

GENETICS

TOWARDS A FRAMEWORK OF SNP INTERACTION

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The forthcoming SNP whole genome association studies will draw a lot of attention. I already have the problem of many interacting SNPs where I am suggesting to divide significant results in 3 compartments - local (LD effects), longrange (cis transcription factor effects) and pathway effects (gene family, system wide effects). The main problem are false positives that can even not be overcome by techniques like FDR. Yea, yea.

