[Title TBD]

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**Introduction**

There is increasing evidence that complex traits are impacted by both a small number of loci of large effect and also many sites of extremely small effect (Boyle et al. 2017). From this “omnigenic” model of many (or “all”) loci affecting a given trait, it follows that a given locus itself affects many traits to small effect, suggesting universal pleiotropy. Theoretical work has found that under universal pleiotropy, as the number of traits increases, adaptation becomes increasingly difficult, since mutations are likely to have deleterious side effects on other traits this is known as the “cost of complexity” (Orr 2000).

Despite this apparent complexity, there is substantial evidence that adaptive evolution, and in particular rapid adaptation, is a pervasive phenomenon (Messer & Petrov 2013; Colosimo et al. 2005; Hoekstra et al. 2006; Levy et al. 2015). How can populations possibly adapt to their environment despite this complex genetic architecture? There are two non-exclusive possibilities. The first possibility is that pleiotropy is limited. This can take on two possible forms: (1) mutations are modular and affect a small number of related traits or (2) mutations reflect “partial pleiotropy” (Lourenço et al. 2011), affecting a small number of traits, though these traits are unrelated. In either of these scenarios, rapid adaptation can proceed because there are enough mutations that have relatively limited side-effects. The second possibility, consistent with the idea of universal pleiotropy, is that mutations affect many traits, but only a small subset of these traits matter to fitness in the environment. Thus, adaptation is possible because few traits matter to fitness.

There have been many attempts to disentangle which of these models are more correct, which has produced a lot of scientific debate (Paaby & Rockman 2013). Moreover, with increasing technological advances, we have the ability to measure an increasingly large number of traits, including gene expression, proteomics, and morphology, and to understand the genetic basis of these traits using Genome Wide Association Studies and Quantitative Trait Locus mapping. However, merely measuring more traits and understanding their associated genetic variants does not get at the crux of the question regarding the ability for organisms and populations to adapt. It is not necessarily straightforward to group measured traits in such a way that makes them relevant to the process of adaptation. Perhaps even the important and relevant phenotypes are not yet measurable. Thus, a new conceptual approach is needed to understand the pleiotropy that matters to adaptation.

One common framework used to model and understand phenotypic evolution is Fisher’s Geometric model(Fisher 1930) (see Fig 1A). In this model, traits are represented by orthogonal axes in a *d*-dimensional space, with the number of dimensions, *d,* indicating the number of traits that have independent contribution to fitness. Organisms are represented by points in this space, with their position determined by their phenotype, the organism’s particular combination of trait values. The fitness of an organism in a particular environment is determined by a function of the organism’s position and the position of the optimum combination of traits in that particular environment (hereafter “the optimum”). Any such function can be considered, but typically a simple Gaussian function is assumed for mathematical convenience, and has some empirically-supported properties, including diminishing-returns epistasis (de Visser et al. 1999; Chou et al. 2011) (but see (Wiser et al. 2013)). Thus, evolution can be seen as proceeding through “adaptive walks” from an ancestral organism that occupies some location in phenotype space. Genetic mutations can cause phenotypic changes, moving the mutant to a new location in this space. If this new location is favored by the fitness function, then it may increase in frequency and give rise to additional mutations.

Using this general framework, estimating the number of independent traits needed to explain the behavior of adaptive mutants is equivalent for estimating the number of dimensions in Fisher’s model. Previous work has aimed to measure the dimensionality of this space for mutations in general (and more specifically deleterious mutations), rather than the dimensionality of adaptation. These studies primarily fall into three categories. One class of methods derives the dimensionality of the space from the distribution of fitness effects(Martin & Lenormand 2006) (Fig 1B). Assuming the ancestor is at the optimum, a Gaussian mutation distribution in phenotype space, and a multivariate Gaussian distribution for the fitness function, Martin and Lenormand (Martin & Lenormand 2006) derive the expected distribution of fitness effects (DFE) taking the form of a gamma distribution. One can then derive the effective dimensionality of the system utilizing the moments of the DFE. Using directed mutation and mutation-accumulation techniques, these methods find that phenotypic dimensionality is relatively low (less than three dimensions) for the model organisms considered.

