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A Covering Method for Detecting Genetic Associations between Rare Variants and Common Phenotypes

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Abstract

Genome wide association (GWA) studies, which test for association between common genetic markers and a disease phenotype, have shown varying degrees of success. While many factors could potentially confound GWA studies, we focus on the possibility that multiple, rare variants (RVs) may act in concert to influence disease etiology. Here, we describe an algorithm for RV analysis, RARECOVER. The algorithm combines a disparate collection of RVs with low effect and modest penetrance. Further, it does not require the rare variants be adjacent in location. Extensive simulations over a range of assumed penetrance and population attributable risk (PAR) values illustrate the power of our approach over other published methods, including the collapsing and weighted-collapsing strategies. To showcase the method, we apply RARECOVER to re-sequencing data from a cohort of 289 individuals at the extremes of Body Mass Index distribution (NCT00263042). Individual samples were re-sequenced at two genes, FAAH and MGLL, known to be involved in endocannabinoid metabolism (187Kbp for 148 obese and 150 controls). The RARECOVER analysis identifies exactly one significantly associated region in each gene, each about 5 Kbp in the upstream regulatory regions. The data suggests that the RVs help disrupt the expression of the two genes, leading to lowered metabolism of the corresponding cannabinoids. Overall, our results point to the power of including RVs in measuring genetic associations.

Introduction

The Common Disease, Common Variant (CDCV) hypothesis [1–3] postulates that the etiology of common diseases is mediated by commonly occurring genomic variants in a population. This has served as the basis for genome wide association (GWA) studies that test for association between individual genomic markers and the disease phenotype. Using genome-wide panels of common SNPs, GWA studies have been successful in identifying hundreds of statistically significant associations for many common diseases as well as several quantitative traits [4–7]. Nevertheless, the success of GWA studies has been mixed. Significant genetic loci have not been detected for several common diseases that are known to have a strong genetic component [4]. Additionally, for many common diseases, associations discovered in GWA studies can account for only a small fraction of the heritability of the disease. While many factors could potentially confound GWA studies, we focus on the possibility that multiple, rare variants may act in concert to influence disease etiology.

The alternative to the CDCV hypothesis, the ‘Common Disease, Rare Variant (CDRV)’ hypothesis has been the topic of much recent debate [8], and has shown promise in explaining disease etiology in multiple studies. For example, rare variants (RVs) have been implicated in reduced sterol absorption and, consequently, lower plasma levels of LDL [9,10] and colorectal cancer [11]. While some studies have shown RVs to increase risk, a recent study indicates that RVs also act ‘protectively’, with multiple RVs in renal salt handling genes showing association with reduced renal salt resorption and reduced risk of hypertension [12]. Additionally, rare mutations in IFIH1 have been shown to act protectively against type 1 diabetes [13].

The aforementioned studies and others focused on re-sequencing of the coding regions of candidate genes using Sanger sequencing (see Table 1 in Schork et al. [8] for a summary). Recent technological advances in DNA sequencing have made it possible to re-sequence large stretches of a genome in a cost-effective manner. This is enabling large-scale studies of the impact of RVs on complex diseases. However, several properties of rare variants make their genetic effects difficult to detect with current approaches. Bodmer and Bonilla provide an excellent review of the properties of RVs, and the differences between rare, and common variant analysis [14]. As an example, if a causal variant is rare ($10^{-4} \leq MAF \leq 10^{-1}$), and the disease is common, then the allele’s Population-Attributable-Risk (PAR), and consequently the odds-ratio (OR), will be low. Additionally, even highly penetrant RVs are
We focus on the problem of detecting multiple rare variants (RVs) that act together to influence disease phenotypes. In considering this problem, we argue that the detection of causal rare variants must necessarily be different from typical single-marker analysis used for common variants and propose a novel algorithm, RARECOVER, to accomplish this analysis. RARECOVER combines a disparate collection of RVs, each with very low effect and modest penetrance. Extensive simulations over a range of values for penetrance and population attributable risk (PAR) illustrate the power of our approach over other published methods, including the collapsing and weighted-sum strategies. To showcase the method, we applied RARECOVER to data from 289 individuals at the extremes of Body Mass Index distribution (NCT00263042), sequenced around the FAAH and MGLL genes. RARECOVER analysis identified exactly one significantly associated region in each gene, each about 5Kbp in the upstream regulatory regions. The data suggests that the RVs help disrupt the expression of the two genes leading to lowered metabolism of the corresponding endocannabinoids previously linked with obesity. Overall, our results point to the power of including RVs in measuring genetic associations, and suggest that whole genome, DNA sequencing-based association studies investigating RV effects are feasible.

