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Logistic Regression

Logistic Regression

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Example: Brand Preference for Orange Juice

- ✓We would like to predict what customers prefer to buy: Citrus Hill or Minute Maid orange juice?
- ✓The Y (Purchase) variable is <u>categorical</u>: 0 or 1
- ✓The X (LoyalCH) variable is a numerical value (between 0 and 1) which specifies the how much the customers are loyal to the Citrus Hill (CH) orange juice
- ✓Can we use Linear Regression when Y is categorical?

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Example: Credit Card Default Data

- ✓We would like to be able to predict customers that are likely to default
- ✓Possible X variables are:
  - ✓Annual Income
  - ✓Monthly credit card balance
- ✓The Y variable (Default) is <u>categorical</u>: Yes or No
- ✓How do we check the relationship between Y and X?

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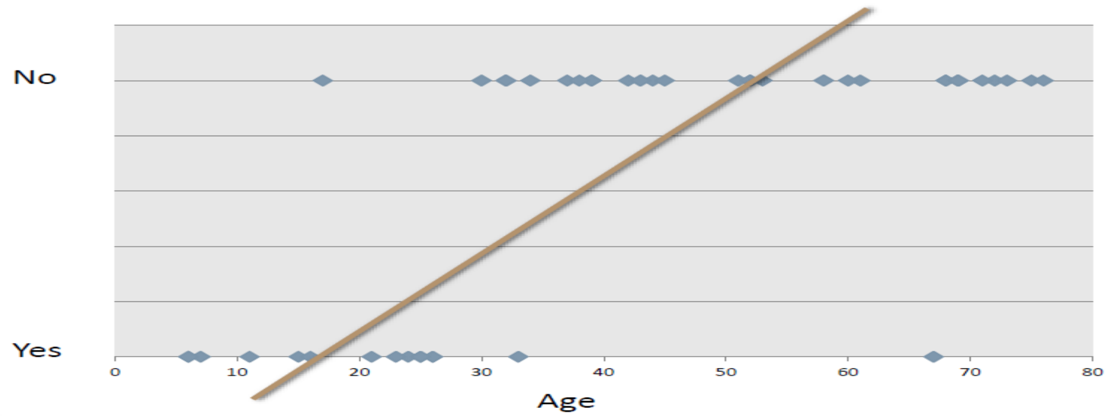
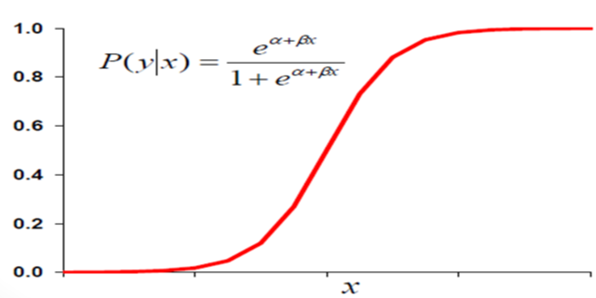
Why Not Linear?



Logistic Regression

- ✓We want a model that predicts probabilities between 0 and 1, that is, S-shaped.
- ✓There are lots of S-shaped curves. We use the logistic model:
- ✓Probability = 1/[1+exp(B0+B1x) or log[p/(1-p)] =B0+B1x
- ✓The function on left, log[p/1-p], is called the logistic function



Logistic Regression

- ✓ Logistic regression models the logit of the outcome
  =Natural logarithm of the odds of the outcome
  =ln(probability of the outcome(p)/probability of not having the outcome(1-p)

$$\ln\left(\frac{P}{1-P}\right) = \alpha + \beta_1 x_1 + \beta_2 x_2 + \dots \beta_i x_i$$

- ✓ B= log odds ratio associated with predictors
- ✓ Exp(B) = Odds Ratio.
- ✓ The betas themselves are log-odds ratios. Negative values indicate a negative relationship between the probability of "success" and the independent variable; positive values indicate a positive relationship
- ✓ Increase in log-odds for a one unit increase in x with all the other x's constant

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Logistic Regression

Model equation	$P_i = \text{Prob}(Y_i=0) = \frac{e^{L_i}}{(1+e^{L_i})}$ Where, $L_i = a+b_1X_{1i}+b_2X_{2i}+\dots+b_pX_{pi}$
Assumption	Y_i and Y_j independent for all $i \neq j$
Parameters to be Estimated	$a, b_1, b_2, \dots, b_p$
Method of Estimation	Maximum Likelihood

- ✓ Maximum Likelihood Estimator:
  - ✓ Starts with arbitrary values of the regression coefficients and constructs an initial model for predicting the observed data.
  - ✓ Then evaluates errors in such prediction and changes the regression coefficients so as make the likelihood of the observed data greater under the new model
  - ✓ Repeats until the model, converges, meaning the differences between the newest model and the previous model are trivial.
- ✓ The idea is that you "find report as statistics" the parameters that most likely to have produced your data

