Computing the Least-Core and Nucleolus for Threshold Cardinality Matching Games[⋆]

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Abstract. In this paper, we study the algorithmic issues on the least-core and nucleolus of threshold cardinality matching games (TCMG). We first show that for a TCMG, the problems of computing least-core value, finding and verifying least-core payoff are all polynomial time solvable. We also provide a general characterization of the least core for a large class of TCMG. Next, based on Gallai-Edmonds Decomposition in matching theory, we give a concise formulation of the nucleolus for a typical case of TCMG which the threshold T equals 1. When the threshold T is relevant to the input size, we prove that the nucleolus can be obtained in polynomial time in bipartite graphs and graphs with a perfect matching.

1 Introduction

One of the important problems in cooperative games is how to distribute the total profit generated by a group of agents to individual participants. The prerequisite here is to make all the agents work together, *i.e.*, form a grand coalition. To achieve this goal, the collective profit should be distributed properly so as to minimize the incentive of subgroups of agents to deviate and form coalitions of their own. This intuition is formally captured by several solution concepts, such as the *core*, the *least-core*, and the *nucleolus*, which will be the focus of this paper.

The algorithmic issues in cooperative games are especially interesting since the definitions of many solution concepts would involve in an exponential number of constraints [11]. Megiddo [9] suggested that finding a solution should be done by an efficient algorithm, *i.e.*, within time polynomial in the number of agents. Deng and Papadimitriou [5] suggested the computational complexity be taken into consideration as another measure of fairness for evaluating and comparing different solution concepts. Subsequently, various interesting complexity and algorithmic results have been investigated [4, 6, 7].

[⋆] The work is partially supported by National Natural Science Foundation of China (NSFC) (NO. 61170062, 61222202, 61433014, 61173009, 11271341). Full version can be seen at: `http://arxiv.org/abs/1409.5987`.

T.-Y. Liu et al. (Eds.): WINE 2014, LNCS 8877, pp. 474–479, 2014.

Matching game is one of the most important combinatorial cooperative games which has attracted much attention [2,3,7]. Kern and Paulusma [7] presented an efficient algorithm for computing the nucleolus for cardinality matching games. Then Biró, Kern, and Paulusma [2] developed an efficient algorithm for computing the nucleolus for matching games on weighted graphs when the core is nonempty. Chen, Lu and Zhang [3] further discussed the fractional matching games. We follow the stream and study the least-core and nucleolus of a natural variation of matching games, called threshold matching games [1].

In this paper, we aim at computing the least-core and the nucleolus for the threshold matching games on unweighted graph, especially when the core is empty. Firstly, we show that for an arbitrary threshold value, the least-core can be obtained in polynomial time through separation oracle technique. By linear program duality, we further provide a general characterization of the least core for a large class of threshold cardinality matching games, which can be used to simplify the sequence of linear programs of the nucleolus. Secondly, we discuss the algorithms for the nucleolus. Especially, when the threshold being one (which is called *edge coalitional games*), we know that finding the least-core and the nucleolus can be done efficiently based on a clear description of the least-core. When the threshold value is relevant to the input size, we prove that the least-core and the nucleolus can also be computed in polynomial time for the games on two typical graphs, the graphs with a perfect matching or bipartite graphs. To our surprise, in all the cases considered, the least-core and the nucleolus do not depend on the value of the threshold. We conjecture our method can be generalized into dealing with general graphs.

2 Preliminaries and Definitions

A cooperative game $\Gamma = (N, v)$ consists of a player set $N = \{1, 2, \cdots, n\}$ and a value function $v : 2^N \to R$ with $v(\emptyset) = 0$. $\forall S \subseteq N$, $v(S)$ represents the profit obtained by S without the help of others. We use $x = (x_1, x_2, \cdots, x_n)$ to represent the payoff vector while x_i is the payoff for player i. For convenience, let $x(S) \triangleq \sum_{i \in S} x_i$. The *core* of Γ is defined as: $\mathcal{C}(\Gamma) := \{x \in R^n : x(N) = v(N) \text{ and } x(S) \geq v(S), \forall S \subseteq N\}$.

