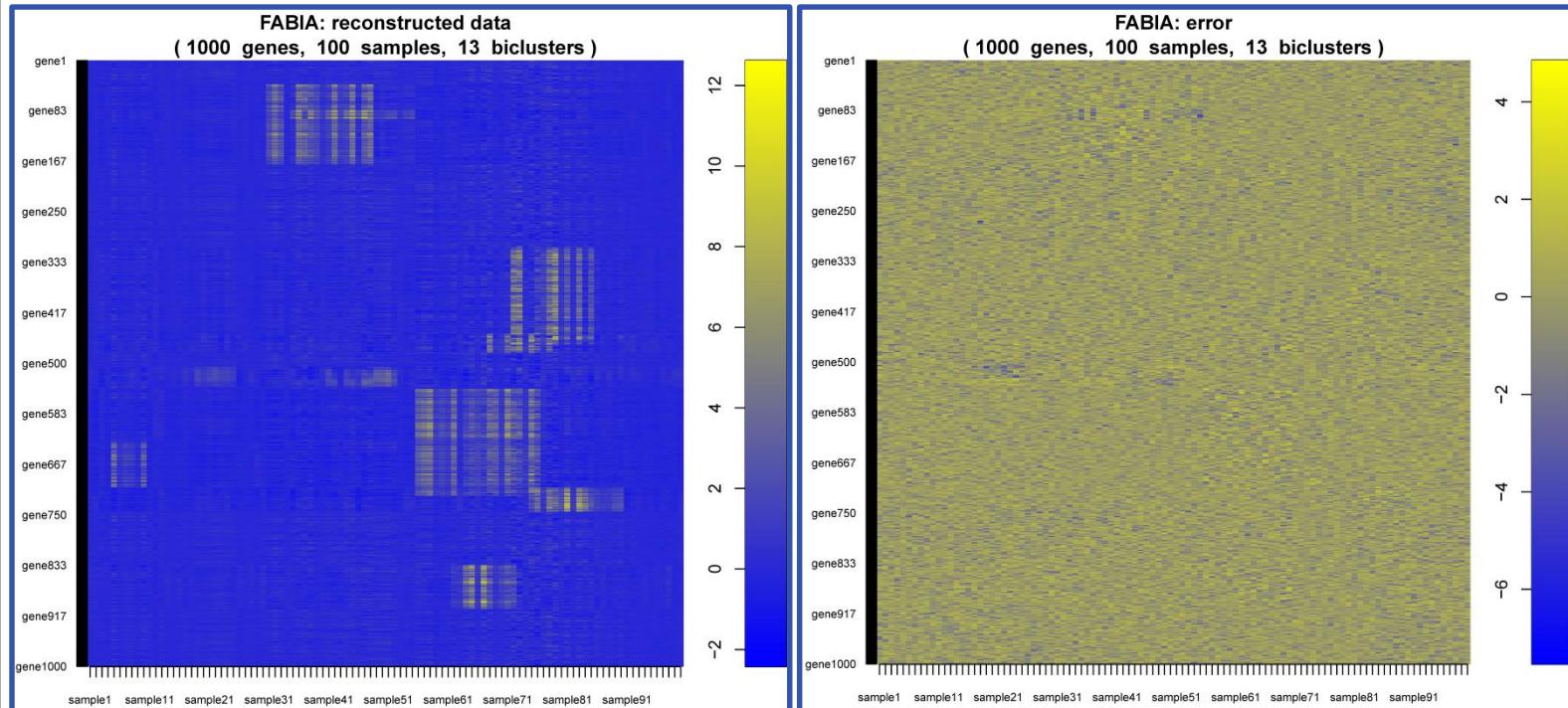
NMF sparseness constraint.
 Not all blocks are detected: too much sparseness enforced
 → difficult to properly adjust the sparseness parameter



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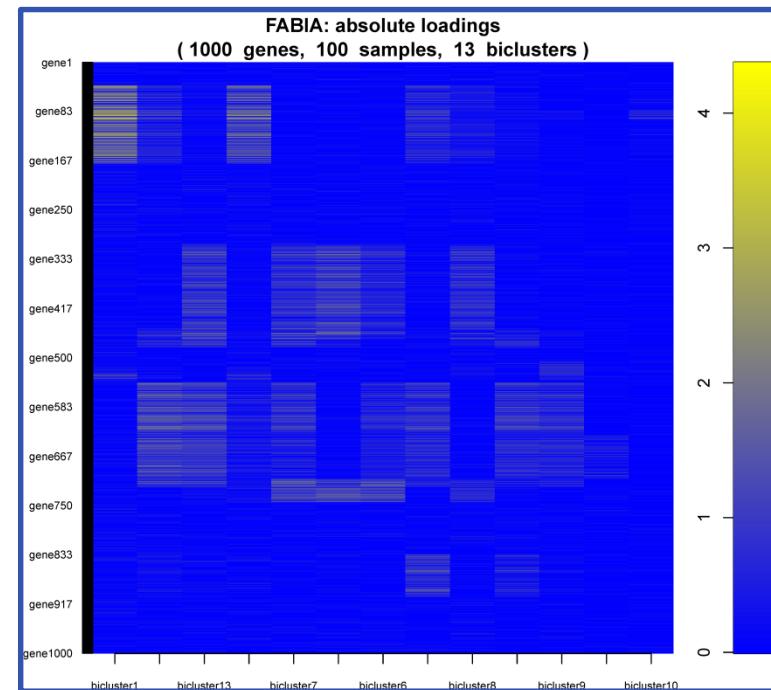
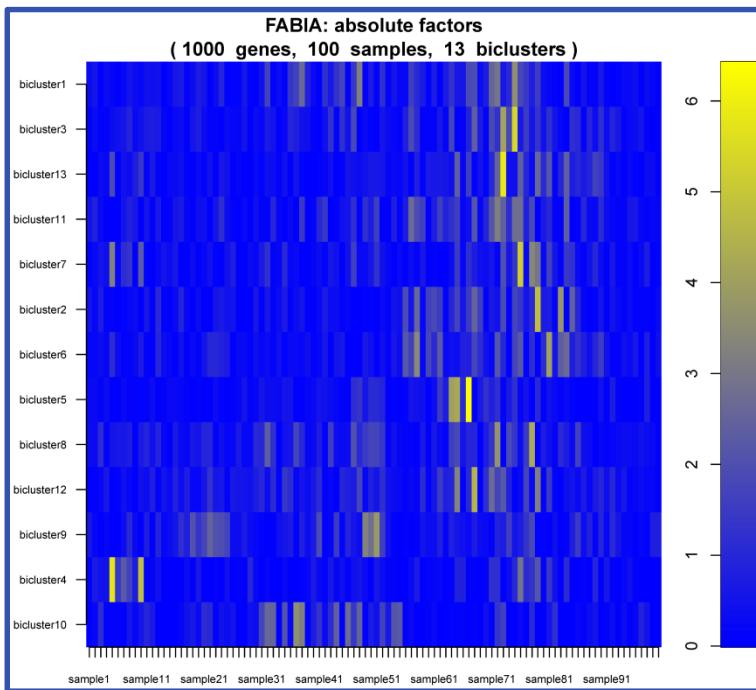
biclustering with FABIA



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biclustering with FABIA



Locally Linear Embedding

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Locally linear embedding (LLE) computes low-dimensional, neighborhood-preserving embeddings / representations.
LLE performs nonlinear mappings. The objective is

$$\varepsilon(\mathbf{W}) = \sum_i \left\| \mathbf{x}_i - \sum_{j=1}^k W_{ij} \mathbf{x}_j \right\|^2 \quad \sum_{j=1}^k W_{ij} = 1$$

Optimized by constrained least squares using neighbors \mathbf{x}_j of \mathbf{x}_i
The solutions of this problem are invariant to rotations, rescalings, and translations of \mathbf{x}_i

Down-projection optimizes $\Phi(\mathbf{Y}) = \sum_i \left\| \mathbf{y}_i - \sum_{j=1}^k W_{ij} \mathbf{y}_j \right\|^2$
where the W_{ij} are fixed

The representation of \mathbf{x}_i by its neighbors is transferred to \mathbf{y}_i

$$\Phi(\mathbf{Y}) = \sum_{ij} M_{ij} \mathbf{y}_i^T \mathbf{y}_j \quad \delta_{ij} : 1 \text{ for } i=j, 0 \text{ otherwise}$$

$$M_{ij} = \delta_{ij} - W_{ij} - W_{ji} + \sum_k W_{ki} W_{kj}$$

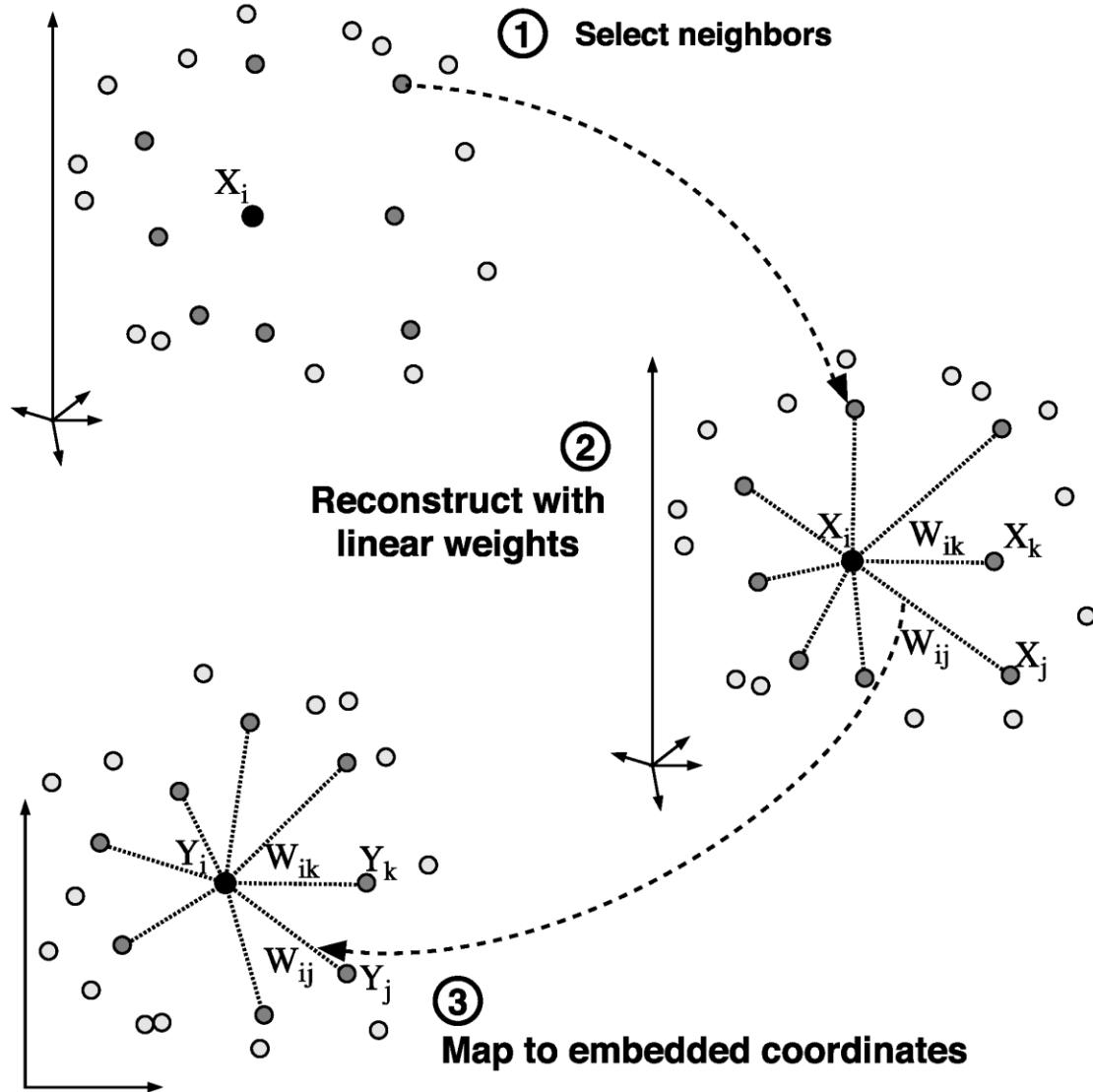
$$\mathbf{M} = (\mathbf{I} - \mathbf{W})^T (\mathbf{I} - \mathbf{W})$$

optimal embedding: bottom d eigenvectors of \mathbf{M} , except the last one

Locally Linear Embedding

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steps of the LLE method



Locally Linear Embedding

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Given: \mathbf{X} : n by m matrix consisting of n data items in m dimensions, dimension of embedding space l , k number of neighbors, distance measure

