

Engineering Self-Organization: From Networking to Synthetic Biology

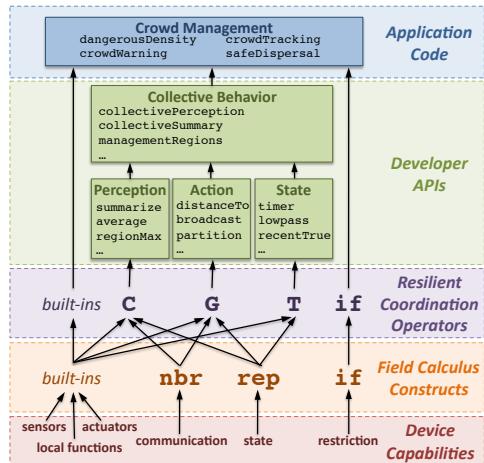
Jacob Beal

Dagstuhl Seminar 15402:
Self-assembly and Self-
organization in Computer
Science and Biology
September, 2015

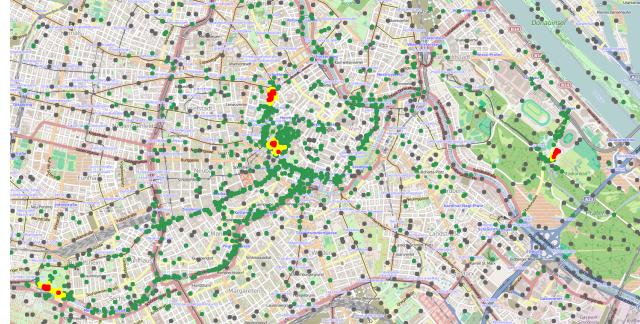
Engineering Aggregates

Aggregate Programming

Field Calculus, Spatial Computing



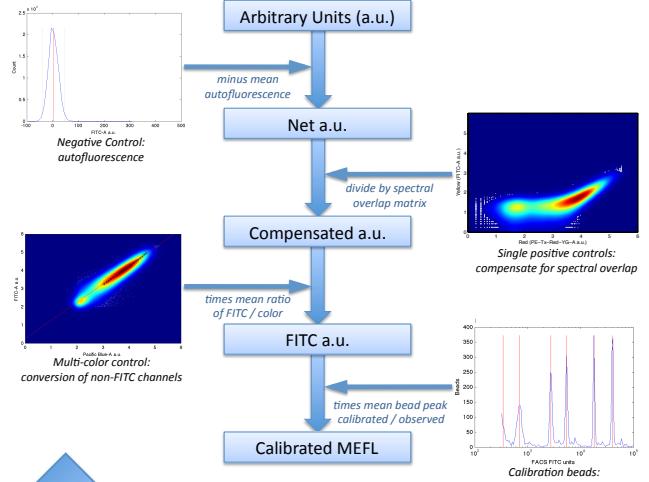
Resilient Networking



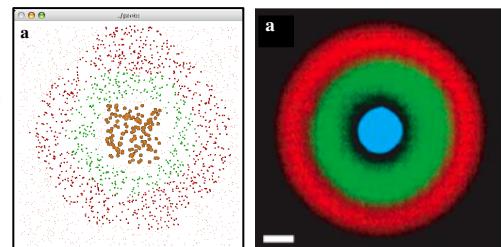
Beal et al., Computer, 2015,
Beal & Bachrach, IEEE Int.Sys. 2006,
Beal & Bachrach, SCW, 2008

Synthetic Biology Analytics & Design

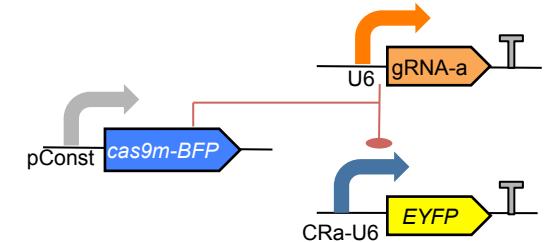
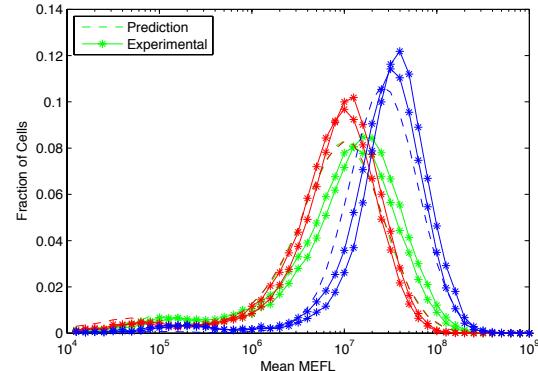
Calibrated Flow Cytometry



Spatial Patterning



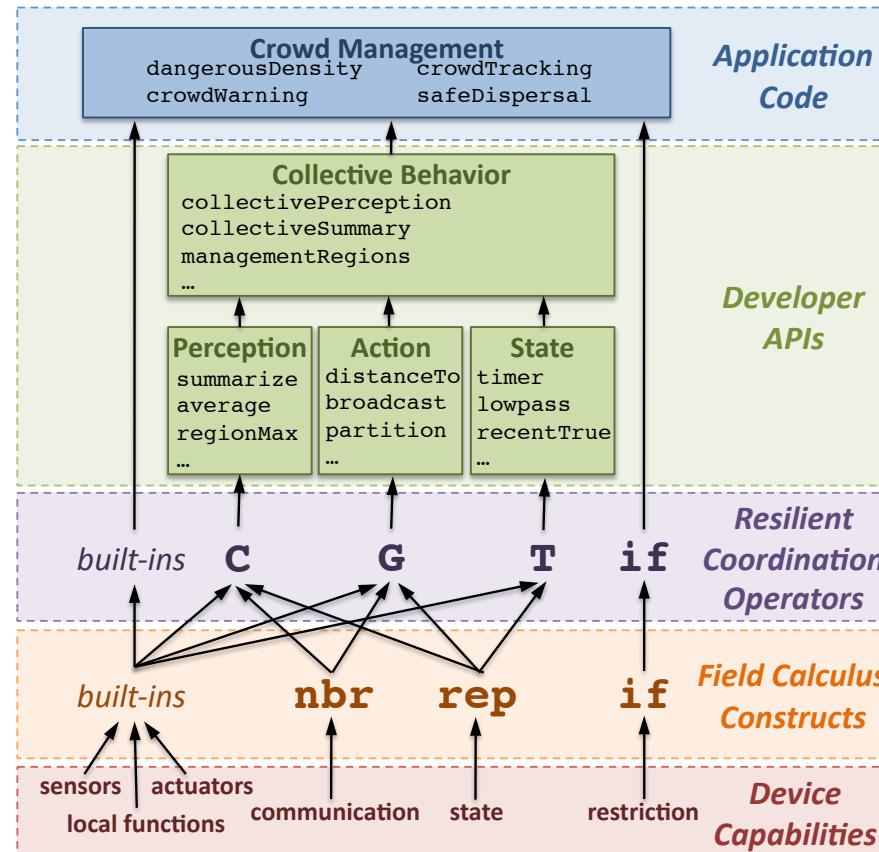
Precision Organism Engineering High-Performance Devices



Kiani et al., Nat. Meth., 2014,
Beal et al., ACS Syn.Bio., 2012,
Beal et al., ACS Syn.Bio., 2014

Aggregate Programming

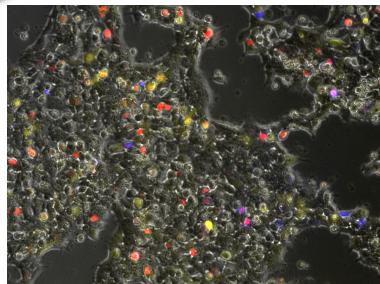
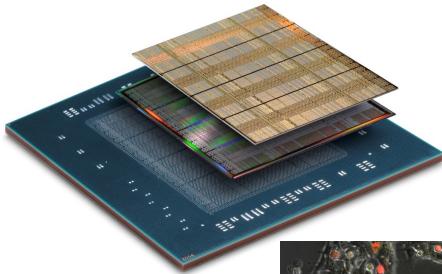
Restrict your development environment...



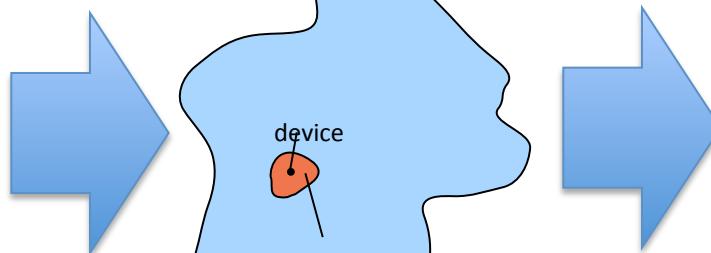
... to contain only resilient distributed systems.

Dealing with challenging platforms

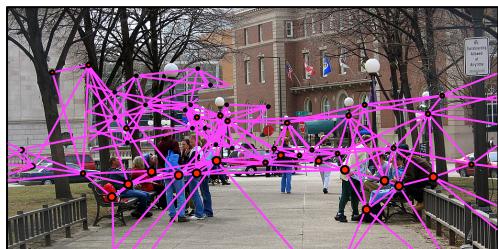
Emerging Computational Platforms



Computational Field Programming Models

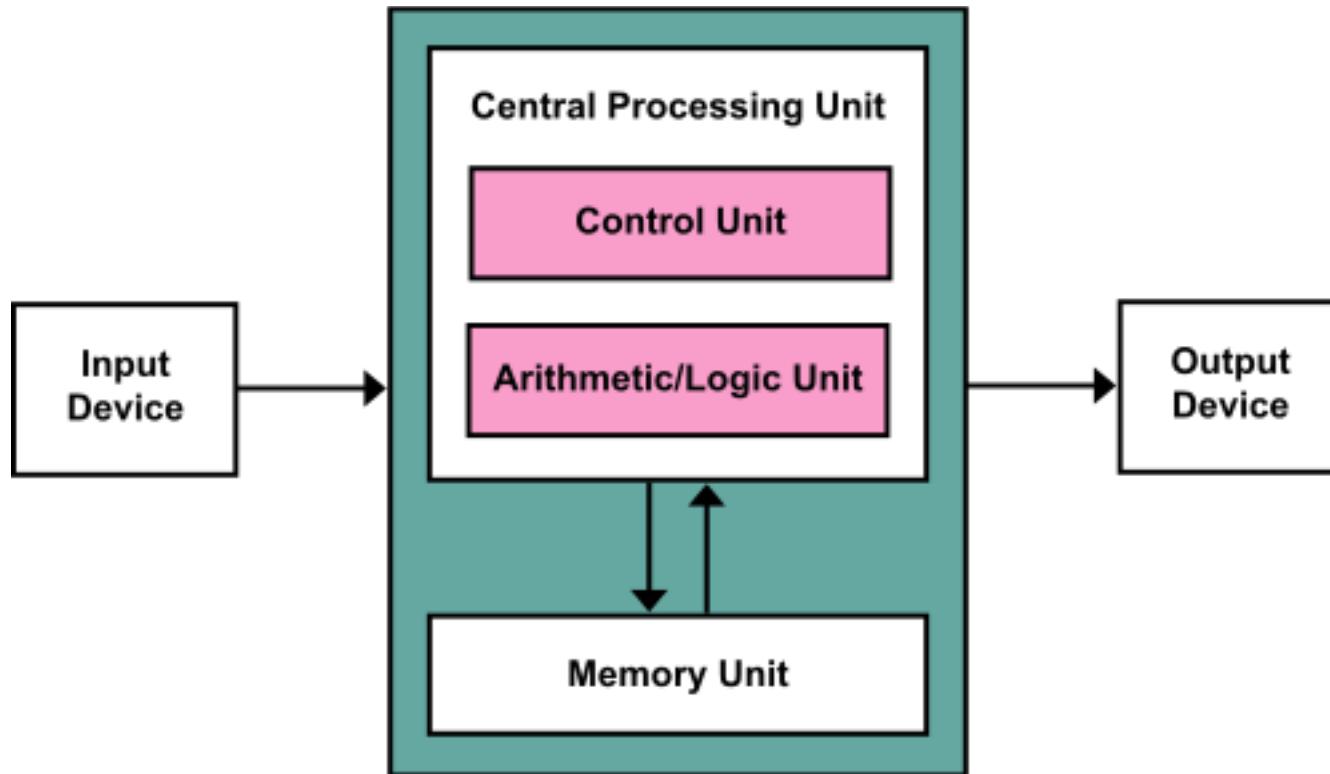


Inherently Resilient Distributed Systems



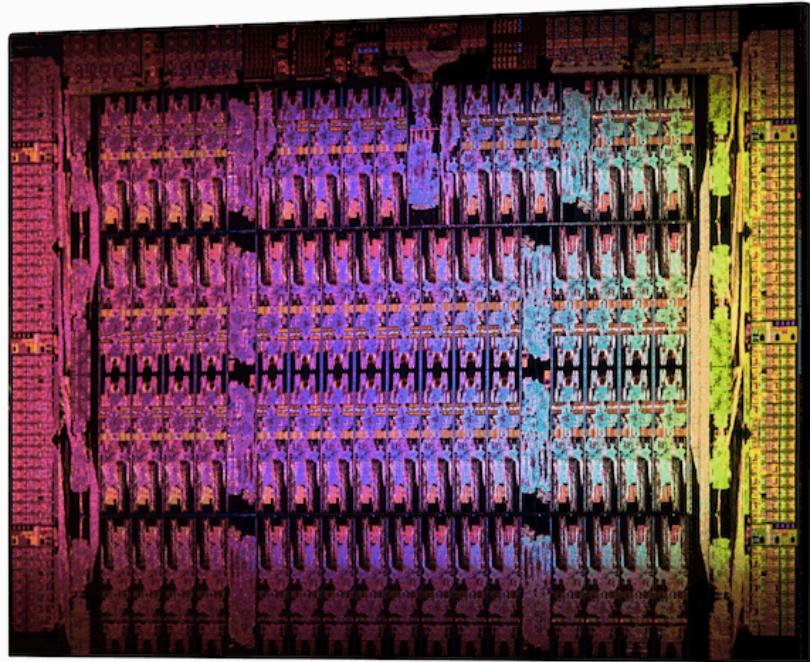
Pay a little efficiency, get a lot of programmability and resilience

Traditional Monolithic Computing

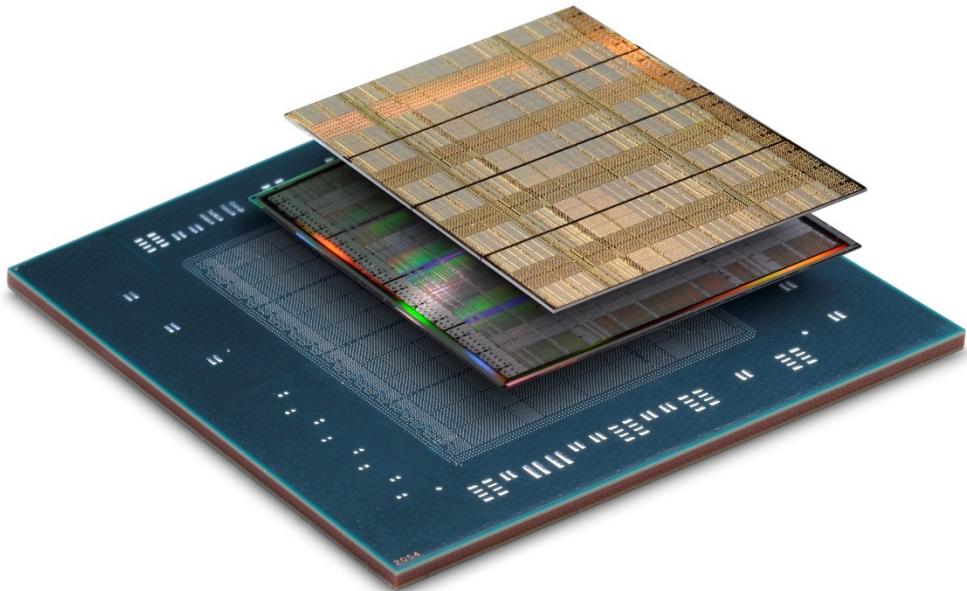


*The venerable von Neumann model is
breaking down in several ways...*

The End of Moore's Law



Intel Xeon Phi: 61 cores



Xilinx Virtex-7: 2M Logic cells

High-performance computing = mesh

Networked Devices Everywhere

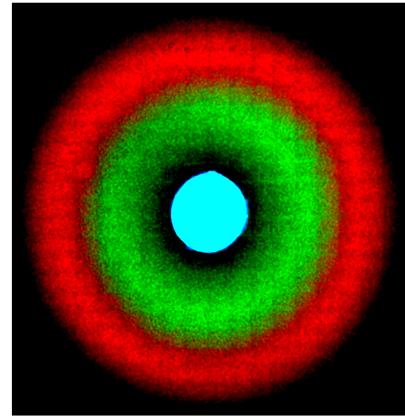


New Computational Materials

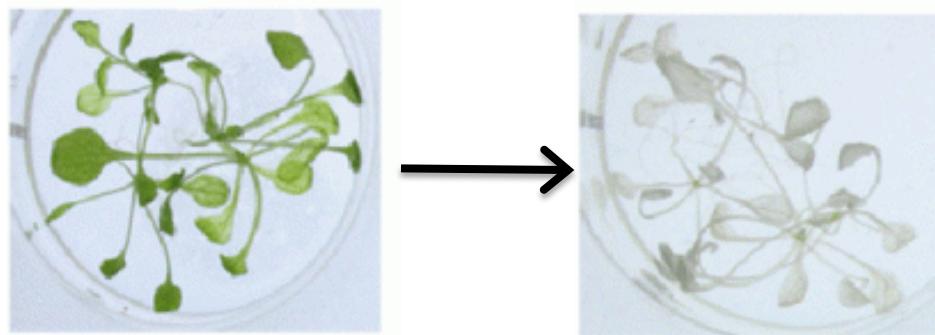
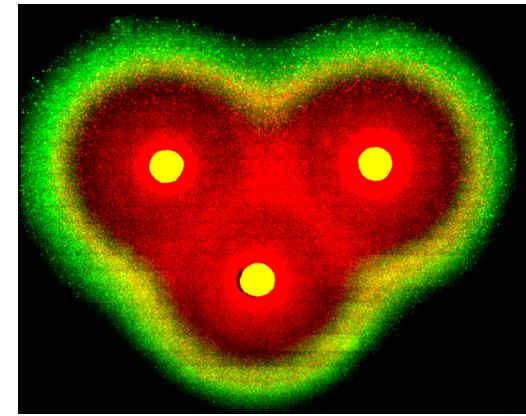
- Synthetic Biology:



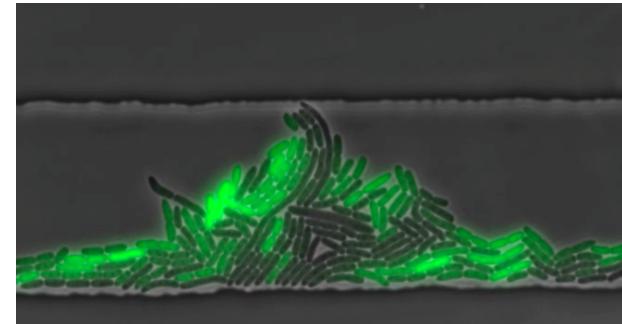
[Levskaya]



[Weiss]



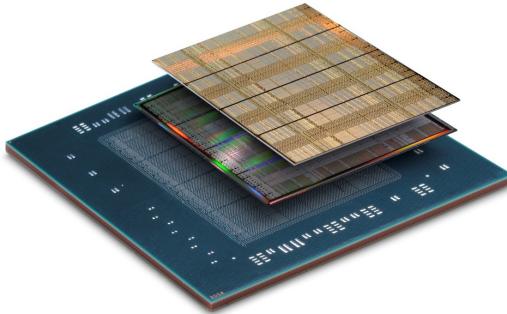
[Medford]



[Hasty]

Other emerging areas too, including nanoassembly, active materials...

