# Genetic Architecture of Transcriptome Regulation

Heather E. Wheeler, Hae Kyung Im 2015-04-30 12:41:51

# 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

	Estimate	Std. Error	t value	Pr(> t )
$\overline{(Intercept)}$	-0.08	0.09	-0.94	0.35
X	1.86	0.10	19.51	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 (R Core Team 2015), and we used package knitcitations (Boettiger 2014) to make the bibliography.

### 4 Results and discussion

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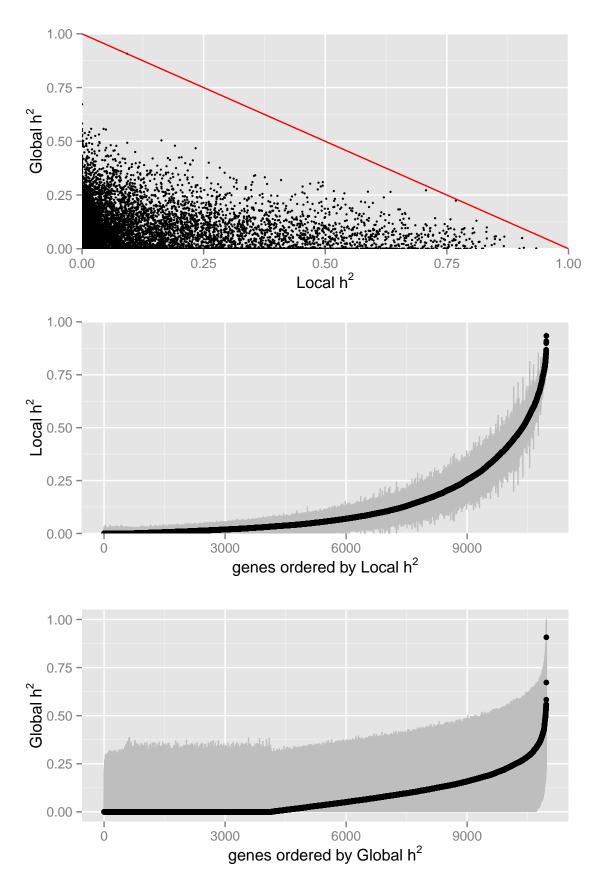


Figure 1: DGN-WB joint heritability. Local h^2 is estimated with SNPs within 1 Mb of each gene. Global h^2 is estimated with SNPs that are eQTLs in the Framingham Heart Study on other chromosomes (FDR < 0.05).