

1 Supplementary Information for Genome-Wide
2 Gene-Environment Interactions [on Quantitative Traits](#)
3 using Family Data

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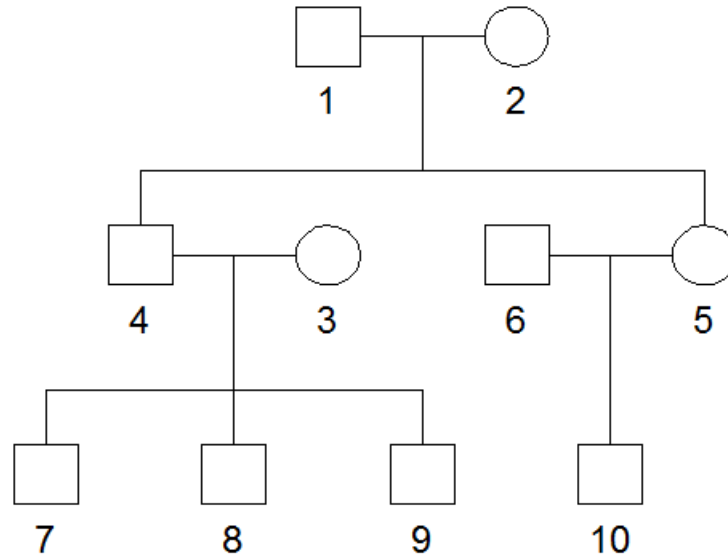
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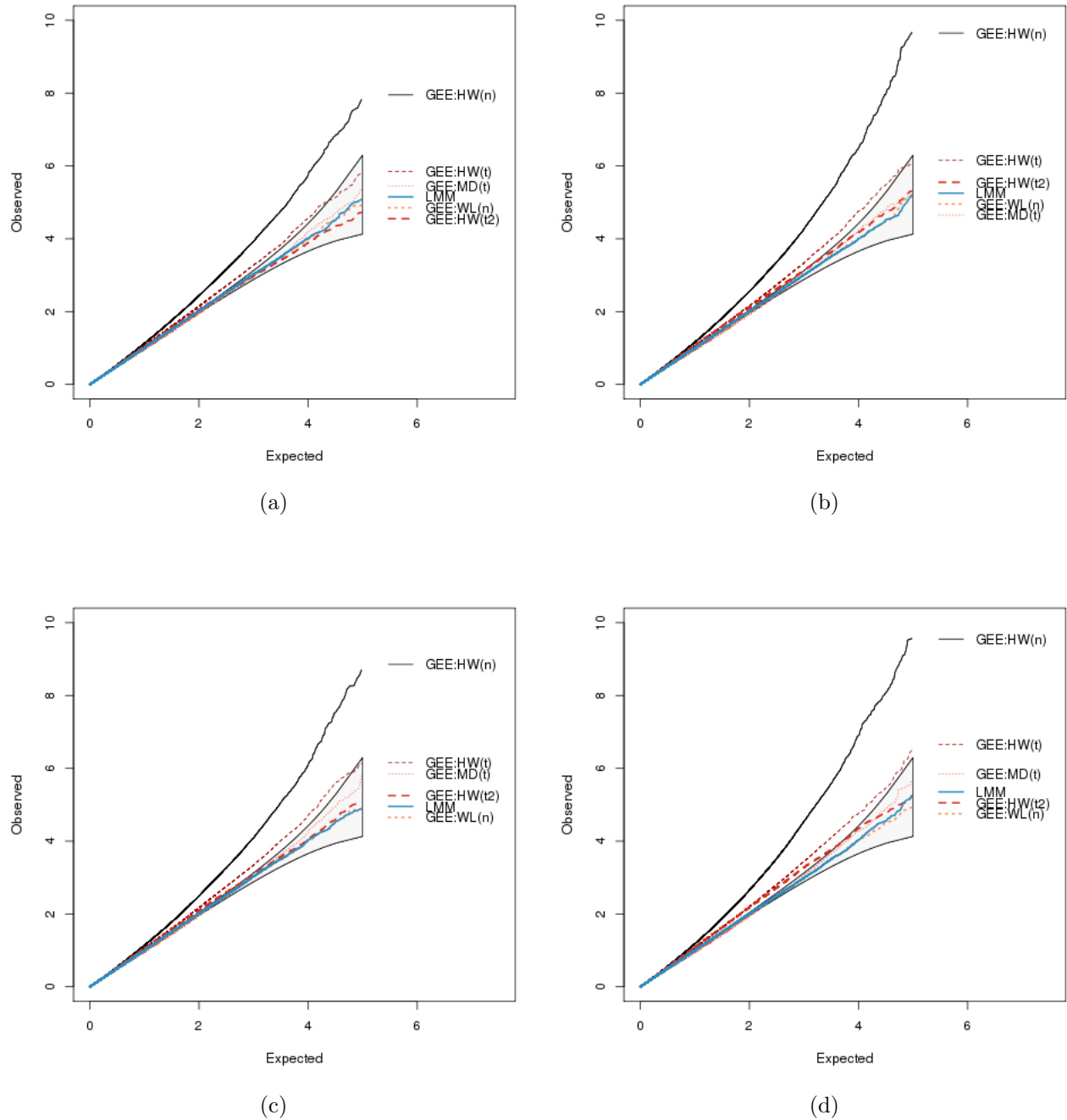
