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Using Multiple Measures for Quantitative Trait Association Analyses: Application to Estimated Glomerular Filtration Rate (eGFR)

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Abstract

Studies of multiple measures of a quantitative trait can have greater precision and thus statistical power compared to single measure studies, but this has rarely been studied in the relation to quantitative trait measurement error models in genetic association studies. Using estimated glomerular filtration rate (eGFR), a quantitative measure of kidney function, as an example we constructed measurement error models of a quantitative trait with systematic and random error components. We then examined the effects on precision of the parameter estimate between genetic loci and eGFR resulting from varying the correlation and contribution of the error components. We also compared the empirical results from 3 genome-wide association studies (GWAS) of kidney function in 9049 European Americans: a single measure, a 3-measure model of the same biomarker of kidney function, and a 6-measure model of different biomarkers of kidney function. Simulations showed that given the same amount of overall errors, inclusion of measures with less correlated systematic errors led to greater gain in precision. The empirical GWAS results confirmed that both the 3- and 6-measure models detected more eGFR-associated genomic loci with stronger statistical association than the single-measure model despite some heterogeneity among the measures. Multiple measures of a quantitative trait can increase the statistical power of a study without additional participant recruitment. However, careful attention must be paid to the correlation of systematic errors and inconsistent associations when different biomarkers or methods are used to measure the quantitative trait.

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Keywords

repeated measures; kidney function; glomerular filtration rate; biomarkers; genome-wide association study; GWAS

Introduction

Genome-wide association studies (GWAS) have discovered many robust, albeit modest, genetic associations for quantitative traits.(1) This is facilitated through large consortia that are comprised of many individual studies to attain appropriate statistical power. While increasing sample size can enhance statistical power by increasing the precision of the genetic parameter estimate, another way to increase the precision is to increase the number of phenotype measures per individual. In epidemiological studies, multiple measures of a phenotype within an individual can represent either: 1) repeated measures from a single assessment method, (e.g. weight over multiple years) or 2) multiple measures assessed using different methods (e.g. weight, percent body fat, waist-to-hip circumference to represent obesity). The impact of multiple measures on the precision of the genetic parameter, and hence the required sample size, will depend on the systematic and random errors of the phenotypic measurement and the correlations between the measures within each individual. Formulas and procedures exist for calculating sample size for detecting associations with correlated data.(2, 3) However, the impact of different types of measurement errors and the application of multiple measure models in GWAS remains to be evaluated.

We therefore performed a simulation study, along with examination of an empirical dataset, to assess how different types of measurement errors affect the precision of the genetic parameter estimate in genetic association analyses of multiple measures. Both the simulation and the empirical studies were based on estimated glomerular filtration rate (eGFR), a quantitative marker of kidney function. GFR is often estimated using serum creatinine (eGFR_{scr}) because the direct measure of GFR is often impractical in both clinical and research settings.(4) Other biomarkers, such as serum cystatin C (CysC), beta trace protein (BTP), and beta-2 microglobulin (B2M), have also been used as kidney function biomarkers. (5–8) In the estimation of GFR, there will be systematic errors that are the properties of each biomarker, and there will also be random errors due to day-to-day physiological change and laboratory measurement errors.

In the simulation study, we examined the impact of systematic and random errors, along with increasing the number of phenotypic measures, on the precision of the genetic parameter estimate. In the empirical data analysis, we aimed to answer the following questions: (1) to what extent do the longitudinal measures of eGFR based on serum creatinine increase the precision of the genetic parameter estimate; and (2) does the addition of measures based on non-creatinine biomarkers provide further gain in the precision and reduce bias in detecting genetic associations?

Materials and Methods

Simulation Study

GFR Measurement Error Model—In our GFR measurement error models, the observed outcome, Y_{ij} (representing eGFR or any other biomarker-based kidney function index), was determined by three latent components: 1) an individual's average stable true GFR (tGFR); 2) systematic errors (ϵ_S), including biomarker specific inter-individual variability, unrelated to the true GFR and not accounted for in the GFR estimating equation; and 3) random errors (ϵ_R), such as laboratory measurement errors and within-individual day-to-day physiological variations in GFR or biomarker levels. For the j^{th} and k^{th} observations of individual i , the correlation between the outcomes, (Y_{ij}, Y_{ik}) , was determined by tGFR and systematic errors, which may or may not be correlated within an individual depending on the method of measurement. In our specification of the measurement error model, the three latent components of the outcome (tGFR, systematic errors and random errors) were assumed to be independent with standard normal distribution, Normal (0, 1). Figure 1 presents a GFR measurement error model of two measures. Details of the specification of the measurement error model are described in the Supplementary Methods section.

