Chapter 8
A Game-Theoretic Approach to Pairwise Clustering and Matching

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Abstract Clustering refers to the process of extracting maximally coherent groups from a set of objects using pairwise, or high-order, similarities. Traditional approaches to this problem are based on the idea of partitioning the input data into a predetermined number of classes, thereby obtaining the clusters as a by-product of the partitioning process. In this chapter, we provide a brief review of our recent work which offers a radically different view of the problem and allows one to work directly on non-(geo)metric data. In contrast to the classical approach, in fact, we attempt to provide a meaningful formalization of the very notion of a cluster in the presence of non-metric (even asymmetric and/or negative) (dis)similarities and show that game theory offers an attractive and unexplored perspective that serves well our purpose. To this end, we formulate the clustering problem in terms of a non-cooperative "clustering game" and show that a natural notion of a cluster turns out to be equivalent to a classical (evolutionary) game-theoretic equilibrium concept. Besides the game-theoretic perspective, we exhibit also characterizations of our cluster notion in terms of optimization theory and graph theory. As for the algorithmic issues, we describe two approaches to find equilibria of a clustering game. The first one is based on the classical replicator dynamics from evolutionary game theory, the second one is a novel class of dynamics inspired by infection and immu-

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nization processes which overcome their limitations. Finally, we show applications of the proposed framework to matching problems, where we aim at finding correspondences within a set of elements. In particular, we address the problems of point-pattern matching and surface registration.

8.1 Introduction

Clustering is the problem of organizing a set of data elements into groups in a way that each group satisfies an internal coherency and external incoherency property. Researchers have focused their attention on this problem for many decades due to its broad applicability, and recently a new wave of excitement has spread across the machine learning community mainly because of the important development of spectral methods. At the same time, there is also growing interest around fundamental questions pertaining to the very nature of the clustering problem (see, e.g., [1, 31, 60]). Yet, despite the tremendous progress in the field, the clustering problem remains elusive and a satisfactory answer even to the most basic questions is still to come.

The vast majority of the existing approaches deal with a very specific version of the problem, which asks for *partitioning* the input data into coherent classes. Even the classical distinction between hierarchical and partitional algorithms [28] seems to suggest the idea that partitioning data is, in essence, what clustering is all about (as hierarchies are but nested partitions). The partitional paradigm is attractive as it leads to elegant mathematical and algorithmic treatments and allows us to employ powerful ideas from such sophisticated fields as linear algebra, graph theory, optimization, statistics, information theory, etc. However, there are several (far too often neglected) reasons for feeling uncomfortable with this oversimplified formulation. Probably the best-known limitation of the partitional approach is the typical (algorithmic) requirement that the number of clusters be known in advance, but there is more than that.

To begin, the very idea of a partition implies that *all* the input data will have to get assigned to some class. There are various applications for which it makes little sense to force all data items to belong to some group, a process which might result either in poorly-coherent clusters or in the creation of extra spurious classes. As an extreme example, consider the classical figure/ground separation problem in computer vision which asks for extracting a coherent region (the figure) from a noisy background [24, 49]. More recently, motivated by practical applications arising in document retrieval and bioinformatics, a conceptually identical problem has attracted some attention within the machine learning community and is generally known under the name of one-class clustering [16, 23].

The second intrinsic limitation of the partitional paradigm is even more severe as it imposes that each element cannot belong to more than one cluster. There are a variety of important applications, however, where this requirement is too restrictive. Examples abound and include, e.g., clustering micro-array gene expression

data (wherein a gene often participate in more than one process), clustering documents into topic categories, perceptual grouping, and segmentation of images with transparent surfaces. Typically, this is solved by relaxing the constraints imposed by crisp partitions in such a way as to have "soft" boundaries between clusters.

Finally, stemming from a natural assumption for central clustering frameworks, clustering approaches have traditionally worked under the assumption that the similarities satisfy metric properties, i.e., they are symmetric, non-negative, and satisfy the triangle inequality. However, recently there has been a strong interest in relaxing these requirements [27, 46, 59]. This is due to the fact that in many applications non-metric similarities arise naturally [25, 58]. More fundamentally, some researches argue that human perception does not satisfy metric properties [27]. While the literature presents many approaches that lift the assumption of non-negativity and triangle inequality [27, 46], little progress has been made in relaxing the symmetry constraint. Note, however, that the limited progress in grouping with asymmetric affinities is not due to the lack of interest. In fact, there are many practical applications where asymmetric (or, more generally, non-metric) similarities do arise quite naturally. For example, such (dis)similarity measures are typically derived when images, shapes or sequences are aligned in a template matching process. In image and video processing, these measures are preferred in the presence of partially occluded objects [27]. Other examples include pairwise structural alignments of proteins that focus on local similarity [5], variants of the Hausdorff distance [18], normalized edit-distances, and probabilistic measures such as the Kullback–Leibler divergence. A common method to deal with asymmetric affinities is simply to symmetrize them, but in so doing we might lose important information that reside in the asymmetry (see, e.g., [12]). As argued in [27], the violation of metricity is often not an artifact of poor choice of features or algorithms, but it is inherent in the problem of robust matching when different parts of objects (shapes) are matched to different images (compare this with the analysis presented in Chap. 2 concerning non-Euclidean data). The same argument may hold for any type of local alignments. Corrections or simplifications of the original affinity matrix of the type described in the previous chapters may therefore destroy essential information, and is therefore important to devise algorithms which are able to work directly on the original data.

Although probabilistic model-based approaches do not suffer from several of the limitations mentioned above, here we suggest an alternative strategy. Instead of insisting on the idea of determining a partition of the input data, and hence obtaining the clusters as a by-product of the partitioning process, we propose to reverse the terms of the problem and attempt instead to derive a rigorous formulation of the very notion of a cluster. We found that game theory offers a very elegant and general perspective that serves well our purposes. Hence, in this chapter we describe a game-theoretic framework for clustering [38, 43, 52] which has found applications in fields as diverse as computer vision and bioinformatics. The starting point is the elementary observation that a "cluster" may be informally defined as a maximally coherent set of data items, i.e., as a subset of the input data C which satisfies both an *internal* criterion (all elements belonging to C should be highly similar to each other) and an *external* one (no larger cluster should contain C as a proper subset).

We then formulate the clustering problem as a non-cooperative *clustering game*, where the notion of a cluster turns out to be equivalent to a classical equilibrium concept from (evolutionary) game theory, as the latter reflects both the internal and external cluster conditions mentioned above. The clustering game is defined as follows: Assume a pre-existing set of objects O and a (possibly asymmetric and even negative) matrix of affinities A between the elements of O. Two players with complete knowledge of the setup play by simultaneously selecting an element of O. After both have shown their choice, each player receives a payoff, monetary or otherwise, proportional to the affinity that the chosen element has with respect to the element chosen by the opponent. Clearly, it is in each player's interest to pick an element that is strongly supported by the elements that the adversary is likely to choose. As an example, let us assume that our clustering problem is one of figure/ground discrimination, that is, the objects in O consist of a cohesive group with high mutual affinity (figure) and of non-structured noise (ground). Being non-structured, the noise gives equal average affinity to elements of the figures as to elements of the ground. Informally, assuming no prior knowledge of the inclination of the adversary, a player will be better-off selecting elements of the figure rather than of the ground.

Within this framework, clusters correspond to the ESSs of our non-cooperative game. The hypotheses that each object belongs to a cluster compete with one-another, each obtaining support from compatible edges and competitive pressure from the others. Competition will reduce the population of individuals that assume weakly supported hypotheses, while allowing populations assuming hypotheses with strong support to thrive. Eventually, all inconsistent hypotheses will be driven to extinction, while all the surviving ones will reach an equilibrium whereby they will all receive the same average support, hence exhibiting the internal coherency characterizing a cluster. As for the extinct hypotheses, they will provably have a lower support, thereby hinting to external incoherency. The stable strategies can be found using *replicator dynamics*, a classic formalization of a natural selection process [26, 57], or more powerful algorithms.

Our game-theoretic formulation of the clustering problem overcomes the aforementioned limitations of the majority of the clustering approaches in the literature. Indeed, it makes no assumption on the underlying (individual) data representation: like graph-based clustering, it does not require that the elements to be clustered be represented as points in a vector space; it makes no assumption on the structure of the affinity matrix, being able to work with asymmetric and even negative similarity functions alike; it does not require a priori knowledge on the number of clusters (since it extracts them sequentially); it leaves clutter elements unassigned; it allows extracting overlapping clusters [53]; it generalizes naturally to hypergraph clustering problems, i.e., in the presence of high-order affinities [44], in which case the clustering game is played by more than two players.

Outline The chapter is organized as follows. We provide basic game-theoretic notions and notation in Sect. 8.2. Section 8.3 presents the idea of the clustering game and provides different characterizations thereof. In Sect. 8.4, we describe algorithms

that can be used to find clusters according to the proposed framework. In Sects. 8.5 and 8.6, we present two effective applications of our clustering framework to the problem of matching, which is central to any recognition task where the object to be recognized is naturally divided into several parts, and the problem of surface alignment, which is a fundamental step in the reconstruction of three-dimensional objects.

8.2 Notations and Theoretical Background

According to classical game theory [21], a game of strategy between two players can be formalized as a triplet $\Gamma = (P, S, \pi)$, where $P = \{1, 2\}$ is the set of two "players" (or agents), $S = \{1, \ldots, n\}$ is a set of *pure strategies* (or actions) available to each player, and $\pi : S^2 \to \mathbb{R}$ is a *payoff function*, which assigns a utility to each *strategy profile* $(s_1, s_2) \in S^2$, which is an (ordered) pair of pure strategies played by the different players.[1] The payoff function can also be represented as a 2-dimensional matrix $A = (a_{ij}) \in \mathbb{R}^{n \times n}$ such that $a_{ij} = \pi(i, j)$.

Evolutionary game theory originated in the early 1970s as an attempt to apply the principles and tools of game theory to biological contexts, with a view to model the evolution of animal, as opposed to human, behavior (see the classical work by J. Maynard Smith [35] who pioneered the field). It considers an idealized scenario whereby individuals are repeatedly drawn at random from a large, ideally infinite, population to play a two-player game. In contrast to classical game theory, here players are not supposed to behave rationally or to have complete knowledge of the details of the game. They act instead according to an inherited behavioral pattern, or pure strategy, and it is supposed that some evolutionary selection process operates over time on the distribution of behaviors. Here, and in the sequel, an agent with preassigned strategy $j \in S$ will be called a *j-strategist*. The state of the population at a given time t can be represented as an n-dimensional vector $\mathbf{x}(t)$, where $x_j(t)$ represents the fraction of j-strategists in the population at time t. Hence, the initial distribution of preassigned strategies in the population is given by $\mathbf{x}(0)$. The set of all possible states describing a population is given by

$$\Delta = \left\{ \mathbf{x} \in \mathbb{R}^n : \sum_{j \in S} x_j = 1 \text{ and } x_j \geq 0 \text{ for all } j \in S \right\}$$

which is called the *standard simplex*. Points in the standard simplex are also referred to as *mixed strategies* in game theory. As time passes, the distribution of strategies in the population changes under the effect of a selection mechanism which, by analogy with Darwinian process, aims at spreading the fittest strategies in the population

[1] We note that although we restrict ourselves to games where all players share the same set of pure strategies and payoff function, in more general settings each agent can well be associated to its own pure strategy set and payoff function.

to the detriment of the weakest ones which, in turn, will be driven to extinction (we postpone the formalization of one such selection mechanism to Sect. 8.4). For notational convenience, we drop the time reference t from a population state and we refer to $\mathbf{x} \in \Delta$ as a population rather than population state. Moreover, we denote by $\sigma(\mathbf{x})$ the *support* of $\mathbf{x} \in \Delta$:

$$\sigma(\mathbf{x}) = \{j \in S : x_j > 0\}$$

which is the set of strategies that are alive in a given population $\mathbf{x}$.

