

Executable Biology

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Modeling of biological objects (e.g. cells) and processes (e.g. pathways) as interacting computer programs.

Biology

-complex natural systems

Computer Science

-complex engineered systems

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- primacy of system

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- primacy of method (“algorithm”)

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-*numeric; stochastic:*
continuous variables

Science of approximation:
bounds errors

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-*symbolic; causalistic:*
discrete events

Science of abstraction:
preserves properties

Computational Science

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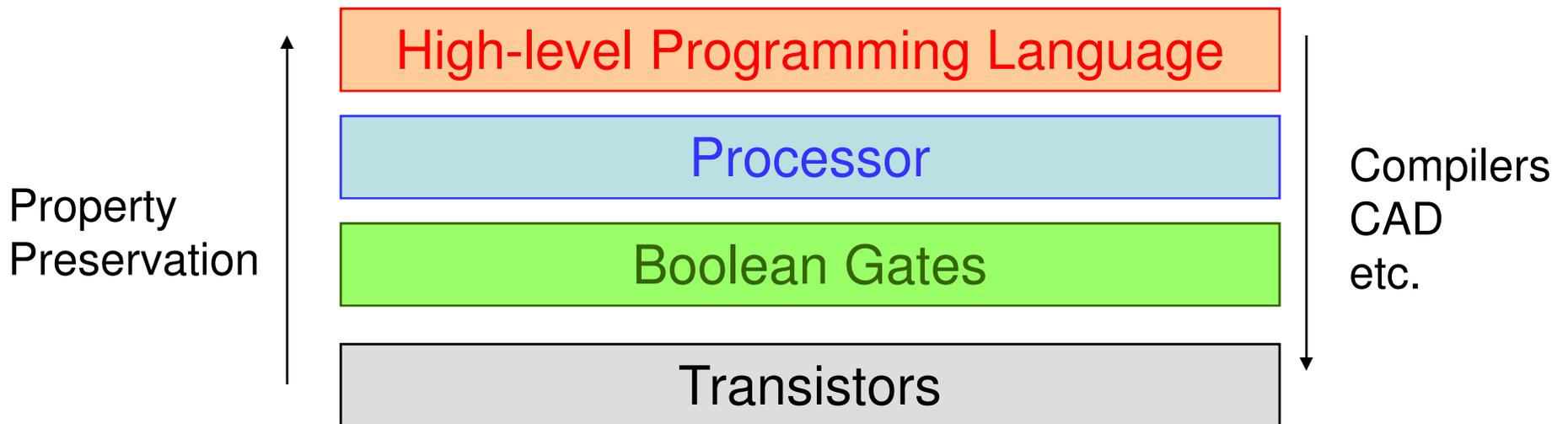
Science of abstraction:
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The Essence of Computer Science

