

1135-05-1935

Robin Anderson, Saint Louis University, **Shuliang Bai**, University of South Carolina, **Fidel Barrera-Cruz*** (fidelbc@math.gatech.edu), Georgia Institute of Technology, **Éva Czabarka**, University of South Carolina, **Giordano Da Lozzo**, University of California, Irvine, **Natalie L. F. Hobson**, Sonoma State University, **Jephian C.H. Lin**, Iowa State University, **Austin Mohr**, Nebraska Wesleyan University, **Heather C. Smith**, Georgia Institute of Technology, **László A. Székely**, University of South Carolina, and **Hays Whitlatch**, University of South Carolina.

Crossing number and the tangle crossing number analogies.

A tanglegram consists of a pair of rooted binary plane trees with the same number of leaves, and a perfect matching between the two leaf-sets. These structures are of use in phylogenetics and are represented with straightline drawings where the leaves of the two plane binary trees are on two parallel lines and only the matching edges can cross. The tangle crossing number of a tanglegram is the minimum crossing number over all such drawings and is related to biologically relevant quantities, such as the number of times a parasite switched hosts.

In this talk we present results for tanglegrams which parallel known theorems for the crossing number of graphs. We show that removing any matching edge from a tanglegram of size n results in a drop of the tangle crossing number by at most $n - 3$, and this is sharp. We also show that the maximum tangle crossing number of a tanglegram of size n , denoted $\gamma(n)$, satisfies $\frac{1}{2}\binom{n}{2}(1 - o(1)) \leq \gamma(n) < \frac{1}{2}\binom{n}{2}$. Finally we present an algorithm for computing non-trivial lower bounds on the tangle crossing number in $O(n^4)$ time. (Received September 25, 2017)