

Methods for the Randomization of Metabolic Networks

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TBI

Outline

- Main Goal and Model

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- Overall Randomization Scheme

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- Main Goal and Model
- Overall Randomization Scheme
- Methods to create large sample-spaces

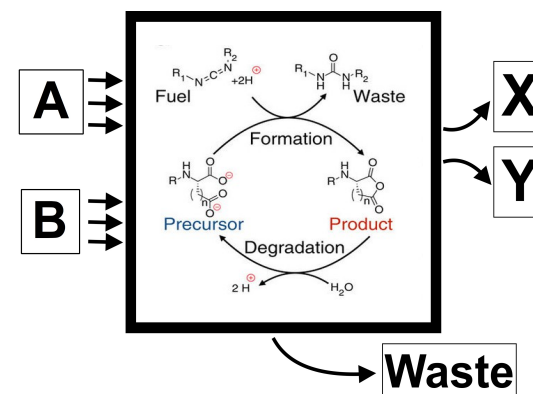
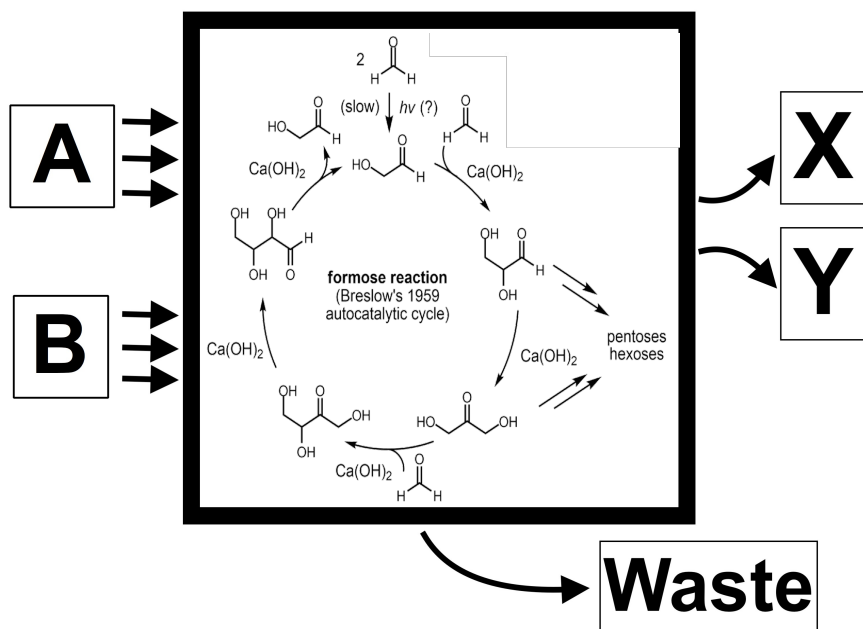
The Main Goal

The Creation of randomized CRNs as statistical background models.

Requirements:

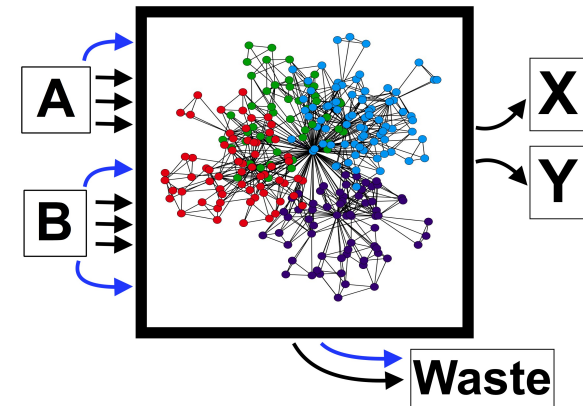
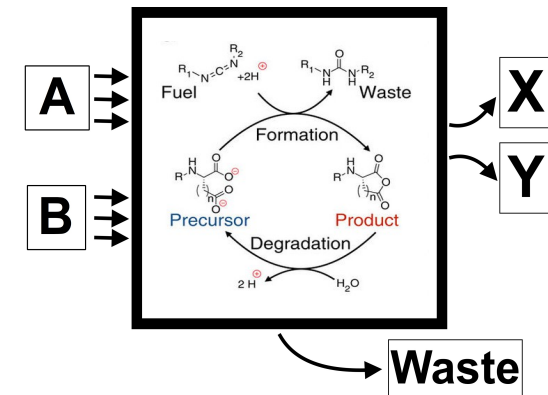
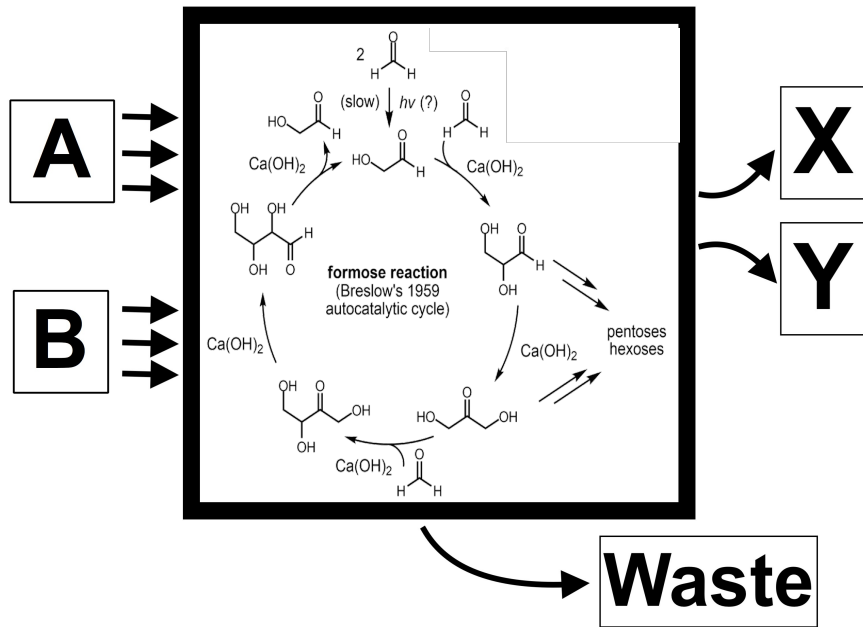
- 1) **Reference Network**
- 2) Keeping its **function**

The Main Goal