We will find it useful to define the following function $u : \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R}$:

$$u\big(\mathbf{y}^{(1)}, \mathbf{y}^{(2)}\big) = \sum_{(s_1,s_2)\in S^2} \pi(s_1, s_2) \prod_{i\in\{1,2\}} y_{s_i}^{(i)} = {\mathbf{y}^{(1)}}^{\top} A \mathbf{y}^{(2)}. \tag{8.1}$$

We will also write $\mathbf{e}^j$ to indicate the n-vector with $x_j = 1$ and zero elsewhere. Now, it is easy to see that the expected payoff earned by a j-strategist in a population $\mathbf{x} \in \Delta$ is given by

$$u\big(\mathbf{e}^j, \mathbf{x}\big) = (A\mathbf{x})_j = \sum_{s\in S} a_{js}, x_s,$$

while the expected payoff over the entire population is given by

$$u(\mathbf{x}, \mathbf{x}) = \mathbf{x}^{\top} A \mathbf{x} = \sum_{j\in S} x_j (A\mathbf{x})_j.$$

Given a population $\mathbf{x}$, we denote by $\tau_-(\mathbf{x})$ the set of pure strategies that perform worse than average, i.e.,

$$\tau_-(\mathbf{x}) = \big\{j \in S : u\big(\mathbf{e}^j, \mathbf{x}\big) < u(\mathbf{x}, \mathbf{x})\big\},$$

by $\tau_+(\mathbf{x})$ the set of strategies performing better than the average, i.e.,

$$\tau_+(\mathbf{x}) = \big\{j \in S : u\big(\mathbf{e}^j, \mathbf{x}\big) > u(\mathbf{x}, \mathbf{x})\big\},$$

and finally by $\tau_0(\mathbf{x})$ the set of strategies performing as the average, i.e.,

$$\tau_0(\mathbf{x}) = \big\{j \in S : u\big(\mathbf{e}^j, \mathbf{x}\big) = u(\mathbf{x}, \mathbf{x})\big\}.$$

A fundamental notion in game theory is that of an equilibrium [57]. Intuitively, an evolutionary process reaches an equilibrium $\mathbf{x} \in \Delta$ when every individual in the population obtains the same expected payoff and no strategy can thus prevail upon the other ones. Formally, $\mathbf{x} \in \Delta$ is a *Nash equilibrium* if

$$u\big(\mathbf{e}^j, \mathbf{x}\big) \leq u(\mathbf{x}, \mathbf{x}), \quad \text{for all } j \in S. \tag{8.2}$$

In other words, at a Nash equilibrium every agent in the population performs at most as well as the overall population expected payoff. This can also be compactly written

as $\tau_+(\mathbf{x}) \cap S = \emptyset$. A Nash equilibrium $\mathbf{x} \in \Delta$ can be equivalently characterized by the condition that

$$u(\mathbf{y}, \mathbf{x}) \leq u(\mathbf{x}, \mathbf{x}) \tag{8.3}$$

for all $\mathbf{y} \in \Delta$. We say that a Nash equilibrium $\mathbf{x}$ is *strict* if (8.3) holds with strict inequality for all $\mathbf{y} \in \Delta \setminus \{\mathbf{x}\}$.

Within a population-based setting, the notion of a Nash equilibrium turns out to be too weak as it lacks stability under small perturbations. This motivated J. Maynard Smith, in his seminal work [35], to introduce a refinement of the Nash equilibrium concept generally known as an Evolutionary Stable Strategy (ESS). Formally, assume that in a population $\mathbf{x} \in \Delta$, a small share ε of mutant agents appear, whose distribution of strategies is $\mathbf{y} \in \Delta$. The resulting post-entry population is then given by $\mathbf{w}_\varepsilon = (1 - \varepsilon)\mathbf{x} + \varepsilon\mathbf{y}$. Biological intuition suggests that evolutionary forces select against mutant individuals if and only if the expected payoff of a mutant agent in the postentry population is lower than that of an individual from the original population, i.e.,

$$u(\mathbf{y}, \mathbf{w}_\varepsilon) < u(\mathbf{x}, \mathbf{w}_\varepsilon). \tag{8.4}$$

Hence, a population $\mathbf{x} \in \Delta$ is said to be *evolutionary stable* if inequality (8.4) holds for any distribution of mutant agents $\mathbf{y} \in \Delta \setminus \{\mathbf{x}\}$, granted the population share of mutants ε is sufficiently small. It can be shown [57] that $\mathbf{x}$ is an ESS equilibrium if and only if it is a Nash equilibrium and the additional stability property $u(\mathbf{x}, \mathbf{y}) > u(\mathbf{y}, \mathbf{y})$ holds for all $\mathbf{y} \in \Delta \setminus \{\mathbf{x}\}$ such that $u(\mathbf{y}, \mathbf{x}) = u(\mathbf{x}, \mathbf{x})$.

8.3 Clustering Games

An instance of the clustering problem can be described by an edge-weighted graph, which is formally defined as a triplet $G = (V, E, \omega)$, where $V = \{1, \ldots, n\}$ is a finite set of *vertices*, $E \subseteq V \times V$ is the set of oriented edges and $\omega : E \to \mathbb{R}$ is a real-valued function which assigns a weight to each edge. Within our clustering framework, the vertices in G correspond to the objects to be clustered, the edges represent neighborhood relationships among objects, and the edge-weights reflect similarity among linked objects. Note that in our framework no assumption is made on the similarity function.

Given a graph $G = (V, E, \omega)$, representing an instance of a clustering problem, we cast it into a two-player *clustering game* $\Gamma = (P, V, \pi)$ where the players' pure strategies correspond to the objects to be clustered and the payoff function π is proportional to the similarity of the objects/strategies $(v_1, v_2) \in V^2$ selected by the players:

$$\pi(v_1, v_2) = \begin{cases} \omega(v_1, v_2) & \text{if } (v_1, v_2) \in E, \\ 0 & \text{otherwise.} \end{cases} \tag{8.5}$$

Our clustering game will be played within an evolutionary setting wherein the two players, each of which is assumed to play a pre-assigned strategy, are repeatedly drawn at random from a large population. Here, given a population $\mathbf{x} \in \Delta$, x_j ($j \in V$) represents the fraction of players that is programmed to select j from the objects to be clustered. A dynamic evolutionary selection process, as the one described in Sect. 8.4, will then make the population $\mathbf{x}$ evolve according to a Darwinian survival-of-the-fittest principle in such a way that, eventually, the better-than-average objects will survive and the others will get extinct. It is clear that the whole dynamical process is driven by the payoff function π which, in our case, has been defined in (8.5) precisely to favor the evolution of highly coherent objects. Accordingly, the support $\sigma(\mathbf{x})$ of the converged population $\mathbf{x}$ does represent a cluster, the non-null components of $\mathbf{x}$ providing a measure of the degree of membership of its elements. Indeed, the expected population payoff $u(\mathbf{x}, \mathbf{x})$ can be regarded as a measure of the cluster's internal coherency in terms of the average similarity of the objects forming the cluster, whereas the expected payoff $u(\mathbf{e}^j, \mathbf{x})$ of a player selecting object $j \in V$ in $\mathbf{x}$ measures the average similarity of object j with respect to the cluster.

We claim that, within this setting, the clusters of a clustering problem instance can be characterized in terms of the ESSs of the corresponding (evolutionary) clustering game, thereby justifying the following definition.

Definition 8.1 (ESS-cluster) Given an instance of a clustering problem $G = (V, E, \omega)$, an *ESS-cluster* of G is an ESS of the corresponding clustering game.

For the sake of simplicity, when it will be clear from context, the term ESS-cluster will be used henceforth to refer to either the ESS itself, namely the membership vector $\mathbf{x} \in \Delta$, or to its support $\sigma(\mathbf{x}) = C \subseteq V$.

The motivation behind the above definition resides in the observation that ESS-clusters do incorporate the two basic properties of a cluster, i.e.,

- *Internal coherency*: elements belonging to the cluster should have high mutual similarities;
- *External incoherency*: the overall cluster internal coherency decreases by introducing external elements.

The rest of this section is devoted to provide support to this claim.

8.3.1 A Combinatorial Characterization

In this section, we provide a complete combinatorial characterization of the clusters under our game-theoretic framework, or more generally of evolutionary stable strategies of two-person symmetric games, which we derived from the dominant set framework [38].

Let $S = \{1, \dots\}$ be the set of the objects to be clustered, let A be the objects' similarity matrix and let $C \subseteq S$ be a non-empty subset of objects. The *(average) weighted in-degree* of $i \in S$ with respect to C is defined as:

$$\text{awindeg}_C(i) = \frac{1}{|C|} \sum_{j \in C} a_{ij},$$

where $|C|$ denotes the cardinality of C. Moreover, if $j \in C$ we define

$$\phi_C(i, j) = a_{ij} - \text{awindeg}_C(j),$$

which is a measure of the similarity of object i with object j with respect to the average similarity of object j with elements in C. The *weight* of i with respect to C is

$$W_C(i) = \begin{cases} 1 & \text{if } |C| = 1, \\ \sum_{j \in C \setminus \{i\}} \phi_{C \setminus \{i\}}(i, j) W_{C \setminus \{i\}}(j) & \text{otherwise,} \end{cases}$$

while the *total weight* of C is defined as

$$W(C) = \sum_{i \in C} W_C(i).$$

Intuitively, $W_C(i)$ gives us a measure of the support that object i receives from the objects in $C \setminus \{i\}$ relative to the overall mutual similarity of the objects in $C \setminus \{i\}$. Here positive values indicate that i has high similarity to $C \setminus \{i\}$.

A non-empty subset of objects $C \subseteq S$ such that $W(T) > 0$ for any non-empty $T \subseteq C$ is said to be a *dominant set* if:

1. $W_C(i) > 0$, for all $i \in C$,
2. $W_{C \cup \{i\}}(i) \leq 0$, for all $i \notin C$.

The two previous conditions correspond to the two main properties of a cluster: the first regards internal homogeneity, whereas the second regards external heterogeneity. The above definition represents our formalization of the concept of a cluster, when A is the similarity matrix describing the clustering problem.

The *weighted characteristic vector* $\mathbf{x}^C$ of a set $C \subseteq S$ is defined as

$$x_i^C = \begin{cases} \frac{W_C(i)}{W(C)} & \text{if } i \in C, \\ 0 & \text{otherwise.} \end{cases}$$

Theorem 8.1 *If $C \subseteq S$ is a dominant set with respect to affinity matrix A, then $\mathbf{x}^C$ is an ESS for a two-player game with payoff matrix A.*

Conversely, if $\mathbf{x}$ is an ESS for a two-person game with payoff matrix A, then $C = \sigma(\mathbf{x})$ is a dominant set with respect to A, provided that $C = \tau_0(\mathbf{x})$.

Proof See [52]. □

This result provides a generalization of the dominant set framework [38] to asymmetric affinities.

8.3.2 A Link to Optimization Theory

If we restrict our attention to symmetric payoff functions, then the notions of Nash equilibrium and ESS have a natural interpretation in terms of optimization theory. Let A be a symmetric payoff matrix and consider the following constrained program, also known as *standard quadratic program* [9]:

$$\begin{aligned} &\text{maximize} && u(\mathbf{x}, \mathbf{x}) = \mathbf{x}^T A \mathbf{x} \\ &\text{subject to} && \mathbf{x} \in \Delta \subset \mathbb{R}^n. \end{aligned} \tag{8.6}$$

A point $\mathbf{x}$ satisfies the Karush–Kuhn–Tucker (KKT) conditions for problem (8.6), i.e., the first-order necessary conditions for local optimality [34], if there exists $n+1$ real constants (Lagrange multipliers) $\mu_1, \ldots, \mu_n$ and λ, with $\mu_i \geq 0$ for all $i = 1, \ldots, n$, such that

$$(A\mathbf{x})_i - \lambda + \mu_i = 0,$$

and $\sum_{i=1}^{n} x_i \mu_i = 0$. Note that, since both x_i and μ_i are nonnegative for all $i = 1, \ldots, n$, the latter condition is equivalent to saying that $i \in \sigma(\mathbf{x})$ implies $\mu_i = 0$. Hence, the KKT conditions can be rewritten as

$$u\left(\mathbf{e}^i, \mathbf{x}\right) = (A\mathbf{x})_i \begin{cases} = \lambda & \text{if } i \in \sigma(\mathbf{x}), \\ \leq \lambda & \text{otherwise,} \end{cases}$$

for some real constant λ.

It is immediate to see that $\lambda = u(\mathbf{x}, \mathbf{x})$. In fact,

$$u(\mathbf{x}, \mathbf{x}) = \sum_{i \in \sigma(\mathbf{x})} x_i u\left(\mathbf{e}^i, \mathbf{x}\right) = \sum_{i \in \sigma(\mathbf{x})} x_i \lambda = \lambda.$$

Therefore, we have that $\mathbf{x}$ satisfies the KKT condition if for all $i = 1, \ldots, n$, $u(\mathbf{e}^i, \mathbf{x}) \leq u(\mathbf{x}, \mathbf{x})$, which indeed corresponds to the Nash equilibrium condition. Hence, under symmetric payoff matrices, the Nash condition is equivalent to the necessary condition for local optimality in (8.6). Moreover, as shown in the following theorem, ESS equilibria can be characterized in terms of strict local solutions of (8.6).

