Model Genetation and Model Selection

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- Bank credit scoring as the example of the problem that requests feature generation.
- 2 Table of primitive functions.
- **3** Genetic and exhaustive generation algorithms.
- Robust feature selection.

The goal is to show how the dimensions reduction algorithms could be robust.

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Client's application & history
↓
Client's score: probability of fraud / default
↓
Accept (refuse) the application
↓
Make the agreement
↓
Client's history
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- Application
- Behavioral
- Collection

Number of the records:

- $\sim 10^4$ for long-term credits,
- $\sim 10^6$ point-of-sale credits,
- $\sim 10^7$ for churn analysis.

Type of detection

Fraud: deliquency 90+ on 3rd

$$0 \longrightarrow 30+ \longrightarrow 60+ \longrightarrow 90+ \longrightarrow 120+$$

Default: deliquency 90+ on any, but 1st

- Create the data set (the design matrix and the target vector)
- Map ordinal and nominal-scaled features to the binary ones
- Make the regression model
- Test it (multi-collinearity, stability, pooling, etc., see Basel-II)
- Determine the cut-off, according to the bank policy

- Loans of 90+ delinquency, default cases, applications
- The fraud cases are rejected
- Overall number of cases $\sim 10^4\text{--}10^6$
- Default rate \sim 8–16%
- Period of observing: no less 91 days after approval
- Number of source variables \sim 30–50
- Number records with missing data > 0, usually very small
- Number of cases with outliers > 0, $3\sigma^2$ -cutoff

Variable	Туре	Categories	
Loan currency	Nominal	3	
Applied amount	Linear		
Monthly payment	Linear		
Term of contract	Linear		
Region of the office	Nominal	7	
Day of week of scoring	Linear		
Hour of scoring	Linear		
Age	Linear		
Gender	Nominal	2	
Marital status	Nominal	4	
Education	Ordinal	5	
Number of children	Linear		
Industrial sector	Nominal	27	
Salary	Linear		
Place of birth	Nominal	94	
Car number shown	Nominal	2	

Scale conversion and grouping

• Applicant's industry, nominal scale

Nominal	Tourism	Banking	Education
John	1	0	0
Thomas	0	1	0
Sara	0	0	1

• Applicant's education, ordinal scale

Ordinal	Primary	Secondary	Higher
John	1	0	0
Thomas	1	1	0
Sara	1	1	1

Problem statement, the data

1 The data set:
$$\mathbf{x} \in \mathbb{R}^n$$
, $y \in \mathbb{R}$,

$$D = \{(\mathbf{x}_i, y_i)\};$$

2 the design matrix $X \in \mathbb{R}^{m \times n}$,

$$X = [\mathbf{x}_1^\mathsf{T}, \dots, \mathbf{x}_m^\mathsf{T}]^\mathsf{T};$$

3 dependent variable $\mathbf{y} \sim \text{Bernoulli}(\boldsymbol{\sigma})$;

$$\mathbf{y} = [y_1, \ldots, y_m]^{\mathsf{T}},$$

4 the model

$$\mathbf{y} = \boldsymbol{\sigma}(\mathbf{w}) + arepsilon, \quad \boldsymbol{\sigma}(\mathbf{w}) = rac{1}{1 + \exp(-X\mathbf{w})}$$

Since

$$p(\mathbf{y}|\mathbf{w}) = \prod_{i=1}^m p_i^{y_i} (1-p_i)^{1-y_i}.$$

the quality criterion is the log likelihood function

$$-\ln P(D|\mathbf{w}) = -\sum_{i \in \mathcal{L}} (y_i \ln \mathbf{w}^\mathsf{T} \mathbf{x}_i + (1 - y_i) \ln(1 - \mathbf{w}^\mathsf{T} \mathbf{x}_i)) = S(\mathbf{w}).$$