Find neighbors in \mathbf{X} space

```
for ( $i = 1$  ;  $i \geq n$  ;  $i++$ ) do
    compute the distance from  $\mathbf{x}_i$  to every other point  $\mathbf{x}_j$ 
    find the  $k$  smallest distances
    assign the corresponding points to be neighbors of  $\mathbf{x}_i$ 
end for
```

Solve for reconstruction weights \mathbf{W}

```
for ( $i = 1$  ;  $i \geq n$  ;  $i++$ ) do
    create matrix  $\mathbf{Z}$  consisting of all neighbors of  $\mathbf{x}_i$  [d]
    subtract  $\mathbf{x}_i$  from every row of  $\mathbf{Z}$ 
    compute the local covariance  $\mathbf{C} = \mathbf{Z}^T \mathbf{Z}$  [e]
    solve linear system  $\mathbf{C}\mathbf{w} = \mathbf{1}$  for  $\mathbf{w}$  [f]
    set  $W_{ij} = 0$  if  $j$  is not a neighbor of  $i$ 
    set the remaining elements in the  $i$ -th row of  $\mathbf{W}$  equal to  $\mathbf{w} / \sum_j (w_j)$ ;
end for
```

Compute embedding coordinates \mathbf{Y} using weights \mathbf{W}

```
create sparse matrix  $\mathbf{M} = (\mathbf{I} - \mathbf{W})^T(\mathbf{I} - \mathbf{W})$ 
find bottom  $l + 1$  eigenvectors of  $\mathbf{M}$  (corresponding to the  $d + 1$  smallest eigenvalues)
set the  $q$ -th column of  $\mathbf{Y}$  to be the  $q + 1$  smallest eigenvector (discard the bottom eigenvector  $\mathbf{1} = (1, 1, 1, \dots)$  with eigenvalue zero)
```

Result \mathbf{Y} : n by l matrix consisting of $l < m$ dimensional embedding coordinates.

Locally Linear Embedding

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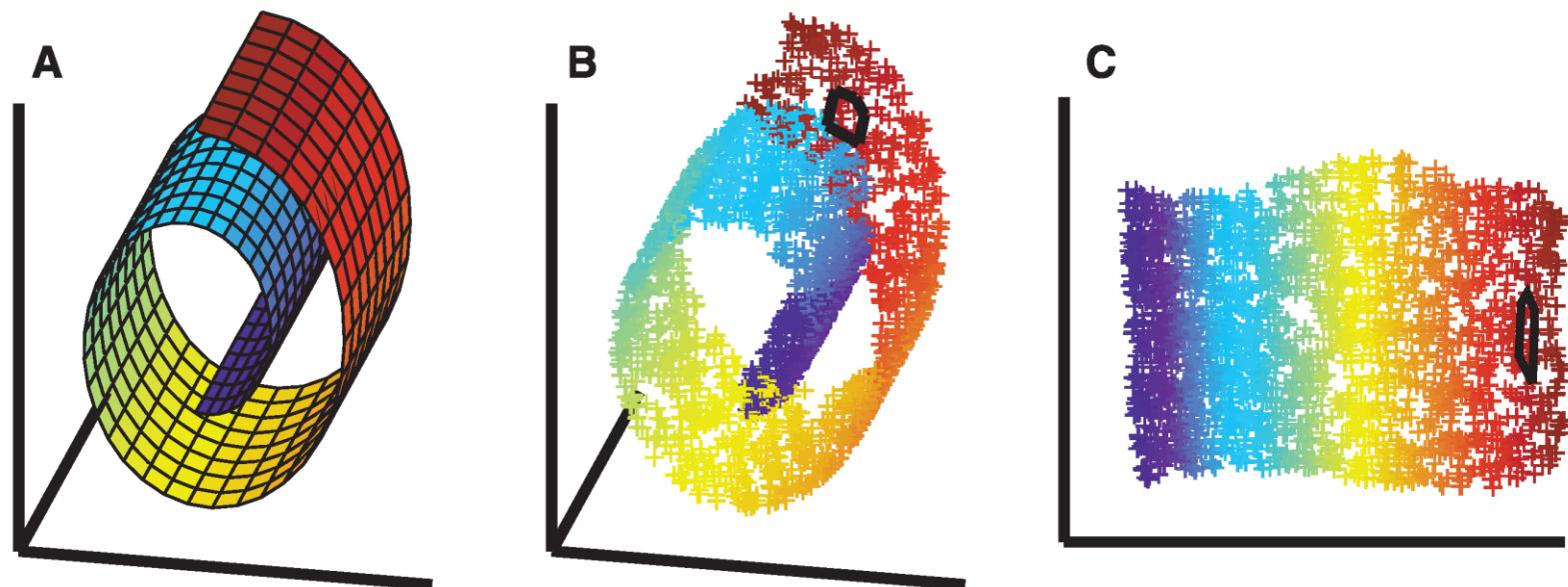
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- [a] Notation \mathbf{x}_i and \mathbf{y}_i denote the i -th row of \mathbf{X} and \mathbf{Y} (in other words the data and embedding coordinates of the i -th point),
 \mathbf{M}^T denotes the transpose of matrix \mathbf{M} ,
 \mathbf{I} is the identity matrix,
 $\mathbf{1}$ is a column vector of all ones
- [b] This can be done in a variety of ways, for example above we compute the k nearest neighbors using Euclidean distance. Other methods such as epsilon-ball include all points within a certain radius or more sophisticated domain specific and/or adaptive local distance metrics.
- [c] Even for simple neighborhood rules like KNN or epsilon-ball using Euclidean distance, there are highly efficient techniques for computing the neighbors of every point, such as KD trees.
- [d] \mathbf{Z} consists of all rows of \mathbf{X} corresponding to the neighbors of \mathbf{x}_i but not \mathbf{x}_i itself
- [e] If $k > m$, the local covariance will not have full rank, and it should be regularized by setting $\mathbf{C} = \mathbf{C} + \epsilon\mathbf{I}$ where \mathbf{I} is the identity matrix and ϵ is a small constant of order 1e-3 trace(\mathbf{C}). This ensures that the system to be solved in step 2 has a unique solution.

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LLE for Swiss Roll data

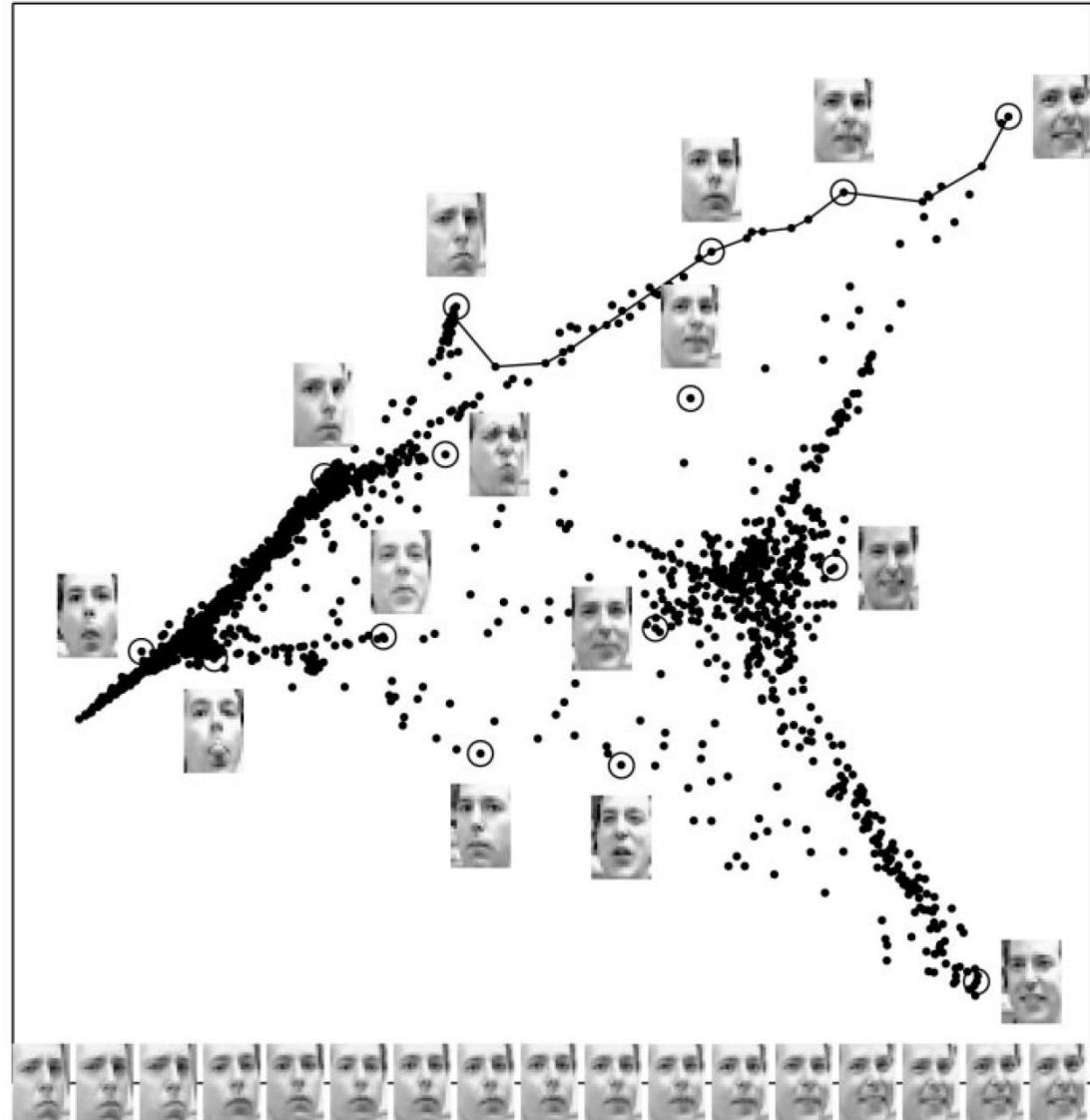


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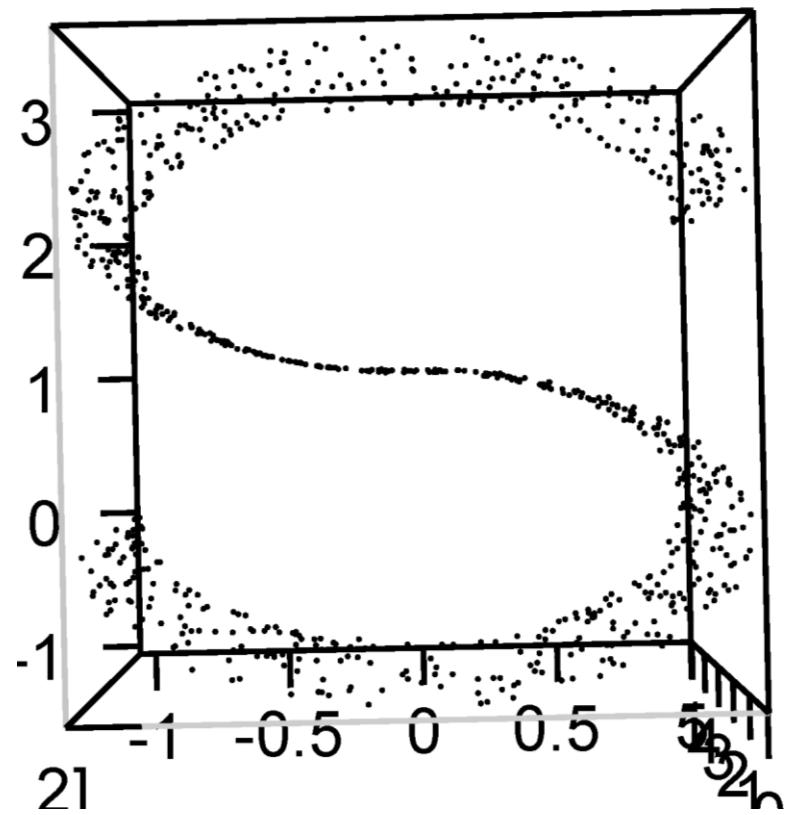
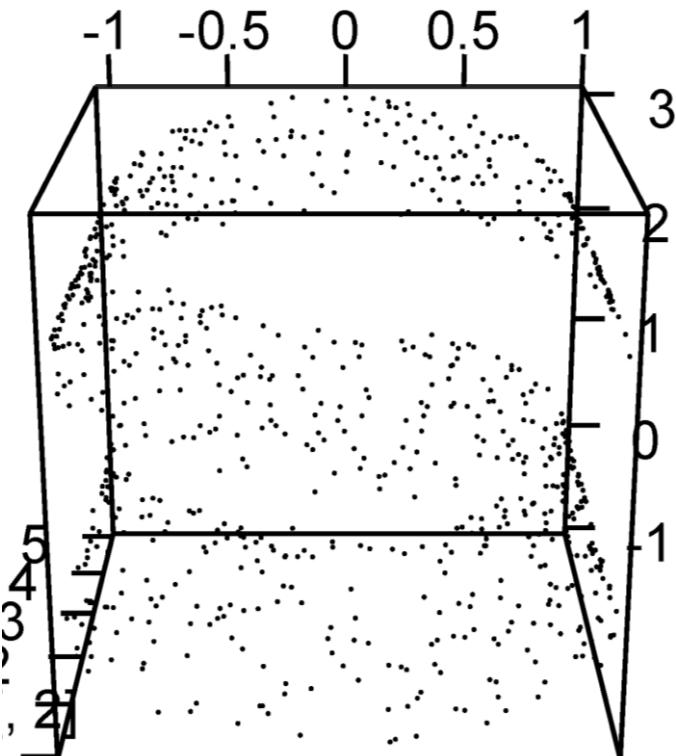
LLE for
face
images



