**Improving Polygenic Risk Score Prediction by Phenotype-Agnostic Dimensionality Reduction**

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**Abstract**

**Motivation:** The progress in sequencing technologies enables early detection of genetic diseases and the development of personalized medicine. The missing heritability problem stands that the variance explained by genetic variation is typically small compared to family-based heritability estimates. As such, it is highly desirable to develop improved models for polygenic risk score (PRS) prediction.

**Results:** In this study, we propose a new approach for computing PRS that enlarges the heritability variance explained of complex traits. Our method is not limited to an additive model and can incorporate high-dimensional genomic interaction. We used a two stages approach. The first stage is a phenotypic-agnostic, an unsupervised approach to dimensionality reduction. The second stage is training a prediction model using a supervised machine learning algorithm. Our approach enables to compute PRS without the need for variables selection techniques, whereas maintaining a computationally feasible model. Moreover, the first stage, which is computational resource intense, is independent of phenotype, i.e., its output can be used as an input for a prediction model for any chosen trait or disease, and therefore can be trained only once. We evaluated the approach using two dimensionality reduction models, Deep Autoencoder and Principal Component Analysis, and two phenotype prediction models, Deep Neural Network and Extreme Gradient Boosting. The models were trained using the UK Biobank dataset with over 340K subjects and 460K SNPs. Moreover, we evaluated the approach on two phenotypes, height, and hypertension, and compared the results to the PRS baseline model. Our model results outperform the base model results in both phenotypes.

**Availability and Implementation:** The data underlying this article were provided by the UK Biobank under license. Data will be shared on request via application to the UK Biobank. The trained dimensionality reduction models are now available in: <https://github.com/nadavlab/genotyping_dimensionality_reduction>

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**Supplementary Information:** [Supplementary data](https://oup.silverchair-cdn.com/oup/backfile/Content_public/Journal/bioinformatics/38/18/10.1093_bioinformatics_btac509/1/btac509_supplementary_data.zip?Expires=1666304004&Signature=kaWls9~M7-tR~XNhc6YICdilYArrxJx1TAFz2rowZ5~cZfaw~3aEc44idxqRodIZJ7BgA0Yevihnzwo6Rmc0H17oXdRDI6dXuCKEOElhU1p0Uf5sSa5ZvD~Nq-qqkR0FVriazbn2XaaHzsfej7GL9P3CJlFpzPb1CWyqzPSVE7lDaebJCtLWpcQ7lRp9zlbpI-wIF9nHvZXMaXuMauPyoFbmGw5UdWASB4DuyJbFA6ba6OrUzq7ht~lQkooMSLvBwrpcZ3YjffjYMrcrImV3RuqyocU8D8JSHCEIE55vTwwURfra~9HLodlrlGi1tIqtlo0F1Gc32d-XPkq9GJgCMQ__&Key-Pair-Id=APKAIE5G5CRDK6RD3PGA) are available in the [Supplementary\_Data](https://oup.silverchair-cdn.com/oup/backfile/Content_public/Journal/bioinformatics/38/18/10.1093_bioinformatics_btac509/1/btac509_supplementary_data.zip?Expires=1666304004&Signature=kaWls9~M7-tR~XNhc6YICdilYArrxJx1TAFz2rowZ5~cZfaw~3aEc44idxqRodIZJ7BgA0Yevihnzwo6Rmc0H17oXdRDI6dXuCKEOElhU1p0Uf5sSa5ZvD~Nq-qqkR0FVriazbn2XaaHzsfej7GL9P3CJlFpzPb1CWyqzPSVE7lDaebJCtLWpcQ7lRp9zlbpI-wIF9nHvZXMaXuMauPyoFbmGw5UdWASB4DuyJbFA6ba6OrUzq7ht~lQkooMSLvBwrpcZ3YjffjYMrcrImV3RuqyocU8D8JSHCEIE55vTwwURfra~9HLodlrlGi1tIqtlo0F1Gc32d-XPkq9GJgCMQ__&Key-Pair-Id=APKAIE5G5CRDK6RD3PGA).docx file.

**Keywords:** UK Biobank; Polygenic Risk Score; Machine Learning; Dimensionality Reduction; Population Genetics

**Introduction**

In recent years, much has been said about the difficulty in finding the full heritability variance of a trait (Maher, 2008; Manolio *et al.*, 2009). Genome‐Wide Association Studies (GWAS) (Collins *et al.*, 1998) attempt to identify genetic loci associated with a complex trait by ranking the loci by statistical significance (p-values) of association with the trait. The most widely tested markers in GWAS are single nucleotide polymorphisms (SNPs), which are genetic variations of a single base pair that show natural variation in the population (Collins *et al.*, 1998; Lewis and Knight, 2012).

The identification of top-ranking SNPs with trait association has led to new types of models that predict polygenic risk scores (PRS). PRS method aggregates information from SNPs across the genome, by weighted the sum of the trait-associated alleles, into a single score that can be used as a trait value or disease risk prediction per subject (Euesden *et al.*, 2015; Torkamani *et al.*, 2018; Yanes *et al.*, 2020; Collister *et al.*, 2022). The growth and progress in sequencing technologies in recent years have resulted in enabling the early detection of genetic diseases and the development of personalized medicine strategies (Chatterjee *et al.*, 2016; Torkamani *et al.*, 2018).

However, it was found that the genetic variation explained by the trait-associated SNPs does not match the expectation from previous family studies. That is, only a small fraction of the genetic risk can be explained by those identified SNPs (van der Sluis *et al.*, 2010). For example, for height phenotype, more than 80% of the variation within a population is attributable to additive genetic factors, but previous studies were able to find only a small fraction of this variation (Visscher *et al.*, 2006). This problem is called the "missing heritability" and has been studied in recent years (Maher, 2008; Manolio *et al.*, 2009).

