# Stochastic model of nucleation Becker-Döring Model

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#### Motivation

Becker-Döring model

Stochastic Becker Döring model

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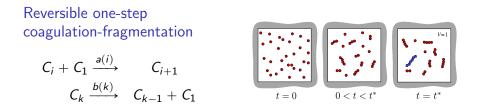
### Key questions

- What is a nucleus? How large should it be?
- How is lag phase related to nucleation?
- What is the time scale of nucleation formation? What is the variability of this step?
- How to include (stochastic) unfavorable aggregation steps in a coagulation-fragmentation model?

#### Motivation

#### Becker-Döring model

Stochastic Becker Döring model

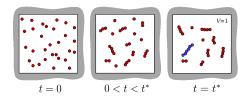


- First used in the work Kinetic treatment of nucleation in supersaturated vapors by physicists Becker and Döring (1935).
- Traditionally used as an infinite set of Ordinary Differential Equations. More recently used as a finite state-space Markov Chain.

Reversible one-step coagulation-fragmentation

$$C_i + C_1 \xrightarrow{a(i)} C_{i+1}$$

$$C_k \xrightarrow{b(k)} C_{k-1} + C_1$$

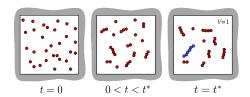


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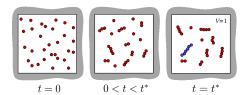


- Purely kinetic model (law of mass-action) : no space, no polymer structure (but size-dependent kinetic rates).
- Indirect interaction between polymer C<sub>i</sub>, i ≥ 2 via the available number of monomers C<sub>1</sub>.

$$C_1(t) + \sum_{i \geqslant 2} iC_i(t) = \text{constant}$$

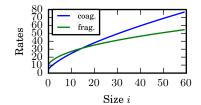
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Typical (in physics literature) coefficients are :

$$a_i = i^{\alpha}$$
,  $b_i = a_i \left( z_s + \frac{q}{i^{\gamma}} \right)$ ,  $\alpha, \gamma \in (0, 1)$ .



#### What is a nucleus? What is its size?

Schematically, there is two different conceptual ways to think of a nucleus :

- 1) As a fixed cluster size, (mainly) depending on structural properties
- 2) As a varying cluster size, depending on thermodynamic quantities (and concentration of monomers).

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Within BD model, both definition are compatible. The size of a cluster evolves "roughly" as

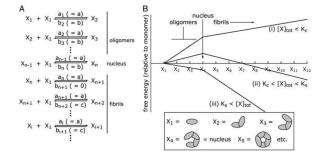
$$\frac{d}{dt} < i >= a(i)c_1(t) - b(i) = a(i)\left(c_1(t) - \frac{b(i)}{a(i)}\right)$$

Motivation **BD** SBD

# Use of BD-like model in protein nucleated-polymerization models

# Irreversible nucleation step, "piecewise constant" rates

Powers & Powers, Biophys. J. 91, 2006



#### How is lag phase related to nucleation?

The lag phase of spontaneous polymerization experiment is usually decomposed in two phases

- ▶ 1) A nucleation phase ( t or  $t^N$ )
- 2) (if it exists) an auto-catalytic phase ( $e^t$ )

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The nucleation phase is much slower, and is believed to more subject to *inherent stochastic* fluctuations

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However, we often measure a mixture of both (tenth time of polymerization curves)

#### Concentration-dependence in BD model

 Based on scaling arguments, one can show that for b<sub>i</sub> = 0 (irreversible nucleation),

$$\inf\{t \ge 0 : c_n(t) \ge \delta m \mid c_i(t=0) = m\delta_{i=1}\} \simeq \frac{1}{m}.$$

while for " $b_i \rightarrow \infty$ " (pre-equilibrium nucleation),

$$\inf\{t \ge 0 : c_n(t) \ge \delta m \mid c_i(t=0) = m\delta_{i=1}\} \simeq \frac{1}{m^n}.$$

Motivation **BD** SBD

# Use of BD-like model in protein nucleated-polymerization models

pre-equilibrium nucleation step, constant rates

$$\begin{cases} \frac{dc_1}{dt} = -(ac_1 - b)y, \\ \frac{dy}{dt} = Kc_1^n (+Q(m - c_1(t))), \\ \frac{dz}{dt} = (ac_1 - b)y, . \end{cases}$$

Ferrone et al., Bophys. J. 32, 1980

$$\begin{array}{l} y = \sum_{i \ge n} c_i \\ z = \sum_{i \ge n} i c_i \\ a(i) = a, \ b(i) = b \\ Q = \text{secondary} \\ \text{nucleation mechanism} \\ (\text{fragmentation,} \\ \text{heterogeneous} \\ \text{nucleation...}) \end{array}$$

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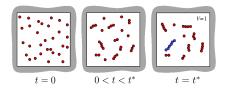
Motivation BD SBD

#### Stochastic Becker-Döring model

Reversible one-step coagulation-fragmentation

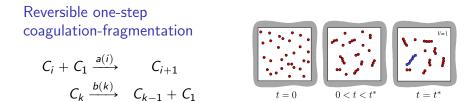
$$C_i + C_1 \xrightarrow{a(i)} C_{i+1}$$

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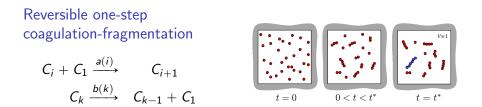
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# Stochastic Becker-Döring model



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- Yet with a large number of particles, one may expect the stochasticity to averaged out. Under which condition(s) the nucleation phase is "stochastic"?