Fundamentally different models



Isolate Systems
Extremely High FLOPs



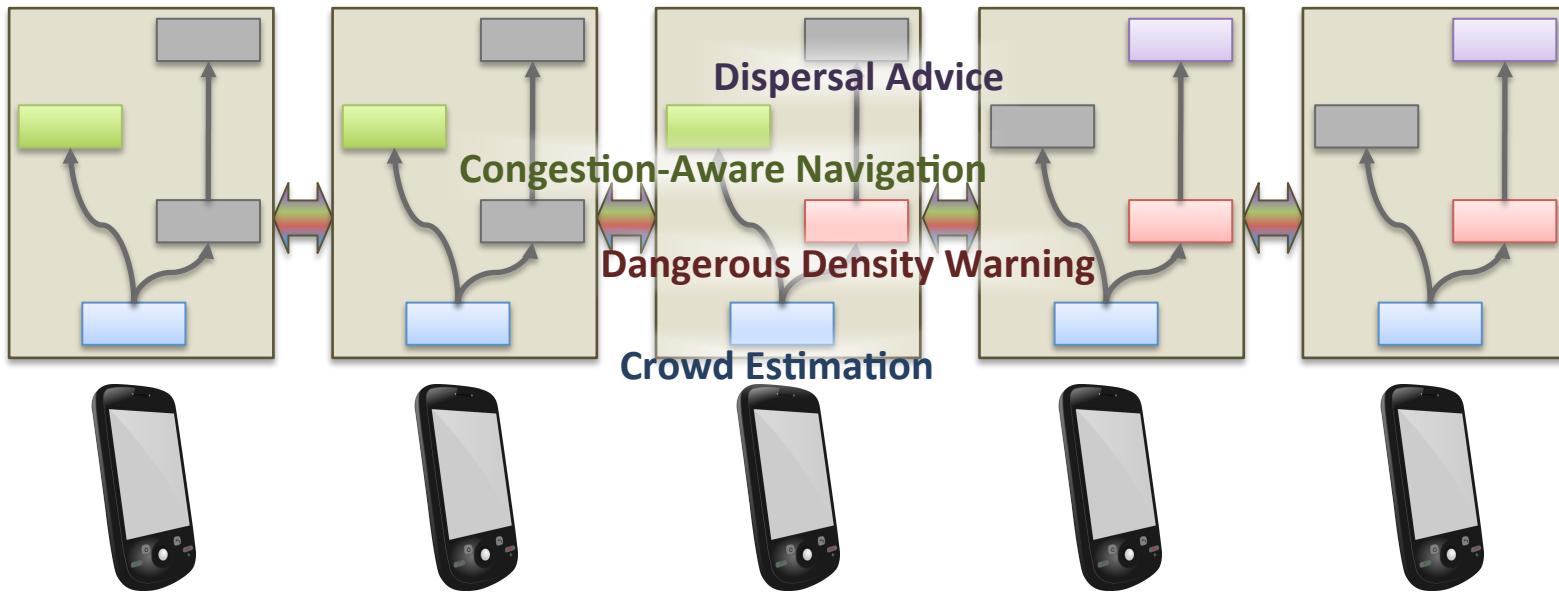
High Dispersion
Moderate FLOPs



High Resolution Sense/Act
Abysmal FLOPs

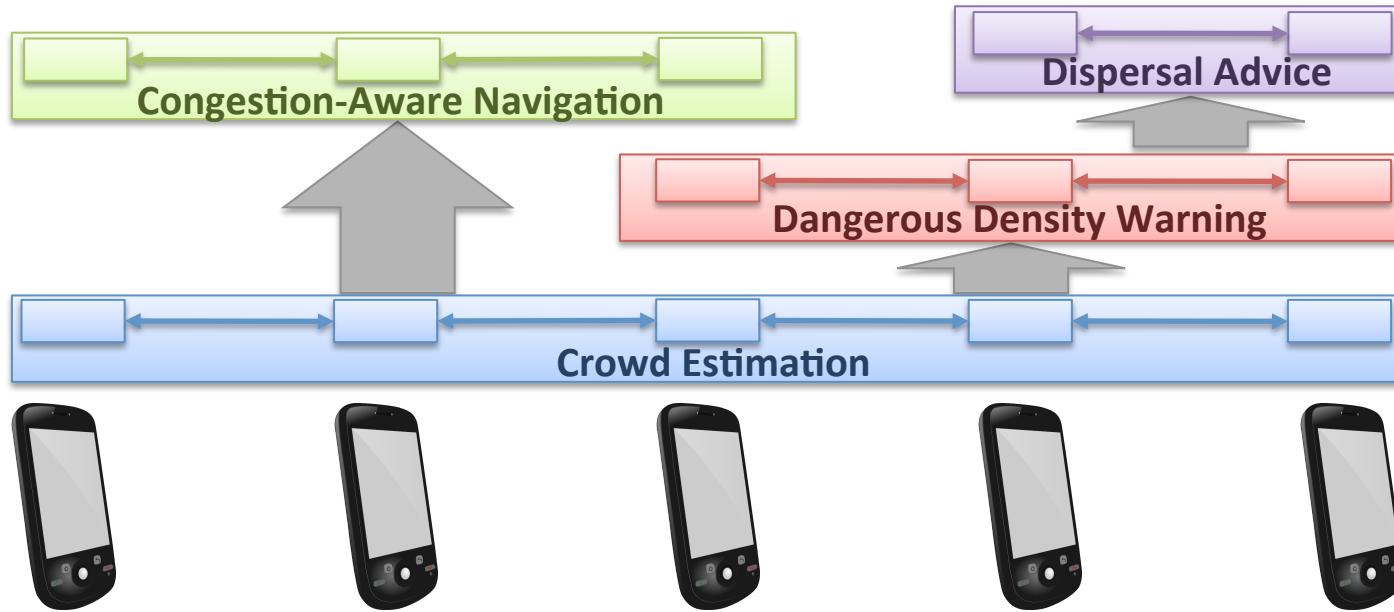
*How can we program aggregates adaptively & efficiently?
Are there commonalities that cross substrates?*

Device-Centric Programming



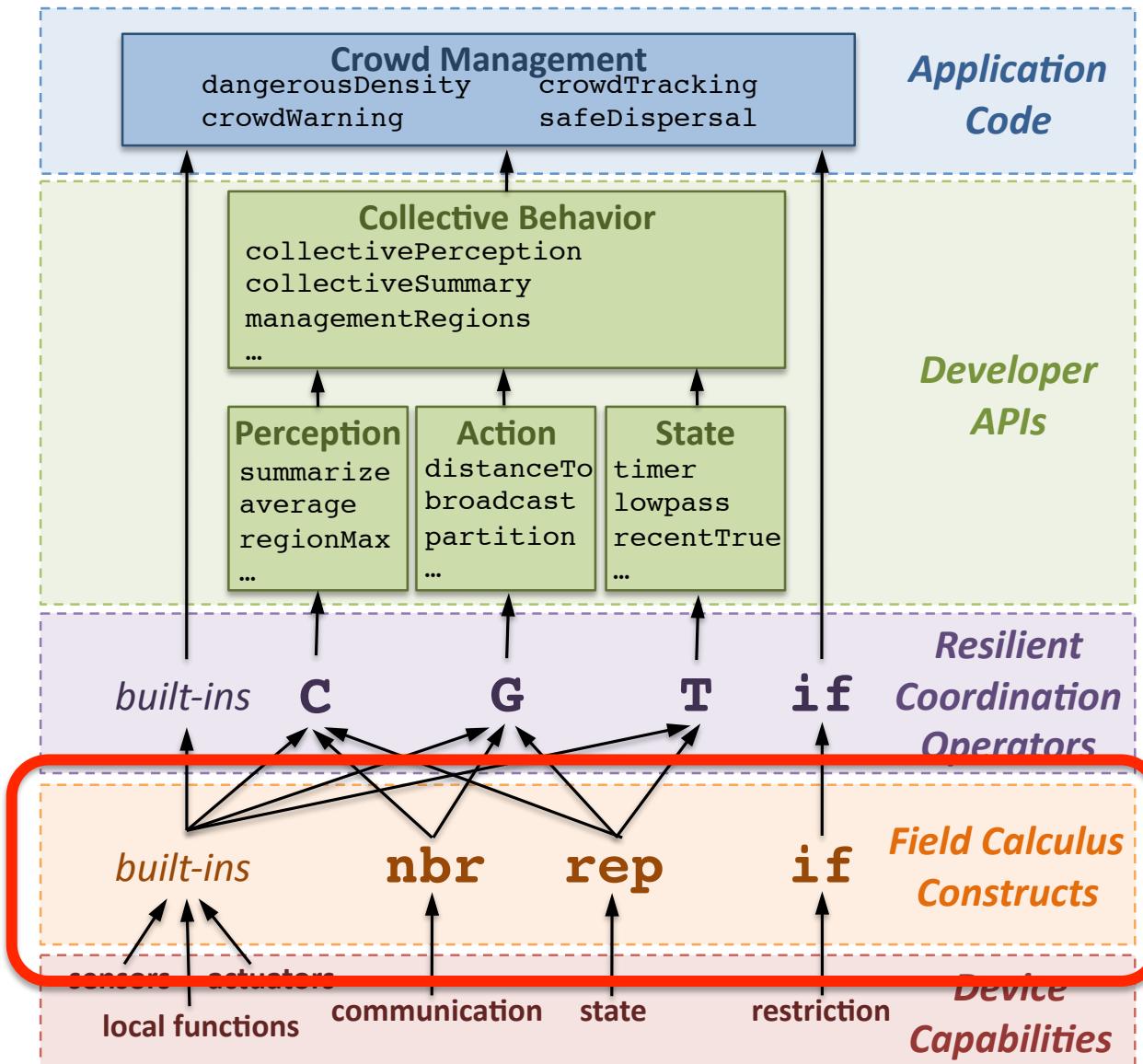
- Explicit design of adaptation and communication
- Complex per-device multi-service application
- Intractable to ensure correct behavior

Aggregate Programming

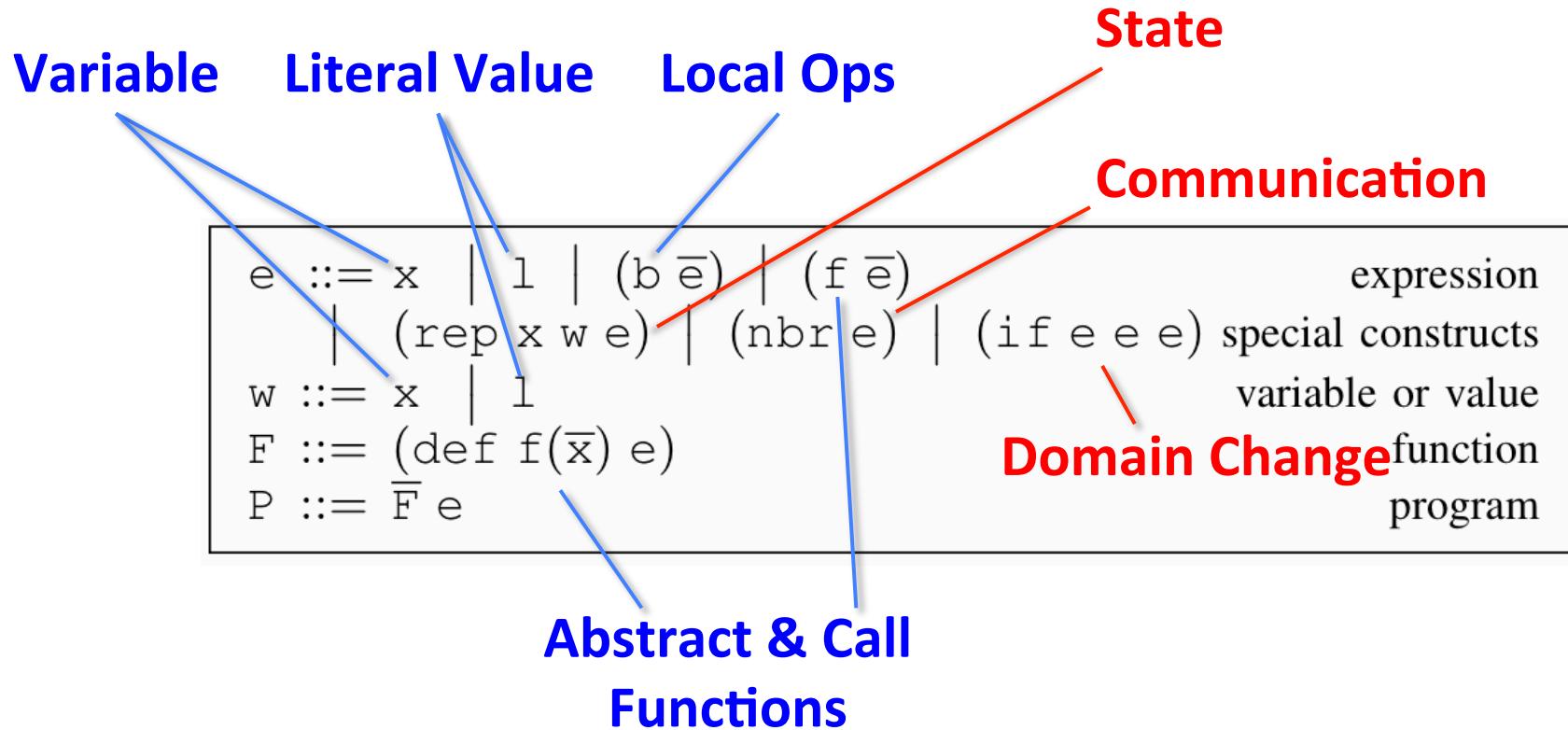


- Implicit adaptation and communication
- Code each collective service independently
- Compose via scope and information flow

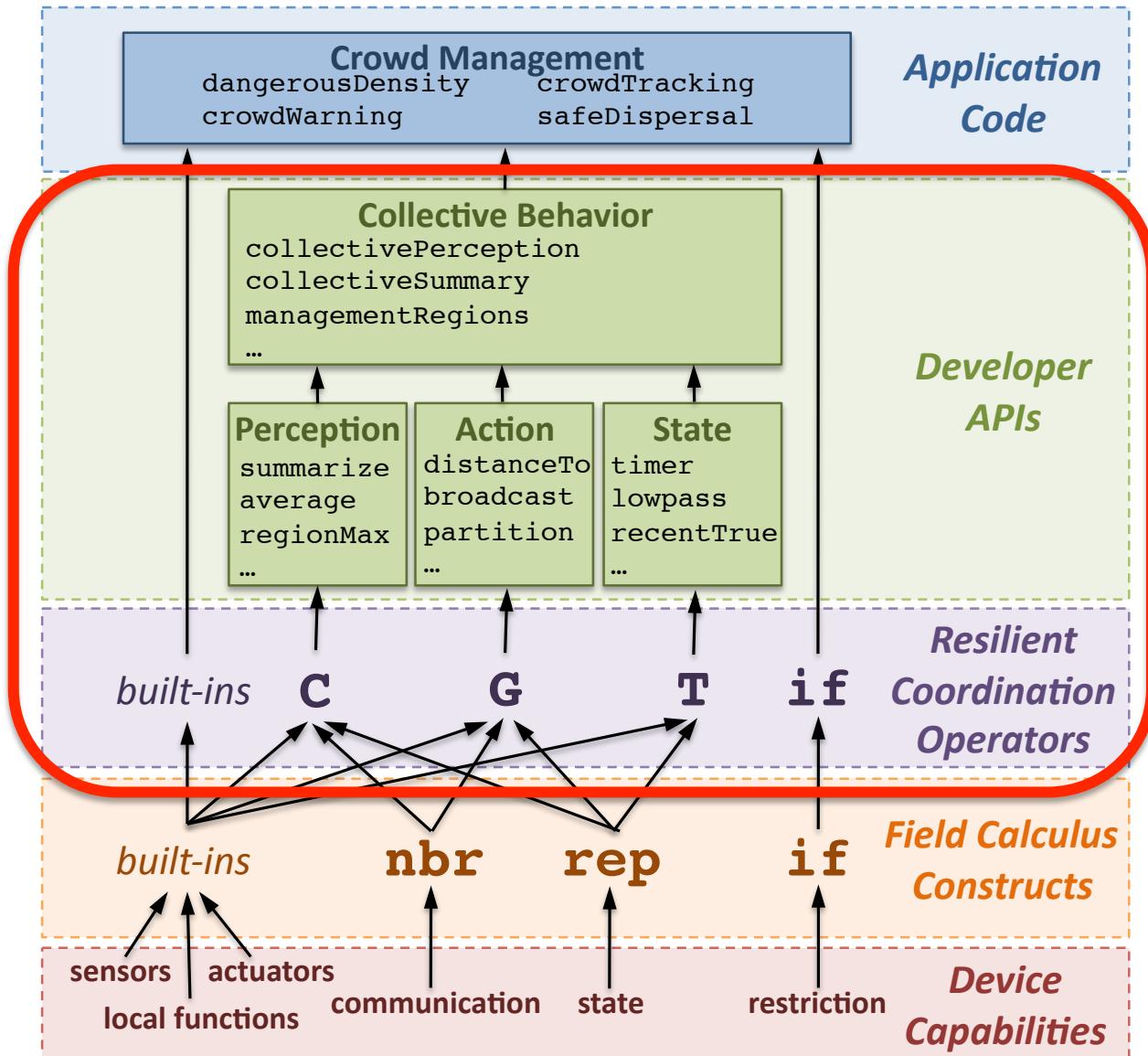
Aggregate Programming Stack



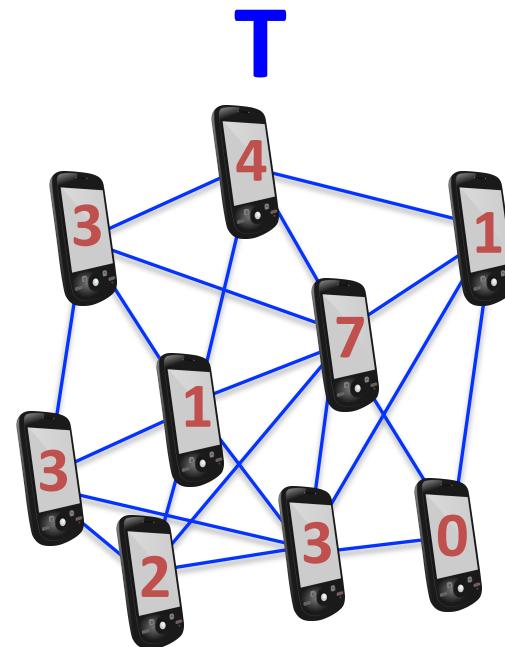
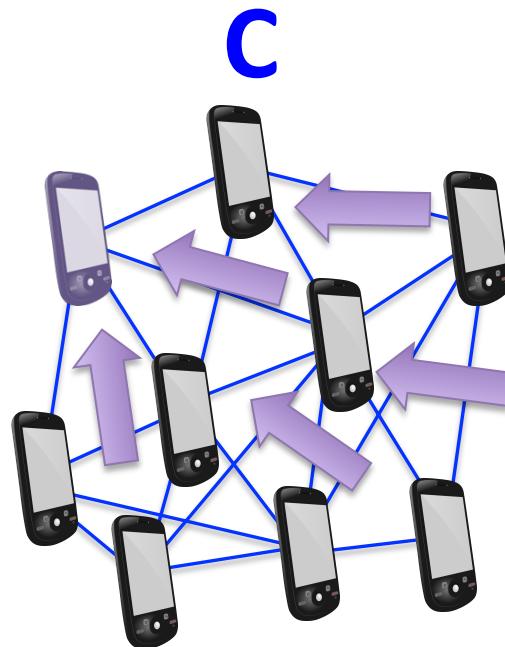
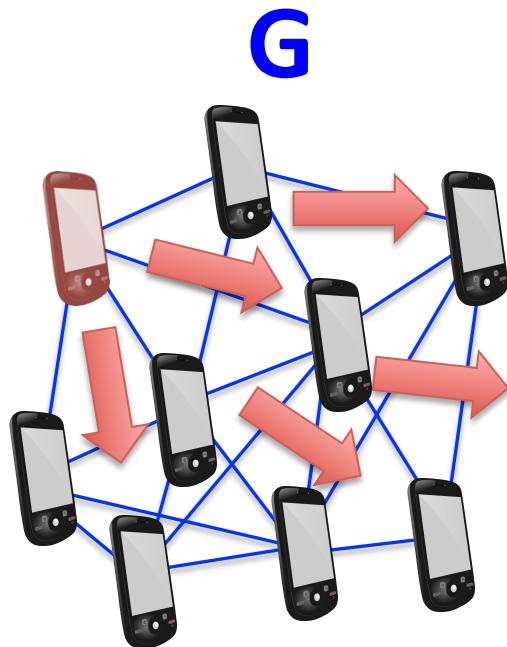
Field Calculus



Aggregate Programming Stack



Self-Stabilizing Building Blocks



Information spreading Information collection Short-term memory

Resilience by construction: all programs from these building blocks are also self-stabilizing!