1. Algorithms

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2. Towers of Abstraction

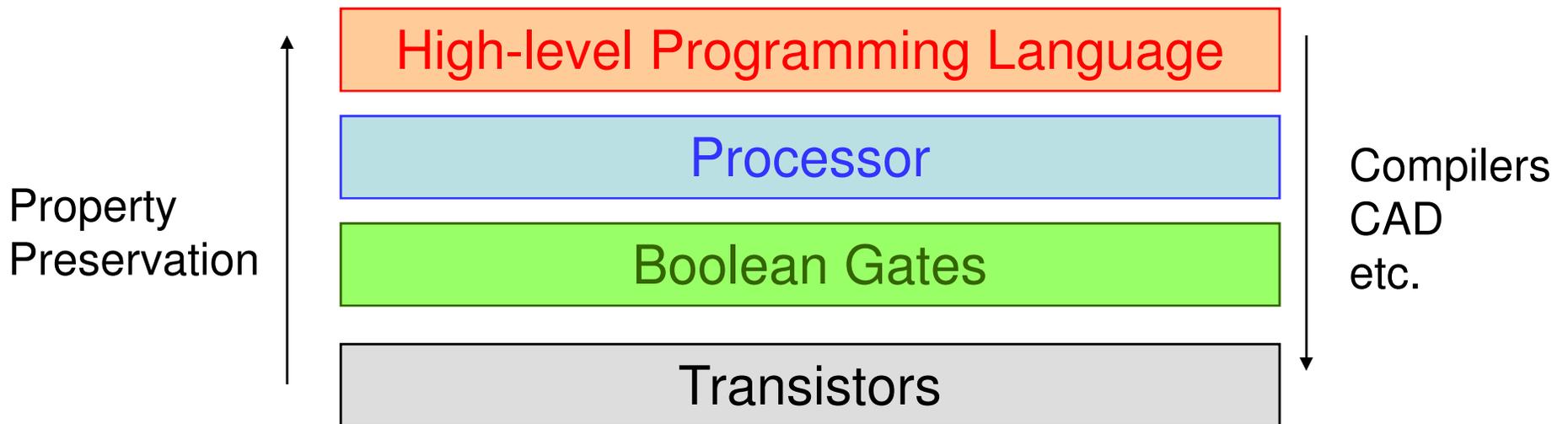


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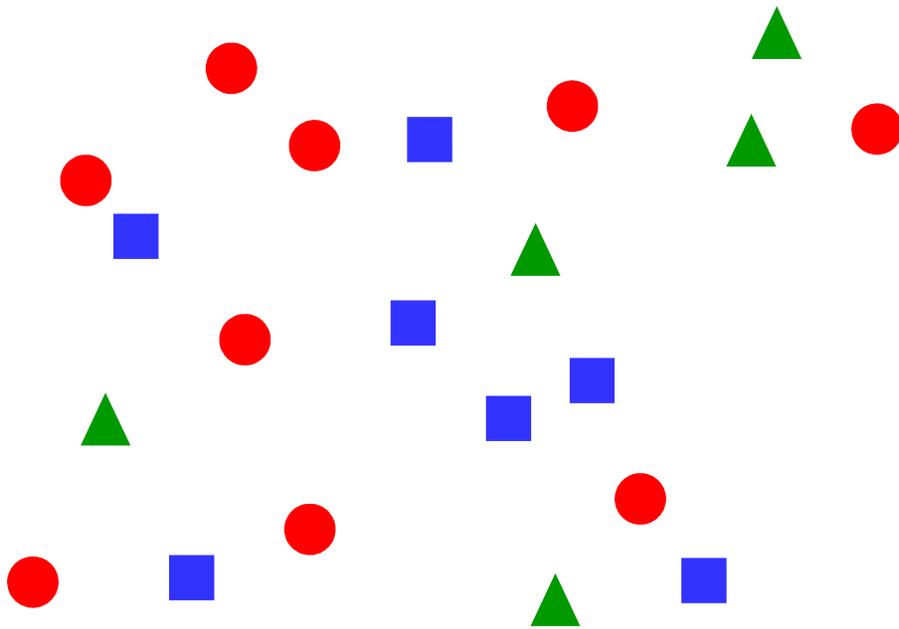
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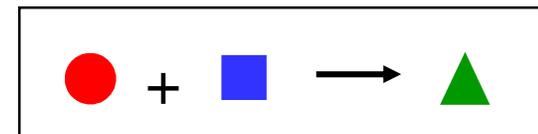
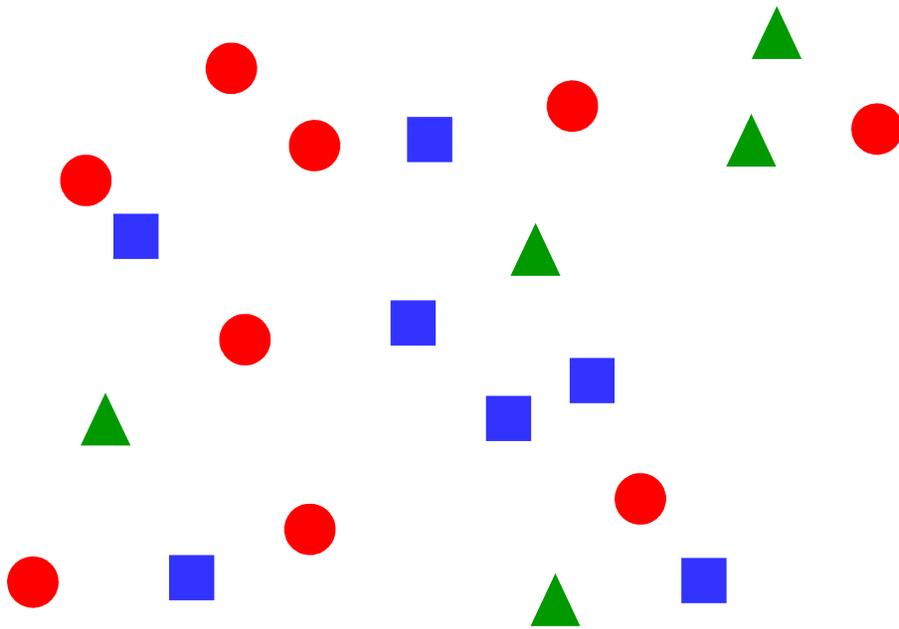
Cloud
Virtual Machine



