# Analysing the microRNA-17-92/Myc/E2F/RB Compound Toggle Switch by Theorem Proving

### Giampaolo Bella and Pietro Liò @ Catania and Cambridge

Under the auspices of British Council's grant Computer-assisted verification for safety properties of genetic networks underlying liver regeneration"

# Motivation

Genetic networks stretch human intuition

 Big problem: miRNA target prediction
 How 'bout miRNA influence on network regulation

 Tools from

 Computational analysis (differential eqs, ...)

Computer-aided visualization (GNA, VisualGNA,...)

OFormal/symbolic approaches

Pen-and-paper (Petri nets, Pi-calculus,...)

Computer-aided (model checking)

Use theorem proving!

# Model Checking vs Theorem Proving

### Pros

- Press-button tool
- May validate properties quickly

### Cons

- Only handles small systems
- State explosion

### Pros

- Handles unboundedsize systems
- OVery expressive

### Cons

- Needs human intervention
- Steep learning curve

PLOS COMPUTATION/

# Predictive Modeling of Signaling Crosstalk during *C. elegans* Vulval Development

#### Jasmin Fisher<sup>1\*</sup>, Nir Piterman<sup>1</sup>, Alex Hajnal<sup>2</sup>, Thomas A. Henzinger<sup>1,3</sup>

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**BIOINFORMATICS** 

### Model Checking Genetic Regulatory Networks with Parameter Uncertainty

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### Temporal logic patterns for querying dynamic models of cellular interaction networks

Pedro T. Monteiro  $^{1,2,3},$  Delphine Ropers  $^1,$  Radu Mateescu  $^1,$  Ana T. Freitas  $^2$  and Hidde de Jong  $^{1,\ast}$ 

### Analysis of Genetic Regulatory Networks: A Model-Checking Approach

### Grégory Batt<sup>1\*</sup>, Hidde de Jong<sup>1</sup>, Johannes Geiselmann<sup>2</sup>, and Michel Page<sup>1,3</sup>

 

 Model Checking Genetic Regulatory Networks

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 using GNA and CADP

 Robustness analysis and tuning of synthetic gene networks
 égory Batt <sup>1</sup>,\*, Boyan Yordanov <sup>2</sup>, Ron Weiss <sup>3</sup> and Calin Belta <sup>1</sup>
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 215-224 (2005)

 BIOINFORMATICS
 Holder Checking Genetic Regulatory Networks

### A general computational method for robustness ana with applications to synthetic gene networks

Aurélien Rizk, Gregory Batt, François Fages and Sylvain Soliman INRIA Paris-Rocquencourt, 78153 Le Chesnay Cedex, France Received on January 7, 2009 215

Toward Integration of Systems Biology Formalism: The Gene Regulatory Networks Case

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### The trail we've walked so far

- Analogies computer/genetic networks
- General model for gene/protein networks
- Formal analysis of the genetic toggle
- Extensions with miRNAs
- Towards analysis of compound toggle featuring miRNA-17-92

### The main theorem

### The complete guarantees

- "Bistability: the toggle may only reach two stable states s.t. either protein prevails"
  - 1. BistabilityA: protein A may exceed its second threshold while B doesn't exceed its own
  - 2. BistabilityB: protein B may exceed its second threshold while A doesn't exceed its own
  - 3. NonInstability: both proteins may not exceed their respective second thresholds at the same time

# The microRNA-17-92/Myc/E2F/RB compund toggle switch



# The tool: Isabelle

- Generic, interactive, user-driven proof-assist
- May use HOL as meta-language
- Its simplifier does conditional term rewriting
- Its automatic provers do classical reasoning
- Proof attempts may fail due to either insufficient skill or sound counterexamples

### **General model: basics**

typedecl gene
typedecl protein
typedecl mirna

# datatype event = Produces gene protein | Triggers protein gene | Inhibits protein gene | Degrades protein | Expresses gene mirna | Silences mirna gene

# General model : initial polymerase

### $\mathbf{consts}$

initialpolymerase :: int

axioms
initialpolymerase\_value [iff]:
 initialpolymerase > 0

### General model : induced polymerase

### $\mathbf{consts}$

inducedpolymerase :: gene  $\Rightarrow$  event list  $\Rightarrow$  int

### primrec

### General model : current polymerase

### $\mathbf{constdefs}$

 $currentpolymerase :: gene \Rightarrow event list \Rightarrow int$ currentpolymerase x nt ==initialpolymerase + inducedpolymerase x nt

### General model : protein concentration

### Verifying the general model

lemma inducedpolymerase\_Produces: inducedpolymerase x (Produces x Y # nt) = inducedpolymerase x nt apply simp done

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lemma currentpolymerase\_Triggers: currentpolymerase x (Triggers Y y # nt) = (if x=y then currentpolymerase x nt + 1 else currentpolymerase x nt) apply (simp add: currentpolymerase\_def) done

## Verifying the general model

lemma inducedpolymerase\_Produces: inducedpolymerase x (Produces x Y # nt) = inducedpolymerase x nt apply simp done

lemma currentpolymerase\_Triggers: currentpolymerase x (Triggers Y y # nt) = (if x=y then currentpolymerase x nt + 1 else currentpolymerase x nt) apply (simp add: currentpolymerase\_def) done

lemma concentration\_Degrades: concentration X (Degrades Y # nt) = (if X=Y then concentration X nt - 1 else concentration X nt) apply simp done

# Modelling the genetic toggle

- Model is set of all possible evolutions
- Each evolution is a list
- Model defined by structural induction

### Modelling the genetic toggle

- Model is set of all possible evolutions
- Each evolution is a list
- Model defined by structural induction
- Qualitative model amenable to TP
  Birth and death factors abstracted away
  Inductive model subsumes stochastic one

### A model toggle: base and production

inductive\_set comptoggle :: event list set where

- base: []  $\in$  comptoggle
- / e2fpr: [ ne2  $\in$  comptoggle; currentpolymerase e2f ne2 > 0 ]]  $\implies$  Produces e2f E2F # ne2  $\in$  comptoggle

### miRNA is expressed and silences...

/ micrex: [ ne4  $\in$  comptoggle; currentpolymerase microRNA1792 ne4 > 0 ]]  $\implies$  Expresses microRNA1792 miR1792 # ne4  $\in$  comptoggle

/ miRsi: [ ne11  $\in$  comptoggle; Expresses microRNA1792 miR1792  $\in$  set ne11 ]  $\implies$  Silences miR1792 e2f # ne11  $\in$  comptoggle

### Myc regulates and degrades...

/ Myctr1: [ ne5  $\in$  comptoggle; concentration Myc ne5  $\geq$  threshold 1 Myc ]]  $\implies$  Degrades Myc # Triggers Myc microRNA1792 # ne5  $\in$  comptoggle

### **Conclusions and developments**

- TP opens up genetic networks to logicians
- Tool support scales up linearly to larger networks
- Toggle switch analysed, now completing holistic analysis of compound toggle
- More and more flavours of TP expected!