

General Blind Source Signal Separation

Problem Statement

Find the separation of a set of source signals from a given set of mixed signals.

The mixed signals is represented as a column vector x ; $x \in R^n$, $n \in N$.

You have no information about how the mix happened between the sources, nor do you know any information about the source.

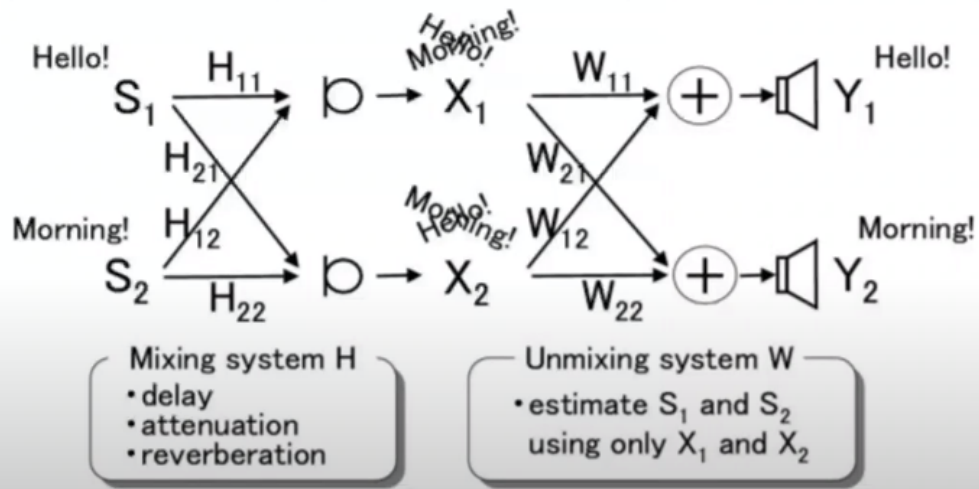
You can assume the following:

- The number of independent sources is equal to the number of mixtures (the number of independent sources is also n).
- Independent sources are non-gaussian signals and that they are mutually independent.

Source signal S

Observed signal X

Unmixed signal Y



Encoding function

we have n independent sources $s_1(t) s_2(t) \dots s_n(t)$ represented as a vector

$$s(t) = [s_1(t) s_2(t) \dots s_n(t)]^T.$$

A ; $A \in R^{n \times n}$, is called the mixing matrix, represents the mixture coefficients where $-5.0 \leq a_{ij} \leq 5.0$ for $1 \leq i, j \leq n$ and $i, j \in N$.

$$x(t) = As(t),$$

To find the source signals, we want to optimize the following equation,

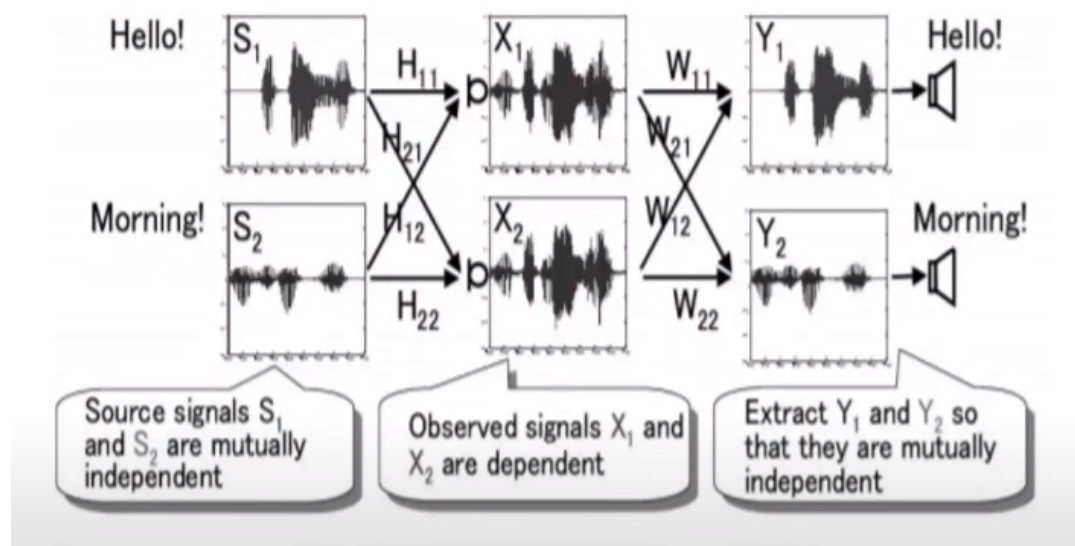
$$y(t) = Bx(t),$$

$$y(t) = [y_1(t) y_2(t) \dots y_n(t)]^T$$

$$B \in R^{n \times n}, -5.0 \leq b_{ij} \leq 5.0$$

B as a chromosome, we can just flatten the matrix to a one dimensional vector, where each gene correspond to an entry in the matrix B , if $n = 2$ then a chromosome for B is

$b_{1,1}$	$b_{1,2}$	$b_{2,1}$	$b_{2,2}$
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Selection method

Initial population

We choose the size of the population, let it be k , then we generate k random candidate solutions (chromosomes).

