Nomenclature and Conventions in Comprehensive Multidimensional Chromatography – An Update

Comprehensive two-dimensional chromatography necessitates additional nomenclature over and above that used in classical one dimensional (1D) chromatography. The use of two (or more) columns requires various parameters on these separate dimensions to be adequately identified. This is achieved by use of a superscript preceding the respective symbol. Also, the process of coupling different dimensions leads to specific terminology, which we report here. A number of recent examples where specific nomenclature related to retention indices, estimation of first dimension retention times, and the definition of modulation ratio, are included. This article and its predecessor aims to establish a basis for suitable nomenclature and conventions in this rapidly advancing area.

In 2003 Schoenmakers *et al.* published a position paper in *LC•GC Europe* (1) defining various nomenclature and conventions in comprehensive multidimensional chromatography. This paper was the outcome of a session organized to discuss the terminology and nomenclature used in this emerging field, during the First International Symposium on Comprehensive Multidimensional Gas Chromatography (GC×GC), held on 6–7 March in Volendam, the Netherlands.

This first symposium was the progenitor to eight further symposia so far, with the 9th GC×GC scheduled for Riva del Garda, Italy, in May 2012. Many of the listed conventions and nomenclature were based on practices that had appeared in the literature up to that time – and admittedly this was largely in the field of GC×GC. Perhaps not surprisingly, unanimous agreement was reached on many of these definitions, terms and symbols, and the need to ensure that establishing a basic 'set of conventions' was appreciated. Most of the terms were logical and this aided acceptance and understanding among chromatographers.

At that time, there were relatively few reports on LC×LC or other comprehensively coupled separation methods. Since this first meeting, many LC×LC developments have been introduced, with a number of different implementation formats, and the review of Stoll *et al*. in 2007 should be referred to (2). In addition, the 2003 paper included some proposals for nomenclature and conventions that were recommended even though they had not been used in the literature. According to Scopus, that paper has been cited almost 90 times in subsequent literature (becoming the most highly cited paper in *LC•GC Europe*), and so has been accorded good acceptance within the chromatography community.

It is time to update the earlier review with various terms and conventions that have been described since that time in this rapidly advancing field of chromatographic analysis. In addition, comments on methods for derivation of various parameters for comprehensive multidimensional chromatography experiments will be included. The more extensive literature on LC×LC in recent years has resulted in a range of new terminologies being added to the lexicon of comprehensive two-dimensional chromatography and this justifies the addition of terms peculiar to that experimental arrangement.

For completeness, the Tables of the earlier review will be reproduced here and additions included where appropriate.

There still remains some lingering confusion or inconsistency over the use of the words “comprehensive” and “orthogonal,” and of the multiplex sign (×) as a short notation for comprehensive two-dimensional (2D) separations. Hence, as in the 2003 paper, the background to, and further comment on, these aspects will be included.

Comprehensiveness

An important discussion surrounded the argument of when a 2D separation can be called comprehensive. Three criteria were established, based essentially on the definitions formulated earlier by Giddings (3). There is a need to clearly distinguish between classical (heart-cut) 2D separations and comprehensive 2D separations. Also, some practitioners use the term ‘comprehensive GC analysis’ to mean ‘analysing everything’.

However, when a specific part of the sample is removed prior to (by selective sample preparation) or during the analysis (for example, solvent vent or a split-flow arrangement), it is still possible to refer to the separation as comprehensive. In that instance it is good practice to specify the fraction of the sample that is analysed. For example, a comprehensive 2D separation of a specific plant extract will refer to theselected extract, which acknowledges the inherent limitations of extraction selectivity (not all the components may be extracted equally). In such an instance the sample can be redefined as that well-defined fraction of the initial material to be analysed. Thus the extract (and not the plant) is the sample to be analysed by comprehensive 2D chromatography. Similarly, the sample can be a serum obtained from whole blood, a distillation fraction obtained from crude oil, or a specific fraction obtained from a chromatographic separation, etc. Therefore, the guiding principle (3) is that a 2D separation can be called comprehensive if:

