

Possible Projects

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Blind Subspace Deconvolution



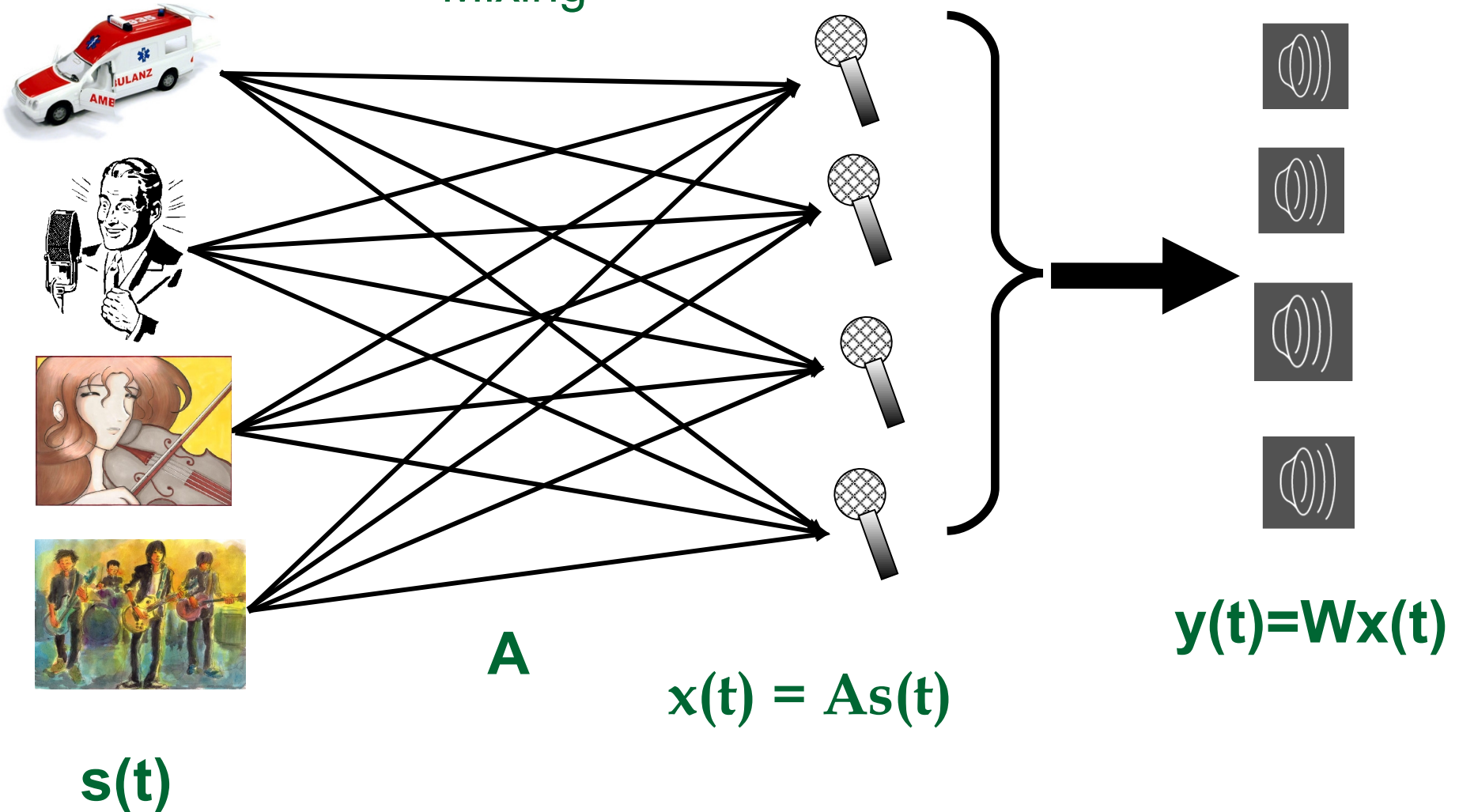
Independent Component Analysis

Sources

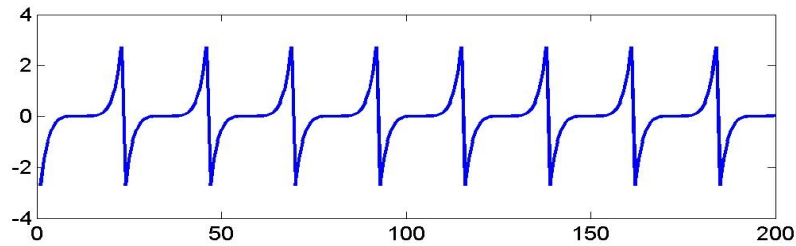
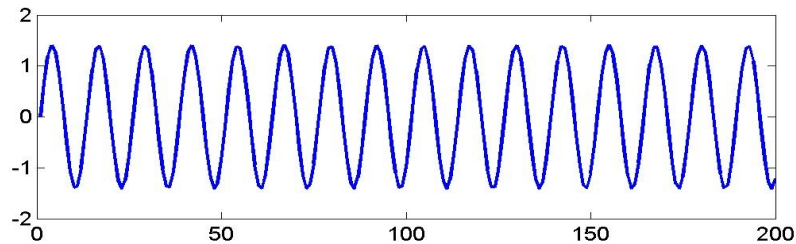
Mixing

