Parameter Identification, Experimental Design and Model Falsification for Biological Network Models Using Semidefinite Programming

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Abstract

One of the most challenging tasks in systems biology is parameter identification from experimental data. In particular, if the available data are noisy, the resulting parameter uncertainty can be huge and should be quantified. In this work, a set-based approach for parameter identification in discrete time models of biochemical reaction networks from time series data is developed. The basic idea is to determine an outer approximation to the set of parameters for which trajectories are consistent with the available data.

In order to approximate the set of consistent parameters a feasibility problem is derived. This feasibility problem is used to verify that complete parameter sets cannot contain consistent parameters. This method is very appealing because instead of checking a finite number of distinct points, complete sets are analyzed. With this approach, model falsification simply corresponds to showing that the set of consistent parameters is empty. Besides parameter identification, a novel set-based method for experimental design is presented. This method yields reliable predictions on the information content of future measurements also for the case of very limited *a priori* knowledge and uncertain inputs. The properties of the method are presented using a discrete time model of the MAP kinase cascade.

1 Introduction

Experimental design, parameter identification and model falsification are important tasks one has to deal with when constructing models of biological systems. Unfortunately, there are several open problems. In parameter identification and model falsification, sparse and noisy data sets as well as non-convexity of the underlying optimization problem are challenging. For experimental design, classical approaches require a detailed *a priori* knowledge about the parameter values, which is typically not available at the beginning of the modeling process, where experimental design can have the largest impact.

In this paper, a set-based approach is presented to overcome the problems related to noisy data and non-convexity for a class of implicit nonlinear discrete time systems with bounded measurement error. The method is based on the outer approximation of the set of consistent parameters (SCP), the set of parameters consistent with all available experimental data. Additionally, the application of the proposed approach to the analysis of biochemical reaction networks is illustrated with a case study.

Classical parameter identification approaches are based on the definition of the objective function and a successive modification of the parameter vector to minimize the objective and thus the difference between system and model response [17]. For the modification of the parameters, gradient-based methods are commonly applied. Hence, these standard approaches check a finite number of distinct points in parameter space. Even in cases where global optimization methods (e.g. clustering-methods, simulated annealing, or differential evolution) are employed [3, 18, 22] it can usually not be guaranteed that the optimal parameter vector is obtained with a finite number of iterations.

In particular for the task of model falsification these classical approaches are deficient as they check only a finite number of points in parameter space. Even if exhaustive Monte-Carlo simulations [21] are employed, which use a random sampling in the parameter space, only falsification probabilities are obtained. In cases where no parameter values are found for which the model reproduces the experimental data, it cannot be guaranteed that no such parameter values exist.

Furthermore, especially if the information content of the measured data is small, the remaining parameter uncertainties may be large and need to be quantified in order to evaluate the quality of the obtained model. This can be done via a practical identifiability analysis and the computation of the confidence intervals. Parameter confidence intervals are traditionally computed using the Fisher information matrix [2] or bootstrapping methods [13]. The Fisher information matrix is computed from the local sensitivity of the output with respect to the parameters. Hence confidence intervals computed using the Fisher information matrix are only valid locally and moreover rely on the assumption that the correct parameter is known, what is clearly not the case. Bootstrapping methods on the other hand are non-deterministic methods and use stochastic elements as well as repeated simulations and repeated solving of the parameter estimation problem. By this it is possible to account for nonlinearity of the identification problem. However, they require detailed knowledge about measurement noise distributions and noise properties (e.g. ergodicity). Hence, their application is in some situations questionable as the prerequisites on the noise are difficult to verify [14].

Another method to perform practical identifiability analysis is based on the calculation of the SCP [14, 16]. The main advantages are that the SCP can be used to derive rigorous bounds on the parameter uncertainties. Secondly, only boundedness of the noise has to be assumed. Furthermore, in case the SCP is provided as a reduced search area for conventional optimization-based methods, a tremendous speed-up to the parameter estimation is possible.

To compute the SCP, set-based methods have been developed during the last decade [11]. In particular Kieffer *et al.* [14] developed methodologies employing set inversion, interval analysis, and constraint propagation. These methods work well if the system has a particular structure, e.g. if it is cooperative

[12, 29], or if the dependency of the output on the parameters is known explicitly. However, if the mapping is not known, the results can get very conservative due to the strong relaxation required by interval arithmetics. One method to obtain good outer bounds for the SCP of systems of ordinary differential equation has been developed by Tucker *et al.* [25], which also uses constraint propagation. Unfortunately, one basic assumption is that the derivatives of the concentrations can be determined. For common measurements techniques used in molecular biology, the noise level typically prohibits the direct determination of measurement derivatives.

In the work of Küpfer *et al.* [16] a novel formulation of the computation of the SCP as feasibility problem is proposed and applied to compute infeasibility certificates for complete regions in parameter space. The feasibility problem is brought to a computationally efficient form by a relaxation to a semidefinite program (SDP) [20]. Related approaches have also been applied to perform global sensitivity and uncertainty analysis for (bio-)chemical reaction networks [10, 28].

The drawback of Küpfer's approach is that only information about the steady state of the system can be employed for the parameter identification and that only polynomial vector fields are considered. In this paper we extend the application of the earlier proposed methods to perform parameter estimation for discrete time systems with rational right hand side for which measurements of the time courses are available. The extention to time course data is crucial and in parallel to this work a first method for parameter identification and model discrimination has been proposed by Borchers *et al.* [4], considering polynomial vector fields. Additionally to the extensions on the theoretical side also a more extensive algorithm than in [16] is applied to approximate the SCP. The proposed parameter identification method is directly applicable to the model falsification problem by trying to establish emptiness of the SCP.

Besides the improvement of the parameter identification method a first set-based experimental design method is presented in this paper. The main goal of experimental design is to select the most informative experiments for parameter identification based on *a priori* knowledge [2, 15]. In this work, we focus on removing the constraint that a good estimate of the real parameters has to be available for selecting the experiments. This can lead to wrong predictions of the information content. Instead, it is assumed that only an *a priori* consistent parameter set is known.

This problem has also been considered by Asprey *et al.* [1] who developed a robust experimental design method based on the Fisher information matrix. In contrast to their work the experimental design approach proposed here uses as design criterion the expected volume of the SCP, a non-local measure. Furthermore, input uncertainties are taken into account as they are common in biological applications.