Theorem 8.2 *Strict local maximizers of* (8.6) *are ESS equilibria of a two-player game with payoff matrix A and vice versa.*

Proof See [26]. □

8.3.3 A Link to Graph Theory

Let $G = (V, E)$ be an undirected graph without self-loops, where $V = \{1, 2, \ldots, n\}$ is the set of vertices and $E \subseteq V \times V$ the set of edges. We define the *order* of a graph G as the cardinality of V. Two vertices $u, v \in V$ are *adjacent* if $(u, v) \in E$. A subset C of vertices in G is called a *clique* if all its vertices are mutually adjacent. It is a *maximal clique* if it is not a subset of other cliques in G. It is a *maximum clique* if it has maximum cardinality. The cardinality of a maximum clique of G is also called *clique number* and it is denoted by $\omega(G)$. The *adjacency matrix* of G is the $n \times n$ symmetric matrix $A_G = (a_{ij})$, where $a_{ij} = 1$ if $(i, j) \in E$, $a_{ij} = 0$ otherwise.

The adjacency matrix of an undirected graph can be regarded to as the similarity matrix of a clustering problem, and therefore our framework can be used to find the clusters. Due to this link to graph theory, it is interesting to see the interpretation of our game-theoretic notion of cluster in this context.

Consider the following constrained quadratic program:

$$\begin{aligned} &\text{maximize} && f_\alpha(\mathbf{x}) = \mathbf{x}^T (A_G + \alpha I)\mathbf{x} \\ &\text{subject to} && \mathbf{x} \in \Delta \subset \mathbb{R}^n, \end{aligned} \tag{8.7}$$

where n is the order of G, I the identity matrix, α is a real parameter, and where Δ is the standard simplex of the n-dimensional Euclidean space.

In 1965, Motzkin and Straus [36] established a connection between the maximum clique problem and the program in (8.7) with $\alpha = 0$. Specifically, they related the clique number of G to global solutions $\mathbf{x}^*$ of the program through the formula $\omega(G) = (1 - f_0(\mathbf{x}^*))^{-1}$, and showed that a subset of vertices C is a maximum clique of G if and only if its characteristic vector $\mathbf{x}^C \in \Delta$ is a global maximizer of f_0 on Δ.[2] Pelillo and Jagota [40] extended the Motzkin–Straus theorem by providing a characterization of maximal cliques in terms of local maximizers of f_0 in Δ.

A drawback of the original Motzkin–Straus formulation is the existence of "spurious" solutions, i.e., maximizers of f_0 over Δ that are not in the form of characteristic vectors. This was observed empirically by Pardalos and Phillips [37] and formalized later by Pelillo and Jagota [40]. In principle, spurious solutions represent a problem since, while providing information about the order of the maximum clique, they do not allow us to easily extract its vertices. Fortunately, there is a straightforward solution to this problem which has been introduced by Bomze [8]. He, indeed, suggested to adopt the formulation in (8.7) and basically proved that for $0 < \alpha < 1$ all local maximizer of (8.7) are strict and in one-to-one correspondence with the characteristic vectors of the maximal cliques of G.

There is an interesting relation between our notion of cluster and graph theory that arises if we consider $A_G + \alpha I$ as the similarity matrix. As seen in the previous section, the first order necessary conditions for $\mathbf{x}$ to be a local maximizer of (8.7)

[2] In the original paper, Motzkin and Straus proved the "only-if" part of this theorem. The converse, however, is a straightforward consequence of their result [40].

coincide with the conditions for $\mathbf{x}$ to be a Nash equilibrium. Hence, local maximizers of (8.7) are indeed Nash equilibria, but the converse does not necessarily hold. On the other hand, we have that $\mathbf{x}$ is an ESS if and only if it is a strict local maximizer of (8.7). Since strict local maximizer are in one-to-one correspondence with the maximal cliques of G, we have that the support of an ESS is indeed a maximal clique. Consequently, there exists a one-to-one relation between maximal cliques of a graph G and ESS-clusters of a clustering game with payoff matrix $A_G + \alpha I$ when $0 < \alpha < 1$ as stated by the following proposition.

Proposition 8.1 *Let $G = (V, E)$ be an undirected graph with adjacency matrix A_G and $0 < \alpha < 1$. A mixed strategy $\mathbf{x}$ is an ESS of a symmetric two-player game with payoff matrix $A_G + \alpha I$ if and only if it is the characteristic vector of a maximal clique of G.*

Proof ESSs of $A_G + \alpha I$ are in one-to-one correspondence with the strict local maximizers of (8.7) [26] and $\mathbf{x}$ is a strict local maximizer of $f_\alpha(\mathbf{x})$ if and only if it is the characteristic vector of a maximal clique of G [8]. Hence, the result follows. □

Finally, an extension of this result to the case of directed graphs can be found in [52].

8.4 Algorithms

In the previous section, we introduced a game-theoretic notion of cluster, but we only mentioned at the way clustering effectively takes place. Summarizing, the intuition is to let non-rational individuals play the clustering game under an evolutionary setting, until the distribution of strategies reaches an equilibrium, which in turn provides us with a cluster. In order this to work, however, we have to specify some selection mechanisms that effectively drives the population to equilibrium, which, resembling a Darwinian process, spreads the fittest strategies in the population to the detriment of the weakest one, which in turn will be driven to extinction. The section starts introducing the replicator dynamics, i.e., the standard dynamics developed in evolutionary game theory. Afterwards, we present a new class of dynamics that have several desired features and are computationally more appealing than the replicator dynamics.

8.4.1 Replicator Dynamics

In evolutionary game theory, the assumption is made that the game is played over and over, generation after generation, and that the action of natural selection will

result in the evolution of the fittest strategies. A general class of evolution equations is given by the following set of ordinary differential equations [57]:

$$\dot{x}_i = x_i(t) g_i(\mathbf{x}) \tag{8.8}$$

for $i = 1, \ldots, n$, where a dot signifies derivative with respect to time and $g = (g_1, \ldots, g_n)$ is a function with open domain containing Δ. Here, the function g_i ($i \in S$) specifies the rate at which pure strategy i replicates. It is usually required that the growth function g is *regular* [57], which means that it is Lipschitz continuous and that $g(\mathbf{x})^\top \mathbf{x} = 0$ for all $\mathbf{x} \in \Delta$. The former condition guarantees us that the system of the differential equation (8.8) has a unique solution through any initial population state. The latter condition, instead, ensures that the simplex Δ is invariant under (8.8), namely, any trajectory starting in Δ will remain in Δ.

A point $\mathbf{x}$ is said to be a *stationary* (or equilibrium) point for our dynamical systems, if $\dot{x}_i = 0$ ($i \in S$). A stationary point $\mathbf{x}$ is (Lyapunov) *stable* if for every neighborhood U of $\mathbf{x}$ there exists a neighborhood V of $\mathbf{x}$ such that $\mathbf{x}(0) \in V$ implies $\mathbf{x}(t) \in U$ for all $t \geq 0$. A stationary point is said to be *asymptotically stable* if any trajectory starting in its vicinity will converge to it as $t \to \infty$.

Payoff-monotonic game dynamics represent a wide class of regular selection dynamics for which useful properties hold. Intuitively, for a payoff-monotonic dynamics the strategies associated to higher payoffs will increase at a higher rate. Formally, a regular selection dynamics (8.8) is said to be *payoff-monotonic* if

$$g_i(\mathbf{x}) > g_j(\mathbf{x}) \quad \Leftrightarrow \quad u\big(\mathbf{e}^i, \mathbf{x}\big) > u\big(\mathbf{e}^j, \mathbf{x}\big)$$

for all $\mathbf{x} \in \Delta$ and $i, j \in S$.

Although this class contains many different dynamics, it turns out that they share a lot of common properties. To begin, they all have the same set of stationary points. Indeed, $\mathbf{x} \in \Delta$ is a stationary point under any payoff monotonic dynamics if and only if $u(\mathbf{e}^i, \mathbf{x}) = u(\mathbf{x}, \mathbf{x})$ holds for all $i \in \sigma(\mathbf{x})$ [57].

A well-known subclass of payoff-monotonic game dynamics is given by

$$\dot{x}_i = x_i \left(f\big(u\big(\mathbf{e}^i, \mathbf{x}\big)\big) - \sum_{j \in S} x_j f\big(u\big(\mathbf{e}^j, \mathbf{x}\big)\big) \right),$$

where $f(u)$ is an increasing function of u. These models arise in modeling the evolution of behavior by way of imitation processes, where players are occasionally given the opportunity to change their own strategies [57].

When f is the identity function, that is, $f(u) = u$, we obtain the standard continuous-time *replicator equations*,

$$\dot{x}_i = x_i \big(u\big(\mathbf{e}^i, \mathbf{x}\big) - u(\mathbf{x}, \mathbf{x})\big), \tag{8.9}$$

whose basic idea is that the average rate of increase $\dot{x}_i / x_i$ equals the difference between the average fitness of strategy i and the mean fitness over the entire population.

Another popular model arises when $f(u) = e^{ku}$, where k is a positive constant. As k tends to 0, the orbits of this dynamics approach those of the standard, first-order replicator model, slowed down by the factor k; moreover, for large values of k, the model approximates the so-called best-reply dynamics [26].

The replicator dynamics, and more in general any payoff monotonic dynamics, have the following properties[26, 57]:

Theorem 8.3 *Under any payoff monotonic dynamics the following hold true*:

- *A Nash equilibrium is a stationary point*;
- *A strict Nash equilibrium is asymptotically stable*;
- *A stationary point* $\mathbf{x}^*$ *that is the limit of an interior orbit, i.e., such that* $\sigma(\mathbf{x}(t)) = S$ *for all* $t \geq 0$ *and* $\lim_{t\to\infty} \mathbf{x}(t) = \mathbf{x}^*$, *is a Nash equilibrium*;
- *A stable stationary point is a Nash equilibrium*;
- *An ESS is asymptotically stable*.

In general, the converses of the implications in Theorem 8.3 do not hold.

Furthermore, if we restrict our focus to symmetric payoff matrices, i.e., $A = A^\top$, then stronger properties hold, as stated in the following theorem.

Theorem 8.4 *If* $A = A^\top$ *then the following hold*:

- $u(\mathbf{x}, \mathbf{x})$ *is strictly increasing along any non-constant trajectory of* (8.9). *In other words, for all* $t \geq 0$ *we have* $\dot{u}(\mathbf{x}, \mathbf{x}) > 0$, *unless* $\mathbf{x}$ *is a stationary point. Furthermore, any such trajectory converges to a* (*unique*) *stationary point*;
- $\mathbf{x}$ *is asymptotically stable if and only if* $\mathbf{x}$ *is an ESS*.

In order to implement the continuous-time replicator dynamics, one can resort to some iterative method like, e.g., the Runge–Kutta method, to find an approximate solution to the ordinary differential equations. Alternatively, one can adopt the discrete-time counterpart of (8.9), known as discrete-time replicator dynamics, which (assuming non-negative payoffs) is given by

$$x_i(t+1) = x_i(t)\frac{u(\mathbf{e}^i, \mathbf{x})}{u(\mathbf{x}, \mathbf{x})},$$

for $i \in S$. This equation is known to possess many of the dynamical properties of the continuous-time dynamics [57].

8.4.2 Infection and Immunization Dynamics

In order to overcome some computational problems afflicting standard evolutionary dynamics, we introduce a new class of evolutionary dynamics, inspired by infection and immunization processes.

