

Step 1:
Launch GenIQ.
Click "Start a New Project."

GenIQ

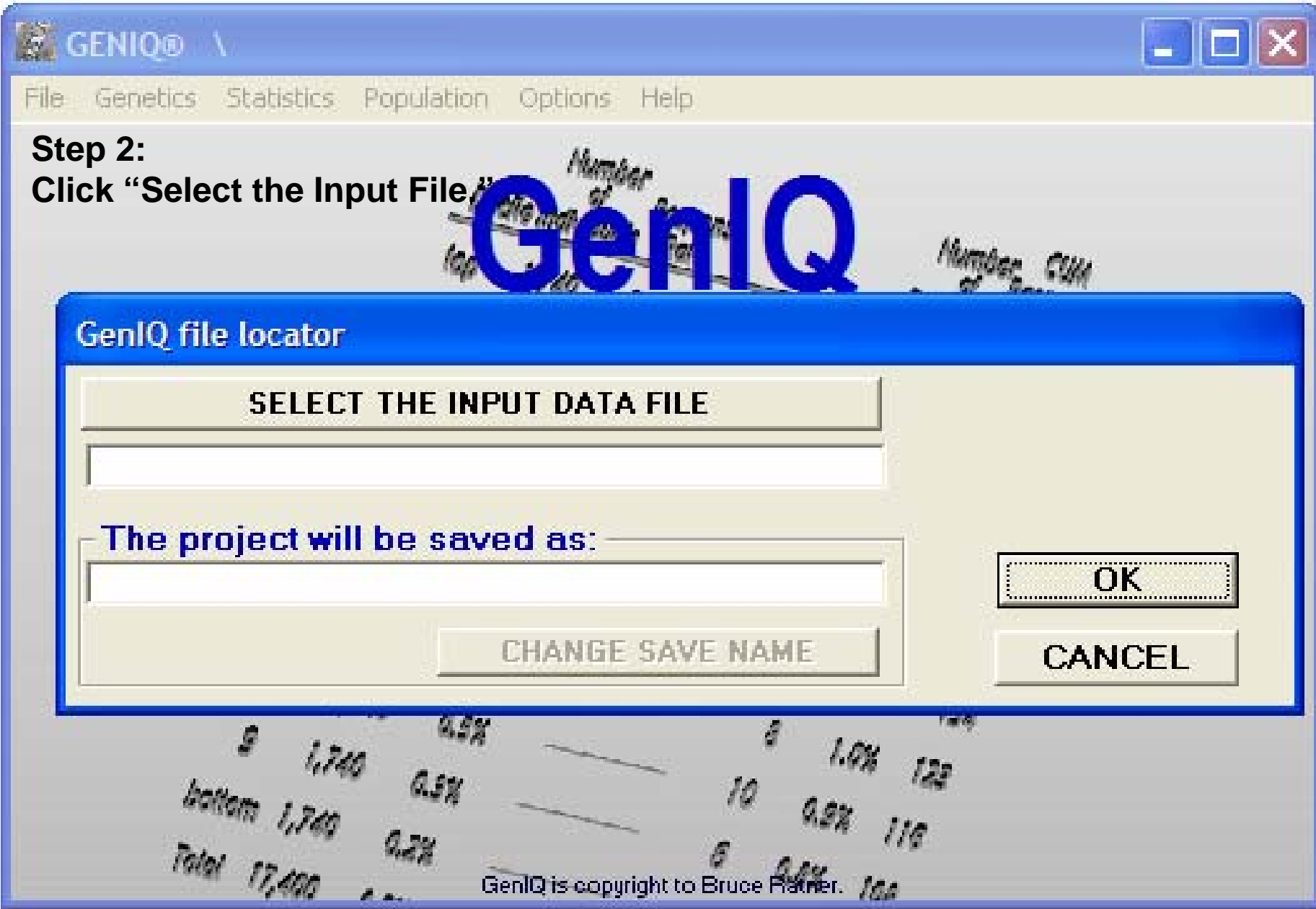
Genetic Modeling for Database Marketing

START A NEW PROJECT

OPEN EXISTING PROJECT

	Number of Responses	Response Rate	CUM of Responses	CUM Response Rate
1	100	2.1%	100	2.1%
2	1,740	1.6%	1,840	1.6%
3	1,740	1.0%	3,580	1.0%
4	1,740	0.8%	5,320	0.8%
5	1,740	0.7%	7,060	0.7%
6	1,740	0.6%	8,800	0.6%
7	1,740	0.5%	10,540	0.5%
8	1,740	0.5%	12,280	0.5%
9	1,740	0.2%	14,020	0.2%
bottom	1,740	0.2%	15,760	0.2%
Total	17,400	1.0%	17,400	1.0%

GenIQ is copyright to Bruce Ratner.



