Haplotype reconstruction via Bayesian linear models with unknown design

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The topic is the reconstruction of the unknown matrices SS and  $\square$  for the multivariate linear model  $Y = \square$  warepsilon under the assumption of binary entries  $s_{ij} \in \{0,1\}$  for SS and  $\square$  matrix. While a frequentist method has recently been proposed for this purpose, a Bayesian approach also seems desirable. In contrast to the point estimates provided by this frequentist method, our proposed hierarchical model delivers a posterior that permits quantifying uncertainty. Since matching permutations in both SS and  $\square$  matching all constraints on sample from the hierarchical model enforcing all constraints.