Let $\mathbf{x} \in \Delta$ be the *incumbent* population state, $\mathbf{y}$ be the *mutant* population invading $\mathbf{x}$ and let $\mathbf{z} = (1-\varepsilon)\mathbf{x}+\varepsilon\mathbf{y}$ be the population state obtained by injecting into $\mathbf{x}$ a small share of $\mathbf{y}$-strategists. Then the *score function* of $\mathbf{y}$ versus $\mathbf{x}$ (introduced in [10]) is given by

$$h_{\mathbf{x}}(\mathbf{y}, \varepsilon) = u(\mathbf{y}, \mathbf{z}) - u(\mathbf{x}, \mathbf{z}) = \varepsilon u(\mathbf{y}-\mathbf{x}, \mathbf{y}-\mathbf{x}) + u(\mathbf{y}-\mathbf{x}, \mathbf{x}).$$

Following [11], we define the *(neutral) invasion barrier* $b_{\mathbf{x}}(\mathbf{y})$ of $\mathbf{x} \in \Delta$ against any mutant strategy $\mathbf{y}$ as the largest population share $\varepsilon_{\mathbf{y}}$ of $\mathbf{y}$-strategists such that for all smaller positive population shares ε, $\mathbf{x}$ earns a higher or equal payoff than $\mathbf{y}$ in the post-entry population $\mathbf{z}$. Formally,

$$b_{\mathbf{x}}(\mathbf{y}) = \inf\big\{\varepsilon \in (0,1) : h_{\mathbf{x}}(\mathbf{y}, \varepsilon) > 0\big\} \cup \{1\}.$$

Given populations $\mathbf{x}, \mathbf{y} \in \Delta$, we say that $\mathbf{x}$ is *immune* against $\mathbf{y}$ if $b_{\mathbf{x}}(\mathbf{y}) > 0$. Trivially, a population is always immune against itself. Note that $\mathbf{x}$ is immune against $\mathbf{y}$ if and only if either $u(\mathbf{y}-\mathbf{x}, \mathbf{x}) < 0$ or $u(\mathbf{y}-\mathbf{x}, \mathbf{x}) = 0$ and $u(\mathbf{y}-\mathbf{x}, \mathbf{y}-\mathbf{x}) \leq 0$. If $u(\mathbf{y}-\mathbf{x}, \mathbf{x}) > 0$, we say that $\mathbf{y}$ is *infective* for $\mathbf{x}$. Hence, the set of infective strategies for $\mathbf{x}$ is given by

$$\Upsilon(\mathbf{x}) = \big\{\mathbf{y} \in \Delta : u(\mathbf{y}-\mathbf{x}, \mathbf{x}) > 0\big\}.$$

Consider $\mathbf{y} \in \Upsilon(\mathbf{x})$; clearly, this implies $b_{\mathbf{x}}(\mathbf{y}) = 0$. If we allow for an invasion of a share ε of $\mathbf{y}$-strategists as long as the score function of $\mathbf{y}$ versus $\mathbf{x}$ is positive, at the end we will have a share of $\delta_{\mathbf{y}}(\mathbf{x})$ mutants in the postentry population, where

$$\delta_{\mathbf{y}}(\mathbf{x}) = \inf\big\{\varepsilon \in (0,1) : h_{\mathbf{x}}(\mathbf{y}, \varepsilon) \leq 0\big\} \cup \{1\}.$$

Note that if $\mathbf{y}$ is infective for $\mathbf{x}$, then $\delta_{\mathbf{y}}(\mathbf{x}) > 0$, whereas if $\mathbf{x}$ is immune against $\mathbf{y}$, then $\delta_{\mathbf{y}}(\mathbf{x}) = 0$. Further note that all the above concepts can be straightforwardly extended to contests with more than two participants and/or correlated individual behavior, where the score functions may be nonlinear in ε; see, e.g., [11] and references therein. In our two-person context, score functions are (affine-)linear, so that there is a simpler expression for $\delta_{\mathbf{y}}(\mathbf{x})$:

$$\delta_{\mathbf{y}}(\mathbf{x}) = \begin{cases} \min\{\frac{u(\mathbf{x}-\mathbf{y}, \mathbf{x})}{u(\mathbf{y}-\mathbf{x}, \mathbf{y}-\mathbf{x})}, 1\} & \text{if } u(\mathbf{y}-\mathbf{x}, \mathbf{y}-\mathbf{x}) < 0, \\ 1 & \text{otherwise.} \end{cases} \tag{8.10}$$

It can be proven [42] that if we allow a population $\mathbf{x}$ to be invaded by an infective strategy $\mathbf{y}$, and the extent of this infection is $\delta_{\mathbf{y}}(\mathbf{x})$, then the postentry population will become immune against $\mathbf{y}$. In formal terms, given $\mathbf{y} \in \Upsilon(\mathbf{x})$ and $\mathbf{z} = [1 - \delta_{\mathbf{y}}(\mathbf{x})]\mathbf{x} + \delta_{\mathbf{y}}(\mathbf{x})\mathbf{y}$, we have that $\mathbf{z}$ is immune against $\mathbf{y}$. The core idea of our method consists in selecting a strategy $\mathbf{y}$ which is infective for the current population $\mathbf{x}$. By allowing for invasion as shown before, we obtain a new population $\mathbf{z}$ which is immune to $\mathbf{y}$. This idea suggests the following class of new dynamics which for evident reasons is called *Infection and Immunization Dynamics* (InImDyn):

$$\mathbf{x}(t+1) = \delta_{\mathscr{S}(\mathbf{x})}(\mathbf{x})\big[\mathscr{S}(\mathbf{x}) - \mathbf{x}\big] + \mathbf{x}, \tag{8.11}$$

where $\mathbf{x}$ should be regarded to as $\mathbf{x}(t)$ and $\mathscr{S} : \Delta \to \Delta$ is a *strategy selection* function, which returns an infective strategy for $\mathbf{x}$ if it exists, or $\mathbf{x}$ otherwise:

$$\mathscr{S}(\mathbf{x}) = \begin{cases} \mathbf{y} & \text{for some } \mathbf{y} \in \Upsilon(\mathbf{x}) \text{ if } \Upsilon(\mathbf{x}) \neq \emptyset, \\ \mathbf{x} & \text{otherwise.} \end{cases} \tag{8.12}$$

By reiterating this process of *immunization*, we aim at reaching a population state $\mathbf{x}$ that cannot be infected by any other strategy. If this is the case then $\mathbf{x}$ is a fixed point under dynamics (8.11), but also a Nash strategy:

Theorem 8.5 *Let $\mathbf{x} \in \Delta$ be a strategy. Then the following statements are equivalent*:

(a) $\Upsilon(\mathbf{x}) = \emptyset$, *i.e., there is no infective strategy for* $\mathbf{x}$;
(b) $\mathbf{x}$ *is a Nash strategy*;
(c) $\mathbf{x}$ *is a fixed point under dynamics* (8.11).

Proof See [42]. □

The following result shows that the average payoff is strictly increasing along any non-constant trajectory of the dynamics (8.11), provided that the payoff matrix is symmetric.

Theorem 8.6 *Let $\{\mathbf{x}(t)\}_{t\geq 0}$ be a trajectory of* (8.11). *Then for all $t \geq 0$,*

$$u\big(\mathbf{x}(t+1), \mathbf{x}(t+1)\big) \geq u\big(\mathbf{x}(t), \mathbf{x}(t)\big),$$

with equality if and only if $\mathbf{x}(t) = \mathbf{x}(t+1)$, provided that the payoff matrix is symmetric.

Proof See [42]. □

Theorem 8.6 shows that by running InImDyn, under a symmetric payoff function, we strictly increase the population payoff unless we are at a fixed point, i.e., have already reached Nash equilibrium. This, of course, holds for any selection function $\mathscr{S}(\mathbf{x})$ satisfying (8.12). However, the way we choose $\mathscr{S}(\mathbf{x})$ may affect the efficiency of the dynamics. The next section introduces a particular selection function that leads to a well-performing dynamics for our purposes.

Depending on how we choose the function $\mathscr{S}(\mathbf{x})$ in (8.11), we may obtain different dynamics. One in particular, which is simple and leads to nice properties, consists in allowing only infective pure strategies or their respective co-strategies. This way, our equilibrium selection process closely resembles a vertex-pivoting method, as opposed to interior-point approaches like replicator dynamics or best-response dynamics [26].

If $\mathbf{x}$ is not fixed under (8.11), i.e., is not a Nash strategy, straightforward intuition renders selection of an infective strategy in a way easier than it could seem at first

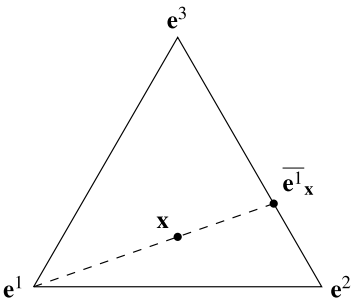


Fig. 8.1 Example of a co-strategy of the pure strategy $\mathbf{e}^1$ with respect to $\mathbf{x}$

glance. Let $\mathbf{x}$ be the current population and let $\mathbf{y}$ be a strategy. The *co-strategy* of $\mathbf{y}$ with respect to $\mathbf{x}$ is given by

$$\overline{\mathbf{y}}_{\mathbf{x}} = (1 - \bar{\varepsilon})\mathbf{x} + \bar{\varepsilon}\mathbf{y},$$

where

$$\bar{\varepsilon} = \min\{\varepsilon \in \mathbb{R} : (1 - \varepsilon)\mathbf{x} + \varepsilon\mathbf{y} \in \Delta\} \leq 0.$$

For any strategy $\mathbf{y}$, if both $u(\mathbf{y} - \mathbf{x}, \mathbf{x})$ and $\bar{\varepsilon}$ are nonzero, then either $\mathbf{y} \in \Upsilon(\mathbf{x})$ or $\overline{\mathbf{y}}_{\mathbf{x}} \in \Upsilon(\mathbf{x})$ in an exclusive sense.

In Fig. 8.1, we can see that the co-strategy of $\mathbf{e}^i$ with respect to $\mathbf{x}$ is the intersection between the simplex boundary and the half line originated in $\mathbf{e}^i$ and passing through $\mathbf{x}$. In this case, $\bar{\varepsilon} = x_i/(x_i - 1)$.

Consider the strategy selection function $\mathscr{S}_{\text{Pure}}(\mathbf{x})$, which finds a pure strategy i maximizing $|u(\mathbf{e}^i - \mathbf{x}, \mathbf{x})|$, and returns $\mathbf{e}^i$, $\overline{\mathbf{e}^i}_{\mathbf{x}}$ or $\mathbf{x}$ according to whether $i \in \tau_+(\mathbf{x})$, $i \in \tau_-(\mathbf{x}) \cap \sigma(\mathbf{x})$ or $i \in \tau_0(\mathbf{x})$: Let $\mathscr{M}(\mathbf{x})$ be a (randomly or otherwise selected) pure strategy such that

$$\mathscr{M}(\mathbf{x}) \in \arg\max\{u(\mathbf{e}^i - \mathbf{x}, \mathbf{x}) : i \in \tau_+(\mathbf{x})\} \cup \{u(\mathbf{x} - \mathbf{e}^i, \mathbf{x}) : i \in \tau_-(\mathbf{x}) \cap \sigma(\mathbf{x})\}.$$

Then $\mathscr{S}_{\text{Pure}}(\mathbf{x})$ can be written as

$$\mathscr{S}_{\text{Pure}}(\mathbf{x}) = \begin{cases} \mathbf{e}^i & \text{if } i = \mathscr{M}(\mathbf{x}) \in \tau_+(\mathbf{x}), \\ \overline{\mathbf{e}^i}_{\mathbf{x}} & \text{if } i = \mathscr{M}(\mathbf{x}) \in \tau_-(\mathbf{x}) \cap \sigma(\mathbf{x}), \\ \mathbf{x} & \text{otherwise.} \end{cases}$$

For obvious reasons, we refer to InImDyn with selection function $\mathscr{S}_{\text{Pure}}(\mathbf{x})$ as *Pure InImDyn*.

Note that the search space for an infective strategy is reduced from Δ to a finite set. Therefore, it is not obvious that $\mathscr{S}_{\text{Pure}}(\mathbf{x})$ is a well-defined selection function, i.e., it satisfies (8.12). However, one can prove [42] than there exists an infective strategy for $\mathbf{x}$ if and only if $\mathscr{S}_{\text{Pure}}(\mathbf{x})$ is infective for $\mathbf{x}$.

Another property that holds for our new dynamics, which is shared also by the replicator dynamics, is the characterization of ESS equilibria in terms of asymptotically stable points of the dynamics under symmetric payoff matrices.

Algorithm 1: FindEquilibrium($A, \mathbf{x}, \tau$)

Require: $n \times n$ payoff matrix A, $\mathbf{x} \in \Delta$ and tolerance τ.
  while $\varepsilon(\mathbf{x}) > \tau$ **do**
    $\mathbf{y} \leftarrow \mathscr{S}_{\text{Pure}}(\mathbf{x})$
    $\delta \leftarrow 1$
    if $\pi(\mathbf{y} - \mathbf{x}) < 0$ **then**
      $\delta \leftarrow \min[\frac{\pi(\mathbf{x}-\mathbf{y}|\mathbf{x})}{\pi(\mathbf{y}-\mathbf{x})}, 1]$
    end if
    $\mathbf{x} \leftarrow \delta(\mathbf{y} - \mathbf{x}) + \mathbf{x}$
  end while
  return $\mathbf{x}$

Theorem 8.7 *A state* $\mathbf{x}$ *is asymptotically stable for* InImDyn *with* $\mathscr{S}_{\text{Pure}}$ *as strategy selection function if and only if* $\mathbf{x}$ *is an ESS, provided that the payoff matrix is symmetric.*

Proof See [42]. □

This selection function exhibits the nice property of rendering the complexity per iteration of our new dynamics linear in both space and time, as opposed to the replicator dynamics, which have quadratic space/time complexity per iteration.

