# 24    Parameterized Counting

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We look at the counting versions (both exact and approximate) of many parameterized problems whose decisions versions are fixed parameter tractable. We describe examples of fixed parameter tractable problems, whose counting versions are also fixed parameter tractable, as well as examples whose counting versions are W[1]-hard.

# 25    News on the ICALP'2001 paper by Liming Cai and David Juedes

Gerhard J. Woeginger

The paper "Subexponential parameterized algorithms collapse the W-hierarchy" by L. Cai and D. Juedes (Proceedings of ICALP'2001, Springer LNCS 2076, pp. 273-284, 2001) states the following main result: *In case some MAX SNP-hard problem can be solved in subexponential time, then W[1]=FPT*. On thursday Aug/02/2001 (during the Dagstuhl seminar on parameterized complexity) a working group of ten people met, and discussed, and tried to understand the arguments of this paper. The talk summarizes the observations and conclusions of this working group.

(1) The proof of Lemma 3 (pages 278 and 279) is fatally flawed. The removal of the conflicting unit clauses $(x)$ and $(\neg x)$ messes up the calculations of the argument.

(2) There is no easy repair of the proof of Lemma 3. It can be shown that if for some $c \geq 3$ and some $r > 1/2$ the problem MAX c-SAT$^{(r,1)}$ is contained in XP, then P=NP. For that reason, any argument along the lines of the current proof should be doomed.

(3) The whole proof of the main result of Cai and Juedes breaks down.

(4) There might be hope to save the main result by centering the argument not around MAX c-SAT, but around the following parameterized variant of Vertex

Cover: Given a graph $G = (V, E)$ and a parameter $k$, does there exist a vertex cover with $k \log |V|$ vertices?

# 26   Open Problems

Benny Chor

Constructing phylogenetic (or evolutionary) trees from biological data is a classical problem in biology, and it still is a major challenge today. Most realistic formulations of the problem, which take errors into account, give rise to hard computational problems. Here, we concentrate on one specific method: quartet based tree reconstruction.

The input is a list of $m$ quartets over $n$ species. Each quartet is an unrooted binary tree on four species. A given quartet is consistent with a binary unrooted tree $T$ if the subtree induced by $T$ on the four leaves is the same as the given quartet. The goal is to construct a binary tree with the $n$ species in its leaves, such that the total number of the satisfied quartets is maximized.

For a full input list ($m = \binom{n}{4}$, where each 4 tuple of species is represented by one quartet) it is easy ($O(n^4)$ time) to solve the decision problem "is there a tree satisfying all $m$ quartets?". For smaller values of $m$, however, even the decision problem is NP complete. The corresponding maximization problem is MAX SNP hard.

Currently, the best EXACT algorithm runs in time $O(m3^n)$. Values of $n$ in the range 20 to 30 are of significant biological interest (e.g. when considering mammalian evolution). A trivial randomized algorithm (pick a random binary tree) satisfies $m/3$ of quartets. This algorithm is easily derandomized.

From the point of view of parameterized complexity, it is known that given the full list ($m = \binom{n}{4}$), answering "is there a tree which satisfies all but $k$ quartets" is in FPT (dependence on $k$ is $4^k$).

Interesting problems:

1. Smaller exponent for an exact algorithm (e.g. $2^n$ instead of $3^n$).
2. A different parameterized approach, capable of handling a fixed proportion $cm$ quartets' errors.
3. An FPT algorithm for satisfying $k + (m/3)$ quartets.