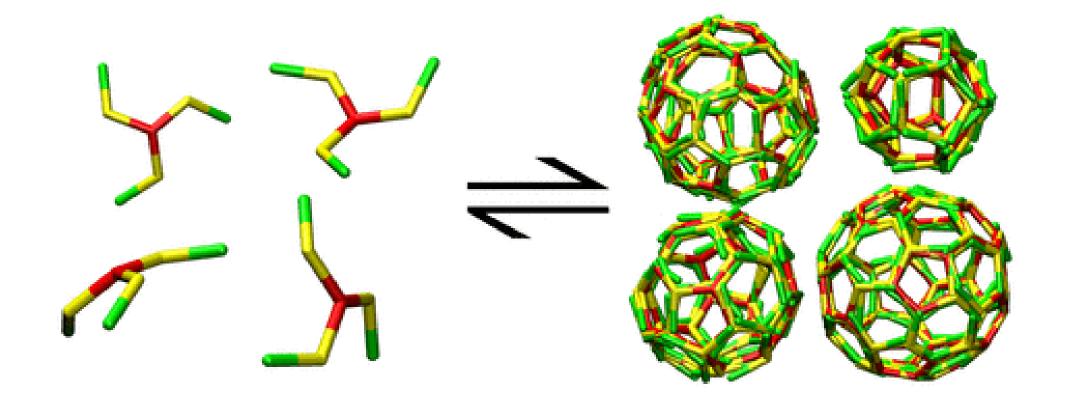
Optimization of Kinetic Self-Assembly Rate Constants

