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Bachelor in Chemical and Biochemical Engineering

Comparisons of the Adsorption Equilibrium of Benzene Derivatives in Reversed-Phase Liquid Chromatography

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Abstract

The isotherm behaviour of three benzene derivatives, Valerophenone (VPhn), Butyl Benzoate (BBzt) and tert-butylbenzene (tBBz), as well as two binary mixtures VPhn+tBBz and BBzt+tBBz were studied. To try to describe to explain the isotherm data, the multi-layer multi-component model was used, a model recently developed by a research group led by Prof. Andreas Seidel-Morgenstern in the Max Planck Institut for Dynamics of Complex Technical Systems (MPI). The main goal of this work is to obtain experimental validation to this model, which until now only existed in paper. The results showed that this model can describe well the isotherm data for both single and multi component systems. Since multi component experiments consume lots of time and resources, cross-checks between the fitted parameters of single and multi components were performed to see if single parameters could describe well the multi component isotherms. The results show that the cross check is not bad, although it's always needed some mixture data. Some further work can be done to determine the minimum amount of multi-component data that gives a good description of the mixtures' isotherm behaviours.

Resumo

Foi estudado o comportamento isotérmico de três derivados do benzeno, Valerofenona (VPhn), Benzoato de Butilo (BBzt) e *tert* Butilbenzeno (tBBz), assim como duas misturas binárias, VPhn+tBBz e BBzt+tBBz. Para tentar explicar os dados isotérmicos, o modelo multi-camada multi-component foi usado, modelo recentemente desenvolvido por um grupo de investigação liderado pelo Prof. Andreas Seidel-Morgenstern no Instituto Max Planck para Dinâmica de Complexos Sistemas Técnicos (MPI). O principal objetivo deste trabalho é obter validação experimental para este modelo que, até agora, só existia em papel. Os resultados mostram que este modelo consegue escrever bastante bem as isotérmicas dos compostos puros e dos sistemas binários. Tendo em conta que o protocolo experimental para os sistemas binários é muito complexo e requer muito tempo e recursos, os parâmetros calculados para os compostos puros foram usados nos sistemas binários e vice-versa, para ver se os primeiros conseguiriam, por si só, descrever as isotérmicas dos sistemas binários. Esta validação experimental não foi má, embora seja sempre preciso dados experimentais das misturas. Este trabalho pode ser continuado com o objetivo de determinar a quantidade mínima de dados experimentais das misturas de forma a obter uma boa descrição das isotérmicas destas.

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Acronyms

BBzt ButylBenzoate.

BC Breakthrough Curve.

ELI Extended Langmuir Isotherm.

FA Frontal Analysis.

FACP Frontal Analysis by Characteristic Point.

HPLC High Performance Liquid Chromatography.

IAST Ideal Adsorbed Solution Theory.

IUPAC International Union of Pure and Applied Chemistry.

LC Liquid Chromatography.

LSQ Least Squares.

MLMC Multi-Layer Multi-Component.

NPLC Normal-Phase Liquid Chromatography.

RPLC Reversed-Phase Liquid Chromatography.

tBBz tert-ButylBenzene.

TLC Thin-Layer Chromatography.

VPhn ValeroPhenone.

Nomenclature

C^{sat}	saturation concentration (mg/ml)
C_0	concentration of the feed ($mmol/ml$)
c_i	concentration of the component i ($mmol/ml$)
c_i^{eq}	concentration of component i in solution after equilibrium (mg/ml)
c_i^{init}	initial concentration of component i (mg/ml)
$K_{1,i}$	first constant of component i (min)
$K_{2,i}$	second constant of component i (min)
M_{acc}	accumulated moles of solute inside the column ($mmol$)
m_{ads}	moles of adsorbent (mg)
n	number of layers
q	moles of solute per volume of stationary phase ($mmol/ml$)
q_i^{eq}	mass concentration of component i in volume of adsorbent after equilibrium (mg/ml)
q_{MAX}	maximum adsorbed moles in a monolayer per volume of adsorbent ($mmol/ml$)
$t_{0,f}$	front dead time (min)
$t_{0,r}$	rear dead time (min)
$t_{infl,f}$	front (or loading) inflexion time (min)
$t_{infl,r}$	rear (or elution) inflexion time (min)
V_0	column void volume (ml)
$V_{0,sys}$	void volume of the system without column (ml)
V_{ads}	volume of adsorbent (ml)
V_{sol}	volume of solution (ml)

Chapter 1

Introduction

1.1 Chromatography: from Ancient to Modern Times

The experiment which gave birth to Chromatography is well known. In 1902, the Russian botanist M. S. Tswett managed to separate plant pigments with proper solvents and adsorbents [7, 14]. In former studies of his work about the separation of α- and β-carotenes, it was seen that he tried hundreds of combinations of stationary and mobile phases and understood that the most important characteristics of the chromatographic process are the purity of the adsorbent and the particle size distribution [7]. He also knew the three ways to realize a chromatographic process: elution, frontal analysis and displacement.

30 years had to pass before someone could reproduce Tswett experiment, accomplished by Kuhn and Lederer. After that, the development of preparative and adsorption chromatography started to grow at a high rate.

1.2 Normal-/Reversed-Phase Chromatography

According to the IUPAC, liquid chromatography (LC) is a mean of separating components in mixtures by distributing them between two phases, in which one of the phases moves freely (mobile phase) through the other, which is fixed (stationary phase), and it's called liquid chromatography because the mobile phase is a liquid. Since its invention, many types of LC were born, such as microbore LC, preparative LC and high performance LC (HPLC), but the emphasis will be in the normal- (NPLC) and reversed-phase (RPLC) chromatography.

Normal-phase LC is the oldest type of chromatography, discovered by Tswett [8],

and it's still the predominant technique for thin-layer chromatography (TLC) and low-pressure dry-column LC. Its main characteristic is the stationary phase being more polar than the mobile phase. Since the stationary phase (usually inorganic adsorbents like silica gel) is more polar than the mobile phase, the retention time increases when the polarity of the mobile phase decreases and vice-versa. After the appearance of RPLC, NPLC started losing ground because RPLC offers much more selectivity, even with mixtures in which the two compounds have minor differences in their molecule sizes. That's why RPLC is usually chosen when working with HPLC. Either way, NPLC is much better in isomers separation [8].

In reversed-phase LC the stationary phase is less polar than the mobile phase, quite hydrophobic, so the retention time increases when the polarity of the mobile phase increases and vice-versa. In RPLC, the separation is determined almost entirely by molecular size and polarity, so it easily separates molecules with similar polarity but different carbon numbers. However, since the stationary phase is hydrophobic (usually C18 or C8), the mobile phase cannot be only water. If only water is used, chances are high that the solutes never elute from the stationary phase, ruining the analysis. Usually, at least 5-10% of organic solvent (methanol, acetonitrile and tetrahydrofuran) has to be mixed with water.

With all these chromatographic methods, the main problem is to choose the best combination for the process studied, so it's important to answer these simple questions: is it needed only organic solvents as mobile phase? Are the components isomers? Is the objective separation or analysis? After answering these main questions, it's much easier to choose the best method.

1.3 Liquid Adsorption - The Isotherm Models

In chromatographic processes, the understanding of what happens inside the column is critical. Each component has different behaviours, regarding retention time, type of adsorption (monolayer or multilayer) and affinity with solid phase, with different packings, different mobile phases and mobile phase ratios (if they are a mixture). If a Frontal Analysis was to be performed with a broad range of concentrations and after the calculation of the adsorbed masses in the stationary phase, one could plot the adsorbed mass concentration in the solid phase, q_0, as a function of the concentration of the inlet, C_0, and obtain several types of curves. Below are represented the most common curves:

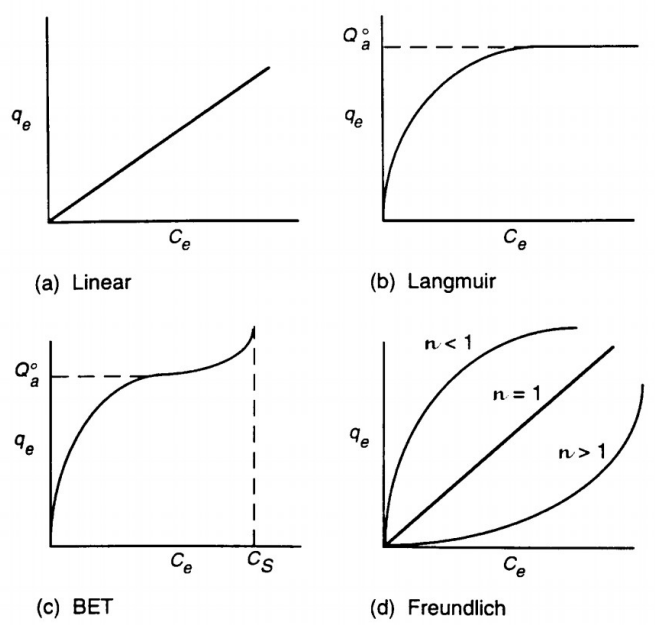


Figure 1.1: The four most common Isotherm behaviours [19]

Figure 1.1 (a) is the simplest case of adsorption, when the adsorbed mass is directly proportional to the bulk concentration. In very dilute concentrations, all compounds follow this behaviour, however it's not usual to see a compound with linear behaviour in a broad range of inlet concentrations.

The curve presented in Figure 1.1 (b) has a concave shape, meaning, in low concentrations, the increase in q_0 is practically linear, but as the concentration of the inlet increases even more, q_0 reaches a maximum, the saturation concentration of solute in the stationary phase. This type of curve is usually called the Langmuir Isotherm since it was Irving Langmuir who developed the first model that described very well this curvature. However, his work was based in a theoretical background and several assumptions had to be made to reach a good mathematical model and, in solid-liquid adsorption, many times some of those assumptions are invalid and the model is not well fitted to the experimental data.

Figure 1.1 (c) is first concave and then turns to convex shape. It shows that it has Langmuirian behaviours for lower concentrations, but if the concentration continues to increase, it suddenly surpasses the maximum adsorbed capacity. In fact, in lower concentrations it occurs only monolayer adsorption, which means, the solute is only adsorbed directly in the solid phase surface, and in higher concentrations the adsorption starts to be multilayer, all the active sites are covered with solute and now the molecules adsorb on top of the previously adsorbed molecules. It's most commonly called a BET behaviour. The BET Isotherm Model can describe, depending on it's parameters, the concave shape, the convex shape (monolayer adsorption) and multilayer adsorption.

In Figure 1.1 (d), when $n > 1$, is shows a convex shape. That happens when the affinity of the solute with the stationary phase always increases with the increasing of C_0, never

to reach a saturation concentration. Of course it only applies in C_0 ranging from 0 to C^{sat}. The most common model that describes this adsorption behaviour is the Freundlich Model, despite its empirical nature. This model can describe three types of shape: the concave, the convex and the linear shape, depending on the values of it's parameters. Furthermore, the convex shape is also usually called an anti-Langmuirian shape.

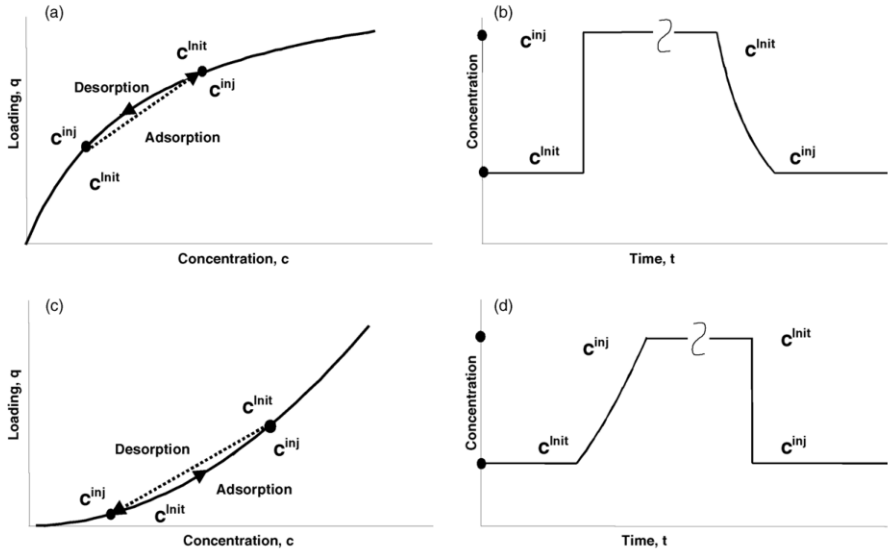


Figure 1.2: Elution Profiles [25]

In Figure 1.2 is seen the most common isotherms (Langmuirian and anti-Langmuirian) and their elution profiles. Figure 1.2 (b) shows a very steep front and a diffuse rear. It's logic because components which follow a langmuirian behaviour tend to adsorb more in lower concentrations. That can be seen in Figure 1.2 (a) where the slope, in lower concentrations, is much bigger than in higher concentrations. It means that, when the step response is interrupted, the concentration starts to decrease and the retention time increases, forming the "long tail" seen in the figure. Figure 1.2 (d) is exactly the opposite, has a very diffuse front and a very sharp rear. The way of thinking is the same as before, only that is exactly the inverse, since it adsorbs more in higher concentrations, when the step response is turned on it forms the "long tail" and when it's shut down the retention time decreases abruptly, forming that very sharp rear.

1.3.1 Multi Component Isotherms

1.3.1.1 Extended Langmuir Isotherm

The extended langmuir isotherm (ELI) was first developed in 1930 by Butler and Ockrent. This model considers competitive behaviour between species and was based in all the langmuir model assumptions. After this model development, several researchers modified the ELI to try and have more accurate and precise approaches for description

of binary mixtures, such as Jain and Snoeyink in 1973 and [9]. One setback about these models is that they always assume only monolayer adsorption.

1.3.1.2 Ideal Adsorbed Solution Theory and some Derivations

The ideal adsorbed solution theory (IAST) is a powerful tool for predicting multi-component isotherms with only the single component isotherms. The biggest model assumption is that the adsorbates are thermodynamically ideal, which means that, for two components A and B, the interactions between A and B are no different than those between A and A and B and B. With this assumption and good isotherm models to describe the pure components' behaviours, the mixture equilibrium data can be directly predicted from the pure component data. Usually the predictions are quite good, but a major setback is that it needs, for each combination of concentration points of A and B, to solve numerically the equations associated with this model. To get very good equilibrium mixture data, the numerical calculation can take lots of time.

There are several derivations of the IAST. Among them are the non-ideal adsorbed solution theory (NIAST), the heterogeneous ideal adsorbed solution theory (HIAST) and the predictive real adsorbed solution theory (PRAST). Several works were published, [3, 23, 24] regarding these new derivations to try and improve the IAST.