1. Every part of the sample is subjected to two different (independent) separations;
2. Equal percentages (either 100% or lower) of all sample components pass through both columns and eventually reach the detector; and

3. The separation (resolution) obtained in the first dimension is essentially maintained.

The third criterion can never be met completely, but chromatographers have learned to live with arbitrary distinctions in similar contexts (for example, the extra-column contribution to peak broadening must be kept negligible). Clearly Giddings understood that criterion 3 was a key to differentiate the heart-cut process from what he envisioned as the proper comprehensive separation experiment, but he will not have conceived how the column chromatography experiment could be conducted to ensure the 1D separation was fully maintained. Blumberg and Klee (4) have recently revisited this definition and re-cast it as “An n-dimensional (nD) analysis is one that generates n-dimensional displacement information”.

One way that the qualifier “essentially maintained” (point 3) may be translated into practical terms is to specify that a reduction in the apparent ^{1}D resolution (observed by projecting a specific peak pair in the comprehensive 2D chromatogram on the ^{1}D axis) should not exceed some fixed limit (for example, 10%). However, this has not been paid due attention in the literature. The most important aspect of preserving resolution in the first dimension is the number of ^{2}D chromatograms recorded across the width of a ^{1}D peak, with three or four normally referred to as the minimum target number. It should be noted that the desire to “essentially maintain” the separation achieved in the first-dimension may not coincide with the optimum conditions of analysis. For example, Horie *et al.* (5) and Vivó Truyols *et al.* (6) independently came to the conclusion that around two “cuts” per ^{1}D peak is optimal for achieving efficient LC×LC separations.

In the earlier paper, the second criterion was reported to give rise to much discussion. Most delegates felt that the term “comprehensive” should not be reserved for instances in which every analyte is completely (100%) transferred to the ^{2}D column and then recorded at the detector — provided that the “split factor” *x* (%) is equal for all components. If (apart from a single intensity factor of *x*) the obtained chromatogram is identical to the one obtained with 100% transfer, then the term comprehensive may be used. In simple words, a “faithful representation” of the sample must be obtained in truly comprehensive 2D chromatography. In practice, it is not easy to obtain such a faithful representation if the transfer factor is not 100%. By selecting time fractions for transfer to the ^{2}D column (for example, sending the effluent to waste during 90% of the time), the fractions of individual peaks will vary. This may result in the comprehensive 2D chromatography experiment being a qualitative process, rather than a quantitative method. When flow splitters are used, gas chromatographers hardly need to be reminded of the danger of discrimination such devices entail. If in doubt (i.e., when some discrimination may occur), it is better to speak of near-comprehensive 2D separations.

The sub-sampling interfaces (i.e. those that sample less than 100% of the injected material and can sample or modulate each solute to a different amount) include diaphragm and early (differential) flow modulators in GC, and instances where the volume transferred to, for example, dual sampling loops in LC exceed the break-through volume of the loop.

A final point worth making is that "comprehensive gas (or liquid) chromatography" is not the same as "comprehensive two-dimensional gas (or liquid) chromatography." The former is an imprecise usage of language that should be avoided. Shorter, unambiguous abbreviations are discussed below. Likewise, it is noted that sometimes the literature includes terms such as "comprehensive GC×GC chromatography". This is also an imprecise use and should be avoided.

Table 1: Examples of abbreviations involving the multiplex (×) sign.

