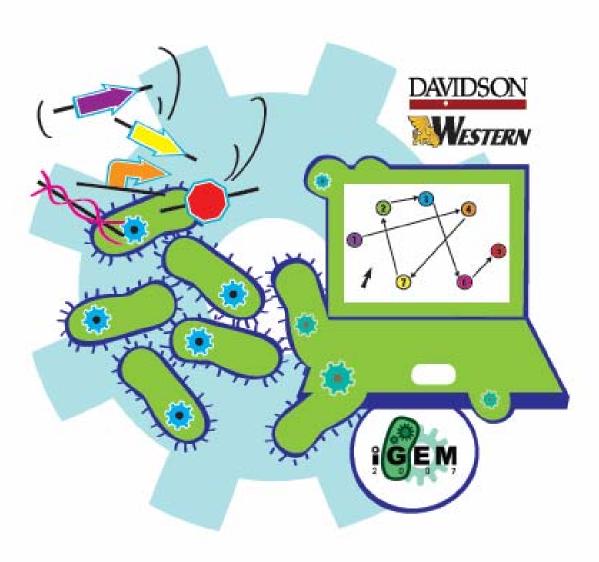
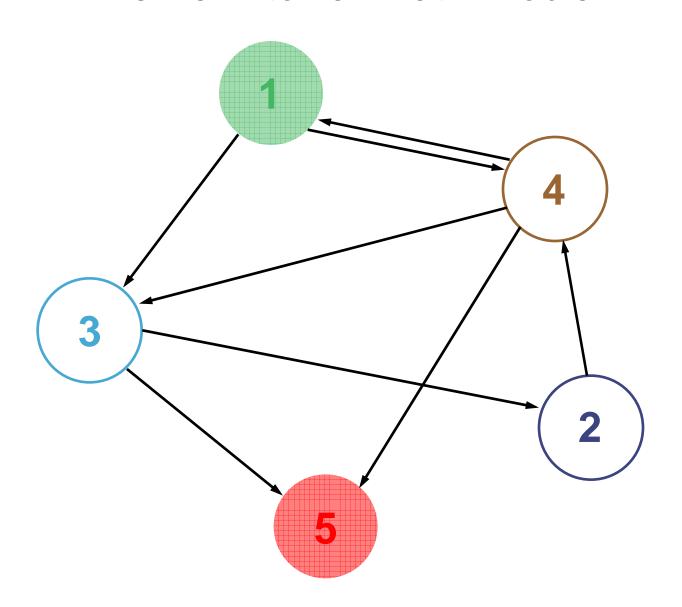
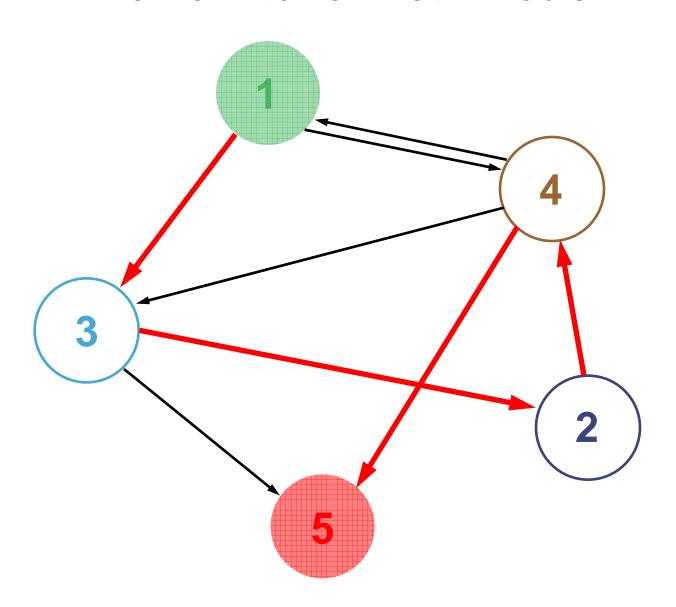
Solving the Hamiltonian Path Problem with Living Hardware