1.3.2 A Novel Generic Model: the Multi-Layer Multi-Component Isotherm

Until now, there's a lack of models that can describe correctly the behaviour of two components in a liquid adsorption process. Some studies were made using the Extended Langmuir Isotherm and some modified models [1] but with no good results. Another study was performed using a modification of the Extended Langmuir Isotherm that was successful to predict competition between species and active sites [9]. However, the latter is basically a direct application of the Extended Langmuir Model, meaning that it assumes only monolayer adsorption, an assumption that is not valid in many cases in Liquid Adsorption.

In the attempt to develop a model that can explain some phenomena that the known models can't, a research group from Max Planck Institut for Dynamics of Complex Technical Systems led by Professor Andreas Seidel-Morgenstern presented in 2016 in the Fundamentals of Adsorption (FOA) Conference the Multi-Layer Multi-Component (MLMC) Isotherm Model [10], a model based entirely on a theoretical background.

The main goal of this work is to apply this model to isotherm data of three components and two binary mixtures using the three components studied to obtain experimental validation and prove, or not, if this model and it's assumptions fit reasonably to the experimental data.

1.4 Experimental Approaches

The adsorption phenomenon varies with the mobile and stationary phases and with the component being studied. Hence, there's no way to determine adsorption isotherms in a theoretical way only, it's needed lots of experimental work. Since Chromatography was born, a significant number of experimental methods were developed, with the static methods at first and more recently the dynamic methods.

The main focus of this work resides in the dynamic methods, so the static methods will not be referred in high detail.

1.4.1 Static Methods

To measure adsorption isotherms with static methods, only the initial and the equilibrium concentrations are needed, $c_i(t = 0)$ and $c_i(t \to \infty)$ respectively.

1.4.1.1 Batch Method

In the Batch Method, a vessel is loaded with adsorbent of mass m_{ads} and it's added a certain volume of solution V_{sol} with known initial concentrations of all components, c_i^{init}. After solution addition, the equilibrium state has to be reached, so a long time has to pass before that happens. After equilibrium establishment, the amount adsorbed of each solute can be calculated using the mass balance:

$$V_{sol}c_i^{init} = V_{sol}c_i^{eq} + V_{ads}q_i^{eq} \tag{1.1}$$

Several experiments have to be done changing c_i^{init} to obtain enough data to determine the solutes' isotherms. A significant number of experiments are required and it's highly recommended to use a range of concentrations from zero to the saturation concentration of each solute. As easily seen, this method requires a huge experimental work and takes lots of time. It's also not that accurate because it's difficult to know how long it takes to reach equilibrium [15].

1.4.2 Dynamic Methods

1.4.2.1 Frontal Analysis

With the evolution of on-line detection using UV detectors and off-line analysis, frontal analysis is now the preferred method for determination of adsorption isotherms. It's called a dynamic method because it needs the outlet profile which is a function of time. With this technique the uncertainty of how long it takes to reach equilibrium state is avoided and the accuracy increases significantly when using the entire breakthrough curve (BC) for determination of the accumulated mass in the column.

This method consists in a large impulse injection, large enough for the column to be fully equilibrated with the solute. In this case the equilibrium state is reached when the BC reaches a "plateau value", the time when the outlet concentration becomes constant. Logically, this plateau value is the concentration of the injection and gives the information that no more solute is being adsorbed.

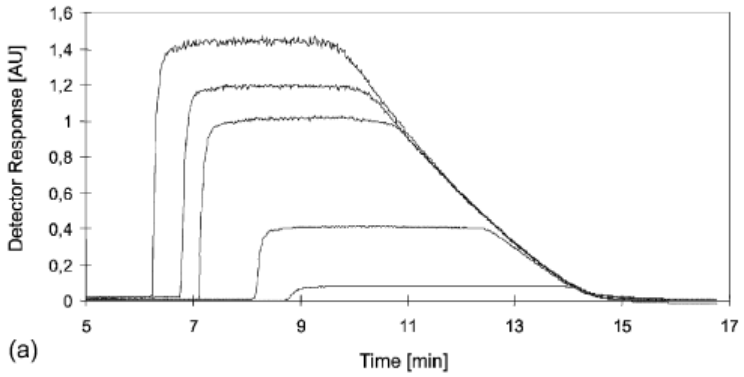


Figure 1.3: Example of a single step FA experiment [15]

The most important things in a BC are the inflection points of both loading and elution parts and the plateau value. The plateau value indicates that the column is equilibrated with the solute and the inflection points give the retention time of the component.

Since the experimental part of this work was made in an HPLC system, there are dead volumes (capillaries, pump, mixer volumes, etc.) which have to be considered in order to correctly calculate the adsorbed mass, so another experiment is required without the column. The main goal is to obtain another BC but now the inflection points will indicate the "dead time", which multiplied by the flow rate give the dead volume. This is of utmost importance because the true retention time will be $t_{infl,f} - t_{0,f}$ or $t_{infl,r} - t_{0,r}$.

Another way to use this technique is using a multi-step gradient, which means, instead of eluting after reaching the plateau value, the injection concentration is increased and is performed for all the concentrations used to calculate the isotherms. With the HPLC system this is easily performed, only one solution close to the saturation concentration and mobile phase need to be prepared, the rest is achieved using the capabilities of the system, reducing labour work.

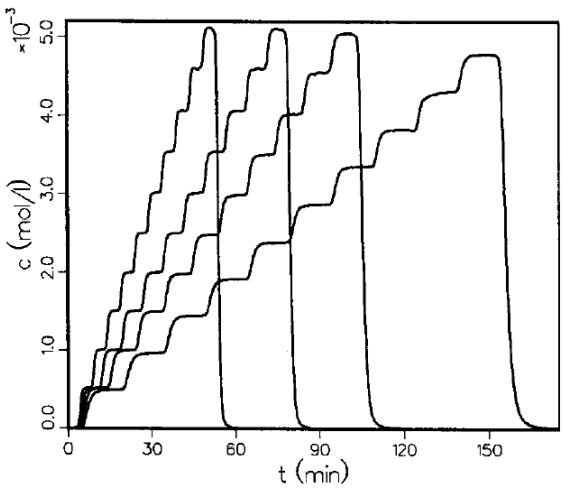


Figure 1.4: Example of a multi-step FA [15]

With all the information given above, it's easy to understand how Frontal Analysis is, until now, the best experimental method to determine adsorption isotherms, both from pure components and mixtures, because the accuracy is extremely higher and the time spent preparing and performing experiments is significantly reduced.

CHAPTER 2

MATHEMATICAL DESCRIPTIONS

2.1 Frontal Analysis

As said before, Frontal Analysis is an on-line experimental method that's used to calculate the accumulated mass inside a chromatographic column using only the inlet and outlet profiles.

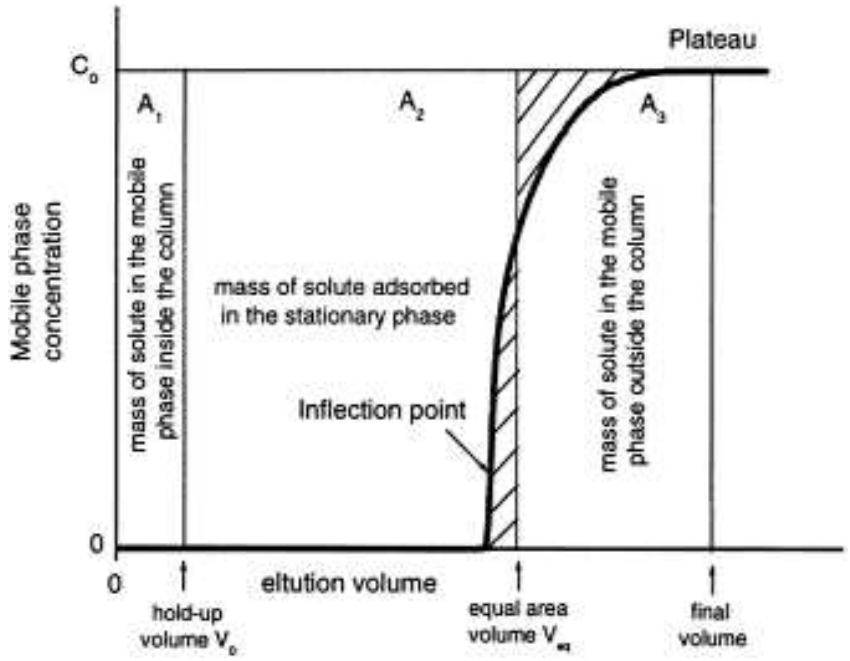


Figure 2.1: Frontal Analysis procedure for accumulated mass calculation [6]

In Figure 2.1 is shown the outlet profile of a frontal analysis experiment. The main goal is to obtain the equal area volume V_{eq} by means of numerical integration of the BC, so it becomes easy to calculate the accumulated mass with the following expression:

$$M_{acc} = C_0 * (V_{eq} - V_0) \tag{2.1}$$

With M_{acc}, C_0 and V_0 being the accumulated mass in the stationary phase[1] (A_2 area), the injected concentration of solute and the column hold-up volume, respectively. One further experiment needs to be done to calculate the volume of stationary phase inside the column to obtain the concentration of solute in the stationary phase, q_0, as:

$$q = \frac{M_{acc}}{V_{ads}} \tag{2.2}$$

As explained before, this method has to be performed with several injected concentrations to have enough data to fit the best isotherm model considering the adsorption behaviour of the target compound.

2.2 Linear Isotherm

The linear isotherm is the most basic isotherm, because the adsorbed mass concentration is linearly proportional to the liquid concentration, which means:

$$q = H.c \tag{2.3}$$

With H being the proportionality constant, usually called the Henry constant.

2.3 Langmuir Isotherm

The Langmuir Isotherm is well known and widely used both in gas and liquid adsorption. This model was developed entirely in a theoretical background, and has this form:

$$q = q_{MAX} \frac{K.c}{1 + K.c} \tag{2.4}$$

With q, q_{MAX}, K and c being the adsorbed mass concentration in the solid, the adsorbed mass concentration if all the active sites were to be occupied, the equilibrium constant and concentration in the bulk liquid, respectively.

[1] only in this case M_{acc} is the accumulated mass in the stationary phase, from here onwards M_{acc} is as described in the nomenclature

This model has several assumptions that need to be verified for the model to work, which are:

- The solid surface has to be homogeneous
- each active site can hold only one molecule
- there are no interactions between adjacent molecules

This model works particularly well in almost all cases for gases, but for liquids one has to be very careful while using this simplified form of the model because in liquid adsorption monolayer adsorption is quite rare and usually there are interactions with adjacent molecules.

2.4 Freundlich Isotherm

The Freundlich Isotherm is an empirical model that tries to have in account heterogeneity of the surface and the interaction between adjacent adsorbed molecules.

$$\frac{q}{q_{MAX}} = K_f.c^n \tag{2.5}$$

Where K_f and n are parameters to be fitted. This model works well in lower and intermediate concentrations, but fails in high concentrations. As shown in Figure 1.1 (d), it can fit well on several types of behaviour, linear, langmuirian and anti-langmuirian, depending only on the parameter n.

2.5 BET Isotherm

The BET Model, developed by Brunaut, Emmer and Teller, hence the name, is an improvement of the langmuir model to describe the phenomenon of multilayer adsorption this way:

$$q = \frac{q_{MAX}(K_a.c)c}{(1 - K_b.c)(1 - K_b.c + K_a.c)} \tag{2.6}$$

Where K_a and K_b are the equilibrium constant with the surface and the equilibrium constant with the second layer on wards, respectively. This model, depending on the parameters, can describe also langmuirian and anti-langmuirian behaviours in monolayer adsorption.

2.6 Multi-Component Isotherms

2.6.1 Extended Langmuir Isotherm

This model, as stated in the name, is a derivation of the langmuir isotherm for single components in which comprises competition between components.

$$q_i = \frac{K^0_{L,i} C_i}{1 + \sum a^0_{L,i} C_{e,i}} \tag{2.7}$$

Where K^0_L and a^0_L are the equilibrium constant and the activity coefficient, respectively. Other modifications to the ELI stated in the previous chapter account for competition (Jain and Snoeyink) and the other one accounts for molecular lateral interactions (Schay).

Jain and Snoeyink proposed an adding term to the ELI that counts for competition for binary mixtures only:

$$\begin{aligned} q_1 &= \frac{(Q^0_{m,1} - Q^0_{m,2}) a^0_{L,1} C_1}{1 + a_{L,1} C_1} + \frac{Q^0_{m,2} a^0_{L,1} C_1}{1 + a_{L,1} C_1 + a_{L,2} C_2} \\ q_2 &= \frac{Q^0_{m,2} a^0_{L,2} C_2}{1 + a_{L,1} C_1 + a_{L,2} C_2} \end{aligned} \tag{2.8}$$

Schay, in 1957, introduced an interaction factor, η, to account for interactions between adjacent molecules. This factor is to be used with both single component and multi component data. This factor is calculated minimizing this function:

$$\eta_i = \frac{100}{n - p_i} \sum_{i=1}^{n} \left[\frac{(q_{meas} - q_{calc})^2}{q_{meas}} \right]_i \tag{2.9}$$

This factor, combining with isotherm data from the ELI gives quite good results, although is only good for monolayer adsorption.

2.6.2 Ideal Adsorbed Solution Theory

This model is based on predicting multi-component isotherm data with single component equilibrium data. The calculation procedure is the following:

$$q = \sum_{i=1}^{N} q_i \tag{2.10}$$

$$z_i = \frac{q_i}{q} \tag{2.11}$$

$$C_i = z_i C_i^0 \tag{2.12}$$

$$\frac{1}{q} = \sum_{i=1}^{N} \frac{z_i}{q_i^0} \tag{2.13}$$

$$\frac{\pi_m A}{RT} = \int_0^{q_1^0} \frac{dlnC_1^0}{dlnq_1^0} dq_1^0 = \frac{\pi_1^0 A}{RT} = \int_0^{q_j^0} \frac{dlnC_j^0}{dlnq_j^0} dq_j^0 = \frac{\pi_j^0 A}{RT} = ... \text{ for } j = 2, 3, ..., N \tag{2.14}$$

Where q is the sum of the component adsorbed concentrations, q_i is the adsorbed concentration of component i, z_i the molar fraction in the stationary phase, C_i^0 is the single component concentration that produces the same spreading pressure as the mixture and q_i^0 the adsorbed concentration in equilibrium with C_i^0, π is the spreading pressure, A is the specific surface area of adsorbent, R is the ideal gases constant and T is the absolute temperature. The subscript m means mixture.

The multi component isotherms can be calculated solving these equations for each concentration of each component.

