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Peak detection methods for GC × GC: An overview

L.L.P. van Stee [1,*], U.A.Th. Brinkman

Division of BioAnalytical Chemistry, VU University Amsterdam, De Boelelaan 1083, 1081 HV Amsterdam, The Netherlands

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ABSTRACT

The literature on methods for peak detection and integration for comprehensive two-dimensional gas chromatography (GC × GC) is reviewed with a focus on methods for the detection of individual peaks. These methods are of importance to make GC × GC generally applicable for identification and subsequent quantification of target compounds, and for non-target screening strategies, such as used in, e.g. food, biological, environmental and metabolomics studies, as well. There are three main groups of technique: methods based on 1D peak integration and subsequent automated clustering, multivariate methods and graphical methods. The principles, merits and demerits of each technique are discussed.

Contents

1. Introduction

The use of comprehensive two-dimensional gas chromatography (GC × GC) is rapidly becoming more widespread also outside academia, especially since much improved hardware is now commercially available. Basically, GC × GC has three main benefits compared to one-dimensional GC (1D-GC): (*i*) if a sample

* Corresponding author. Tel.: +31 (0)88 866 15 04; fax: + 31 (0) 88 866 69 70
E-mail address: leo@vanstee.eu (L.L.P. van Stee).
[1] Present address: Triskelion BV, Utrechtseweg 48, 3704 HE Zeist, The Netherlands.

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contains a number of classes of structurally related compounds, a group-type separation can often be effected; (*ii*) in most cases a better separation between individual compounds can be realised; (*iii*) if GC × GC can separate the analytes of interest from the bulk of the sample matrix, sample preparation can be simplified.

Petrochemistry was the first area in which GC × GC was widely applied, and today the technique is regularly used, e.g., to monitor and improve refinery processes. While for petrochemicals improved group-type separation is the main benefit, the higher separation efficiency by itself has been found to be extremely valuable in many other areas: GC × GC is increasingly being used today for the analysis of complex environmental, food and biological samples. The chemical diversity of the compounds in these samples is often large and the resulting chromatograms are therefore usually less structured than petrochemical samples; consequently, in most cases, the quantification of individual compounds rather than groups is required.

As will be explained in more detail below, in GC × GC the signal of an individual compound is split into several peaklets (also called pulses or modulations) which have to be combined to reconstruct the complete GC × GC peak. Automating this combination process, i.e. 2D peak detection, is a challenging problem – especially when large sample series and many analytes are involved. Indeed, peak detection – which is the subject matter of the present review – is a much more complex problem in GC × GC than in 1D-GC. Other chemometric techniques such as retention time alignment, feature finding – i.e. finding distinct differences in large series of samples for e.g. metabolomics studies, visualisation, optimisation, background correction, etc.—are also more complex than in 1D-GC. For a discussion of techniques that deal with this wide range of topics, the reader is referred to publications such as [1–9] and references therein.

2. GC × GC: principles and visualisation

In multidimensional gas chromatography, a second column is connected to the outlet of the first column, to enable a second separation with different selectivity. A device that can trap and release compounds eluting from the first column is inserted between the two columns. In one type of multi-dimensional GC, so-called heart cutting (GC–GC, a single fraction of typically 30–60 s of length eluting from the first column is trapped and re-analysed on the second column; the remaining sections of the chromatogram are diverted via a waste port. The chromatogram of the second separation has the same format as a normal 1D chromatogram and data analysis can be performed using standard methods. If there are a few key components in a sample which cannot easily be separated from each other and/or interfering matrix compounds, GC–GC is a rewarding strategy. However, there are two main disadvantages: (i) during trapping of the fraction of interest the resolution achieved on the first column is lost, and (ii) the procedure rapidly becomes very time-consuming and complicated if more than a few fractions have to be re-analysed; that is, non-target screening is very impractical.

In contrast to GC–GC, in which usually only a *single* fraction is re-injected onto the second column, in GC × GC *many* fractions comprising the *entire* 1D chromatogram are re-analysed, whence the often used term 'comprehensive two-dimensional gas chromatography', or GC × GC. A typical set-up of such a system consists of a regular GC system with two columns coupled in series by a modulator. The modulator is a device used to repeatedly trap, concentrate and, next, release compounds eluting from the first dimension column [10–13]. The length of the trapped fractions is chosen such that loss of the first-dimension resolution is minimised. Consequently, the sampling rate has to be high enough to allow several measurements to be made across each first-dimension peak. Peak widths in the first-dimension separation – which is usually carried out on a conventional capillary column of 15–30 m length – typically are 10–30 s; the second separation should therefore be completed in 2–8 s if one wants to have at least four sampling points across a 1D peak. Such fast separations can only be realised on short capillary columns of 1–2 m length, and preferably with a narrow bore and a thin film in order to maximise the plate number. All sample constituents are now subjected to two separations based on mutually different retention principles. A schematic illustration is shown in Fig. 1a and b: for each individual compound injected onto the first-dimension column several discrete peaklets show up in the second-dimension chromatograms. As regards data analysis, this peak-into-peaklet splitting is the major difference between 1D-GC and GC × GC.

The result of a GC × GC analysis is a collection of many short second-dimension chromatograms. In principle, each second-dimension run can be stored as a separate data file. However, since the basics of most software were developed for 1D chromatography, it is common practice to record all short chromatograms sequentially in a single file.

The raw GC × GC data can of course be visualised as a conventional chromatogram (see Fig. 1b). However, interpretation will then be very difficult because, from the raw data, one cannot easily tell which peaklets belong to the same compound. In addition, any structure present in the chromatogram that can aid interpretation is not visible. These features only show up after so-called demodulation. Basically, demodulation implies cutting of the sequential GC × GC

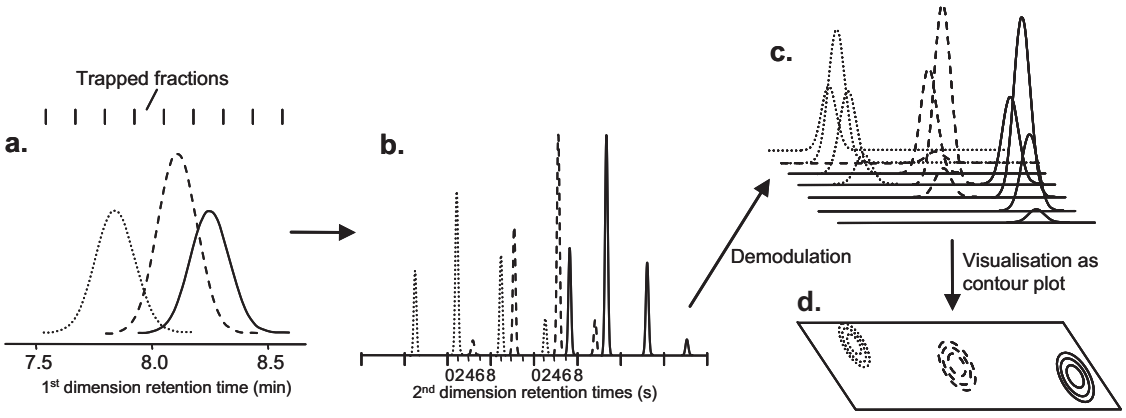

Fig. 1. Schematic depiction of a GC × GC separation. Three peaks showing partial overlap after the first-dimension separation (**a**) are modulated (8 s modulation time) and detected as several discrete peaklets for each compound (**b**). The result of demodulation and visualisation is shown in **c** and **d**, respectively.