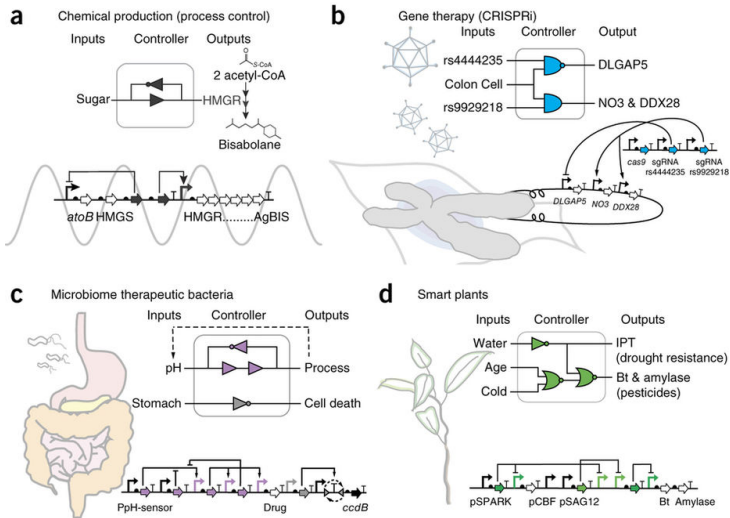


Engineering Genetic Circuits

Chris J. Myers

Lecture 11: Principles of Genetic Circuit Design

Potential Uses of Synthetic Genetic Circuits



(Courtesy of Brophy/Voight, Nature Methods, 2014)

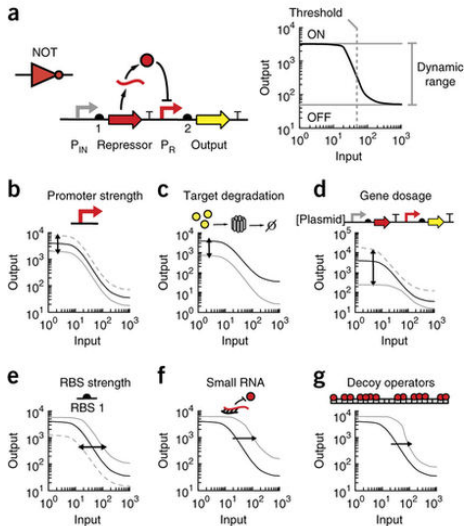
Challenges to Genetic Circuit Design

- Require precise balancing of regulators to generate a correct response.
- Can be difficult to screen for correct performance.
- Few tools available to measure circuit performance other than fluorescent reporters, which are limited for measuring dynamics.
- Sensitive to environment, growth conditions, and genetic context.
- Assembly of large genetic circuits is difficult and often has errors.

Overview

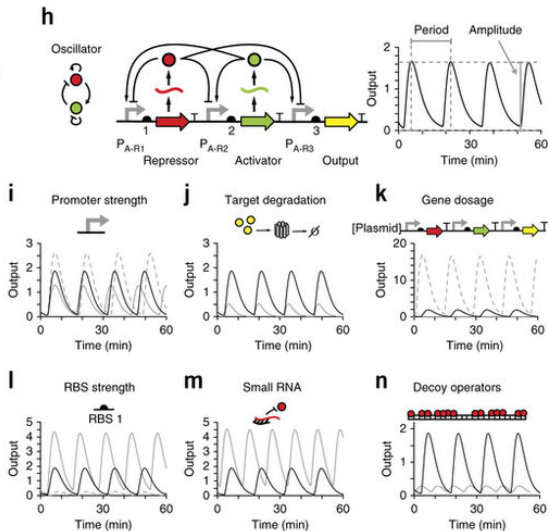
- Methods of modifying circuit behavior.
- Common failure modes from connecting circuits.
- Circuit performance within the context of a living cell.
- Alternative regulatory mechanisms for genetic logic gates.