2.6.3 MLMC Model

The first assumption is that all the layers have langmuirian behaviour. For single component, the model takes this form:

$$\begin{aligned} \hat{q}_1 &= q_{MAX} \frac{K_1.c}{1 + K_1.c} \\ \hat{q}_i &= \hat{q}_{i-1} \frac{K_i.c}{1 + K_i.c} \end{aligned} \tag{2.15}$$

With $i = 1, 2, ..., n$, being n the number of layers. The derivation of this model when the number of layers is infinite can be found in the literature [10]. The final form is:

$$q = q_{MAX} \frac{K_1.c(1 + K_2.c)}{1 + K_1.c} \tag{2.16}$$

Other assumption made is that, for $2 \leq i \leq n$, $K_i = K_{i+1} = ... = K_n$. Since K_i is an equilibrium constant and depends on the interaction between the molecule and the surface, from the second layer onwards the surface (the molecules themselves) is always the same. This model can take different shapes, depending on the relationship between K_1 and K_2:

- $K_1 = K_2$: linear shape
- $K_1 > K_2$: convex shape
- $K_1 < K_2$: concave shape

When it comes to multi-component, another assumption is made. For better understanding, let's assume a mixture with components A and B and A* and B* are molecules already adsorbed. So, when another A or B molecule adsorbs on top of A* or B*, the interactions, regardless of the combinations possible, are the same, which means:

$$\mathrm{AA^*} \Leftrightarrow \mathrm{AB^*} \Leftrightarrow \mathrm{BA^*} \Leftrightarrow \mathrm{BB^*}$$

Applying the assumptions stated, the general form of the model for n layers and i components is:

$$q_i = \sum_{j=1}^{n} q_{i,j} = \sum_{j=1}^{n} \left[q_{MAX} \left(\prod_{k=0}^{j-1} \frac{\Psi_k}{1+\Psi_k} \right) \frac{K_{i,j}.c_i}{1+\Psi_j} \right] \tag{2.17}$$

With $\Psi_j = \sum_i K_{i,j} c_i$.
In this work two derivations will be used:

$$q_i = \frac{q_{MAX}}{1+\Psi_1} (K_{1,i}.c_i + \Psi_1.K_{2,i}.c_i) \tag{2.18}$$

For infinite number of layers, and:

$$q_i = \frac{q_{MAX}}{1+\Psi_1} \left[K_{1,i} c_i + \Psi_1 \left\{ 1 - \left(\frac{\Psi_2}{1+\Psi_2} \right)^{n-1} \right\} K_{2,i} c_i \right] \tag{2.19}$$

For a finite number of layers. In this derivation other shapes can be achieved:

- $K_1 < K_2$: S-Shape
- $K_1 > K_2$: langmuirian shape

At a first sight it seems a very promising work when it comes to describe adsorption behaviours, for single and multi-components, and this work will try to determine if all the assumptions are reasonable in all conditions or if they are violated in real cases.

Chapter 3

Experimental Protocol

Three components were used, Valerophenone (VPhn), tert-Butylbenzene (tBBz) and Butylbenzoate (BBzt). All of these components were acquired from Sigma Aldrich. These components were chosen for having similar molecular sizes but different functional groups, expecting to have different interactions with the stationary phase. To be certain, a FA experiment was performed with a ternary mixture of the three components. The binary mixtures VPhn with tBBz and BBzt with tBBz were chosen. The solvents used, both for preparation of solutions and mobile phase for analysis, were 50% of demineralized water and 50% of 2-Propanol HPLC grade bought from VWR Chemicals.

The type of liquid chromatography used for all the frontal analysis experiments was reversed-phase and were performed in a HPLC system which all compartments are from the Dionex Ultimate 3000 series produced by Thermo Scientific. The system had a degasser, a pump, one capillary and one cylindrical static mixers with a total volume of 400 μl (50 for capillary mixer and 350 for cylindrical mixer). For FA the mixer was not used, but for analysis it was. The column had a silica gel packing with C18 chains with 5μm of particle diameter, the length was 50 mm and the diameter was 4.6 mm. Since the main goal is to obtain isotherm data, the temperature was controlled and maintained at 27 ºC.

For the determination of dead volumes in the HPLC system, a frontal analysis experiment with fraction collection was performed. After analysis of the results, The obtained dead volume of the system was 0.9645 ml.

The column properties, such as void volume, stationary phase volume and total porosity had to be studied. Having that in mind, the Blue Dextran colorant was used because it's known to have no affinity with the stationary phase. One setback is that the colorant molecule is too big to enter the particle pores, so it could be only calculated the external porosity. To determine the total porosity of the column, water was used because the molecular size is much smaller than the pore size. Although water is invisible in the UV,

a small injection can induce perturbations in the baseline, and with those perturbations it's possible to see the time in which the injected water comes out of the column. With the water and the colorant retention times it's possible to calculate all the parameters mentioned above, presented below:

Table 3.1: Column Properties

ϵ_T	V_0 (ml)	V_S (ml)	V_T (ml)
0.497	0.413	0.418	0.831

For the single components, two solutions were prepared, one close to the saturation concentration, and the other a dilution of 1:5 of the first for each component. Two 10-step gradient Frontal Analysis for each component and each solution were performed in a HPLC system, which was programmed to increase the inlet concentration by 10% of the solution concentration each 7 minutes, starting at 10% and ending at 100%. The flow rate was 2 ml/min, with a total experiment time of 91 minutes, including elution. For those experiments, the outlet had to be collected in fractions, two per minute, because BBzt had a significant amount of impurities, so only the fractionation could give the pure BC for BBzt. For the other components, fraction collection was performed as well for the experimental protocol to be consistent. The fraction collector is a part of Dionex Ultimate 3000 series and also produced by Thermo Scientific. The prepared solutions are shown below:

Table 3.2: Solutions Concentrations for Single Components

Dilution	C_{tBBz} (mol/L)	C_{VPhn} (mol/L)	C_{BBzt} (mol/L)
Mother Liquor	0.090	0.230	0.218
Dilution 1:5	0.018	0.046	0.043

For each mixture, three solutions were prepared. The components in each solution were mixed according to a molar ratio of 1/1, 1/3 and 3/1, close to the saturation concentration, with the numerator representing VPhn or BBzt and the denominator tBBz. For

each ratio, three frontal analysis were made with 33, 67 and 100% of the mother liquor. In each frontal analysis the outlet was fractionated, one fraction each 0.15 minutes, in a total of 93 fractions. The flow rate was 2 ml/min and the injection time was 7 minutes, with a total experiment time of 25 minutes, including elution. Below it is shown a table with the prepared solutions:

Table 3.3: Concentrations used for Binary Mixtures

BBzt + tBBz			VPhn + tBBz		
Ratios	C_{BBzt} (mol/L)	C_{tBBz} (mol/L)	Ratios	C_{VPhn} (mol/L)	C_{tBBz} (mol/L)
3/1	0.1345	0.0448	3/1	0.1596	0.0552
1/1	0.0899	0.0898	1/1	0.0874	0.0907
1/3	0.0342	0.1029	1/3	0.0339	0.1055

To determine the saturation concentrations, solubility tests were performed. These solubility tests were a rough way to determine the range of concentrations that could be used for the determination of the isotherm parameters. The components were weighted in a mass flask respecting the molar ratios as good as possible and then it was added solvent until the solution turned homogeneous.

Regarding the analysis of all the samples collected for every experiment, the HPLC auto-sampler was used. For single components, the injection volume was 1 μl, the analysis time per sample was 2.5 minutes with a flow rate of 3 ml/min. For mixtures, the injection volume was 1 μl, the analysis time per sample was 2.5 minutes and the flow rate was 3 ml/min. For every analysis of every sample, the injection was always repeated twice, to check for reproducibility. UV signal was used for component detection. For single components the wavelengths used were 260, 280, 330 and 360 nm and for mixtures 215, 230, 254 and 280 nm.

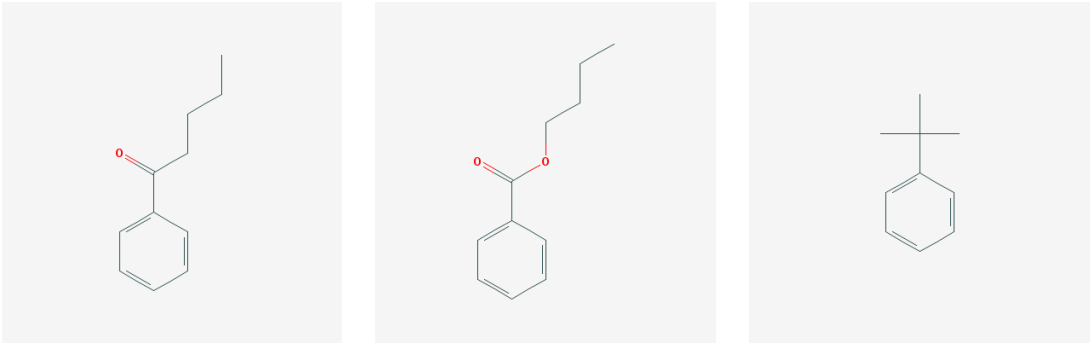
After the analysis, the BC were obtained with the units being absorbance units per minute, so they had to be converted for concentration units, moles per liter, and that was done recurring to calibration curves. "By eye", it was chosen a volume range where the plateaus of all BC were very well defined. For single components it was a multi-step experiment, so the volume range starts 5ml before the next injection volume. For mixtures, the range was from 10 to 15 ml. The determination of a volume range for the well defined plateaus is to calculate the average and to reach, with a quite good precision, to the correct plateau value. After that, knowing the plateau values and the

inlet concentrations for every experiment, a function can be fitted to those data. In this work, the third order polynomial function passing through the origin (when x^0 term doesn't exist) and the power function were used for single components and mixtures, respectively. The fitting was performed with the help of the MatLab software, using the *lsqcurvefit* function. This function uses the Least Squares algorithm for curve fitting.

Chapter 4

Data Analysis

As said in section 3, the components were chosen for having similar molecular sizes but different functional groups. The molecular forms are:



(a) Valerophenone (b) Butyl Benzoate (c) tert-Butylbenzene

Figure 4.1: Molecular Structure of the three components used

4.1 Pure Components Isotherms

For each component, two frontal analysis experiments were performed, one for lower concentrations and another for higher concentrations, close to saturation. With this experimental method, a wide range of concentrations was achieved and a good amount of data was obtained for further calculations.

4.1.1 Valerophenone

Below the two profiles obtained are presented:

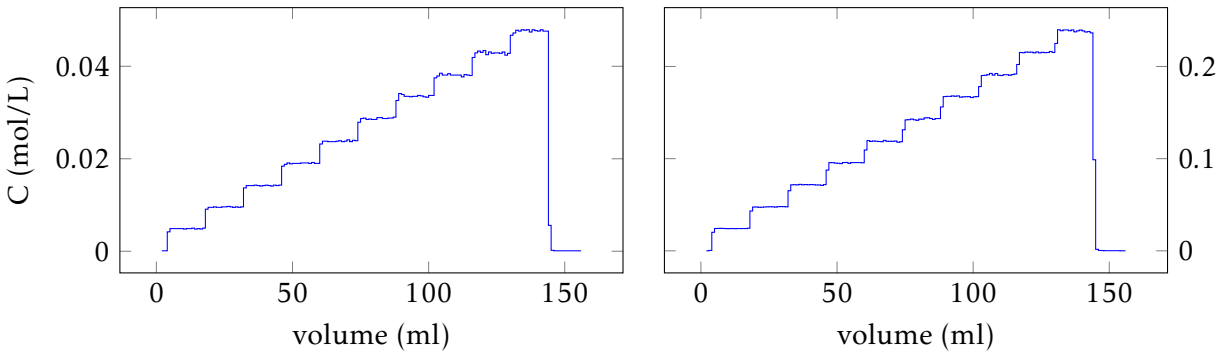


Figure 4.2: Valerophenone Raw Data

These plots represent the chromatograms obtained using the software *Chromeleon* after converting the absorbance units for molar concentrations, so each plateau represents a percentage of the mother liquor's concentration. The next step is to calculate the accumulated moles in the column.

The approach used was to divide the data in injection times: since the injection time was 7 minutes or an injection volume of 14 ml because the flow rate was 2 ml/min, and the first injection was at 2 ml, the first BC is from 2 to 16 ml, the second from 16 to 30 and so on until the last step is reached.

The next step is to calculate the accumulated moles of each BC. For that, numerical methods have to be used, and in this work it was used the trapezoids method with the help of MatLab. It was also used the equal area method explained in section 2.1. To better demonstrate the calculation method let's assume that, since the concentrations of the mother liquors are known, the concentration of each plateau can be expressed in this form:

$$C_i = j.C_0 \tag{4.1}$$

Where $i = 1, ...,$ number of plateaus and $j = 0.1, 0.2, ..., 1$ represents the mother liquor fractionation for each step.

Now that the concentrations are known, it's possible to calculate the equal area volume with this expression:

$$(InjVol_{i+1} - EqualVol_i)(C_i - C_{i-1}) = \int_{InjVol_i}^{InjVol_{i+1}} BC(V)dV \tag{4.2}$$

With this expression being valid only from the second BC onwards. For the first BC the C_{i-1} is 0. After obtaining this value, it's easy to calculate the accumulated moles in that injection:

$$M_{acc,p,i} = (C_i - C_{i-1})(EqualVol_i - InjVol_i - V_{0,sys}) \tag{4.3}$$

Being, again, valid only from the second BC onwards. the index p means partial accumulated moles, the accumulated moles in each injection increase.

Since, until now, this process only calculates the accumulated moles in each step increase, not the actual accumulated moles inside the column, the way to do that is to add the accumulated moles of the previous steps, so:

$$\begin{aligned} M_{acc,1} &= M_{acc,p,i} \\ M_{acc,i} &= \sum_{k=1}^{i} M_{acc,p,k} \end{aligned} \tag{4.4}$$

The accumulated moles inside the column calculated represent the moles in the bulk liquid that are always inside the column and the moles adsorbed in the stationary phase. Knowing this, it's easy to calculate the molar concentration of solute in the adsorbent the following way:

$$q_i = \frac{M_{acc,i} - C_i.V_0}{V_s} \tag{4.5}$$

This process was applied in both experiments referred, and now, since the adsorbed moles calculated are specific for each concentration, the data can be agglomerated in a single plot to see the entire isotherm data [1]:

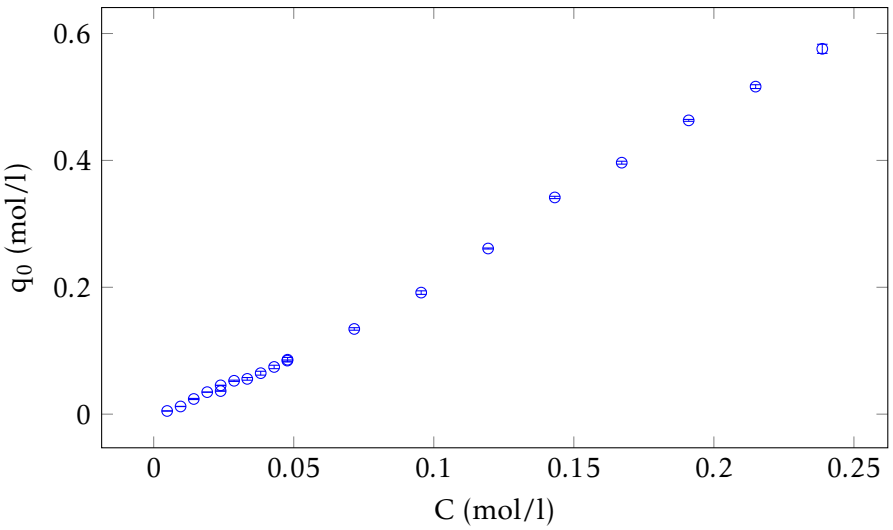


Figure 4.3: Valerophenone Isotherm Data

As explained in section 3, the analysis of the samples were always duplicated and the isotherm data was calculated considering the average of these two points, so technically

there are three points available for calculation, the lower, average and higher values, so it's possible to calculate the isotherm data with those data and obtain the error bars showed in Figure 4.3. The sizes of the error bars show that the reproducibility of the analysis was very good.