Sho Takeshita

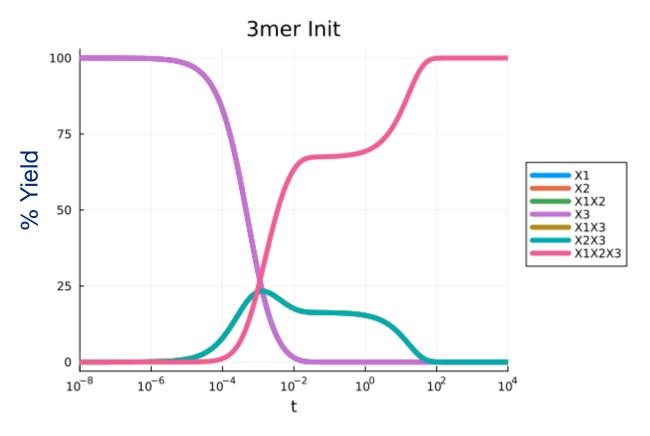
Johnson Lab



Self-assembly is ubiquitous for living systems

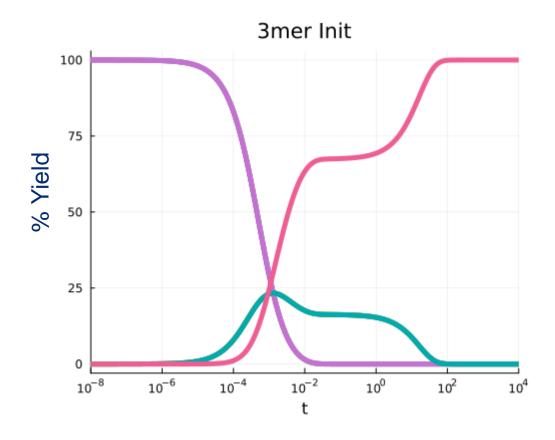


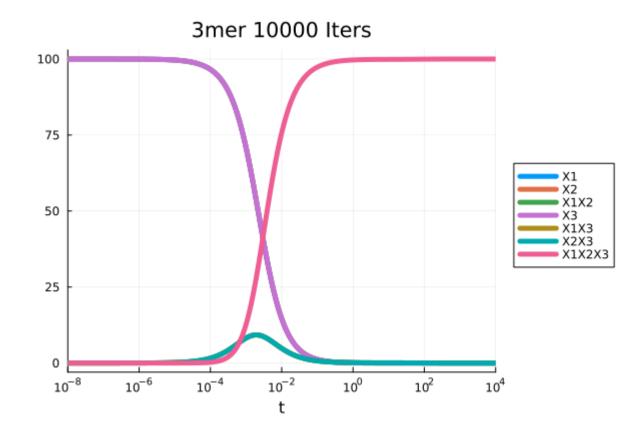
Kinetic Trapping



- Experiments and protein design
- Trapping leads to max yield taking too long

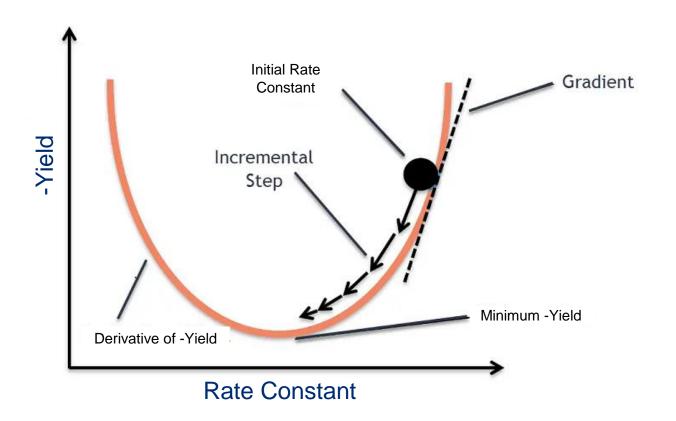
Goal is optimization





Calculating gradients is challenging

- Need to calculate gradient w.r.t rates to navigate large parameter space
- There is no explicit function of the yield – can't get analytical gradients
- Automatic differentiation!
 - Uses chain rule
 - Iteratively updates the rate constants until solution obtained

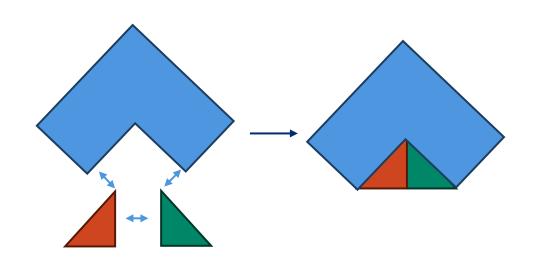


Past Work

- Previously done in Python using AutoDiff, but inefficient for large systems (A. Jhaveri, S. Loggia, Y. Qian, M.E. Johnson (2024))
- Limited to 7mers with 256GB
- Need to study bigger systems Jhaveri et al. showed it works well, but limited by computational resources

Fully connected hetero-n-mers

Fully Connected



Rate Growth

$$X1 + X2 \stackrel{k1}{\rightleftharpoons} X1X2$$

$$X1 + X3 \stackrel{k1}{\rightleftharpoons} X1X3$$

$$X2 + X3 \stackrel{k1}{\rightleftharpoons} X2X3$$

$$X1 + X2X3 \stackrel{k3}{\rightleftharpoons} X1X2X3$$

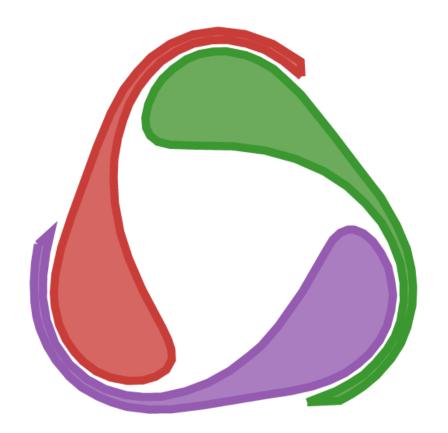
$$X2 + X1X3 \stackrel{k3}{\rightleftharpoons} X1X2X3$$

$$X3 + X1X2 \stackrel{k3}{\rightleftharpoons} X1X2X3$$

 Subunits of the same size n share association and dissociation rates



- Designed for performance for scientific applications
- Python is slow and costly in memory
- Has convenient libraries Catalyst!



