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Multi-stage Multi-component Transfer Rate Morphological Population Balance Model for Crystallisation Processes

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Abstract

A model was proposed for single crystals for modeling the non-equilibrium crystal growth (CrystEngComm, 2018, **20**, 5143-5153). It describes mathematically and digitally the non-equilibrium growth behavior of single crystals using multi-component transfer rate models, as well as considering multi-component phase equilibria, adsorption, orientation and crystallization of individual molecules on crystal faces. In this paper, the model for single crystal growth is extended to modeling a population of crystals in a crystalliser by incorporating it into morphological population balance equations. The resulting modeling approach, i.e. the multi-stage multi-component transfer rate morphological population balance is able to predict the spatial and temporal distribution of multi-components inside crystals during the course of crystallisation as well as the multi- component composition in the product crystals. The new modeling approach is introduced by reference to a case study of NaNO₃ batch cooling crystallization in water.

Keywords: Morphological Population Balance model; multi-component mass transfer; non-equilibrium; crystal shape; crystal composition

Nomenclature									
Subscript		р	Order of solid mass transfer rate equation						
i	Component number	$Q_{i,j,k}^{ads}$	Adsorption equilibrium equation						
j	Moment number	$Q_{i,j,k}^{S}$	Solid phase and						
k	Face number	$R_{i,j,k}^{L}$	Liquid phase mass transfer equation						
Variable and Parameter		$R^{S}_{\!\!i,j,k}$	Solid phase mass transfer equation						
Ą	Area of face k, m ²	$S_{j,k}^{ads} \\$	Summation relation of mole fractions in adsorption layer						
С	Total number of components	$S_{j,k}^{\rm L}$	Summation relation of mole fractions in liquid						
F	Total number of faces	S _{i,j,k}	Component mole number in the crystal						
G _k	Facet growth rate, m/s	t	Time, s						
H _i	Component mole fraction change rate, s ⁻¹	V	Crystal volume, m ³						
K _{i,k}	Langmuir constant of adsorption	X	Vector of facet normal distances						
$\mathbf{K}_{\mathrm{i},\mathrm{k}}^{\mathrm{r}}$	Equilibrium ratio of component mole fraction (adsorption layer to solid)	X _k	Facet normal distance from the crystal center						
$k_{i,k}^d$	liquid phase mass transfer coefficient, $mol/(m^2s)$	$x_{i,j,k}^{\rm I}$	Liquid component molar fraction on the interface						
$k_{i,k}^{r}$	mass transfer coefficient from adsorbed solute to crystallized solute, mol/(m ² s)	$x_{i,j}^{L}$	Component molar fraction in the solution bulk						
$\mathbf{l}_{i,j,k}$	Component mole fraction in solution, mol	Y	Vector of component mole fractions						
M _i	Mole weight, kg/mol	\boldsymbol{y}_i	Component mole fraction in the crystal						
$M^{I}_{i,j,k}$	Mass balance equation of interface	$y_{i,j,k}^{I}$	Solid component molar fraction on the interface						
$M_{i,j}^{L}$	Mass balance equation of liquid	$y_{i,j,k}^{S}$	Component molar fraction in the formed crystal layer						
$M^{S}_{i,j,k}$	Mass balance equation of solid	$\boldsymbol{Z}_{i,j,k}$	Component molar fraction in the adsorption layer						
$N_{i,j,k}^L$	Mass transfer rate in liquid,	Ψ	Crystal population number density,						

	mol/s	#/m ^F ,	F	is	the	number	of
		indepe	nder	t fac	es		
$N_{i,i,k}^{S}$	Mass transfer rate in solid, $\rho_{\rm i}$	Component density, kg/m ³					
1, ј, к	mol/s						