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LLE on the "S" curve data

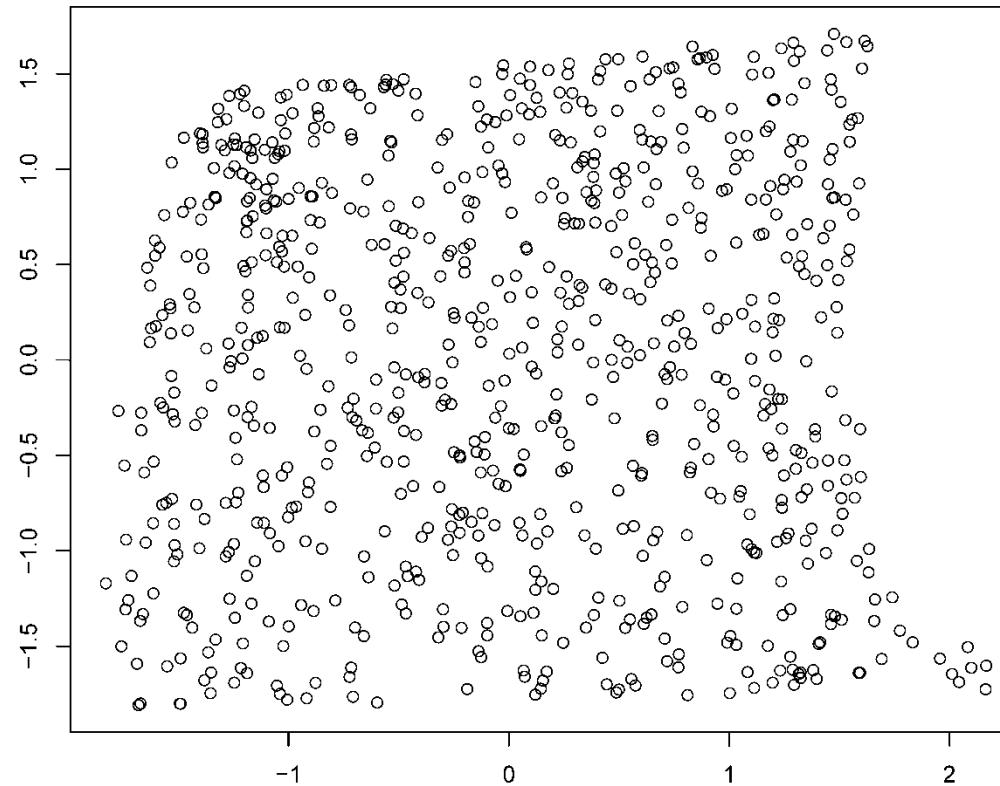


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LLE on the "S" curve data

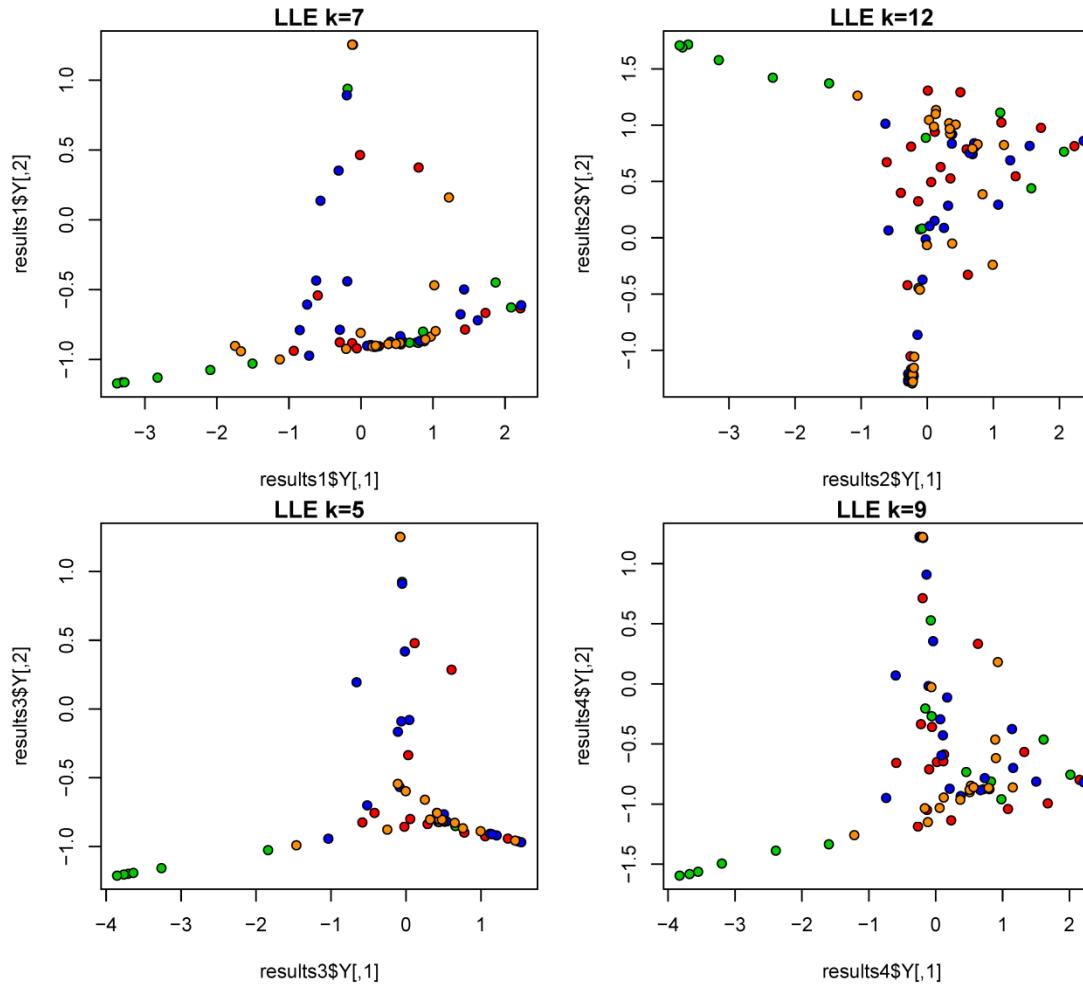
LLE embedded data



Locally Linear Embedding

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LLE applied to multiple tissues: 101 features with largest variance.
 results are worse than with other methods: observations not on manifold



Isomap

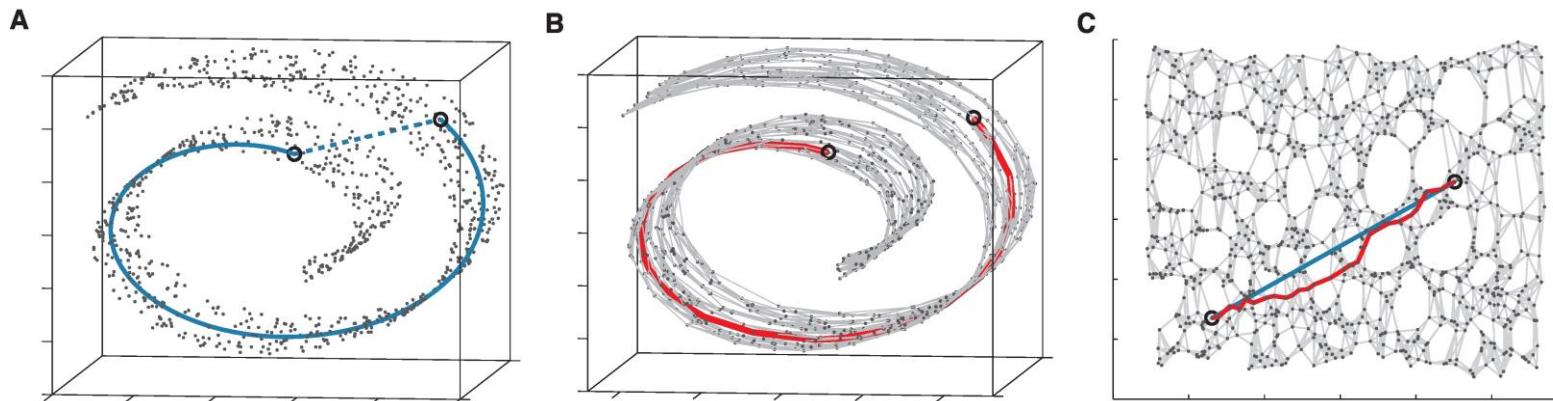
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Isomap is a low-dimensional embedding method which computes a quasi-isometric, low-dimensional embedding. Isomap is similar to LLE and a non-linear projection

- geodesic distance induced by a neighborhood
- geodesic distances:
 - shortest distances on a manifold
 - shortest path by Dijkstra's algorithm
 - sum of edge weights
- largest l eigenvectors of geodesic distance matrix are coordinates in projected space



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doubly centered geodesic distance matrix $\tau(\mathbf{D})$

$$\tau(\mathbf{D}) = -\frac{1}{2} \mathbf{H} \mathbf{D}^2 \mathbf{H}$$

where $\mathbf{D}^2 = D_{ij}^2 = D_{ji}^2$ is the element-wise square of the geodesic distance matrix

$$\mathbf{H} \text{ is the centering matrix } \mathbf{H} = \mathbf{I}_n - \frac{1}{n} \mathbf{1} \mathbf{1}^T \quad \mathbf{1} = (1, 1, \dots, 1)^T \in \mathbb{R}^n$$

objective of Isomap: $E = \|\tau(\mathbf{D}_X) - \tau(\mathbf{D}_Y)\|_{L^2}$

\mathbf{D}_Y matrix of Euclidean distances in the projected space

\mathbf{D}_X matrix of geodesic distances

τ converts distances to inner products

The objective can be minimized by setting the coordinates \mathbf{y}_i to the top l eigenvectors of the matrix $\tau(\mathbf{D}_X)$

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Given: distances $d(\mathbf{x}_i, \mathbf{x}_j)$ between pairs from n data points in an m -dimensional space X , parameter k or parameter e

Construct neighborhood graph

Define the graph G over all data points by connecting points \mathbf{x}_i and \mathbf{x}_j if they are closer than e (e -Isomap), or if i is one of the k nearest neighbors of j (k -Isomap). Closeness and neighborhood is measured by $d(\mathbf{x}_i, \mathbf{x}_j)$.

Set edge lengths equal to $d(\mathbf{x}_i, \mathbf{x}_j)$.