A payoff vector in $\mathcal{C}(\Gamma)$ guarantees that any coalition S cannot get more profit if it breaks away from the grand coalition. When $\mathcal{C}(\Gamma) = \emptyset$, there is a nature relaxation of the core: the *least-core*. Given $\varepsilon \leq 0$, an imputation x is in the *ε-core* of Γ, if it satisfies $x(S) \geq v(S) + \varepsilon$ for all $S \subset N$. Let $\varepsilon^* := \sup\{\varepsilon | \varepsilon\text{-core of } \Gamma \text{ is nonempty}\}$. The ε^*-core is called the least-core of Γ, denoted by $\mathcal{LC}(\Gamma)$, and the value ε^* is called the $\mathcal{LC}(\Gamma)$ value. Obviously, the optimal solution of the following linear program LP_1 is exactly the value and the imputations in $\mathcal{LC}(\Gamma)$:

$$LP_1 : \quad \begin{array}{ll} \max & \varepsilon \\ \text{s.t.} & \begin{cases} x(S) \geq v(S) + \varepsilon, & \forall S \subset N \\ x_i \geq v(\{i\}), & \forall i \in N \\ x(N) = v(N). & \end{cases} \end{array}$$

Now we turn to the concept of the *nucleolus*. Given any payoff x, the excess of a coalition S under x is defined as $e(x,S) = x(S) - v(S)$, which can be viewed as the satisfaction degree of the coalition S under the given x. The *excess vector* is the vector $\theta(x) = (e(x,S_1), e(x,S_2), \cdots, e(x,S_{2^n-2}))$, where $S_1, \cdots, S_{2^n-2}$ is a list of all nontrivial subsets of N that satisfies $e(x,S_1) \leq e(x,S_2) \leq \cdots \leq e(x,S_{2^n-2})$. The nucleolus of the game $\varGamma$, denoted by $\eta(\varGamma)$, is the payoff x that lexicographically maximizes the excess vector $\theta(x)$.

Kopelowitz [8] proposed that $\eta(\varGamma)$ can be computed by recursively solving the following sequential linear programs $SLP(\eta(\varGamma))$ $(k = 1, 2, \cdots)$:

$$LP_k: \quad \begin{array}{ll} \max & \varepsilon \\ \text{s.t.} & \begin{cases} x(S) = v(S) + \varepsilon_r, & \forall S \in \mathcal{J}_r \quad r = 0, 1, \cdots, k-1 \\ x(S) \geq v(S) + \varepsilon, & \forall S \in 2^N \setminus \cup_{r=0}^{k-1} \mathcal{J}_r \\ x_i \geq v(\{i\}), & \forall i \in N \\ x(N) = v(N). & \end{cases} \end{array}$$

Initially, we set $\mathcal{J}_0 = \{\emptyset, N\}$ and $\varepsilon_0 = 0$. The number ε_r is the optimal value of the r-th program LP_r, and $\mathcal{J}_r = \{S \subseteq N : x(S) = v(S) + \varepsilon_r, \forall x \in X_r\}$, where $X_r = \{x \in R^n : (x, \varepsilon_r)$ is an optimal solution of $LP_r\}$. We call a coalition in $\mathcal{J}_r$ *fixed* since its allocation is fixed to a number. Kopelowitz [8] showed that this procedure converges in at most n steps.

We now introduce the definitions of threshold matching games. For a weighted graph $G = (V, E; w)$ and a threshold $T \in R^+$, the corresponding *threshold matching game* (TMG) is a cooperative game defined as $\varGamma = (V, w; T)$. We have the player set V and $\forall\ S \subseteq V$,

$$v(S) \triangleq \begin{cases} 1, & \text{if } w(M) \geq T, \text{ where } M \text{ is the maximum weight matching of } G[S] \\ 0, & \text{otherwise} \end{cases}$$

where $G[S]$ is the induced subgraph by S on G, $w(M) = \sum_{e \in M} w(e)$. By Theorem 1 in [6], when $\mathcal{C}(\varGamma) \neq 0$, the core and the nucleolus can be given directly. However, when $\mathcal{C}(\varGamma) = 0$, the least-core and the nucleolus is hard to compute [1].

In the following we restrict ourselves to *threshold cardinality matching game* (TCMG) $\varGamma = (V; T)$ based on unweighted graph $G = (V, E)$. That is, $\forall S \subseteq N$, $v(S) = 1$ if the size of a maximum matching in $G[S]$ is no less than T, and $v(S) = 0$ otherwise.

