Establishing Baseline Performance Scores for the CAGEN Robust Gene Response Challenge

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CAGEN - Critical Assessment of Genetically Engineered Networks

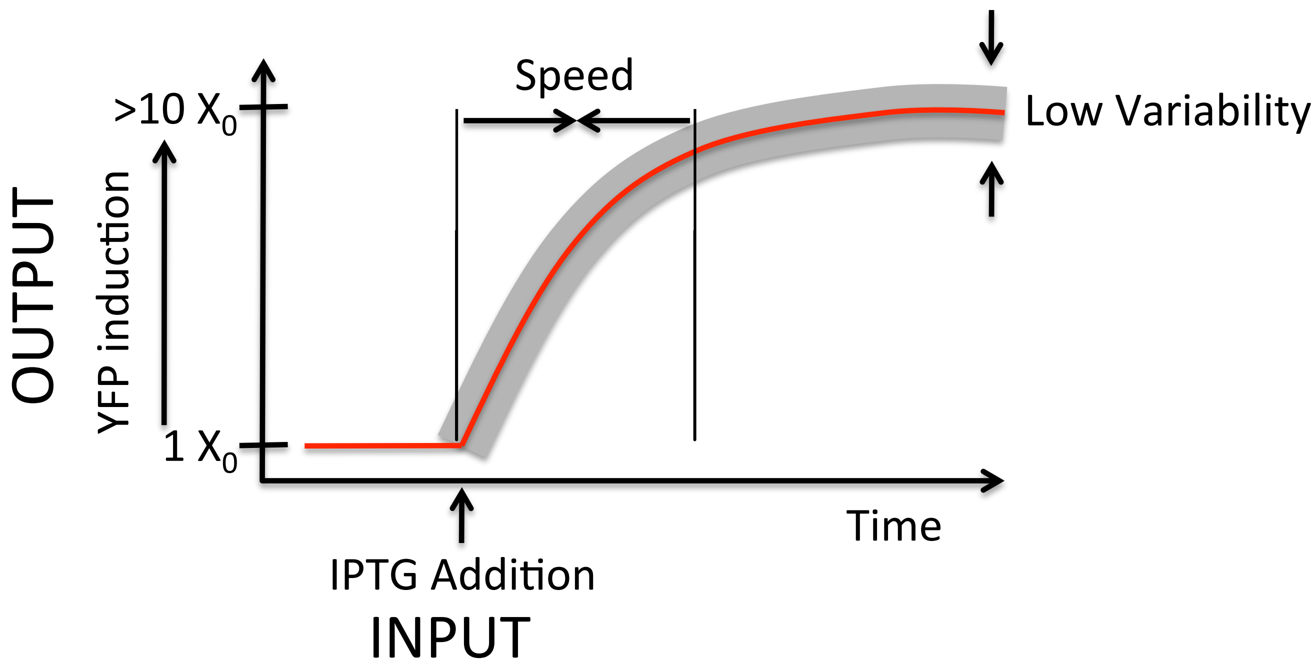
- Systematize the design of genetic networks (robustness, connectability)