Applying building blocks:

Example API algorithms from building blocks:

distance-to (source)	max-likelihood (source p)
broadcast (source value)	path-forecast (source obstacle)
summarize (sink accumulate local null)	average (sink value)
integral (sink value)	region-max (sink value)
timer (length)	limited-memory (value timeout)
random-voronoi (grain metric)	group-size (region)
broadcast-region (region source value)	recent-event (event timeout)
distance-avoiding-obstacles (source obstacles)	

Since based on these building blocks, all programs built this way are self-stabilizing!

Complex Example: Crowd Management

```
(def crowd-tracking (p)
  ;; Consider only Fruin LoS E or F within last minute
  (if (recently-true (> (density-est p) 1.08) 60)
    ;; Break into randomized "cells" and estimate danger of each
    (+ 1 (dangerous-density (sparse-partition 30) p))
    0))

(def recently-true (state memory-time)
  ;; Make sure first state is false, not true...
  (rt-sub (not (T 1 1)) state memory-time))
(def rt-sub (started s m)
  (if state 1 (limited-memory s m)))

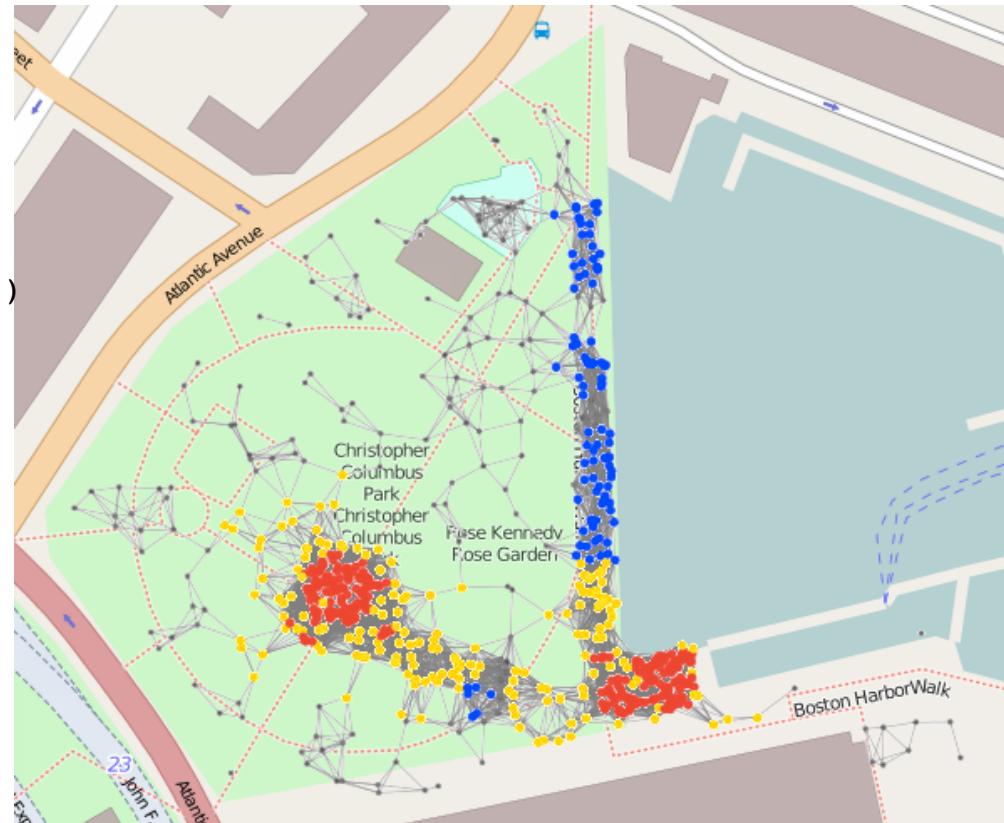
(def dangerous-density (partition p)
  ;; Only dangerous if above critical density threshold...
  (and
    (> (average partition (density-est p)) 2.17)
    ;; ... and also involving many people.
    (> (summarize partition + (/ 1 p) 0) 300)))
```

*18 lines non-whitespace code
10 library calls (21 ops)*

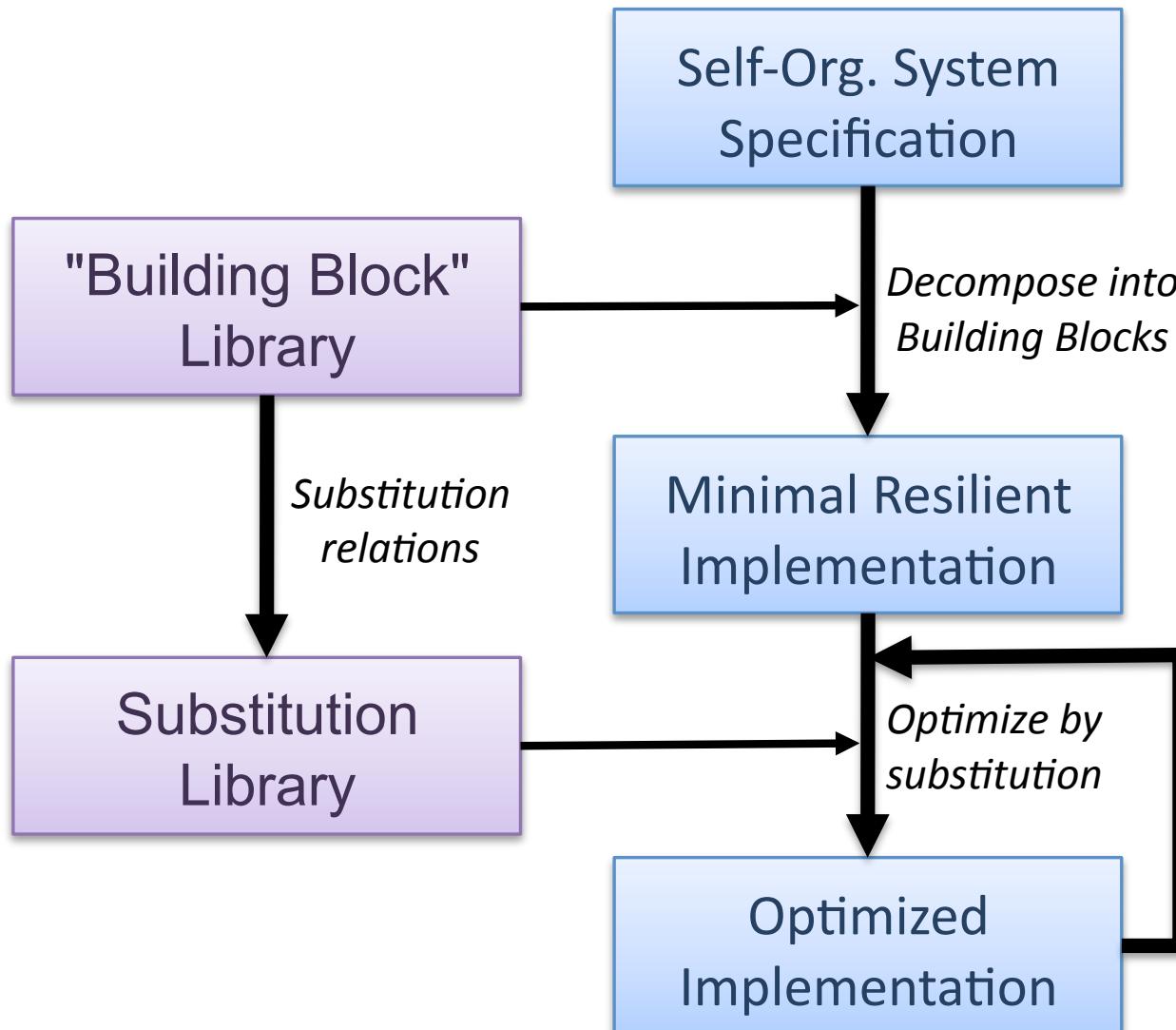
IF: 3 G: 11 C: 4 T: 3

```
(def crowd-warning (p range)
  (> (distance-to (= (crowd-tracking p) 2))
      range))

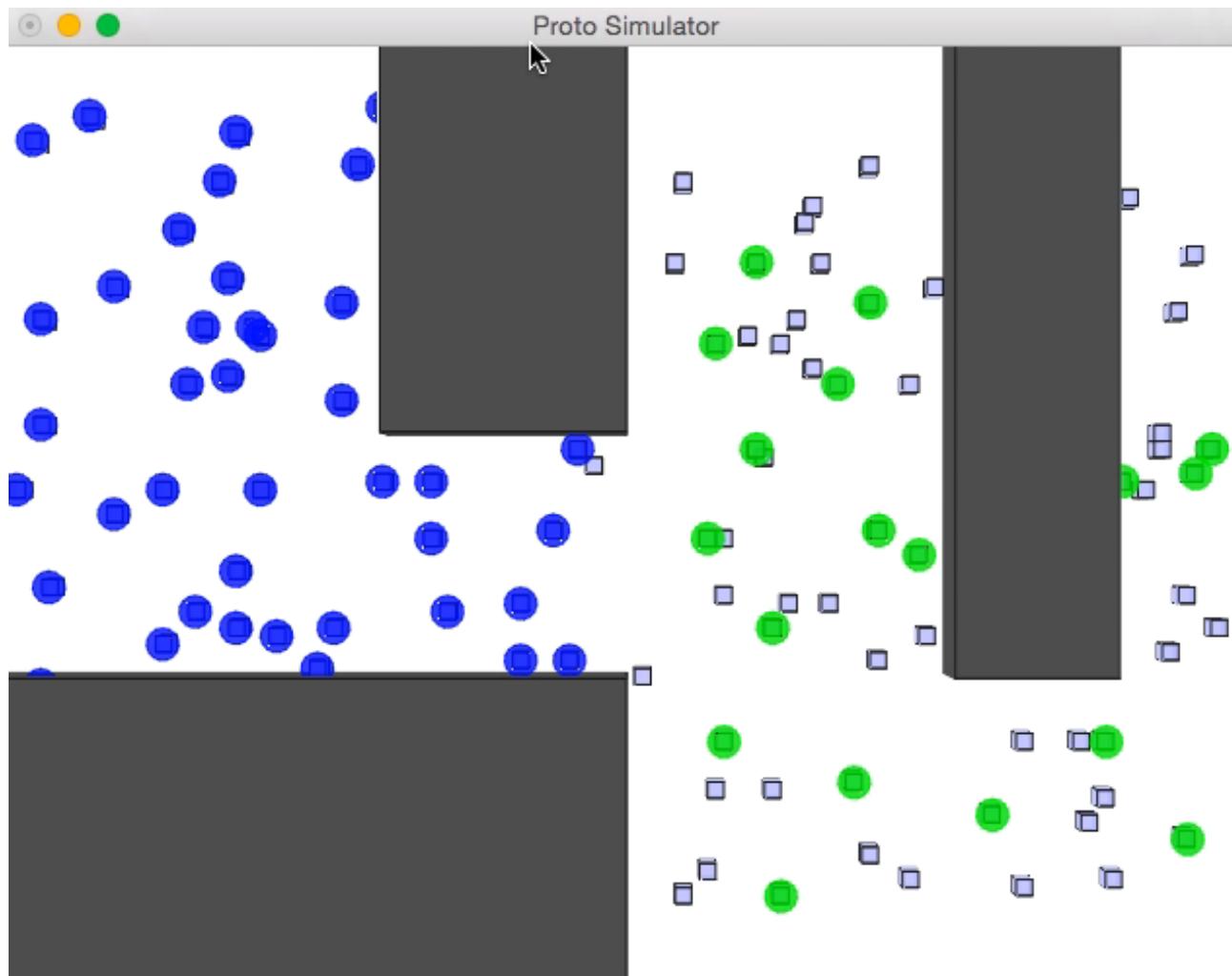
(def safe-navigation (destination p)
  (distance-avoiding-obstacles
    destination (crowd-warning p)))
```



Optimization of Dynamics

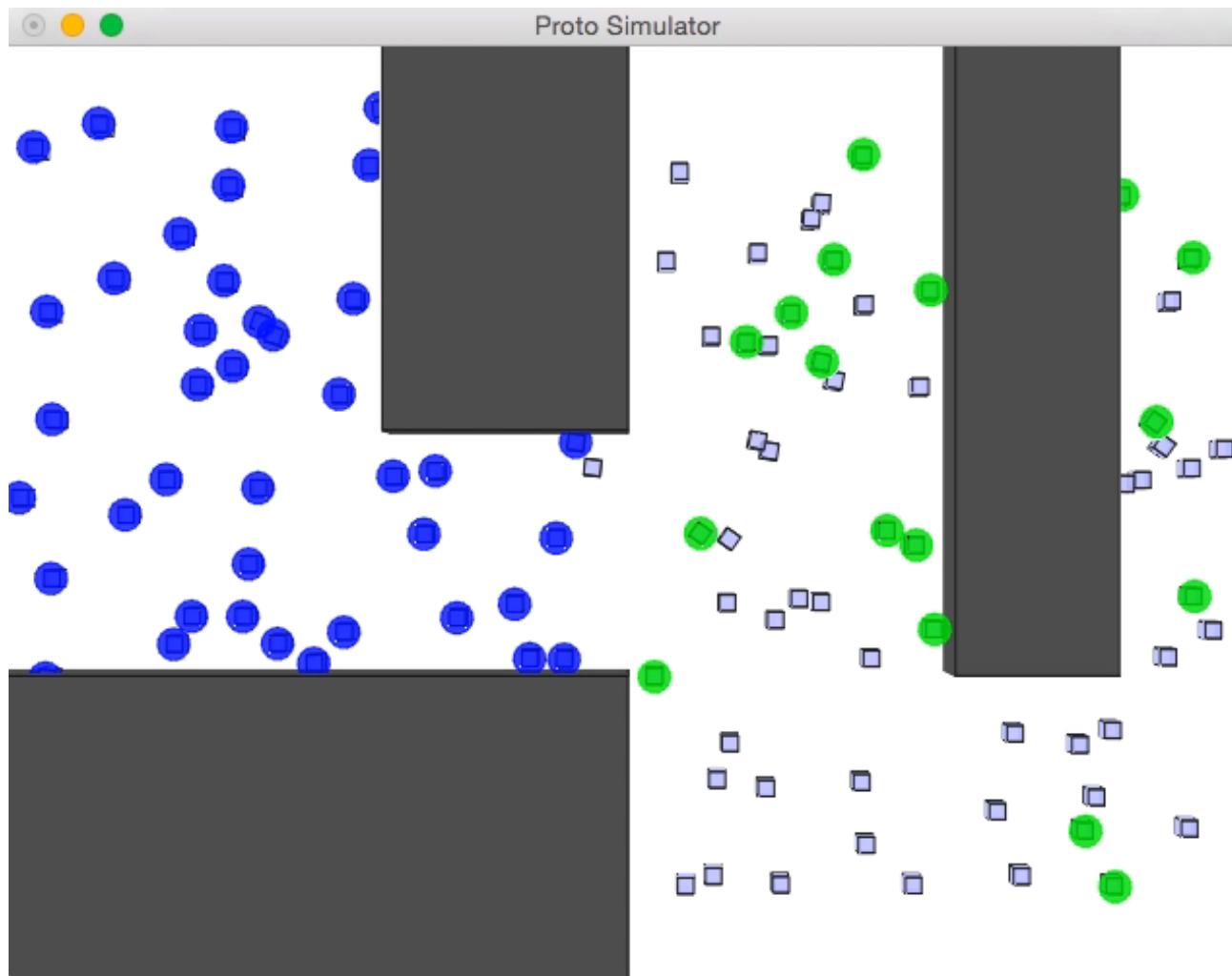


Optimization Example: Crowd Alert



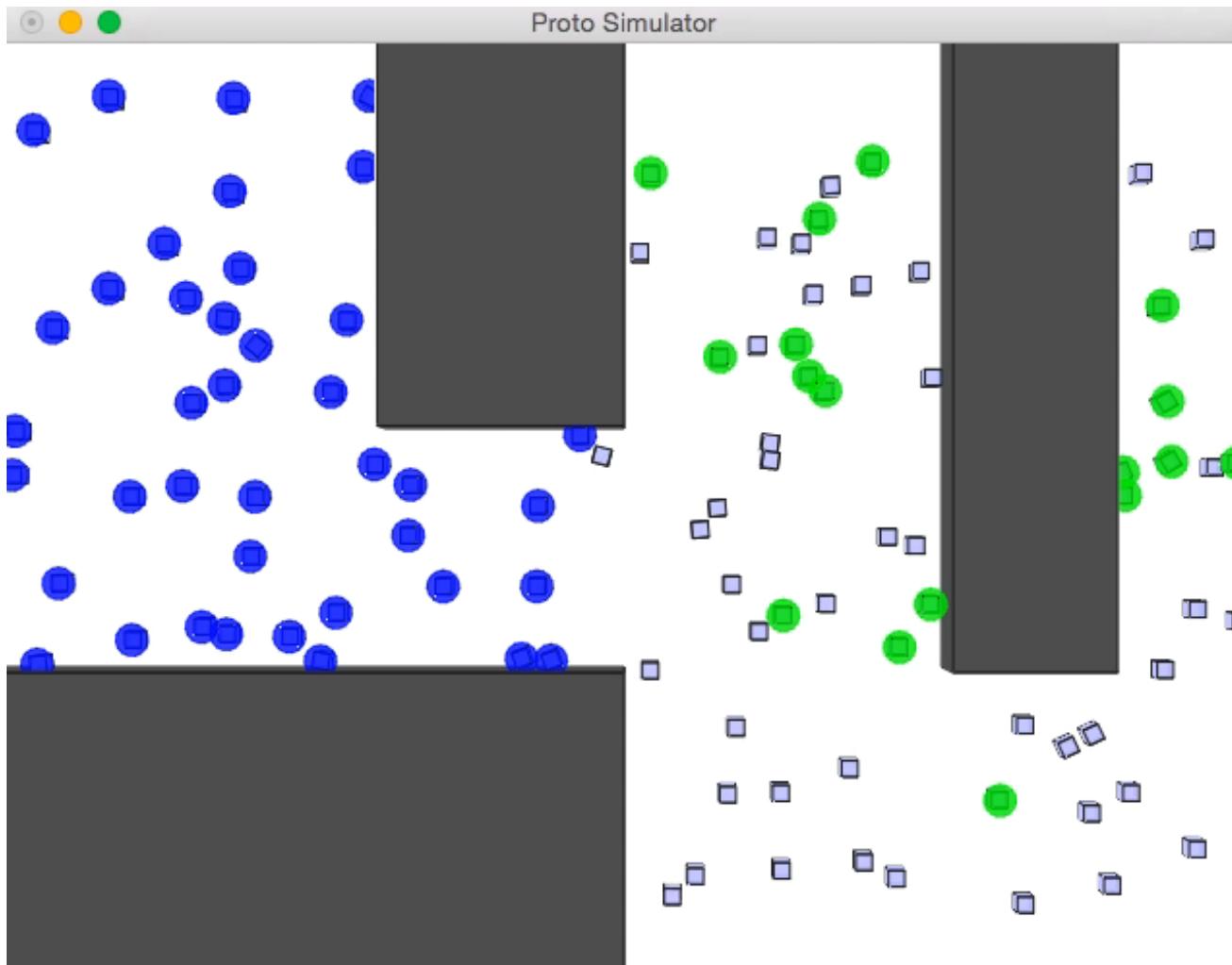
Naïve algorithm: when stationary, fine...

