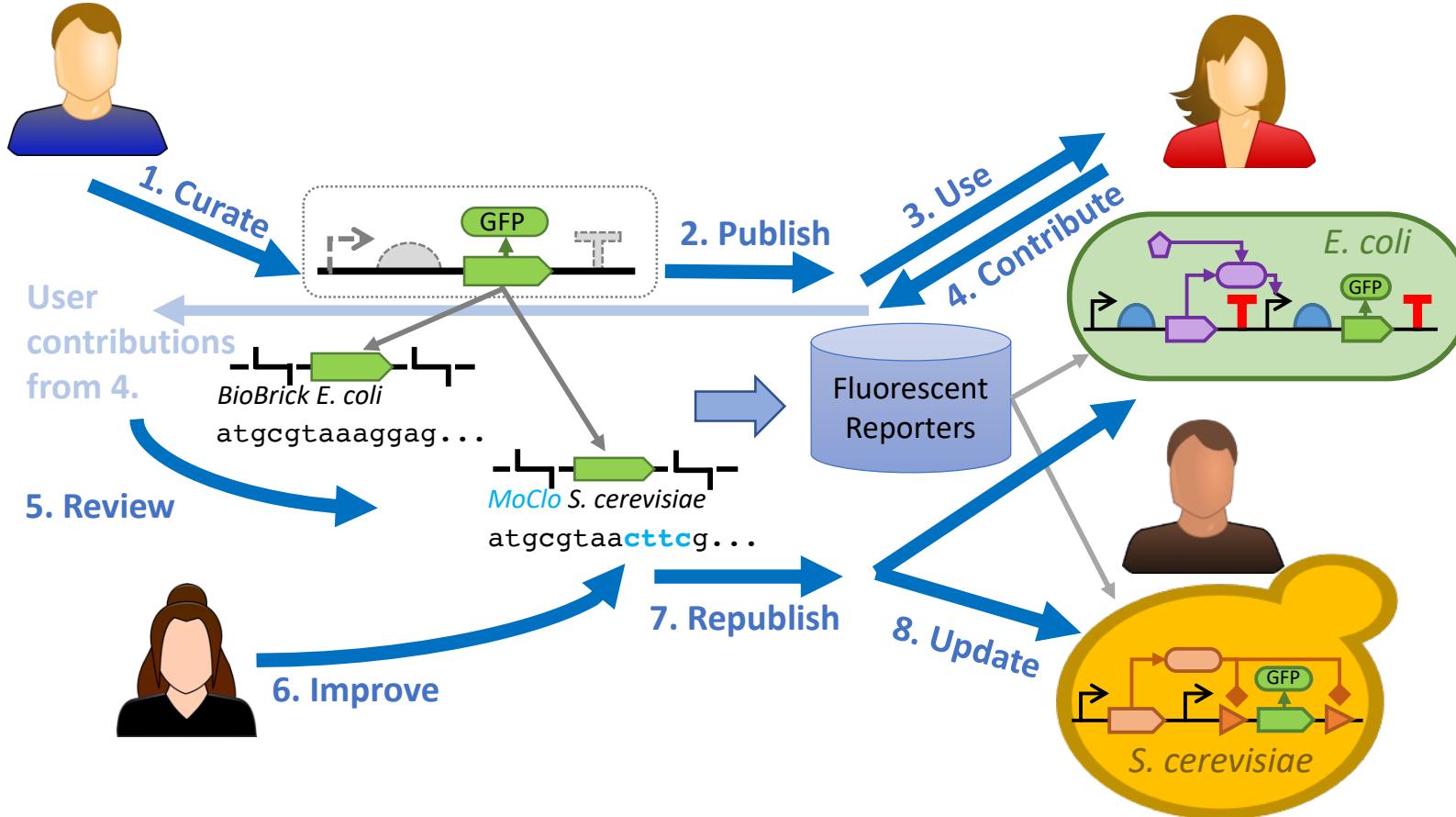


Steps Towards Functional Synthetic Biology

Ibrahim Aldulijan, Jacob Beal, Sonja Billerbeck, Jeff Bouffard, Gaël Chambonnier, Nikolaos Delkis, Isaac Guerreiro, Martin Holub, Daisuke Kiga, Jacky Loo, Paul Ross, Vinoo Selvarajah, Noah Sprent, Gonzalo Vidal, Alejandro Vignoni



Stats from the prototype used to build the 2022 iGEM Distribution:

- Four automated stages of validation & build planning
- 493kb of designs
- 346 parts in 13 packages
- 569 machine-generated intermediates & composites
- 87 pull requests, 571 commits in 7 weeks
- 15 contributors at 11 institutions in 8 countries
- Most contributors were not programmers, many had never used git before

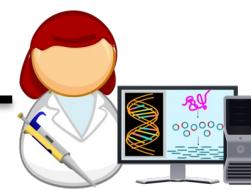
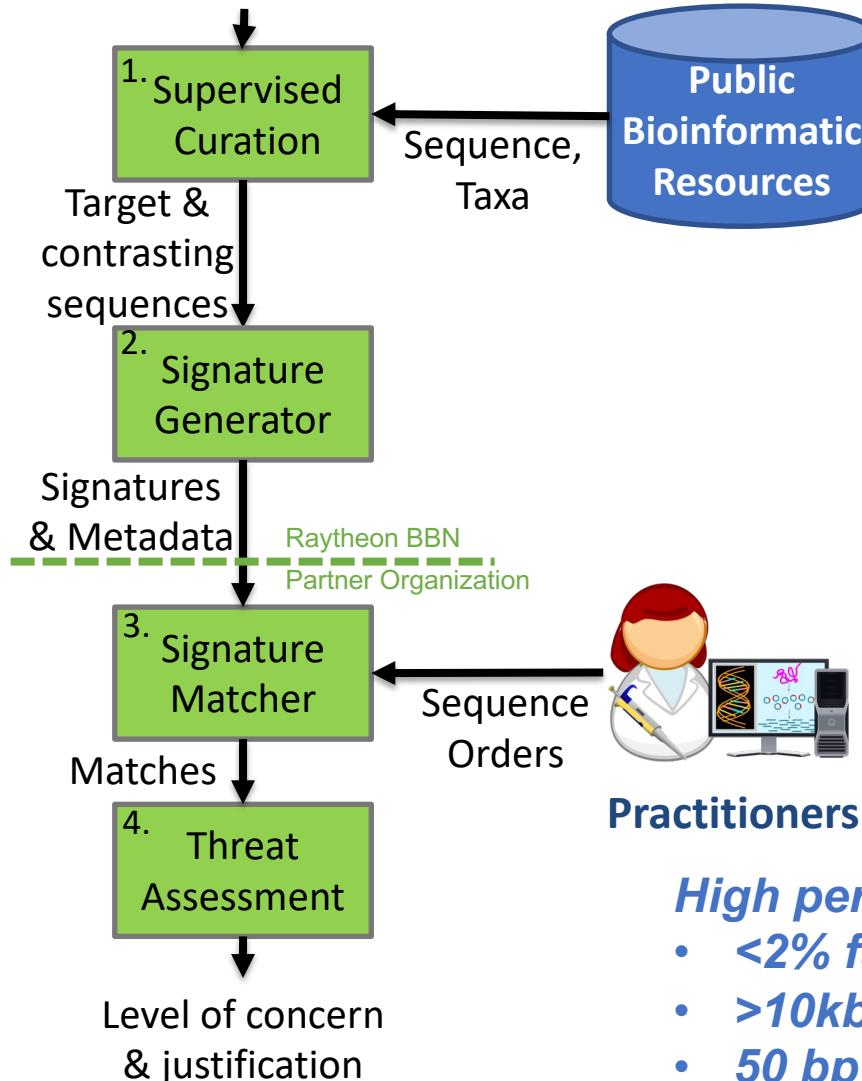
Adapting Malware Detection to DNA Screening

Dan Wyschogrod, Jeff Manthey, Tom Mitchell, Steven Murphy, Adam Clore, Jacob Beal



Synthesis Provider(s)