Methods of Modifying Circuit Behavior



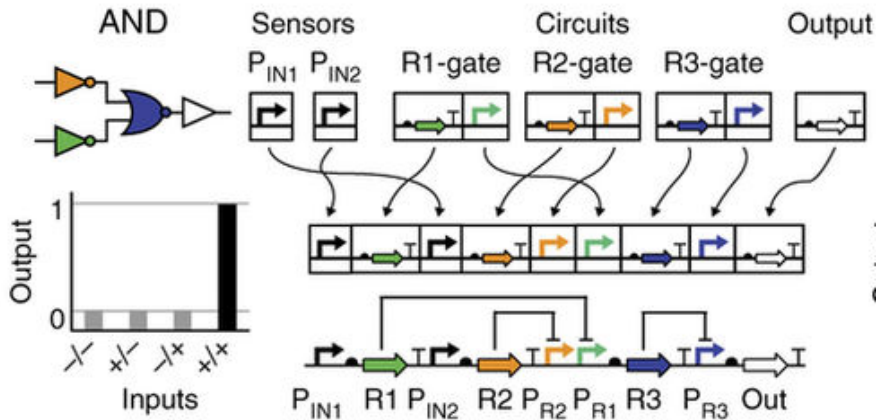
(Courtesy of Brophy/Voight, Nature Methods, 2014)

Methods of Modifying Circuit Behavior (cont)



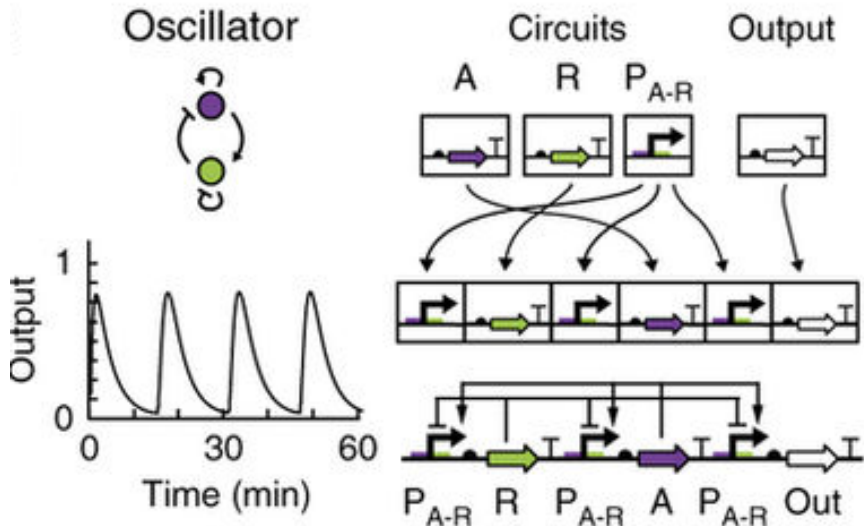
(Courtesy of Brophy/Voigt, Nature Methods, 2014)

Connecting Circuits: AND Gate Example



(Courtesy of Brophy/Voight, Nature Methods, 2014)

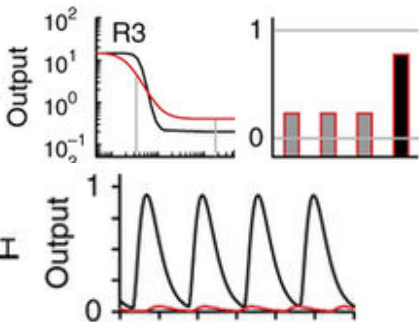
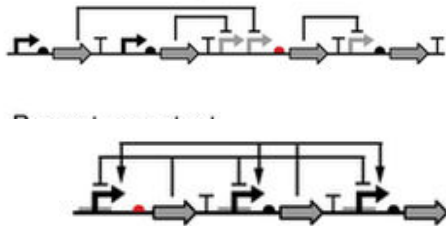
Connecting Circuits: Oscillator Example



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Mismatched Response Functions

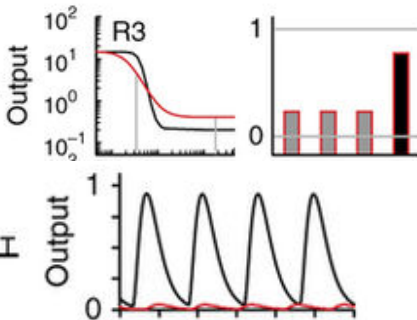
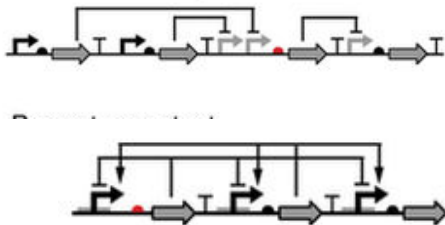
Mismatched response functions