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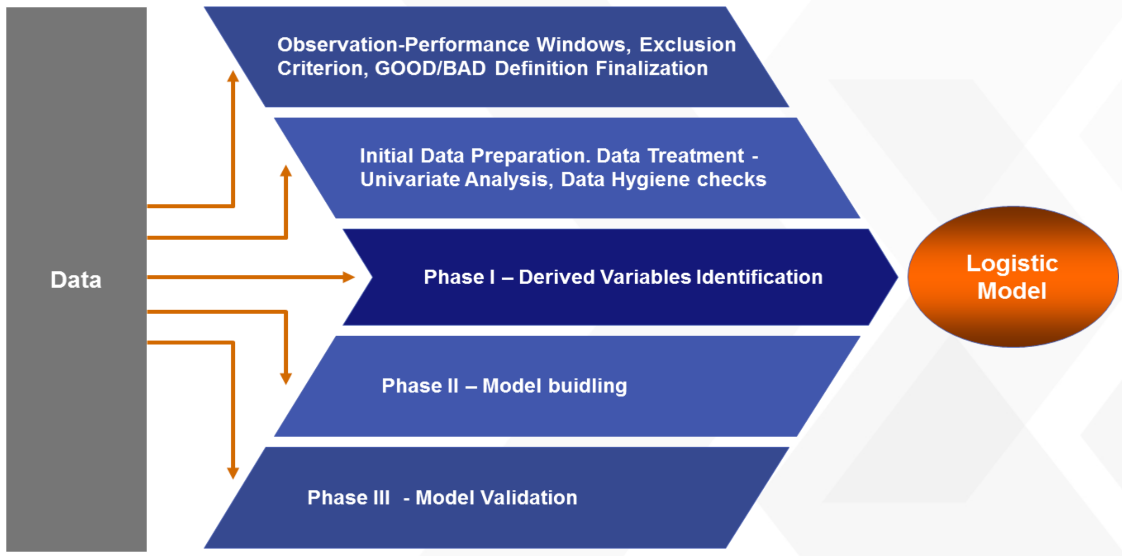
Modeling Methodology – Logistic Model Development



Target variable(GOOD/BAD) Definition Finalization

Obs-Perf Windows

Observation window is where the Xs (independent vars) come from. Performance window is where the Y (dependent var) comes from.

Observation Window — Mar'04 — *Xs* — Mar'05

Performance Window — May05 — *Y* — Oct'05

Exclusion Criterion

Observations from the population that need to be excluded. Necessary to weed out data bias and to ensure model utility.

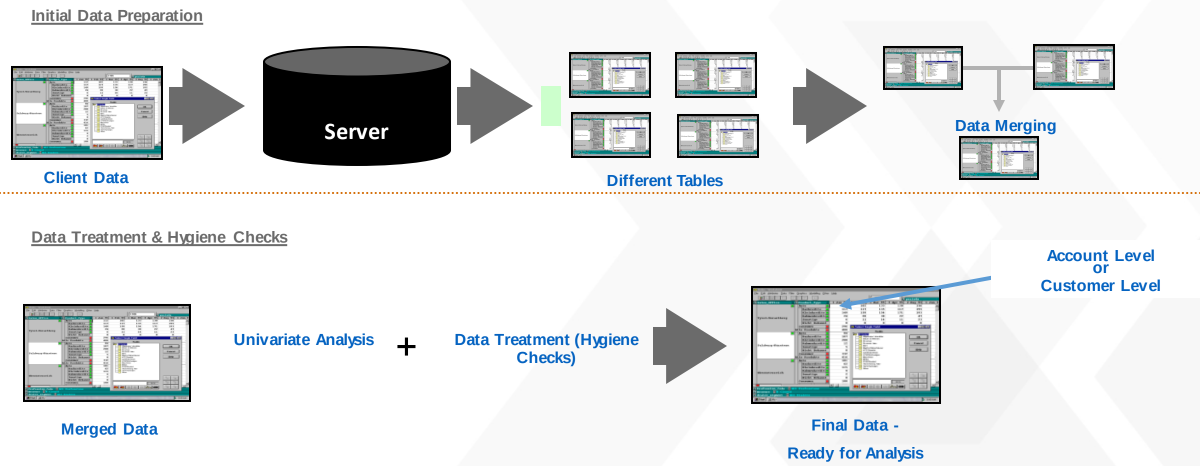
e.g. – Inactive accounts at observation point to be excluded, Accounts charged off within performance window to be excluded.