Optimization Example: Crowd Alert



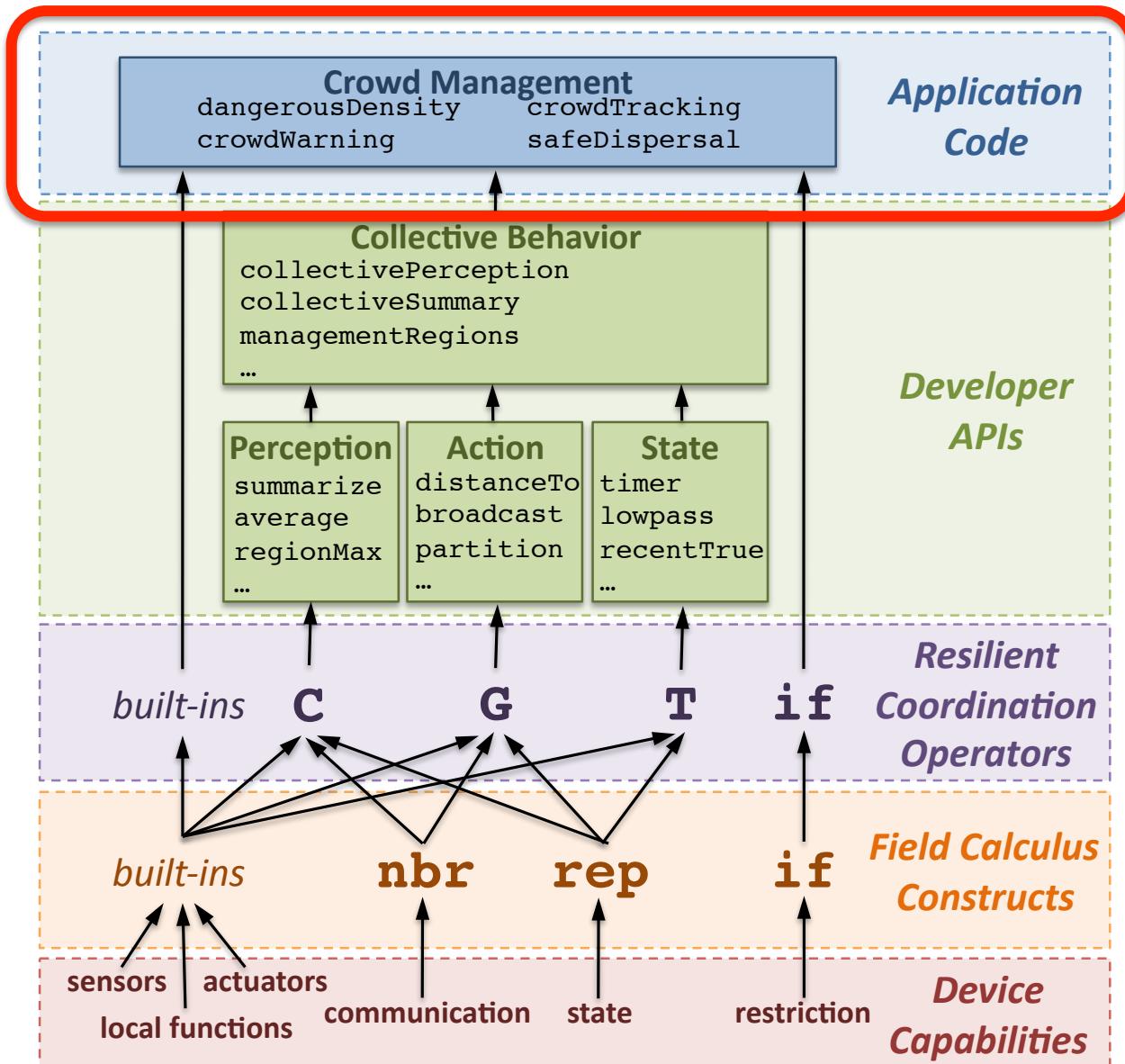
... but dynamics can't keep up with fast mobility.

Optimization Example: Crowd Alert

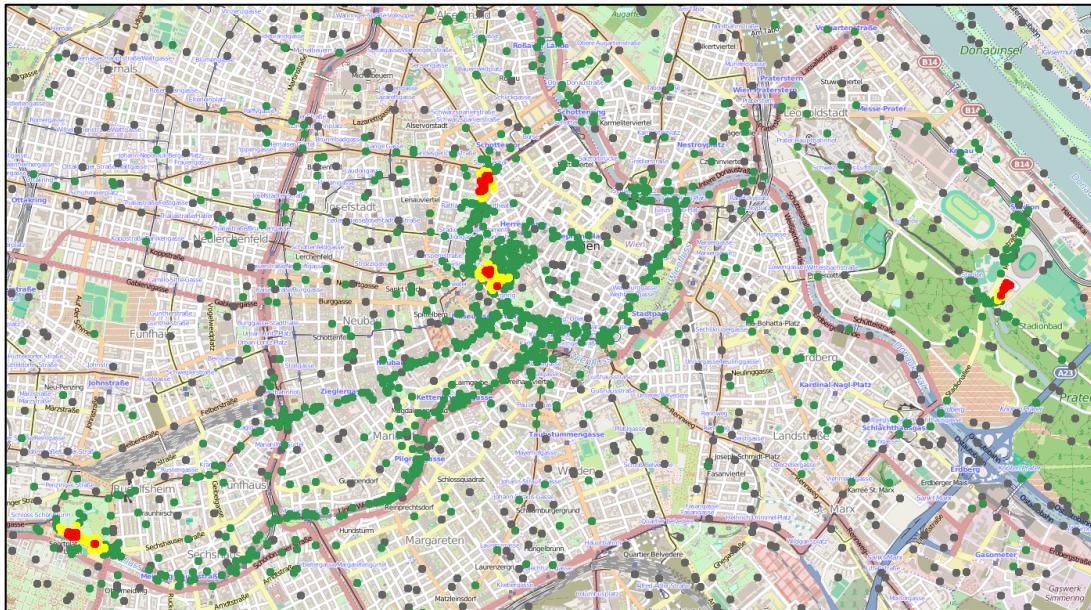


Optimized dynamics, however, work well.

Aggregate Programming Stack



Crowd Safety Services

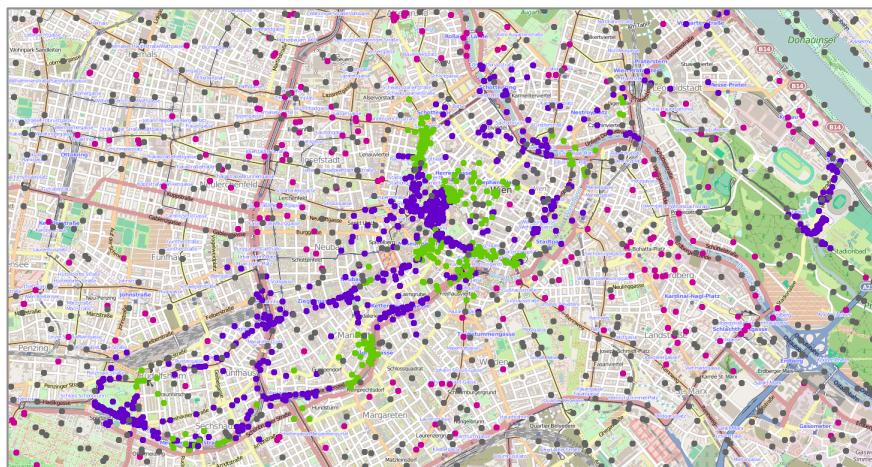


```

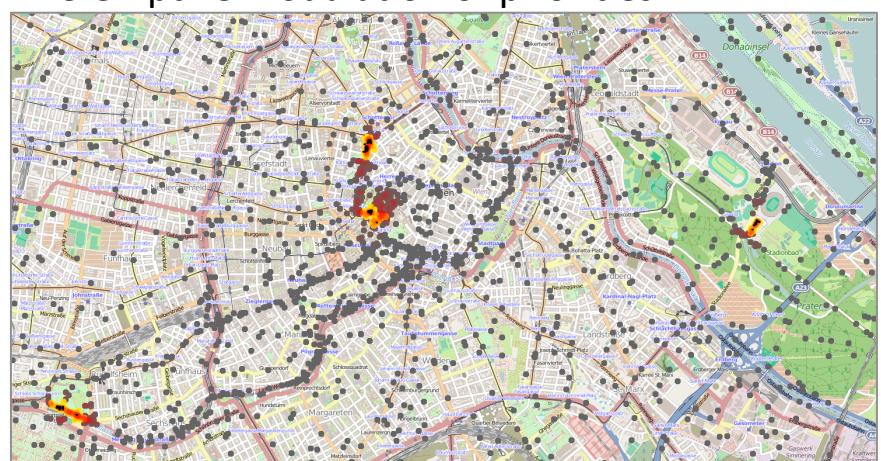
def dangerousDensity(p, r) {
    let mr = managementRegions(r*2, () -> { nbrRange });
    let danger = average(mr, densityEst(p, r)) > 2.17 &&
        summarize(mr, sum, 1 / p, 0) > 300;
    if(danger) { high } else { low }
}
def crowdTracking(p, r, t) {
    let crowdRgn = recentTrue(densityEst(p, r)>1.08, t);
    if(crowdRgn) { dangerousDensity(p, r) } else { none };
}
def crowdWarning(p, r, warn, t) {
    distanceTo(crowdTracking(p,r,t) == high) < warn
}