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Mismatched Response Functions

Mismatched response functions

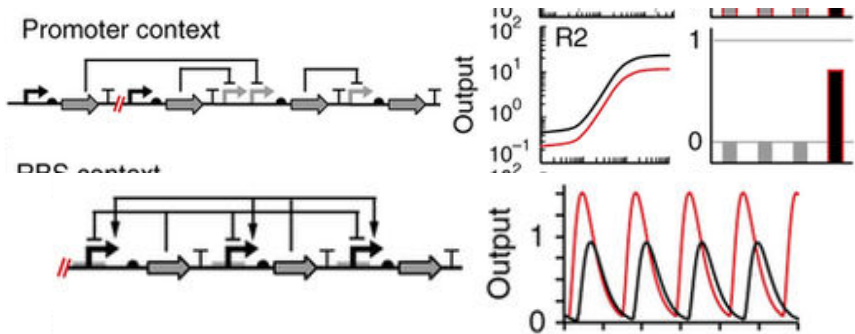


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

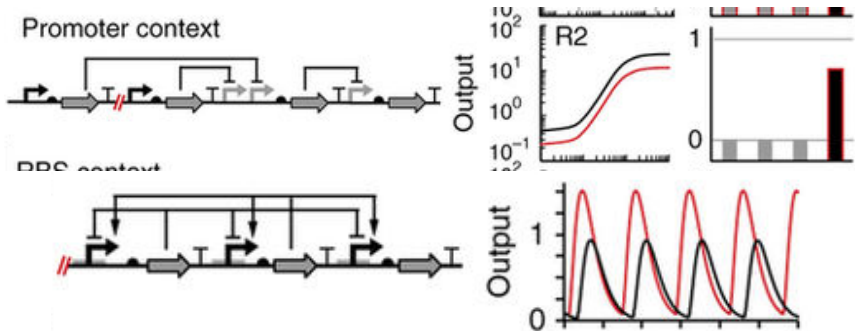
Select RBSs and promoters to achieve the required expression levels.

Failure Modes: Promoter Context



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Promoter Context

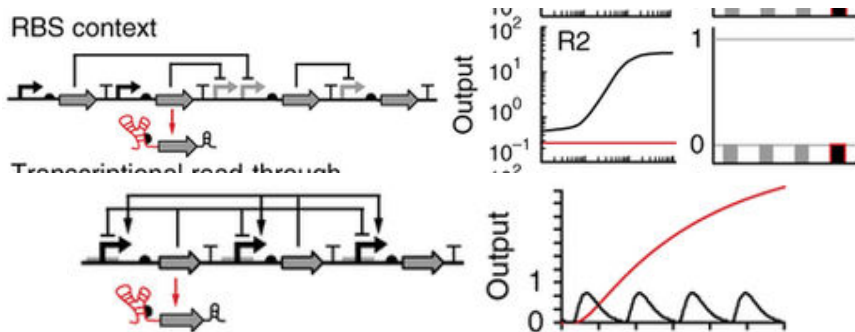


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

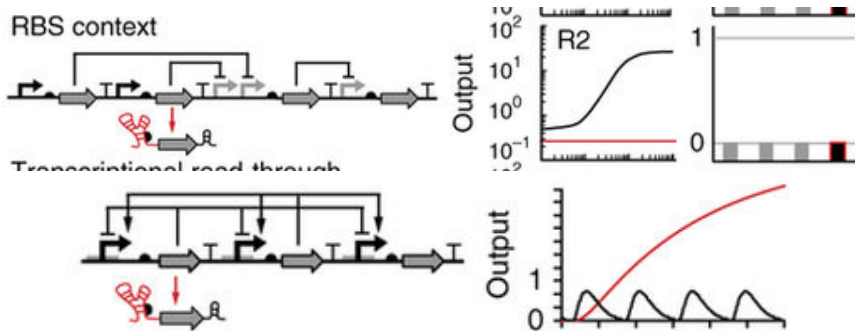
Insulator sequences standardize the DNA sequences flanking promoters.