Theorem 8.8 *Given the iterate* $\mathbf{x}^{(t)}$ *and its linear transformations* $A\mathbf{x}(t)$ *and* $A^{\top}\mathbf{x}(t)$*, both space and time requirement of one iteration step is linear in* n*, the number of objects.*

Proof See [45]. □

The only step of quadratic complexity is the first one, where we need to compute $A\mathbf{x}(0)$ and $A^{\top}\mathbf{x}(0)$. Even this can be reduced to linear complexity, if we start from a pure strategy $\mathbf{e}^i$, in which case we have $A\mathbf{x}(0) = A_i$ and $A^{\top}\mathbf{x}(0) = (A^{\top})_i$. Note that the latter is impossible, e.g., for the replicator dynamics.

The algorithmic procedure for finding an equilibrium using InImDyn with $\mathscr{S}_{\text{Pure}}$ is summarized in Algorithm 1. Note that as stopping criterion we compute the following quantity:

$$\varepsilon(\mathbf{x}) = \sum_i \min\left\{x_i, \pi\left(\mathbf{x} - \mathbf{e}^i|\mathbf{x}\right)\right\}^2 < \tau, \tag{8.13}$$

which measures the degree of violation of the Nash conditions. Indeed, $\varepsilon(\mathbf{x}) = 0$ if and only if $\mathbf{x}$ is a Nash equilibrium.

8.5 Game-Theoretic Matching

The problem of finding correspondences within a set of elements, or features, is central to any recognition task where the object to be recognized is naturally divided into several parts. In this context, graph-based representations have been used with considerable success due to their ability to capture concisely the relational arrangement of object primitives, in a manner which can be invariant to changes in object viewpoint. However, applications in which estimating a set of correspondences is a central task toward the solution range from object recognition, to 3D registration, to feature tracking, to stereo reconstruction [7, 30, 33]. Several matching algorithms have been proposed in the literature. Some can just be classified as ad hoc solutions to specific problems, but the vast majority cast the problem into an energy minimization framework and extract approximate optimizers of an objective function within a set of feasible correspondences. In general, the overall goal is to maximize the global or local coherence of the matched pairs with respect to some compatibility. In most cases, the objective function can be written as a monotonic transformation of the sum of pairwise interactions between matching hypotheses. This can be either the similarity between matched features, as in the graph-matching case [4, 19, 55], and often the set of feasible correspondences can be defined using only unary and binary relations. For instance, it is possible to guarantee a global one-to-one match and structural coherence using the association graph technique described by Barrow and Burstall [6]. Also adjacency and hierarchical constraints can be enforced on a local pairwise basis, as shown by the many techniques that cast the matching problem to an equivalent clique search in an auxiliary association graph [39, 41, 51]. Formulations that satisfy these conditions range from bipartite matching, to subgraph isomorphism, to quadratic assignment, to edit-distance, and include a dual form of parameter estimation approaches such as Hough transform and RANSAC.

The previous sections introduced a novel game-theoretic clustering approach. In this section, we will build from that framework to introduce a matching approach based on the game-theoretic selection of correspondences between features to be matched. The first part will be devoted to the introduction of the novel selection process, while the second and third part will show applications of this frameworks to two important computer vision tasks.

We present a game-theoretic approach to correspondence estimation derived from the clustering approach presented in the previous section. The proposed approach is quite general since it can be applied to any formulation where both the objective function and the feasible set can be defined in terms of unary and pairwise interactions. The main idea is to model the set of possible correspondences as a set of game strategies. Specifically, we formulate the matching problem as a non-cooperative game where the potential associations between the items to be matched correspond to strategies, while payoffs reflect the degree of compatibility between competing hypotheses. A distinguishing feature of the proposed framework is that it allows one to naturally deal with general many-to-many matching problems even in the presence of asymmetric compatibilities.

8.5.1 Matching as a Non-cooperative Game

Before going into the details of the proposed framework, we need to introduce some notations and definitions that will be used throughout. Let O_1 and O_2 be the two sets of features that we want to match, we define the set of *feasible associations* $\mathbb{A} \subseteq O_1 \times O_2$ the set of relations between O_1 and O_2 that satisfy the unary constraints. Hence, each feasible association represents a possible matching hypothesis. We assume that we can compute a set of *pairwise compatibilities* $C : \mathbb{A} \times \mathbb{A} \to \mathbb{R}^+$ that measure the support that one association gives to the other. Here, the self compatibilities, i.e., the compatibilities that an association gives to itself, are assumed to be zero.

In this formulation, a *submatch* (or simply a *match*) is intuitively a set of associations, which satisfies the pairwise feasibility constraints, and two additional criteria: *high internal compatibility*, i.e., the associations belonging to the match are mutually highly compatible, and *low external compatibility*, i.e., associations outside the match are scarcely compatible with those inside. This definition of match allows us to abstract from the specific problem, since domain-specific information is confined to the definition of the compatibility function. Further, we are able to deal with many-to-many, one-to-many, many-to-one, and one-to-one relations in a uniform way, as we do not impose restriction on the way the associations are selected, but incorporate the constraints with the compatibilities.

The proposed approach generalizes the association graph technique described by Barrow and Burstall [6] to a context where structural constraints are continuous. Further, the approach can be seen as a proper generalization of [39] since, in case of symmetric 0,1 supports, the solutions of the ESSs maximize the same objective function.

We define a *matching game* as a clustering game over the associations. Assume that we have two sets of objects O_1 and O_2, and a compatibility function C. Let $O = \{1, \ldots, n\}$ be the enumeration of the set of associations $\mathscr{A}$, where $n = |\mathscr{A}|$. In the matching game, the set of feasible correspondences O forms the set of *pure strategies* (in the language of game-theory) available to the players and $A = (a_{ij})$ is an $n \times n$ payoff (or utility) matrix [56], where c_{ij} is the payoff that a player gains when playing the strategy i against an opponent playing strategy j. Within our matching setting, Nash equilibria are good candidates for a match, as they satisfy both the internal and external compatibility criteria. In fact, any association $i \in \sigma(\mathbf{x})$ of a Nash equilibrium $\mathbf{x}$ receives from $\mathbf{x}$ the same expected payoff $(A\mathbf{x})_i = \mathbf{x}^T A\mathbf{x}$, while associations not in $\sigma(\mathbf{x})$ receive a lower or equal support from associations of the match. Note, however, that the external criterion is not strict: there could exist associations not in $\sigma(\mathbf{x})$ that earn a payoff equal to $\mathbf{x}^T A\mathbf{x}$ like associations in the group, which may lead to a non-isolated Nash equilibrium and, thus, to an ambiguous match. Therefore, here we undertake an evolutionary game-theoretic analysis of the possible strategies available to each player.

8.5.1.1 Enforcing Hard Constraints

A main characteristic of the proposed approach is that associations pairs that have zero compatibility cannot be in the same selected submatch. This means that pairwise constraints can be enforced by forcing to zero the compatibility between associations that do not satisfy the constraints.

Theorem 8.9 *Consider a matching-game with compatibilities* $A = (a_{ij})$ *with* $a_{ij} \geq 0$ *and* $a_{ii} = 0$. *If* $\mathbf{x} \in \Delta$ *is an ESS then* $a_{ij} > 0$ *for all* $i, j \in \sigma(\mathbf{x})$.

For a proof see [3].

Theorem 8.9 shows that if we set a non-positive compatibility between two associations, then there exists no match containing them. This provides a way for expressing hard constraints in our matching framework such as one-to-one or one-to-many correspondences.

8.5.2 Point-Pattern Matching

In this set of experiments, our goal is to test the ability of the proposed framework to match corresponding features points between two instances of the same image with modified scale and orientation. The feature points are extracted from each image with the SIFT algorithm [33]. SIFT features are known to be highly repeatable under a large class of affine transformations and are very resilient to splitting or joining. Under these conditions, we need a very selective matcher which enforces a common global transformation to all the matched features. In [33], Lowe gauges the coherence of the transformation using RANSAC. This, however, requires a global threshold for the consensus, which limits the precision of the estimation.

The experiments were performed on the Aloi database [22]. For each run we selected 20 images and randomly deformed them with an affine transformation with a scale variation between 0.5 and 2 and a rotation between 0.5 and 2.0 radians. We extracted the SIFT features from the original and transformed image and picked as candidate associations all the pairs with sufficiently similar descriptors. Each candidate association represents a single transformation and supports only associations with similar transformations. To measure the support between two associations, we project the first point of one association with the transformation of the other association. Then we measure the distance between the transformed point and the corresponding point in the first association. We repeat the operation reversing the role of the two associations obtaining the two distances d_1 and d_2. The support is, then, $e^{-\max(d_1,d_2)}$. Once the best match is extracted, we have two alternatives to compute the final transformation: the first is an unweighted approach where we compute a simple average of the transformation parameters related to the associations in the match. The second approach weighs the transformation parameters with the proportion of the population playing the related strategy at equilibrium.

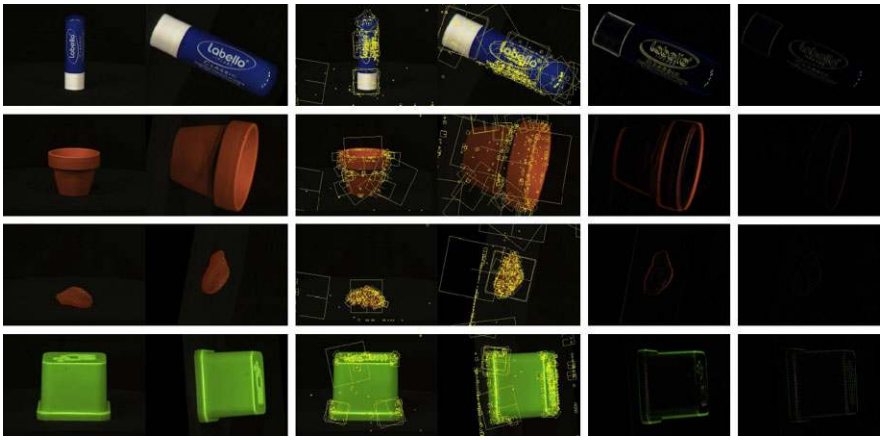


Fig. 8.2 Point pattern matching: the *first two columns* show the original images, the *third* and *fourth columns* show the extracted features, and the *fourth* and *fifth* show the allineation error using the transforms estimated using RANSAC (*fifth*) and our approach (*sixth*)

We compare our approach with RANSAC, where we determine the associations to agree within tolerance if $\max(d_1, d_2) < 5$ pixels. the value of 5 pixels was experimentally determined to be the one which gave the best results. Note that this threshold on the error limits the accuracy of RANSAC, while our approach, being parameter-less, does not suffer from this drawback.

Figure 8.2 shows the original images (first two columns), the extracted features (third and fourth columns), and the transformation error obtained using the two approaches (last two columns). The error is the difference between the original image transformed with the estimated transformation and the second image. The fifth column shows the error obtained using the transformation estimated with RANSAC, while the sixth column shows the difference using the transformation estimated using the weighted version of our approach. As can be seen our approach estimates the transformation with higher accuracy than RANSAC. So much so that the difference images are almost completely black. This is mainly due to the lack of a lower bound on the precision of the transformation, which for RANSAC is enforced by the consensus threshold.

Figure 8.3 plots the error in the estimation of translation, scale and rotation as we increase the variations in scale and orientation. The average and standard deviations are computed over 140 images. As can be seen, the weighted and unweighted versions of our approach have similar performance, with the weighted version exhibiting slightly lower error. On the other hand RANSAC show errors an order of magnitude larger in all conditions.