GOOD/BAD Definition

Definition of Y. How do we define a Good/Bad?

e.g. – Bad definition of 90+ ever + major derog (that includes Bankrupt, Charge offs, Repossessions, but excluding Fraud) within the Performance window. Goods are defined as anything other than a Bad.

Initial Data Preparation. Data Treatment -Univariate Analysis, Data Hygiene checks



Phase I – Derived Variable Identification

Raw variables could of few types – Demographic, Product Related, Behavioral, etc.

From the Raw variables (populated in the dataset) – New variables are *Derived*.

Why Derived Variables?

- ✓ **New business relevant variables could be created by certain combinations of raw variables. *E.g. Utilization is a derived variables that is created from balance & credit limit.***
- ✓ **In certain cases aggregation variables make more sense rather than stand-alone ones. *E.g. Average payments in last 3 months, Maximum delinquency level in last 6 months…***
- ✓ **New variables creation ensures that we capture all the nuances of data.**

Phase II(a) – Fine classing

- ✓Fine classing is a process that allows us to determine which characteristics are worthy of consideration in the development of the model.
- ✓Each characteristic is investigated to determine the underlying good/bad trends in the data at attribute level for discrete data and in small bands for continuous data.
- ✓This process brings out the information values of the variables telling us ability of the variable to separate the goods and bads.

Log Odds (Weight of Evidence):

Log of Odds represents the proportion of Goods vis-à-vis proportion of Bads in a particular attribute. ***Weight of Evidence = ln(g/b)***

Information Value:

Information Value (IV) is a measurement of how well the characteristic can differentiate between 'good' & 'bad' and whether that characteristic should be considered for modeling.

Phase II(a) – Fine classing (contd…)

Information Value:

Let g and b denote the proportion of goods and the proportion of bads for a given attribute. The following descriptive statistics are used to describe the Information Value (IV) of a particular attribute.

Information Value = [(g – b) ln(g/b)]

IV <0.03 Not Predictive **– do not consider for modeling**
IV 0.03 – 0.1 Predictive **– consider for modeling**
IV >0.1 Very Predictive **– use in modeling**

Phase II(a) - Fine classing output

TABLE=TOTAL SAMPLE

acct_age	TOTAL ACCTS	ROW % TOTAL	NO. GOODS	ROW % GOODS	NO. BADS	ROW % BADS	ODDS	LOG(LN) ODDS	MARG. INFO VALUE	ROW CHI-SQUARE
Total	17204	100.00	15255	100.00	1949	100.00	1.00	0.00	0.00	0

TABLE=MARGINAL CLASSINGS

acct_age	TOTAL ACCTS	ROW % TOTAL	NO. GOODS	ROW % GOODS	NO. BADS	ROW % BADS	ODDS	LOG(LN) ODDS	MARG. INFO VALUE	ROW CHI-SQUARE
2 - 9	2065	12.00	1686	11.05	379	19.45	0.57	-0.56	0.05	101.442
10 - 16	1934	11.24	1662	10.89	272	13.96	0.78	-0.25	0.01	14.405
17 - 23	1786	10.38	1537	10.08	249	12.78	0.79	-0.24	0.01	12.139
24 - 34	1989	11.56	1743	11.43	246	12.62	0.91	-0.09	0.00	2.139
35 - 46	1919	11.15	1697	11.12	222	11.39	0.98	-0.02	0.00	0.110
47 - 66	1729	10.05	1599	10.48	130	6.67	1.57	0.45	0.02	24.985
67 - 86	1768	10.28	1675	10.98	93	4.77	2.30	0.83	0.05	64.817
87 - 121	1758	10.22	1627	10.67	131	6.72	1.59	0.46	0.02	26.307
122 - 177	1744	10.14	1581	10.36	163	8.36	1.24	0.22	0.00	6.823
178 - 422	512	2.98	448	2.94	64	3.28	0.90	-0.11	0.00	0.699

INFORMATION VALUE = 0.153

TOTAL CHI-SQUARE VALUE = 253.866 WITH 9 DF
Acct_age IS SIGNIFICANT AT THE 0 % LEVEL

Phase II(b) - Coarseclassing

- ✓Coarseclassing is the grouping together of attributes of characteristics with similar performance (log odds) in the fineclassing output into coarser groups.
- ✓This allows statistically valid groupings to be modeled and allows for fluctuations within characteristics to be smoothed out. These coarse groupings are called 'dummy variables'.
- ✓In continuous variables dummies can be used to smooth a trend within a variable that deviates from the trend.

Important DOs

- Try to make classes with around 5% of the population. Classes with less than 5% might not be a true picture of the data distribution and might lead to model instability.
- Business inputs from the SMEs in the markets are essential for coarseclassing process as fluctuations in variables can be better explained and classes make business sense.

