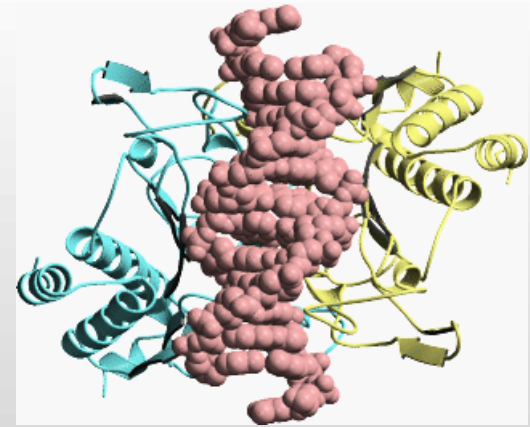


Background - Reversible Associations

Reversible Systems:

Self-association, hetero-association, or multiple reactions ($A + A + B \rightleftharpoons A_2B$)



The concentration in one component affects the concentration of another

Reactions can be fast (diffusion controlled) or slow (kinetically limited)

...and they observe mass action laws

Background - Reversible Associations



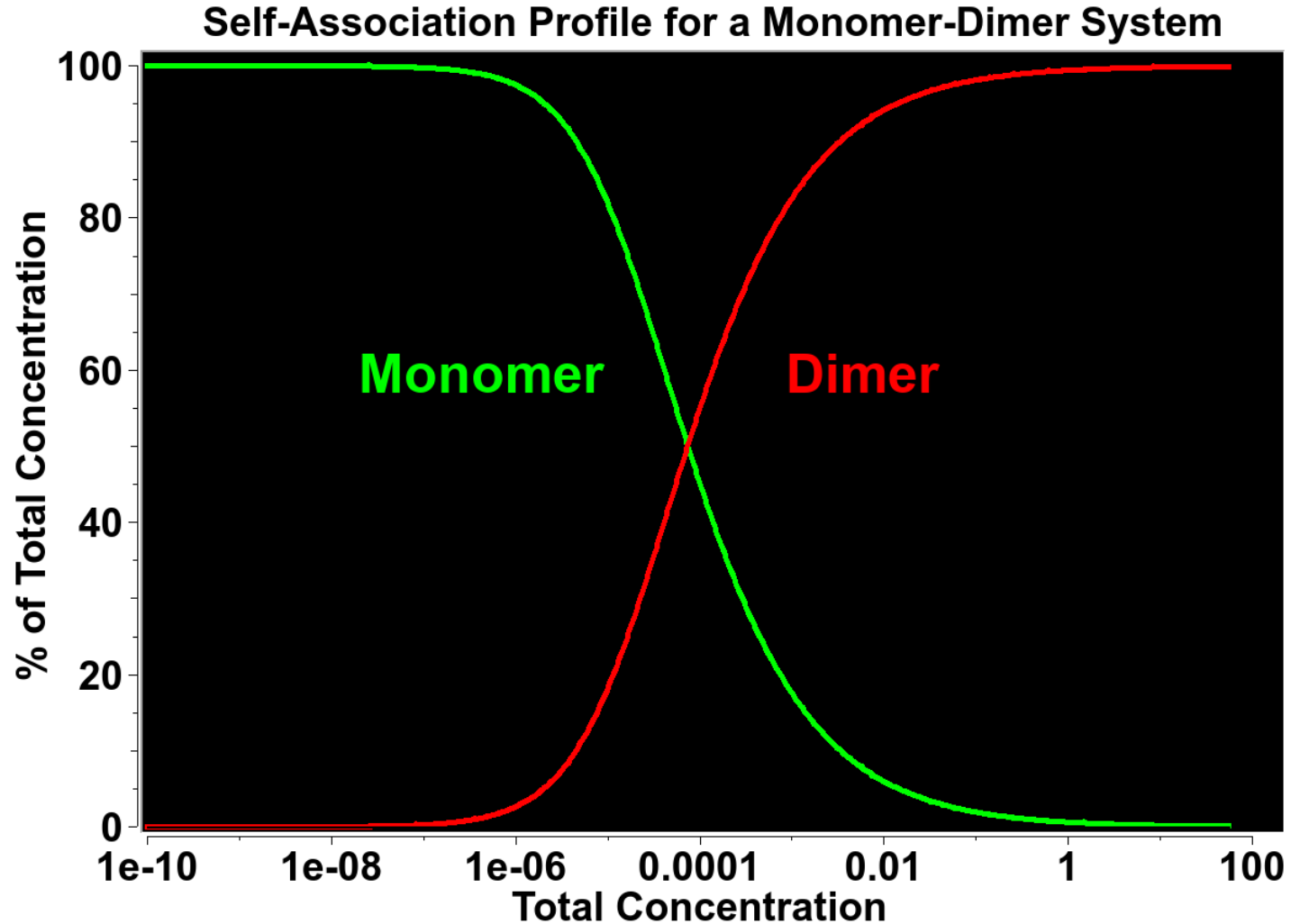
Equilibrium Constant:
$$K_a = \frac{[M_n]}{[M]^n} \quad K_d = \frac{[M]^n}{[M_n]}$$