Firstly, it has been shown that some factors can substantially influence the power of PRS prediction. Association testing's power is directly affected by the sample size of the data which served as a base to identify statistical significance SNPs, the effect size weighting methods, and the selection of the p-value threshold for including in the PRS calculation (Dudbridge, 2013; Chatterjee *et al.*, 2013).

Secondly, the main limitation of standard PRS, is that it assumes independence between SNPs, i.e., trait-associated SNPs are mostly discovered using single-locus analysis, where variants are evaluated individually for association with phenotypes. In this type of analysis, factors with interaction effects but no marginal effects will not include in the PRS calculation (Culverhouse *et al.*, 2002; Moore, 2003). Thus, PRS will exclude a single locus with miscorrelation to the phenotype. While in recent years much has been discussed about an increase in the heritability variance of a phenotype when combining them within gene-gene interaction technique (Culverhouse *et al.*, 2002; Moore, 2003; Lehner, 2007; Cordell, 2009; McKinney and Pajewski, 2012).

However, there is a big challenge when combining gene-gene interaction. In the phase of detecting factors that display interaction effects, a major challenge could be the limited sample size compared to the huge amount of genetic loci, and the computational capacity needed for that. For complex diseases, we might also expect not only two-locus interactions but higher-level interactions (multilocus genotype combinations). This will lead to additional challenges such as the huge amount of parameters of the models, and to accurately estimate these parameters, extremely large data sets would be required (Cordell, 2009).

Regression-based methods are widespread data-mining methods for detecting gene–gene interactions (Cordell, 2009) and for the prediction of complex traits (Makowsky *et al.*, 2011; Dudbridge, 2013; Khera *et al.*, 2018; Lello *et al.*, 2019). For example, the Plink tool (Purcell *et al.*, 2007), which provides an option to assume an allelic model for both the main effects and the interactions, using a regression model. Regression-based methods were criticized due to their inability to deal with a high-dimensional dataset that may contain multilocus genotype combinations, nonlinear problems, and sparse data and therefore were replaced by more sophisticated machine-learning models (Moore and Williams, 2002; McKinney *et al.*, 2006; Cordell, 2009).

Artificial Neural Networks (ANNs) have become practical data mining models in the study of associations between genomic data and complex phenotypes, because of their capability of learning linear as well as nonlinear phenotype-genotype relationships. Moreover, these models can also take into account gene-gene interactions in addition to the main effects (McKinney *et al.*, 2006; González-Recio *et al.*, 2014). Not only that ANN models do not rely on most of the prior assumptions that underlie parametric models, but also, they can capture complex signals from the data and deliver better predictive accuracy (Ehret *et al.*, 2015).

As large genomic datasets accumulate, it is now possible to train even deeper and more complex models to gain insights and perform difficult genomic tasks (Danilevsky and Shomron, 2021). However, due to the ANNs' lack of interpretability, one of their limitations is that such models usually do not use for inferring the effects of SNPs on phenotypes. In high-dimensional genomic data, ANNs typically have more parameters (weights) than samples, and they may be too computationally demanding when the number of neurons is large (Ehret *et al.*, 2015).  Moreover, one of their limitations is that they require a sample size larger than the number of features, and may even require a sample size in the range of the number of features squared (Hua *et al.*, 2005; Figueroa *et al.*, 2012).

Therefore, many studies used variable selection techniques in which only subsets of SNPs are used as predictors (Ehret *et al.*, 2015; Bellot *et al.*, 2018; Peng *et al.*, 2021). While other studies demonstrated that traits are influenced by both common and rare SNPs with small effects (Gibson, 2012). Such a feature selection is performed using prior knowledge, for example selecting only SNPs in proximity to genes that are suspected to be related or associated with the phenotype of interest. Another approach for SNPs subsetting is to select only SNPs with a direct effect on the phenotype (Thomas *et al.*, 2020).

In the field of genetics, autoencoder, which is a type of [ANN](https://en.wikipedia.org/wiki/Artificial_neural_network), can be used to reduce the gene space by combining multilocus genotypes into a smaller number of variables (Xie *et al.*, 2017). Part of its advantages is that it is a nonparametric model, i.e. no hypothesis about the value of a statistical parameter is made, and it is free of any assumed genetic model.

Another family of models, which are not based on Neural Networks architecture, that may capture non-linear interactions between loci are Random Forest (RF), Gradient Boosted Trees (GBT), and Extreme Gradient Boosting (XGBoost). These algorithms have been used in the genetic analysis of complex diseases because of their capability to combine different predictors sequentially, i.e. taking into account interaction structures in the data (Goldstein *et al.*, 2010; Chen and Ishwaran, 2012; Paré *et al.*, 2017; Romagnoni *et al.*, 2019; Thomas *et al.*, 2020; Bracher-Smith *et al.*, 2022). The advantage of boosting algorithms is that they can facilitate the drawbacks associated with large datasets. Previous genome-wide studies have shown that such models can perform better than linear methods and deliver better predictive accuracy (González-Recio and Forni, 2011; González-Recio *et al.*, 2013).

Boosting models iteratively learn from residual estimates from previous estimators. As iterations increase, the selected SNP should contribute less at each iteration. Moreover, this model performs variable selection, as some SNPs may not be selected at all (González-Recio *et al.*, 2014). In high-dimensional data such as genomic data, some suggested methods subset features even before applying machine-learning algorithms (Romagnoni *et al.*, 2019). However, previous works have shown that a model using the entire genome had better predictive performance than a model that selects features first. The reason for the lower performance of such models is that when SNPs are excluded from the model, a substantial amount of information may be lost, and that cannot be compensated (Thomas *et al.*, 2020).

