

Institut für Diskrete Mathematik

Vortrag im Seminar für Kombinatorik und Optimierung

Freitag 1. Dezember, 15:00

Hörsaal BE01, Steyrergasse 30, Erdgeschoss

Tangle Crossing Numbers and the Tanglegram Kuratowski Theorem

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A tanglegram of size n is a triplet (L, R, M) where L and R are rooted binary trees with n leaves each, and M is a perfect matching between the two sets of leaves. Two tanglegrams (L_1, R_1, M_1) and (L_2, R_2, M_2) are the same if there is a pair of treeisomorphisms (ϕ, ψ) mapping L_1 to L_2 and R_1 to R_2 such that matched pairs of leaves get paired to matched pairs of leaves. Tanglegrams are used in phylogenetics, where for example they can represent the phylogenetic trees of parasites and hosts, where the matching gives which parasite infects which host.

A tanglegram layout (i.e. the way tanglegrams are usually drawn) is as follows: draw the two rooted binary trees in the plane with straight lines and without crossing edges such that the leaves of L are on the line x = 0 and L is drawn in the semiplane $x \leq 0$, the leaves of R are drawn on the line x = 1 and R is drawn in the semi-plane $x \geq 1$, and the edges of the matching are drawn with straight line. The crossing number of a layout is the number of unordered pairs of matching edges that cross and the tangle crossing number of a tanglegram is the minimum crossing number over all of its layouts. The tangle crossing number is related to a number of biologically important quantities, e.g. the number of times parasites switched hosts. I will present some results about the tangle crossing number, including a Kuratowski type theorem.

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