File S1

Appendix: Dynamic Bayesian Testing of Sets of Variants in Complex Diseases

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Additional Power Comparison Results

Datasets are generated in the same way as described in the main text, except that each dataset only contains 50 SNPs, such that there are 30% disease variants in each dataset. Figure S1-S3 show the power of our method compared to existing methods with maximum MAF bounded at 0.01, 0.05, and 0.5, respectively. Figure S4 shows the power comparison between BEAM3 and SKAT on simulated datasets of 100,000 SNPs containing 100 disease variants.

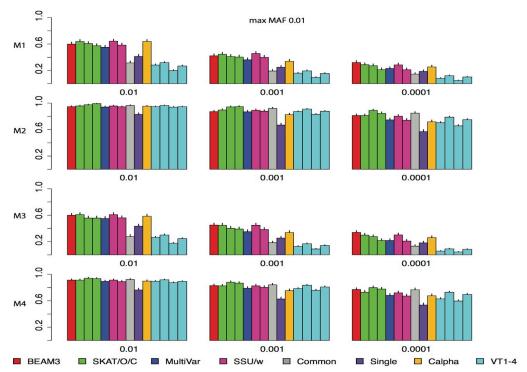


Figure S1. Comparison on datasets with 30% disease variants and MAF bounded at 0.01 on 4 disease models. x: significance. y: power for 4 models.

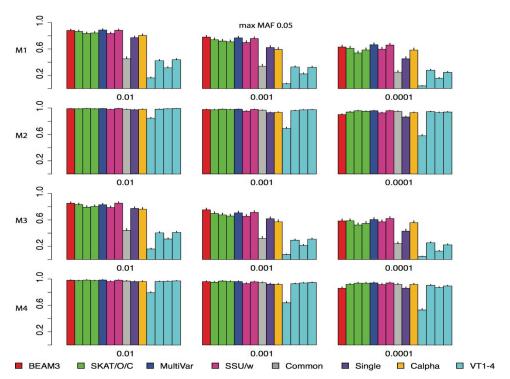


Figure S2. Comparison on datasets with 30% disease variants and MAF bounded at 0.05 on 4 disease models. x: significance. y: power for 4 models.

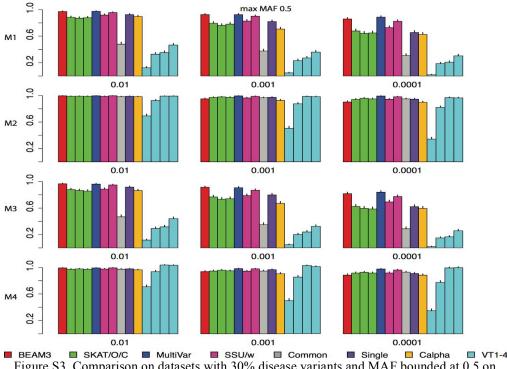


Figure S3. Comparison on datasets with 30% disease variants and MAF bounded at 0.5 on 4 disease models. x: significance. y: power for 4 models.

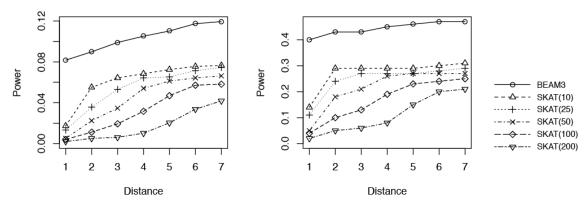


Figure S4. Power comparison between BEAM3 and SKAT on simulated datasets of 100,000 SNPs. "Distance": maximum allowed # of SNPs between the center of a reported significant SNP set (data-wide p-value 0.01) and the nearest true disease variant, such that the true variant is counted towards power. SKAT: in the parenthesis shows the number of SNPs per set.