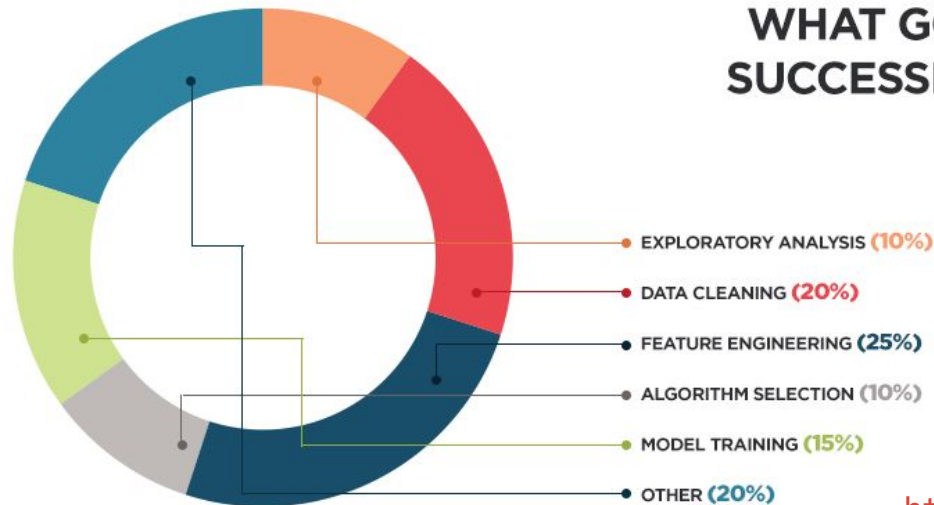


feature engineering

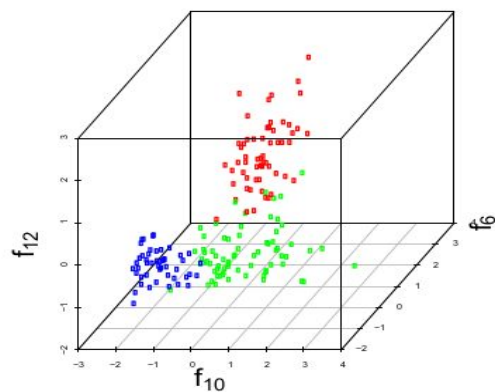
Q: how do you get the most out of your data, for predictive modelling?

Data scientists typically spend a lot of time doing “feature engineering”...

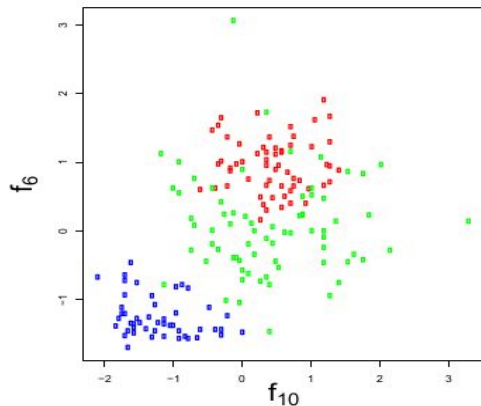


<https://elitedatascience.com/feature-engineering>

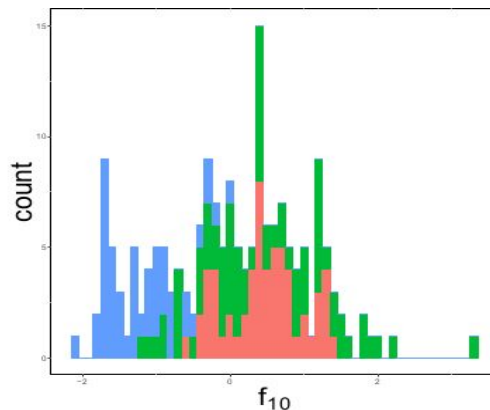
# More features = good?



(a) 3 features:  $f_{10}$ ,  $f_6$ ,  $f_{12}$ .



(b) 2 features:  $f_{10}$ ,  $f_6$ .



(c) 1 feature:  $f_{10}$ .

Figure 1.1: Wine dataset projected across varying numbers of features. Wine contains three classes, 13 features, and 178 instances.

from Andrew Lensen's PhD thesis, VUW, 2019

[e.g. plot 3d demo](#)

an imaginary example...