Evaluation of Datasets with Complete Data—Using four models (summarized in Table 1), we investigated the impact of varying 1) the overall measurement errors, and 2) the correlation between the systematic errors, $(\epsilon_{Sij}, \epsilon_{Sjk})$, on the gain in precision of the genetic parameter estimate in multiple measure models. We assumed the causal SNP explained 0.5% of tGFR variance without measurement errors. The contribution of tGFR to the variance of the outcome, Y_{ij} , was set to 0.7 in models 1 and 2, and reduced to 0.5 in models 3 and 4. Therefore, the percentage of the variance of Y_{ij} explained by the SNP was 0.35% for models 1 and 2 and 0.25% for models 3 and 4, similar to the modest effect size of the index SNPs in eGFR GWAS results (9). The setting of 0.7 for the contribution of tGFR in models 1 and 2 was based on unpublished data from the Modification of Diet in Renal Disease (MDRD) Study and the African American Study of Kidney Disease (AASK). In these two studies, the correlation between eGFR and tGFR, estimated from urinary clearance of ^{125}I -iothalamate (gold standard), was approximately 0.9 in patients with chronic kidney disease. This implies the contribution of tGFR to the variance of eGFR was approximately 0.81 ($=0.9^2$). In the general population the contribution of tGFR to eGFR variance would be lower (10).

In models 1 and 2, the contribution of random errors to the variance of the outcome was set at 0.1 based on the estimates of within-individual variation in serum creatinine (11) and measured GFR (11, 12). Therefore, the contribution of systematic errors to the variance of the outcome was set to 0.2 ($=1 - 0.7 - 0.1$). The contributions of systematic errors in models 3 and 4 were kept at the same level. The systematic errors, $(\epsilon_{Sij}, \epsilon_{Sjk})$, where $j \neq k$, were assumed to be uncorrelated in models 1 and 3, and have a covariance of 0.5 in models 2 and 4.

From the GFR measurement error model parameters described above, we estimated the observed covariance of the outcomes and the residual variance of a generalized least square (GLS) regression model (Table 1). GLS is a common method for modeling multiple

correlated continuous outcomes and can estimate the association between a predictor and the outcomes taking into account correlated residuals. In this paper, we reserve the term “errors” to refer to the latent error components in the measurement error model and use “residuals” to refer to the portion of the outcome unexplained by predictor(s) in a GLS regression model.

We expressed the gain in precision of the genetic parameter estimate in a multiple measure model over a single measure model in term of the estimated “change in equivalent sample size”. The formula for the estimate of the gain in precision is provided in Supplementary Methods section. This measure is relevant in situations where an investigator might be deciding between increasing power through additional recruitment of study participants (thus increasing Y_i) or adding another outcome measure in the existing population (adding Y_{ik}). Equivalent sample size was defined as the sample size in a single measure ordinary least square (OLS) regression that would provide the same power as a multiple measure model using GLS given the same effect size and alpha level.

Evaluation of Datasets with Data Missing Completely at Random—Based on the above measurement error models, we simulated datasets with sample sizes of either 3,000 or 6,000 to assess the impact of randomly missing data on the gain of precision in the genetic parameter estimate in multiple-measure models. The mechanism of missing completely at random (MCAR) (15) was deemed to be appropriate for this study because our focus was the gain in precision of the parameter estimate instead of evaluating biases in parameter estimate. Each dataset had three repeated outcome measures, Y_{i1} , Y_{i2} , and Y_{i3} , with a variance of 1 and a constant modest SNP effect size ($\beta=0.075*SD$ of Y_{ij}). If the SNP has an allele frequency of 35%, it would explain about 0.25% of the variance of Y_{ij} , similar to the SNP effects in models 3 and 4 in Table 1. Missing data rates in scenario 1 were 10% for the second measure and 25% for the third measure. The rates increased to 20% and 40% in scenario 2. With each missing data scenario, we simulated datasets with correlations between Y_{ij} and Y_{ik} ranging from 0.5 to 0.8. Since the SNP effect was assumed to be constant across the outcome measures, the change in the correlations between Y_{ij} and Y_{ik} was assumed to be solely due to the change in the correlation of systematic errors (ϵ_S). Residuals were generated with a distribution of Normal(0, 1) and then transformed to have the desired correlation by multiplying the Cholesky decomposition of a variance-covariance matrix. Supplementary Table 1 presents the simulation parameters. Ten thousand iterations were performed for datasets with a sample size of 3,000, and 6,000 iterations were performed for datasets with a sample size of 6,000.