**Materials and Methods**

**Phenotype and Genotype Data**

In this study, we used the UK Biobank data (Allen *et al.*, 2014) with 487,409 samples and 93,095,623 SNPs from the imputed data set. In addition, clinical and physiologic phenotypes including height and hypertension, and socio-demographic covariates including age (Data-Field 21003), ethnic group (Data-Field 22006), sex (Data-Field 22001), genotype measurement batch (Data-Field 22000), and the center where the patient's examination was performed (Data-Field 54). In contrast to other UK Biobank PRS studies, we did not use the 40 PCA variables (Data-Field 22009) which were calculated by the UK Biobank based on all the data set due to information leakage concerns.

**Preprocessing**

Quality control was implemented on participants and SNPs using Plink2 tool (Purcell *et al.*, 2007). SNPs’ quality control was performed by eliminating variants with duplicate ID, missing values (keep only genotyped SNPs with a dosage of 0, 1, or 2), variants that deviate from Hardy–Weinberg equilibrium (HWE) by p-value < 1e-6, and variants with minor allele frequency (MAF) < 0.001. SNPs quality control operations were carried out in the order of mention, according to the default Plink2 order. Subjects’ quality control was performed by eliminating family-related subjects as described in (Sheppard *et al.*, 2021). In addition, we used only subjects from those that were European Caucasians ancestry to prevent population stratification (Lewis and Knight, 2012).

SNPs were coded as 0,1,2 for homozygote for the minor allele, heterozygote, and homozygote for the alternative allele, assuming additive allele effects. The samples were randomly split into 85% training set and 15% test set. From the training set, 1000 random samples were taken to serve as the validation set. We chose a relatively low validation set size because we wanted to maximize the number of samples on which the model can be trained. Such a large dataset in high dimension, could not be loaded to memory at once. Therefore, we decided to split the data into chunks of 1,000 samples each. We used iterative algorithms such that in each iteration the model was updated based on a batch of 1,000 samples.

**Phenotypes**

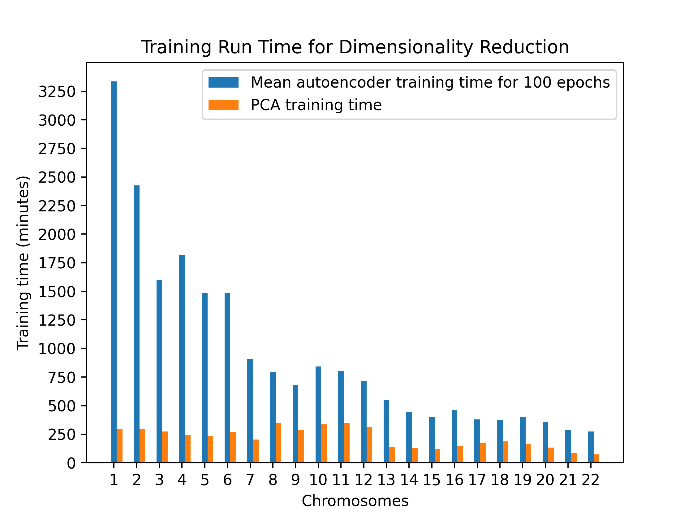
To examine the quality of the complex trait prediction models, we used two phenotypes, one quantitative and one binary trait. Height is a continuous trait, highly heritable, and classic polygenic trait (Lango Allen *et al.*, 2010). Hypertension was used as a binary trait, as it is a common disease that has a complex multifactorial etiology (Moore and Williams, 2002).

The new variables after dimensionality reduction, which were used as an input for the trait prediction model, were min-max normalized to be between zero and one. The trait prediction model was adjusted using the covariates listed above. We used the socio-demographic categorical features: sex, genotype measurement batch, and the patient's assessment center as dummy variables. Age was min-max normalized to be between zero and one. In addition, for each model, we also filtered samples that had a missing value for the phenotype of interest.

**Dimensionality Reduction**

For the dimensionality reduction process, we have trained separate dimensionality reduction models for each of the 22 chromosomes (without the sex chromosomes) due to the existing resource limit. We have used two models: Deep Auotoencoder (autoencoder) (Rumelhart *et al.*, 1985) and Principal Component Analysis (PCA) (Hotelling, 1933). Other dimensionality reduction alternative methods exist, like Truncated Singular Value Decomposition (SVD) (Golub and Reinsch, 1971) and Lsomap (Tenenbaum *et al.*, 2000), and can be easily adapted. However, we chose the two mentioned as they are broadly used and can be trained using an iterative process using batch processing. We have chosen to reduce the dimension of the SNPs to 10% of the input SNPs amount in each chromosome, a percentage that is adjusted to the computational power available resources and allows the union later on of the variables from all the chromosomes for the prediction model. For the autotencoder this was achived by setting the number of neurons in the encoding layer to 10% of the input SNPs amount. For PCA, we used the first 10% prinicpal components.

The dimensionality reduction phase is independent of phenotype, i.e. training does not require labels and its output can be used as an input for any type of prediction model and any chosen trait or disease. The dimensionality reduction models were evaluated using the validation set according to the coefficient of determination metric (see evaluation metrics section). The training run time of the dimensionality reduction phase is shown in Figure 1.



**Figure 1. Training running times of the dimension reduction models (in minutes).** For the autoencoder model, the times shown are the average running time per 100 epochs for the 600 epochs that the model was trained.