1000 cases, half are ♀ / ♂, 30% have heart disease

frequency of the antecedent  
(l.h.s), overall

fraction of cases where the  
consequent (r.h.s.) was true

	Rule	$fr$	$\phi$
1	smoking $\rightarrow$ heart disease	120	0.400
2	sports $\rightarrow \neg$ heart disease	400	0.800
3	coffee $\rightarrow \neg$ heart disease	240	0.700
4	stress $\rightarrow$ heart disease	150	0.300
5	pine bark extract $\rightarrow \neg$ heart disease	1	1.000
6	female $\rightarrow \neg$ heart disease	352	0.704
7	female, stress $\rightarrow$ heart disease	100	0.385
8	stress, smoking $\rightarrow$ heart disease	100	0.500
9	smoking, coffee $\rightarrow$ heart disease	96	0.400
10	smoking, sports $\rightarrow$ heart disease	20	0.333
11	female, sports $\rightarrow \neg$ heart disease	203	0.808

simple  
dependencies

independencies

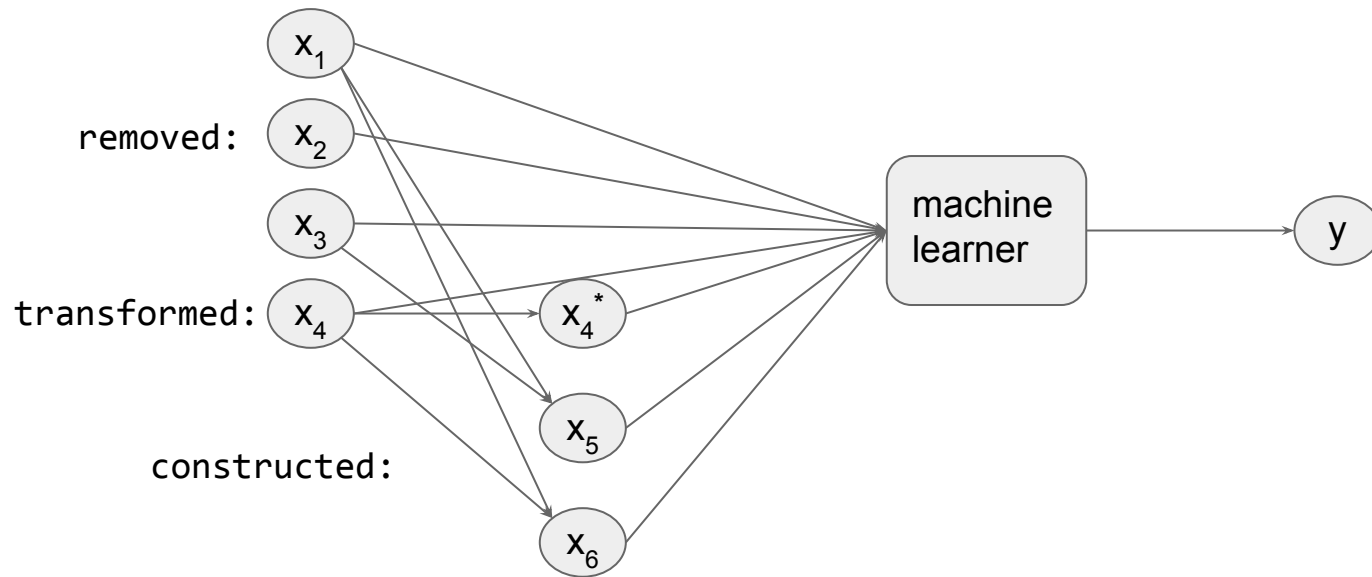
spurious (too few)

spurious (too *small*)