Author Summary

We focus on the problem of detecting multiple rare variants (RVs) that act together to influence disease phenotypes. In considering this problem, we argue that the detection of causal rare variants must necessarily be different from typical single-marker analysis used for common variants and propose a novel algorithm, RARECOVER, to accomplish this analysis. RARECOVER combines a disparate collection of RVs, each with very low effect and modest penetrance. Extensive simulations over a range of values for penetrance and population attributable risk (PAR) illustrate the power of our approach over other published methods, including the collapsing and weighted-sum strategies. To showcase the method, we applied RARECOVER to data from 289 individuals at the extremes of Body Mass Index distribution (NCT00263042), sequenced around the FAAH and MGLL genes. RARECOVER analysis identified exactly one significantly associated region in each gene, each about 5Kbp in the upstream regulatory regions. The data suggests that the RVs help disrupt the expression of the two genes leading to lowered metabolism of the corresponding endocannabinoids previously linked with obesity. Overall, our results point to the power of including RVs in measuring genetic associations, and suggest that whole genome, DNA sequencing-based association studies investigating RV effects are feasible.
Methods

Modeling RV association

We define a locus as a genomic region of fixed size (nucleotides). Let $S$ denote the set of RVs in the locus. We abuse notation slightly by using $S$ to also denote the locus itself. A case-control study at $S$ includes a set of individual genotypes. For genotype $I$, and RV $x \in S$, let $I_x \in \{0, 1, 2\}$ denote the number of minor alleles that genotype $I$ carries for variant $x$. Extending the notation to subsets, $C \subseteq S$ of RVs, define $I_C = \sum_{x \in C} I_x$. For a subset $C \subseteq S$, denote a union-variant $A_C$ as follows: individual $I$ has the allele $A_C = 1$ if and only if $I_C > 0$. Otherwise, $A_C = 0$. The union-variant is a virtual construct that helps combine the effect of multiple RVs.

For an individual chosen at random, and $C \subseteq S$, let $X_{\text{corr}}(A_C, D)$ denote an association test statistic between the union-variant $A_C$ and the disease status $D$. Here, we will use Pearson’s $\chi^2$ as the test-statistic, but the method remains unchanged for other measures. Using this notation, the collapsing strategy described by Li and Leal [15] uses the test-statistic $X_{\text{corr}}(A_S, D)$ to associate a locus $S$ with the disease. Instead, we define the association statistic for locus $S$ by

$$X_{\text{corr}}(S, D) = \max_{C \subseteq S} X_{\text{corr}}(A_C, D) \quad (1)$$

The RareCover method

Our method, RareCover, accepts a locus containing a set $S$ of RVs in a window of fixed size (nucleotides). It returns the test-statistic, $X_{\text{corr}}(S, D)$, a $p$-value on the statistic, and the subset $C \subseteq S$ of RVs that contribute to the union variant. The window size $C \subseteq S$ is a parameter. When the input locus is larger than the window size, RareCover looks at overlapping windows of size $C \subseteq S$, where each window is shifted one RV away from the previous window. For each window, the $X_{\text{corr}}$ statistic is output, along with a non-adjusted $p$-value.

The computation for the $X_{\text{corr}}$ statistic on a single window is described in the Algorithm below. Given a set $S$ of RVs over $n$ individuals, the naive computation for computing $X_{\text{corr}}(S, D)$ needs $\sim n^2$ [28] computations. A reduction from the MAX-COVER problem can be used to show that the problem is NP-hard, indicating that no provably efficient algorithm is likely [28]. Similar reductions can also be used to show the hardness result for a variety of other proposed association statistics. Therefore, we employ a greedy heuristic that is fast ($\sim |S|n$ computations), and does well in practice. In each step, (see Algorithm), we select the variant that adds the most to the statistic, until no further improvement is possible. On a standard Linux workstation, the computation is fast, about 100 windows per second.

```plaintext
procedure RareCover $(S, Q)$
Set $C = \emptyset$, $u = \emptyset$
repeat
Set $C = C + \{u\}$
Select $C \in S - C$ that maximizes $X_{\text{corr}}(S_{C + \{u\}}, D)$
while $(X_{\text{corr}}(S_{C + \{u\}}, D) - X_{\text{corr}}(S_C, D) \geq Q)$
return $X_{\text{corr}}(S_C, D)$.

The RareCover method for detecting locus association. $C$ describes the current subset of ‘causal’ SNPs. Initially $C$ is empty. In each iteration, the RV $u$ that maximizes the test statistic is chosen, and added to $C$. When the improved statistic $X_{\text{corr}}(S_{C + \{u\}}, D)$ is not significantly better than the current statistic $(X_{\text{corr}}(S_C, D))$, the method stops, and outputs $C$.
```

Computing significance. While the test-statistic is a $\chi^2$ test on the union-variant $A_C$, significance cannot be computed directly, as $C$ is optimized over many possibilities. The multiple-tests will increase the statistic for non-associated loci as well. We compute significance by applying RareCover to permutations of the case-control genotypes.