Observation

Estimation



Independent Component Analysis

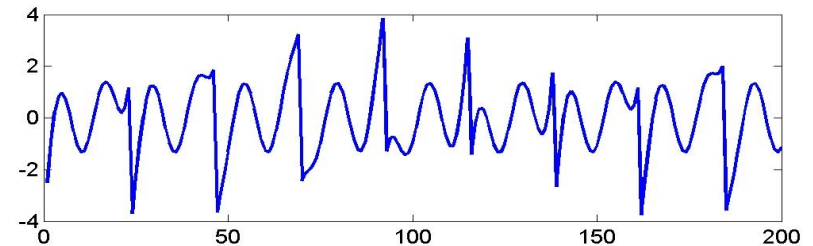
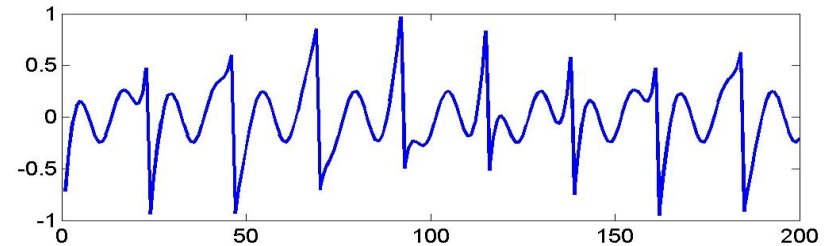


Independent signals

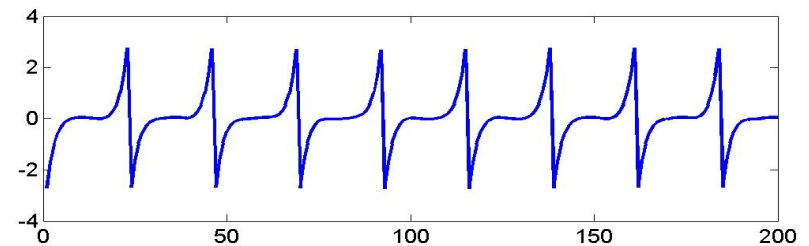
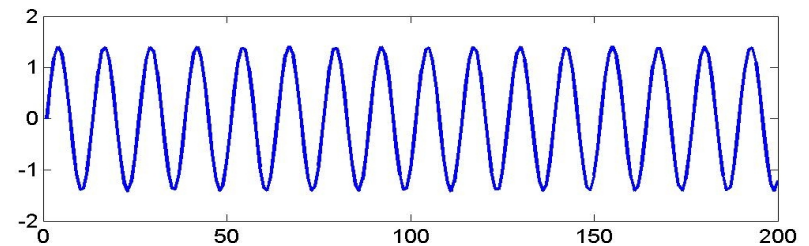
$$x_1(t) = a_{11}s_1(t) + a_{12}s_2(t)$$

$$x_2(t) = a_{21}s_1(t) + a_{22}s_2(t)$$

$$WA = \begin{bmatrix} \text{white} & \text{gray} \\ \text{gray} & \text{white} \end{bmatrix}$$



Mixtures



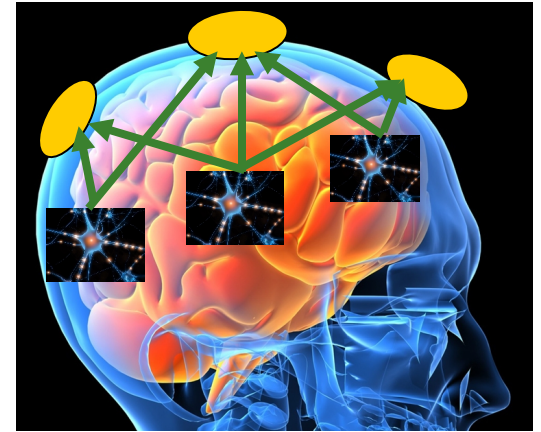
ICA estimation

Some ICA Applications

- Medical signal processing – fMRI, ECG, EEG
 - Brain Computer Interfaces
 - Image denoising
 - Modeling of the hippocampus, place cells
 - Modeling of the visual cortex
 - Microarray data processing
 - Decomposing the spectra of galaxies
 - Blind deconvolution
 - Feature extraction
 - Face recognition
 - Time series analysis
 - Financial applications
 - Clustering
 - Classification
-

ICA Applications, Removing Artifacts from EEG

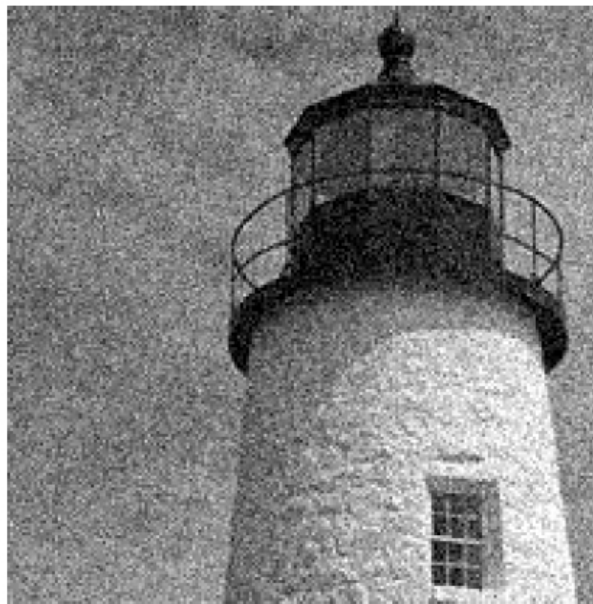
- EEG ~ *Neural cocktail party*
- Severe **contamination** of EEG activity by
 - ❑ eye movements,
 - ❑ blinks,
 - ❑ muscle,
 - ❑ heart, ECG artifact
 - ❑ vessel pulse
 - ❑ electrode noise
 - ❑ line noise, alternating current (60 Hz)
- ICA can effectively **detect, separate and remove** activity in EEG records from a wide variety of artifactual sources.
(Jung, Makeig, Bell, and Sejnowski)



