

# Efficient Analysis of Population Protocols and Chemical Reaction Networks

Doctoral Defense

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Martin Helfrich 

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# Introduction: Motivation



*“Population protocols and chemical reaction networks are **formal models** in which **many simple entities interact** resulting in a **hard to analyse** system.”*

# Introduction: Use Cases

## Epidemiology

### Sensor Networks



### Social Networks



### Robot Swarms



### Drug Discovery

## Self-Organizing Systems

## Goal of Thesis:

Enable efficient (or “practical”) analysis of these models via:

1. Theoretical results
2. New efficient analysis methods
3. Easily accessible tools

# Introduction: Thesis Overview

## Goal of Thesis:

Enable efficient (or “practical”) analysis of these models via:

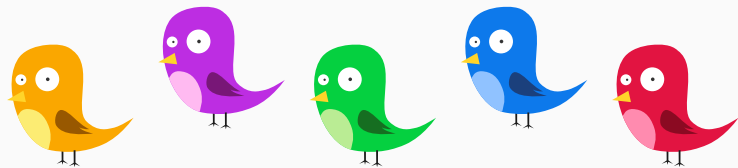
1. Theoretical results
2. New efficient analysis methods
3. Easily accessible tools

## Results of Thesis:

- **Efficient verification of population protocols**  
→ in this talk: focus on tool [Peregrine](#)
- **Synthesis of efficient population protocols**  
→ not in this talk
- **Efficient transient analysis of chemical reaction networks**  
→ in this talk: focus on segmental simulation idea

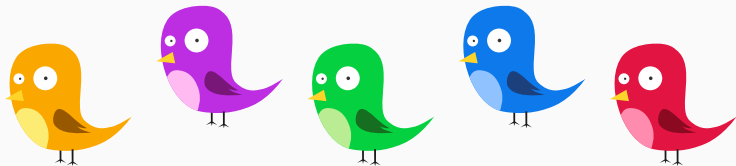
# Population Protocols

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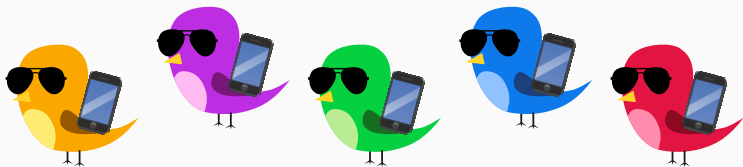
- Anonymous **mobile agents** with very few resources



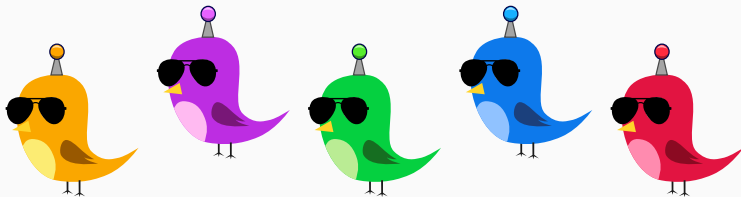
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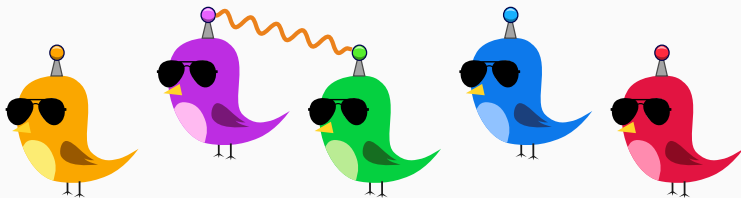
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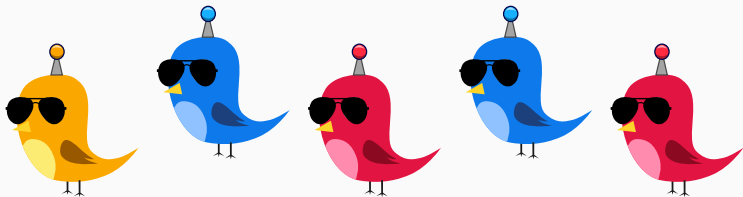
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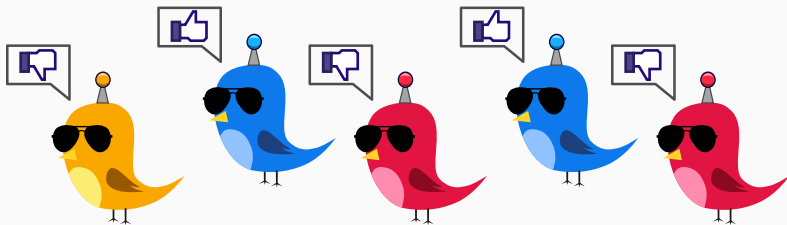
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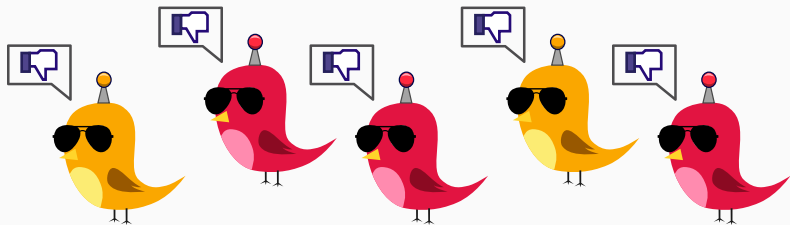
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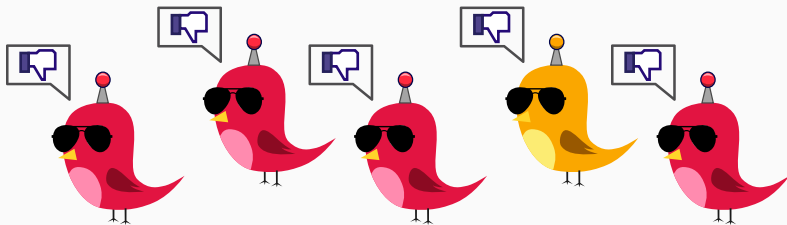


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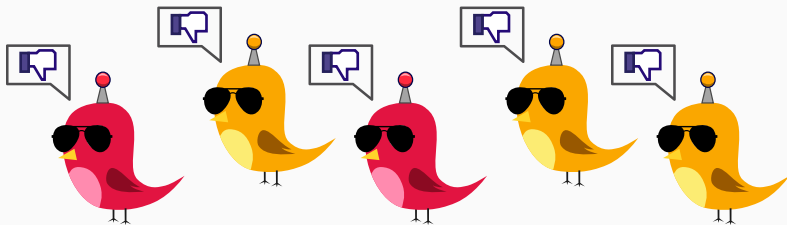




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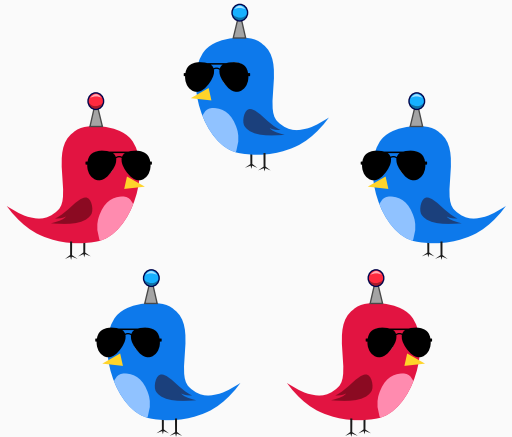


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# Population Protocols: Example

At least as many blue birds as red birds?