The remainder of the paper is structured as follows: In Section 2 the problems of parameter identification and model falsification are formulated and the theoretical background as well as the applied algorithms are presented. Section 3 contains an explanation of the experimental design approach and the method for selecting the most informative measurements. In Section 4 the developed algorithms are illustrated by an application to the experimental design, SCP estimation and model falsification for a simple model of the MAP kinase cascade.

Mathematical notation: The space of real symmetric $n \times n$ matrices is denoted as $\mathcal{S}^n$. $\mathcal{I}(a, b)$ denotes the integer set $\{a, a+1, \ldots, b\}$. The positive semidefiniteness of a quadratic matrix $X \in \mathcal{S}^n$ is denoted $X \succeq 0$ and the trace of X by $\mathrm{tr}(X)$.

2 Parameter Identification and Model Falsification

2.1 Problem Statement

Consider an implicit nonlinear discrete time dynamical model for a biochemical reaction network given by the system of implicit difference equations

$$\Sigma : \begin{cases} 0 = F(x^{(k+1)}, x^{(k)}, u^{(k)}, p), \quad x^{(0)} = x_0 \\ 0 = H(y^{(k)}, x^{(k)}, p), \end{cases} \tag{1}$$

where $y^{(k)} \in \mathbb{R}^{n_y}$ is the output vector, $x^{(k)} \in \mathbb{R}^{n_x}$ the state vector, $u^{(k)} \in \mathbb{R}^{n_u}$ the input vector at the k–th time point, and $p \in \mathbb{R}^{n_p}$ a constant parameter vector to be estimated. In this paper, only rational functions F and H are considered, but extensions to piecewise polynomial or general smooth non-linear functions are possible [10]. Many modelling frameworks for biochemical reaction networks rely exclusively on polynomial or rational functions, which stem from the law of mass action, the Michaelis-Menten mechanism or Hill-type reaction rates with integer Hill coefficients. However, the approach proposed in this paper is not applicable to generalized mass action networks [27], which are a less commonly used formalism to describe biochemical reaction networks.

Discrete time models of reaction networks arise from discrete time modelling [8] or via time discretization of differential equation models [7]. The advantage of discrete compared to continuous time models is the strictly algebraic mapping from $x^{(k)}$ to $x^{(k+1)}$.

We will assume that the input $u^{(k)}$ is known to be contained in a compact set $\mathcal{U}^{(k)} \subset \mathbb{R}^{n_u}$. In addition, there are constraints on the state variables, given by $x^{(k)} \in \mathcal{X}^{(k)} \subset \mathbb{R}^{n_x}$. Such constraints are often available from conservation laws or maximal production rates for individual chemical species.

The output of the system Σ is available through possibly erroneous measurements. The measurements are given by

$$\bar{y}^{(k)} = y^{(k)} + e^{(k)}, \quad k \in \mathcal{I}(0, N), \tag{2}$$

in which $\bar{y}^{(k)} \in \mathbb{R}^{n_y}$ is the measured output, $e^{(k)} \in \mathbb{R}^{n_y}$ the unknown measurement error, and $N+1$ the number of measurement points. We assume that the measurement error at each time point is known to be contained in a known compact set $\mathcal{E}^{(k)} \subset \mathbb{R}^{n_y}$. Then one can determine the set

$$\mathcal{Y}^{(k)} = \left\{ y \in \mathbb{R}^{n_y} \;\middle|\; \exists e \in \mathcal{E}^{(k)} : \bar{y}^{(k)} = y + e \right\}, \tag{3}$$

which by construction contains the actual output $y^{(k)}$ of the system at each time point k.

Let us introduce the notation $y^{(0,k)} = (y^{(0)}, \ldots, y^{(k)})$, $k > 0$, for an output sequence of the model Σ, and similarly $u^{(0,k)}$, $x^{(0,k)}$, $e^{(0,k)}$, and $\bar{y}^{(0,k)}$ for input,

state, measurement error, and measured output sequences, respectively. Moreover, we consider sets of sequences denoted by $\mathcal{U}^{(0,k)} = \{u^{(0,k)} \mid u^{(i)} \in \mathcal{U}^{(i)}, i = 0,\dots,k\}$, $\mathcal{X}^{(0,k)} = \{x^{(0,k)} \mid x^{(i)} \in \mathcal{X}^{(i)}, i = 0,\dots,k\}$, $\mathcal{E}^{(0,k)} = \{e^{(0,k)} \mid e^{(i)} \in \mathcal{E}^{(i)}, i = 0,\dots,k\}$, and $\mathcal{Y}^{(0,k)} = \{y^{(0,k)} \mid y^{(i)} \in \mathcal{Y}^{(i)}, i = 0,\dots,k\}$.

We call a parameter vector $p \in \mathbb{R}^{n_p}$ consistent with $(\Sigma, \mathcal{U}^{(0,N-1)}, \mathcal{X}^{(0,N)}, \mathcal{Y}^{(0,N)})$, if there exist $u^{(0,N-1)} \in \mathcal{U}^{(0,N-1)}$ and a solution $x^{(0,N)} \in \mathcal{X}^{(0,N)}$ of Σ such that $y^{(0,N)} \in \mathcal{Y}^{(0,N)}$.

The first problem that is considered in this paper is to compute the set of consistent parameters.

Problem 1 *Given the model Σ, the set of input sequences $\mathcal{U}^{(0,N-1)}$, the set of accessible states $\mathcal{X}^{(0,N)}$, and the set of output sequences $\mathcal{Y}^{(0,N)}$, compute the set $\mathcal{P}^* \subset \mathbb{R}^{n_p}$ of all parameters which are consistent with $(\Sigma, \mathcal{U}^{(0,N-1)}, \mathcal{X}^{(0,N)}, \mathcal{Y}^{(0,N)})$.*

For models of typical biochemical networks, the set $\mathcal{P}^*$ usually cannot be determined explicitly. In this work, we focus on the computation of an outer approximation $\bar{\mathcal{P}}^* \supseteq \mathcal{P}^*$, which is guaranteed to contain all consistent parameters. In this way, upper bounds on the parameter uncertainty resulting from uncertain measurement data can be obtained.

The second problem under consideration is the task of model falsification. In the proposed framework, the model falsification problem is simply the problem of proving that the set of consistent parameters is empty. If this is the case, the model structure Σ cannot reproduce the experimental data for any values of the parameters p.