Introduction

Crystallization is a chemical engineering separation process widely used for product purification. During crystallization, the so-called impurities are mainly left in the solution, while the product component such as a drug active pharmaceutical ingredient (API) is purified. Since a crystal is a well-structured solid particle with multiple faces, each being selective in adsorbing and crystallizing individual components, one could imagine that inside each crystal, in each face direction, at any size dimensional location, the composition of the multi-components would vary. In a recent study ¹ a modeling technique for single crystals was proposed that allows the spatial distribution of multiple compounds inside the crystal to be estimated any time during crystallization. In addition, the facet growth rate in the model was not related directly to supersaturation or impurities like the models used by previous researchers such as Kubota². Instead, it depends on the amount of materials transferred, adsorbed or crystallized onto the crystal faces and the material density. As a result, the solid-liquid phase equilibrium assumption Borsos et al.³ is unnecessary because inclusion of impurities and the evolution of crystal composition can be directly calculated. Simultaneous prediction of both composition and shape of a crystal can be achieved.

The new modeling method proposed by authors ¹ only achieved simulation for single crystals. In this paper, the method is extended to a crystal population in a stirred crystallizer. This was achieved by incorporating it into morphological population balance equations⁴. The new modeling technique is called multi-stage multi-component transfer rate morphological population balance equations (M³PBE). The remaining of this article is organized as follows. Firstly, a brief introduction of the multi-component mass transfer rate based model for single crystals will be given.

Then the integration into morphological population balance equation will be described. Afterwards the M³PBE model will be applied to simulate the composition, shape and size distribution of NaNO₃ crystal population in the presence of KNO₃ impurities. And finally conclusions will be drawn.



Brief Introduction to Single Crystal Model

Fig. 1 Schematic diagram of non-equilibrium stage model of a single crystal on a face.

Fig. 1 depicts the interface model between one face k (k = 1...F) of a crystal, and the liquid phase at time j. Let's examine the kinetic and thermodynamic phenomena involved for a component i that initially in the body liquid phase to crystallize on this crystal phase k. It can be considered as involving three steps. First, component i diffuses (or mass transfers) from the solution bulk to the interface, as a result of the driving force, i.e. concentration difference between the bulk solution and the interface, $x_i^L - x_i^I$. Here it is assumed that the bulk solution is well mixed so the composition of i in the bulk solution is uniform. Secondly, between the liquid phase and the solid phase there is an interface layer. Suppose the interface is so thin that there is no mass transfer resistance and the layer is homogeneous and we denote the composition of i component in it as z_i . In addition, it is assumed that the interface layer is formed by component adsorption, and the adsorption is fast that x_i^I and z_i can be assumed in adsorption equilibrium. In this paper the adsorption equilibrium is modeled with Langmuir adsorption isotherms. Thirdly, the adsorbed component i is integrated onto the crystal face. In here, the diffusion of component i in the solid phase is neglected. In the solid phase it is modeled like a "reaction" process that the adsorbed solute molecule i is included into the crystal. The driving force of this step is the difference between the adsorption molar fraction ($z_{i,k}$) and the equilibrium molar fraction that depends on the solid interface molar fraction ($y_{i,k}^I$). Here k is the kth face of the crystal, k=1,2,...,F. Therefore, for component i, on face k, the interface model equations are as follows,

$$R_{i,j,k}^{L} \equiv N_{i,j,k}^{L} - k_{i,k}^{d} A_{k} (x_{i,j}^{L} - x_{i,j,k}^{I}) = 0$$
⁽¹⁾

$$Q_{i,j,k}^{ads} \equiv z_{i,j,k} - \frac{K_{i,k} x_{i,j,k}^{l}}{1 + \sum_{m=1}^{C-1} K_{m,k} x_{m,j,k}^{I}} = 0$$
(2)

$$\mathbf{R}_{i,j,k}^{s} \equiv \mathbf{N}_{i,j,k}^{s} - \mathbf{k}_{i,k}^{r} \mathbf{A}_{k} (\mathbf{z}_{i,j,k} - \mathbf{K}_{i,k}^{r} \mathbf{y}_{i,j,k}^{I})^{p} = 0$$
(3)