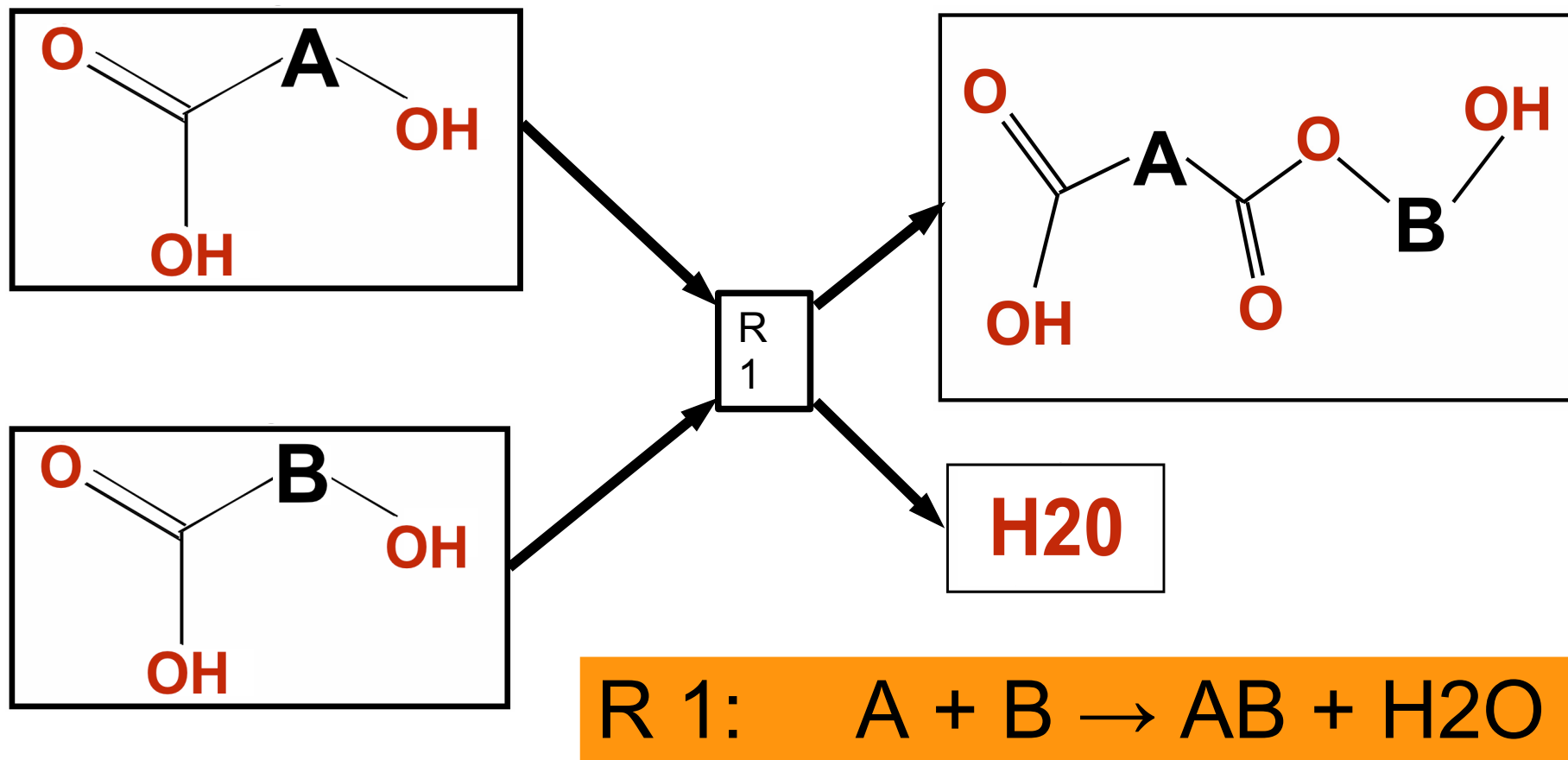
- 1) Formose catalytic cycle <https://commons.wikimedia.org/wiki/File:Formose.png>
- 2) Tena-Solsona et.al, *Non-equilibrium dissipative supramolecular materials with a tunable lifetime*