```

Dissemination of new versions

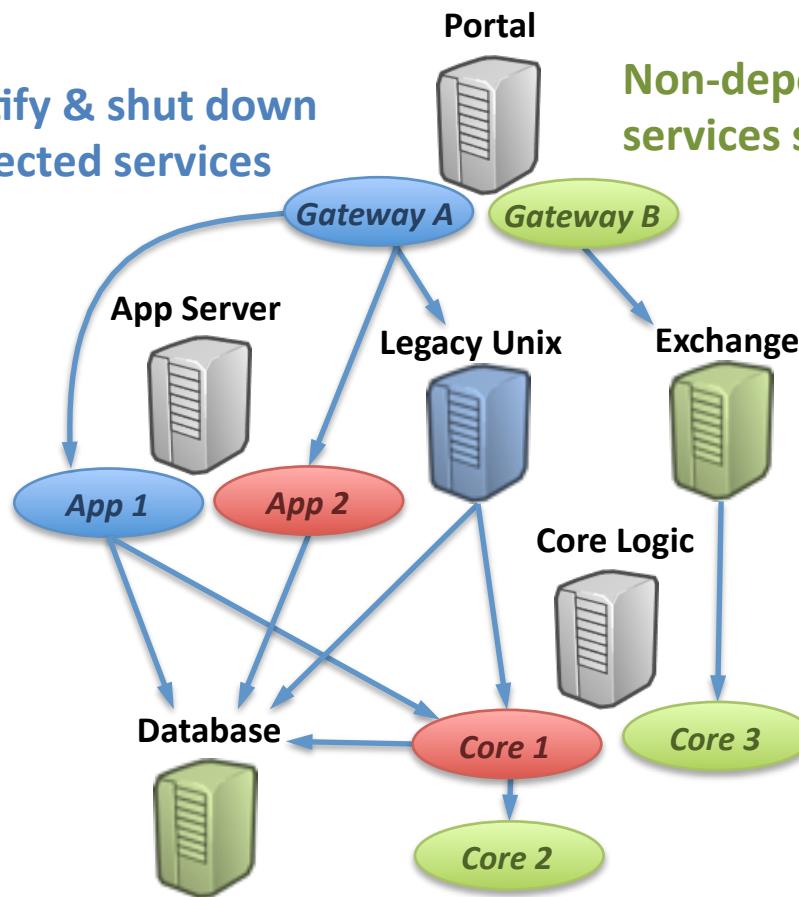


Pre-emptive modulation of priorities



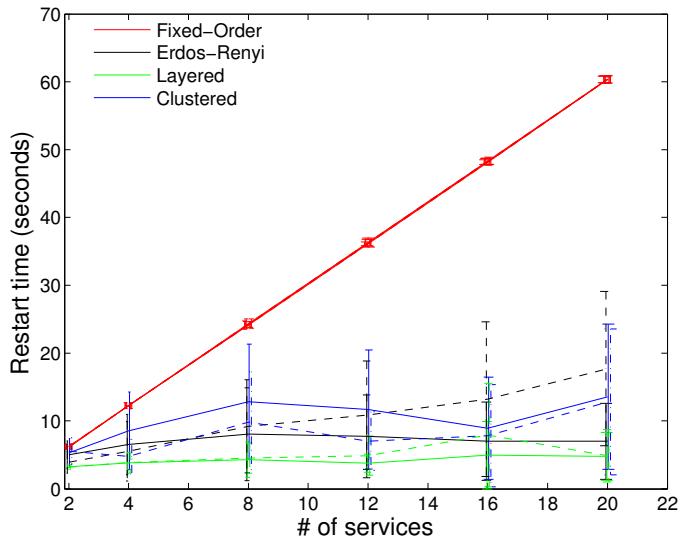
Dependency-Directed Recovery

Identify & shut down
affected services

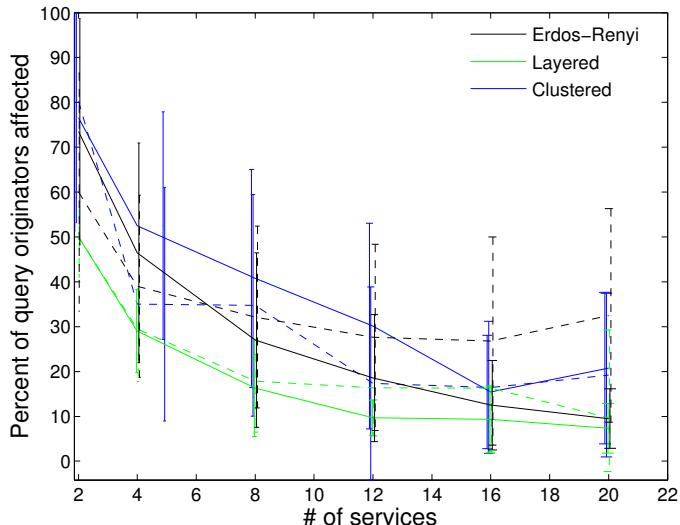


Non-dependent
services still run

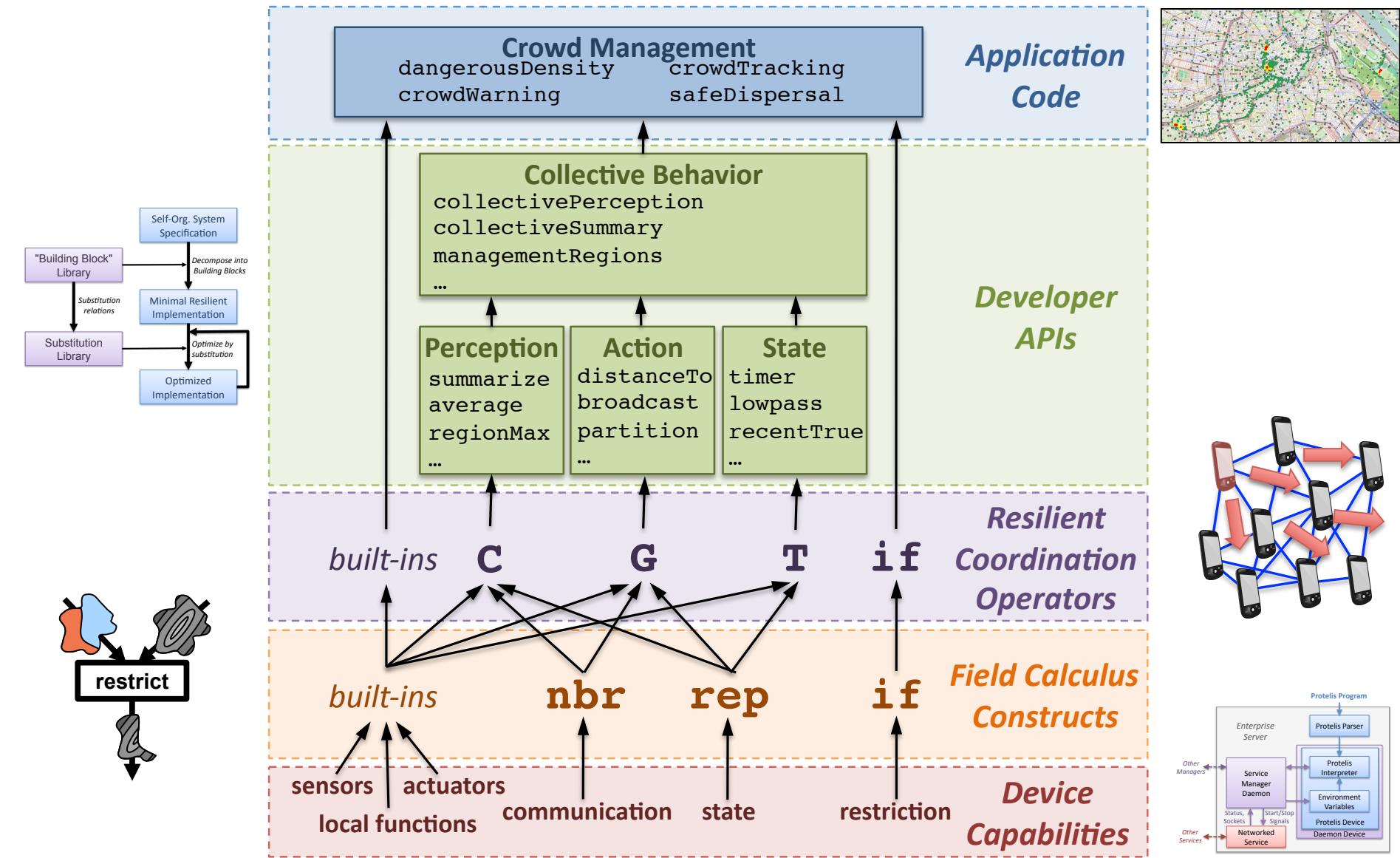
Dramatically better recovery time



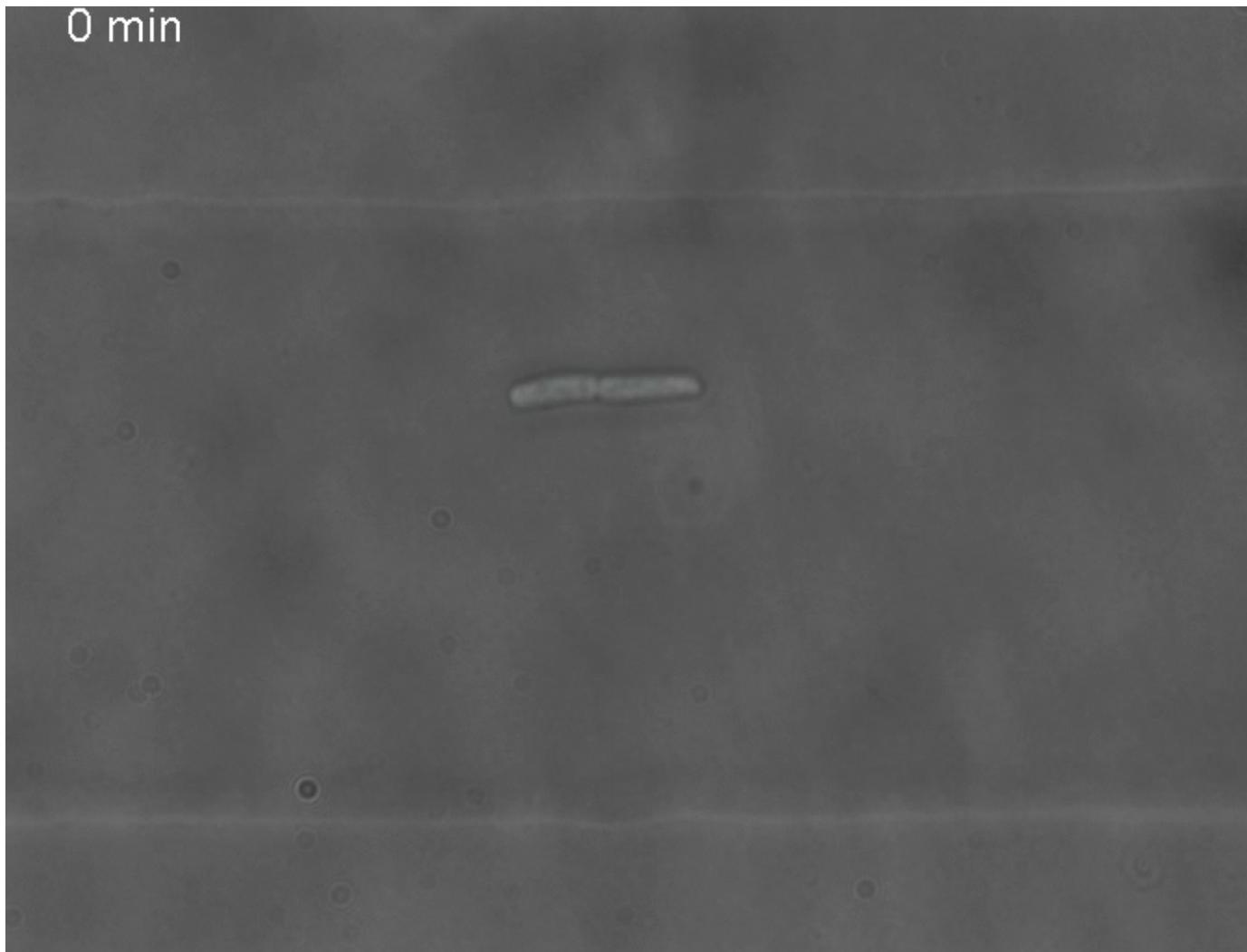
Fewer services disrupted



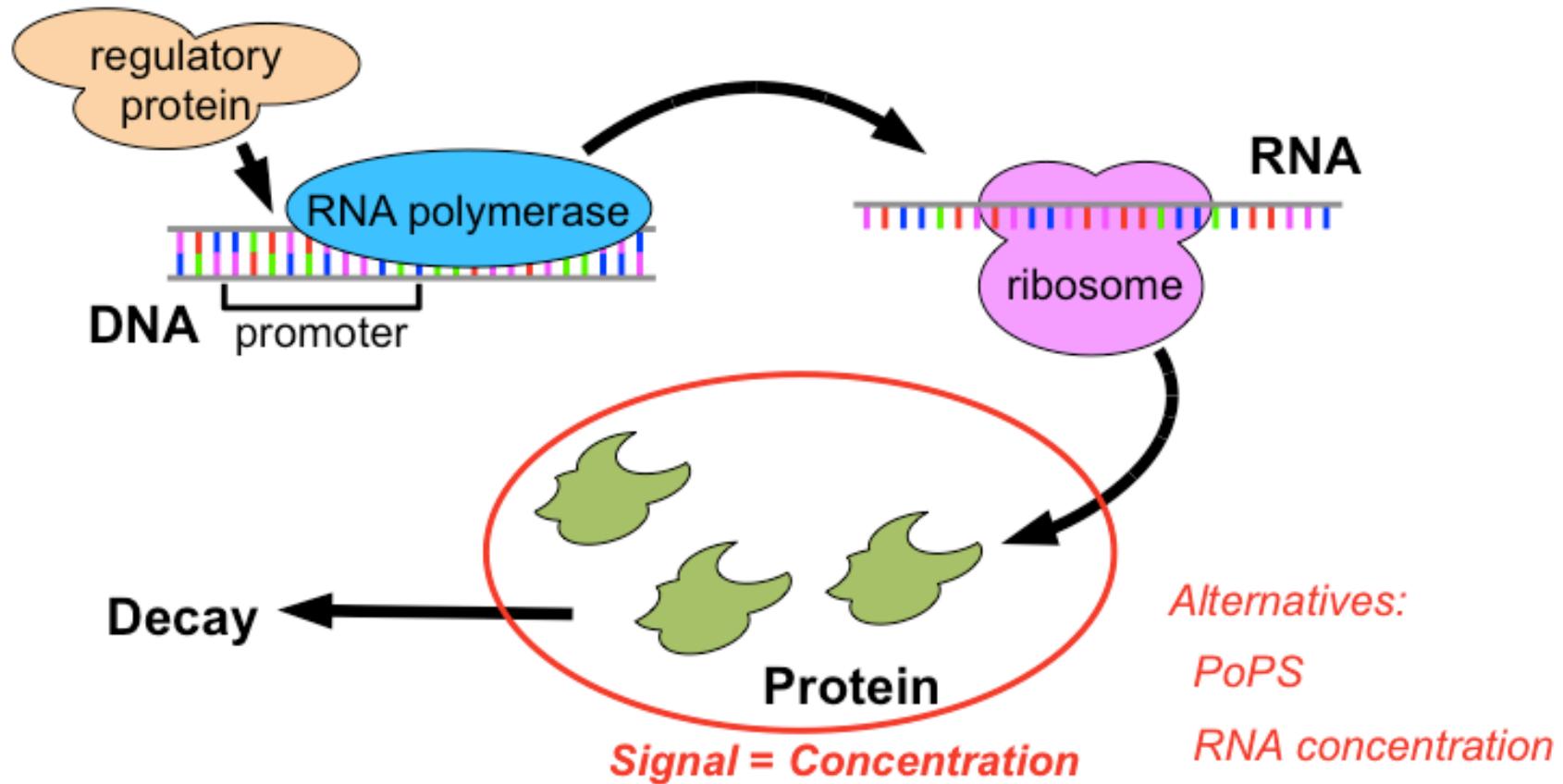
Summary: Aggregate Methodology



Now let's go to biology...

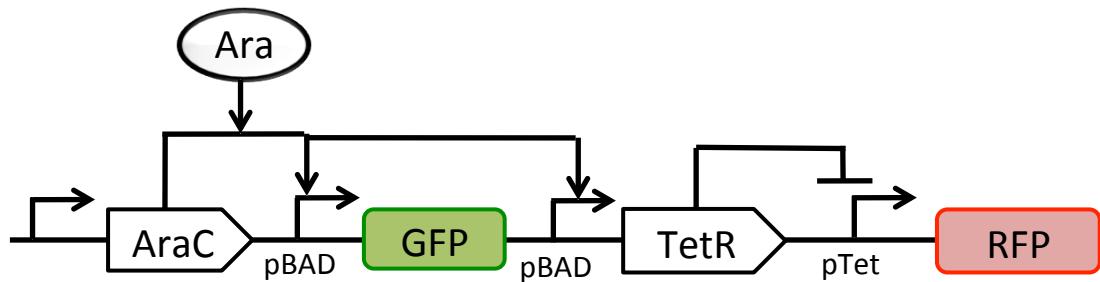


Transcriptional Logic Computations

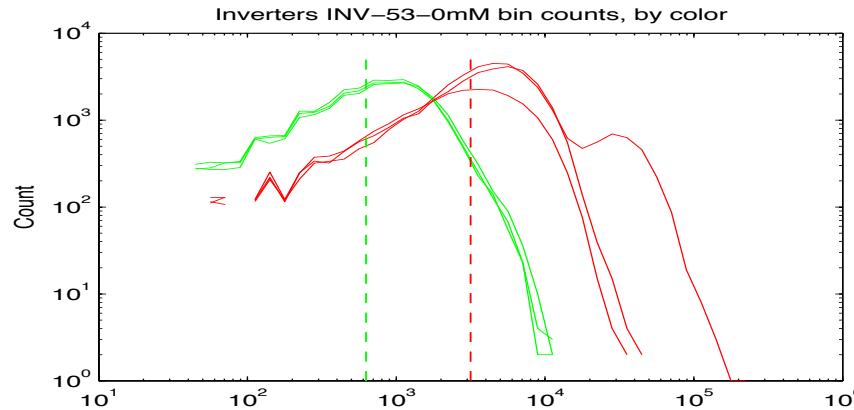


Stabilizes at *decay = production*

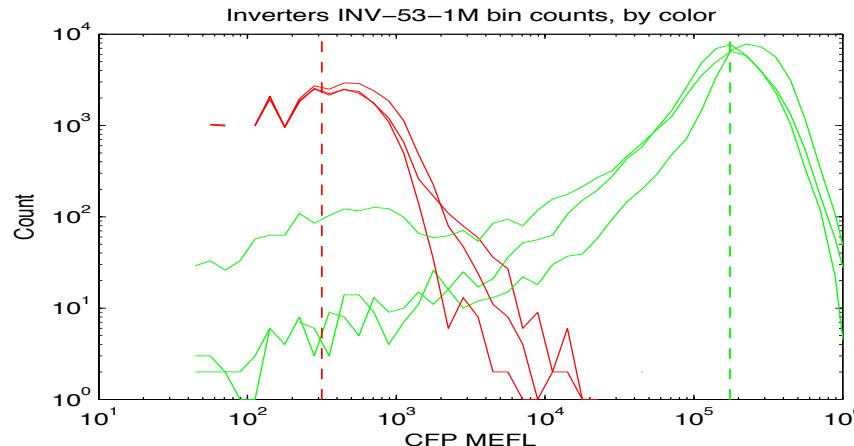
Simple Circuit Example



“Off”

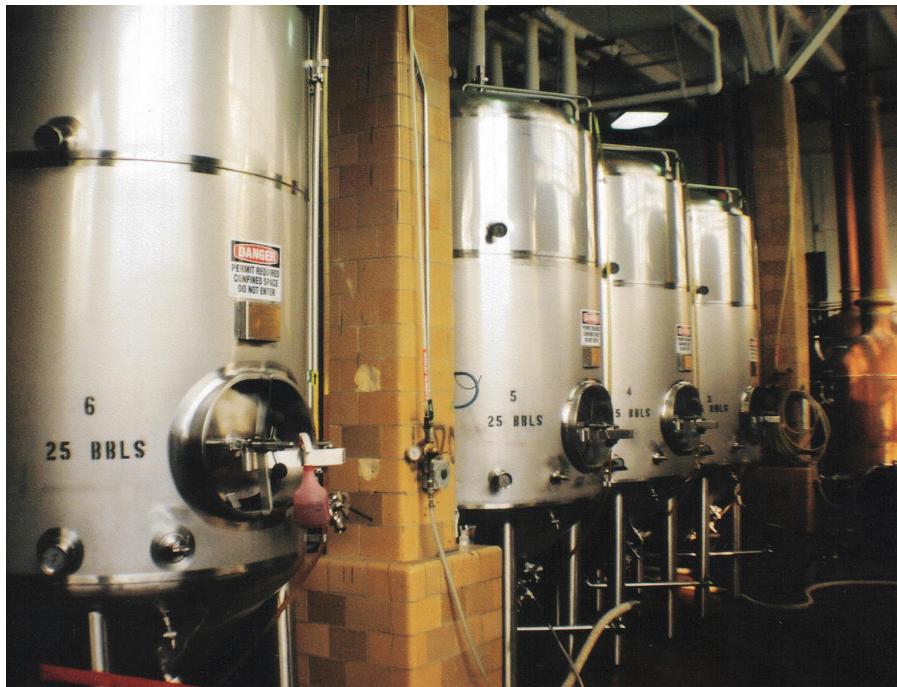


“On”

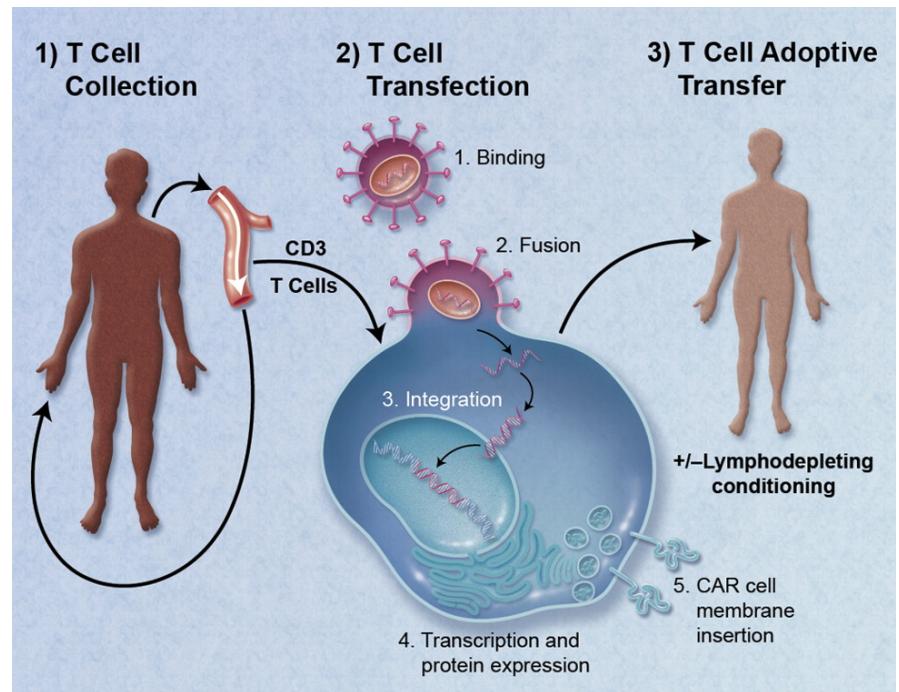


Application Examples

Fermentation control

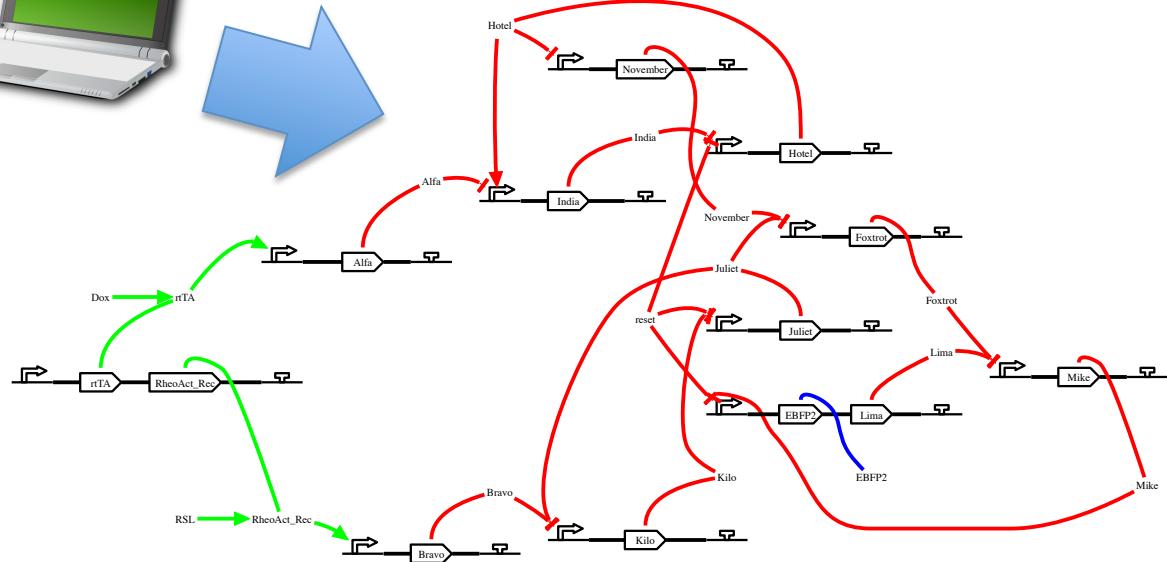
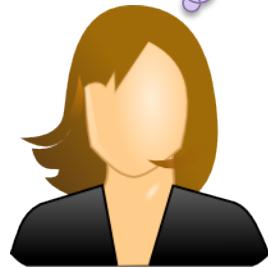


CAR T-cell Therapy



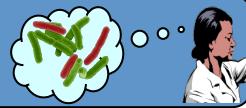
High-Level Genetic Circuit Design

Make drug when
Arabinose shows
up before IPTG



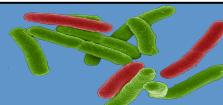
Why a tool-chain?

