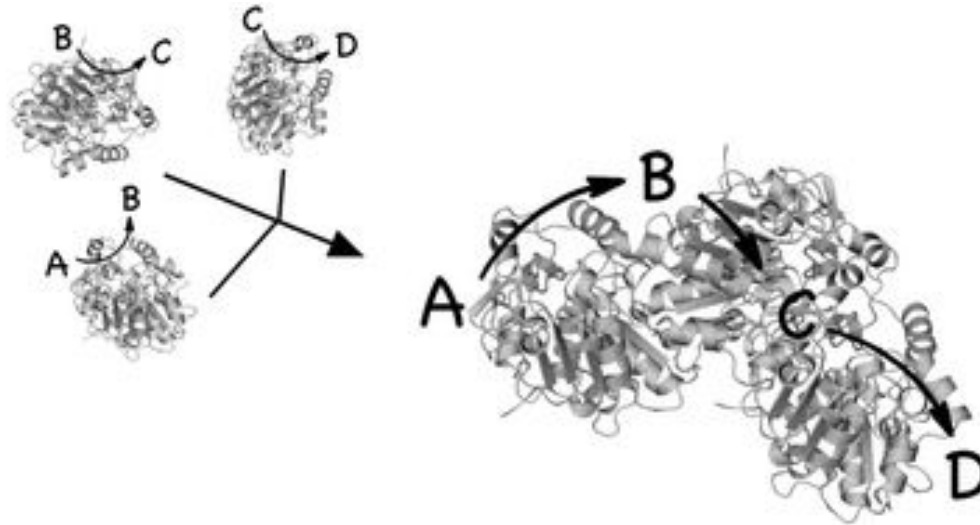


Synergy or Transport in Enzyme Assembly

Alexus Locke
Apratim Jash

Multi-Step Enzymatic Reactions Catalyze Metabolic Processes

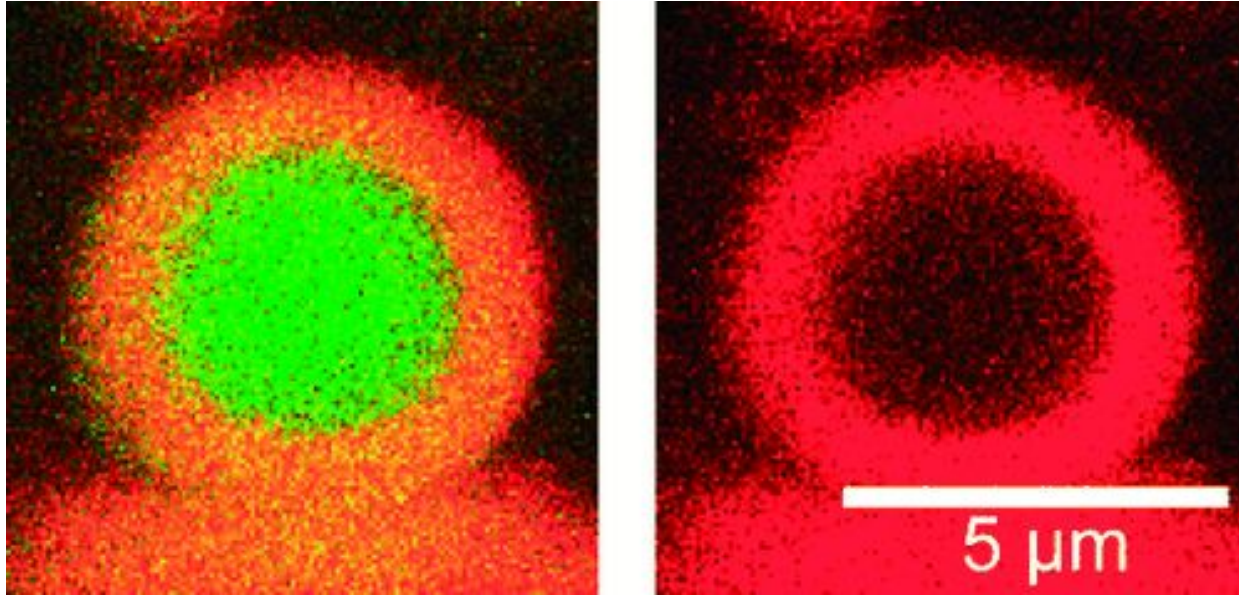
“...many crucial cellular functions such as biosynthesis and cellular signaling are controlled by multi-step enzymatic reactions that take place simultaneously with unsurpassed efficiency and specificity”¹