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11 Washington, Seattle, WA; Group Health Research Institute, Group Health
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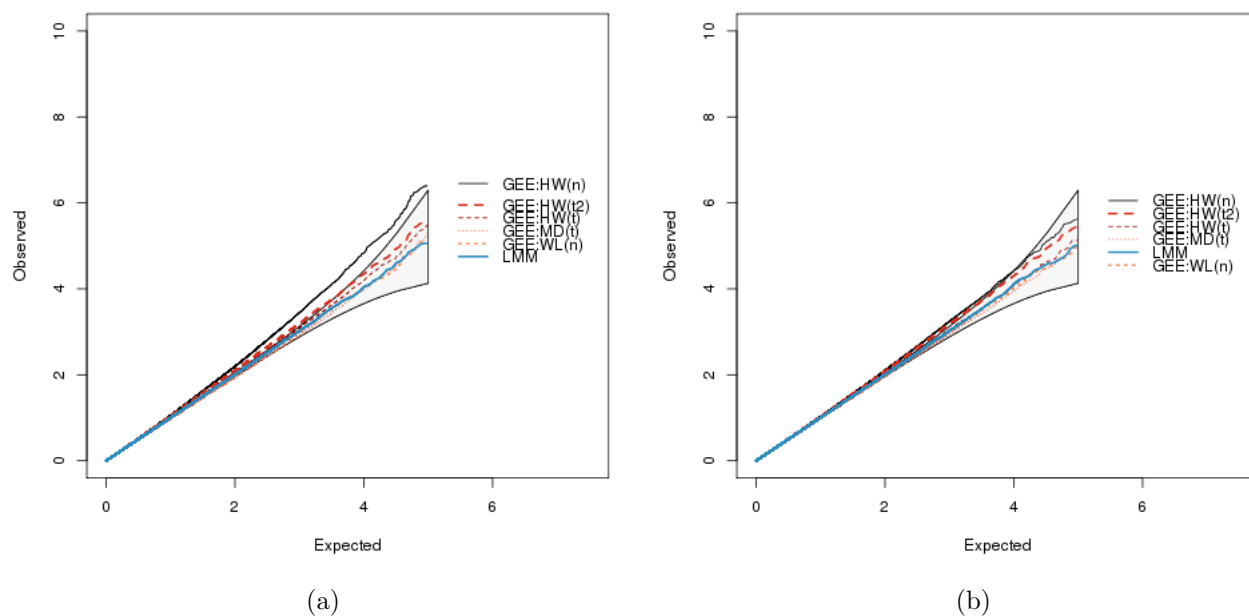
13 **Supplementary Figures**