Kinetics:
$$K_a = \frac{k_{on}}{k_{off}}$$

$$[M] + [M_n] = C_{total}$$

Solve polynomial:
$$[M] + K_A [M]^n - C_{total} = 0$$

Background - Reversible Associations



A Model for Reversible Reactions

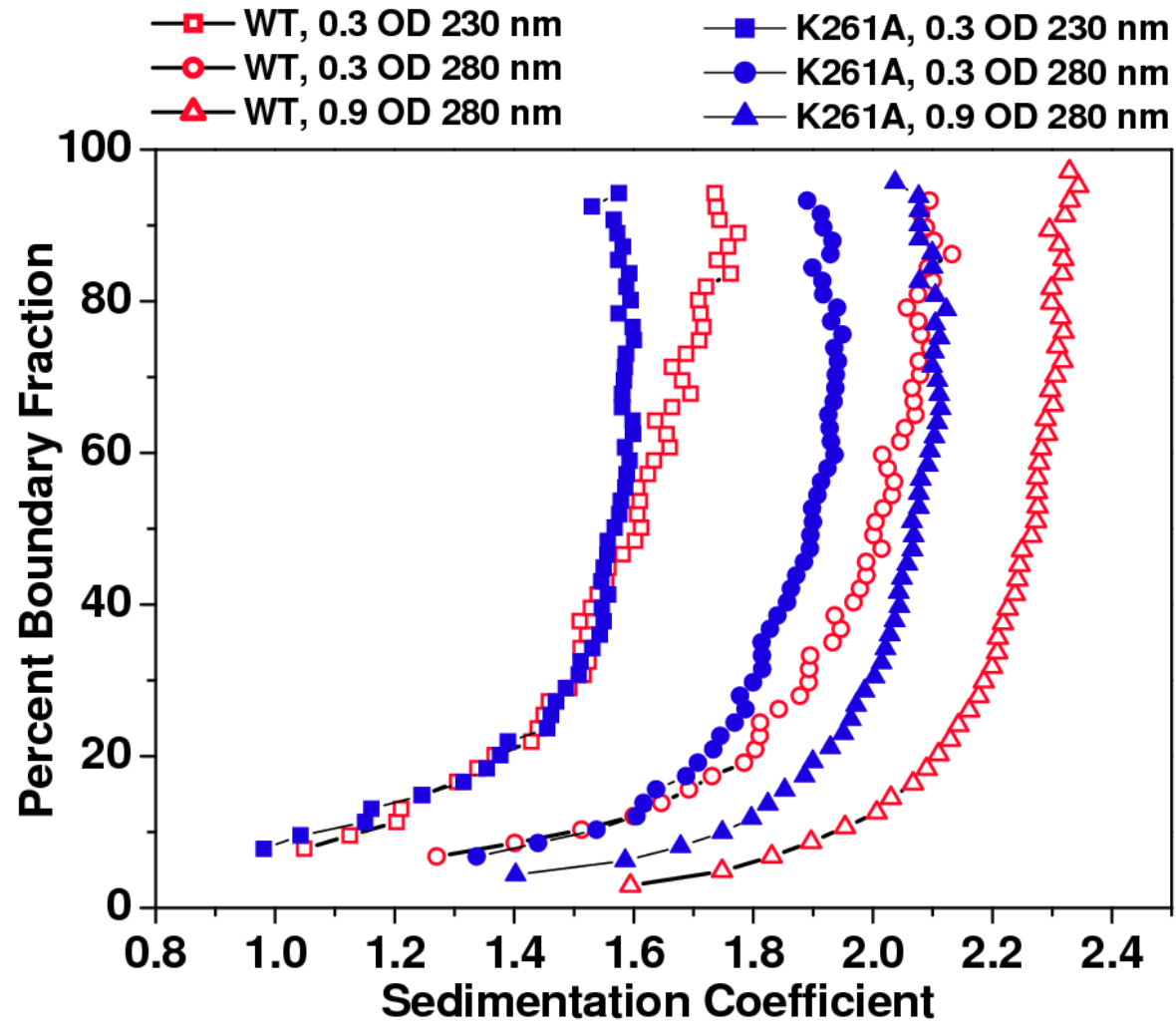
In the gradient, the *weight-average* sedimentation coefficient and the *gradient-average* diffusion coefficient are observed:

$$\bar{s} = \frac{\sum_{j=1}^m s_j C_j}{C_T} = \frac{\sum_{j=1}^m s_j K_j C_1^j}{C_T} \quad \bar{D} = \frac{\sum_{j=1}^m D_j (\partial C_j / \partial r)}{\sum_{j=1}^m (\partial C_j / \partial r)} = \frac{\sum_{j=1}^m j D_j K_j C_1^{j-1}}{\sum_{j=1}^m j K_j C_1^{j-1}}$$

Claverie, J.-M., Dreux, H., and R. Cohen (1975). Sedimentation of Generalized Systems of Interacting Particles. I. Solutions of Systems of Complete Lamm Equations. Biopolymers 14:1685-1700

Todd GP, Haschemeyer RH. General solution to the inverse problem of the differential equation of the ultracentrifuge. Proc Natl Acad Sci U S A. 1981 78(11):6739-43.

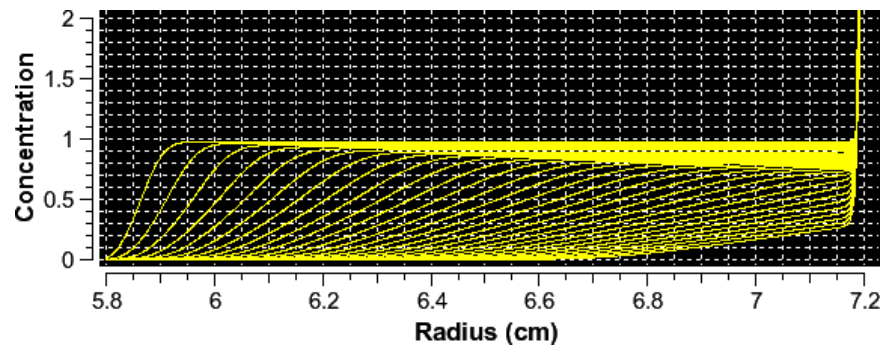
Monomer-Dimer Interface Mutation Analysis



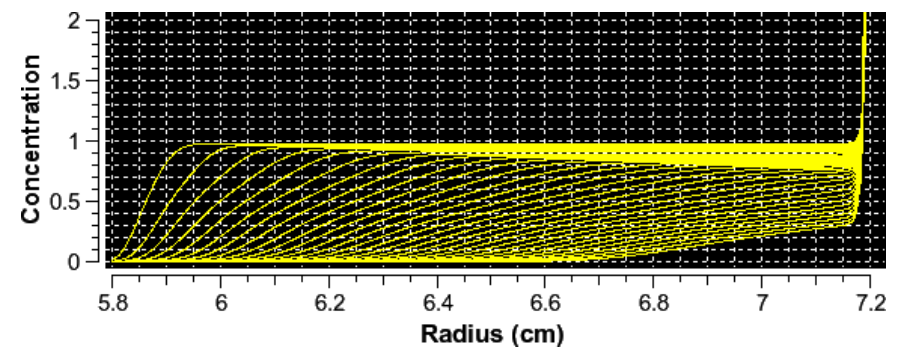
Models for Reacting Systems:

Monomer – Trimer Equilibrium, Monomer MW = 50 kDa

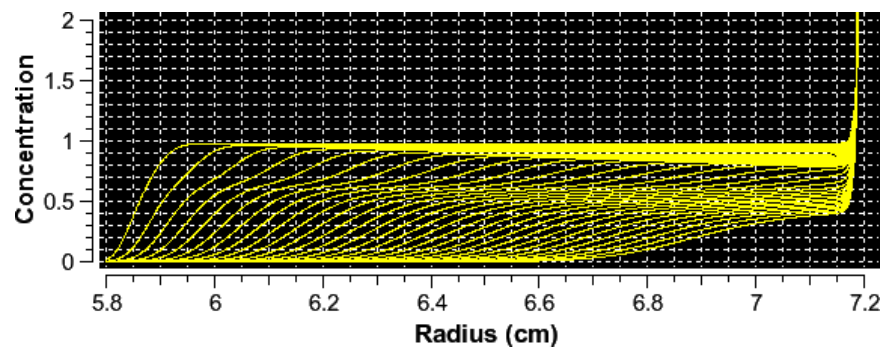
$K_{\text{off}} = 1.0/\text{sec}$



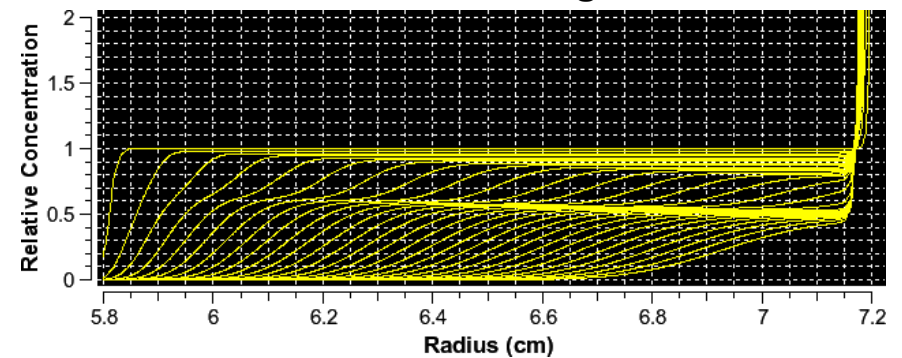
$K_{\text{off}} = 1.0 \times 10^{-3}/\text{sec}$



$K_{\text{off}} = 1.0 \times 10^{-4}/\text{sec}$



non-interacting



Models for Reacting Systems:

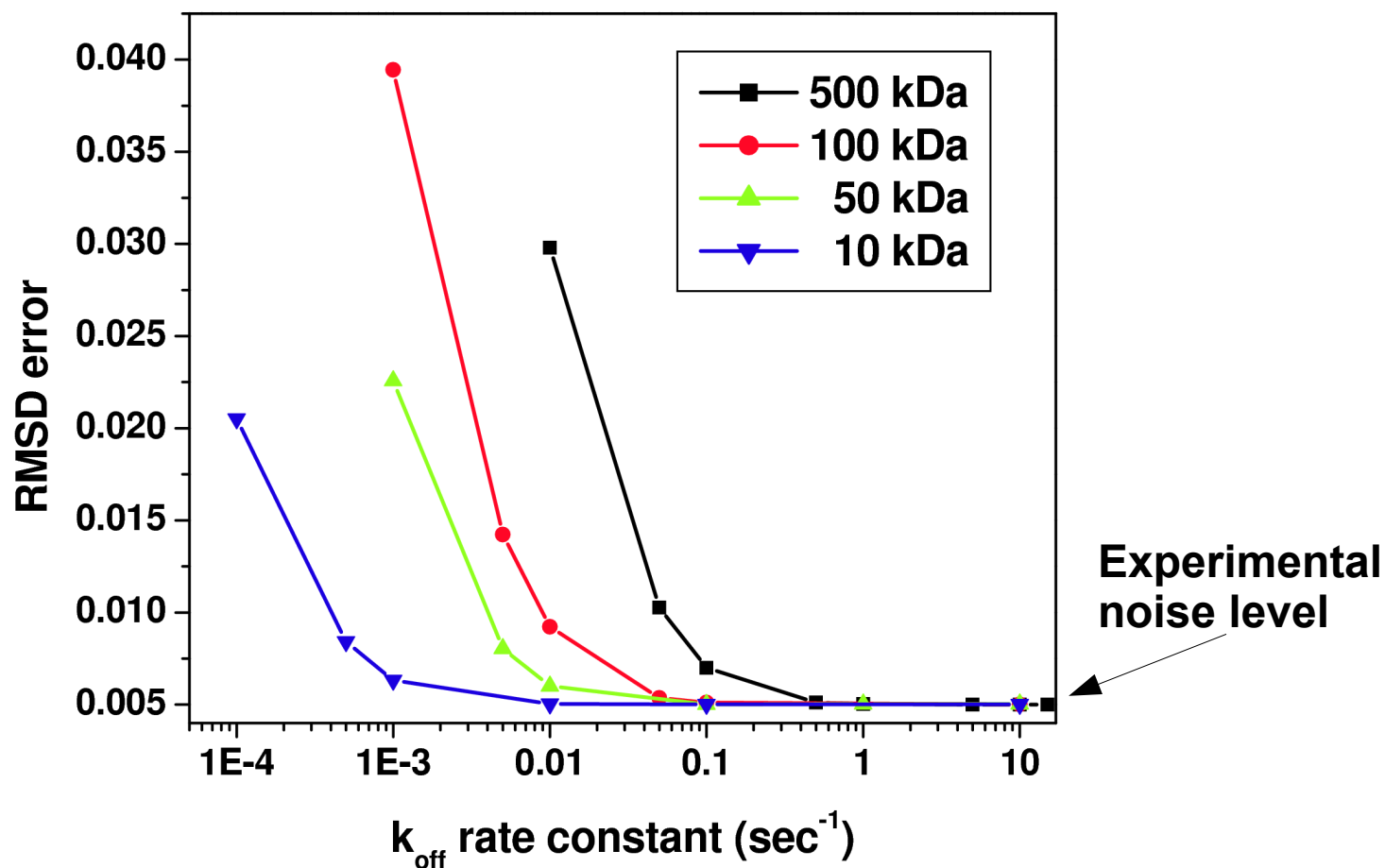
The magnitude of the measurable off-rate depends on rotor speed and sedimentation coefficient:

$$s \sim \frac{M}{f}$$

Faster rotor speed, higher molecular weight and globular shape will favor the measurement of faster rate constants.

