

ADAM – Analysis of Dynamic Algebraic Models

<http://dvd.vbi.vt.edu>

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<http://dvd.vbi.vt.edu/cgi-bin/git/adam.pl>

VIRGINIA BIOINFORMATICS INSTITUTE
AT VIRGINIA TECH

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Analysis of Dynamic Algebraic Models (ADAM) 1.0

ADAM uses a combination of simulation and algorithms to analyze the dynamics of discrete biological systems. It can analyze **Logical Models** (in [GINSim](#) format), **Polynomial Dynamical Systems (PDS)**, and **Probabilistic Boolean (or multistate) Networks**. For small enough networks (deterministic or probabilistic), ADAM simulates the complete state space of the model and finds all attractors (steady states and limit cycles) together with statistics about the size of components. For larger networks, ADAM computes fixed points for both deterministic and probabilistic networks, and limit cycle of the length specified by the user for deterministic networks. You can follow our [step-by-step tutorial](#) or read the [user guide](#). It is important that you follow the format specified in the

1) Model

Model Type:

☐ Logical Model (GINsim file) ☒ PDS ☐ Probabilistic Network ☐ Petri Net

Enter number of states per node:

$f_3 = x_1 \cdot x_2 + x_3^2$

2) Analysis

Select the type of network:

☐ Conjunctive/Disjunctive (Boolean rings only)
☒ Simulation (suggested for nodes ≤ 11)
☐ Algorithms (suggested for nodes > 11)

Simulation: For $n < 12$. Enumerates all possible states. Outputs at minimum fixed points and number of components. See 'Small Networks Options' for other output options.

3) Options

☒ Dependency graph ☐ Feedback Circuit ☒ Print probabilities ☒ State space graph

Select the **updating scheme** for the functions (only for Logical Model or PDS):

☒ Synchronous
☐ Sequential

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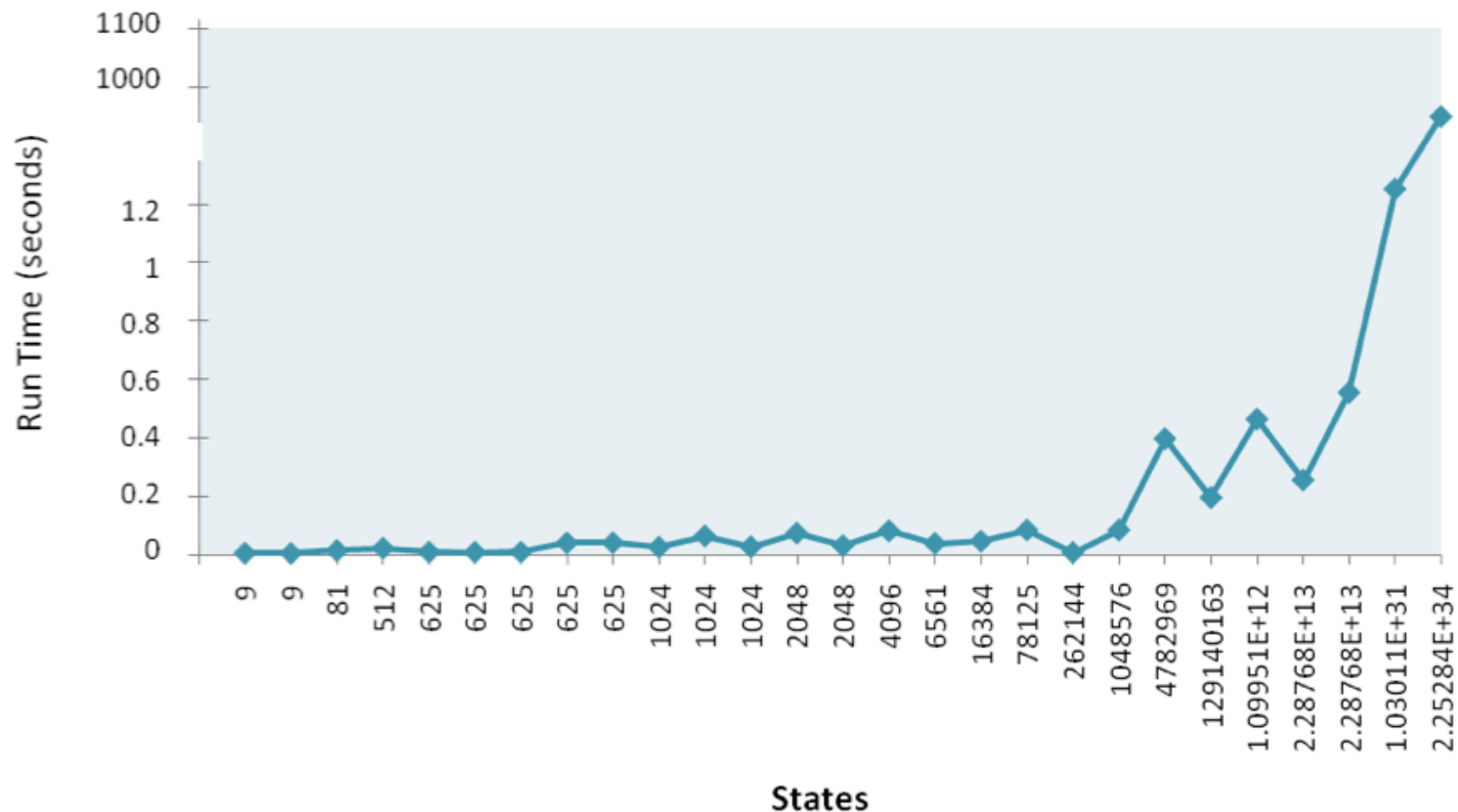
- Attractor = solution to system of equations
- ADAM uses computer algebra system *Macaulay2*
- Gröbner basis computations
 - Worst case: doubly-exponential
 - Equations for biological systems are sparse: Gröbner basis computation work extremely well
- Other algorithm for special networks like *conjunctive networks*

