Genetic Architecture of Transcriptome Regulation

Heather E. Wheeler[1], Nicholas Knoblauch[2], GTEx Consortium, Nancy J. Cox[3], Dan L. Nicolae[1], Hae Kyung Im[1]

2015-05-13 12:26:40 [1]Department of Medicine, University of Chicago, [2]Committee on Genetics, Genomics, and Systems Biology, University of Chicago, [3]Division of Genetic Medicine, Vanderbilt University

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)	-0.09	0.1	-0.89	0.38
x	2.19	0.1	22.51	0.00

Table 1: This is a GLM summary table.

3.3 Plots

3.4 Citations

The relationship was first described by Reference 1. However, there are also opinions that the relationship is spurious [2]. We used R for our calculations [3], and we used package `knitcitations` [4] to make the bibliography.

4 Results and discussion

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References

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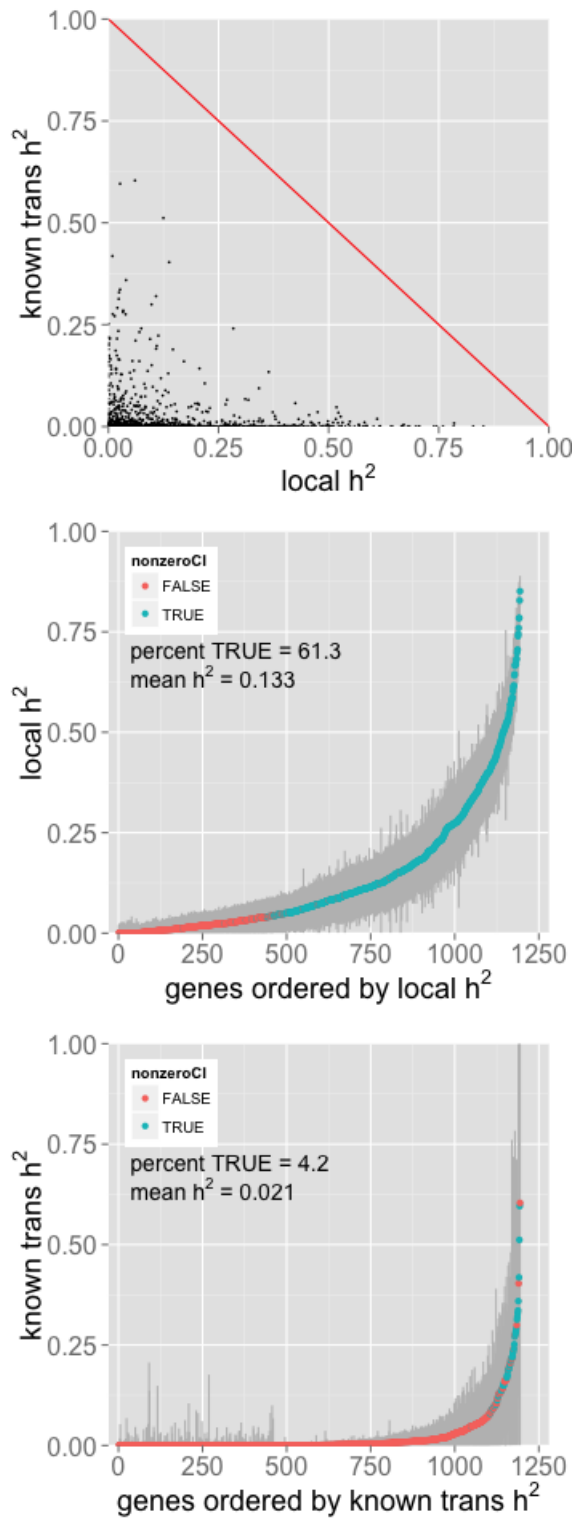