Models for Reacting Systems:

Range of measurable k_{off} rate constants for different MW



Genetic Algorithm Optimization:

**Genetic Algorithms (also called evolutionary programming)
provide a stochastic optimization method**

Holland J, Adaption in Natural and Artificial Systems, 1975, U. of Michigan Press

Based on nature – evolutionary paradigm

Mutation, recombination, deletion, insertion, crossover operators

Random number generators are used to manipulate operators

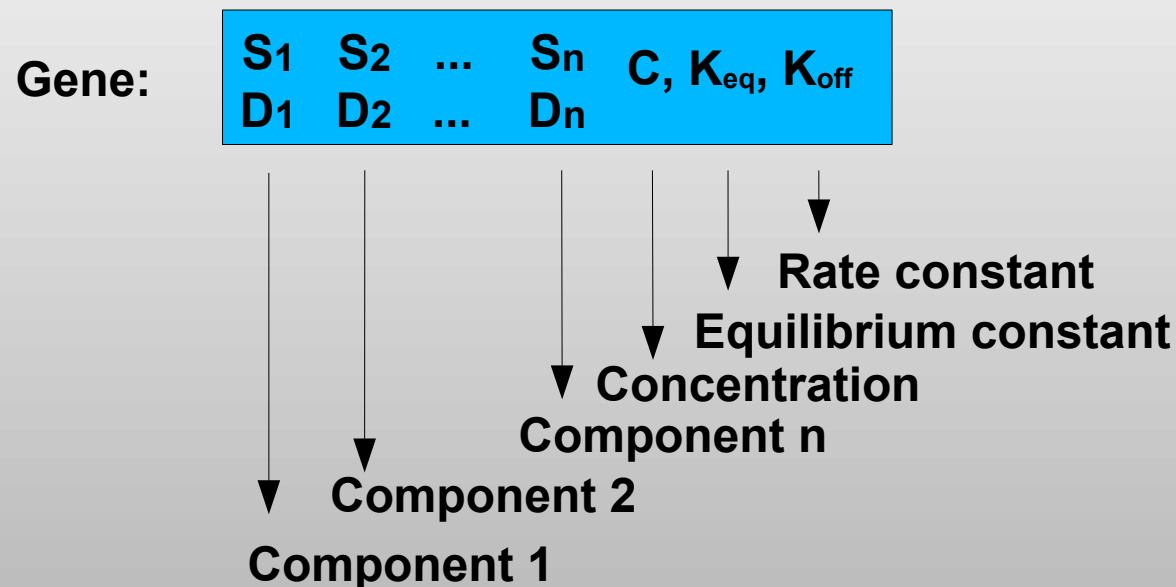
Generational Model – survival of the fittest (...fitting function)

Generation → iterations, genes → parameter strings, bases → s, D, K_d, k_{off}

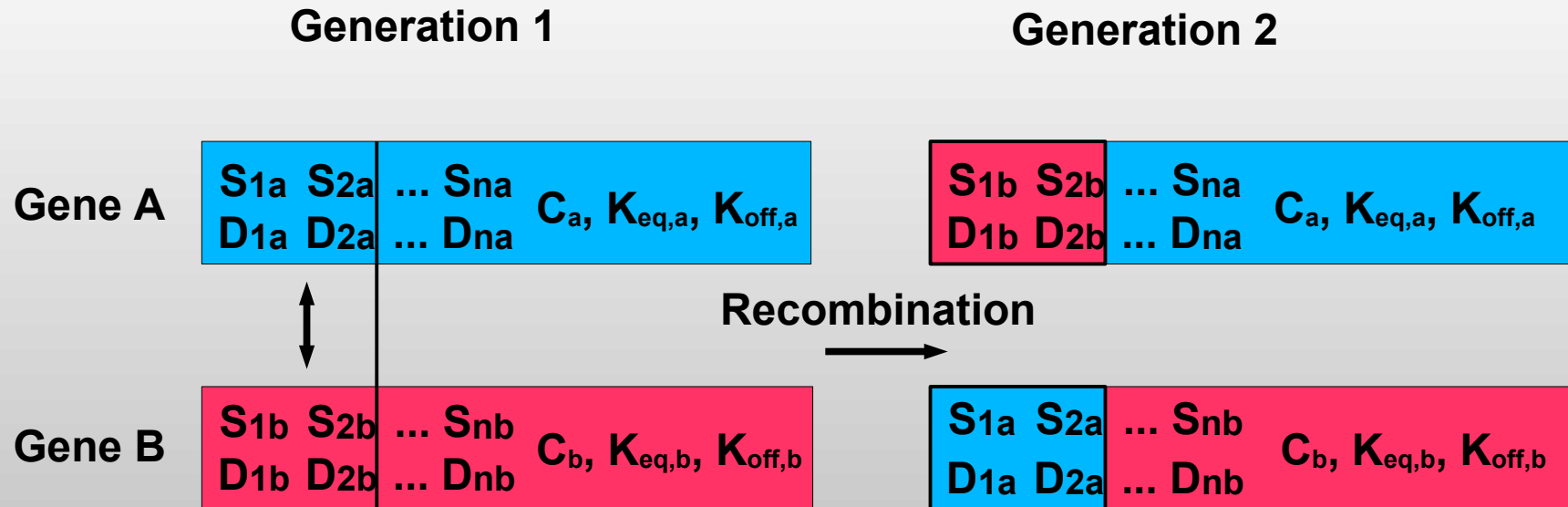
Use a Monte Carlo analysis to determine confidence level from noisy data

Genetic Algorithm Optimization:

Genes are strings of parameters, each gene consists of a pair of corresponding sedimentation and diffusion coefficients, loading concentration, equilibrium constants and rate constants.