How it works

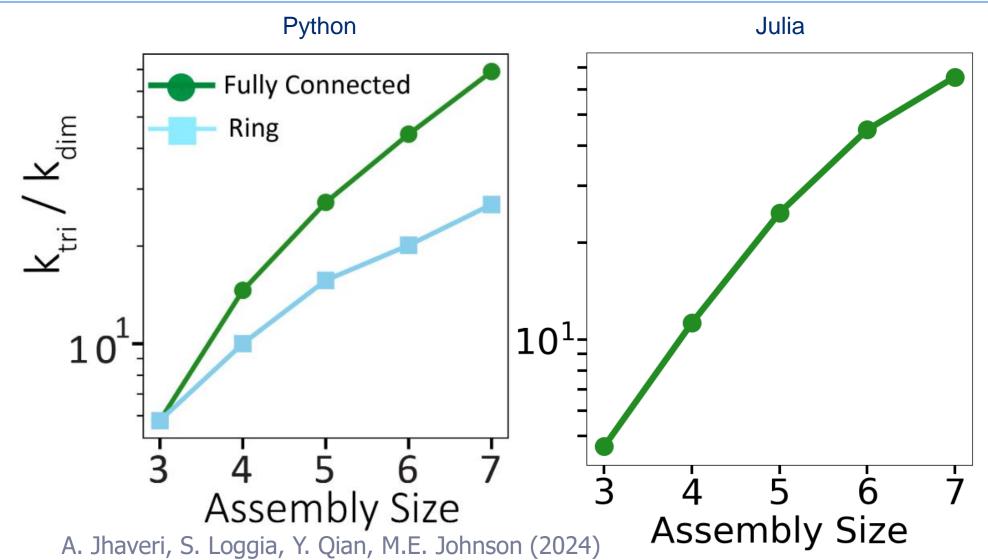
- Give program an nmer and initial rates and concentrations
- Generates reaction network
- Constructs differential equations
- Optimizes using AutoDiff

$$\begin{array}{c} X1 + X2 \stackrel{k1}{\rightleftharpoons} X1X2 \\ X1 + X3 \stackrel{k1}{\rightleftharpoons} X1X3 \\ X2 + X3 \stackrel{k1}{\rightleftharpoons} X2X3 \\ X1 + X2X3 \stackrel{k3}{\rightleftharpoons} X1X2X3 \\ X2 + X1X3 \stackrel{k3}{\rightleftharpoons} X1X2X3 \\ X3 + X1X2 \stackrel{k3}{\rightleftharpoons} X1X2X3 \end{array}$$