With each dataset, we performed three analyses: 1) an OLS regression using the first measure (Y_{i1}) as outcome, 2) a GLS regression using Y_{i1} and Y_{i2} as outcomes, and 3) a GLS regression using Y_{i1} , Y_{i2} , and Y_{i3} as outcomes. Changes in equivalent sample size were calculated using equation 3 based on the variance of the SNP parameter estimates generated in the simulations. To obtain the 95% interval of the variance of the SNP parameter estimate, we sampled the standard errors (SE) of the SNP parameter estimates in the single and multiple measure models separately, then calculated the square of the ratio of the SEs. After repeating this procedure 1000 times, we obtained the 0.025 and 0.975 percentile for the 95% interval. SAS 9.2 PROC GLM was used for OLS regression, and PROC MIXED with the repeated statement was used for GLS regression. A template of the

SAS macro for running the association analysis was included in the Supplementary Materials.

Empirical Data

Study Population—The ARIC Study is a prospective observational cohort study of 15,792 middle age adults (baseline age between 45 and 64) in four US communities. Details of the study design were reported previously (16). Since the known genomic risk loci for reduced eGFR were detected in populations of European ancestry, only the ARIC European American cohort (n=9,049) was included in this analysis.

Phenotype and Genotype in Empirical Dataset—In the ARIC study, the following measures of kidney function were available: three repeated measures of serum creatinine (SCr) at visits 1, 2, and 4 and measures of serum cystatin C (CysC), beta trace protein (BTP), and beta-2 microglobulin (B2M) at visit 4 (Supplementary Figure 1). The Supplementary Methods section reports the measurement methods of these biomarkers and the calculation of the outcome measures: eGFR based on serum creatinine (eGFR_{scr}) and cystatin C (eGFR_{cys}) and scaled BTP and B2M. Over two million imputed single nucleotide polymorphisms (SNPs) were evaluated in the analysis. Details on genotyping and quality control are reported in the Supplementary Methods section.

GWAS Statistical Analysis—Three genome-wide scans were performed: 1) a single-measure model using eGFR_{scr} at visit 1 as outcome, 2) a 3-measure model using eGFR_{scr} at visits 1, 2, and 4 as outcomes, and 3) a 6-measure model using the three repeated measures of eGFR_{scr} and the measures of eGFR_{cys}, scaled BTP and scaled B2M as outcomes. Covariates included age, gender, study center, and the first 10 principal components with significant association with the outcome (p<0.05). The 3- and 6-measure models additionally included visit as a categorical covariate. The single-measure model was analyzed using ProbABEL (17). The multiple-measures models were analyzed using SAS 9.2 PROC MIXED with the repeated statement and a pre-specified variance-covariance matrix to optimize performance. The Supplementary Methods section reports the generation of this variance-covariance matrix.

We calculated the genomic control factor (λ_{GC}) for the results of each genome-wide scan to assess possible test statistic inflation and corrected the p-values when $\lambda_{GC} > 1$. (18) The model comparisons were based on the genomic control corrected p-value (PValGC).

In addition, for the index SNPs of 16 known eGFR loci (9), we performed separate regression analyses using standardized outcome measures to obtain standardized SNP parameter estimates and standard errors of the single measure model and the 3- and 6-measure models.

Comparisons of the Single- and Multiple-Measure Models in the Empirical Dataset—The assumption of constant effect size across measures did not hold in the empirical data because the association between a SNP and a biomarker could change over time, and the association between a SNP and different biomarkers could vary. Therefore, we did not use the change in equivalent sample size as a metric for comparison in the empirical

study. Instead we compared the effect estimates of the index SNPs of the 16 known eGFR loci from the single-, 3-, and 6-measure models and the change in standard error due to multiple measures. Next, we compared the GWAS results of the three models with respect to the number of loci with $P_{ValGC} < 5 \times 10^{-8}$. Only SNPs with minor allele frequency (MAF) $> 5\%$ were included.

