

Fuzzy Matching in Symbolic Systems Biology

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Motivation

- Symbolic systems biology aims to explore biological processes as whole systems instead of small and independent elements.
- The objective is to define formal models closer to the biologists mindsets.
- It is equally important to be able to compute with, analyze, and reason about these networks of biomolecular interactions at multiple levels of detail.
- Such models may suggest new insights and understanding of complex biological mechanisms.

Motivation

- Biological interactions can be handled with rule-based modeling in a natural way.
- We will focus on **Pathway Logic**, based on **Maude** formal language.
- It defines system states and rules specifying the manners in which the state changes along time.
- It supports many kinds of analysis: simulation, search, model checking, and meta-analysis.

Motivation: Terms

- The **basic data structure** in Pathway Logic is a set of *locations*.
 $\{L \mid S\} \{L' \mid S'\} \dots$
- Each location is a pair with the location identifier and a *soup* of elements in the location.
 $[E - M] E' \dots$
- For example,
 $\{CLc \mid [Mek1 - act] [Erk1 - act\ phos(Y\ 204)] \}$
 $\{NUc \mid Maz [Tp53-gene - on] Rb1 Chek1 Chek2 Myc Tp53 NProteasome\}$

Motivation: Rules

- Rules are usually unconditional.
- They are composed of reactants, products, and controls:
 - *Controls* are the occurrences that appear in the rule's premise and conclusion.
 - *Reactants* are the occurrences that appear in the premiss but not the conclusion.
 - *Products* are the occurrences that appear in the conclusion but not the premise.

Motivation: Rules

- Rules have the following form:

```
r1 [632c.Akts.by.Ilk]:
  {CLc | clc [Ilk - act] Akts}
=> {CLc | clc [Ilk - act] [Akts - phos(FSY)]} .
```

- With the following meaning:
 - CLc** corresponds to the cytoplasm.
 - The protein **Ilk** is activated.
 - A protein in the **Akts** family is found.
 - The variable **clc** matches the rest of the elements in the set.
 - After the reaction **Akts** will be phosphorylated on **FSY**.

Motivation: Rules

- The rule

```
r1 [632c.Akts.by.Ilk]:
  {CLc | clc [Ilk - act] Akts}
=> {CLc | clc [Ilk - act] [Akts - phos(FSY)]} .
```

can be understood as:

```
cr1 [632c.Akts.by.Ilk]:
  {CLc | clc Akts}
=> {CLc | clc [Akts - phos(FSY)]}
if clc' [Ilk - act] := clc .
```

Motivation: Modifications

- Some aspects might be more or less general depending on the rule.
- For example, we can use the `Akts` family or a specific member, like `Akt1`.
- We can indicate the reaction is phosphorylated (`phos(FSY)`) or phosphorylated in a particular location (`phos(Y 123)`).

Motivation

- The point now is: **how to build a model from some data?**
- Starting from an initial state, the Pathway Logic model is obtained by a symbolic reasoning process to derive instances of rules.
- These instances are derived from a rule knowledge base relevant to the given initial state.
- **Why instances?**
- Because the reactions are, in some cases, slightly different from the particular rules.

Motivation

- Some examples of what can go wrong are:
 - The state contains [Akts - act phos] and the rule premise requires [Akts - phos].
 - A rule requires Akts (the family) to be present and the state contains Akt1 (a member of the family).
 - The state contains [Akts - Yphos] and the rule premise requires [Akt - phos].
- In the last two cases the rule is “**more general**” than the state, so it should match somehow.
- However, the notion of generality is not the one used in Maude language, involving variables of a given sort and ground terms.

Motivation: Families and Products

- Note that we have information about **families**:

```
op Akts : -> AktS [ctor metadata "(\  
  (type Family)\  
  (members Akt1 Akt2 Akt3))"] .
```

- As well as for the corresponding **products**:

```
op FSY : -> Site [ctor metadata "(\  
  (FamilyName Akts)\  
  (epitopes \  
    \"Akt1 phos(S473)\"  
    \"Akt2 phos(S474)\"  
    \"Akt3 phos(S472)\")")"] .
```

Motivation

- Maude standard matching mechanism cannot deal with these problems.
- Thus far this was solved by hand.
- So we propose a notion of *fuzzy matching* to deal with them.
- This matching has been implemented at the metalevel and integrated with Pathway Logic via Full Maude.
- The current version does not really implement matching; it adds generic rules that will work with standard matching.

Fuzzy matching: Forwards and backwards analysis

- We perform *forwards* and *backwards* analysis.
- Forwards analysis works from initial states.
- Backwards analysis works from reached states.

