Computers and Chemical Engineering 63 (2014) 82–90

Contents lists available at ScienceDirect

Computers and Chemical Engineering

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

A qualitative comparison between population balances and stochastic models for non-isothermal antisolvent crystallization processes

Giuseppe Cogoni[a], David Widenski[b], Massimiliano Grosso[a,*], Roberto Baratti[a], José A. Romagnoli[b]

[a] Dipartimento di Ingegneria Meccanica, Chimica e dei Materiali, Università di Cagliari, Cagliari, Italy
[b] Department of Chemical Engineering, Louisiana State University, Baton Rouge, LA, United States

ARTICLE INFO

Article history:
Received 12 July 2013
Received in revised form 3 December 2013
Accepted 2 January 2014
Available online 10 January 2014

Keywords:
Crystallization
Stochastic modeling
Population balance
Antisolvent and temperature effects

ABSTRACT

The goal of the present work is to model the crystal growth processes mediated by both antisolvent feed and temperature variations through the time evolution of the Particle Size Distribution (PSD). The study is carried out by exploiting two different approaches. In the first approach a population balance equation (PBE) model is devised, where crystal nucleation and growth phenomena are developed taking into account rigorous first principle assumptions. The second approach is based on a phenomenological stochastic formulation leading to a global Fokker–Planck Equation (FPE) governed by a limited number of parameters, describing the time evolution of the probability density function representing the crystal PSD. Validations against experimental data are presented for the NaCl–water–ethanol ternary system. The pros and cons of both approaches are discussed.

1. Introduction

Antisolvent aided crystallization is an advantageous separation technique when the solute is highly soluble or heat sensitive. The driving force in crystal formation is the supersaturation that establishes the thermodynamic equilibrium for the solid–liquid separation. In crystallization operations in general, and in antisolvent crystallization in particular, control of the crystal size and the crystal size distribution is a crucial issue and several factors can affect the size and the widening of the size distribution. Modeling of antisolvent crystallization processes has been tackled, for example, in the systems paracetamol (Trifkovic, Sheikhzadeh, & Rohani, 2008; Zhou et al., 2006) and sodium chloride (Nowee, Abbas, & Romagnoli, 2008a, 2008b). Recently, cooling has been combined with antisolvent crystallization, and the joint process has been modeled for lovastatin (Nagy, Fujiwara, & Braatz, 2008) and for acetylsalicylic acid (Lindenberg, Krattli, Cornel, Mazzotti, & Brozio, 2009). Crystallization theory states that the temperature influence is extremely important for the growth rate because it is correlated with the kinetic of the growth rate and nucleation rate as well as the solvent composition that is affected by the antisolvent feed rate (Mullin, 2001).

The development of effective mathematical models describing the crystal growth dynamics is a crucial issue toward finding the optimal process performance and to control the crystal size and distribution. Typically, mathematical models based on population balance equations (PBE) are taken into account to describe the time evolution of crystal particles size distributions. Randolph and Larson (1988) first implemented the population balance approach. Since then there have been a number of applications. Examples are the crystallization of: citric acid (Caillet, Sheibat-Othman, & Fevotte, 2007), lovastatin (Nagy, Fujiwara, et al., 2008), paracetamol (Nagy, Chew, Fujiwara, & Braatz, 2008; Trifkovic et al., 2008; Worlitschek & Mazzotti, 2004), potassium aluminium (Nowee, Abbas, & Romagnoli, 2007), potassium chloride (Mohameed, Abu-Jdayil, & Al Khateeb, 2002), ammonia sulphate (Abbas, Nowee, & Romagnoli, 2006; Abbas & Romagnoli, 2006, 2007) and sodium chloride (Nowee et al., 2008a, 2008b). In general, PBEs are widely used as a modeling framework for the study of different applications as: adsorption of impurities (Févotte & Févotte, 2010), jet crystallizers (Woo, Nagy, Tan, & Braatz, 2009) and phase transitions (Févotte & Alexandre, 2007). Multidimensional population balance models also have been proposed for crystals whose growth is not homogeneous across each size axis (Ma, Tafti, & Braatz, 2002; Puel, Févotte, & Klein, 2003). Population balance models have been used to optimize crystallization operating conditions for various systems (Nagy, Fujiwara, & Braatz, 2007; Nowee et al., 2008a; Trifkovic et al., 2008). Computational fluid dynamics (CFD) models have been combined with population balance models for modeling mixing effects

* Corresponding author. Tel.: +39 0706755075.
E-mail address: massimiliano.grosso@dimcm.unica.it (M. Grosso).

0098-1354/$ – see front matter © 2014 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.compchemeng.2014.01.001

in crystallization systems (Woo, Tan, & Chow, 2006; Woo et al., 2009; Zauner & Jones, 2000).

At the core of the structured population dynamics, the number of crystals in a semi-batch crystallizer is increased by nucleation and decreased by dissolution or breakage. In structured population balances, the crystals are classified by their size. Therefore, population balance-based approaches provide more detailed information regarding the crystal size distribution in the crystallization unit. However, such a detailed description demands a great deal of knowledge on the thermodynamic properties associated with the solute and solvent to be incorporated into the structured population balances.

