Material-Sparing Methods for Early Crystallization Development Using the Technobis Crystalline[™]

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Challenges in Early Crystallization Process Development

□ Material-Sparing Workflow for Kinetic Screening in a Crystalline

Generation of a Kinetic Map to Inform Early Process Design







Challenges in Early Crystallization Development



Industrial Crystallization

Most active pharmaceutical ingredients (APIs) are solids.

Why do we use crystallization?

SEPARATION of a solid mass from solvents/solutions, reaction mixtures

QUALITY CONTROL Removal of impurities and control of the right polymorph

PARTICLE ENGINEERING to enhance downstream unit operations like filtration and drying, and address drug product requirements







What Can Happen if Crystallization is Not Designed Well





Fast cooling, no seeding







Multistage cooling profile with seeding



Crystallization Development Road Map





Thermodynamic and Kinetic Aspects of Crystallization

Thermodynamics:

- Provide the driving force for crystallization (chemical potential).
- Often simplified as equilibrium solubility.
- Phase diagrams are the maps we use to design crystallizations.
- Helpful for knowing maximum yield and polymorphic forms.

Kinetics:

- Describe how fast things will happen.
- Rate equations that depend on supersaturation.
- Helpful for knowing particle characteristics such as size, shape, and filterability.



Solubility Curve and Metastable Zone Width Measurement



We all wish for this simple curve using crystal 16 data but often encounter complicated profiles



The Real-Life Phase Diagram...



Process parameters such as temperature, solvent composition or reagent level

Metastable Limit

Primary nucleation point (aka 'cloud point')

Kinetic Event

Dependent on route to the end conditions

- Temperature rates
- Addition rates
- Agitation / mixing
- Foreign matter / seed
- Reactor shape / size



Crystallization Design Workflow





Problem Statement

- It's very difficult to accurately predict crystallization behavior without performing extensive experimental screenings.
- Polymorphism, changes across different scales, changing kinetic values of growth and secondary nucleation, impurities, stability, processability, dissolution behavior, stirring effects, etc.

Approach Explored

- Crystalline[™]-based experiments allow for greater amounts of data and information to be collected for the early development of crystallization processes in a material sparing fashion.
- We explored these methods on two compounds through Pfizer-Rowan collaboration.



Material-Sparing Workflow to Measure Kinetics in the Crystalline



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Data Collection



Data Collection

Collecting imaging data near the onset of nucleation:



- Capture rates of 1 image/second.
- Analysis to obtain the total number and size of crystals in a picture.

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Navigating Crystal Overlap

As crystallization progresses, overlapping crystals will be seen as a single entity – not representative anymore!





Data Flow – What Do We Need?





Model Description



General Batch Crystallization Model

The Crystalline experiment can be tracked using a general population balance model for batch crystallization (initial conditions for the moments needed):



Problem: the Crystalline does not measure population moments, only their projections as crystal number and size!

Moments on Camera

The 8 mL vials used for the Crystalline have external dimensions of 17 x 60 mm.

Camera captures a small volume within. We'll call this θ .





Moments on Camera

The captured volume is much larger than that found in most PATs (back lighting, large capture area, large image depth). We get a 2D projection containing >100 crystals, with a certain size.

• The crystalline provides a particle size distribution, where size is the diameter of the equivalent circle:





Moments on Camera

<u>Assuming crystals have cubical habit</u> (requirement for the presented methods), their 2D projection on camera is not a strong function of their orientation:



http://www.malinc.se/math/linalg/ rotatecubeen.php

• We can estimate area (k_a) and volume (k_v) shape factors, that translate size from the Crystalline (L, as equivalent circle diameter) into area and volume of the cubical crystals:

$$k_a = \frac{3}{2}\pi \qquad k_v = \left(\frac{\pi}{4}\right)^{3/2}$$



Moments on Camera → Overall Crystallizer Moments

For each image, we can now calculate the number, length, area, and volume of the crystals on camera (making the cubical habit assumption to get the projection of the crystal in the third dimension):



• Note: Because the crystalline only measures counts and size, *L*_{tot}, *A*_{tot} and *V*_{tot} are not independent!



General Crystallization Model → Crystalline[™] - Specific Model

We can now adapt the batch crystallization model to use those projected moments instead:



J.M. Schall, G. Capellades, A.S. Myerson. CrystEngComm 2019, 21, 5811-5817.



General Crystallization Model → Crystalline[™] - Specific Model

We can now adapt the batch crystallization model to use those projected moments instead:





Data Processing



Back to the Data Flow





Processing Crystalline Data

To ensure that the methods are not user-sensitive, we have automated data cropping, outlier detection, and calculation of initial conditions for parameter estimation.



- Cropped range covering 70% of the event, from base line to the highest crystal count.
- Outlier removal based on deviation from a moving average.

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Processing Crystalline Data – Excel Template

Assumptions / Comments

Crystalline measures particle size as the diameter of the equivalent circle with the same projected area as the crystal

Although it reports particle size, area is the most reliable reading, which can be re-calculated as A= IN;"(3/2)"n"L;²

Methods rely on the samples collected on camera being representative of the crystal concentration and size in suspension, on working with cubical crystals, and on the assumptions of constant habit and negligible agglomeration

Especially when using the overhead hook for stirring, the stirrer may show up on camera and decrease the signal in certain pictures. An outlier removal algorithm has been implemented that removes pictures with less than 70% of the crustals from a moving average (see 3b below).

