A method for identifying hamiltonian viruses

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Abstract

A virus is a local configuration that prevents a graph (digraph) from possessing a given property P. We give an exact and a genetic algorithm for deciding whether a given structure is a virus for the hamiltonian property. These algorithms can be used for identifying families of non hamiltonian digraphs.

Key words: digraph, digraph properties, virus, hamiltonicity, non-hamiltonicity, genetic algorithm, algorithms.

1 Introduction

It is well known that the problem to decide when a graph (digraph) is hamiltonian is NP-complete [4]. A method, based on an exact and a genetic algorithm, is presented for identifying hamiltonian viruses. The method is supported by a theorem, characterizing local structures as hamiltonian virus [3, 5].

As a consequence we can derive a procedure for deciding whether a given digraph is non-hamiltonian. This procedure is of the same complexity of the problem of deciding if a given digraph is hamiltonian, but the interest of the procedure is the fact of using a local structure.

A "yes" answer to the hamiltonicity problem in a given digraph (or graph) can be verified by checking in polynomial time that a sequence of vertices given by an oracle is a hamiltonian cycle (or circuit). In case of non-hamiltonian digraphs, as stated in [6] pages 28, 29, there is no known way of verifying a "yes" answer to the complementary problem of deciding if a digraph is non-hamiltonian. A solution to this problem is to provide a hamiltonian virus, in the sens of [5, 3] (see definition below) whose presence in the digraph can be also checked in polynomial time, as it will be mentioned at the end of this section. In case the non-hamiltonian digraph does not contain hamiltonian viruses, it must have a particular structure, as can be seen in Theorem 2.

The virus notion has been used in random generation of digraphs without certain properties [9, 8]. With respect to the hamiltonicity problem, it can be important to detect hamiltonian viruses present in a digraph, particularly "small" virus classes for which our method shows a good behaviour. Additionally, the identification of hamiltonian viruses in a digraph can be useful in order to eliminate them by adding the required (minimal) number of arcs.

1.1 Terminology

Let P be a property defined on all digraphs and let $\mathbf{N}$ be the set of nonnegative integers.

Definition 1 *[5] A* digraph virus *is a 5-uple* (H, T^-, T^-, f^+, f^-) *where* $H = (V(H), E(H))$ *is a digraph, (with a non empty vertex set),* T^-, T^- *are parts of the vertex set of* H*, and* f^-, f^- *are mappings from* T^+, T^- *to* $\mathbf{N}$ *respectively.*

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A digraph virus (H, T^+, T^-, f^+, f^-) *is* present *in a digraph* D *if* D *has a proper induced subdigraph* $\tilde{H}$ *isomorphic to* H *(for convenience we identify* $\tilde{H}$ *with* H*), such that the equalities* $d_D^+(x) = f^+(x) + d_H^+(x)$ *on each vertex* x *of* T^+ *and* $d_D^-(x) = f^-(x) + d_H^-(x)$ *on each vertex* x *of* T^-*, hold.*

A digraph virus V *is a* virus for a digraph property P *if every digraph where* V *is present, lacks property* P*. The cardinality of* V *is defined as the order of* H*.*

In a similar way of [5, 3] we define a graph virus (H, T, f) where $H = (V(H), E(H))$ is a graph, $T \subseteq V(H)$ and f is a mapping from T to N.

Lemma 1 *[5] If a digraph of order* n *has no virus of order* $h < n$ *for some property* P*, then it has no virus of order less than* h *for* P*.*

Equivalently, a virus for a property P is present in viruses of larger order for that property.

Remark 1 *If a digraph contains viruses then some virus of order* $n - 1$ *must be present.*

Some properties are characterized by viruses; more precisely, a property P is characterized by a class of viruses $\mathcal{V}$ if the following assertions are equivalent:

(*i*) G does not have property P

(*ii*) a virus $V \in \mathcal{V}$ is present in G

In general, the class of all viruses for property P establishes only that $(ii) \Rightarrow (i)$. In [3], it is proven that the properties "G is connected" and "G is strongly connected" are characterized by viruses.