Abbreviation	Location
GC×GC	Comprehensive two-dimensional gas chromatography
GC×GC–FID	Comprehensive two-dimensional GC with flame-ionization detection
GC×GC–MS	Comprehensive two-dimensional GC with mass spectrometry detection
GC×GC–'X'	Comprehensive two-dimensional GC with 'X' detection
LC×LC	Comprehensive two-dimensional liquid chromatography
LC×SEC	Comprehensive two-dimensional (liquid × size-exclusion) chromatography
LC×GC	Comprehensive two-dimensional (liquid × gas) chromatography
SFC×GC	Comprehensive two-dimensional (supercritical-fluid × gas) chromatography
GC×GC×GC	Comprehensive three-dimensional gas chromatography
LC–GC×GC	On-line liquid chromatography — comprehensive two-dimensional gas chromatography
SFC–GC×GC	On-line supercritical-fluid chromatography — comprehensive two-dimensional gas chromatography
SFC×SFC	Comprehensive two-dimensional supercritical-fluid chromatography
CE×CE	Comprehensive two-dimensional capillary electrophoresis
LC×CE	Comprehensive two-dimensional (liquid chromatography × capillary electrophoresis)
LC×GC×GC	Comprehensive three dimensional (liquid × gas × gas) chromatography
LC×LC×CE	Comprehensive three dimensional (liquid×liquid) chromatography×capillary electrophoresis
DGC×DGC	Comprehensive dynamic GC×GC
IC×LC	Comprehensive two-dimensional (ion×reversed-phase liquid) chromatography
Generic abbreviations for the technique. Whilst these have been noted in the literature, no agreement has not been adopted on their use, and so they are presented without comment.	
C2DC; CMDC; C2DS; CMDS	Comprehensive two-dimensional chromatography; Comprehensive multidimensional chromatography; Comprehensive two-dimensional separation; Comprehensive multidimensional separation

[4]Table 1: Examples of abbreviations involving the multiplex (×) sign. [Click to Enlarge]

The Multiplex Sign

To abbreviate the term "comprehensive 2D" the multiplex sign (×) may be used (7). This is a clear distinction from conventional "linear" or "heart-cut" 2D separations, which are usually abbreviated with a hyphen (or n-dash) (for example, GC–GC, LC–GC). The multiplex sign can be used as an abbreviation for a number of different comprehensive 2D separation techniques. Some examples are listed in Table 1. Hyphens are

conventionally used to indicate the coupling of a chromatographic system to any kind of detector: as in GC with flame-ionization detection (GC–FID), GC coupled with Fourier-transform infrared spectroscopy (GC–FTIR), or GC with atomic-emission detection (GC–AED), although usage such as GC/MS is often noted), and to indicate on-line coupled ("hyphenated" or "coupled-column") systems (such as on-line solid-phase extraction in combination with LC, SPE–LC). This illustrates that hyphens are used in several different ways and that the meaning of the symbol is not unambiguously defined. However, in all three instances the hyphen indicates that the systems are coupled on-line.

Other variants to coupled instrument notations include GC(FID) for "simple" (single-channel) detectors and LC/MS or LC//MS for off-line combinations, and even variations within abbreviations for GC with time-of-flight mass spectrometry, such as GC–TOF/MS, GC–TOF–MS or GC–TOF MS for this instrumental arrangement are noted. A detailed discussion of such notations and obtaining some consensus in their use is beyond the scope of the present paper. For a discussion on the notation of chromatography–MS systems see the glossary of terms proposed by Murray (8).

Because MS is a technique to separate ions generated on-line with the separation step, one can argue that GC×MS and LC×MS are comprehensive 2D separation methods. This argument is most realistic when a soft ionization method is used, which results in minimal fragmentation of parent ions. This has been used, for example, for GC×FIMS (field ionization MS), or other similarly soft ionization methods, with data displayed on largely independent axes of retention and ion mass (which predominantly generate molecular ions).
Every analyte component is then indeed separated in two dimensions. If MS acquisition takes place sufficiently fast to meet the requirements of comprehensiveness and if discrimination at the MS inlet is avoided, the '×' sign may arguably be used. For conventional gas chromatography–mass spectrometry with electron ionization, a hyphen is more appropriate. The abbreviation GC×2GC is suggested for a comprehensive two-dimensional gas chromatography system with two parallel second-dimension (2D) columns (9). According to the guidelines given above for use of the word "comprehensive," this is applicable to such a system, provided that the sample is distributed across the two 2D columns without any discrimination. An example of a comprehensive three dimensional separation (GC×GC×GC) has been noted (10).