A second class of methods uses drift load(Poon & Otto 2000; Tenaillon et al. 2007). These also assume that populations are relatively close to the optimum, but instead explicitly use distance from an optimum as a metric to quantify the phenotypic dimensionality. Intuitively, this is accomplished by observing that large populations are able to effectively purge most deleterious mutations. However, small populations are unable to remove mildly deleterious mutations that drift to fixation, thus carrying a “drift load”. Moreover, the number of such deleterious mutations available to a population can be worked out as a function of the number of phenotypic dimensions, assuming some mutation distribution. Combining these relationships, this class of methods can then observe the fitness of populations across a gradient of effective population sizes to estimate the effective number of phenotypic dimensions. From this set of measurements, researchers found that there were relatively many dimensions (more than five) for the organisms observed.

Attempting to reconcile the different measures of phenotypic dimensionally observed by the two classes of methods, Lourenco(Lourenço et al. 2011) conducted analysis that suggests that DFE approaches are downwardly biased by universal pleiotropy assumptions, and that methods using drift load are relatively insensitive to the pleiotropy of mutations. Lourenco proposes a model of “partial pleiotropy” to explain the observed differences, suggesting that single mutations only affect a small subset of traits, but that mutations altogether affect many traits.

A third class of methods utilizes datasets generated to study epistasis (Fig 1C). Assuming a Gaussian mutation distribution around the ancestor and additive effects of mutations in phenotype space, epistasis is expected to be reflected in the nonlinearity of the phenotype to fitness map. Previous studies have used the distribution of angles between pairs of mutations (Weinreich & Knies 2013) and approximate Bayesian computation(Blanquart & Bataillon 2016) on epistasis datasets to understand phenotypic dimensionality.

These approaches require the use of strict mathematical assumptions to derive tractable mathematical expressions and predictions. Most (if not all) of these assumptions are likely to be violated. It is unlikely that the ancestor is optimally fit, since adaptation is constantly proceeding (Wiser et al. 2013). Moreover, assuming additivity of mutants in phenotype is likely to be wrong. This is particularly clear in the extreme example of pairs of loss of function mutations in the same pathway. Finally, a local Gaussian distribution for mutations in phenotypic space is also unlikely loss of function mutations can drastically change the expression of proteins and thus move a cell’s phenotype very far from the initial set of phenotypes. Additionally, there have been calls for the use of partial pleiotropy in these models to reconcile conflicting conclusions by some of these studies(Lourenço et al. 2011; Bataillon & Bailey 2014).

Recent technological advances allow us to measure the fitness of many mutants with high precision in a high-throughput manner (Levy et al. 2015) and take an approach that removes the necessity for some of these assumptions. In particular, this allows for fitness measurements of a large collection of mutants in a range of conditions (Venkataram et al. 2016; Li et al. 2018). Our approach builds on the phenotypic intuition supplied by Fisher’s geometric model and takes advantage of this new technology by measuring this dimensionality using subtle environmental perturbations (Fig 1D). That is, we slightly change the environment that mutant linages grow in, and use precise measurements of their fitness relative to the ancestor to triangulate both the mutants and the optima that represent the optimal combination of phenotypes in a given environment. We find the space that best fits our data for each number of dimensions, and then evaluate which number of dimensions gives us the best ability to predict withheld data using cross validation.

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**Figure 1. Fisher’s geometric model and approaches to infer dimensionality. A.** In Fisher’s geometric model, traits have independent effects on fitness, and mutations are represented by vectors in phenotype space, where the new mutant genotype is represented by a new location. Fitness is determined by the distance from the optimum (denoted by gray circle). Thus, everything the same distance away from the origin as the ancestor is neutral (on dashed line), and everything closer is adaptive. **B.** Estimating the number of dimensions using the distribution of fitness effects assumes a fixed mutation distribution and that the ancestor is optimally fit. **C.** Estimating the number of dimensions using epistasis data assumes a mutation distribution and also that the effect of mutations on phenotype is additive, i.e. the vector representing a double mutation is the sum of the vectors of the subsequent single mutations. **D.** Our approach. We use subtle environmental perturbations to triangulate mutants and conditions. Relative fitness measurements give us information about the distance between a mutant and the condition’s optimum, relative to the distance between the ancestor and that optimum.

**Methods**

We consider an explicit model of phenotypic evolution based on Fisher’s Geometric Model (Fisher 1930). In this model, phenotypes are depicted as orthogonal axes in a *d*-dimensional space, with the number of dimensions, *d,* representing the number of traits possibly relevant in this space. Organisms are depicted as points in this *d*-dimensional space, with their position determined by the combination of phenotypes represented by that particular organism. An organism’s absolute fitness in a particular environment is determined by a function of its distance from an optimal phenotype.

