ON THE ALGEBRAIC GEOMETRY
OF POLYNOMIAL DYNAMICAL SYSTEMS

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Abstract. This paper focuses on polynomial dynamical systems over finite fields. These systems appear in a variety of contexts, in computer science, engineering, and computational biology, for instance as models of intracellular biochemical networks. It is shown that several problems relating to their structure and dynamics, as well as control theory, can be formulated and solved in the language of algebraic geometry.

Key words. Polynomial dynamical system, inference of biochemical networks, control theory, computational algebra.

1. Introduction. The study of the dynamics of polynomial maps as time-discrete dynamical systems has a long tradition, in particular polynomials over the complex numbers leading to fractal structures. An example of more recent work using techniques from algebraic geometry includes the study of the algebraic and topological entropy of iterates of monomial mappings \( f = (f_1, \ldots, f_n) \) over subsets of \( \mathbb{C}^n \) [10].

The study of iterates of polynomial mappings (or, more generally, rational maps) over the \( p \)-adic numbers originally arose in Diophantine geometry [2]. For more recent work see, e.g., [27]. Finally, there is a long tradition of studying the iterates of polynomial maps \( f : \mathbb{F}_q \rightarrow \mathbb{F}_q \) over finite fields, primarily using techniques from combinatorics and algebraic number theory (see, e.g., [22, 23]).

The general case of finite dynamical systems

\[
f = (f_1, \ldots, f_n) : \mathbb{F}_q^n \rightarrow \mathbb{F}_q^n,
\]

with \( f_i \in \mathbb{F}_q[x_1, \ldots, x_n] \) has long been of interest in the special case \( q = 2 \), which includes Boolean networks and cellular automata. They are of considerable interest in engineering and computer science, for instance. Since the 1960s they are also being used increasingly as models of diverse biological and social networks.

The underlying mathematical questions in these studies for different fields are similar. They relate primarily to understanding the long-term behavior of the iterates of the mapping. In the case of monomial mappings, the matrix of exponents is usually the right mathematical object to analyze by using different methods based on the ground field. Generally, one would like to be able to use some feature of the structure of the coordinate functions \( f_i \) to deduce properties of the structure of the phase space of the system \( f \) which represents the system's dynamics. For finite systems, i.e.,

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polynomial dynamical systems $f$ over a finite field $k$, the phase space $P(f)$ has the form of a directed graph with vertices the elements of $k^n$. There is an edge $v \rightarrow w$ in $P(f)$ if $f(v) = w$. Since the graph has finitely many vertices it is easy to see that each component has the structure of a directed limit cycle, with trees (transients) feeding into each of the nodes in the cycle.

**Example 1.1.** Let $f : \mathbb{F}_3^2 \rightarrow \mathbb{F}_3^2$ be given by $f(x_1, x_2) = (1 - x_1 x_2, 1 + 2x_2)$. The phase space of $f$ has two components, containing two limit cycles: one of length two and one of length three. See Figure 1 (right). The dependency relations among the variables are encoded in the dependency graph in Figure 1 (left).

In this case the information of interest is the number of components, the length of the limit cycles, and, possibly, the structure of the transient trees. It is also of interest to study the sequence of iterates $f^r$ of $f$.

In recent years interest in polynomial dynamical systems over general finite fields has arisen also because they are useful as multistate generalizations of Boolean network models for biochemical networks, such as gene regulatory networks. In particular, the problem of network inference from experimental data can be formulated and solved in this framework. The tools used are very similar to those developed for the solution of problems in the statistical field of design of experiments and which led directly to the new field of algebraic statistics. (This connection is made explicit in [21].) Analyzing finite dynamical systems models of molecular networks requires tools that provide information about network dynamics from information about the system. Since the systems arising in applications can be quite high-dimensional it is not feasible to carry out such an analysis by exhaustive enumeration of the phase space. Thus, the studies of polynomial dynamics mentioned earlier become relevant to this type of application. Finally, an important role of models in biology and engineering is their use for the construction of controllers, be it for drug delivery to fight cancer or