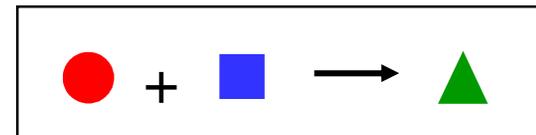
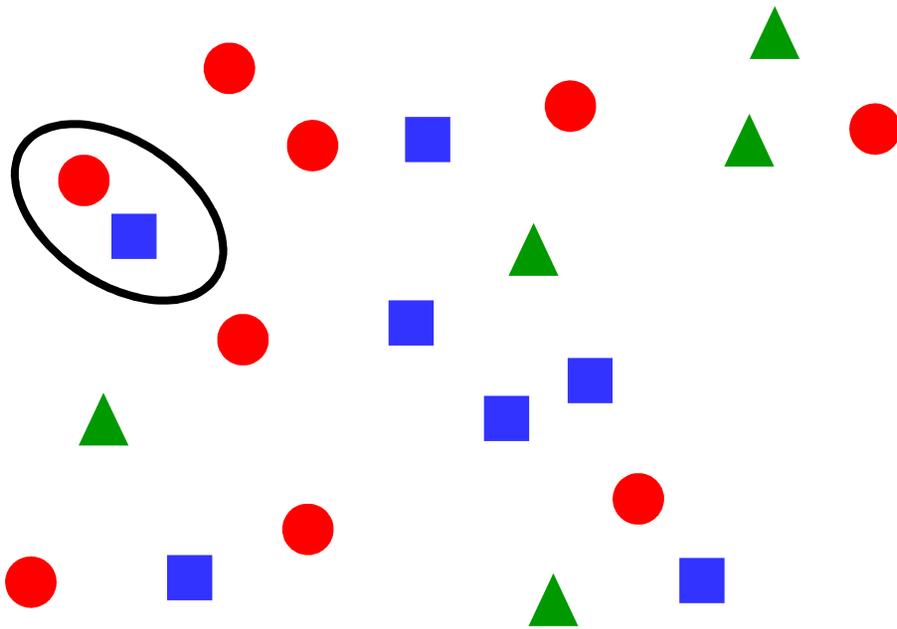
Markovian Population Models