Phase II(b): Dummy creation & correlation

Dummy Creation

✓Fineclassing & Coarseclassing procedure helps in identifying the dummies to be created.

✓Dummying is the process of assigning a binary outcome to each group of attributes in each predictive characteristic.

Dummy Correlation Check

✓Once dummies are created – we need to run the correlation check on these dummies.

✓This is done to take care of any significant multi-collinearity effects that may exist among the dummies.

✓Correlation coefficient cut-off for dummy correlation is set at 0.5

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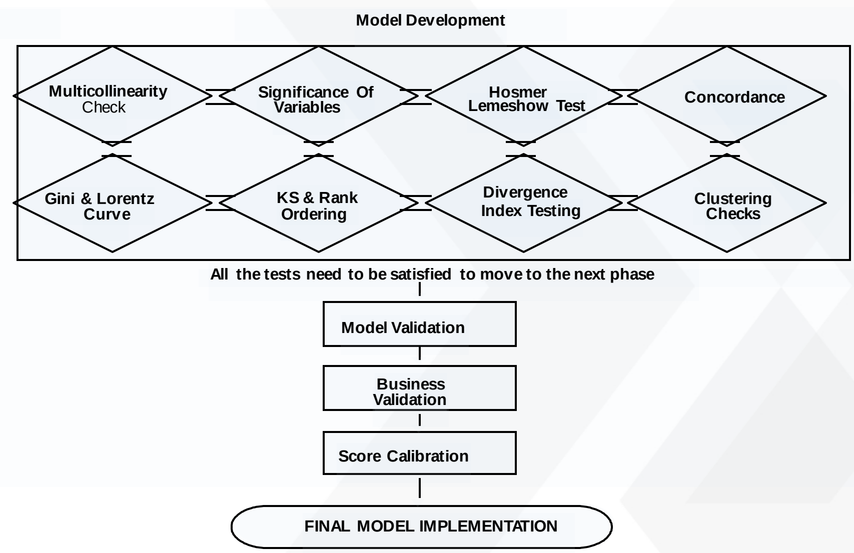
Phase II(c): Model Building



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Multicollinearity

What is Multicollinearity?

Multicollinearity is a phenomenon when there is a linear relationship between a set of variables.

Why is Multicollinearity a problem ?

Multicollinearity affects the parameter estimates making them unreliable.

How to detect Multicollinearity?

Variance Inflation Factor (VIF) = $1/(1-R^2)$

How to remove Multicollinearity ?

- **Look into Variance proportions table for the row with highest CI**
- **Identify variables with highest factor loadings in the row**
- **Drop the variable which is least significant**

VIF>1.75 => Multicollinearity

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Variable Significance

Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	0.6010	0.1423	17.8279	<.0001
d1_cons_cd_grt_1	1	1.0016	0.1326	57.0378	<.0001
d3_max_cdlevel	1	-1.0768	0.2338	21.2164	<.0001
d1_Payment_method	1	1.6529	0.1449	130.1012	<.0001
d3_OTB_jun04	1	0.6993	0.1176	35.3416	<.0001
d2_crlimit_may04	1	0.3627	0.1156	9.8523	0.0017
d2_avg_pay_bal	1	0.4720	0.1084	18.9700	<.0001
d2_max_payment	1	0.2424	0.1110	4.7691	0.0290
d4_age	1	0.4141	0.1094	14.3331	0.0002

Chi – Square value for each explanatory variable – the chi-square value indicates the level of significance, i.e – the impact of independent (explanatory) variable on the dependent variable.

The p-value cut-off should be decided in discussion with the business. Ideally the p-value<0.0001. However in case of smaller population size p-value could be <0.05 or p-value<0.1.

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Hosmer Lemeshow

Null Hypothesis: The expected values from the model = The observed values from the population

Alternative Hypothesis: The expected values from the model not equal to The observed values from the population

- ✓Hosmer Lemeshow Goodness of Fit test involves dividing the data into approximately 10 groups of roughly equal size based on the percentiles of the estimated probabilities.
- ✓The discrepancies between the observed and expected number of observations in these groups are summarized by the Pearson chi-square statistic, which is then compared to chi-square distribution with *t* degrees of freedom, where *t* is the number of groups minus 2.

Partition for the Hosmer and Lemeshow Test

Group	Total	Good = 1 Observed	Good = 1 Expected	Good = 0 Observed	Good = 0 Expected
1	924	756	753.27	168	170.73
2	1002	918	920.21	84	81.79
3	1058	997	1002.64	61	55.36
4	981	947	945.00	34	36.00
5	884	859	860.25	25	23.75
6	923	905	904.36	18	18.64
7	931	921	919.35	10	11.65
8	786	778	779.30	8	6.70
9	734	731	729.17	3	4.83
10	953	950	948.44	3	4.56

Hosmer and Lemeshow Goodness-of-Fit Test

Chi-Square	DF	Pr > ChiSq
2.6543	8	0.9541

For a robust model – we need to *accept* the null hypothesis. Hence, *Higher the p-value better the model fit*.