4.1.2 Butyl Benzoate

For Butyl Benzoate, the chromatograms already converted to molar concentrations are as followed:

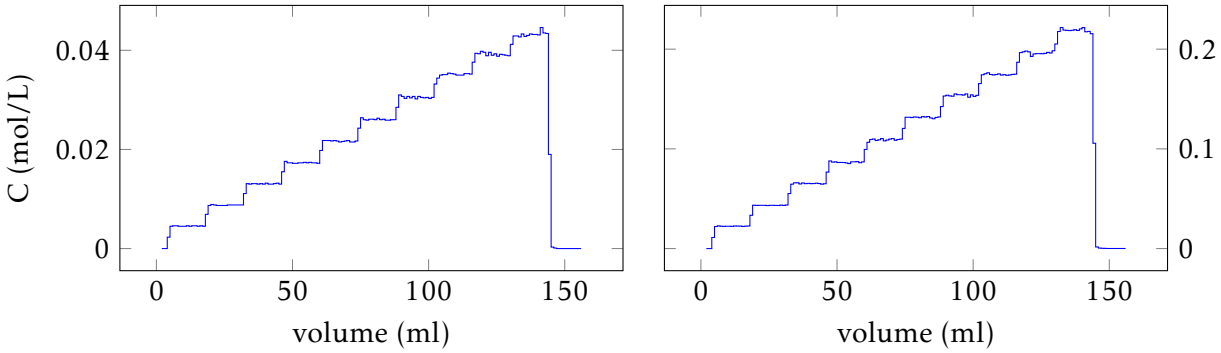


Figure 4.4: Butyl Benzoate Raw Data

After proceeding the same way as for Valerophenone, the final isotherm data is presented:

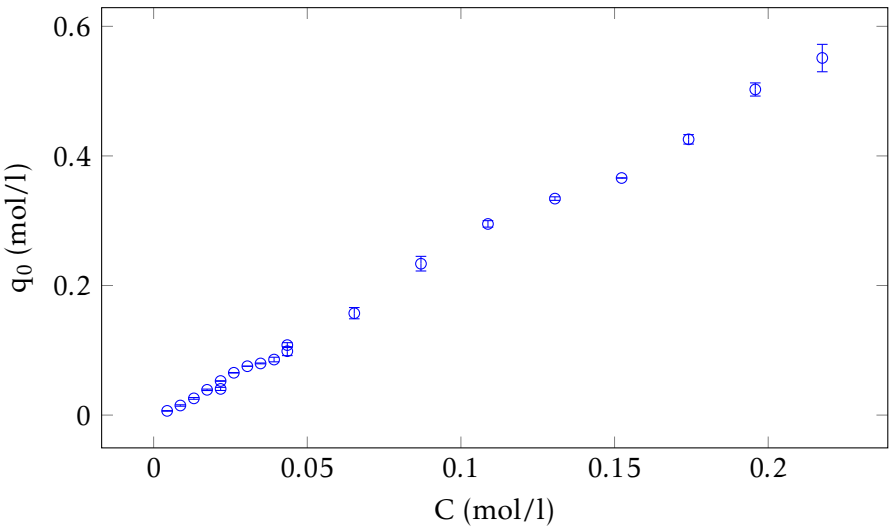


Figure 4.5: Butyl Benzoate Isotherm Data

[1] the calculation method was applied to all the components, so the next sections will have only the final data

Again, the error bars show that a good reproducibility was achieved.

4.1.3 tert-Butylbenzene

For tert-Butylbenzene, everything was made the same way:

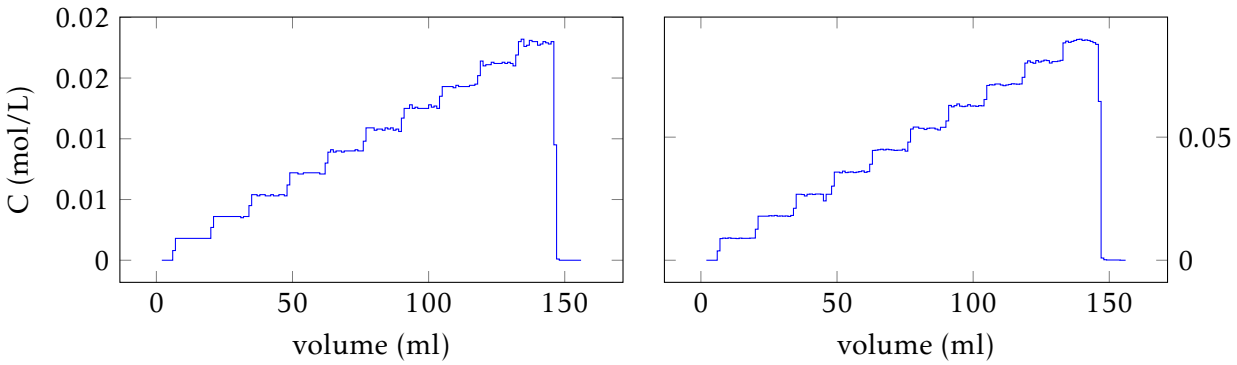


Figure 4.6: tert-Butylbenzene Raw Data

Which can be determined the following isotherm data:

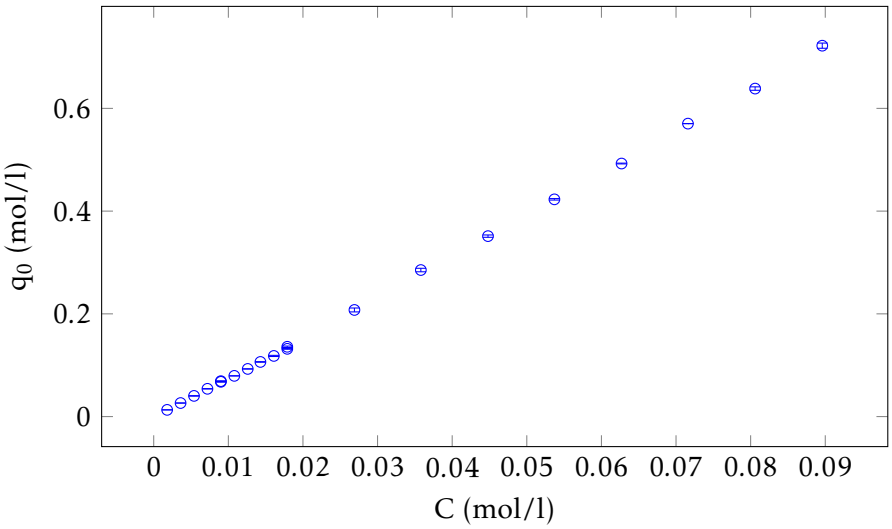


Figure 4.7: tert-Butylbenzene isotherm data

The almost undetectable error bars show a very good reproducibility of the analysis.

4.1.4 Parameter Estimation

Now that the isotherm data is determined, the last thing to do is to fit an isotherm model to obtain the isotherm parameters. To reach that objective, the MLMC derivation with a finite number of layers was used. Because the goal is to compare these parameters to those of the multi components, the single components were fitted two at a time, VPhn with tBBz and BBzt with tBBz to match with the mixtures' components. Since all components have identical molecular size (they are all benzene derivatives), the MLMC model assumes that q_{MAX} and n are constant, so the three components should be fitted altogether. However, if the fittings are done separately, it's possible to compare the same parameters and see if they are identical or not. That being sad, the problem has to be divided in two objective functions to be minimized. For i =BBzt, tBBz the objective function is:

$$ObjFun_{BBzt,tBBz} = \sum_{i} \sum_{j=1}^{20} \left(q_{calc,i,j} - q_{exp,i,j} \right)^2 \tag{4.6}$$

And for i =VPhn, tBBz:

$$ObjFun_{VPhn,tBBz} = \sum_{i} \sum_{j=1}^{20} \left(q_{calc,i,j} - q_{exp,i,j} \right)^2 \tag{4.7}$$

For solving this minimization problem, again MatLab was used. The function used was *fmincon*, which deals with constrained non-linear minimization. The algorithm used was the Active Set Algorithm. A good explanation for this algorithm can be found on-line in the MatLab documentation [22].

For each minimization problem, the parameters to be adjusted are q_{MAX}, n and K_1 and K_2 for each component, with a total of six parameters. The only constraint used was that all parameters have to be greater than or equal to zero. The next figure shows the fitting results for BBzt and tBBz:

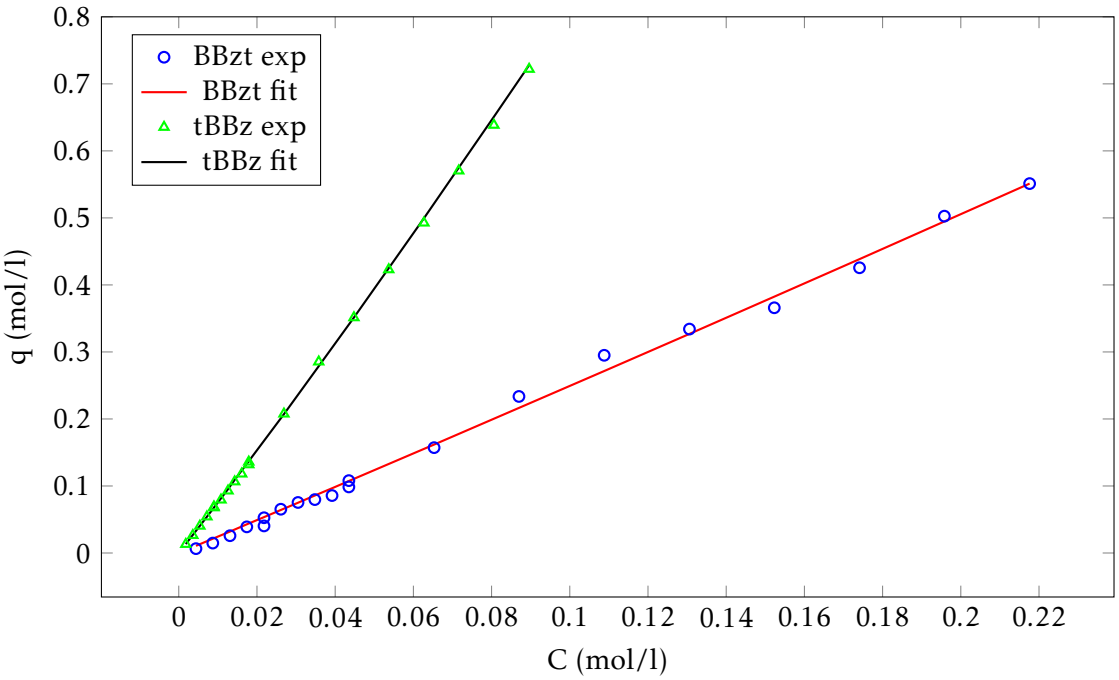


Figure 4.8: MLMC Model fitted for BBzt and tBBz

And for VPhn and tBBz:

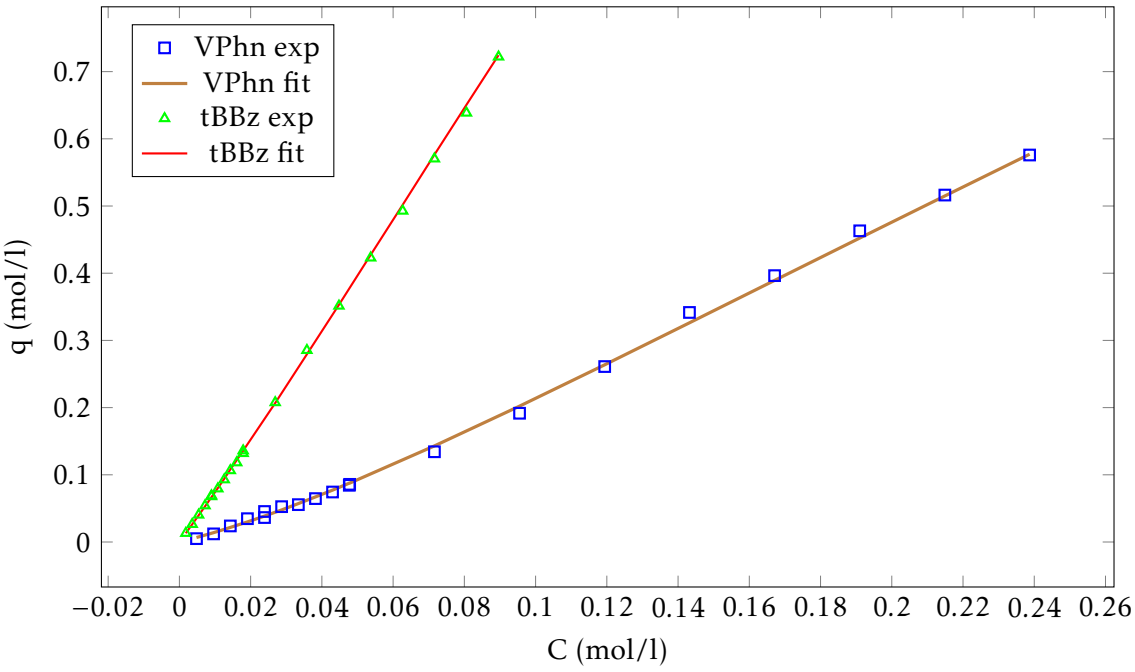


Figure 4.9: MLMC Model fitted for VPhn and tBBz

The estimated parameters for both fittings can be shown in the table below:

Table 4.1: Estimated parameters for each fitting

VPhn and tBBz			BBzt and tBBz		
Constants	VPhn	tBBz	Constants	BBzt	tBBz
K_1	0.568	3.096	K_1	1.117	3.413
K_2	10.245	5.602	K_2	1.314	4.672
q_{MAX}	2.352		q_{MAX}	2.192	
n	2.647		n	9.998	
ObjFun	8.799×10^{-4}		ObjFun	2.124×10^{-4}	

By having two objective functions that share some parameters, like K_1 and K_2 of tBBz, n and q_{MAX}, it would be expected that those parameters would be equal, or at least identical. When it comes to q_{MAX}, the values are quite close, which means that the model's assumption that $q_{MAX}$is always the same if the molecules have identical size and the stationary phase remains the same is not violated. Regarding $K_1$and $K_2$of tBBz, the values are somewhat close to each other, which was expected. The number of layers should be the same for both fittings but it is not. The difference is quite big because above 10, the number of layers doesn't change much, so it can be considered infinite. Since this work is based on RPLC, the stationary phase is hydrophobic, so the less polar the solutes are, the bigger the affinity with the adsorbent. Saying that, and looking at Figure 4.1, the molecules will bind with the carbon chain (an alkane), the least polar site [20]. As stated in [20], ketones are more polar than esters or alkenes, so probably VPhn, after binding in the surface with the butane chain, acts as a terminator, since the part that's not bidden is polar, which explains the reduced number of layers compared with BBzt and tBBz.

