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Joseph C Watkins* (jwatkins@math.arizona.edu), Department of Mathematics, University of Arizona, Tucson, AZ 85716, **Xavier Didelot** (xavier.didelot@gmail.com), Oxford Centre for Gene Function, University of Oxford, 1 South Parks Road, Oxford, OX1 3TG, and **Jesse E Taylor** (jtaylor@math.asu.edu), Department of Mathematics, Arizona State University, tempe, AZ 85287. *The Wright-Fisher Diffusion Process and an Application to Queues and Bacterial Recombination.*

In this talk, we will develop, using a duality argument, an identity stating that the Laplace transform of the length of a contiguous bacterial recombination region equals the probability of choosing a given allele in a stationary population evolving according to the one-dimensional Wright-Fisher diffusion model. Beyond giving us an improved inferential strategy for parameter estimation in bacterial recombination, the matching of the selection and recombination parameters in the identity also suggests the existence of an intriguing connection between ancestral recombination graphs and ancestral selection graphs. (Received August 17, 2010)