Failure Modes: RBS Context



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: RBS Context



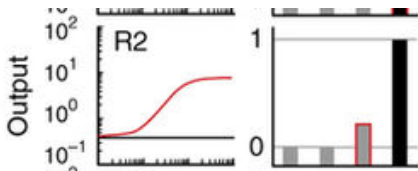
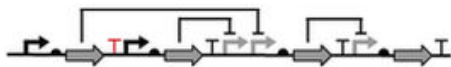
(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

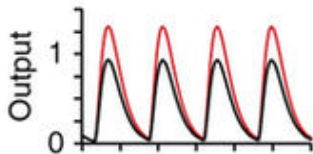
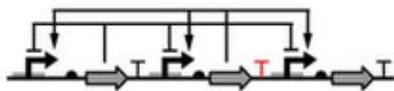
5' UTR can be cleaved with ribozymes to standardize RBS accessibility.

Failure Modes: Transcriptional Read Through

Transcriptional read-through



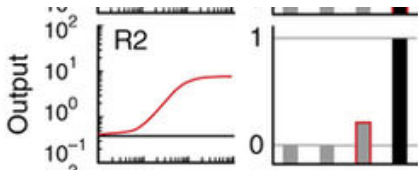
Port junction interference



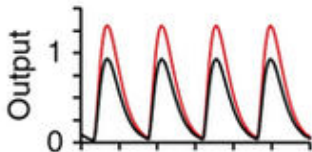
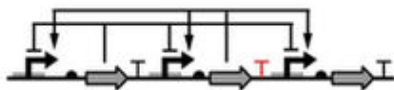
(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Transcriptional Read Through

Transcriptional read-through



Port junction interference

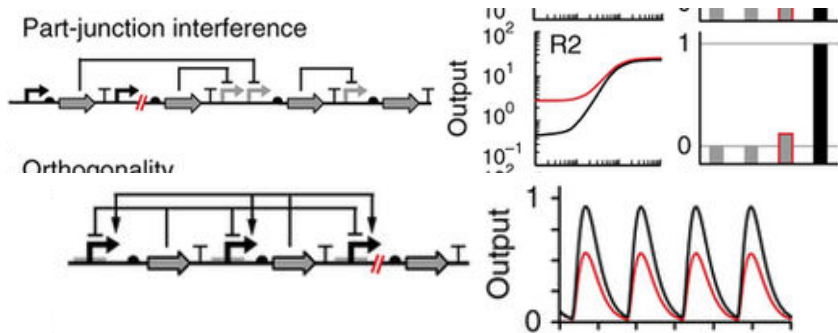


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

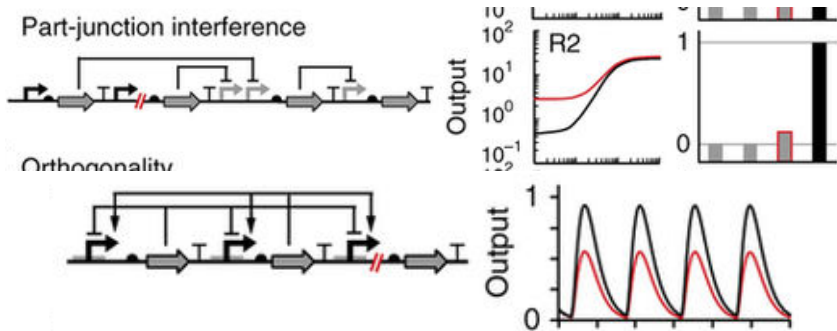
Use strong, tandem terminators.