Selection

"using the helpful parts of biological evolution, and replacing the parts that might not work for us"

Tournament selection.

We choose the size of the tournament that is 20% of k , which is the size of the population, and round it to the nearest power of two.

We choose the probability p such that $0 < p < 1$ of each selection, and distribute the probabilities for each position in the tournament to be chosen as follows,

$$p \propto ((1 - p)^{\alpha_i}); \alpha_i \text{ is the fitness for chromosome } i$$

This keeps running until we have our population complete (number of selection = k), then the selected parents are passed to crossover and mutate.

Crossover

- Multiline crossover
- Multiline with random crossover

Mutation

We chose a mutation rate of 0.01, where we change a certain gene to a random value m ; $-5 \leq m \leq 5$

Fitness function

"The nearer the individual to the solution of the optimization problem, the more fit is the individual"

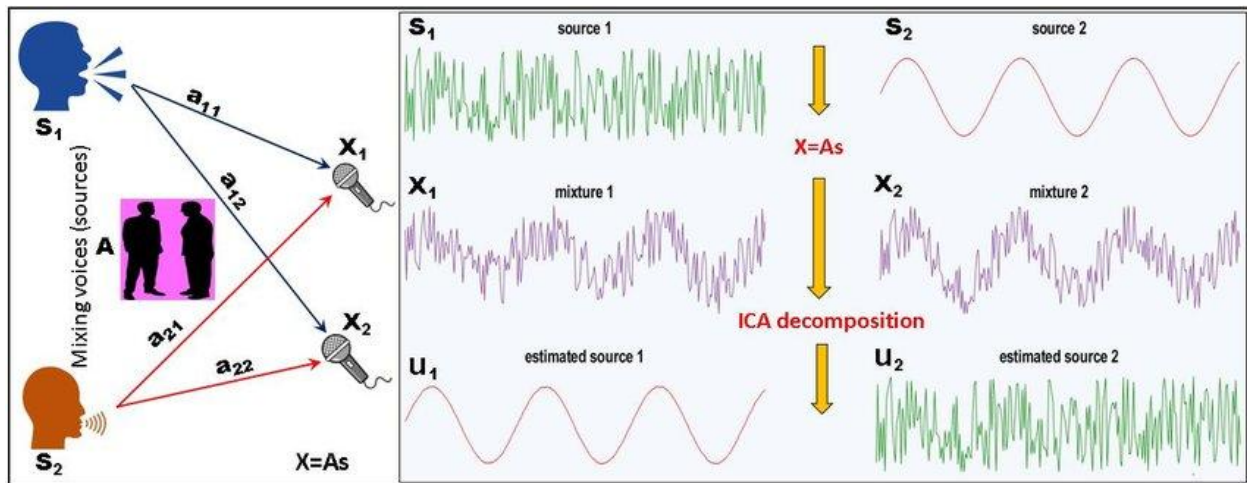
maximization of the kurt sum, minimize the mutual information

- Kurt is used to show the independency of the components of the source signals.
- Mutual information (MI) is used to show how much common information between two random variables X and Y.

"In optimization, it is more convenient to solve minimization problems. However, the opposite perspective would be valid, too."

let $M \in R^{n \times n}$, $n \in N$, and it's entries are the $MI(y_i, y_j)$

$$f(y) = \sum_{i=1}^n |kurt(y_i)| + \sum_{i=1, j=1, i \neq j}^n 100e^{-10m_{ij}}, \text{ for all } m_{ij} < 0.2$$



Ref

- [Medical Imaging Signals And Systems](#)
- [A Genetic Algorithm for Blind Source Separation Based on Independent Component Analysis](#)
- [Signal separation](#)
- [Cocktail party](#)
- [Independent component analysis](#)
- [Medical imaging](#)
- [A real-time blind source separation scheme and its application to reverberant and noisy acoustic environments](#)
- [Blind Signal Separation: Statistical Principles](#)
- [Dynamic Programming Algorithms for Computing Optimal Knockout Tournaments](#)
- [Independent component analysis: algorithms and applications](#)
- [What is mean by the non-gaussianity in the independent component analysis\(ICA\)?](#)
- [Independent Component Analysis \(ICA\) | by Shawhin Talebi](#)
- [A Short Introduction to ICA](#)
- [Projection pursuit](#)