4.2 Multi-Component Isotherms

In this section, the raw data of the mixtures were analysed. In this case, the calculation method was different because it was performed only single step FA for each mixture and each ratio. A good example for a single step FA is shown in Figure 1.3. In terms of calculation the equal area method was used, but now, since each experiment had an elution part, the accumulated moles could be calculated in two different ways, so the further fitting of the isotherm data could be more precise.

In Figure 1.3 there is a loading and an elution part. It's seen two inflection points in which it's possible to obtain two equal area volumes.

As explained earlier in section 3.2 the value range used to calculate the plateaus for all BC of mixtures was from 10 to 15 ml. Using these values, equal area volumes were determined, but first it's needed to calculate the inlet concentrations for each mixture and each ratio. Assuming that there are $i = 1, 2$ mixtures, $j = 1, 2, 3$ ratios, $k = 1, 2$ components and being $f = 0.33, 0.67, 1$ the inlet fractionation for each ratio, described in section 3.2, then the inlet concentrations for each mixture, ratio and component are:

$$C_{i,j,k,f} = f.C_{0,i,j,k} \tag{4.8}$$

And the equal area volumes are:

$$\begin{aligned} (15 - EqVol_{load,i,j,k,f})C_{i,j,k,f} &= \int_{2+V_{0,sys}}^{15} BC_{i,j,k,f}(V)dV \\ (EqVol_{elut,i,j,k,f} - 10)C_{i,j,k,f} &= \int_{10}^{V_{end}} BC_{i,j,k,f}(V)dV \end{aligned} \tag{4.9}$$

With the subscripts $load$ and $elut$ meaning loading and elution, respectively. After this, is quite easy to calculate the accumulated moles in each part of the BC:

$$\begin{aligned} Macc_{load,i,j,k,f} &= (EqVol_{load,i,j,k,f} - 2 - V_{0,sys})C_{i,j,k,f} \\ Macc_{elut,i,j,k,f} &= (EqVol_{elut,i,j,k,f} - 16 - V_{0,sys})C_{i,j,k,f} \end{aligned} \tag{4.10}$$

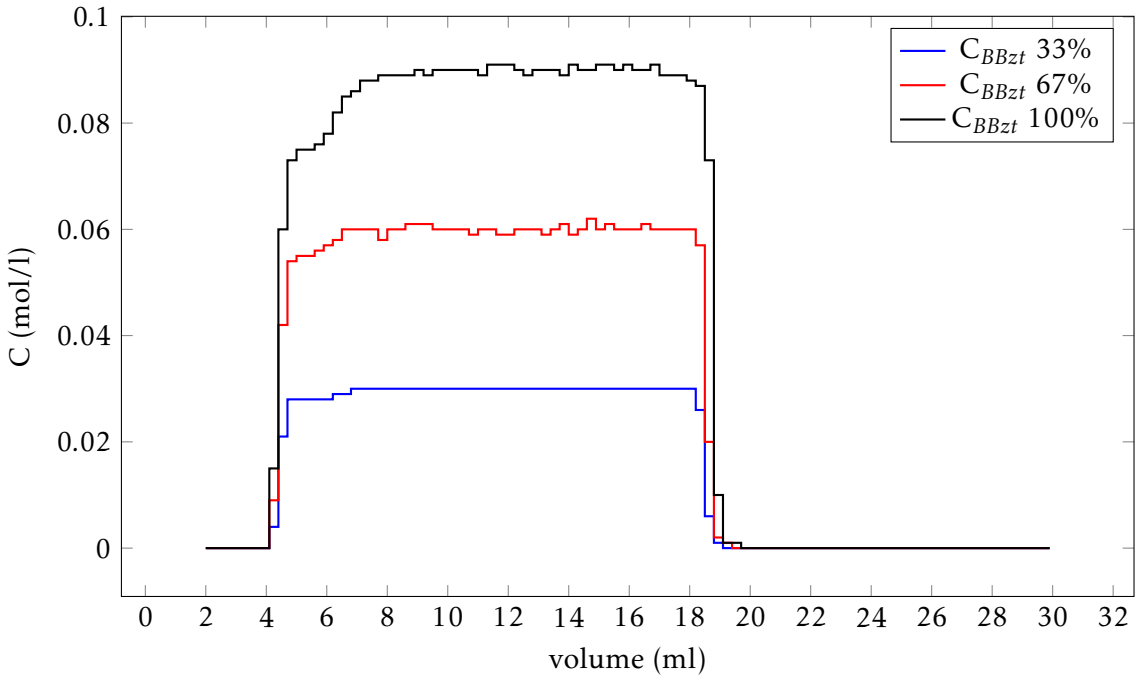
Now that the accumulated moles are calculated, the remaining step is to calculate the adsorbed moles:

$$
\begin{aligned}
q_{load,i,j,k,f} &= \frac{Macc_{load,i,j,k,f} - C_{i,j,k,f}}{V_{ads}} \\
q_{elut,i,j,k,f} &= \frac{Macc_{elut,i,j,k,f} - C_{i,j,k,f}}{V_{ads}}
\end{aligned}
\tag{4.11}
$$

These two adsorbed moles should be the same. However, since every experimental work has some experimental error, it's not quite the same, although really close.

4.2.1 Butyl Benzoate and tert-Butylbenzene

In here it's presented the raw data already converted for molar concentrations.



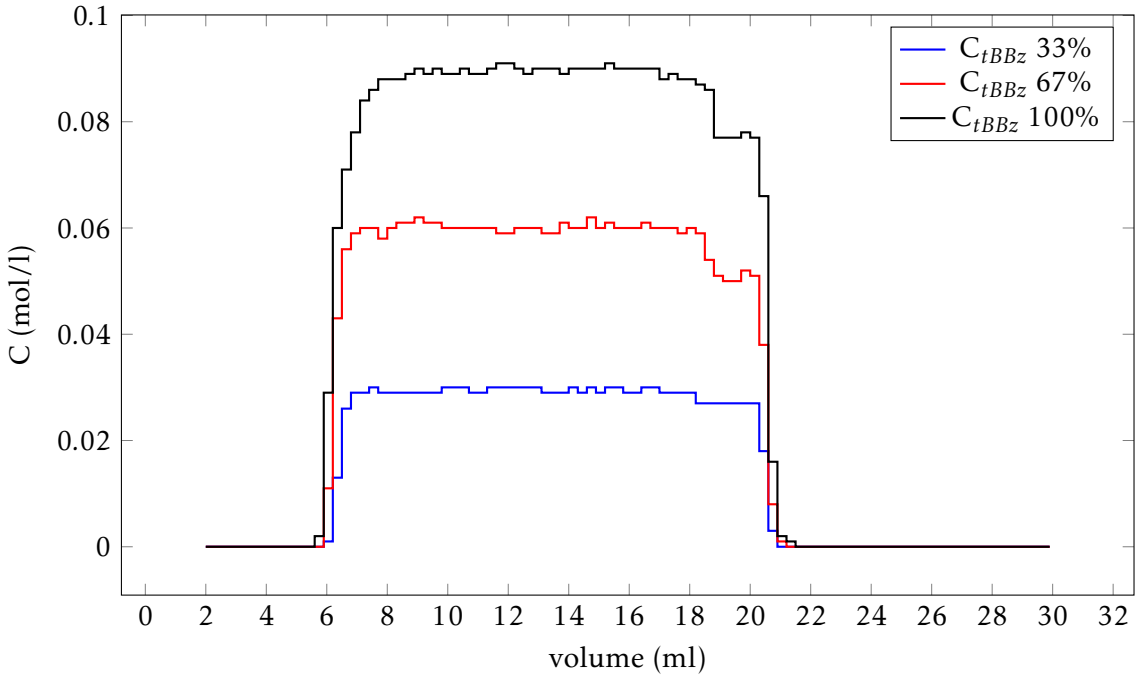


Figure 4.10: BCs for BBzt and tBBz with 1/1 Ratio

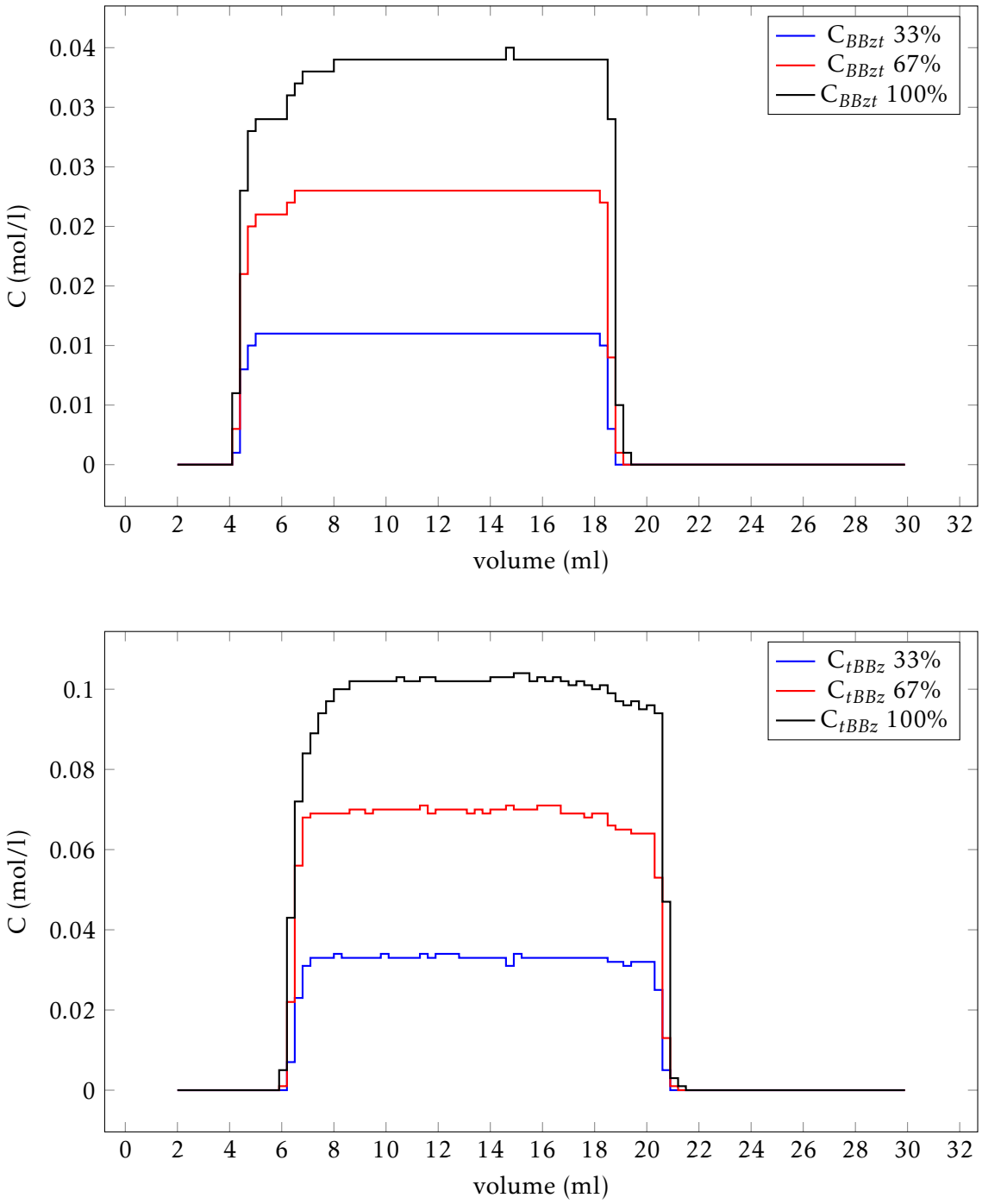


Figure 4.11: BCs for BBzt and tBBz with 1/3 Ratio

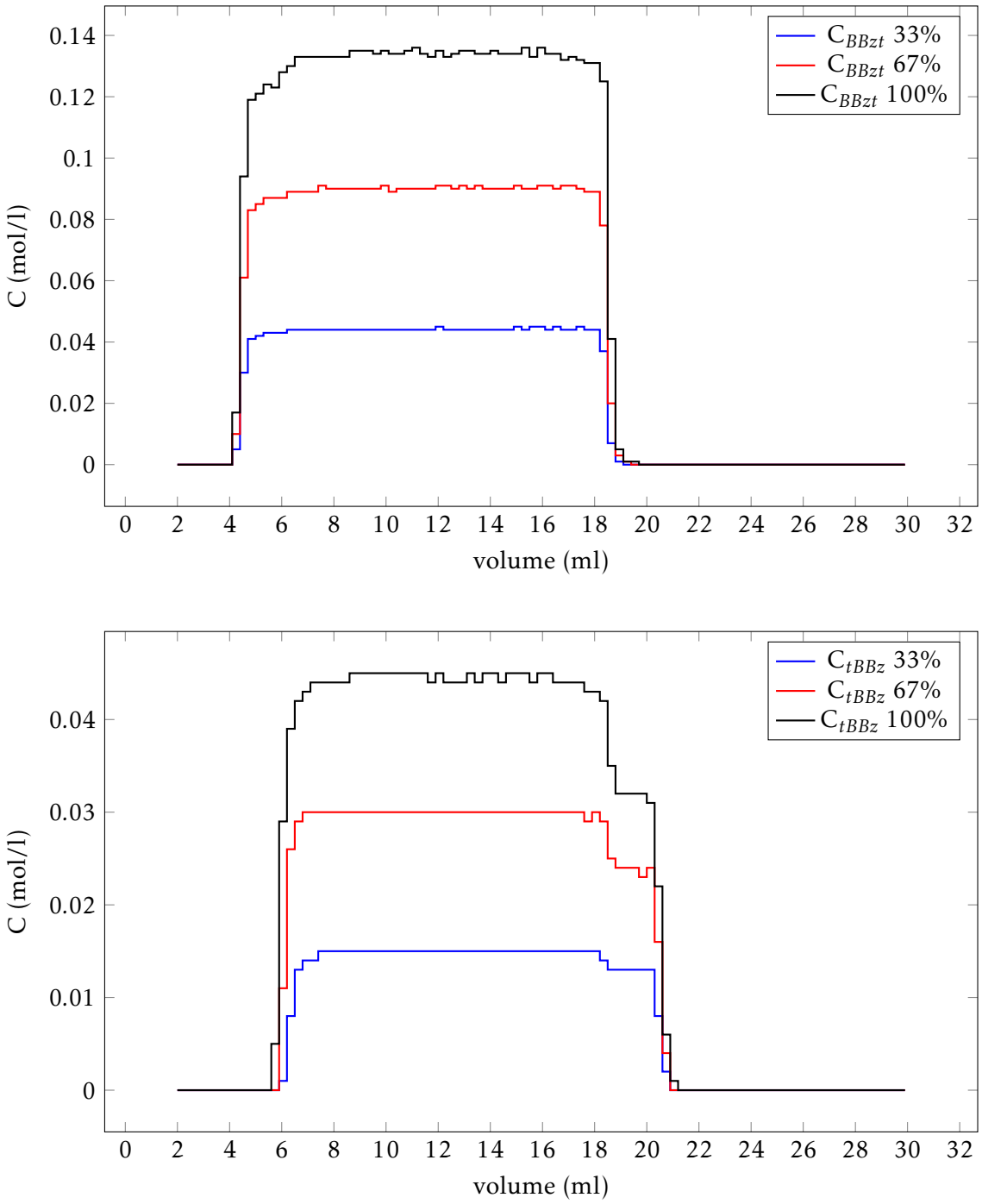


Figure 4.12: BCs for BBzt and tBBz with 3/1 Ratio

These BC are after fraction collection and analysis. As clearly seen, every BC has more than one plateau, meaning that there is competition between both components. Competition is a quite self explanatory name, means that the molecules are competing with each other for the active sites, changing the equilibrium concentration of each component, hence the two plateaus.

