

Alzheimer's disease dataset description

Alzheimer's disease in a China sample that consisted of 257 Alzheimer's disease patients and 242 age-matched controls. They used denaturing high performance liquid chromatography (DHPLC) to screen the NEP gene for SNPs and then each candidate SNP was confirmed by DNA sequencing.

R6 indicates -204 G>C, N4 indicates IVS3+106T>G, N6 indicates C .401 A>G, N11 indicates I V S10 - 5 C >T, N15 indicates I V S15+144 T >A, N18 indicates I V S17 - 294 C >T, N22 indicates I V S22+36 C >A, N24 indicates 3'UT R159 C >T.

Four iterations were completed in the IECS workflow. The pattern of the simultaneous mutation of SNP (IV S22+36C>A) and SNP (3'UT R159C>T) was extracted in the first round; the IV S17 - 294C>T mutation pattern was extracted in the second round; the simultaneous mutation pattern of IV S3 + 106T >G, IV S10 - 5C>T, and 3 'UT R159C>T was extracted in the third round; and the IV S22 + 36C>A mutation pattern was extracted in the fourth round. Please refer to Table 2 for the results of the QCA analysis.

The followed is display the four-round iteration process and the results calculated by fsQCA3.0 and SPSS22 software and the consistency threshold is 0.8.

Round 1

QCA solution

```
--- TRUTH TABLE SOLUTION ---
frequency cutoff: 1
consistency cutoff: 1
Assumptions:
```

	raw coverage	unique coverage	consistency
~R6*~N4*~N11*~N15*N22*N24	0.0972763	0.0583658	1
~R6*~N6*~N11*~N15*N18*~N22*~N24	0.0233463	0.0194553	1
~R6*~N4*~N6*~N11*~N15*~N18*N22	0.0389105	0.0116732	1
~R6*N4*~N6*~N11*~N15*N18*~N22	0.0077821	0.00389105	1
~R6*N4*~N6*~N15*N18*N22*~N24	0.0116732	0.0116732	1
~R6*N4*~N6*~N11*N15*N22*N24	0.0077821	0.00389105	1
~R6*N6*~N11*~N15*N18*N22*N24	0.0155642	0.00389105	1
~R6*N4*~N6*N11*~N15*~N18*~N22*N24	0.0155642	0.0155642	1
~R6*~N4*~N6*~N11*N15*N18*~N22*N24	0.0077821	0.0077821	1
~R6*~N4*~N6*N11*N15*N18*N22*~N24	0.00389105	0.00389105	1
R6*~N4*~N6*N11*~N15*N18*~N22*N24	0.00389105	0.00389105	1
~R6*N4*N6*N11*N15*~N18*~N22*N24	0.00389105	0.00389105	1
R6*~N4*N6*N11*~N15*N18*N22*N24	0.00389105	0.00389105	1
~R6*~N6*~N11*~N15*~N18*N22*N24	0.0311284	0	1
~R6*N4*~N6*~N11*~N18*N22*N24	0.0077821	0	1
solution coverage: 0.202335			
solution consistency: 1			

The pattern (N22*N24) is extracted from the prime implicants

(~R6*~N4*~N11*~N15*N22*N24) with the greatest raw coverage in the solution.

The pattern is tested with chi-square test in the source dataset.

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	7.304 ^a	1	.007	.008	.005
Continuity Correction ^b	6.533	1	.011		
Likelihood Ratio	7.499	1	.006		
Fisher's Exact Test					
Linear-by-Linear Association	7.289	1	.007		
N of Valid Cases	499				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 25.22.

b. Computed only for a 2x2 table

52 compatible samples are excluded from the current dataset and there are 447 samples left for the next round of calculation.