- Facilitate applications, for ex. in agriculture, medicine

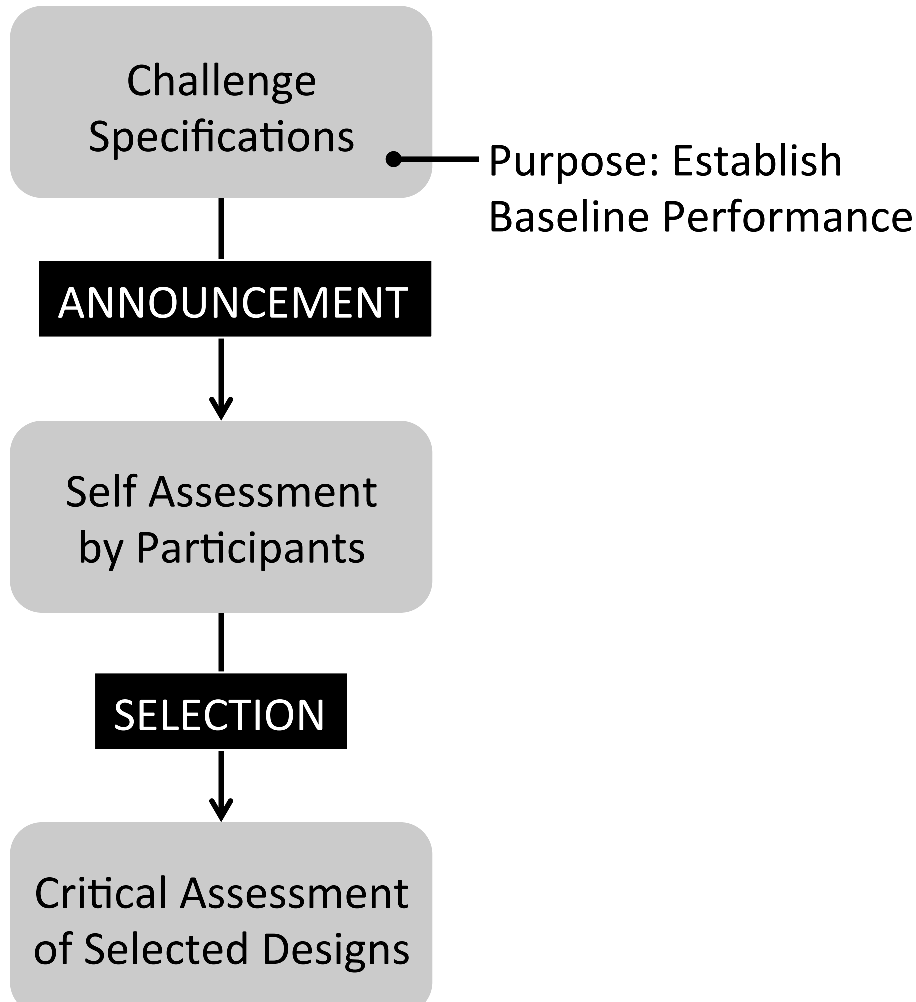
CAGEN Challenge #1 : Robust Gene Response

Induce OUTPUT (YFP) in response to INPUT (IPTG), so that,

1) Detectable: >10 fold induction
2) Robust: Low variability across cells & temperatures
3) Fast: Quick response



Purpose
Establish Baseline Performance



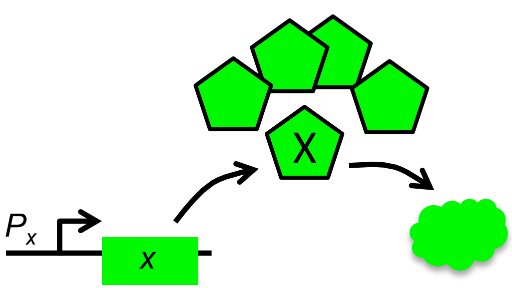
Performance metric to score robustness and speed of designs