Now, the only thing left is to determine the isotherm data, calculated as explained above and presented below:

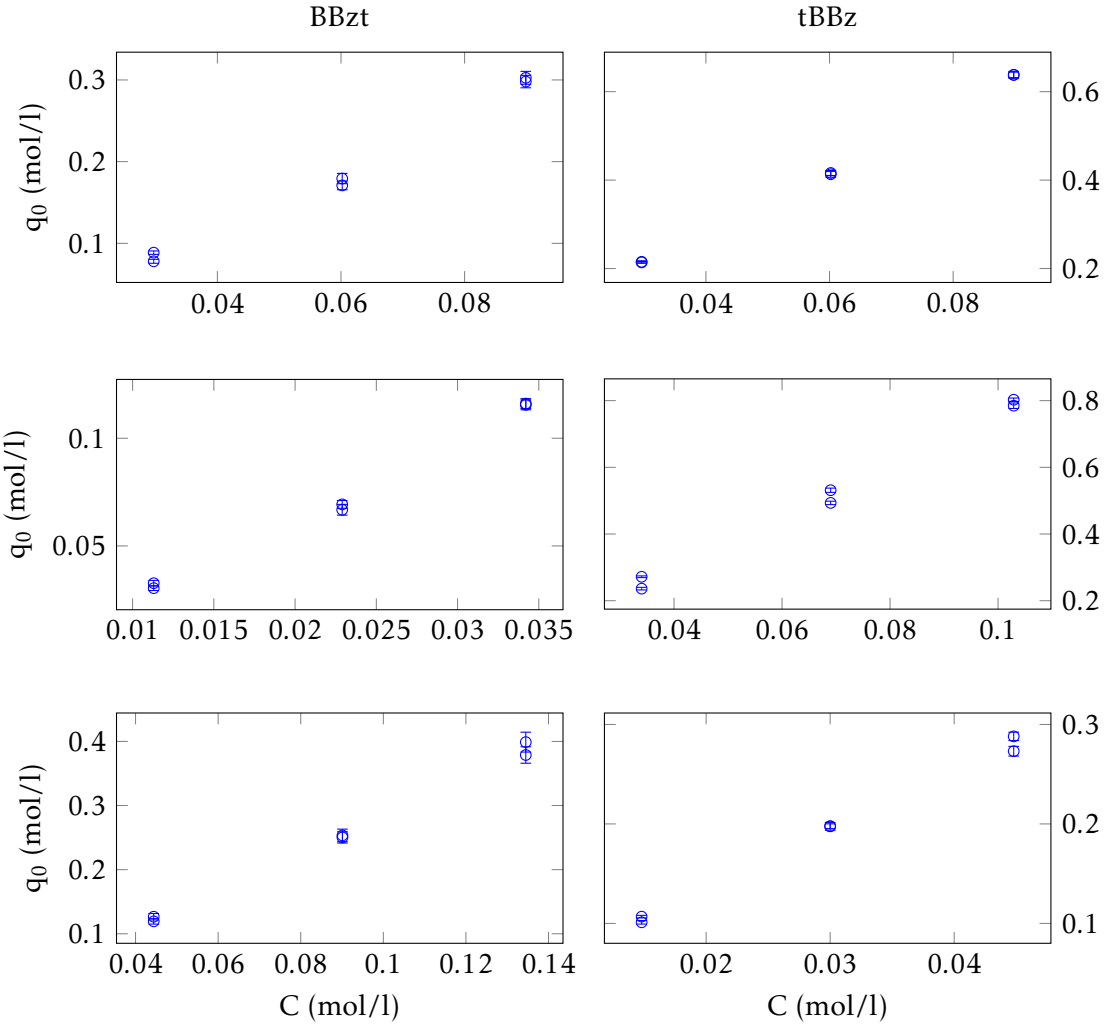


Figure 4.13: Isotherm data for BBzt and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

The error bars were calculated the same way as in section 4.1.

4.2.2 Valerophenone and tert-Butylbenzene

For this mixture, all calculation procedures were the same. Below it's shown the raw data already converted for molar concentrations.