We must find the active set $\mathcal{A}\subset\mathcal{J}$ and the model parameters $\bm{w}_{\mathcal{A}},$ such that

$$egin{aligned} & \hat{oldsymbol{w}} = rg\min_{oldsymbol{w} \in \mathbb{R}^{|\mathcal{A}|}} S(oldsymbol{w}|\mathcal{A}, D_{\mathcal{L}}) \quad ext{and} \ & \hat{\mathcal{A}} = rg\min_{\mathcal{A} \subseteq \mathcal{J}} S(\mathcal{A}|\hat{oldsymbol{w}}, D_{\mathcal{T}}), \end{aligned}$$

where $\mathcal{I} = \mathcal{L} \sqcup \mathcal{T}$. Indexes of

- the objects, $\{1, \ldots, i, \ldots, m\} = \mathcal{I}$, split $\mathcal{I} = \mathcal{L} \sqcup \mathcal{T}$;
- the features $\{1,\ldots,j,\ldots,n\} = \mathcal{J}$, denote by \mathcal{A} the active set.

Error function for the binomial distribution hypothesis

Let the dependent variable **y** is distributed binomially:

$$\mathbf{y} \sim \mathcal{B}(f, 1-f).$$

The likelihood function

$$p(D|w,B,f) = \prod_{i\in\mathcal{I}} f_i^{y_i}(1-f_i)^{1-y_i},$$

and the error function

$$S(\mathbf{w}) = \frac{1}{2} (\mathbf{w} - \mathbf{w}_{\mathsf{MP}})^{\mathsf{T}} A(\mathbf{w} - \mathbf{w}_{\mathsf{MP}}) + \sum_{i \in \mathcal{I}} y_i \ln f_i + (1 - y_i) \ln (1 - f_i).$$

The covariance matrix B^{-1} is estimated using Newton-Raphson method iteratively:

$$\mathbf{w}_{k+1} = \mathbf{w}_k - (X^{\mathsf{T}}BX)^{-1}X^{\mathsf{T}}(\mathbf{f} - \mathbf{y}) = (X^{\mathsf{T}}BX)^{-1}X^{\mathsf{T}}B(X\mathbf{w}_k - B^{-1}(\mathbf{f} - \mathbf{y}))$$

ROC-curve as the quality criterion



We have an initial model defined by the set A; append the generated set of the features and estimate their significance.

 $\begin{array}{lll} \xi = & 1 & 2 & 3 & \dots & c, \quad c \text{ is the number of categories}, \xi \in C; \\ & \downarrow & \downarrow & \downarrow & \downarrow \\ x_j = & \gamma_1 & \gamma_2 & \gamma_3 & \dots & \gamma_c, \quad |\Gamma| \text{ is the number of groups}, \gamma \in \Gamma. \end{array}$

We must find the function

$$h: C \to \Gamma$$
.

The optimization problem is

$$(h,|\mathsf{\Gamma}|) = rg\max_{h\in H} S(w)_{\mathcal{A}\cup j}.$$

List of primitive functions

Description	In	N in	Out	N out	Comm	Param
Nominal to binary	nom	1	bin	1–4	-	Yes
Ordinal to binary	ord	1	bin	1–4	-	Yes
Linear to linear segments	lin	1	lin	1–4	-	Yes
Linear segments to binary	lin	1	bin	1–4	-	Yes
Get one column of n-matrix	bin	1–4	bin	1	-	Yes
Conjunction	bin	2–6	bin	1	Yes	-
Disjunction	bin	2–6	bin	1	Yes	-
Negate binary	bin	1	bin	1	-	-
Logarithm	lin	1	lin	1	-	-
Hyperbolic tangent sigmiod	lin	1	lin	1	-	-
Logistic sigmoid	lin	1	lin	1	-	-
Sum	lin	2–3	lin	1	Yes	-
Difference	lin	2	lin	1	No	-
Multiplication	lin,bin	2–3	lin	1	Yes	-
Division	lin	2	lin	1	No	-
Inverse	lin	1	lin	1	-	-
Polynomial transformation	lin	1	lin	1	-	Yes
Radial basis function	lin	1	lin	1	-	Yes
Monomials: $x\sqrt{x}$, etc.	lin	1	lin	1	-	-