Crossover/Recombination



Mutation

Generation 1

S ₁	S ₂	...	S _n	C, K _{eq} , K _{off}
D ₁	D ₂	...	D _n	



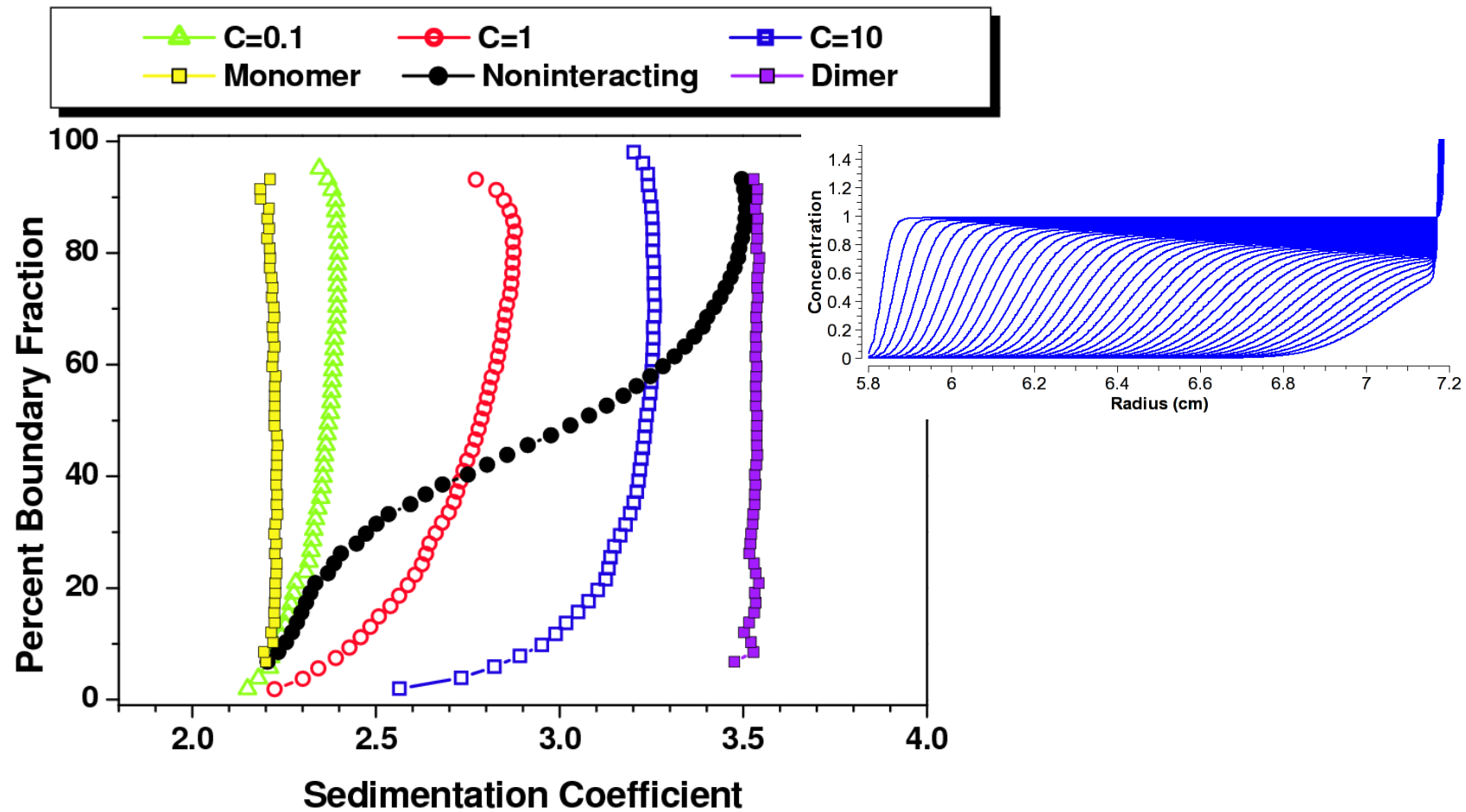
Generation 2

S ₁	S ₂	...	S _n	C	K _{eq}	K _{off}
D ₁	D ₂	...	D _n			

Mutation Event
(within linear constraints)
maintaining molecular weight, shape constraints

Diagnostics: van Holde – Weischet Analysis

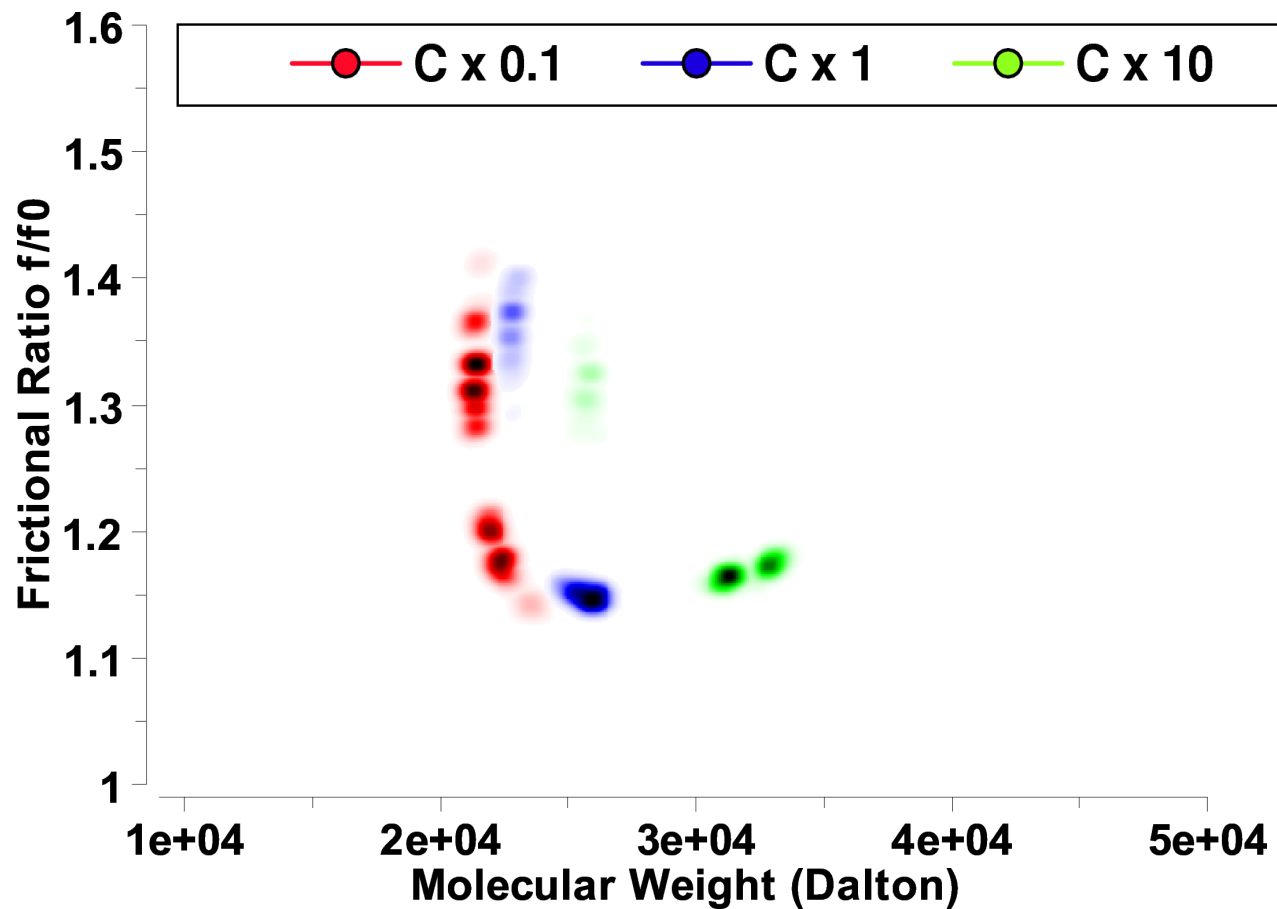
Example 1: Simulated Monomer – Dimer Equilibrium