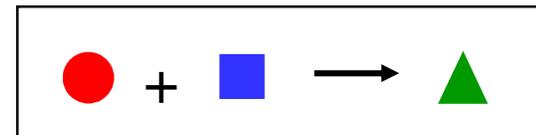
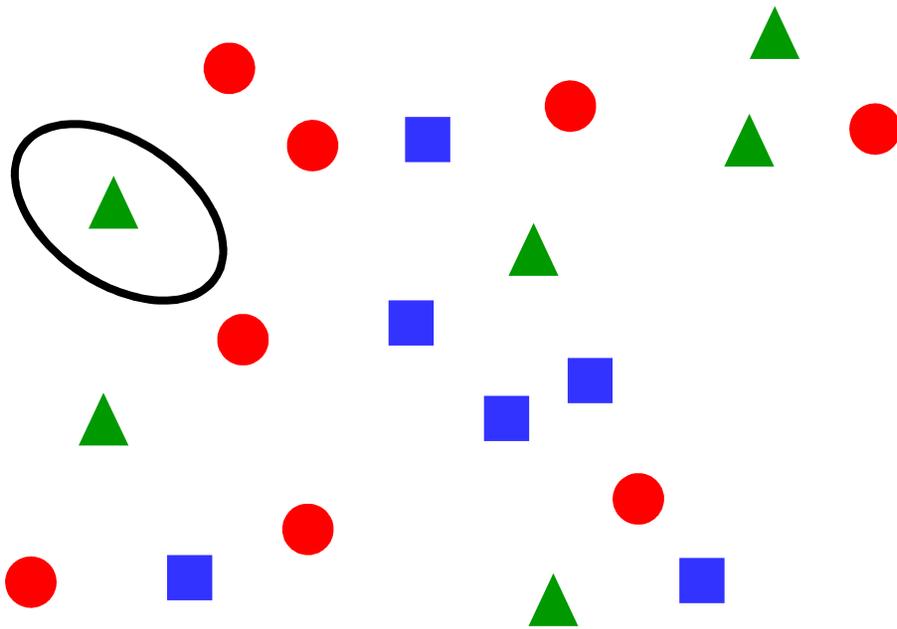
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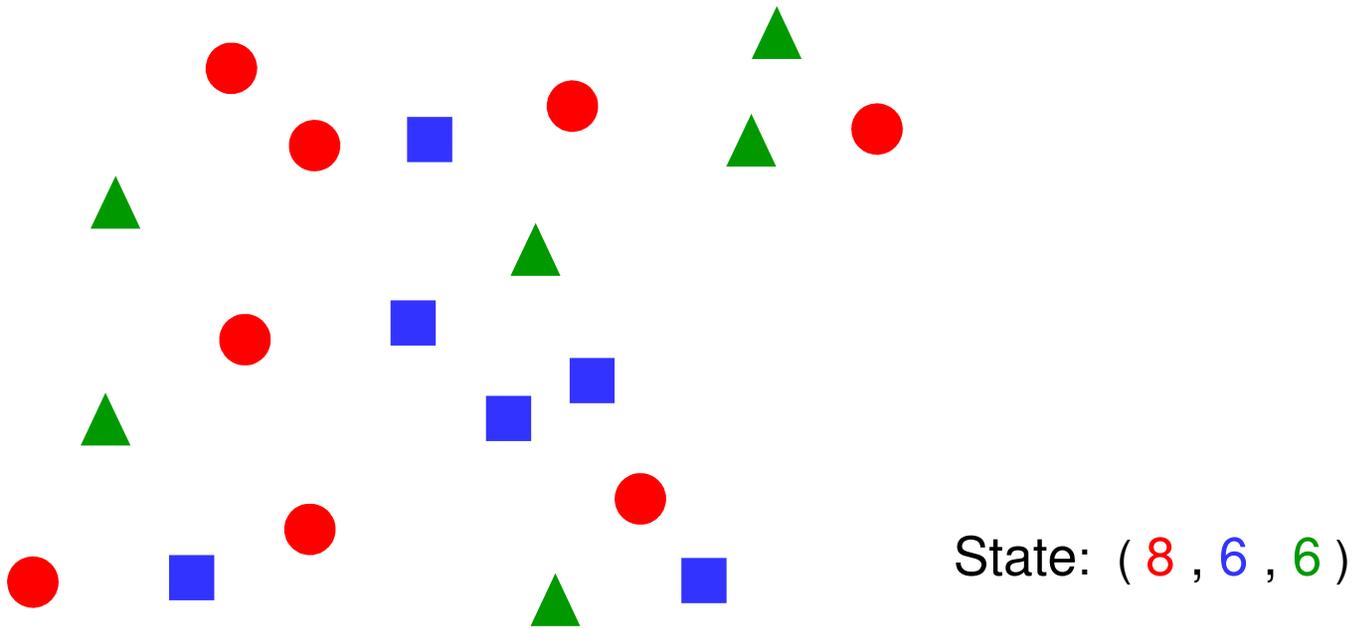
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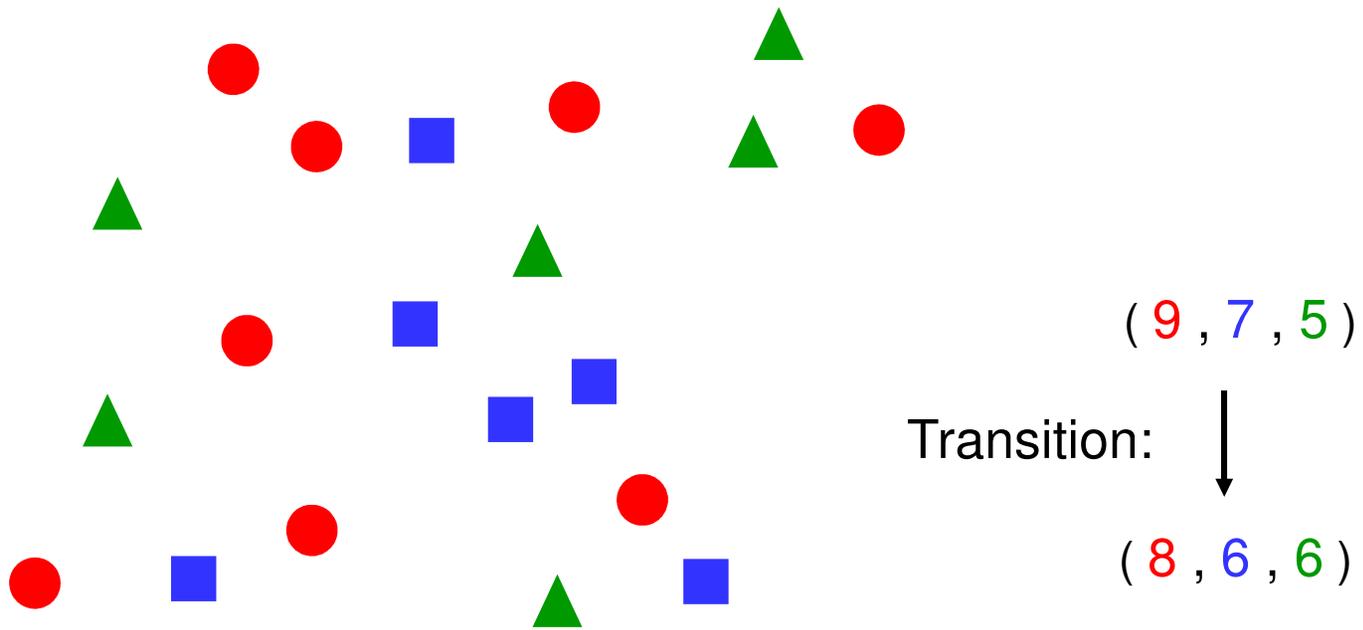
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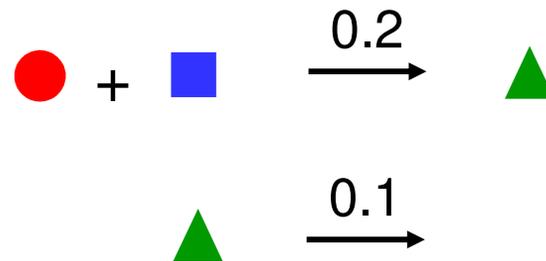
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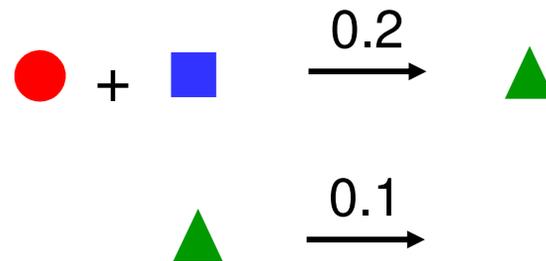