The number of permuted trials required to achieve genome-wide significance can be large. We make the computation tractable using two ideas: first, empirical tests show that the $\chi^2$ statistic on $A_C$ correlates tightly with the permutation $p$-value (Figure 1). Note that the saturation at the end is due to limited trials. Let $t$ denote the value of $X_{\text{corr}}$ for a window, $S$. When $t$ is less than a pre-determined threshold $(\tau)$, no permutation test is done, as the window is unlikely to be significant. When $t \geq \tau$, the statistic is recomputed after permuting case and control labels (default 10^4 permutations), and a $p$-value is computed as the fraction of the permuted samples whose $X_{\text{corr}}$ value matches or exceeds $t$. To save time on this computation, we run permutations in a data-driven fashion. We run a maximum of 10^4 permutations, but stop as soon as we obtain 2 samples for which the RareCover statistic exceeds $t$.

$$p \text{-val}(t) = \begin{cases}
\frac{2}{k^2} & \text{if 2 samples match or exceed } t \\
10^{-14} & \text{otherwise}
\end{cases} \quad (2)$$

Both, the parameter $\tau$, and the maximum number of iterations can be adjusted, based on desired level of significance, and the size of the genomic region. Here, we set parameter $\tau = 20$, which corresponds to a permutation adjusted $p$-value of $10^{-15}$ in Figure 1. This ensures fast computation with no loss of power (See Results).

RareCover for genomic regions. RareCover can also be applied to a locus containing a single gene. The definition of a
gene varies; it sometimes includes only the coding exons, or it can include all exons including UTRs, and even regulatory regions. While the scanning window approach of RareCover can be applied unchanged for any genic locus, we must correct for multiple windows at a locus. Given a genic locus, we permute cases and controls multiple times and score every window in the locus. Then, the adjusted (locus) P-value of a window with "Xcorr" value t is the fraction of all permuted windows in the locus with an "Xcorr" score of t or higher.

**RareCover parameters.** RareCover is a model-free approach, and has only 2 parameters: the window size W, and a convergence cut-off Q (see procedure above). Empirical tests by simulation show that the performance is similar despite large variations in window size 5-10Kbp, as well as a choice of Q. Hence, no explicit training was performed, and the parameters were set to W=5Kbp, and Q=0.5. The performance of RareCover was extensively tested over a wide range of simulation parameters.

### Parameters for RV simulation

Consider a locus with a set S of rare-variants. Let a subset C of RVs be causal, in the sense that a mutation at any s ∈ C increases the likelihood of disease. For an individual, I, we use AC and A_C as short-forms of the events \( AC = 1 \) (or \( AC > 0 \)), and \( A_C = 0 \), respectively. Similarly, events \( D, \overline{D} \) reflect case-control status for the individual. We work with the following 3 parameters for power calculations:

1. **Disease prevalence** in the population, denoted by \( P_D \).
2. **Penetrance** of the locus, denoted by \( p = \Pr(D | A_C) \).
3. **Locus-PAR**, denoted by \( R = \Pr(A_C | D) \).

Note that the PAR for a variant is often described by the following (Ex: Bodmer and Bonilla, 1999 [14])

\[
R = \frac{K - y}{K} = 1 - \frac{y}{K} \tag{3}
\]

where \( K \) is the number of individuals with the phenotype, and \( y \) is the number of individuals that show the phenotype, but do not have the variant allele. In our terminology

\[
R = 1 - \frac{\Pr(\overline{A_C} \cap D)}{P_D} = 1 - \Pr(\overline{A_C} | D) = \Pr(A_C | D) \tag{3}
\]

The choice of these parameters is intuitive as we expect an RV to have moderate penetrance, but very low PAR (\( \Pr(A_C | D) \)). However, the multiple RVs in C have roughly additive effect, leading to moderate locus-PARs. These parameters are tightly related to other, more common measures of locus association, such as the Odds-Ratio (OR), as shown below:

\[
\text{OR}(S) = \frac{\Pr(D | A_C)}{\Pr(D | \overline{A_C})} = \frac{\rho}{1 - \rho} \frac{\Pr(D | \overline{A_C})}{\Pr(D | A_C)} \tag{3}
\]

To compute \( \Pr(D | A_C) \), we start with a Bayesian relation for computing the likelihood of a genotype containing a causal RV as

\[
\Pr(A_C) = \frac{\Pr(A_C | D) \Pr(D)}{\Pr(D | A_C)} = \frac{RP_D}{\rho} \tag{4}
\]

Then,

\[
\Pr(D | A_C) = \Pr(\overline{A_C} | D)P_B = \frac{(1 - R)P_D}{\Pr(\overline{A_C})} = \frac{(1 - R)P_D}{1 - \frac{RP_D}{\rho}} \tag{5}
\]

and,

\[
\Pr(D | \overline{A_C}) = 1 - \Pr(D | A_C). \tag{6}
\]

### Simulating constant sized populations (CP)

We simulate multiple case-control studies over a range \( P_D, \rho, R \). A simulation of \( N \) individuals begins with the division of the individuals into \( \frac{N}{2} \) cases and \( \frac{N}{2} \) controls. Once this is done two additional steps take place.

1. Generate a set of RVs for the simulated locus containing causal, and neutral RVs.
2. Simulate the genotypes for each individual.

We start by generating causal RVs. As RVs do not show high LD, we can model the population by generating each RV independently. We adapt Pritchard’s argument that the frequency distribution of rare, deleterious, RVs must follow Wright’s model under purifying selection [29]. Therefore, the allele frequencies \( p \) are sampled according to:

\[
f(p) = p^{\beta_S - 1} (1 - p)^{\beta_N - 1} e^{\sigma (1 - p)} \tag{7}
\]

where

- \( p \), allelic frequency
- \( \sigma \), selection coefficient
- \( \beta_S \), rate of mutation from normal allele to causal
- \( \beta_N \), rate of repair from causal allele to normal

We choose \( \sigma = 30.0, \beta_S = 0.2, \beta_N = 0.002 \) [29]. Note that we do not control the number of causal RVs, \( |C| \), directly, in our simulation. Recall that

\[
\Pr(A_C | D) = 1 - \Pr(\overline{A_C} | D) = 1 - \prod_{i \in C} \Pr(\overline{A_{(i)} | D})\tag{5}
\]

Further,

\[
\Pr(\overline{A_{(i)} | D}) = 1 - \Pr(A_{(i)} | D) = 1 - \frac{(\Pr(A_{(i)} | D)\Pr(D | A_{(i)}))}{\Pr(D)} \tag{7}
\]

Therefore, setting a value for R limits the size of the causal RV.

\[
R = \Pr(A_C | D) = 1 - \prod_{n \in C} \left( 1 - \frac{\rho_i P_D}{\rho} \right) \tag{8}
\]

Further, the sampling procedure occasionally generates SNPs with a high individual PAR. These variants would show up as being significant even with a single marker analysis. Therefore, these are discarded. The procedure SIMULATERV describes the method to generate causal RVs. To generate neutral RVs, we use Fu’s model of allele distributions [30] on a coalescent, which suggests that the number of mutations that affect \( i \) individuals in a population with mutation rate \( \theta \) is given by \( \theta/i \). For the purposes of our simulation we use \( \theta = 5.0 \).
Simulating genotypes

For both cases and controls, each RV is sampled independently. For non-causal variants \( s \in S - C \), the probability of picking a minor allele is \( \pi_s \), for both case and control individuals. To sample alleles from causal SNPs, recall that under the union model, \( \Pr(D|A_{(s)}) = \Pr(D|A_C) = \rho \) for all \( s \in C \). Therefore, the minor allele frequencies are given by

\[
\Pr(A_{(s)}|D) = \frac{\rho \pi_s}{P_D} \quad \Pr(A_{(s)}|\bar{D}) = \frac{(1-\rho)\pi_s}{(1-P_D)}
\]

We assume HW equilibrium to sample genotypes for case and control individuals.

Simulating populations with bottleneck and recent expansion (BRE)

Recently, Kryukov and colleagues [31] described a demographic model that explicitly models European ancestry. The population is assumed to be relatively stable for a long period, but is followed by a bottleneck, and rapid expansion after the bottleneck (about 7500–9000 years ago, with 20–25 years per generation). They validate their model by comparing observed versus predicted allelic frequencies. To this model, they add ‘causal’ (mostly deleterious) mutations using a distribution of selection coefficients from a gamma distribution. The causal alleles are associated with a change in a quantitative trait (QT). The QT values are normally distributed. Individuals carrying any causal mutation have QT values drawn from a Normal distribution with a shifted mean. For Rare variant analysis, individuals are chosen from the lower (Control) and upper (Case) tails of the QT distribution.

For our study, the authors provided us with individual genotypes simulated according to their demographic model, with causal mutations contributing to the following shifts: 0.125\( \sigma \) (Low), 0.25\( \sigma \) (Medium), 0.5\( \sigma \) (High). The highest and lowest 5%, and 10% of the QT distributions were used for the Case and Control populations. For the 5% population (500 controls, 500 cases), the locus PAR varied as 0.01–0.05. For the 10% populations, the number of individuals is larger (1000 controls, 1000 cases), but the PAR values decrease to 0.013 (Low), 0.017 (Medium), and 0.02 (High).

Reimplementing alternative strategies

For the purposes of comparison, we reimplemented the collapsing statistic proposed by Li and Leaf [15] as well as the weighted-sum statistic used by Madsen and Browning [16]. Both publications discuss the separation of variants into groups based upon function (i.e. non-synonymous coding SNPs) or other property. However, because we are performing our studies on model free, unannotated data, we do not perform any such grouping.

As a result, the CMC approach proposed by Li and Leaf [15] is equivalent to collapsing all variants in the locus and calculating the association. Li and Leaf show that the assignment of variants to functional groups, separately collapsing these groups, and finally performing a multivariate analysis improves power to detect causal loci. However, separation of variants into groups is inexact and the authors show that errors in group assignment can confound tests for significance. Additionally, performing this separation on a genome wide scale may be intractable.