A point that may have been noted by authors in recent years is the lack of consistency in the expression used for the abbreviation GC×GC. Of 15 journals checked, eleven used GC×GC and four used GC × GC. Other infrequent and inaccurate uses include GCXGC, and GCxGC (that is, using the normal font as either capital or lower case, instead of the multiplex sign). There appears to be consensus that GC×GC without spaces should be used.

Table 2: Definitions of orthogonality in different fields of science.	
Field	**Definition of Orthogonality**
Mathematics*	Of two vectors or functions: perpendicular; having an inner product equal to zero.
	Of a set of vectors or functions: such that the inner product of any two iszero if and only if the two are distinct.
Statistics*	Of a set of variates: statistically independent.
	Of an experimental design: such that the variates under investigation can be treated as statistically independent.
Chemistry (esp. Instrumental Analysis)	Of two instrumental dimensions that possess different mechanisms of analysis; for separation dimensions, where elution times in the two dimensions can be treated as statistically independent.

[5]Table 2: Definitions of orthogonality in different fields of science. [Click to Enlarge].

Orthogonality

"Orthogonality" remains one of the terms used most inconsistently in the literature on 2D separations. This is quite unlike the precise definitions in mathematics and statistics. In the chemical literature, orthogonality concepts are often associated with multidimensional instrumental chemical analysis and especially with separation science, where it has been used informally to indicate merely different separations (coupled separation dimensions) or mechanisms (hyphenated with detection), rather than those that are "perpendicular" or "independent."

In the Volendam discussion, no reasons were found for such a broad and peculiar interpretation of the word. A sensible definition for "orthogonality" in separation science is listed together with definitions from mathematics and statistics in Table 2. The analytical definition implies that completely independent analysis processes are used, or in separation science that independent retention mechanisms apply in the two dimensions.

Whether or not orthogonal separation mechanisms (orthogonal separations) lead to good separations depends on the sample, its components and the specific physical-chemical manner in which the retention mechanisms are exploited. For example, if ^{1}D separates according to boiling point, while ^{2}D is only able to separate according to stereo-selectivity, then only stereo-isomers in the sample will exhibit an orthogonal 2D separation. Sometimes it is noted that authors refer to the 'degree of orthogonality' in a separation. For instance, LC×LC comprising different LC mechanisms – such as, reversed-phase and normal phase; size-exclusion and reversed-phase should meet this criterion. Note in contrast with the GC×GC experiment both dimensions have an underlying analyte boiling point mechanism. The presumed 'orthogonal' column set comprising a non-polar ^{1}D stationary phase with a polar ^{2}D stationary phase has led some authors to refer to a polar×non-polar stationary phase column set as non-orthogonal. There should be no justification for this designation. There is still scope for a rational basis and agreement for determining the 'extent of orthogonality'.

In the following section, some recent studies that support certain concepts in GC×GC are

further exemplified. The following sections refer to the nomenclature and terms reported in Table 3.

Table 3(a): Nomenclature suggested for comprehensive two-dimensional (gas) chromatography.