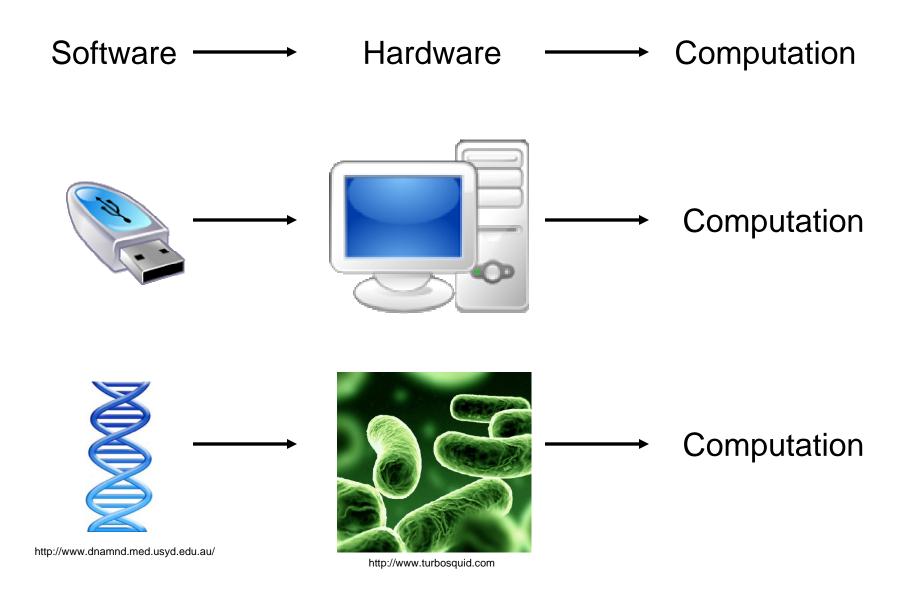
The Hamiltonian Path Problem



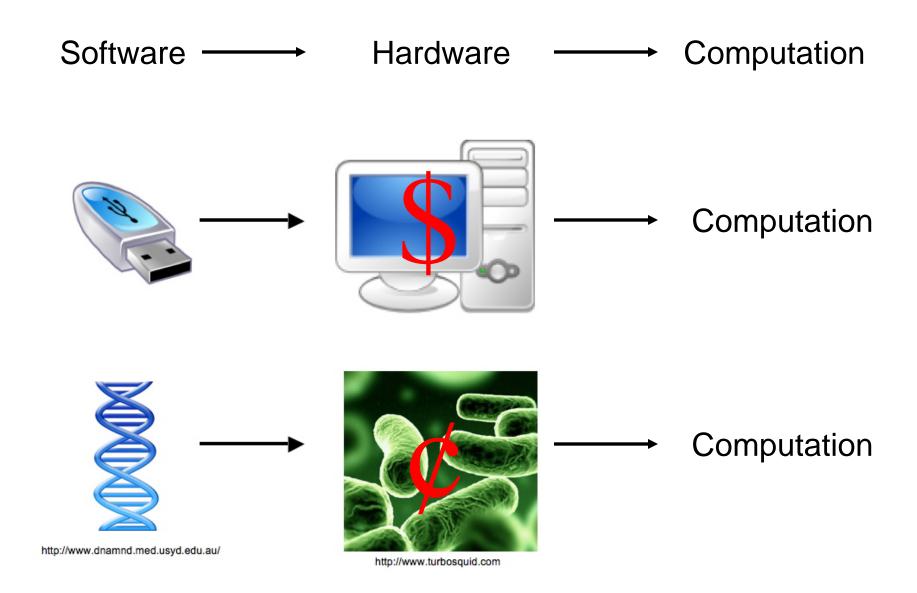
The Hamiltonian Path Problem



Advantages of Bacterial Computation

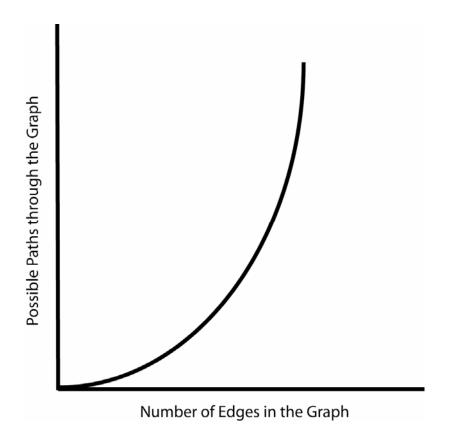


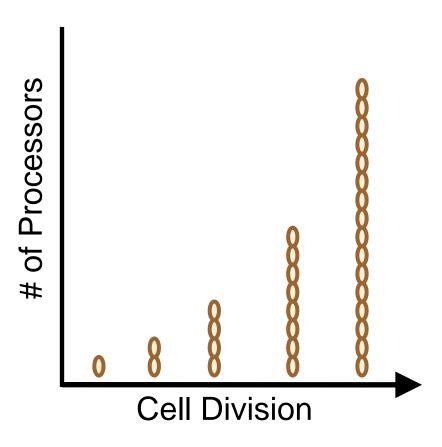
Advantages of Bacterial Computation



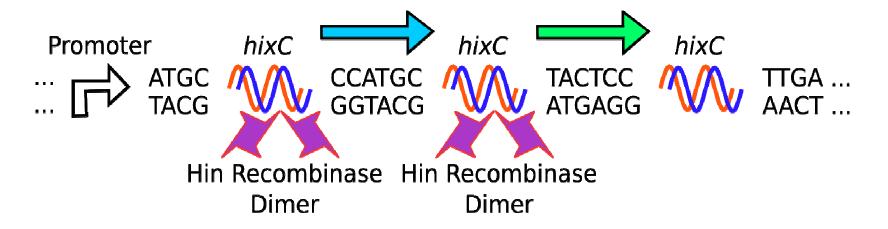
Computational Complexity

- Non-Polynomial (NP)
- No Efficient Algorithms

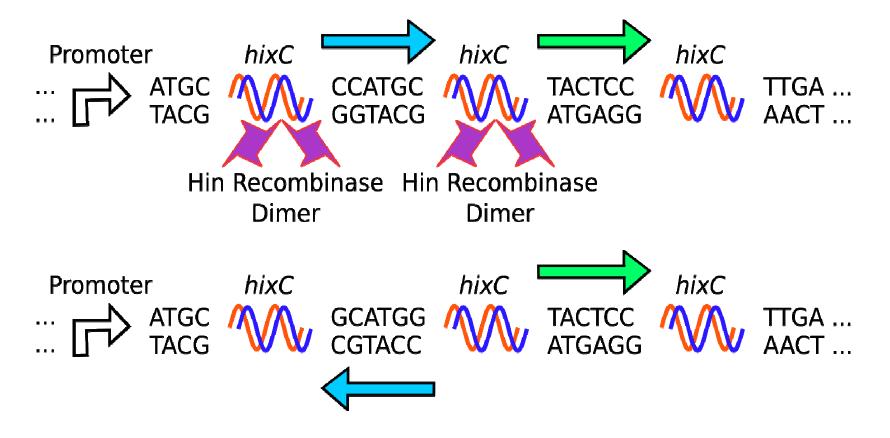




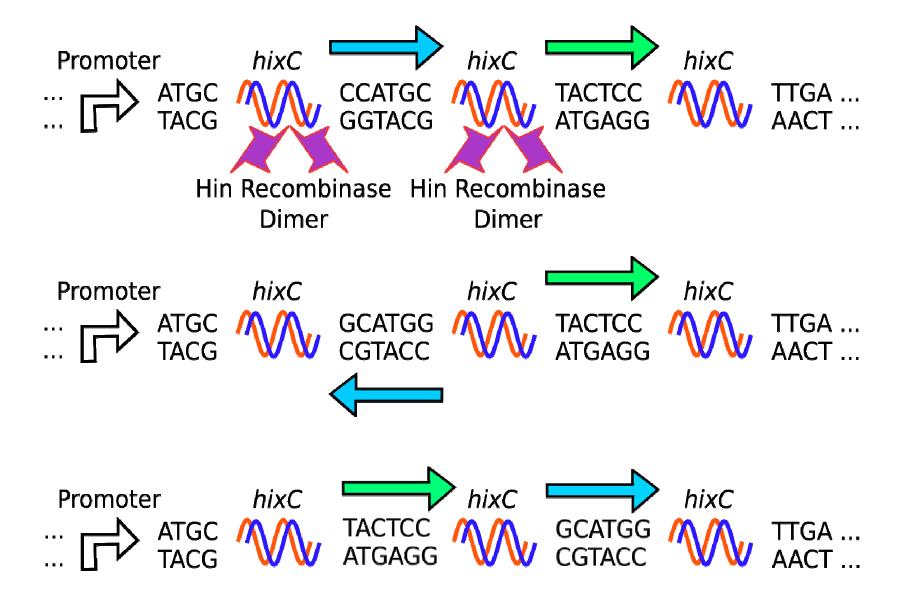
Flipping DNA with Hin/hixC

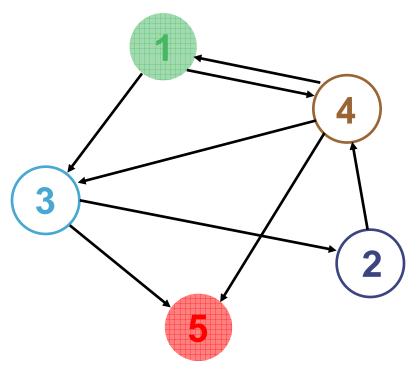


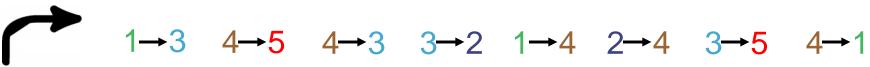
Flipping DNA with Hin/hixC

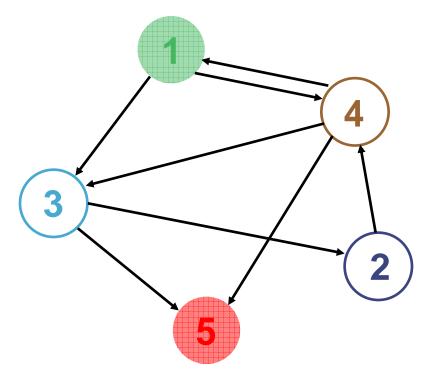


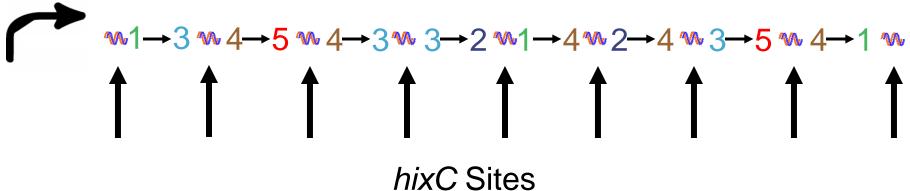
Flipping DNA with Hin/hixC

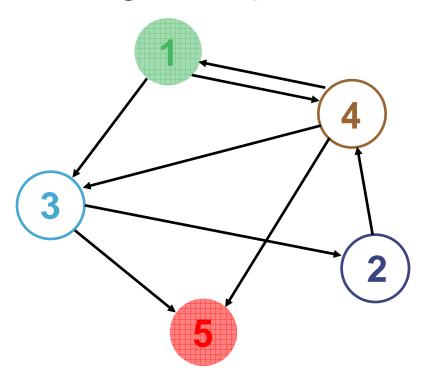




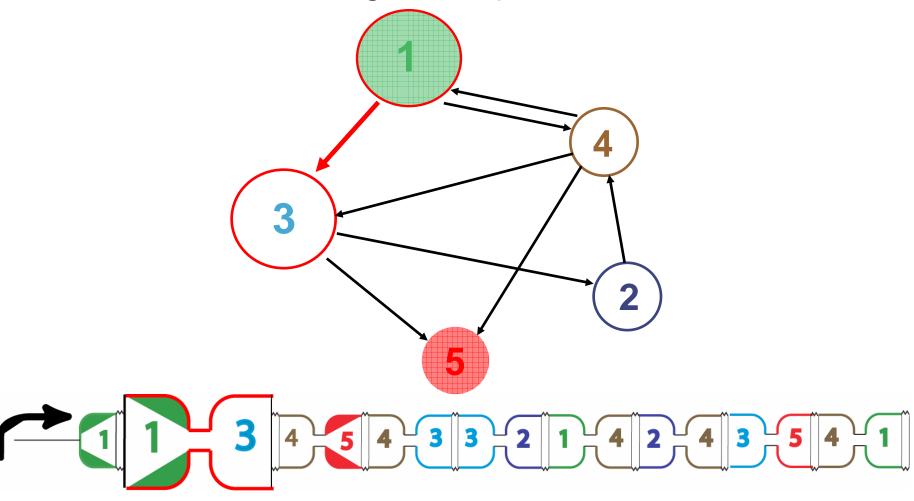




