

COMP 571: Homework #5  
Spring 2016

*Assigned on April 13, 2016*

*Due at 11:00 pm on April 22, 2016.*

*Attach your solutions as a single PDF file to an email to both TAs in the course (do not copy the instructor on the email).*

*The Honor Code applies to all homework sets. Sign the pledge on your solutions.*

The paper “Population genomic analysis of outcrossing and recombination in yeast,” by Ruderfer *et al.* (Nature Genetics, 38(9): 1077-1081, 2006) describes an HMM-based method for estimating the rate of recombination from sequence data. Describe formally the method that they propose and discuss the assumptions underlying the method. In particular, you need to describe the HMM formally, and discuss its underlying assumptions.