Term	Definition
Modulator	Interface device between the two columns in a comprehensive two-dimensional separation system that accumulates or samples narrow bands from the eluate of the first column for fast re-injection into the second column.
Modulation time or Modulation period (P_M)	The duration of a complete cycle of modulation in a comprehensive two-dimensional separation system (equals the data conversion time of each second dimension chromatogram, *i.e.*, the time between two successive injections into the second column).
Modulation frequency (f_M)	Number of modulations per unit of time.
Modulator temperature (T_M)	The temperature of the modulation zone used in thermal modulation.
Modulation number (n_M)	The number of modulated peaks recorded for a given first-dimension peak.
Modulation ratio (M_R)	The ratio of the peak width at baseline (^1w_b) for the first dimension peak to the modulation period (P_M).
Modulation phase (Φ; F_M)	The pattern of modulated peaks caused by the time relationship between the shape of the analyte peak and the pulsing process of the modulator in a comprehensive two-dimensional separation system (18).
In-phase modulation	The modulation phase that produces a symmetrical sequence of peaks with a single maximum peak pulse (18).
Out-of-phase modulation	Any phase that produces a non-symmetrical peak-pulse distribution (18).
180° out-of-phase modulation	The modulation phase that produces a symmetrical sequence of peaks with two equal maximum peak pulses (18).
Single-stage modulation	Accumulation and focusing during one series of processes at one location in the modulator.
Dual-stage modulation	Accumulation and focusing during two successive series of processes at two locations in the modulator.
Focusing effect	Reduction of the band width (in time, distance and/or volume units) (= band width without modulation/band width with modulation).
Sensitivity enhancement (= peak-amplitude enhancement)	Ratio between peak height with and without modulation (note: sensitivity refers to the signal, not to the noise!).*
Zone compression	The effect of reducing a chromatographic peak (width) in space or time to give a higher concentration within a chromatography column.
Separation space	The region within the two-dimensional GC×GC plot in which compounds are, or may be, distributed.
Wrap-around	The occurrence of second dimension peaks in subsequent modulation sequences, caused by second-dimension retention times that exceed the modulation period of a comprehensive two-dimensional system (19).
Iso-volatility curves	The observation of reduced retention of a solute on a ^{2}D column in GC×GC as the temperature of the oven increases, seen as a decreasing retention time ^2t_R band in the 2D plot.
Column set	The combination of columns used for a given comprehensive 2D chromatography experiment.
Column set relative diameter ratio	The relative change in cross sectional area for the ^{1}D to ^{2}D columns of the column set = $^1d_c/^2d_c$.
Chromatogram structure	The observed ordering of chemically related compounds in the plane of a comprehensive two-dimensional separation.
Colour plot	Two-dimensional plot representing a comprehensive two-dimensional separation, in which the colour represents the signal intensity of the components in the separation system.**
Contour plot	Two-dimensional plot representing a comprehensive two-dimensional separation, in which similar signal intensities of components are connected by means of a line.**
Apex plot	Two-dimensional plot representing a comprehensive two-dimensional separation, in which peak apexes of second-dimension peaks are displayed by a symbol in the ^{2}D space. This may also be simplified to the peak apexes of individual components. **
Cryogenic / thermal modulation	GC×GC system in which the interface operates by changes in temperature compared with the oven temperature, either by setting an elevated or cooler temperature.
Diaphragm modulation	GC×GC system in which the interface operates by periodically selecting a small sub-fraction of the ^{1}D peak to be transferred to the ^{2}D column using a diaphragm system.
Flow modulation	GC×GC system in which the interface operates by a flow switching mechanism; normally a higher flow is maintained for the ^{2}D column.

* A reduction in the detection limit may also be achieved. This reduction is proportional to the product of the sensitivity enhancement and the noise.
** The x-axis represents the first-dimension retention time, the y-axis the second-dimension retention time of the separation system.

[6]Table 3(a): Nomenclature suggested for comprehensive two-dimensional (gas) chromatography. [Click to Enlarge]

Table 3(b): The following terms are not advised usage.

Comprehensive (gas or liquid) chromatography	The word "comprehensive" has been assigned a meaning for 2D (or multi-dimensional) separations, not for 1D separations or chromatography in general.
Comprehensive GC×GC (or LC×LC) chromatography	This is a pleonasm. GC×GC or LC×LC suffices.
Normal phase (column set)	There is no apparent agreement on the use of such a term for GC×GC. This supposedly refers to a column set whose first phase and second phases constitute non-polar and polar phases, respectively. Whilst this phase combination might have been one that was originally widely used, the likely confusion with LC definition of 'normal phase' makes its use unsuitable.
Reverse-phase (or Inverse phase) column set	This presumably refers to a column set whose first and second phases constitute polar and non-polar phases respectively. Its use is not recommended.