 $R_{i,j,k}^{L}$, $Q_{i,j,k}^{ads}$ and $R_{i,j,k}^{S}$ represent the liquid phase mass transfer, adsorption equilibrium and solid phase mass transfer equations of component i, on face k, at moment j respectively; $k_{i,j,k}^{d}$ is the liquid phase mass transfer coefficient in mol/(m²s), where the superscript d denotes that the mass transfer coefficient is due to molecular diffusion. $k_{i,j,k}^{r}$ is the mass transfer coefficient from adsorbed solute to crystallized solute in mol/(m²s),where superscript r denotes that the mass transfer coefficient $k_{i,j,k}^{r}$ equation is in the form of a kinetic expression. $K_{i,k}^{r}$ is the equilibrium ratio of component i on crystal face k. p is the order, $K_{i,k}$ is the simplified Langmuir constant of adsorption of component i on crystal face k. According to Karpiński's suggestion, assigning the reaction order p = 2 would be the most appropriate choice in light of the BCF (Burton, Cabrera and Frank) growth theory.⁵

The component molar fraction in the bulk liquid phase can be expressed as the

molar fractions of components in the liquid phase as:

$$\mathbf{x}_{i,j,k}^{L} = \frac{\mathbf{l}_{i,j,k}}{\sum_{n=1}^{C} \mathbf{l}_{n,j,k}}$$
(4)

wherein $x_{i,j,k}^{L}$ is the molar fraction of component i in the solution at moment j on face k, $l_{i,j,k}$ is the mole number of component i in the solution at moment j on face k.

In this model, the diffusion in the solid phase is neglected. Therefore, the growth of crystal is assumed to be purely layer-by-layer stacking of crystallized material. Therefore, the solid composition related to the mass transfer is equal to the composition of the crystal layer that formed in the last moment (i = 1, 2, ..., C).

$$Q_{i,j,k}^{S} \equiv y_{i,j,k}^{I} - y_{i,j,k}^{S} = 0$$
(5)

And the component molar fractions in the crystal layer formed at moment j can be expressed by:

$$y_{i,j,k}^{S} = \frac{s_{i,j,k} - s_{i,j-1,k}}{\sum_{n=1}^{C} (s_{n,j,k} - s_{n,j-1,k})}, j \ge 2$$
(6)

wherein $s_{i,j,k}$ is the mole number of component i in the crystal at moment j on face k

The inclusion of these three steps are inspired by the work of Karpiński⁵ and Martins and Rocha⁶ on crystal growth of a single solute. The first and the third steps are described by corresponding rate equations that depend on the mass transfer driving force while the second step is assumed to follow the adsorption equilibrium.

With the interface model introduced above, it can now consider the temporal change of a crystal in the course of crystallization. If the process is divided into discretized moments, each moment can be regarded as a "stage" in the time space. Then the crystal growth in time can be described in the same way as the stage model of a distillation columns⁷. Fig. 1shows the details of a stage model. On the stage, j represents the jth moment, or the jth stage. The entering and leaving arrows represent the status of the solution and crystal at moment j-1 and j, or at stage j-1 and stage j. The state of a stage is described by a series of variables shown in Fig. 1, including

total moles of liquid and solid, L and S (mol), component moles of liquid and solid 1 and s (mol), enthalpy (J/mol), temperature (K). These variables are related to each other by equations. At the moment j, i.e. at stage j, mass and heat transfer takes place between the solution and the solid crystal face. The transfer rates of mass and heat are denoted as N (mol/s) and e (J/s). The superscripts L and S represent liquid and solid phases, and the subscripts i and j represent component i and stage j respectively. The model can also consider feeding (e.g. adding seeds) and heat exchange with the streams $f_{i,j}^L$ and Q_j^L . In this paper the focus is placed on crystal growth modeling so heat transfer is neglected. If there is no feeding after the crystallization begins, the mass balance equations for liquid phase, solid phase and interface can be written in turn as:

$$\mathbf{M}_{i,j}^{L} \equiv \mathbf{l}_{i,j} - \mathbf{l}_{i,j-1} + \sum_{k=1}^{F} \mathbf{N}_{i,j,k}^{L} \Delta t = 0$$
(7)

$$\mathbf{M}_{i,j,k}^{S} \equiv \mathbf{s}_{i,j,k} - \mathbf{s}_{i,j-1,k} + \mathbf{N}_{i,j,k}^{S} \Delta t = 0$$
(8)

$$\mathbf{M}_{i,j,k}^{\mathrm{I}} \equiv \mathbf{N}_{i,j,k}^{\mathrm{L}} \Delta t - \mathbf{N}_{i,j,k}^{\mathrm{S}} \Delta t = 0 \tag{9}$$

