Journal of Chromatography A, 1325 (2014) 204–212

Contents lists available at ScienceDirect

Journal of Chromatography A

journal homepage: www.elsevier.com/locate/chroma

Rapid determination of thermodynamic parameters from one-dimensional programmed-temperature gas chromatography for use in retention time prediction in comprehensive multidimensional chromatography

Teague M. McGinitie[a], Heshmatollah Ebrahimi-Najafabadi[a,b], James J. Harynuk[a,*]

[a] Department of Chemistry, University of Alberta, Edmonton, Alberta, T6G2G2, Canada
[b] Department of Medicinal Chemistry, School of Pharmacy, Guilan University of Medical Sciences, Rasht, Iran

ARTICLE INFO

Article history:
Received 18 October 2013
Received in revised form 2 December 2013
Accepted 3 December 2013
Available online 17 December 2013

Keywords:
Comprehensive two-dimensional gas chromatography
Gas chromatography
Retention time
Prediction
Thermodynamics

ABSTRACT

A new method for estimating the thermodynamic parameters of $\Delta H(T_0)$, $\Delta S(T_0)$, and ΔC_P for use in thermodynamic modeling of GC×GC separations has been developed. The method is an alternative to the traditional isothermal separations required to fit a three-parameter thermodynamic model to retention data. Herein, a non-linear optimization technique is used to estimate the parameters from a series of temperature-programmed separations using the Nelder–Mead simplex algorithm. With this method, the time required to obtain estimates of thermodynamic parameters a series of analytes is significantly reduced. This new method allows for precise predictions of retention time with the average error being only 0.2 s for 1D separations. Predictions for GC × GC separations were also in agreement with experimental measurements; having an average relative error of 0.37% for ^1t_r and 2.1% for ^2t_r.

1. Introduction

Predictive models of GC retention can be useful for several tasks including the optimization of separation conditions [1] and the identification of unknown peaks in chromatograms [2]. With comprehensive techniques such as GC × GC becoming more prevalent, predictive models that can provide accurate retention information for these separation modes (ideally in both separation dimensions) are also required. The complexity associated with optimizing a comprehensive two-dimensional separation (e.g. GC × GC) is exponentially greater than that for the optimization of a one-dimensional separation. This complexity arises due to the interdependence of the separation conditions in the two dimensions. Consequently, changes made to one dimension (i.e. column geometry, column chemistry, temperature, or flow) will affect the conditions experienced by analytes in both dimensions of the separation [3]. Given the large number of variables that could be optimized in a GC × GC separation it would be advantageous to use predictive models to aid in the optimization process.

Predictive modeling could also be used as a tool to interpret the information contained within the structured retention patterns observed in GC × GC. Using a model of chromatographic retention for one- or multi-dimensional separations, an extra layer of information to confirm the identity of a compound could be provided. This ability to identify compounds in a sample on the basis of retention information and mass spectral data would be particularly useful in distinguishing structural isomers which are often difficult (or impossible) to distinguish by mass spectrometry alone. The need for such interpretive tools is clear when one considers that GC × GC chromatograms frequently contain thousands (or even tens of thousands) of peaks eluting across a two-dimensional plane [4].

A variety of models exist for the prediction of retention behavior in 1D GC and while the field of GC × GC is relatively new, several attempts have already been made to create predictive models suitable for multidimensional gas chromatography. One of the first predictive models to be adapted to GC × GC used calculated vapour pressures derived from the Kovats retention indices in order to estimate retention times [5]. This work introduced the usage of isovolatility curves to estimate the retention of analytes in the second dimension. Western and Marriott [6] then refined this technique through the use of timed injections of alkane standards. Since then there have been several variations of this technique for use in

* Corresponding author. Tel.: +1 780 492 8303; fax: +1 780 492 8231.
E-mail address: james.harynuk@ualberta.ca (J.J. Harynuk).

0021-9673/$ – see front matter
http://dx.doi.org/10.1016/j.chroma.2013.12.008

GC × GC of which most are centered on the use of relating retention index to an analyte's partition coefficient in order to model retention behavior. Several authors including Vendeuvre [7], Pang [8], Arey [9] and Seeley [10] have adapted these methods in various ways.

RI-based models have the advantage of an extensive library of RI data from which to work, at least for some stationary phases. However, the generation of isovolatility curves remains technically difficult on most instruments and can be time consuming [11]. Furthermore, it has been argued that the use of alkanes as retention index standards is not necessarily appropriate for the second dimension in GC × GC [12]. Despite these limitations for GC × GC, the popularity of RI models remains high, with several new studies conducted within the last few years [13,14] and a recent review by von Muehlen and Marriott [15].

With the rise of GC × GC, thermodynamic modeling of retention times is being revisited by several research groups. Zhu et al. used thermodynamics predicted from isovolatility curves to predict the retention indices of alcohols [16]. While Lu et al. estimated enthalpic and entropic parameters to predict retention times for a variety of pyridines [17]. The manner by which these estimations were performed worked incredibly well for optimizing a specific separation on the instrument used to collect the data. However, it is unclear how easily predictions could be ported from one system to another. Thewalim et al. used a two-parameter thermodynamic model to estimate retention times for various column sets [18]. Dorman et al. also used a thermodynamic model based on ΔH and ΔS to predict the retention times of select components from the Grob mixture in a GC × GC separation [19], and Zhu et al. have used thermodynamic modeling to predict retention times of alkanes and PAHs in GC × GC separations [20].