Compute shortest paths by Floyd's algorithm

```

for ( $i = 1$  ;  $i \geq n$  ;  $i++$ ) do
  for ( $j = 1$  ;  $j \geq n$  ;  $j++$ ) do
    Initialize  $d_G(\mathbf{x}_i, \mathbf{x}_j) = d(\mathbf{x}_i, \mathbf{x}_j)$  if  $i, j$  are linked by an edge;  $d_G(\mathbf{x}_i, \mathbf{x}_j) = \infty$ , otherwise.
    end for
  end for
  for ( $k = 1$  ;  $k \geq n$  ;  $k++$ ) do
    for ( $i = 1$  ;  $i \geq n$  ;  $i++$ ) do
      for ( $j = 1$  ;  $j \geq n$  ;  $j++$ ) do
         $d_G(\mathbf{x}_i, \mathbf{x}_j) = \min\{d_G(\mathbf{x}_i, \mathbf{x}_j), d_G(\mathbf{x}_i, \mathbf{x}_k) + d_G(\mathbf{x}_k, \mathbf{x}_j)\}.$ 
      end for
    end for
  end for

```

define shortest path matrix \mathbf{D}_X by $[\mathbf{D}_X]_{ij} = d_G(\mathbf{x}_i, \mathbf{x}_j)$

Construct l -dimensional embedding

Compute λ_p as the p -th eigenvalue (in decreasing order) of the matrix $\tau(\mathbf{D}_X)$, and v_{pi} as the i -th component of the p -th eigenvector.

set $y_{ij} = \sqrt{\lambda_i} v_{ji}$.

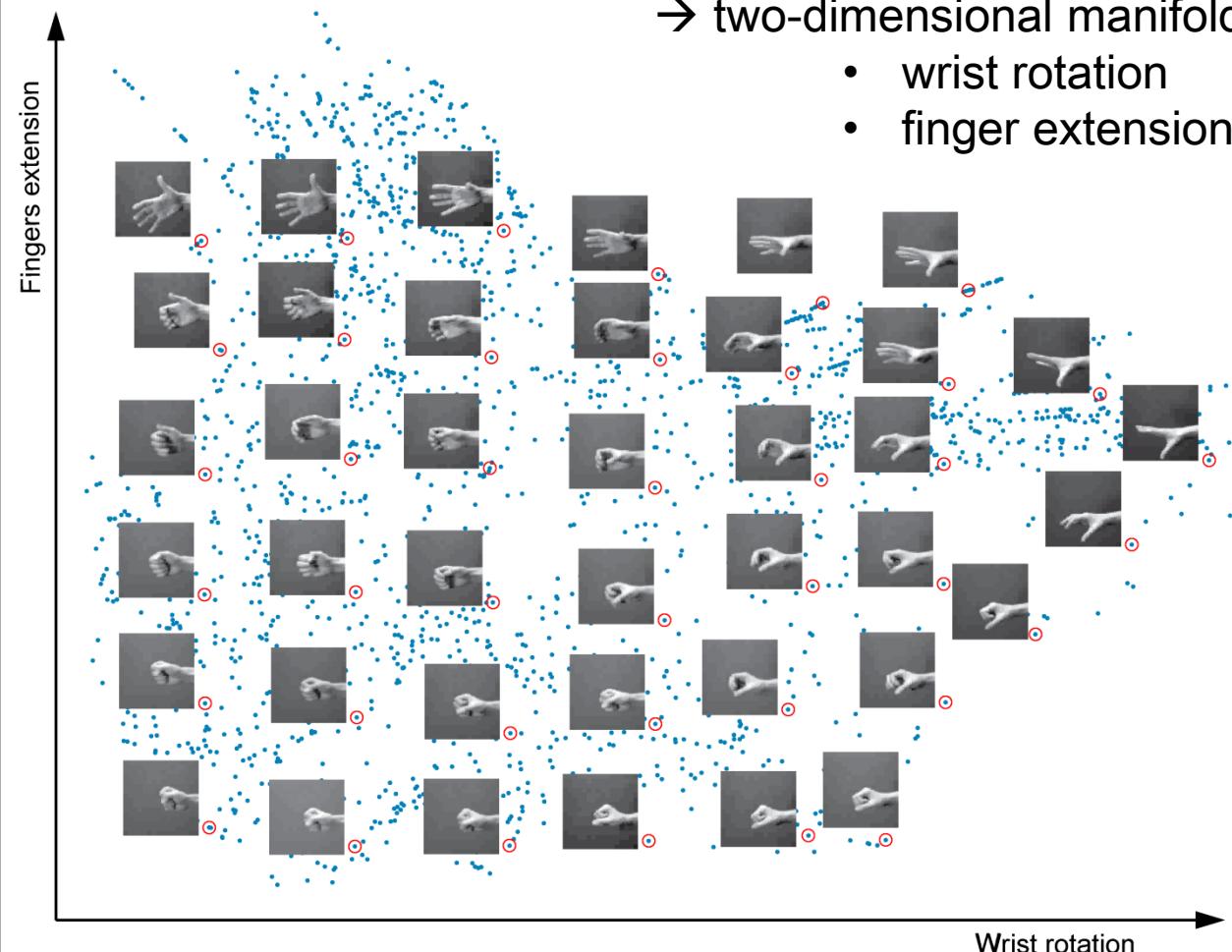
Result \mathbf{Y} : coordinate vectors \mathbf{y}_i in a l -dimensional ($l < m$) Euclidean space

Y

Isomap

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Isomap ($k=6$), $n=2000$ images of a hand opening and closing movements at different wrist orientations



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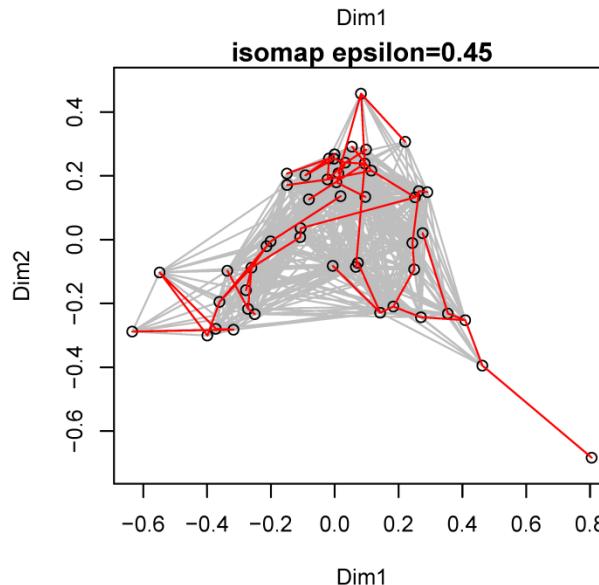
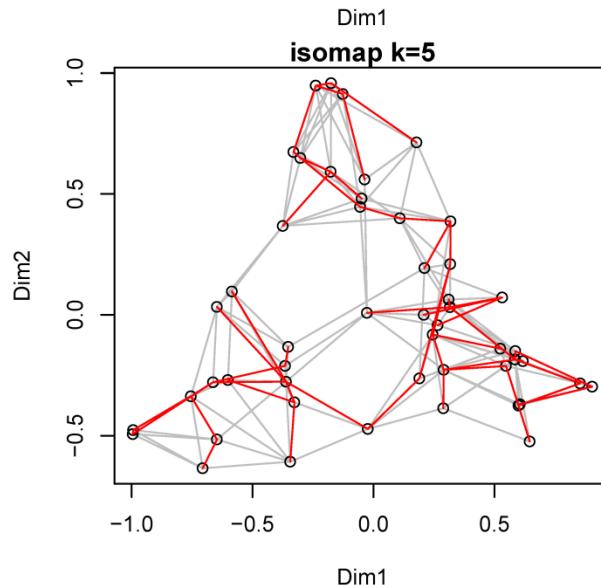
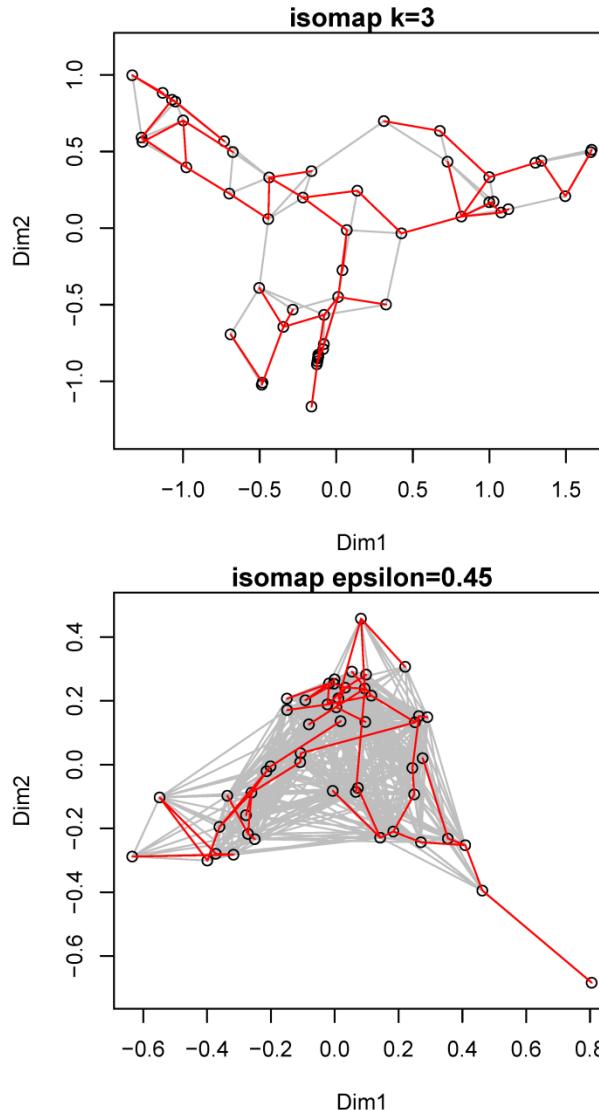
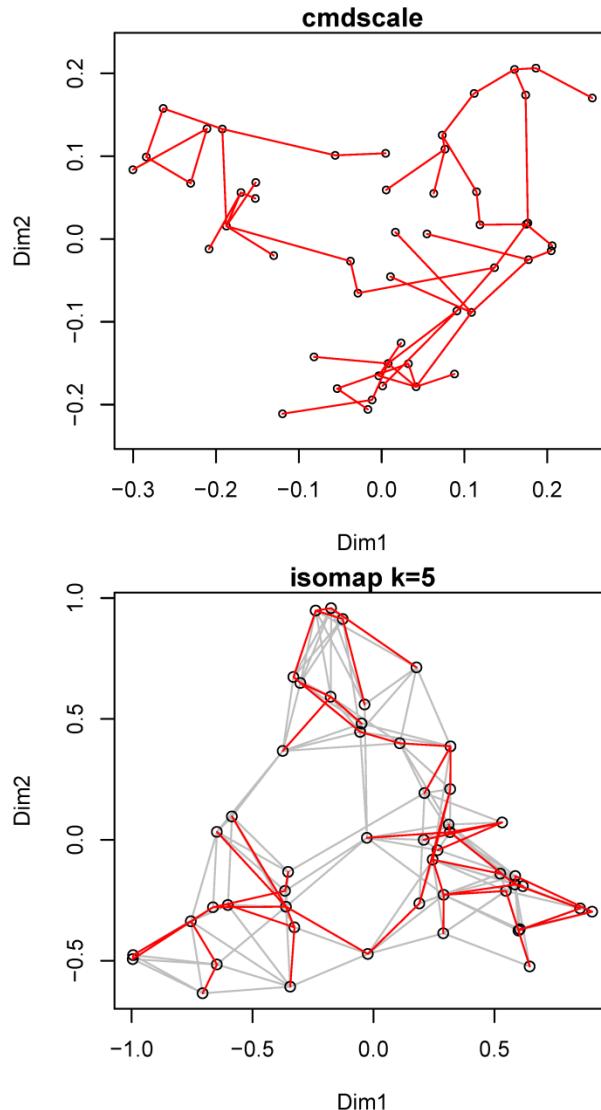
6.8.2 Examples

tree counts in 1-hectare plots in the Barro Colorado Island

- 50 plots of 1 hectare with counts of trees on each plot
- quadrants are located in a regular grid
- 225 tree species (at least 10 cm in diameter at breast height)
- counts in each one hectare square of forest