Problem 2 *Given the model Σ, $\mathcal{U}^{(0,N-1)}$, $\mathcal{X}^{(0,N)}$, and $\mathcal{Y}^{(0,N)}$, determine whether the set of consistent parameters $\mathcal{P}^*$ is empty or not.*

2.2 Theoretical background

2.2.1 Infeasibility certificates

In this section a method to compute an outer approximation to the set of consistent parameters is derived. For this purpose, we introduce the feasibility problem

$$(P): \begin{cases} \text{find} & y^{(0,N)} \in \mathcal{Y}^{(0,N)},\ x^{(0,N)} \in \mathcal{X}^{(0,N)}, \\ & u^{(0,N-1)} \in \mathcal{U}^{(0,N-1)},\ p \in \mathcal{P}, \\ \text{s.t.} & F(x^{(k+1)}, x^{(k)}, u^{(k)}, p) = 0, \quad k \in \mathcal{I}(0, N-1) \\ & H(y^{(k)}, x^{(k)}, p) = 0, \quad k \in \mathcal{I}(0, N). \end{cases}$$

This feasibility problem is in the following used for the classification of a parameter test set $\mathcal{P} \subset \mathbb{R}^{n_p}$. If (P) is infeasible, $\mathcal{P}$ does not contain consistent parameters. Unfortunately, (P) is a nonlinear feasibility problem and in general non-convex and therefore NP-hard to solve.

Küpfer *et al.* [16] proposed a framework for relaxing a polynomial non-convex feasibility problem to a semidefinite program (SDP) [26], and apply it to parameter estimation for steady state measurements. Due to inherent convexity of SDPs, these problems can be solved computationally efficiently, e.g. via primal-dual interior point methods. In the following, we present an

approach which is based on the work of Küpfer *et al.* [16], and extends this work to dynamical measurements.

For the relaxation of (P) to a SDP, the original feasibility problem is first rewritten as a quadratic feasibility problem. Therefore, all equations and constraints appearing in (P) have to be polynomial. If all sets are convex polytopes and the functions F and H are polynomial in all of their arguments, this is fulfilled. In case that F and/or H are rational in their arguments, one can just multiply each equation with its least common denominator. In order to rewrite (P) as a quadratic problem, the vector $\xi \in \mathbb{R}^{n_\xi}$ is introduced, which consists of the monomials appearing in F and H, i.e.

$$\xi = (1,\ y_{i_y}^{(k)},\ x_{i_x}^{(k)},\ u_{i_u}^{(k)},\ p_{i_p},\ y_{i_y}^{(k)} x_{i_x}^{(k)},\ x_{i_x}^{(k)} p_{i_p}, \ldots)^T \tag{4}$$

for all $i_y \in \mathcal{I}(1, n_y)$, $i_x \in \mathcal{I}(1, n_x)$, $i_u \in \mathcal{I}(1, n_u)$, $i_p \in \mathcal{I}(1, n_p)$, $k \in \mathcal{I}(0, N)$ [20]. Using the monomial vector ξ, the equality constraints

$$\begin{aligned} F(x^{(k+1)}, x^{(k)}, u^{(k)}, p) = 0, \qquad & k \in \mathcal{I}(0, N-1) \\ H(y^{(k)}, x^{(k)}, p) = 0, \qquad & k \in \mathcal{I}(0, N) \end{aligned} \tag{5}$$

can be transformed to

$$\xi^T Q_i \xi = 0, \quad i \in \mathcal{I}(1, n_x N + n_y(N+1)), \tag{6}$$

with $Q_i \in \mathcal{S}^{n_\xi}$. Note that for higher order terms in ξ, additional constraints have to be introduced. These lead to additional equations of the form

$$\xi^T Q_i \xi = 0, \quad i \in \mathcal{I}(n_x N + n_y(N+1) + 1, c), \tag{7}$$

where again $Q_i \in \mathcal{S}^{n_\xi}$, and c is the total number of equality constraints.

In order to simplify notation, $\mathcal{Y}^{(k)}$, $\mathcal{X}^{(k)}$, $\mathcal{U}^{(k)}$, and $\mathcal{P}$ are restricted to polyhedral sets. Then the constraints $y^{(0,N)} \in \mathcal{Y}^{(0,N)}$, $x^{(0,N)} \in \mathcal{X}^{(0,N)}$, $u^{(0,N-1)} \in \mathcal{U}^{(0,N-1)}$, and $p \in \mathcal{P}$ can be written as

$$B\xi \geq 0, \tag{8}$$

with $B \in \mathbb{R}^{n_b \times n_\xi}$, and n_b is the number of constraints which jointly describe the sets $\mathcal{Y}^{(0,N)}$, $\mathcal{X}^{(0,N)}$, $\mathcal{U}^{(0,N-1)}$, and $\mathcal{P}$.

The original feasibility problem (P) can then be restated as

$$(QP): \begin{cases} \text{find} & \xi \in \mathbb{R}^{n_\xi} \\ \text{subject to} & \xi^T Q_i \xi = 0, \quad i \in \mathcal{I}(1, c) \\ & B\xi \geq 0 \\ & \xi_1 = 1. \end{cases}$$

A relaxation to a SDP is classically done by introducing the matrix $X = \xi\xi^T$ and dropping the appearing non-convex constraint $\operatorname{rank}(X) = 1$ [9]. This leads to the relaxed feasibility problem

$$(RP): \begin{cases} \text{find} & X \in \mathcal{S}^{n_\xi} \\ \text{subject to} & \operatorname{tr}(Q_i X) = 0, \quad i \in \mathcal{I}(1, c) \\ & BXe_1 \geq 0 \\ & BXB^T \geq 0 \\ & \operatorname{tr}(e_1 e_1^T X) = 1 \\ & X \succeq 0, \end{cases}$$

with $e_1 = (1, 0, \ldots, 0)^T \in \mathbb{R}^{n_\xi}$. Note that the relaxation may induce additional solutions. To reduce conservatism, the redundant constraint $BXB^T \geq 0$ is added, which is satisfied by every solution of (QP) and (P).

From (RP) one can derive the Lagrange dual problem,

$$(DP): \begin{cases} \text{maximize} & \nu_1 \\ \text{subject to} & e_1\lambda_1^T B + B^T\lambda_1 e_1^T + B^T\lambda_2 B \\ & +\lambda_3 + \nu_1 e_1 e_1^T + \sum_{i=1}^{c} \nu_{2,i} Q_i = 0 \\ & \lambda_1 \geq 0,\ \lambda_2 \geq 0,\ \lambda_3 \succeq 0, \end{cases}$$

with the Lagrange multipliers $\lambda_1 \in \mathbb{R}^{n_b}$, $\lambda_2 \in \mathcal{S}^{n_b}$, $\lambda_3 \in \mathcal{S}^{n_\xi}$, $\nu_1 \in \mathbb{R}$ and $\nu_2 \in \mathbb{R}^c$ [28]. Using the dual problem, one can obtain an infeasibility certificate for the original problem.