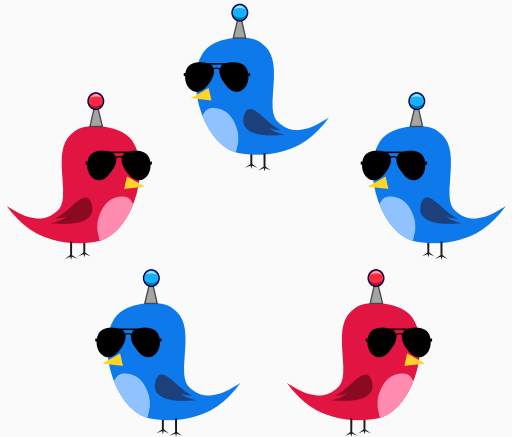


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## Protocol:

- 4 states: blue/red, large/small
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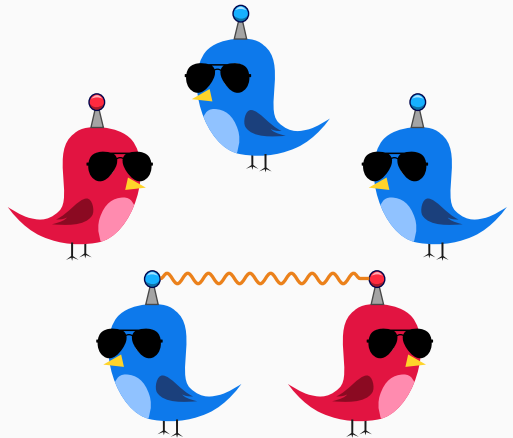


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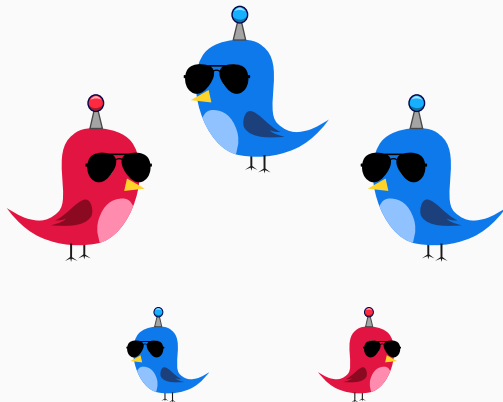


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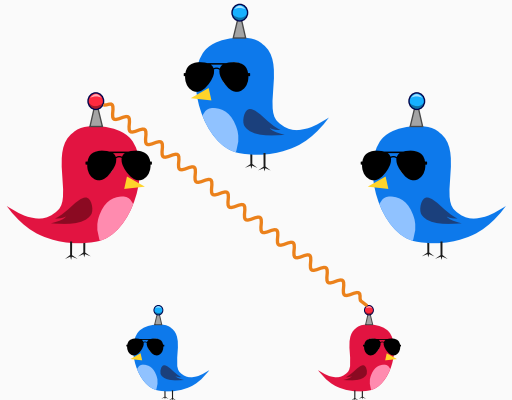


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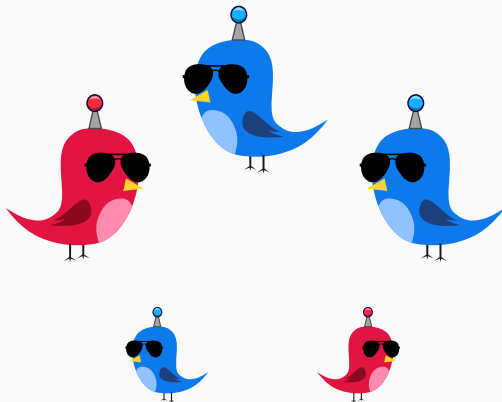


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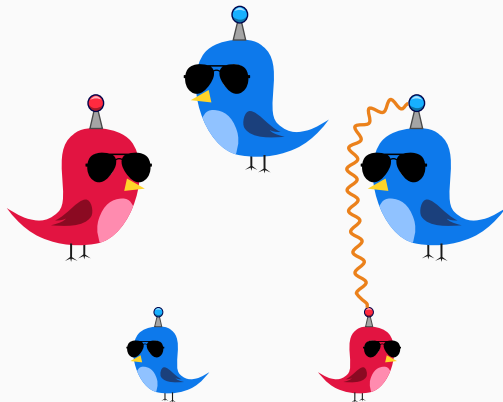


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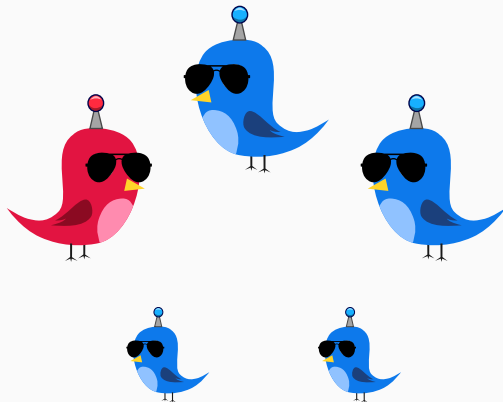


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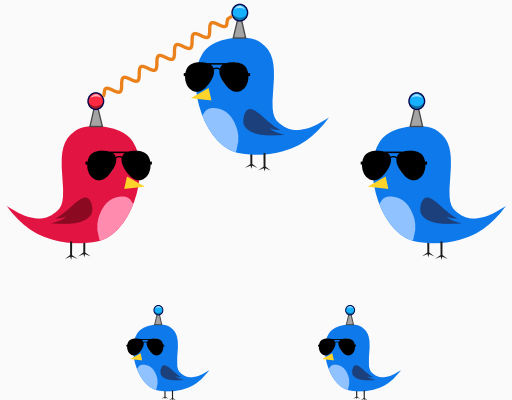


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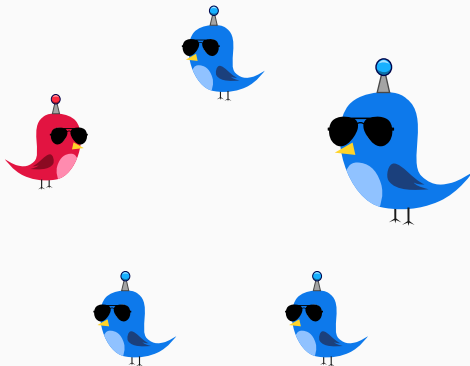


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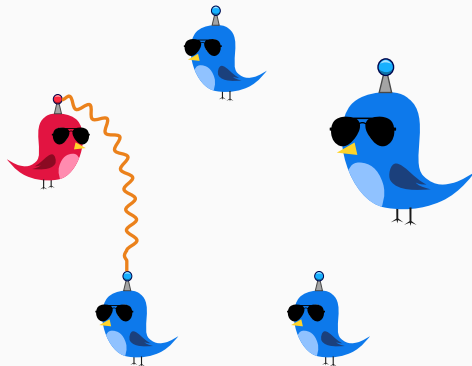