Isomap

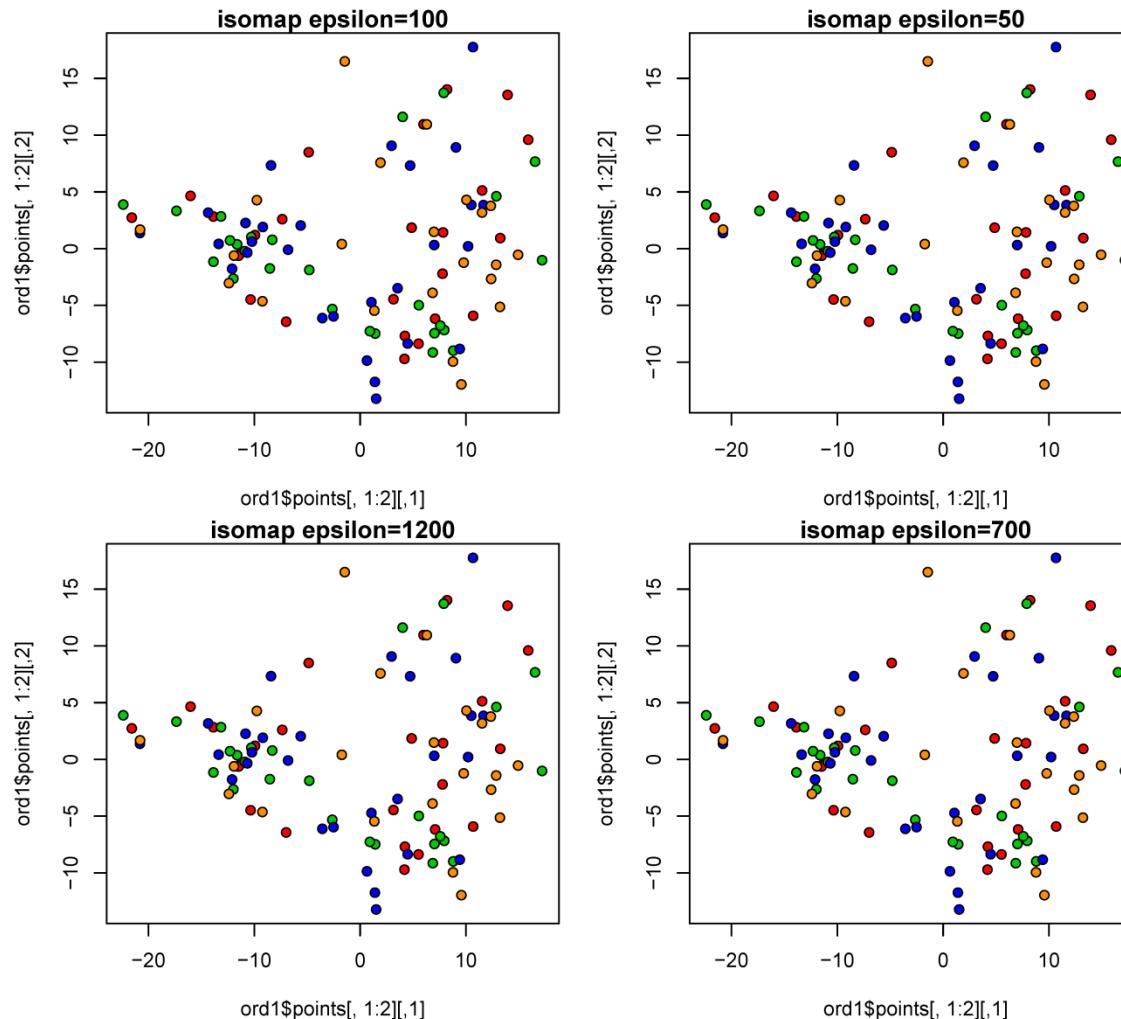
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Isomap for the multiple tissues data: results not as good as with other methods: observations not on a manifold



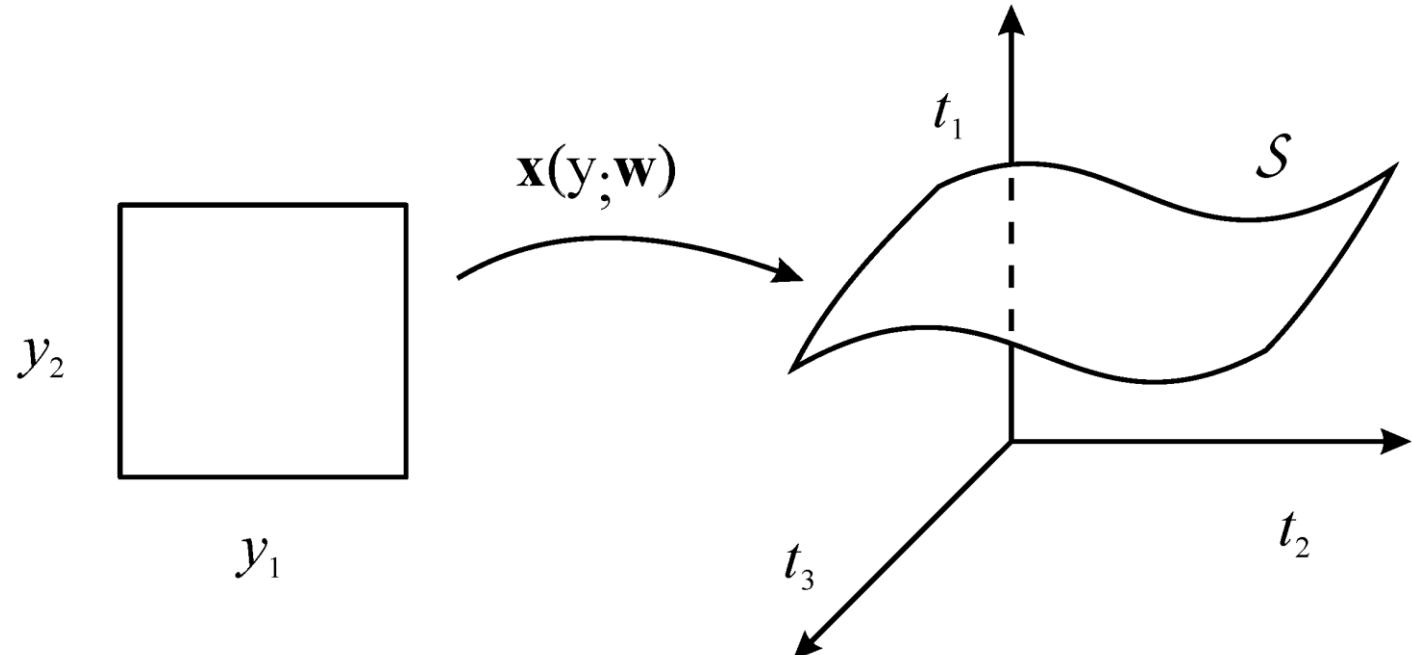
Generative Topographic Mapping

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generative topographic mapping (GTM) is a non-linear latent variable model as an alternative to SOMs to overcome their disadvantages.

GTM is similar to factor analysis as it also maps from the latent space to the observations space.

Latent variables $y \in \mathbb{R}^l$ are mapped to observations $x \in \mathbb{R}^m$, $m > l$



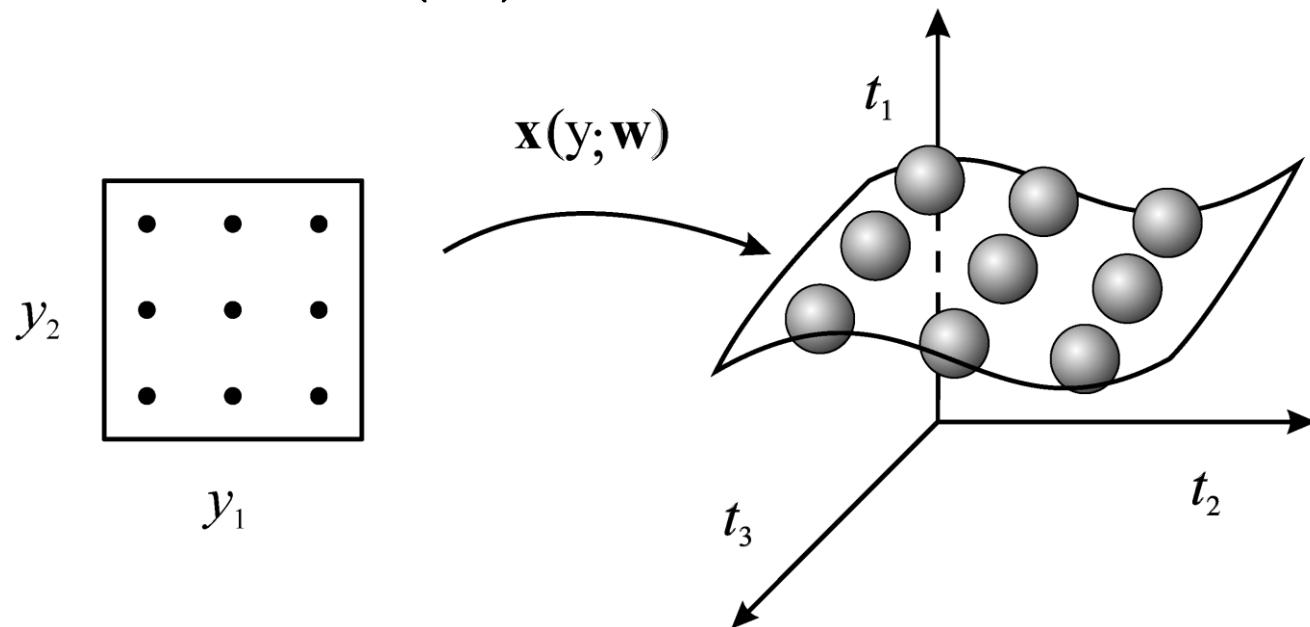
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latent-variable space: distribution $p(\mathbf{y})$
 observation space: distribution $p(\mathbf{x} | \mathbf{w})$

If points are mapped from a l -dimensional to a m -dimensional space:
 probability masses would vanish \rightarrow Gaussian ball in m -dim. space:

$$p(\mathbf{t} | \mathbf{y}, \mathbf{w}, \beta) = \left(\frac{\beta}{2\pi} \right)^{m/2} \exp -\frac{\beta}{2} \|\mathbf{x}(\mathbf{y}, \mathbf{w}) - \mathbf{t}\|^2$$



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distribution in the m -dimensional space is obtained by integrating over all \mathbf{x} that contribute to a density at \mathbf{t} :

$$p(\mathbf{t} \mid \mathbf{w}, \beta) = \int p(\mathbf{t} \mid \mathbf{x}, \mathbf{w}, \beta) p(\mathbf{x}) d\mathbf{x}$$