Proposition 1 *Let ν_1^* be the optimal cost of (DP). If $\nu_1^* = \infty$, then the original feasibility problem (P) is infeasible.*

This follows directly from weak duality. Note that any feasible solution to (DP) with $\nu_1^* > 0$ implies that (DP) is unbounded from above and Proposition 1 applies. We call such a solution an *inconsistency certificate*, because it gives a guarantee that $\mathcal{P}$ does not contain consistent parameters. For a more detailed discussion we refer to [28].

2.2.2 Reduction of Computational Complexity

The advantage of the formulation using the Lagrange dual is that the problem is convex and can be solved efficiently, as long as the number of optimization variables of (DP) is trackable. However, the number of optimization variables can be problematic already for small scale systems, if a large number of measurement points needs to be considered. The reason is that the number of optimization variables n_o is of order $\mathcal{O}^2((n_y+n_x+n_u+n_p)N)$ and thus grows quadratically in the number of uncertain variables and the number of time points. Furthermore, the dominating time for solving these problems is the cost for solving a linear program, which is of order $\mathcal{O}^3(n_o)$ [5]. Thus the effort for solving (DP) grows to the sixth order in the number of uncertain variables and time steps. This is of relevance in particular if the considered system or the number of measurement points are large.

To reduce the computational effort with respect to the number of time points, the original feasibility problem (P) can be split. This is done by splitting the sequences of input, state, and output variables in subsequences, such that several feasibility problems, each considering only a subset of time points, are constructed.

The resulting feasibility problems are given by

$$(P_j): \begin{cases} \text{find} & y^{(j,j+m)} \in \mathcal{Y}^{(j,j+m)},\ x^{(j,j+m)} \in \mathcal{X}^{(j,j+m)}, \\ & u^{(j,j+m-1)} \in \mathcal{U}^{(j,j+m-1)},\ p \in \mathcal{P}, \\ \text{s.t.} & F(x^{(k+1)}, x^{(k)}, u^{(k)}, p) = 0, \quad k \in \mathcal{I}(j, j+m-1) \\ & H(y^{(k)}, x^{(k)}, p) = 0, \quad k \in \mathcal{I}(j, j+m), \end{cases}$$

where $m+1$, with $1 \leq m \leq N$, is the number of sequential measurement points taken into account in the optimization problem (P_j). Since a solution of (P)

satisfies the constraints where the complete sequences from 0 to N are taken into account, we observe that if (P) is feasible, then also (P_j), $j = 0, \ldots, N-m$, are feasible. Because the reverse is in general false, considering (P_j), $j = 0, \ldots, N-m$, instead of (P) corresponds to a relaxation. Each feasibility problem (P_j) can be relaxed to its dual problem (DP_j), as shown above for (P). Using the (DP_j) we obtain:

Proposition 2 *Let $\nu_{j,1}^*$ be the optimal cost of (DP_j). If*

$$\sup\left\{\nu_{j,1}^* \mid \forall j \in \mathcal{I}(0, N-m)\right\} = \infty,$$

then the original feasibility problem (P) is infeasible.

This result follows again from weak duality.

Note that splitting the original problem along the time axis solves only part of the problem, the question how m should to chosen remains. As a rule of thumb, we suggest that with increasing measurement uncertainties and a decreasing number of measured variables, m should increase in order to maintain a comparable estimation quality.

Remark 1 *As the number of optimization variables and the computational complexity for solving (P_j) strongly increases with the number of states and parameters of the system, it is so far not possible to consider large scale systems. To change this, an in depth analysis of the structure of (P_j) has to be performed in the future to reduce the computation time.*

2.3 SCP computation and model falsification

Using the Lagrange dual problems (DP_j), a certificate for the inconsistency of (P), for a given set of parameters $\mathcal{P}_i$, can be computed. This allows to exploit (DP_j) to determine an outer approximation $\bar{\mathcal{P}}^*$ to the set of consistent parameters $\mathcal{P}^*$. In this work, this is done via a multi-dimensional bisection algorithm.

Therefore, at first an initial set $\mathcal{P}_0$, with $\mathcal{P}^* \subseteq \mathcal{P}_0$, has to be determined. In many practical applications, finding a set $\mathcal{P}_0$, with $\mathcal{P}^* \subseteq \mathcal{P}_0$, is not a restriction. A suitable set $\mathcal{P}_0$ can often be determined from physical insight into the problem. For instance in biochemical reaction networks all parameters are in general positive, hence already lower bounds are found.

Starting from the initial set $\mathcal{P}_0$, a recursive bisection of $\mathcal{P}_0$ is performed. For each of the resulting subsets $\mathcal{P}_i$ arising in the bisection, the corresponding dual problems (DP_j) are analyzed and it is tried to compute inconsistency certificates for $\mathcal{P}_i$. Successful computation of an infeasibility certificate assures that $\mathcal{P}_i$ does not intersect the SCP. If no certificate can be obtained, $\mathcal{P}_i$ is bisected, and it is tried to obtain an infeasibility certificate for the subsets. An approximation $\bar{\mathcal{P}}^*$ of the SCP is finally given by

$$\bar{\mathcal{P}}^* = \mathcal{P}_0 \setminus \bigcup_I \mathcal{P}_I, \tag{9}$$

where $\mathcal{P}_I$ are the sets for which an inconsistency certificate could be obtained.

The implementation of the algorithm is outlined as follows:

`Algorithm:` $\mathcal{P}$ `= Analyze-`$\mathcal{P}(\mathcal{U}, \mathcal{X}, \mathcal{Y}, \mathcal{P})$

1. If $V(\mathcal{P}) < \epsilon$, return $\mathcal{P} = \mathcal{P}$

2. Check feasibility of $DP_j(\mathcal{U}, \mathcal{X}, \mathcal{Y}, \mathcal{P})$, $\forall j \in \mathcal{I}(0, N-m)$

3. If $\sup\left\{\nu_{1,j}^* \mid j \in \mathcal{I}(0, N-m)\right\} = \infty$, return $\mathcal{P} = \emptyset$

4. If $\sup\left\{\nu_{1,j}^* \mid j \in \mathcal{I}(0, N-m)\right\} \neq \infty$:

   4.1. Bisection of $\mathcal{P}$ in $\mathcal{P}_1$ and $\mathcal{P}_2$

   4.2. $\mathcal{P}_1$ = Analyze-$\mathcal{P}(\mathcal{U}, \mathcal{X}, \mathcal{Y}, \mathcal{P}_1)$

   4.3. $\mathcal{P}_2$ = Analyze-$\mathcal{P}(\mathcal{U}, \mathcal{X}, \mathcal{Y}, \mathcal{P}_2)$

   4.4. Return $\mathcal{P} = \mathcal{P}_1 \cup \mathcal{P}_2$

This algorithm is called recursively until the weighted volume

$$V(\mathcal{P}) = \int_{\mathcal{P}} w(p)dp \tag{10}$$

of a test set $\mathcal{P}$ is smaller than a tolerance ϵ. Here, $w(p) \geq 0$ is a weighting function used to assess the importance of different regions in parameters space. For a more detailed discussion of this bisection algorithm we refer to [11]. The algorithm is implemented in `Matlab`. For solving the dual problems (DP_j) the open source toolbox `SeDuMi` is used [23].