The summation of the compositions of components of either the liquid phase, or the solid phase, or for the adsorption phase should be 1. It is called the summation equation. The solid phase summation equations can be obtained from the summation of $Q_{i,j,k}^{S}$ so they are not independent equations and won't be listed here.

$$S_{j,k}^{L} \equiv \sum_{i=1}^{C} x_{i,j,k}^{I} - 1 = 0$$
(10)

$$S_{j,k}^{ads} \equiv \sum_{i=1}^{C} Z_{i,j,k} - 1 = 0$$
(11)

There are C+6CF unknown quantities for each stage j. These are the component liquid mole number ($l_{i,j}$: C in number), the solid mole number ($s_{i,j,k}$: CF), the liquid composition at the interface ($x_{i,j,k}^{I}$: CF), the solid composition at the interface ($y_{i,j,k}^{I}$: CF), the adsorption phase composition at the interface ($z_{i,j,k}$: CF), the mass transfer rate ($N_{i,j,k}^{L}$: CF and $N_{i,j,k}^{S}$: CF). The C+6CF independent equations that permits these unknown quantities include: component material balances for the liquid ($M_{i,j}^{L}$: C in

number), component material balances for the solid ($M^{S}_{i,j,k}$: CF), component material balances around the interface ($M_{i,j,k}^{I}$: CF), the liquid phase mass transfer rate equations $(R^{L}_{i,j,k} : (C-1)F)$, the solid phase mass transfer rate equations $(R^{S}_{i,j,k} : CF)$, the interface solid component model $(Q^{S}_{i,j,k}: CF)$, the interface adsorption equilibrium $(Q^{ads}_{i,j,k}: (C-1)F)$, the summation equations $(S^{L}_{j,k}: F \text{ and } S^{ads}_{j,k}: F)$. If the component molar numbers of solution and crystal at the last moment are known and the mass transfer rate can be obtained, the component molar numbers of solution and crystal at the present moment can be calculated in accordance with mass balance. Therefore the number of equations is equal to the number of variables so the equations can be solved using an appropriate numerical solution algorithm. In our model, the "streams" between stages are not countercurrent but concurrent. Therefore our model can be solved stage by stage, which is more convenient than solving non-equilibrium stage models for a distillation column. By solving the equations, the component mass transfer rates to each of the crystal face can be obtained. Then a particular facet crystal growth rate can be calculated by summing up all the component mass transfer rates (in mol/s) to that face divided by the component densities and molar weights and the face area. The change of the crystal composition can also be calculated according to the component solid mole number.

The M³PBE Model

After the non-equilibrium stage model for a single crystal is introduced above, the attention is turned to incorporating the model to Morphological Population Balance Equation. Population Balance Equation (PBE) is the most common method to model the size distribution of a crystal population. Ma et al. proposed Morphological Population Balance Equation (M-PBE) model to simulate the shape distribution or multi-dimensional size distribution of crystals.⁴

The compositions of components should be incorporated into the number population density distribution and then M-PBE can be extended to multi-stage multi-component transfer rate morphological population balance equations (M³PBEs)

model as Eq. (12):

$$\frac{\partial \Psi(\mathbf{X}, \mathbf{Y}, t)}{\partial t} + \sum_{k=1}^{F} \frac{\partial}{\partial x_{k}} \left(G_{k}(\mathbf{X}, \mathbf{Y}) \Psi(\mathbf{X}, \mathbf{Y}, t) \right) + \sum_{i=1}^{C-1} \frac{\partial}{\partial y_{i}} \left(H_{i}(\mathbf{X}, \mathbf{Y}) \Psi(\mathbf{X}, \mathbf{Y}, t) \right) = 0$$
(12)

wherein Ψ is the number population density function of crystal, **X** is the vector of normal distances from the crystal faces to the geometric center of a crystal with elements x_k (k=1,2,...,F). F is the number of crystal faces. **Y** is the vector of mole fraction of crystal components, with elements y_i (i=1,2,...,C-1). C is the number of chemical components. t is time. G_k is the facet growth rate of face k and H_i is the mole fraction change rate of component i.