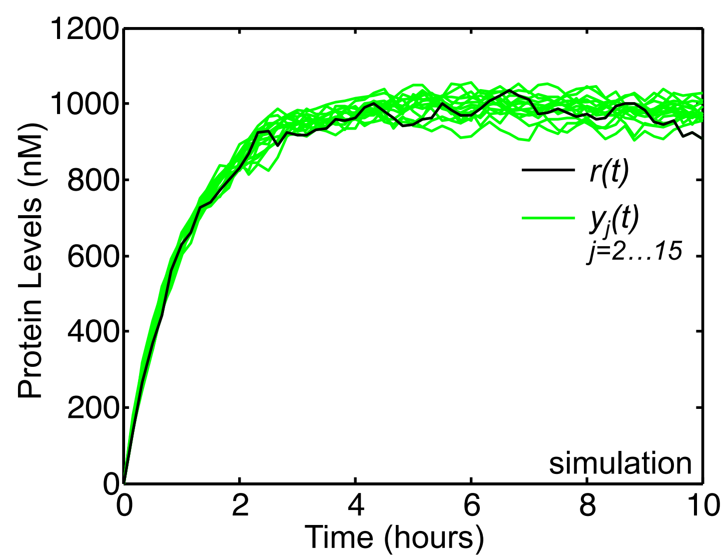
Time integral of square error

Worst Case

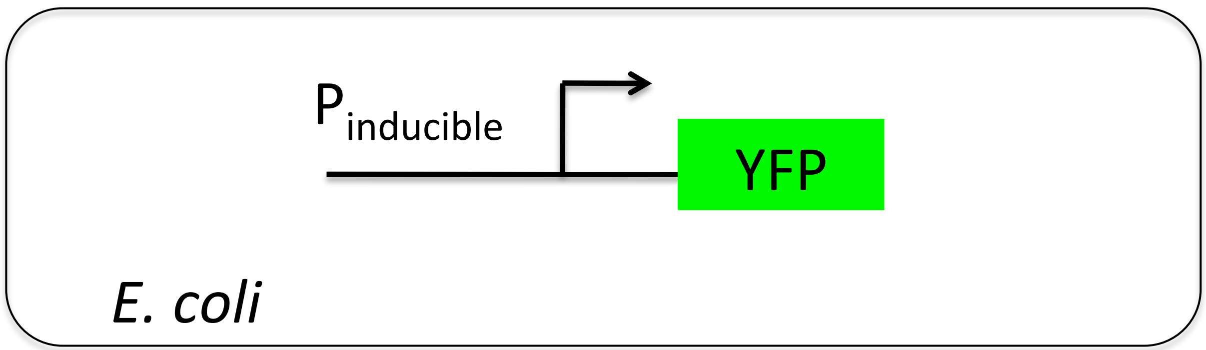
$$S = \frac{\max_j \int_{T_1}^{T_2} |y_j(t) - r(t)|^2 dt}{M^2}$$

Normalizing factor
(equilibrium amplitude of reference trace)



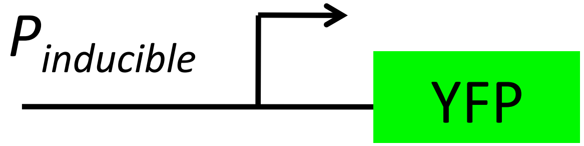


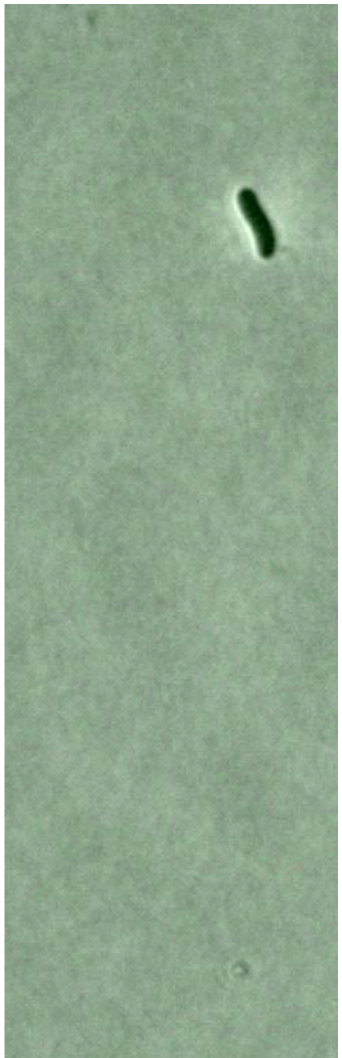
Single cell dynamics are measured for a simple reference design, for different temperatures