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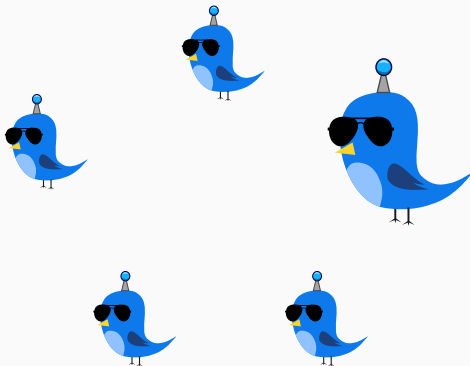


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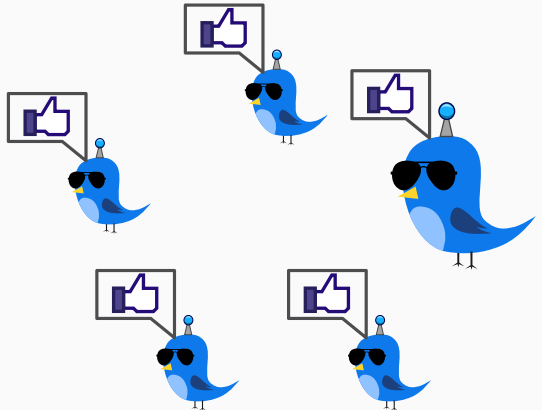


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## Correctness properties:

$$\left( \text{blue}_{\text{large}} \geq \text{red}_{\text{large}} \right) \implies \text{FG} \left( \text{red}_{\text{small}} + \text{red}_{\text{large}} = 0 \right)$$
$$\left( \text{blue}_{\text{large}} < \text{red}_{\text{large}} \right) \implies \text{FG} \left( \text{blue}_{\text{small}} + \text{blue}_{\text{large}} = 0 \right)$$

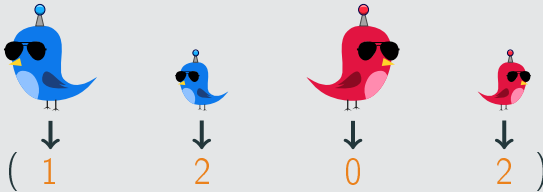
"Birds converge to color of majority."



# Population Protocols: Verification Idea

## Definition: Configuration

A vector describing the number of agents per state:

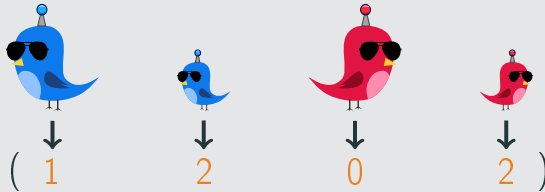


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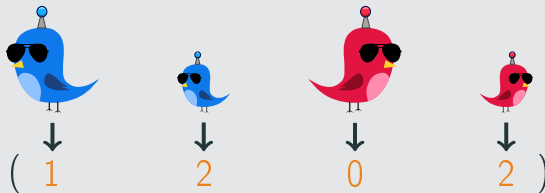
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Correctness proofs are typically structured in **stages** that trap the system in progressively more constrained subsets of configurations.

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→ **Idea:** Formalize structure as **stage graph!**

# Population Protocols: Stage Graphs

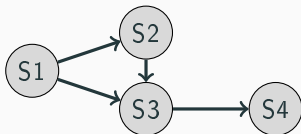
## Definition: Stage Graph

A **stage graph** for  $\varphi_{\text{pre}} \Rightarrow FG\varphi_{\text{post}}$  is a finite DAG satisfying:

1. Each node is an inductive set of configurations, called **stage**.

*"It is impossible to leave stages."*

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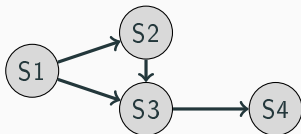
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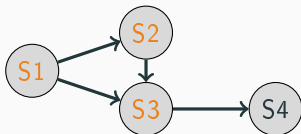
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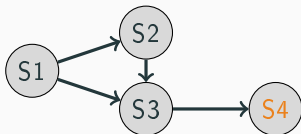
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4. In stages without successors, all configurations satisfy  $\varphi_{\text{post}}$ .  
*"Finally, the postcondition holds forever."*

Example:



## Theory

A population protocol is correct if and only if there is a stage graph proving it.



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A stage graph that is described using only Presburger formulas.

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# Population Protocols: Results

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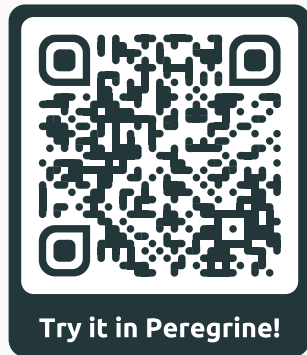
## Practice

- Most systems have small stage graphs
- Most systems make progress by “killing” transitions

→ Use heuristics to efficiently construct Presburger stage graphs

## Stage graphs:

- Can be **efficiently constructed** for most protocols
- **Certify** liveness properties
- Are independently **checkable**
- **Explain** how the protocol works
- Give **speed** guarantees
- Help to find **counter examples**



# Chemical Reaction Networks

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# Chemical Reaction Networks

## Example: Viral Infection

|                       |  |  |
|-----------------------|--|--|
| <b>Species:</b>       | RNA, DNA, V, P   |  |
| <b>Initial state:</b> | (1 × RNA)  |  |
| <b>End time:</b>      | 200s   |  |
| <b>Reactions:</b>     | $\text{DNA} + \text{P} \xrightarrow{0.00001} \text{V}$ $\text{RNA} \xrightarrow{1000} \text{RNA} + \text{P}$ $\text{DNA} \xrightarrow{0.025} \text{DNA} + \text{RNA}$ $\text{RNA} \xrightarrow{1} \text{DNA} + \text{RNA}$ | $\text{RNA} \xrightarrow{0.25} \emptyset$ $\text{P} \xrightarrow{2} \emptyset$ |

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Similar to population protocols but:

- Variable number of molecules
- Continuous time (,i.e., behaves like CTMC not DTMC)
- **Focus on modeling** systems (instead of designing them)

How does the system evolve?

## How does the system evolve?

### Transient analysis:

- Hard because of complex dynamics, state-space explosion, stochasticity, stiffness, multimodality, ...
- Two approaches:
  - Direct (numerical)
  - Indirect (using many trajectories)

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### This work

- **Goal:** Efficiently compute many simulations
- **Idea:** Use memoization!

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- Sample one reaction at a time

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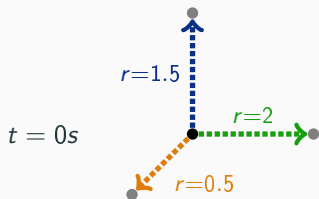
- Sample one reaction at a time

$t = 0s$       ●  
                          $S_{init}$

Start in initial state.

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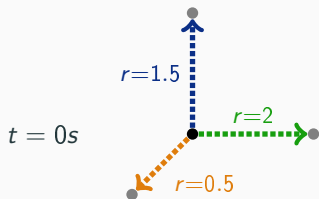
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Compute rate of all reactions.