We have trained a fully connected autoencoder model with TensorFlow Python package (Abadi *et al.*, 2016). Each chromosome’s autoencoder was designed as an encoder with two hidden layers when the second one being the feature compress layer (bottleneck), and a decoder with one hidden layer. We have chosen to add dropout layers to prevent overfitting, and because this technique is known for its ability to efficiently combine many different neural network architectures (Srivastava *et al.*, 2014). Each hidden layer had a dropout layer with a rate of 0.1, except for the bottleneck. The number of neurons in each hidden layer was 20%, 10%, and 20% of the input SNP amount respectively. We have done a hyperparameters tunning using the validation set for the activation functions and for the learning rate, where the best configuration was chosen according to the RMSE metric. The tuning was done on chromosome 22, assuming that the training on the other chromosomes will behave similarly and due to the long-running times. We trained our model using the Adam optimizer (Kingma and Ba, 2014), MSE loss function, with a batch size of 250 over 600 epochs. The chosen activation functions were PReLU (He *et al.*, 2015) for the hidden layers and linear for the output layer, and the best learning rate was 1e-5.

The second method for dimensionality reduction we used was PCA implemented by Scikit-learn package in Python (Pedregosa *et al.*, 2011). We projected the SNPs data of each individual in each chromosome using the first 10% principle components.

**Phenotype Prediction**

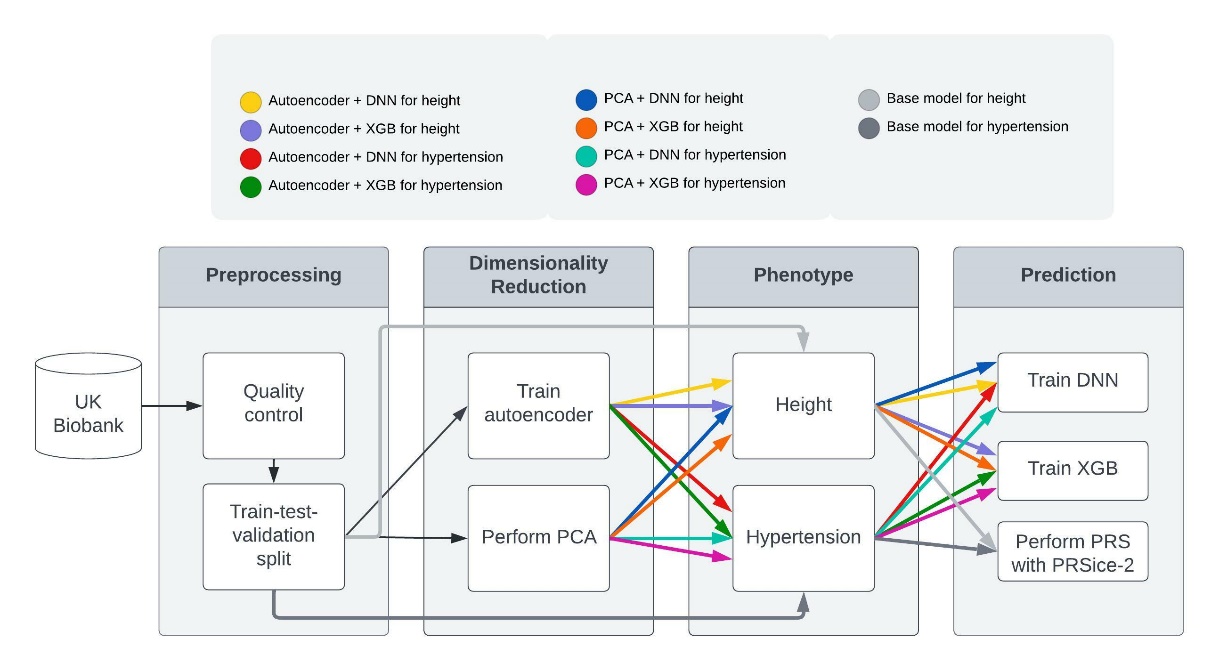
We concatenated the new representations of each chromosome and adjusted them to the covariates matrix. The combined dataset was used as the input for the phenotype prediction model. We have used two models for prediction: Deep Neural Network (DNN) (Werbos, 1982) and XGBoost (XGB) (Chen and He, 2015; Chen and Guestrin, 2016) since they can be trained using an iterative process and following the advantages discussed in the introduction section. We have trained the two prediction models for each phenotype and input variables driven by different dimensionality reduction models separately (see Figure 2). Each model has its hyperparameters tuned, where the best configuration (Table 1) was chosen using the validation set according to the RMSE metric for height and Log-loss metric for hypertension. Then the models were evaluated on the test set by different evaluation metrics. The training running times of the different models are shown in Table 2 (see resources section for information about the resources consumed).

**Table 1.** **Best configurations.** For each model, the chosen configuration is based on hyperparameters tuning. The best configuration was chosen using the validation set according to the RMSE metric for height and Log-loss metric for hypertension.

|  |  |  |  |
| --- | --- | --- | --- |
| Phenotype | Configuration | Hyperparameter tuned | Chosen hyperparameter value |
| Height | Autoencoder + DNN | DNN hidden layers' activation function | Relu |
| PCA + DNN | DNN hidden layers' activation function | Prelu |
| Autoencoder + XGB | Tree's max depth | 5 |
| PCA + XGB | Tree's max depth | 5 |
| Hypertension | Autoencoder + DNN | DNN hidden layers' activation function | Prelu |
| PCA + DNN | DNN hidden layers' activation function | Prelu |
| Autoencoder + XGB | Tree's max depth | 2 |
| PCA + XGB | Tree's max depth | 2 |

**Table 2.** **Training running times of the trait prediction models in minutes.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **PCA** | | **Autoencoder** | | **Dimensionality Reduction model** |
| **XGB** | **DNN** | **XGB** | **DNN** | **Prediction model** |
| 1958 | 1924 | 1776 | 1892 | Height |
| 537 | 2474 | 692 | 2021 | Hypertension |



**Figure 2.** **A schematic overview of the study’s framework.** The dimensionality reduction phase was independent of the phenotype, i.e., its output can be used as an input for any type of prediction model and any trait or disease. Therefore, it can be trained only once. Then, we trained and compared multiple pipelines for height and hypertension phenotypes prediction. Note that the dimensionality reduction phase was trained for each chromosome separately. Then, the variables from all chromosomes were merged, adjusted to the covariate matrix, and used as input for the prediction models.

