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Margaret I Doig*, margaretdoig@creighton.edu. *Computational grid Floer homology: explorations of crossing change and knot genus.*

We present a recent program designed to calculate knot genus and other related invariants using grid Floer homology, and we use it to explore the typical effect of a random crossing change on a knot's genus. We also outline possible applications in studying the stability of naturally occurring knots such as those found in proteins and DNA. We provide instructions for accessing the program via web browser in the hopes that others may use it for investigating questions in low-dimensional topology. (Received September 16, 2019)