

Compound identification in GC-MS by simultaneously evaluating mass spectrum and retention index

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Table S1. Results of the five times of 5-fold cross validation for analysis of the query dataset containing retention indices acquired on standard non-polar column. Each datum is the average of the results of a 5-fold cross validation with its standard deviation.

| | CV 1 | CV 2 | CV 3 | CV 4 | CV 5 |
|--------------------|-----------|-----------|-----------|-----------|-----------|
| a | 0.05±0.02 | 0.05±0.03 | 0.06±0.03 | 0.04±0.03 | 0.04±0.03 |
| b | 23±6 | 25±8 | 23±7 | 21±8 | 24±6 |
| w | 0.66±0.02 | 0.71±0.08 | 0.64±0.08 | 0.69±0.04 | 0.67±0.03 |
| Training error (%) | 11.5±0.1 | 11.5±0.2 | 11.4±0.3 | 11.4±0.2 | 11.5±0.4 |
| Testing error (%) | 11.8±0.4 | 11.9±0.8 | 11.9±0.9 | 11.9±0.7 | 12.0±1.8 |

Table S2. Results of the five times of 5-fold cross validation for analysis of the query dataset containing retention indices acquired on standard polar column. Each datum is the average of the results of a 5-fold cross validation with its standard deviation.

| | CV 1 | CV 2 | CV 3 | CV 4 | CV 5 |
|--------------------|-----------|-----------|-----------|-----------|-----------|
| a | 0.02±0.01 | 0.02±0.01 | 0.03±0.02 | 0.02±0.01 | 0.01±0.01 |
| b | 26±7 | 32±3 | 26±6 | 29±1 | 26±7 |
| w | 0.72±0.07 | 0.67±0.07 | 0.73±0.13 | 0.73±0.09 | 0.75±0.05 |
| Training error (%) | 13.7±0.2 | 13.7±0.5 | 13.7±0.5 | 13.7±0.6 | 13.7±0.2 |
| Testing error (%) | 14.3±1.0 | 14.1±2.0 | 14.3±1.8 | 14.3±2.3 | 14.4±1.4 |