# Graph Polynomials Motivated by Gene Assembly

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The interlace polynomial was discovered by Arratia, Bollobás, and Sorkin by studying DNA sequencing methods. Its definition can be traced from 4-regular graphs (the Martin polynomial), to circle graphs and finally to arbitrary graphs.

Our interest in these polynomials came from the study of ciliates, an ancient group of unicellular organisms. They have the remarkable property that their DNA is stored in two vastly different types of nuclei. The two versions of the versions of the gene can be elegantly modelled using a 4-regular graph.

We give an overview of the polynomials involved, their basic properties, and their relation to the Tutte polynomial.

Joint work with Robert Brijder.

**References.**

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[2] R. Brijder, H.J. Hoogeboom, The Algebra of Gene Assembly in Ciliates. In: *Discrete and Topological Models in Molecular Biology* (N. Jonoska, M. Saito, eds.), Natural Computing Series, Springer, 289–307, 2014.