1. <https://doi.org/10.1371/journal.pone.0097103>

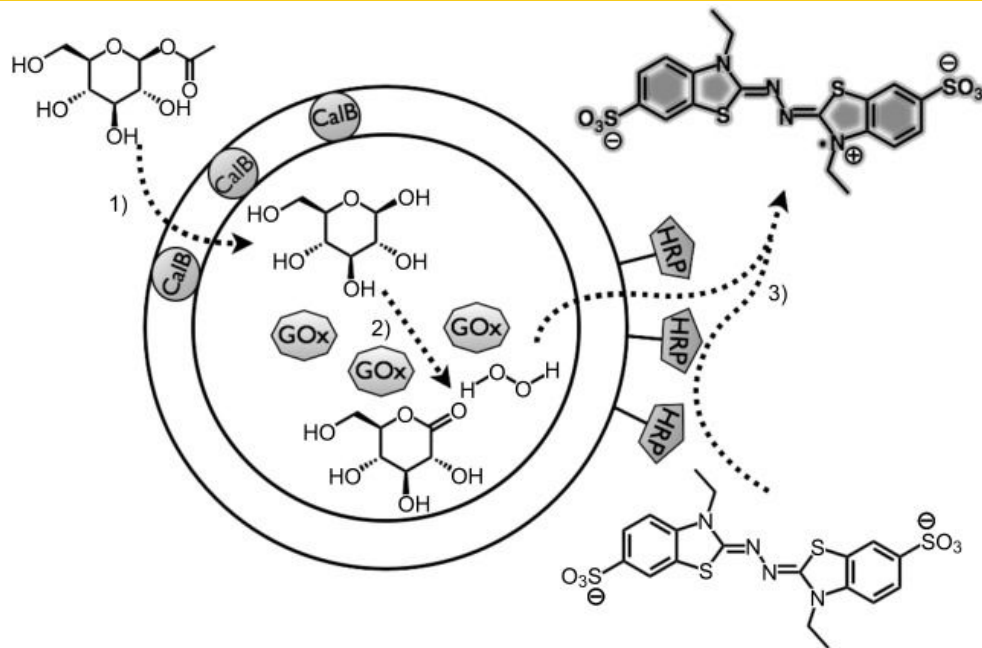
2. <https://doi.org/10.1039/C1SM06452E>

Use of Vesicles to Mimic Complex Enzyme Systems



Cross-sectional images of the giant vesicle observed by confocal laser scanning microscopy

Advances in the Design of Complex Enzymatic Systems



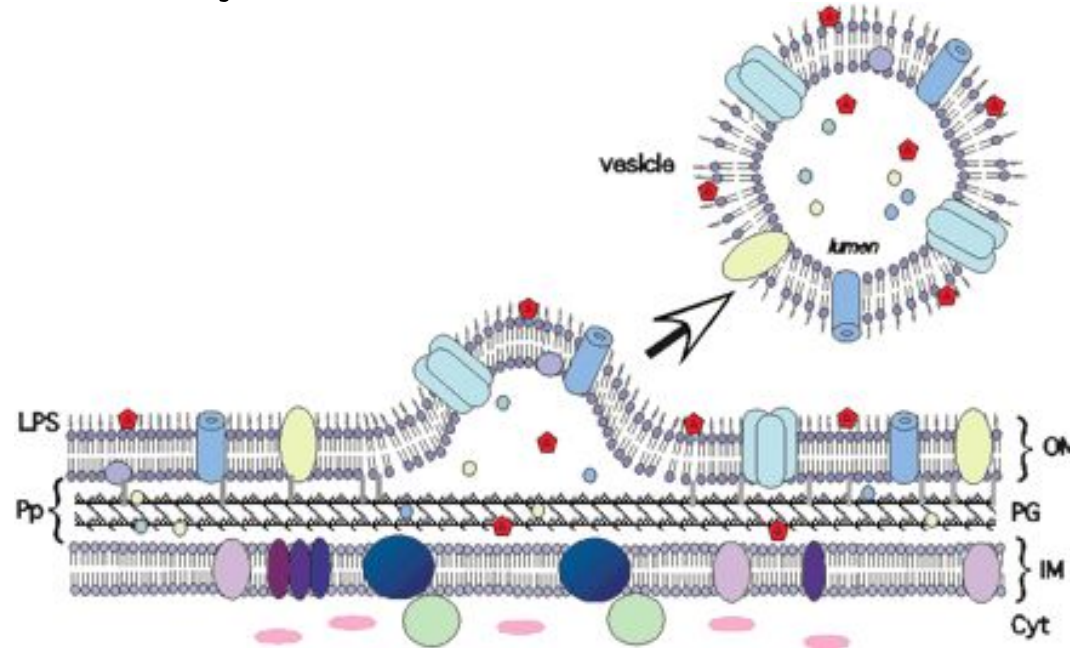
Schematic representation of the multistep reaction. 1) Monoacetylated Glucose 2) Oxidation of glucose to gluconolactone by GOx in the inner aqueous compartment, providing a molecule of hydrogen peroxide. 3) Hydrogen peroxide is used by HRP to convert ABTS to ABTS.+ . HRP is tethered to the polymersome surface.

