Discussion

Comments on the "classical equations" given in J. Chromatogr. A 1024 (2004) 195–207

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Recently, Bicchi et al. [1] published a paper on direct resistively heated column GC for high-speed analysis. In the Column Evaluation section (Section 3.1), the authors give three "classical equations". I would like to draw attention to the fact that all three equations as given in the paper are wrong:

1.1. Resolution (*R*)

The text specifies w_b used in the resolution equation as

$$w_b = \frac{w_{b2} - w_{b1}}{2}$$

However, in the universally accepted retention equation (see, e.g., No. 3.10.01 of the IUPAC Chromatography Nomenclature [2] w_b is the average peak width at base and not the difference of the two peak widths. In other words, the correct expression should be

$$w_b = \frac{w_{b1} + w_{b2}}{2}$$

1.2. Separation number (SN)

The equation as given in the paper is incorrect: a (-1) term is missing in the right-hand side. The correct expression is [2]:

$$SN = \frac{t_{R2} - t_{R1}}{w_{b1} + w_{b2}} - 1$$

It is a minor point, but the authors' definition is not precise. According to the paper, this term expresses "the number of well-separated peaks within any homologue pair". Actually, the definition of the separation number specifies that *n*-alkanes, and not any homologous series, should be used.

1.3. Maximum number of peaks (*n*)

Authors give the following equation:

$$n = \frac{\Delta t}{w_b}$$

without specifying the meaning of Δt. In GC, generally, this symbol is used for the difference of the retention times corresponding to two consecutive peaks, i.e.,

$$\Delta t = t_{R2} - t_{R1}$$

and obviously, this is not what the authors meant: according to their definition *n* means "the maximum number of peaks that can be separated on a given column". On the other hand, if $\Delta t = t_{R2} = t_{R1}$, then $n = R$.

Also, the definition of w_b in connection with this expression ("equal to four times the standard deviation of the peak") is not precise: of which peak? If *n* expresses the "maximum number of peaks" one can separate on the column, then obviously the standard deviation

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of the individual peaks will be different: much smaller for the first peak than for the last peak considered. In addition, the "maximum number of peaks" depends on the time frame of the chromatogram, and this must be specified.

References

[1] C. Bicchi, C. Brunelli, C. Cordero, P. Rubiolo, M. Galli, A. Sironi, J. Chromatogr. A 1024 (2004) 195–207.
[2] Pure Appl. Chem. 65 (1993) 819–872.