There given

- the measured features $\Xi = \{\xi\}$,
- the expert-given primitive functions $G = \{g(\mathbf{b}, \xi)\}$,

$$g: \xi \mapsto x;$$

- the generation rules: $\mathcal{G} \supset G$, where the superposition $g_k \circ g_l \in \mathcal{G}$ w.r.t. numbers and types of the input and output arguments;
- the simplification rules: g_u is not in \mathcal{G} , if there exist a rule

$$r: g_u \mapsto g_v \in \mathcal{G}.$$

The result is

the set of the features $X = {\mathbf{x}_1, \dots, \mathbf{x}_j, \dots, \mathbf{x}_n}.$

The number of features exceeds the number of clients!

- Frac(Period of residence, Undeclared income)
- **Frac**(**Seg**(Period of employment), Term of contract)
- And(Income confirmation, Bank account)
- **Times(Seg**(Score hour), **Frac(Seg**(Period of employment), Salary))

- 1 Select random nodes in two features,
- 2 exchange the corresponded subtrees,
- S modify the function at a random node for another one from the primitive set.
- Any modification must result an admissible superposition.



1. Consider cartesian product $G \times \Xi$ of the set of non-generated variables Ξ the primitives G. Denote by a_{ι} the superpositions $g_{\nu}(\xi_{u})$ 2. Product superpositions a_{ι} no more than P times

$$a_{\iota}=g_{v}(\xi_{u}), \hspace{1em}$$
 where the index $\hspace{1em} \iota=(v-1)U+u$

and

$$x_j = \prod \underbrace{a_{\iota_1} \dots a_{\iota_p}}_{p \text{ times}}, \text{ where } \iota \in \{1, \dots, UV\}, p \in \{1, \dots, P\}.$$

In the other words

$$\xi_u \xrightarrow{g_v} g_v(\xi_u) \equiv a_\iota \xrightarrow{\Pi^{\rho}} x_j, \qquad j \in \mathcal{J}.$$

Consider the linear models as the polynomial with a monomial $a_{\iota} = g_{\nu}(\xi_{u})$

$$f(\mathbf{w},\mathbf{x}) = \sum_{\iota=1}^{UV} w_{\iota}a_{\iota} + \sum_{\iota=1}^{UV} \sum_{\kappa=1}^{UV} w_{\iota\kappa}a_{\iota}a_{\kappa} + \sum_{\iota=1}^{UV} \sum_{\kappa=1}^{UV} \sum_{\tau=1}^{UV} w_{\iota\kappa\tau}a_{\iota}a_{\kappa}a_{\tau} + \cdots$$

Let $G = \{g_1, \ldots, g_l | g = g(\mathbf{b}, \cdot, \ldots, \cdot)\}$ such that there are given

- the function $g: (\mathbf{b}, x) \mapsto x'$,
- its parameters **b** (the empty set is allowed),
- number of arguments v(g) of the function g and the order of the arguments (zero arguments is allowed),
- domain dom(g) and codomain cod(g).

Consider the model $f(\mathbf{w}, \mathbf{x})$ as a superposition

$$f(\mathbf{w}, \mathbf{x}) = (g_{i(1)} \circ \cdots \circ g_{i(K)})(\mathbf{x}), \text{ where } \mathbf{w} = [\mathbf{b}_{i(1)}^{\mathsf{T}}, \dots, \mathbf{b}_{i(K)}^{\mathsf{T}}]^{\mathsf{T}}.$$

The admissible superposition f

is the superposition, which satisfies

$$\operatorname{\mathsf{cod}}(g_{i(k+1)})\subseteq\operatorname{\mathsf{dom}}(g_{i(k)}), ext{ for any } k=1,\ldots,K-1.$$

- The vertex V_i corresponds to the primitive function g_{s(i)}.
- The number of outgoing nodes from the vertex V_i equal the number of arguments of v(g_{s(i)}).
- The order of the outgoing nodes from the vertex V_i equals the order of the arguments of g_{s(i)}.
- The leaves of the tree Γ_f corresponds to the independent variables x_i and constants; they are treated as the primitives g(Ø).