## Gillespie's stochastic simulation algorithm (SSA) [9]

- Sample one reaction at a time



Time until the next reaction:  $\Delta t \sim EXP(0.5+2+1.5)$

Probability of reactions:  $\frac{0.5}{4}$ ,  $\frac{2}{4}$ ,  $\frac{1.5}{4}$



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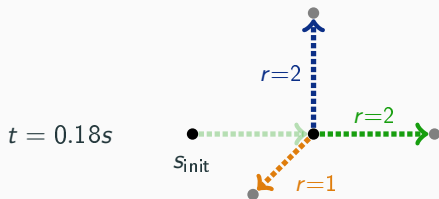
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Apply change to both time and state, then repeat.

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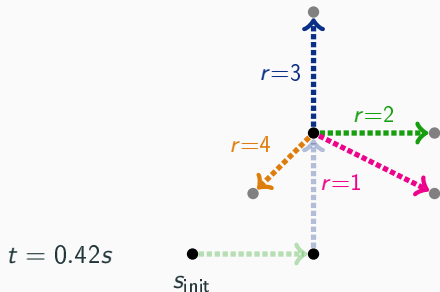


Time until the next reaction:  $\Delta t \sim EXP(1+2+2)$

Probability of reactions:  $\frac{1}{5}, \frac{2}{5}, \frac{2}{5}$

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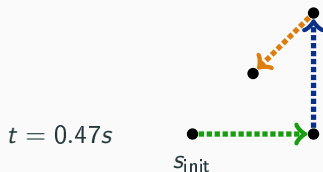


Time until the next reaction:  $\Delta t \sim EXP(4+2+3+1)$

Probability of reactions:  $\frac{4}{10}, \frac{2}{10}, \frac{3}{10}, \frac{1}{10}$

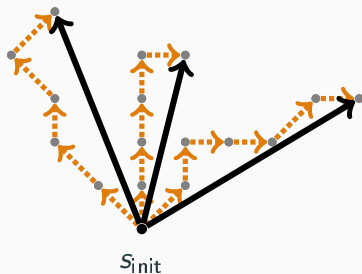
## Gillespie's stochastic simulation algorithm (SSA) [9]

- Sample one reaction at a time
- May take a long time



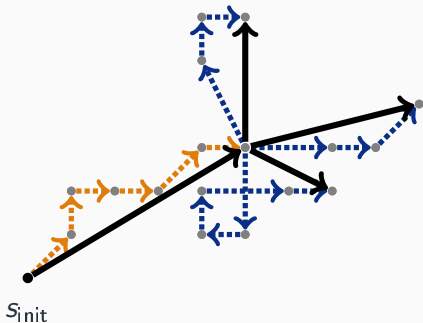
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Precompute  $k$  short trajectories (called **segments**) for each state.  
→ Simulate by sampling segments instead of single reactions.



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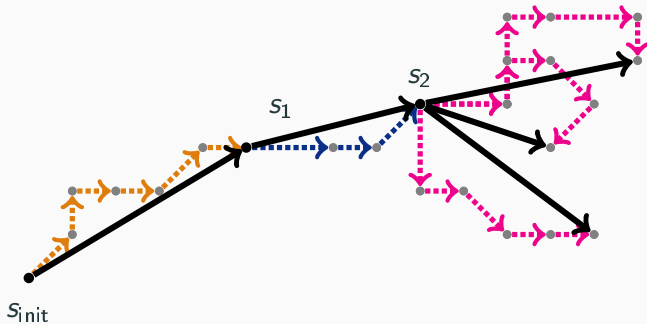
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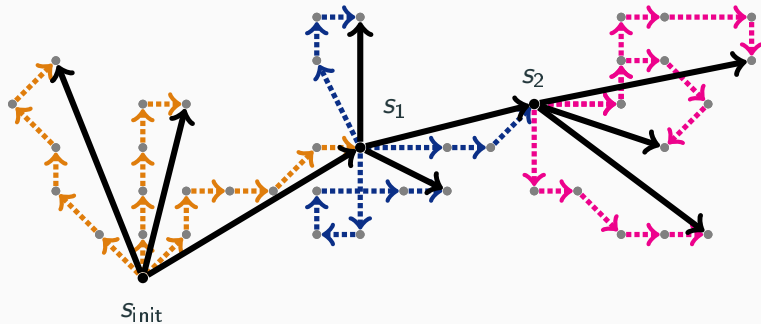
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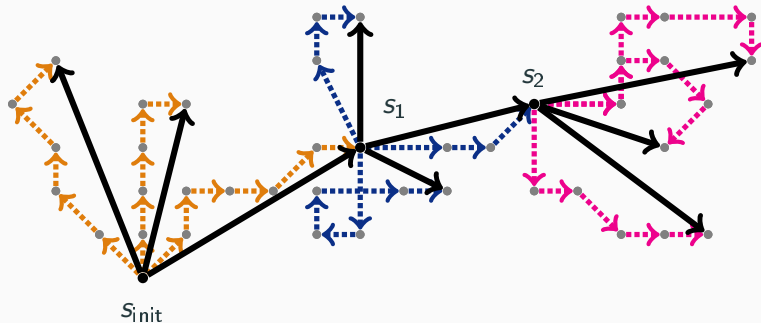
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# CRN: Segmental Simulation

Precompute  $k$  short trajectories (called **segments**) for each state.

→ Simulate by sampling segments instead of single reactions.



- much faster!
- **Problem:** many states → too inefficient

# CRN: Abstraction-Based Segmental Simulation

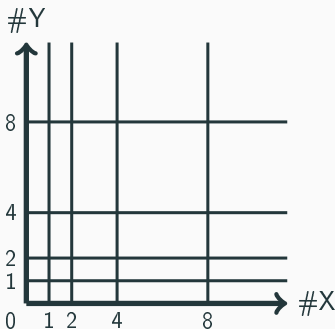
- **Idea:** Do not treat every state separately!

# CRN: Abstraction-Based Segmental Simulation

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- States with similar species counts have similar propensities  
→ their behavior is similar

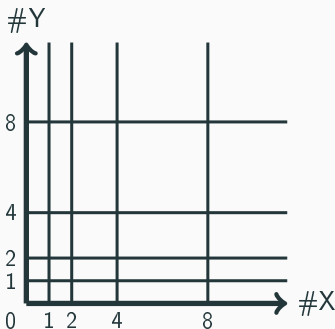
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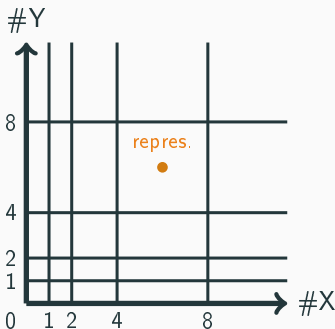
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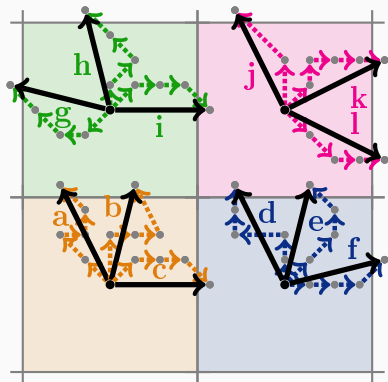
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Only precompute  $k$  segments for each representative.



