

# SMT Solving and modeling for biology

Denis Kuperberg  
CNRS, LIP, ENS Lyon

GdT Plume  
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# Part 1

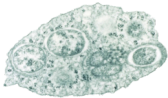
## Wolbachia-induced infertility in mosquitoes

With

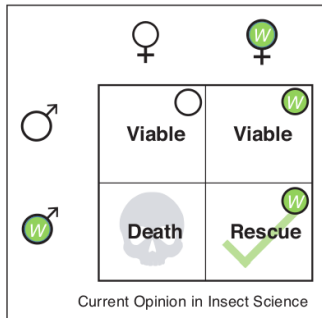
Sylvain Charlat, Alice Namias , Mathieu Sicard, Mylène Weill



# Cytoplasmic Incompatibility

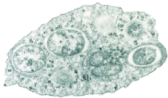


**VS**

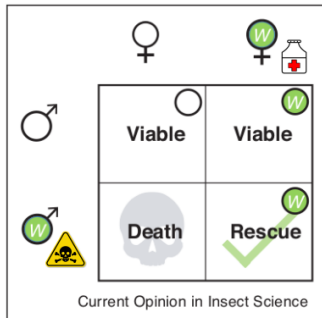


Credit: [Namias et al 2022]

# The toxin/antidote hypothesis














**VS**



Credit: [Namias et al 2022]

# Different Wolbachia strains

	♀	♀ W	♀ W
♂	 Viable	 Viable	 Viable
	 Death	 Rescue ✓	
	 Death		 Rescue ✓

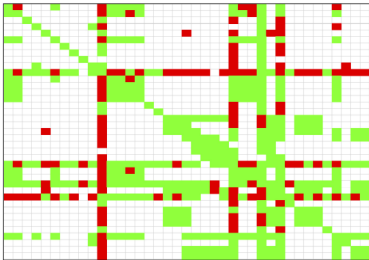
# Different Wolbachia strains

	♀	♀ W	♀ W
♂	Viable	Viable	Viable
W♂	Death	Rescue	?
W♂	Death	?	Rescue

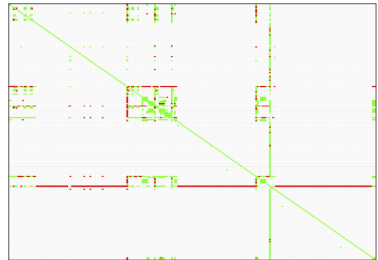
**Hypothesis:** each strain has its own cocktail.

# The data

39 lines with phenotypic and molecular data



239 lines with phenotypic data



# Optimizing the parameters

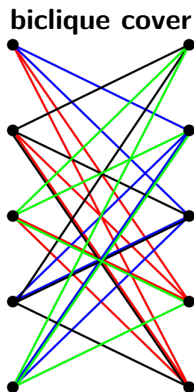
How many kind of toxins needed ?



# Optimizing the parameters

How many kind of toxins needed ?

NP-complete [Nor et al 2012]:

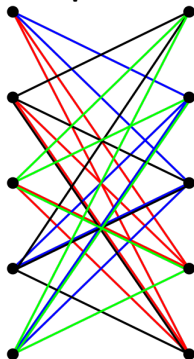


# Optimizing the parameters

How many kind of toxins needed ?

NP-complete [Nor et al 2012]:

**biclique cover**



*Variant:* quantitative model

# Using SAT/SMT Solver

**Before SAT solving** [Nor et al 2012]:

- ▶ ad-hoc heuristics for  $19 \times 19$  matrix
- ▶ fill missing data manually
- ▶ approximate results

# Using SAT/SMT Solver

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- ▶ ad-hoc heuristics for  $19 \times 19$  matrix
- ▶ fill missing data manually
- ▶ approximate results

## **With minisat/Z3** (this work):

- ▶ deal with  $239 \times 239$  matrix
- ▶ robust to missing data
- ▶ explore various models and questions

# Results

## Boolean

Toxs per strain	Types
1	14
2	10
3	9

## Quantitative

Levels	Types
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*And more:*

- ▶ test robustness
- ▶ predict missing data
- ▶ find cells discriminating models

# Perspectives

- ▶ Confront predictions with new data
- ▶ Prescribe tests to discriminate models
- ▶ Find correlations with genetic data
- ▶ Evolutionary explanations