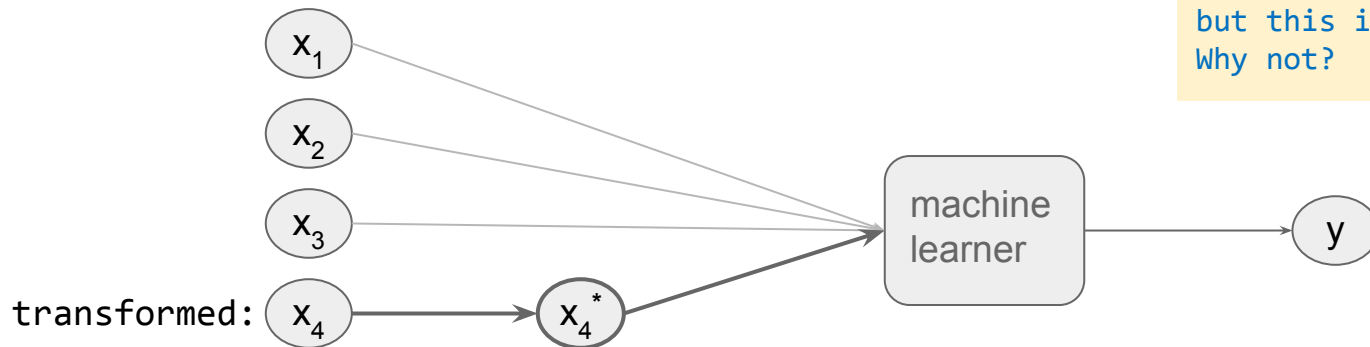
non-monotonicity!

superfluous  
variables

# changes to features



# one-to-one



for example

- clipping
- normalization
- discretization
- mathematical transformations such as logarithm  $\log(x)$ , reciprocal function  $1/x$ , exponentiation  $\exp(x)$ , etc...

aside: if  $x_1 \in \{\text{dog, cat, ferret}\}$  it is tempting to transform into

dog  $\rightarrow$  1

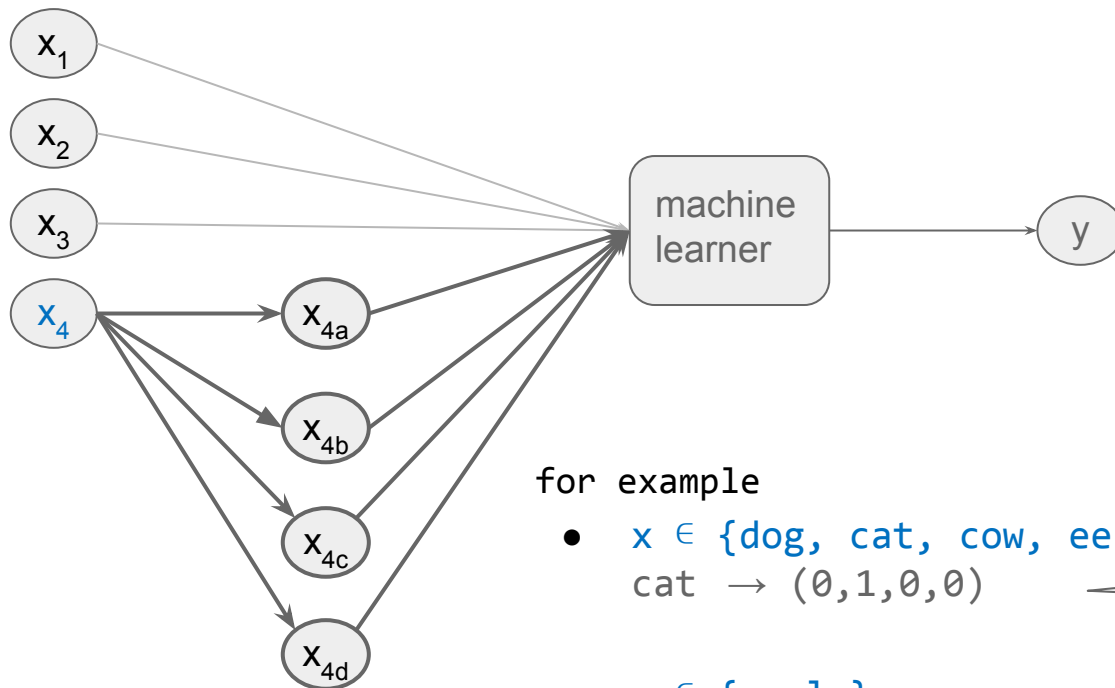
cat  $\rightarrow$  2

ferret  $\rightarrow$  3

but this is *not* a good idea.  
Why not?