One difference between the M³PBEs and the previous morphological population balance equations is that the face growth rate is calculated with the mass transfer rates from the non-equilibrium stage model rather than the conventional growth rate kinetics equations, as Eq. (13) shows:

$$G_{k}(\mathbf{X}, \mathbf{Y}) = \frac{\sum_{i=1}^{C} \left[N_{i,k}(\mathbf{X}, \mathbf{Y}) M_{i} / \rho_{i} \right]}{A_{k}(\mathbf{X})}$$
(13)

wherein $N_{i,k}$ is the mass transfer rate of component i on face k, in mol/s. M_i is the molar weight and ρ_i is the density of component i. $A_k(\mathbf{X})$ is the area of face k, which can be obtained according to the geometric information of the crystal. If k stands for a symmetric-related face group, A_k should be the sum of all the face areas in that group.

The mole fraction change rate of component i can also be calculated with the mass transfer rates as Eq. (14) shows:

$$H_{i}(\mathbf{X}, \mathbf{Y}) = \frac{1}{V(\mathbf{X})\sum_{i=1}^{C} (y_{i}\rho_{i} / M_{i})} \left(\sum_{k=1}^{F} N_{i,k}(\mathbf{X}, \mathbf{Y}) - y_{i} \sum_{i=1}^{C} \sum_{k=1}^{F} N_{i,k}(\mathbf{X}, \mathbf{Y}) \right)$$
(14)

wherein $V(\mathbf{X})$ is the crystal volume.

With the H and G specified, Eq. (10) can be numerically solved using the high resolution algorithm proposed by Gunawan, Fusman and Braatz⁸.

In summary, the framework of our method is as Fig. 2 shows. For each discretized moment, we firstly solve the stage model according to the amount of each

component in the liquid and solid phase at that moment. Then we can get the mass transfer rate and calculate the facet growth rate and mole fraction change rate. Afterwards, the M³PBE equation can be solved using the high resolution algorithm ⁸ and then the data of amount of each component in the liquid and solid phase at that moment can be updated and the calculation can be iterated moment by moment until the desired duration of crystallization processes is reached.



Fig. 2 Framework of method

Case study

Simulation scenario

In Shu's work¹, the single crystal model was applied to modelling a single NaNO₃ crystal growth from aqueous solution in the presence of impurity KNO₃. In the case study of this work we choose the same material but now it is for the whole crystal population in the crystallizer.

Fig. 3 is the equilibrium morphology of a NaNO3 crystal which was predicted by

Benages-Vilau⁹ and also observed by Wu et al.¹⁰ As Fig. 3 shows, a NaNO₃ crystal is rhombohedral with six faces. These faces can be classified into three groups of crystallographically equivalent faces, i.e. two {104}, two { $\overline{1}14$ } and two { $0\overline{1}4$ }. the values of α , β , and γ are 90.57°, 102.72°, and 102.72°. Wu et al. also measured the crystal face specific growth kinetics of all the three faces.



Fig. 3 Equilibrium and experimental morphology of a NaNO3 crystal

Benages-Vilau et al. studied the morphology change of NaNO₃ from aqueous solution in the presence of K^+ or Li⁺ ions. They found that the addition of these impurities led to a sudden decrease of the {104} face and caused the morphology change¹¹.