For the task of model falsification also the above described algorithm is applied. If $\mathcal{P}_0$ can be certified to be inconsistent, i.e. the algorithm returns the empty set, we have a guarantee that no parameter value $p \in \mathcal{P}_0$ exists for which the model can fit the experimental data, and the model Σ is falsified.

Remark 2 *Applying the proposed method does not require an a priori identifiability analysis. If parameters p_j are not identifiable from the data, the uncertainty in these parameters will not decrease during SCP computation. Hence, identifiability can be studied in a rigorous way using the proposed algorithm.*

3 Experimental Design

3.1 Problem Statement

Besides the evaluation and analysis of measured data, it is of interest to predict the information content I of future experiments to perform experimental design.

Generally, experimental design aims at determining an experimental setup which allows gaining a maximal amount of additional information with respect to parameter identification [2] or model falsification [6]. In this paper, we focus on the comparison of the expected information content of different sets of input sequences $\mathcal{U}_1^{(0,N-1)}, \ldots, \mathcal{U}_M^{(0,N-1)}$, in which $\mathcal{U}_i^{(0,N-1)}$ denotes a set of experimentally feasible sequences of stimuli.

Compared to traditional approaches it is not assumed that a good approximation of the correct parameter is known, a set-based information criterion is used, and the fact that inputs can not be forced precisely is taken into account. The last point is of particular relevance in biological applications and experiments.

As a measure for information content of an experiment we consider the volumetric ratio of the falsified and the initial parameter set. The proposed method is hence related to D-optimal experimental design, where the determinate of the covariance matrix is minimized [1].

The experimental design problem can be stated as follows:

Problem 3 *Given the model Σ, an a priori consistent parameter set $\mathcal{P}_0$, and M sets of feasible input sequences $\mathcal{U}_i^{(0,N-1)}$, $i \in \mathcal{I}(1,M)$, determine the set of input sequences $\mathcal{U}_{i^*}^{(0,N-1)}$ for which the expected information content $[I](\mathcal{U}_{i^*}^{(0,N-1)}, \mathcal{P}_0)$ is maximal.*

3.2 Theoretical Background

In order to select the most informative experiments, the expected information content $[I](\mathcal{U}_i^{(0,N-1)}, \mathcal{P}_0)$ for a given set of input sequences $\mathcal{U}_i^{(0,N-1)}$ and an *a priori* consistent parameter set $\mathcal{P}_0$ has to be defined. Therefore, at first the information content of a particular experiment $\left(u^{(0,N-1)}, \bar{y}^{(0,N)}\right)$ is defined as,

$$I(p, u^{(0,N-1)}, e^{(0,N)}) = \frac{V\left(\mathcal{P}_0 \setminus \mathcal{P}^*\left(u^{(0,N-1)}, \bar{y}^{(0,N)}\right)\right)}{V\left(\mathcal{P}_0\right)}, \tag{11}$$

where $V(\mathcal{P})$ is the weighted volume of a set as defined in (10). This information content depends on the input $u^{(0,N-1)}$ and, via the measured output $\bar{y}^{(0,N)}$, on the system parameter p and the measurement noise $e^{(0,N)}$. The expected information content $[I](p, u^{(0,N-1)})$ is obtained by marginalization over $e^{(0,N)}$ according to the formula

$$[I](p, u^{(0,N-1)}) = \frac{\int_{\mathcal{E}^{(0,N)}} I(p, u^{(0,N-1)}, e^{(0,N)})\, de}{V(\mathcal{E}^{(0,N)})}. \tag{12}$$

Because the parameter p and the precise input sequence $u^{(0,N-1)}$ are unknown, further marginalization using the *a priori* information $p \in \mathcal{P}^0$ and the set of feasible input sequences $\mathcal{U}_i^{(0,N-1)}$ is performed. This yields

$$[I](p, \mathcal{U}_i^{(0,N-1)}) = \frac{\int_{\mathcal{U}_i^{(0,N-1)}} I(p, u^{(0,N-1)})\, du^{(0,N-1)}}{V(\mathcal{U}_i^{(0,N-1)})}, \tag{13}$$

the expected information content for a given set of input sequences $\mathcal{U}^{(0,N-1)}$ and the parameter p, and

$$[I](\mathcal{P}_0, \mathcal{U}_i^{(0,N-1)}) = \frac{\int_{\mathcal{P}_0} [I](p, \mathcal{U}_i^{(0,N-1)})\, dp}{V(\mathcal{P}_0)}, \tag{14}$$

the expected information content for the feasible set of input sequences $\mathcal{U}_i^{(0,N-1)}$ and the set of *a priori* consistent parameters $\mathcal{P}_0$.

The information measure $[I](\mathcal{P}_0, \mathcal{U}_i^{(0,N-1)})$ can now be used to determine the most informative set of input sequences:

Proposition 3 *Let $[\bar{I}](\mathcal{U}_i^{(0,N-1)}, \mathcal{P}_0)$ be the expected information content for $u \in \mathcal{U}_i^{(0,N-1)}$. If*

$$[\bar{I}](\mathcal{U}_{i^*}^{(0,N-1)}, \mathcal{P}_0) \geq [\bar{I}](\mathcal{U}_i^{(0,N-1)}, \mathcal{P}_0)\ \forall i \in \mathcal{I}(1,M), \tag{15}$$

then $\mathcal{U}_{i^*}^{(0,N-1)}$ *is the maximal informative set of input sequences with respect to parameter identification.*

3.3 Approximation of information measure

Unfortunately, neither the expected information content nor the set of consistent parameters for a given measurement $\mathcal{P}^*$ can be computed, therefore, $[I](\mathcal{P}_0,\mathcal{U}_i^{(0,N-1)})$ is approximated by $[\bar{I}](\mathcal{P}_0,\mathcal{U}_i^{(0,N-1)})$.