Monomer MW = 20 kDa, $K_d = C \times 1$, $k_{off} = 1 \times 10^{-3}/\text{sec}$, $f/f_0 = 1.25$ (both)

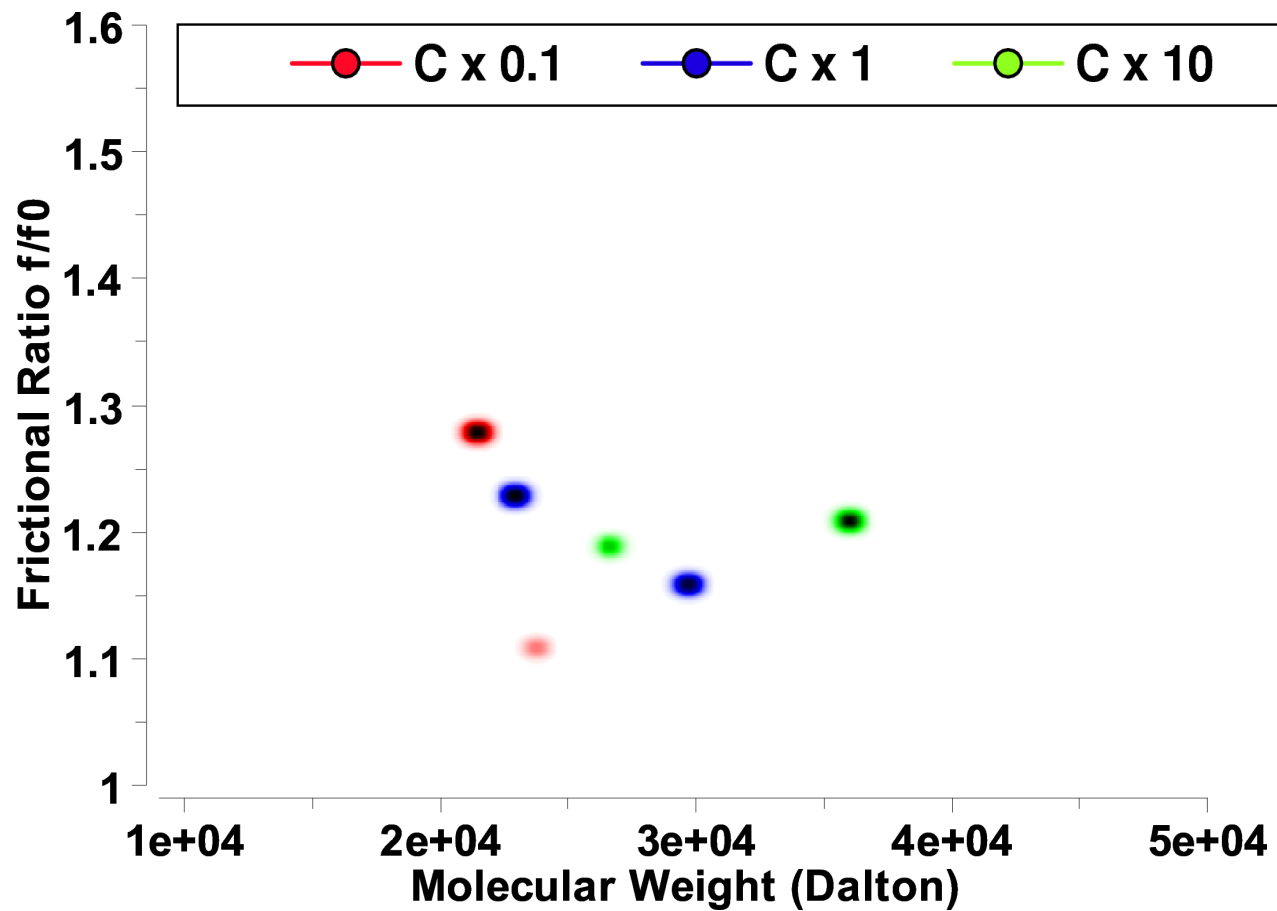
2DSA Monte Carlo Analysis

Monomer – Dimer Equilibrium, Monomer MW = 20 kDa



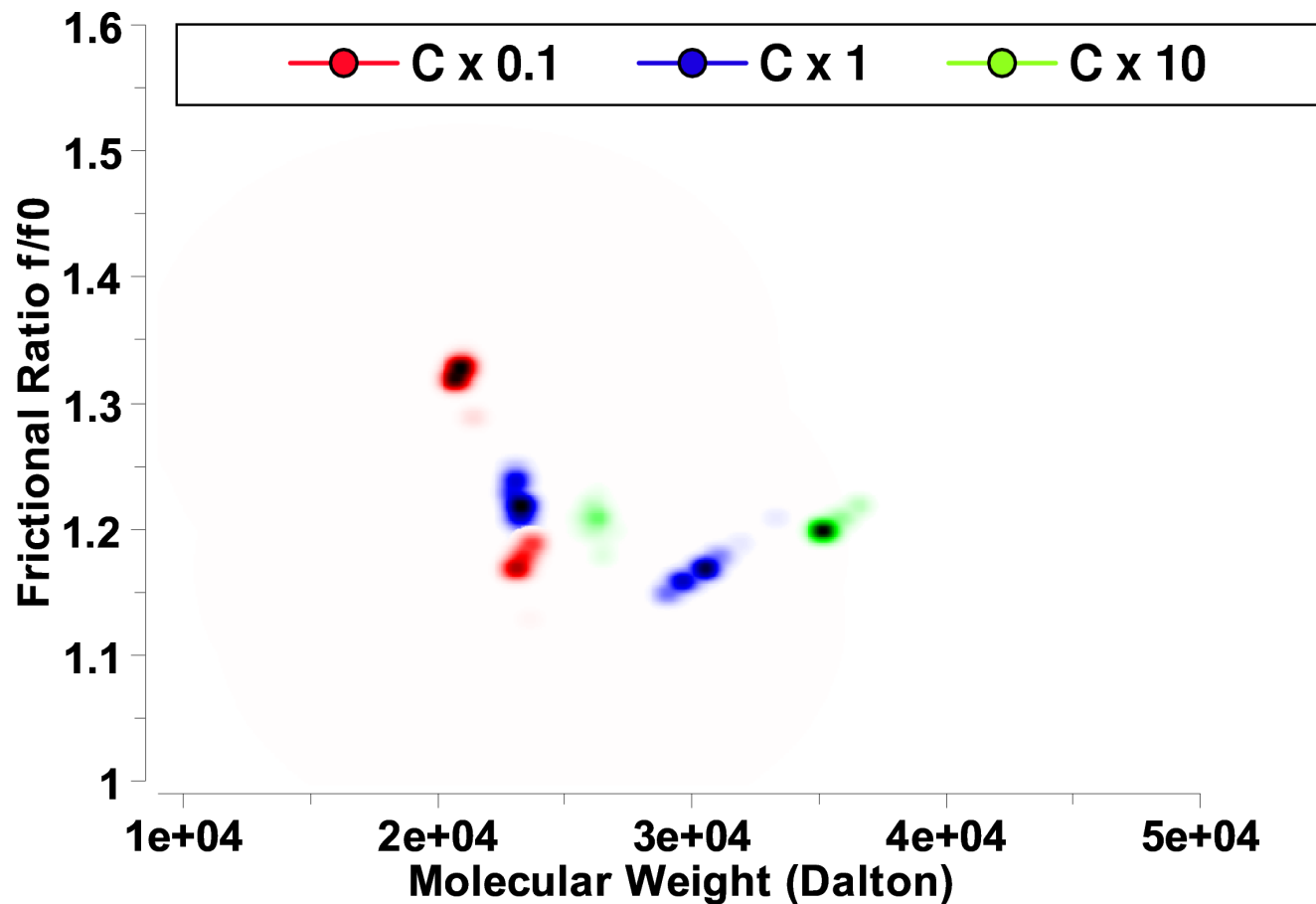
Genetic Algorithm Analysis

Monomer – Dimer Equilibrium, Monomer MW = 20 kDa



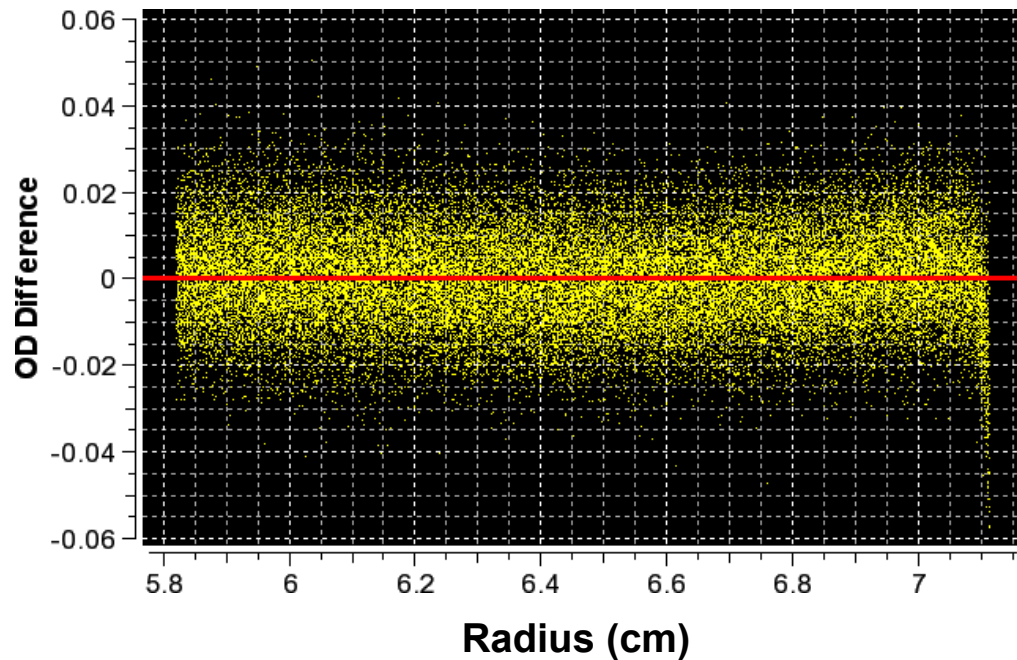
Genetic Algorithm Monte Carlo Analysis

