Feature selection

Victor Kitov

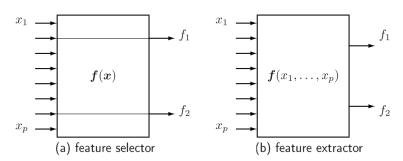
v.v.kitov@yandex.ru

Yandex School of Data Analysis



Feature selection

Feature selection is a process of selecting a subset of original features with minimum loss of information related to final task (classification, regression, etc.)



Applications of feature selection

- Why feature selection?
 - increase predictive accuracy of classifier
 - improve optimization stability by removing multicollinearity
 - increase computational efficiency
 - reduce cost of future data collection
 - make classifier more interpretable
- Not always necessary step:
 - some methods have implicit feature selection:

Applications of feature selection

- Why feature selection?
 - increase predictive accuracy of classifier
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- Not always necessary step:
 - some methods have implicit feature selection:
 - decision trees and tree-based (RF, ERT, boosting)
 - L1 regularization

Types of features

Define f - the feature, $F=\{f_1,f_2,...f_D\}$ - full set of features, $\tilde{F}=F\backslash\{f\}.$

Strongly relevant feature:

$$p(y|f,\tilde{F}) \neq p(y|\tilde{F})$$

• Weakly relevant feature:

$$p(y|f, \tilde{F}) = p(y|\tilde{F}), \text{ but } \exists S \subset \tilde{F} : p(y|f, S) \neq p(y|S)$$

Irrelevant feature:

$$\forall S \subset \tilde{F}: p(y|f,S) = p(y|S)$$

Types of features

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Irrelevant feature:

$$\forall S \subset \tilde{F}: p(y|f,S) = p(y|S)$$

Aim of feature selection

Find minimal features subset $S \subset F$ such that $P(y|S) \approx P(y|F)$, i.e. leave only relevant and non-redundant features.

Categorization of feature selection algorithms

- Completeness of search:
 - Complete
 - exhaustive search complexity is 2^D.
 - may be not exhaustive under certain conditions on $J(S)^1$
 - Suboptimal
 - deterministic
 - random (deterministic with randomness / completely random)
- Integration with final predictor
 - independent (filter methods)
 - uses predictor quality (wrapper methods)
 - is embedded inside predictor (embedded methods)

 $^{^{1}}J(S)$ is a score of feature subset S.

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 - Feature subset generation
 - Feature importance estimation
- 2 Simultaneous feature selection specification

Individual feature importances approach

- Estimate importances for individual features $I(f_1), I(f_2), ... I(f_D)$.
- Generate feature subset based on importances.

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Incomplete search with suboptimal solution

• Order features with respect to feature importances I(f):

$$I(f_1) \ge I(f_2) \ge \dots \ge I(f_D)$$

option 1: select top m

$$\hat{F} = \{f_1, f_2, ... f_m\}$$

option 2: select best set from nested subsets:

$$S = \{\{f_1\}, \{f_1, f_2\}, ...\{f_1, f_2, ...f_D\}\}$$

$$\hat{F} = \arg\max_{F \in S} J(F)$$

- Comments:
 - simple to implement
 - when features are correlated, it will take many redundant features

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Application of feature importances

- Feature importances can be used:
 - for feature selection
 - for rescaling features for adapting their impact on the model:
 - e.g.: in K-NN, in linear methods with regularization
 - for adapting feature sampling probability in random forest, extra random trees.

Correlation

• two class:

$$\rho(f,y) = \frac{\sum_{i} (f_{i} - \bar{f})(y_{i} - \bar{y})}{\left[\sum_{i} (f_{i} - \bar{f})^{2} \sum_{i} (y_{i} - \bar{y})^{2}\right]^{1/2}} = \frac{a}{b}$$

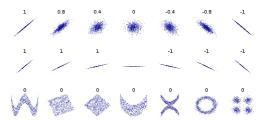
• multiclass $\omega_1, \omega_2, ...\omega_C$ (micro averaged $ho(f, y_c) \, c = 1, 2, ...C)$

$$R^{2} = \frac{\sum_{c=1}^{C} \left[\sum_{i} (f_{i} - \bar{f})(y_{ic} - \bar{y}_{c}) \right]^{2}}{\sum_{c=1}^{C} \sum_{i} (f_{i} - \bar{f})^{2} \sum_{i} (y_{ic} - \bar{y}_{c})^{2}} = \frac{\sum_{c} a_{c}^{2}}{\sum_{c} b_{c}^{2}}$$

- Benefits:
 - simple to compute
 - applicable both to continuous and discrete features/output.
 - does not require calculation of probability density function.