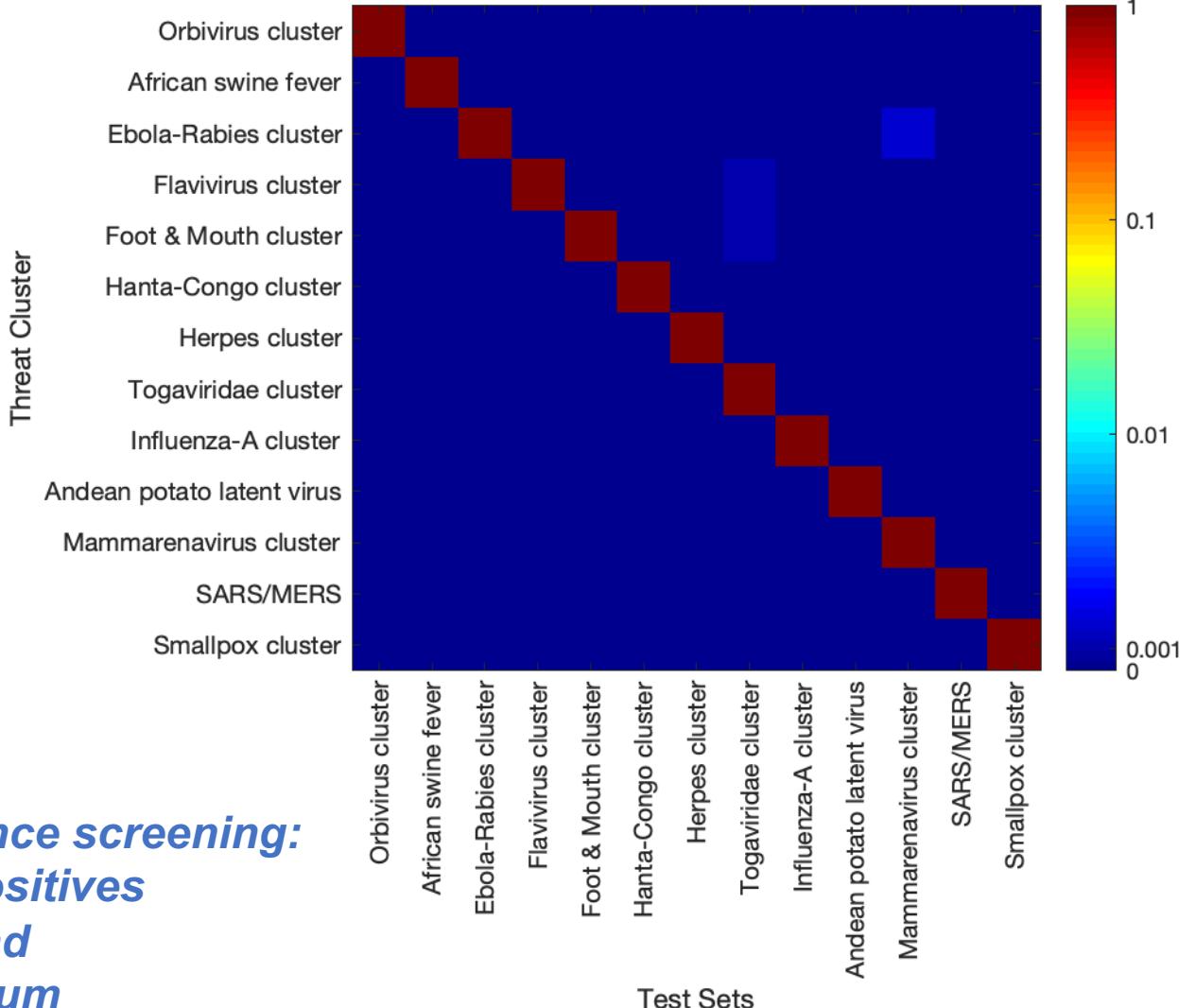
Blacklist & Whitelist



Practitioners

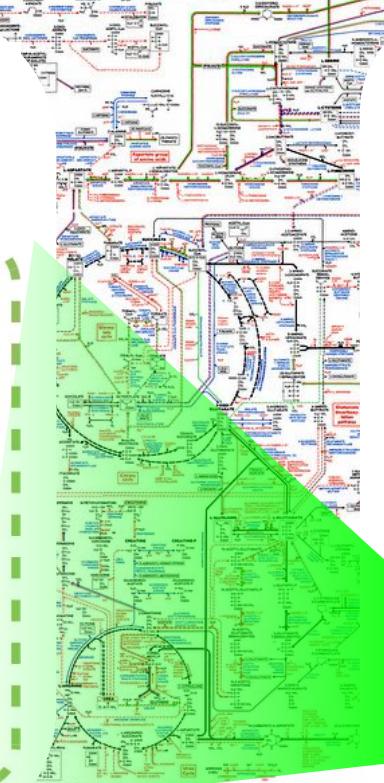
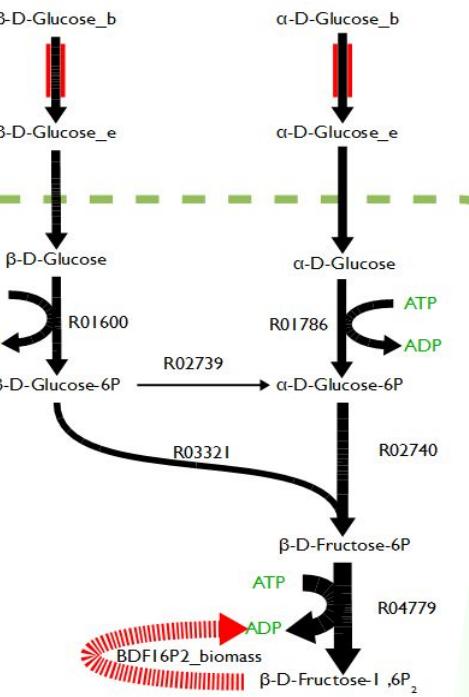
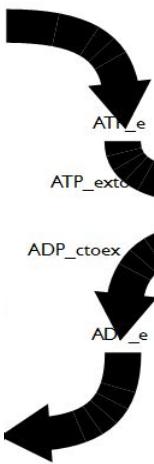
High performance screening:

- <2% false positives
- >10kb/second
- 50 bp minimum



All possible metabolic phenotypes How to use this knowledge?