[7]Table 3(b): The following terms are not advised usage. [Click to Enlarge].

Retention Indices, *I*

I values have been reported for ^{1}D and ^{2}D data in GC×GC, and the experiment can be conducted in a number of ways. ^{1}D data are best acquired by using a 'split T' before the ^{2}D column, with ^{1}D retention data ($^{1}t_{R}$) recorded with an FID. However, such an arrangement must lead to an incorrect assessment of the actual $^{1}t_{R}$ value due to added retention on the short transfer line that connects the ^{1}D column to the FID. Others have used the retention time of the largest modulated peak (or the modulation time of this peak) in the GC×GC result as a surrogate for the $^{1}t_{R}$ value, and then used this for deducing the ^{1}I values (11).

A method for ^{2}I in GC was reported by using a suite of alkanes injected periodically through the first injector, which requires them to pass through the entire first column (12). The interference caused by co-injected solvent was a drawback to the method. A solid-phase micro-extraction (SPME) method with appropriate alkane sampling was then described (9), with again injection into the first injector. The constraint of passing alkanes through the ^{1}D column was overcome by delivering alkanes directly to the end of the ^{1}D column just prior to the modulator, so that any alkane could be introduced to the ^{2}D column at any time. The use of a second injector made this possible, with SPME again used for sampling the alkanes so that no solvent was introduced.

In all cases, the sequentially injected alkanes describe a so-called 'iso-volatility' plot within the 2D separation space, which refers to the observation that the injected component defines an exponential reduction in $^{2}t_{R}$ as temperature increases. Interpolation (or sometimes extrapolation) between successive alkanes in the pseudo-isothermal 2D analysis gives the ^{2}I value. The method is not straightforward and demands some attention to the details of the experiment. However, one can predict that once the 2D space has been defined by suitable alkane elution patterns to derive an equivalent ^{2}I space, the ^{2}I value of any solute should be easily deduced.

Apparent $^{1}t_{R}$ Values from Modulated $^{2}t_{R}$ Peaks

The modulated peaks that are generated from the GC×GC experiment can be used to estimate the apparent $^{1}t_{R}$ value on the ^{1}D column. We choose to call this $^{1}t_{R,app}$ because it is a derived value rather than a directly measured quantity. A model describing the resulting distribution of 2D peaks, based on a 1D Gaussian peak shape, can be fitted to the ^{1}D peak (13, 14). The prediction of $^{1}t_{R,app}$ also has to include measurement of the solute hold time in the modulator, which we choose to call th, and must also account for the $^{2}t_{R}$ value.

Note that the t_h value is not simply the same as the modulation time or modulation period (P_M; in some literature, this has been proposed as the second dimension cycle time ^2t_c). The total retention time of a modulated peak in the experiment should take into account all retention contributions to the total. It might be thought that a simple formula such as:

$$t_{R,tot} = {}^1t_R + {}^2t_R + t_h \quad [1]$$

will account for the different contributions to the total. However, an accurate ^1t_R value cannot be easily defined for a single modulated peak – due to the manner in which the first peak is sampled in the experiment. There is no specific ^1t_R value for the segment or part of the $_1$D peak that is sampled, but rather a range of retention times for the segment of the sampled peak. However, ^1t_R values can be estimated by applying a Gaussian or exponentially modified Gaussian (EMG) function to the distribution of modulated peaks for the component, and deriving the peak maximum for this reconstructed ^{1}D peak.