Let $G = (V, E)$ be a graph. Given $A \subseteq V$, we use $\mathcal{B}$ and $\mathcal{D}$ denote the set of even components and odd components in $G \setminus A$, respectively. A set $A \subseteq V$ is called a *Tutte set* if each maximum matching M^* of G can be decomposed as $M^* = M_{\mathcal{B}} \cup M_{A,\mathcal{D}} \cup M_{\mathcal{D}}$, where $M_{\mathcal{B}}$ $(M_{\mathcal{D}})$ induces a perfect (nearly perfect) matching in any component $B \in \mathcal{B}$ $(D \in \mathcal{D})$, and $M_{A,\mathcal{D}}$ is a matching which matches every vertex in A to some vertex in an odd component in $\mathcal{D}$.

Lemma 1 (Gallai-Edmonds Decomposition) [10] *Given $G = (V, E)$, one can construct a Tutte set $A \subseteq V$ in polynomial time such that*

1. *all odd components $D \in \mathcal{D}$ are factor-critical;*
2. *$\forall D \in \mathcal{D}$ there is a maximum matching M^* of G which does not completely cover D (we say M^* leaves D* uncovered*).*

3 Least-Core of TCMG

Throughout this section, let $\Gamma = (V;T)$ be the TCMG defined on an unweighted graph $G = (V,E)$ with threshold $T : 1 \leq T \leq v^*$. Since both testing the core nonemptiness and finding a core member can be done efficiently, we focus on the case where $\mathcal{C}(\Gamma) = \emptyset$.

From a subtle analysis, we can conclude that the least-core $\mathcal{LC}(\Gamma)$ of TCMG can be characterized as the optimal solution of the following linear program LP_1^T:

$$LP_1^T : \quad \begin{array}{ll} \max \varepsilon & \\ \text{s.t.} & \begin{cases} x(M_T) \geq 1+\varepsilon, & \forall M_T \in \mathcal{M}_T \\ x(V) = 1 & \\ x_i \geq 0, & i = 1,2,\cdots,n. \end{cases} \end{array}$$

We can show that least-core can be solved efficiently by ellipsoid method with a polynomial time separation oracle.

Theorem 1. *If $\Gamma = (V;T)$ is a TCMG with empty core, then the problems of computing the $\mathcal{LC}(\Gamma)$ value, finding a $\mathcal{LC}(\Gamma)$ member and checking if an imputation is in $\mathcal{LC}(\Gamma)$ are all polynomial time solvable.*

In the following, we further provide a characterization of the least core of TCMG under some conditions. Denote $\mathcal{M}_T = \{M_1, M_2, \cdots, M_m\}$ be the set of all matchings whose sizes are exact T, and let $a_1, a_2, \cdots, a_m$ be the the indicator vectors of the set of vertices that are covered by the matchings in $\mathcal{M}_T$. We have the following result which is quite useful in the algorithm design for the nucleolus in next sections.

Theorem 2. *Let $\Gamma = (V;T)$ be a TCMG with empty core. If $(\frac{2T}{n}, \cdots, \frac{2T}{n})_n$ is a convex combination of $a_1, a_2 \cdots, a_m$, then the value of $\mathcal{LC}(\Gamma)$ is $\varepsilon = \frac{2T}{n} - 1$ and $(\frac{1}{n}, \cdots, \frac{1}{n})_n \in \mathcal{LC}(\Gamma)$.*

4 Nucleolus of TCMG

We firstly consider the *edge coalitional game* (ECG) $\Gamma^1 = (V;1)$ defined on an unweighted graph $G = (V,E)$, *i.e.*, the TCMG with threshold $T = 1$. When $\mathcal{C}(\Gamma^1) = \emptyset$, the linear program for $\mathcal{LC}(\Gamma^1)$ is as follows:

$$LP_1^1 : \quad \begin{array}{ll} \max & \varepsilon \\ \text{s.t.} & \begin{cases} x_i + x_j \geq 1+\varepsilon, & \forall e = (i,j) \in E \\ x(V) = 1 & \\ x_i \geq 0, & i = 1,2,\cdots,n. \end{cases} \end{array}$$

According to Gallai-Edmonds Decomposition, every graph can be decomposed into A, $\mathcal{B}$, $\mathcal{D}$. Let $\mathcal{D}_0$ be the set of singletons in $\mathcal{D}$ ($\mathcal{D}_0$ may be empty). Let G_0 be a bipartite graph with vertex set $A \cup \mathcal{D}_0$ and edge set consisting of edges with two endpoints in A and $\mathcal{D}_0$ separately. Find a maximum matching M_0 in G_0. Denote the matched vertices in A and $\mathcal{D}_0$ by A_1 and $\mathcal{D}_{01}$ with respect to M_0. Let $A_2 = A \setminus A_1$ and $\mathcal{D}_{02} = \mathcal{D} \setminus \mathcal{D}_{01}$.