Correlation for non-linear relationship

- Correlation captures only linear relationship.
- Example: consider X-random variable, with $\mathbb{E}X = 0$, $\mathbb{E}X^3 = 0$ and random variable $Z = X^2$. Then X, Z are uncorrelated but dependent.
- Other examples of data and its correlation:



Correlation between ranks. 12/30

Definitions

• Entropy² of random variable Y:

$$H(Y) := -\sum_{y} p(y) \ln p(y)$$

Conditional entropy of Y after observing X:

$$H(Y|X) := -\sum_{x} p(x) \sum_{y} p(y|x) \ln p(y|x)$$

• Kullback-Leibler divergence for two p.d.f. P(x) and Q(x): $KL(P||Q) := \sum_{x} P(x) \ln \frac{P(x)}{Q(x)}$

 $^{^2}$ measures level of uncertainty of r.v. Y

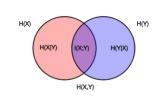
Mutual information

Mutual information measures how much r.v. X and Y share information between each other:

$$MI(X,Y) := \sum_{x,y} p(x,y) \ln \left[\frac{p(x,y)}{p(x)p(y)} \right] = KL(p(x,y)||p(x)p(y))$$

Properties:

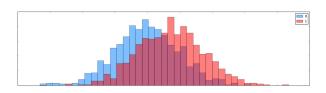
- MI(X, Y) = MI(Y, X)
- $MI(X, Y) = KL(p(x, y)||p(x)p(y)) \ge 0$
- MI(X, Y) = H(Y) H(Y|X)
- $MI(X, Y) < \min \{H(X), H(Y)\}$
- X, Y- independent <=> MI(X, Y) = 0 (for discrete r.v.)
- X completely identifies Y, then $MI(X,Y) = H(Y) \le H(X)$



Mutual information for feature selection

- Normalized variant $NMI(X, Y) = \frac{MI(X, Y)}{H(Y)}$ equals
 - zero, when P(Y|X) = P(Y)
 - \bullet one, when X completely identifies Y.
- Properties of MI and NMI:
 - identifies arbitrary non-linear dependencies
 - requires calculation of probability distributions
 - continuous variables need to be discretized

importance based on probabilistic distance



Measure of feature f importance - distance between p(f|y=0) and p(f|y=1), e.g. total variation:

$$\int |p(x|y=1) - p(x|y=0)| dx$$

Relief criterion: 1-NN

INPUT:

Training set $(x_1, y_1), (x_2, y_2), ...(x_N, y_N)$ Number of neighbours KDistance metric $\rho(x, x')$ # usually Euclidean

for each object x_n, y_n :

calculate nearest neighbour of the same class $x_{s(n)}$

calculate K nearest neighbour of class $x_{d(n)}$

for each feature f_i in $f_1, f_2, ... f_D$:

calculate importance
$$R(f_i) = \frac{1}{N} \sum_{n=1}^{N} \frac{|x_n^i - x_{d(n)}^i|}{|x_n^i - x_{s(n)}^i|}$$

OUTPUT:

feature importances R

Relief criterion: K-NN

INPUT:

Training set $(x_1,y_1),(x_2,y_2),...(x_N,y_N)$ Number of neighbours KDistance metric $\rho(x,x')$ # usually Euclidean

for each object x_n, y_n :

calculate K nearest neighbours of the same class y_n :

$$X_{s(n,1)}, X_{s(n,2)}, ... X_{s(n,K)}$$

calculate K nearest neighbours of class other than y_n :

$$X_{d(n,1)}, X_{d(n,2)}, ... X_{d(n,K)}$$

for each feature f_i in $f_1, f_2, ... f_D$:

calculate importance
$$R(f_i) = \frac{1}{N} \sum_{n=1}^{N} \sum_{k=1}^{K} \frac{|x_n^i - x_{d(n,k)}^i|}{|x_n^i - x_{s(n,k)}^i|}$$

OUTPUT:

 $\overline{feature importances} R$

Tree feature importances

- Tree feature importances (clf.feature_importances_ in sklearn).
 - Consider feature f
 - Let T(f) be the set of all nodes, relying on feature f when making split.
 - efficiency of split at node t: $\Delta I(t) = I(t) \sum_{c \in childen(t)} \frac{n_c}{n_t} I(c)$
 - feature importance of $f: \sum_{t \in T(f)} n_t \Delta I(t)$
- Alternative: difference in decision tree prediction quality for
 - original validation set
 - ② validation set with j-th feature randomly shuffled

Feature importances from linear model

- Feature importances from linear classification:
 - fit linear classifier with regularization to data
 - features should be normalized
 - retrieve w (clf.coef_ in scikit-learn)
 - **3** importance of feature f_i is equal to $|w_i|$.