Round 2

QCA solution

--- TRUTH TABLE SOLUTION ---

frequency cutoff: 1

consistency cutoff: 1

Assumptions:

	raw coverage	unique coverage	consistency
~R6*~N6*~N11*~N15*N18*~N22*~N24	0.0271493	0.0226244	1
~R6*N4*~N6*~N11*~N15*N18*~N22	0.00904977	0.00452489	1
~R6*N4*~N6*~N15*N18*N22*~N24	0.0135747	0.0135747	1
~R6*~N4*~N6*~N11*~N15*~N18*N22*~N24	0.0135747	0.0135747	1
~R6*N4*~N6*N11*~N15*~N18*~N22*N24	0.0180995	0.0180995	1
~R6*~N4*~N6*~N11*N15*N18*~N22*N24	0.00904977	0.00904977	1
~R6*~N4*~N6*N11*N15*N18*N22*~N24	0.00452489	0.00452489	1
R6*~N4*~N6*N11*~N15*N18*~N22*N24	0.00452489	0.00452489	1
~R6*N4*N6*N11*N15*~N18*~N22*N24	0.00452489	0.00452489	1
solution coverage: 0.0995475			
solution consistency: 1			

The pattern (N18) is extracted from the prime implicants

(~R6*~N6*~N11*~N15*N18*~N22*~N24) with the greatest raw coverage in the solution.

The pattern is tested with chi-square test in the source dataset.

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	4.979 ^a	1	.026	.026	.017
Continuity Correction ^b	4.410	1	.036		
Likelihood Ratio	5.049	1	.025		
Fisher's Exact Test					
Linear-by-Linear Association	4.969	1	.026		
N of Valid Cases	499				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 32.49.

b. Computed only for a 2x2 table

26 compatible samples are excluded from the current dataset and there are 421 samples left for

the next round of calculation.

Round 3

QCA solution

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--- TRUTH TABLE SOLUTION ---
frequency cutoff: 1
consistency cutoff: 1
Assumptions:
```

	raw coverage	unique coverage	consistency
~R6*~N4*~N6*~N11*~N15*~N18*N22*~N24	0.0147059	0.0147059	1
~R6*N4*~N6*N11*~N15*~N18*~N22*N24	0.0196078	0.0196078	1
~R6*N4*N6*N11*N15*~N18*~N22*N24	0.00490196	0.00490196	1
solution coverage: 0.0392157			
solution consistency: 1			

The pattern (N4*N11*N24) is extracted from the prime implicants

(~R6*N4*~N6*N11*~N15*~N18*~N22*N24) with the greatest raw coverage in the solution.

The pattern is tested with chi-square test in the source dataset.

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.013 ^a	1	.909	1.000	.561
Continuity Correction ^b	.000	1	1.000		
Likelihood Ratio	.013	1	.909		
Fisher's Exact Test					
Linear-by-Linear Association	.013	1	.909		
N of Valid Cases	499				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.79.

b. Computed only for a 2x2 table

7 compatible samples are excluded from the current dataset and there are 414 samples left for the next round of calculation.

Round 4

QCA solution

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--- TRUTH TABLE SOLUTION ---
frequency cutoff: 1
consistency cutoff: 1
Assumptions:
```

	raw coverage	unique coverage	consistency
~R6*~N4*~N6*~N11*~N15*~N18*N22*~N24	0.0150754	0.0150754	1
solution coverage: 0.0150754			
solution consistency: 1			

The pattern (N22) is extracted from the prime implicants

(~R6*~N4*~N6*N11*~N15*~N18*N22*~N24) with the greatest raw coverage in the solution.

The pattern is tested with chi-square test in the source dataset.

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	9.708 ^a	1	.002	.002	.001
Continuity Correction ^b	8.886	1	.003		
Likelihood Ratio	9.977	1	.002		
Fisher's Exact Test					
Linear-by-Linear Association	9.688	1	.002		
N of Valid Cases	499				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 30.55.

b. Computed only for a 2x2 table

6 compatible samples are excluded from the current dataset and there are 408 samples left for the next round of calculation.

Round 5

QCA has no solution

*** ERROR(Quine-McCluskey): The 1 Matrix is Empty. ***

Algorithm: Quine-McCluskey

--- TRUTH TABLE SOLUTION ---

frequency cutoff: 1

consistency cutoff: 1

Assumptions: