

Reasoning over Biological Networks using Maximum Satisfiability

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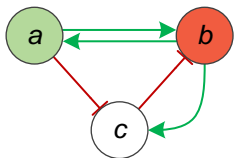
Current State of Systems Biology

- High-throughput methods
 - Large sets of comprehensive data
- Models are incomplete
- Data is inconsistent
- Aberrant measurements
- We propose a SAT-based framework to
 - Detect inconsistencies
 - Repair inconsistencies
 - Predict unobserved variations

- 1 Modelling
 - Influence Graphs
 - Sign Consistency Model
 - Maximum Satisfiability
- 2 Reasoning
 - Checking Consistency
 - Repairing
 - Predicting
- 3 Experimental Evaluation
 - Setup
 - Results
- 4 Concluding Remarks

Influence Graphs

- Biological networks are represented by influence graphs
- An **influence graph** is a directed graph $G = (V, E, \sigma)$
 - V is a set of vertices representing the **genes**
 - E is a set of edges representing the **interactions** between the genes
 - $\sigma : E \rightarrow \{+, -\}$ is a (partial) **labelling** of the **edges**
- An **experimental profile** $\mu : V \rightarrow \{+, -\}$ is a (partial) **labelling** of the **vertices**
 - Each vertex is also classified as **input** or **non-input**

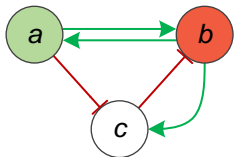


$$\sigma = \left\{ \begin{array}{ll} a \rightarrow b = +, & a \rightarrow c = -, \\ b \rightarrow a = +, & b \rightarrow c = +, \\ c \rightarrow b = - & \end{array} \right\}$$
$$\mu = \{a = +, \quad b = -\}$$

Sign Consistency Model

- The labelling $\mu(v)$ of a non-input vertex v is **consistent** if
 - There is at least one **influence** that explains its sign
 - One edge $u \rightarrow v$ such that $\mu(u) \cdot \sigma(u \rightarrow v) = \mu(v)$
- An influence graph $G = (V, E, \sigma)$ and an experimental profile μ are **mutually consistent** if
 - There are **total labellings** σ' and μ' (**total extensions** of σ and μ)
 - Such that $\mu'(v)$ is consistent for every non-input vertex v

Example



$$\sigma = \left\{ \begin{array}{ll} a \rightarrow b = +, & a \rightarrow c = -, \\ b \rightarrow a = +, & b \rightarrow c = +, \\ c \rightarrow b = - & \end{array} \right\}$$
$$\mu = \{a = +, \quad b = -\}$$

- The graph and profile are **inconsistent**
 - $\mu(a) = +$ while $\mu(b) \cdot \sigma(b \rightarrow a) = -$
- Why?
 - Incomplete model
 - Aberrant measurements
- **Repairing** (restoring consistency)
 - $\mu(a) = -$ or $\mu(b) = +$ (**cardinality-minimal** repairs)
 - Make a and b inputs (**subset-minimal** repair)

Maximum Satisfiability

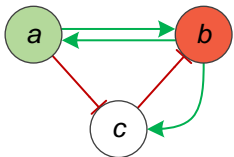
- Boolean Satisfiability (SAT)
 - Given a propositional formula φ , find an assignment to the variables that satisfies all clauses in φ
- Maximum Satisfiability (MaxSAT)
 - Optimization version of SAT
 - Find an assignment that maximizes (minimizes) the number of satisfied (unsatisfied) clauses
- Partial MaxSAT
 - Given a propositional formula $\varphi = \varphi_h \cup \varphi_s$, find an assignment to the variables that satisfies all hard clauses (φ_h) and the maximum number of soft clauses (φ_s)

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Checking Consistency

- SAT solution for checking consistency
- 4 types of variables
 - vertices (lvt_{x_v}) – 1 unit clause for each vertex with known label (μ)
 - inputs (inp_v) – 1 unit clause for each vertex
 - edges ($ledg_{uv}$) – 1 unit clause for each edge with known label (σ)
 - influences ($infl_{uv}$) – 2 constraints for each influence
- Ensuring consistency
 - 2 constraints for each vertex
- SAT call reveals whether the graph and profile are mutually consistent or not

Example



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$$\mu = \{a = +, \quad b = -\}$$

$lvtx_a \quad \neg lvtx_b$ (no unit clause for vertex c)

$\neg inp_a \quad \neg inp_b \quad \neg inp_c$

$ledg_{ab} \quad \neg ledg_{ac} \quad ledg_{ba} \quad ledg_{bc} \quad \neg ledg_{cb}$