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Concordance

Association of Predicted Probabilities and Observed Responses

Percent Concordant	79.0
Percent Discordant	19.1
Percent Tied	1.9
Pairs	3627468

- ✓Concordance is used to assess how well scorecards are separating the good and bad accounts in the development sample.
- ✓The higher is the concordance, the larger is the separation of scores between good and bad accounts.
- ✓The concordance ratio is a non-negative number, which theoretically may lie between 0 and 1.

Concordance Determination:

Among all pairs formed from 0 & 1 observations from the dependent variable, the % of pairs where the probability assigned to an observation with value 1 for the dependent variable is greater than that assigned to an observation with value 0.

Percentage of concordant pairs should be *at least greater than 60*.

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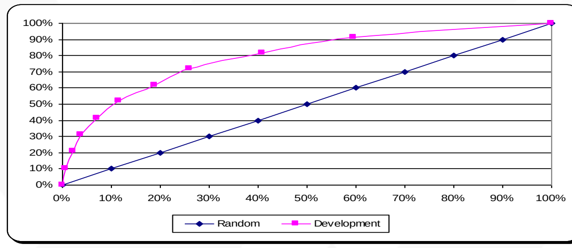
Lorenz Curve, Gini, KS

Lorenz curve indicates the lift provided by the model over random selection.

Gini coefficient represents the area covered under the Lorenz curve. A good model would have a Gini coefficient between 0.2 - 0.35



Lorenz Curve

Kolmogorov-Smirnoff (KS) statistic is defined as the absolute difference of cumulative % of Goods and cumulative % of Bads.

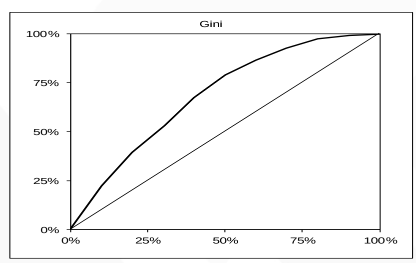
KS statistic value *should not be less than 20*. Higher the KS – better is the model.

Lorenz Curve, Gini, KS

Template for calculating Gini and KS coefficient for measuring discriminatory power of a rating

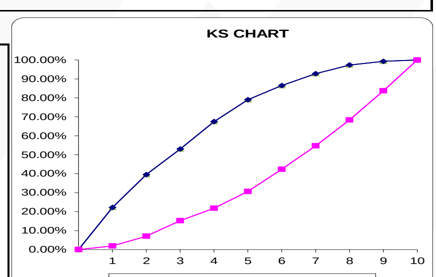
GINI-coefficient:	0.62
KS	0.48

Rating class	# of customers Good	Bad	Total	Bad rate	Accumulated pop. Bad	Good	Total	GINI area	KS
					0.00%	0.00%	0.00%		
1	12	92	104	88.46%	22.17%	1.93%	10.02%	1.11%	20.24%
2	32	72	104	69.23%	39.52%	7.06%	20.04%	3.09%	32.46%
3	51	56	107	52.34%	53.01%	15.25%	30.35%	4.77%	37.76%
4	41	60	101	59.41%	67.47%	21.83%	40.08%	5.86%	45.64%
5	55	48	103	46.60%	79.04%	30.66%	50.00%	7.27%	48.38%
6	73	31	104	29.81%	86.51%	42.38%	60.02%	8.29%	44.13%
7	77	26	103	25.24%	92.77%	54.74%	69.94%	8.89%	38.04%
8	85	19	104	18.27%	97.35%	68.38%	79.96%	9.52%	28.97%
9	96	8	104	7.69%	99.28%	83.79%	89.98%	9.85%	15.49%
10	101	3	104	2.88%	100.00%	100.00%	100.00%	9.98%	0.00%
Total	623	415	1,038	39.98%				68.65%	48.38%



Important: Rating Classes need to go from worst to best; in the example "1" is the worst rating class

In statistics, the Kolmogorov–Smirnov test (K–S test) is a nonparametric test for the equality of continuous, one-dimensional probability distributions that can be used to compare a sample with a reference probability distribution (one-sample K–S test), or to compare two samples (two-sample K–S test). The two-sample KS test is one of the most useful and general nonparametric methods for comparing two samples, as it is sensitive to differences in both location and shape of the empirical cumulative distribution functions of the two samples.



Rank Ordering

Rank Ordering is a test to validate whether the model is able to differentiate the Goods from the Bads across the population breakup.