The tree for the superposition $\sin(\ln x_1) + \frac{x_2^3}{2}$

The superposition depth d(f) is

maximum depth of the tree Γ_f , number of the nodes V from the root to the most distanced leaf.

The superposition complexity C(f) is

the number of all admissible subtrees of the tree Γ_f .

$$(x) = (x) + (x)$$

Given: $G = \{g_u, h_v | u \in U, v \in V\}$ is a set of the primitive functions of one and two arguments, $\mathbf{x} = \{x_j | j \in J\}$ — independent variables.

$$\begin{array}{ll} \textbf{Step 1:} \ \mathcal{F}_1 = \left\{ f_s^{(1)} \right\} = \{ g_u(x_j) \} \cup \{ h_v(x_j, x_k) \}, \\ k \in \mathcal{J}, \ s \in \left\{ 1, \ldots, |\mathcal{U}| \cdot |\mathcal{J}| + |\mathcal{V}| \cdot |\mathcal{J}|^2 \right\}. \end{array}$$

Step k:

(Gen) Append to ${\mathcal F}$ the set

$$\mathcal{F}^{(k)} = \left\{ f_{s}^{(k)} \right\} = \left\{ g_{u} \left(f_{s'}^{(k-1)} \right) \right\} \cup \left\{ h_{v} \left(f_{s''}^{(k-1)}, f_{s'''}^{(k-1)} \right) \right\},$$

(Rem) which does not contain the superpositions, isomorphic to $g_u\left(f_s^{(k)}\right)$ and $h_v\left(f_s^{(k)}, f_{s'}^{(k)}\right)$ form the sets $\mathcal{F}^{(k)} \dots \mathcal{F}^{(1)}$.

Exhaustive search in the set of the generalized linear models

$$\mu(\mathbf{y}) = \mathbf{w}_0 + \alpha_1 \mathbf{w}_1 \mathbf{x}_1 + \alpha_2 \mathbf{w}_2 \mathbf{x}_2 + \ldots + \alpha_R \mathbf{w}_R \mathbf{x}_R$$

Here $\alpha \in \{0,1\}$ is the structural parameter.

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Find a model defined by the set $\mathcal{A}\subseteq\mathcal{J}$:

Exhaustive search in the set of the generalized linear models

$$\mu(\mathbf{y}) = \mathbf{w}_0 + \alpha_1 \mathbf{w}_1 \mathbf{x}_1 + \alpha_2 \mathbf{w}_2 \mathbf{x}_2 + \ldots + \alpha_R \mathbf{w}_R \mathbf{x}_R$$

Here $\alpha \in \{0,1\}$ is the structural parameter.

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Find a model defined by the set $\mathcal{A}\subseteq\mathcal{J}$:

Discrete genetic algorithm for feature selection (simple ver.)

- **()** There are set of binary vectors $\{\mathbf{a}_1, \ldots, \mathbf{a}_P\}$, $\mathbf{a} \in \{0, 1\}^n$;
- 2 get two vectors $\mathbf{a}_p, \mathbf{a}_q, p, q \in \{1, \dots, P\}$;
- ${f 3}$ chose random number $\nu \in \{1, \ldots, n-1\};$
- **4** split both vectors and change their parts:

$$[a_{p,1},\ldots,a_{p,\nu},a_{q,\nu+1},\ldots,a_{q,n}] \rightarrow \mathbf{a'}_p,$$

$$[a_{q,1},\ldots,a_{q,\nu},a_{p,\nu+1},\ldots,a_{p,n}] \rightarrow \mathbf{a'}_q;$$

- **5** choose random numbers $\eta_1, \ldots, \eta_Q \in \{1, \ldots, n\}$;
- **6** invert positions η_1, \ldots, η_Q of the vectors $\mathbf{a'}_p, \mathbf{a'}_q$;
- 7 repeat items 2-6 P/2 times;
- 8 evaluate the obtained models.