FBA



○ ● ○ ... ○ ● C_{med}

Neural layer

○ ● ○ ... ○ ● V_{in}

Neural layer

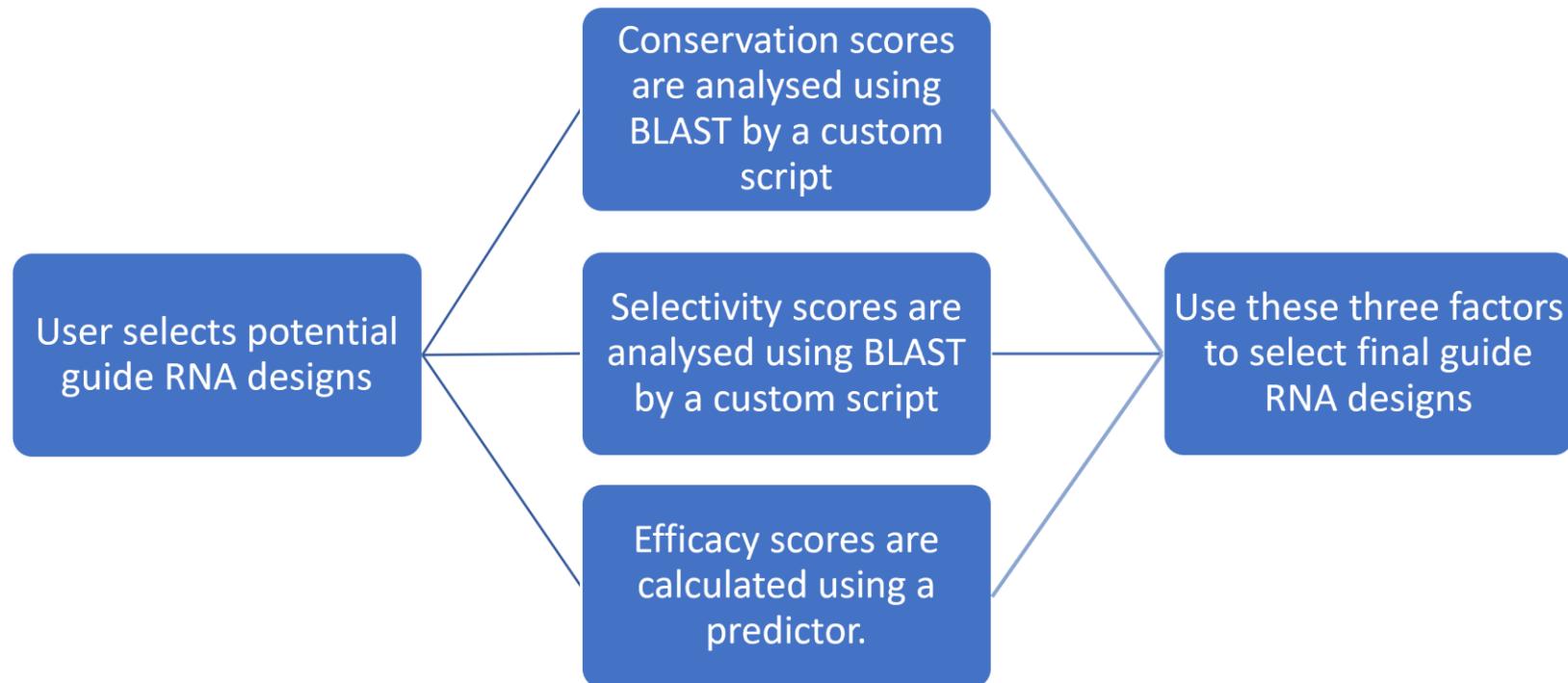
○ ● ○ ... ○ ● V_0

Mechanistic layer

○ ● ○ ... ○ ● V_f

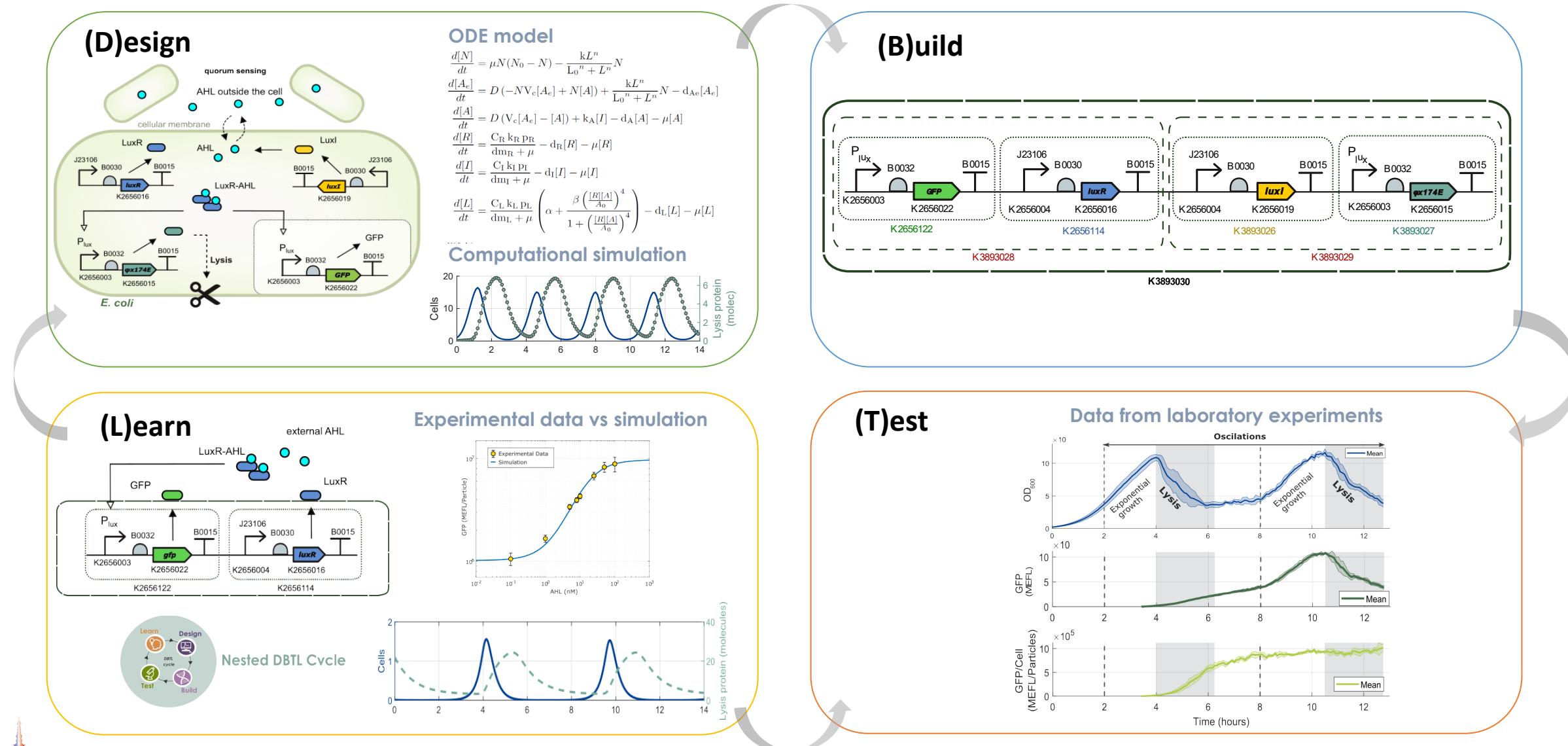
Developing a scoring system to optimise the design of CRISPR Cas12 diagnostics

Akashaditya Das, Ana Pascual Garrigos, Dr. Jennifer C Molloy, Dr. James W Ajioka



DBTL bioengineering cycle: developing a population oscillator

Andrés Arboleda-García, Iván Alarcon-Ruiz, Yadira Boada, Jesús Picó, Eloisa Jantus-Lewintre




Computer-aided enhancement of genetic design data

Matthew Crowther & Angel Goni-Moreno

Interdisciplinary Computing and Complex Biosystems (ICOS) Research Group - School of Computing Science

Centro de Biotecnología y Genómica de UPM-INIA/CSIC



Exploring advantages and limitation of discrete modeling of biological network motifs

- Convert ODEs to discrete model using defined rules
- Compare the simulation results between original and converted model
- Explore new logical rules in discrete modeling and apply this method to larger networks in the future

$$\frac{dS}{dt} = -k_b SI$$

$$\frac{dI}{dt} = k_b SI - k_g I$$

$$\frac{dR}{dt} = k_g I$$

Element	Positive	Negative
S		(S,I)
I	(S,I)	I
R	I	

Fig.2. Conversion for a basic disease outbreak model(SIR)