We have trained a fully connected DNN model with TensorFlow Python (Abadi *et al.*, 2016). The network was designed with two hidden layers and each hidden layer had a dropout layer with a rate of 0.1. The number of neurons in each hidden layer was 20% and 10% of the input variables amount respectively. We have tuned the hidden layers' activation function for each model (Table 1), and we have chosen a linear output layer's activation function for height and sigmoid for hypertension. We trained our model using the Adam optimizer (Kingma and Ba, 2014) with a batch size of 50 over 80 epochs. The learning rate used was 1e-7 and the loss function was MSE for height and binary-cross-entropy for hypertension.

For the second prediction model, we have trained XGB model with xgboost Python package. XGB can be used for regression for height as well as for classification for hypertension. We have trained the model in batch processing using the "xgb\_model" parameter which allows training continuation. For each batch of 1000 samples, the model built one gradient boosted tree, using a 0.2 subsample ratio of columns and a 0.01 minimum loss reduction required to make a further partition on a leaf node. We tuned the maximal depth of the tree for each model separately (Table 1), and we trained our model for 20 epochs for hypertension and 40 epochs for height prediction until convergence. The learning rate used was 1e-3 and the evaluation metric was RMSE for height and binary-cross-entropy for hypertension.

**The Base Model, Phenotype Prediction using PRSice-2**

The base model was executed for each phenotype separately on the original SNPs, before the dimensionality reduction process (see Figure 2). First, we performed GWAS (Collins *et al.*, 1998; Marees *et al.*, 2018) using Plink2 tool (Purcell *et al.*, 2007) on the training set. In this method, trait-associated SNPs are discovered using single-locus analysis, where each variant, adjusted to the covariate, is evaluated individually for association with a phenotype.

Then, we performed PRS analyses (Choi *et al.*, 2020; Collister *et al.*, 2022) using PRSice-2 software (Choi and O’Reilly, 2019). In the classic PRS calculation method, only SNPs with a GWAS association p-value below a certain threshold are included in the calculation. The PRSice-2 software searches for a p-value threshold that generates the PRS best-fit which maximizes the phenotypic variation. In order to compute PRS we have used the training set and omitted SNPs that had constant dosage. Additionally, the p-value and the coefficients obtained from GWAS results for each SNP. Consider SNPs with a p-value smaller than the tested threshold, , a list of the number of the effective allele observed for each SNP, assuming an additive model. Additionally, a list of the regression coefficients for height and log-odds ratio for hypertension , the PRS is computed as follows:

Then, to adjust the PRS to the covariate matrix, we trained a linear regression for height and logistic regression for hypertension using Scikit-learn package in Python (Pedregosa *et al.*, 2011). The predictors were the PRS obtained from the PRSice-2 software and the covariate matrix. The model was evaluated on the test set by the same metrics mentioned above and compared to the new approach we suggest.

**Evaluation Metrics**

For evaluating and comparing the conserved information of dimensionality reduction models, we compare the correct SNPs values and the reconstructed SNPs values obtained from the decoder models. We did that using the coefficient of determination (R2) metric, calculated using the weighted variance aggregation, implemented by Scikit-learn package in Python (Pedregosa *et al.*, 2011).

For evaluating and comparing the different algorithms for complex trait prediction we have chosen the metrics according to the type of phenotype. For height, a quantitative phenotype, we have used R2 and Root Mean Square Error (RMSE). Consider samples, a list of correct values , and a list of predicted values obtained from the estimated model , the RMSE is calculated as follows:

The R2 is calculated as follows:

For hypertension, a binary phenotype, with unequal distribution between the two classes, we have used the Average Precision metric. Since the ratio between the number of samples in the different classes was 23%-77%, and to compare the results on a range of metrics, we also used for evaluation Area Under the Receiver Operating Characteristics (ROC AUC) and Cross Entropy Loss (Log Loss) metrics. Consider samples, a list of estimated probabilities obtained from the estimation model and a list of correct values , the Log Loss is calculated as follows:

Considering optional threshold, the Average Precision is calculated as follows:

Whereas Precision is the proportion of the true positive samples of the overall predicted positive observations and recall, is the portion of the true positive samples from the overall predicted negative observations.

**Resources**

The training of the prediction models was made on a high-performance computing cluster. For the DNN prediction models, we used an Intel Xeon Silver 4214 CPU @ 2.20GHzp processor and Nvidia's RTX-2080 GPU. We allocated for each DNN model a job with 6 hyper-threading and 80G RAM. For the XGB prediction models, we used an AMD EPYC 7702P 64-Core CPU. We allocated for each XGB model a job using 4 hyper-threading and 15G RAM.

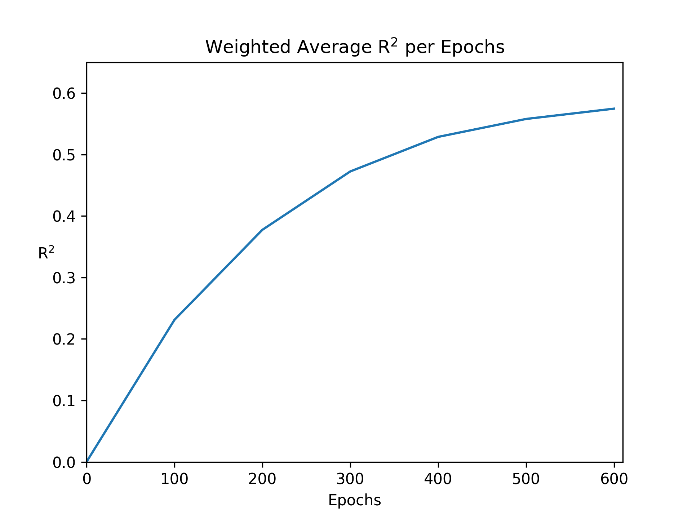
**Results**

**Preprocessing Results**

After quality control, 341,985 samples and 467,429 SNPs were used in the analyses (see supplementary table S2). The hypertension phenotype comprised 266,001 controls and 75,984 cases. The training set included 289,688 samples, the test set 51,297 samples and the validation set 1000 samples. In addition, for the height outcome prediction 745 samples were filtered out due to phenotype missingness. For hypertension outcome prediction, no additional samples had a missing phenotype.

**Dimensionality Reduction Results**

The Dimensionality Reduction results were evaluated using the validation set, for each chromosome and each dimensionality reduction model. The weighted average R2 for the autoencoder achieved 0.5745, and for the PCA achieved 0.6642, where each chromosome’s R2 is weighted according to the number of SNPs in it (see supplementary table S1). The autoencoder's R2 yielded overall lower results in all chromosomes than PCA's results. As shown in Figure 1, the average time for training the autoencoder for 100 epochs was much longer than the total time needed for training the PCA. In Figure 3 it can be seen the weighted average R2 value dependent on the number of epochs for the autoencoder model. We trained the autoencoder for 600 epochs until it seemed to reach a plateau.



**Figure 3.** **The weighted average R2 value dependent on the number of epochs for the autoencoder model.**

**Predictive Ability Compared to the Base Model across Different Traits**

The number of features in the prediction model input matrix was 42,870, including 42,742 variables from the dimension reduction process unioned from all 22 chromosomes, and 128 variables from the covariate matrix. The covariate matrix included age, sex, 105 dummy variables of the genotype measurement batch, and 21 dummy variables of the assessment center. Our new approach performance was then compared with the base model. The optimal p-value threshold using PRSice-2 software was 1, both for height and hypertension, meaning all the SNPs were taken into account in the computing of the PRS. Table 3 details the results on the test set for height phenotype prediction, and Table 4 for hypertension phenotype prediction.

**Table3 .** **Prediction results on height phenotype using the test set.** The RMSE metric is presented in centimeters.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **---** | **PCA** | | **Autoencoder** | | **Dimensionality Reduction model** |
| **Base model** | **XGB** | **DNN** | **XGB** | **DNN** | **Prediction model** |
| 6.031 | 6.436 | **5.785** | 6.435 | 5.914 | RMSE |
| 0.574 | 0.515 | **0.608** | 0.515 | 0.591 | R2 |

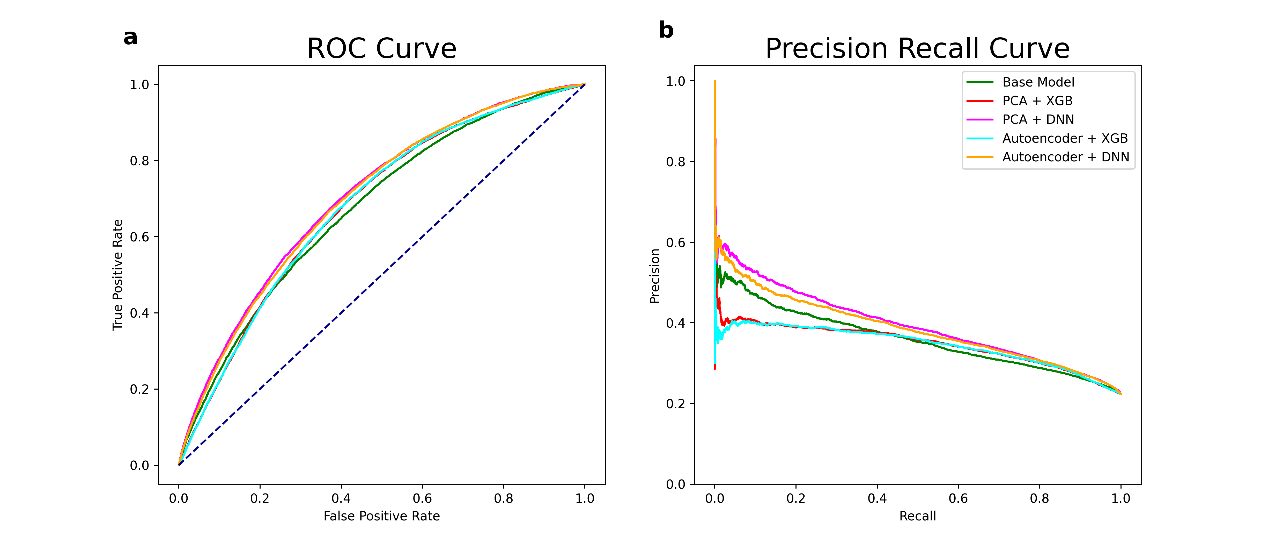
**Table4 .** **Prediction results on hypertension phenotype using the test set.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **---** | **PCA** | | **Autoencoder** | | **Dimensionality Reduction model** |
| **Base model** | **XGB** | **DNN** | **XGB** | **DNN** | **Prediction model** |
| 0.566 | 0.505 | **0.490** | 0.505 | 0.492 | Log-loss |
| 0.675 | 0.681 | **0.705** | 0.681 | 0.700 | ROC AUC |
| 0.360 | 0.347 | **0.394** | 0.345 | 0.384 | Average Precision |

When examining the prediction performance of the different models, we can observe that our model results outperform the base model results both in height and hypertension phenotypes.