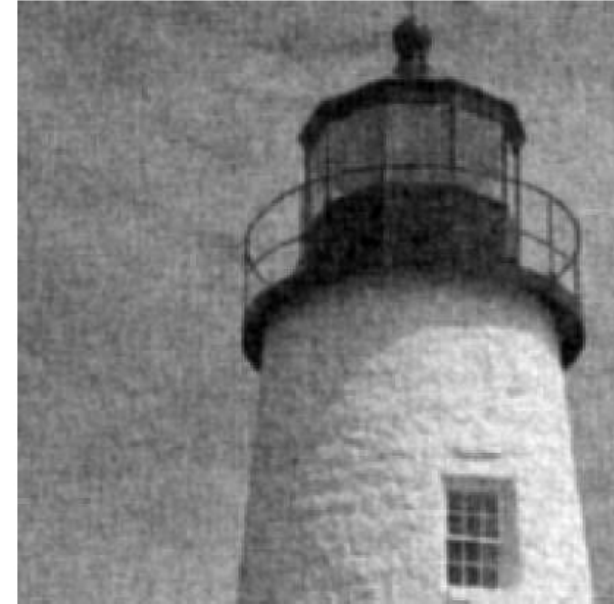
ICA for Image Denoising (Hoyer, Hyvarinen)



original



noisy



Wiener filtered



median filtered

ICA denoised



ICA for Microarray data processing

$$\mathbf{X}^T = \text{Microarray Data Matrix} = \begin{bmatrix} \mathbf{A} \\ \mathbf{a}_k \end{bmatrix} * \begin{bmatrix} \mathbf{S} & \mathbf{s}_k \end{bmatrix}$$

$$\mathbf{X}^T \in \mathbb{R}^{M \times N}$$

M = number of experiments

N = number of genes

Assumption:

- each experiment is a mixture of **independent expression modes** ($\mathbf{s}_1, \dots, \mathbf{s}_K$).
- some of these modes (e.g. \mathbf{s}_k) can be related to the difference between the classes.
- $\rightarrow \mathbf{a}_k$ correlates with the class labels

Generalizations

- **Blind Deconvolution**

- $x(t) = A_1 s(t-1) + A_2 s(t-2) + \dots + A_k s(t-k)$
- After FFT we have to do ICA in the frequency space

- **Independent Subspace Analysis**

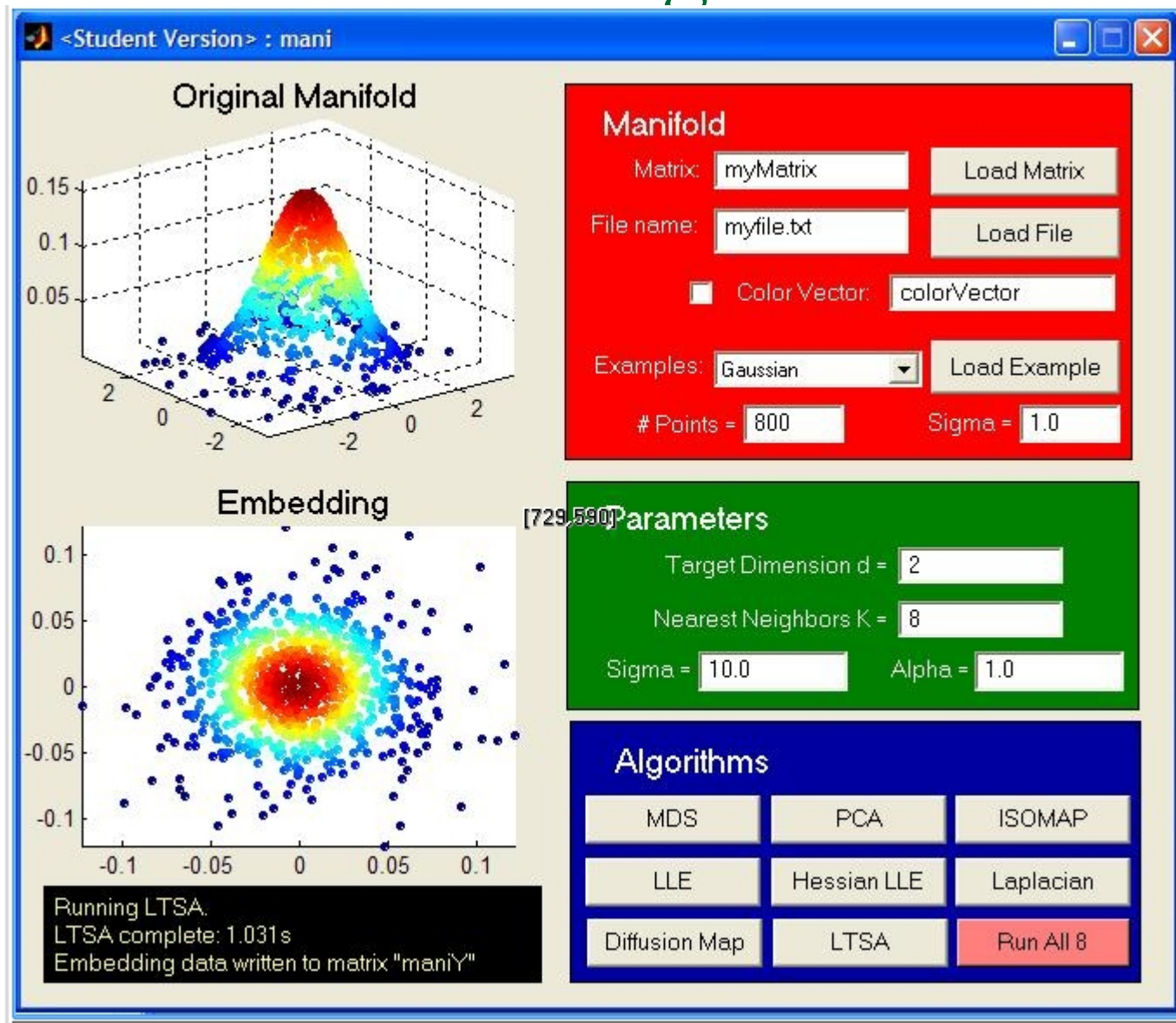
- ***Blind Subspace Deconvolution using FFT???***