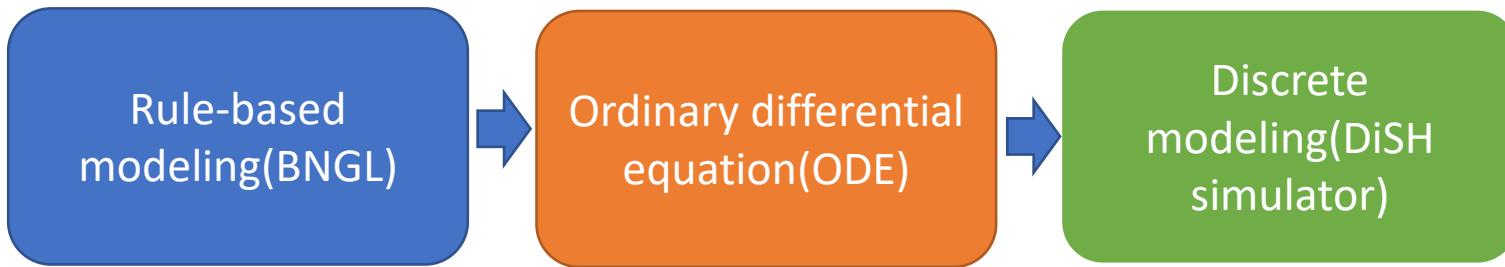


Fig.1. Conversion from BNGL model to discrete model

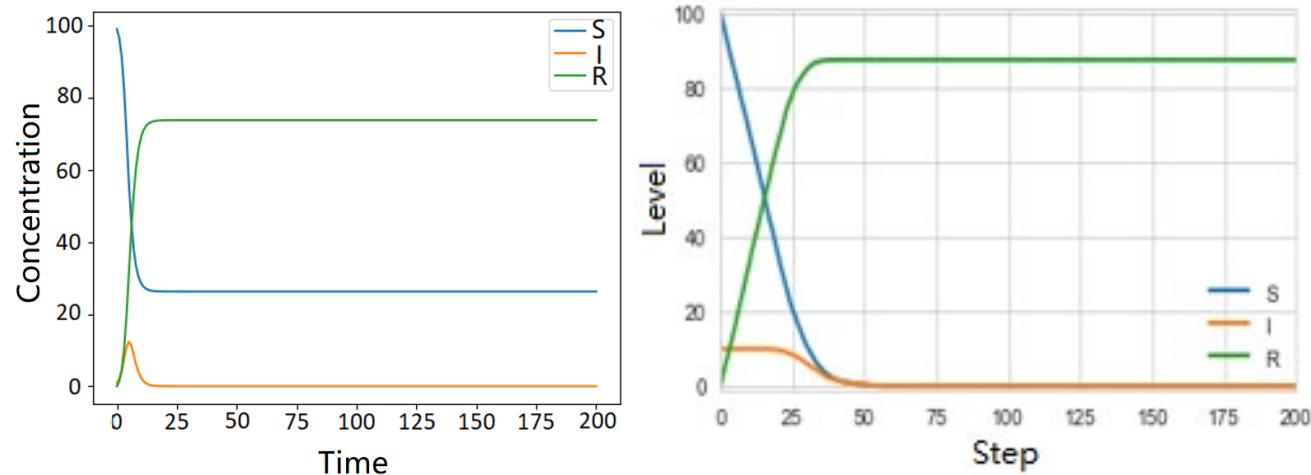
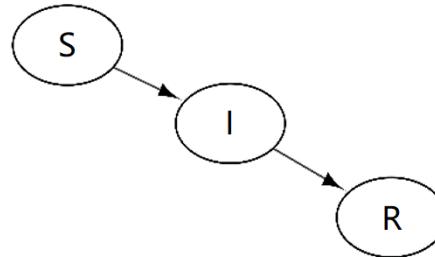


Fig.3. Simulation results for ODE and discrete modeling in SIR model

A Conceptual Interactive Microfluidic Design and Control Workflow

Grant #2211040

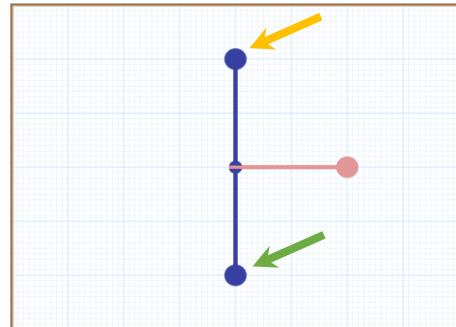
Yangruirui(Ron) Zhou, Douglas Densmore

Contact: yrrzhou@bu.edu

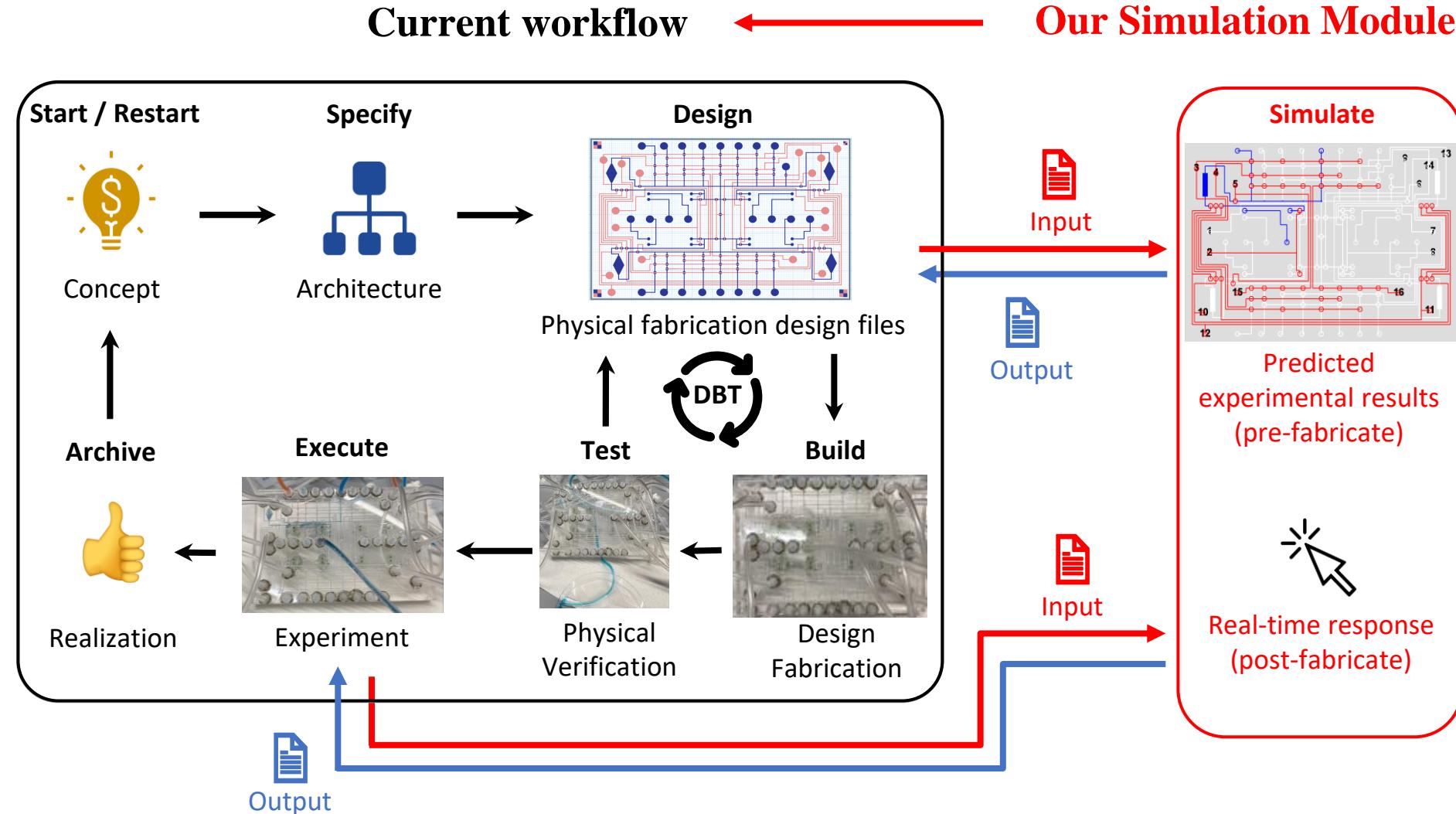
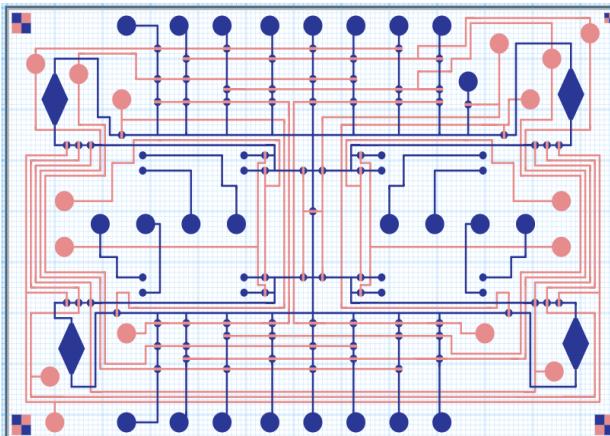
Biological Design Center, Boston University, Boston, Massachusetts, USA