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The nucleation phase is "stochastic" for unfavorable aggregation

Reversible one-step coag.-frag.

$$C_i + C_1 \xleftarrow{a_i \\ b_{i+1}/\varepsilon} C_{i+1}$$

Using pre-equilibrium hypothesis, in the unfavorable aggregation limit, the leading order of the first assembly time of a cluster of size N is

$$< T > \approx_{\varepsilon \to 0} \frac{1}{\varepsilon^{N-2}} \frac{\prod_{k=2}^{N-1} b_k}{\prod_{k=1}^{N-1} a_k \prod_{k=0}^{N-1} (M-k)}$$

Also, in the asymptotic  $\varepsilon \to 0$  the first assembly time T is an exponential distribution.

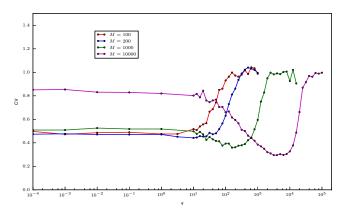
Motivation BD SBD

#### **Unfavorable** aggregation : 1) scaled reaction rates

Reversible one-step coag.-frag.

Y. et al., JCP, 144, 2016

$$C_i + C_1 \xrightarrow[b_{i+1}/\varepsilon]{a_i} C_{i+1}$$



Reversible one-step coag.-frag.

Y. et al., JCP, 144, 2016

$$C_i + C_1 \xrightarrow[b_{i+1}/\varepsilon]{a_i} C_{i+1}$$

This behavior can be used to couple a first part, very unfavorable, to a second part, favorable or irreversible

$$C_1, Y, Z \mapsto \left\{ \begin{array}{ccc} C_1 - n, Y + 1, Z + n & \text{at rate} & \alpha(C_1) \,, \\ C_1 - 1, Y, Z + 1 & \text{at rate} & pC_1Y \,, \\ C_1, Y + 1, Z & \text{at rate} & qZ \,. \end{array} \right.$$

Then, for "small  $\alpha$ ", and large volume, the lag time is composed of the convolution of an Exponential variable of rate  $\alpha$  and a deterministic time given by the ODE

$$\begin{cases} \frac{dc_1}{dt} = -pc_1y \ (-n\alpha(c_1)) \ .\\ \frac{dy}{dt} = qz \ (+\alpha(c_1)) \ , \quad y = \sum_{i \ge n} c_i \ ,\\ \frac{dz}{dt} = pc_1y \ +(n\alpha(c_1)) \ , \quad z = \sum_{i \ge n} ic_i \ . \end{cases}$$

Szavits-Nossan et al., PRL 113, 2014  $Y = \sum_{i \ge 2} C_i, \ Z = \sum_{i \ge 2} iC_i$ 

$$C_1, Z \mapsto \left\{ \begin{array}{ll} C_1 - 2, Z + 2 & \text{at rate} & \varepsilon^{\nu} \alpha(\varepsilon C_1)^2 \,, \\ C_1 - 1, Z + 1 & \text{at rate} & p(C_1 \varepsilon)(Z \varepsilon) \,. \end{array} \right.$$

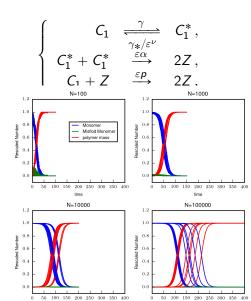
Then, for  $\nu > 1$ , and  $\varepsilon \rightarrow 0$ , the lag time converges "essentially" to an exponential distribution (in the time scale  $\varepsilon^{\nu} t$ )

Doumic et al., SIAM J. App. Math., 76(6) (2016)  $Z = \sum_{i \ge 2} iC_i$ 

$$\begin{cases} \frac{dc_1}{dt} = -pc_1 z \left(-2\alpha c_1^2\right).\\ \frac{dz}{dt} = pc_1 z \left(+2\alpha c_1^2\right), \quad z = \sum_{i \ge n} ic_i. \end{cases}$$

Motivation BD SBD

#### **Unfavorable** aggregation : 1) scaled reaction rates

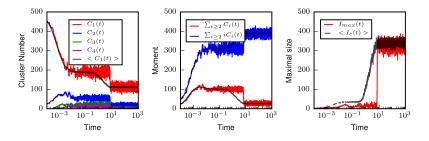


Adapted from *Eugène et al.,JCP*, 144(17), 2016 and Doumic et al., SIAM J. App. Math., 76(6) 2016

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Then, for the
rescaled process
\varepsilon(C_1(t), C_1^*(t), Z(t))
we observ
"translated
trajectory" as
\varepsilon \rightarrow 0
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#### **Unfavorable** aggregation : 2) Large nucleus size

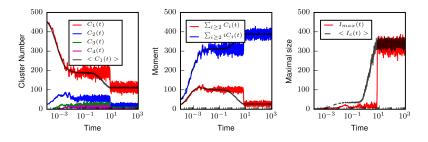
The classical nucleation theory considers small excess of monomers (supersaturated solution) which corresponds to very large nucleus size. In the stochastic setting, there is a phase transition in **finite random time** 



The transition phase is abrupt and corresponds to the rapid formation of a **single** large cluster

#### Unfavorable aggregation : 2) Large nucleus size

The classical nucleation theory considers small excess of monomers (supersaturated solution) which corresponds to very large nucleus size. In the stochastic setting, there is a phase transition in **finite random time** 



The scaling limit of this random time for large number / (vanishingly small) supersaturated density is an open problem.

# Summary

- Different definitions of nucleus consistent in BD model
- Concentration-dependence of nucleation (and lag) phase
- Variability in nucleation phase

Thanks for your attention !