Manifold learning using time processes



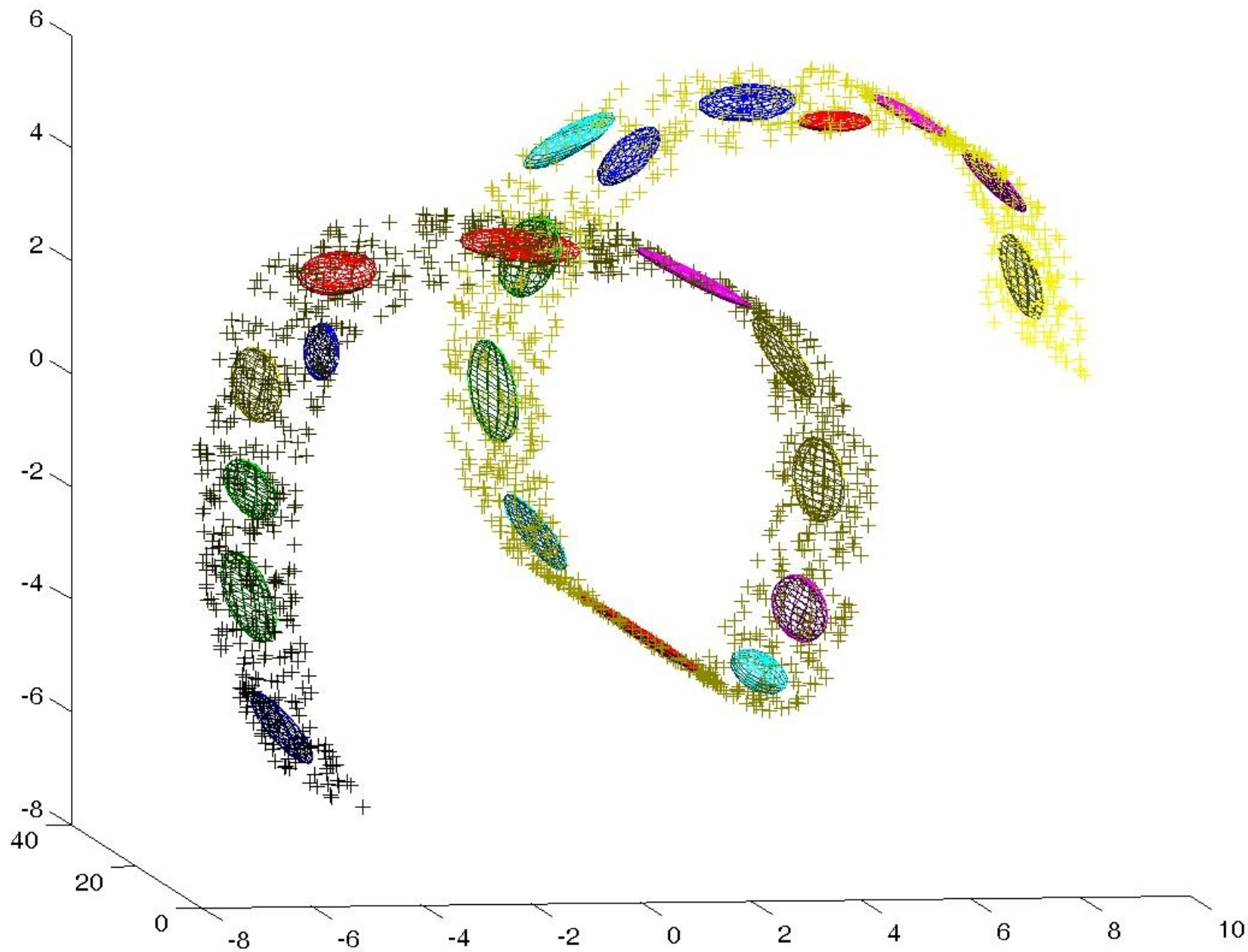
Manifold learning

<http://www.math.umn.edu/~wittman/mani/>

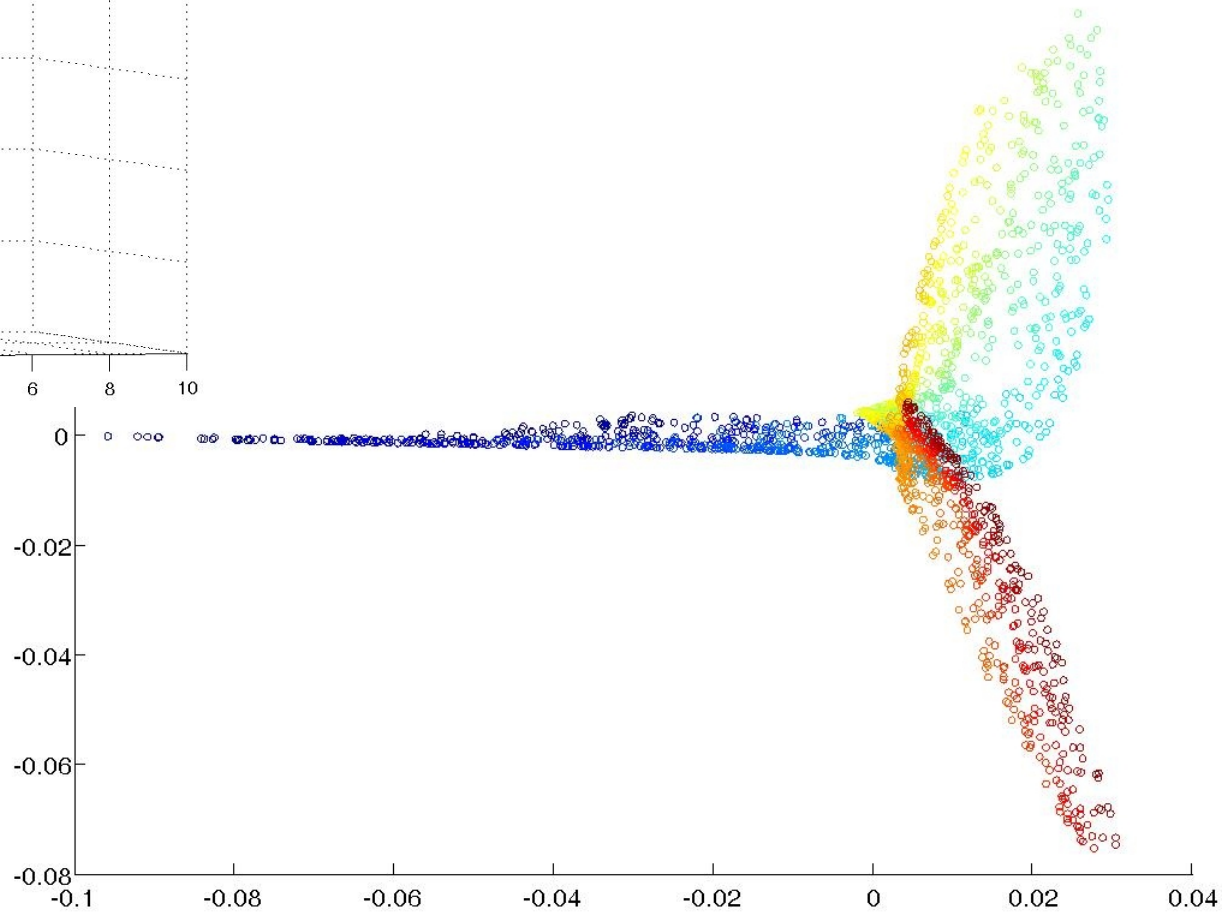
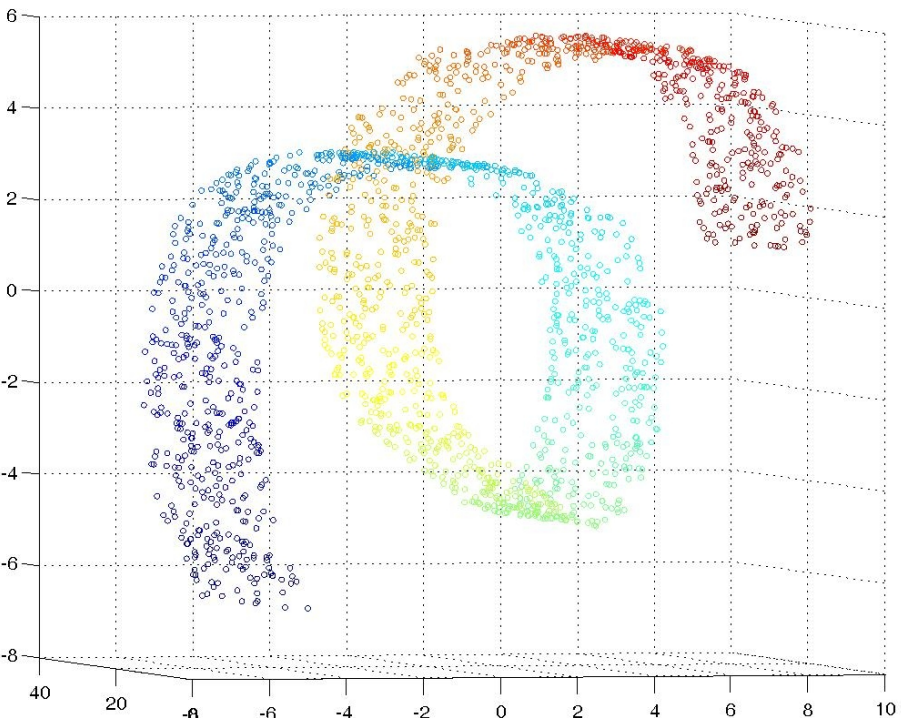


Manifold learning

- The algorithms usually assume iid sample.
 - ***Can we exploit time correlations???***
 - E.g. using Hidden Markov Models in the Variational Bayesian Mixture Factor Analyzer model (vbMFA, Beal & Ghahramani)...
-