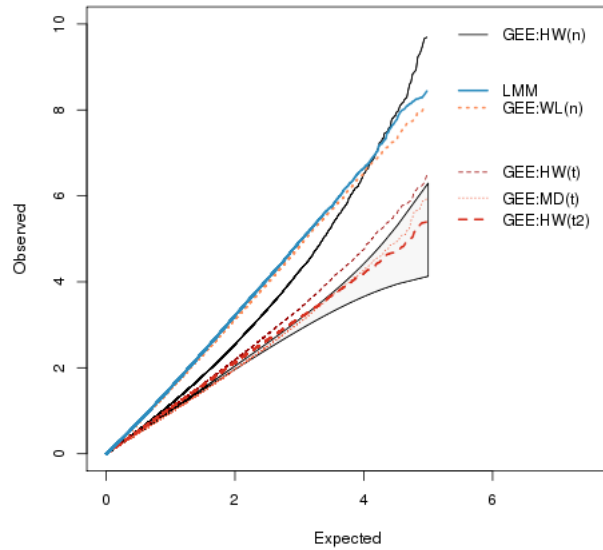
Supplementary Figure 1: Sample pedigree for three-generational family generated in simulations.



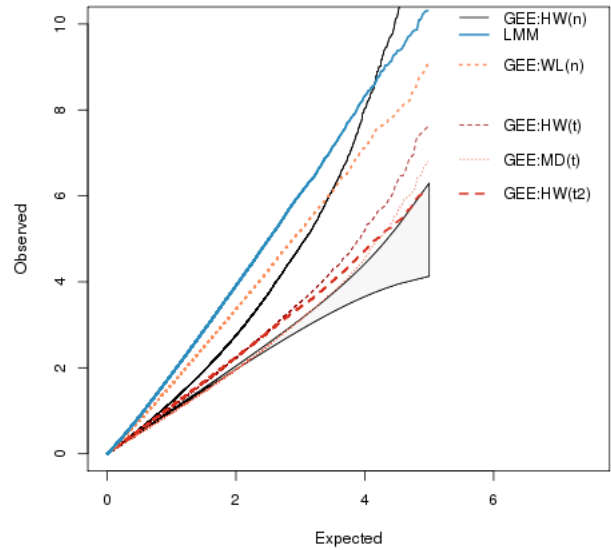
Supplementary Figure 2: Quantile-quantile plots of $-\log_{10}(\text{p-values})$, with each plot derived from one million simulations. Simulated data in the top row are from 200 nuclear families, each of size 5, while data in the bottom row are from 100 three-generational families, each of size 10. Subfigures (a) and (c) assume a single cross-sectional measurement with $\text{MAF}=0.10$ and $\text{P}(\text{exposure})=10\%$, while subfigures (b) and (d) assume four longitudinal measurements with $\text{MAF}=0.05$ and $\text{P}(\text{exposure})=5\%$. GEE models use either sandwich (HW), Mancl & DeRouen (MD), or Wang & Long (WL) standard error estimates, with reference distribution being normal (n), t with Satterthwaite estimates of degrees of freedom (t), or approximate estimates of degrees of freedom (t2).



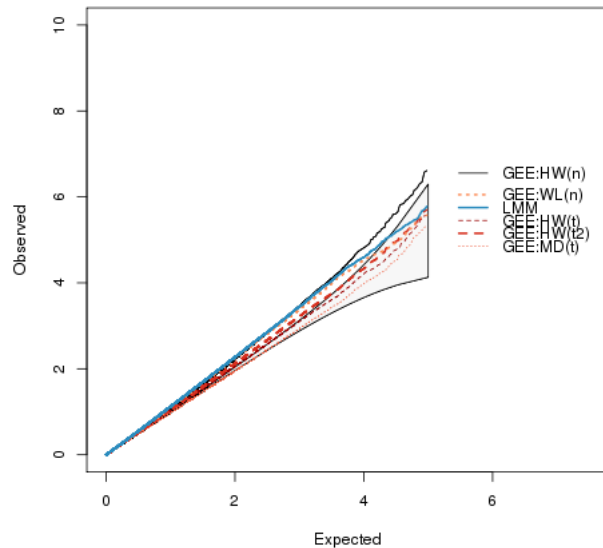
Supplementary Figure 3: Quantile-quantile plots of $-\log_{10}(\text{p-values})$, with each plot derived from one million simulations. Simulated data are single cross-sectional measurements from 100 three-generational families, each of size 10. Subfigure (a) assumes $\text{MAF}=0.10$ and $\text{P}(\text{exposure})=40\%$, while subfigure (b) assumes $\text{MAF}=0.40$ and $\text{P}(\text{exposure})=40\%$. GEE models use either sandwich (HW), Mancl & DeRouen (MD), or Wang & Long (WL) standard error estimates, with reference distribution being normal (n), t with Satterthwaite estimates of degrees of freedom (t), or approximate estimates of degrees of freedom (t2).



(a)



(b)



(c)

Supplementary Figure 4: Quantile-quantile plots of $-\log_{10}(\text{p-values})$, with each plot derived from one million simulations. Simulated data are from 100 three-generational families, each of size 10. Models are mis-specified because outcome variance is twice as high among exposed participants as it is among unexposed participants. Subfigure (a) assumes a single cross-sectional measurement with $\text{MAF}=0.10$ and $\text{P}(\text{exposure})=10\%$; subfigure (b) assumes four longitudinal measurements with $\text{MAF}=0.05$ and $\text{P}(\text{exposure})=5\%$; and subfigure (c) assumes a single cross-sectional measurement with $\text{MAF}=0.10$ and $\text{P}(\text{exposure})=40\%$. GEE models use either sandwich (HW), Mancl & DeRouen (MD), or Wang & Long (WL) standard error estimates, with reference distribution being normal (n), t with Satterthwaite estimates of degrees of freedom (t), or approximate estimates of degrees of freedom (t2).