Thermodynamic-based models are attractive for several reasons, first thermodynamic models can account for changing operating conditions while maintaining accuracy, assuming that the model accurately accounts for the temperature dependence of the thermodynamic parameters over the range of temperatures studied [21]. This is an advantage over models based on specific properties (such as RI) which have a dependence on oven temperature and ramp rate [22]. The second advantage that thermodynamic models hold is that they do not require determinations of isovolatility curves. As our previous research has shown, accurate prediction of ${}^1t_r$ and ${}^2t_r$ for a molecule in GC×GC is possible using thermodynamics provided that the molecule's thermodynamic parameters are known for each stationary phase involved [23].

Regardless of the advantages thermodynamic modeling offers, its widespread usage is hampered by the unavailability of a library or other repository of thermodynamic data for a wide range of molecules. Without a library of thermodynamic data for a large cross section of analytes on a variety of stationary phases, thermodynamic predictions will largely remain in the realm of academic curiosities and small custom applications. Towards this end, we have previously outlined a standardized approach to estimate an analyte's thermodynamic parameters in a way that permits their use in inter-laboratory studies [24]. The same research introduced an automated method for the collection of thermodynamic data which reduced the required operator time necessary to perform careful manual injections to gather data.

Despite these refinements, the collection of thermodynamic data remains a time-consuming endeavor. Using our previous approach, a minimum of six isothermal separations performed in triplicate were required to obtain accurate thermodynamic parameters for a single compound. While it may be possible to run a solution that contains several analytes of interest, the nature of isothermal chromatography limits the utility of this approach. To date, the work of Dorman et al. [19] appears to be the only example of an approach that uses temperature-programmed separations to obtain thermodynamic data for a two-parameter thermodynamic model of the GC separation. The problem with two-parameter thermodynamic models of GC separations is that the enthalpy (ΔH) and entropy (ΔS) of the GC process are assumed constant; however, these terms are in fact observed to be temperature-dependent over the range of temperatures commonly experienced by an analyte in temperature-programmed GC separations. For more accurate predictions over the range of temperatures typical of temperature-programmed GC, the change in adiabatic molar heat capacity (ΔC_P) must be considered in order to account for the temperature-dependence of (ΔH) and (ΔS).

Herein we demonstrate a method whereby thermodynamic information for a three-parameter model of the GC process can be rapidly collected and calculated for multiple analytes based on data obtained from a series of temperature-programmed separations. This rapidly collected data can then be used with existing models for the prediction of GC or GC × GC separations.

2. Theory

In order to accurately predict retention in a gas chromatographic separation it is necessary to estimate the changes in enthalpy and entropy of the analyte at some reference temperature, $\Delta H(T_0)$ and $\Delta S(T_0)$, respectively, as well as the change in its adiabatic molar heat capacity, ΔC_P. In previous works [21,23,25–29] these parameters have been estimated through a series of isothermal separations from which a regression of the partition coefficient, K, against temperature, T, provides estimates for $\Delta H(T_0)$, $\Delta S(T_0)$, and ΔC_P through Eqs. (1)–(4) [21].

$$K(T) = e^{A + \frac{B}{T} + C\ln(T)} \tag{1}$$

$$A = \frac{\Delta S(T_0) - \Delta C_P In(T_0) - \Delta C_P}{R} \tag{2}$$

$$B = -\frac{\Delta H(T_0) - \Delta C_P T_0}{R} \tag{3}$$

$$C = \frac{\Delta C_P}{R} \tag{4}$$

These thermodynamic estimates are then used in a time summation model based on the method of Snijders et al. [30] to arrive at the retention time. The difference between the Snijders approach and ours is that at each step the value of the partition coefficient is recalculated based on the thermodynamic parameters for the compound, and the model is adapted for GC and GC × GC predictions [23]. In brief, the distance traveled by an analyte which is initially at a position x_n along the column during a brief interval of time is calculated. The time interval is sufficiently small for both the carrier gas velocity and retention factor of the analyte to be assumed constant. Thus, at the end of interval n, the analyte is at position $x_{(n+1)}$. Then, the local velocity of the carrier gas and partition coefficient are recalculated based on the new position in the column and changes in oven temperature and/or inlet pressure and the distance traveled in the subsequent time interval is calculated. The process repeats until the total distance traveled by the analyte exceeds the length of the column.

In this study, a nonlinear optimization procedure is used to estimate the thermodynamic parameters that would be required for an analyte to exhibit the retention times observed in a series of temperature-programmed separations. Here we combined the previously used time summation model with the Nelder–Mead simplex algorithm [31]. However, any other optimization technique such as genetic algorithms, particle swarm optimization, or Quasi-Newton techniques could in principle be used to minimize the error values of the predicted retention times. The Nelder–Mead