Our implementation of the model makes some inherent assumptions about the fitness function that determines fitness in each environment. First, it assumes that each trait contributes independently to fitness in any given environment – this can be done by transforming the space if considering a single optimum (Martin & Lenormand 2006), but is not generally true if the interactions between traits differ between conditions. Second, each trait is rescaled such that they have equal effect on fitness in a given condition. We assume this scaling holds for all conditions.

*Simulation Methods*

To test our method for estimating the phenotypic space from fitness data, we perform a simulation study. First, we simulate data that fits our phenotypic model and then feed the corresponding data into our method to infer the phenotype space and number of fitness-relevant phenotypes. To do this, we simulate an n−dimensional phenotype space by randomly placing the ancestor on the surface of the n−ball of unit distance. Then, we randomly generate “mutants” by sampling uniformly within the n−ball, to simulate only adaptive mutations. Finally, we randomly sample locations for the optima for new conditions in a ball of smaller radius, to simulate subtle environmental perturbations. We now have a set of mutants and conditions, for which we can generate relative fitness data by calculating a fitness function on this phenotype space for each mutant in each condition. For simplicity and consistency with previous literature, we start with a Gaussian function of distance.

To keep our simulation data realistic, we also simulate Gaussian measurement noise to ensure our estimation can properly handle realistic levels of noise from fitness measurement studies (Venkataram et al. 2016).

*Estimation Methods*

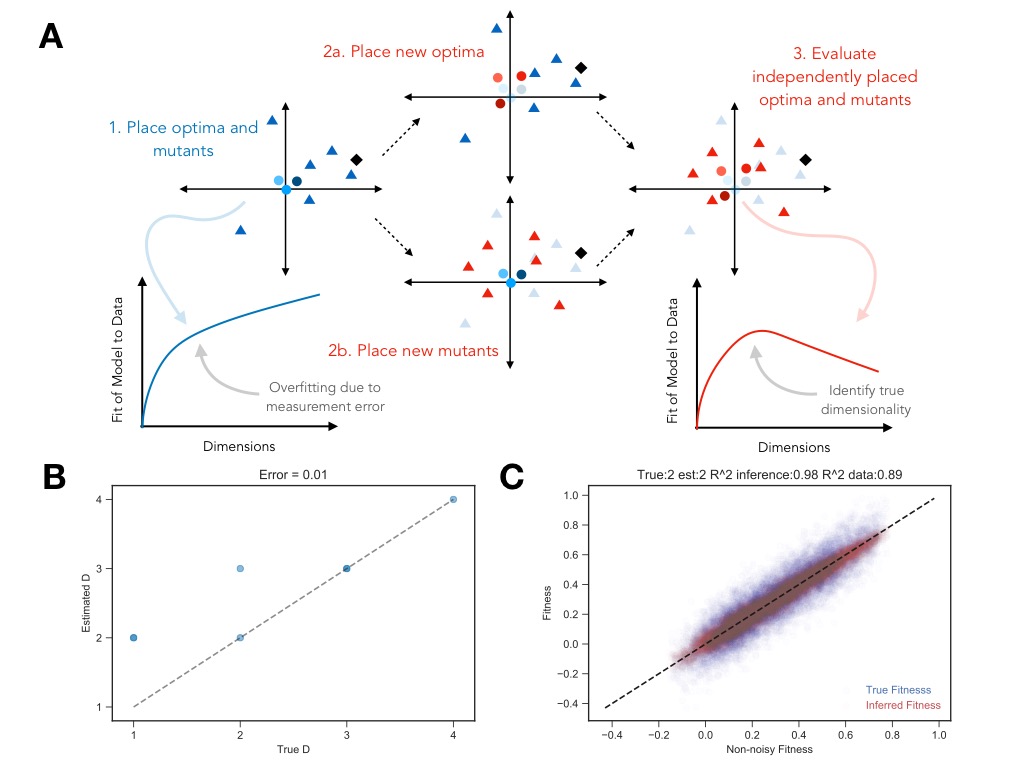
To infer the phenotypic space of our model from a set of mutants, we use an optimization technique on the relative fitness values of the set of mutants across subtle environmental perturbations. For a given number of traits *D*, we aim to find the positions of mutants, optima, and the ancestor that best fits our relative fitness data. We do this by finding the parameters that minimize the function:

where ,, and represent the locations of the mutants, optima, and ancestor, respectively. is the measured relative fitness of mutant in condition with a relative measure of the measurement uncertainty (see SI).