First of all, $\mathcal{P}^*$ is outer approximated by $\bar{\mathcal{P}}^*$ using the algorithm presented in Section 2.3. This yields a lower bound on the information content of a particular measurement,

$$\bar{I}(p, u_i^{(0,N-1)}, e^{(0,N)}) = \frac{V\left(\mathcal{P}_0 \setminus \bar{\mathcal{P}}^*\left(u^{(0,N-1)}, \bar{y}^{(0,N)}\right)\right)}{V\left(\mathcal{P}_0\right)}. \tag{16}$$

Using this approximation, the integral defining the expected information content $[I](\mathcal{U}_i^{(0,N-1)}, \mathcal{P}_0)$ is approximated via a Monte-Carlo approach,

$$[\bar{I}](\mathcal{P}^0,\mathcal{U}_i^{(0,N-1)}) = \frac{1}{s_p s_u s_e} \sum_{j_1=1}^{s_p} \sum_{j_2=1}^{s_u} \sum_{j_3=1}^{s_e} \bar{I}(p_{j_1}, u_{j_2}^{(0,N-1)}, e_{j_3}^{(0,N)}), \tag{17}$$

in which p_{j_1}, $u_{j_2}^{(0,N-1)}$, and $e_{j_3}^{(0,N)}$ are obtained by drawing random samples from $\mathcal{P}_0$, $\mathcal{U}_i^{(0,N-1)}$, and $\mathcal{E}^{(0,N)}$, respectively.

Basically, the system is simulated for different parameters, input sequences, and measurement errors. Based on these artificial data, the SCP is determined and used to approximate the expected information content.

It has to be emphasized that the quality of the approximation of $[\bar{I}](\mathcal{U}_i^{(0,N-1)}, \mathcal{P}_0)$ strongly depends on s_p, s_u, and s_e, the number of samples. These numbers should be chosen sufficiently high, such that convergence of $[\bar{I}](\mathcal{P}^0,\mathcal{U}_i^{(0,N-1)})$ is observed. Depending on the non-linearity of the system, the required number of samples can vary strongly.

Remark 3 *In this work we focus on the sets themselves and not on the probability distribution on the sets. Therefore, no weighting, corresponding to an a priori probability of the measurements disturbances and the a priori consistent parameters is considered. An extension is straight forward and uses the a priori probabilities of the different variables.*

4 Example

In order to illustrate the proposed experimental design, parameter identification, and model falsification scheme, a simple time discrete model of the MAP kinase cascade is analyzed, as illustrated in Figure 1. The MAPK cascade plays a crucial role in cell differentiation, proliferation, and other signal transduction pathways [19].

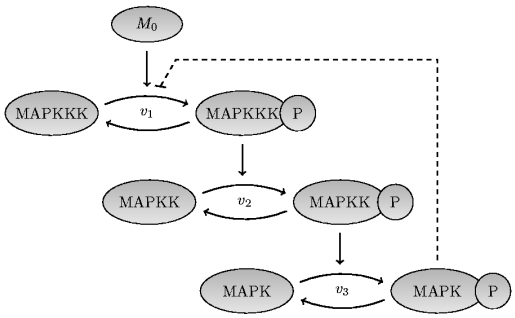

Figure 1: Illustration of the MAP-kinase-cascade.

4.1 Model of the MAPK cascade

The model of the MAPK cascade considered here is build up of the three different kinases MAPKKK, MAPKK, and MAPK which are unphosphorylated in the absence of signal. Phosphorylation and associated activation is performed by the upstream kinase. The difference equations describing the system dynamics are

$$\begin{aligned} x_1^{(k+1)} &= x_1^{(k)} + \Delta T\ v_1^{(k+1)}, \quad x_1^{(0)} = x_{1,0}, \\ x_2^{(k+1)} &= x_2^{(k)} + \Delta T\ v_2^{(k+1)}, \quad x_2^{(0)} = x_{2,0}, \\ x_3^{(k+1)} &= x_3^{(k)} + \Delta T\ v_3^{(k+1)}, \quad x_3^{(0)} = x_{3,0}, \end{aligned} \tag{18}$$

in which x_1 is the concentration of MAPKKK-P, x_2 is the concentration of MAPKK-P, and x_3 is the concentration of MAPK-P, all given in nM. Production and degradation of the different kinases are not considered because these happen on a slower timescale. Using mass conservation, the unphosphorylated states have been eliminated to reduce the model order.

In the following, it is distinguished between two different models for the reaction fluxes:

Model 1: The first model of the MAPK cascade is a simple chain of phosphorylations. M_0 controls the activation of MAPKKK, MAPKKK-P controls the activation of MAPKK, and so on. The reaction fluxes v_i are modelled using mass-action kinetics,

$$\begin{aligned} v_1^{(k)} &= k_1 \left(M_1 - x_1^{(k)}\right) u^{(k)} - k_{-1} x_1^{(k)} \\ v_2^{(k)} &= k_2 \left(M_2 - x_2^{(k)}\right) x_1^{(k)} - k_{-2} x_2^{(k)} \\ v_3^{(k)} &= k_3 \left(M_3 - x_3^{(k)}\right) x_2^{(k)} - k_{-3} x_3^{(k)}. \end{aligned} \tag{19}$$

The concentration of the enzyme M_0 can be interpreted as the input to the system and is denoted by u.

Model 2: In the second model, besides the phosphorylation cascade included in model 1, also a feedback inhibition from MAPK-P onto the phosphorylation of MAPKKK is considered (dashed line in Figure 1). This yields the modified

reaction flux v_1,

$$v_1^{(k)} = k_1 \left(M_1 - x_1^{(k)} \right) \frac{u^{(k)}}{1 + k_4 x_3^{(k)}} - k_{-1} x_1^{(k)}. \tag{20}$$

v_2 and v_3 are equivalent to those in model 1. The modification of v_1 yields a rational system which can be transformed to a polynomial one by multiplication with the denominator $1 + k_4 x_3^{(k)}$, as explained in Section 2.2.1.

The two discrete time models are the time discretization, using an implicit Euler scheme, of the continuous time models, describing the signaling pathways. The nominal parameter values are given in Table 1.

In the following, model 1 is assumed to describe the process and measurement data are generated using model 1. Besides parameter identification for model 1 a goal is to falsify model 2.

