Genetic Architecture of Transcriptome Regulation

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1 Abstract

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2 Introduction

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3 Methods

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3.1 Equations

The deterministic part of the model is defined by this **in-line equation** as $\mu_i = \beta_0 + \beta_1 x$, and the stochastic part by the **centered equation**:

$$\frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu_i)^2/(2\sigma^2)}$$

3.2 Tables

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## Warning: package 'knitr' was built under R version 3.1.2
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.05	0.11	0.45	0.65
x	2.10	0.11	19.72	0.00

Table 1: This is a GLM summary table.

3.3 Plots

3.4 Citations

The relationship was first described by Halpern et al. (2006). However, there are also opinions that the relationship is spurious (Keil *et al.* 2012). We used R for our calculations (**???**), and we used package `knitcitations` (Boettiger 2014) to make the bibliography.

4 Results and discussion

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References

Boettiger, C. (2014). *knitcitations: Citations for knitr markdown files.* Retrieved from http://CRAN.R-project.org/package=knitcitations

Halpern, B.S., Regan, H.M., Possingham, H.P. & McCarthy, M.A. (2006). Accounting for uncertainty in marine reserve design. *Ecol Letters*, **9**, 2–11. Retrieved from http://dx.doi.org/10.1111/j.1461-0248.2005.00827.x

Keil, P., Belmaker, J., Wilson, A.M., Unitt, P. & Jetz, W. (2012). Downscaling of species distribution models: a hierarchical approach (R. Freckleton, Ed.). *Methods Ecol Evol*, **4**, 82–94. Retrieved from http://dx.doi.org/10.1111/j.2041-210x.2012.00264.x