can get the original feature into a more useful range for the learner

# one-to-many



might make it  
easier / more  
natural for the  
machine  
learner to work  
with

for example

- $x \in \{\text{dog, cat, cow, eel}\}$ :

cat  $\rightarrow (0, 1, 0, 0)$

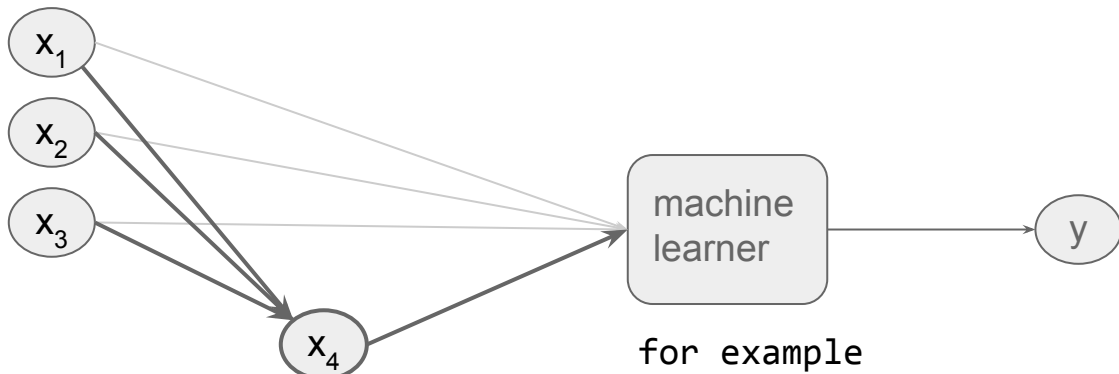
"one-hot"  
encoding

- $x \in \{\text{reals}\}$ :

$x \rightarrow (x, x^2, x^3, x^4)$

polynomial  
expansion

# many-to-one



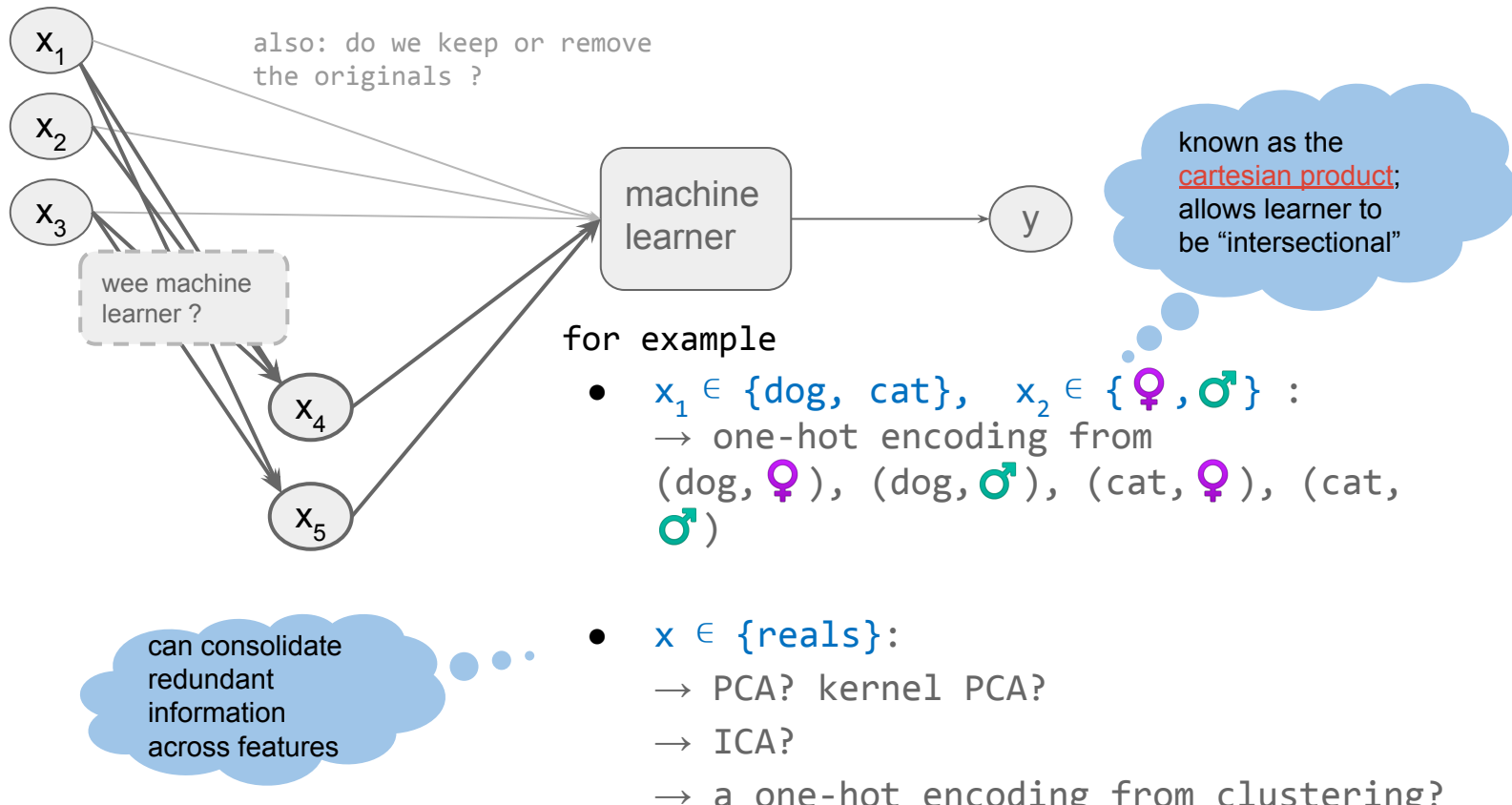
put basic features together to construct new features that can capture **relationships** between the basic features – the idea is to augment the feature space with these too