Results

Effect of Multiple Measures on Change in Equivalent Sample Size Assuming Complete Data

Figure 2A shows the relationship between the change in equivalent sample size and the number of outcome measures in the four models described in Table 1. Figure 2B shows the reciprocal of equivalent sample size as required sample size. Equivalent sample size may be more intuitive when an investigator only has the option of obtaining new measures given a fixed sample size; whereas the change in required sample size may be useful when an investigator have the option of varying both the numbers of measures or participants. For these results, we varied the following parameters: 1) the number of outcome measures, 2) the total measurement errors, and 3) the correlation between systematic errors.

Under the assumptions of no missing data and constant effect size across measures, adding additional outcome measures always led to a gain in estimated equivalent sample size. Assuming an uncorrelated residual variance, σ^2 , of 0.3 as in model 1, an increase of up to 10 measures led to 37% gain in equivalent sample size; however, this gain leveled off around five or six measures.

The relative gain in equivalent sample size with each additional measure was determined by the uncorrelated residual variance, σ^2 , as shown in equation 2. For a fixed total measurement error, as in models 1 and 2, the model with less correlated systematic errors, ϵ_S , had relatively higher uncorrelated residual variance, σ^2 , and resulted in more gain in equivalent sample size. For example, in model 1, the addition of a second measure led to an 18% gain in equivalent sample size but only 11% in model 2. Model 3 outperformed model 4 for the same reason.

Next, we also compared the impact of varying both the total measurement error and the correlation between systematic errors. Comparing models 2 and 3, model 2 had lower overall measurement errors but higher correlated residuals due to correlated systematic errors. The higher correlated residuals in model 2 led to a smaller gain in precision than model 3 with each additional measure. After the fifth measure, model 3 exceeded model 2 in estimated equivalent sample size. Supplementary Table 2 presents the changes in equivalent sample size with 95% confidence interval for sample sizes of 3000 and 10,000. Even though the estimate of the expected gain in equivalent sample size with additional measures is independent of the sample size when assuming complete data, the 95% confidence intervals of the estimate are narrower with larger sample size.

Effect of Multiple Measures on Change in Equivalent Sample Size Assuming Data Missing Completely At Random

Supplementary Table 3 shows the change in expected equivalent sample size when the data were missing completely at random. Similar to the results based on complete data, the gain in equivalent sample size was higher when the residuals were less correlated. As expected, higher missing data rate resulted in less gain in equivalent sample size with each additional outcome measure. When the outcome measures had a correlation of 0.5, the gains in equivalent sample size for adding a second measures with 0%, 10% and 20% missing data were 33%, 30% and 27% respectively. Even with a missing data rate as high as 40%, there was still gain in equivalent sample size.

Application to Kidney Function Measures in ARIC

Supplementary Table 4 reports the sample sizes, means, standard deviations, and correlations of the outcome measures of kidney function in the empirical study. The correlations between eGFR_{scr} across the three visits ranged from 0.63 to 0.69. The correlations between eGFR_{scr} and measures of kidney function based on other biomarkers were lower. The lowest correlation was 0.34 between eGFR_{scr} at visit 1 and scaled BTP at visit 4, and the highest correlation was 0.72 between eGFR_{cys} and scaled B2M both at visit 4.

Comparison of the results for 16 known eGFR-associated SNPs

We tested for the associations between kidney function and the index SNPs (with the SNP with the lowest p-value) at 16 known eGFR-associated loci using 1) a single-measure model with eGFR_{scr} at visit 1 as the outcome, 2) a 3-measure model including eGFR_{scr} from visits 1, 2, and 4; 3) a 6-measure model including both the repeated and the multiple measures of kidney function derived from different biomarkers; 4) a single-measure model with eGFR_{scr} at visit 4 as the outcome and the comparison of this results with a 4-measure model including all four measures of kidney function at visit 4.