For data points $\{\mathbf{t}_1, \dots, \mathbf{t}_n\}$, the log likelihood is

$$\log \mathcal{L} = \sum_{i=1}^n \ln p(\mathbf{t}_i \mid \mathbf{w}, \beta)$$

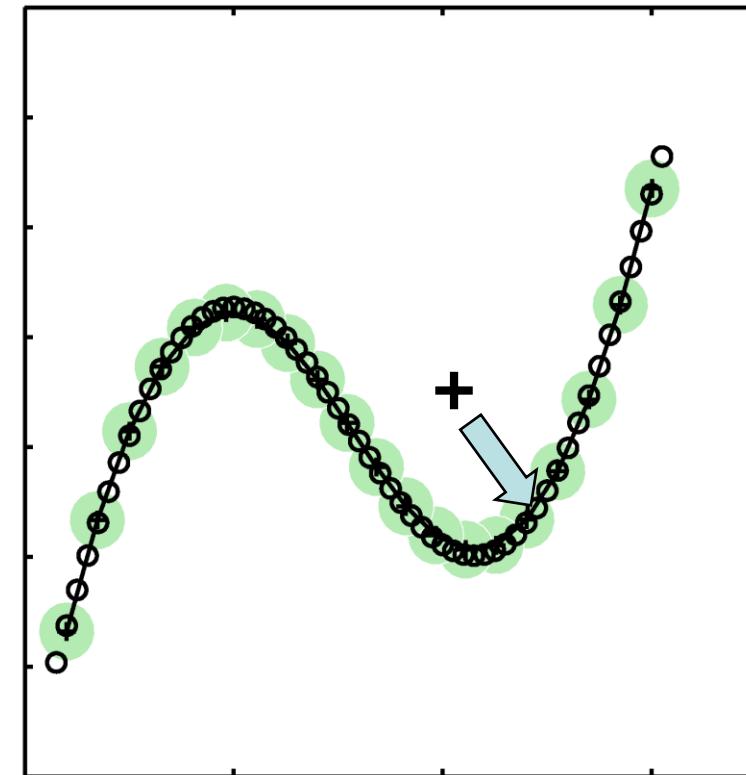
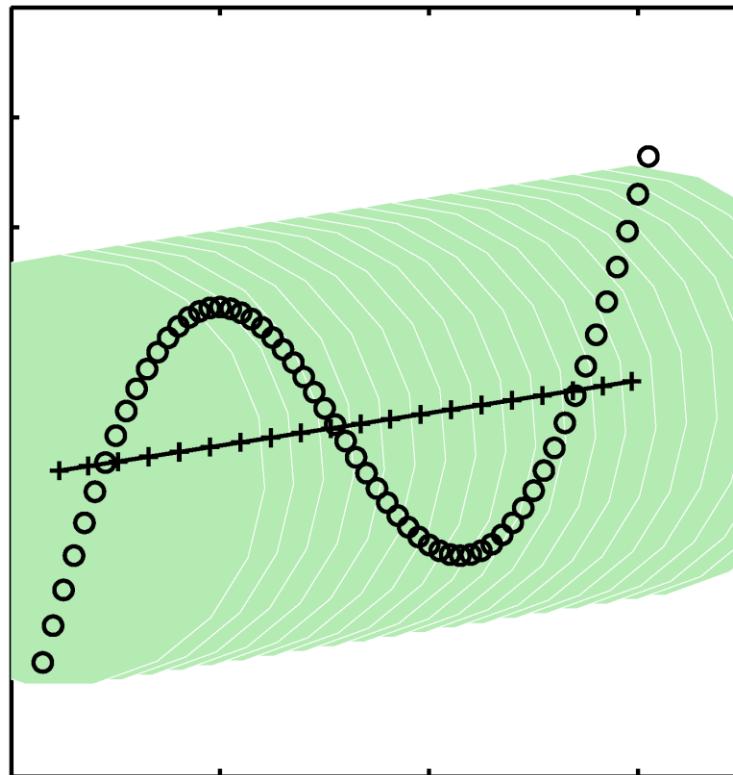
$$p(\mathbf{y}) = \frac{1}{L} \sum_{j=1}^L \delta(\mathbf{y} - \mathbf{y}_j)$$

$$p(\mathbf{t} \mid \mathbf{w}, \beta) = \frac{1}{L} \sum_{j=1}^L p(\mathbf{t} \mid \mathbf{y}_j, \mathbf{w}, \beta)$$

kernel density estimate or constraint Gaussian mixture model in the m -dim. space with centers mapped from an l -dim. space

Generative Topographic Mapping

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Toy problem involving data (o) generated from a 1-dimensional curve embedded in 2 dimensions, together with the projected latent points (+) and their Gaussian noise distributions (filled circles). The initial configuration is shown on the left, and the result on the right.

t-Distributed Stochastic Neighbor Embedding



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***t*-distributed stochastic neighbor embedding (t-SNE)** models each high-dimensional observations by a two- or three-dimensional representation: similar observations are represented by nearby projections and dissimilar observations distant representations.

stochastic neighbor embedding (SNE) the similarity is the conditional probability $p_{j|i}$ that x_i would pick x_j as its neighbor

$$\text{For } \{x_1, \dots, x_n\} \text{ we obtain } p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2/2\sigma_i^2)}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2/2\sigma_i^2)}$$

For low-dimensional projections a conditional probability is computed

$$q_{j|i} = \frac{\exp(-\|\mathbf{y}_i - \mathbf{y}_j\|^2)}{\sum_{k \neq i} \exp(-\|\mathbf{y}_i - \mathbf{y}_k\|^2)}$$

objective is the Kullback-Leibler divergence between P and Q :

$$KL(P||Q) = \sum_{i \neq j} p_{j|i} \log \frac{p_{j|i}}{q_{j|i}} \quad \text{minimized by gradient descent}$$

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objective for the SNE:

- difficult to optimize
- crowding problem

For example in 10 dimensions, it is possible to have 11 data points that are mutually equidistant but there is no way to model this faithfully in a two-dimensional map

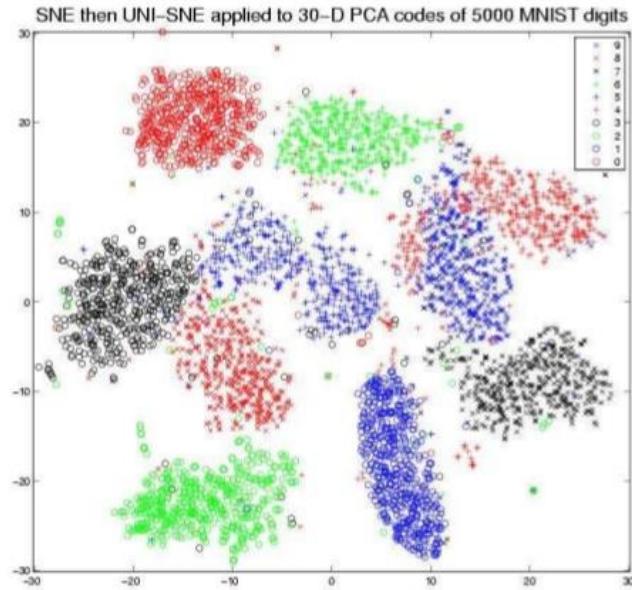
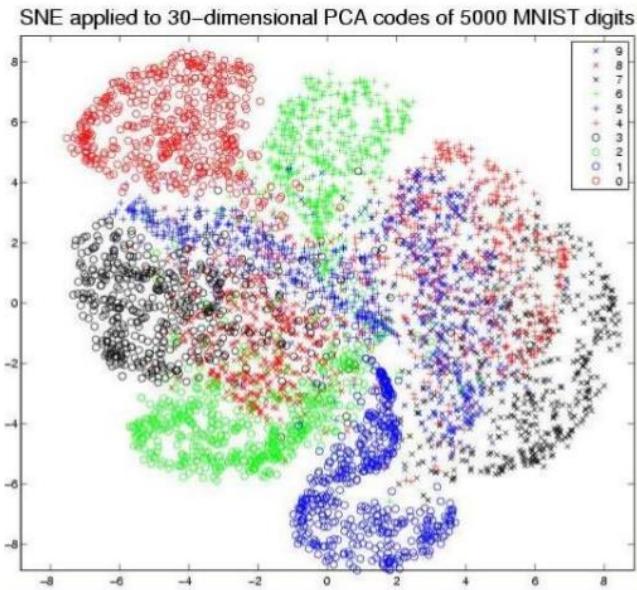
t-distributed stochastic neighbor embedding, solves these SNE problems by

- objective of the SNE is symmetrized → simpler gradients
- objective uses Student's *t*-distribution → heavy-tailed which reduces the crowding problem and simplifies the optimization

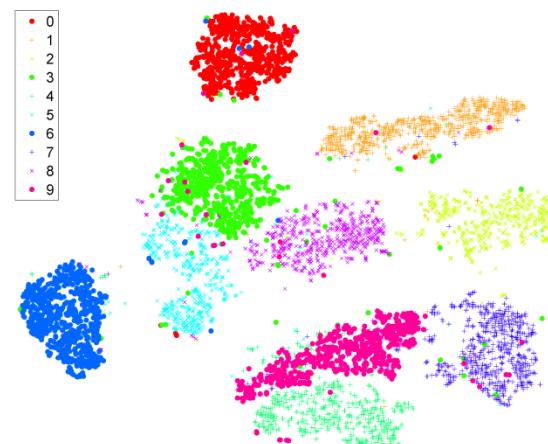
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Crowding



t-SNE



(a) Visualization by t-SNE.

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Symmetry:

$$p_{ij} = \frac{p_{j|i} + p_{i|j}}{2n}$$

Heavy-tails using the Student's *t*-distribution:

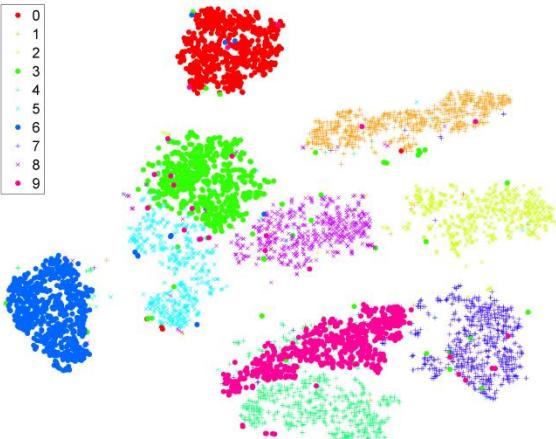
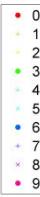
$$q_{ij} = \frac{(1 + \|y_i - y_j\|^2)^{-1}}{\sum_{k \neq l} (1 + \|y_k - y_l\|)^{-1}}$$

Optimization via gradient descent

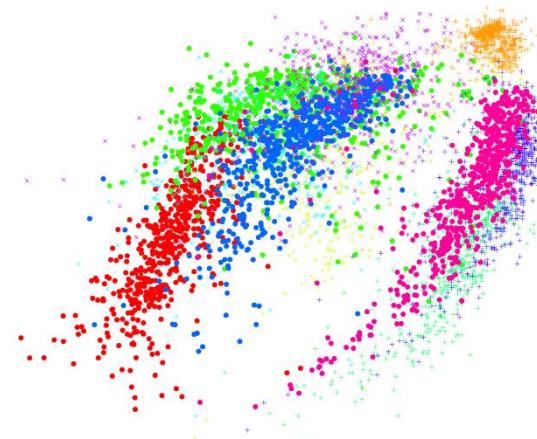
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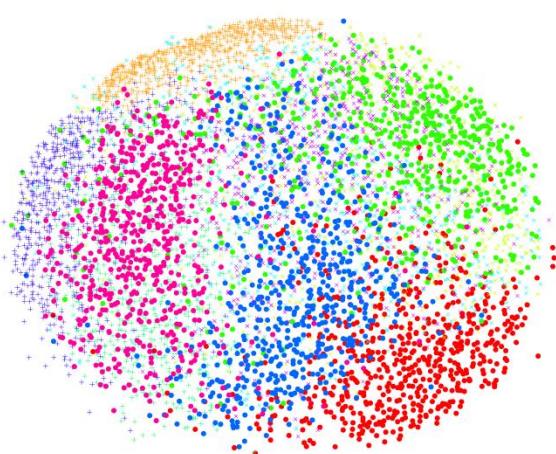
6,000 handwritten digits from the MNIST data set:
t-SNE is compared to Sammon's mapping, Isomap, and LLE.



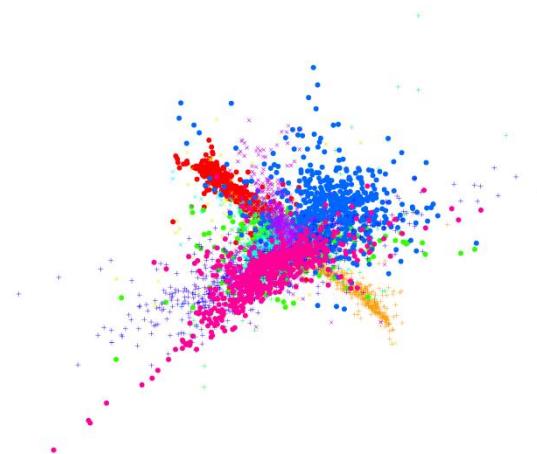
(a) Visualization by t-SNE.



(c) Visualization by Isomap.



(b) Visualization by Sammon mapping.