for example

- $x \in \{\text{TRUE}, \text{FALSE}\}$ :  
 $(x_1 \text{ and } x_2) \text{ or } x_3$
- $x \in \{\text{reals}\}$ :  
 $(x_1 + x_2) * x_3$



# many-to-many



# many-to-one is a.k.a. “feature construction”

- we can also put basic features together to make constructed features that might capture **relationships** between the basic features – the idea is to augment the feature space with these too

*E.g.* Given base features  $[X_1, X_2, X_3]$

linear constructions:

$$X_c = X_1 + X_2,$$

or 
$$X_c = 4X_1 + 3X_2 + 6X_3,$$

...

nonlinear constructions:

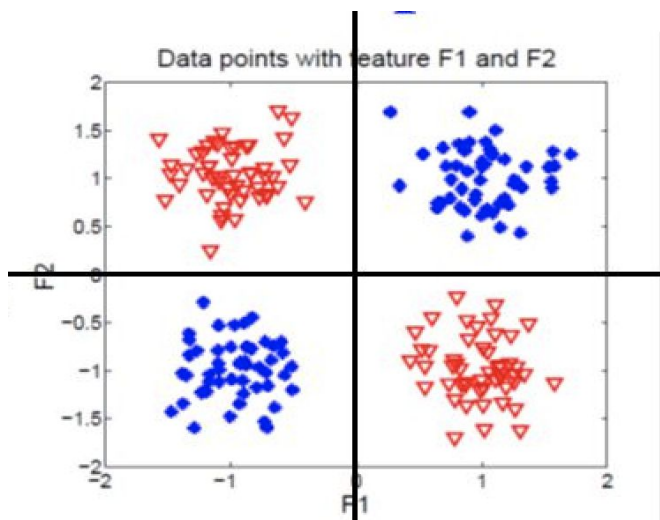
$$X_c = X_1 * X_2,$$

or 
$$X_c = X_1 * X_2^2$$

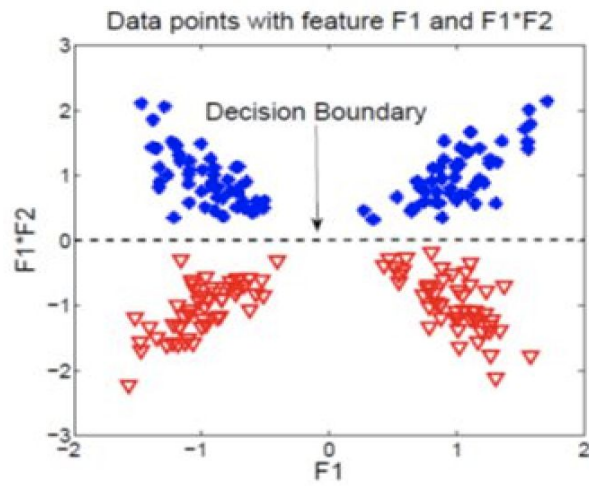
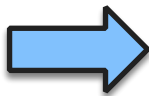
# feature construction

the quality of such constructed features can drastically affect the learning performance

- -ve: Feature interactions introduce errors and add complexity
- +ve: more meaningful features that lead to more concise and accurate machine learning models



$$F_3 = F_1 * F_2$$



# components of a feature construction system

Automatic feature construction systems need the following two components:

- a **search strategy** to search the space of possible functions (of original features)
- an **evaluation mechanism** to measure the goodness of a candidate function

# operators for constructing new features

## Boolean features:

- $x_1, x_2 \in \{\text{TRUE}, \text{FALSE}\}$ 
  - e.g.  $x_3 \leftarrow \text{not}(x_1)$
  - e.g.  $x_4 \leftarrow \text{xor}(x_1, x_2)$

⇒ logical operators like negation, conjunctions, disjunctions,...