In an attempt to quantify the sensitivity of the approach to noise, we added an increasing amount of Gaussian noise to the rotated and scaled images before we computed the SIFT features. This introduces an increasing number of outliers as well as missing feature points. Figure 8.4 plots the Frobenius norm of the difference between the ground truth and the estimated transformation matrices as the standard

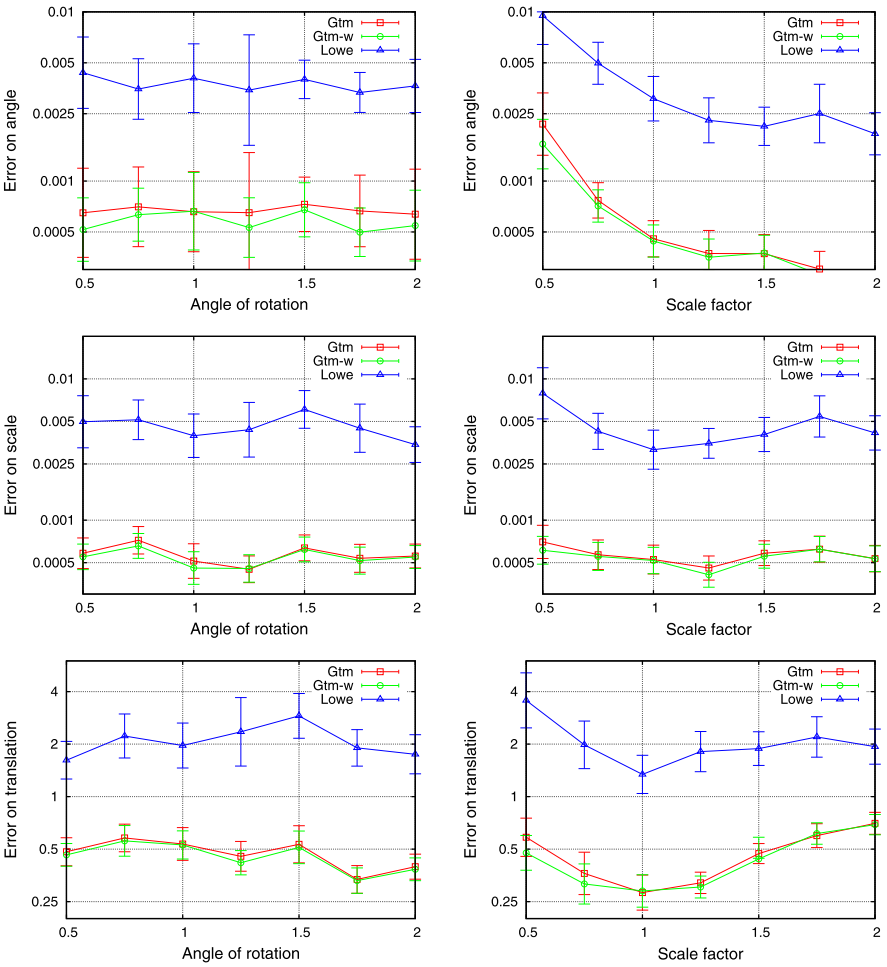


Fig. 8.3 Point pattern matching: error in the estimation of translation, scale and rotation as we increase the variations in scale and orientation. The *plots in the first column* show the error in rotation angle, scale and translation as a function of the rotation angle. The *plots in the second column* show the errors as a function of the scale factor

deviation of the Gaussian noise increases. For each noise level we selected 20 images and randomly deformed them with an affine transformation with a scale variation between 0.5 and 2 and a rotation between 0.5 and 2.0 radians. From the plot we can see that our approach maintains a much lower error as compared to RANSAC even at high noise levels. Further, we can see that, while the rate with which the error increases with noise is similar for RANSAC and the unweighted version of our approach, the weighted version appears to provide much lower error even with a high level of noise.

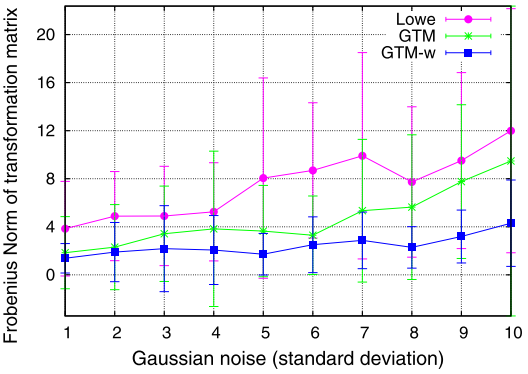


Fig. 8.4 Point pattern matching: sensitivity to noise. The *plot* displays the Frobenius norm of the difference between exact and estimated transformation errors under an increasing amount of Gaussian noise

8.6 Game-Theoretic Surface Alignment

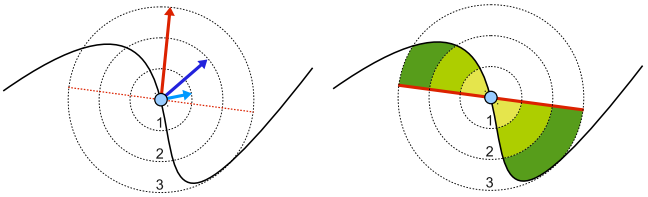
Surface registration is a fundamental step in the reconstruction of three-dimensional objects. This is typically a two step process where an initial coarse motion estimation is followed by a refinement.

Coarse registration techniques can be roughly organized into three main classes: global methods, feature-based methods and technique based on RANSAC [20] or PROSAC [14] schemes. Global methods, such as PCA [15] or Algebraic Surface Model [50], exploit some global property of the surface and thus are very sensitive to occlusion. Feature-based approaches aim at the localization and matching of interesting points on the surfaces. They are more precise and can align surfaces that exhibit only partial overlap. Nevertheless, the unavoidable localization error of the feature points prevents them from obtaining accuracies on par with fine registration methods.

A completely different coarse registration approach is the one taken by RANSAC-based techniques. DARCES [13] is based on the random extraction of sets of mates from the surfaces and their validation based on the accuracy of the estimated transformation. The more recent Four Points Congruent Sets method [2] follows a similar route, but filters the data to reduce noise and performs early check in order to reduce the number of trials.

A recent and extensive review of many different methods can be found in [48].

In this section, we present a novel technique that allows obtaining a fine surface registration in a single step, without the need of an initial motion estimation. The main idea of our approach is to cast the selection of correspondences between points on the surfaces in a game-theoretic framework. This process yields a very robust inlier selection scheme that does not depend on any particular technique for selecting the initial strategies as it relies only on the global geometric compatibility between correspondences. This context diverges from the general matching scheme presented in the previous section in that only a few correspondences a sought. In fact, contrary to the tradition of graph matching, inlier selection processes are tuned to very low false positive correspondences, admitting in converse a large amount of false negatives.



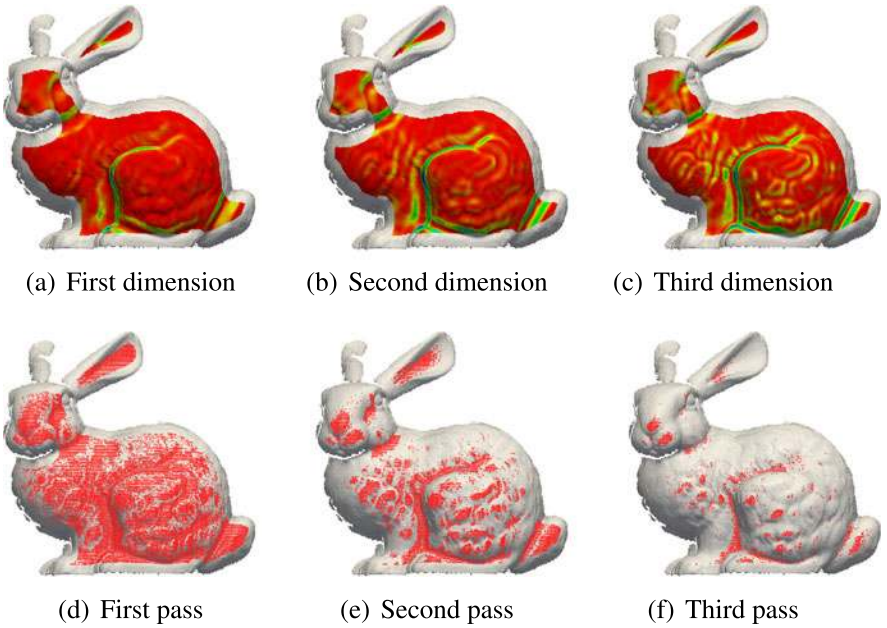
(a) Normal Hash (b) Integral Hash

Fig. 8.5 Example of the two basic Surface Hashes proposed

In principle, by adopting our matching approach, all the points from both surfaces to registered could be used to build the matching strategies; in practice, however, this would lead to a very big set of candidates with a huge portion of outliers. We solve the problem by adopting very loose yet repeatable descriptors, and by adopting a game-theoretic approach to select only the distinctive points. In the remaining of this section, we will introduce the point selection process, then the matching process used to perform surface alignment and finally we will experimentally characterize its performance with respect to the state-of-the-art.

8.6.1 Interest Point Selection

Given the large number of points contained in typical 3D objects, it is not practical for any matching algorithm to deal with all of them. In addition, the isolation of a relatively small number of interest points can enhance dramatically the ability of the matcher to avoid false correspondences. We do this using a novel set of robust descriptors and a game-theoretic feature-selection approach. The *Normal Hash* (see Fig. 8.5(a)) is obtained by setting a reference on the average surface normal over a patch that extends to the largest scale (red arrow in figure) and then, for each smaller scale, calculating the dot product between the reference and the average normal over the reduced patches (blue arrows in figure). The rationale behind this measure lies in the observation that at the largest scale the average normal is more stable with respect to noise and that the dot product offers a concise representation of the relation between the vectors obtained at various scales. The *Integral Hash* (see Fig. 8.5(b)) is similar in spirit to the Normal Hash. In this case, we search for the best fitting plane (in the least squares sense) with respect to the surface patch associated to the largest scale. Then we calculate the volume enclosed between the surface and such a plane. In practice, it is not necessary to evaluate this volume accurately: even naive approximations, such as the sum of the distances of the surface points from the plane, have been shown empirically to provide a reasonable approximation. Note that Normal Hashes evaluated over n scales yield descriptor vectors of length $n - 1$ (since the larger scale is used only to calculate the reference normal), while Integral Hashes provide n-dimensional vectors. In Fig. 8.6, a Normal Hash of dimension 3 (respectively from (a) to (c)) evaluated over 4 scales is shown. Note that the descriptor is



(a) First dimension (b) Second dimension (c) Third dimension

(d) First pass (e) Second pass (f) Third pass

Fig. 8.6 Example of a 3-dimensional Normal Hash and the related detection process

not defined at the points for which the larger support is not fully contained in the surface, i.e., points close to the surface boundary.

In order to obtain discriminant descriptors, we screen out features exhibiting descriptors that are too common over the surface. This is in essence an anomaly detection problem and it is done eliminating the common strategy detected through a clustering game where the strategy set S corresponds to the set of all the surface points and the payoff matrix is defined by

$$\pi_{ij} = e^{-\alpha|d_i - d_j|}, \tag{8.14}$$

where d_i and d_j are the descriptor vectors associated to surface point i and j, and α is a parameter that controls the level of selectivity. We can initialize the set of retained features to the whole surface and run a sequence of Matching Games, eliminating the extracted clusters, until the desired number of points are left. At this point, the remaining features are those characterized by less-common descriptors which are more likely to represent good cues for the matching. It should be noted that by choosing large values for α the payoff function decreases more rapidly with the growth of the distance between the Surface Hashes, thus the Matching Game becomes more selective and fewer points survive. In the end, this results in a blander decimation and thus in a larger ratio of retained interest points. By converse, a small value for α leads to a more greedy filtering and thus to a more selective interest point detector. In Fig. 8.6 (from (d) to (f)), we show three steps of the evolutive interest point selection with respect to the 3-dimensional Normal Hash shown

from (a) to (c). In Fig. 8.6(d), we see that after a single pass of the Matching Game most of the surface points are still considered interesting, while after respectively two and three passes only very distinctive points (belonging to areas with less common curvature profile) are left.

8.6.2 Isometry-Enforcing Game

We will refer to the points belonging to the first surface with the term *model points*, while we will use the term *data points* with respect to the second surface. This distinction is captious since there is no actual difference in role between the two surfaces; however, it is consistent with the current registration literature and helps in defining an order within matches.

Given the set of all model points M and the set of all data points D, we need to construct a set of *matching strategies* $S \subset M \times D$ constructed on the selected interest points. To this end, we perform a discriminative point selection from the model surface, and from this we create the set S by selecting the k most similar points from the whole data model D, where the similarity is gauged through the Euclidean distance of the descriptors. There is, thus, an asymmetry in the role of the surfaces, where only the model M is sub-sampled through the discriminative point selection process, and than it drives the creation of the strategy S. When not otherwise stated, in our experiments we set k to be equal to 5. Limiting the number of correspondences per source feature to a constant value, we limit the growth of the number of strategies to be linear with the number of model points selected.

Since the set of strategies S is built by proposing several attainable matches for each considered model point, while the correct match is not guaranteed to be within the best k selected matches, it is obvious that the number of outliers in S will be far superior to the number of correct correspondences. In order to extract this minority of correct matches buried into S, our framework must exploit the consistency of any pair of those strategies with respect to some property.