Solution Similarity

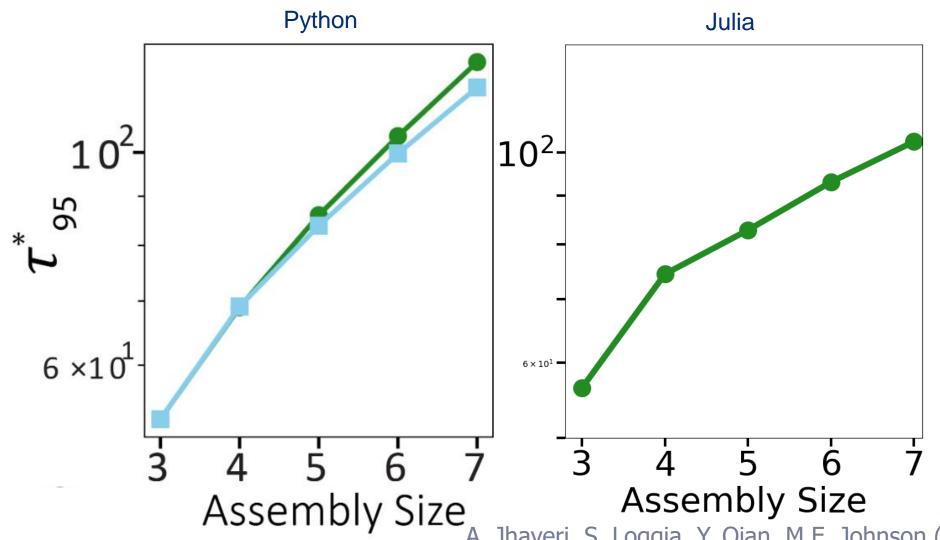


Optimal ratio over assembly size



1

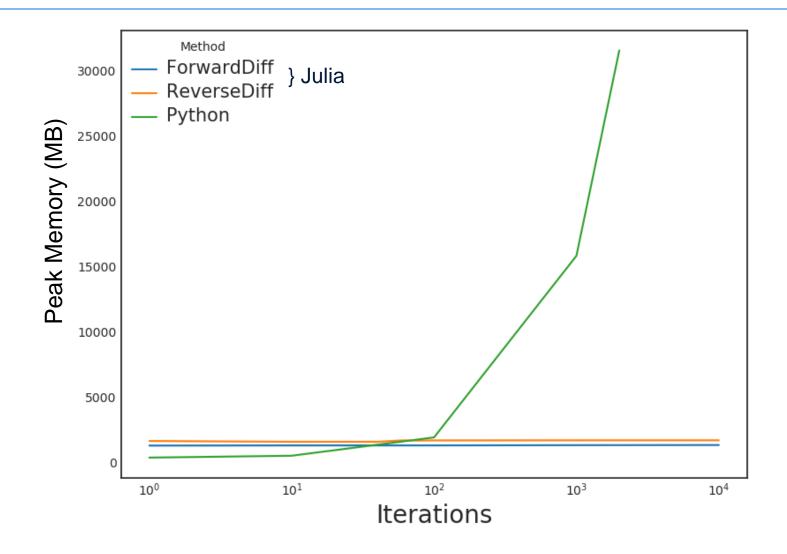
Time to reach 95% yield over assembly size