Fuzzy matching

- We first define a notion of $P > P'$, read “ P is more general than P' .”
- Generality is measured with respect to the knowledge base.
- For example $\text{phos} > \text{Yphos} > \text{phos}(\text{Y } 123)$, where
 - phos says phosphorylation on some site.
 - Yphos says phosphorylation on a tyrosine site.
 - $\text{phos}(\text{Y } 123)$ says phosphorylation a tyrosine site at position 123.
- For simplicity, $P > P'$ also holds if $P = P'$.

Fuzzy matching

- This notion is easily extended to locations.
- In this case we have

$$\{L \mid [P - \text{mods}]\} \gg \{L \mid [P' - \text{mods}']\}$$

- It holds if $P > P'$ and $m_i > m'_i$, with m_i an element of mods and m'_i an element of mods' .

Forward matching

- Given a rule of the form

$$\begin{aligned}
 & r1 \{L \mid \text{CONT} [P - \text{mods} \text{ mods0}]\} \\
 & \Rightarrow \{L \mid \text{CONT} [P - \text{mods} \text{ mods1}]\} \\
 & \quad \text{if } \text{CONT}' [Q - \text{qmods}] := \text{CONT} .
 \end{aligned}$$

where `mods` and/or `qmods` may be empty, and `mods0` or `mods1` may be empty but not both.

- And a state

$$\{L \mid [Q' - \text{qmods}'] [P' - \text{mods}' \text{ mods0}] \}$$

Forward matching

- The rule fuzzy forward matches the term if
 $\{L \mid [P - \text{mods}]\} \gg \{L \mid [P' - \text{mods}']\}$
 and
 $\{L \mid [Q - \text{qmods}]\} \gg \{L \mid [Q' - \text{qmods}']\}$
- In this case, the result of applying the rule will be
 $\{L \mid [Q' - \text{qmods}'] [P' - \text{mods}' \text{ mods}1]\}$

Forward matching

- In our previous example, given the rule


```
cr1 [632c.Akts.by.Ilk]:
    {CLc | clc Akts}
    => {CLc | clc [Akts - phos(FSY)]}
    if clc' [Ilk - act] := clc .
```
- It can be fuzzily applied to the state


```
{CLc | clc Akt1 [Ilk - act]}
```
- Obtaining as result


```
{CLc | clc [Akt1 - phos(FSY)]}
```

Backwards matching

- Given a reached state, we can also use fuzzy matching to collect information about the source state.
- In this case we have the same rule schema:

```

cr1 {L | CONT [P - mods mods0]}
=> {L | CONT [P - mods mods1]}
    if CONT' [Q - qmods] := CONT .
  
```

- And the collected state:

```
{L | [P' - mods' mods1] }
```

Backwards matching

- The rule fuzzy backwards matches the term if $\{L \mid [P - \text{mods}]\} \gg \{L \mid [P' - \text{mods}']\}$
- And the source term will be $\{L \mid [P' - \text{mods}' \text{ mods0}] [Q - \text{qmods}]\}$

Backwards matching

- Assume we want to reach `[Eif4ebp1 - phos(S 65)]` in `CLc`.
- The state contains `[Akts - act phos(FSY) phos(KTF)]` in the `CLc`.
- In this case the rule `819c` fuzzy matches by refining the modifications in `Akts` to match the available occurrence:

```
r1 [819c.Eif4ebp1.by.Akts]:
  {CLc | clc [Akts - act] Eif4ebp1}
=> {CLc | clc [Akts - act] [Eif4ebp1 - phos(S 65)] } .
```

Implementation

- We have implemented fuzzy matching as an extension of Full Maude language.
- This extension allows users to perform some analysis that the standard Pathway Logic implementation does not support.
- In particular, it supports *narrowing*.
- It also allows us to manipulate the modules in the database.
- However, these changes are not integrated with the Pathway Logic Assistant.

Implementation

- The current implementation does not really implement a matching function.
- It instantiates the rules so the Maude standard matching algorithm.
- This simple approach allows us to evaluate the usefulness of fuzzy matching.
- However, it presents a bad performance:
 - The transformation itself takes time.
 - The obtained module is huge in general, so the execution is also slow.

Conclusions

- We proposed a notion of fuzzy matching that captures the fuzziness of experimental results.
- It allows rules to be matched by specializing or generalizing occurrences to match.
- We presented a prototype that implements this notion of matching.

Ongoing work

- The current implementation of the system modifies the rules in the module so Maude standard matching works as fuzzy matching.
- This has the advantage of producing all possible concrete rules.
- However, it also generates very large models and many irrelevant rules.
- Our aim is to instantiate by need, starting with an initial state of interest.
- Once implemented, we want to integrate it with the Pathway Logic Assistant.
- Finally, we want to apply the algorithm to relevant examples and analyze how it behaves.

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