Overall, for most of the 16 index SNPs, the multiple measure models resulted in lower association p-values due to the gain in precision of the beta estimates of the SNP effect (Supplementary Figure 3, Supplementary Table 5). The standard error reduction of the multiple-measures models over the single-measure model was 12% for the 3-measure model and 21% for the 6-measure model. Compared with the single-measure model, the 3-measure model had 15 index SNPs with lower p-values; five of them were at least one order of magnitude lower. Again, compared with the single-measure model, the 6-measure model has 12 index SNPs with lower p-value; seven of them were at least one order of magnitude lower. The 6-measure model resulted in larger pvalue than the single measure model at four loci due to weaker associations of the index SNPs with the non-creatinine biomarkers at *TFDP2* and *ANXA9* and opposite effect directions of the index SNPs with scaled BTP at *PIP5K1B* and *DAB2*. Supplementary Figure 4 shows the standardized beta estimates of the 16 index SNPs when regressed separately against the outcomes calculated from the four biomarkers at visit 4 of the ARIC study. For 8 of the 16 index SNPs, the beta estimates against eGFR_{scr} were larger than those against the non-creatinine-based outcomes. For the index SNPs of three loci (*ATXN2*, *PIP5K1B*, and *DAB2*), the beta estimates against scaled

BTP were in opposite directions from the estimates against the other three outcomes. Supplementary Table 6 presents the 95% confidence intervals of the estimates and p-values. Compared with the single measure model of eGFRscr at visit 4 versus the 4-measure model at visit 4, all the beta estimates were in the same direction. The standard error reduction from the four model was approximately 18%. However, only nine of the 16 SNPs had lower p-values in the 4-measure model (Supplementary Table 7).

GWAS Results

To determine whether the additional outcome measures would result in the identification of additional kidney loci in genome-wide scans, we performed three GWAS analyses. With respect to loci that reached genome-wide significance ($P_{ValGC} < 5 \times 10^{-8}$), the single-measure model identified one locus (*NAT8*), the 3-measure model identified three loci (*NAT8*, *SHROOM3*, and *SPATA5L1*), and the 6-measure model identified two loci (*NAT8*, *SHROOM3*, Supplementary Table 8). All loci had previously been discovered and replicated in a much larger sample.(9) One of the significant loci from the 3-measure model of eGFRscr, *SPATA5L1*, was not significant in the 6-measure model. This locus has been suspected to be a genetic locus related to creatinine production rather than kidney function, as evidenced by the lack of association with non-creatinine kidney function biomarkers.(9) One of the genes in this locus, *GATM*, encodes the rate-limiting enzyme in creatinine biosynthesis (19). This 6-measure model result suggests that the non-creatinine-based biomarkers reduced biases due the correlated systematic errors of the creatinine-based outcomes.

Discussion

Using both simulated and empirical datasets, we showed that increasing the number of outcome measures per individual led to gains in equivalent sample size, thus a gain in power, in genetic association analyses when the genetic effects were similar across measures. In addition, less correlated systematic errors led to greater gains in equivalent sample size. The marginal gain decreased with each additional measure and leveled off around the addition of the fifth or sixth measure. Lui and Cumberland made similar observations in the situation of 2-group complete balanced data.(20) The gain in equivalent sample size was relatively robust to data missing completely at random as the gain persisted even when the missing data rate was as high as 40%.

The results from our simulation study were corroborated by the results from the empirical study of multiple measures of kidney function in the ARIC study. We showed that inclusion of eGFRscr from 3 separate study visits (the 3-measure model) was more powerful than the single-measure model using eGFRscr at visit 1. However, the addition of other biomarkers of kidney function, including eGFRcys, scaled BTP and scaled B2M, did not make the 6-measures model more powerful than the 3-measures model despite additional gain in the precision of the SNP parameter estimates due to the heterogeneity of SNP associations with the different biomarkers. While longitudinal repeated measures of a trait can be used to estimate change over time, our study focused on the use of repeated measures to detect

associations that are similar across multiple measures. We estimated the mean effect over time and not change over time.

When studying multiple measures of an outcome, one can consider either repeated measures using the same method or multiple measures of an underlying trait using different methods, such as the use of different biomarkers for kidney function in this work. The contrast between these two scenarios was represented by the results of the 3-measure model and the 6-measure model from our empirical study. For repeated measures of the same outcome, correlated systematic errors between the multiple measures of the outcome may limit the gain in precision of the SNP parameter estimate. When using multiple measures based on different methods to represent one underlying trait, some measures may contain additional measurement errors, which reduce the statistical power of the study. In the kidney function empirical study, the inclusion of additional non-creatinine-based outcomes did not identify more loci with lower p-values. The non-creatinine-based outcomes may have more measurement errors due to the lack of population-based equations for calculating eGFR based on these biomarkers. Therefore, regardless of the number of measures, well-measured phenotypes that minimize measurement errors are important for detecting associations, a topic that has been studied extensively.(21)