Figure 1: DGN-WB joint heritability (h^2). Local h^2 is estimated with SNPs within 1 Mb of each gene. Global h^2 is estimated with SNPs that are eQTLs in the Framingham Heart Study on other chromosomes (FDR < 0.05).
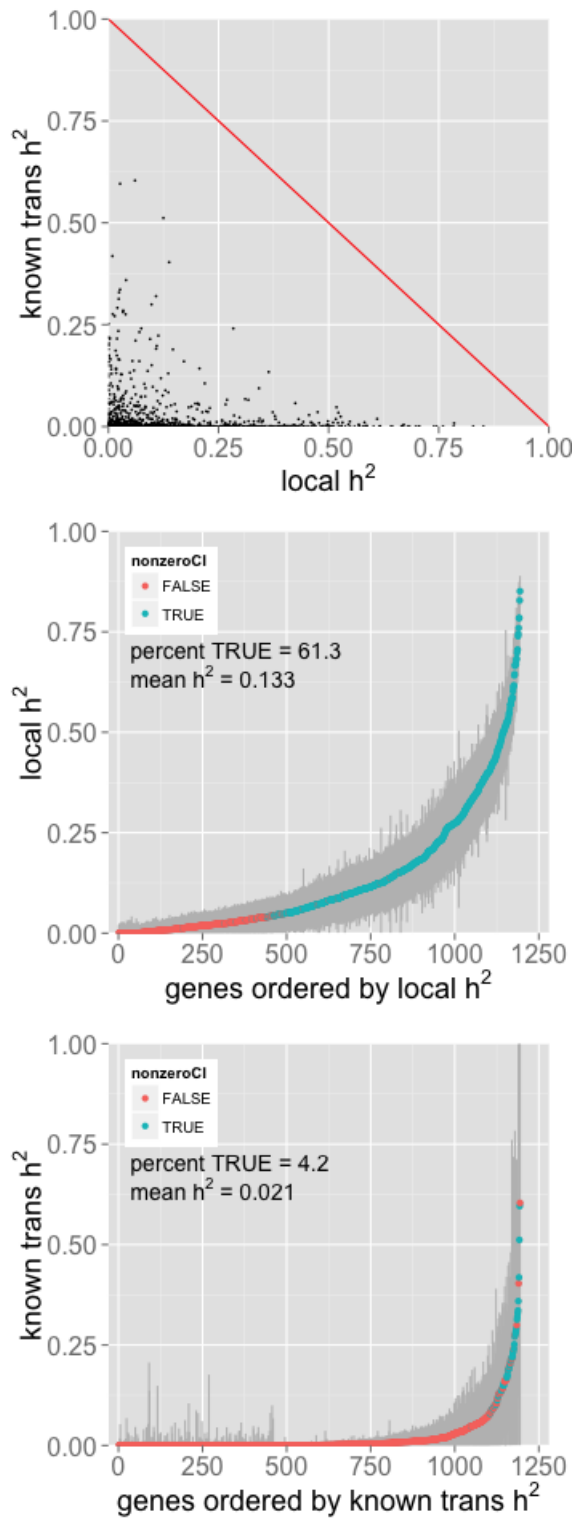
Figure 2: DGN-WB joint heritability (h^2) with known trans-eQTLs. Local h^2 is estimated with SNPs within 1 Mb of each gene. Known trans h^2 is estimated with SNPs that are trans-eQTLs in the Framingham Heart Study for each gene (FDR < 0.05).