Figure 2: DGN-WB joint heritability (h^2) with known trans-eQTLs. Local h^2 is estimated with SNPs within 1 Mb of each gene. Known trans h^2 is estimated with SNPs that are trans-eQTLs in the Framingham Heart Study for each gene (FDR < 0.05).
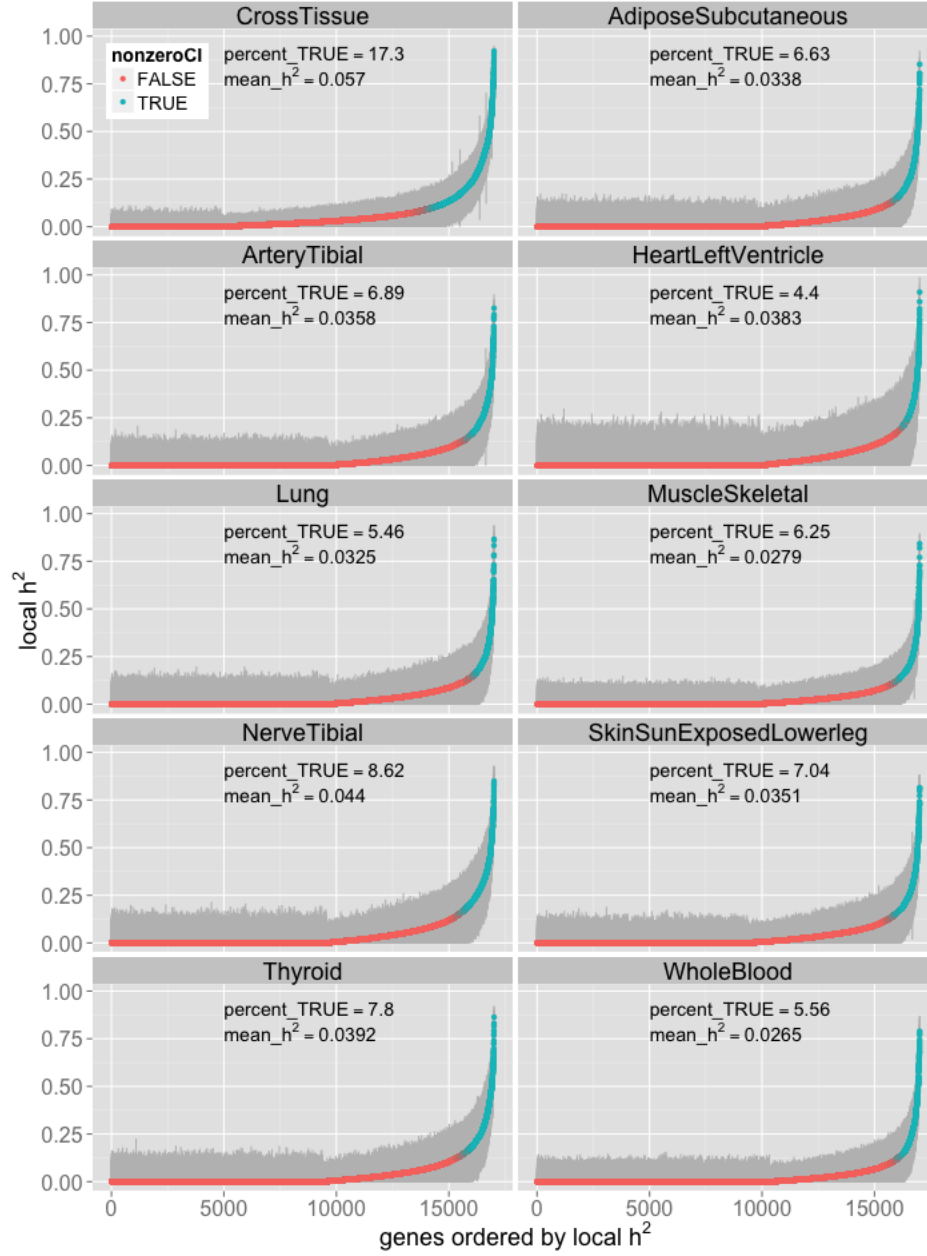
Figure 3: Cross-tissue heritability (h^2) compared to tissue-wide h^2. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-wide local h^2 is estimated using the measured gene expression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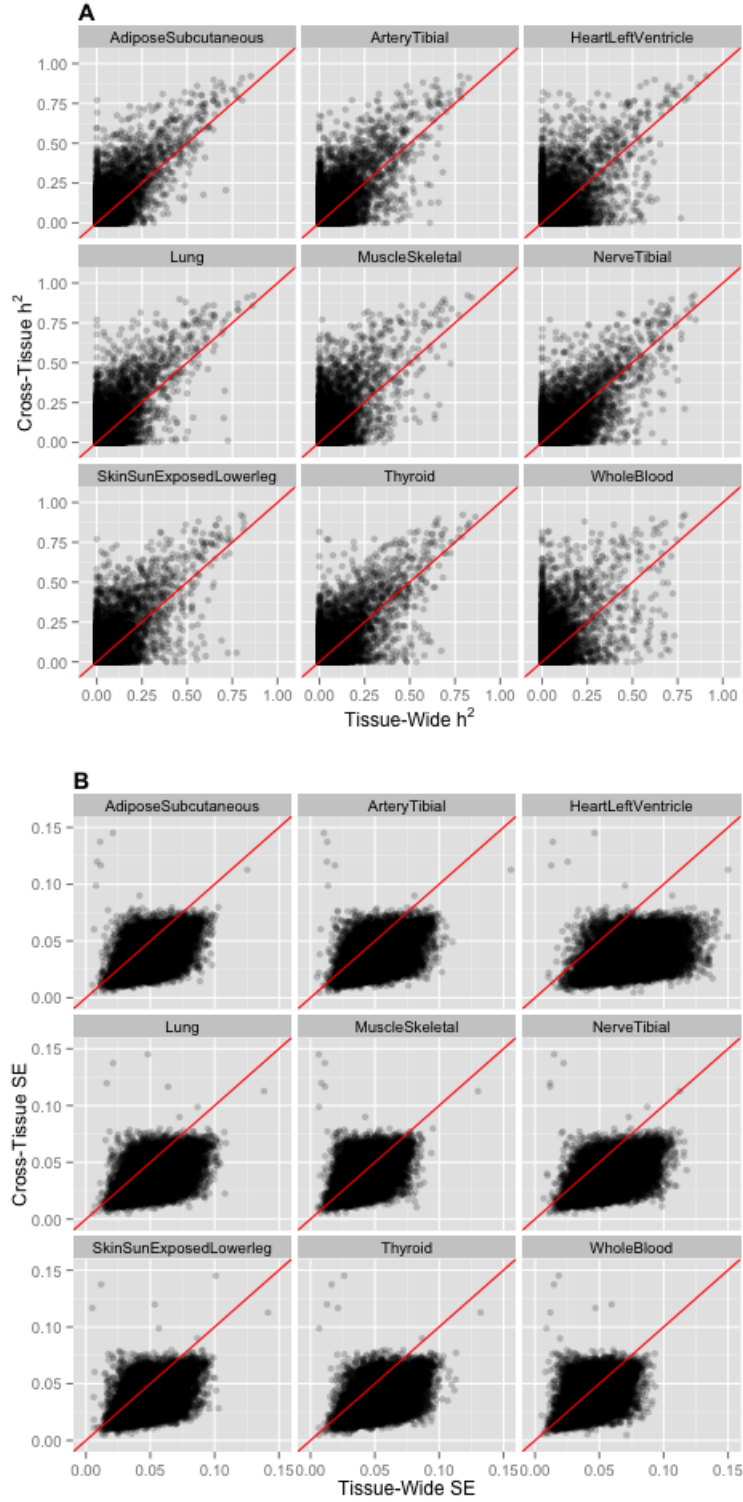