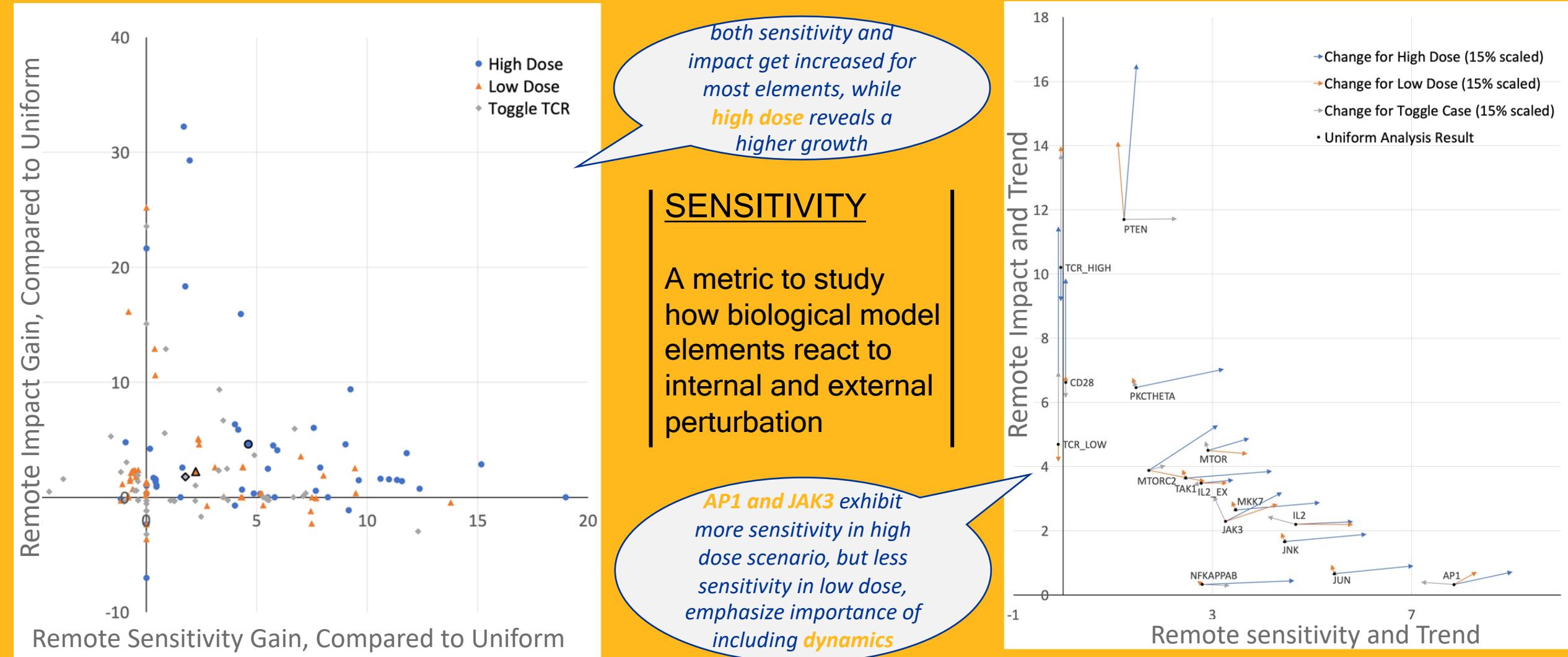
Left to right?
Boston to Paris?
(constraints: weather, transport,...)

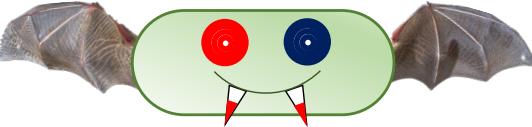


More Complex?
More Constraints?

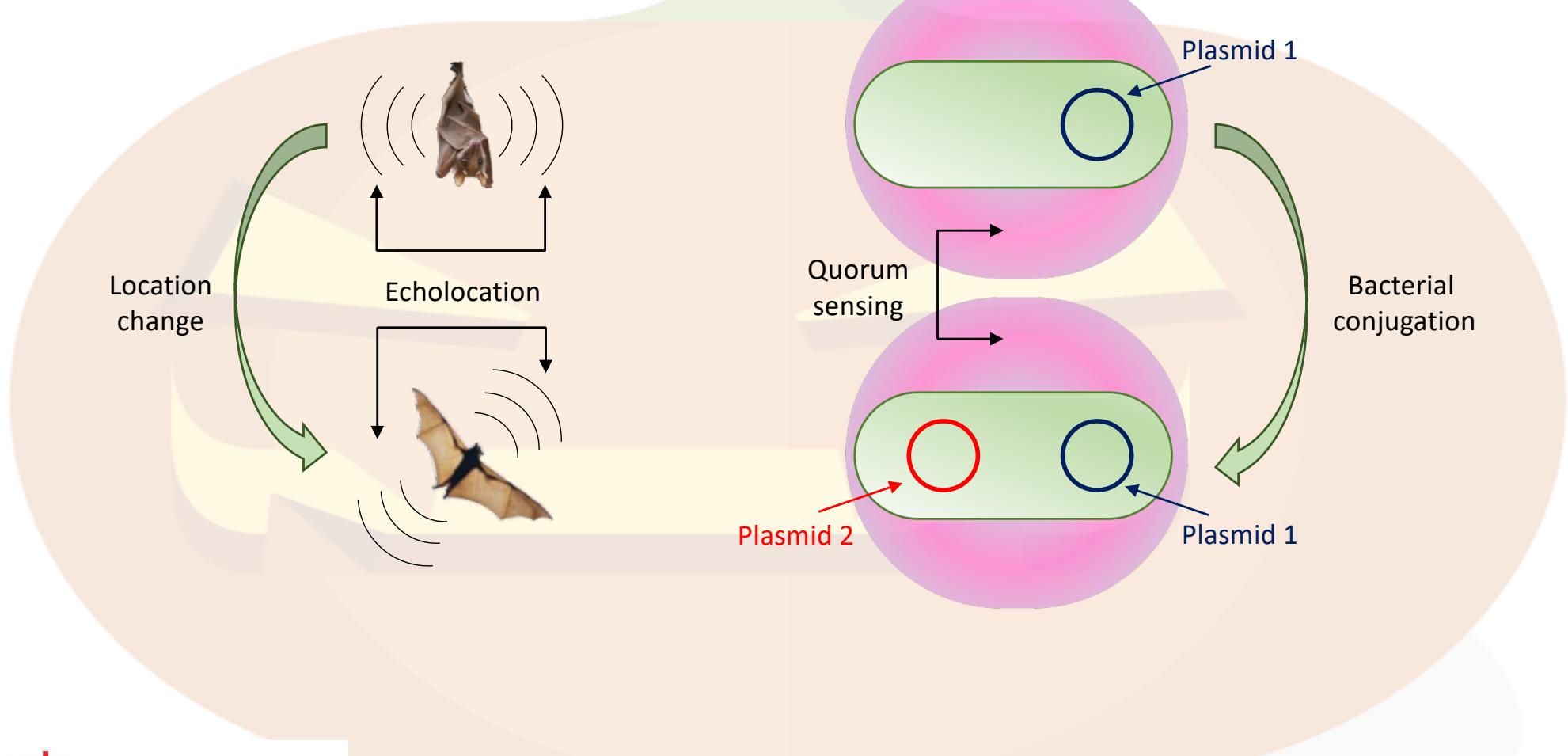
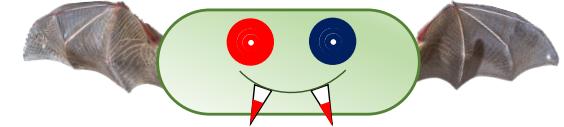