Organism Level Description

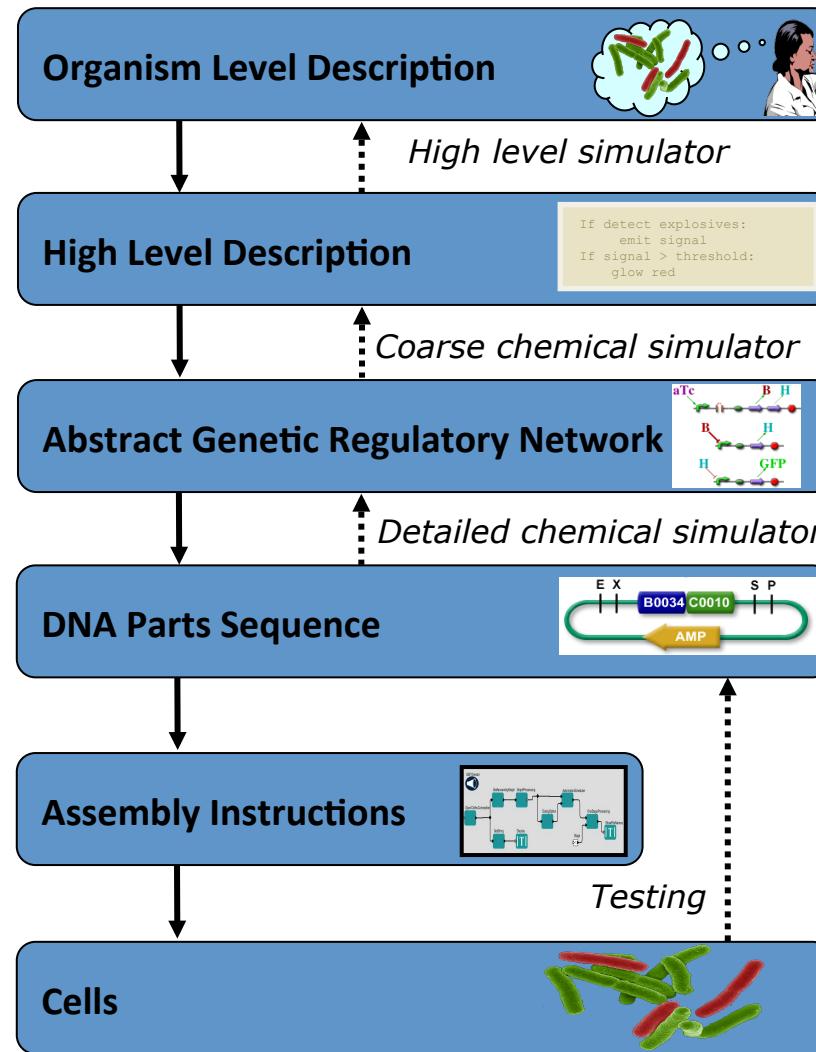


*This gap is too big
to cross with a
single method!*

Cells



TASBE tool-chain



Collaborators:



Ron
Weiss



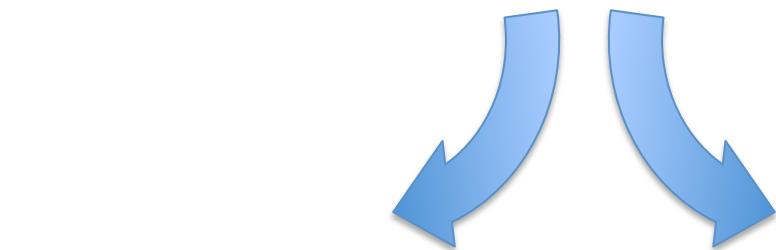
Douglas
Densmore

*Modular architecture
also open for flexible
choice of organisms,
protocols, methods, ...*

A Tool-Chain Example

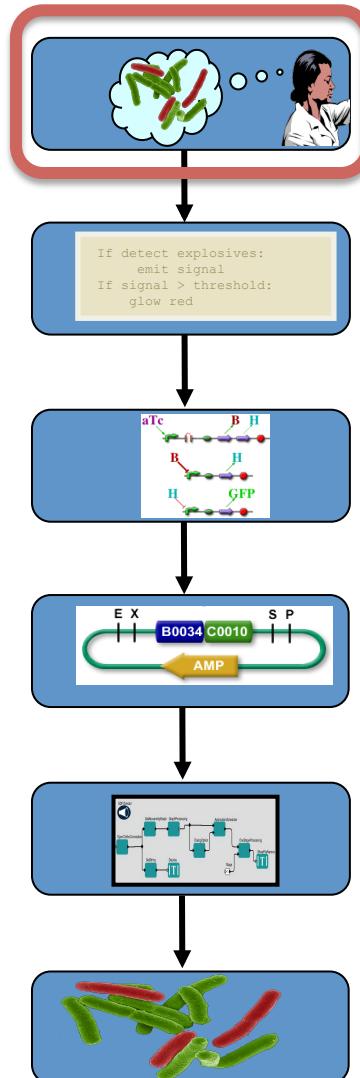
A high-level program of a system that reacts depending on sensor output

```
(def simple-sensor-actuator ()
  (let ((x (test-sensor)))
    (debug x)
    (debug-2 (not x))))
```



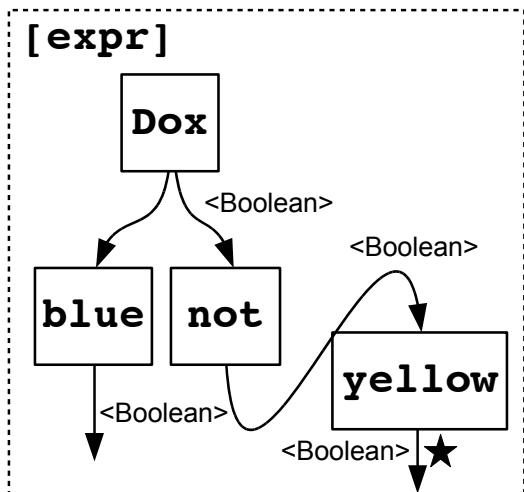
Mammalian Target

E. coli Target

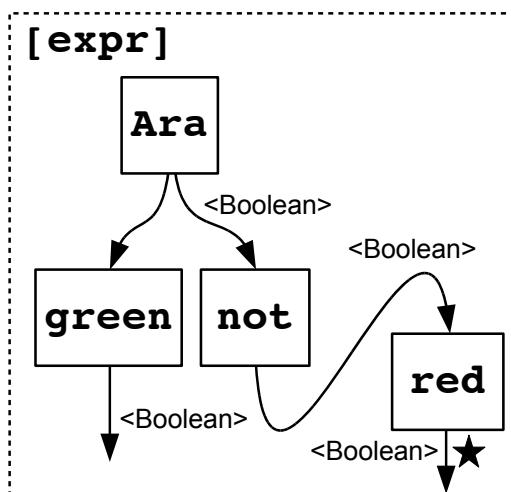


A Tool-Chain Example

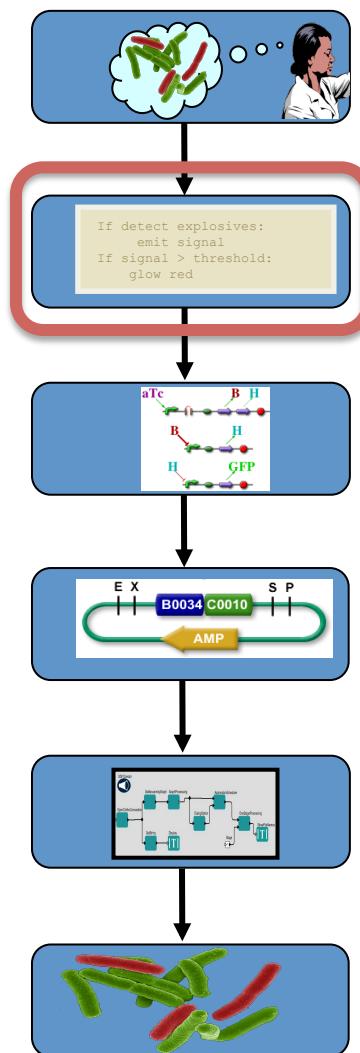
Program instantiated for two target platforms



Mammalian Target

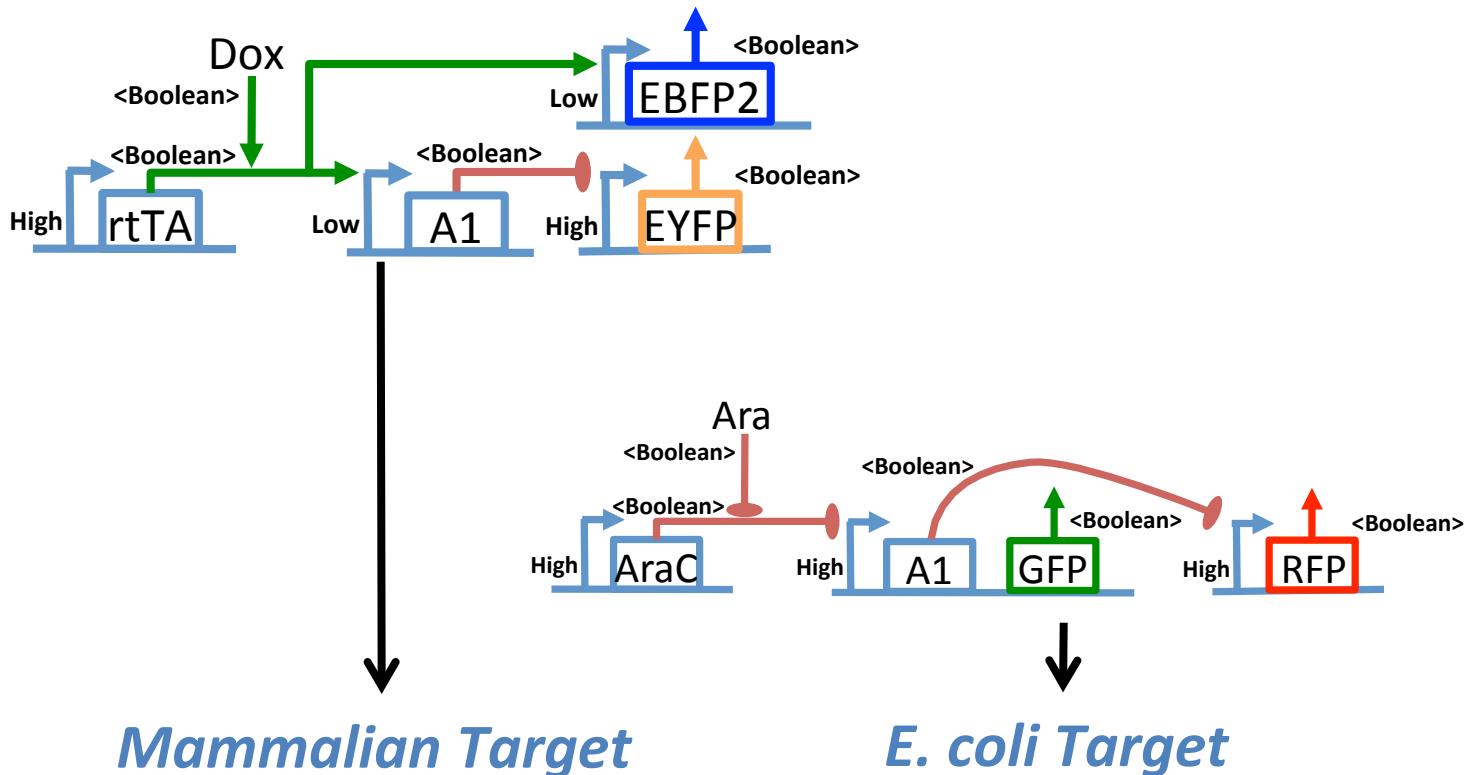


E. coli Target

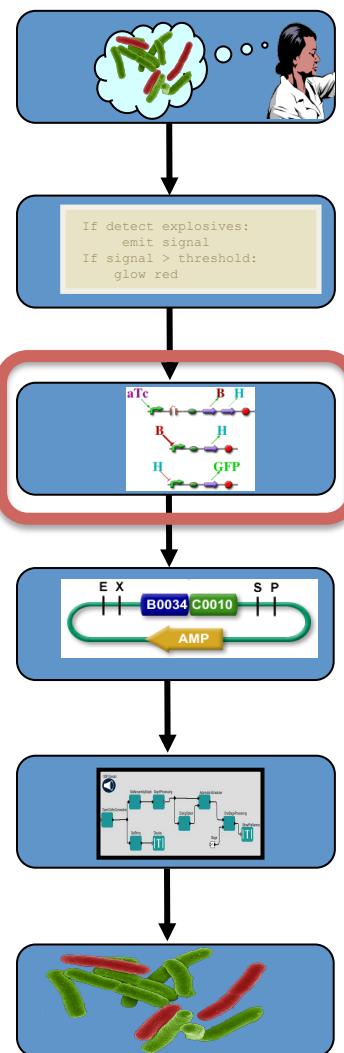


A Tool-Chain Example

Abstract genetic regulatory networks

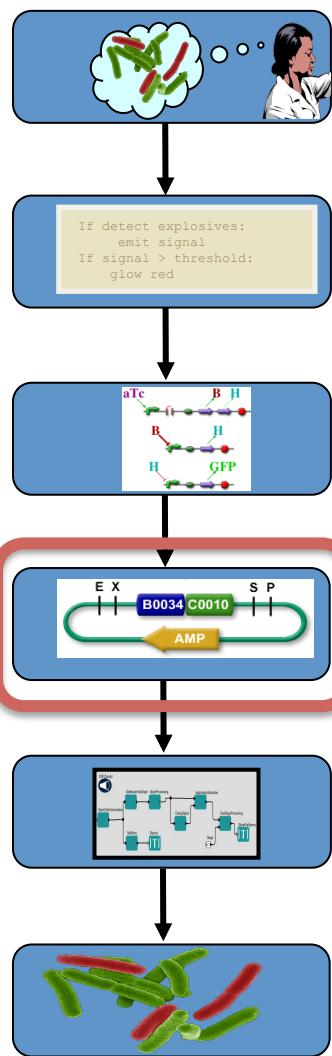
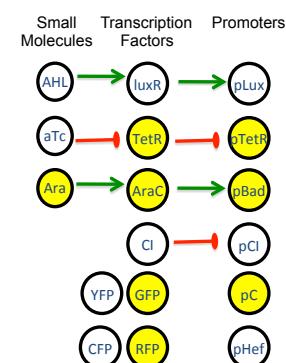
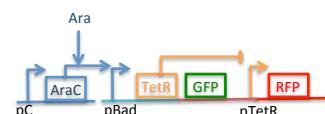
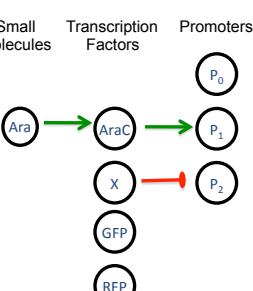
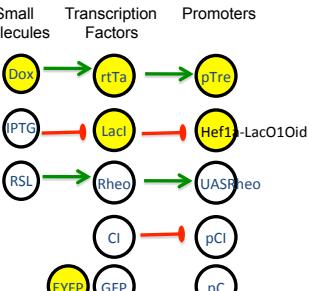
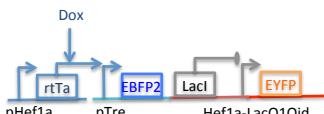
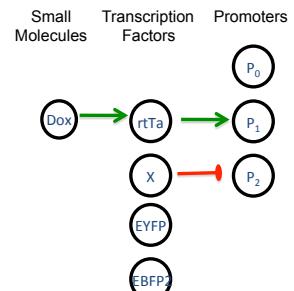


[Beal et al, ACS Syn. Bio. 2012]



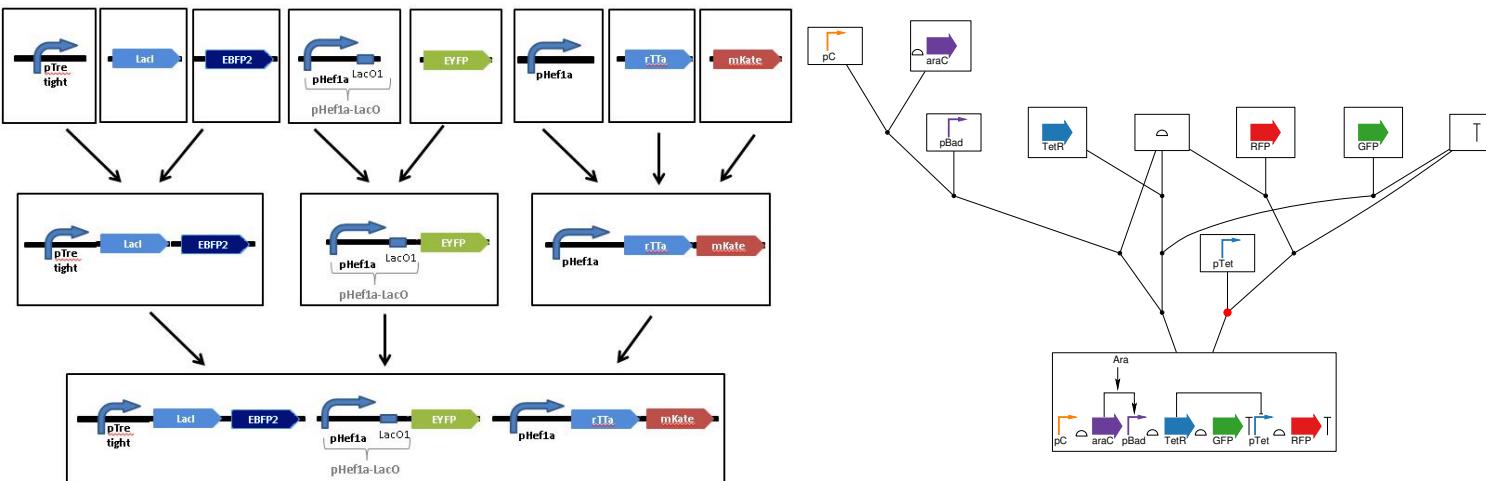
A Tool-Chain Example

Automated part selection using database of known part behaviors



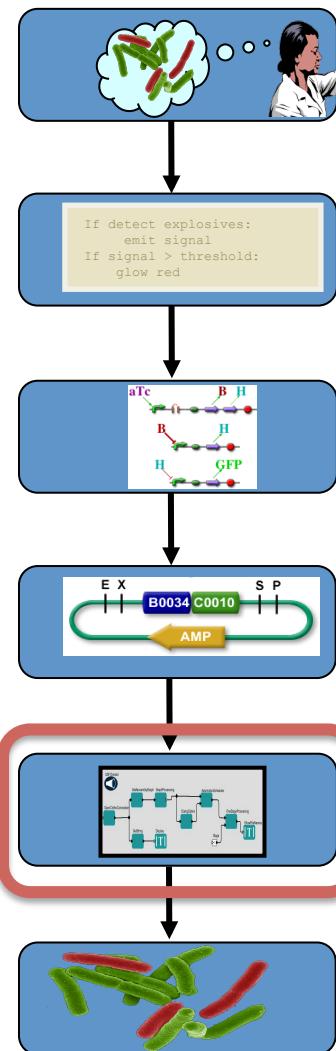
A Tool-Chain Example

Automated assembly step selection for two different platform-specific assembly protocols



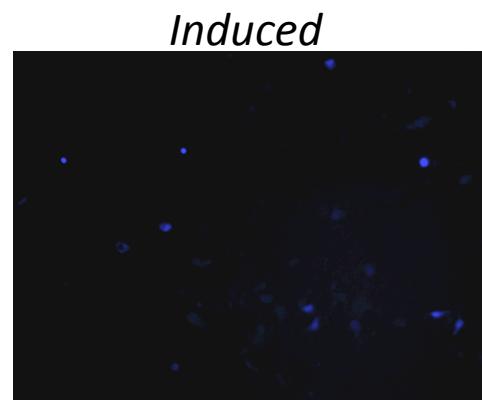
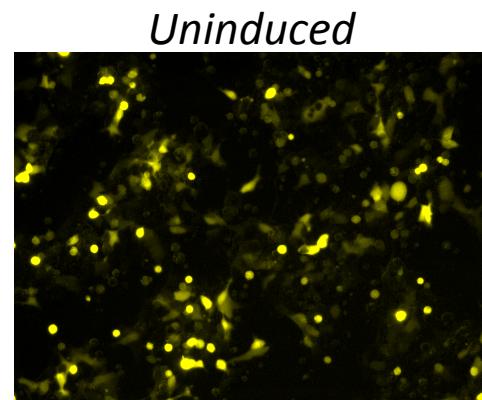
Mammalian Target

