

# Kinetic parameter estimation in biochemical reaction networks using observability extensions



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## Introduction

Accurate & reliable **parameter estimation** [1]

- Vital part of mathematical modeling
- Bottleneck in systems biology
- Becoming feasible (better measurements)

## Problem statement

**Kinetic reaction model** (ode's)

$$\frac{dc}{dt} = N \cdot r(c), \quad y = h(c)$$

- Measurement  $y$ 
  - Some reaction rates  $r_i$
  - Some species concentrations  $c_i$
- Reaction kinetics
 
$$r = \hat{r} \frac{c_1^{\nu_1}}{K_1^{\eta_1} + c_1^{\eta_1}} \cdots \frac{c_n^{\nu_n}}{K_n^{\eta_n} + c_n^{\eta_n}}$$
- Known: Reaction & Hill-term orders  $\nu$  &  $\eta$

Aim: Infer the parameters  $\mathbf{K}$  &  $\hat{r}$   
based on measurement  $y$  (output)

## Method

### 1. Model extension [2]

Introduce new dynamic variables for

- Reactions rates
  - Denominators (Hill variables)
- $$\frac{d}{dt} \log(r) \Rightarrow \dot{r} = f(c, m, r)$$
- $$m = K^\eta + c^\eta \Rightarrow \dot{m} = f(c)$$
- ⇒ Extended system:  
Parameter independent & linear output
- $$\dot{x} = f(x), \quad y = C \cdot x$$
- ⇒ Initial conditions  $\hat{x}_0 \triangleq$  parameters

### 2. State reconstruction [3]

Use measurement to estimate new states

- Non-linear observer with error-gain  $L$
- Caution:  $L$  ill-conditioned if not well observable

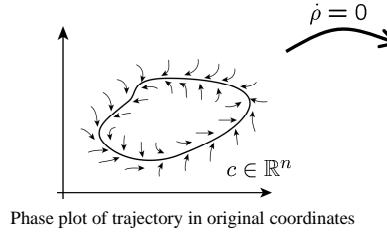
### 3. Parameter estimation

Use definition of extended variables

- Reaction rates ⇒ nominal rates  $\hat{r}$
- Hill variables ⇒ Hill constants  $K$

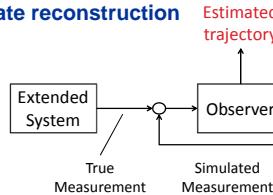
## Illustration of the method

### 1. Model extension

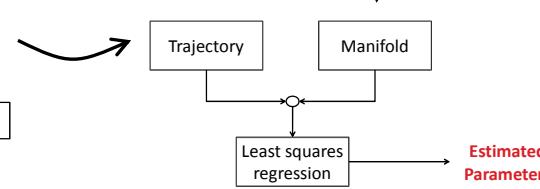


Trajectory in extended coordinates moves on low-dimensional manifold

### 2. State reconstruction



### 3. Parameter estimation



- Model extension
  - Higher dimensional space
  - ⇒ Trajectory on manifold
  - Shape of manifold
  - Defined by parameters
  - According definition extended variables
  - Regression on observed trajectory
  - ⇒ Identifies parameters

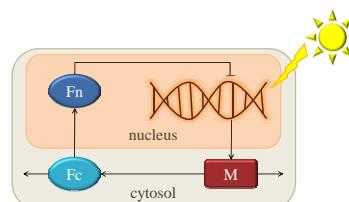
## Example

Circadian rhythm in *neurospora*

- Oscillations according to day-night cycle

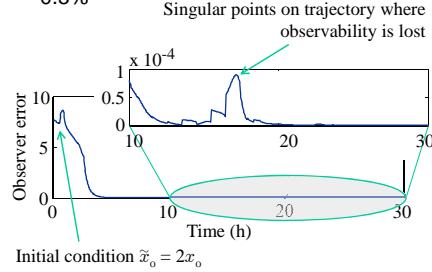
### Model [3]

- Dynamic gene regulation model
- 3 species, 3 mass action & 3 Hill reactions ⇒ 9 unknown parameters



## Results

- Observer converged
- Parameter estimate accurate, error < 0.5%



## Important Advantages

- Decoupling of state & parameter estimation
- Identifiability can be analyzed in terms of observability
- Measurement of all states (species concentrations) not generally necessary

## Conclusion

- Allows us to identify models & experiments for which the estimation is possible
- Very accurate estimation under noise free conditions

Parameter estimation can benefit from observability based approach

## Outlook

- Application to models of metabolic pathways, signal transduction and gene regulation
- Hybrid observer design: Continuous simulation & discrete updates
- Treating noise: e.g. Kalman Filters, error propagation, ...

## References

- (1) Peifer, M & Timmer, J, *IET Syst Biol*, 1(2):78–88 (2007)
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- (3) Vargas, A & Moreno, JA, *Int J Contr*, 78:247–253 (2005)
- (4) Leloup, JC, Gonze, D, & Goldbeter, A, *J Biol Rhythms*, 14(6):433–444 (1999)

## Acknowledgements

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