On the other hand, in [10] it is shown that the viruses for property "G is bipartite" do not characterize this property. In a similar way in [10] it is shown that the viruses for the property "G has a perfect matching" do not characterize this property; moreover, a characteristic property of the graphs without perfect matching and no viruses for the property "G has a perfect matching" is also given in [10] .

In [5, 7] it is shown that the hamiltonian property is not characterized by its viruses, at least for digraphs.

Deciding the existence of "small" hamiltonian viruses can be useful, if the following metaconjecture is true for the hamiltonian property:

> For many important properties there exist viruses of small order in *almost all* instances in which the property is not present.

This metaconjecture is useful because the presence (or absence) of a hamiltonain virus of order k inside a digraph of order n can be detected by a procedure in $O(n^k)$ time. If k is a small number (say, less than or equal to 3) then, an *almost surely* correct answer to the question *does* G *have property* P*?* can be given by a procedure with "small" time complexity. There are two examples in favor of this metaconjecture. It is proved for non strongly connected graphs in [2] and graphs without perfect matching in [3] that "almost all" of them contain a virus of smallest order of the class; "almost" should be understood here in its usual probabilistic sense meaning a proportion tending to 1 as the number of vertices tends to infinity.

Our paper is structured as follows: in section 1 we give an introduction to our approach, based on previous results. Section 2 contains the characterization of hamiltonian viruses. Section 3 and Section 4 presents an exact and a genetic algorithm, for deciding whether a given uple is a hamiltonian virus. The paper concludes with Section 5 where some open questions related to the notion of hamiltonian viruses are posed.

2 Viruses for "hamiltonian" property

The following theorem is an extension of the one given in [3] about viruses with $T^+ = T^-$.

Theorem 1 *[5]* (H, T^+, T^-, f^+, f^-) *is a virus for the property "D is hamiltonian" if and only if for every set of disjoint paths* $P_1, \cdots, P_r$ *covering* $V(H)$ *there exists a path* $P_j = (x_j^1, \ldots, x_j^{q(j)})$*, with* $q(j) \geq 1$ *such that either* $f^-(x_j^1) = 0$ *or* $f^+(x_j^{q(j)}) = 0$*.*

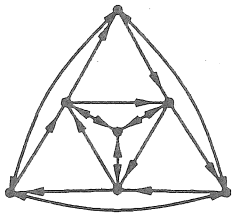

Figure 1: A non-hamiltonian digraph W without virus

Thus, for each $x \in T^-$ (resp. T^-) only the fact whether $f^-(x)$ (resp. $f^-(x)$) is strictly greater than 0 or not matters and we can simplify the notation to $V = (H, T^+, T^-)$. In this case, $V = (H, T^+, T^-)$ is present in a digraph D if and only if there is a copy $\tilde{H}$ (which we also denote by H) in D with $T^+ = \{x : d_H^+(x) = d^+(x)\}$ and $T^- = \{x : d_H^-(x) = d^-(x)\}$. This means that the vertices in T^+ send no edge outside $V(H)$ and the vertices in T^- receive no edge from the outside of $V(H)$.

The following theorem is also proved in [5]

Theorem 2 *[5] A digraph D has no viruses for the hamiltonian property if and only if it has the following structure: for each vertex x the remaining part $D \setminus x$ has a covering by vertex disjoint paths $P_1, \ldots, P_r$ such that each of them constitutes a circuit with x.*

The digraph W in figure 1 shows that there exist non hamiltonian digraphs without any virus. In W there are no hamiltonian viruses of order 6. Then by Remark 1, W does not have viruses.

Definition 2 *Let $H = (V(H), E(H))$ be a proper induced subdigraph of a given digraph D. We define the 3-uple V_D* associated to *H in D as follows: $V_D = V_{D(H)} = (H, T_D^+, T_D^-)$, where $T_D^+ = \{x \in V(H) : N^+(x) \cap (V(D) \setminus V(H) = \emptyset\}$ and $T_D^- = \{x \in V(H) : N^-(x) \cap (V(D) \setminus V(H) = \emptyset\}$.*

Thus V_D is a virus present in D.