The weighted-sum statistic proposed by Madsen and Browning [16] is used to detect association between a pre-defined group and a disease state. To compare fairly we defined the group of mutations as all mutations at a locus. We reimplemented the weighting approach based upon allele frequency as well as the sum and ranking approach to determine a score. Finally, we implemented a single-marker test as a bi-allelic \( \chi^2 \)-statistic with 1d.f. The tests were used to score windows over a wide range of simulation parameters to better understand how RARECOVER performed in comparison to the collapsing, and weighted strategies. For each strategy, a \( p \)-value of significance was established by doing 10\(^3\) randomized trials using permuted case and control data. All three methods were run on the same sets of permuted data, and the \( p \)-values were used to compare. Code for all methods is available upon request from the authors.

MSMB gene resequencing

Recently, Yeager and colleagues [32] resequenced a ~97Kbp region including the micro-seminoprotein-\( \beta \) (MSMB) gene (chr10:51, 168, 025–51, 265, 101) for 36 prostate cancer cases, 26 controls, plus another 8 CEPH individuals. While the number of individuals is too small to derive rare variants, we used the predicted genotypes supplied by the authors for RV analysis. For this analysis, we used 26 + 8 individuals together as controls, and all 284 variants with MAF < 5% were used as input to RARECOVER.

CRESCENDO data

In a recently submitted study 40 LR-PCR amplicons (Harmsen et al., unpublished) were used to re-sequence 31Kbp from the FAAH locus (NCBI36 chr1:46621328–46653043) and 157Kbp from the MGLL locus (NCBI36 chr3:128880456–129037011). A total of 289 individuals were selected for sequencing from two tails of the BMI distribution of the CRESCENDO cohort (http://clinicaltrials.gov/ct/show/NCT00263042). 147 individuals had BMI lower than 30 kg/m\(^2\) and 142 individuals a BMI greater than 40 kg/m\(^2\). DNA sequencing libraries were prepared, and sequenced as previously described in Harmsen, 2009 [33] with the following modifications: sequencing libraries were indexed by 4nt barcode located downstream of the adapter [34] and between one and six libraries were loaded per lane of the Illumina GAII instrument. The reads obtained from several lanes were merged, aligned and the variant called using MAQ mapmerger, map and cnsvview+SNPFilter options respectively [35]. All samples had an average coverage greater than 60 \( \times \). Allowing for a minimum coverage of 3 reads and a minimum base quality (Phred \( \geq 10 \)), a raw set of 1451 single nucleotides variants (SNVs) were identified in the population. The SNVs were filtered for Hardy Weinberg Equilibrium in the controls (\( p < 0.001 \)) and genotyping rate \( \geq 90\% \) of the samples to obtain a final set of 1393 SNVs (220 FAAH, 1173 MGLL). Of these, 165 + 935 = 1100 SNVs had MAF \( \leq 0.1 \), and were selected for RV analysis. The list and location of the RVs identified by RARECOVER as supporting the association is available in Supplemental Table S1.
Results

Simulations (CP)
We simulated cases and controls for a collection of sample sizes, ranging from \( n = 100 \) to over \( n = 5000 \) individuals with equal numbers of cases and controls. The MAF for rare variants ranged from \( 10^{-4} \) to \( 10^{-1} \). Throughout, we assume the disease prevalence in the population to be \( P_D = 0.05 \). The PAR for the locus was set to \( R \in \{0.1, 0.2\} \). The penetrance, \( \rho \) was varied in the interval \( [0.075, 0.25] \), corresponding to OR values of 1.6–7. The dependence on parameters is somewhat non-trivial. To see this, note that \( \frac{\rho}{P_D} \) is a lower bound on relative risk. Reducing \( P_D \) would increase the relative risk, only making association easier. In other words if the disease incidence is low, and a causal variant is low frequency, then the presence of the causal variant is a strong indicator of disease status.

The results of the simulation are shown in Figure 2. For each choice of parameters \( (\rho, R, \alpha, \gamma) \), 100 case-control studies were sampled as described in Methods. The data-set was tested using RARECOVER, collapsing, weighted-sum heuristics, as well as single-marker tests.

To enable a fair comparison, the 4 methods were applied to \( 3 \times 10^4 \) randomizations of the same data-set, obtained by permuting cases and controls. The \( p \)-value is similar to a False Discovery Rate calculation. The span of a typical human gene is about 10Kbp, and will contain about 100 rare-variants, implying fewer than 100 distinct windows per gene. If we assume 100 candidate genes for a phenotype, we would have \( 10^4 \) candidate windows. A \( p \)-value, or FDR of \( \times 10^{-4} \) could therefore be considered significant at the genome-wide level. A test score was considered significant if it was higher than each of the \( 3 \times 10^4 \) permutations, giving the 95% confidence interval of the \( p \)-value as \( [0, 0.0001] \). The power of a test for a specific choice of parameters is the fraction of (100) tests that had a significant score. Consider the sample point in Figure 2, with \( \rho = 0.25, R = 0.1 \), and a sample of 1280 individuals. The power of RARECOVER is over 96%, which can be contrasted with the low power of the weighted-sum [16], and collapsing heuristics. For any choice of parameters, RARECOVER shows better performance than the other methods.