Limitations

- Thermodynamic and mechanical instability of liposomes
- Low permeability of polymersomes
- Tedious and multiple-step syntheses and conjugations of polymersomes

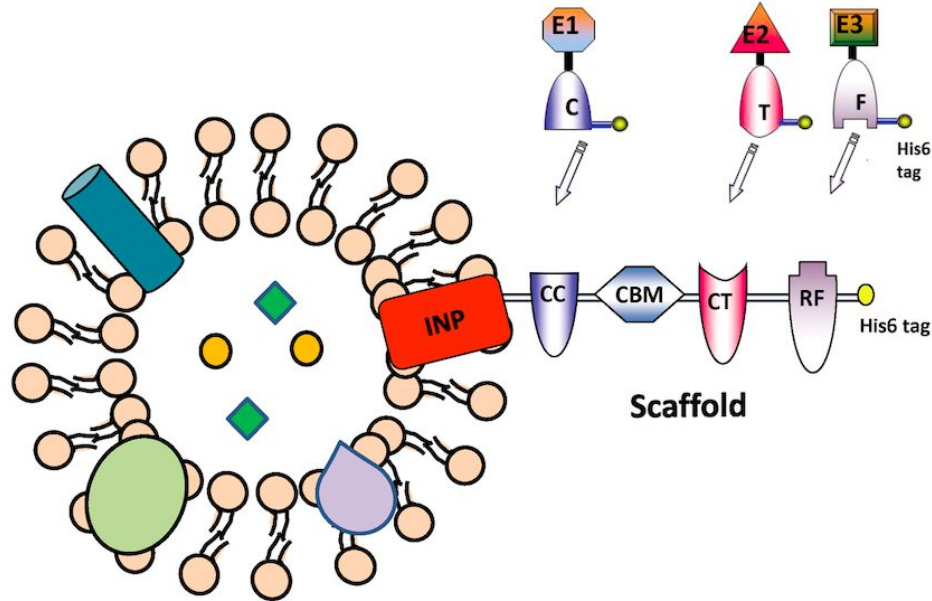
Park et al. Approach

OMVs as synthetic nanoreactors



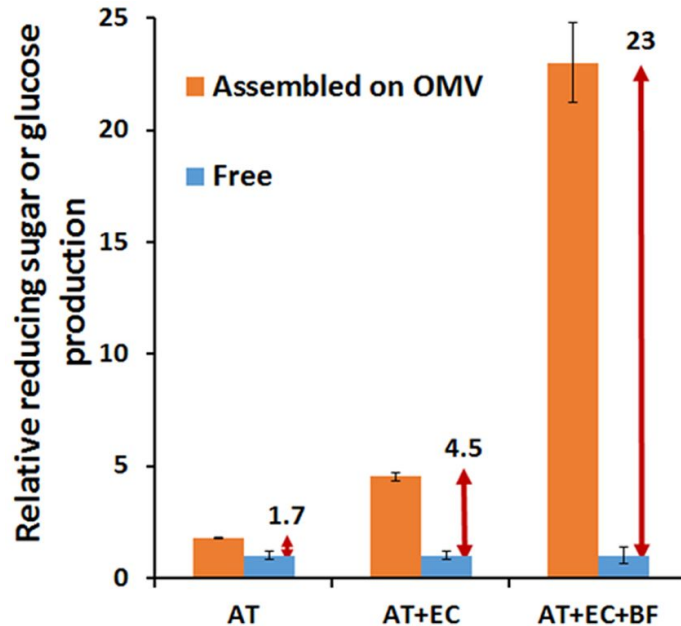
Model of vesicle biogenesis. OM vesicles are proteoliposomes consisting of OM phospholipids and LPS, a subset of OM proteins, and periplasmic (luminal) proteins. (LPS) Lipopolysaccharide; (Pp) periplasm; (OM) outer membrane; (PG) peptidoglycan; (IM) inner membrane; (Cyt) cytosol.