Failure Modes: Part Junction Interference



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Part Junction Interference

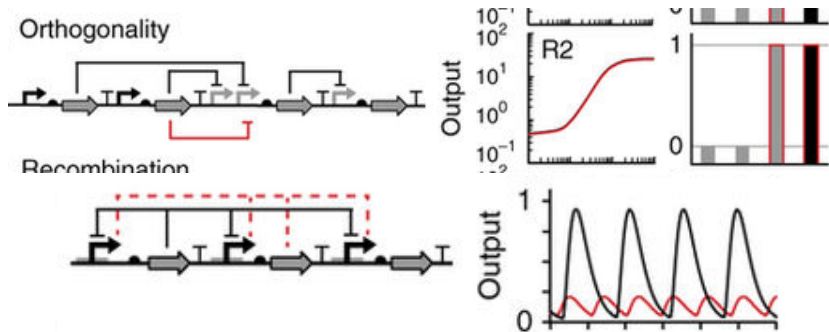


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

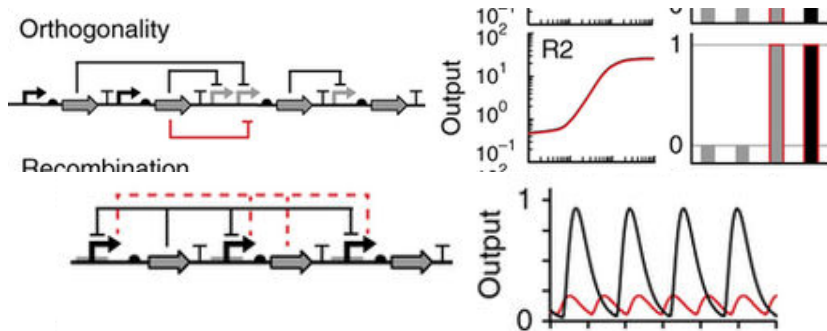
Scan for unintended functional sequences.

Failure Modes: Orthogonality



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Orthogonality

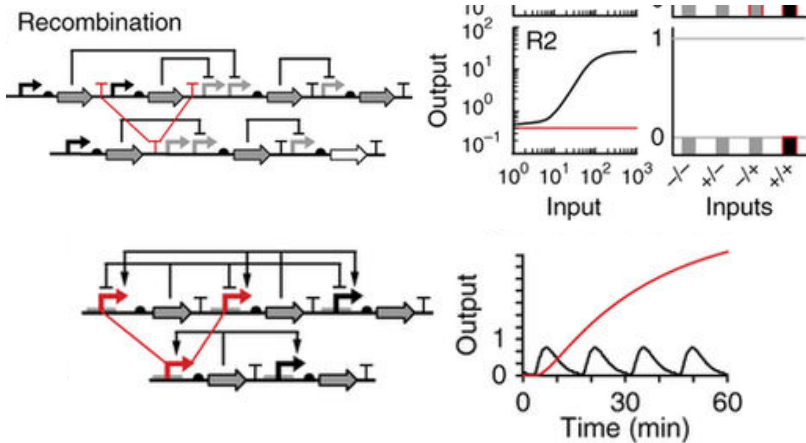


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

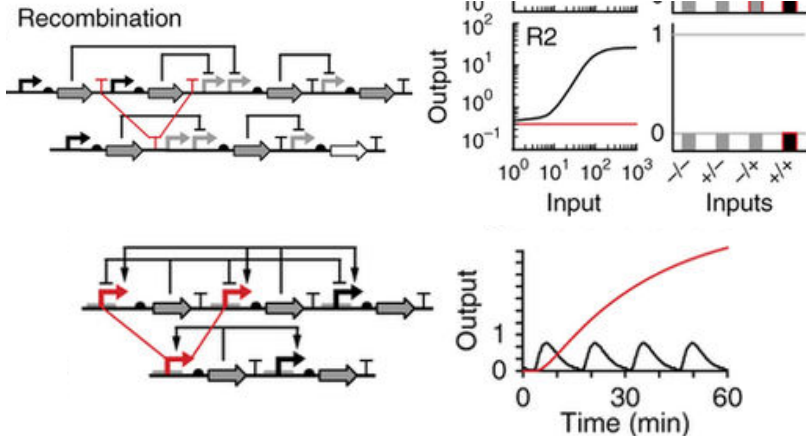
Screen parts to test every combination of promoter and regulatory element.

Failure Modes: Recombination



(Courtesy of Brophy/Voight, Nature Methods, 2014)

Failure Modes: Recombination

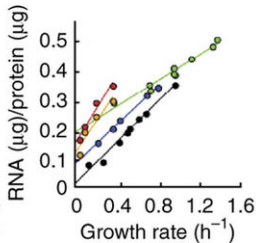
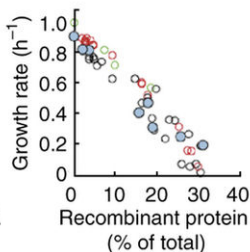
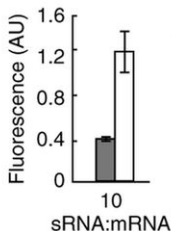
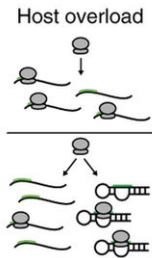