Monomer – Dimer Equilibrium, Monomer MW = 20 kDa

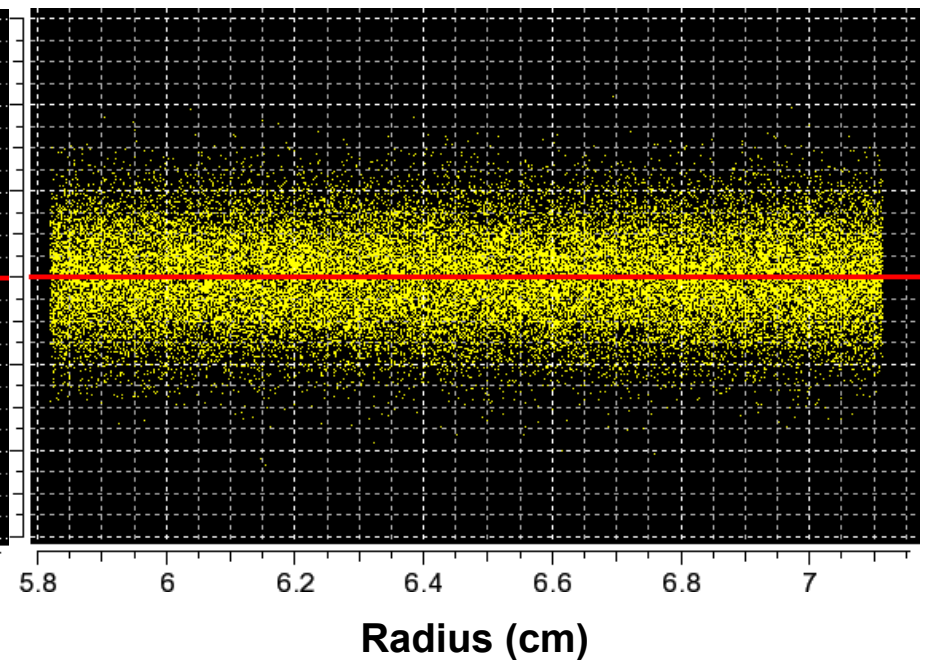


UltraScan Model Builder for Reacting Systems - Dimer:

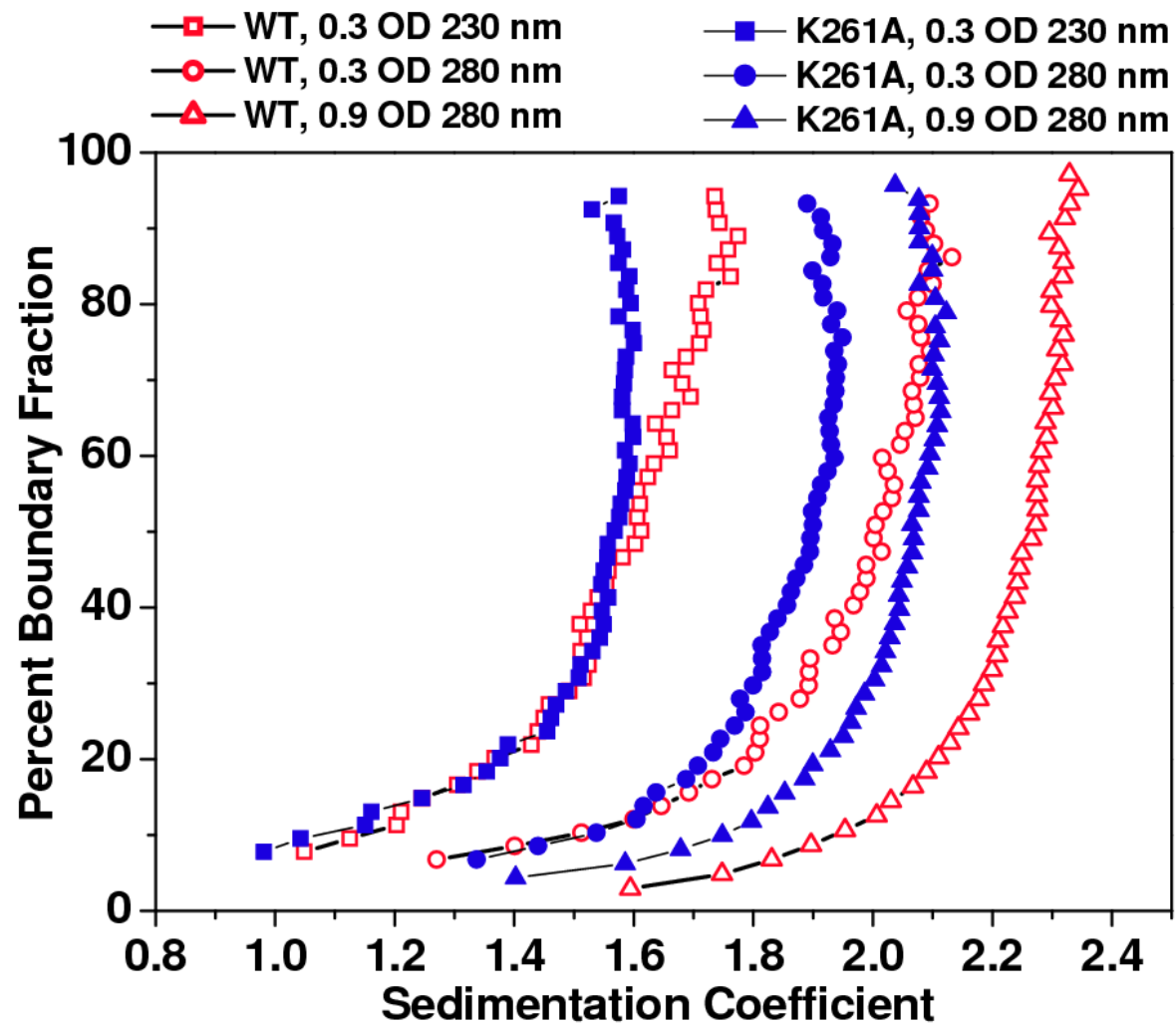
GA-MC Non-Interacting Fit



GA Reversible Model Fit



Monomer-Dimer Interface Mutation Analysis



Monomer-Dimer Interface Mutation Analysis Velocity Results

Parameter:	wildtype, 0.3 OD	K261A, 0.3 OD
K_d (μM)	10.4 (9.62, 11.4)	17.1 (15.9, 18.4)
k_{off} ($\times 10^{-5} \text{ sec}^{-1}$)	72.7 (26.5, 118.9)	84.0 (46.4, 121.6)
f/f_0 (monomer)	1.31 (1.28, 1.34)	1.33 (1.32, 1.35)
f/f_0 (dimer)	1.35 (1.33, 1.37)	1.43 (1.42, 1.45)

SV fitting results for C-RING1B wildtype and K261A mutant to a reversible monomer-dimer equilibrium model that allows for the presence of a contaminant. Values in parentheses represent 95% confidence intervals.