Synergistic assembly of multiple enzymes



Functional assembly of multiple enzymes on engineered bacterial outer membrane vesicles (OMVs). A trivalent scaffold containing three orthogonal cohesin domains, DocC (from *C. cellulolyticum*), DocT (from *C. thermocellum*) and DocF (from *R. flavefaciens*), and one cellulose-binding module, is displayed onto OMVs using the ice nucleation protein (INP) anchor. The specific interaction between each cohesin-dockerin pair enables the sequential assembly of three dockerin-tagged cellulases (E1, E2 and E3) onto the OMVs at their corresponding position (C, T or F).

Key Results and Conclusions from Paper



- 23-fold increase in conversion of cellulose to glucose
- Increase in conversion is due to the synergy developed between the three enzymes

Production of reducing sugars (AT and AT+EC) or glucose (AT+BC+RF) from PASC by enzyme-assembled OMVs or the same amount of free enzymes.

Our Model

Aim of this Study

To determine the possibility of enzyme spatial organization being the sole cause of enhanced production of glucose

Methodology and Governing Equations

Diffusion Control: Random Walk

- Diffusion time \gg reaction time
- Reaction rates only depend on physical movements of the molecules

$$k = \frac{1}{\text{average reaction time}} = \frac{\text{average steps to the reaction}}{\text{time per step}}$$

Kinetic Control: Tau Leaping

- Conversion is instantaneous
- Reaction rates ignored as diffusion effects are negligible

$$\text{rate} = \frac{V_{\max} \cdot [S]}{K_M + [S]}$$

Assumptions

1. No side reactions occur.
2. Enzymes can be react with another substrate outside of its intended one and be deactivated.

Random Walk for Diffusion Control

Success v. Failure:

- Success: producing C within defined number of random steps
- Failure:
 - Max steps were taken without producing C
 - A interacted with E3 before E2, deactivating E3

```
Walk 1 completed in 636441 steps, A reached E3 before E2. Simulation failed :(
Successful! A+E2 -> B
Successful! B+E3 -> C
Walk 2 completed in 668645 steps.

Walk 3 completed in 1000000 steps, no reaction
Walk 4 completed in 355551 steps, A reached E3 before E2. Simulation failed :(
Walk 5 completed in 1000000 steps, no reaction
```

Next Steps for Diffusion Control

- Run simulation more to determine rate constants
- Plot relationship between overall reaction and varying r_a and r_b

$$k = \frac{1}{\text{average reaction time}} = \frac{\text{average steps to the reaction}}{\text{time per step}}$$

