MCMC scheme also estimates missing genotypes

- SeattleSNP data; 48 genes, 48 individuals, average ~80 SNPs per gene.

Error rates for imputing missing data:

PHASE v2.0 (NR)	PHASE v2.0 (R)	Naïve Gibbs	HAP	Straw
3.1%	2.8%	4.2%	6.3%	18.3%