(Courtesy of Brophy/Voight, Nature Methods, 2014)

SOLUTION:

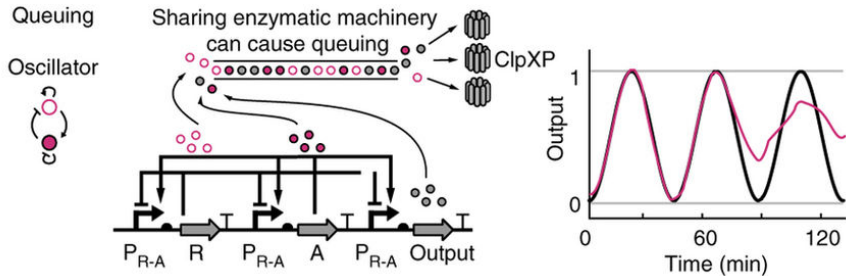
Use large libraries of parts with enough sequence diversity.

Host Context Issues: Host Overload



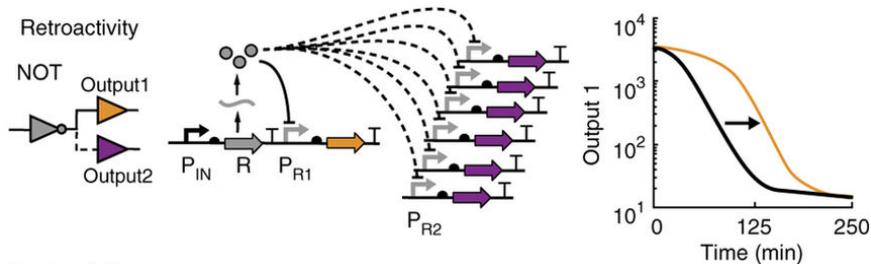
(Courtesy of Brophy/Voight, Nature Methods, 2014)

Host Context Issues: Queuing



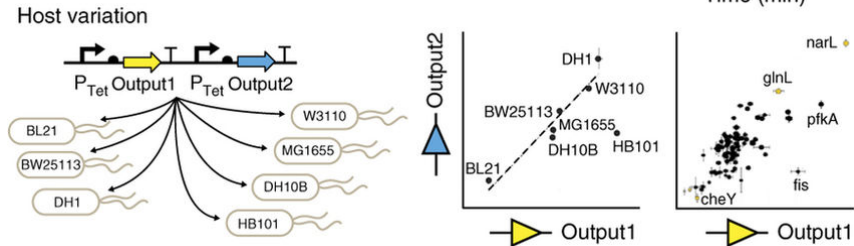
(Courtesy of Brophy/Voight, Nature Methods, 2014)

Context Issues: Retroactivity



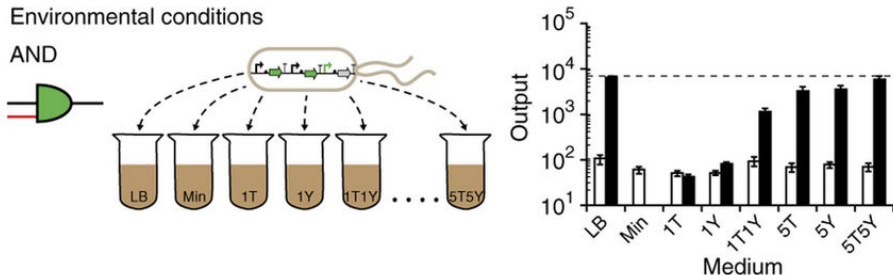
(Courtesy of Brophy/Voight, Nature Methods, 2014)

Context Issues: Host Variation



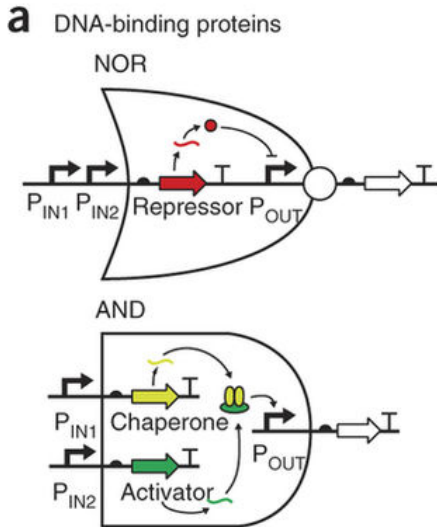
(Courtesy of Brophy/Voigt, Nature Methods, 2014)