Our phenotypic model differs somewhat from the one proposed by Madsen and Browning. In their model, the PAR for each causal variant is assumed to be equal, and is equal to the groupwise PAR divided by the number of causal variants. We also applied the tests to this model, using 1000 cases, and 1000 controls, and groupwise PAR values at 0.02, 0.1, 0.25. The power of the MB test at these values was computed to be 0.68, 1 respectively, while the power of RARECOVER on the data sets is 0.01, 0.975, 1 (Supplemental Figure S1).

An advantage of the RARECOVER approach is that it does not depend upon MAF, or the density of RVs in a region. This is partly because it combines the effects of multiple associating RVs that associate, and discards the RVs that do not associate. By contrast, other methods combine all RVs, albeit with different weights. While RARECOVER does not recover all of the causal RVs, it always recovered a significant subset of the causal RVs in our simulations. See Figure 3, which summarizes the results for \( \rho = 0.25, R = 0.1 \). Let \( C^* \) correspond to the simulated causal RVs, while \( C \) corresponds to the set returned by RARECOVER. Thus, \( \frac{|C \cap C^*|}{|C^*|} \) corresponds to the fraction of causal RVs recovered.

With modest sample size, more than 50% of the RVs are recovered, and help provide a direct interpretation of the genetic association. A somewhat unexpected aspect is that the number of causal RVs, \( \langle C^* \rangle \), and also, \( \langle C \rangle \) increases with an increasing sample size. For larger samples, we can recover a larger number of the low frequency variants, and the causal set has a larger mix of low frequency RVs. As we only consider RVs with MAF \( > 10^{-4} \), the number saturates by 10K individuals.

Simulated BRE populations
The 4 methods were also applied to the data sets provided by Kryukov et al., as explained in Methods. The cases and controls are chosen from the extremes of a population of 10,000 phenotyped individuals to reflect current population cohorts. As the locus PARs are very small (0.01–0.03), we work with a nominal
p-value cut-off of 0.01. As before, power is defined as the fraction of 1000 simulations on which the test met the p-value cut-off. In addition to the 4 methods, we also plot the power of the true causal mutations to illustrate their small effect.

Figure 4 shows the results upon choosing the 5%, and 10% extremes for different levels of phenotypic association. RARECOVER outperforms other methods over the different tests, and is comparable to the results of selecting the true causal mutations. As suggested previously, increasing PAR values, and population sizes, increase the power of RARECOVER, as with all methods. However, the power of RARECOVER does not appear to be affected by the specifics of the demographic simulation.

The allele frequency spectrum of the CP and BRE models is shown in Figure 5. There are significant differences in allele frequency spectra in the two cases. In the CP case, there is a bias in the cases among alleles with lower frequency. High frequency causal variants represent an easier case, as they can be detected by single marker analysis. To eliminate these cases, we discarded high frequency causal variants from the simulations, which partly explains the bias in CP, relative to BRE. In the CP (respectively, BRE) models, the average number of variants per 5Kbp window was 52.48 (respectively, 38.09), with 27.02 (respectively, 19.61) causal variants. The performance of RARECOVER is robust against different demographic models, and depends mainly upon locus PAR, and sample size.

Running time

The running time of RARECOVER increases linearly with the number of SNPs, and the number of individuals, as shown in Figure 6. For a population of 10,000 individuals, the running time goes from 80ms to 311ms on a standard Linux desktop, as the number of SNPs in the window increases from 10 to 50. The times shown here do not include the cost of reading and writing the data, which incurs a fixed additional cost (about 250ms. See Supplemental Figure S2). The total running time is at most 2× that of a single marker test.

On the FAAH data (289 individuals), the running time for a window of 5Kbp was computed to be 0.01 seconds. Consider a genome-wide scan with \( W_G \) windows. To achieve genome-wide significance, we would need \( 0.01W_G \) randomizations for each window, which could be computationally intensive.

However, we run RARECOVER in two passes, using the XCORR statistic on the union-variant as a filter (Figure 1). The permutation test is only applied to the fraction \( w < 1 \) of the \( W_G \) windows for which the XCORR statistic exceeds a threshold \( \text{Xcorr}(A_C, D) > t \).

Therefore the RARECOVER computation is executed on \( W_G + wW_G^2 \) windows. As discussed in the methods, \( W_G \approx 10^4 \). For \( w = 10^{-4.5} \) (corresponding to \( t = 20 \) in Figure 1), the total time is

\[
0.01(10^4 + 10^{0.5-10^4}) \approx 416s
\]

If the number of candidate windows is larger (\( W_G \approx 10^6 \)), and a conservative filter is chosen (corresponding to \( t = 25 \)), the running time increases to 90 hrs., easily accomplished on a small cluster.

Results on resequencing data

MSMB data. A RARECOVER analysis of the 284 variants did not identify anything significant. A 5Kbp window starting at chr10:51253758 has a nominal p-value of 0.06. The 9 SNPs selected by RARECOVER cover 12 cases and 0 control individuals. If we apply RARECOVER after including common variants, the same region has a nominal p-value of 0.002 due to a common variant that occurs in 26 cases, and 16 controls. This window lies not in MSMB but in a neighboring gene, NCOA4, also a candidate gene for prostate cancer risk [32]. A larger population sequencing will help resolve if this is a true association.