Tau Leaping for Kinetic Control

R1: $A + E2 \rightarrow B$

R2: $B + E3 \rightarrow C$

R3: E2 degrades

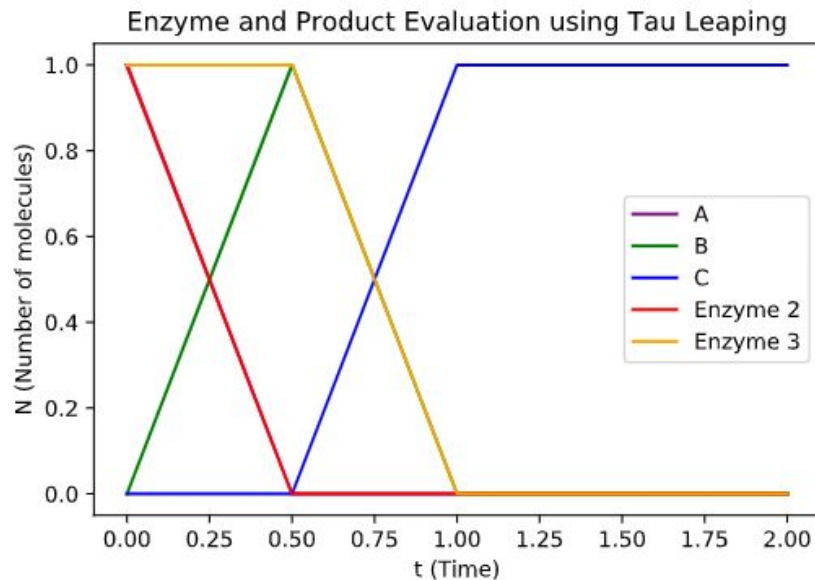
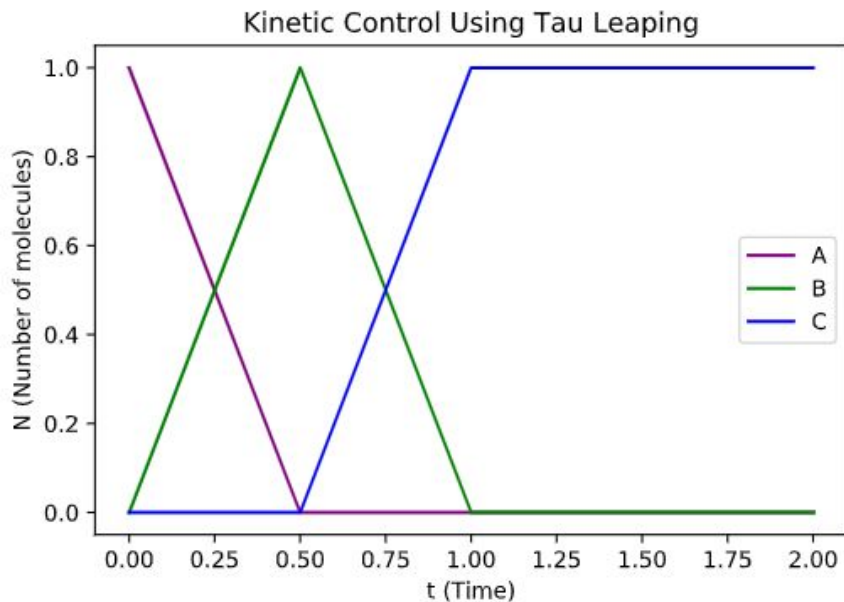
R4: E3 degrades

ELEMENTS

REACTIONS

	R1	R2	R3	R4
A	-1	0	0	0
B	1	-1	0	0
C	0	1	0	0
E2	-1	0	-1	0
E3	0	-1	0	-1

Preliminary Results



Project Next Steps

- Finalize Diffusion Controlled System
- Run combined Python Script for a Diffusion and Kinetic System
- Analyze results to determine if spatial organization is a viable possibility for the concentration increase received by Park et al.

Questions?

References

1. Park, M. et al. (2014). Positional assembly of enzymes on bacterial outer membrane vesicles for cascade reactions. PLoS One, 9(5).
2. Schoffelen, S. & van Hest, J. C. M. (2012). Multi-Enzyme Systems: Bringing Enzymes Together in Vitro. Soft Matter, 8(6), 1736–1746.
3. Nomura, S. M., et al. (2003). Gene Expression within Cell-Sized Lipid Vesicles. ChemBioChem, 4(11), 1172–1175.
4. Van Dongen, S. F. M., et al. (2008). A Three-Enzyme Cascade Reaction through Positional Assembly of Enzymes in a Polymersome Nanoreactor. Chemistry - A European Journal, 15(5), 1107–1114.
5. Kuehn, M. J. (2005). Bacterial Outer Membrane Vesicles and the Host-Pathogen Interaction. Genes & Development, 19(22), 2645–2655.
6. Cao, Y., Gillespie, D. T., & Petzold, L. R. (2006). Efficient step size selection for the tau-leaping simulation method. The Journal of chemical physics, 124(4), 044109.
7. Conrado, R. J., Mansell, T. J., Varner, J. D., & DeLisa, M. P. (2007). Stochastic reaction–diffusion simulation of enzyme compartmentalization reveals improved catalytic efficiency for a synthetic metabolic pathway. Metabolic engineering, 9(4), 355–363.