GENETICS

BEST OF TWO WORLDS

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Finally, linkage and association data can be used together after downloading new software using genotype inference.

> It reduces the number of genotyping reactions and increases the power of genome-wide association studies. Our method combines sparse marker data from a linkage scan and high-resolution SNP genotypes for several individuals to infer genotypes for related individuals.

Sure, we

- could already test association only in linked families
- knew that linkage genome scans will improve the power of association
- could evaluate by stepc if a polymorphisms explains a linkage result
but this seems to be the best recycling for our old fashioned linkage data. Yea, yea.