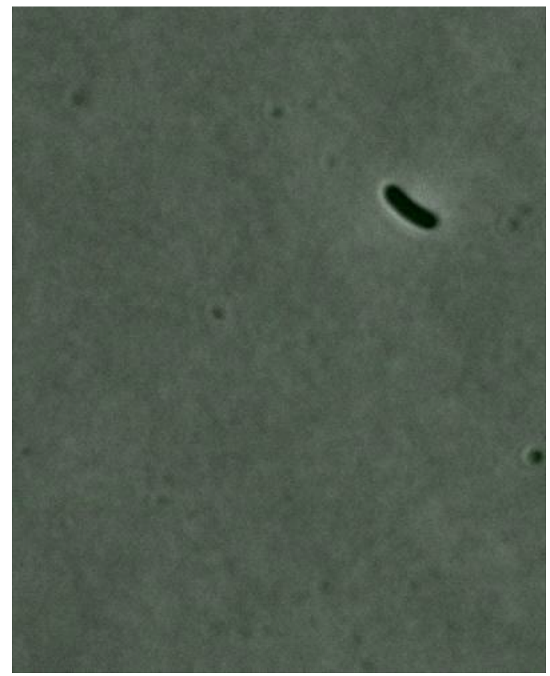


		30 °C	32 °C	34 °C
#1	#1 P_{lac} *yfp* IPTG	?	?	?
#2	#2 P_{lac} *cI-yfp* IPTG	?	?	?