- ✓The population is divided into the deciles in the descending order of predicted values (Good/Bad as the case might be).
- ✓A model that rank orders, predicts the highest number of Goods in the first decile and then goes progressively down.

Models have to rank order completely across development as well as Validation samples.

decile	Bad	Good
1	3	915
2	6	912
3	7	910
4	13	905
5	19	898
6	30	888
7	30	888
8	61	856
9	78	840
10	167	750
Total	414	8762

ranking	sat_rank
SATISFACTORY	all

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Divergence Index Test

Good	_FREQ_	ave	variance		Ho: Bad Score => Good Score	p- value
	41338	752.67	4070.44		Null Hypothesis is Rejected	
0	856	654.55	10578.1225	DI	T - Statistic	
1	40482	754.75	3725.8816	**1.4038**	**-28.398**	**<0.0001**

Divergence Index is an indicator of how well the means of the goods and bads are differentiated.

Null Hypothesis: The means of Good accounts / population = The means of Bad accounts / population

Alternative Hypothesis: The means of Good accounts / population is not equal to the means of Bad accounts / population

For a robust model – we need to *reject* the null hypothesis. Hence, *lower the p-value better the model*.

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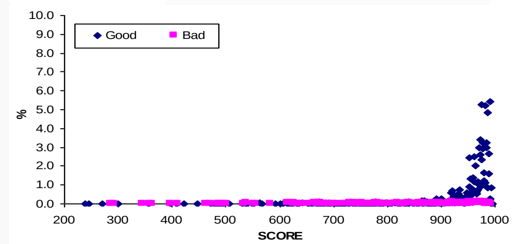
Clustering check

The concept behind Clustering check is that a good model should be sensitive enough to differentiate between 2 Good/Bad accounts.

i.e the model should be able to identify differences between seemingly same type of accounts/sample observations and assign them different scores.



A good model should not have significant clustering of the population at any particular score and the population must be well scattered across.

Ideally the clustering should be as low as possible. A thumb-rule would be to contain the clustering so that it is *within 5-6%*.

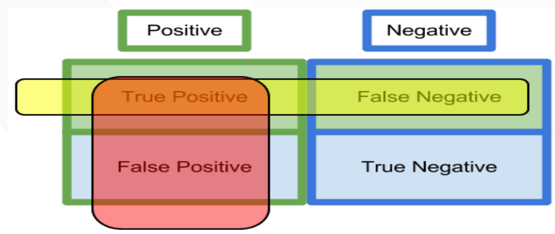
Other Metrics

Coefficient's signs & stability	**Coefficients signs** must match in the models run on both the samples. **Stability** (significance and parameter estimates should be within 95% Confidence limits of parameter estimates) in the models run on both the samples.
Divergence Index	$D = \frac{x_1 - x_2}{s}$ is a commonly employed measure of the separation achieved by a model. It is related to a t-distribution (multiply by (G+B) ½) if the two population variances are equal. This measure how well the means of the respondents and non-respondents are differentiated. A t statistic > |6| shows a high level of differentiation.
Somers' D	It is used to determine the strength and direction of relation between pairs of variables. Its values range from -1.0 (all pairs disagree) to 1.0 (all pairs agree). It is defined as $(n_c - n_d)/t$ where n_c is the number of pairs that are concordant, n_d the number of pairs that are discordant, and t is the number of total number of pairs with different responses.
Gamma	The Goodman-Kruskal Gamma method does not penalize for ties on either variable. Its values range from -1.0 (no association) to 1.0 (perfect association). Because it does not penalize for ties, its value will generally be greater than the values for Somer's D.
Kendall's Tau-a	It is a modification of Somer's D that takes into the account the difference between the number of possible paired observations and the number of paired observations with a different response. It is defined to be the ratio of the difference between the number of concordant pairs and the number of discordant pairs to the number of possible pairs $(2(n_c - n_d)/(N(N-1))$. Usually Tau-a is much smaller than Somer's D since there would be many paired observations with the same response.

Confusion Metrics

CONFUSION MATRIX

	p' (Predicted)	n' (Predicted)
p (Actual)	True Positive	False Negative
n (Actual)	False Positive	True Negative



sensitivity = recall = tp / (tp + fn)
specificity = tn / (tn + fp)
precision = tp / (tp + fp)

Sensitivity/recall – how good a test is at detecting the positives.
Specificity – how good a test is at avoiding false alarms.
Precision – how many of the positively classified were relevant.