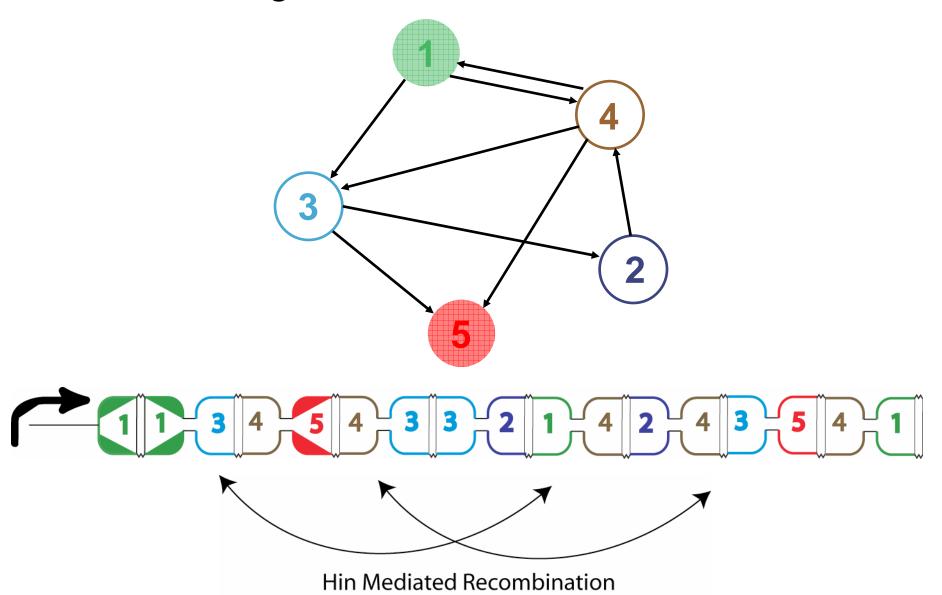




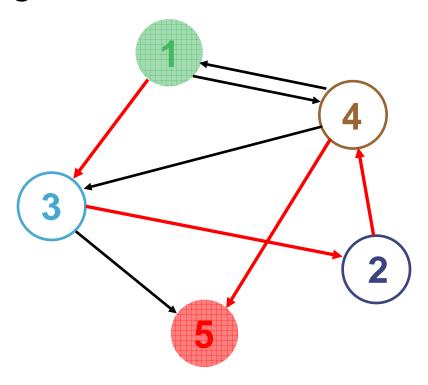




Using Hin/hixC to Solve the HPP



Using Hin/hixC to Solve the HPP





Solved Hamiltonian Path

Predicting Outcomes of Bacterial Computation

How Many Plasmids Do We Need?

Probability of at least *k* solutions on *m* plasmids for a 14-edge graph

	<i>k</i> = 1	5	10	20
m = 10,000,000	.0697	0	0	0
50,000,000	.3032	.00004	0	0
100,000,000	.5145	.0009	0	0
200,000,000	.7643	.0161	.000003	0
500,000,000	.973	.2961	.0041	0
1,000,000,000	.9992	.8466	.1932	.00007

k = actual number of occurrences

 λ = expected number of occurrences

 $\Lambda = m$ plasmids * # solved permutations of edges ÷ # permutations of edges

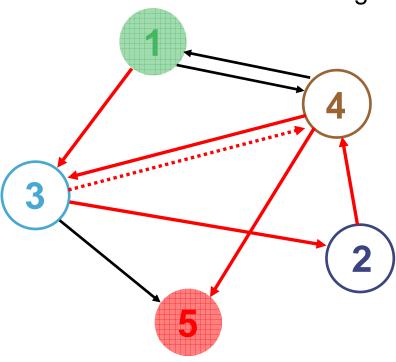
Cumulative Poisson Distribution:

P(# of solutions
$$\geq k$$
) = $1 - \sum_{x=0}^{k-1} \frac{e^{-\lambda} \cdot \lambda^x}{x!}$