CRESCEUNDO cohort data. As described earlier, the CRESCEUNDO cohort subjects selected for sequencing were individuals at the extremes of BMI distribution. We applied RARECOVER to overlapping windows of length 5Kbp over the region (as described in Methods), to analyze the impact of RVs (For the purposes of comparison the performance of all methods can be seen in Supplemental Figure S4). The permutation based p-values for two genes are plotted in Figure 7. For both loci, we
found a single region of approximately \(5000\) bp, that was enriched in strongly associating variants.

The FAAH enzyme (1p33) is known to hydrolyze anandamide (AEA), and other fatty acid amides. The region with the most significant association, located \(\frac{1}{2}\) \(5705\)/C/C/C1/C1/C1 \(716\)/C/C1/C1/C1 upstream of the FAAH transcription start site (TSS), contains 31 RVs. RARECOVER selected a subset of 16 RVs, with a union-variant that appears in 23 cases, and 0 controls (nominal permutation \(p\)-value \(0.002\)). The locus specific \(p\)-value for the window is \(0.009\). Analyzing the locus for functional significance, the locus falls within a retroviral Long-Term-Repeat (LTR). Insertion of retroviral elements, followed by adaptation of the viral regulatory elements is a well known mechanism for gene regulation. A recent analysis of the FAAH core promoter (\(\pm 100\) bp upstream) in human T-cells identified a C/EBP site which (through a STAT3 tethering) mediated the leptin regulation of FAAH expression [36]. Surprisingly, the leptin mediated regulation of FAAH was observed in immune cells, but not a model of neuronal cells [37]. Our results suggest that an alternative regulatory region 1Kbp upstream of the TSS is disrupted by RVs in obese individuals. A scan for transcription factor binding sites reveals many relevant transcription factor binding sites, including one for C/EBP (data not shown).

The enzyme monoacylglycerol lipase (MGLL), encoded by the MGLL gene located on chromosome 3q21.3, is a presynaptic enzyme that hydrolyzes 2-arachidonoylglycerol (2-AG), the most abundant endocannabinoid found in the brain. The RARECOVER scan on 935 RVs identified a single window enriched with associated RVs. The window lies immediately upstream of the gene, suggesting that the causal RVs have a regulatory function. At the most significant locus (chr3: \(129030871\) – \(129035531\), upstream of MGLL TSS), 10 of 24 RVs were selected, with the union RV present in 36 cases, and 8 controls. While the nominal \(p\)-value is \(0.002\), the locus adjusted \(p\)-value is at the margin of significance, at \(0.05\). The locus contains a known LINE element and a promoter for RNA polymerase II. Mutations in this promoter could easily interfere with binding affinity for RNA Polymerase II and affect subsequent transcription/translation.

In our analysis, we only considered RVs (MAF \(\leq 0.1\)). Harismendy et al. have reported on the connection between common variant, and RV associations in a recently submitted study. Their
Figure 5. Allele frequency spectra in various demographic models. BRE refers to the simulation of population under bottleneck followed by recent expansion from Kryukov et al.; CP refers to the simulation under a constant population size. The allele frequencies in CP are biased toward rare variants in cases, while there is little bias in BRE. The performance of RARECOVER is robust to data sets with different allele frequency spectra.
doi:10.1371/journal.pcbi.1000954.g005

Figure 6. Running time of RARECOVER as a function of sample size, and number of SNPs. As RARECOVER is a greedy approach, the running time increases linearly with an increase in number of SNPs, and individuals. The running time shown here does not include the time for disk input and output of the data, which incurs a fixed additional cost of ~250ms to each run. The total running time is about twice that of single marker tests.
doi:10.1371/journal.pcbi.1000954.g006
results suggest that common variants do not identify significant associations in FAAH, but identify 2 regions with significantly associated SNPs at the MGLL locus. LD between the significant common variants and the MGLL union-variant is low, with the highest $r^2$ value of 0.29. This suggests that the rare and common variations might have independent, additive effects on the phenotype.

**Discussion**

We described a novel method for Rare variant analysis with greatly improved power of detecting associations, relative to other published methods. RareCover utilizes the specific properties of RVs as compared to common variants, and applies a greedy approach to picking a subset of RVs, that best associate with the phenotype. It is a natural extension of previous methods, which either collapsed all RVs at a locus, or collapsed them after weighting different SNPs differently. Our algorithm is similar in orientation to the greedy solutions for the combinatorial problems of identifying set-cover and test-cover (See for example, Lovasz [38]). However, it is specifically designed for case-control analysis. The power of the method is extensively analyzed against different values of locus PAR, penetrance, and sample size. RareCover easily outperforms other methods which group, and collapse SNPs. The weighting approaches are reasonable, given that most causal RVs have functional significance, and likely to have moderately high penetrance, which one would not expect in a non-causal RVs. However, a large number of non-causal RVs, even with small weights, can dilute the association of the causal RVs. Also, it is difficult to identify different groupings of RVs, and to set appropriate weights for different groups.