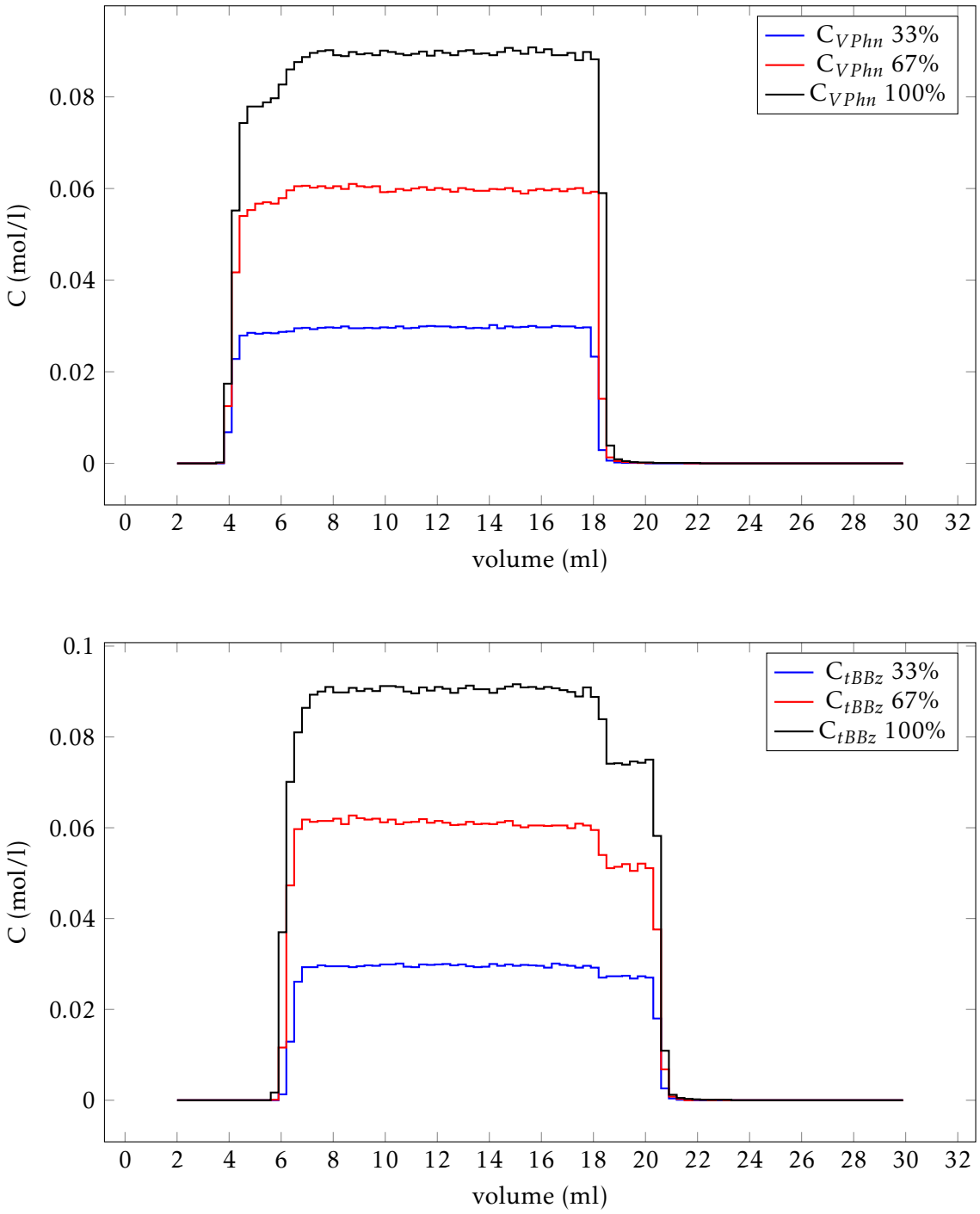


Figure 4.14: BCs for VPhn and tBBz with 1/1 Ratio

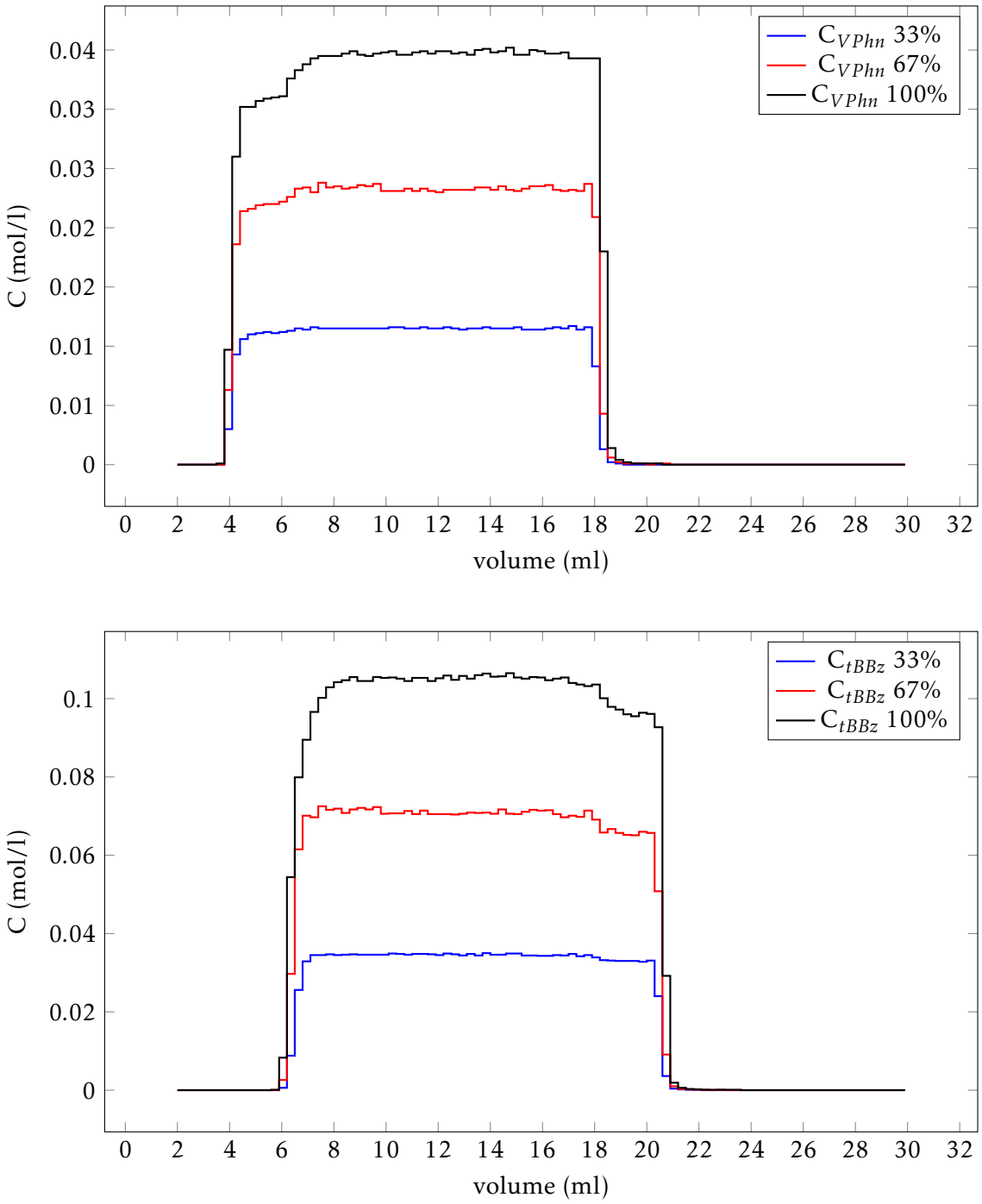


Figure 4.15: BCs for VPhn and tBBz with 1/3 Ratio

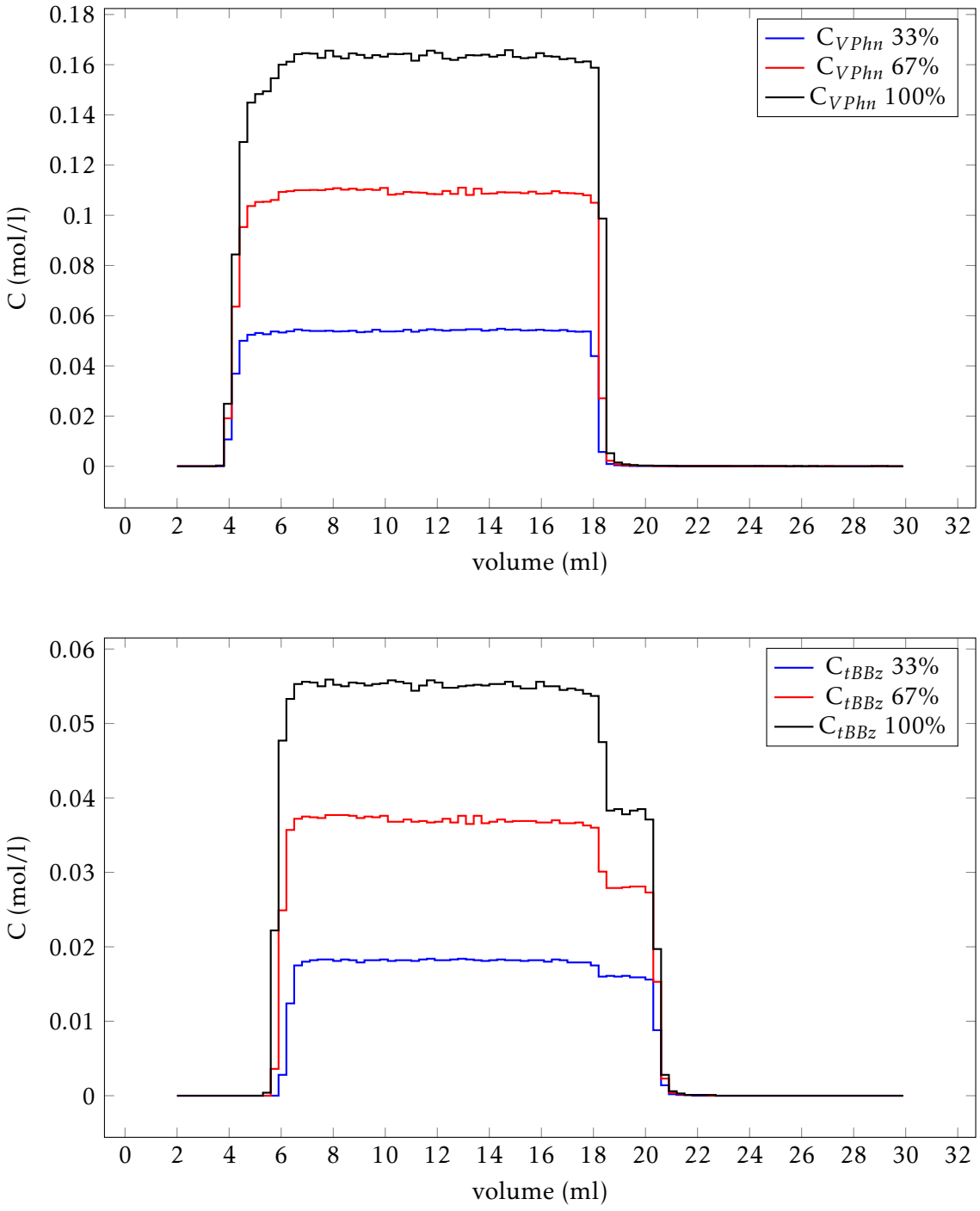


Figure 4.16: BCs for VPhn and tBBz with 3/1 Ratio

Again, with this data is easy to calculate the isotherm data, presented below:

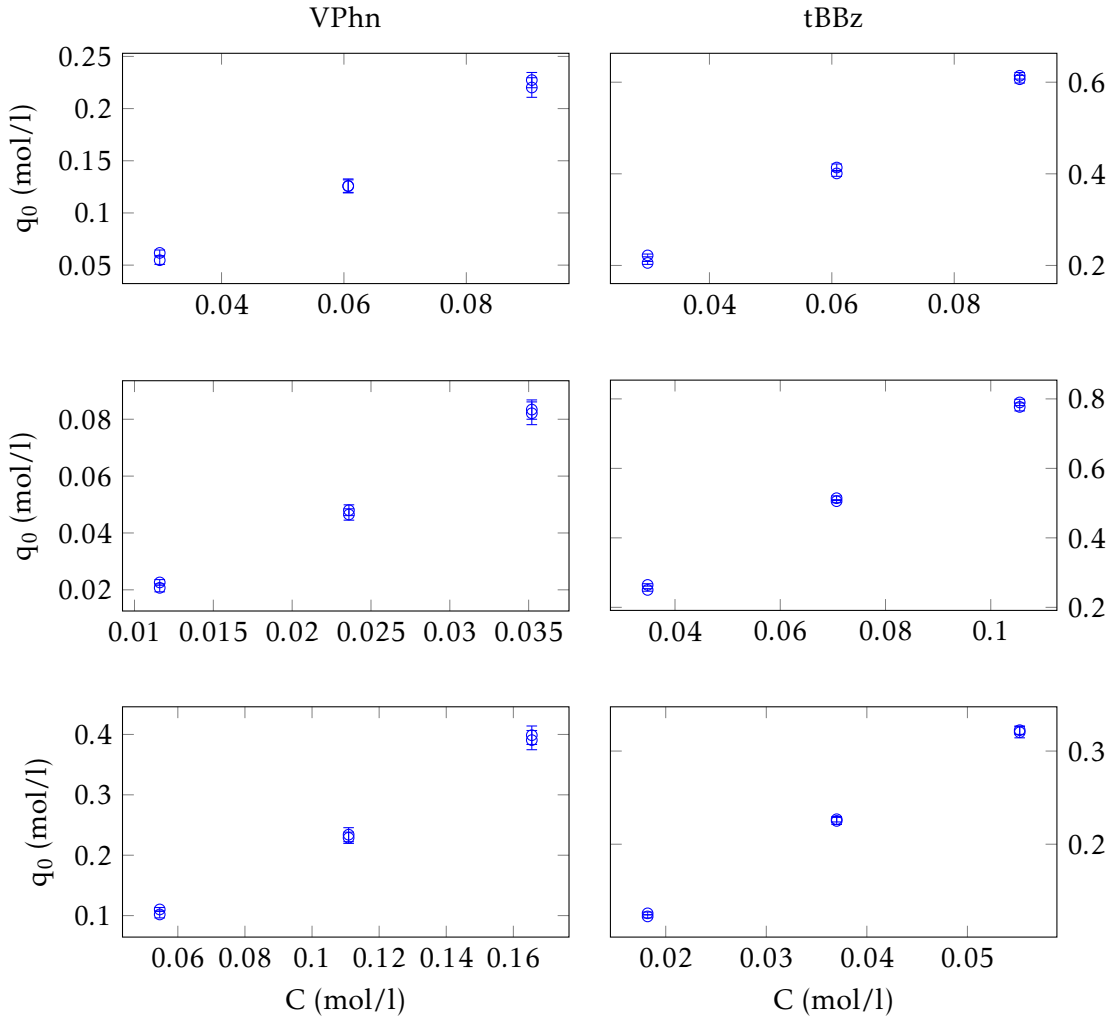


Figure 4.17: Isotherm data for VPhn and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

4.2.3 Parameter Estimation

To estimate the model parameters in the mixtures data, MatLab and the same algorithm for the single components were used. Each mixture data was fitted separately so later the parameters could be compared and analysed. Considering the reasons stated, two objective functions were used:

$$ObjFun_i = \sum_j \sum_k \left(q_{calc,i,j,k} - q_{i,j,k}\right)^2 \tag{4.12}$$

With i, j and k being the mixtures, ratios and components, respectively.

Again, q_{MAX} and n are assumed constant in each mixture and adding K_1 and K_2 of each component, there's a total of 6 parameters for each minimization problem. After fitting, the results can be seen below:

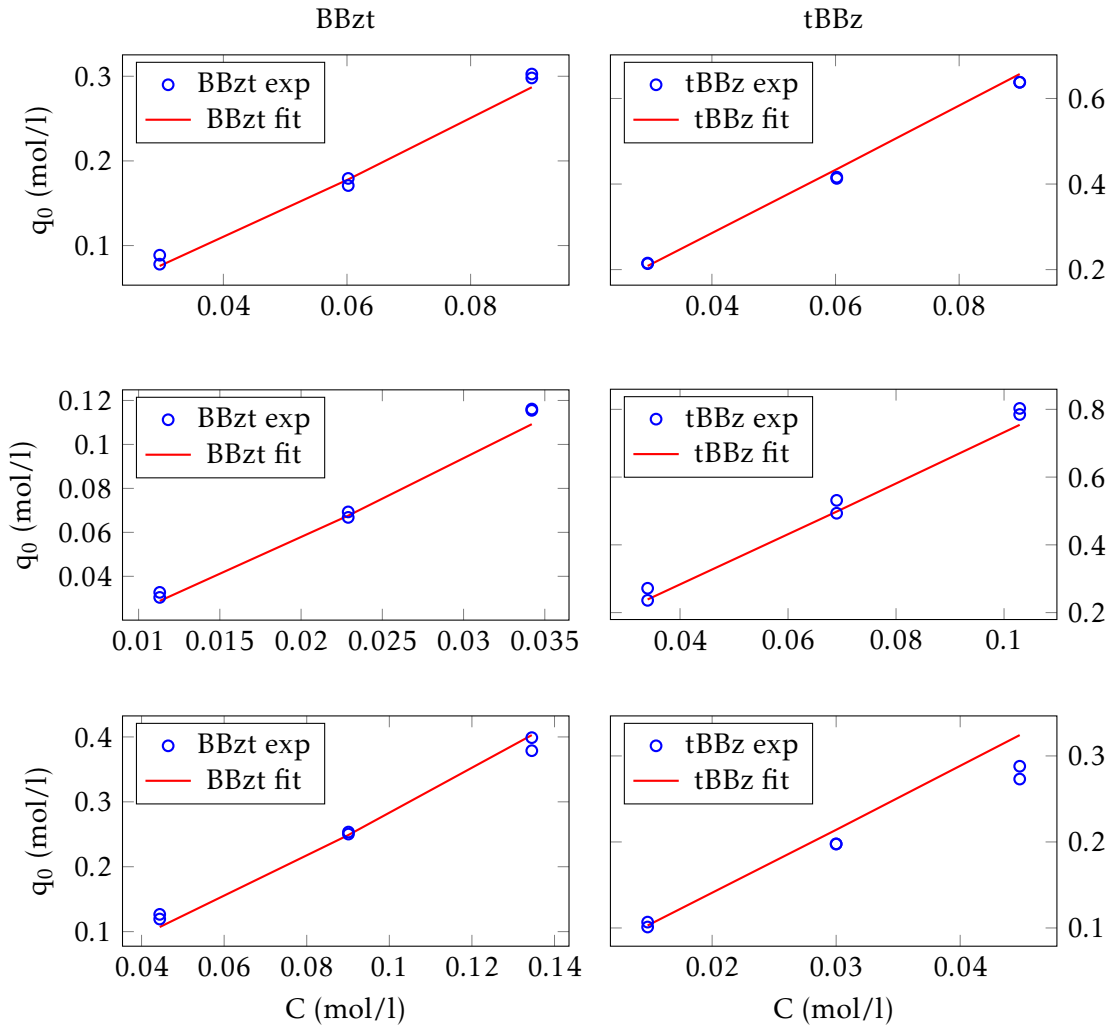


Figure 4.18: Fitted model for BBzt and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

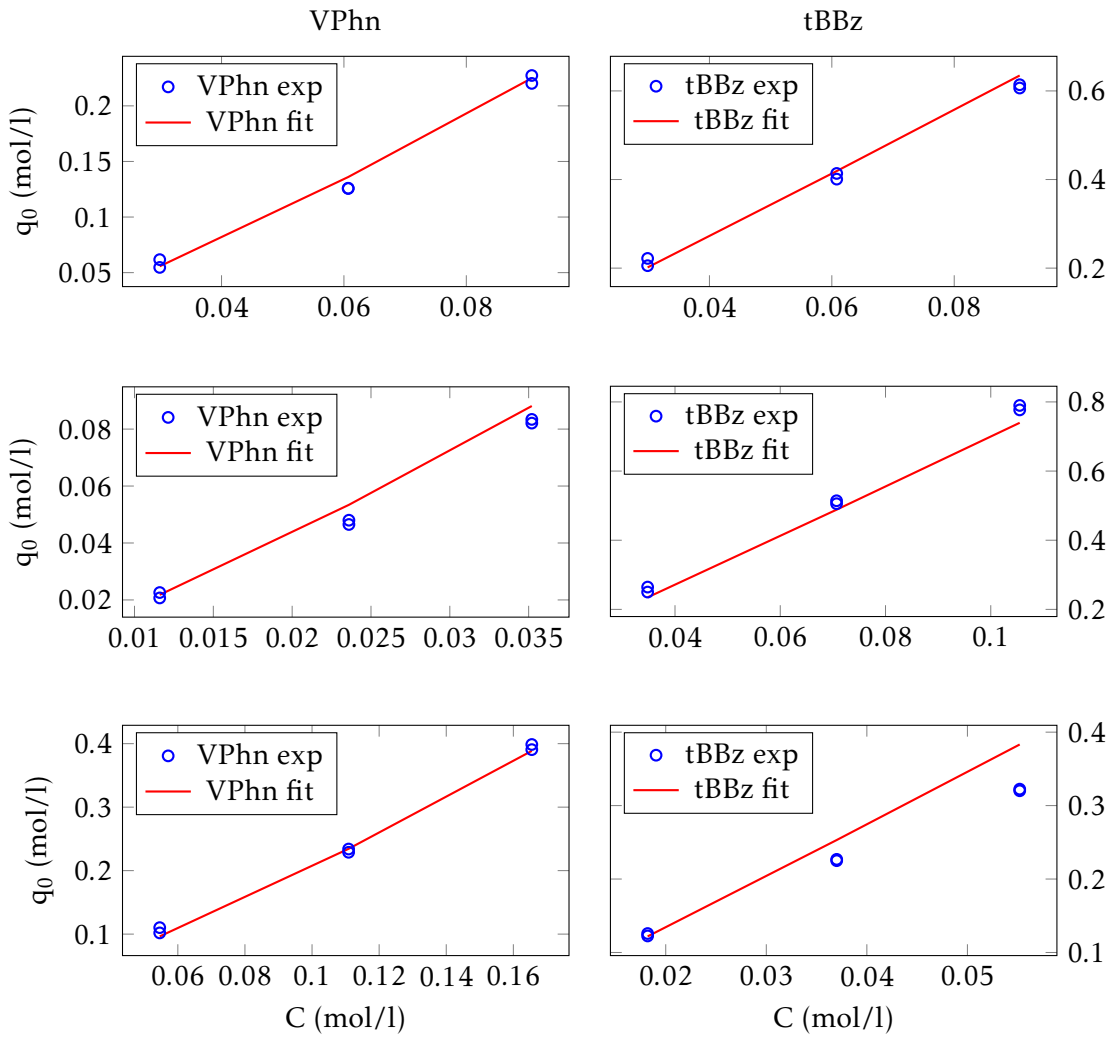


Figure 4.19: Fitted model for VPhn and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

In this table, the parameter's values can be seen:

Table 4.2: Estimated parameters for each mixture

VPhn + tBBz			BBzt + tBBz		
Constants	VPhn	tBBz	Constants	BBzt	tBBz
K_1	1.866	9.782	K_1	2.58	9.115
K_2	5.539	11.352	K_2	6.068	10.829
q_{MAX}	0.661		q_{MAX}	0.736	
n	21.405		n	10.195	
ObjFun	0.0175		ObjFun	0.0134	

By looking at these data, the values of n, as explained above, have practically the same influence, the $K_1$and K_2values for tBBz are pretty close, as well as the q_{MAX}values.