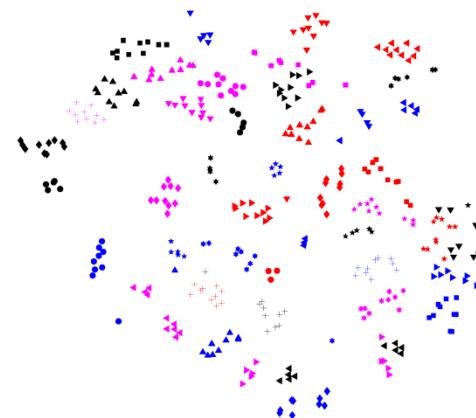
(d) Visualization by LLE.

t-Distributed Stochastic Neighbor Embedding

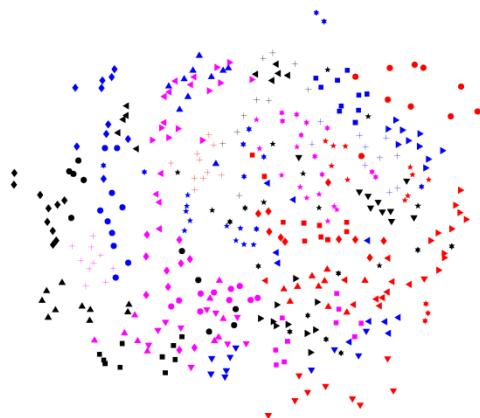
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faces from the Olivetti data base:

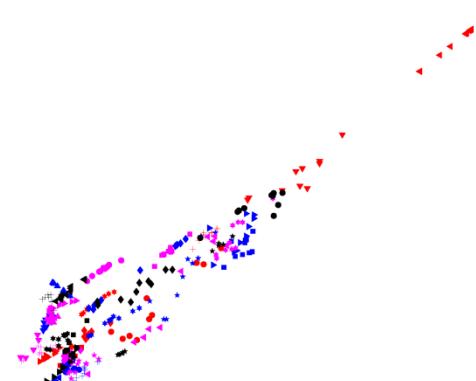
t-SNE is compared to Sammon's mapping, Isomap, and LLE.



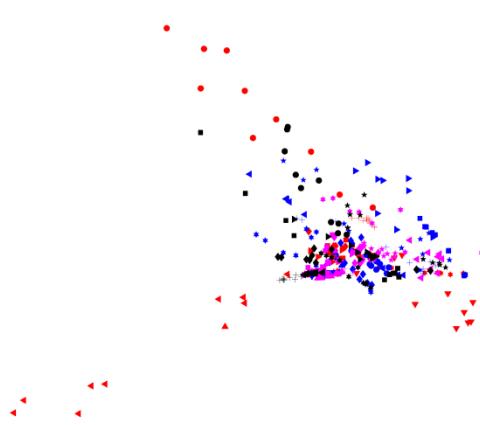
(a) Visualization by t-SNE.



(b) Visualization by Sammon mapping.



(c) Visualization by Isomap.



(d) Visualization by LLE.

t-Distributed Stochastic Neighbor Embedding

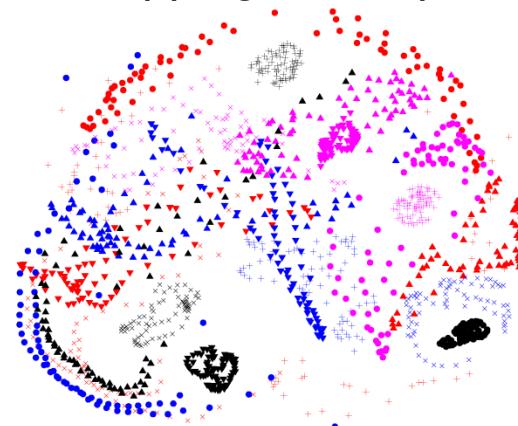
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COIL-20 data set:

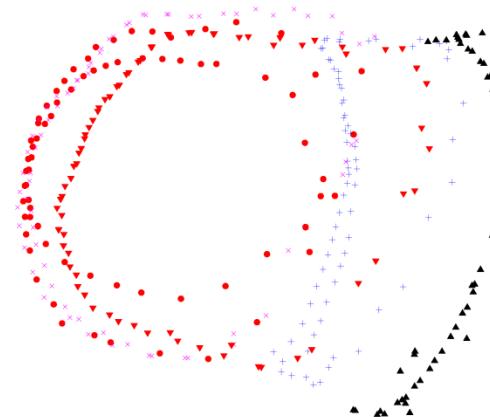
t-SNE is compared to Sammon's mapping, Isomap, and LLE.



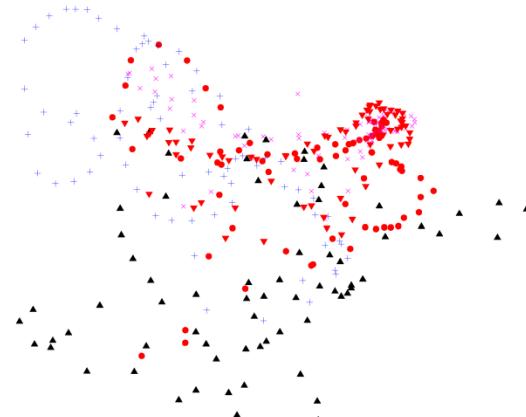
(a) Visualization by t-SNE.



(b) Visualization by Sammon mapping.



(c) Visualization by Isomap.

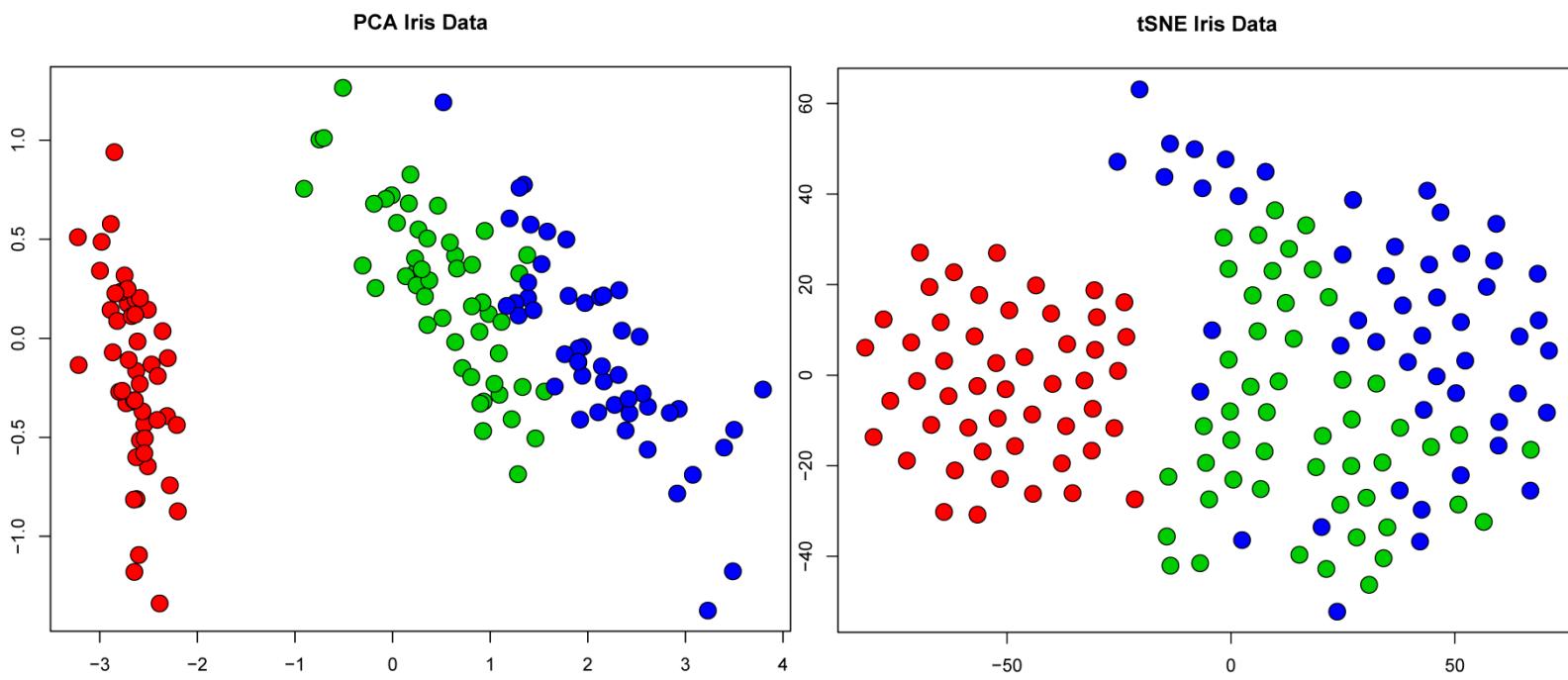


(d) Visualization by LLE.

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iris data set



t-Distributed Stochastic Neighbor Embedding

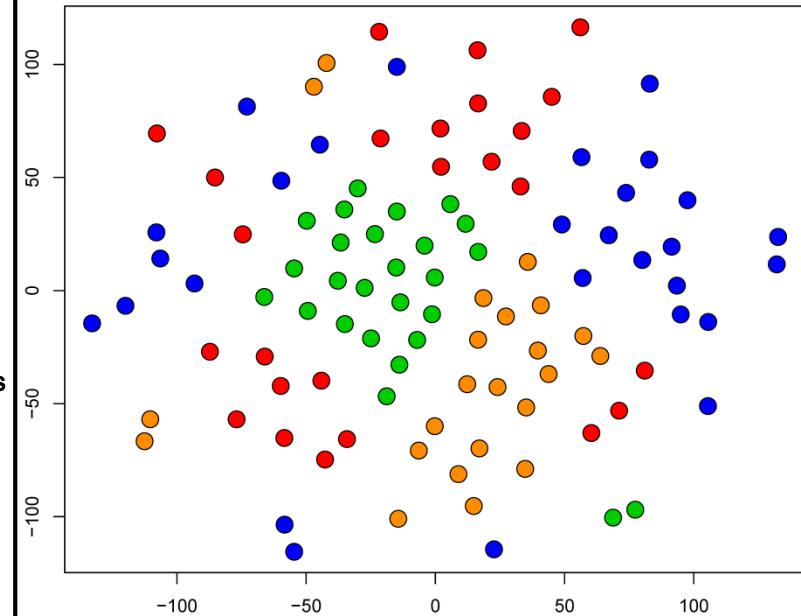


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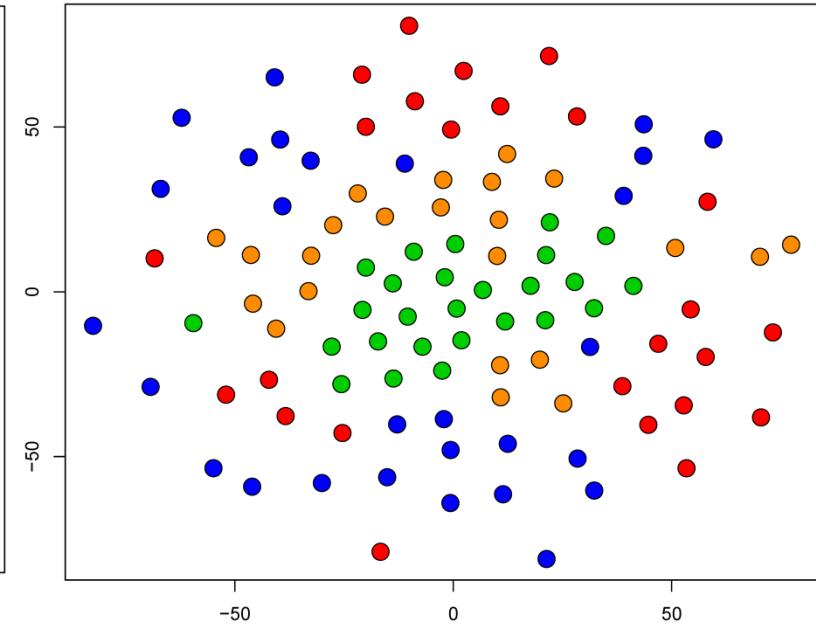
multiple tissues data: features with largest variance

The results are not as good as with other methods because the observations are not located on a 2-dimensional manifold.

tSNE Multiple Tissues Data: perplexity=30



tSNE Multiple Tissues Data: perplexity=50



Self-Organizing Map

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Self-Organizing Map (SOM) or Kohonen map:

SOMs comprise two objectives:

- clustering (see next subsection)
- down-projecting.