Performance



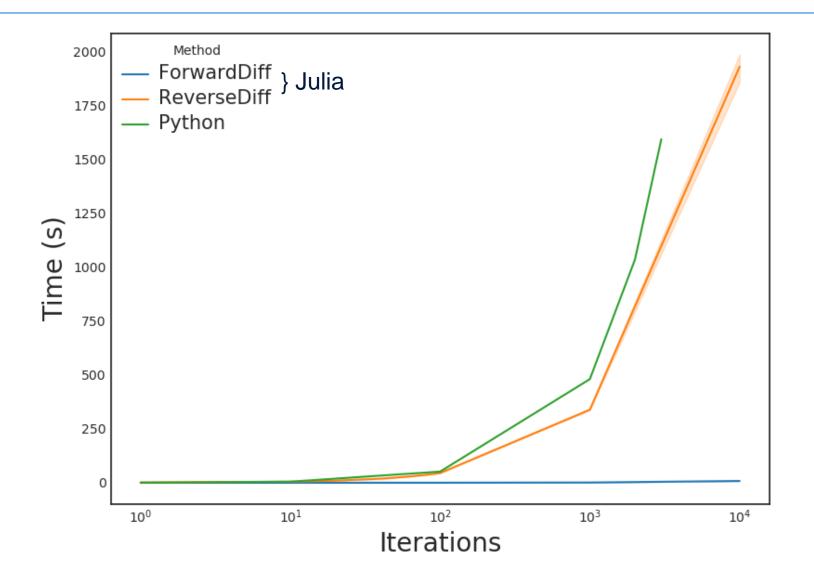
Memory Performance Over Iterations



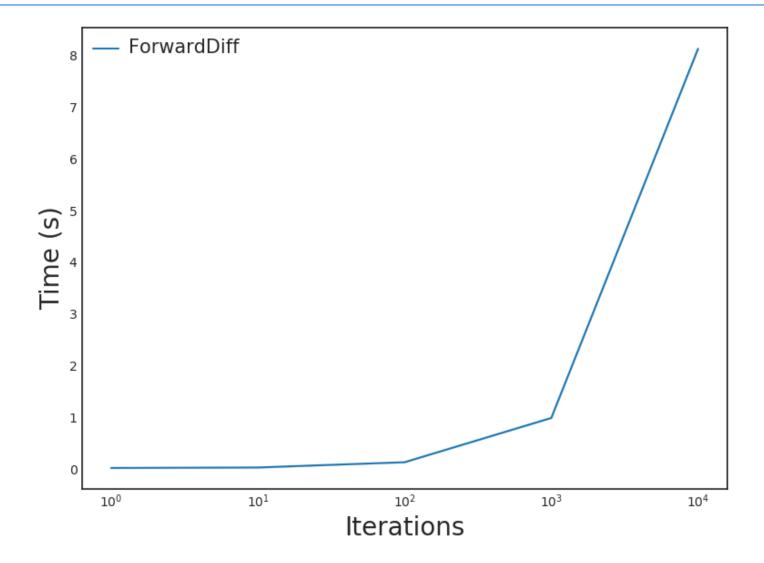
Memory Performance Over Iterations



Time Performance Over Iterations



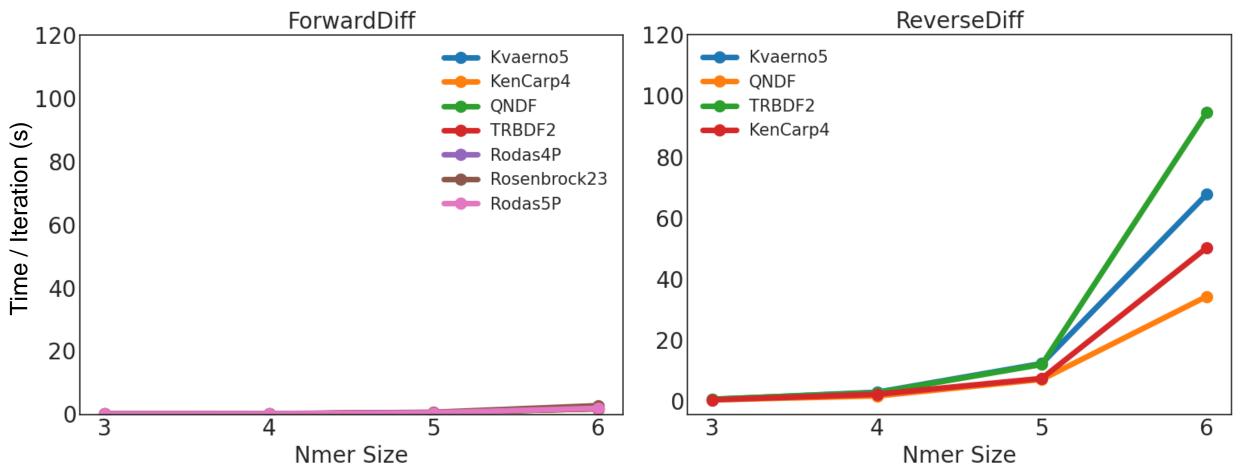
Time Performance Over Iterations



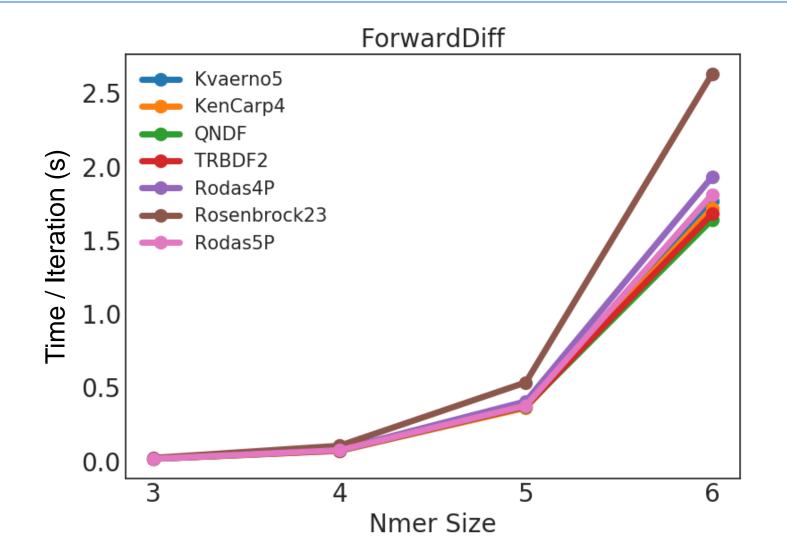
Integrator Performance



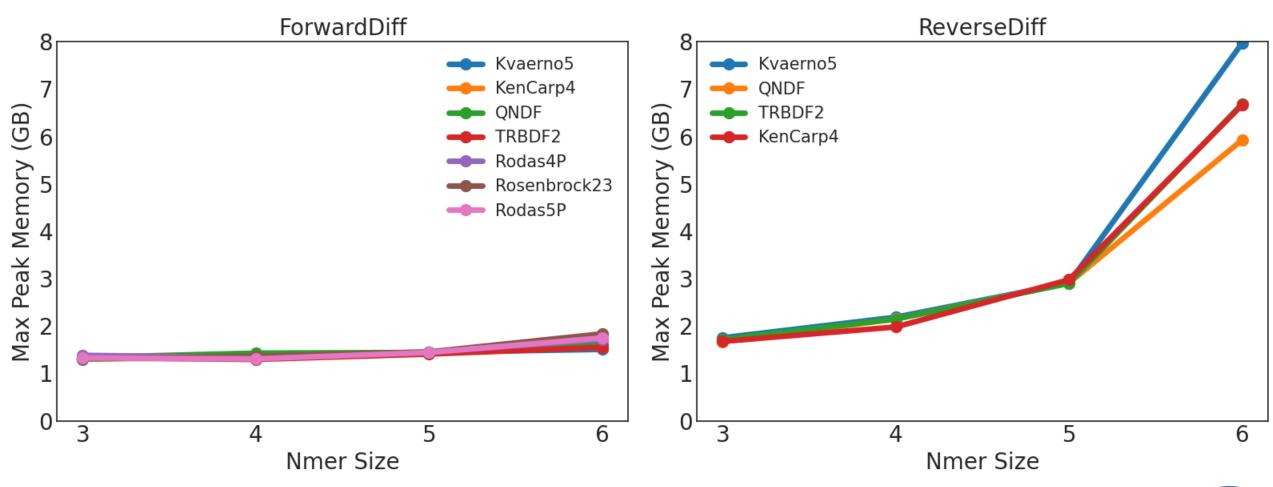
Time Performance of Integrators