An alternative and novel approach to deal with particulate systems characterized by mean crystal size (MCS) and crystal size distribution (CSD) was formulated and implemented recently and it is based on modeling the growth process in terms of a Fokker–Planck Equation (FPE) (Galan, Grosso, Baratti, & Romagnoli, 2009; Grosso, Cogoni, Baratti, & Romagnoli, 2011; Grosso, Galan, Baratti, & Romagnoli, 2009). In this approach, the fluctuations of the particle state due to different uncertainty sources (e.g., turbulence at micro-scale mixing, temperature fluctuations, etc.) during the crystallization can be modeled as a random process. Thus, in an effort to explain the observed macroscopic behavior of crystal growth in antisolvent aided crystallization, the Fokker–Planck equation (FPE) is incorporated as the centerpiece of the approach. Models based on Fokker–Planck equations have been used in atmospheric sciences (Egger, 1981; Vallis, 1988), financial market dynamics (Michael & Johnson, 2003), polymerization (Matsoukas & Lin, 2006; Hosseini, Bouaswaig, & Engell, 2012, 2013), among others. Pertaining the latter topic, the FPE approach has been recently used in the framework of the emulsion polymerization (Hosseini et al., 2013), and it was shown that the addition of a stochastic term in the growth term representing the evolution of the particles leads to a better description of the experimental data. Within this context, the use of FPE represents a new direction in developing a population balance model, taking into account the natural fluctuations present in the crystallization process, and allowing a novel description, in a compact form, of the PSD in time.

In this work the comparative analysis between the different approaches to model the time evolution of the Particle Size Distribution (PSD), is presented. The study is solely focused on the growth process. The mathematical modeling for both approaches includes the influence of the two operating parameters, antisolvent feedrate and temperature. These operating variables are used in a direct manner for the population balance approach, where the model is based on first principle assumptions. On the other hand, the phenomenological parameters appearing in the FPE models are formulated considering a polynomial relationship in the model parameters dependencies with the input manipulated variables (antisolvent flowrate and temperature) toward a global model to be used within all possible operating regimes. In this formulation, the input-parameter models should have simple linear or quadratic dependences. Validations against experimental data are presented for the NaCl–water–ethanol crystallization system for both models.

2. Experimental work

2.1. Experimental set-up

The experimental rig is comprised of a 1 l jacketed reactor connected to a Thermo Scientific® cooling/heating bath circulator that provides to keep constant the temperature inside the reactor by an embedded PID controller and a thermocouple wired inside the reactor. The antisolvent is added using a Masterflex® peristaltic pump calibrated for each experiment. The crystal size distribution is determined from the pictures of the samples taken from the reactor using a digital camera mounted in a stereo-microscope and then processed by means of sizing computer software (Amscope®).

2.2. Experimental procedure

At the start-up condition, the crystallizer is loaded with an aqueous solution of NaCl made up of 34 g of NaCl dissolved in 100 g of water. The temperature is kept constant throughout the run, using three different values for the temperature, respectively 10 °C (hereafter referred as low temperature: LT), 20 °C (medium temperature: MT), and 30 °C (high temperature: HT). The ethanol was added to the aqueous NaCl solution using a calibrated peristaltic pump. Three different anti-solvent flow-rates were implemented: $u_0 = 0.7$ ml/min (hereafter referred as low feed rate: LFR), $u_0 = 1.5$ ml/min (medium feed rate: MFR) and $u_0 = 3.0$ ml/min (high feed rate: HFR). Thus a full factorial experimental design of nine experiments was performed. Along the operation, 8 ml samples were taken in an infrequent fashion. Samples were then vacuum filtered over filter paper and then dried into an oven, at least for 24 h, with a constant temperature of 50 °C. The crystal size distribution is determined by visual inspection of images taken using a digital camera mounted in a stereo-microscope (Wild Heerbrugg polarizing light microscope with 5 MP AmScope camera) at 25× magnification. The captured images, for each sampling time during the batch run, are then processed by means of a sizing computer software (Amscope®). Typically, for each time, the number of crystals analyzed for each crystal sample ranged between 150 and 300. Such large number of measurements is motivated to allow an efficient estimation of the experimental average crystal size $M_{1,\mathrm{exp}}$ at each kth operating condition of the full factorial design (thus $k = 1, \ldots, 9$) and at sampling time $t_{j,k}$

$$M_{1,\mathrm{exp}}(t_{j,k}) = \frac{1}{n_{j,k}} \sum_{i=1}^{n_{j,k}} L_i \tag{1}$$

where in Eq. (1), $n_{j,k}$ is the number of crystals measured in the kth experience at time t_j and L_i is the ith crystal measurement.

3. Population balance approach

The developments of rigorous mathematical models describing the crystal growth dynamics in crystallization processes are based-on population balances (Randolph & Larson, 1988). The idea of population balances has been widely used the modeling of particulate systems in chemical engineering, with applications including crystallization (Lindenberg et al., 2009; Nagy, Fujiwara, et al., 2008; Nowee et al., 2007, 2008a, 2008b; Randolph & Larson, 1988; Trifkovic et al., 2008; Zhou et al., 2006), manufacture of pharmaceutical API (Lindenberg et al., 2009; Nagy, Fujiwara, et al., 2008; Nagy et al., 2007; Nowee et al., 2008a, 2008b; Trifkovic et al., 2008; Worlitschek & Mazzotti, 2004; Zhou et al., 2006), and polymerization (Crowley, Meadows, Kostoulas, & Doyle, 2000; Thompson & Stevens, 1977).

A population balance allows for the tracking of a distribution of particles as they grow in solution. Traditionally, a complete population balance crystallization model is comprised of a population balance with corresponding crystallization kinetics, mass balance, and solubility model (Nowee et al., 2008a, 2008b). Here, the crystal growth is assumed as size independent and with negligible attrition and agglomeration. As a further assumption, the only internal coordinate that uniquely identifies the crystal is its size, L. Within these assumptions the PBE has the following form:

$$\frac{\partial n(L,t)}{\partial t} + \frac{n(L,t)}{V(t)}\frac{dV(t)}{dt} + G\frac{\partial n(L,t)}{\partial L} - B\delta(L - L_0) = 0 \tag{2}$$