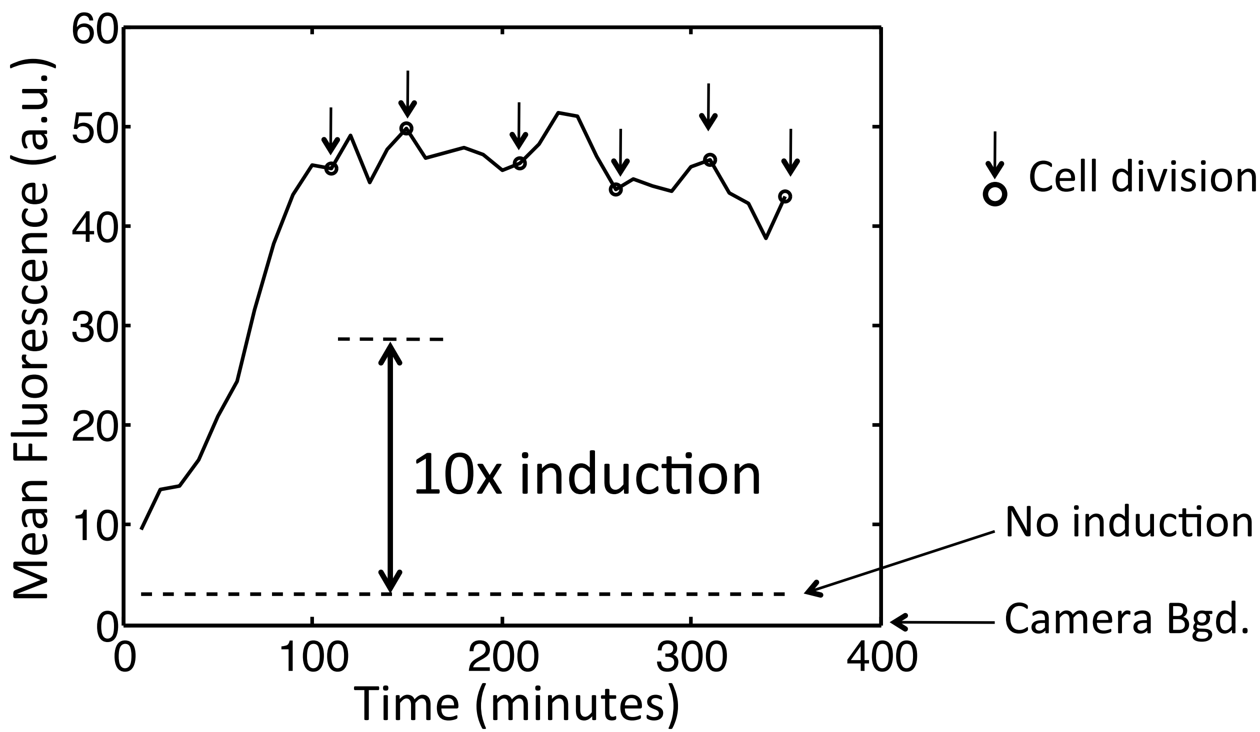
Movies





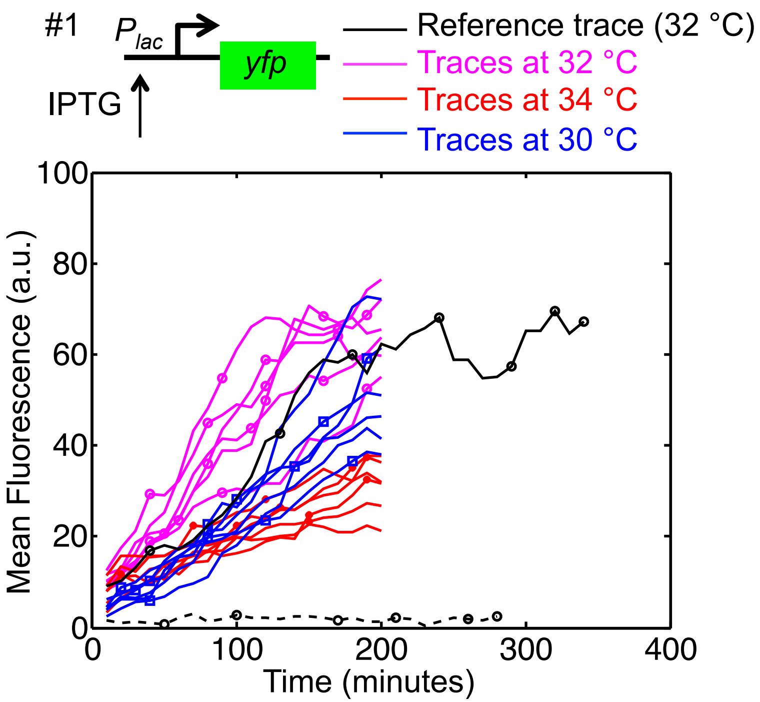


Reference trace exhibits > 10x induction

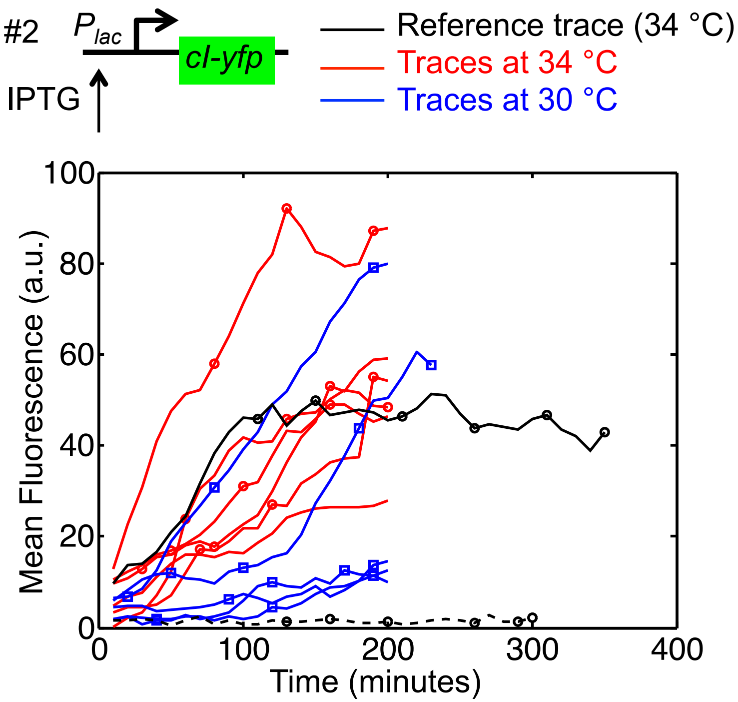


Performance scores for inducible protein expression circuits

S = 0.27

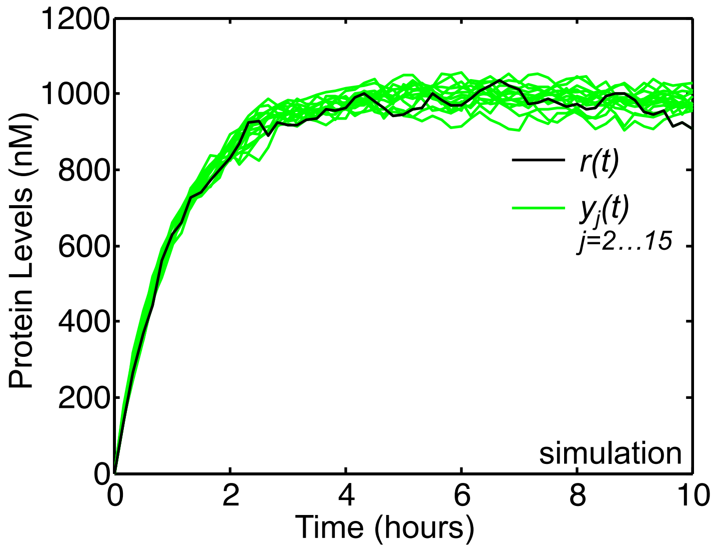


S = 0.29

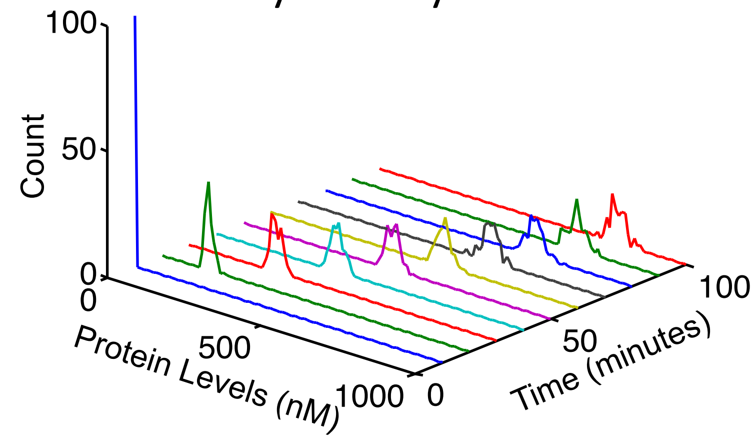


Population level metric to estimate performance score

Single-Cell Dynamics/ Microscopy



Population Dynamics/ Flow Cytometry