4.3 Experimental Validation

To determine the isotherm data for single components two 10-step FA analysis were performed. In this work fraction collection had to be used because of impurities in BBzt, but usually it is not needed, only UV signal is required. Meanwhile, the experimental work for mixtures is much more complex: fraction collection is inevitable and to obtain good data, several ratios with several FA per ratio have to be performed and further fraction analysis has to be made, which consumes lots of time and resources, being very prone to human errors too. It would be good if the MLMC model could describe the isotherm behaviour for mixtures with only experimental data for the single components. In this section, cross-check of the parameters for single and multi-component systems will be presented, to see if the isotherms are well predicted with only the single component data.

The first thing to check is how good single component parameters can describe multi component behaviour:

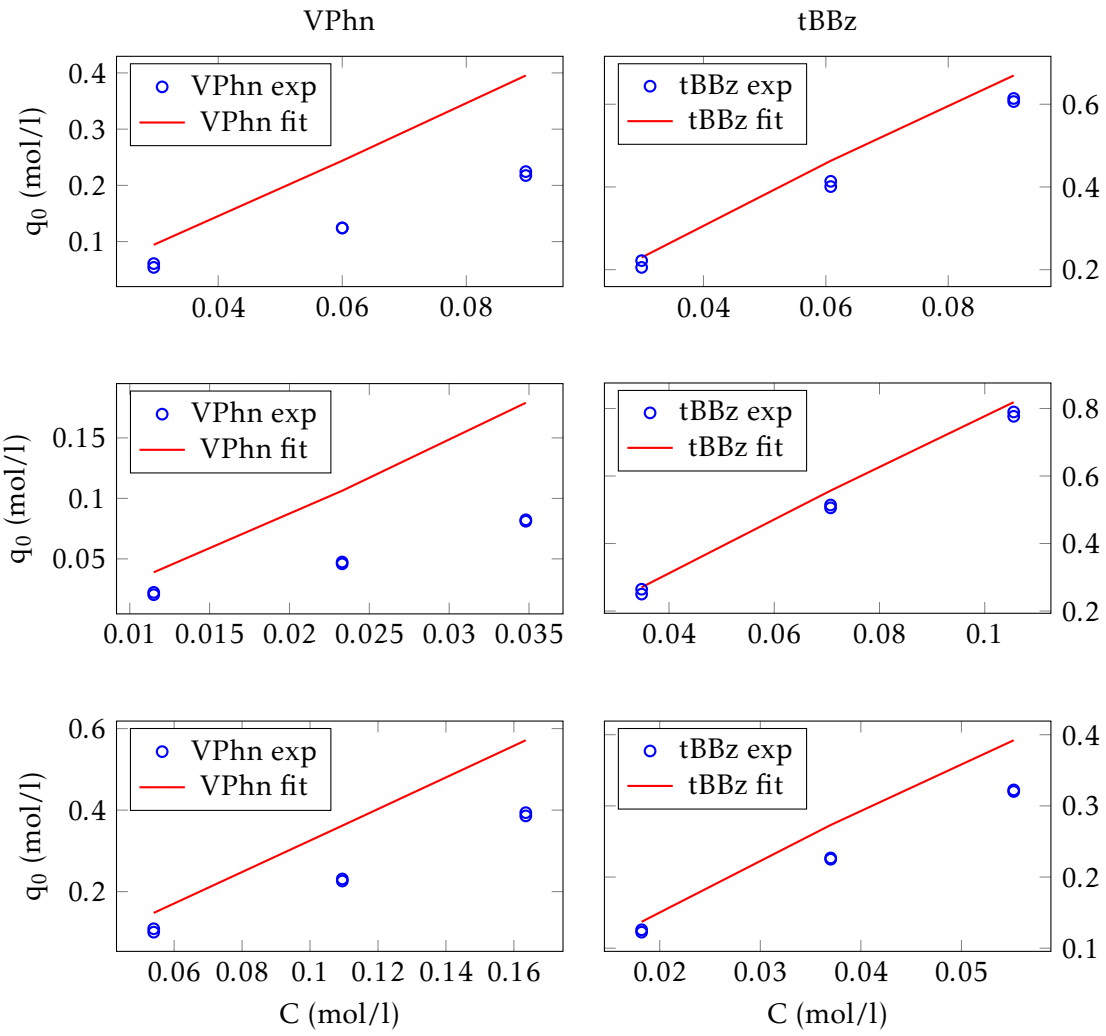


Figure 4.20: Cross-check for VPhn and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

For this multi component system, the correlation coefficient (R^2) was 0.937. As seen, the single component parameters fit tBBz data very well but not VPhn data. For this component, more mixture data should be included in the fitting to obtain better behaviour descriptions.

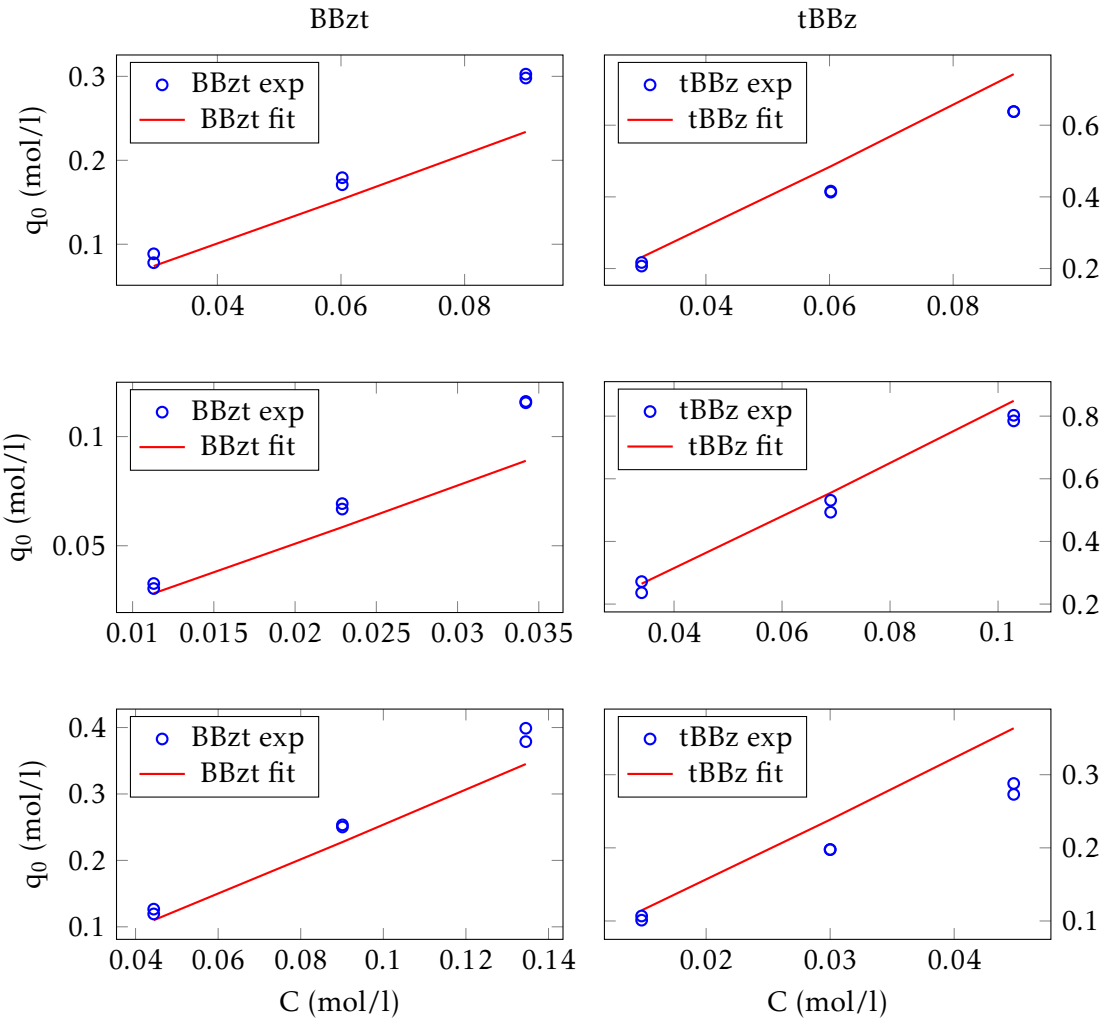


Figure 4.21: Cross-check for BBzt and tBBz. Each row represents 1/1, 1/3 and 3/1 ratios, respectively.

For the multi component system above, the single component parameters fit quite well for tBBz and for BBzt, showing a very good R^2 of 0.981.

After using the single component parameters in the multi component systems, now it'll be presented the inverse, multi component parameters in the single component systems:

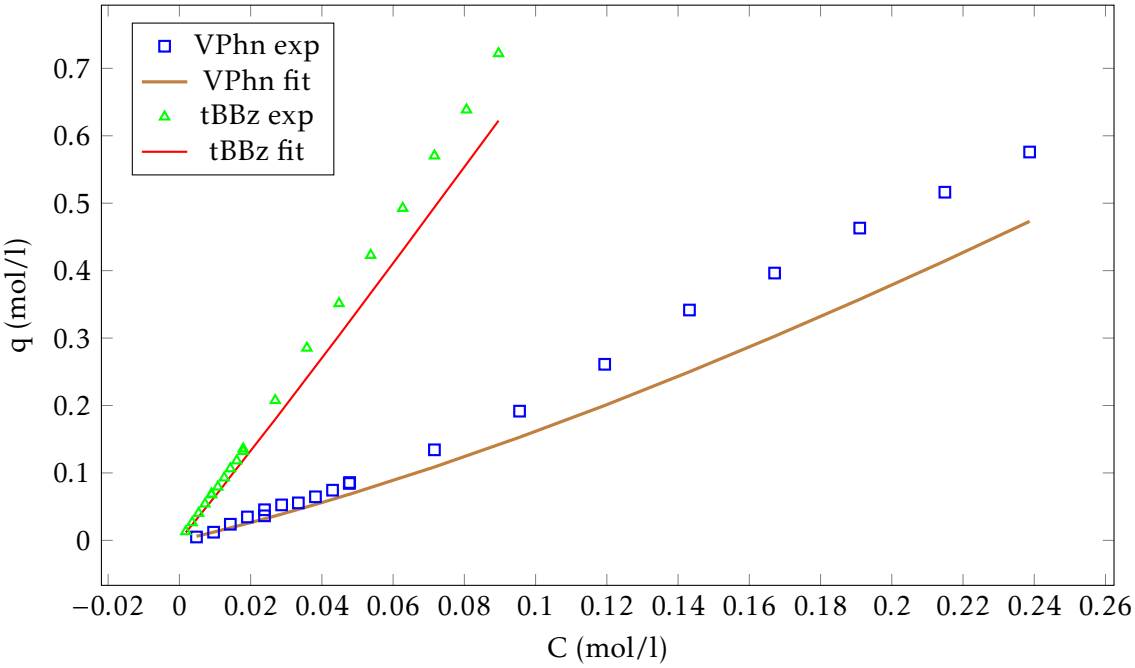


Figure 4.22: Cross-check for VPhn and tBBz

For VPhn and tBBz, the fitting is not bad in total, although for VPhn the tendency is not a good match. In the data it's detected a little curvature, suggesting an s-shape and the predicted data show a too accentuated anti-langmuirian curvature. For tBBz, the fitting is quite good. The slope is not the same, but the tendency quite matches and in low concentrations the fitting is quite good. The global R^2 for this cross check was 0.941.

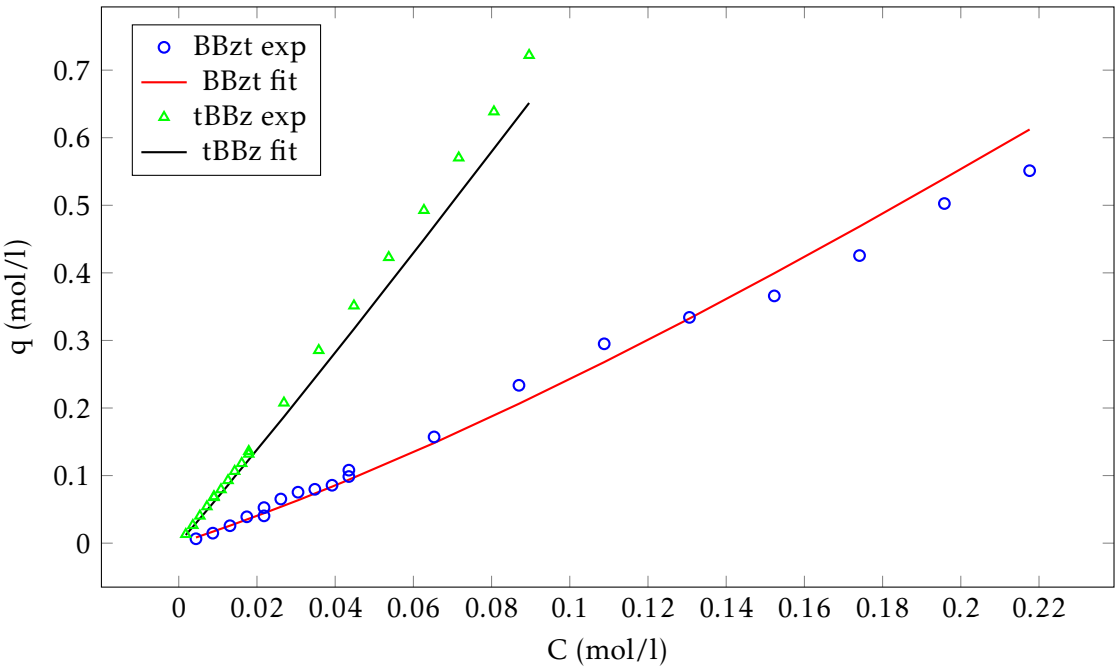


Figure 4.23: Cross-check for BBzt and tBBz

For BBzt and tBBz, the fittings are quite good, with an R^2 of 0.98. For BBzt, the tendency of the experimental data and fitted data is quite similar. For tBBz, the same happens as above, with the tendency being the same, although the slope is not, but for lower concentrations the fitting is quite good.

Chapter 5

Conclusions

In overall, the results of this work were quite successful.

The MLMC model could be fitted in both single and multi component systems separately. However, when parameters were compared and analysed, some big deviations were noticed, particularly in the number of layers. These deviations have logical explanations, but more experimental data is needed to be certain of these theories. When trying to study the predictability of multi component isotherm behaviours with single component parameters, it was quite good, for BBzt and tBBz but not for VPhn. Probably some unknown behaviour occurs when VPhn and tBBz are mixed.

When it comes to the cross check data, it was quite successful for tBBz and BBzt, but not that much for VPhn. One solution is to obtain more data from the multi component system, more concentration points for each ratio and more ratios, which is not practical at all, especially because the experimental work required is quite extensive, complex and consumes lots of time and resources. Another solution is to try and analyse single component data with some mixture data and fit altogether. Mixing multi component with single component data could give a better prediction of the mixture isotherms and help to reduce experimental work.

Since single component data is always needed, further work could be done in the attempt of determining the minimum amount of mixture data to add to the single data in order to guarantee good precision description with minimum resources and time consumption.

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