A few studies have used repeated measures in the setting of genome-wide association studies and have found mixed results with respect to the gain in efficiency. Rasmussen-Torvik et al.(22) compared the results from using the average of 4 repeated measures of fasting glucose over 12 years (N=5,782) to the results from 4 separate GWASs of fasting glucose from each study visit (N ranged from 8,372 at visit 1 to 6,421 at visit 4) and found that, despite a smaller sample size, the results from the analysis of the average fasting glucose values were stronger. the p-values of the index SNP at five candidate regions were lower by three to eight orders of magnitude, mostly due to reduction in standard errors. This suggests the average of a trait can reduce intra-individual variations and lead to stronger statistical associations. On the other hand, Malhotra et al. conducted genome-wide association studies of body mass index (BMI) that used up to 17 repeated measures and the maximum BMI (from 1965 to 2004) in 1,120 Pima Indians.(23) No genome-wide significant loci were identified. Of the 20 top SNPs reported from the repeated measure analysis, nine had p-values that were lower than their corresponding p-values from the analysis using the maximum BMI, and the differences in p-values were less than two orders of magnitude. The gain in efficiency from the repeated measures was not apparent, which is possible if maximum BMI captures an individual's overall disposition toward obesity better than repeated measures of BMI over a very long period of time where BMI might fluctuate greatly.

One limitation of our work is that we only used GLS for analyses of multiple outcome measures and did not evaluate other methods. Ferreira and Purcell proposed the use of canonical correlation analysis for analyzing correlated outcomes in GWA studies.(24) Coin et al proposed using multiple phenotypes as predictors and a genetic variant as outcome in a regression model.(25) Both of these methods require the use of complete data. In addition, as it was shown in the GFR measurement error model, the correlation between measures can come from two sources: the true measure of the trait of interest and correlated systematic

errors, which does not help the detection of genetic associations of the trait. Therefore, the application of methods for combining multiple measures requires some assumptions and understanding of the measurement error model of the trait of interest.

Other limitations of this work include the assumption of one tGFR and constant covariance of outcomes in the measurement error models. The underlying latent trait may change over time, and the covariance structure among outcome measures may be complex. However, the basic conclusion of this work holds for multiple latent traits and complex covariance structures. Regardless of the specific covariance structure, correlated systematic errors reduce the gain in precision when using multiple measures.