Receiver Operating Characteristic Curve: Plot of TPR(Sensitivity) vs FPR(1- Specificity)

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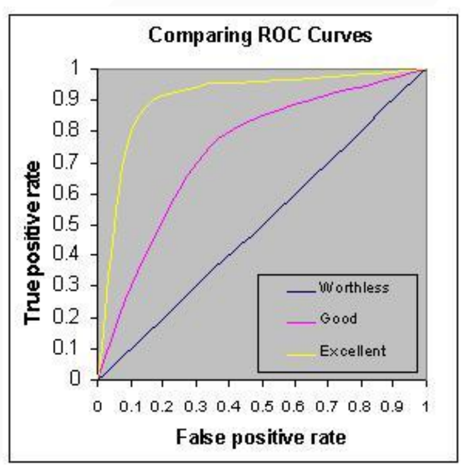
ROC Curve

- *ROC* = *Receiver Operating Characteristic*
- Started in electronic signal detection theory (1940s - 1950s)
- Plot of TPR(Sensitivity) vs FPR(1- Specificity)
- Can be used in machine learning applications to assess classifiers



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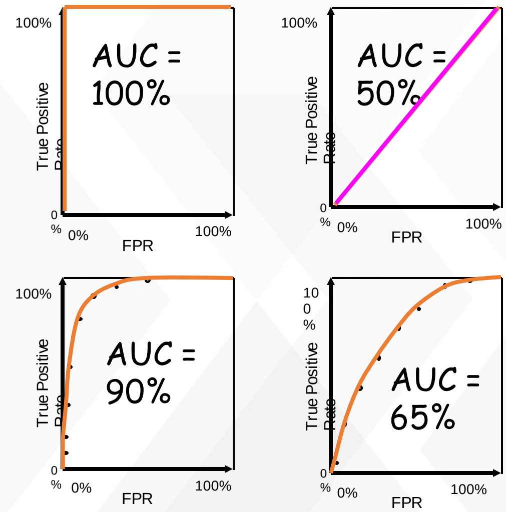
ROC Curve - AUC

- *Overall measure* of model performance
- In classification,
- AUC = Concordance+0.5*Ties

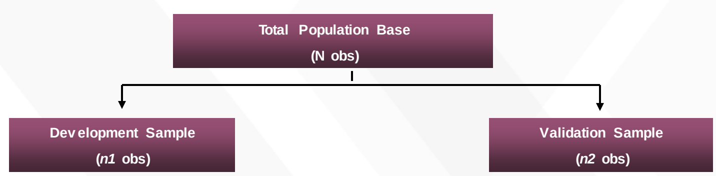


Phase III: Model-Validation

Validation could be done in 2 ways:

✓ **Validation Re-run**

✓ **Scoring the Validation sample**



Validation Re-run

- ➢ Rerun the model on the validation sample.
- ➢ Check the chi-sq values and level of significances and p-values for each explanatory variable.
- ➢ The p-values should not change significantly from the development sample to the validation sample.
- ➢ Check the signs of the parameter estimates. They should not change from development sample to the validation sample.
- ➢ Check rank ordering. Both Development and validation samples should rank order.

Validation sample scoring

- ➢ Score the validation sample using the parameter estimates obtained from the scorecard developed on the development sample.
- ➢ Check rank ordering. Both development and validation samples should rank order.

Model Evaluation

- Model validity refers to the stability and reasonableness of the logistic regression coefficients.
- The plausibility and usability of the fitted logistic regression function.
- The ability to generalize inferences drawn from the analysis.
- For model validation following statistical measures can be compared between the development and validation sample.
  - Coefficient sign's & Stability
  - Concordance/Somer's D
  - Decile Analysis/Rank Ordering
  - ROC Curve/Gini Coefficient
  - Kolmogorov–Smirnov test (K–S test)
  - Classification Matrix

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Steps to check stability of model between training and validation

Check	Test	Results
• Predictive power	Overall Gini	The overall Gini measure is 70%*, which is very good.
• Consistency in rank-ordering	Visual assessment of bar charts	Model rank-orders response consistently.
• Variable validity	Statistical significance of variables Plausibility of coefficient signs	All model variables are significant. Direction of all variables' effects plausible.
• Model stability	Out-of-sample stability of coefficients Multicollinearity tests (correlation and VIF)	New data would yield quasi identical model. No dangerous levels of correlated variables found.
• Model calibration	Correlation with actual bad rate	High correlation between predicted and actual bad rate

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Appendix

Rare events description and example

Rare Events:

- Certain group or event happens very rarely and so its incidence in the data is very sparse and effort needs to be made to make sure they are well represented in the sample.
- Use **stratified sampling** method for rare events.
- Keep all (or most) of the observations for the rare events but sample the non-rare events more heavily.
- Calculation adjustment needs to be done to determine actual ratio between the rare and other events .
- Examples- Fraud, email campaigns , churn etc

Sampling Techniques when there is Low Response Rate (rare events)

Biased Sampling

Biased sampling is a non-random sampling procedure that incorporates a systematic bias/error in sample selection. It generates a statistical sample of a population where some members of the population are more likely to be included than others. This would imply that some members are underrepresented or overrepresented relative to others in the population.