False Positives



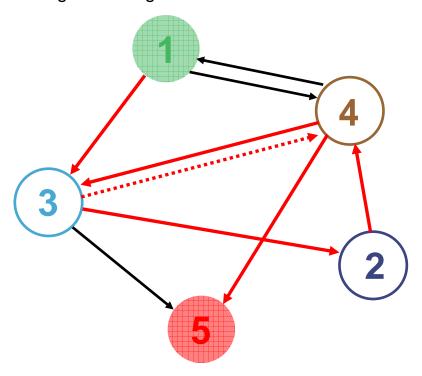
Extra Edge



False Positives



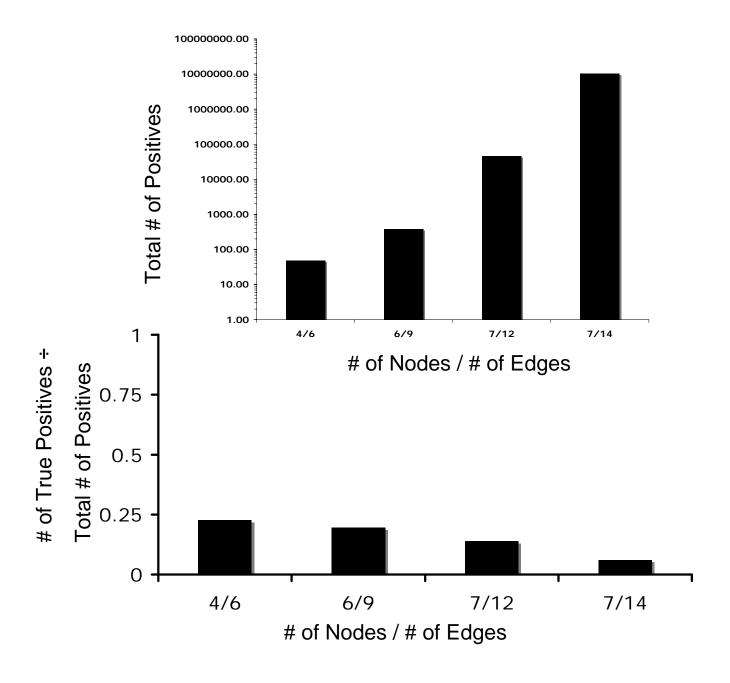
PCR Fragment Length



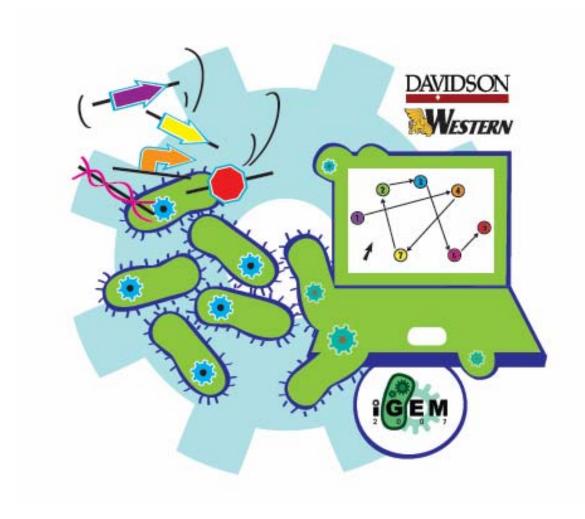


PCR Fragment Length

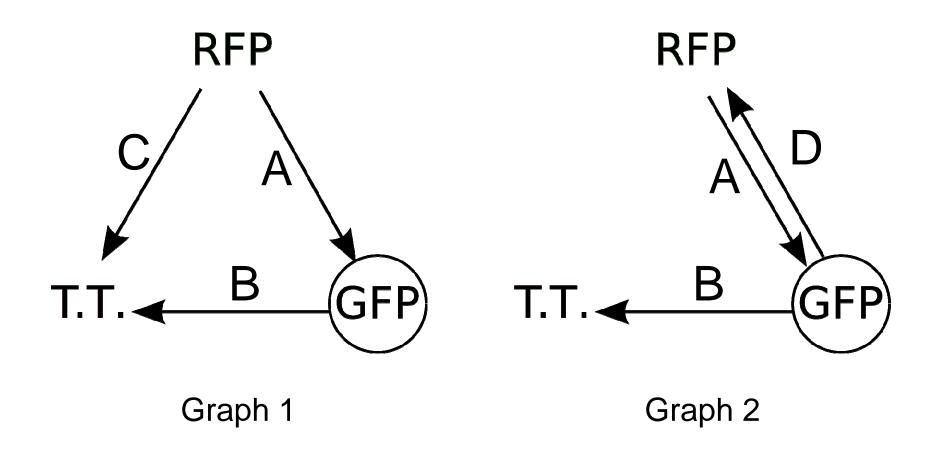
Detection of True Positives



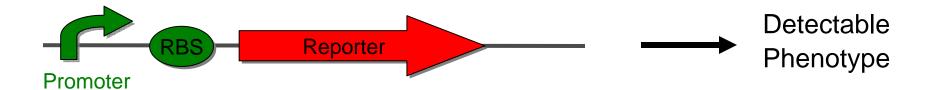
Building a Bacterial Computer

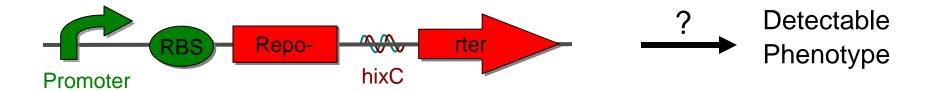


Choosing Graphs

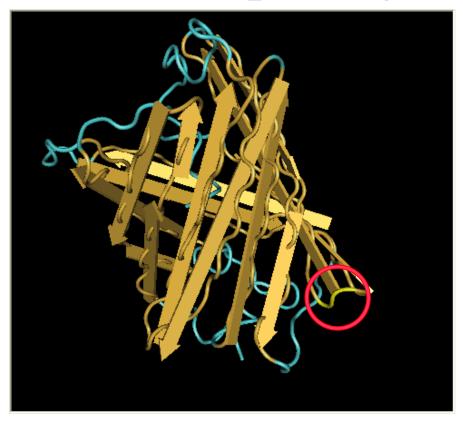


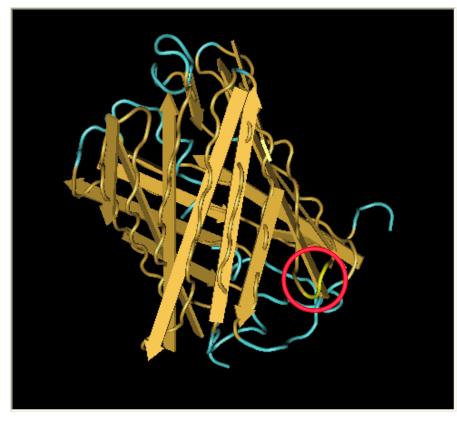
How to Split a Gene





Splitting Reporter Genes

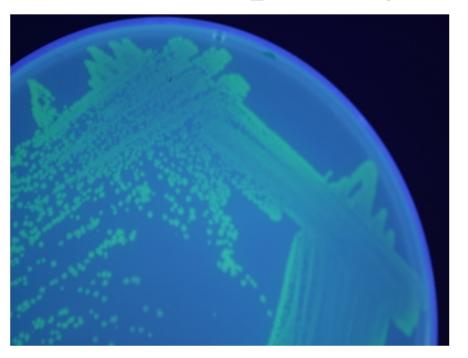


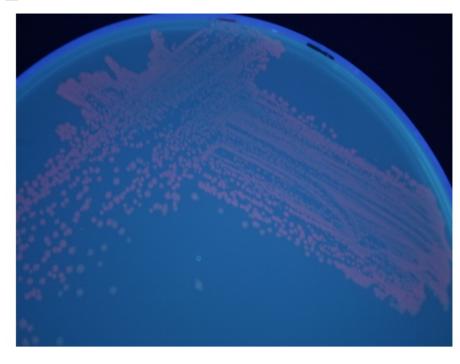


Green Fluorescent Protein

Red Fluorescent Protein

Splitting Reporter Genes





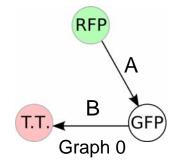
GFP Split by *hixC*

RFP Split by *hixC*

HPP Constructs

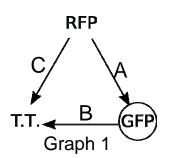
Graph 0 Construct:

GFP1 R0085 B0034 I715022J44000 I715023B0034 I715019J44000 I715020



Graph 1 Constructs:

R0085 B0034 I715022J44000 I715023B0034 I715019J44000 I715020B0010 B0012 J44000 I715023B0010 B0012 J44000 RFP2 GFP1 R0085 B0034 I715022J44000 I715023B0034 I715019J44000 I715023B0010 B0012 J44000 I715020B0010 B0012 J44000 GFP1



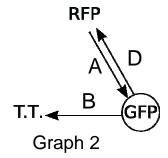
BAC

DBA

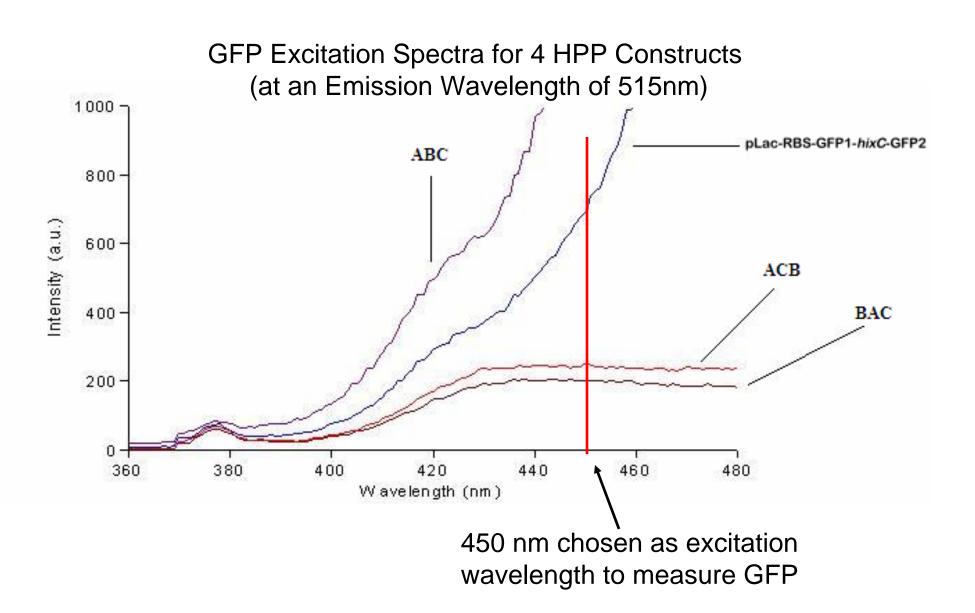
ACB

Graph 2 Construct:

RFP1 GFP2 R0085 B0034 I715022J44000 I715020B0034 I715022J44000 I715020B0010 B0012 J44000 I715023B0034 I715019J44000

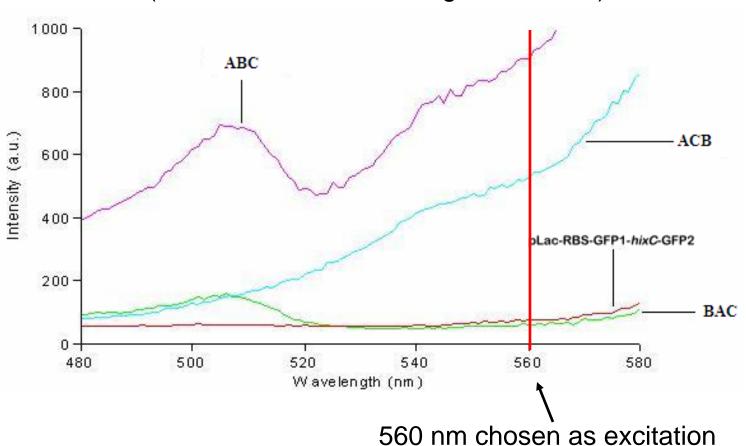


Measuring Fluorescence



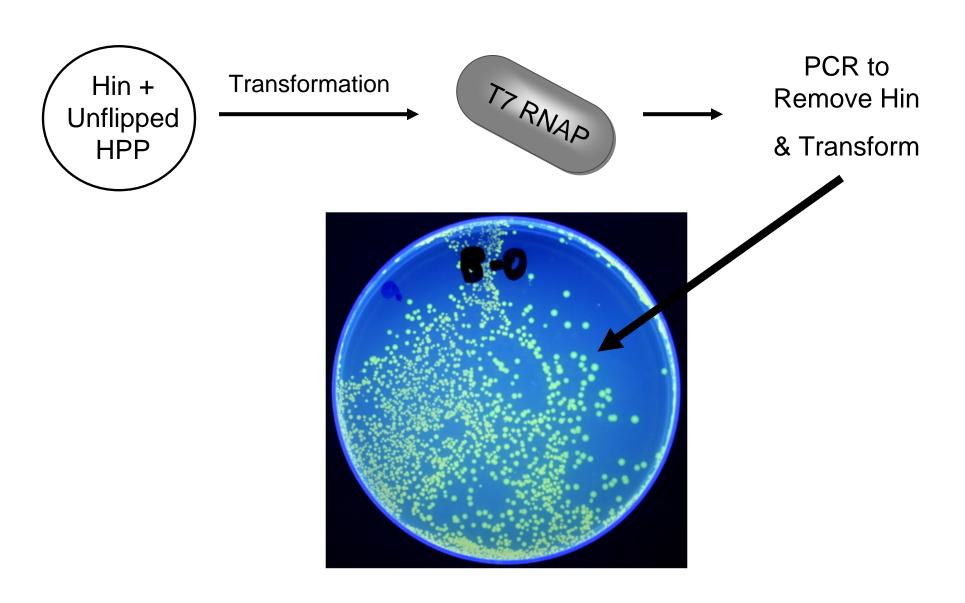
Measuring Fluorescence

RFP Excitation Spectra for 4 HPP Constructs (at an Emission Wavelength of 608nm)