For height phenotype, the deep learning classifier trained on the output from the dimensionality reduction process achieved the best R2 score of 0.608 after the PCA process and 0.591 after the autoencoder process. For these models, the RMSE for height prediction was 5.785-5.914 centimeters. The XGB model shows a worse R2 score than the base model. While in the DNN model, the model that included the variables after PCA produced better prediction than after Autoencoder, in XGB the results are quite the same for both types of dimensionality reduction models. Thus, our model result shows that although the weighted average R2 for the autoencoder was significantly lower than PCA, the prediction results of the first one can reach a compromise with the second one.

For hypertension phenotype, both DNN and XGB prediction results surpass those of the base model results according to ROC AUC and Log-Loss metrics. Based on the Average Precision metric, the base model outperforms the XGB model, but not the DNN model. The deep learning classifier trained on the variables driven by the dimensionality reduction process achieved the best ROC AUC score of 0.705 after the PCA process and 0.7 after the autoencoder process. The PCA and the autoencoder performed quite similarly according to the ROC AUC and Log-loss metrics, while there is a slight gap of 0.01 in favor of the PCA in the Average Precision metric. Overall, the DNN classifier surpasses the results of both the base model and the XGB model, as seen in the receiver operating characteristic curve (ROC) and the precision-recall curve (Figure 4).

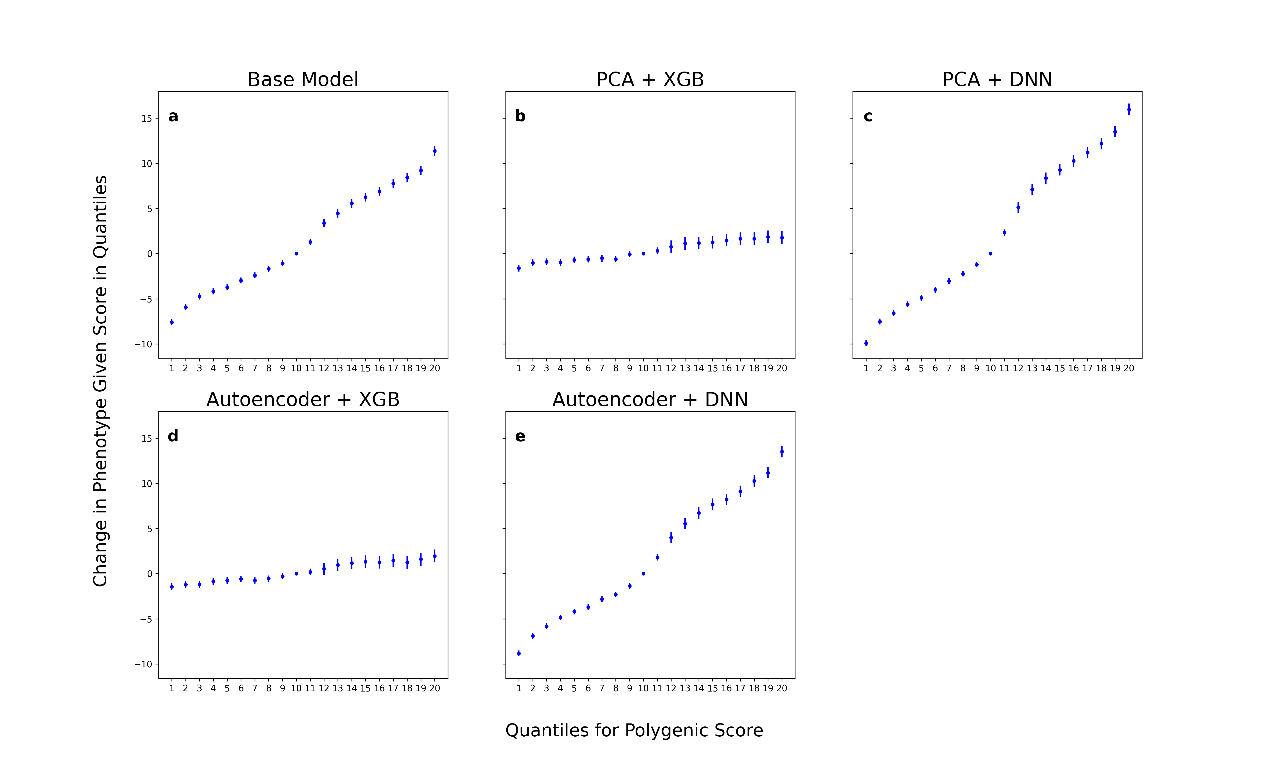


**Figure 4.** **Plots for hypertension phenotype**. **a.** Receiver Operating Characteristic curve (ROC). **b.** Precision-Recall curve.