E. coli Target

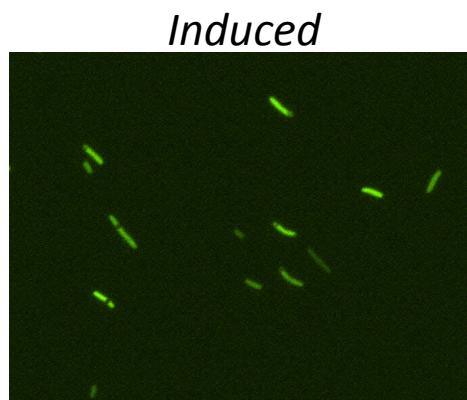
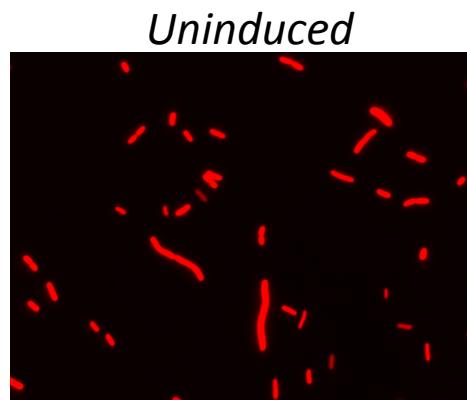


A Tool-Chain Example

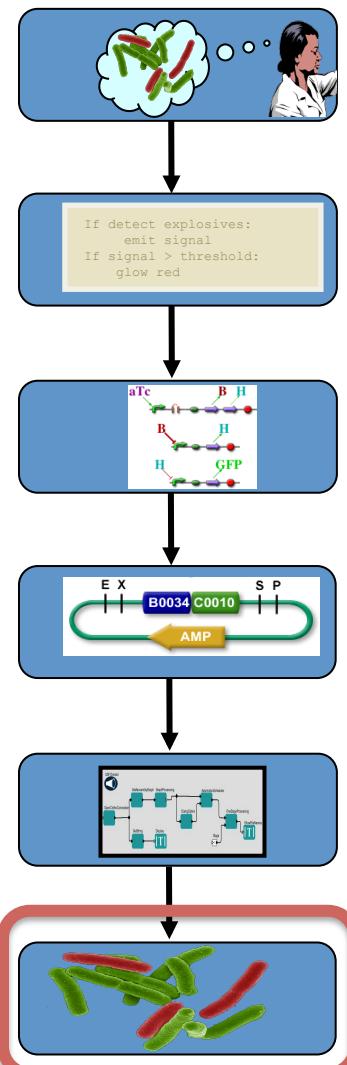
Resulting cells demonstrating expected behavior



Mammalian Target

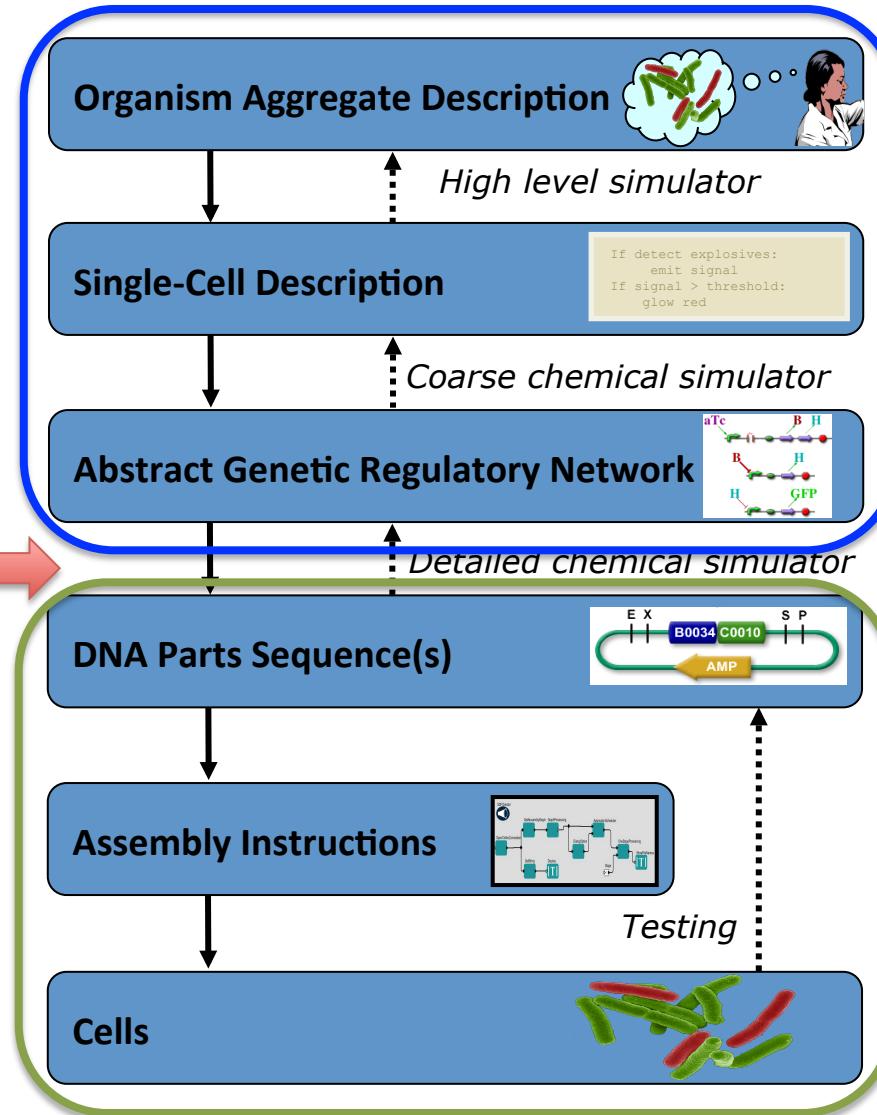


E. coli Target



The Tool-Chain Approach:

Gap!



Proto BioCompiler

[Beal et al, PLoS ONE 2011]

Alternate 2nd stages:
SBROME, CELLO, GEC, ...

Next-Gen Synthesis,
Organick, Antha, MAGE,
microfluidics, ...

Complex Designs: Barriers & Emerging Solutions

- Barrier: Characterization of Devices
 - Emerging solution: TASBE characterization method
- Barrier: Availability of High-Gain Devices
 - Emerging Solution: combinatorial device libraries based on CRISPR, TALs, miRNAs, recombinases, ...
- Barrier: Predictability of Biological Circuits
 - Emerging solution: EQuIP prediction method

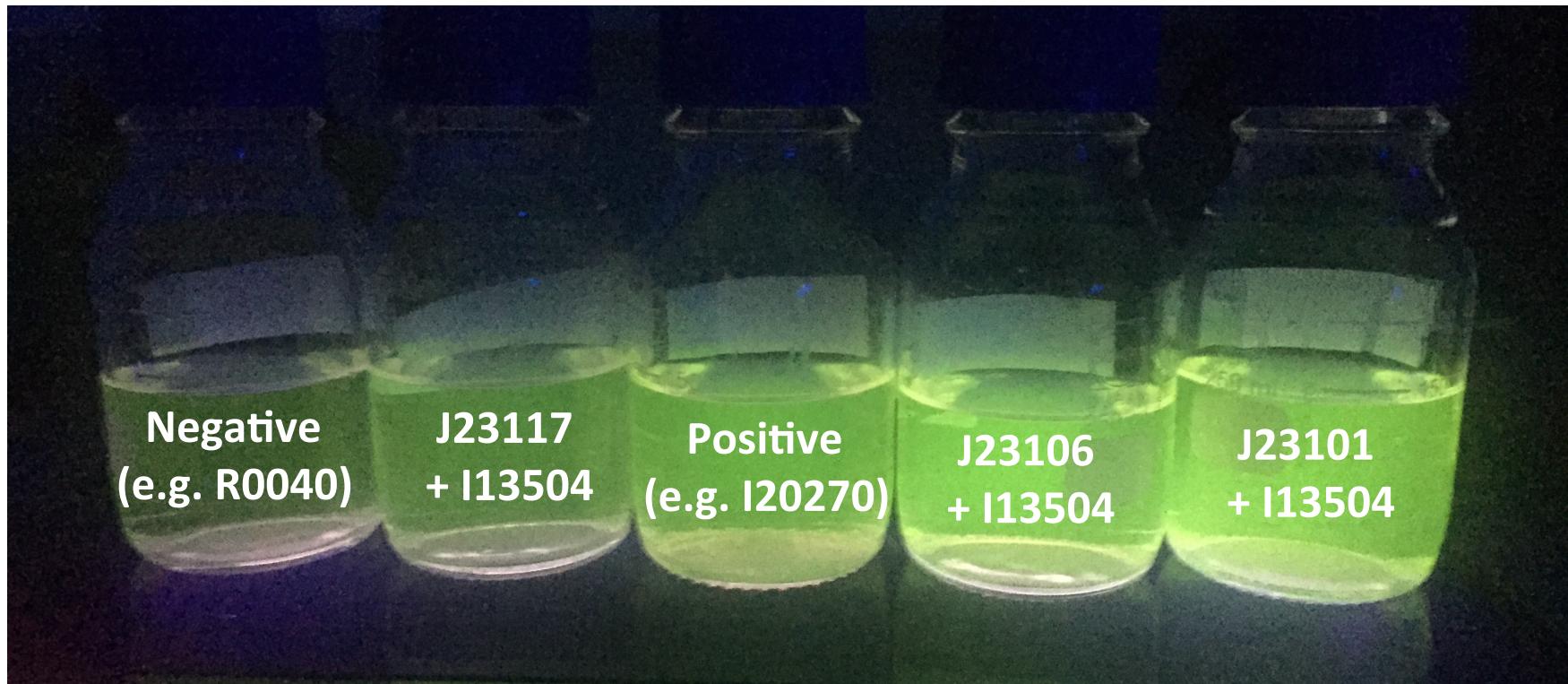
Characterization & reproducibility

iGEM Interlab Study:

Build three constitutive GFP constructs

Culture & measure fluorescence

3 biological replicates (Extra: x 3 technical rep.)



2015 iGEM Interlab Study Participation

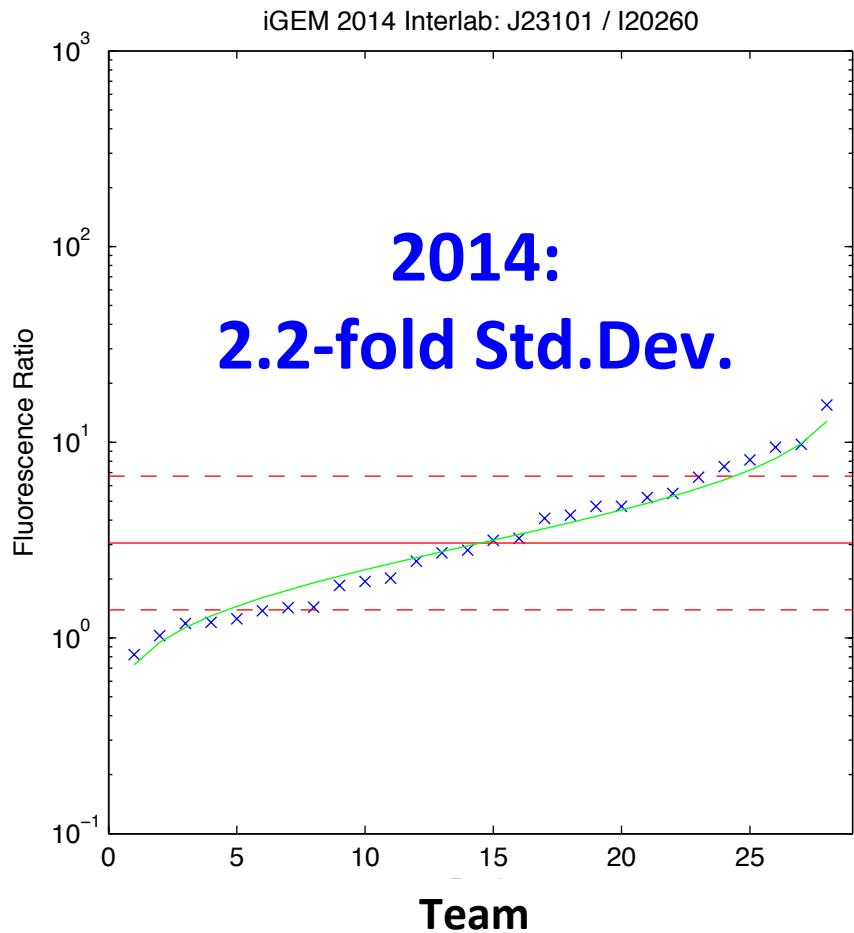


Participating Teams

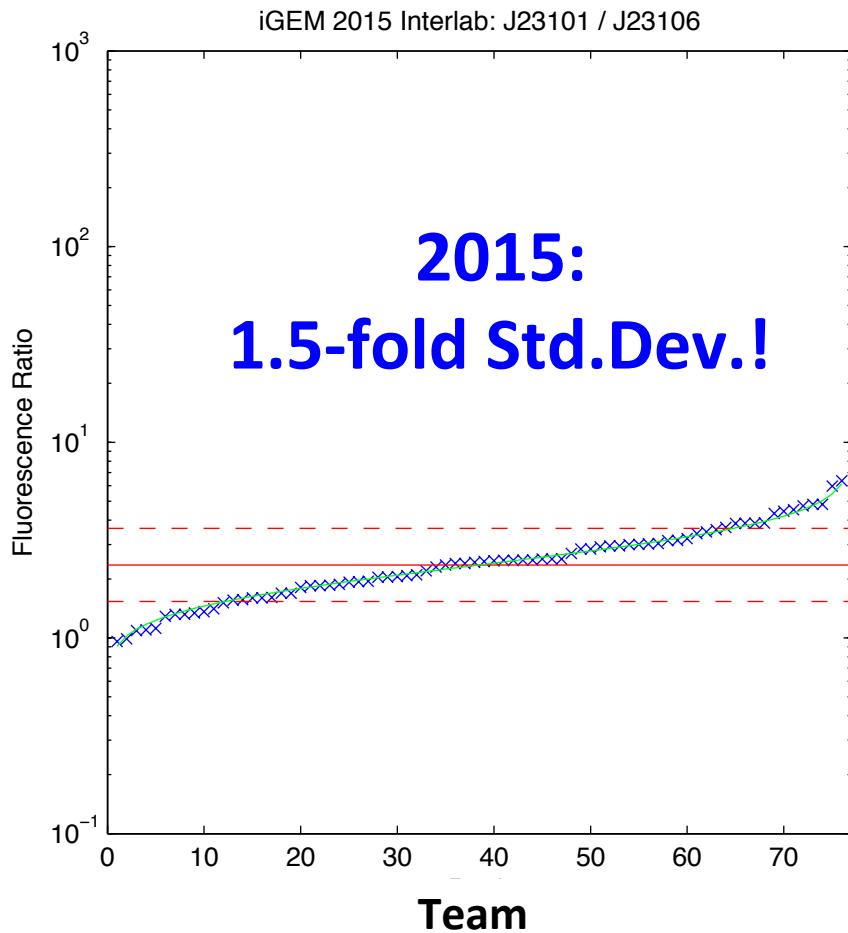
Aalto-Helsinki	Birkbeck	CU Boulder	Glasgow	London Biohackspace	NJAU_China	Rock Ridge Virginia	TecCEM HS	Tufts	Waterloo
Aix-Marseille	BIT	Czech_Republic	Harvard_BioDesign	LZU	Northeastern	SCUT	Tec_Monterrey	UCL	William and Mary
Amoy	Boston University	Duke	Hong_Kong-CUHK	Marburg	NRP-UEA	SDU-Denmark	Tokyo Tech	UCLA	WLC-Milwaukee
ANU-Canberra	Brasil-USP	Edinburgh	HUST-China	METU_Turkey	NTNU-Trondheim	SPSingapore	Toronto	UC San Diego	WPI-Worcester
ATOMS-Turkiye	Cairo_Egypt	EPF_Lausanne	HZAU-China	Minnesota	NU_Kazakhstan	Stanford-Brown	Trento	UFMG_Brazil	UMaryland
Austin_UTexas	Carnegie Mellon	ETH Zurich	IISER_Pune	MIT	OUC-China	Stockholm	TrinityCollegeDublin	Utah_State	Vanderbilt
BHSE_Beijing	CityU_HK	Exeter University	KU Leuven	Nanjing_NFLS	Oxford	SYSU-Software	TU Delft	Vilnius-Lithuania	Waterloo
Bielefeld	Cork	Freiburg	Leicester	Nankai	Paris-Saclay	SZMS_15_Shenzhen	TU_Eindhoven	William and Mary	WLC-Milwaukee
BIOSINT Mexico	CSU_Fort_Collins	Gifu	Lethbridge	NEAU-China	Pasteur	TecCEM	Tuebingen	WPI-Worcester	UFMG_Brazil

High sensitivity to protocol

2014: J23101 (High) vs. I20260 (Med)



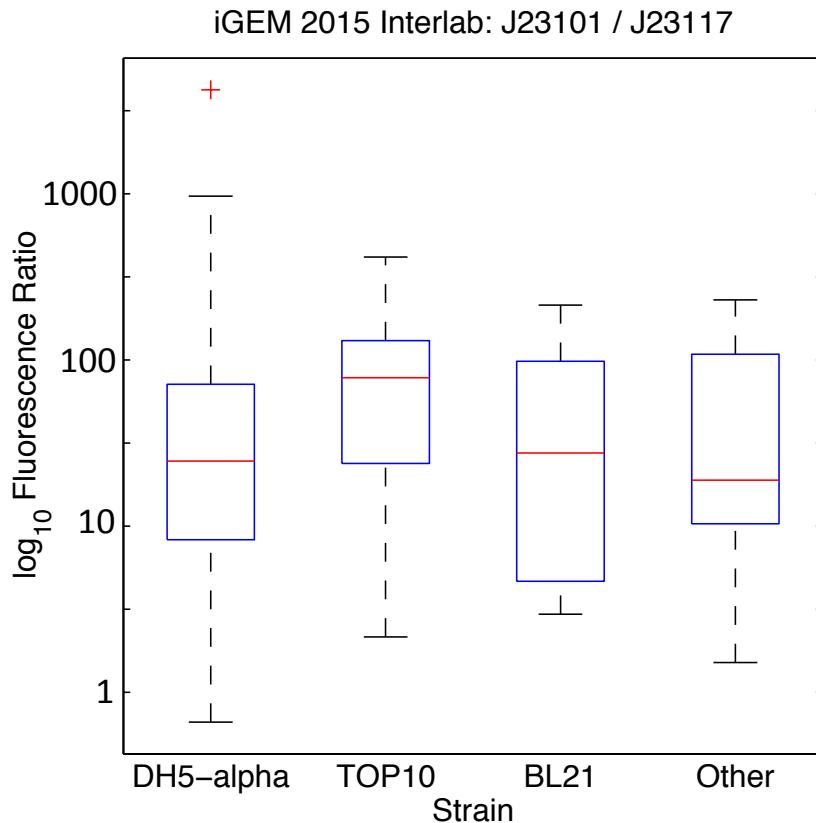
2015: J23101 (High) vs. J23106 (Med)



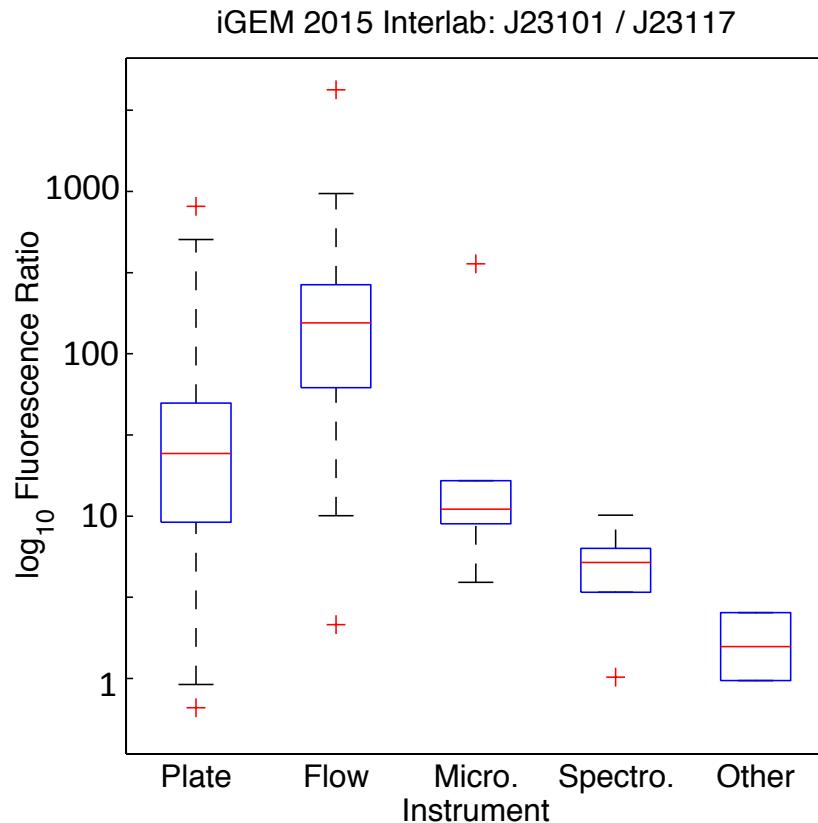
More specific protocol → tighter distributions

Instrument issues drive variation!

