From DNA sequencing to exact weighted independent sets

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What do a variant of DNA sequencing, discrete assignment under a fixed number of cost scenarios and the exact perfect matching problem in bipartite graphs have in common? They are all polynomially equivalent. However, the computational complexity of these problems is unknown. The question about the complexity of the exact perfect matching problem, when the weights are encoded in unary, has been raised in 1982 by Papadimitriou and Yannakakis, and remains an open problem to date.

In this talk, I will introduce a problem closely related to the exact perfect matching problem: the so-called exact weighted independent set problem (denoted by EXACT-WIS). This is the problem of determining whether a given vertex-weighted graph contains an independent set whose weight equals a given integer. I will explain its relation to the exact perfect matching problem and discuss several complexity results for EXACT-WIS and its restricted version (where the independent set is required to be of maximum size), for particular graph classes.

On the negative side, I will present the first non-trivial NP-hardness result: EXACT-WIS is strongly NP-complete for cubic bipartite graphs. On the positive side, I will distinguish several graph classes where EXACT-WIS can be solved in pseudo-polynomial time. As a corollary, this results in pseudo-polynomially solvable cases of the exact perfect matching problem.