If $\mathcal{D}_{02} = \emptyset$, by making use of Theorem 2, the least-core value and an imputation in the least-core can be obtained directly:

Proposition 1 *Given an ECG* $\Gamma^1 = (V; 1)$*, if* $\mathcal{D}_{02} = \emptyset$*, then the value of* $\mathcal{LC}(\Gamma^1)$ *is* $\varepsilon = \frac{2}{n} - 1$ *and* $(\frac{1}{n}, \cdots, \frac{1}{n})_n \in \mathcal{LC}(\Gamma)$*.*

When $\mathcal{D}_{02} \neq \emptyset$, we cannot find such a convex combination. But if we delete $\mathcal{D}_{02}$ from G, we can find a convex combination in $G' = G[V \setminus \mathcal{D}_{02}]$ by using the similar argument Proposition 1. Denote Γ' to be the corresponding ECG defined on G' and the value of $\mathcal{LC}(\Gamma')$ is $\frac{2}{n'} - 1$ where $n' = n - |\mathcal{D}_{02}|$. Consider the following imputation $\widetilde{x}$:

$i \in V$	$i \in V(\mathcal{B})$	$i \in V(A)$ and $\mathcal{D}_{02} \to i$	$i \in V(A)$ and $\mathcal{D}_{02} \nrightarrow i$	$i \in V(\mathcal{D}_{01})$ and $\mathcal{D}_{02} \to i$	$i \in V(\mathcal{D}_{01})$ and $\mathcal{D}_{02} \nrightarrow i$	$i \in V(\mathcal{D}_{02})$
$\widetilde{x}_i$	$\frac{1}{n'}$	$\frac{2}{n'}$	$\frac{1}{n'}$	0	$\frac{1}{n'}$	0

Here, $\mathcal{D}_{02} \to i$ (or $\mathcal{D}_{02} \nrightarrow i$) represents i is reachable (or unreachable) from $\mathcal{D}_{02}$ by M_0-alternating path in G_0. We can easily check that the imputation $\widetilde{x}$ with $\varepsilon = \frac{2}{n'} - 1$ is feasible, *i.e.*, the value of $\mathcal{LC}(\Gamma^1)$ is also $\frac{2}{n'} - 1$.

We then focus on the computation of nucleolus. Since we have seen $\varepsilon_1 = \frac{2}{n'} - 1$, we can prove LP^1_k in $SLP(\eta(\Gamma^1))$ can be rewritten as:

$$LP^1_k: \quad \begin{array}{ll} \max & \varepsilon \\ \text{s.t.} & \begin{cases} x(e) = \frac{2}{n'} - \varepsilon_1 + \varepsilon_r, & e \in E_r, r = 1, \cdots, k-1 \\ x_i = -\varepsilon_1 + \varepsilon_r, & i \in V_r, r = 1, \cdots, k-1 \\ x(e) \geq \frac{2}{n'} - \varepsilon_1 + \varepsilon, & e \in E \setminus \bigcup_{r=1}^{k-1} E_r \\ x_i \geq -\varepsilon_1 + \varepsilon, & i \in V \setminus \bigcup_{r=1}^{k-1} V_r \\ x(V) = 1, \ x_i \geq 0, & i \in V. \end{cases} \end{array}$$

Initially set $E_0 = V_0 = \emptyset$ and $\varepsilon_0 = 0$. The number ε_r is the optimal value of the r-th program LP^1_r, and $E_r = \{e \in E : x(e) = 1 + \varepsilon_r, \forall x \in X_r\}$, $V_r = \{i \in N : x_i = 1 - \frac{2}{n'} + \varepsilon_r, \forall x \in X_r\}$, where $X_r = \{x \in R^n : (x, \varepsilon_r) \text{ is an optimal solution of } LP^1_r\}$. Therefore, the size of the linear programs in LP^1_1 and $SLP(\eta(\Gamma^1))$ are all polynomial. It follows that the least-core and the nucleolus of ECG can be computed efficiently.

Theorem 3. *Given an ECG* $\Gamma^1 = (V; 1)$*, the nucleolus* $\eta(\Gamma^1)$ *can be obtained in polynomial time.*

Now we consider the general case $\Gamma^T = (V; T)$ with arbitrary threshold $1 \leq T \leq v^*$. In the following theorem, we firstly show that for the graphs with a perfect matching, the least-core of Γ^T is independent of T. Then we use this characterization to prove that the nucleolus of Γ^T can be obtained in polynomial time and $\eta(\Gamma^T)$ is also independent of T.