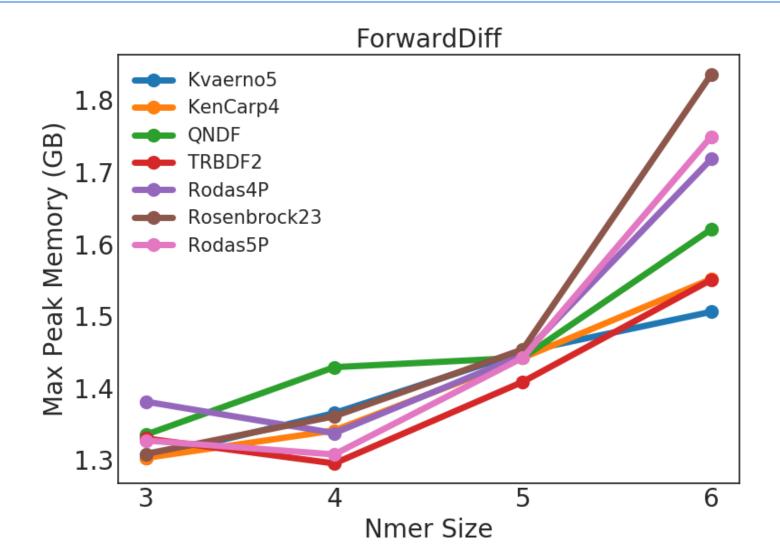
Time Performance of Integrators



Memory Performance of Integrators



Memory Performance of Integrators



Summary

- Solutions are reasonable and similar to the Python version
- Julia performs better than Python
- ForwardDiff is more efficient than ReverseDiff
- QNDF is optimal for ReverseDiff
- More testing for ForwardDiff integrators

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Questions