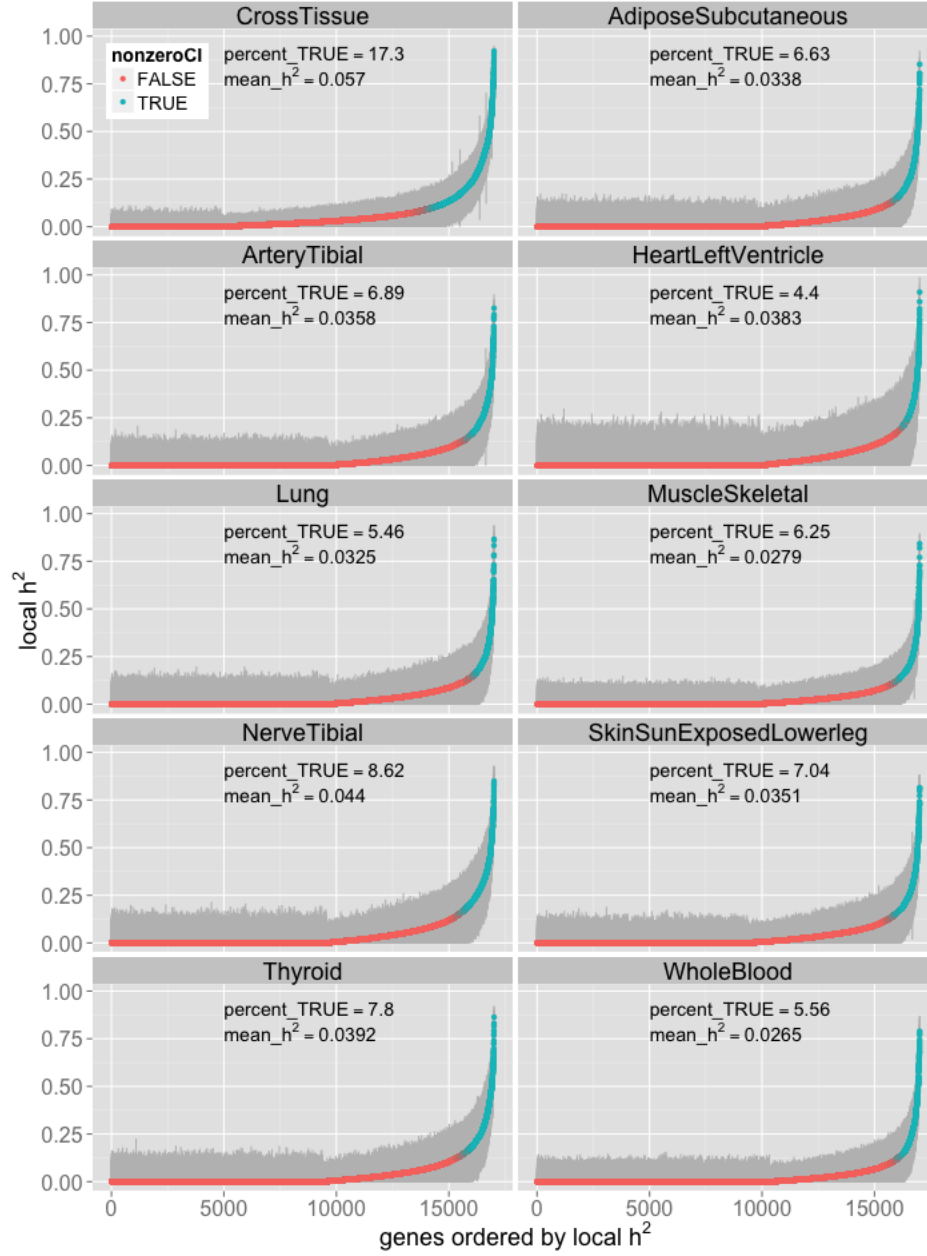
Figure 3: Cross-tissue heritability (h^2) compared to tissue-wide h^2. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-wide local h^2 is estimated using the measured gene expression for each respective tissue and SNPs within 1 Mb of each gene.
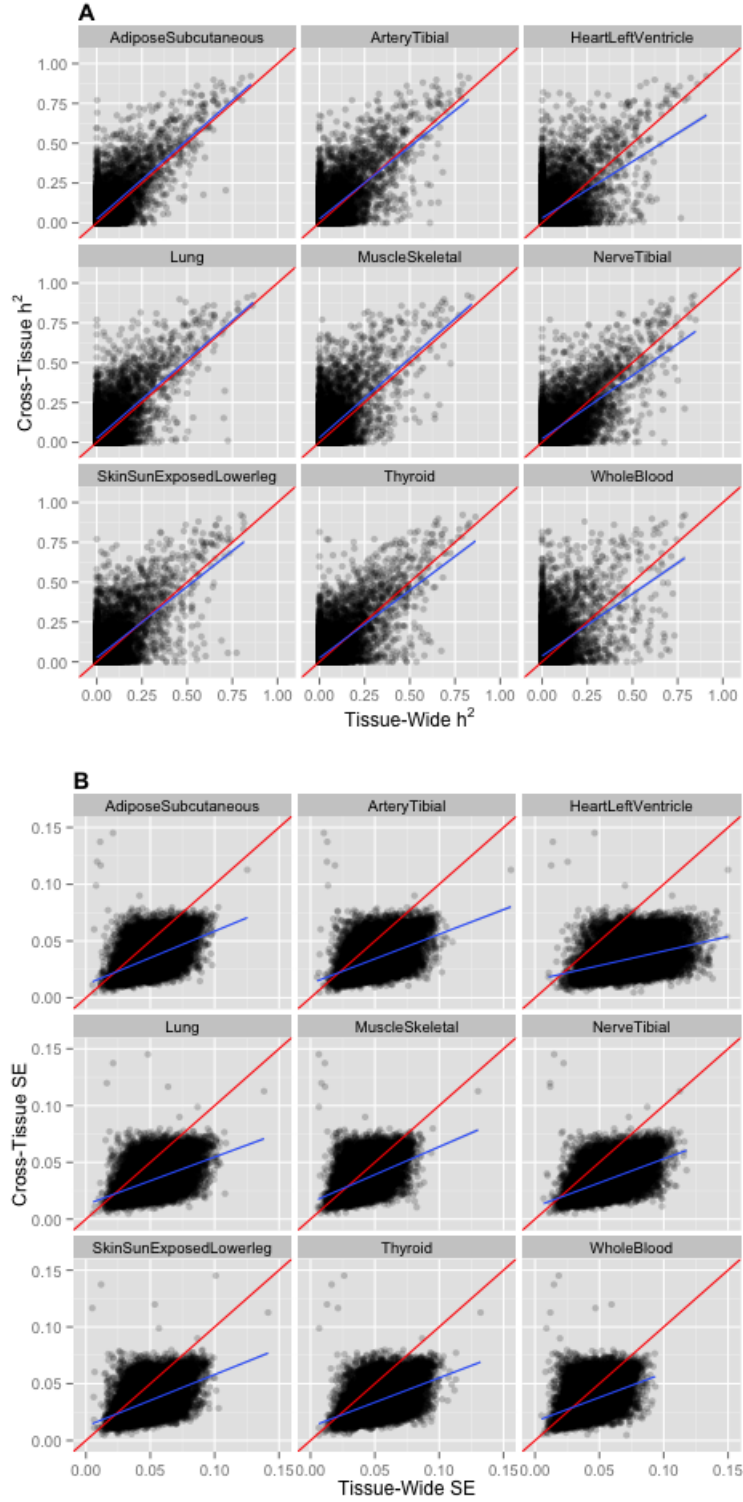
Figure 4: Cross-tissue and tissue-wide comparison of heritability (h^2, **A**) and standard error (SE, **B**). Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-wide local h^2 is estimated using the measured gene expression for each respective tissue and SNPs within 1 Mb of each gene.
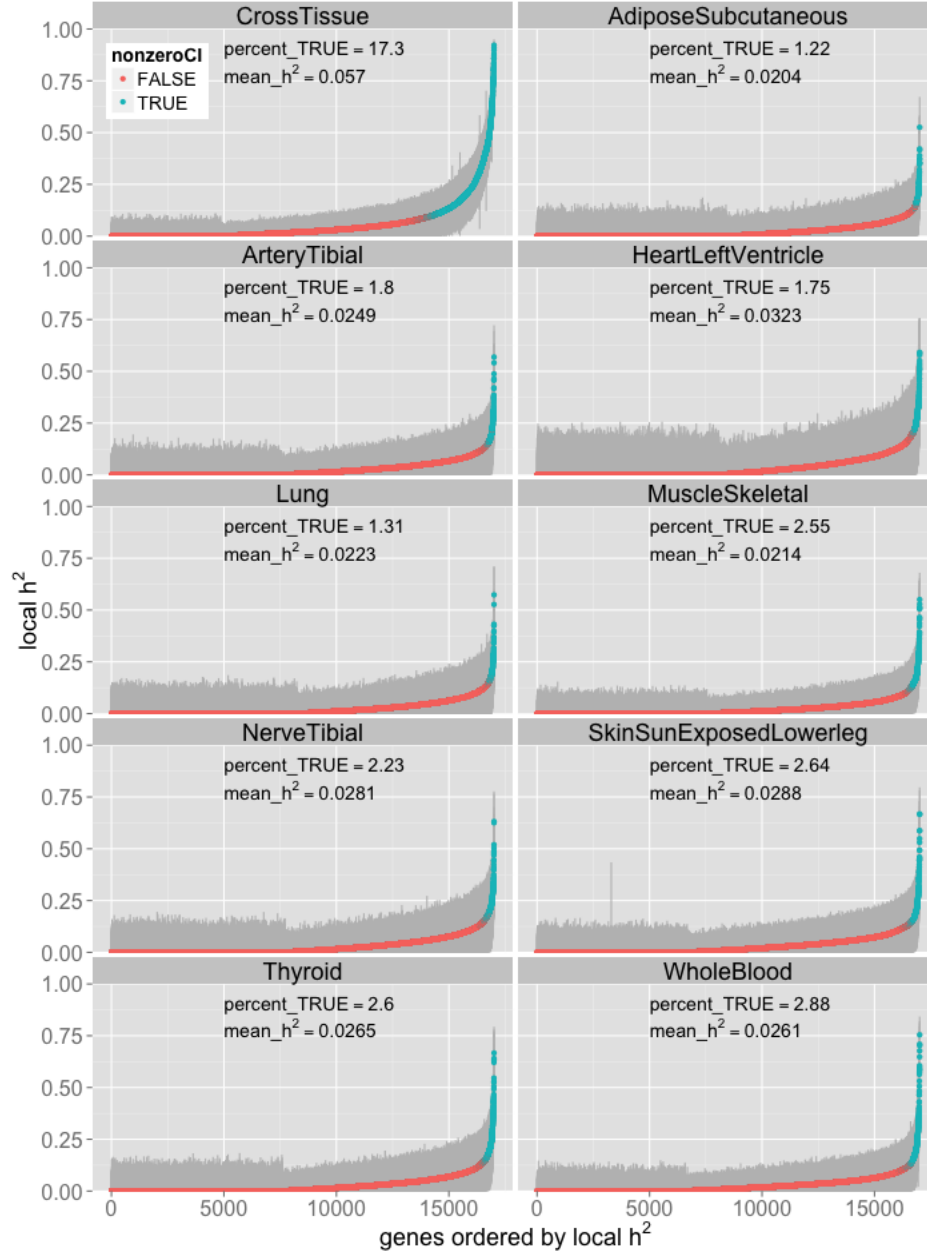
Figure 5: Cross-tissue heritability (h^2) compared to tissue-specific h^2. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-specifc local h^2 is estimated using the tissue-specific component (residuals) of the mixed effects model for gene expression for each respective tissue and SNPs within 1 Mb of each gene.