Let $H = (V(H), E(H))$ be a proper induced subdigraph of a given digraph D. We will show that, in order to prove the existence of hamiltonian viruses, where the first component is isomorphic to H, it is sufficient to consider the 3-uple V_D associated to H in D.

¿From Lemma 1, a given digraph D has a hamiltonian virus if the 3-uple V_D associated to $H = D - x$ in D is a hamiltonian virus for some vertex x of D. Otherwise the digraph D does not contain hamiltonian viruses.

Remark 2 *¿From Theorem 1 and Theorem 2 the set of digraphs can be partioned into the following disjoint classes:*

- hamiltonian digraphs.

- non-hamiltonian digraphs without hamiltonian viruses. They have the structure given in Theorem 2 with, of course, $r \geq 2$, for each x.

- (non-hamiltonian) digraphs with hamiltonian viruses.

Theorem 3 *Let $D = (V, E)$ be a digraph and let $H = (V(H), E(H))$ be a proper induced subdigraph of D. Assume that $V = (H, T^+, T^-)$ is a hamiltonian virus present in D, then the 3-uple $V_D = (H, T_D^+, T_D^-)$ associated to H in D is a hamiltonian virus present in D.*

Proof : Let $P_1, \ldots, P_r$ be a set of disjoint paths covering $V(H)$. Since V is a hamiltonian virus then there exists a path, saying $P_j = (x_j^1, \ldots, x_j^{q(j)})$, with $q(j) \geq 1$ such that either $f^-(x_j^1) = 0$ or $f^+(x_j^{q(j)}) = 0$. Without loss of generality, let us assume $f^+(x_j^{q(j)}) = 0$. Hence, by definition of T_D^- we have $x_j^{q(j)} \in T_D^-$. Therefore V_D is a hamiltonian virus. □

Remark 3 *Let $D = (V, E)$ be a digraph and let $H = (V(H), E(H))$ be a proper induced subdigraph of D. If the 3-uple $V_D = (H, T_D^+, T_D^-)$ associated to H in D is a hamiltonian virus then:*

1. Any 3-uple $V = (H, T^+, T^-)$ present in D with $T_D^- \subseteq T^-$, $T_D^+ \subseteq T^+$ is a hamiltonian virus.

2. There may exist 3-uples (H, T^+, T^-) with $T^+ \subset T_D^+$ or $T^- \subset T_D^-$ present in D that are hamiltonian viruses. For example: let D be the digraph constituted by the symmetric circuit $C_4 = (bcdeb)$ with the symmetric edge ab. The 3-uples V_D associated to C_4 and (C_4, T^+, T^-) with $T^+ = \{e, c\}$, $T^- = T_D^-$ are hamiltonian viruses.

Remark 4 *Let $D = (V, E)$ be a digraph and let $H = (V(H), E(H))$ be a proper induced subdigraph of D. If (H, T^+, T^-) is a hamiltonian virus present in D then:*
$(H \setminus S, T^+, T^-)$ where $S = \{x \in V(H) \setminus (T^+ \cup T^-) : xy \notin E, yx \notin E \ \forall \ y \in V(T^+ \cup T^-)\}$ is a hamiltonian virus present in D.

Proof : Directly from Theorem 1.

□

3 An exact decision algorithm

Let $H = (V(H), E(H))$ be a digraph. In this section an algorithm is presented for deciding whether a given 3-uple (H, T^+, T^-) associated to H is a hamiltonian virus. The algorithm is based on Theorem 1 for characterizing hamiltonian viruses. The main idea is to determine a set of paths with initial and terminal vertex in the complement of T^- and T^+ w.r.t $V(H)$ respectively, which covers $V(H)$. If there is no such covering, then the 3-uple is not a hamiltonian virus.

3.1 The problem

¿From Theorem 1 and Theorem 3, the 3-uple (H, T^+, T^-) associated to H is not a hamiltonian virus if and only if there exists a set of disjoint paths $P_1, \ldots, P_r$ covering $V(H)$ such that for every path $P_j = (x_j^1, \ldots, x_j^{q(j)})$, $1 \leq j \leq r$, the following condition holds:

$$x_j^1 \notin T^- \quad and \quad x_j^{q(j)} \notin T^+ \tag{1}$$

A covering has to be found verifying (1), in case of not finding the 3-uple candidate that is effectively a hamiltonian virus.