LTSA Failure



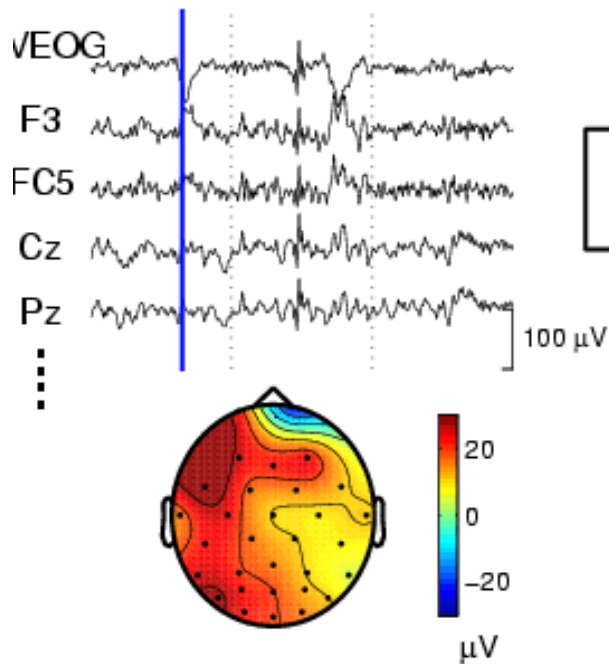
Thanks for the attention!