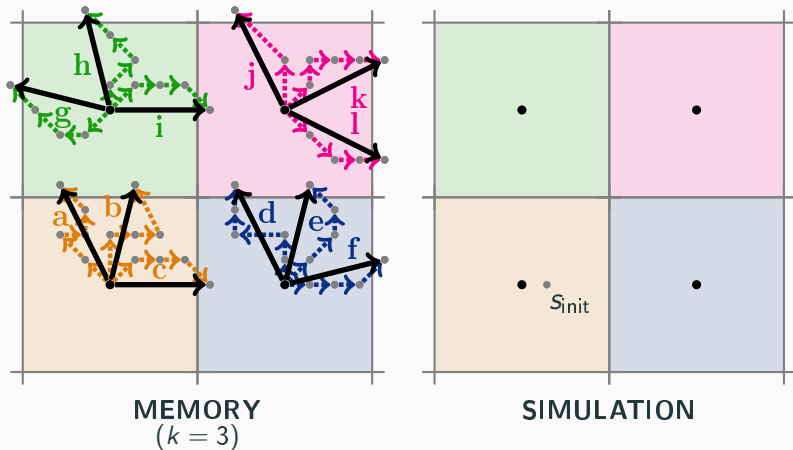
**MEMORY**  
( $k = 3$ )

Segments end when they leave the abstract state.

→ Intuition: "*significant change*"

# CRN: Abstraction-Based Segmental Simulation

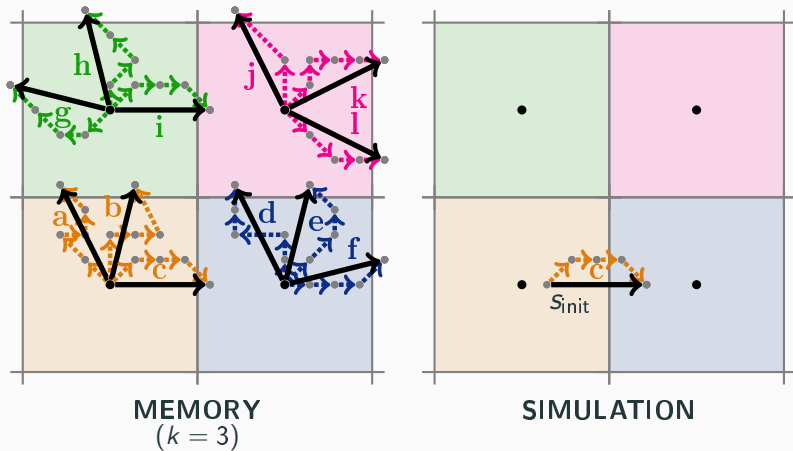
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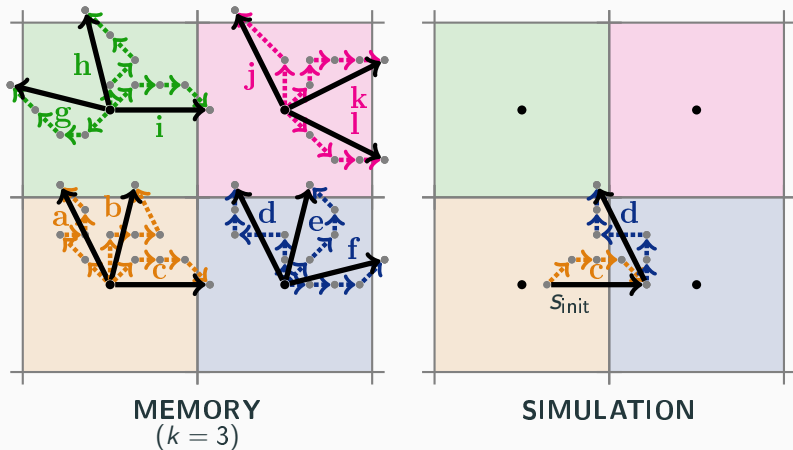
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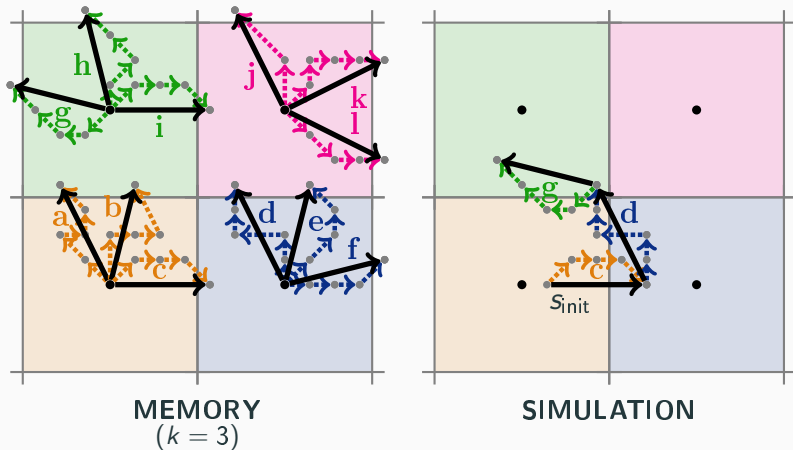
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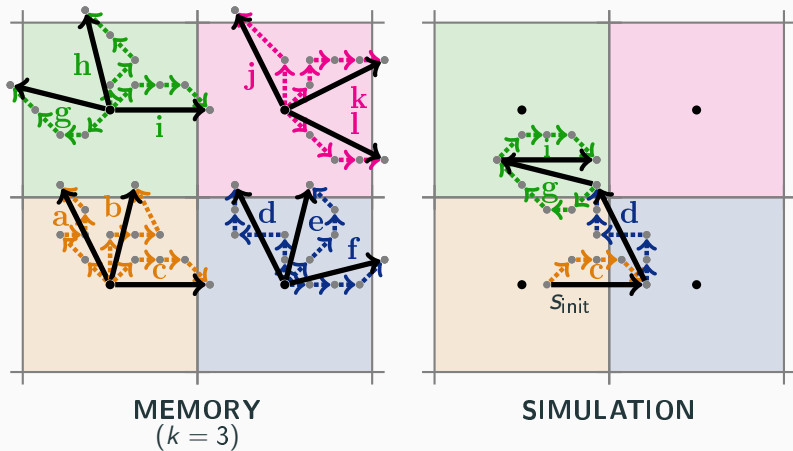