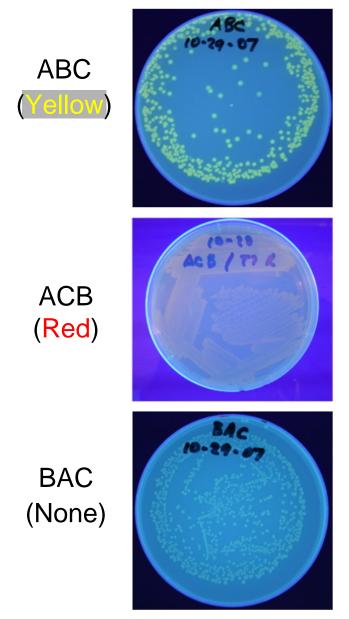


560 nm chosen as excitation wavelength to measure RFP

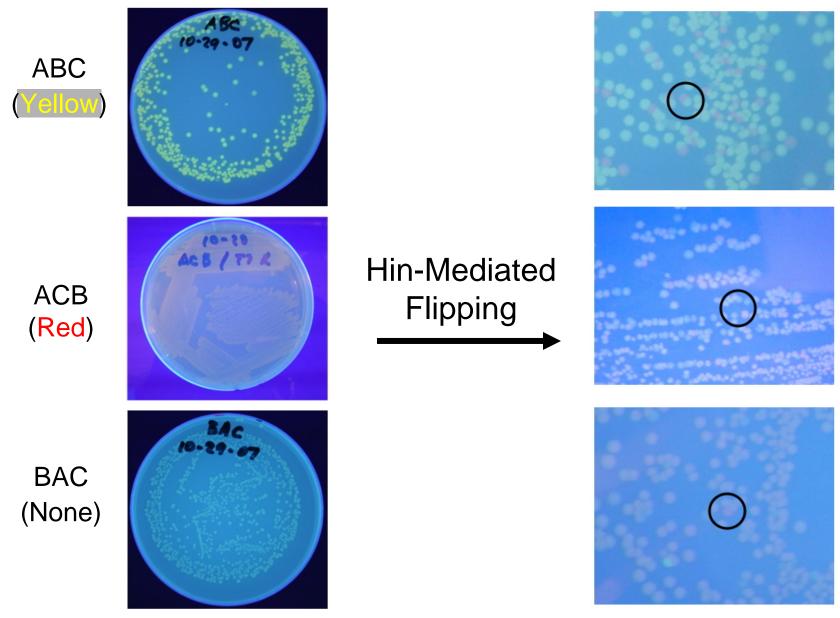
Coupled Hin & HPP Graph



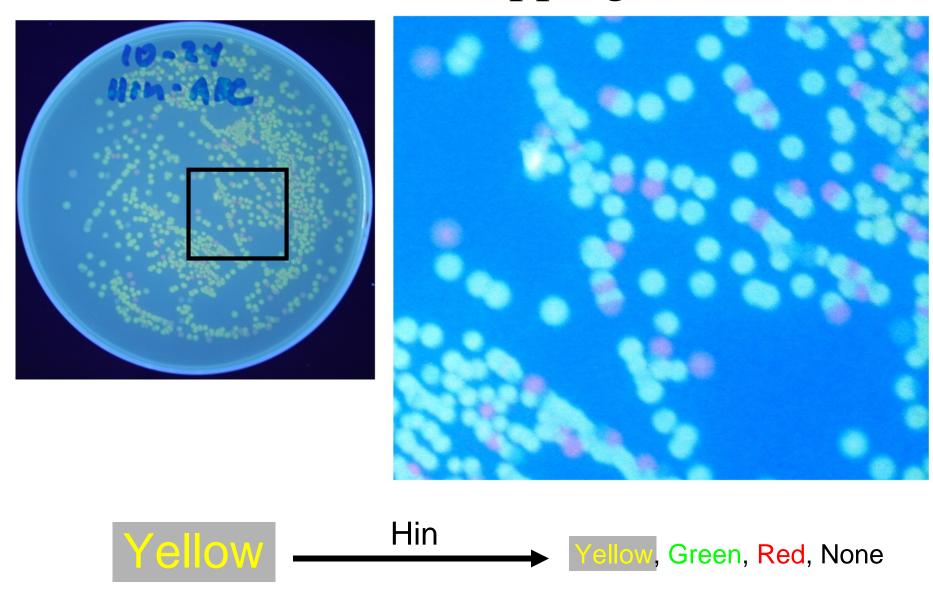
Flipping Detected by Phenotype



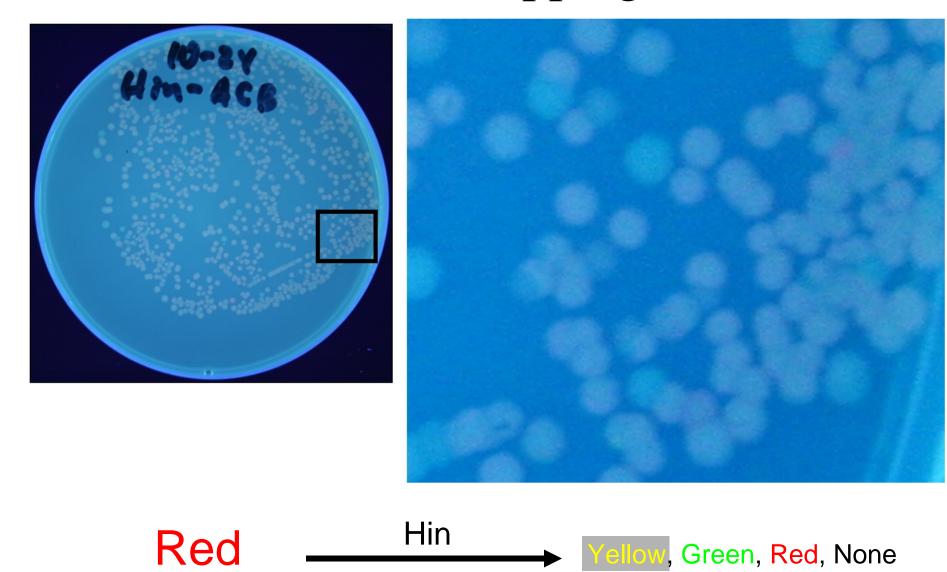
Flipping Detected by Phenotype



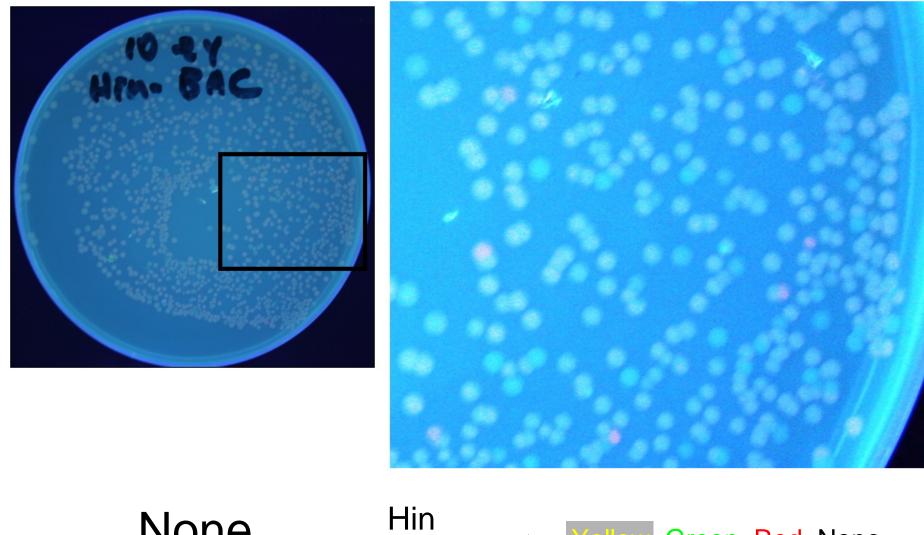
ABC Flipping



ACB Flipping

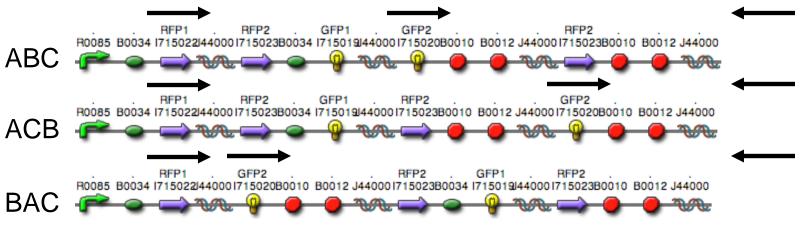


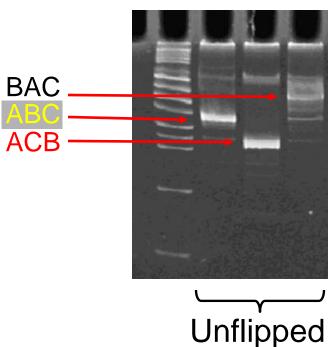
BAC Flipping



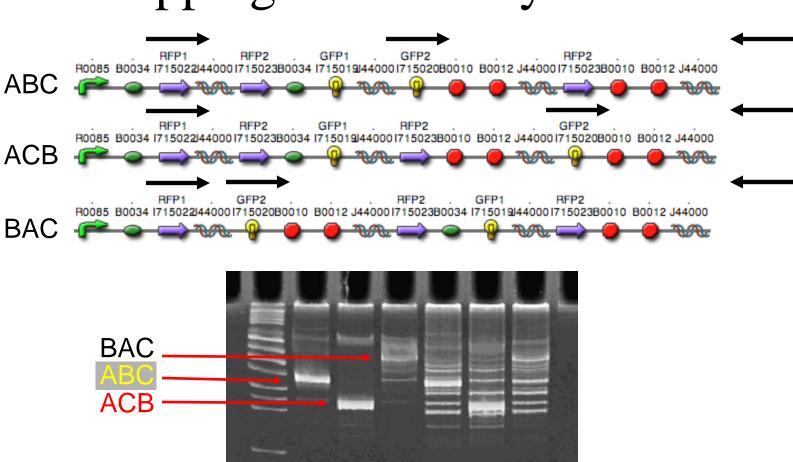
None Yellow, Green, Red, None

Flipping Detected by PCR





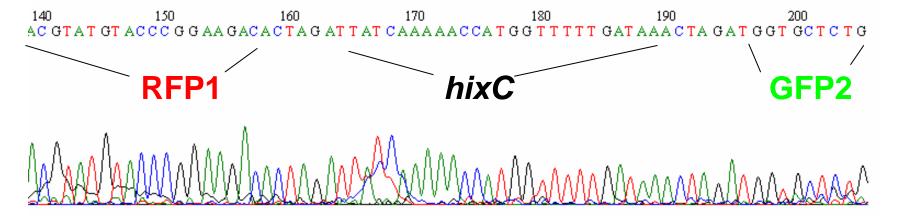
Flipping Detected by PCR



Unflipped Flipped

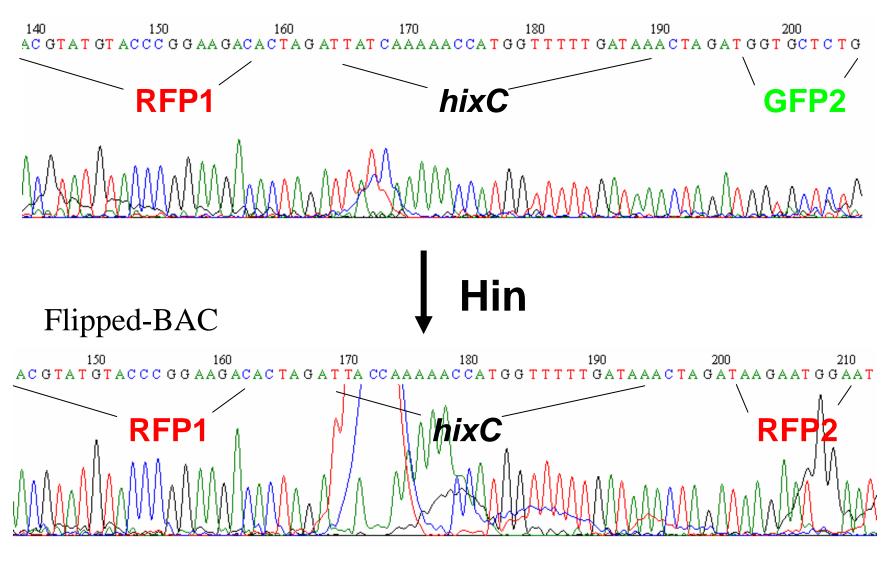
Flipping Detected by Sequencing

BAC



Flipping Detected by Sequencing

BAC



Conclusions

- Modeling revealed feasibility of our approach
- GFP and RFP successfully split using hixC
- Added 69 parts to the Registry
- HPP problems given to bacteria
- Flipping shown by fluorescence, PCR, and sequence
- Bacterial computers are working on the HPP and may have solved it

Living Hardware to Solve the Hamiltonian Path Problem





Students: Oyinade Adefuye, Will DeLoache, Jim Dickson, Andrew Martens, Amber Shoecraft, and Mike Waters, Jordan Baumgardner, Tom Crowley, Lane Heard, Nick Morton, Michelle Ritter, Jessica Treece, Matt Unzicker, Amanda Valencia

Faculty: Malcolm Campbell, Todd Eckdahl, Karmella Haynes, Laurie Heyer, Jeff Poet