Step 2:

Click "Select the Input File"

Number of
GenIQ
Number CUM

GenIQ file locator

SELECT THE INPUT DATA FILE

The project will be saved as:

CHANGE SAVE NAME

OK

CANCEL

9 1,740 0.5%
bottom 1,740 0.5%
Total 17,400 0.2%

5 1.0% 122
10 0.9% 116
5 0.8% 100

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Look in:



demo_dat1b.sas7bdat

**Step 3:
Choose the data file.
Then click "Open."**



Recent



Desktop



My Documents



My Computer



My Network Places

File name:

Files of type:

Open

Cancel

Step 4:
Click "OK."



GenIQ file locator

SELECT THE INPUT DATA FILE

C:\Program Files\GenIQ\Examples\demo_dat1b.sas7bdat

The project will be saved as:

C:\Program Files\GenIQ\Examples\demo_dat1b.sas7bgmx

CHANGE SAVE NAME

OK

CANCEL

\$	1,740	0.5%	\$	1.0%	123
bottom	1,740	0.5%	10	0.2%	116
Total	17,400	0.2%	5	0.1%	106

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LOADING FILE NOW.

Identify VARS

- Target Y
- Predictor X
- Deselect

Set holdout %

◀ ▶ 50

VARIABLE NAME	Abr	USAGE	TYPE	Comment
response	x1	Y	Numeric	OK
hi_balance	x2	X	Numeric	OK
no_bal_decr	x3	X	Numeric	OK
no_of_trans	x4	X	Numeric	6 missing
recency_mos	x5	X	Numeric	OK
mos_on_file	x6	X	Numeric	OK
tranx_active	x7	X	Classes[3]	OK

Step 5:

- Select Identification of Variables:
Target Variable, and Predictor Variables.
- Select Handling of Data:
Missing Data, and % for Holdout.
- Then, click "OK."

OK

CANCEL

HOW SHOULD MISSING DATA BE TREATED

Quasi Complete-
Case Analysis

(Casewise Deletion on NumVars)

Complete-Case
Analysis

(Casewise Deletion)

All-Case
Analysis

(Genetic Imputation)

BUSY....PLEASE STAND BY

Identify VARS

- Target Y
- Predictor
- Deselect

Set holdout

50

OK

CANCEL

HOW SHOULD MISSING DATA BE TREATED

Quasi Complete-Case Analysis

(Casewise Deletion on NumVars)

Complete-Case Analysis

(Casewise Deletion)

All-Case Analysis

(Genetic Imputation)

RESPONSE RATE?

The sample response rate is 8.701%

If the sample is biased, please enter the TRUE POPULATION response rate.

8.7013

OK

Cancel

Step 6:

Accept or change sample response rate.
Then click "OK."

Step 7:
 Click "SET DEFAULTS."
 Then click "OK."

GENETIC ALPHABET SELECTOR

SET DEFAULTS	CLEAR	OK	CUSTOM FUNCTIONS	HELP
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ARITHMETIC operations					CIRCULAR functions			NUMERIC MATERIAL					
+	-	x	÷	^	 ÷ 	Sin	Cos	Tan	0.1	2	Pi	Rand	
Abs	Fra	Int	Mod	Sqn		Asin	Acos	Atn	1	3	e		
Ln	Exp	Log	10^x	Exp-		Csec	Sec	Cot	10	4	True	π	
√	Crt	Lsr	Bqr	Atn2		Acsc	Asec	Acot	100	5	False		

LOGICALS		{CRISP, fuzzy}					HYPERBOLIC functions			CUSTOM functions			
<	≤	=	>	≥	≠	≅	Sinh	Cosh	Tanh	Fn	Fn	Fn	Fn
AND	OR	NOT	EQV	IMP	XOR		Asnh	Acsh	Atnh	Fn	Fn	Fn	Fn
and	or	not	eqv	imp	xor		Csch	Sech	Coth	Fn	Fn	Fn	Fn
Blwn	ifT	if<=	Xltr				Acsch	Asch	Acth	Fn	Fn	Fn	Fn

Step 8:

Click “Run GenIQ” bar at the bottom.

POPULATION AND BREEDING CONTROLS

Genetic POPULATION size
Models/Gen. ◀ ▶ 250

Stop when
Decile 1 Cum Lift is > 999
OR generations = ▶ 100

BREEDING PROBABILITIES

PROBABILITIES		%
Crossover	◀▶	80
Terminal Selection	◀▶	20
Mutation (I/R/P)	◀▶	20
Editing	◀▶	2