Repeat R times; here P, Q, R are the parameters of the algorithm and n is the number of the corresponding model features.

Discrete genetic algorithm for grouping

- **1** There are set of binary vectors $\{\mathbf{a}_1, \ldots, \mathbf{a}_P\}$, $\mathbf{a} \in \{1, \ldots, k\}^n$;
- 2 get two vectors $\mathbf{a}_p, \mathbf{a}_q, p, q \in \{1, \dots, P\}$;
- 3 chose random number $\nu \in \{1, \ldots, n-1\};$
- **4** split both vectors and change their parts:

$$[a_{p,1},\ldots,a_{p,\nu},a_{q,\nu+1},\ldots,a_{q,n}]
ightarrow \mathbf{a'}_p,$$

$$[a_{q,1},\ldots,a_{q,\nu},a_{p,\nu+1},\ldots,a_{p,n}] \rightarrow \mathbf{a'}_q;$$

- **6** choose random numbers $\eta_1, \ldots, \eta_Q \in \{1, \ldots, n\}$;
- **(**) replace values in positions η_1, \ldots, η_Q of the vectors $\mathbf{a'}_p, \mathbf{a'}_q$ for random values from $\{1, \ldots, k\}$;
- 7 repeat items 2-6 P/2 times;
- 8 evaluate the obtained models.

Repeat R times; here P, Q, R are the parameters of the algorithm and k is desired number of categories.

What is the optimal feature set?



Multicorrelation and Variance Inflation Factor

- Extract *j*-th column from the design matrix *X*,
- make regression $X_{\mathcal{J}\setminus\{j\}}$ on $\mathbf{y} \equiv X_{\{j\}}$,
- for the feature number *j*

$$\mathsf{VIF}_j = \frac{1}{1 - R_j^2}$$

where the determination coefficient

$$R_j^2 = 1 - rac{\|\mathbf{x}_j - \mathbf{f}(\mathbf{x}_1, \dots, \mathbf{x}_{j-1}, \mathbf{x}_{j+1}, \dots, \mathbf{x}_n)\|^2}{\|\mathbf{x}_j - \tilde{\mathbf{x}}_j\|^2};$$

here $\tilde{\mathbf{x}}_j$ is average vector for \mathbf{x}_j .

Make singular values decomposition of the design matrix X

$$X = U\Lambda V^{\mathsf{T}},$$

where $UU^{\mathsf{T}} = I_m$, $V^{\mathsf{T}}V = I_n$, a Λ is the diagonal matrix with elements $\lambda_1 > \lambda_2 > \ldots > \lambda_r$, r is the rank of X, in our case r = n. The matrix $X^{\mathsf{T}}X$ is considered as the estimation of the correlation matrix.

$$X^{\mathsf{T}}X = V\Lambda^{\mathsf{T}}U^{\mathsf{T}}U\Lambda V^{\mathsf{T}} = V\Lambda^{2}V^{\mathsf{T}},$$
$$X^{\mathsf{T}}XV = V\Lambda^{2}.$$

Find the conditional indexes

$$\eta_j = rac{\lambda_{\max}}{\lambda_j}.$$

Obtain the variances of the parameters w

$$Var(\mathbf{w}) = \sigma^2 (X^T X)^{-1} = \sigma^2 (V^T)^{-1} \Lambda^{-2} V^{-1} = \sigma^2 V \Lambda^{-2} V^T,$$

where σ^2 is the variance of the residuals. The variance of w_j is *j*-th diagonal element of $Var(\mathbf{w})$. Match the conditional index η_i and corresponding coefficients q_{ij}

$$\sigma^{-2}\mathbf{var}(w_i) = \sum_{j=1}^n \frac{v_{ij}^2}{\lambda_j^2} = (q_{i1}+q_{i2}+\ldots+q_{in}),$$