Dynamic Behavior Alters Influences and Sensitivities in Biological Networks





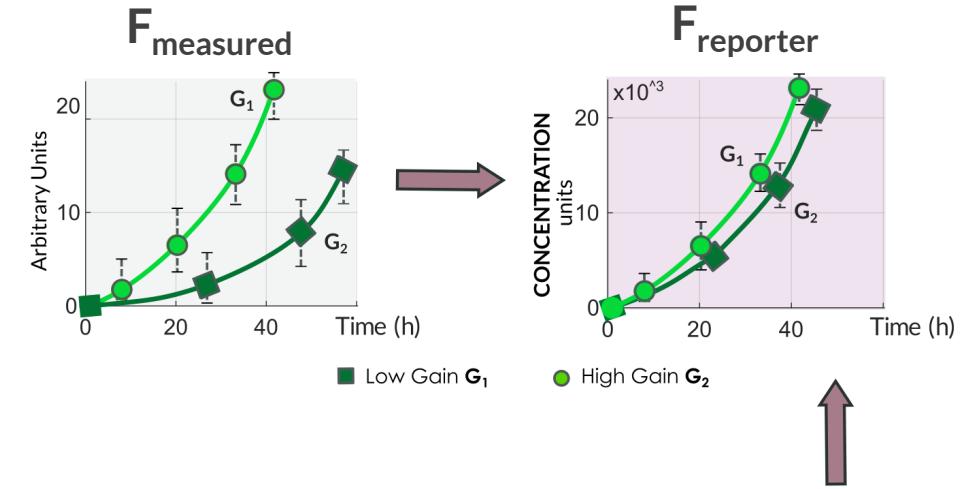
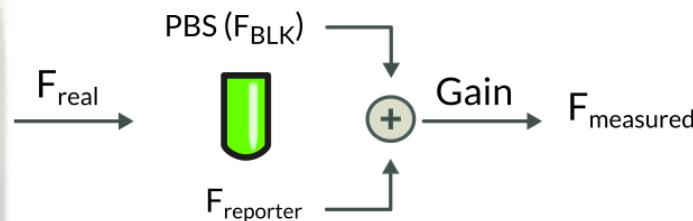
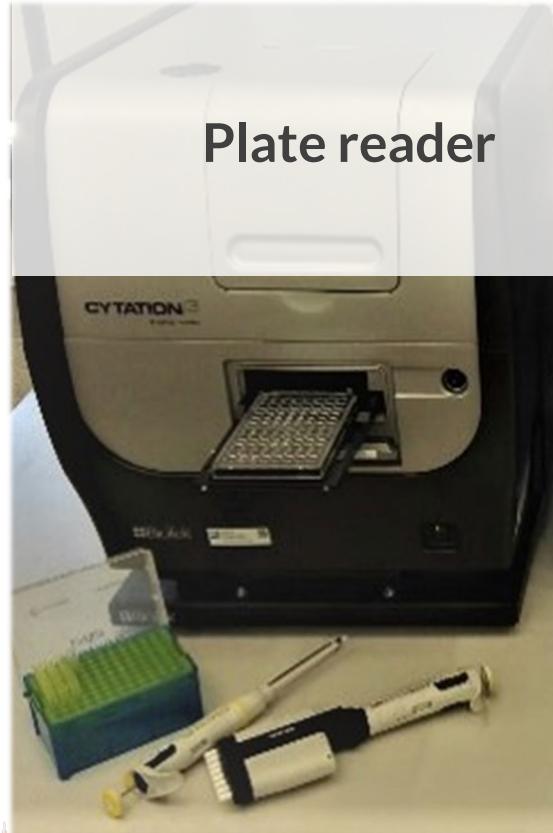
Bat algorithm for cells



PLATERO

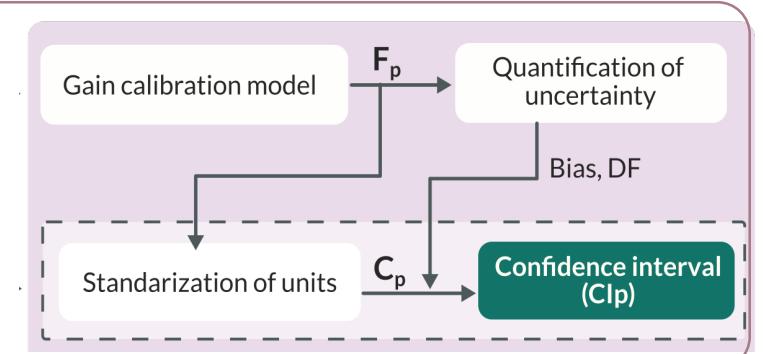
A Plate Reader Calibration Protocol to work with different instrument gains & asses measurement uncertainty

Yadira Boada, Alba González-Cebrián, Joan Borrás-Ferrís, Jesús Picó, Alberto Ferrer, Alejandro Vignoni

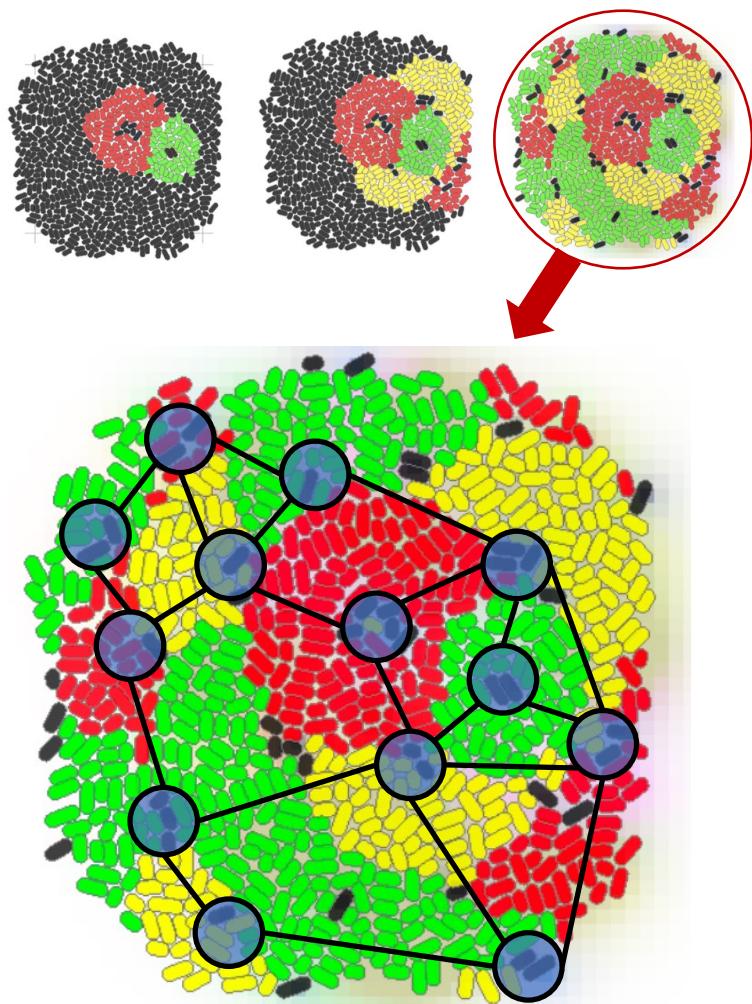


PLATERO MATLAB TOOLBOX:

- Measurements at **different gains compatible** between them, even in the same experiment
- Conversion Arbitrary to Concentration Units
- Analysis and prediction of uncertainty



Solving graph 3-coloring (gro remix version)



Algorithm

1. The circuit initiates by instantiating two leaders (cells) that are assigned different colors.
2. These cells emit QS signals to mark their color (node) zone and prohibit adjacent zones from using the same color.
3. A third color is assigned to a different leader adjacent to the previously selected ones (by choosing the color excluded by the other two signals), and in turn emits its own QS signals.
4. Leaders keep being chosen and assigned a color of which they do not receive signals, completing the colony coloring, and therefore, the graph coloring.