Our application of the method on the CRESCENDO individuals, generates plausible hypotheses on the role of FAAH and MGLL in of obesity. The genetic association of FAAH with obesity is interesting because many previous studies with common variants have failed in identifying significant associations. We investigated the hypothesis that allelic heterogeneity due to multiple RVs, influences the obesity phenotype. Second, the low LD between RVs and causal variants implies that if an RV is significantly associated, it is likely to have functional significance. Our simulations confirmed that RVs identified by RareCover were enriched in the causal RVs. In analyzing FAAH and MGLL, we identified exactly one small, functionally significant region, at each locus with significant association. This suggests that multiple rare variations help influence the regulation of the two genes. Recently, Sipe and colleagues collected metabolite expression levels on 8 metabolites from 96 severely obese subjects and 48 normal weight subjects [39]. Comparing against our FAAH data, we find that the levels of AEA (anandamide) are highest in obese individuals that carry an RV identified by RareCover, and lowest in individuals that are non-obese, and do not carry the causal RV. As FAAH helps metabolize AEA (anandamide), this result is consistent with the hypothesis of the RVs disrupting FAAH expression. The data on all metabolite expression will be published elsewhere (Harismendy et al., unpublished).

Nevertheless, our study also raises many methodological questions. Our approach is greedy, in that it selects the most discriminating RV at each step. Theoretically, it is possible that a collection of RVs, that are individually less discriminating, are jointly more strongly correlated. In that case, RareCover will not identify them. We implemented an approach based on simulated annealing to find an optimal subset of SNPs. However, in our simulations with the union model, the greedy method worked as well as the more complex optimization, and was significantly faster. Recall that in the simple Union model, the penetrance does not change upon inclusion of additional SNPs, but the PAR increases. Other, more complex models are possible. For example, we could have a threshold model, in which the penetrance increases with a minimum number of rare alleles. Or, we could
have additive models, where the penetrance increases as a function of the number of rare alleles. As more re-sequencing data becomes available, these will be the focus of additional investigation. A second issue is that our definition of a locus is set arbitrarily as a window of fixed length, much like in other methods. However, empirical tests with a small range of window-sizes did not significantly change the results. It is possible that a dynamic assignment of the size of the locus could increase power, but at the cost of additional computations.

In this study, we analyze only the rare variants. While the **RareCover** algorithm can work unchanged with rare and common variants, a correct test for power of such an approach would require a biological model that combines the effect of RV and common variants. It is hard to speculate on such models in the absence of empirical data. However, preliminary results on comparing common and rare variants at the MGLL locus suggest an independent, additive effect.

GWA studies have shown that identifying the genetic basis of disease depends upon many factors. For this reason, algorithms have been devised to deal with population substructure issues, epistatic interactions between loci, as well as rare variant analysis. Our results indicate that RV analysis is useful in many contexts, and novel methods may have to be developed to include the effect of RVs in all of the above.

## Supporting Information

### Figure S1

Madsen and Browning models. RareCover performance on the phenotypic models proposed by Madsen and Browning. In this model, the PAR for each causal variant is assumed to be equal, and is equal to the groupwise PAR divided by the number of causal variants. The power of RareCover and other methods is applied on populations with 1000 cases, and 1000 controls, and groupwise PAR values at 0.02, 0.1, and 0.25.

Found at: doi:10.1371/journal.pcbi.1000954.s001 (0.46 MB TIF)

### Figure S2

RareCover running time including I/O. Running time of RareCover as a function of number of individuals, and number of SNPs, including time for input and output of data. The time for input and output dominates when the number of individuals is less than 2000. Otherwise, the time increases linearly with an increase in number of SNPs, and number of individuals.

Found at: doi:10.1371/journal.pcbi.1000954.s002 (1.51 MB TIF)

### Figure S3

RareCover on MGLL. Performance of RareCover on MGLL. The most significant window (described by the box) appears upstream of the MGLL gene, near the promoter region.

Found at: doi:10.1371/journal.pcbi.1000954.s003 (0.55 MB TIF)

### Figure S4

Method comparison. Performance of RareCover the weighted-sum statistic, and collapsing on the FAAH and MGLL. Some peaks are replicated in only a subset of methods. RareCover is the only method that identifies a significant hit in a region in MGLL containing common variants associated with the disease phenotype. Common variants were excluded from this analysis.

Found at: doi:10.1371/journal.pcbi.1000954.s004 (1.62 MB TIF)

### Table S1

Detailed SNP information for the windows highlighted in Figure 3 and Figure S3. The columns indicate the SNP id, position, and relative risk of each SNP within the selected 5000 bp windows. Case Matches refers to the number of case samples that carry the SNP, and similarly for Control Matches. The worksheets containing raw data give the genotype at each SNP (0, 1, or 2) within each 5000 bp window as well as disease status. Individual ids have been removed.

Found at: doi:10.1371/journal.pcbi.1000954.s005 (0.15 MB XLS)

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## Author Contributions


## References