Theorem 4. *Suppose* $G = (V, E)$ *is a simple graph which has a perfect matching and* $\Gamma^T = (V; T)$ *is a TCMG defined on* G*. Let* $\Gamma^1 = (V; 1)$ *be the corresponding ECG defined also on* G*. Then the value of* $\mathcal{LC}(\Gamma^T)$ *is* $\varepsilon^T_1 = \frac{2T}{n} - 1$ *and* $\mathcal{LC}(\Gamma^T) = \mathcal{LC}(\Gamma^1)$*. Furthermore,* $\eta(\Gamma^T) = \eta(\Gamma^1)$*.*

Let $G = (L, R; E)$ be a bipartite graph with vertex set $L \cup R$ and edge set E. Find a maximum matching M^* in G. Denote the matched vertices in L and R as L_1 and R_1 with respect to M^* respectively. Let $L_2 = L \setminus L_1$ and $R_2 = R \setminus R_1$. If both L_2 and R_2 are empty, it is reduced to the situation in Theorem 4. So we assume at least one of L_2 and R_2 is not empty. If we delete L_2 and R_2 from G, we can find the least-core value and an imputation in least-core by Theorem 4. Denote Γ' to be the corresponding TCMG defined on G' where G' is the induced subgraph by $(L \cup R) \setminus (L_2 \cup R_2)$ in G. Then the value of $\mathcal{LC}(\Gamma')$ is $\frac{2T}{n'} - 1$ where $n' = n - |L_2| - |R_2|$. It is obvious that $\frac{2T}{n'} - 1$ is an upper bound of the value of $\mathcal{LC}(\Gamma^T)$. Actually, we can show that this is actually the value of the least-core in the bipartite graphs.

Theorem 5. *Suppose* $G = (L, R; E)$ *is a bipartite graph and* $\Gamma^T = (V; T)$ *is a TCMG defined on* G. *Let* $\Gamma^1 = (V; 1)$ *be the corresponding ECG defined also on* G. *Then the value of* $\mathcal{LC}(\Gamma^T)$ *is* $\varepsilon_1^T = \frac{2T}{n'} - 1$ *and* $\mathcal{LC}(\Gamma^T) = \mathcal{LC}(\Gamma^1)$, *here* $n' = n - |L_2| - |R_2|$. *Furthermore,* $\eta(\Gamma^T) = \eta(\Gamma^1)$.

References

1. Aziz, H., Brandt, F., Harrenstein, P.: Monotone cooperative games and their threshold versions. In: Proceedings of the 9th International Conference on Autonomous Agents and Multiagent Systems, vol. 1, pp. 1107–1114 (2010)
2. Biró, P., Kern, W., Paulusma, D.: Computing solutions for matching games. International Journal of Game Theory 41(1), 75–90 (2012)
3. Chen, N., Lu, P., Zhang, H.: Computing the nucleolus of matching, cover and clique games. In: Proceedings of the 26th AAAI Conference on Artificial Intelligence (2012)
4. Deng, X., Fang, Q., Sun, X.: Finding nucleolus of flow game. Journal of Combinatorial Optimization 18(1), 64–86 (2009)
5. Deng, X., Papadimitriou, C.H.: On the complexity of cooperative solution concepts. Mathematics of Operations Research 19(2), 257–266 (1994)
6. Elkind, E., Goldberg, L.A., Goldberg, P.W., Wooldridge, M.: Computational complexity of weighted threshold games. In: Proceedings of the National Conference on Artificial Intelligence, vol. 22, p. 718 (2007)
7. Kern, W., Paulusma, D.: Matching games: the least-core and the nucleolus. Mathematics of Operations Research 28(2), 294–308 (2003)
8. Kopelowitz, A.: Computation of the kernels of simple games and the nucleolus of n-person games. Technical report, DTIC Document (1967)
9. Megiddo, N.: Computational complexity of the game theory approach to cost allocation for a tree. Mathematics of Operations Research 3(3), 189–196 (1978)
10. Plummer, M.D., Lovász, L.: Matching theory. Access Online via Elsevier (1986)
11. Schmeidler, D.: The nucleolus of a characteristic function game. SIAM Journal on Applied Mathematics 17(6), 1163–1170 (1969)