Using a global optimization technique to find the parameter values minimize this score for each number of dimensions,

To estimate the number of dimensions and avoid overfitting, we use a cross validation scheme (Fig 2). That is, we divide our data into 5 distinct sets (500 mutants into 5 groups of 100 and 60 conditions into 5 groups of 12). For each “fold” of the data, we exclude a set of mutants and conditions to use as a test set and first use the computational method to estimate the best space for the remaining set of data (See step 1 of Fig 2A.) for each value of D (the number of dimensions) we are interested in. If we were to only do this, we would expect the fit to continually increase as we increase the number of dimensions, because we will begin to fit measurement noise. Next, we fix this space and use only the locations of the original set of mutants as information to find the best location for the conditions in the test set (step 2a of Fig 2A), and separately, use the locations of the original set of conditions to find the best location for the mutants in the test set (step 2b). Finally, we evaluate the relative fitness values predicted from the estimated locations of the mutants and conditions in the test set that were placed independently (step 3). The model that has the best fit of the test set’s relative fitness values to the measured values is the correct number of dimensions that was not over-fit to the original data. This is repeated for each of the 5 test sets to ensure the best model prevails regardless of choice of test set.

**Results**



**Figure 2. Cross validation scheme and simulation results. A.** A representation of the cross validation scheme. First, we place a “training” set of optima and mutants in each d-dimensional space. Here, the fit of the model to the data will continuously increase as we add more dimensions. Second, we hold this space constant and place new optima using the information of the mutants in the training set and separately place new mutants using the optima in the training set. Finally, we evaluate the predicted fitness of the “test” set, which consists of the new, independently-placed optima and mutants. The fit of the model with the test set should decrease at some critical number of dimensions, representing where overfitting of the training set occurred, and serving as an estimate for the true underlying dimensionality. **B.** Comparison of the estimated dimensionality and true dimensionality across various simulations with simulated measurement error of (. **C.** Visualization of the fit of the model to true underlying simulated data compared to the “true” fitness with measurement error. Shown in red is the fit of the inferred fitness to the simulated data without noise (). Shown in blue is the fit of the true measured fitness with error to the simulated data without noise ().

*Result 1: In simplest cases, our method works*

*R1a: we capture the correct number of dimensions*

*R1b: we capture a reasonable space*

*R1c: we capture “true” fitness better than the simulated error*

Our computational method accurately estimates the true number of dimensions using this method (Fig 2B), particularly for a low number of dimensions in preliminary simulations. Moreover, it seems like our method, if anything, is prone to overestimating the number of dimensions, indicating that we should be confident that a result is an upper bound on the true underlying dimensionality.

In addition to our models estimating the true dimensionality of simulated data well, it is also able to accurately estimate the relative fitness of test data (Fig. 2C), fitting the underlying simulated data better than the noisy measurements passed into the model. This means that our cross validation scheme properly accounts for measurement error and finds the true underlying fitness values.

*Result 2: Sensitivity of our method to isotropy of selection and mutation*

The ability to detect the influence depends on the dispersion of mutants and optima in trait space, precision of measurement, and the combination of the two. If mutants and optima are less dispersed (mutants have similar phenotypes and conditions have subtle differences), then more precise measurements are needed (and vice versa). Because our model assumes that each trait contributes equally to fitness, traits that have lower contribution (in un-rescaled space) will also have the effect of lowering the dispersion of mutants in the dimension corresponding with that trait.

*[TBD] but 2a could be selection and 2b could be mutation. Maybe show some figure to explain rescaling in terms of fitness. Probably include something about measurement error in here (and how measurement error x anisotropy effect sensitivity)*

*Result 3: Identification of classes of mutations with outlier behavior*

Our method for inferring the space inherently relies on how the collection of mutants behave over a collection of conditions. How well can we detect the behavior of particular mutants and conditions? That is, is our method only good for inferring the commonalities but not particular behavior, and if so, how can we know that (and which) particular behaviors are not picked up?

*Result 4: Application to Hillenmeyer data?*

**Discussion**

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