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Modeling PCR in Natural Convection Systems[1] KEVIN DORFMAN, University of Minnesota, EHUD YARIV, GUY BEN DOV, Technion, Israel — Polymerase chain reaction (PCR) is a biochemical protocol for making many copies of a DNA template by thermal cycling between a hot temperature (where the strands are separated) and a cool temperature (where primers are annealed). In natural convection PCR, the requisite thermal cycling is provided by a buoyancy-driven circulating flow of the carrying buffer between a lower hot plate (at the denaturing temperature) and an upper cold plate (at the annealing temperature). We present a multi-component convection-diffusion-reaction model for natural convection-driven PCR when both primers and PCR enzyme are in excess. The evolution of the DNA population achieves a stationary state, wherein the problem is recast as an eigenvalue problem for computing the exponential amplification rate. With a realistic choice of parameters, the model predicts a doubling time on the order of two minutes, in agreement with experiments and much slower than the fluid cycling time. In contrast to what might be expected, the doubling time increases monotonically with the diffusion coefficient.

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