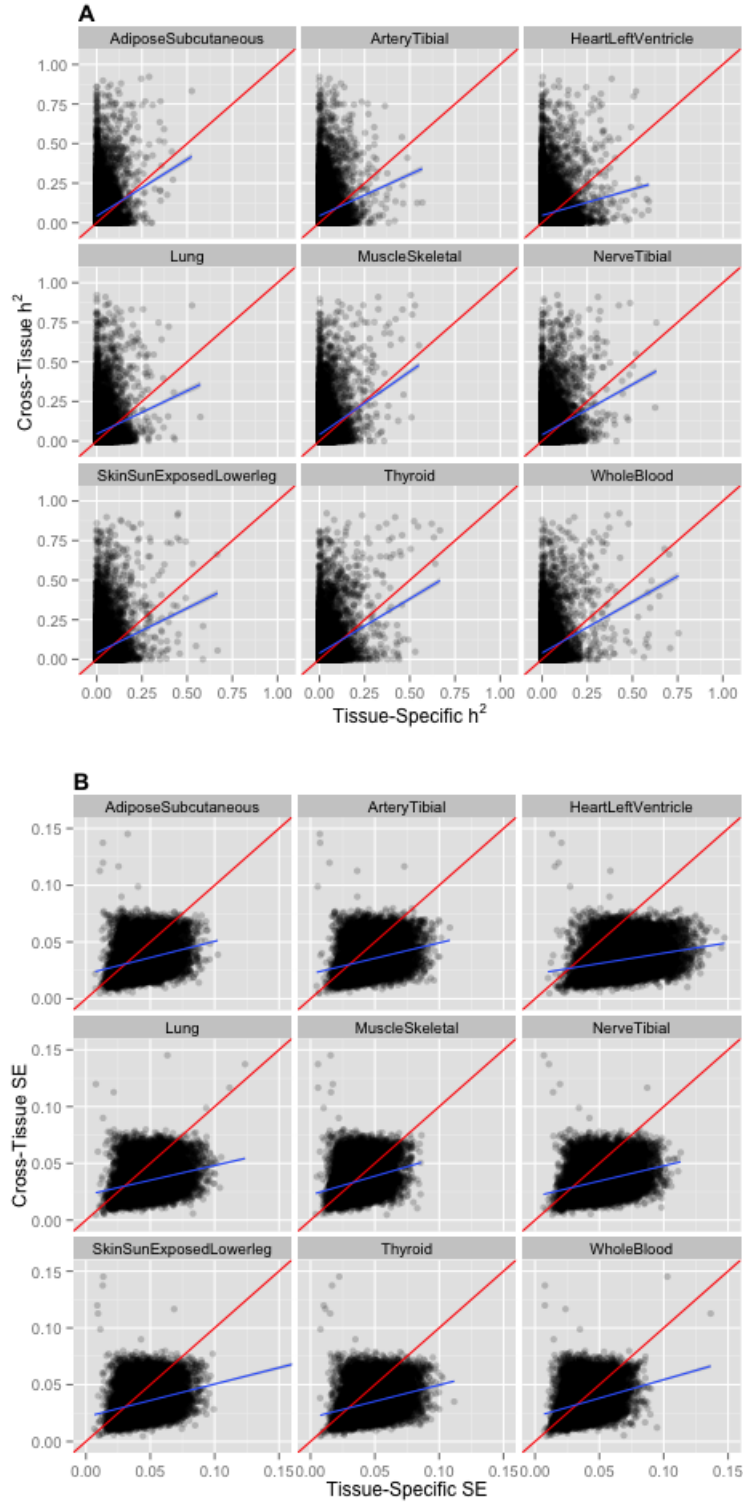
Figure 6: Cross-tissue and tissue-specific comparison of heritability (h^2, **A**) and standard error (SE, **B**) estimation. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-specifc local h^2 is estimated using the tissue-specific component (residuals) of the mixed effects model for gene expression for each respective tissue and SNPs within 1 Mb of each gene.