For SOMs the objective function **cannot** be expressed as a single scalar function like an energy or an error function.

lack of a scalar objective / cost function:

- no theoretical basis for choosing learning parameters
- no assurance to achieve topographic ordering
- no proofs of convergence
- models cannot be compared
- overfitting not detected
- stopping of training is difficult to determine
- quality of the solution is hard to assess
- no probability density for further processing by other methods

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$\mathbf{y}_k \in \mathbb{R}^l$ equidistantly fill a hypercube associated with $\mathbf{w}_k \in \mathbb{R}^m$, which are the parameters of the SOM

Data points that are neighbors should be neighbors in the projection preserve **neighborhood relation**: **topologically ordered maps** (TOMs)

on-line update rule:

$$k = \arg \max_s \mathbf{x}^T \mathbf{w}_s$$

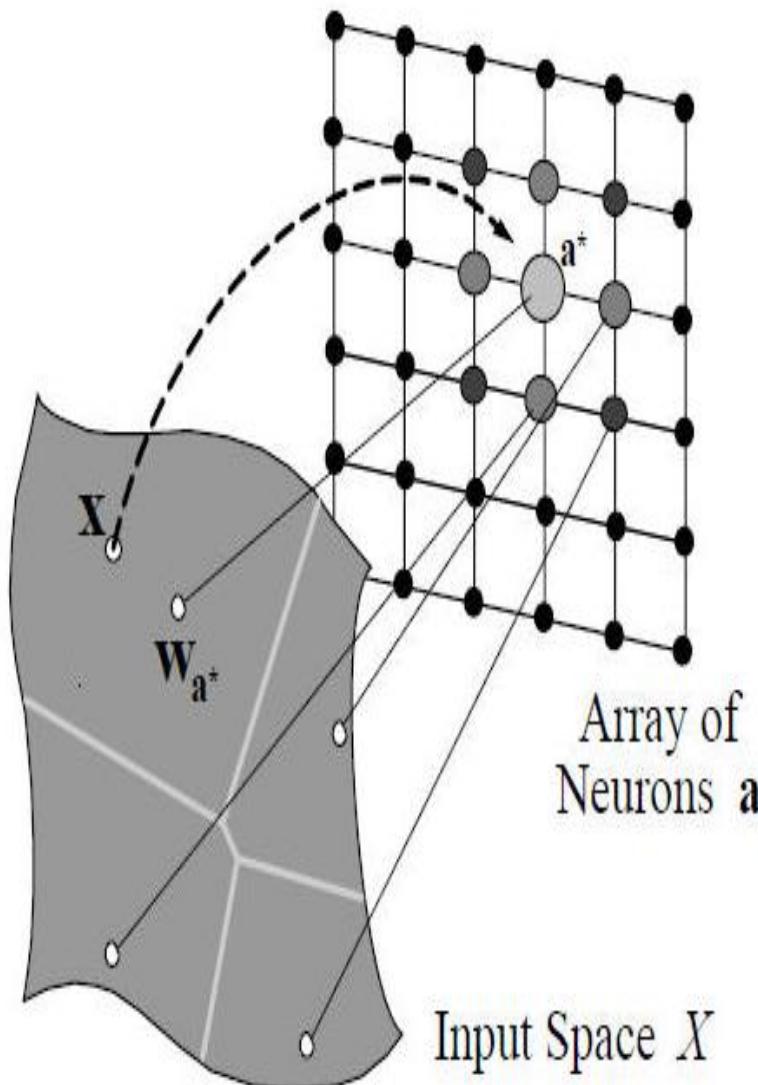
$$(\mathbf{w}_t)^{\text{new}} = \mathbf{w}_t + \eta \delta(\|\mathbf{y}_t - \mathbf{y}_k\|) (\mathbf{x} - \mathbf{w}_t)$$

where η is the learning rate, δ is the window function which is largest for $\mathbf{y}_t = \mathbf{y}_k$ and is decreasing with the distance to \mathbf{y}_k .

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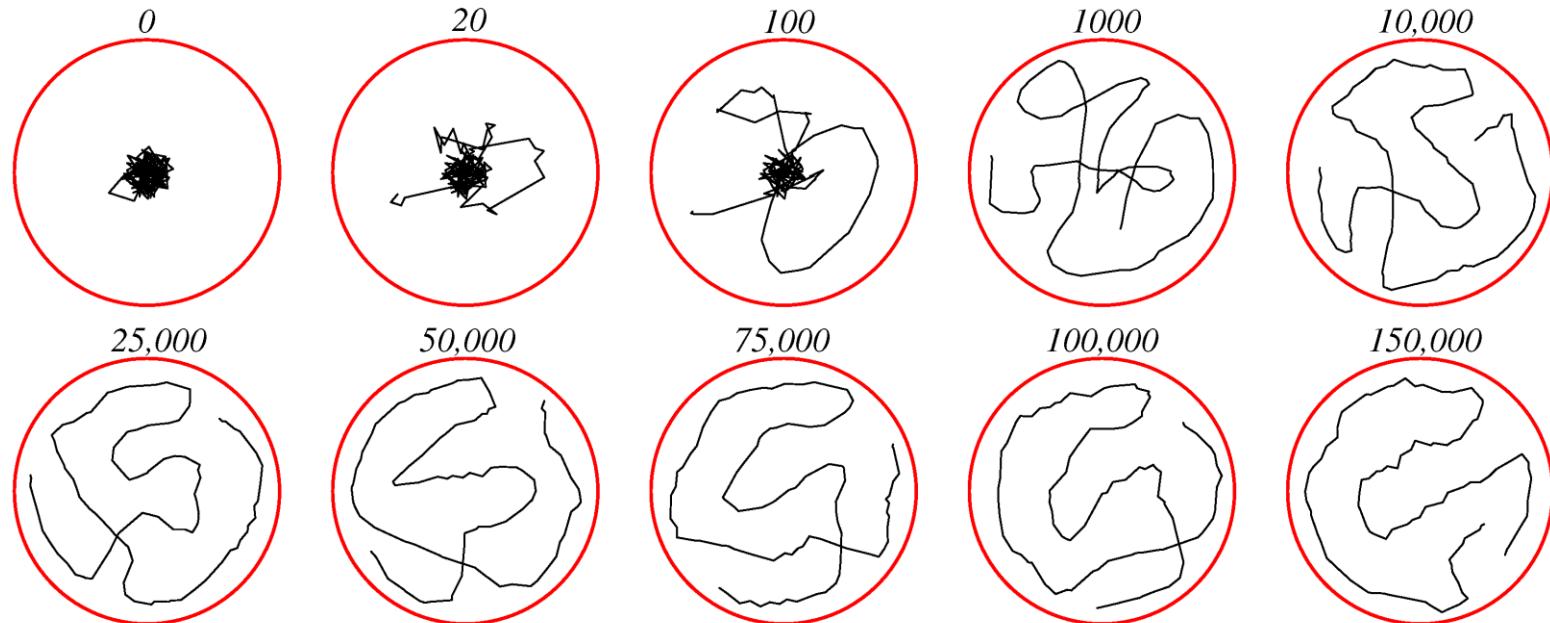
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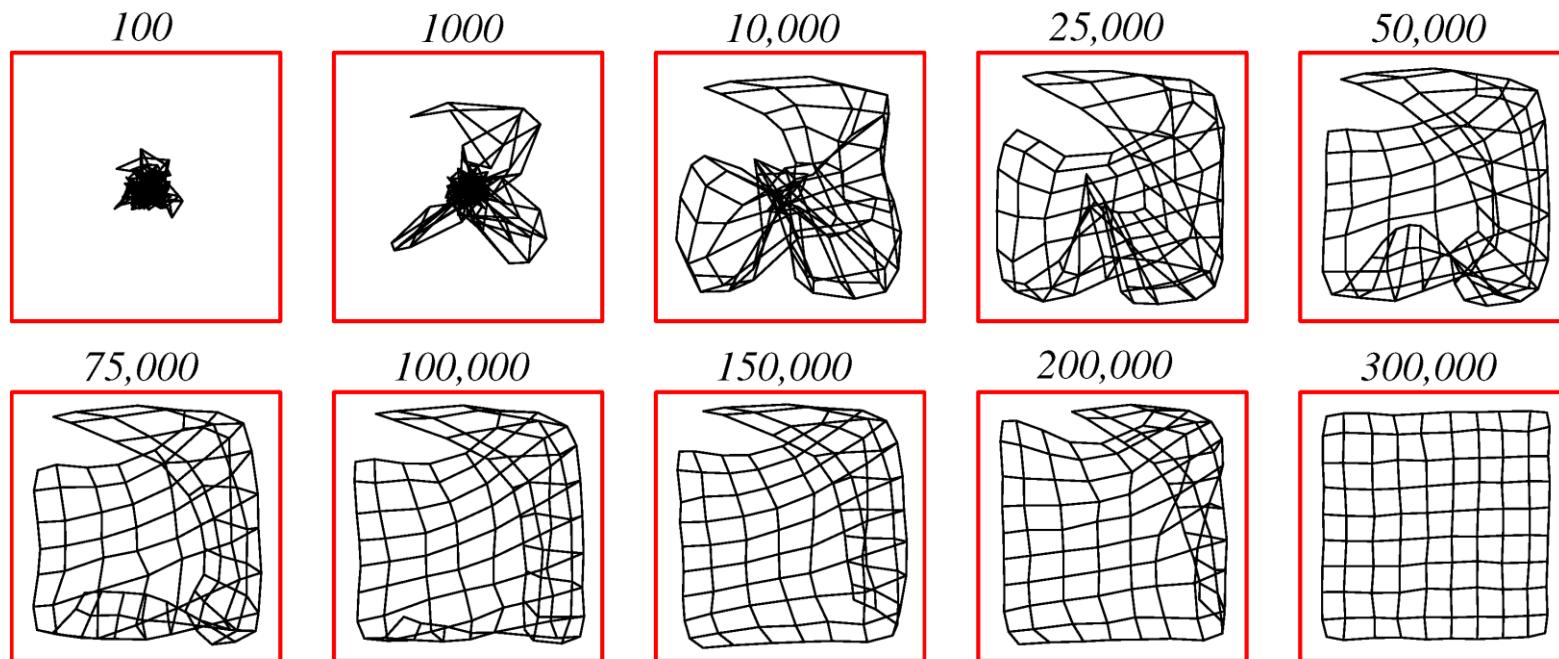
Example 1: one-dimensional representation of a two-dimensional space



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Example 2: square data space to a square (grid) representation space

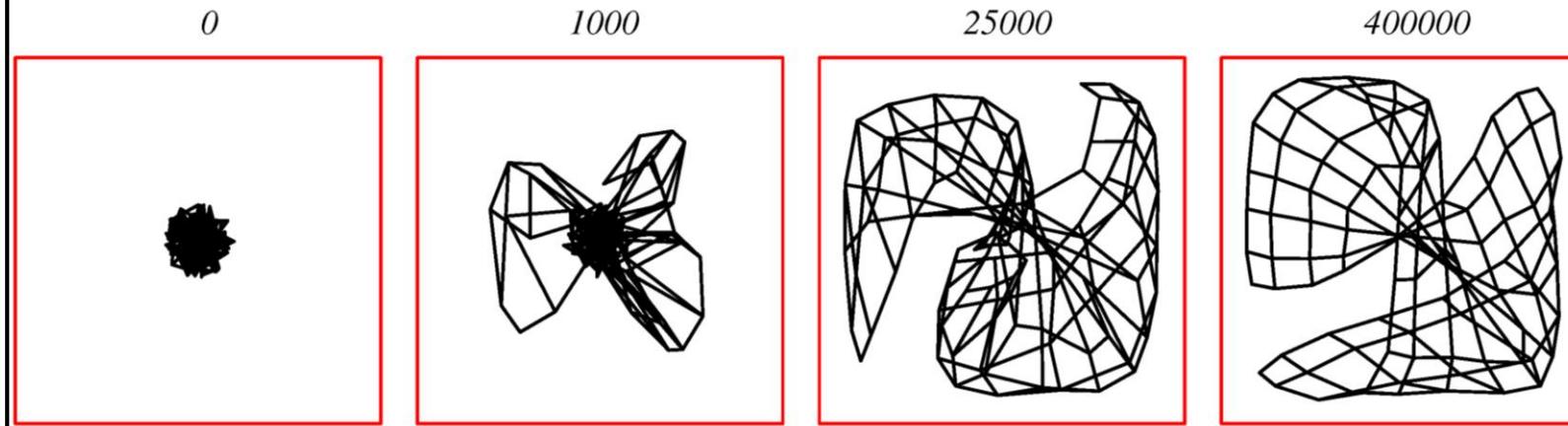


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Example 2 with different initialization. Kinks in the map do not vanish even if more patterns are presented – that is a local minimum



Self-Organizing Map

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Example 2 with a non-uniformly sampling: the density at the center was higher than at the border