$$S = \frac{\max_j \int_{T_1}^{T_2} |y_j(t) - r(t)|^2 dt}{M^2}$$

$$\boxed{S = \frac{\int_{T_1}^{T_2} \sigma^2(t) dt}{M^2}}$$

Future Work
Refined single-cell measurements using μfluidics

Challenge Specifications

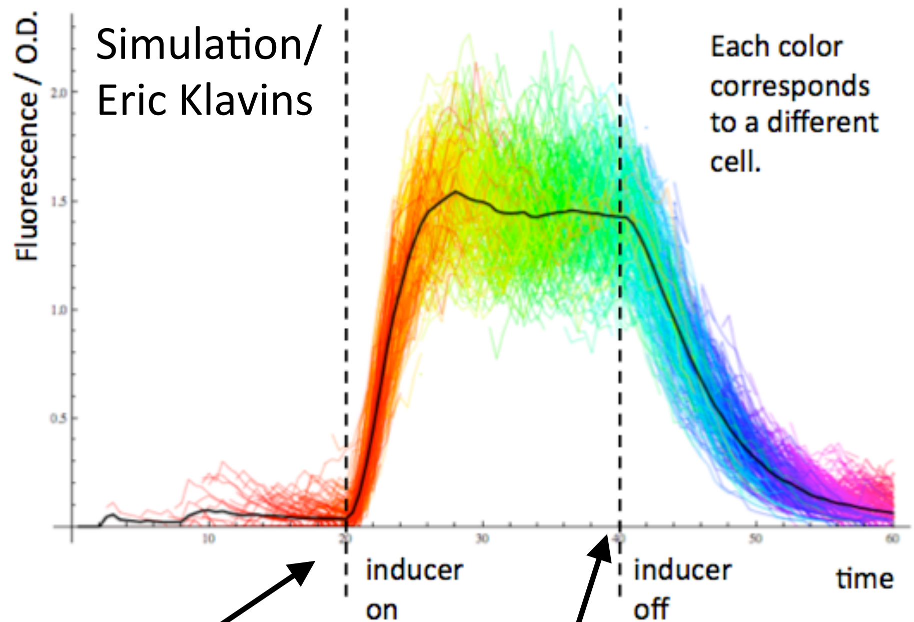
Baseline for Critical Assessment

↓

Self Assessment by Participants

↓

Critical Assessment of Selected Designs



Benefit #1.
Exact induction time measurement.

Benefit #2:
Similar decay time measurement.