Figure 4: Cross-tissue and tissue-wide comparison of heritability (h^2, **A**) and standard error (SE, **B**). Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-wide local h^2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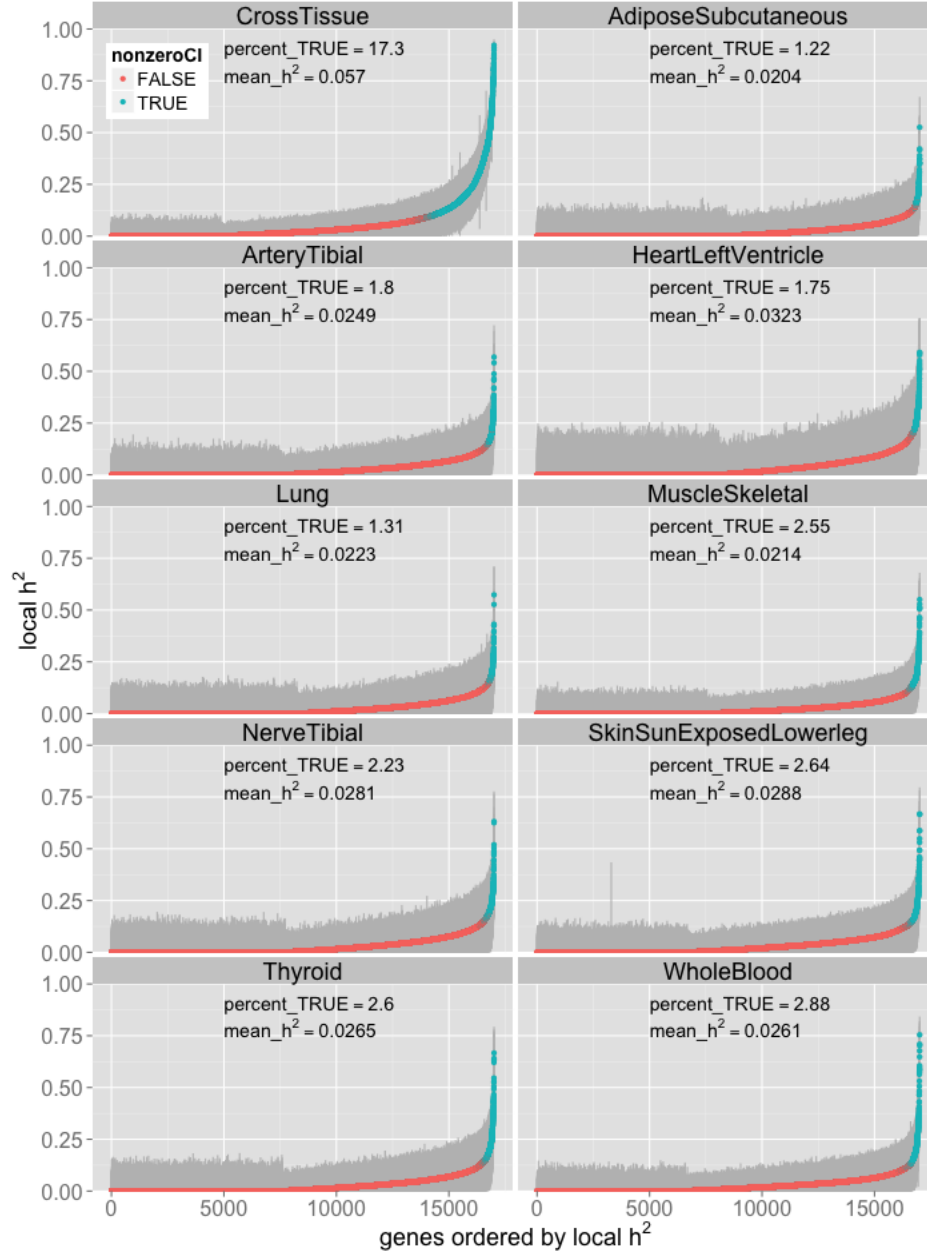
Figure 5: Cross-tissue heritability (h^2) compared to tissue-specific h^2. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-specifc local h^2 is estimated using the