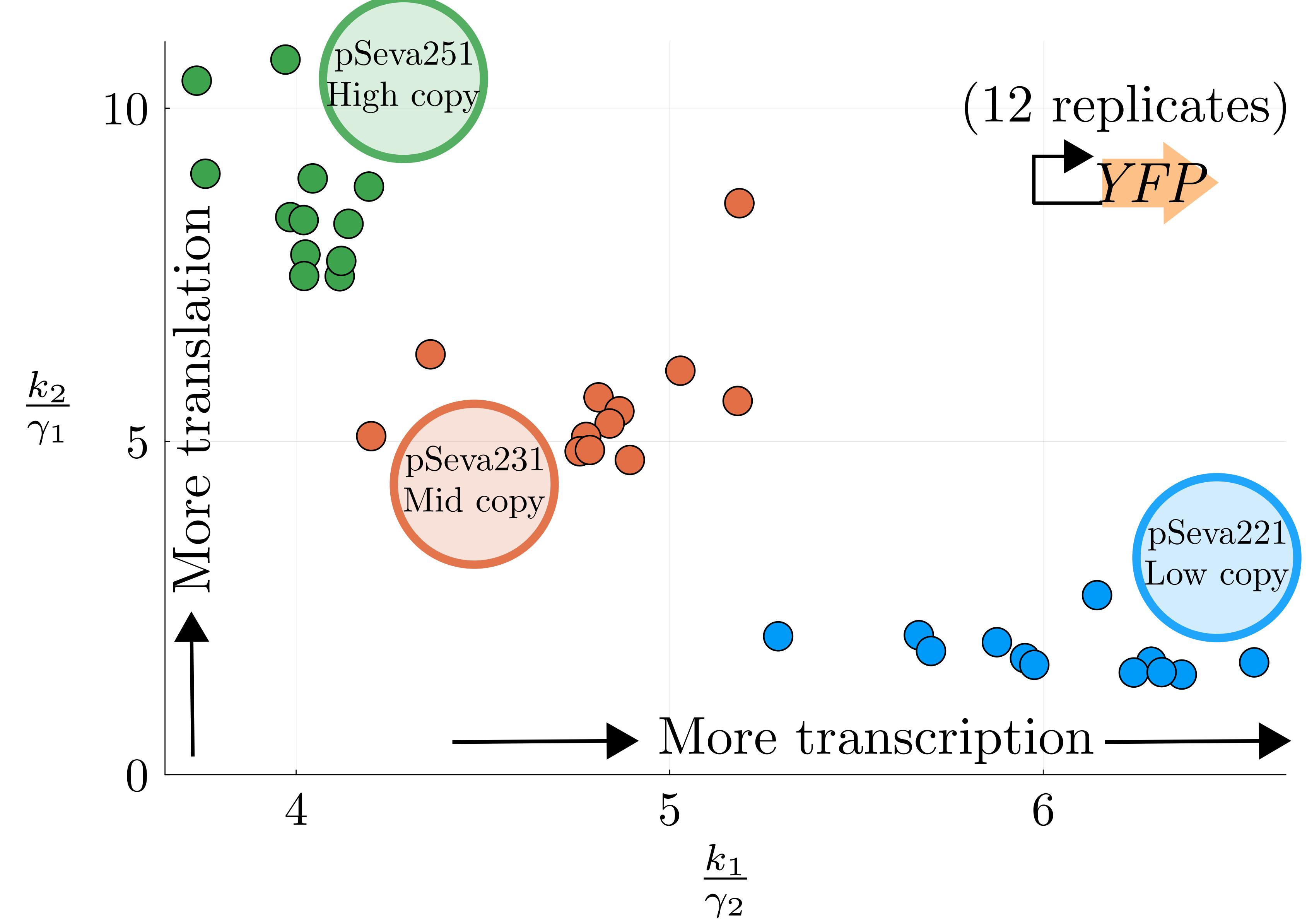
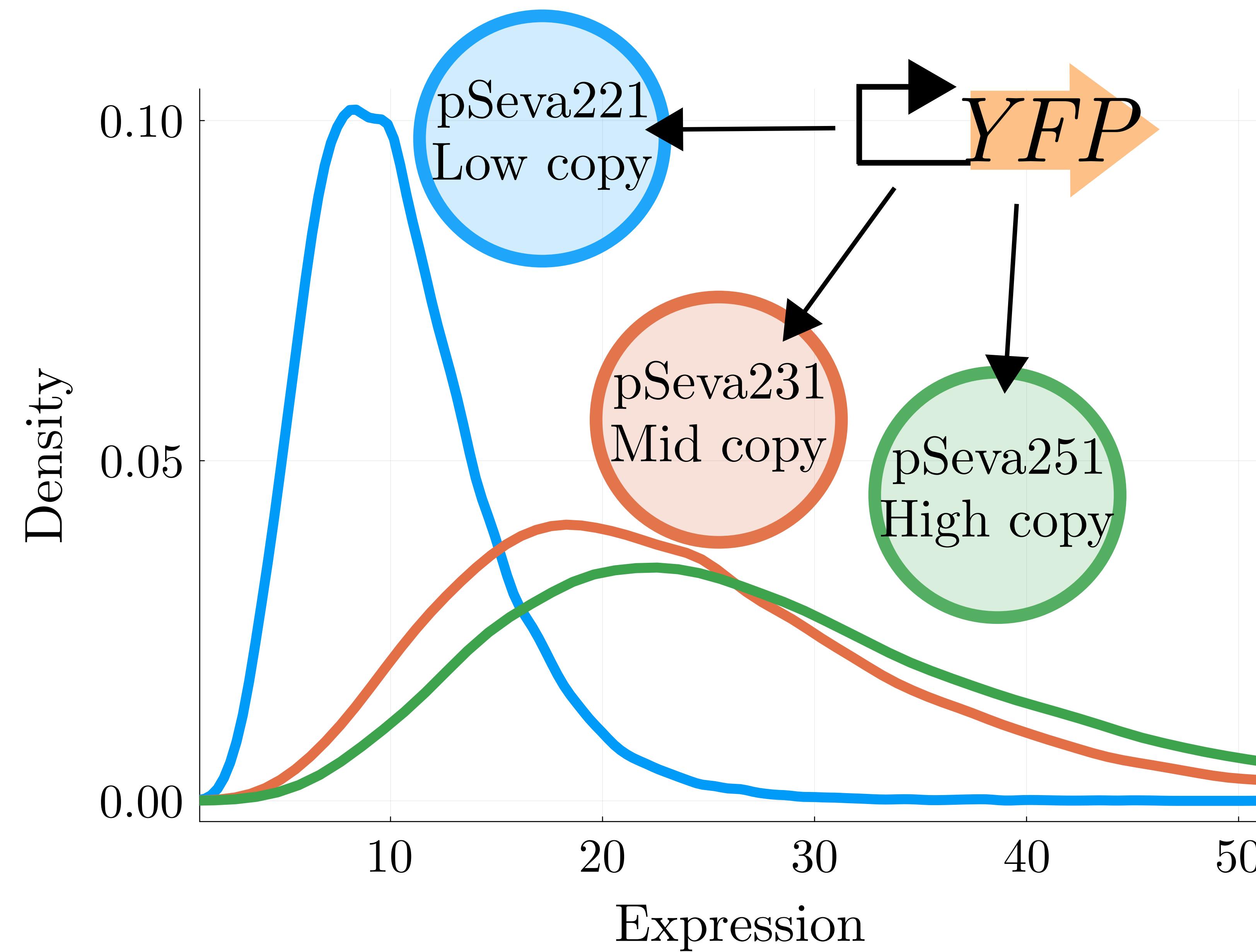
Probabilistic programming for synthetic gene networks

Lewis Grozinger (presenting)