The Modulation Ratio; M_R

The modulation ratio was introduced (15) as a means to quantify the relationship between P_M, to the peak width at baseline on the first column (^1w_b). In many cases the time available for the ^{2}D separation is equal to P_M. In some cases (for example, when using gradient-elution LC for ^{2}D in the LC×LC experiment) the available time may be shorter. The obvious question to ask is how does one decide upon the appropriate P_M to use? Note here that in LC, the time available to the ^{2}D separation has been termed 2tc, the second dimension cycle time. LC normally does not involve a focusing 'modulation' step (nor a time-compression effect as in flow modulation in GC), so modulation period P_M might not be interchangeable with ^2t_c for LC×LC.

The modulation ratio (M_R) is defined as $4^1\sigma$ / P_M, where $4^1\sigma$ is the measure of ^1w_b. The modulation ratio is approximately equal to the number of second-dimension chromatograms ("cuts" or "slices") recorded for each ^{1}D peak. For a given ^{1}D peak, the modulation time will be shorter than the peak width at base if $M_R > 1$. M_R can easily be established, since both P_M and ^1w_b are or should be known and this can aid in method set-up (16). The number of modulated peaks recorded (the modulation number, n_M) depends on the magnitude (injected mass) of the component, the modulation phase, the modulation period relative to the peak width and the sensitivity of detection of the 2D peaks for the compound. Thus, n_M cannot be rigorously defined.

A number of experimental parameters can be set based on the desired M_R value and the value of P_M derived from the ^1w_b value. For instance, P_M determines the maximum value

of 2tR that can be recorded without wrap-around. Under non-programmed conditions ^2t_R is related to ^2k and ^2t_M (or the equivalent term $^2t_0$ in size-exclusion chromatography).

Other Definitions

In Table 3 a number of other relevant definitions are collected. Several of these are specifically derived from the field of GC×GC, but their use need not be exclusive for this technique. For example, the word modulator may equally well be used to describe the intermediate stage in a number of other comprehensive multidimensional chromatography methods. One result from the Volendam discussion was that a modulator does not necessarily need to incorporate a focusing effect; in fact there is no rationale for insisting that focusing is necessary according to the definitions of comprehensive multidimensional chromatography. However, GC×GC is most readily accomplished in practice with the aid of focusing. The latter is easily achieved by thermal modulation in GC×GC, but the increasingly popular method of flow modulation does not rely on a focusing effect in space. However, it does have a compression effect in time. Focusing is also not usually encountered in the comprehensive 2D combination of two liquid-phase separation methods.

Table 4: Non-exhaustive list of symbols suggested for use in GC×GC (and other comprehensive 2D separation methods).

Symbols	Definition
^1d_c, ^2d_c	Internal diameters of the first- and second-dimension columns (respectively) used in a comprehensive two-dimensional system.
^{1}D, ^{2}D	First dimension and second dimension of a C2DC system
1D, 2D	One dimensional or two-dimensional system
^1t_R, ^2t_R	Retention times of a peak in the first and second dimension of a comprehensive two-dimensional system (respectively). Note that ^2t_R can potentially differ for each modulated peak of a given injected component.
^1t_M, ^2t_M	Hold-up times (or "dead" times) of the first and second columns of a comprehensive two-dimensional system (respectively).
^1k, ^2k	Retention factors of a peak eluting from the first-and second-dimension columns of a comprehensive two-dimensional system (respectively)
^1I, ^2I	Retention indices of a peak eluting from the first- and second-dimension columns of a comprehensive two-dimensional system (respectively)
^1N, ^2N	The numbers of theoretical plates of the first and second columns of a comprehensive two-dimensional system (respectively).
$^1N_{eff}$, $^2N_{eff}$	The numbers of effective plates of the first and second columns of a comprehensive two-dimensional system (respectively).
$^1\sigma$, $^2\sigma$	Standard deviations of a peak eluting from the first-and second-dimension columns of a comprehensive two-dimensional system (respectively).
^1w_b, ^2w_b	Peak widths at base of a peak eluting from the first-and second-dimension columns of a comprehensive two-dimensional system (respectively).
^1R_s, ^2R_s	Resolution values of a peak pair eluting from the first and second column of a comprehensive two-dimensional system (respectively).
^1n_c, ^2n_c	Peak capacities of the first and second columns of a comprehensive two-dimensional system (respectively) [the use of n_c is advised to avoid confusion with n that is sometimes used for theoretical plates]
^1d_f, ^2d_f	Film thicknesses of the first and second columns of a comprehensive two-dimensional system (respectively).
$^1\bar{u}$, $^2\bar{u}$	Average linear velocities in the first and second columns of a comprehensive two-dimensional system (respectively).
^1T_e, ^2T_e	Elution temperatures for a peak eluting from the first dimension and second dimension of a comprehensive two-dimensional GC system (respectively). (note that ^1T_e and ^2T_e will be essentially the same due to the very fast elution of components on ^{2}D for the GC×GC experiment, defining isothermal elution)
T_M	Modulator temperature
P_M	Modulation period
M_R	Modulation ratio
$^1t_{R,app}$	Apparent first dimension retention time of the component on the first dimension
t_h	Hold time of the peak in the modulator
As_{2D}	Two-dimensional peak asymmetry