Markovian Population Models

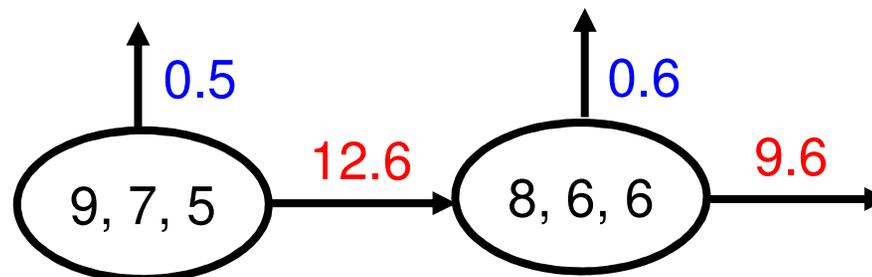


Syntax: stoichiometric equations (finite object)

Markovian Population Models



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Semantics: CTMC (infinite object)

Syntax: Guarded Commands

Dimension n : state $(x_1, \dots, x_n) \in S$
state space $S = \mathbb{N}^n$

$n = 3$

Finite set of guarded commands:

each consists of

1. guard $G \subseteq S$
2. update function $u: G \rightarrow S$
3. rate function $\alpha: G \rightarrow \mathbb{R}^+$

$$\begin{aligned} G_1: x_1 \geq 1 \wedge x_2 \geq 1 \\ u_1(x_1, x_2, x_3) = (x_1 - 1, x_2 - 1, x_3 + 1) \\ \alpha_1(x_1, x_2, x_3) = 0.2 \cdot x_1 \cdot x_2 \end{aligned}$$

$$\begin{aligned} G_3: x_3 \geq 1 \\ u_3(x_1, x_2, x_3) = (x_1, x_2, x_3 - 1) \\ \alpha_3(x_1, x_2, x_3) = 0.1 \cdot x_3 \end{aligned}$$

Syntax matters!