ICA decomposition

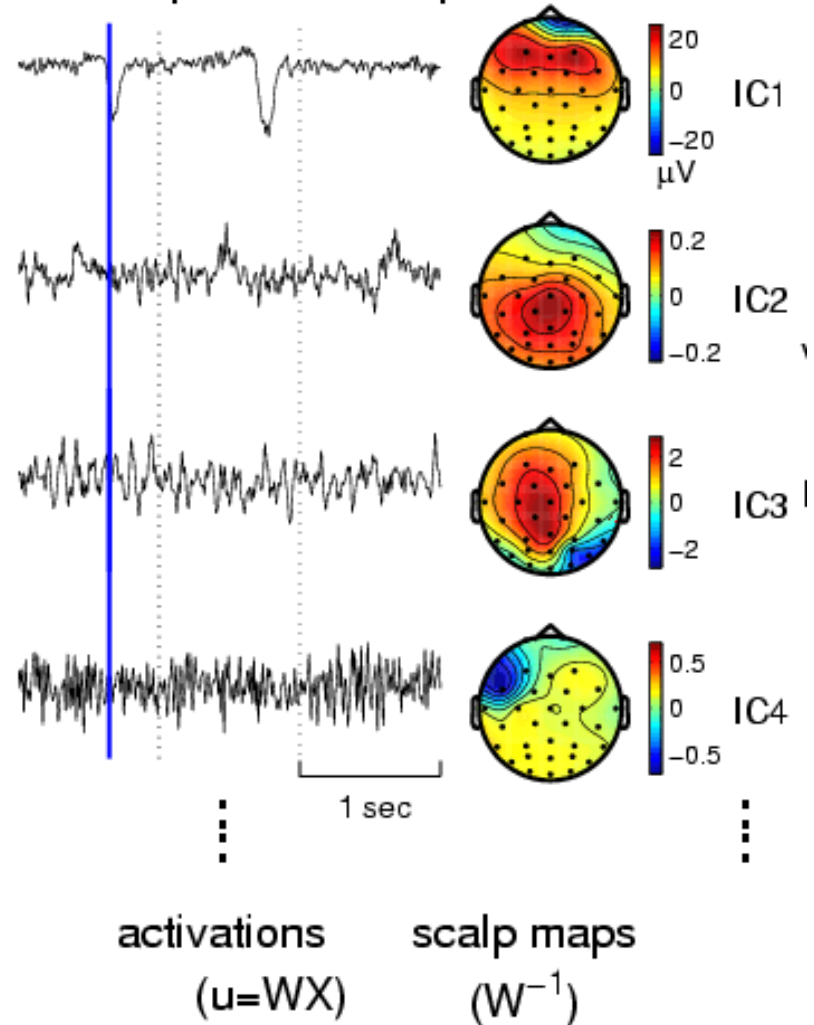


EEG Scalp Channels

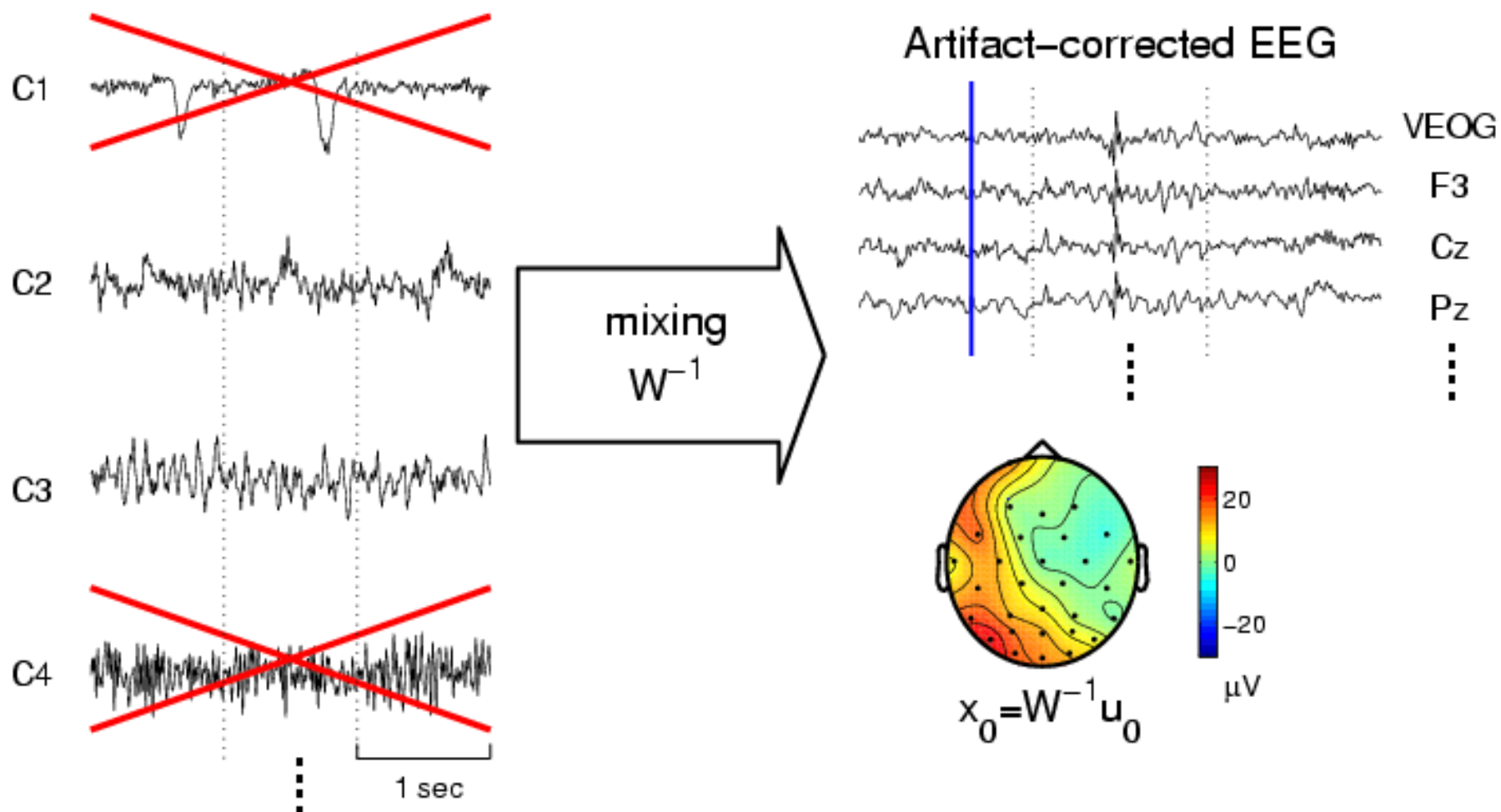


unmixing
(W)

Independent Components