In order to define a suitable payoff function, we need to assign to each pair of matching strategies a payoff that is inversely proportional to a measure of violation of the rigid-transformation constraint. This violation can be expressed in several ways, but since all the rigid transformations preserve Euclidean distances, we choose this property to express the coherence between matching strategies. Clearly, this isometry constraint is looser than the rigid-transformation constraint as it cannot prevent specular flips of the surfaces, but the global consistency provided by the game-theoretic framework ensures that only rigid alignments will prevail.

Definition 8.2 Given a function $\pi : S \times S \to \mathbb{R}^+$, we call it an *isometry-enforcing payoff function* if for any $((a_1, a_2), (b_1, b_2))$ and $((c_1, c_2), (d_1, d_2)) \in S \times S$ we have that $||a_1 - b_1| - |a_2 - b_2|| > ||c_1 - d_1| - |c_2 - d_2||$ implies $\pi((a_1, a_2), (b_1, b_2)) < \pi((c_1, c_2), (d_1, d_2))$.

An isometry-enforcing payoff function is a function that is monotonically decreasing with the absolute difference of the Euclidean distances between respective model and data points of the matching strategies compared. In other words, given two matching strategies, their payoff should be high if the distance between the model points is equal to the distance between the data points, and it should decrease as the difference between such distances increases.

Given a set of matching strategies S and an enumeration $O = \{1, \ldots, |S|\}$ over it, an *isometry-enforcing game* is a clustering game where the population is defined as a vector $\mathbf{x} \in \Delta^{|S|}$ and the payoff matrix $A = (a_{ij})$ is defined as $a_{ij} = \pi(s_i, s_j)$, where $s_i, s_j \in S$ are enumerated by O and π is a symmetric one-to-one isometry-enforcing payoff function. Intuitively, $\mathbf{x}_i$ accounts for the percentage of the population that plays the ith matching strategy.

In theory, any rigidity-enforcing payoff function can be used to perform surface registration. Throughout the experimental section, we adopted

$$\pi\big((a_1, b_1), (a_2, b_2)\big) = \left(\frac{\min(|a_1 - a_2|, |b_1 - b_2|)}{\max(|a_1 - a_2|, |b_1 - b_2|)}\right)^{\lambda}, \tag{8.15}$$

where a_1, a_2, b_1, and b_2 are respectively the two model (source) and data (destination) points in the compared matching strategies. This is derived from a *Lipschitz distance*, providing a *relative* measure of distortion of the global Euclidean metric. Parameter λ allows making the enforcement of the conservation of the Euclidean distance more or less strict.

Since, contrary to the matching setup, in the inlier selection framework we are only interested in a few good correspondences, even after converging to an ESS, we select only a small set of the support to estimate the rigid transformation. In particular, we keep only strategies whose population proportion is more than a given ration of the maximum surviving population.

8.6.3 Application to Surface Alignment

In order to explore the role of both the discriminant feature detector and the matching technique, we designed a wide range of experimental validations. First, we analyzed the sensitivity of the descriptor to several sources of noise and the influence of the number of scales (and thus of the size of the descriptor vector). Further, we studied the sensitivity of the matching algorithm to its parameters, with the goal of identifying an optimal parameterization (if any) and assess the stability of the method. Also a number of comparative test were made. Specifically, we analyzed the performance obtained by using our matcher with different feature detectors and the overall comparison with respect to other well-know registration pipelines.

All the experiments were performed on a personal computer equipped with an Intel Core i7 processor and 8 GB of memory. The dataset used, where not differently stated, was built upon publicly available models; specifically the Bunny [54], the

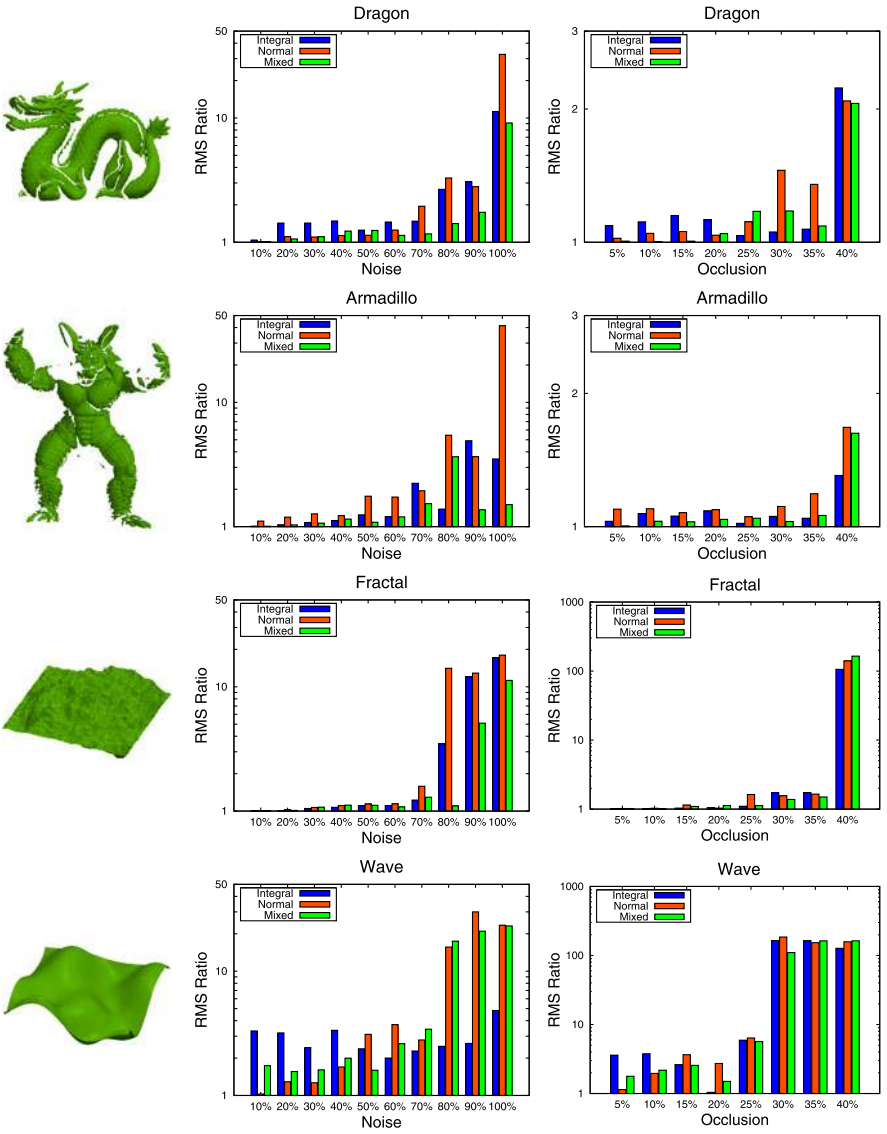


Fig. 8.7 Comparison of different descriptors using real and synthetic objects

Armadillo [32], and the Dragon [17] from the Stanford 3D scanning repository. To further assess the shortcomings of the various approaches, we used two synthetic surfaces representative of as many difficult classes of objects: a wave surface and a fractal landscape (see Fig. 8.7). Since a ground truth was needed for an accurate quantitative comparison, we generated virtual range images from the models and

then applied additive Gaussian noise to them. The descriptor used was a mixed Surface Hash with 3 scales.

8.6.3.1 Sensitivity Analysis of the Descriptor

The performance of different descriptors was tested for various levels of noise and occlusion applied to two surfaces obtained from real range scans ("armadillo" and "dragon" from Stanford) and two synthetic surfaces designed to be challenging for coarse and fine registration techniques ("fractal" and "wave"). The noise is a positional Gaussian perturbation on the point coordinates with its level (σ) expressed in terms of the percentage of the average edge length, while occlusion denotes the percentage of data and model surfaces removed. The RMS Ratio in the charts is the ratio of the root mean square error (RMS) obtained after registration and the RMS of ground truth alignment. The Normal and Integral Hashes were calculated over 3 levels of scale and the "Mixed" Hash is simply the juxtaposition of the previous two.

In Fig. 8.7, we see that all the descriptors obtain good results with real range images and the registration "breaks" only with very high levels of noise (on the same order of magnitude of the edge length). Interestingly, the Mixed Hash always obtains the best performance, even with high level of noise: This higher robustness is probably due to the orthogonality between the Normal and Integral Hashes. The behavior with the "fractal" synthetic surface is quite similar, by contrast all the descriptors seem to perform less well with the "wave" surface. This is due to the lack of distinctive features on the model itself, which indeed represents a challenge for any feature based registration technique [47]. The performance obtained with respect to occlusion is similar: all the descriptors achieve fairly good results and are resilient to high levels of occlusion (note that 40 percent occlusion is applied both to data and model). Overall the Mixed Hash appears to be consistently more robust. Since we found that the descriptors calculated over 3 levels of scale break at a certain level of noise, we were interested in evaluating if their performance can be improved by increasing their dimension.

In Fig. 8.8, we present the results obtained with different levels of scale for the Mixed Hash. The graphs show the average over all the surfaces and the associated RMS. It is interesting to observe that by reducing the scale level the technique becomes less robust, whereas its performance increases dramatically when the number of scales increases. With a scale level of 5 our approach can deal even with surfaces subject to Gaussian positional noise of σ greater than the edge length. Unfortunately, this enhanced reliability comes with a drawback: by using larger levels of scale the portion of boundary that cannot be characterized grows. In the right half of Fig. 8.8, the shrinking effect is shown for scale levels from 2 to 5.

8.6.3.2 Sensitivity to the Parameters of the Matcher

The game-theoretic matching technique presented basically depends on four parameters:

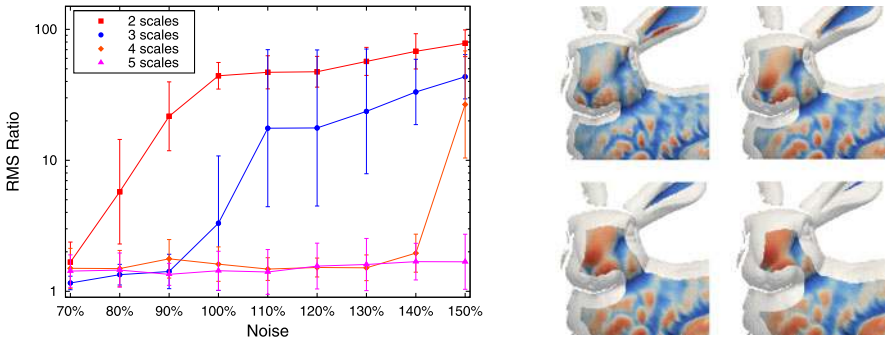


Fig. 8.8 Effect of scale on the matching accuracy

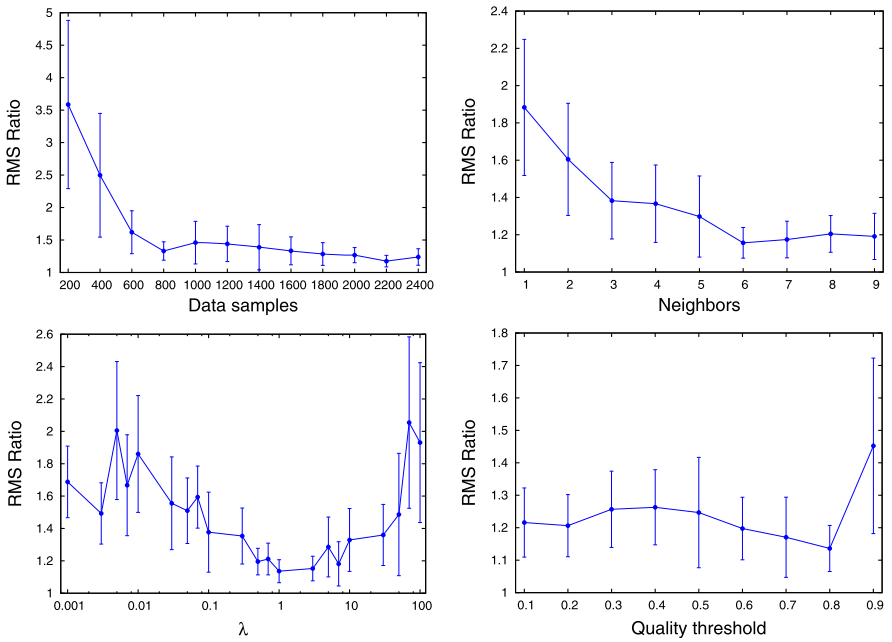


Fig. 8.9 Analysis of the sensitivity of the Game-Theoretic Matcher with respect to the parameters of the algorithm

- The number of points sampled from the model object;
- The number k of neighbors considered when building the initial set of candidates;
- The selectivity λ for the rigidity-enforcing payoff (8.15);
- The quality threshold used to deem a strategy as non-extinct upon convergence.