## Nominal/Categorical features:

- $x_1 \in \{\text{dog}, \text{cat}\}, x_2 \in \{\text{rain}, \text{snow}\} \dots$ 
  - e.g.  $x_3 \in \{(\text{dog}, \text{rain}), (\text{dog}, \text{snow}), (\text{cat}, \text{rain}), (\text{cat}, \text{snow})\}$

⇒ cartesian product

## Numerical features:

- $x_1 \in \{\text{ints}\}, x_2 \in \{\text{reals}\}, \dots$ 
  - $x_4 \leftarrow \min(x_1, \text{mean}(x_2, x_3))$

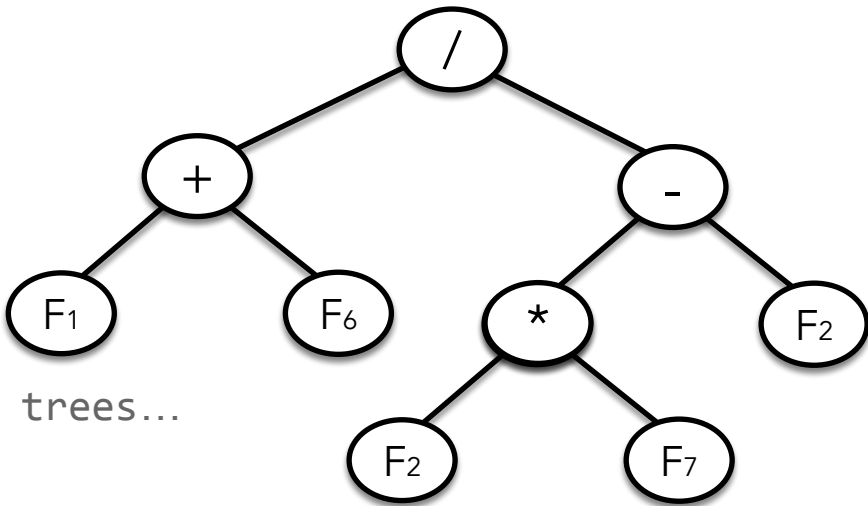
⇒ add, multiply, max, average, equals, ...

# can we construct new features automatically with Genetic Programming?

Genetic Programming is a **flexible** way to make mathematical and logical functions

warning: there **isn't much structural (topological) information** in the search space of possible functions

→ yes it's possible,  
but be prepared to spend a  
lot of compute time trying out dud trees...



# evaluating new features

- Not all constructed features are good!...
- Apply the usual feature selection techniques to remove redundant and irrelevant features
  - Q: what are the “usual” techniques?