Methodology

1.Create two datasets, one having events and other having non-events data.
2. All the events are used in modeling.
3. From non-events base data, pick up that many observations randomly such that event rate based on all events and random selection of non-events data be equal to desired event rate.
Post the model is developed, the bias is adjusted using a correction factor (ratio of log of odds of sample to log of odds of population).

Assigning Weights

ML estimator for logistic regression gives equal weight to type 1 and type 2 error
If only a few percent of the sample are response (mirroring the population), estimator focuses on predicting "non-response"
However, biggest economic impact (loss) is caused by response accounts
By changing weight to 50:50, model tries to better predict "response", and economic performance of model can be improved

Methodology

1.Calculate the response percentage in the overall population
2. Then compute(decide) the weights such that the sample would have the response and non-response in the same proportions
3. Create weight variable as follows
multiplier=(**100**-response-percent)/response-percent;
if response_flag =1 then weight.= multiplier;
else weight.=1;

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Bias adjustment when we use Biased Sampling

If the event rate is as low as 0.05% then the event rate is increased to about 5% (desired event rate).
How would we increase: by keeping all the events data and part of non-events is randomly picked from non-events such that new event rate is about 5%.

Whenever a bias sample is used in the model development, it's suggested to carry out 'Bootstrapping' and 'Jacknifing' at the time of model validation. These two practices would help to check if there is any bias in the parameter estimation.

p_s is the sample response rate (e.g., 5%); p_p is the actual population response rate (historical or, better, predicted future).

Logit score

$$Y = c + \beta_1 X_1 + \beta_2 X_2 + \ldots$$

Logistic score (Biased)

$$P = \frac{1}{1 + e^{-Y}} = \frac{e^{Y}}{e^{Y} + 1}$$

Calibrated Score

$$P^* = \frac{P * P_p * (1-P_s)}{P * P_p * (1-P_s) + (1-P) * (1-P_p) * P_s}$$

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Calibration adjustment when we use Biased Sampling

Logit score

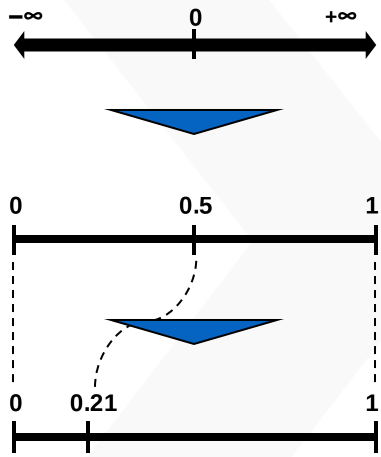
$$Y = c + \beta_1 X_1 + \beta_2 X_2 + \dots$$

Logistic score

$$P = \frac{1}{1 + e^{-Y}} = \frac{e^{Y}}{e^{Y} + 1}$$

Calibrated Score

$$P^* = \frac{\frac{p_p}{p_s} P}{\frac{p_p}{p_s} P + \frac{1 - p_p}{1 - p_s} (1 - P)}$$



- Logit score is unbounded
- For the average case (X value is sample mean for each X), Y is typically 0*
- If "response" was coded as 1, then higher Y is higher probability of response

- Logistic score is bounded between 0 and 1
- P = 0.5 typically corresponds to the sample response rate*
- If "response" was coded as 1, then higher P is higher probability of response

- P* is bounded between 0 and 1 (i.e., 0% and 100%)
- However, numerical value now corresponds to the estimated Probabilities

* Assuming model was built on a sample with 50/50 split between response and non-response cases

** p_s is the sample response rate (e.g., 50%); p_p is the actual population response rate (historical or, better, predicted future).

Boot Strapping & Jackknifing – Validation

Boot Strapping

Bootstrapping is the practice of estimating properties of an estimator (such as its variance) by measuring those properties when sampling from an approximating distribution. One standard choice for an approximating distribution is the empirical distribution of the observed data. In the case where a set of observations can be assumed to be from an independent and identically distributed population, this can be implemented by constructing a number of resamples of the observed dataset (and of equal size to the observed dataset), each of which is obtained by random sampling with replacement from the original dataset.

Jackknifing

Jackknifing, which is similar to bootstrapping, is used in statistical inferencing to estimate the bias and standard error in a statistic, when a random sample of observations is used to calculate it. The basic idea behind the jackknife estimator lies in systematically recomputing the statistic estimate leaving out one observation at a time from the sample set. From this new set of "observations" for the statistic an estimate for the bias can be calculated and an estimate for the variance of the statistic.

SOURCE: Wikipedia Images

Q&A

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