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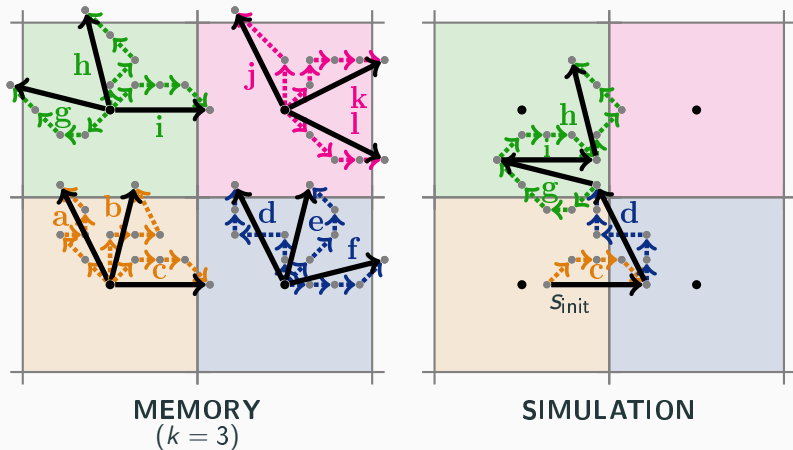
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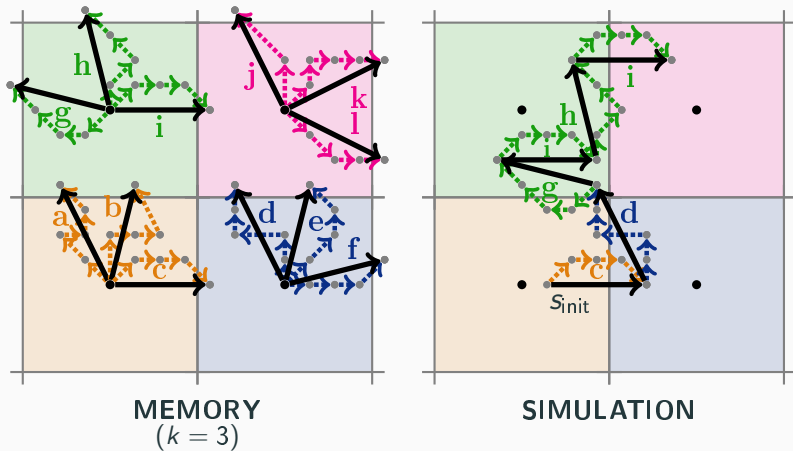
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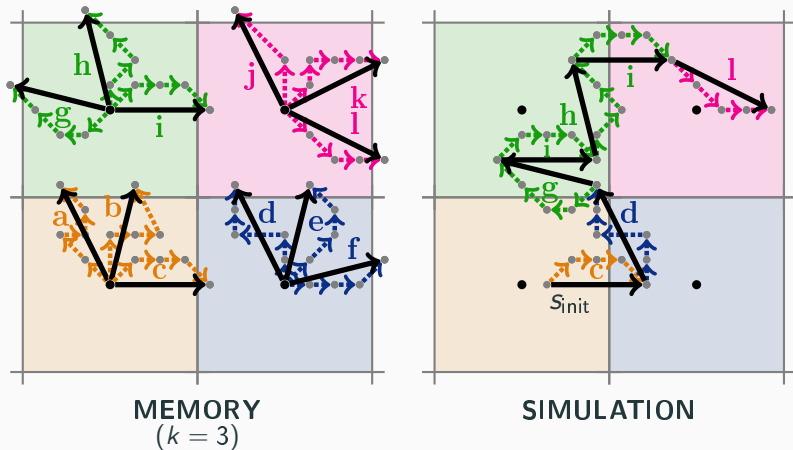
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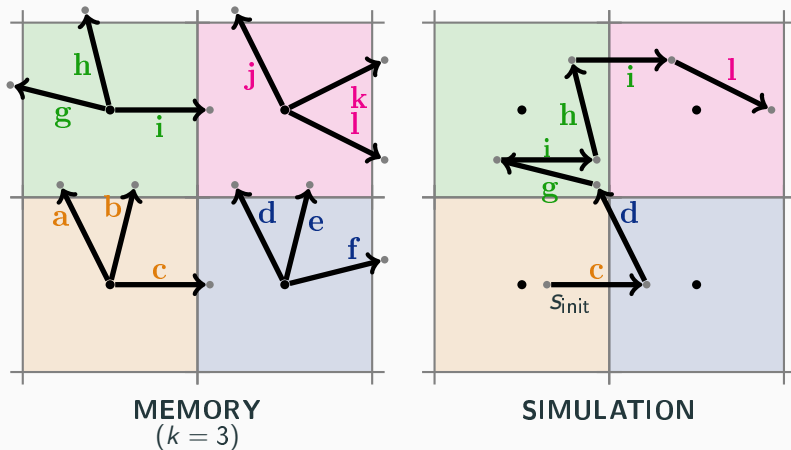
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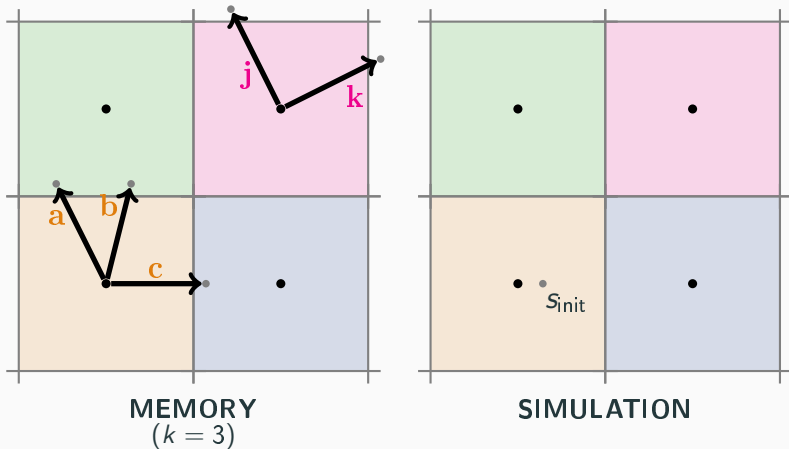