GWAS provide a systematic, unbiased way to identify genes and pathways underlying a biological process.(26, 27) Very large sample sizes have been used to increase the precision of the genetic parameter estimates, thus increasing the power to identify loci of modest effect sizes.(28) Increasing sample size through additional participant recruitment can be expensive and sometimes not feasible. Therefore, using multiple measures of an outcome is another way to increase the statistical power of a study, especially for population-based cohort studies that have often collected multiple measures for prospective analyses of an outcome. Our findings can inform the choice of measures in the design of a multiple measure study.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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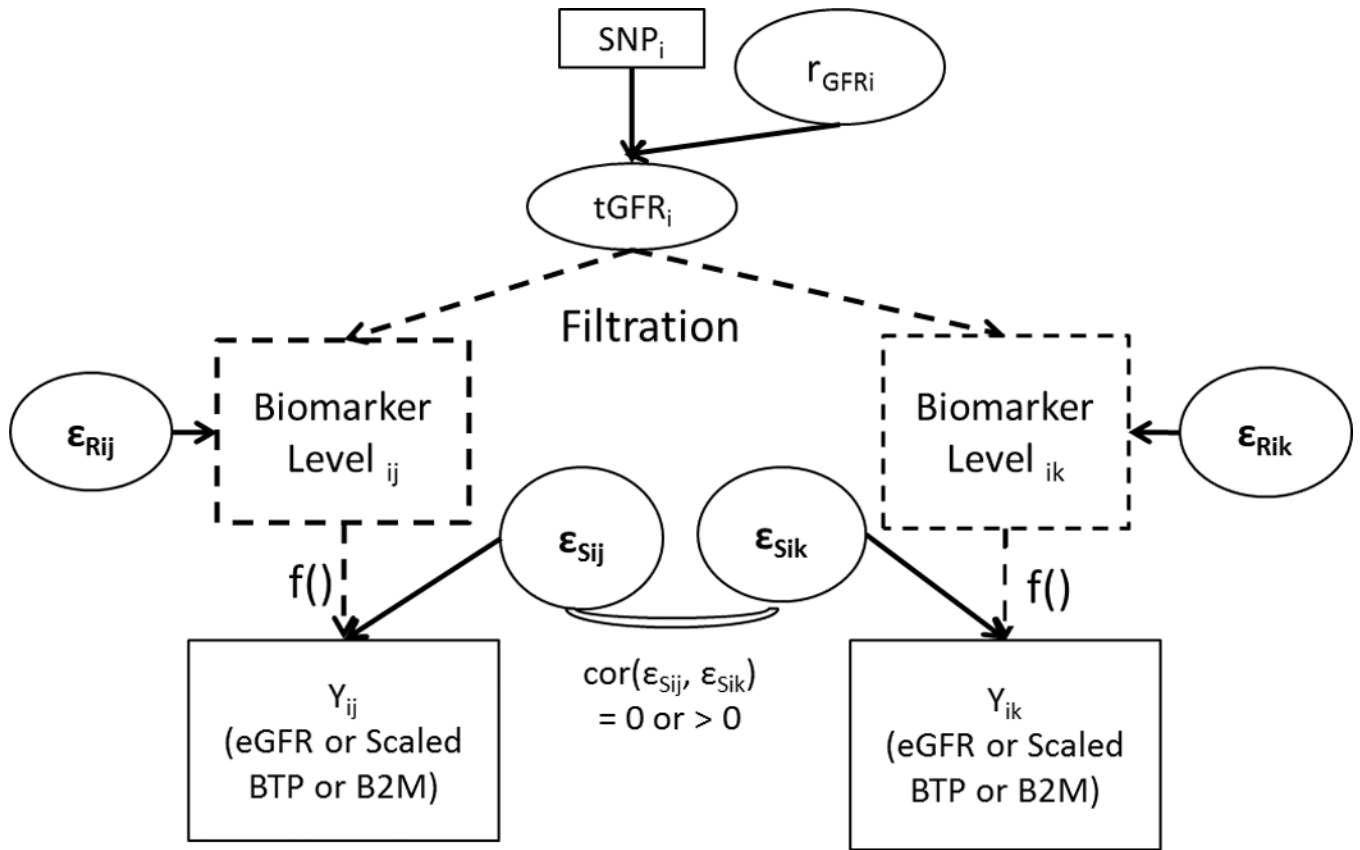


Figure 1. GFR Measurement Error Model. The SNP effect is assumed to act solely through tGFR. Y_{ij} is a function of tGFR, systematic errors (ϵ_s) and random errors (ϵ_r). The elements with dotted lines shows the process of estimating GFR based on biomarker levels and are not part of the measurement error model.

Notations and assumptions:

- tGFR: true GFR, average stable GFR, standardized to $N(0, 1)$
- i: individual
- j or k: observation within an individual
- r_{GFR} : tGFR level not explained by the SNP
- Y_{ij} : outcome in regression model, calculated from biomarker level using an equation, $f()$, representing estimated GFR
- ϵ_s : systematic errors in Y_{ij}
- ϵ_r : random errors in Y_{ij}
- $\epsilon_s, \epsilon_r \sim N(0, 1)$