3.2 The algorithm

In order to find the path covering $V(H)$ satisfying (1), the algorithm performs the following two steps:

1. Building the set P of all paths satisfying (1)
2. Looking for a covering of $V(H)$ using the paths found in the previous step.

3.2.1 Building the set of paths

The recursive function **FIND_PATHS** (a_path: *path*) builds all the paths beginning by the initial path a_path. For each vertex **v** of $\overline{T^-}$ a call to **FIND_PATHS**((v)) is made.

```
P := ∅;
FIND_PATHS (c: path)
    {
    if (last_vertex(c) ∈ T+ bar)
        P := P ∪{c}
```

```
    for each successor s of last_vertex(c)
        if (s ∉ c) FIND_PATHS( c + (s));
    }
```

+ denotes the path concatenation operation.

3.2.2 Looking for the covering

The search of a covering is a Branch and Bound implemented by the recursive function **COVER**. The two parameters of **COVER** (covered: *vertex_list*, disjoint_paths: *path_list*) memorize the state of the search of the covering in the tree of all the possibilities.
The parameter **covered** is the list of the vertices already covered in the actual state and the parameter **disjoint_paths** is the list of paths which are disjoint from **covered**, and also which can be used to continue the search for a covering.
The list **disjoint_paths** allows to prune the number of branches by reducing the number of paths available to go further. Moreover, a bound can be determined if this list does not contain "enough" vertices. The branches and bounds are defined as follows:
BRANCHES:

- USE the first path of **disjoint_paths**
- DON'T USE the first path of **disjoint_paths** and forget it

BOUNDS:

- SUCCESS if **covered** covers all the vertices of $V(H)$
- FAILURE if the set of all vertices of all the paths of **disjoint_paths** does not contain all the vertices needed to complete the covering.

To start the search, the initial call is **COVER**((), P): no vertex is covered and all the paths could be used.

```
virus := true;
COVER (covered: vertex_list, disjoint_paths: path_list)
    {
    if | covered |=| V(H) |
        virus := false:
        exit:
    if | covered ∪( ⋃_{x∈disjoint_paths} V(x)) |=| V(H) |
        x1 := first_path (disjoint_paths);
        COVER(covered ∪V(x1), {x ∈ disjoint_paths / x ∩ x1 = ∅});
        COVER(covered , disjoint_paths -{x1});
    }
```

The **virus** variable contains the result. If **virus** = true the tested configuration is a virus.

3.2.3 Complexity

The first step of the algorithm (building the list of all the paths) takes the greatest time and memory space. The number of paths could be huge: in the worst case, a complete digraph H of order N with $T^- = T^+ = \emptyset$ has N = $\sum_{l=1}^{n} l!$ paths (all the arrangements of any size of n elements).Then this number could be reduced to 2^n (the number of parts of a set of n elements) because the order of the vertices in the path is not important in the search for the covering. The path is stored if the set of its vertices is not already present. This check take 2^{N^2} steps. The second part (looking for the covering) in the worst case consists in building all the

coverings of a set of n elements that is: $\sum_{r=1}^{n} B_{r,n} = B_n$ where $B_{r,n}$ is the number of ways of splitting a set of n elements into r parts. We know that

$$B_n \sim \frac{1}{e\sqrt{\beta}} \exp(n(\beta - 1 + \beta^{-1}))$$

[11] where β is defined by $\beta e^{\beta} = n$.This maximum bound is huge, but in practice, a rapid answer is possible with a configuration up to 15 vertices.

4 A genetic algorithm

We also propose a genetic algorithm for deciding whether a given 3-uple (H, T^+, T^-) associated to H is a hamiltonian virus.

The idea is to focus this problem as an adaptation of the Traveling Salesman Problem (TSP). The vertices are seen as towns, and a special distance between two towns is defined.

4.1 How to focus the problem of a hamiltonian circuit as a TSP

It is easy to adapt the TSP to find a hamiltonian circuit in a digraph H: A circuit C is represented by a chromosome of n = | $V(H)$ | genes. Each gene represents a vertex. The chromosome represents the sequence of vertices visited. It is a path representation. For example the chromosome C = (3 5 2 1 4) naturally represents the circuit 3-5-2-1-4-3.