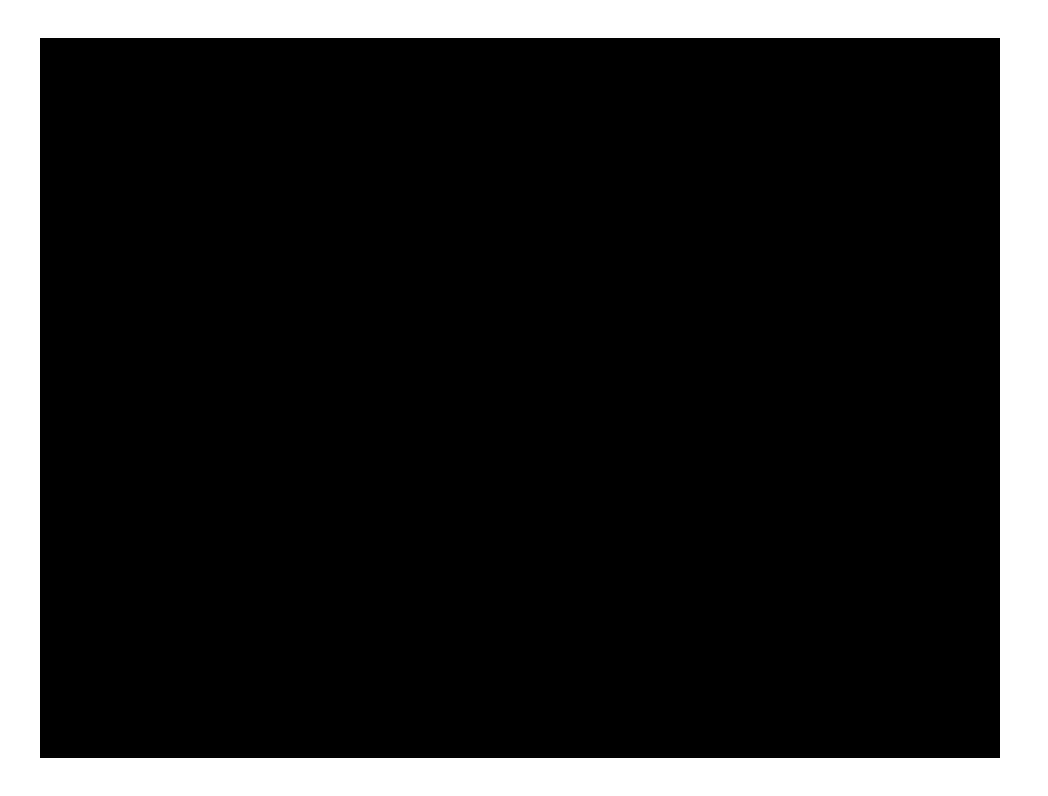
Living Hardware to Solve the Hamiltonian Path





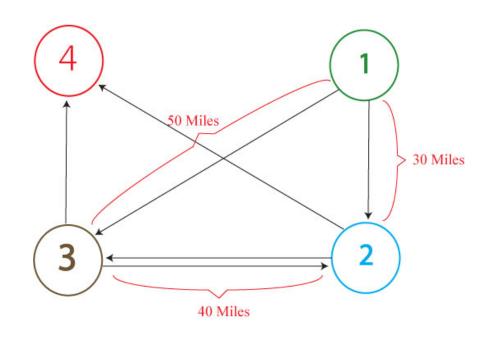


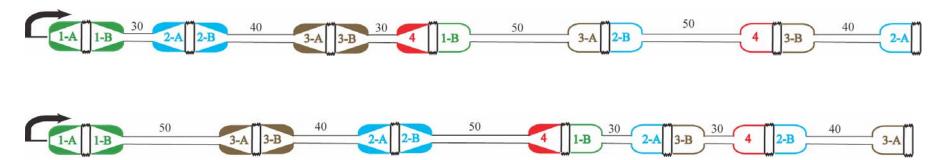
Acknowledgements: Thanks to The Duke Endowment, HHMI, NSF DMS 0733955, Genome Consortium for Active Teaching, Davidson College James G. Martin Genomics Program, Missouri Western SGA, Foundation, and Summer Research Institute, and Karen Acker (DC '07). Oyinade Adefuye is from North Carolina Central University and Amber Shoecraft is from Johnson C. Smith University.



Extra Slides

Traveling Salesperson Problem





Another Gene-Splitting Method

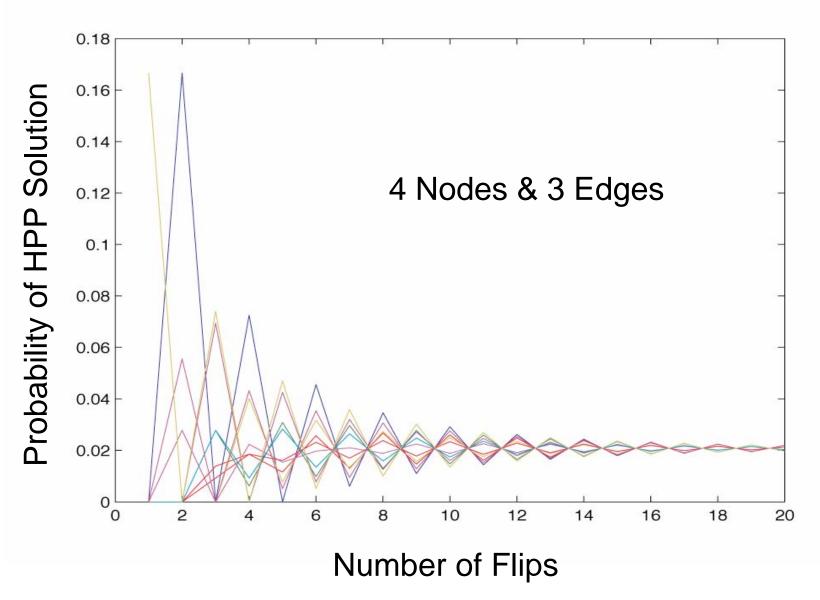
Other Attempts at Gene Splitting

Reporter Gene	Status	
Kanamycin Resistance	Failed	
Tetracycline Resistance	Failed	
Chloramphenicol Resistance	Undetermined (Issues in building)	
Cre Recombinase	Undetermined (Issues in testing)	

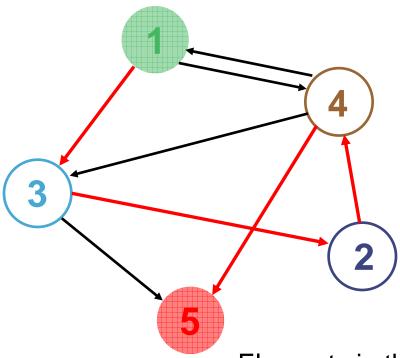
Normalized Fluorescence Measurements

Construct	Observed Color on UV Box	Green (450/515)	Red (560/608)
pLac-RBS-RFP	Red	7	263
pLac-RBS-RFP-RBS-GFP	Red	144	370
pLac-GFP1-hixC-GFP2	Green	136	0
pLac-RBS-RFP1-hixC-RFP2	None	0	147
pLac-RBS-GFP1-hixC-RFP2	None	11	2
pLac-RBS-RFP1-hixC-GFP2	None	13	2
AB (R1-hixC-R2-G1-hixC-G2)	Green	72	18
ABC (R1-hixC-R2-G1-hixC-G2)	Yellow	340	255
ACB (R1-hixC-R2-G1-hixC-R2)	Red	1	143
BAC (R1-hixC-G2)	None	11	3
DBA (R1-hixC-G2)	Hybrid green	15	3

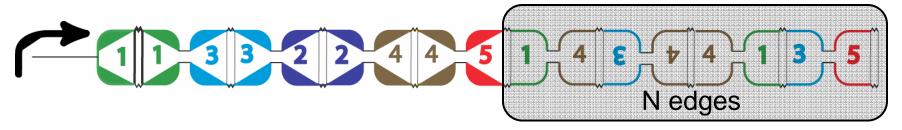
Starting Arrangement



True Positives



Elements in the shaded region can be arranged in any order.



Number of True Positives = N! * 2N