The Main Goal



- 1) Formose catalytic cycle <https://commons.wikimedia.org/wiki/File:Formose.png>
- 2) Tena-Solsona et.al, *Non-equilibrium dissipative supramolecular materials with a tunable lifetime*
- 3) <https://www.taylorintime.com/wp-content/uploads/2016/02/Brain-network.png>

Molecule- and CRN-model (MØD¹)



[1] Jakob L. Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler: „A software package for chemically inspired graph transformation.“ CoRR, abs/1603.02481, 2016.

Main Problem

- CRNs are heavily constrained
- randomized CRNs should be tailored to the Reference Network

Our Strategy

- 1) Create a large sample space
from species and reactions of the
Reference CRN

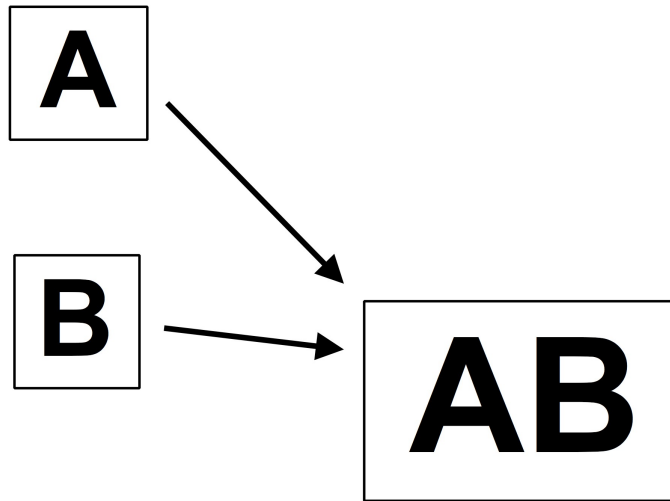
Our Strategy

- 1) Create a large sample space
from species and reactions of the
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- 2) Randomly pick a set of reactions
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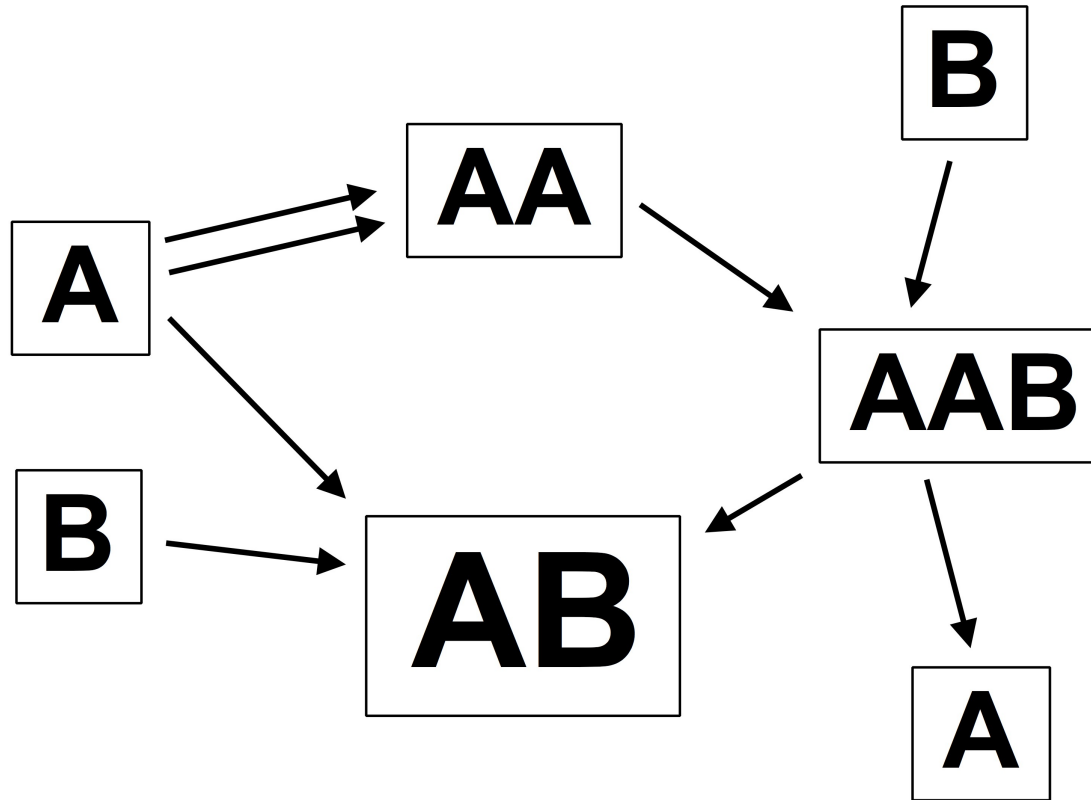
Our Strategy

- 1) Create a large sample space
from species and reactions of the
Reference CRN
- 2) Randomly pick a set of reactions
of sufficient size
- 3) Enumerate pathways that
preserve the reference function