It is assumed that the concentrations of all three phosphorylated kinases are measurable,

$$y^{(k)} = (x_1^{(k)}, x_2^{(k)}, x_3^{(k)})^T + e^{(k)}, \tag{21}$$

in which e is the uniformly distributed measurement noise with $e \in \mathcal{E}^{(0,N)}$ and

$$\mathcal{E}^{(0,N)} = \left\{ e^{(0,N)} \,\middle|\, -\bar{e} \leq e^{(k)} \leq \bar{e}, \forall k \in \mathcal{I}(0,N) \right\}, \tag{22}$$

in which $\bar{e} = (0.02, 100, 100)^T$ nM. This absolute error corresponds to a relative error of 15 % and is realistic for Western Blots which are typically used to measure protein concentrations [24].

To reduce the problem size and to simplify the visualization of the result it is assumed that the ratios of forward to backward reaction rates $r_i = k_i/k_{-i}$ are known, for instance from previously performed steady state measurements. Furthermore, the total amount of the different kinases M_i is considered to be known. Therefore, for both models just the absolute values, here k_{-i} for $i = 1, 2, 3$, are in the following considered as uncertain,

$$p = (k_{-1}, k_{-2}, k_{-3})^T. \tag{23}$$

The initial set $\mathcal{P}^0$ for the estimation is set to

$$\mathcal{P}_0 = \{p \in \mathbb{R}^3 \mid 10^{-3} \leq p_i \leq 10, \forall i \in \{1,2,3\}\}. \tag{24}$$

Thus initial parameter uncertainties of four orders of magnitudes are considered. This is realistic for biological systems.

4.2 Experimental Design for the MAPK cascade

Before any experiment is performed, the experiment with the highest expected information content is selected using model 1 and the set of *a priori* consistent parameters $\mathcal{P}_0$. Experimental constraints are that measurements can only be performed at eight different points in time, $N = 7$, and only pulses in M_0 with a nominal concentration of 10^{-3} nM are feasible. The design variable is the pulse length yielding

$$\mathcal{U}_i^{(1,7)} = \left\{ u^{(1,7)} \,\middle|\, \begin{array}{l} u^{(k)} \in \mathcal{U}^h, \forall k \in \mathcal{I}(1,i), \\ u^{(k)} \in \mathcal{U}^s, \forall k \in \mathcal{I}(i+1), \\ u^{(k)} \in \mathcal{U}^l, \forall k \in \mathcal{I}(i+2,7) \end{array} \right\}, \forall i = \mathcal{I}(1,7), \tag{25}$$

Table 1: Actual parameter values.

Parameter	Value	Units	Parameter	Value	Units
k_1	5	1/(min nM)	k_{-1}	0.05	1/min
k_2	2	1/(min nM)	k_{-2}	0.1	1/min
k_3	0.001	1/(min nM)	k_{-3}	0.1	1/min
k_4	0.1	1/nM	ΔT	4	min
M_0	0.001	nM	M_1	3	nM
M_2	1200	nM	M_3	1200	nM

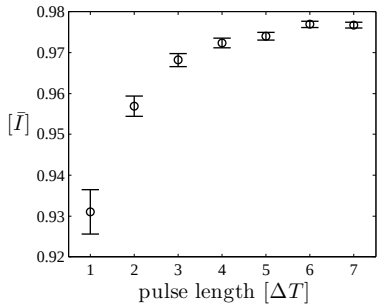

Figure 2: Expected information content $[\bar{I}]$ and corresponding variance for the different set of input sequences, $\mathcal{U}_1^{(1,7)}, \ldots, \mathcal{U}_7^{(1,7)}$. Discretization $\Delta T = 4$ min (Table 1).

in which $\mathcal{U}^l$ and $\mathcal{U}^h$ denote the set of low and high enzyme concentration,

$$\begin{aligned} \mathcal{U}^l &= \left\{ u \,\middle|\, 0 \leq u \leq 0.1 \cdot 10^{-3} \right\}, \\ \mathcal{U}^h &= \left\{ u \,\middle|\, 0.9 \cdot 10^{-3} \leq u \leq 1.1 \cdot 10^{-3} \right\}. \end{aligned} \tag{26}$$

Here an input uncertainty of 10^{-4} nM is considered, which may arise from errors in pipettation, filtration, and measurement. Furthermore, uncertainty and inaccuracies in the stimulus removal time are modeled by assuming the input directly after switching off as unknown with the bound $u^{(i+1)} \in \mathcal{U}^s = \left\{ u \,\middle|\, 0 \leq u \leq 1.1 \cdot 10^{-3} \right\}$.

For all sets of input sequences $\mathcal{U}_i^{(1,7)}$ the expected information content is computed. This is done according to (17) using the explained Monte-Carlo method. For the weighting function (10), used to determine the information content of a single artificial measurement, $w = \prod_{i=1}^{3} p_i^{-1}$ is chosen. This enforces a uniform weighting on the logarithmically scaled axes. The resulting expected information content for the different input sequences is depicted in Figure 2. The highest expected information content is obtained for a step length of six and the lowest one for a step length of 1. For a step length of 6, the expected amount of the parameter set $\mathcal{P}_0$ which can be qualified as inconsistent is 97.7 %. For a step of length one, it is only 93.1 %. The corresponding difference in the expected size of the consistent parameters $\bar{\mathcal{P}}^*$ is thus approximately a factor of three.

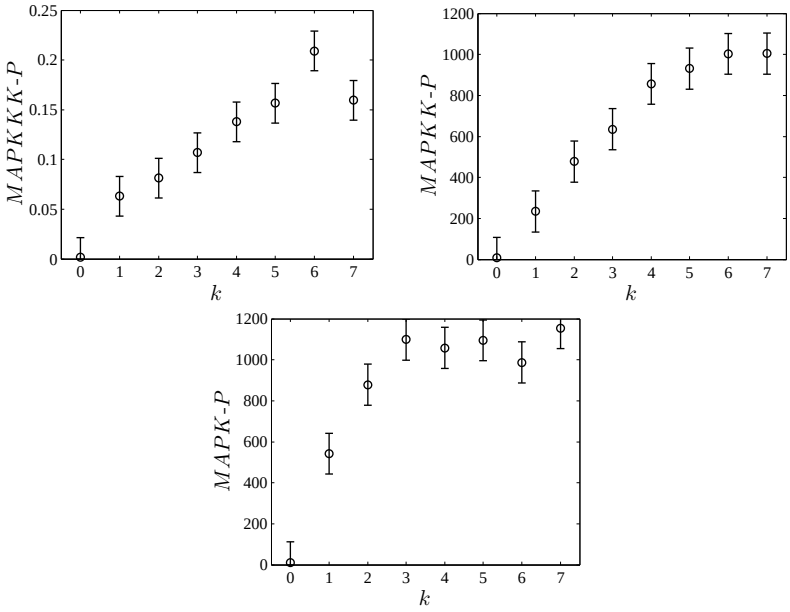

Figure 3: Artificial experimental data for MAPKKK-P, MAPKK-P and MAPK-P and corresponding error bounds.

