SFB 680
MOLECULAR BASIS OF
EVOLUTIONARY INNOVATIONS

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Fitness landscape of an E. coli lac promoter

We infer a large fitness landscape from high-throughput sequence data from the E. coli lac promoter region with ~200k sequences. The sequences are associated with measurements of transcriptional activity. Utilizing linear regression and L1 regularization (LASSO), we find the best linear and quadratic approximations to fit the data. We find the fitness landscape to be largely smooth and additive, with a small amount of epistasis. Our method also reveals the locations of binding sites, and their interactions without any prior knowledge and without any difficult optimization steps.

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Institute for Theoretical Physics, Zülpicher Str. 77, Conference Room,

Host: Joachim Krug

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