Initially 1000 pure NaNO₃ crystals are loaded in the crystallizer as crystal seeds and the crystallization temperature was kept at 25°C. KNO₃ was assumed to be adsorbed on {104} face only. The initial solution consists of 181.14g of NaNO₃, 0.21g of KNO₃ (the molar ratio of NaNO₃/KNO₃ is 1000) and 188.86g of H₂O. The initial distributions of face normal distances of {104}, { $\overline{1}$ 14} and { $0\overline{1}$ 4} are in Gaussian distribution as Eq. (15):

$$\Psi(\mathbf{X}, \mathbf{y}, 0) = \frac{1}{(2\pi)^{3/2} \sigma_1 \sigma_2 \sigma_3} e^{-\frac{1}{2} \left[\left(\frac{\mathbf{x}_1 - \mu_1}{\sigma_1} \right)^2 + \left(\frac{\mathbf{x}_2 - \mu_2}{\sigma_2} \right)^2 + \left(\frac{\mathbf{x}_3 - \mu_3}{\sigma_3} \right)^2 \right]}$$
(15)

wherein $\Psi(\mathbf{X}, \mathbf{y}, \mathbf{0})$ is the initial number density distribution function, \mathbf{x}_1 , \mathbf{x}_2 and \mathbf{x}_3 stand for the of face normal distances of {104}, { $\overline{1}14$ } and { $0\overline{1}4$ }. μ_1 , μ_2 and μ_3 are the mean values of corresponding face normal distances and σ_1 , σ_2 and σ_3 are the standard deviations. Their values are 100 µm, 300 µm, 300 µm, 25 µm, 50 µm and 50 µm respectively. The initial distribution curves of the normal distances of {104}, { $\overline{1}14$ } and { $0\overline{1}4$ } are as Fig. 4 shows.



Fig. 4 Initial distribution of facet normal distances

Model parameters

In our previous work, we discussed the determination of parameter values of the model ¹. The liquid mass transfer coefficients can be calculated based on correlation equation given by Geankoplis ¹² and the necessary property parameters of diffusivity, density and viscosity aqueous NaNO₃ and KNO₃ can be found in the work of Graber et al. ¹³. Other parameters corresponding to NaNO₃ can be regressed according to the solubility data ^{14 15}, and the facet growth rate measurement given by Wu et al.¹⁰. Their

values are in Table 1.

Parameter	{104}	{114}	$\{0\overline{1}4\}$
$K_{i,k}$	77.68	109.32	114.78
$K^{\mathrm{r}}_{\mathrm{i},\mathrm{k}}$	0.927	0.947	0.950
$k^{r}_{i,k}(10^{3} \text{mol} \cdot \text{m}^{-2} \cdot \text{s}^{-1})$	0.650	1.520	1.801

Table 1 Model parameters corresponding to NaNO₃

Because the measurement data of growth of NaNO₃ crystals in the presence of KNO₃ impurity are unavailable, the parameters corresponding to KNO₃ cannot be regressed. According to the experiment results of Benages-Vilau et al., the addition of KNO₃ impurity poisoned the {104} face growth rate¹¹. Therefore, in our previous work, KNO₃ was assumed to affect the {104} face only and the parameters corresponding to other faces are assumed to be 0. The values of $K_{i,k}$, $K^{r}_{i,k}$ and $k^{r}_{i,k}$ for KNO₃ on face {104} are assumed to be 776.8, 0.9805 and 64.97 mol•m⁻²•s⁻¹ respectively. The sensitivity of these parameters value were also discussed.¹ In the following simulation, we will use the same parameter values.

Simulation result

With M³PBE, we can calculate the time-depended joint number density distribution of the three normal distances and the overall KNO₃ concentration of the crystals. Since it is hard to show a 4-dimensional distribution, we transformed the simulated distribution into three 2-dimensional joint distribution of one of the three normal distances and the overall KNO₃ concentration as Fig. 5 shows. All the crystals are initially pure so the initial distributions are 1-dimensional peaks. During the crystallization, KNO₃ goes into the crystals so the distributions change into 2-dimensional surfaces. As NaNO₃ is consumed, the growth rates decreases.