an imaginary example...  
1000 cases, half are men/women, 30% have heart disease

		frequency of the antecedent (l.h.s.), overall	fraction of cases where the consequent (r.h.s.) was true
Rule		$fr$	$\phi$
1	smoking $\rightarrow$ heart disease	120	0.400
2	sports $\rightarrow$ $\neg$ heart disease	400	0.800
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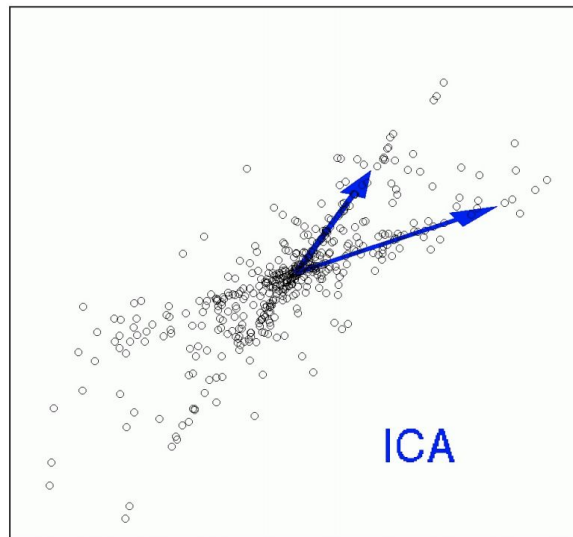
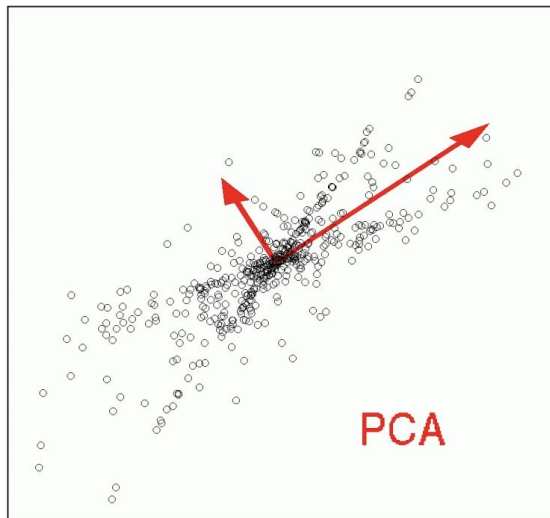
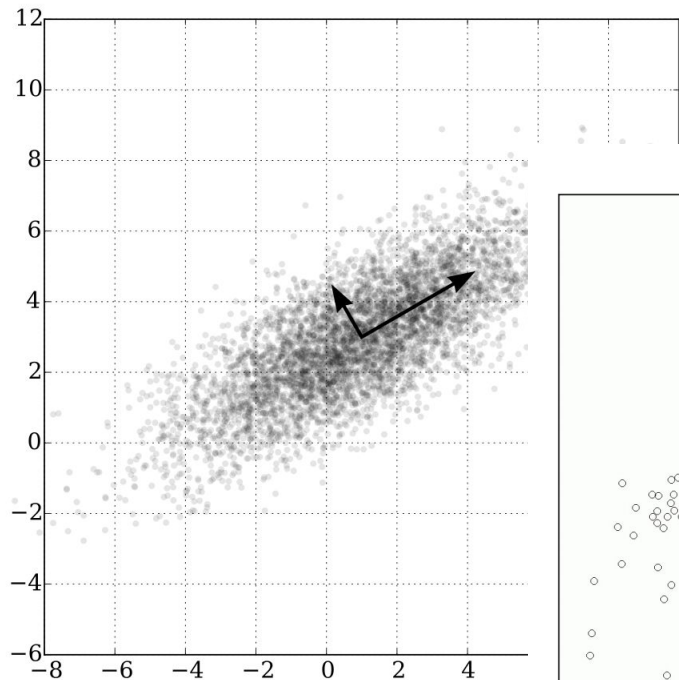
non-monotonicity!

superfluous variables

# Some specific “many to many” feature methods:

## PCA (Principal Components Analysis)

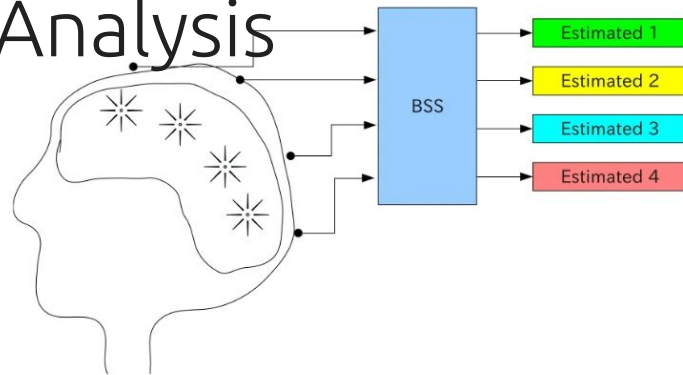
- PCA
- ICA
- Kernel PCA





# ICA - Independent Components Analysis

- PCA and ICA both create new components that are **linear combinations** of the originals



- ICA assumes the observed data arose as a linear combination of independent components (that are sadly unknown)
  - **Goal of ICA:** recover the components from  $X$  by finding a linear transformation
- it's like PCA but we're looking for components that are as **statistically independent** as possible
- PCA removes correlation, but doesn't usually find those independent components that might actually underly the data
- why might it be good to find truly independent components?

# kernel PCA

- Kernel PCA combines a specific mathematical view of PCA with **kernel** functions, creating a **nonlinear extension** of PCA
- Perform PCA on data that has been transformed into a high-dimensional setting – “blessing of dimensionality” (!)