Conditional index	$var(w_1)$	$var(w_2)$		$var(w_n)$
η_1	q_{11}	q_{21}		q_{n1}
η_2	q_{12}	q 22		q_{n2}
:	÷	÷	•••	÷
η_n	q_{1n}	q_{2n}		q_{nn}

Таблица: The decomposition of **var** (w_i)

- the bigger q_{ij} the bigger impact of *j*-th parameter into the variance of *i*-th parameter;
- the bigger values of η_j mean there is a dependency between the features;
- the *i*-th feature in involved in the multicorrelation if η_j is larger and q_{ij} exceeds a given threshold.

Add stage: Add the feature, which brings minimum to the error function $S(\mathbf{w})$

$$j^* = \arg \min_{j \in \mathcal{J} \setminus \mathcal{A}_{k-1}} S(\mathbf{w} | \mathcal{D}_{\mathcal{L}}, f_{\mathcal{A}_{k-1} \cup \{j\}}).$$

$$\mathcal{A}_k = \mathcal{A}_{k-1} \cup \{j^*\}$$

until $S(f_{\mathcal{A}_k}|\mathbf{w}^*, \mathcal{D})$ exceeds its minimum value on this stage but no more than a given ΔS_{Add} .

Del stage: Dell the feature according to the Belsley method:

$$i^* = \sum_{g=1}^t \left[\eta_g^2 > \eta_t \right]$$

$$j^* = \arg \max_{j \in \mathcal{A}_{k-1}} \sum_{g=t-i^*+1}^t q_g^j$$

 $\mathcal{A}_k = \mathcal{A}_{k-1} igcar{j^*}{j^*}$

until $S(f_{\mathcal{A}_k} | \mathbf{w}^*, \mathcal{D})$ exceeds its minimum value on this stage but no more than a given ΔS_{Del} . Repeat Add and Del stages until the value of the error function $S(f_{\mathcal{A}_k} | \mathbf{w}^*, \mathcal{D})$ became stable. The plot shows how the error function $S(\mathbf{w})$ varies during the steps. The control sample set C is used.



For given feature set $\mathcal{A} \in \mathcal{J}$ perform N-fold cross-validation procedure: $\mathcal{I} = \mathcal{L} \sqcup \mathcal{C}$. Treat the obtained values of the error function $S(\mathbf{w}|\mathcal{C})$ as realization of corresponding random variable. Estimate the expectation and variance:

$$ES = \frac{1}{N} \sum_{i=1}^{N} S_i,$$

$$DS = \frac{1}{N} \sum_{i=1}^{N} (S_i - ES)^2,$$

where N — number of folds (splits) and S_i is computed on the *i*-th split.



Red dots show the minimum expectation *ES* for the corresponding number of features |A|.

Algorithms	$S_{\mathcal{L}}$	$S_{\mathcal{C}}$	AIC	BIC	Cp	$\lg \kappa$	k
Genetic	0.073	0.107	-1152	-1072	337	13	26
GMDH	0.146	0.194	-1076	-1045	745	6	10
Stepwise	0.128	0.154	-1092	-1055	644	7	12
Ridge	0.111	0.146	-819	-330	832	33	160
Lasso	0.121	0.147	-1089	-1034	611	5	18
Stage	0.071	0.096	-1157	-1077	324	9	26
FOS	0.106	0.135	-1105	-1044	527	7	20
LARS	0.098	0.095	-1102	-1017	492	7	28
Evidence	0.097	0.123	-1118	-1054	469	5	21

See

mvr.svn.sourceforge.net/viewvc/mvr/lectures/Strijov2012IAM.METU.Part3.pdf

or for short

bit.ly/K3i8zJ

The next

- 1 model comparison,
- multimodelling.