The fitness function F(C) is the length of the tour .

$$F(C) = \sum_{i=0}^{n-1} distance(X_i, X_{i+1}) \text{ , } with\ X_n = X_0$$

The distance is defined as follow:

$$distance(X,Y) = \begin{cases} 0\ if\ (X,Y)\ is\ an\ arc\ of\ H \\ 1\ \ otherwise \end{cases}$$

The genetic algorithm is used to **minimize** the fitness.

4.2 Hamiltonian circuit and hamiltonian virus

The following lemma establishes a relationship between the problems of deciding if a digraph is hamiltonian and the one of deciding if a given 3-uple is a hamiltonian virus.

Lemma 2 *Let (H, T^+, T^-) be a given 3-uple and let $H^1 = (V^1, E^1)$ be a digraph with $V^1 = V(H)$ and $E^1 = E(H) \cup (\overline{T^+} \times \overline{T^-})$. Then (H, T^+, T^-) is not a hamiltonian virus if and only if H^1 has a hamiltonian circuit which contains at least an arc $(X,Y) \in (\overline{T^+} \times \overline{T^-})$.*

Proof : Let C be a hamiltonian circuit of H^1. Let $(X_+^i, X_-^i) \in$ C, $1 \leq i \leq l$, the arcs belonging to $(\overline{T^+} \times \overline{T^-})$. ¿From this circuit we can construct the following covering of $V(H)$:
$(X_-^1, \ldots, X_+^2), \ldots (X_-^i, \ldots, X_+^{i+1}) , \ldots (X_-^l, \ldots, X_+^1)$. All the paths start from a vertex of $\overline{T^-}$ and end with a vertex of $\overline{T^+}$. i.e satisfy condition (1)(see 3.1)

Reciprocally, let $C_1, \ldots, C_i, \ldots C_l$ be a covering of $V(H)$ satisfying condition (1).

If $C_i = (X_i^-, \ldots, X_i^+)$, $1 \leq i \leq l$,then
$X_1^- \xrightarrow{C_1} X_1^+ X_2^- \xrightarrow{C_2} X_2^+ \ldots\ldots X_{l-1}^+ X_l^- \xrightarrow{C_l} X_l^+$ is a hamiltonian circuit of $V(H^1)$ because for all $1 \leq i \leq l$ we have $(X_i^+, X_{i+1}^-) \in (\overline{T^+} \times \overline{T^-})$ with $X_{l+1}^+ = X_1^-$. □

Based on this lemma, we design a new fitness function F(C) and a new distance in order to determine whether a structure is a virus:

$$F(C) = \sum_{i=0}^{n-1} distance(X_i, X_{i+1}) + penality$$

with $X_n = X_0$ and penality $\neq 0$ if C does not contain arcs in $(\overline{T^+} \times \overline{T^-})$.

The new distance function is defined to add the virtual connections $(\overline{T^-} \times \overline{T^-})$:

$$distance(X,Y) = \begin{cases} 0 \; if \; (X,Y) \; is \; an \; arc \; of \; H \\ 0 \; if \; X \in \overline{T^+} \; and \; Y \in \overline{T^-} \\ 1 \quad otherwise \end{cases}$$

We are looking for a **null length** tour. Thanks to the penality we are sure that such a tour contains at least a sequence $X_i X_{i+1}$ with $X_i \in \overline{T^-}$ and $X_{i-1} \in \overline{T^-}$.
For example if the chromosome $C = (X_0 \; X_1 \; \ldots \; X_9)$ has a fitness value null, then it as a structure such as:
$C : X_0 \overset{arc}{\rightarrow} X_1 \overset{arc}{\rightarrow} X_2 \overset{+-}{\rightarrow} X_3 \overset{arc}{\rightarrow} X_4 \overset{arc}{\rightarrow} X_5 \overset{arc}{\rightarrow} X_6 \overset{+-}{\rightarrow} X_7 \overset{arc}{\rightarrow} X_8 \overset{arc}{\rightarrow} X_9$,
Where $\overset{arc}{\rightarrow}$ denotes the presence of an arc, and $\overset{--}{\rightarrow}$ denotes a couple in $(\overline{T^+} \times \overline{T^-})$
this chromosome C represents the covering of V(H) with the two paths:
$X_7 \rightarrow X_8 \rightarrow X_9 \rightarrow X_0 \rightarrow X_1 \rightarrow X_2$ and $X_3 \rightarrow X_4 \rightarrow X_5 \rightarrow X_6$.