To save memory: Work with **summaries** instead of segments.



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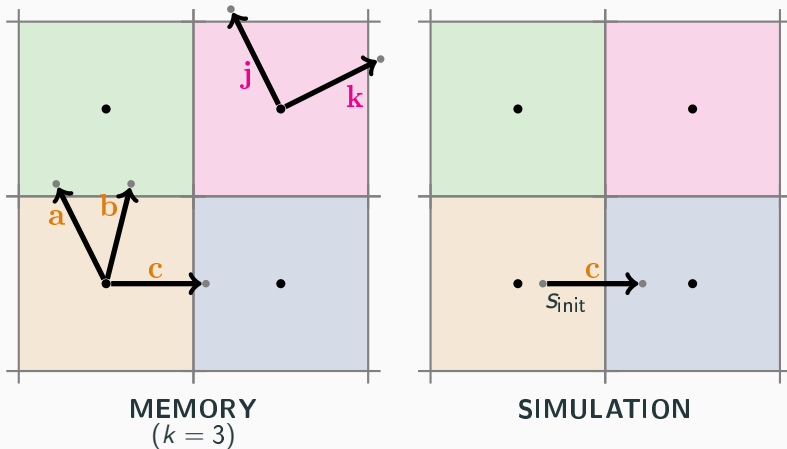
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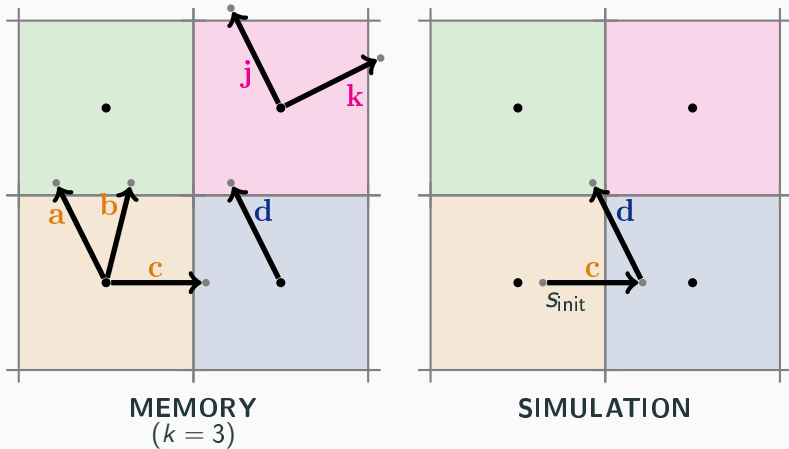
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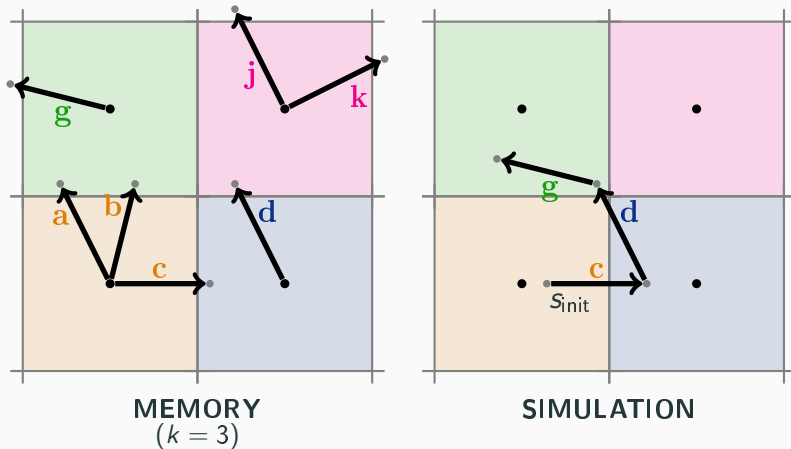
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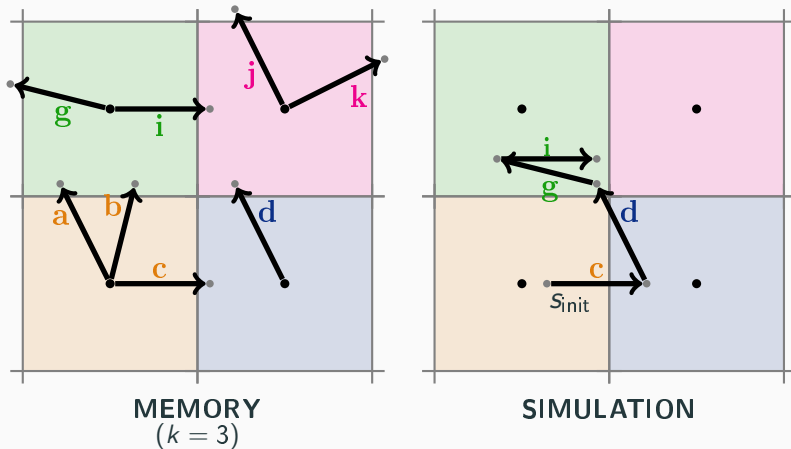
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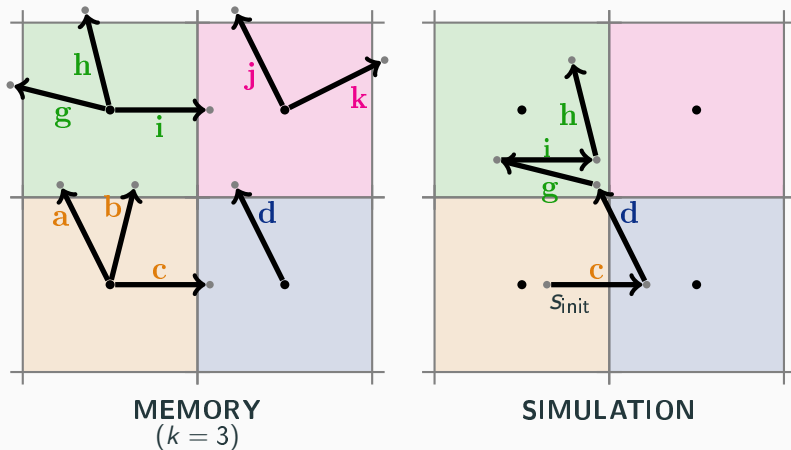
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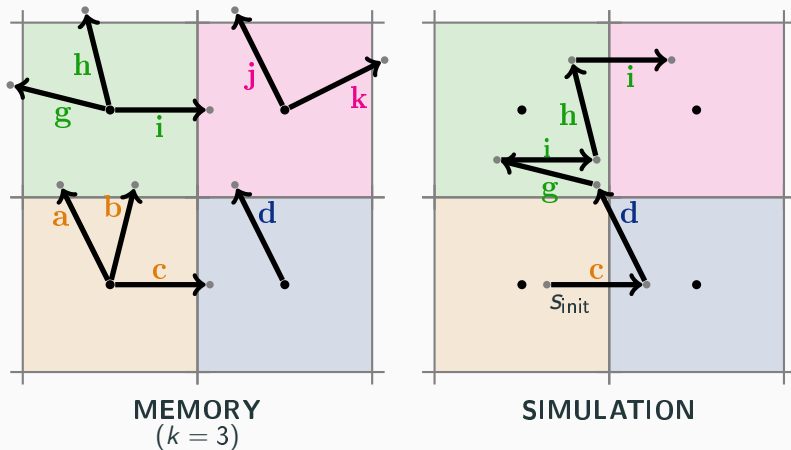
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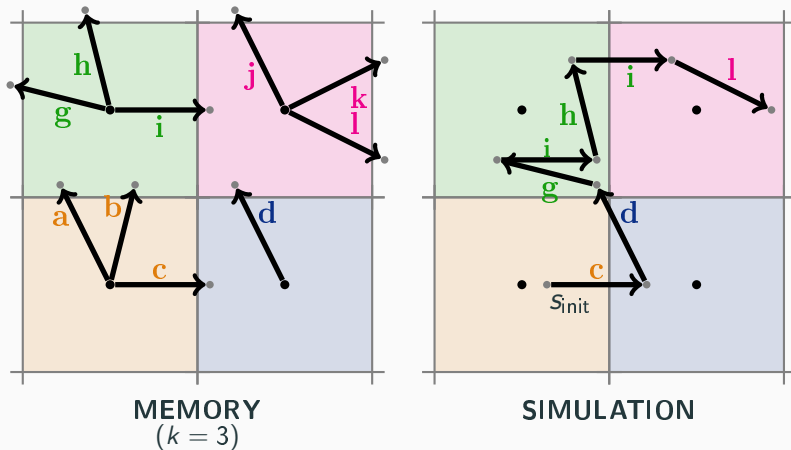
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## Segmental simulation:

- Reuses previous simulations to generate new ones
- Is an approximate simulation technique
- Accurately captures dynamics of most systems
- Speeds up transient analysis (up to 4000x faster)
- Efficiently predict the behavior of CRNs



Thank you



THANK YOU!