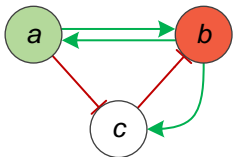
$infl_{ba} \longrightarrow (lvtx_b \wedge ledg_{ba}) \vee (\neg lvtx_b \wedge \neg ledg_{ba})$

$\neg infl_{ba} \longrightarrow (lvtx_b \wedge \neg ledg_{ba}) \vee (\neg lvtx_b \wedge ledg_{ba})$

$inp_a \vee (lvtx_a \longrightarrow infl_{ba})$

$inp_a \vee (\neg lvtx_a \longrightarrow \neg infl_{ba})$

Example



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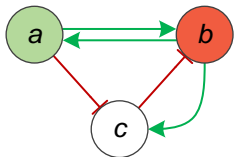
$\neg inp_a \quad \neg inp_b \quad \neg inp_c$

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$$\begin{aligned} infl_{ba} &\longrightarrow (lvtx_b \wedge ledg_{ba}) \vee (\neg lvtx_b \wedge \neg ledg_{ba}) \\ \neg infl_{ba} &\longrightarrow (lvtx_b \wedge \neg ledg_{ba}) \vee (\neg lvtx_b \wedge ledg_{ba}) \end{aligned}$$

$$\begin{aligned} inp_a &\vee (lvtx_a \longrightarrow infl_{ba}) \\ inp_a &\vee (\neg lvtx_a \longrightarrow \neg infl_{ba}) \end{aligned}$$

Example



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$$\begin{aligned} & inp_a \vee (lvtx_a \longrightarrow infl_{ba}) \\ & inp_a \vee (\neg lvtx_a \longrightarrow \neg infl_{ba}) \end{aligned}$$

- **Partial MaxSAT** solution for repairing
- Only cardinality-minimal repairs
- 3 types of repair operations
 - flip vertices signs
 - make vertices inputs
 - flip edges signs
- Converting encoding into MaxSAT
 - Clauses corresponding to what we are repairing are made **soft** (only unit clauses)
 - The remaining clauses are **hard**
- MaxSAT call identifies the set of repairs (**unsatisfied clauses**)

- What is common to all (optimal) solutions
- **Backbone** of the formula
- **Intersection** of all repairs (predicting under inconsistency)
 - Enumeration (feedback loop)
 - Only **1 blocking clause** (the current prediction)
 - Only a **subset** of the **variables** is relevant

Predicting under Inconsistency

Input: Partial MaxSAT Formula \mathcal{F}

Output: Predicted Repairs of \mathcal{F} , *prediction*

```
(out, opt, sol) ← MaxSAT( $\mathcal{F}$ ) // compute initial solution
optimum ← opt
prediction ← Get-Repairs(sol)

while |prediction| ≠ 0 do
  (out, opt, sol) ← MaxSAT( $\mathcal{F} \cup [\neg \text{prediction}]$ ) // block current prediction
  if out == UNSAT or opt > optimum then
    break
  prediction ← prediction ∩ Get-Repairs(sol) // update prediction

return prediction
```

- Either the prediction is reduced or the algorithm terminates
- At most n iterations ($n = \text{number of repair operations} = \textit{optimum}$)

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- SAT/MaxSAT vs ASP (Gebser et al. 2010, 2011)
- Instances
 - Randomly generated
 - GRN of *E. coli* along with 2 experimental profiles
- Timeout: 600 seconds
- Intel Xeon 5160 (3.00 GHz, 4 GB)
- ASP: *clasp*, *gringo*
- SAT: MINISAT, *minibones*
- MaxSAT: MSUNCORE

Consistency Checking, Predicting under Consistency

- SAT vs ASP
- Trivial for both approaches

Repairing, Predicting under Inconsistency

- MaxSAT vs ASP
- ASP could not solve the hardest instances

		<i>Solved (%)</i>	<i>Time</i>
<i>Repair</i>	ASP	2448 (87)	20471
	MaxSAT	2814 (100)	994
<i>Predict</i>	ASP	2440 (87)	14181
	MaxSAT	2814 (100)	8422

Concluding Remarks

- New SAT/MaxSAT framework for reasoning over biological networks
- SAT/MaxSAT approach more competitive than ASP approach
- Future
 - Minimal inconsistent cores (MICs)
 - More types of repair operations (e.g. add edges)
 - Subset-minimal repairs
 - Improve prediction under inconsistency

Questions?