To the Editor:

I am writing to you to correct our mistake in our article ("A Submerged Membrane Reactor for Continuous Phenol Hydroxylation Over TS-1") published in the *AIChE Journal*, DOI 11514, 2008; 54(7):1842-1849.

Recently we have identified an error in our article, which is "TS-1 catalyst (average particle size, 200 nm; BET surface area, 95 $m^2 \cdot g^1$; the Si/Ti molar ratio, 9) was provided by Baling Petrochemical Co., SINOPEC". (p 1843) should be replaced by "TS-1 catalyst (average particle size, 200 nm; BET surface area, 408 $m^2 \cdot g^1$; the Si/Ti molar ratio, 59) was provided by Baling Petrochemical Co., SINOPEC".

I apologize for any inconvenience.

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To the Editor:

In a recent article on the operation of seeded batch crystallizers,[1] my co-authors and I used the method of moments to model crystallizer operation and also reported the final crystal-size distribution function at the end of the batch. It was subsequently brought to my attention that we did not explain how the final crystal-size distributions were calculated, and that our method may be of interest to other researchers since researchers working with moment models seldom report final crystal-size distribution functions, and it is well-known that the crystal-size distribution function cannot be recovered exactly from a finite number of moments. Therefore, I would like to briefly explain how the final crystal-size distribution function was calculated.

From the integration of the equations in the method of moments model, the nucleation and growth rates as a function of time can be determined. In principle, since the calculation must only be performed once (not repeatedly for the optimization) to determine the final crystal-size distribution one could simply solve the partial differential equation

$$\frac{\partial f}{\partial t} + G(t)\frac{\partial f}{\partial L} = 0$$

subject to the initial condition that the crystal-size distribution is equal to the seed crystal size distribution and the left boundary condition

$$f(0,t) = \frac{B(t)}{G(t)}$$

However, there is a simpler way for the assumptions that were made in the article. The final crystal-size distribution will be the sum of contributions from the seeds and the nuclei. The final seed crystal-size distribution will have the same shape as the initial seed crystal-size distribution—it will simply be shifted to the right by an amount equal to $\int_0^{t_f} G(t)\mathrm{d}t$. For the nuclei, at some time t^* during the batch, the value of the crystal size distribution at the left boundary ($L = 0$) will be given by $f(0,t^*) = B(t^*)/G(t^*)$. At the end of the batch, this point in the crystal-size distribution will have shifted to the right by an amount equal to $\int_{t^*}^{t_f} G(t)\mathrm{d}t$. So if $B(t)$ and $G(t)$ are known, one can plot $B(t)/G(t)$ vs. $\int_t^{t_f} G(t')\mathrm{d}t'$ to determine the crystal-size distribution function of the nuclei, and then add in the contribution from the seeds. (The smallest seed-grown crystal will always be larger than the largest nucleated crystal under the assumptions that we used.) Of course, this only works for the very restricted set of assumptions (no breakage or agglomeration, size-independent growth, etc.) that were considered in the article. If these assumptions were not valid, it would be necessary to solve the full partial differential equation. However, then of course the simple method of moments could not be applied either.

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Literature Cited

1. Ward JD, Yu CC, Doherty MF. A new framework and a simpler method for the development of batch crystallization recipes. *AIChE J*. 2011;57:606–617.

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