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**Jie Zheng\*** ([zhengj@ncbi.nlm.nih.gov](mailto:zhengj@ncbi.nlm.nih.gov)), Lister Hill Center, 8600 Rockville Pike, Bethesda, MD 20894-0001. *Computational Analysis of Variation in Human Meiotic Recombination Hotspots.*

Meiotic recombinations tend to occur within narrow spans of genomic sequences which are called "hotspots". Large-scale single nucleotide polymorphism (SNP) data from the HapMap project enable us to computationally infer historical recombination hotspots for the whole human genome. Existing methods such as LDhat assume that recombination hotspots are homogeneous across the population; however, there is increasing evidence (e.g. from sperm typing) of polymorphism of recombination hotspots. In this talk, I will present results of our ongoing work that confirm the polymorphism, as well as association between hotspots and neighboring sequence variation that we have identified computationally. This is a project in collaboration with Teresa M. Przytycka from NCBI, Pavel P. Khil and R. Daniel Camerini-Otero from NIDDK, National Institutes of Health.

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