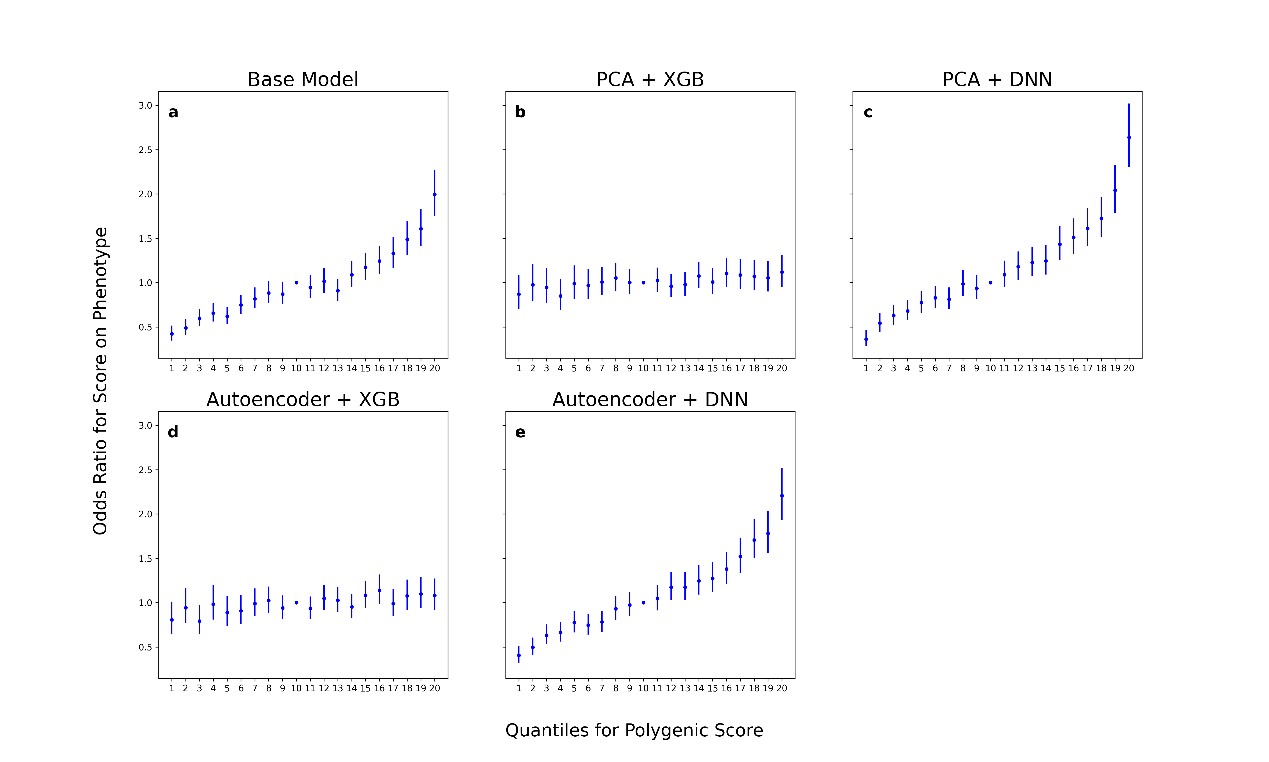
In order to examine how trait values vary with increasing predicted phenotype target and to measure the elevated disease risk among individuals with the highest predicted values, we visualized the results using a quantile plot (Figures 5 & 6). The predicted phenotype was first split into 20 quantiles of increasing values, i.e. 20 equally sized quantiles, each comprising 5% of the predicted values sample distribution. Then, the quantiles as dummies were adjusted to the covariate matrix and were used as a predictor of the phenotype in linear or logistic regression models. The y-axis takes values of the coefficients for height prediction and odds ratio for hypertension prediction.

For height phenotype, the quantile plots (Figure 5) reflect an S-shape, which means that the trait values are more spread out between quantiles at the tails, as expected in a normally distributed target trait. The trend in coefficients is significantly steeper in the DNN models than in the XGB and the base models. That is, the variation in the coefficients for the different quantiles in the DNN models has a wider range, and therefore we can assume that there is a stronger correlation between the quantile and the phenotype.

For hypertension phenotype, the quantile plots (Figure 6) of the DNN and the base model reflect a disease risk increase sharply in the right tail of the distribution. The plots are asymmetrical, with a marked inflection at the upper end, as expected when the cases are enriched in the higher quantiles. However, in the XGB prediction model, the plots are more symmetrical, which shows a lack of division for disease risk between the different quantiles.



**Figure 5.** **Quantile plot for height phenotype.** The y-axis takes values of the coefficients of the quantiles. The error bars represent a 95% confidence interval.



**Figure 6. Quantile plot for hypertension phenotype.** The y-axis represents the odds ratio for the phenotype. The error bars represent a 95% confidence interval.

**Discussion**

We suggest a more adequate approach for predicting individual trait value or disease risk using all available SNPs, an alternative to feature selection while taking into account SNPs interactions as predictors. The new approach can be used in the development of personalized medicine strategies and for improving healthcare. Moreover, this new approach can be generalized to any clinical and physiologic phenotypes without the need to train the dimensionality reduction part more than once.

We showed that our method is capable of predicting an individual’s trait value or disease risk better than the PRS base model. We have found that dimensionality reduction using PCA, in addition to being a faster procedure, and although it only learns linear patterns, can serve as a good basis for phenotype prediction. The autoencoder process approach sometimes became equal to PCA, but mostly shows slightly worse results. However, we wish to underline the potential of autoencoder, that by design can learn and represent non-linear relationships. In the data set we have used, the dimensionality shrinkage of the SNPs using a linear method yielded the best results, but perhaps an autoencoder may be more useful with a larger number of samples. For the trait prediction model, our results showed that the deep learning methods are capable to predict phenotype with higher performance than boosting algorithms like XGBoost.

We acknowledge some limitations of the current work. First, the model was trained and evaluated using individuals of European descent only, hence, adjustments to the model may need to be made for other ancestral groups. Second, due to limitations in the computational power resources available to us, our model was estimated using one validation set. We assume that the estimation of the model using k-fold cross-validation can lead to more stable, accurate, and comprehensive results. Third, We trained and evaluated our method using data from the UK Biobank data, however, a better evaluation would have used an external independent dataset.

**Acknowledgments**

This research has been conducted using the UK Biobank resource under Application Number 56774. We would like to thank Dr. Jonathan Rosenblatt for the fruitful discussion along the way.

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