Context Issues: Environmental Conditions



(Courtesy of Brophy/Voight, Nature Methods, 2014)

DNA Binding Proteins

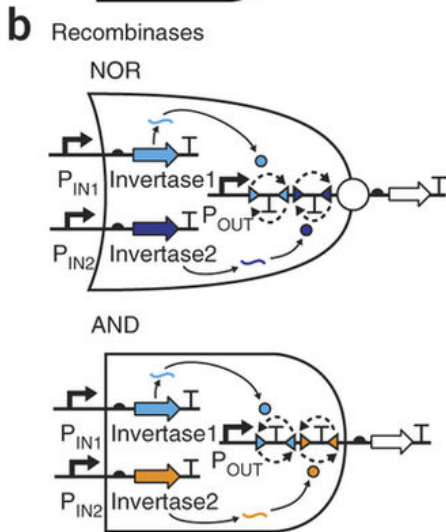


(Courtesy of Brophy/Voight, Nature Methods, 2014)

Challenges with DNA Binding Proteins

- Expanding protein libraries is difficult, since they must be orthogonal.
 - zinc-finger proteins
 - transcription activator-like (TAL) effectors
 - TetR and LacI homologs.
- Even when individual transcription factors are nontoxic, multiple regulators may be toxic.
- Circuits are dependent on growth rate, since dilution rate affects steady-state concentration of regulators.
- Response functions are often suboptimal and difficult to control (high OFF states and low dynamic ranges).

Recombinases

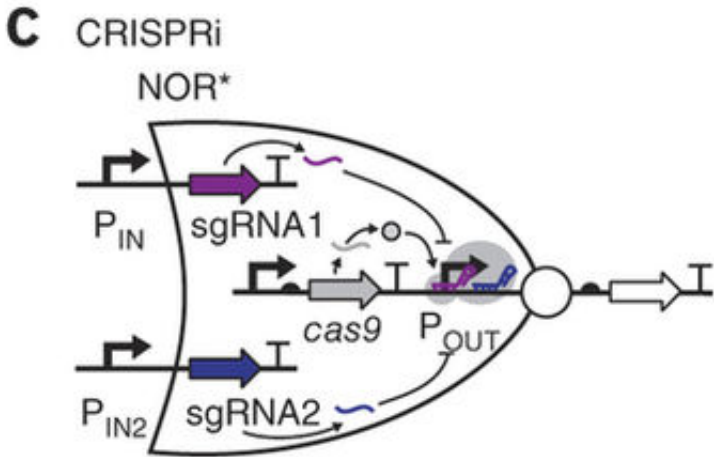


(Courtesy of Brophy/Voight, Nature Methods, 2014)

Recombinases: Advantages/Disadvantages

- Tyrosine recombinases (Cre, Flp, FimBE) - require host-specific factors, can be reversible and irreversible.
- Serine integrases - catalyze unidirectional reactions to invert DNA without host factors and often have excisionases to return to original orientation.
- Advantages:
 - Ideal for memory storage since they flip DNA permanently.
 - All two-input logic gates have been built using serine integrases.
- Disadvantages:
 - Reactions can be slow and generate mixed populations.
 - Reversing the state change requires extra circuitry.

CRISPRi



(Courtesy of Brophy/Voight, Nature Methods, 2014)