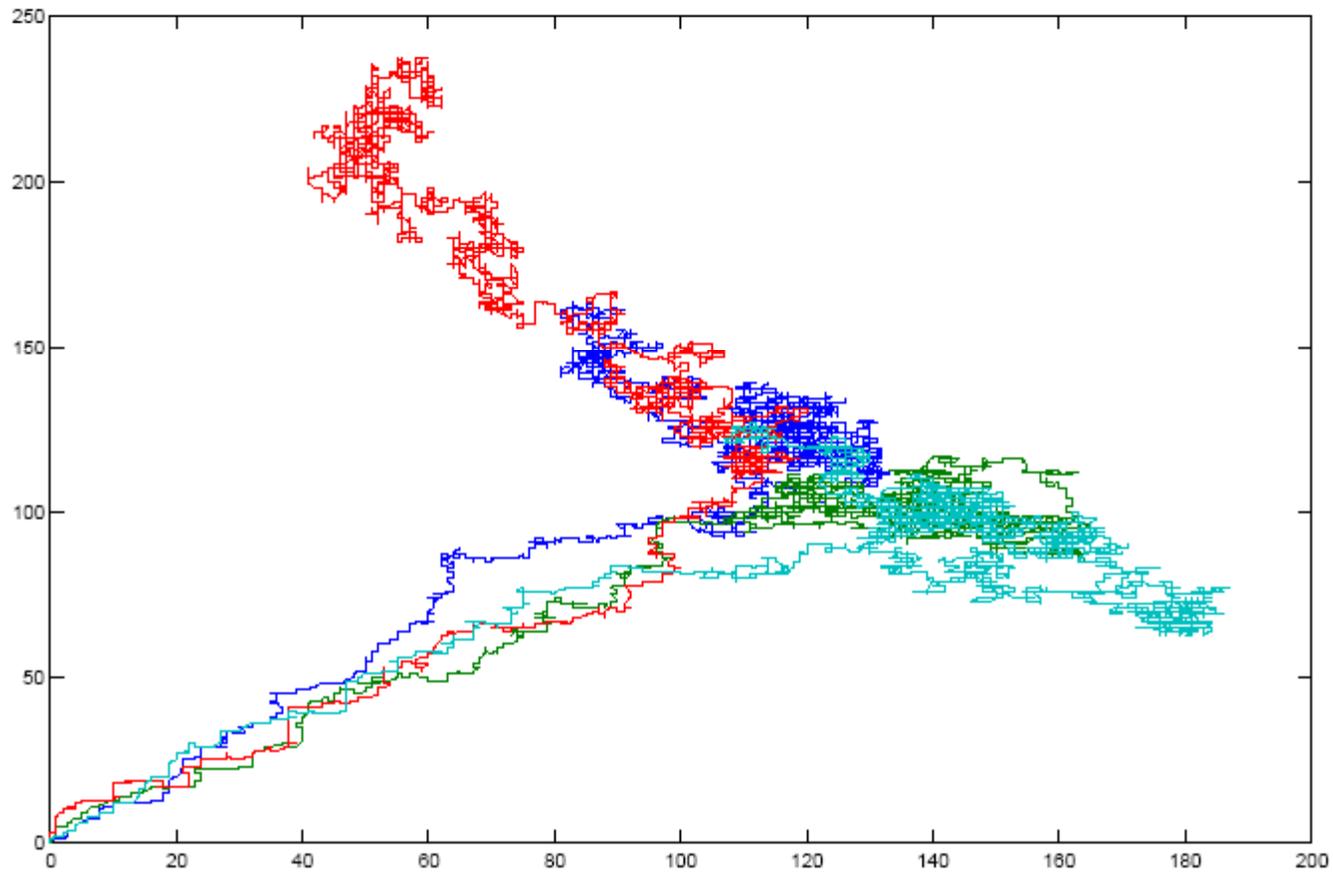
1. Composition and compositionality
2. Expressiveness and succinctness
3. Executability
4. Encapsulation and abstraction

e.g. Petri nets: not compositional
 Stoichiometric equations: not expressive
 Rate matrices: not succinct
 Differential equations: not executable