(a)



(b)



(c)

Fig. 5 Joint number density of crystal KNO₃ concentration and facet normal distance. (a) Facet normal distance of {104} and crystal KNO₃ concentration; (b) Facet normal distance of { $\overline{114}$ } and crystal KNO₃ concentration; (c) Facet normal distance of { $0\overline{14}$ } and crystal KNO3 concentration

The concentration distribution curves at different moments are shown in Fig. 6. It can be seen that the movement of the curve peak as crystallization goes on, which indicates the increasing rate of overall KNO₃ concentration in crystals, decreases because of the consumption of KNO₃.



Fig. 6 Time-dependent crystal KNO3 concentration distribution

Another simulation was carried out for NaNO₃ crystallization without KNO₃ impurities. Except the initial amount of KNO₃ in solution, all other initial conditions are the same as the case above. The comparison of facet normal distance distributions are shown in Fig. 7. The increasing rate of normal distances of {104} face in the case with KNO₃ (solid curve in the first figure) is significantly smaller than that in the case without KNO₃ (dash curve in the first figure) because KNO₃ poisoned the growth of {104} face. On the other hand the normal distances of the other two faces of the two cases are very similar under the assumption that the impurity doesn't affect these two faces and the parameters corresponding to KNO₃ on these two faces are assigned as 0.





Fig. 7 Comparison of facet normal distance distribution of crystallization with and without KNO₃: Different colors represents different moments. Solid curves represent crystallization with KNO₃

impurities and Dash curves represent crystallization without KNO3 impurities

Further Discussion

M³PBEs provide unprecedented modeling capability fully based on first principle equations. The model parameter values can be obtained via three approaches: direct experimental measurement using instrument, estimation using molecular simulation (for some parameters), as well as model identification using data from crystallization experiments and an optimization approach together with the M3PBEs model.

The most reliable approach is direct experimental measurement using instrument. For instance, $k_{i,k}^{d}$, the liquid phase mass transfer coefficient can be measured by solid dissolution¹⁶. There are also correlations available for its estimation like the correlation given by Geankoplis, which can be used to predict the mass-transfer coefficients from liquid phase to the surface of small catalyst particles, microorganisms and other solids or liquid drops¹². Solubility data could be used to estimate mass transfer coefficients, for

instance, $K_{i,k}$ (Langmuir constant of adsorption) and $K^{r}_{i,k}$ (the equilibrium ratios) were correlated with the solubility data; if $K_{i,k}$ can be obtained, $K^{r}_{i,k}$ can be calculated using the correlation relations.¹

For some parameters, currently they may not be easily measured in experiments, but molecular simulation could be an alternative approach to estimate their values. For example, the parameters corresponding to mass transfer from adsorption layer to solid phase, $k_{i,k}^{r}$ (the mass transfer coefficient from adsorbed solute to crystallized solute) and r (the reaction order) canbe calculated with molecular simulation.

A not so rigorous but nevertheless practical method for estimation of parameter values is via model identification. Data from crystallization experiments and analysis of crystal shape and composition can be used, together with an optimization method to estimate the parameter values.

It should be noted that there may be errors in measurements or estimation of the parameter values. Therefore a sensitivity of parameters was discussed in the previous work¹. The focus of the current paper is on building the M³PBE modeling framework, future research could include developing new instrument and methods for accurate measurement and estimation of parameter values.

Future work should also consider the integration of M³PBE with computational fluid dynamics in order to model large scale industrial processes, as well as more effective numerical solutions methods that can reduce the solution time of equations.

Conclusion

The proposed multi-stage multi-component transfer rate morphological population balance equations (M³PBEs) enable the temporal and spatial distribution of multiple components inside individual crystals of a population in a crystallizer, as well as crystal shape and multi-dimensional size distributions to be modeled. The potential use of the new modeling technique in estimation of a drug's stability, modeling co-crystallization of two or multiple components, as well as in dealing with other challenging crystallization processes such as chiral drug separation via

crystallization is open for future exploration. Future research should also investigate M³PBEs integration with computational fluid dynamics for use in large scale crystallizers, new instrument and methods for parameter measurement and estimation, as well as more efficient mathematical algorithms for solution of M³PBEs equations.

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