tissue-specific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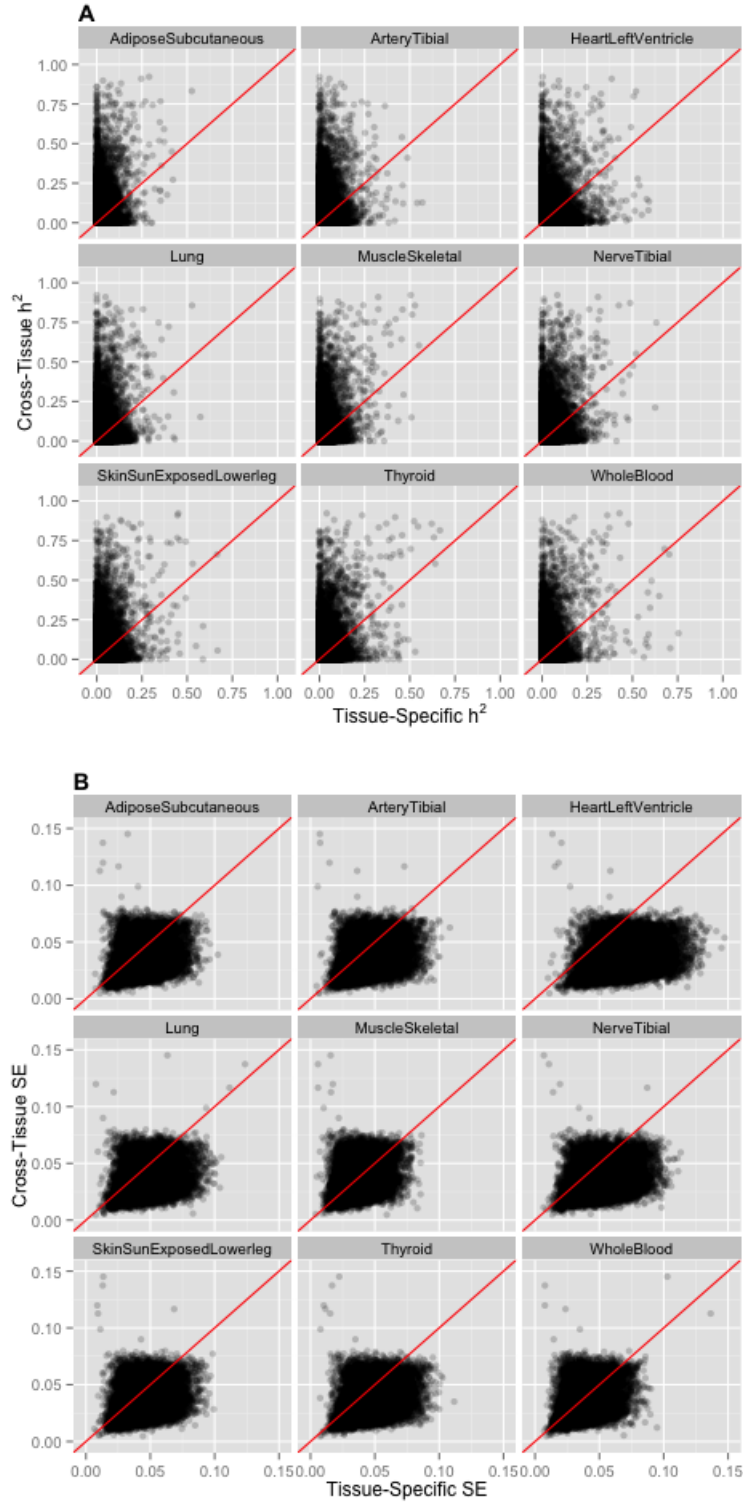
Figure 6: Cross-tissue and tissue-specific comparison of heritability (h^2, **A**) and standard error (SE, **B**) estimation. Cross-tissue local h^2 is estimated using the cross-tissue component (random effects) of the mixed effects model for gene expression and SNPs within 1 Mb of each gene. Tissue-specifc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

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