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 - Sequential search subset generation
 - Genetic search subset generation

Simultaneous feature selection specification

- Need to specify:
 - quality criteria J(S) for any feature subset S
 - typically: quality of model with these features (wrapper approach)
 - feature subset generation method $S_1, S_2, S_3, ...$

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Sequential search

- Sequential forward selection algorithm:
 - init: $k = 0, F_0 = \emptyset$
 - while k < max_features:</p>
 - $f_{k+1} = \operatorname{arg\,max}_{f \in F} J(F_k \cup \{f\})$
 - $F_{k+1} = F_k \cup \{f_{k+1}\}$
 - if $J(F_{k+1}) < J(F_k)$: break
 - k=k+1
 - return F_k
- Variants:
 - sequential backward selection
 - up-k forward search
 - down-p backward search
 - up-k down-p composite search
 - up-k down-(variable step size) composite search

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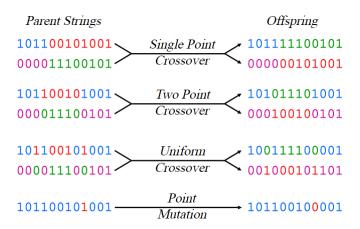
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Genetic³ algorithms

- Each feature set $F = \{f_{i(1)}, f_{i(2)}, ... f_{i(K)}\}$ is represented using binary vector $[b_1, b_2, ... b_D]$ where $b_i = \mathbb{I}[f_i \in F]$
- Genetic operations:
 - $crossover(b^1,b^2)=b$, where $b_i=egin{cases} b_i^1 & \text{with probability } \frac{1}{2} \\ b_i^2 & \text{otherwise} \end{cases}$ $mutation(b^1)=b$, where $b_i=egin{cases} b_i^1 & \text{with probability } 1-\alpha \\ \neg b_i^1 & \text{with probability } \alpha \end{cases}$
 - for some small α .

³Name inspired by genetic inheritance in biology.

Genetic operations: demo



Genetic algorithms

INPUT:

population size B and expanded population size B' parameters of mutation and crossover maximum number of iterations T, minimum quality change ΔJ

ALGORITHM:

generate
$$B$$
 feature sets $S_1, S_2, ... S_B$ randomly. set $t=1$, $P^0=\{S_1, S_2, ... S_B\}$, $J^0=J(P^0)$ while $t<=T$ and $|J^t-J^{t-1}|>\Delta J$: modify P^{t-1} using crossover and mutation: $S_1', S_2', ... S_{B'}'= \mathrm{modify}(P^{t-1}|\theta)$ order transformed sets by decreasing quality: $J(S_{i(1)}^{t}) \geq J(S_{i(2)}^{t}) \geq ... J(S_{i(B')}^{t})$ set next population to consist of best representatives: $P^t=\{S_{i(1)}', S_{i(2)}', ... S_{i(B)}'\}$ set $J^t=\max_{S\in P^t}J(S)$ $t=t+1$

 $\underline{\text{OUTPUT}}$: suboptimal set of feature sets P^t

Modifications of genetic algorithm

- Preserve best features and best feature subsets:
 - Augment P'^t with K best representatives from P^{t-1} .
 - Make mutation probability lower for good features (that frequently appear in inside representatives).
- Increase breadth of search:
 - Crossover between more than two parents
- To prevent convergence to local optimum:
 - simultaneously modify several populations and allow rare random transitions between them.

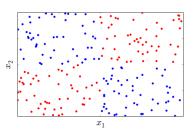
Importance in context

Individually features do not affect y:

$$p(y|x^2) = p(y), \quad p(y|x^2) = p(y)$$

but may be relevant together:

$$p(y|x^1, x^2) \neq p(y)$$



Which methods will extract features relevant in context but itrrelevant individually?