How to Use

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1- Export the PSD data from the Crustalline, only at the region where the temperature was constant. It does not need to start right at the point where temperature became constant. You just need a range that captures the crustallization event. This should give one file per crustallization event.

2 - Copy and paste the Crystalline PSD output in the highlighted cells, one tab per crystallization event. Check that temperature was constant throughout

3 - Compare the plotted figures - was the event captured correctly? Is there any change in slope or an increase in noise towards the end of the event that would have to be cropped? Was that cropped right by the template?

3.a - if the outlier removal is too severe, you can adjust the percent change allowed here (default is 30% deviation from moving average):

Accepted deviation from moving average: 30% (recommend 30%, use 100% to turn off outlier removal) 0.7

Correction factor:

3.b - Note that outlier removal is set on a moving average

4 - Copy the values in columns DR and DT to gPROMS for parameter estimation - you'll be using number and area only, but still need initial conditions for N, L, A, and V. Your initial conditions, as the average of the first ten points, are in rU20 - U23. For fast crystallizing systems, make sure those average



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Processed Data

We get trends for number, length, area, and volume of crystals on camera:



 Because length, area, and volume are not independent (all calculated from the crystal area that the equipment sees), <u>only number and area</u> <u>are used for parameter estimation</u>.



Parameter Estimation - Example



Acetaminophen from Ethanol-Water

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Kinetic data collected at 10 °C, at constant solvent composition (25% ethanol in water), for different starting supersaturations. 4 replicate events at each concentration:



- With 4 camera modules, the entire screening can be completed in one day (4 concentrations x 4 replicates -> 16 events).
- While data is noisy, trends with supersaturation can be clearly seen beyond the repeatability of the methods.

Parameter Estimation

Best fit and parameters for Acetaminophen in Ethanol-Water:

Parameter	Value	Units
k _b	$(2.08 \pm 0.03) \cdot 10^5$	g ⁻¹ s ⁻¹
b	2	-
j	1	-
k_g	2.31 ± 0.02	μm/s
g	1	-
θ	5.45 ± 0.09	mg/picture

 $B = k_b \sigma^b M_{T,s}^j$





40 mg/g Exp — 40 mg/g Fit

▲ 60 mg/g Exp — 60 mg/g Fit

200

160

120

80

40

Crystals / Picture

• 50 mg/g Exp — 50 mg/g Fit

70 mg/g Exp — 70 mg/g Fit

- Estimated θ is reasonable when converting from mass to volume.
- Note: depth may be underestimated, as effective 2D area is not 2.6 mm x 1.9 mm (crystals at picture's edges may not be analyzed)

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Model Validation

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Pfizer

CSPE Lab

To validate reproducibility, experiments were repeated at the Pfizer site (Groton, CT), with their Crystalline:

• Camera magnification is 2.8 µm/pixel instead of our 4 µm/pixel. New dimensions:



 The 2D area being captured is 2.4 mm² instead of 4.9 mm² (effective area may be lower, edge effect). We expect θ to drop by at least 50%.

Model Validation

Rowan University

🔁 Pfizer

CSPE Lab

To validate reproducibility, experiments were repeated at the Pfizer site (Groton, CT), with their Crystalline:

• Using parameters estimated at Rowan to predict Pfizer data (adjusting θ only):



- θ for the 2.8 µm/pixel magnification converged at 2.26 ± 0.02 mg/picture.
- 59% drop in θ when capture area drops by 51% \rightarrow Effects of different depth, and edge effects.

Application: Systematic Process Development







Systematic Crystallization Process Development

- Classifying APIs by their kinetic properties using Crystalline[™]-based experiments allows greater amounts of data and information to be collected for the early development of crystallization processes in a material sparing fashion.
- gPROMS FormulatedProducts[™]-based modeling allows for the development of a parameter estimation framework that can provide quick and accurate k_b and k_a values for nucleation and growth respectively.

Objectives

Can we use k_b and k_g (nucleation and growth constants) to model crystallization behavior independent of supersaturation and suspension density?

- Reduce the number of unknowns and variables.
- Model crystallization events.
- Identify trends.
- Make data-based predictions.



API Selection





Rathi, S.; Chavan, R. B.; Shastri, N. R. Drug Delivery and Translational Research 2019, 10 (1), 70-82.

Model Compounds





The Workflow



Big Picture – Systematic Crystallization Process Development

Trends between k_b and k_g values plotted against each other for different systems could tell a variety of stories.

- How similar are solvent-dependent kinetics, compared to differences across solutes?
- Pure solvents vs mixed solvents how much difference is there in kinetic effects?
- How much of a correlation exists between nucleation and growth?
- Quick comparison of new compounds with established systems
- Residence time and initial pot conditions for continuous crystallization
- Identification of critical parameters, and streamlining development stages: are solvent or temperature effects significant for this compound? Do we need to investigate those at the larger scale?





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Griffin Fountain