## First Author:

- Checking Qualitative Liveness Properties of Replicated Systems with Stochastic Scheduling (CAV'20) [3]
- Peregrine 2.0: Explaining Correctness of Population Protocols Through Stage Graphs (ATVA'20) [8]
- Abstraction-Based Segmental Simulation of Chemical Reaction Networks (CMSB'22) [10]

## Non-first Author:

- Succinct Population Protocols for Presburger Arithmetic (STACS'20) [2]
- Fast and Succinct Population Protocols for Presburger Arithmetic (SAND'22) [5]

## Others (not part of thesis):

- Automata Tutor v3 (CAV20) [7]
- Decision Power of Weak Asynchronous Models of Distributed Computing (PODC'21) [4]
- Fast and succinct population protocols for Presburger arithmetic (Journal of Comp. and Sys. Sciences 2023) [6]

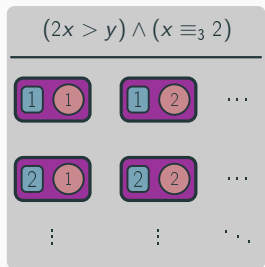
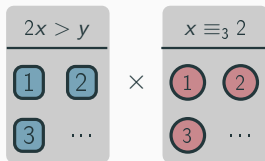
# Population Protocol: Synthesis

## Our result

For every quantifier-free Presburger formula  $\varphi$  there is a population protocol which

- has  $\mathcal{O}(\text{POLY}(|\varphi|))$  states,  
→ *succinct*
- for  $n$  agents stabilizes in  $\mathcal{O}(n^2 \log n)$  expected interactions, and  
→ *fast*
- can be constructed efficiently.

$$(2x > y) \wedge (x \equiv_3 2)$$



# Population Protocol: Synthesis Idea

## Idea:

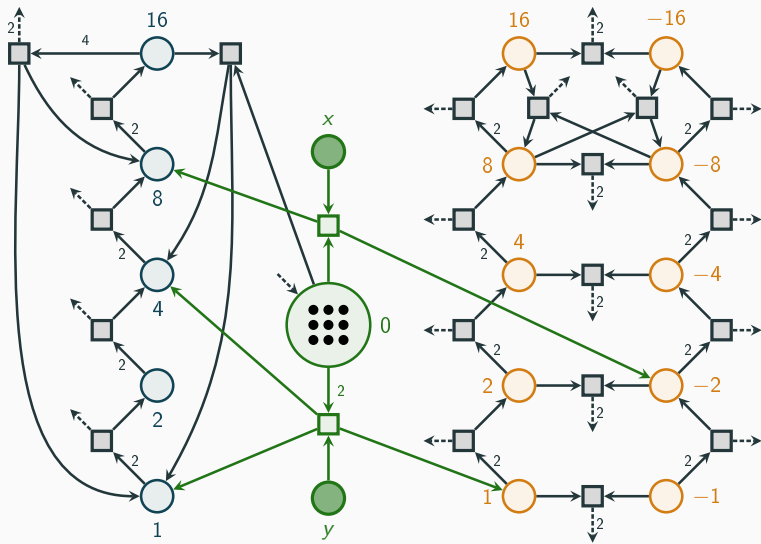
- **Binary** value representation  
(instead of unary)
- Agents participate in computation of only **one** atomic formula  
(instead of in all)

## Population Computer

Like population protocol but easier to design because:

- k-way transitions
- Helper agents
- More flexible output definition

# Population Protocol: Synthesis (Fast and Succinct)



$$8x + 5y \equiv_{11} 4$$

$\vee$

$$y - 2x \geq 5$$



- [1] Angluin, D., Aspnes, J., Diamadi, Z., Fischer, M.J., Peralta, R.: Computation in networks of passively mobile finite-state sensors. p. 290–299. PODC '04, Association for Computing Machinery, New York, NY, USA (2004). <https://doi.org/10.1145/1011767.1011810>
- [2] Blondin, M., Esparza, J., Genest, B., Helfrich, M., Jaax, S.: Succinct Population Protocols for Presburger Arithmetic. In: Paul, C., Bläser, M. (eds.) 37th International Symposium on Theoretical Aspects of Computer Science (STACS 2020). Leibniz International Proceedings in Informatics (LIPIcs), vol. 154, pp. 40:1–40:15. Schloss Dagstuhl–Leibniz-Zentrum für Informatik, Dagstuhl, Germany (2020). <https://doi.org/10.4230/LIPIcs.STACS.2020.40>
- [3] Blondin, M., Esparza, J., Helfrich, M., Kučera, A., Meyer, P.J.: Checking qualitative liveness properties of replicated systems with stochastic scheduling. In: Lahiri, S.K., Wang, C. (eds.) Computer Aided Verification. pp. 372–397. Springer International Publishing, Cham (2020). [https://doi.org/10.1007/978-3-030-53291-8\\_20](https://doi.org/10.1007/978-3-030-53291-8_20)

- [4] Czerner, P., Guttenberg, R., Helfrich, M., Esparza, J.: Decision power of weak asynchronous models of distributed computing. p. 115–125. PODC'21, Association for Computing Machinery, New York, NY, USA (2021).  
<https://doi.org/10.1145/3465084.3467918>,  
<https://doi.org/10.1145/3465084.3467918>
- [5] Czerner, P., Guttenberg, R., Helfrich, M., Esparza, J.: Fast and Succinct Population Protocols for Presburger Arithmetic. In: Aspnes, J., Michail, O. (eds.) 1st Symposium on Algorithmic Foundations of Dynamic Networks (SAND 2022). Leibniz International Proceedings in Informatics (LIPIcs), vol. 221, pp. 11:1–11:17. Schloss Dagstuhl – Leibniz-Zentrum für Informatik, Dagstuhl, Germany (2022). <https://doi.org/10.4230/LIPIcs.SAND.2022.11>
- [6] Czerner, P., Guttenberg, R., Helfrich, M., Esparza, J.: Fast and succinct population protocols for presburger arithmetic. *Journal of Computer and System Sciences* **140**, 103481 (2024).  
<https://doi.org/https://doi.org/10.1016/j.jcss.2023.103481>,  
<https://www.sciencedirect.com/science/article/pii/S0022000023000867>

- [7] D'Antoni, L., Helfrich, M., Kretinsky, J., Ramneantu, E., Weininger, M.: Automata tutor v3. In: Lahiri, S.K., Wang, C. (eds.) *Computer Aided Verification*. pp. 3–14. Springer International Publishing, Cham (2020). [https://doi.org/10.1007/978-3-030-53291-8\\_1](https://doi.org/10.1007/978-3-030-53291-8_1)
- [8] Esparza, J., Helfrich, M., Jaax, S., Meyer, P.J.: Peregrine 2.0: Explaining correctness of population protocols through stage graphs. In: Hung, D.V., Sokolsky, O. (eds.) *Automated Technology for Verification and Analysis*. pp. 550–556. Springer International Publishing, Cham (2020). [https://doi.org/10.1007/978-3-030-59152-6\\_32](https://doi.org/10.1007/978-3-030-59152-6_32)
- [9] Gillespie, D.T.: Exact stochastic simulation of coupled chemical reactions. *The Journal of Physical Chemistry* **81**(25), 2340–2361 (12 1977). <https://doi.org/10.1021/j100540a008>
- [10] Helfrich, M., Češka, M., Křetínský, J., Martiček, Š.: Abstraction-based segmental simulation of chemical reaction networks. In: Petre, I., Păun, A. (eds.) *Computational Methods in Systems Biology*. pp. 41–60. Springer International Publishing, Cham (2022). [https://doi.org/10.1007/978-3-031-15034-0\\_3](https://doi.org/10.1007/978-3-031-15034-0_3)