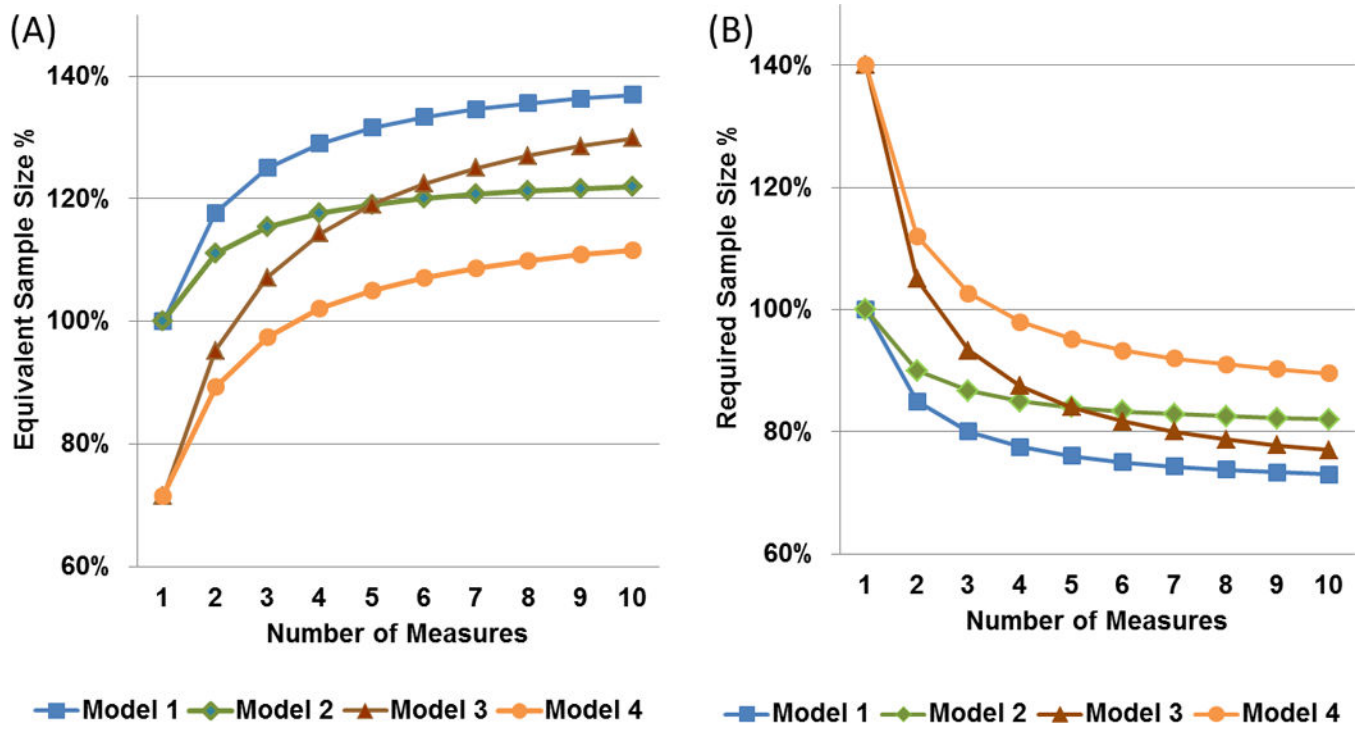


Figure 2. (A) Change in equivalent sample size % in the four measurement error models. The equivalent sample sizes of models 3 and 4 were indexed to the sample size of model 1 accounting for the smaller beta of the genetic parameter estimate due to the smaller contribution of tGFR. (B) Change in required sample size (=1/equivalent sample size)% from the four measurement error models.

Table I

GFR Measurement Error Models.

Model	Overall Measurement Errors	Systematic errors correlated	% tGFR variance explained by SNP	GFR Measurement Error Model Parameters (unobserved)				Estimates based on GFR Measurement Error Model Parameters				
				w_1^2	w_2^2	w_3^2	$\text{cov}(\epsilon_{Sij}, \epsilon_{Rjk})$	% of Var(Y _{ij}) explained by SNP	τ^2	σ^2	$\text{cov}(Y_{ij}, Y_{ik})$	
1	Less	No	0.5	0.7	0.2	0.1	0	0	0.35	0.69	0.30	0.70
2	Less	Yes	0.5	0.7	0.2	0.1	0.5	0	0.35	0.79	0.20	0.80
3	More	No	0.5	0.5	0.2	0.3	0	0	0.25	0.49	0.50	0.50
4	More	Yes	0.5	0.5	0.2	0.3	0.5	0	0.25	0.59	0.40	0.60

Notation and formula used:

w_1^2 , w_2^2 , and w_3^2 are the contributions of tGFR, systematic errors, and random errors to the variance of the outcome, Y_{ij}

% of Var(Y_{ij}) explained by SNP = % of tGFR variance explained by SNP * w_1^2

$\tau^2 = w_1^2 - \% \text{ of Var}(Y_{ij}) \text{ explained by SNP} + w_2^2 * \text{cov}(\epsilon_{Sij}, \epsilon_{Rjk})$

$\sigma^2 = w_2^2 * (1 - \text{cov}(\epsilon_{Sij}, \epsilon_{Rjk})) + \text{cov}(\epsilon_{Rij}, \epsilon_{Rjk})$

$\text{cov}(Y_{ij}, Y_{ik}) = w_1^2 + w_2^2 * \text{cov}(\epsilon_{Sij}, \epsilon_{Sjk})$