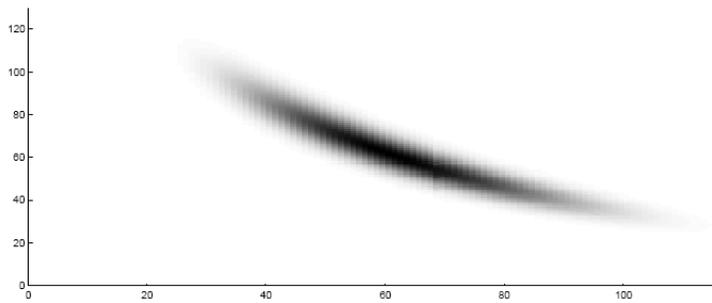
Guarded Commands

- compositional
- expressive and succinct
- executable
- counterexample-guided abstraction refinement
- model checking

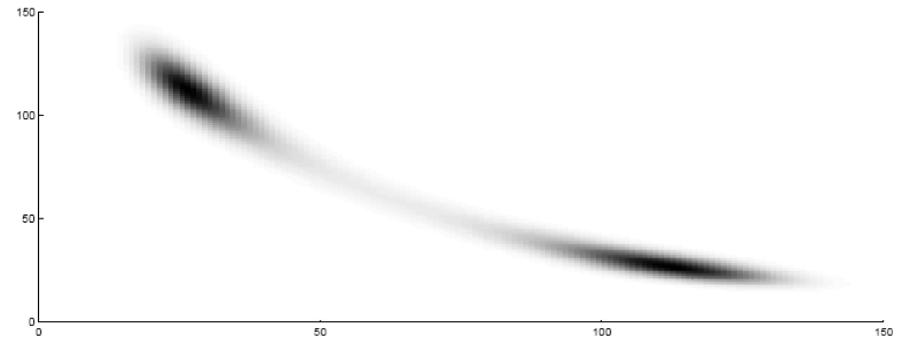
Genetic Toggle Switch: Four Simulation Runs



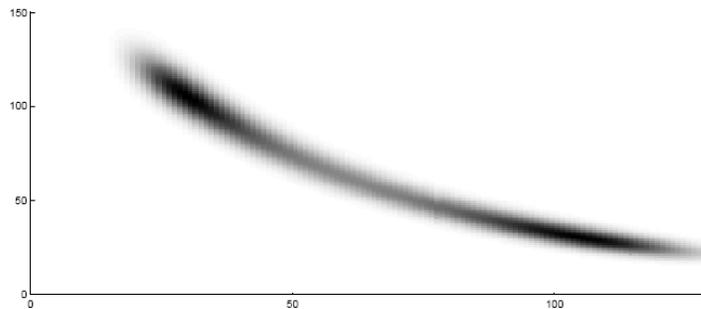
Genetic Toggle Switch: Model Checking [DHMW09]



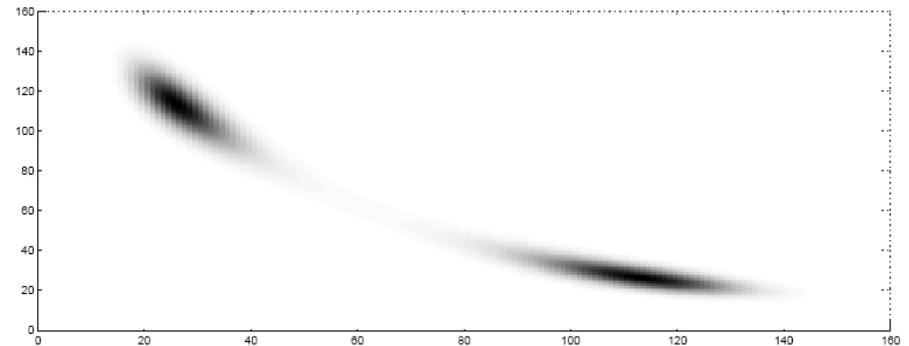
$t = 5000$



$t = 30000$



$t = 15000$



$t = 50000$

Bacteriophage λ Model [DHMW09]