4.3 Parameter Identification

For the examination of the properties of the developed scheme for the SCP computation an artificial experiment is now performed. To generate artificial measurement data, model 1 is simulated using the nominal parameter values and the nominal input sequence with a pulse length of six. The resulting output is corrupted by random measurement noise according to (22). The obtained artificial experimental data are depicted in Figure 3. The approximated information content of this measurement is 0.994, thus 99.4 % of $\mathcal{P}_0$ could be shown to be inconsistent with the measurement data.

For the artificial experimental data depicted in Figure 3, the set of consistent parameters of model 1 is computed using the algorithm outlined in Section 2. The obtained result is shown in Figure 4.

In order to evaluate the effect of the experimental design on the estimated SCP, also for the input with the lowest expected information content an artificial experiment is performed and the corresponding SCP approximated. The results can be found in Figure 5. Here 98.6 % of $\mathcal{P}_0$ can be ruled out and hence the volume of the remaining parameter set consistent with the experimental data differs by a factor of 2.4. This can be seen, also in case of extreme limited *a priori* knowledge, the proposed experimental design approach can help to select the most informative experiments.

To rate the quality of the obtained outer approximation $\bar{\mathcal{P}}^*$ of the SCP using the proposed algorithm, 1000 plausible points in parameter space are computed using a sampling-based approach. A detailed analysis uncovers that 70.7 % of the hypercubes that $\bar{\mathcal{P}}^*$ is built of contain at least one parameter sample and

thus $\bar{\mathcal{P}}^*$ is a fairly good approximation of the SCP.

Compared to the sampling-based approach the main advantage of our method is that an outer approximation of the SCP is obtained. Thus all consistent parameters have to be contained in $\bar{\mathcal{P}}^*$. The traditional approach on the other hand yields an inner approximation of the SCP and important solutions can be missed. The computation time of both approaches is comparable for this example.

4.4 Model Falsification

In the previous subsections it has been shown how the proposed method can be applied for SCP computation. In this section the focus lies on the falsification of models. Therefore, for model 2 the SCP is computed using the artificial experimental data shown in Figure 3, which are obtained by simulating model 1.

This computation takes here only two minutes until the SCP-computation algorithm returns that $\bar{\mathcal{P}}^*$ is empty. Hence, no parameter in the considered *a priori* consistent parameter set $\mathcal{P}_0$ can reproduce the measured dynamics within the measurement error bounds. Thus model 2 is falsified.

Compared to standard algorithms which sample the set $\mathcal{P}_0$ the computational effort is small. Additionally and even more important, it can be guaranteed that no consistent parametrisation of model 2 exists. Standard algorithms just provide a falsification probability.

5 Conclusions

In this paper an approach for parameter identification, model falsification, and experimental design using set-based methods based on work of Kuepfer *et al.* [16] is developed. For the classification of complete parameter sets a feasibility problem is defined, which is relaxed to a computationally efficient SDP. Based on this SDP, an algorithm to outer approximate the set of all consistent parameters of discrete time dynamical processes with rational right hand side is developed.

The resulting approximation to the set of consistent parameters directly describes the uncertainty in the parameters resulting from uncertain measurements. The result can also be applied for model falsification. Due to these properties, the proposed approach provides valuable information to the modeler. Furthermore, the set-based approach is applied to define a measure for the information content of a specific experimental measurement. This measure can be used to select the most informative experimental setup with respect to parameter identification, even in case of extremely limited *a priori* information and uncertain input sequences.

To illustrate the method, it is applied to a simple model of the MAPK cascade. This example highlights the advantages of the set-based approach for parameter identification, model falsification, and experimental design over classical methods.

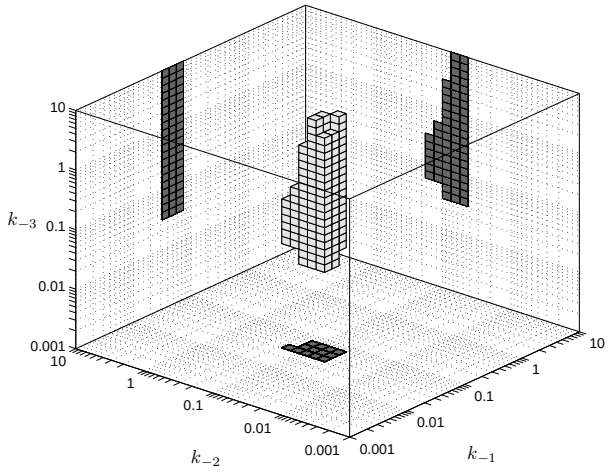

Figure 4: Approximation $\bar{\mathcal{P}}^*$ (light gray) of SCP and the projections of $\bar{\mathcal{P}}^*$ (dark gray) on the planes for the set of input sequences with the highest expected information content, $\mathcal{U}_6^{(1,7)}$.

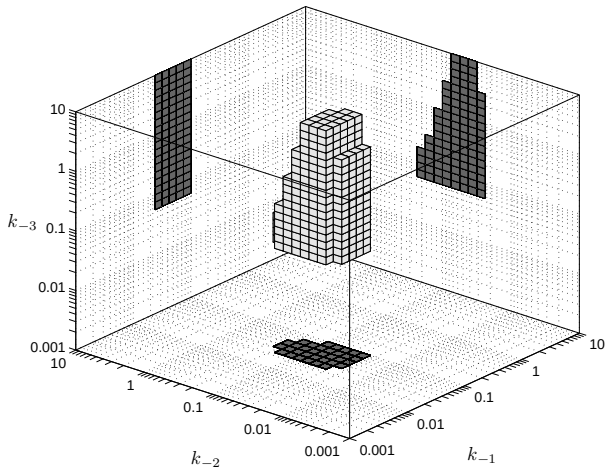

Figure 5: Approximation $\bar{\mathcal{P}}^*$ (light gray) of SCP and the projections of $\bar{\mathcal{P}}^*$ (dark gray) on the planes using for the set of input sequences with the lowest expected information content, $\mathcal{U}_1^{(1,7)}$.

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