# Part 2

## Detection of autocatalytic cycles

With

Sylvain Charlat, Etienne Rajon, Nicolas Lartillot



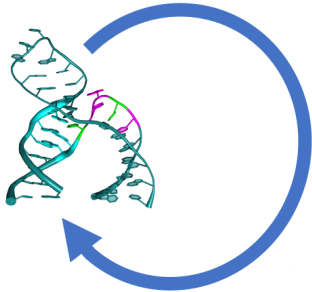
**LBBE**

LABORATOIRE DE BIOMÉTRIE  
ET BIOLOGIE ÉVOLUTIVE



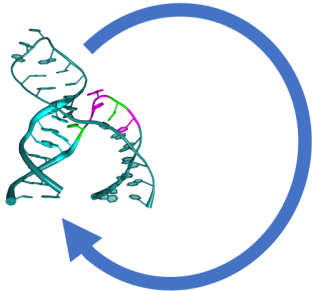
# Origin of Life dichotomy

**Replicator first**

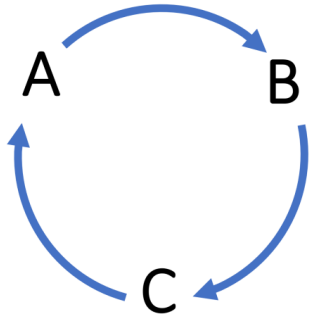


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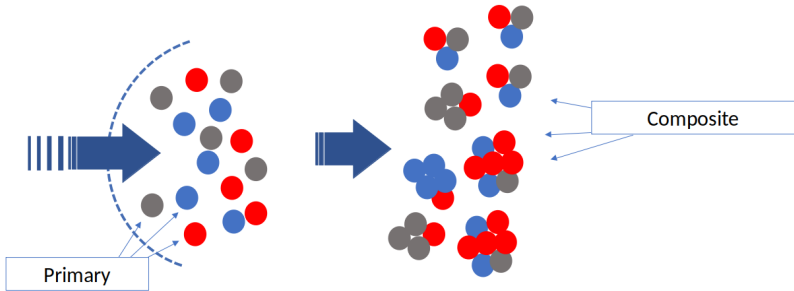
**Replicator first**



**Metabolism first**

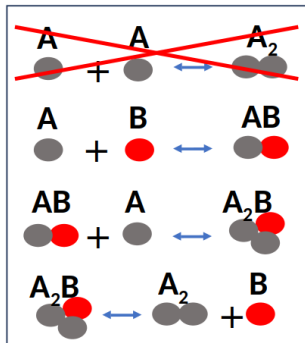


# Soup of chemical reactions

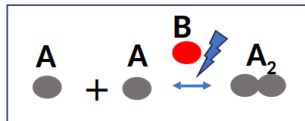


# Spontaneous (auto)catalysis

## Catalysis

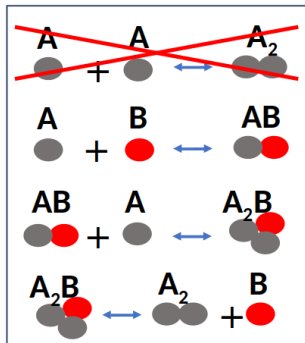


$\Leftrightarrow$

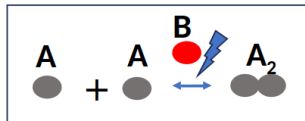


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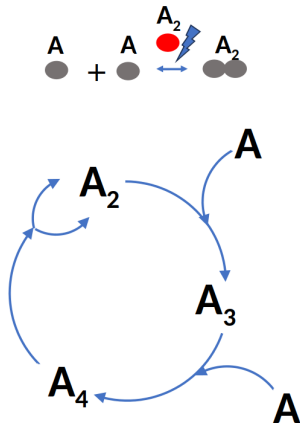
Catalysis



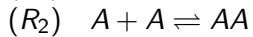
$\parallel$



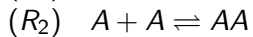
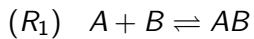
Autocatalysis



## Reaction matrix

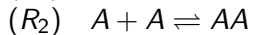


## Reaction matrix



	$R_1$	$R_2$
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$\vec{v} \in \mathbb{R}^2$  flow vector  $\Rightarrow M \cdot \vec{v}$  balance for each entity.



# Autocatalysis via matrices

**Autocatalytic core** [Blockhuis et al 2022]:

Submatrix  $N$  of  $M$  such that

- ▶ each column and line contains  $\text{coef} < 0$  and  $\text{coef} > 0$
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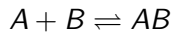
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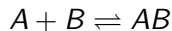
NP-complete ?

## From concentrations to flows



How to compute flow ?

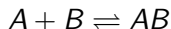
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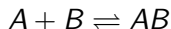
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Concentration vector  $\vec{u} \rightsquigarrow$  flow vector  $\vec{v}$ .



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**Compatible cores:** share the same witness

# What we want

- ▶ design systems
- ▶ sample systems
- ▶ find autocatalytic cores
- ▶ mark consistent cores
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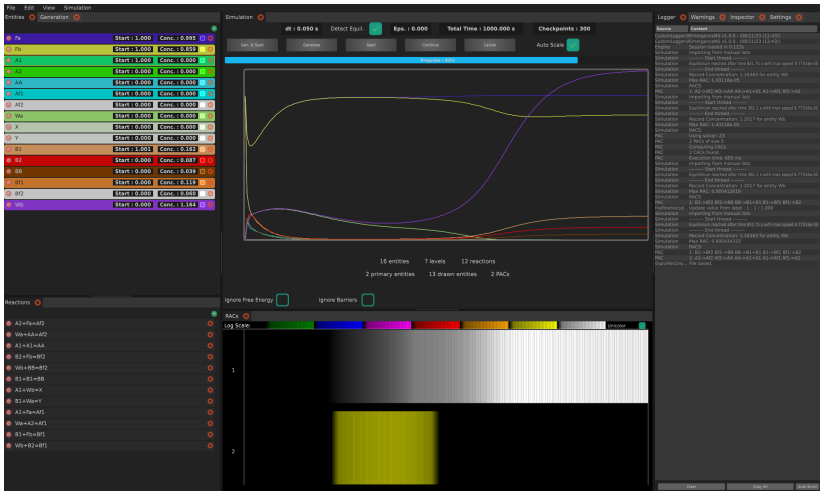


SMT Solver Z3



JUCE OrganicUI

# The program



# Perspectives

- ▶ Spectrum of interactions between cores
- ▶ Quantitative analysis (expectancy of autocatalysis, . . . )
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## **Very long term goals:**

- ▶ Quantify natural selection
- ▶ Criteria for life
- ▶ Possible build-up scenario

Thank you !