Desired precision:	3×10^{-6}
Model checking:	55 min runtime
Gillespie simulation ($\beta = 0.95$):	67 h runtime (3×10^8 runs)

Model Checking CTMCs [DHMW09]

Transient distributions can be efficiently approximated by combining adaptive uniformization with ideas from Computer Science:

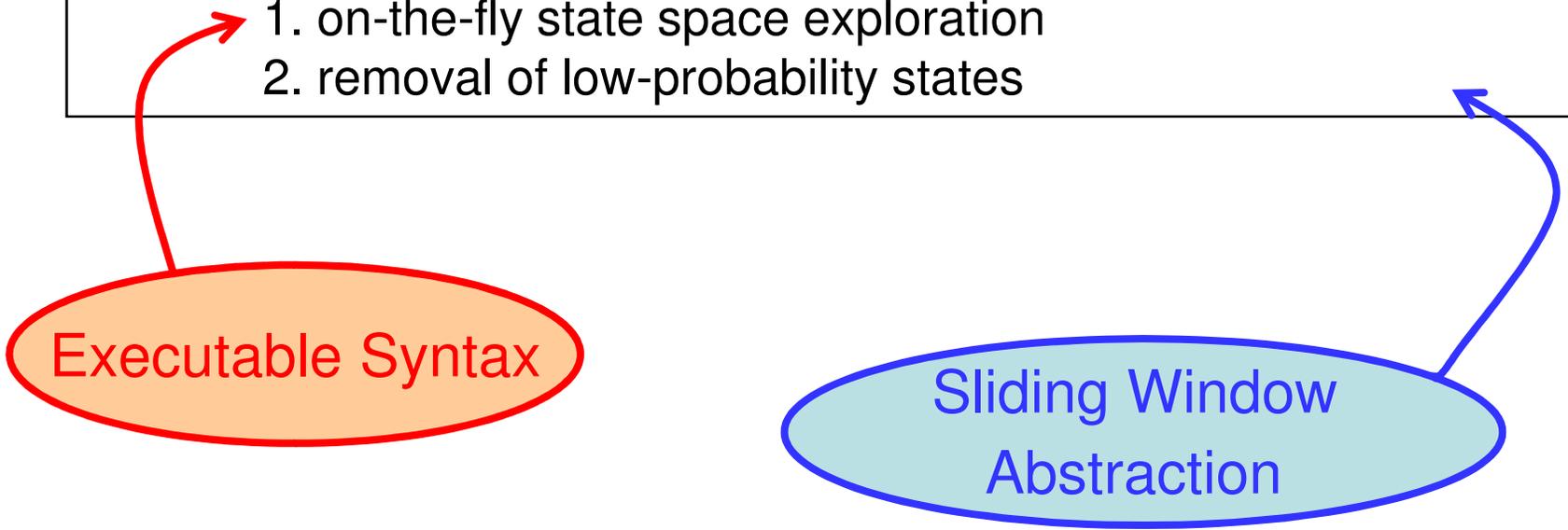
1. on-the-fly state space exploration
2. removal of low-probability states

Model Checking CTMCs [DHMW09]

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1. on-the-fly state space exploration
2. removal of low-probability states

Executable Syntax



Sliding Window
Abstraction

Opportunity and Challenges

1. Computer Science can contribute to biology far more than *algorithms* and *tools*, e.g. modeling principles such as *reactivity*, *compositionality*, *executability*, *hybrid systems*, *property preserving abstraction*, and *model checking*.

Example: bounded asynchrony [FHMP08]

Opportunity and Challenges

1. Computer Science can contribute to biology far more than *algorithms* and *tools*, e.g. modeling principles such as *reactivity*, *compositionality*, *executability*, *hybrid systems*, *property preserving abstraction*, and *model checking*.
2. Computer Science needs to develop more *quantitative* models.

B versus R

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1. Computer Science can contribute to biology far more than *algorithms* and *tools*, e.g. modeling principles such as *reactivity*, *compositionality*, *executability*, *hybrid systems*, *property preserving abstraction*, and *model checking*.
2. Computer Science needs to develop more *quantitative* models.
3. Training of scientists!!!

IST Austria



8 biologists, 4 computer scientists, 1 PhD program