



Estimation of KEGG pathways effects on stature using GWAS summary statistics

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Study

- **Objective** → estimate effect of KEGG pathways on stature
- Cows → 5 000 Danish Holstein, 4 000 Danish red, 4 000 Finnish red




- SNPs → Illumina Bovine 50K imputed to 25.4 million (1000 Bull Genomes)
- Measured trait → stature
- Dependent variable → SNP P-values from GWAS (GCTA)
- Model → $\hat{g} = \mu + Z_p p + e$ (custom in Python)
 - g SNP P-values
 - p KEGG pathway $p \sim N(0, P \hat{\sigma}_p^2)$
 - P covariance expressed by Jaccard index based on genes



Results & Conclusions

- The most significant SNPs



13:78338645
intergenic
closest gene PTGIS



22:48045904
intron
CACNA1D



6:437526698
intergenic
closest gene GBA3

- KEGG with highest impact

mta00945

Stilbenoid, diarylheptanoid and gingerol biosynthesis (467 genes)

- **Pathways** represent metabolic processes determining complex phenotypes
- **Pathways** enable for incorporating effects of genes with lower effects → infinitesimal model
- **Mixed models** allow for covariance modelling