Daniel R. Grayson and Michael E. Stillman. Macaulay2, a soft-ware system for research in algebraic geometry. Available at <http://www.math.uiuc.edu/Macaulay2/>.

Abdul Salam Jarrah, Reinhard Laubenbacher, and Alan Veliz-Cuba. The dynamics of conjunctive and disjunctive boolean network models. Bull Math Biol, 2010.

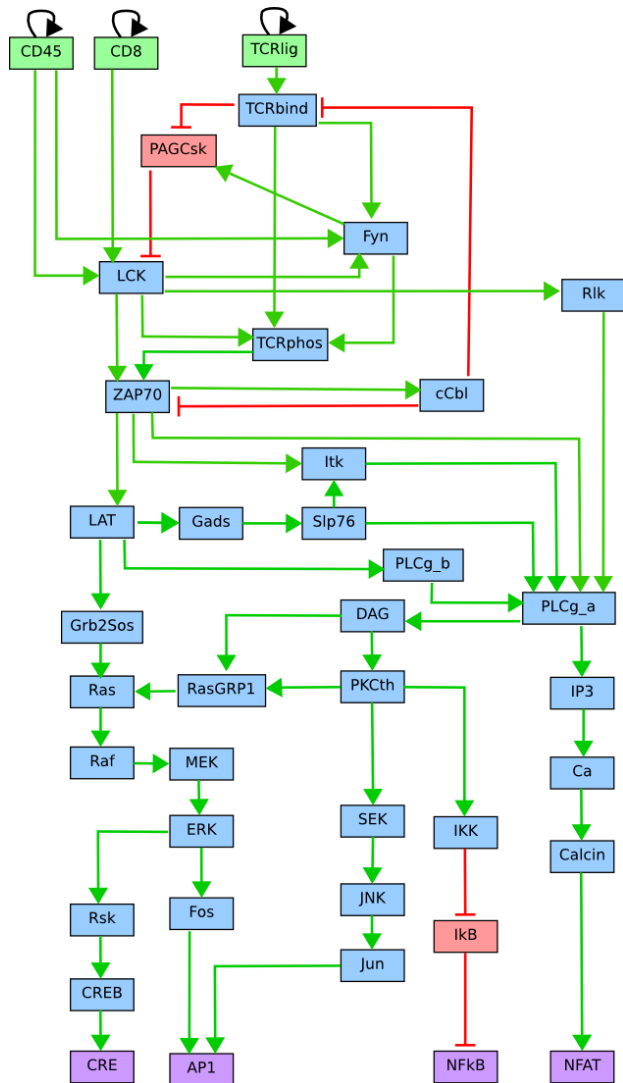
Gröbner Basis Computation Benchmarking

Fixed Point Computations



Logical Models of Biological systems from
http://gin.univ-mrs.fr/GINsim/model_repository.html

Gröbner Basis Computation Benchmarking



- TCR Signaling Pathway
 - 40 genes
 - 2^{40} possible states
 - ADAM computes all seven steady states in less than 1 second