4.3 Characteristics of the genetic algorithm

- We have opted for a steady state algorithm (i.e that uses overlapping populations, only a part $P_{replacement}$ of the population is replaced at each generation)
- The genetic coding uses a path representation.
- We use the edge recombination crossover [13] which preserve the path structure.
- The edge recombination crossover is modified to take into account the orientation of the arcs.
- The initial population is formed randomly but each chromosome is built to have as much as possible a good fitness value. The first "town" is choosed randomly among all the "towns", the next one is choosed randomly among the "towns" connected to the previous "town", if possible. This improvement allows to build an initial population with a best value.

4.4 Experimental results

We ran the algorithm on different examples of hamiltonian digraphs, finding almost always the circuit after less than 200 generations. So, when the algorithm does not find a circuit after 200 generations it could means that the digraph does not contain one. The population size seems to be an important parameter which had to be augmented with the digraph size. Figure 2 shows the behaviour of the algorithm when used to find a hamiltonian circuit for a digraph with 100 vertices and 250 arcs. We also used, see figure 3, the algorithm to decide if a given 3-uple, of order 100 with 250 arcs and with $| T^- | = | T^- | = 90$, is not a virus, by finding a covering. The figures show the evolution of the fitness value of the best individual and the average fitness value of the total population. The evolution stops when the best individual becomes zero, meaning that a circuit (in the first example) or a covering (in the second example) has been found. The most important parameters are the same in both cases, namely population size = 200, $P_{mutation} = 0.05$, and $P_{replacement} = 0.5$.

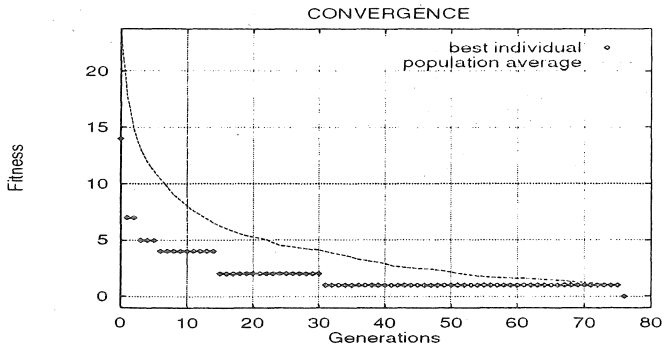

Figure 2: Convergence to zero, a circuit is found

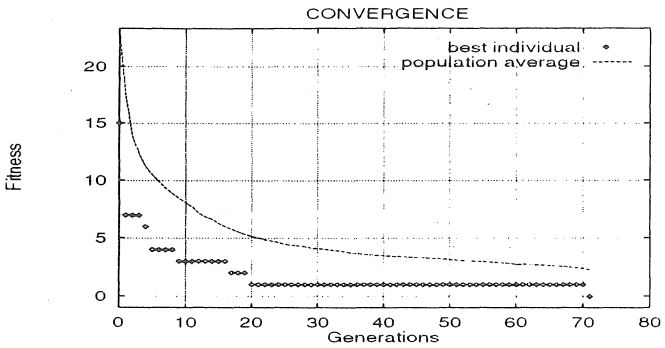

Figure 3: Convergence to zero, a covering is found

5 Remarks and open problems

A digraph D is hypohamiltonian if it has no hamiltonian circuit but every vertex-deleted subdigraph $D - v$ has such a circuit. Hypohamiltonian graphs are defined analogously.

The following conjecture should be true for digraphs:

Conjecture 1 *Every non-hamiltonian digraph without hamiltonian viruses is hypohamiltonian.*

However, as we shall see leter, the following conjecture is false.