[8]Table 4: Non-exhaustive list of symbols suggested for use in GC×GC (and other comprehensive 2D separation methods). [Click to Enlarge].

Symbols

Table 4 lists a number of symbols that are recommended for use in comprehensive 2D separations in general and GC×GC in particular. The use of the superscript prefix 1 or 2 is suggested to distinguish between the ^{1}D and ^{2}D columns. This table has a number of more recent examples of symbols that have been reported for GC×GC. Table 5 reports a selection of nomenclature proposed for aspects of LC×LC according to a recent paper (17), in which the authors state that they endeavour as much as possible to base their nomenclature on that used in the 2003 *LC•GC Europe* article.

Table 5: Additional list of symbols used by Potts et al. (17) for LC×LC.

α	Under-sampling coefficient
β	Under-sampling correction factor
$^1n'_c$	Corrected peak capacity of the first column of a comprehensive two-dimensional system (respectively); $^1n_c/\beta$
^1t_g, ^2t_g	Gradient times of a first dimension and second dimension comprehensive two-dimensional LC system (respectively)
$^1n'_{c,0.9}$	Corrected first dimension peak capacity at 90% of its limiting value (corrected for under-sampling)
$^1n'_{c,2D}$	Corrected (2D) peak capacity (corrected for under-sampling)
$1n'_{c,2D,0.9}$	Corrected (2D) peak capacity at 90% of the limiting value (corrected for under-sampling)
$1n'_{c,2D,max}$	Corrected (2D) peak capacity at the limiting value (corrected for under-sampling)
^2t_c	Second dimension cycle time (sampling time of the first dimension)
$^2t_{g,opt}$	Gradient times of the second dimension of a comprehensive two-dimensional LC system at which corrected (2D) peak capacity is a maximum
t_{re-eq}	Second dimension re-equilibration time: part of the cycle time
$n_{c,2D}$	Theoretical peak capacity of a comprehensive 2D chromatography system (R_S = 1)

[9]Table 5: Additional list of symbols used by Potts et al. (17) for LC×LC. [Click to Enlarge].

Conclusion

Comprehensive 2D separations are increasingly important for the separation of complex mixtures. In this paper, a number of suggestions for definitions, nomenclature and symbols are presented that originated from the community involved with comprehensive 2D gas chromatography (GC×GC), but may be equally applicable for other comprehensive 2D separations. Some examples of studies that illustrate determination of specific parameters in the GC×GC experiment are outlined.

The use of clear, unambiguous and well-defined terms and symbols may assist in better mutual communication between separation scientists, and between separation scientists and the broader scientific community.

References

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