Ángel Goñi-Moreno

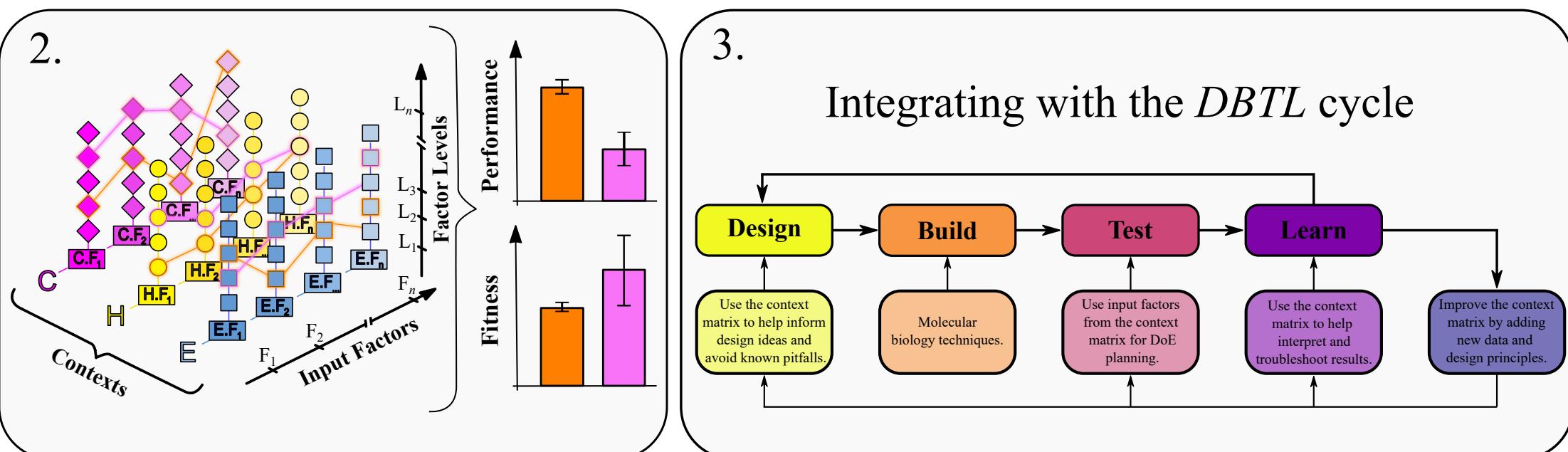
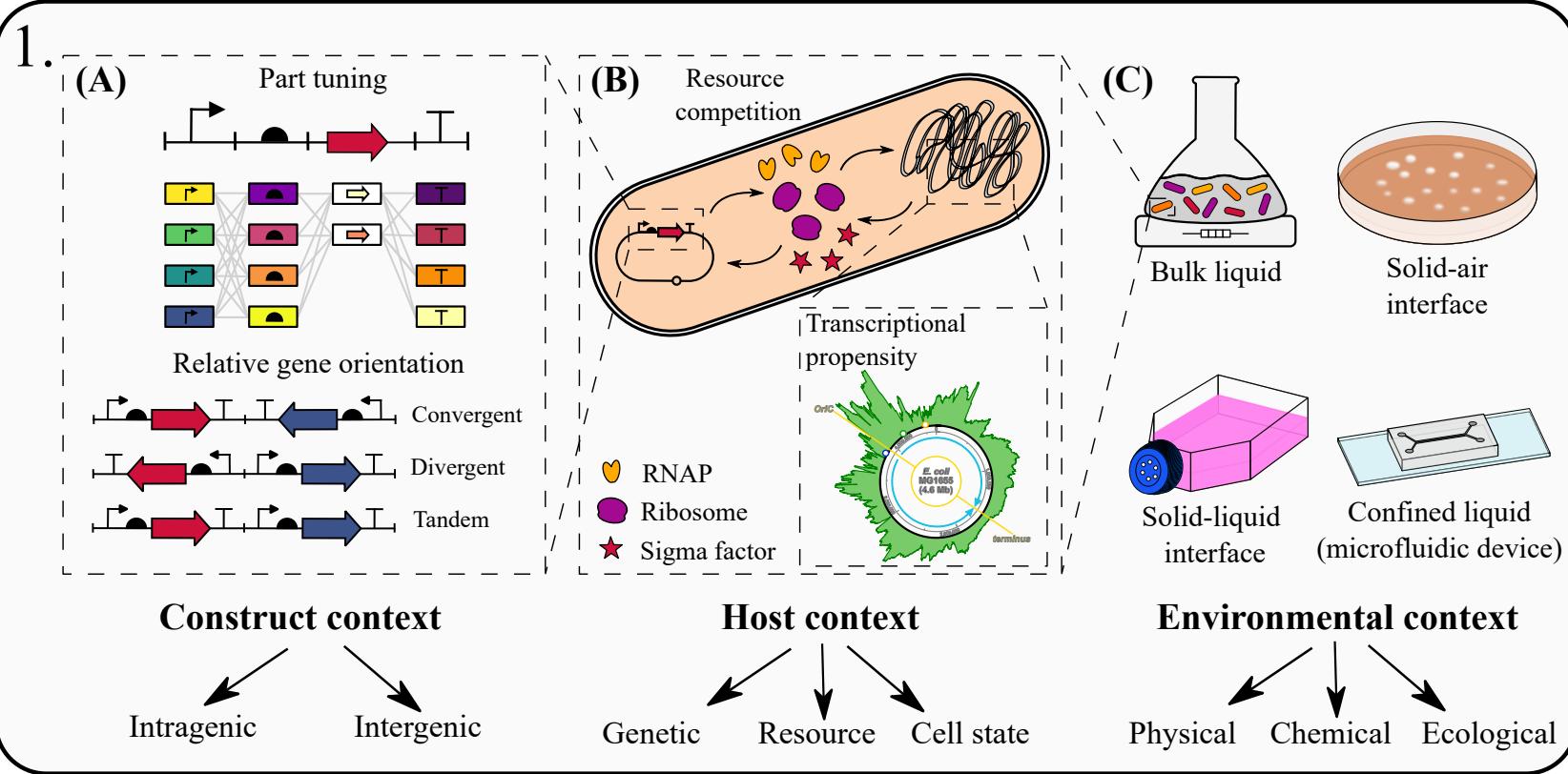
Monday 17:30-18:30
Poster 4102

Cytometry data from different contexts → reveals their effects via probabilistic models



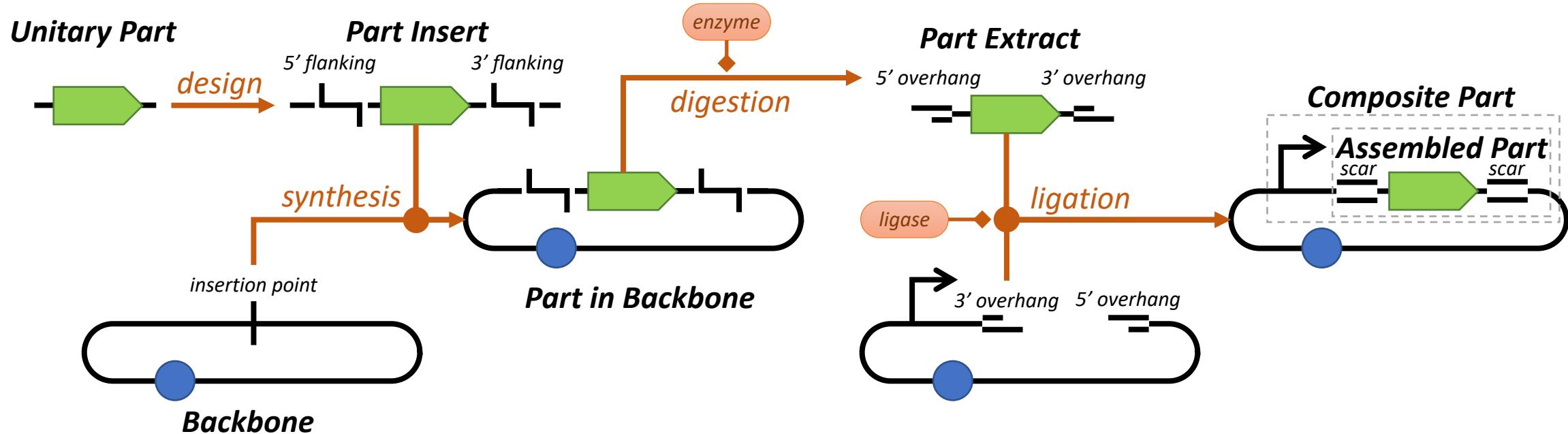
with the goal of using this knowledge in automated design of genetic networks

Towards a framework for context-aware synthetic biology



Standardizing the Representation of Parts and Devices for Build Planning

Jacob Beal, Vinoo Selvarajah, Gael Chambonnier, Traci Haddock-Angelli, Alejandro Vignoni, Gonzalo Vidal, Nicholas Roehner



Standard vocabulary and SBOL representation for digestion/ligation build plans