Set default values

GenIQ FITNESS CONTROL

SELECTION METHOD

- Fitness only
- Fitness & beauty
- Tournament

FITNESS BASED ON

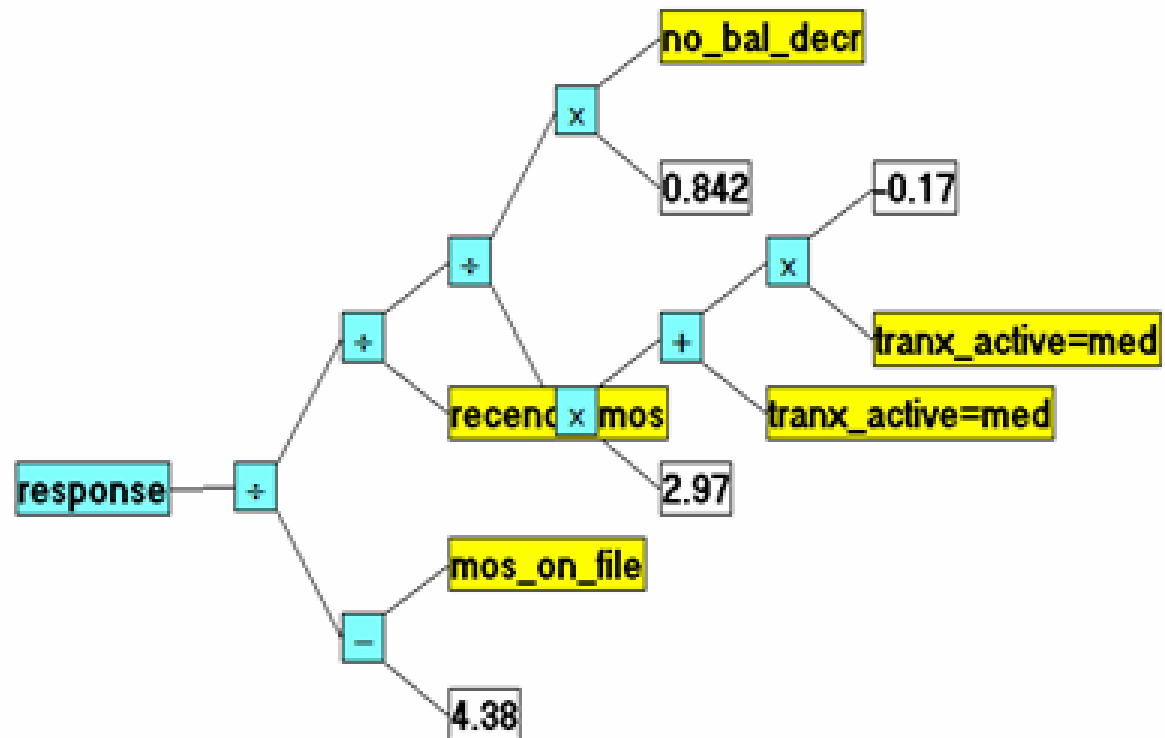
- GenIQ Fitness Function 2.0

Run GenIQ

Step 9:

Let the GenIQ Model, displayed in tree-form in the top-right window, evolve. Click “PAUSE” when you are satisfied with the corresponding ‘optimized’ decile table, as GenIQs objective is to optimize the decile table.

RESPONSE DECILE ANALYSIS				
TRAINING SET sample size = 4597				
Population response = 8.70%				
DECILE	Predicted Response	Resp Rate%	Cum RespR%	Cum Lift
Top	75	16.31	16.30	197
2nd	48	10.44	13.38	154
3rd	40	8.70	11.82	136
4th	47	10.22	11.42	131
5th	34	7.40	10.62	122
6th	34	7.40	10.08	116
7th	41	8.92	9.91	114
8th	29	6.31	9.46	109
9th	27	5.87	9.06	104
Bottom	25	5.44	8.70	100



- The GenIQ Model is conveniently displayed in tree-form; but, it is actually a *computer program!* Accordingly, it is the computer code that represents the final GenIQ Model, i.e., serves as the model equation.
- For the GenIQ Model presented, the model equation/computer code is:

```

x1 = 4.38;
  x2 = mos_on_file;
x1 = x2 - x1;
  x2 = recency_mos;
  x3 = 2.97;
    If tranx_active = "med" Then x4 = 1; Else x4 = 0;
      If tranx_active = "med" Then x5 = 1; Else x5 = 0;
        x6 = -.17;
          x5 = x5 * x6;
            x4 = x4 + x5;
              x3 = x3 * x4;
                x4 = .842;
                  x5 = no_bal_decr;
                    x4 = x4 * x5;
                      If x3 NE 0 Then x3 = x4 / x3; Else x3 = 1;
                        If x2 NE 0 Then x2 = x3 / x2; Else x2 = 1;
                          If x1 NE 0 Then x1 = x2 / x1; Else x1 = 1;
GenIQvar = x1;
GenIQ_Probability = 1 / (1 + Exp(-(-2.688323 + GenIQvar * 88.51257)));

```

GenIQ Predictive Analytics

- The previous nine steps/screen-shots indicate how simple predictive analytics can be. Of course, there is much to be said about each step. But, the message is clear: Building a regression model with GenIQ requires virtually no statistical background, as the [GenIQ provides](#) a machine learning solution to the classical statistical problem of [building predictive regression models](#).
- For more about GenIQ, call Bruce Ratner at 516.791.3544
- [Benefits of GenIQ](#), and [GenIQ: Data Mining Tool](#) are on these links.