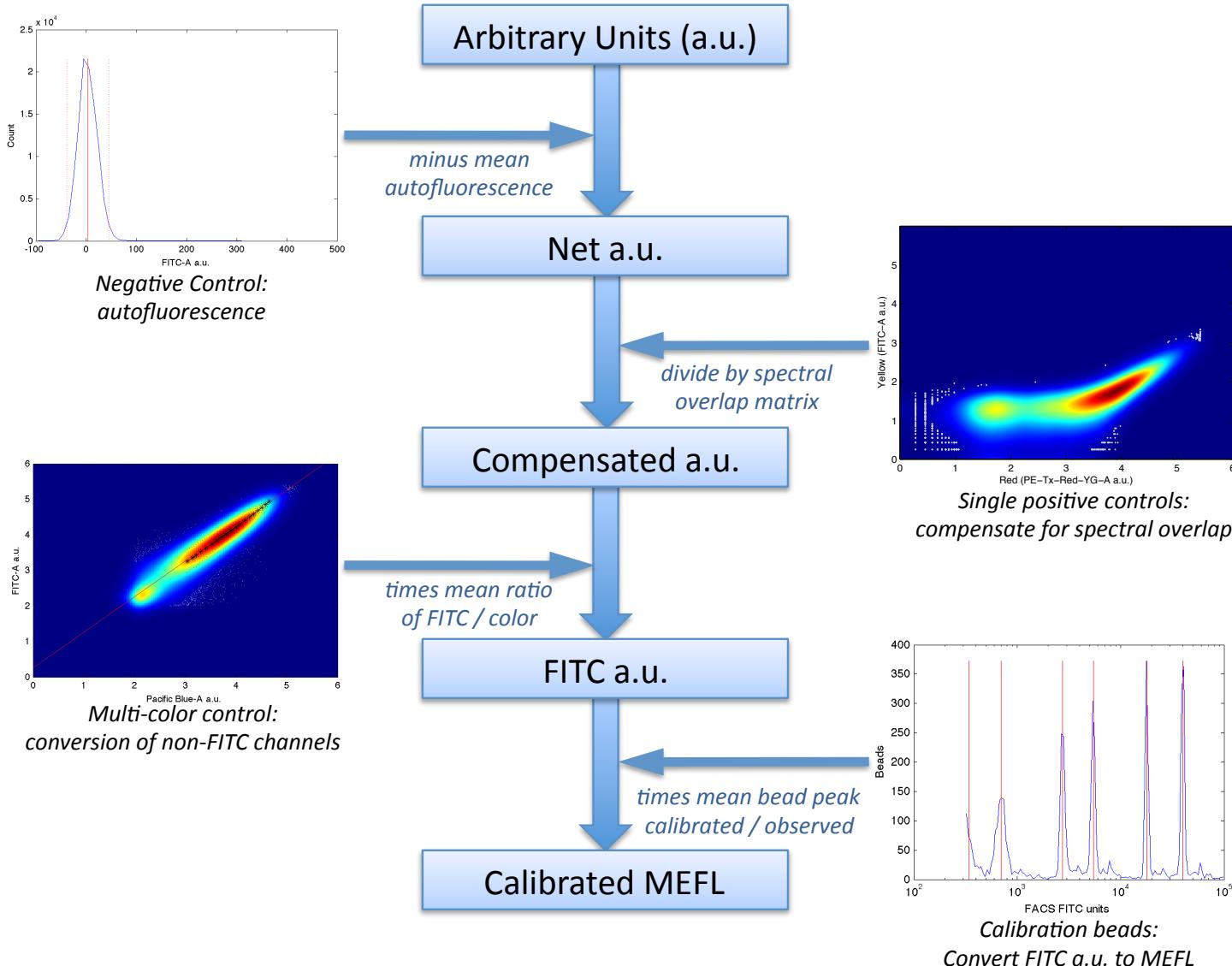
Strain



Instrument

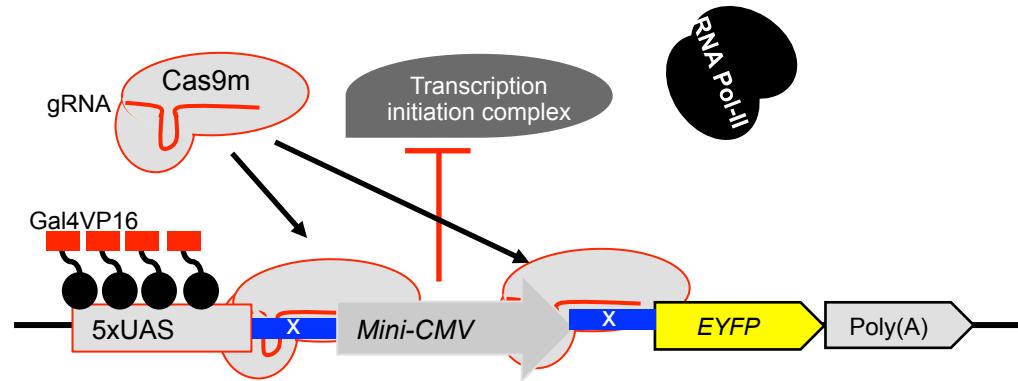


Calibrated Flow Cytometry

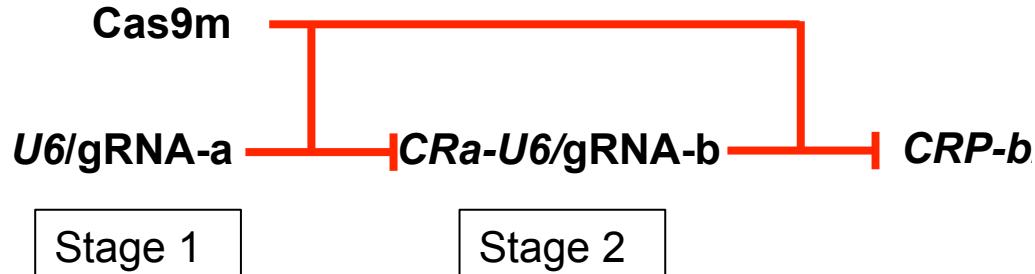


CRISPR Repressor Devices

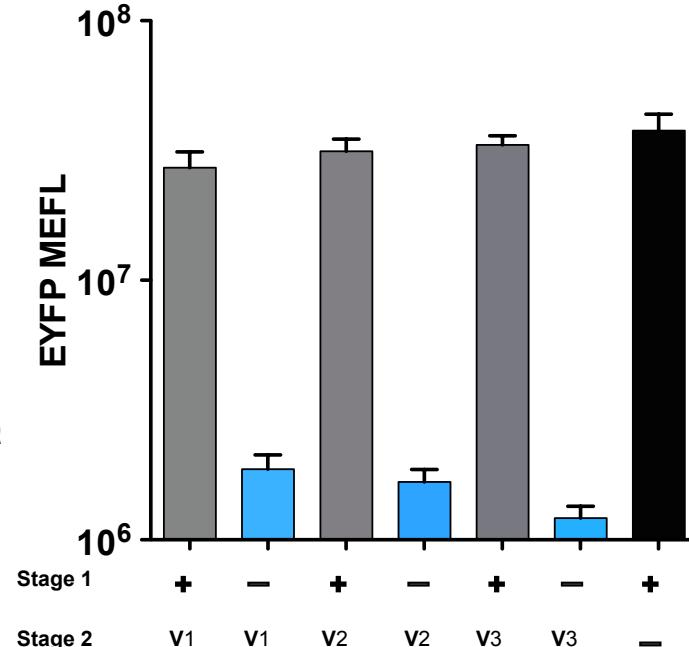
CRISPR system can be used to create high-performance repressors, large libraries



Example: CRISPR cascades

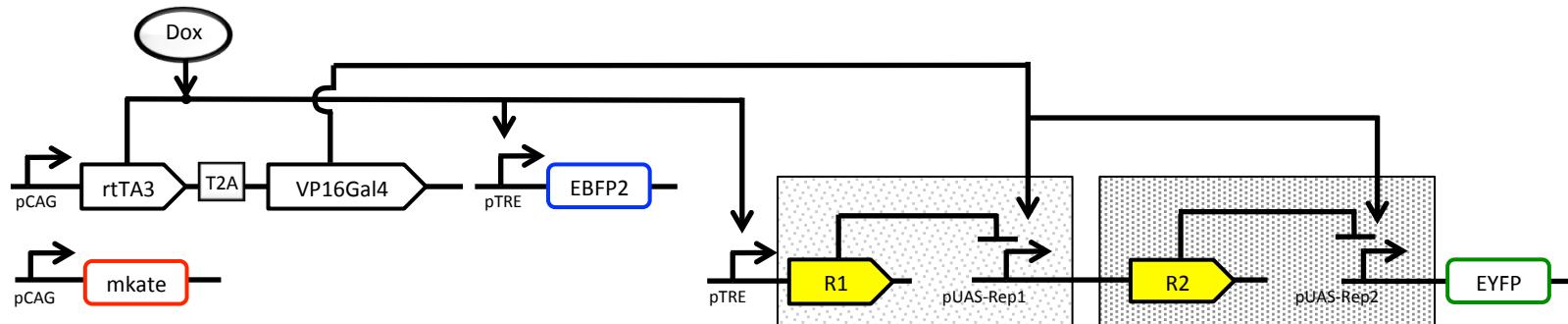


[Kiani et al, Nat.Meth. 2014]

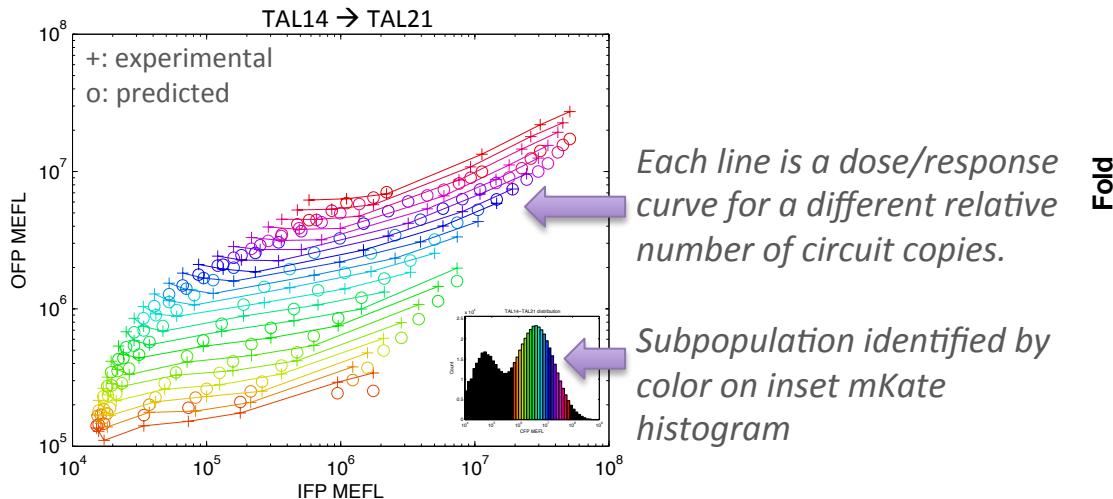


Example: Predicting Repressor Cascades

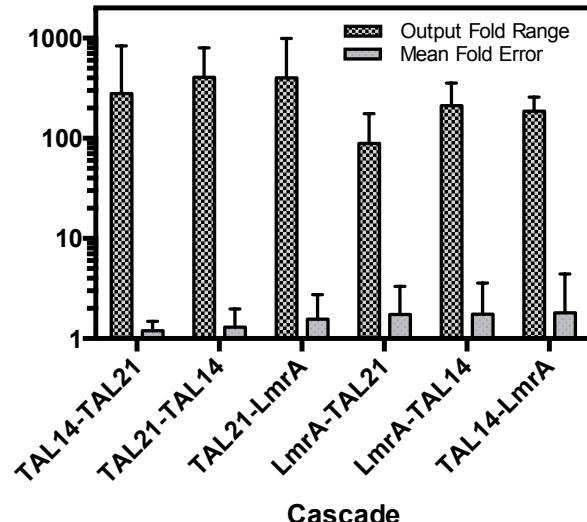
Precision dose-response measurement allows high-precision prediction with quantitative models



Prediction of Repressor Cascade



Range vs. Error for 6 Cascades



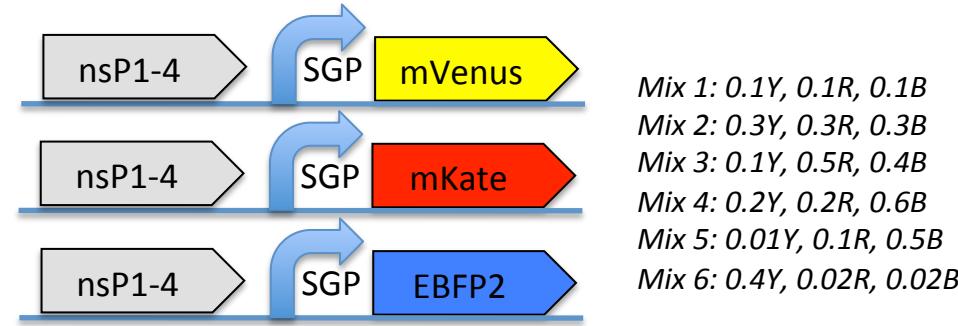
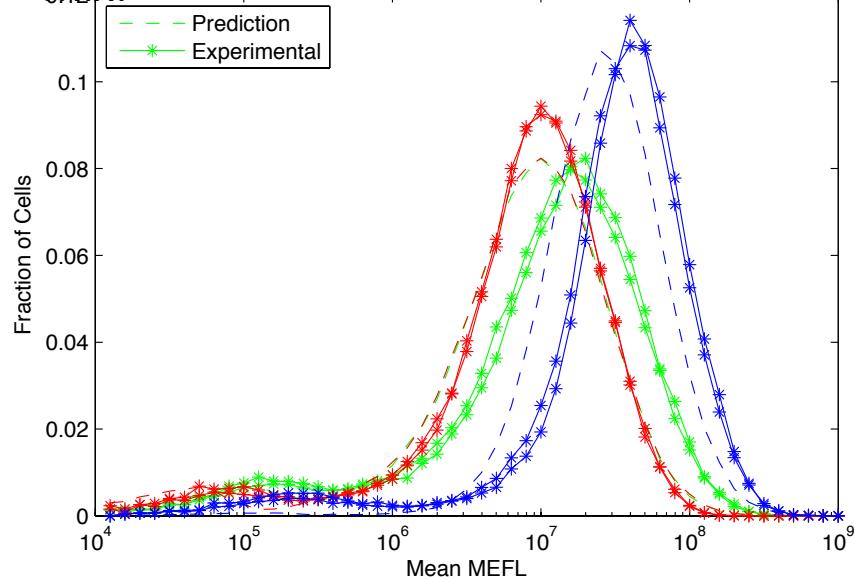
Example: Engineering Replicon Expression

Per-cell measurement of dose-response gives model allowing high-precision control of expression

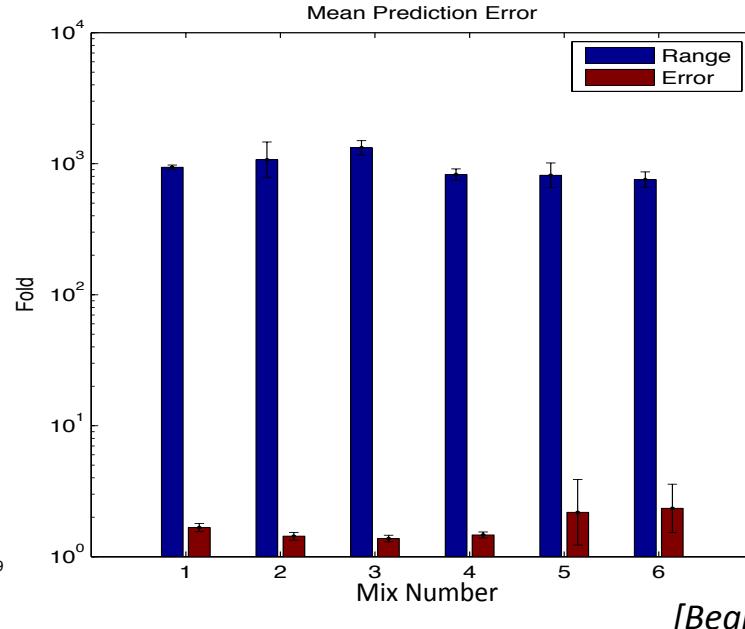
Example:
Prediction of fluorescence vs. time for novel mixtures of 3 Sindbis RNA replicons

Example Prediction of 3-RNA Replicon

Mix:



Range vs. Error for 6 Mixtures



Summary

- Aggregate programming maps from global specifications to local interaction rules
- Field calculus, building block libraries, and substitution relations allow efficient engineering
- Aggregate programming can also be applied to engineering of biological organisms
- New biological devices, measurement, and modeling are starting to enable complex designs

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