The first two parameters are related to the building of the set of strategies S. In Fig. 8.9, it can be seen that optimal results can be achieved with less than 1000 samples and that there is virtually no gain in using more than 6 neighbors.

The third parameter (λ) is related to the level of strictness with respect to the enforcement of the rigidity constraint: Higher values for λ will make the payoff function more steep, thus making the selection process more picky. By contrast, lowering λ will yield a payoff matrix with smaller variance, up to the limit value of 0, when the matrix assumes value 1.0 for all the strategies pairs that do not break the one-to-one constraint and 0 otherwise. As expected, our experiments show that very low or very high values for λ deliver poor results and, while there is clearly a larger variance that what has been captured by the experiments, the optimal value seems to be around 1.

Finally, the fourth parameter sets the ratio (with respect to the most successful match) used to classify a strategy as surviving or extinct. The last experiment of Fig. 8.9 shows that all the tested values below 0.8 give similarly good results. This simply means that there is good separability between extinct and non-extinct strategies, the former being very close to 0.

Overall, we can assess that the matching method has a very limited dependency on its parameters, which can easily be fixed at values that are both safe and efficient. The most influent parameter is probably λ; however, a value of 1.0 (that indeed simplifies equation (8.15) to a simple ratio) appears to be optimal for our test set.

8.6.3.3 Comparison with Full Pipelines

The whole registration algorithm presented can be classified as a coarse method, since it does not require initialization. For this reason, we compared it with several other coarse techniques. Specifically, we implemented the whole Spin Images pipeline [29] and used the implementation supplied by the authors respectively for the MeshHOG/MeshDOG [61] and the Four Points Congruent Sets [2] methods. The latter method was initialized both with the parameters suggested by the authors and also with values for t and s that we manually optimized to get the best possible results from our dataset.

In the first row of Fig. 8.10, we present the results of this comparison. In these experiments, the occlusion is measured with respect to each range image and is applied in opposite directions of the overlapped area. That means that with an occlusion of 10 % the actual overlap is reduced by 20 %. The noise is an additive Gaussian noise with a standard error expressed as a percentage over the average edge length. The occlusion test has been made with noise at level 10 % and the noise test was performed with no occlusion. From the tests our method exhibits better results in both scenarios and breaks only with high levels of occlusion and noise. Note that the 4PCS method with parameters $t = 0.9$ and $s = 500$ does not always give a feasible solution with any occlusion greater than 10 %. With extreme levels of noise the 4PCS seems to get better and obtains lower RMS ratios than our method. The reduction in performance of our method is related to the breaking of the descriptors, that at such high levels of noise do not carry sufficient information any more. A clarification should finally be made about the apparent improvement that 4PCS seems to exhibit as noise increases. In fact, at high noise levels the RMS associated

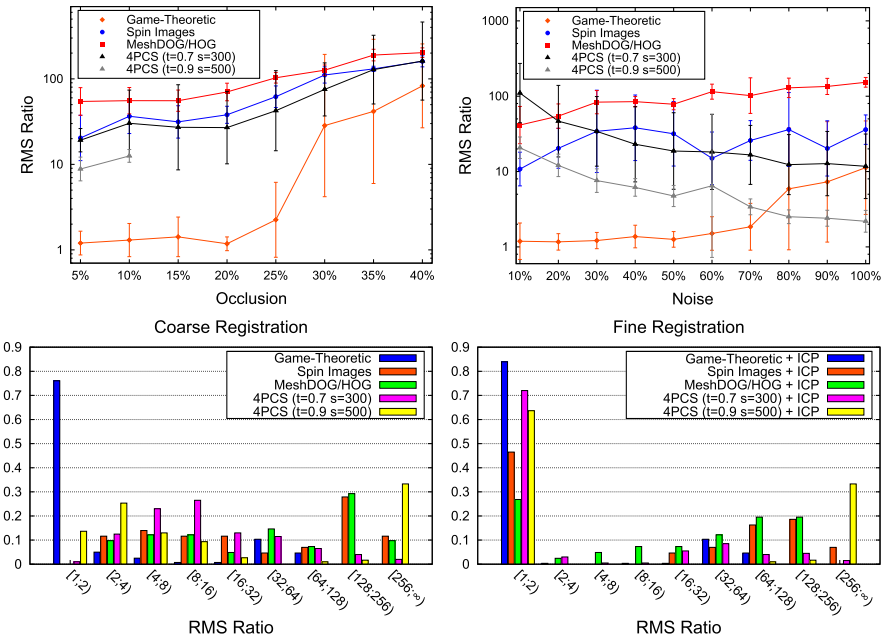


Fig. 8.10 Comparisons between our Game-Theoretic Registration technique and other widely used surface registration pipelines

to ground-truth motion is also high. In such conditions the additional error due to misalignment becomes less relevant in terms of contribution to the overall RMS ratio, which is dominated by random noise. Since 4PCS explores thoroughly the set of feasible motions until a solution with RMS low enough is found (depending on the stop criteria), it is expected to test more alignments when surfaces are noisier and thus yield lower RMS ratio values. However, it is easy to build simple examples where a solution can obtain a low RMS ratio (even lower than one) and still being far from the correct alignment. Figure 8.11 shows an example coarse registration obtained respectively with Spin Images, 4PCS, and the Game-Theoretic registration technique.

These results only indicate that GTR gives a better coarse registration; however, to seek a perfectly fair comparison, it is also needed to measure how much enhancement can be obtained by performing a fine registration step starting from the obtained coarse initialization. To this end, we applied the ICP algorithm starting from the initial motion estimated with the different methods with no occlusion and random noise values below 60 %. The results are shown in the bottom row of Fig. 8.10 with histograms obtained by binning the distance between model points and data surface along the normal vector. Normals that do not intersect the data surface are discarded. The size of the bins grows exponentially. The first histogram shows the distribution obtained from the coarse registration and the second reports

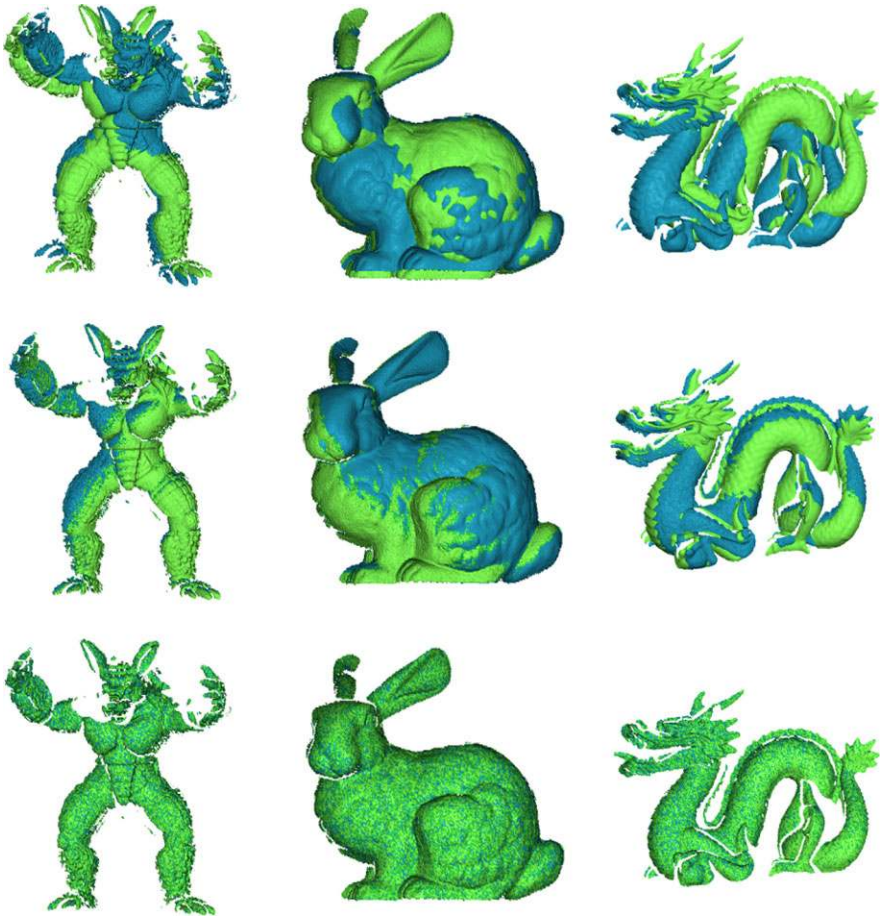


Fig. 8.11 Examples of surface registration obtained respectively with Spin Images (*first row*), MeshDOG (*second row*), 4PCS (*third column*) and our Game-Theoretic Registration technique (*last row*)

the enhancement obtained by applying ICP. Again, the results are favorable to our method, with very few points exhibiting large errors after refinement.

8.6.3.4 Quality of Fine Registration

In addition to the full pipeline comparisons, we also investigated how reliable the proposed approach would be if directly used as a fine registration technique. The goal of this test is two-fold: we want to evaluate our quality as a complete alignment tool and, at the same time, find the breaking point of traditional fine registration techniques.

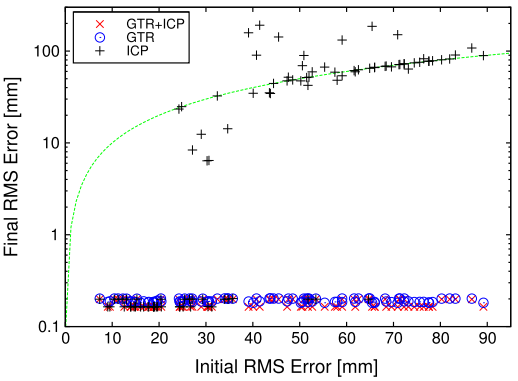


Fig. 8.12 Comparison of fine registration accuracies (the *green dashed line* represents $y = x$)

The method we used for comparison is a best-of-breed ICP variant, similar to the one proposed in [54]. Point selection is based on Normal Space Sampling [47], and point-surface normal shooting is adopted for finding correspondences; distant mates or candidates with back-facing normals are rejected. To minimize the influence of incorrect normal estimates, matings established on the boundary of the mesh are also removed. The resulting pairings are weighted with a coefficient based on compatibility of normals, and finally a 5 %-trimming is used. Each test was performed by applying a random rotation and translation to different range images selected from the Stanford 3D scanning repository. Additionally, each range image was perturbed with a constant level of Gaussian noise with standard deviation equal to 12 % of the average edge length. We completed 100 independent tests and for each of them we measured the initial RMS error between the ground-truth corresponding points and the resulting error after performing a full round of ICP (ICP) and a single run of our registration method (GTR). In addition, we applied a step of ICP to the registration obtained with our method (GTR + ICP) in order to assess how much the solution extracted using our approach was further refinable.

A scatter plot of the obtained errors before and after registration is shown in Fig. 8.12. The final error is on a log-scale, so the dotted curve represent the points with identical initial and final error. We observe that ICP reaches its breaking point quite early; in fact, with an initial error above the threshold of about 20 mm it is unable to find a correct registration. By contrast, GTR is able to obtain excellent alignment regardless of the initial motion perturbation. Finally, applying ICP to GTR decreases the RMS only by a very small amount.

8.7 Conclusions

In this chapter, we have introduced a game-theoretic formulation of the clustering problem which is able to work with non-metric (dis)similarities (even asymmetric and negative ones). Within our framework, the problem of clustering a set of data elements is viewed as a non-cooperative clustering game and classical equilibrium

notions from evolutionary game theory turn out to provide a natural formalization of the notion of a cluster. Our game-theoretic perspective has the following attractive features: it makes no assumption on the underlying (individual) data representation, e.g., spectral clustering, it does not require that the elements to be clustered be represented as points in vector space; it does not require a priori knowledge on the number of clusters (since it extracts them sequentially); it leaves clutter elements unassigned (useful, e.g., in figure/ground separation or one-class clustering problems); it allows extracting overlapping clusters (see, e.g., [53]); and it can naturally handle high-order similarities. Besides the game-theoretic connotation, we have provided also a combinatorial characterization of our notion of a cluster and established conditions under which relations with optimization theory and graph theory exist. Furthermore, we have focused our attention on the algorithmic aspects of computing equilibria in our clustering game. Specifically, we have reviewed a class of dynamics developed within the evolutionary game theory, the replicator dynamics being one representative, that can be used to find equilibria in clustering games. In addition, we have proposed a new class of dynamics for the same purpose that overcomes some limitations of the classical evolutionary dynamics.

Finally, the proposed approach was adapted to address generic matching problems and inlier selection problems, where a low rate of false positive is required, even at the expense of a high number of false negatives. The approach applied to point-pattern matching and 3D reconstruction problems provided performance clearly at the state-of-the-art.

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