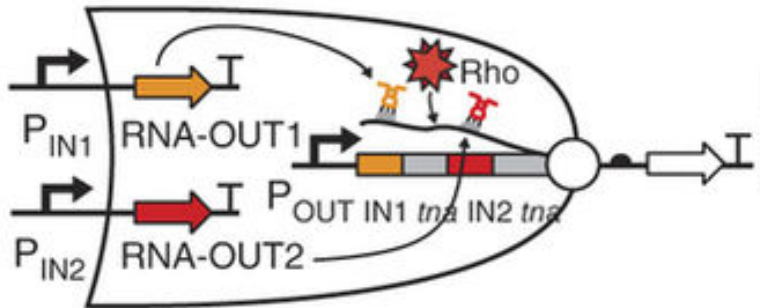
CRISPRi: Advantages/Disadvantages

- *Clustered, regularly interspaced, short palindromic repeat* (CRISPR) function as a bacterial immune system that targets specific DNA sequence motifs for degradation.
- Use a Cas (CRISPR-associated) nuclease and guide RNA to introduce double-strand breaks to specific DNA sequences.
- CRISPR *interference* (CRISPRi) uses dCas9/Cas9_{N-}, which does not have a nuclease, as a transcription factor to repress gene expression by producing a DNA bubble.
- Advantages:
 - Can create orthogonal set of guide sequences to target different promoters.
 - Operate at speeds similar to protein-based circuits.
- Disadvantages:
 - Predicting guide RNA orthogonality is complicated.
 - Toxicity can result if Cas9 binds to and interferes with the host genome.
 - Retroactivity can be an issue since Cas9 is a shared resource.

d

RNA-IN/OUT

NOR*

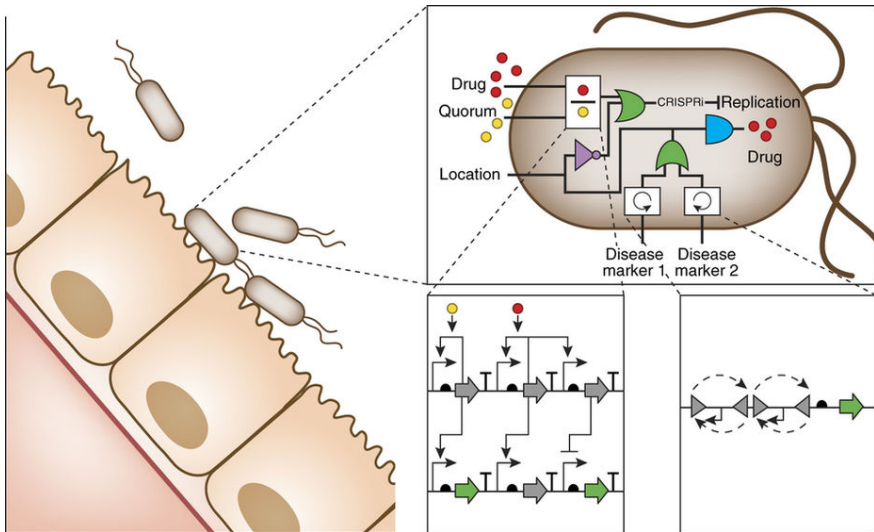


(Courtesy of Brophy/Voight, Nature Methods, 2014)

RNA IN/OUT: Advantages/Disadvantages

- Natural system represses translation with a short non-coding RNA.
- Synthetic system adapted to repress transcription using the transcriptional adapter, *tna*, composed of RBS and CDS for TnaC.
- When TnaC translation is blocked, Rho binds knocking off the RNAP.
- Advantages:
 - Could be used to generate a large set of orthogonal regulators.
 - Have been successfully used for 2/3/4-input NOR gates.
- Disadvantages:
 - Each transcriptional regulator requires the same *tna* regulatory element (~290 bp), which could lead to homologous recombination.

Conceptual Circuit for a Therapeutic Bacterium

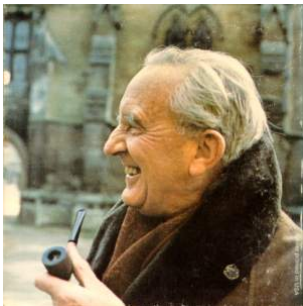


(Courtesy of Brophy/Voight, Nature Methods, 2014)

The Road Ahead

- Standards:
 - Experimental synthetic biologists should be encouraged by journals and funding agencies to share their data using standards and repositories.
 - Computational synthetic biologists need to develop software tools that can easily create models and capture design information using standards.
- Abstraction:
 - Experimental synthetic biologists must determine design details that are critical to achieving a desired phenotypic behavior.
 - Computational synthetic biologists must fall out of love with their models, accept abstraction, and create tools supporting multiple abstractions levels.
- Decoupling:
 - Experimental synthetic biologists need to create libraries of components that are more orthogonal and well characterized.
 - Computational synthetic biologists need to develop design flows that allow the biologically naive to build genetic circuits that actually work.

J. R. R. Tolkien



*Faithless is he that says
farewell when the road darkens.*

Sources

- Brophy/Voight, Nature Methods, 2014.
- Myers, IEEE Transactions on Multi-Scale Computing Systems, 2015.