Conjecture 2 *Every hypohamiltonian digraph has no hamiltonian viruses.*

Notice that the digraph in Figure 1 is hypohamiltonian and without hamiltonian viruses. In [12] Thomassen gives a method for obtaining hypohamiltonian digraphs by forming the cartesian product of cycles. We give here a short summary of his results, in order to give some remarks on Conjecture 1 and Conjecture 2.

Recall that if D_1 and D_2 are digraphs, then the **cartesian product** $D_1 \times D_2$ is the digraphs with vertex set $V(D_1) \times V(D_2)$ such that the edge from (v_1, v_2) to (u_1, u_2) is present if and only if $v_1 = u_1$ and $v_2u_2 \in E(D_2)$, or $v_2 = u_2$ and $v_1u_1 \in E(D_1)$. The directed cycle of length k, $2 \leq k$, is denoted C_k. With this notation Thomassen gives the following theorems:

Theorem 4 *[12] For each $k \geq 3$, $m \geq 1$, $C_k \times C_{mk-1}$ is a hypohamiltonian oriented digraph (i.e. no cycle of length 2). Moreover, $C_3 \times C_{6k+4}$ is hypohamiltonian for each $k \geq 0$.*

Theorem 5 *[12] There is no hypohamiltonian digraph with fewer than six vertices, and for each odd $m \geq 3$, $C_2 \times C_m$ is a hypohamiltonian digraph.*

Conjecture 2 is not true for graphs as it can be deduced from the following theorems:

Theorem 6 *[3] (H, T, f) is a virus for the property "G is hamiltonian" if and only if for every set of disjoint paths $P_1, \cdots, P_r$ covering $V(H)$ there exists a path P_j such that: if P_j consists of just one vertex $\{x_j^1\}$ then $f(x_j^1) \leq 1$ and if $V(P_j) = \{x_j^1, \cdots, x_j^{q(j)}\}$ then $f(x_j^1) = 0$ or $f(x_j^{q(j)}) = 0$.*

This theorem characterizes the hamiltonian viruses for graphs and it is used in [5] to show that:

Theorem 7 *A non-hamiltonian graph with minimum degree less than or equal to 3 contains always a virus for the hamiltonian property.*

Finally, Theorem 8 is used in Corollary 1 to show that the conjecture 2 is false for planar graphs:

Theorem 8 *[12] Every planar hypohamiltonian graph contains a vertex of degree 3.*

Corollary 1 *Every planar hypohamiltonian graph contains always a virus for the hamiltonian property.*

Remark 5 *The hypohamiltonian digraphs $C_3 \times C_{6k-4}$ with $k \geq 0$ (Theorem 4) and the hypohamiltonian digraphs given in Theorem 5 verify Conjecture 2. However the digraph $C_4 \times C_{11}$ i.e. $k = 4$ and $m = 3$ in Theorem 4 no verify Conjecture 2.*

Finally, we suspect that the following conjecture is feasible to be true.

Conjecture 3 *Every non-hamiltonian vertex-transitive digraph without hamiltonian viruses is hypohamiltonian.*

We have proved that the only non-hamiltonian vertex-transitive digraph without hamiltonian viruses and of order 6, is the hypohamiltonian digraph $C_2 \times C_3$. Which is in favour of Conjecture 3.

Other interesting problems concerning hamiltonian virus theory are:

1. Evaluate the complexity of the problem: decide whether a 3-uple (H, T^-, T^-) is a virus for hamiltonian property.
2. The detection of hamiltonian viruses in a digraph and their destruction by minimal changes (addition or removal of arcs, for example) could lead to a moderate change to the graph that gives it the hamiltonian property.
3. Evaluate how close is the hamiltonian property and the property D has no hamiltonian virus of order $< n$. This evaluation is useful to design approximate algorithms for hamiltonicity property, with their asymptotical error probability.
4. The study of sufficient conditions for (detecting) the presence of hamiltonian viruses in a digraph, is an important open problem. For instance, Theorem 7 stated above.
5. New sufficient conditions may arise from virus theory in order to ensure the hamiltonicity of a digraph family.

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