# SNP prioritisation in GWAS with dense marker sets

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## Conclusions

- The empirical density distribution of GWAS based P-values from whole-genome sequencing does not significantly differ from the density distribution of GWAS based P-values from targeted amplicon sequencing
- The empirical density distribution of GWAS based P-values

### Objectives

The comparison of GWAS based Pvalues resulting from different real data structures and SNP densities.

from whole-genome sequencing is significantly different from the density distribution of GWAS based *P*-values from **SNP** microarray

 Intercorrelation between SNPs affects the empirical Pvalue density distribution in GWAS

#### **P-value sets**

- GWAS based on whole-genome sequencing (WGS)
- targeted amplicon sequencing (TAS)
- SNP microarray

## Methods

- Two sample Kolmogorov-Smirnov test for comparison of empirical density distributions of P-values
- Estimation of the proportion of true  $H_0$ : LFDR (Phipson, averaging local FDR) histogram method (Mosig and Nettleton)
- Multiple testing correction:

mean (averaging *P*-values) convest (Langaas, convex decreasing density)



Method of

Method of genotyping	LFDR	Mean	Histogram	Convest	Number of 5000 -					
WGS	0.9999973	0.9999975	1.000000	1.000000	0 -					
Microarray	0.9997295	0.9997317	0.9985244	0.9983977	o.oo TAS data	0.25	0.50	0.75	1.00	
TAS	0.9970516	0.9974642	0.9820944	0.9811121	30 -					
Comparison testMicroarray vs WG	of <i>P</i> -value en SP = 0.001 Mid	npirical densi croarray vs TAS P	ity distribution = 0.630 WGS	<b>DNS → KS</b> vs TAS P = 0.621	Number of nominal P-value	0.25	0.50 P-value	0.75	1.00	