Summed Projection of Selected Components



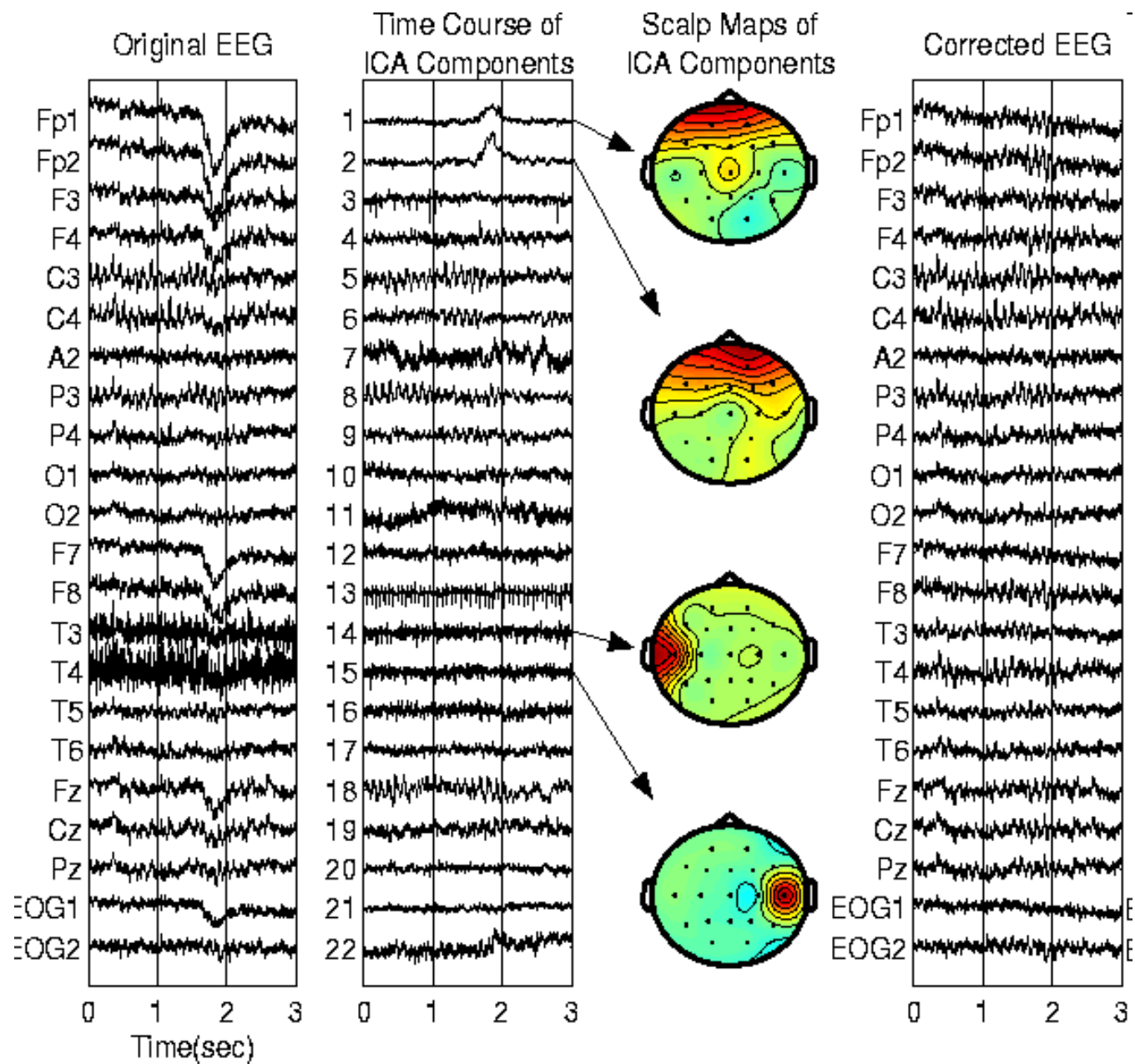


Fig from Jung

ICA for Microarray data processing

(Schachtner et al, ICA07)