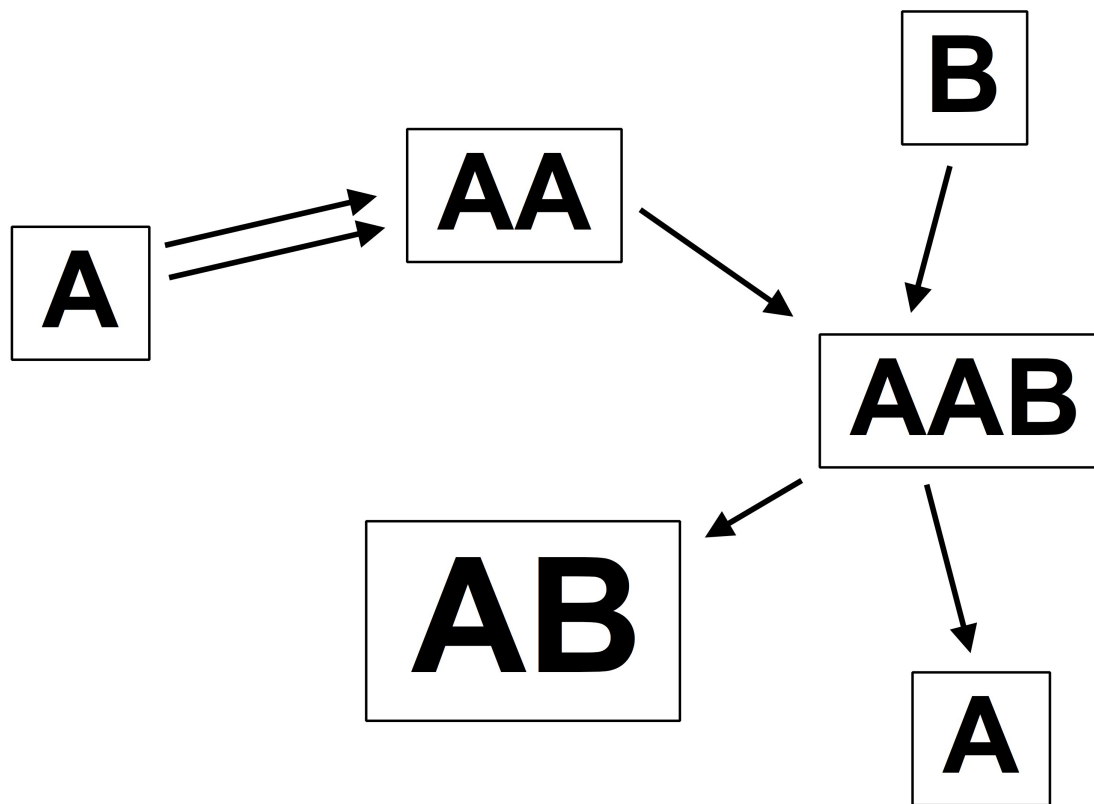
Reaction - Closure



Reaction - Closure

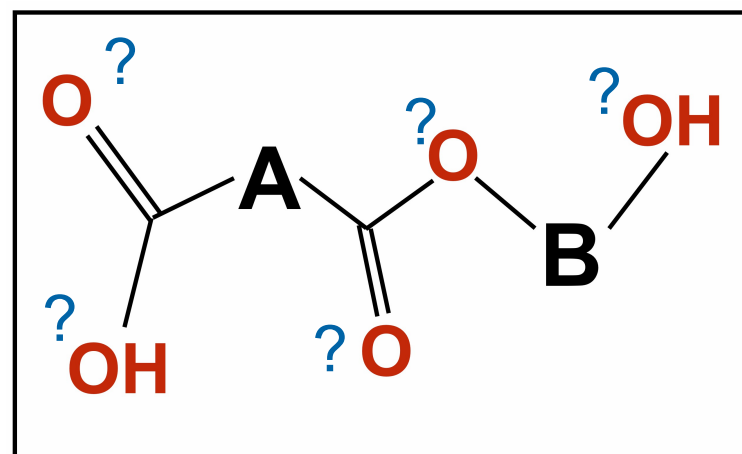
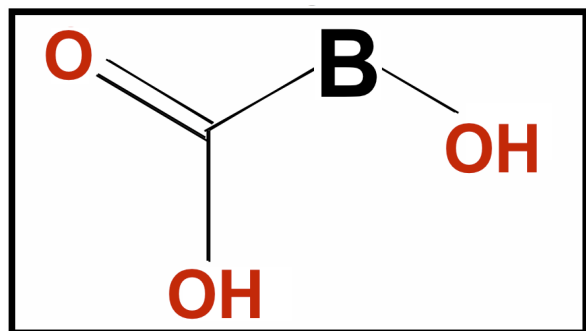
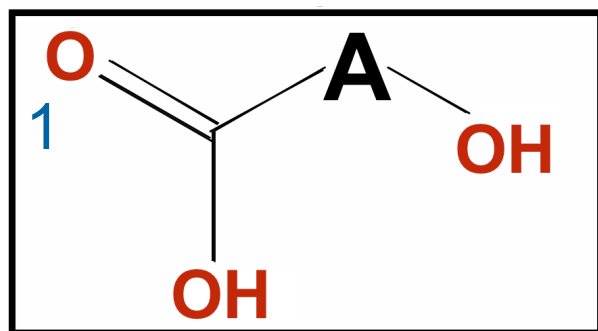


Reaction - Closure



Reaction - Mapping

(atom-atom mapping)



Reaction - Mapping

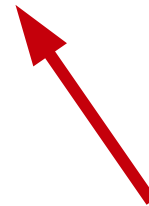
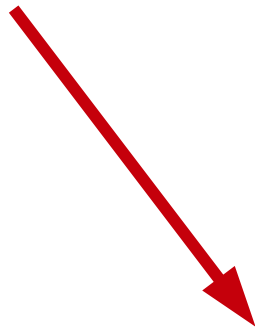
- Integer Linear Programming (ILP)-based Algorithm (First et al. 1969¹)
- Implementation with MØD in mind: ChemRULER (by B. Thiel)

1)First et al. Stereochemically consistent reaction mapping and identification of multiple reaction mechanisms through integer linear optimization. J Chem Inf Model 2012, 52:84–92.

Combined

Add new species by
applying reaction-rules

Find new reaction-maps
and turn them into rules



And Finally...

My Thanks to the people at the **TBI**

And a recommendation for

MedØIDatschgerl(MØD¹)

[1] Jakob L. Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler: „A software package for chemically inspired graph transformation.“ CoRR, abs/1603.02481, 2016.

Classification using bisimulation

- A weak Bisimulation-approach to CRN-equivalence using Nuskell¹
- Equivalence of partitions

1) Stefan Badelt, Seung Woo Shin, Robert F. Johnson, Qing Dong, Chris Thachuk, and Erik Winfree (2017) "A General-Purpose CRN-to-DSD Compiler with Formal Verification, Optimization, and Simulation Capabilities"