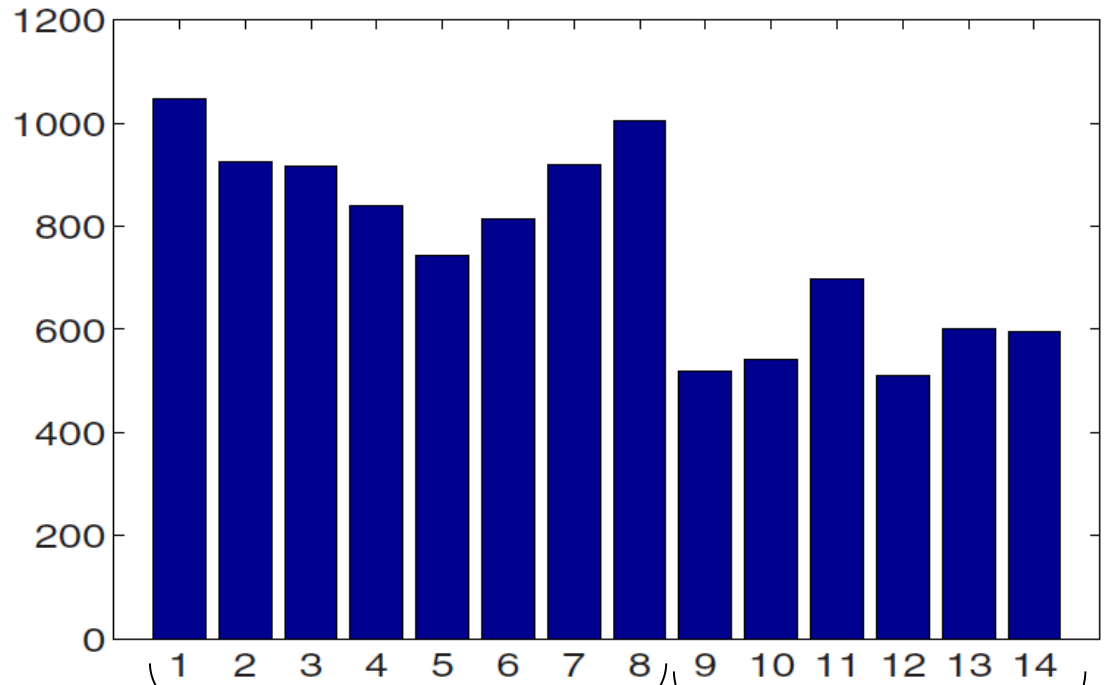
Breast Cancer Data set

M=14 Experiments

N=22283 genes

2 classes

9th column of **A**:



$|\text{Corr}(\mathbf{a}_9, \mathbf{d})|=0.89$, where
 \mathbf{d} is the vector of class labels

Class 1,
weak metastasis

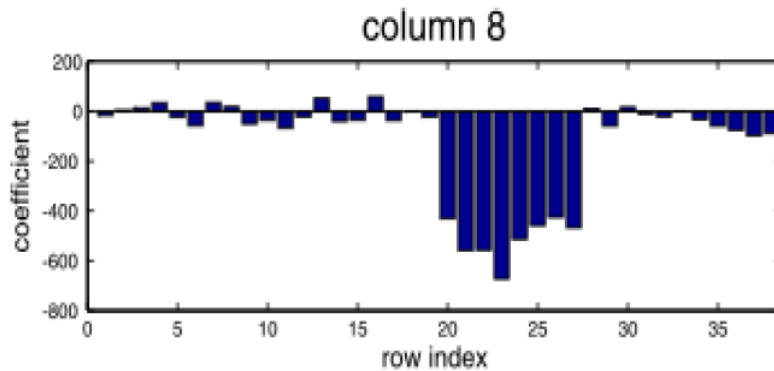
Class 2,
strong metastasis

ICA for Microarray data processing (Schachtner et al, ICA07)

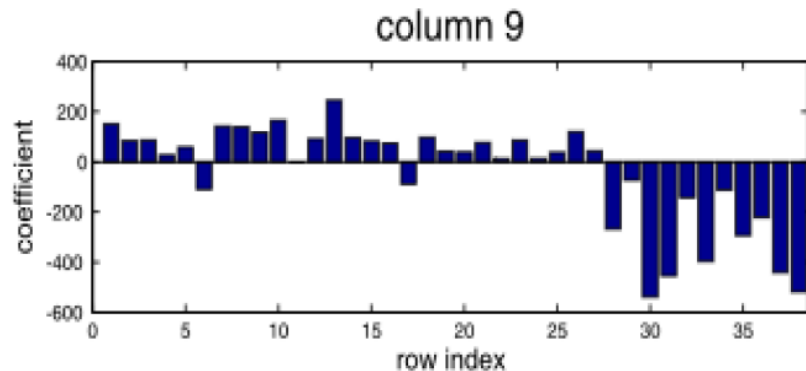
Leukemia Data set M=38 Experiments

N=5000 genes

3 classes: ALL-B, ALL-T, AML



ALL-B ALL-T AML



ALL-B ALL-T AML